OVARIAN CANCER

Evaluation of DNA from the Papanicolaou Test to Detect Ovarian and Endometrial Cancers

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Papanicolaou (Pap) smears have revolutionized the management of patients with cervical cancers by permitting the detection of early, surgically curable tumors and their precursors. In recent years, the traditional Pap smear has been replaced by a liquid-based method, which allows not only cytologic evaluation but also collection of DNA for detection of human papillomavirus, the causative agent of cervical cancer. We reasoned that this routinely collected DNA could be exploited to detect somatic mutations present in rare tumor cells that accumulate in the cervix once shed from endometrial or ovarian cancers. A panel of genes that are commonly mutated in endometrial and ovarian cancers was assembled with new whole-exome sequencing data from 22 endometrial cancers and previously published data on other tumor types. We used this panel to search for mutations in 24 endometrial and 22 ovarian cancers and identified mutations in all 46 samples. With a sensitive massively parallel sequencing method, we were able to identify the same mutations in the DNA from liquid Pap smear specimens in 100% of endometrial cancers (24 of 24) and in 41% of ovarian cancers (9 of 22). Prompted by these findings, we developed a sequence-based method to query mutations in 12 genes in a single liquid Pap smear specimen without previous knowledge of the tumor's genotype. When applied to 14 samples selected from the positive cases described above, the expected tumor-specific mutations were identified. These results demonstrate that DNA from most endometrial and a fraction of ovarian cancers can be detected in a standard liquid-based Pap smear specimen obtained during routine pelvic examination. Although improvements need to be made before applying this test in a routine clinical manner, it represents a promising step toward a broadly applicable screening methodology for the early detection of gynecologic malignancies.

INTRODUCTION

Since the introduction of the Papanicolaou (Pap) test, the incidence and mortality of cervical cancer in screened populations have been reduced by more than 75% (*1*, *2*). In contrast, deaths from ovarian and endometrial cancers have not substantially decreased during that same time period. As a result, more than 69,000 women in the United States were estimated to be diagnosed with ovarian or endometrial cancer in 2012 (*3*). Although endometrial cancer is more common than ovarian cancer, the latter is more lethal. In the United States, about 15,000 and 8,000 women are expected to die each year from ovarian and endometrial cancers, respectively (*3*). Worldwide, more than 200,000 deaths from these tumors are expected this year alone (*4*, *5*).

In an effort to replicate the success of cervical cancer screening, several approaches for the early detection of endometrial and ovarian cancers have been proposed. For endometrial cancers, efforts have focused on cytology and transvaginal ultrasound (TVS). Cytology can indeed indicate a neoplasm within the uterus in some cases, albeit with low specificity (*6*). TVS is used to measure the thickness of the endometrium, because it is known that endometria harboring a cancer are thicker than normal endometria (*7*). As with cytology, screening measurement of the endometrial thickness with TVS lacks sufficient specificity because benign lesions, such as polyps, can also result in a thickened endometrium. Accordingly, neither cytology nor TVS fulfills the requirements for a screening test (*6*, *8*).

Even greater efforts have been made to develop a screening test for ovarian cancer, including the assessment of serum CA-125 levels in conjunction with TVS. CA-125 is a high–molecular weight transmembrane glycoprotein expressed by coelomic- and Müllerian-derived epithelia that is elevated in a subset of ovarian cancer patients with early-stage disease and in some cases before clinical diagnosis (*9*, *10*). The specificity of CA-125 is limited by the fact that it is also elevated in a variety of benign conditions, such as pelvic inflammatory disease, endometriosis, and ovarian cysts (*11*). Although TVS can visualize the ovary, it can only detect large tumors and cannot definitively distinguish benign from malignant tumors. Several clinical screening trials with serum CA-125 and TVS have been conducted, but none have shown a survival benefit. Some have shown an increase in morbidity compared to controls because false-positive tests elicit further evaluation by laparoscopy or exploratory laparotomy (*12*–*14*).

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Accordingly, the U.S. Preventative Services Task Force, the American Cancer Society, the American Congress of Obstetricians and Gynecologists, and the National Comprehensive Cancer Network do not recommend routine screening for endometrial or ovarian cancers in the general population. These organizations warn that "the potential harms outweigh the potential benefits" (*15*–*18*). An exception to this recommendation has been made for patients with a hereditary predisposition to ovarian cancer, such as those with germline mutations in a *BRCA* gene or those with Lynch syndrome. It is recommended that *BRCA* mutation carriers be screened every 6 months with TVS and serum CA-125, starting at a relatively early age. Screening guidelines for women with Lynch syndrome include annual endometrial sampling and TVS beginning between ages 30 and 35 years (*17*, *19*).

The mortality associated with undetected gynecologic malignancies has made the development of an effective screening tool a high priority. An important observation that inspired the current study is that asymptomatic women occasionally present with abnormal glandular cells (AGCs) detected in a cytology specimen as part of their routine cervical cancer screening procedure. Although AGCs are associated with premalignant or malignant disease in some cases (*20*–*24*), it is often difficult to distinguish the AGCs arising from endocervical, endometrial, or ovarian cancer from one another and from more benign conditions.

We reasoned that more sophisticated molecular methods might be able to detect the presence of cancer cells in endocervical specimens at higher sensitivities and specificities than possible with conventional methods. In particular, we hypothesized that somatic mutations characteristic of endometrial and ovarian cancers would be found in the DNA purified from routine liquid-based Pap smears (henceforth denoted as "Pap specimens"; Fig. 1). Unlike cytologically abnormal cells, such oncogenic DNA mutations are specific clonal markers of neoplasia that should be absent in nonneoplastic cells. The experiments described here were carried out to test this hypothesis.

RESULTS

There were four components to this study: (i) establishing the somatic mutations typically present in endometrial and ovarian cancers, (ii) identifying at least one mutation in each tumor from 46 patients with these cancers, (iii) determining whether the mutations identified in these tumors could also be detected in Pap specimens from the same patients, and (iv) developing a technology that could directly assess cells from Pap specimens for mutations commonly found in endometrial or ovarian cancers.

Prevalence of somatically mutated genes in endometrial and ovarian cancers

There are six major histopathologic subtypes of epithelial ovarian cancers (Table 1). The most prevalent subtype is high-grade serous (60% of total), followed by endometrioid (15%), clear cell (10%), low-grade serous carcinoma (8%), mucinous (2%), and transitional cell carcinoma (2%) (*25*–*27*). Most of these cases are found at an advanced stage, and the combined 5-year survival (*3*, *28*) for these malignancies is about 27% (Table 1). Genome-wide studies (*29*–*31*) have identified commonly mutated genes among the most prevalent ovarian cancer subtypes (Table 2).

Such comprehensive studies have not yet been reported for the endometrioid and mucinous subtypes, which collectively represent ~20% of ovarian cancer cases (Table 1). However, commonly mutated genes in the endometrioid and mucinous subtypes have been reported (*32*). In aggregate, the most commonly mutated gene in epithelial ovarian cancers was *TP53*, which was mutated in 69% of these cancers (Table 2). Other highly mutated genes included *ARID1A*, *BRAF*, *CTNNB1*, *KRAS*, *PIK3CA*, and *PPP2R1A* (Table 2).

Among endometrial cancers, the endometrioid subtype is by far the most common, representing 85% of the total (Table 1). Because cancers of this subtype are so frequent and have not been analyzed at a genome-wide level, we evaluated them through whole-exome sequencing. The DNA purified from 22 sporadic endometrioid carcinomas, as well as from matched nonneoplastic tissues, was used to generate 44 libraries suitable for massively parallel sequencing. The clinical aspects of the patients and histopathologic features of the tumors are listed in table S1. Although the examination of 22 cancers cannot provide a comprehensive genome landscape of a tumor type, it is adequate for diagnostic purposes as these only require the identification of the most frequently mutated genes.

Among the 44 libraries, the average coverage of each base in the targeted region was 149.1, with 88.4% of targeted bases represented by at least 10 reads. After applying stringent criteria for the identification of somatic mutations (as described in Materials and Methods), the sequencing data demarcated the tumors into two groups: 10 cancers

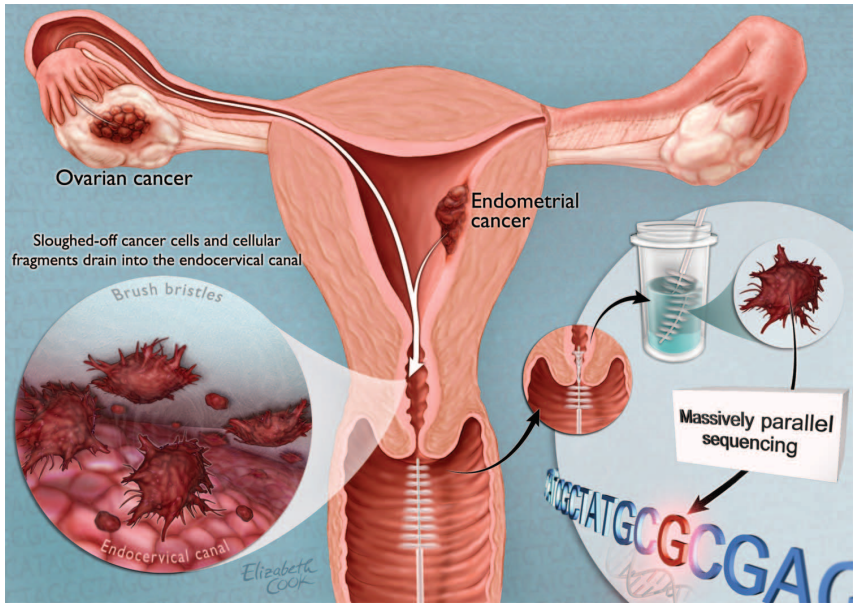


Fig. 1. Schematic demonstrating the principal steps of the procedure described in this study. Tumor cells shed from ovarian or endometrial cancers are carried into the endocervical canal. These cells can be captured by the brush used for performing a routine Pap smear. The brush contents are transferred into a liquid fixative, from which DNA is isolated. By means of massively parallel sequencing, this DNA is queried for mutations that indicate the presence of a malignancy in the female reproductive tract.

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Table 1. Epidemiology of ovarian and endometrial tumors in the United States. The estimated numbers of new cases and deaths in the United States from the major subtypes of ovarian and endometrial cancers are listed. N/A, not available.

Tissue	Type	Subtype	Subtype distribution (%)	Estimated new cases, 2012	5-Year survival (%)	References
Ovarian	Epithelial	High-grade serous	60	13,368	9	(*3*, *25*)
		Endometrioid	15	3,342	71	(*3*, *26*)
		Clear cell	10	2,228	62	(*3*, *26*)
		Low-grade serous	8	1,782	40	(*3*, *25*)
		Mucinous	2	446	65	(*3*, *26*)
		Transitional cell	2	446	57	(*27*, *28*)
		Other	3	668	N/A	(*3*, *25*–*28*)
Endometrial	Type I: endometrioid	Endometrioid	85	40,060	91	(*3*, *26*)
	Type II: non-endometrioid	Papillary serous	10	4,713	45	(*3*, *26*)
		Clear cell	5	2,357	68	(*3*, *36*)

(termed group N, for non–highly mutated) harbored <100 somatic mutations per tumor (median, 32; range, 7 to 50), and 12 cancers (termed group H, for highly mutated) harbored >100 somatic mutations per tumor (median, 674; range, 164 to 4629) (table S1).

The high number of mutations in the group H tumors was consistent with a deficiency in DNA repair. Eight of the 12 group H tumors had microsatellite instability (MSI-H, table S1), supporting this conjecture. Moreover, six of the group H tumors contained somatic mutations in the mismatch repair genes *MSH2* or *MSH6*, whereas none of the group N cancers contained mutations in mismatch repair genes (table S2). Mismatch repair deficiency is common among endometrial cancers, and these tumors occur in 19 to 71% of women with inherited mutations in mismatch repair genes (that is, patients with hereditary nonpolyposis colorectal cancer) (*33*).

A complete list of the 12,795 somatic mutations identified in the 22 cancers is provided in table S2. The most commonly mutated genes included the phosphatidylinositol 3-kinase pathway genes *PTEN* and *PIK3CA* (*34*), the adenomatous polyposis coli pathway genes *APC* and *CTNNB1*, the fibroblast growth factor receptor *FGFR2*, the adapter protein *FBXW7*, and the chromatin-modifying genes *ARID1A* and *MLL2* (Table 2). Genes in these pathways were mutated in both group N and H tumors. Our results are consistent with previous studies of endometrioid endometrial cancer that had evaluated small numbers of genes, although mutations in *FBXW7*, *MLL2*, and *APC* had not been appreciated to occur as frequently as we found them. It was also interesting that few *TP53* mutations (5%) were found in these endometrial cancers (Table 2 and table S2), a finding also consistent with previous studies.

Papillary serous carcinomas of the endometrium account for 10 to 15% of endometrial cancers, and a recent genome-wide sequencing study of this tumor subtype has been published (*35*). The most common mutations in this subtype are listed in Table 2. The least common subtype of endometrial cancers is clear cell carcinoma (*36*), which occurs in <5% of cases. Genes reported to be mutated in these cancers were garnered from the literature (Table 2).

Identification of mutations in tumor tissues

We acquired tumors from 46 cancer patients for whom Pap specimens were available. These included 24 patients with endometrial cancers and 22 with ovarian cancers; their clinical, demographic, and histopathologic features are listed in table S3.

Somatic mutations in the 46 tumors were identified through whole-exome sequencing (table S2) or through targeted sequencing of genes frequently mutated in the most common subtypes of ovarian or endometrial cancer (Table 2). Enrichment for these genes was achieved with a custom solid-phase capture assay composed of oligonucleotides ("capture probes") complementary to a panel of gene regions of interest. For the oncogenes, we only targeted their commonly mutated exons, whereas we targeted the entire coding regions of the tumor suppressor genes.

DNA sequencing libraries were generated from tumors and their matched nonneoplastic tissues, and then captured with the assay described above. In each of the 46 cases, we identified at least one somatic mutation (table S3) that was confirmed by an independent assay, as described below.

Identification of somatic mutations in Pap specimens

In the liquid-based Pap smear technique in routine use today, the clinician inserts a small brush into the endocervical canal during a pelvic exam and rotates the brush so that it dislodges and adheres to loosely attached cells or cell fragments. The brush is then placed in a vial of fixative solution (for example, ThinPrep). Some of the liquid from the vial is used to prepare a slide for cytological analysis or for purification of human papillomavirus (HPV) DNA. In our study, an aliquot of the DNA purified from the liquid was assessed for the presence of DNA from the cancers of the 46 patients. Preliminary studies showed that the fixed cells or cell fragments in the liquid contained >95% of the total DNA in the vial. We therefore purified DNA from the cell pellets when the amount of available liquid was greater than 3 ml (as occurs with some liquid-based Pap smear kits) and, for convenience, purified DNA from both the liquid and cells when smaller amounts of liquid were in the kit. In all cases, the purified DNA was of relatively high molecular weight (95% >5 kb). The average amount of DNA recovered from the 46 Pap specimens was 9.9 ± 14.8 μg (table S3).

We anticipated that, if present at all, the amount of DNA derived from neoplastic cells in the Pap smear fluid would be relatively small

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Table 2. Genetic characteristics of ovarian and endometrial cancers. The frequencies of the commonly mutated genes in ovarian and endometrial cancers are listed.

Tissue	Type	Subtype	Somatically mutated genes (frequency)	Reference
Ovarian	Epithelial	High-grade serous	*TP53* (96%)	(*29*)
			CSMD3 (6%)	(*29*)
			FAT3 (6%)	(*29*)
			BRCA1 (3%)	(*29*)
			BRCA2 (3%)	(*29*)
		Endometrioid	*TP53* (68%)	(*32*)
			ARID1A (30%)	(*32*)
			CTNNB1 (26%)	(*32*)
			PTEN (17%)	(*32*)
			PIK3CA (15%)	(*32*)
			KRAS (10%)	(*32*)
			PPP2R1A (11%)	(*32*)
			CDKN2A (12%)	(*32*)
			BRAF (8%)	(*32*)
		Clear cell	*ARID1A* (57%)	(*30*)
			PIK3CA (40%)	(*30*)
			PPP2R1A (7%)	(*30*)
			KRAS (4.7%)	(*30*)
		Low-grade serous	*BRAF* (38%)	(*31*)
			KRAS (19%)	(*31*)
		Mucinous	*TP53* (56%)	(*32*)
			KRAS (40%)	(*32*)
			PPP2R1A (33%)	(*32*)
			CDKN2A (16%)	(*32*)
			PTEN (11%)	(*32*)
Endometrial	Type I: endometrioid	Endometrioid	*PTEN* (64%)	Current study
			PIK3CA (59%)	Current study
			ARID1A (55%)	Current study
			CTNNB1 (32%)	Current study
			MLL2 (32%)	Current study
			FBXW7 (27%)	Current study
			RNF43 (27%)	Current study
			APC (23%)	Current study
			FGFR2 (18%)	Current study
			KRAS (9%)	Current study
			PIK3R1 (9%)	Current study
			EGFR (14%)	Current study
			AKT1 (5%)	Current study
			NRAS (5%)	Current study
			TP53 (5%)	Current study
	Type II: non-endometrioid	Papillary serous	*TP53* (82%)	(*35*)
			PIK3CA (24%)	(*35*)
			FBXW7 (20%)	(*35*)
			PPP2R1A (18%)	(*35*)
		Clear cell	*TP53* (45%)	(*32*)
			PPP2R1A (33%)	(*32*)
			PIK3CA (29%)	(*32*)
			PTEN (13%)	(*32*)
			PIK3R1 (9%)	(*32*)
			KRAS (5%)	(*32*)

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compared to the DNA derived from normal cells brushed from the endocervical canal. This necessitated the use of an analytic technique that could reliably identify a rare population of mutant alleles among a great excess of wild-type alleles. A modification of one of the Safe-SeqS (Safe-Sequencing System) procedures described in (*37*), in which DNA templates are amplified with modified gene-specific primers, was designed for this purpose (Fig. 2).

In brief, a limited number of polymerase chain reaction (PCR) cycles were performed with a set of gene-specific primers. One of the primers contained 14 degenerate "N" bases (that is, equal probability of being an "A," "C," "G," or "T") located 5′ to its gene-specific sequence, and both primers contained sequences that permitted universal amplification in the next step. The 14 "N" bases formed unique identifiers (UIDs) for each original template molecule. Subsequent PCR products generated with universal primers were purified and sequenced. If a mutation preexisted in a template molecule, that mutation should be present in every daughter molecule containing that UID, and such mutations are called "supermutants" (*37*). Mutations not occurring in the original templates, such as those occurring during the amplification steps or through errors in base calling, should not give rise to supermutants. The Safe-SeqS approach used here is capable of detecting 1 mutant template among 5000 to 1,000,000 wild-type templates, depending on the amplicon and the position within the amplicon that is queried (*37*).

We designed Safe-SeqS primers (table S4) to detect at least one mutation from each of the 46 patients described in table S3. In the 24 Pap specimens from patients with endometrial cancers, a mutation present in the tumor was identified in every case (100%). The median fraction of mutant alleles was 3% and ranged from 0.01 to 80% (Fig. 3 and table S3). Amplifications of DNA from nonneoplastic tissues were used as negative controls in these experiments to define the detection limits of each queried mutation. In all cases, the fraction of mutant alleles was significantly different from the background mutation levels in the negative controls ($P < 0.001$, binomial test). There was no obvious

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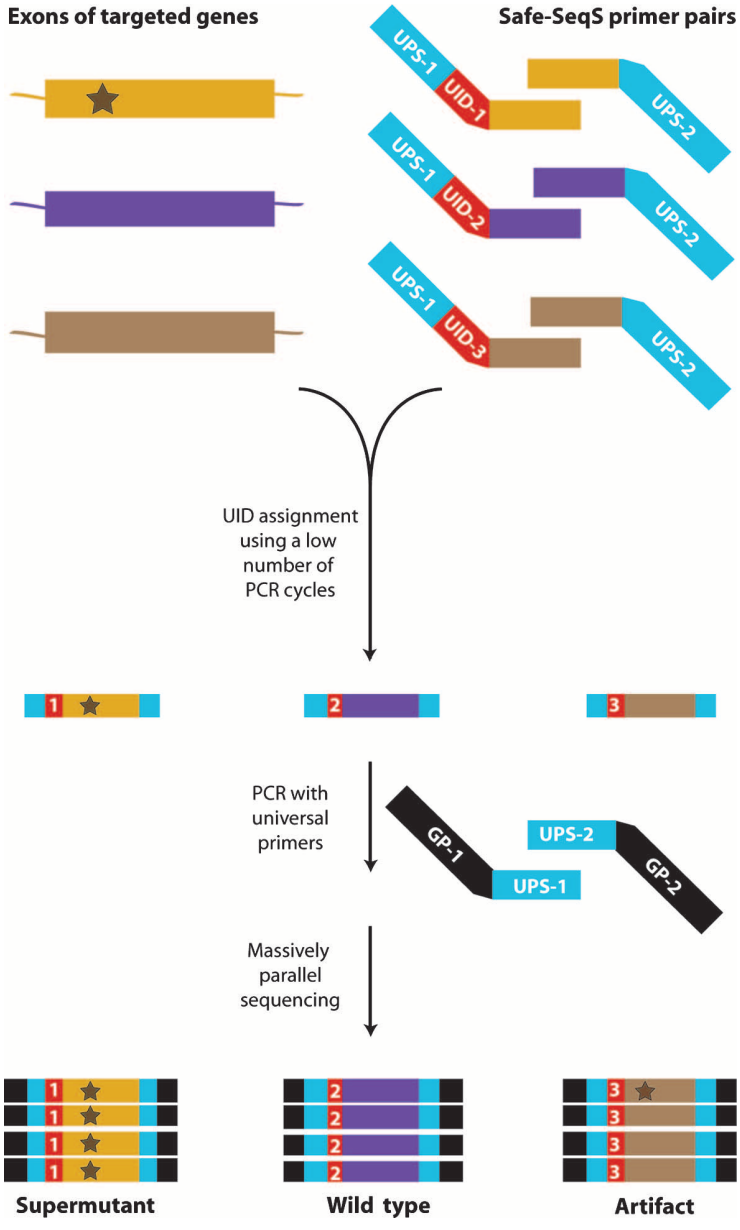


Fig. 2. Diagram of the modified Safe-SeqS assay used, which allowed for the simultaneous detection of mutations in 12 different genes. Top left: DNA templates from three exons of different genes (yellow, purple, and brown rectangles) to be queried for mutations. Note that only one of the templates contains a mutation (star) that exists before any sample preparatory steps or sequencing. Top right: Safe-SeqS primer pairs contain binding sites for universal primers ("UPS," blue), a unique identifier ("UID," red), and gene-specific sequences (colors match the targeted exon). Next, the templates and primers are combined into a single PCR compartment and a UID is attached to each targeted template, along with UPS binding sites, after a low number of PCR cycles ("UID assignment"). The Safe-SeqS primers are removed, and subsequent PCR is performed with primers containing UPS sites, as well as the sequences required for attachment to the sequencing instrument ("GP," black) to prepare the templates for massively parallel sequencing. When mutations preexist in template DNA before sample preparation, all of the sequenced daughter molecules sharing the same UID will contain the same mutation (a "supermutant"). In contrast, artifactual mutations caused by sample preparation or sequencing are unlikely to be observed in most other daughter molecules sharing the same UID ("Artifact"). Note that only one of two DNA strands is depicted for clarity.

correlation between the fraction of mutant alleles and the histopathologic subtype or the stage of the cancer (Fig. 3 and table S3).

In endometrial cancer cases PAP 041 and PAP 083, two mutations found in the tumor DNA were evaluated in the Pap specimens (table S3). In both cases, the mutations were identified in DNA from the Pap specimen (table S3). Moreover, the ratios between the mutant allele fractions of the two mutations in the Pap specimens were correlated with those of the corresponding tumor samples. For example, in the Pap specimen of case PAP 083, the mutant allele fractions for the *CTNNB1* and *PIK3CA* mutations were 0.14 and 0.064%, respectively—a ratio of 2.2. In the primary tumor from PAP 083, the corresponding ratio was 2.0 (79.5 to 39.5%).

Similar analysis of Pap specimen DNA from ovarian cancer patients revealed detectable mutations in 9 of the 22 patients (41%). The fraction of mutant alleles was smaller than in endometrial cancers (median, 0.49%; range, 0.021 to 5.9%; see Fig. 3 and table S3). All but one of the cases with detectable mutations were epithelial tumors; the exception was a dysgerminoma, a malignant germ cell tumor of the ovary (table S3). As with the endometrial cancers, there was no statistically significant correlation between the fraction of mutant alleles and histopathologic criteria. However, most ovarian cancers are detected only at an advanced stage, and this was reflected in the patients assessed in our cohort.

A genetic test for screening purposes

Our results demonstrate that mutant DNA molecules from most endometrial cancers and some ovarian cancers can be found in routinely collected Pap specimens. However, in all 46 cases depicted in Fig. 3, a specific mutation was known to occur in the tumor, and an assay was subsequently designed to determine whether that mutation was also present in the corresponding Pap specimens. In a screening setting, the presence and genotype of tumors would obviously not be known before evaluation. We therefore designed a prototype test based on Safe-SeqS that could assess several genes and could be used in a screening setting (Fig. 2).

This multiplexed approach included 50 primer pairs that amplified segments of 241 to 296 base pairs (bp) containing frequently mutated regions of DNA. The regions to be amplified were chosen from the most commonly mutated genes in endometrial and ovarian cancers (Table 2) and included exons from *APC*, *AKT1*, *BRAF*, *CTNNB1*, *EGFR*, *FBXW7*, *KRAS*, *NRAS*, *PIK3CA*, *PPP2R1A*, *PTEN*, and *TP53*. In control experiments, 46 of the 50 amplicons were shown to provide information on a minimum of 2500 templates, as the number of sequenced templates can be determined directly from Safe-SeqS data (Fig. 2). Given the accuracy of Safe-SeqS, this number was adequate to comfortably detect mutations existing in >0.1% of template molecules (*37*). The regions covered by these 46 amplicons (table S5), encompassing 10,257 bp, were predicted to be able to detect at least one mutation in >90% of either endometrial or ovarian cancers.

This test was applied to Pap specimens from 14 patients with cancer—12 endometrial and 2 ovarian—as well as 14 Pap specimens collected from healthy controls. The two ovarian

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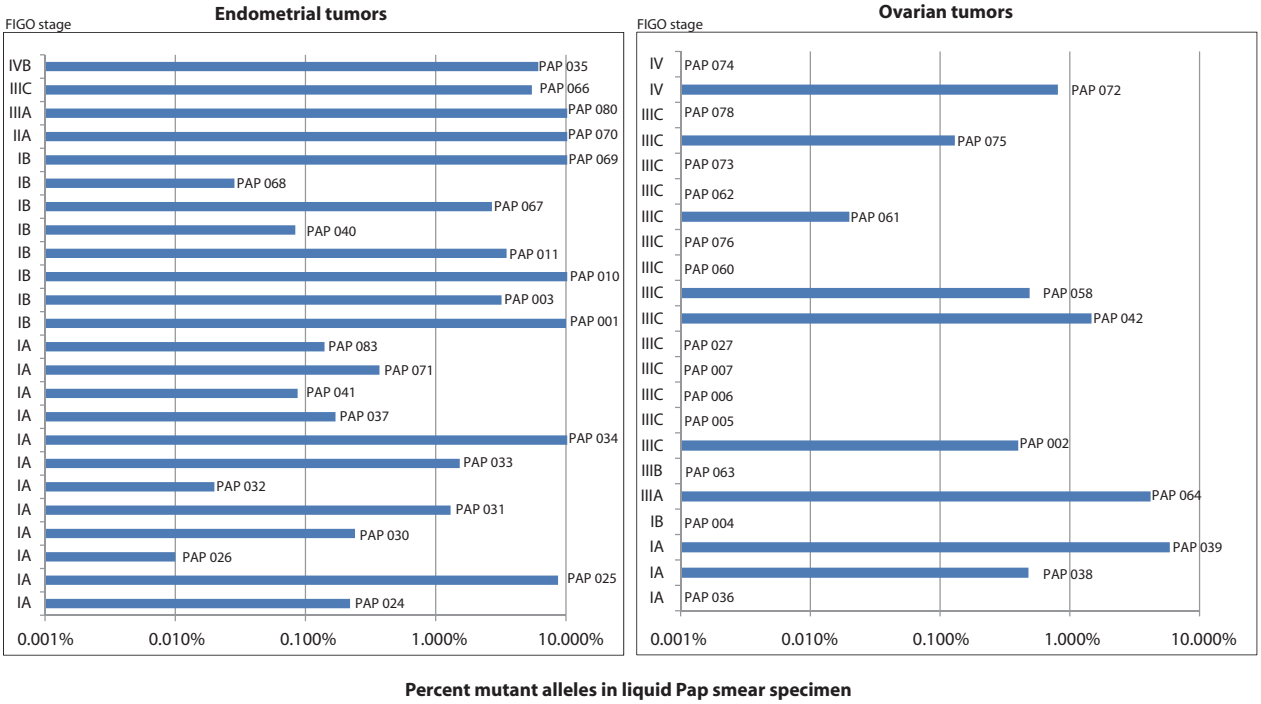


Fig. 3. Percent mutant alleles in liquid Pap smear specimens. The fraction of mutant alleles from each of 46 Pap specimens is depicted. The stage of each tumor is listed on the *y* axis. The *x* axis demonstrates the percent mutant allele fraction as determined by traditional Safe-SeqS. Mutant allele frequencies are higher than 10% in some cases but are depicted at 10% in this figure for clarity. Precise mutation frequencies are reported in table S3 for all samples.

cancers used were stages IA and IV. The endometrial cancers were stage I (n = 10), stage II (n = 1), and stage IV (n = 1). The 14 cancer cases were arbitrarily chosen from those which had mutant allele fractions >0.1% (table S3) and therefore above the detection limit of the multiplexed assay. In all 14 Pap specimens from women with cancer, the mutation expected to be present (table S3) was identified (Fig. 4 and table S6). The fraction of mutant alleles in the multiplexed test was similar to that observed in the original analysis of the same samples, where only one Safe-SeqS primer pair per amplicon was used (tables S3 and S6). No mutations were detected in the 14 Pap specimens from women without cancer (Fig. 4).

DISCUSSION

Georgios Papanicolaou published his seminal work, entitled *Diagnosis of Uterine Cancer by the Vaginal Smear*, in 1943 (*38*). At that time, he suggested that endocervical sampling could in theory be used to detect not only cervical cancers but also other cancers arising in the female reproductive tract, including endometrial carcinomas. The research reported here moves us much closer to that goal. In honor of Papanicolaou's pioneering contribution to the field of early cancer detection, we have named the approach described herein as the "PapGene" test.

An important development from the last several years is the recognition that all human cancers result from mutations in a limited set of genes and an even more limited set of pathways through which these genes act (*39*). The whole-exome sequencing data we present, combined with previous genome-wide studies, provide a compelling example of the common genetic features of cancer (Table 2). Through the analysis of particular regions of only 12 genes (table S5), we could detect at least one driver mutation in most of nine different gynecologic cancers (Table 1). Although several of these 12 genes were tumor suppressors, and therefore difficult to therapeutically target, knowledge of their mutational patterns provides actionable opportunities for cancer diagnostics.

The most important finding in this paper is that diagnostically useful amounts of cells or cell fragments from endometrial and ovarian cancers are present in the cervix and can be detected through molecular genetic approaches. Detection of malignant cells from endometrial and ovarian carcinomas in cervical cytology specimens is relatively uncommon. Microscopic examination cannot always distinguish them from one another, from cervical carcinomas, or from more benign conditions. In our study, 100% of endometrial cancers (n = 24) and 41% of ovarian cancers (n = 22) shed cells into the cervix that could be detected in materials collected as part of routine Pap specimens. In both types of cancer, tumors of low grade were detected (Fig. 3). These findings, in conjunction with technical advances allowing the reliable detection of mutations present in only a very small fraction of DNA templates, are the foundations of the PapGene test.

This study provides proof of principle for endocervical DNA testing for gynecologic cancers, but there are important limitations that must be addressed before this approach can be used in the clinic. The test, even in its current format, appears to be promising as a screening tool for endometrial cancer because the data in Fig. 3 show that even the lowest stage endometrial cancers could be detected through the analysis of DNA in Pap specimens. However, only 41% of ovarian cancers could be detected in Pap specimens, even when the mutations in their tumors were known. In eight of the nine Pap

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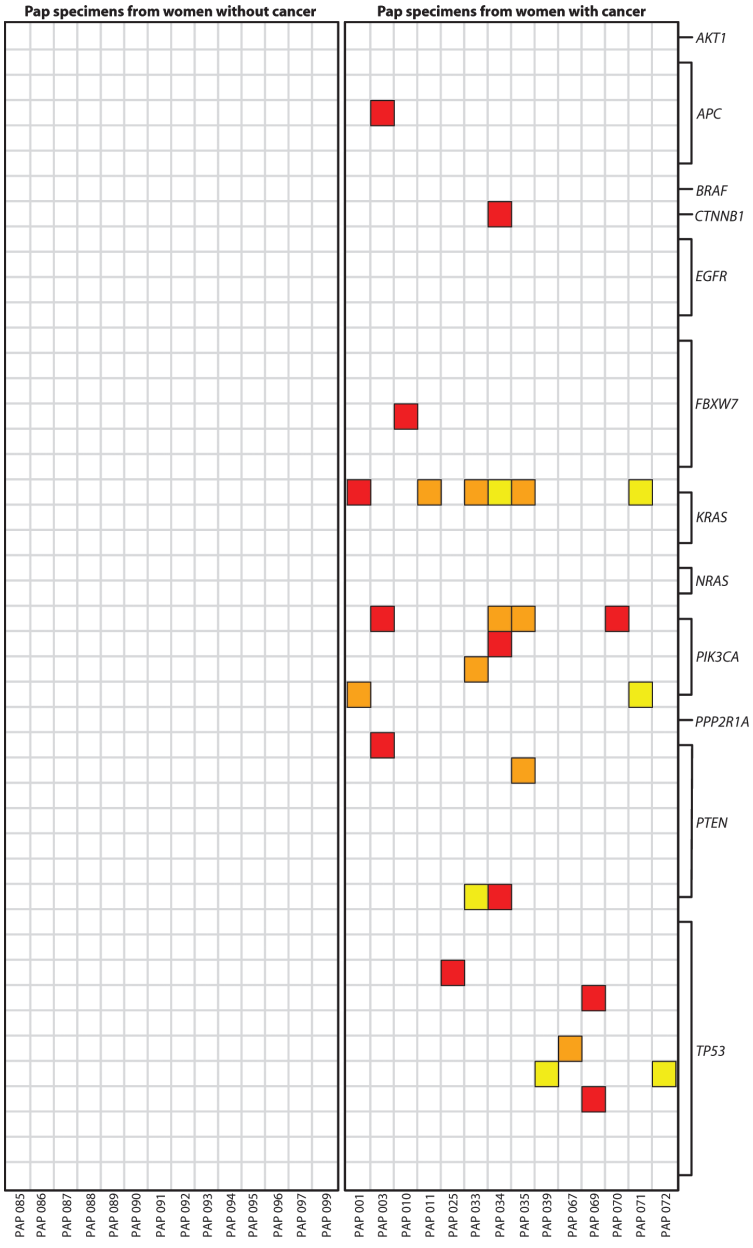


Fig. 4. Heat map depicting the results of multiplex testing of 12 genes in Pap specimens. The PapGene test interrogates 46 gene regions, with each block on the *y* axis representing one region analyzed for the indicated gene. The 28 samples assessed (14 from control women without cancer and 14 from women with cancer) are indicated on the *x* axis. Mutations are indicated as colored blocks, with white indicating no mutation, yellow indicating a mutant fraction of 0.1 to 1%, orange indicating a mutant fraction of 1 to 10%, and red indicating a mutant fraction of >10%.

specimens from ovarian cancer patients that contained detectable mutations, the mutant allele fractions were >0.1% and therefore within the range currently detectable by PapGene testing (table S3). Further improvements in the technology could increase the technical sensitivity of the PapGene test and allow it to detect more ovarian cancers. One improvement would involve an increase in the number of potential gene targets assessed by the PapGene test. Development of an improved collection method may also be important to improve sensitivity. The current method of liquid specimen collection is designed for the detection of cervical cancer and, as such, uses a brush that collects cells from the ectocervix and only minimally penetrates the endocervical canal. A small cannula introduced into the endometrial cavity, similar to the Pipelle endometrial biopsy instrument, could theoretically be used to obtain a more highly enriched sample of cells coming from the endometrium, fallopian tube, and ovary (*40*). Specificity must also be further addressed in the future, and a greater number of healthy controls need to be evaluated, although it is encouraging that none evaluated so far had detectable mutations. This result is consistent with the idea that mutation-based screening should be exquisitely specific because mutations should not be found in normal cells. As noted in the Introduction, specificity is a major limitation of current screening tests in general and for ovarian cancer in particular.

The quantitative nature of the PapGene test also opens the possibility of using it to monitor the response to hormonal agents (for example, progestins) when treating young women with low-risk endometrial cancers. Some of these women choose to preserve fertility, undergoing medical therapy rather than hysterectomy (*41*), and PapGene testing could be performed at regular intervals to monitor them for local cancer recurrence or progression.

Even if tumors were identified at an advanced stage, detection of presymptomatic ovarian cancers could be of benefit. One of the most important prognostic indicators for ovarian cancer is the amount of residual disease after surgical debulking. Initially, debulking was considered optimal if the residual tumor was less than 2 cm. Subsequently, the threshold was reduced to 1 cm, and now, surgeons attempt to remove any visible tumor. With each improvement in surgical debulking, survival has lengthened (*42*). The earlier these advanced-stage ovarian cancers are diagnosed, the lower the overall tumor burden and the higher the chance of optimal debulking. Furthermore, it is possible that a small volume of tumor is likely to be more sensitive to cytotoxic chemotherapy than the large, bulky disease typical of symptomatic high-grade serous carcinoma.

An essential aspect of any screening approach is that it should be relatively inexpensive and easily incorporated into standard medical practice. Evaluation of HPV DNA is already part of routine Pap specimen testing because HPV analysis increases the test's sensitivity (*43*, *44*). The DNA purification component of the PapGene test is identical to that used for HPV, so this component is feasible. The preparation of DNA, multiplex amplification, and sequencing constituting the PapGene test can be performed at a cost comparable to a routine HPV test in the United States today. Note that the increased sensitivity provided by the Safe-SeqS component of the PapGene test can be implemented on any massively parallel sequencing instrument, not just those used in this study. With the reduction in the cost of massively parallel sequencing expected in the future, PapGene testing should become even less expensive.

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There are millions of Pap smear tests performed annually in the United States. Could PapGene testing be performed on such a large number of specimens? We believe so, because the entire DNA purification and amplification process can be automated, just as it is for HPV testing. Although it may now seem unrealistic to have millions of these sophisticated sequence-based tests performed every year, it would undoubtedly have seemed unrealistic to have widespread, conventional Pap smear testing performed when Papanicolaou published his original paper in 1943 (*38*). Even today, when many cervical cytology specimens are screened with automated technologies, at least 2 to 8% of samples require evaluation by a skilled cytopathologist (*45*). In contrast, the analysis of PapGene testing is done completely in silico, and the readout of the test is objective and quantitative.

In sum, these data highlight the high specificity of mutation-based diagnostics paired with the sensitivity of interrogating local-regional bodily secretions for tumor-derived DNA. PapGene testing has the capacity to increase the use of conventional cytology screening through the unambiguous detection of DNA from endometrial and ovarian carcinomas, and lays the foundation for a new generation of screening tests.

MATERIALS AND METHODS

Patient samples

All samples for this study were obtained according to protocols approved by the Institutional Review Boards of The Johns Hopkins Medical Institutions (Baltimore, MD), Memorial Sloan-Kettering Cancer Center (New York, NY), University of Sao Paulo (Sao Paulo, Brazil), and ILSBio, LLC (Chestertown, MD). Demographic, clinical, and pathologic staging data were collected for each case. All histopathology was centrally re-reviewed by board-certified pathologists. Staging was based on 2009 FIGO criteria (*46*). Purified DNA from tumor and normal tissues as well as liquid-based Pap smears were quantified in all cases with quantitative PCR using the primers and conditions previously described (*47*). Unless otherwise indicated, all patient-related values are reported as means ± 1 SD. Additional details are provided in the Supplementary Materials and Methods.

MSI testing

Tumor samples were designated as follows: MSI-high if two or more mononucleotide repeats varied in length compared to the germline DNA; MSI-low if only one locus varied; and microsatellite stable if there was no variation compared to the germ line. Pentanucleotide loci confirmed identity in all cases. Additional details are provided in the Supplementary Materials and Methods.

Preparation and sequencing of captured Illumina DNA libraries

Preparation of Illumina genomic DNA libraries and selection for exomic DNA were performed according to the manufacturer's recommendations. Exomic capture was performed with the SureSelect Human Exome Kit V 4.0 (Agilent), whereas the custom solid-phase capture assay was performed by modification of previously described methods (*48*, *49*). Paired-end sequencing with an Illumina GA IIx Genome Analyzer provided 2 × 75 base reads from each fragment. Known polymorphisms recorded in dbSNP Build 130 (*50*) in the sequence tags that passed filtering were removed from the analysis. Identification of high-confidence mutations was performed as described previously (*30*). Additional details are provided in the Supplementary Materials and Methods.

Assessment of low-frequency mutations

Primers were designed as described previously (*37*) with Primer3 (*51*). Templates were prepared for sequencing as described previously (*37*), with modifications that facilitated the amplification of multiple gene regions in a single well of a 96-well PCR plate. With the primers described in table S4, 66 ng of templates was amplified in two rounds of PCR (Fig. 2) for the single amplicon assays. The multiplexed assays were performed in similar fashion with six independent amplifications—each containing 66 ng of DNA (that is, ~400 ng total)—per sample with the primers described in table S5. High-quality sequence reads were analyzed as previously described (*37*), employing quality scores that reflected the probability that an individual base call was made in error (*52*). The template-specific portion of the reads was matched to a reference sequence set by a custom script (available from the authors upon request). Additional details are provided in the Supplementary Materials and Methods.

SUPPLEMENTARY MATERIALS

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Materials and Methods

Table S1. Summary characteristics of endometrial cancers (endometrioid subtype) studied by whole-exome sequencing.

Table S2. Mutations identified by whole-exome sequencing in 22 endometrioid endometrial cancers.

Table S3. Clinical characteristics and mutations assessed in Pap specimens.

Table S4. Primers used to assess individual mutations in Pap specimens.

Table S5. Primers used to simultaneously assess 12 genes in Pap specimens with the multiplexed Safe-SeqS strategy.

Table S6. Mutations identified in Pap specimens through simultaneous assessment of 12 genes with the multiplexed Safe-SeqS strategy.

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Inostics and PGDx have licensed several patent applications from Johns Hopkins, on which I.K., N.P., K.W.K., B.V., and L.A.D. are inventors. The patents related to the current manuscript are patent WO2012/142,213 titled "Safe Sequencing System," and provisional patent application 61/719,942 titled "Papanicolaou test for ovarian and endometrial cancers." These relationships are subject to certain restrictions under The Johns Hopkins University policy, and the terms of these arrangements are managed by the University in accordance with its conflict-of-interest policies. J.W. was an advisor for MyGenostics Inc. in 2012 and owns company stock. **Data and materials availability:** All data and described custom-written scripts are available from the authors upon request.

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Supplementary Materials for

Evaluation of DNA from the Papanicolaou Test to Detect Ovarian and Endometrial Cancers

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This PDF file includes:

Materials and Methods

Other Supplementary Material for this manuscript includes the following:
(available at www.sciencetranslationalmedicine.org/cgi/content/full/5/167/167ra4/DC1)

Table S1 (Microsoft Excel format). Summary characteristics of endometrial cancers (endometrioid subtype) studied by whole-exome sequencing.
Table S2 (Microsoft Excel format). Mutations identified by whole-exome sequencing in 22 endometrioid endometrial cancers.
Table S3 (Microsoft Excel format). Clinical characteristics and mutations assessed in Pap specimens.
Table S4 (Microsoft Excel format). Primers used to assess individual mutations in Pap specimens.
Table S5 (Microsoft Excel format). Primers used to simultaneously assess 12 genes in Pap specimens with the multiplexed Safe-SeqS strategy.
Table S6 (Microsoft Excel format). Mutations identified in Pap specimens through simultaneous assessment of 12 genes with the multiplexed Safe-SeqS strategy.

Supplementary Materials and Methods

Patient Samples

All samples for this study were obtained according to protocols approved by the Institutional Review Boards of The Johns Hopkins Medical Institutions (Baltimore, MD), Memorial Sloan Kettering Cancer Center (New York, NY), University of Sao Paulo (Sao Paulo, Brazil), and ILSbio, LLC (Chestertown, MD). Demographic, clinical and pathologic staging data were collected for each case. All histopathology was centrally re-reviewed by board-certified pathologists. Staging was based on 2009 FIGO criteria (*46*).

Fresh-frozen tissue specimens of surgically resected neoplasms of the ovary and endometrium were assessed for neoplastic cellularity by a board-certified pathologist. Serial frozen sections were used to guide the trimming of Optimal Cutting Temperature (OCT) compound embedded frozen tissue blocks to enrich the fraction of neoplastic cells for DNA extraction.

Formalin-fixed paraffin embedded (FFPE) tissue samples were assessed by a board-certified pathologist (Propath LLC, Dallas, TX) for tumor cellularity and to demarcate areas of high tumor cellularity. Tumor tissues from serial 10 micron sections on slides from the original tumor block were macrodissected with a razorblade to enrich the fraction of neoplastic cells for DNA extraction.

The source of normal DNA was matched whole blood or non-neoplastic normal adjacent tissue.

Liquid-based Pap smear specimens were collected with cervical brushes and transport medium from a Digene HC2 DNA Collection Device (Qiagen) or ThinPrep 2000 System (Hologic) and stored according to the manufacturer's recommendations.

Unless otherwise indicated, all patient-related values are reported as means ± 1 standard deviation.

DNA Extraction

DNA was purified from tumor and normal tissue, as well as Pap specimens, with an AllPrep kit (Qiagen) according to the manufacturer's instructions. DNA was purified from tumor tissue by adding 3 mL RLTM buffer (Qiagen) and then binding to an AllPrep DNA column (Qiagen) according to the manufacturer's protocol. DNA was purified from Pap specimens by adding five volumes of RLTM buffer when the amount of liquid was ≤3 mL. When the amount of liquid was >3 mL, the cells and cell fragments were pelleted at 1,000 x g for five minutes and the pellets were dissolved in 3 mL RLTM buffer. DNA was quantified in all cases with quantitative PCR, employing the primers and conditions previously described (*47*).

Microsatellite instability testing

Microsatellite instability was detected with the MSI Analysis System (Promega), containing five mononucleotide repeats (BAT-25, BAT-26, NR-21, NR-24 and MONO-

27) and two pentanucleotide repeat loci, per the manufacturer's instructions. After amplification, the fluorescent PCR products were sized on an Applied Biosystems 3130 capillary electrophoresis instrument (Invitrogen). Tumor samples were designated as follows: MSI-high if two or more mononucleotides varied in length compared to the germline DNA; MSI-low if only one locus varied; and microsatellite stable (MSS) if there was no variation compared to the germline. Pentanucleotide loci confirmed identity in all cases.

Preparation and sequence capture of Illumina DNA libraries

Overview. Preparation of Illumina genomic DNA libraries for exomic and targeted DNA captures was performed according to the manufacturer's recommendations. Briefly, 1-3 µg of genomic DNA was used for library preparation with the TruSeqDNA Sample Preparation Kit (Illumina). The DNA was acoustically sheared (Covaris) to a target size of ~200 bp. The fragments were subsequently end-repaired to convert overhangs into blunt ends. A single "A" nucleotide was then added to the 3' ends of blunt fragments to later prevent them from self-ligation; a corresponding "T" on the 3' end of adaptor molecules provided the complementary overhang. After ligation to adaptors, the library was amplified with 8-14 cycles of PCR to ensure yields of 0.5 and 4 µg for exomic and targeted gene captures, respectively.

Exomic enrichment. Exomic capture was performed with the SureSelect Human Exome Kit V 4.0 (Agilent) according to the manufacturer's protocol with the addition of TruSeq index-specific blocks in the hybridization mixture (AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC-XXXXXX-

ATCTCGTATGCCGTCTTCTGCTTGT, where the six base “XXXXXX” region denotes one of 12 sample-specific indexes).

Targeted gene enrichment. Targeted gene enrichment was performed by modifications of previously described methods (*48, 49*). In brief, targeted regions of selected oncogenes and tumor suppressor genes were synthesized as oligonucleotide probes by Agilent Technologies. Probes of 36 bases, tiled in 3-base intervals (that is, 33-base overlaps), were designed to capture both the plus and the minus strands of the DNA. The oligonucleotides were cleaved from the chip by incubating with 3 mL of 35% ammonium hydroxide at room temperature for five hours. The solution was transferred to two 2 mL tubes, dried under vacuum, and redissolved in 400 µL of ribonuclease (RNase)- and deoxyribonuclease (DNase)-free water. Five microliters of the solution was used for PCR amplification with primers complementary to the 12-base sequence common to all probes: 5'-TGATCCCGCGACGA*C-3' and 5'-GACCGCGACTCCAG*C-3', with * indicating a phosphorothioate bond. The PCR products were purified with a MinElute Purification Column (Qiagen), end-repaired with End-IT DNA End-Repair Kit (Epicentre), and then purified again with a MinElute Purification Column. The PCR products were ligated to form concatamers as described (*48*). The major differences between the protocol previously described (*48, 49*) and the one used in the present study involved the amplification of the ligated PCR products and the solid phase capture method as noted below. Biotinylated capture probes were prepared by amplifying 50 ng of ligated PCR products with the REPLI-g Midi Kit (Qiagen) supplemented with 2.5 nmol Biotin-16-dUTP (Roche) in a 27.5 µL reaction incubated at 30°C for 16 hours. After inactivating the polymerase by incubating at 65°C for three mins, the biotinylated

capture probes were purified with QIAquick PCR Purification Columns. For capture, 4-5 µg of library DNA was incubated with 1 µg of the prepared probes in a hybridization mixture as previously described (*48*). The biotinylated capture probes and captured library sequences were subsequently purified with 500 µg Dynabeads MyOne Streptavidin C1 (Invitrogen). After washing as per the manufacturer's recommendations, the captured sequences were eluted with 0.1 M NaOH and then neutralized with 1 M Tris-HCl (pH 7.5). Neutralized DNA was desalted and concentrated with a MinElute Purification Column using a 20 µL elution volume. The eluate was amplified in a 100 µL Phusion Hot Start II (Thermo Scientific) reaction containing 1X Phusion HF buffer, 0.25 mM dNTPs, 0.5 µM each forward and reverse TruSeq primers, and 2 U polymerase with the following cycling conditions: 98℃ for 30 s; 14 cycles of 98℃ for 10 s, 60℃ for 30 s, and 7 2℃ for 30 s; and 72℃ for 5 min. The amplified pool containing enriched target sequences was purified with an Agencourt AMPure XP system (Beckman) and quantified with a 2100 Bioanalyzer (Agilent).

Massively parallel sequencing and somatic mutation identification

After capture of targeted sequences, paired-end sequencing with an Illumina GA IIx Genome Analyzer provided 2 x 75 base reads from each fragment. The sequence tags that passed filtering were aligned to the human genome reference sequence (hg18) and subsequent variant-calling analysis was performed with the ELANDv2 algorithm in the CASAVA 1.6 software (Illumina). Known polymorphisms recorded in dbSNP Build 130 (*50*) were removed from the analysis. Identification of high confidence mutations was performed as described previously (*30*).

Assessment of low-frequency mutations

Primer Design. We attempted to design primer pairs to detect mutations in the 46 cancers described in the text. Primers were designed as described previously (*37*) with Primer3 (*51*). Sixty percent of the primer pairs amplified the expected fragments; in the other 40%, a second or third set of primer pairs had to be designed to reduce primer dimers or non-specific amplification.

Sequencing Library Preparation. Templates were prepared for sequencing as described previously (*37*), with the modifications noted below that facilitated the amplification of multiple gene regions in a single well of a 96-well PCR plate. In brief, each strand of each template molecule was encoded with a 14 base unique identifier (UID) – comprised of degenerate "N" bases (equal probability of being an "A," "C," "G," or "T") - with two to four cycles of amplicon-specific PCR ("UID assignment PCR cycles," see Fig. 2). Both forward and reverse gene-specific primers contained universal tag sequences at their 5' ends, providing the primer binding sites for the second-round amplification, but only the forward primer contained the UID, which was positioned between the 5' universal tag and the 3' gene-specific sequences (Fig. 2). Four "N" bases were additionally included in the reverse primer to facilitate sequencing analysis of paired-end libraries (table S4). The UID assignment PCR cycles were performed on 66 ng of DNA in a 50 µL reaction containing 1X Phusion HF buffer, 0.25 mM dNTPs, 0.5 µM each of forward (containing the 14 "N" bases) and reverse primers, and 2 U of Phusion Hot Start II Polymerase (Thermo Scientific). Carryover of residual UID-containing primers to the second-round amplification, which can complicate

template quantification (*37*), was minimized through a 15 min exonuclease digestion at 37^0C to degrade unincorporated primers. In Kinde *et al*. (*37*), Exonuclease-I (Enzymatics) was chosen to eliminate the residual UID-containing primers, however we found that a different exonuclease – $RecJ_f$ (New England Biolabs) – followed by purification with AMPure XP beads (Beckman) and elution in 10 µL of TE (10 mM Tris-HCl, 1 mM EDTA, pH 8.0), more extensively removed the UID-containing primers and yielded more robust amplification products. The eluted templates were amplified in a second-round PCR with primers containing the grafting sequences necessary for hybridization to the Illumina GA IIx flow cell at their 5' ends (Fig. 2). The reverse amplification primer additionally contained an index sequence between the 5 'grafting and 3' universal tag sequences to enable the PCR products from multiple individuals to be simultaneously analyzed in the same flow cell compartment of the sequencer (*37*). The second-round amplification reactions contained 1X Phusion HF buffer, 0.25 mM dNTPs, 0.5 µM each of forward and reverse primers, and 2 U of Phusion Hot Start II Polymerase in a total of 50 µL. After an initial heat activation step at 98^0 C for 2 minutes, 23 cycles of PCR were performed with the following cycling conditions: 98^0C for 10 s, 65^0C for 15 s, and 72^0C for 15 s. The multiplexed assay was performed in similar fashion utilizing six independent amplifications – each containing 66 ng of DNA (that is, ~400 ng total) – per sample with the primers described in table S5. The PCR products were purified with AMPure XP beads and used directly for sequencing on either Illumina MiSeq or GA IIx instruments, with equivalent results.

Data Analysis. High quality sequence reads were analyzed as previously described (*37*). Briefly, we selected reads that contained high quality basecalls in their UID region

(that is, the first 14 cycles) by utilizing the quality scores generated by the sequencing instrument, which indicate the probability that an individual base call was made in error (*52*). Reads in which each of the 14 bases comprising the UID (representing one original template strand; see Fig. 2) had a quality score ≥15 were grouped by their UIDs and only the UIDs supported by more than one read were retained for further analysis. The template-specific portion of the reads that contained the sequence of an expected amplification primer was matched to a reference sequence set with a custom script (available from the authors upon request). Artifactual mutations – introduced during the sample preparation or sequencing steps – were reduced by requiring that >50% of reads sharing the same UID contained the identical mutation (a "supermutant," Fig. 2). For the 46 assays querying a single amplicon, we required that the fraction of mutant alleles was significantly different from the background mutation levels determined from a negative control (P <0.001, binomial test). As mutations are not known *a priori* in a screening environment, we used a more agnostic metric to detect mutations in the multiplexed assay. A threshold supermutant frequency was defined for each sample as the sum of the mean frequency of supermutants – including only those with average quality scores ≥25 and excluding those at positions with relatively high-frequency variants (such as SNPs or any mutation present at proportions ≥1%) – and six standard deviations of the mean. Only supermutants exceeding this threshold and representing at least two template molecules were designated as mutations and reported in Fig. 4 and table S6.

table S1. Summary Characteristics of Endometrial Cancers (Endometrioid Subtype) Studied by Whole-Exome Sequencing

Case #	Age	Stage (FIGO)	Pathologic stage (TNM class)	Number of mutations	Microsatellite stability status*
PAP 003	53	IB	T1bN0M0	847	MSS
PAP 010	73	IB	T1bN0M1	29	MSS
PAP 011	58	IB	T1bN0M2	579	MSI-H
PAP 024	56	IA	T1aN0	7	MSS
PAP 026	86	IA	T1a	769	MSI-H
PAP 030	73	IA	T1aNx	49	MSS
PAP 031	61	IA	T1aNx	41	MSS
PAP 032	82	IA	T1aNx	9	MSS
PAP 033	68	IA	T1aNX	34	MSS
PAP 034	55	IA	T1aN0	454	MSI-H
PAP 043	55	IB	T1BN0MX	26	MSS
PAP 045	57	IB	T1BN0MX	4,629	MSS
PAP 046	44	IIA	T2ANXMX	40	MSS
PAP 047	53	IA	T1AN0MX	1,767	MSS
PAP 048	62	IIIC	T2AN1MX	394	MSI-H
PAP 049	45	IIB	T2BN0MX	20	MSS
PAP 050	39	IB	T1BN0MX	50	MSS
PAP 052	70	IVB	T1AN1M1	164	MSI-H
PAP 053	66	IB	T1BN0MX	1,102	MSI-H
PAP 054	73	IA	T1ANXMX	413	MSI-H
PAP 055	61	IA	T1AN0MX	1,195	MSS
PAP 057	59	IIB	T2BN0MX	176	MSI-H

* MSI-H: micosatellite unstable; MSS: microsatellite stable. See Materials and Methods for additional details

table S2. Mutations Identified by Whole-Exome Sequencing in 22 Endometrioid Endometrial Cancers

Gene name	Gene description	Gene ID	Case #	Unique reads	Mutant fraction (%)	Chromosome	Chromosome position	Transcript	Nucleotide	Amino acid change
AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase; delta)	ENSG00000026652	PAP003	137	14.6%	chr6	161495247	CCDS5280.1	c.434C>T	p.S145L
HPDL	4-hydroxyphenylpyruvate dioxygenase-like	ENSG00000186603	PAP003	268	14.6%	chr1	45565993	CCDS519.1	c.586G>A	p.D196N
HTR1D	5-hydroxytryptamine (serotonin) receptor 1D	ENSG00000179546	PAP003	416	13.7%	chr1	23393050	CCDS231.1	c.250G>A	p.D84N
HTR2B	5-hydroxytryptamine (serotonin) receptor 2B	ENSG00000135914	PAP003	236	12.3%	chr2	231696614	CCDS2483.1	c.109G>A	p.E37K
HTR4	5-hydroxytryptamine (serotonin) receptor 4	ENSG00000164270	PAP003	79	13.9%	chr5	147844076	CCDS34272.1	c.1136C>T	p.A379V
PFKFB3	6-phosphofructo-2-kinase/fructose-2;6-biphosphatase 3	ENSG00000170525	PAP003	155	12.9%	chr10	6298681	CCDS7078.1	c.373G>A	p.D125N
AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	ENSG00000127914	PAP003	61	18.0%	chr7	91469797	CCDS5622.1	c.2630A>G	p.D877G
ADAM20	ADAM metallopeptidase domain 20	ENSG00000134007	PAP003	141	12.8%	chr14	70059427	CCDS32111.1	c.1951G>A	p.A651T
ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif; 2	ENSG00000087116	PAP003	147	14.3%	chr5	178473718	CCDS4444.1	c.3392A>C	p.E1131A
ADAMTS4	ADAM metallopeptidase with thrombospondin type 1 motif; 4	ENSG00000158859	PAP003	166	18.1%	chr1	159430509	CCDS1223.1	c.1388T>C	p.L463P
ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif; 6	ENSG00000049192	PAP003	452	14.4%	chr5	64483458	CCDS3983.2	c.3315C>A	p.Y1105X
APPL2	adaptor protein; phosphotyrosine interaction; PH domain and leucine zipper containing 2	ENSG00000136044	PAP003	93	14.0%	chr12	104135581	CCDS9101.1	c.206A>G	p.E69G
AP4B1	adaptor-related protein complex 4; beta 1 subunit	ENSG00000134262	PAP003	85	12.9%	chr1	114239599	CCDS865.1	c.1831G>T	p.E611X
APC	adenomatous polyposis coli	ENSG00000134982	PAP003	155	11.0%	chr5	112203538	CCDS4107.1	c.4348C>T	p.R1450X
ADORA2A	adenosine A2a receptor	ENSG00000128271	PAP003	110	16.4%	chr22	23166613	CCDS13826.1	c.395C>T	p.S132L
AMD1	adenosylmethionine decarboxylase 1	ENSG00000123505	PAP003	111	15.3%	chr6	111303034	CCDS5086.1	c.33G>T	p.E11D
AMIGO1	adhesion molecule with Ig-like domain 1	ENSG00000181754	PAP003	214	13.6%	chr1	109852464	CCDS30795.1	c.594G>T	p.K198N
ADIPOR1	adiponectin receptor 1	ENSG00000159346	PAP003	139	18.0%	chr1	201186785	CCDS1430.1	c.37A>G	p.N13D
AGXT2L1	alanine-glyoxylate aminotransferase 2-like 1	ENSG00000164089	PAP003	124	12.1%	chr4	109900447	CCDS3682.1	c.242C>A	p.S81Y
ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog; S. cerevisiae)	ENSG00000085224	PAP003	105	10.5%	chrX	76794306	CCDS14434.1	c.4511G>A	p.R1504Q
ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog; S. cerevisiae)	ENSG00000085224	PAP003	132	13.6%	chrX	76823973	CCDS14434.1	c.3431G>T	p.R1144I
APBB1IP	amyloid beta (A4) precursor protein-binding; family B; member 1 interacting protein	ENSG00000077420	PAP003	253	13.8%	chr10	26891264	CCDS31167.1	c.1373C>A	p.P458H
ALS2CR12	amyotrophic lateral sclerosis 2 (juvenile) chromosome region; candidate 12	ENSG00000155749	PAP003	123	13.8%	chr2	201861663	CCDS2346.1	c.1298A>G	p.D433G
AMOTL2	angiomotin like 2	ENSG00000114019	PAP003	210	11.9%	chr3	135561764	CCDS33860.1	c.1757C>T	p.A586V
ANK3	ankyrin 3; node of Ranvier (ankyrin G)	ENSG00000151150	PAP003	289	16.3%	chr10	61500981	CCDS7258.1	c.9664A>G	p.T3222A
ASB11	ankyrin repeat and SOCS box-containing 11	ENSG00000165192	PAP003	460	11.1%	chrX	15211571	CCDS14164.1	c.949G>A	p.E317K
ASB11	ankyrin repeat and SOCS box-containing 11	ENSG00000165192	PAP003	193	11.9%	chrX	15242526	CCDS35209.1	c.4C>T	p.L2F
ASB5	ankyrin repeat and SOCS box-containing 5	ENSG00000164122	PAP003	238	16.4%	chr4	177379305	CCDS3827.1	c.665A>G	p.Y222C
ANKRD11	ankyrin repeat domain 11	ENSG00000167522	PAP003	679	11.6%	chr16	87876274	CCDS32513.1	c.4177G>A	p.E1393K
ANKRD30A	ankyrin repeat domain 30A	ENSG00000148513	PAP003	85	21.2%	chr10	37548293	CCDS7193.1	c.3479G>T	p.R1160I
ANKRD50	ankyrin repeat domain 50	ENSG00000151458	PAP003	157	16.6%	chr4	125811673	CCDS34060.1	c.2209C>T	p.R737X
ANKRD62	ankyrin repeat domain 62	ENSG00000181626	PAP003	98	13.3%	chr18	12085562	ENST00000314074	c.427G>A	p.A143T
ANO5	anoctamin 5	ENSG00000171714	PAP003	93	11.8%	chr11	22257807	CCDS31444.1	c.2662T>G	p.L888V
MKI67	antigen identified by monoclonal antibody Ki-67	ENSG00000148773	PAP003	315	11.7%	chr10	129794018	CCDS7659.1	c.6076A>G	p.T2026A
ARAP2	ArfGAP with RhoGAP domain; ankyrin repeat and PH domain 2	ENSG00000047365	PAP003	209	12.9%	chr4	35746148	CCDS3441.1	c.4891C>T	p.R1631W
ARGFX	arginine-fifty homeobox	ENSG00000186103	PAP003	228	13.2%	chr3	122787577	CCDS33834.1	c.388C>T	p.R130X
ARMC1	armadillo repeat containing 1	ENSG00000104442	PAP003	123	19.5%	chr8	66702148	CCDS6181.1	c.40G>A	p.A14T
ARMC2	armadillo repeat containing 2	ENSG00000118690	PAP003	225	14.2%	chr6	109381080	NM_032131	c.1748C>T	p.P583L
ARMC5	armadillo repeat containing 5	ENSG00000140691	PAP003	141	14.2%	chr16	31381666	CCDS42155.1	c.1297G>T	p.E433X
ARMCX5	armadillo repeat containing; X-linked 5	ENSG00000125962	PAP003	128	12.5%	chrX	101743783	CCDS14500.1	c.58G>T	p.D20Y
ASGR1	asialoglycoprotein receptor 1	ENSG00000141505	PAP003	171	12.9%	chr17	7022462	ENST00000380920	c.145C>A	p.L49I
ASPHD1	aspartate beta-hydroxylase domain containing 1	ENSG00000174939	PAP003	106	18.9%	chr16	29824693	CCDS10660.1	c.1147G>T	p.D383Y

ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP003	275	11.6%	chr1	26959947	CCDS285.1	c.1934C>A	p.S645X
ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP003	304	16.4%	chr1	26978941	CCDS285.1	c.5965C>T	p.R1989X
ATM	ataxia telangiectasia mutated	ENSG00000149311	PAP003	112	15.2%	chr11	107660298	CCDS31669.1	c.3881T>G	p.I1294S
ATM	ataxia telangiectasia mutated	ENSG00000149311	PAP003	104	13.5%	chr11	107677627	CCDS31669.1	c.5220T>G	p.I1740M
ATOH8	atonal homolog 8 (Drosophila)	ENSG00000168874	PAP003	235	13.6%	chr2	85853409	ENST00000377336	c.1118G>A	p.R373H
ATAD5	ATPase family; AAA domain containing 5	ENSG00000176208	PAP003	123	13.8%	chr17	26186835	CCDS11260.1	c.1610A>C	p.E537A
ATP2A3	ATPase; Ca++ transporting; ubiquitous	ENSG00000074370	PAP003	101	15.8%	chr17	3778337	CCDS11042.1	c.3014C>T	p.S1005L
ATP10B	ATPase; class V; type 10B	ENSG00000118322	PAP003	234	13.7%	chr5	159980478	CCDS43394.1	c.1870C>T	p.L624F
ATP6V0D2	ATPase; H+ transporting; lysosomal 38kDa; V0 subunit d2	ENSG00000147614	PAP003	293	26.3%	chr8	87180337	CCDS6241.1	c.14C>T	p.A5V
ATP4A	ATPase; H+/K+ exchanging; alpha polypeptide	ENSG00000105675	PAP003	131	13.0%	chr19	40738202	CCDS12467.1	c.2137G>A	p.V713M
ATP1A3	ATPase; Na+/K+ transporting; alpha 3 polypeptide	ENSG00000105409	PAP003	294	17.0%	chr19	47184114	CCDS12594.1	c.171A>C	p.K57N
ABCA13	ATP-binding cassette; sub-family A (ABC1); member 13	ENSG00000179869	PAP003	198	13.1%	chr7	48285342	ENST00000319379	c.5368G>T	p.G1790W
ABCA13	ATP-binding cassette; sub-family A (ABC1); member 13	ENSG00000179869	PAP003	221	15.4%	chr7	48422583	ENST00000319379	c.12151G>T	p.D4051Y
ABCA5	ATP-binding cassette; sub-family A (ABC1); member 5	ENSG00000154265	PAP003	146	10.3%	chr17	64810590	CCDS11685.1	c.983G>A	p.G328E
ABCB7	ATP-binding cassette; sub-family B (MDR/TAP); member 7	ENSG00000131269	PAP003	182	15.4%	chrX	74196847	CCDS14428.1	c.1982C>A	p.S661Y
ABCG5	ATP-binding cassette; sub-family G (WHITE); member 5	ENSG00000138075	PAP003	410	11.0%	chr2	43904738	CCDS1814.1	c.1142G>T	p.R381I
AVL9	AVL9 homolog (S. cerevisiase)	ENSG00000105778	PAP003	153	11.8%	chr7	32565083	CCDS34613.1	c.697C>T	p.L233F
BDP1	B double prime 1; subunit of RNA polymerase III transcription initiation factor IIIB	ENSG00000145734	PAP003	244	13.9%	chr5	70855682	CCDS43328.1	c.5548C>T	p.R1850W
BCAM	basal cell adhesion molecule (Lutheran blood group)	ENSG00000187244	PAP003	306	13.4%	chr19	50013718	CCDS12644.1	c.1178C>T	p.A393V
BNC1	basonuclin 1	ENSG00000169594	PAP003	217	17.1%	chr15	81717280	CCDS10324.1	c.2903C>T	p.S968L
BAG3	BCL2-associated athanogene 3	ENSG00000151929	PAP003	103	14.6%	chr10	121426644	CCDS7615.1	c.1588G>A	p.V530M
B3GAT2	beta-1;3-glucuronyltransferase 2 (glucuronosyltransferase S)	ENSG00000112309	PAP003	85	16.5%	chr6	71660693	CCDS4974.1	c.595C>T	p.R199X
B4GALNT2	beta-1;4-N-acetyl-galactosaminyl transferase 2	ENSG00000167080	PAP003	103	13.6%	chr17	44602072	CCDS11544.1	c.1684C>T	p.L562F
BOD1L	biorientation of chromosomes in cell division 1-like	ENSG00000038219	PAP003	297	15.5%	chr4	13212697	CCDS3411.2	c.4925T>C	p.V1642A
BAI3	brain-specific angiogenesis inhibitor 3	ENSG00000135298	PAP003	217	10.6%	chr6	70001650	CCDS4968.1	c.2613G>T	p.M871I
BRCA1	breast cancer 1; early onset	ENSG00000012048	PAP003	155	16.8%	chr17	38499576	CCDS11453.1	c.1498A>C	p.N500H
BRCA2	breast cancer 2; early onset	ENSG00000139618	PAP003	160	10.0%	chr13	31866855	CCDS9344.1	c.9286G>A	p.E3096K
BRMS1L	breast cancer metastasis-suppressor 1-like	ENSG00000100916	PAP003	56	17.9%	chr14	35365562	CCDS32066.1	c.89C>T	p.S30F
BRD3	bromodomain containing 3	ENSG00000169925	PAP003	139	16.5%	chr9	135900297	CCDS6980.1	c.1154C>T	p.S385L
BTBD12	BTB (POZ) domain containing 12	ENSG00000188827	PAP003	204	15.7%	chr16	3598776	CCDS10506.2	c.191A>C	p.K64T
BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	ENSG00000156970	PAP003	105	12.4%	chr15	38280425	CCDS10053.1	c.1519G>T	p.E507X
BBOX1	butyrobetaine (gamma); 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1	ENSG00000129151	PAP003	101	12.9%	chr11	27103802	CCDS7862.1	c.862C>T	p.R288C
BTNL8	butyrophilin-like 8	ENSG00000113303	PAP003	153	13.7%	chr5	180268464	CCDS43413.1	c.322G>T	p.D108Y
CDH12	cadherin 12; type 2 (N-cadherin 2)	ENSG00000154162	PAP003	129	13.2%	chr5	21878113	CCDS3890.1	c.728G>C	p.G243A
CELSR2	cadherin; EGF LAG seven-pass G-type receptor 2 (flamingo homolog; Drosophila)	ENSG00000143126	PAP003	170	10.6%	chr1	109596499	CCDS796.1	c.2275C>T	p.R759C
CANT1	calcium activated nucleotidase 1	ENSG00000171302	PAP003	149	15.4%	chr17	74504984	CCDS11760.1	c.316C>T	p.R106X
CAB39	calcium binding protein 39	ENSG00000135932	PAP003	62	16.1%	chr2	231366271	CCDS2478.1	c.379T>G	p.L127V
CASR	calcium-sensing receptor	ENSG00000036828	PAP003	249	12.0%	chr3	123463395	CCDS3010.1	c.823G>A	p.D275N
CASQ2	calsequestrin 2 (cardiac muscle)	ENSG00000118729	PAP003	157	14.0%	chr1	116112571	CCDS884.1	c.115G>A	p.E39K
CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	ENSG00000175040	PAP003	169	15.4%	chr3	144323696	CCDS3129.1	c.1348G>T	p.E450X
CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	ENSG00000175040	PAP003	88	14.8%	chr3	144323924	CCDS3129.1	c.1576C>T	p.R526W
CBR1	carbonyl reductase 1	ENSG00000159228	PAP003	192	11.5%	chr21	36365173	CCDS13641.1	c.345C>A	p.F115L
CES7	carboxylesterase 7	ENSG00000159398	PAP003	85	15.3%	chr16	54451101	CCDS10755.1	c.-1G>T	p.IVS7-1-1SpliceAcceptor
CASS4	Cas scaffolding protein family member 4	ENSG00000087589	PAP003	268	13.1%	chr20	54460597	CCDS33492.1	c.958A>G	p.T320A
CSNK1G3	casein kinase 1; gamma 3	ENSG00000151292	PAP003	99	24.2%	chr5	122909271	CCDS43355.1	c.15G>T	p.K5N
COMT	catechol-O-methyltransferase	ENSG00000093010	PAP003	159	11.3%	chr22	18336180	CCDS13770.1	c.737C>T	p.S246L
CNOT8	CCR4-NOT transcription complex; subunit 8	ENSG00000155508	PAP003	139	12.9%	chr5	154231505	CCDS4329.1	c.496G>A	p.V166I

CD163L1	CD163 molecule-like 1	ENSG00000177675	PAP003	256	18.0%	chr12	7447675	CCDS8577.1	c.1131T>G	p.N377K
CD40LG	CD40 ligand	ENSG00000102245	PAP003	183	13.7%	chrX	135568885	CCDS14659.1	c.431G>A	p.G144E
CD84	CD84 molecule	ENSG00000066294	PAP003	79	15.2%	chr1	158787379	CCDS1206.1	c.831A>C	p.R277S
ARHGEF9	Cdc42 guanine nucleotide exchange factor (GEF) 9	ENSG00000131089	PAP003	374	12.6%	chrX	62792175	CCDS35315.1	c.1224G>T	p.K408N
CDK5RAP2	CDK5 regulatory subunit associated protein 2	ENSG00000136861	PAP003	290	15.5%	chr9	122255764	CCDS6823.1	c.2584G>A	p.E862K
CADM2	cell adhesion molecule 2	ENSG00000175161	PAP003	151	15.9%	chr3	86198617	CCDS33792.1	c.1308C>A	p.F436L
CDC73	cell division cycle 73; Paf1/RNA polymerase II complex component; homolog (S. cerevisiae)	ENSG00000134371	PAP003	161	12.4%	chr1	191360959	CCDS1382.1	c.226C>T	p.R76X
CNTROB	centrobin; centrosomal BRCA2 interacting protein	ENSG00000170037	PAP003	228	12.7%	chr17	7791750	CCDS32557.1	c.2130G>T	p.K710N
CENPF	centromere protein F; 350/400ka (mitosin)	ENSG00000117724	PAP003	108	13.0%	chr1	212881322	CCDS31023.1	c.3018A>C	p.E1006D
CEP152	centrosomal protein 152kDa	ENSG00000103995	PAP003	182	12.1%	chr15	46835777	CCDS42033.1	c.2960G>A	p.R987Q
CEP164	centrosomal protein 164kDa	ENSG00000110274	PAP003	108	16.7%	chr11	116771552	CCDS31683.1	c.2993G>A	p.R998Q
CEP63	centrosomal protein 63kDa	ENSG00000182923	PAP003	129	10.9%	chr3	135760707	CCDS3086.1	c.1699G>A	p.D567N
CBLN2	cerebellin 2 precursor	ENSG00000141668	PAP003	162	16.7%	chr18	68356520	CCDS11999.1	c.546A>C	p.E182D
CHRNA6	cholinergic receptor; nicotinic; alpha 6	ENSG00000147434	PAP003	101	10.9%	chr8	42731328	CCDS6135.1	c.274G>T	p.D92Y
CHRNB2	cholinergic receptor; nicotinic; beta 2 (neuronal)	ENSG00000160716	PAP003	170	14.1%	chr1	152810305	CCDS1070.1	c.382G>A	p.E128K
CHD4	chromodomain helicase DNA binding protein 4	ENSG00000111642	PAP003	152	13.2%	chr12	6562672	CCDS8552.1	c.4013G>T	p.R1338I
CHD5	chromodomain helicase DNA binding protein 5	ENSG00000116254	PAP003	101	14.9%	chr1	6129030	CCDS57.1	c.1631G>T	p.R544I
C1orf125	chromosome 1 open reading frame 125	ENSG00000162779	PAP003	142	12.0%	chr1	177666299	CCDS30948.1	c.1422A>C	p.E474D
C10orf26	chromosome 10 open reading frame 26	ENSG00000166272	PAP003	148	17.6%	chr10	104562902	CCDS7540.1	c.853G>A	p.D285N
C10orf67	chromosome 10 open reading frame 67	ENSG00000179133	PAP003	90	12.2%	chr10	23673640	NM_153714	c.73T>A	p.S25T
C10orf72	chromosome 10 open reading frame 72	ENSG00000165633	PAP003	178	13.5%	chr10	49985654	CCDS31198.1	c.448G>T	p.E150X
C11orf30	chromosome 11 open reading frame 30	ENSG00000158636	PAP003	106	14.2%	chr11	75835683	CCDS8244.1	c.53G>T	p.R18I
C12orf50	chromosome 12 open reading frame 50	ENSG00000165805	PAP003	102	15.7%	chr12	86904273	CCDS9031.1	c.869G>T	p.R290I
C12orf50	chromosome 12 open reading frame 50	ENSG00000165805	PAP003	174	12.1%	chr12	86907205	CCDS9031.1	c.667G>T	p.E223X
C13orf39	chromosome 13 open reading frame 39	ENSG00000139780	PAP003	112	12.5%	chr13	102136470	CCDS32003.1	c.707A>C	p.K236T
C14orf166B	chromosome 14 open reading frame 166B	ENSG00000100565	PAP003	108	16.7%	chr14	76364492	NM_194287	c.194C>T	p.S65L
C14orf39	chromosome 14 open reading frame 39	ENSG00000179008	PAP003	170	10.0%	chr14	59997868	CCDS9746.1	c.1074G>T	p.Q358H
C17orf104	chromosome 17 open reading frame 104	ENSG00000180336	PAP003	101	10.9%	chr17	40095284	NM_001145080	c.278C>A	p.S93Y
C17orf104	chromosome 17 open reading frame 104	ENSG00000180336	PAP003	161	12.4%	chr17	40102400	NM_001145080	c.2446G>T	p.E816X
C17orf53	chromosome 17 open reading frame 53	ENSG00000125319	PAP003	163	20.2%	chr17	39581370	CCDS11477.1	c.673G>A	p.A225T
C19orf41	chromosome 19 open reading frame 41	ENSG00000161652	PAP003	413	14.3%	chr19	55353375	CCDS12792.2	c.458G>T	p.R153M
C2orf55	chromosome 2 open reading frame 55	ENSG00000196872	PAP003	292	11.6%	chr2	98821054	CCDS42720.1	c.199G>A	p.E67K
C20orf118	chromosome 20 open reading frame 118	ENSG00000101342	PAP003	133	15.0%	chr20	34939758	CCDS33465.1	c.76G>A	p.E26K
C22orf43	chromosome 22 open reading frame 43	ENSG00000189269	PAP003	102	10.8%	chr22	22291553	CCDS42985.1	c.434C>T	p.S145F
C3orf17	chromosome 3 open reading frame 17	ENSG00000163608	PAP003	145	17.2%	chr3	114207150	CCDS33824.1	c.1627A>G	p.I543V
C5orf34	chromosome 5 open reading frame 34	ENSG00000172244	PAP003	242	13.2%	chr5	43542171	CCDS3946.1	c.368T>C	p.V123A
C6orf203	chromosome 6 open reading frame 203	ENSG00000130349	PAP003	71	15.5%	chr6	107467931	CCDS5058.1	c.274A>C	p.K92Q
C7orf25	chromosome 7 open reading frame 25	ENSG00000136197	PAP003	279	14.0%	chr7	42916027	CCDS5466.1	c.998G>A	p.R333Q
C7orf45	chromosome 7 open reading frame 45	ENSG00000165120	PAP003	429	16.8%	chr7	129643215	CCDS5816.1	c.404T>G	p.F135C
C7orf58	chromosome 7 open reading frame 58	ENSG00000106034	PAP003	131	13.0%	chr7	120442961	CCDS34739.1	c.256G>T	p.E86X
C8orf48	chromosome 8 open reading frame 48	ENSG00000164743	PAP003	196	18.9%	chr8	13469262	NM_001007090	c.391A>C	p.N131H
C9orf5	chromosome 9 open reading frame 5	ENSG00000106771	PAP003	99	16.2%	chr9	110893150	CCDS43858.1	c.1023A>C	p.E341D
CXorf65	chromosome X open reading frame 65	ENSG00000204165	PAP003	733	11.9%	chrX	70243128	CCDS35324.1	c.4T>A	p.F2I
CLDN10	claudin 10	ENSG00000134873	PAP003	86	15.1%	chr13	95010398	CCDS9476.1	c.232G>A	p.A78T
CSTF1	cleavage stimulation factor; 3' pre-RNA; subunit 1; 50kDa	ENSG00000101138	PAP003	227	11.5%	chr20	54406159	CCDS13452.1	c.500G>A	p.R167Q
COPB1	coatomer protein complex; subunit beta 1	ENSG00000129083	PAP003	83	13.3%	chr11	14436764	CCDS7815.1	c.2692C>T	p.R898C
CCDC33	coiled-coil domain containing 33	ENSG00000140481	PAP003	197	15.2%	chr15	72413329	CCDS42058.1	c.1993G>A	p.A665T
CCDC54	coiled-coil domain containing 54	ENSG00000138483	PAP003	119	10.1%	chr3	108579765	CCDS2949.1	c.641C>A	p.S214Y
CCDC73	coiled-coil domain containing 73	ENSG00000186714	PAP003	136	12.5%	chr11	32591908	CCDS41630.1	c.2532G>T	p.E844D
COL3A1	collagen; type III; alpha 1	ENSG00000168542	PAP003	156	13.5%	chr2	189582130	CCDS2297.1	c.3761C>A	p.S1254Y
COL4A6	collagen; type IV; alpha 6	ENSG00000197565	PAP003	170	13.5%	chrX	107317826	CCDS14541.1	c.1678C>T	p.R560W
CFI	complement factor I	ENSG00000205403	PAP003	283	15.5%	chr4	110881498	CCDS34049.1	c.1752A>C	p.X584Y
CDAN1	congenital dyserythropoietic anemia; type I	ENSG00000140326	PAP003	161	16.1%	chr15	40814835	CCDS32209.1	c.973C>T	p.L325F

CDAN1	congenital dyserythropoietic anemia; type I	ENSG00000140326	PAP003	292	14.4%	chr15	40815782	ENST00000267892	c.575A>G	p.Q192R
COPS4	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)	ENSG00000138663	PAP003	119	10.9%	chr4	84208623	CCDS3600.1	c.1011G>T	p.K337N
CPNE4	copine IV	ENSG00000196353	PAP003	145	13.1%	chr3	133106957	CCDS3072.1	c.21T>G	p.I7M
COX18	COX18 cytochrome c oxidase assembly homolog (S. cerevisiae)	ENSG00000163626	PAP003	140	11.4%	chr4	74149944	CCDS3554.1	c.485G>A	p.R162Q
CKM	creatine kinase; muscle	ENSG00000104879	PAP003	434	11.1%	chr19	50501931	CCDS12659.1	c.1063G>C	p.D355H
CKM	creatine kinase; muscle	ENSG00000104879	PAP003	224	14.3%	chr19	50510649	CCDS12659.1	c.395G>A	p.R132H
CRY1	cryptochrome 1 (photolyase-like)	ENSG00000008405	PAP003	133	12.8%	chr12	105915933	CCDS9112.1	c.1179T>G	p.N393K
CSMD2	CUB and Sushi multiple domains 2	ENSG00000121904	PAP003	239	15.9%	chr1	33840632	CCDS380.1	c.6640G>A	p.V2214M
CUEDC1	CUE domain containing 1	ENSG00000180891	PAP003	103	12.6%	chr17	53305055	CCDS11599.1	c.752G>A	p.R251Q
CWF19L2	CWF19-like 2; cell cycle control (S. pombe)	ENSG00000152404	PAP003	130	12.3%	chr11	106804733	CCDS8336.1	c.-1T>C	p.IVS4+2-1SpliceDonor
CNGA2	cyclic nucleotide gated channel alpha 2	ENSG00000183862	PAP003	204	13.7%	chrX	150663359	CCDS14701.1	c.1728G>T	p.E576D
CCBL2	cysteine conjugate-beta lyase 2	ENSG00000137944	PAP003	61	16.4%	chr1	89226557	CCDS30766.1	c.65C>A	p.S22Y
CYSLTR2	cysteinyl leukotriene receptor 2	ENSG00000152207	PAP003	232	14.2%	chr13	48179069	CCDS9412.1	c.115G>T	p.E39X
CYP2C8	cytochrome P450; family 2; subfamily C; polypeptide 8	ENSG00000138115	PAP003	95	13.7%	chr10	96786953	CCDS7438.1	c.1395G>T	p.K465N
CYP2S1	cytochrome P450; family 2; subfamily S; polypeptide 1	ENSG00000167600	PAP003	341	11.1%	chr19	46396468	CCDS12573.1	c.669C>A	p.F223L
CYP7B1	cytochrome P450; family 7; subfamily B; polypeptide 1	ENSG00000172817	PAP003	96	24.0%	chr8	65691029	CCDS6180.1	c.623T>G	p.F208C
CRLF3	cytokine receptor-like factor 3	ENSG00000176390	PAP003	173	17.9%	chr17	26143677	CCDS32607.1	c.866G>A	p.R289Q
DCHS2	dachsous 2 (Drosophila)	ENSG00000197410	PAP003	158	12.0%	chr4	155376834	CCDS3785.1	c.7055C>T	p.S2352F
DACT1	dapper; antagonist of beta-catenin; homolog 1 (Xenopus laevis)	ENSG00000165617	PAP003	100	11.0%	chr14	58183064	CCDS9736.1	c.1970C>T	p.A657V
ADAM22	DAVID_ADAM metallopeptidase domain 22	ENSG00000222045	PAP003	159	15.1%	chr7	87648838	CCDS43608.1	c.2383C>T	p.R795X
ASXL3	DAVID_additional sex combs like 3 (Drosophila)	NM_030632	PAP003	133	11.3%	chr18	29574332	NM_030632	c.2966G>A	p.R989Q
Arl13a	DAVID_ADP-ribosylation factor-like 13A	NM_001162490	PAP003	230	13.9%	chrX	100130052	NM_001162490	c.774G>T	p.K258N
ARL15	DAVID_ADP-ribosylation factor-like 15	NM_019087	PAP003	127	18.1%	chr5	53444902	NM_019087	c.349G>T	p.E117X
BIRC8	DAVID_baculoviral IAP repeat-containing 8	ENSG00000180152	PAP003	361	13.6%	chr19	58485327	CCDS12863.1	c.113A>T	p.Q38L
Casp8ap2	DAVID_caspase 8 associated protein 2	NM_001137667	PAP003	110	13.6%	chr6	90629057	NM_001137667	c.908C>T	p.S303L
CLIC1	DAVID_chloride intracellular channel 1	ENSG00000213719	PAP003	85	11.8%	chr6	31812029	CCDS4719.1	c.28T>G	p.L10V
chd7	DAVID_chromodomain helicase DNA binding protein 7	NM_017780	PAP003	195	12.3%	chr8	61927996	NM_017780	c.6158G>A	p.R2053Q
C12orf55	DAVID_chromosome 12 open reading frame 55	ENSG00000165990	PAP003	126	12.7%	chr12	95445168	ENST00000298953	c.1172G>A	p.R391Q
C19orf55	DAVID_chromosome 19 open reading frame 55	NM_001039887	PAP003	483	11.8%	chr19	40947875	NM_001039887	c.727T>G	p.F243V
ARHGAP40	DAVID_chromosome 20 open reading frame 95	NM_001164431	PAP003	204	13.7%	chr20	36708132	NM_001164431	c.1595G>A	p.R532Q
C3orf77	DAVID_chromosome 3 open reading frame 77	NM_001145030	PAP003	147	17.7%	chr3	44260345	NM_001145030	c.1343C>T	p.S448L
C8orf80	DAVID_chromosome 8 open reading frame 80	NM_001010906	PAP003	388	23.2%	chr8	27944694	NM_001010906	c.1893T>A	p.N631K
CDRT1	DAVID_CMT1A duplicated region transcript 1	NM_006382	PAP003	72	15.3%	chr17	15437388	NM_006382	c.1994T>C	p.I665T
ccdc64b	DAVID_coiled-coil domain containing 64B	NM_001103175	PAP003	308	14.0%	chr16	3020721	NM_001103175	c.592C>T	p.R198W
COL6A6	DAVID_collagen type VI alpha 6	NM_001102608	PAP003	234	17.5%	chr3	131769926	NM_001102608	c.2189C>T	p.T730M
Col11a2	DAVID_collagen: type XI: alpha 2	ENSG00000204248	PAP003	557	13.1%	chr6	33241428	CCDS43452.1	c.4368G>T	p.E1456D
COL29A1	DAVID_collagen: type XXIX: alpha 1	NM_153264	PAP003	248	14.1%	chr3	131670592	NM_153264	c.7054G>T	p.E2352X
CNTNAP4	DAVID_contactin associated protein-like 4	NM_138994	PAP003	79	21.5%	chr16	75127096	NM_138994	c.2690G>A	p.R897H
CNTNAP5	DAVID_contactin associated protein-like 5	NM_130773	PAP003	254	12.6%	chr2	124695800	NM_130773	c.131C>T	p.S44F
LOC100271	DAVID_DH and coiled-coil domain-containing protein	NM_001145451	PAP003	90	17.8%	chr2	39011792	NM_001145451	c.401C>A	p.P134H
DNHD1	DAVID_dynein heavy chain domain 1	NM_144666	PAP003	201	12.4%	chr11	6522898	NM_144666	c.4153C>T	p.R1385X
DNAH1	DAVID_dynein: axonemal: heavy chain 1	NM_015512	PAP003	279	10.8%	chr3	52402509	NM_015512	c.10594C>T	p.R3532C
DST	DAVID_dystonin	NM_020388	PAP003	153	11.1%	chr6	56580127	NM_020388	c.5647G>T	p.D1883Y
Epha6	DAVID_EPH receptor A6	NM_001080448	PAP003	64	15.6%	chr3	98016452	NM_001080448	c.295G>A	p.E99K
Epha6	DAVID_EPH receptor A6	NM_001080448	PAP003	87	14.9%	chr3	98937610	NM_001080448	c.3086G>A	p.R1029Q
EPPK1	DAVID_epiplakin 1	NM_031308	PAP003	427	15.9%	chr8	145013163	NM_031308	c.6247T>G	p.F2083V
ETV5	DAVID_ets variant 5	ENSG00000171656	PAP003	99	16.2%	chr3	187257957	CCDS33906.1	c.988G>T	p.D330Y
Fat1	DAVID_FAT tumor suppressor homolog 1 (Drosophila)	NM_005245	PAP003	158	10.1%	chr4	187779351	NM_005245	c.5383C>T	p.R1795X
Fbxo10	DAVID_F-box protein 10	NM_012166	PAP003	92	16.3%	chr9	37505946	NM_012166	c.2651G>A	p.R884Q
Fbxo10	DAVID_F-box protein 10	NM_012166	PAP003	262	17.2%	chr9	37531446	NM_012166	c.320G>A	p.R107Q

FLJ46836	DAVID_FLJ46836 protein	ENSG00000196979	PAP003	229	11.4%	chr9	131944100	ENST00000358748	c.103G>A	p.D35N
GSPT1	DAVID_G1 to S phase transition 1	NM_002094	PAP003	111	20.7%	chr16	11887963	NM_002094	c.1119A>C	p.E373D
GLB1L3	DAVID_galactosidase: beta 1-like 3	NM_001080407	PAP003	483	15.9%	chr11	133686231	NM_001080407	c.1244C>T	p.S415L
LOC100128	DAVID_hypothetical LOC100128310	ENSG00000179253	PAP003	227	14.1%	chr20	59727549	ENST00000317652	c.73G>A	p.D25N
LOC401286	DAVID_hypothetical LOC401286	ENSG00000203689	PAP003	150	15.3%	chr6	167813004	ENST00000366825	c.166C>T	p.L56F
LOC100128	DAVID_hypothetical protein LOC100128554	ENSG00000214043	PAP003	66	21.2%	chr12	125513314	ENST00000397346	c.467G>T	p.R156I
LOC100132	DAVID_hypothetical protein LOC100132731	ENSG00000187695	PAP003	222	16.2%	chr3	130146658	ENST00000344062	c.842T>C	p.L281P
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP003	128	10.9%	chr13	102191633	NM_001146197	c.9415G>T	p.E3139X
Rfx8	DAVID_hypothetical protein LOC731220	NM_001145664	PAP003	205	12.2%	chr2	101401843	NM_001145664	c.253A>G	p.T85A
KIAA0748	DAVID_KIAA0748	NM_001136030	PAP003	66	24.2%	chr12	53643912	NM_001136030	c.536C>A	p.S179Y
KSR2	DAVID_kinase suppressor of ras 2	NM_173598	PAP003	172	11.0%	chr12	116447362	NM_173598	c.1810G>A	p.E604K
KIF4A	DAVID_kinesin family member 4B; kinesin family member 4A	NM_001099293	PAP003	314	15.0%	chr5	154376535	NM_001099293	c.2923G>T	p.E975X
Kif4b	DAVID_kinesin family member 4B; kinesin family member 4A	NM_001099293	PAP003	314	15.0%	chr5	154376535	NM_001099293	c.2923G>T	p.E975X
AQPEP	DAVID_laeverin	ENSG00000172901	PAP003	143	16.1%	chr5	115326682	CCDS4124.1	c.469G>A	p.E157K
LOXHD1	DAVID_lipoxygenase homology domains 1	NM_144612	PAP003	136	16.9%	chr18	42393455	NM_144612	c.3170G>T	p.R1057L
TRANK1	DAVID_lupus brain antigen 1	NM_014831	PAP003	84	13.1%	chr3	36849628	NM_014831	c.6318G>T	p.E2106D
LY6G5C	DAVID_lymphocyte antigen 6 complex: locus G5C	ENSG00000204428	PAP003	63	17.5%	chr6	31756068	CCDS34401.1	c.53G>T	p.S18I
MAML2	DAVID_mastermind-like 2 (Drosophila)	NM_032427	PAP003	227	13.2%	chr11	95465985	NM_032427	c.858G>T	p.E286D
Matn2	DAVID_matrilin 2	NM_002380	PAP003	128	25.8%	chr8	99115048	NM_002380	c.2800A>T	p.K934X
MLL2	DAVID_myeloid/lymphoid or mixed-lineage leukemia 2	NM_003482	PAP003	231	15.2%	chr12	47702400	NM_003482	c.16342C>T	p.R5448X
MLL4	DAVID_myeloid/lymphoid or mixed-lineage leukemia 4	ENSG00000105663	PAP003	84	15.5%	chr19	40903038	NM_014727	c.949G>T	p.G317X
MYO1H	DAVID_myosin IH	NM_001101421	PAP003	106	14.2%	chr12	108318684	NM_001101421	c.355C>A	p.L119I
ND2	DAVID_NADH-ubiquinone oxidoreductase chain 2	ENSG00000198763	PAP003	82	57.3%	chrM	4666	ENST00000361453	c.196G>A	p.A66T
ND5	DAVID_NADH-ubiquinone oxidoreductase chain 5	ENSG00000198786	PAP003	103	62.1%	chrM	12864	ENST00000361567	c.527G>A	p.R176H
NRXN1	DAVID_neurexin 1	NM_001135659	PAP003	299	14.0%	chr2	50619090	NM_001135659	c.2068G>A	p.D690N
Nrk	DAVID_Nik related kinase	NM_198465	PAP003	116	12.9%	chrX	105012405	NM_198465	c.229A>C	p.K77Q
SGK269	DAVID_NKF3 kinase family member	ENSG00000173517	PAP003	86	11.6%	chr15	75212950	CCDS42062.1	c.3529G>A	p.E1177K
NECAB1	DAVID_N-terminal EF-hand calcium binding protein 1	NM_022351	PAP003	209	26.3%	chr8	91962531	NM_022351	c.354G>T	p.K118N
nfe2l2	DAVID_nuclear factor (erythroid-derived 2)-like 2	ENSG00000222043	PAP003	125	13.6%	chr2	177804865	CCDS42782.1	c.712G>T	p.E238X
OR2H1	DAVID_olfactory receptor: family 2: subfamily H: member 1	ENSG00000204688	PAP003	470	11.5%	chr6	29538012	CCDS4660.1	c.487C>A	p.H163N
OR6V1	DAVID_olfactory receptor: family 6: subfamily V: member 1	NM_001001667	PAP003	475	14.3%	chr7	142459788	NM_001001667	c.229C>T	p.P77S
PLSCR5	DAVID_phospholipid scramblase family: member 5	NM_001085420	PAP003	81	14.8%	chr3	147792262	NM_001085420	c.550G>T	p.E184X
PINX1	DAVID_PIN2-interacting protein 1	NM_017884	PAP003	112	12.5%	chr8	10729690	NM_017884	c.25C>T	p.R9W
Patl2	DAVID_protein associated with topoisomerase II homolog 2 (yeast)	NM_001145112	PAP003	224	15.2%	chr15	42747915	NM_001145112	c.1282G>A	p.E428K
PCDHGA11	DAVID_protocadherin gamma subfamily A: 11	NM_018914	PAP003	241	12.9%	chr5	140781820	NM_018914	c.842C>A	p.S281X
Pcdhga6	DAVID_protocadherin gamma subfamily A: 6	NM_018919	PAP003	300	13.3%	chr5	140735381	NM_018919	c.1547C>T	p.A516V
RIN2	DAVID_Ras and Rab interactor 2	NM_018993	PAP003	94	14.9%	chr20	19920894	NM_018993	c.2151A>C	p.E717D
RIMS1	DAVID_regulating synaptic membrane exocytosis 1	NM_014989	PAP003	447	10.5%	chr6	72863428	NM_014989	c.301G>A	p.E101K
RING1	DAVID_ring finger protein 1	ENSG00000204227	PAP003	196	12.2%	chr6	33285714	CCDS34424.1	c.284G>A	p.R95Q
RYR2	DAVID_ryanodine receptor 2 (cardiac)	NM_001035	PAP003	99	10.1%	chr1	235820749	NM_001035	c.3994A>C	p.N1332H
RYR3	DAVID_ryanodine receptor 3	NM_001036	PAP003	196	10.2%	chr15	31775909	NM_001036	c.6059C>T	p.A2020V
SLFN12L	DAVID_schlafen family member 12-like	NM_001145027	PAP003	184	12.5%	chr17	30830846	NM_001145027	c.583G>T	p.D195Y
SERINC5	DAVID_serine incorporator 5	NM_178276	PAP003	76	21.1%	chr5	79497966	NM_178276	c.855A>C	p.E285D
LOC100129	DAVID_similar to tudor domain containing 1	ENSG00000218819	PAP003	81	14.8%	chr2	21218664	ENST00000405799	c.4820T>C	p.V1607A
SCN5A	DAVID_sodium channel: voltage-gated: type V: alpha subunit	NM_001099404	PAP003	87	13.8%	chr3	38597712	NM_001099404	c.2942G>T	p.C981F
SLC4A10	DAVID_solute carrier family 4: sodium bicarbonate transporter: member 10	NM_022058	PAP003	100	16.0%	chr2	162513907	NM_022058	c.2179C>T	p.R727X
STARD9	DAVID_StAR-related lipid transfer (START) domain containing 9	NM_020759	PAP003	413	14.5%	chr15	40771116	NM_020759	c.10048G>A	p.E3350K
SYDE2	DAVID_synapse defective 1: Rho GTPase: homolog 2 (C. elegans)	NM_032184	PAP003	100	13.0%	chr1	85421291	NM_032184	c.1622G>A	p.R541Q
TRAV23DV6	DAVID_T cell receptor alpha variable 23/delta variable 6	ENSG00000211803	PAP003	56	23.2%	chr14	21624577	ENST00000390451	c.9G>T	p.K3N

TRDV1	DAVID_T cell receptor delta variable 1	ENSG00000211804	PAP003	162	17.3%	chr14	21634633	ENST00000390452	c.244C>T	p.R82C
TOP2A	DAVID_topoisomerase (DNA) II alpha 170kDa	NM_001067	PAP003	64	15.6%	chr17	35823064	NM_001067	c.485G>A	p.R162Q
TMEM216	DAVID_transmembrane protein 216	NM_016499	PAP003	85	15.3%	chr11	60918012	NM_016499	c.34C>T	p.R12C
TRIM15	DAVID_tripartite motif-containing 15	ENSG00000204610	PAP003	357	14.6%	chr6	30246758	CCDS4677.1	c.874G>T	p.D292Y
Tbcd	DAVID_tubulin folding cofactor D	NM_005993	PAP003	168	10.1%	chr17	78457213	NM_005993	c.1917G>T	p.E639D
WDR87	DAVID_WD repeat domain 87	NM_031951	PAP003	176	11.4%	chr19	43068608	NM_031951	c.7426G>A	p.E2476K
WDR87	DAVID_WD repeat domain 87	NM_031951	PAP003	295	16.3%	chr19	43071286	NM_031951	c.4748G>A	p.R1583Q
ZNF275	DAVID_zinc finger protein 275	NM_001080485	PAP003	496	15.9%	chrX	152264174	NM_001080485	c.34G>A	p.V12I
ZNF284	DAVID_zinc finger protein 284	NM_001037813	PAP003	175	10.3%	chr19	49282543	NM_001037813	c.1072C>A	p.L358I
ZNF432	DAVID_zinc finger protein 432	ENSG00000221897	PAP003	96	14.6%	chr19	57228894	CCDS12848.1	c.1850G>A	p.R617Q
ZNF564	DAVID_zinc finger protein 564	ENSG00000220949	PAP003	154	15.6%	chr19	12499104	CCDS42505.1	c.818G>T	p.R273I
ZNF793	DAVID_zinc finger protein 793	NM_001013659	PAP003	137	11.7%	chr19	42720476	NM_001013659	c.1076G>T	p.R359I
ZNF836	DAVID_zinc finger protein 836	NM_001102657	PAP003	139	15.8%	chr19	57350824	NM_001102657	c.1924G>A	p.E642K
ZFP92	DAVID_zinc finger protein 92 homolog (mouse)	ENSG00000189420	PAP003	254	11.8%	chrX	152339476	ENST00000338647	c.447G>T	p.E149D
DCAF12L2	DDB1 and CUL4 associated factor 12-like 2	ENSG00000198354	PAP003	212	12.7%	chrX	125126994	CCDS43991.1	c.595G>A	p.A199T
DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	ENSG00000141141	PAP003	84	13.1%	chr17	33058517	CCDS11323.1	c.1213G>T	p.E405X
DHX34	DEAH (Asp-Glu-Ala-His) box polypeptide 34	ENSG00000134815	PAP003	230	12.6%	chr19	52550295	CCDS12700.1	c.865G>A	p.D289N
DOCK2	dedicator of cytokinesis 2	ENSG00000134516	PAP003	84	13.1%	chr5	169030691	CCDS4371.1	c.256C>A	p.P86T
DOCK2	dedicator of cytokinesis 2	ENSG00000134516	PAP003	209	12.0%	chr5	169368128	CCDS4371.1	c.3122C>A	p.S1041Y
DEFB125	defensin; beta 125	ENSG00000178591	PAP003	236	15.3%	chr20	24758	CCDS12989.2	c.171T>G	p.I57M
DBC1	deleted in bladder cancer 1	ENSG00000078725	PAP003	284	11.3%	chr9	120969365	CCDS6822.1	c.2104C>T	p.R702X
DPCD	deleted in primary ciliary dyskinesia homolog (mouse)	ENSG00000166171	PAP003	120	18.3%	chr10	103350998	CCDS7514.1	c.319C>T	p.R107X
DTX3L	deltex 3-like (Drosophila)	ENSG00000163840	PAP003	161	16.1%	chr3	123770824	CCDS3015.1	c.1198G>A	p.E400K
DMP1	dentin matrix acidic phosphoprotein 1	ENSG00000152592	PAP003	117	12.0%	chr4	88803059	CCDS3623.1	c.1105G>A	p.D369N
DNASE1L1	deoxyribonuclease I-like 1	ENSG00000013563	PAP003	513	12.5%	chrX	153285066	CCDS14747.1	c.403C>T	p.P135S
DGKI	diacylglycerol kinase; iota	ENSG00000157680	PAP003	60	16.7%	chr7	136990022	CCDS5845.1	c.734G>T	p.R245I
DGAT2L6	diacylglycerol O-acyltransferase 2-like 6	ENSG00000184210	PAP003	751	15.3%	chrX	69336900	CCDS14397.1	c.338C>A	p.S113Y
DICER1	dicer 1; ribonuclease type III	ENSG00000100697	PAP003	188	16.0%	chr14	94660518	CCDS9931.1	c.1144G>A	p.E382K
DMBX1	diencephalon/mesencephalon homeobox 1	ENSG00000197587	PAP003	189	11.6%	chr1	46745311	CCDS536.1	c.42G>T	p.M14I
DPYSL5	dihydropyrimidinase-like 5	ENSG00000157851	PAP003	522	11.7%	chr2	26975086	CCDS1730.1	c.215C>T	p.T72I
DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	ENSG00000151240	PAP003	105	17.1%	chr10	365516	CCDS7054.1	c.3610C>A	p.L1204M
DPP10	dipeptidyl-peptidase 10 (non-functional)	ENSG00000175497	PAP003	314	15.0%	chr2	116288907	CCDS33278.1	c.1748A>G	p.D583G
DPP6	dipeptidyl-peptidase 6	ENSG00000130226	PAP003	189	13.2%	chr7	154192064	NM_130797	c.888G>T	p.E296D
DIS3L	DIS3 mitotic control homolog (S. cerevisiae)-like	ENSG00000166938	PAP003	191	17.8%	chr15	64412469	CCDS10214.1	c.2681A>G	p.Y894C
DDR2	discoidin domain receptor tyrosine kinase 2	ENSG00000162733	PAP003	146	15.1%	chr1	160991222	CCDS1241.1	c.370C>T	p.R124W
DLG3	discs; large homolog 3 (Drosophila)	ENSG00000082458	PAP003	89	14.6%	chrX	69632004	CCDS14403.1	c.1795G>A	p.D599N
DAAM1	dishevelled associated activator of morphogenesis 1	ENSG00000100592	PAP003	119	11.8%	chr14	58800040	CCDS9737.1	c.92G>A	p.R31Q
DCLRE1B	DNA cross-link repair 1B (PSO2 homolog; S. cerevisiae)	ENSG00000118655	PAP003	363	13.5%	chr1	114255723	CCDS866.1	c.986C>A	p.S329Y
DNAJB9	DnaJ (Hsp40) homolog; subfamily B; member 9	ENSG00000128590	PAP003	119	15.1%	chr7	108000886	CCDS5752.1	c.525A>C	p.K175N
DOPEY1	dopey family member 1	ENSG00000083097	PAP003	120	11.7%	chr6	83920475	CCDS4996.1	c.6383T>G	p.V2128G
DUXA	double homeobox A	ENSG00000204527	PAP003	98	15.3%	chr19	62363852	CCDS33126.1	c.151G>T	p.E51X
DCLK2	doublecortin-like kinase 2	ENSG00000170390	PAP003	81	16.0%	chr4	151381075	CCDS34076.1	c.1775G>A	p.R592Q
DUSP26	dual specificity phosphatase 26 (putative)	ENSG00000133878	PAP003	94	26.6%	chr8	33574491	CCDS6092.1	c.85C>T	p.R29X
DNAH10	dynein; axonemal; heavy chain 10	ENSG00000197653	PAP003	498	13.5%	chr12	122979841	NM_207437	c.12019G>A	p.E4007K
DNAH10	dynein; axonemal; heavy chain 10	ENSG00000197653	PAP003	348	15.2%	chr12	122979928	NM_207437	c.12106A>G	p.K4036E
DNAH5	dynein; axonemal; heavy chain 5	ENSG00000039139	PAP003	78	17.9%	chr5	13788295	CCDS3882.1	c.11706G>T	p.K3902N
DNAH5	dynein; axonemal; heavy chain 5	ENSG00000039139	PAP003	110	10.0%	chr5	13954558	CCDS3882.1	c.1855A>G	p.N619D
DNAH9	dynein; axonemal; heavy chain 9	ENSG00000007174	PAP003	193	10.9%	chr17	11813537	CCDS11160.1	c.13429C>A	p.L4477M
DMD	dystrophin	ENSG00000198947	PAP003	98	15.3%	chrX	31657671	CCDS14233.1	c.7658G>A	p.R2553Q
EFCAB4B	EF-hand calcium binding domain 4B	ENSG00000130038	PAP003	155	23.9%	chr12	3652949	CCDS8522.1	c.595G>T	p.D199Y
EMILIN3	elastin microfibril interfacer 3	ENSG00000183798	PAP003	332	15.7%	chr20	39424271	CCDS13316.1	c.1352G>A	p.G451E
ELP3	elongation protein 3 homolog (S. cerevisiae)	ENSG00000134014	PAP003	212	16.5%	chr8	28023828	CCDS6065.1	c.416G>A	p.R139H
ENAM	enamelin	ENSG00000132464	PAP003	395	12.4%	chr4	71728741	CCDS3544.1	c.2734G>T	p.D912Y
ERMP1	endoplasmic reticulum metallopeptidase 1	ENSG00000099219	PAP003	109	11.9%	chr9	5787929	CCDS34983.1	c.2274A>C	p.K758N

EPC2	enhancer of polycomb homolog 2 (Drosophila)	ENSG00000135999	PAP003	55	18.2%	chr2	149228140	NM_015630	c.634C>T	p.R212W
EPHA1	EPH receptor A1	ENSG00000146904	PAP003	191	11.5%	chr7	142802143	CCDS5884.1	c.2232T>G	p.N744K
EPHA8	EPH receptor A8	ENSG00000070886	PAP003	218	11.0%	chr1	22775621	CCDS225.1	c.484C>T	p.R162W
EPYC	epiphycan	ENSG00000083782	PAP003	73	19.2%	chr12	89882150	CCDS31870.1	c.883C>T	p.R295X
ERO1LB	ERO1-like beta (S. cerevisiae)	ENSG00000086619	PAP003	149	10.7%	chr1	234456400	CCDS31064.1	c.844G>T	p.E282X
EPB49	erythrocyte membrane protein band 4.9 (dematin)	ENSG00000158856	PAP003	117	19.7%	chr8	21981062	CCDS6020.1	c.172C>T	p.R58W
ESR1	estrogen receptor 1	ENSG00000091831	PAP003	257	11.7%	chr6	152461619	CCDS5234.1	c.1613A>G	p.D538G
EIF1	eukaryotic translation initiation factor 1	ENSG00000173812	PAP003	76	17.1%	chr17	37099695	CCDS11403.1	c.171G>T	p.K57N
EIF4G3	eukaryotic translation initiation factor 4 gamma; 3	ENSG00000075151	PAP003	138	15.9%	chr1	21050413	CCDS214.1	c.3529G>A	p.V1177M
EVX2	even-skipped homeobox 2	ENSG00000174279	PAP003	223	11.7%	chr2	176655193	CCDS33333.1	c.658G>A	p.E220K
ERCC3	excision repair cross-complementing rodent repair deficiency; complementation group 3 (xeroderma pigmentosum group B complementing)	ENSG00000163161	PAP003	355	13.5%	chr2	127762755	CCDS2144.1	c.978G>T	p.K326N
FAM111A	family with sequence similarity 111; member A	ENSG00000166801	PAP003	140	12.1%	chr11	58676250	CCDS7973.1	c.533C>T	p.S178L
FAM123A	family with sequence similarity 123A	ENSG00000165566	PAP003	242	13.2%	chr13	24642461	CCDS9312.1	c.940G>A	p.D314N
FAM131B	family with sequence similarity 131; member B	ENSG00000159784	PAP003	118	16.9%	chr7	142766072	CCDS5882.1	c.352G>A	p.D118N
FAM133A	family with sequence similarity 133; member A	ENSG00000179083	PAP003	104	15.4%	chrX	92851578	CCDS14466.1	c.504G>T	p.E168D
FAM149B1	family with sequence similarity 149; member B1	ENSG00000138286	PAP003	237	13.5%	chr10	74662846	NM_173348	c.1271G>A	p.R424Q
FAM172A	family with sequence similarity 172; member A	ENSG00000113391	PAP003	128	11.7%	chr5	93243042	CCDS4069.1	c.676A>C	p.K226Q
FAM184A	family with sequence similarity 184; member A	ENSG00000111879	PAP003	153	13.1%	chr6	119342370	CCDS43499.1	c.2314C>A	p.H772N
FAM196A	family with sequence similarity 196; member A	ENSG00000188916	PAP003	118	22.9%	chr10	128863473	NM_001039762	c.1177C>T	p.R393W
FAM200A	family with sequence similarity 200; member A	ENSG00000221909	PAP003	142	10.6%	chr7	98983340	CCDS5668.1	c.627T>G	p.I209M
FAM26E	family with sequence similarity 26; member E	ENSG00000178033	PAP003	145	14.5%	chr6	116939929	CCDS5108.1	c.377A>G	p.E126G
FAM45B	family with sequence similarity 45; member B	ENSG00000221930	PAP003	98	13.3%	chrX	129457787	ENST00000408950	c.974G>T	p.R325I
FAM47A	family with sequence similarity 47; member A	ENSG00000185448	PAP003	110	16.4%	chrX	34058093	CCDS43926.1	c.2224T>G	p.F742V
FAM55A	family with sequence similarity 55; member A	ENSG00000095110	PAP003	134	16.4%	chr11	113898190	CCDS8372.1	c.928C>T	p.R310C
FAM73B	family with sequence similarity 73; member B	ENSG00000148343	PAP003	71	15.5%	chr9	130851568	CCDS6917.1	c.508G>A	p.D170N
FAM83G	family with sequence similarity 83; member G	ENSG00000188522	PAP003	118	18.6%	chr17	18847703	CCDS42276.1	c.377G>A	p.R126H
FAM84A	family with sequence similarity 84; member A	ENSG00000162981	PAP003	211	13.7%	chr2	14692983	ENST00000381456	c.206G>T	p.R69I
FBXL2	F-box and leucine-rich repeat protein 2	ENSG00000153558	PAP003	125	20.0%	chr3	33375819	CCDS2658.1	c.161G>T	p.R54I
FBXW7	F-box and WD repeat domain containing 7	ENSG00000109670	PAP003	104	10.6%	chr4	153470332	CCDS3777.1	c.1178G>A	p.R393Q
FBXO25	F-box protein 25	ENSG00000147364	PAP003	90	22.2%	chr8	403089	CCDS5953.1	c.926C>T	p.A309V
FBXO8	F-box protein 8	ENSG00000164117	PAP003	131	13.0%	chr4	175395230	CCDS3820.1	c.868C>T	p.R290X
FCER2	Fc fragment of IgE; low affinity II; receptor for (CD23)	ENSG00000104921	PAP003	438	12.1%	chr19	7668127	CCDS12184.1	c.311C>A	p.S104Y
FGF16	fibroblast growth factor 16	ENSG00000196468	PAP003	243	18.5%	chrX	76598581	NM_003868	c.263G>A	p.R88Q
FLRT3	fibronectin leucine rich transmembrane protein 3	ENSG00000125848	PAP003	216	13.9%	chr20	14255494	CCDS13121.1	c.659T>G	p.V220G
FLRT3	fibronectin leucine rich transmembrane protein 3	ENSG00000125848	PAP003	161	18.0%	chr20	14255774	CCDS13121.1	c.379A>C	p.I127L
FSIP2	fibrous sheath interacting protein 2	ENSG00000188738	PAP003	136	16.9%	chr2	186372993	ENST00000344648	c.2567A>C	p.K856T
FBLN2	fibulin 2	ENSG00000163520	PAP003	118	23.7%	chr3	13634630	ENST00000295761	c.1780G>A	p.E594K
FSHR	follicle stimulating hormone receptor	ENSG00000170820	PAP003	84	15.5%	chr2	49043558	CCDS1843.1	c.1906G>T	p.D636Y
FHOD1	formin homology 2 domain containing 1	ENSG00000135723	PAP003	279	16.8%	chr16	65822692	CCDS10834.1	c.2567G>A	p.R856Q
FHOD3	formin homology 2 domain containing 3	ENSG00000134775	PAP003	106	10.4%	chr18	32346421	CCDS32816.1	c.428A>G	p.E143G
FPR2	formyl peptide receptor 2	ENSG00000171049	PAP003	308	16.6%	chr19	56964624	CCDS12840.1	c.901C>T	p.L301F
FPR3	formyl peptide receptor 3	ENSG00000187474	PAP003	253	11.5%	chr19	57019714	CCDS12841.1	c.901C>A	p.L301I
FMR1	fragile X mental retardation 1	ENSG00000102081	PAP003	110	10.0%	chrX	146826752	CCDS14682.1	c.1066T>G	p.L356V
FZD1	frizzled homolog 1 (Drosophila)	ENSG00000157240	PAP003	229	12.2%	chr7	90733452	CCDS5620.1	c.1321G>A	p.E441K
FTSJ3	FtsJ homolog 3 (E. coli)	ENSG00000108592	PAP003	377	12.7%	chr17	59256511	CCDS11644.1	c.418G>A	p.A140T
FKTN	fukutin	ENSG00000106692	PAP003	90	12.2%	chr9	107410039	CCDS6766.1	c.766C>T	p.R256X
FGD3	FYVE; RhoGEF and PH domain containing 3	ENSG00000127084	PAP003	151	10.6%	chr9	94834893	CCDS43849.1	c.1702G>A	p.E568K
FGD6	FYVE; RhoGEF and PH domain containing 6	ENSG00000180263	PAP003	159	14.5%	chr12	94127881	CCDS31878.1	c.1310C>T	p.S437L
GPATCH8	G patch domain containing 8	ENSG00000186566	PAP003	134	18.7%	chr17	39830721	CCDS32666.1	c.4250C>A	p.S1417Y
GPR108	G protein-coupled receptor 108	ENSG00000125734	PAP003	93	14.0%	chr19	6686930	CCDS42479.1	c.280C>T	p.R94C
GPR173	G protein-coupled receptor 173	ENSG00000184194	PAP003	227	14.5%	chrX	53122649	CCDS14349.1	c.121G>A	p.A41T
GPR98	G protein-coupled receptor 98	ENSG00000164199	PAP003	241	12.9%	chr5	90052564	NM_032119	c.9680G>A	p.R3227Q

GPRASP1	G protein-coupled receptor associated sorting protein 1	ENSG00000198932	PAP003	128	14.1%	chrX	101797763	CCDS35352.1	c.2266G>T	p.E756X
GPRASP2	G protein-coupled receptor associated sorting protein 2	ENSG00000158301	PAP003	324	16.7%	chrX	101858155	CCDS14501.1	c.1702C>T	p.R568X
GPRC6A	G protein-coupled receptor; family C; group 6; member A	ENSG00000173612	PAP003	95	15.8%	chr6	117220243	CCDS5112.1	c.2536A>C	p.K846Q
GABRA5	gamma-aminobutyric acid (GABA) A receptor; alpha 5	ENSG00000186297	PAP003	180	12.8%	chr15	24679408	NM_000810	c.211C>T	p.R71C
GABRR3	gamma-aminobutyric acid (GABA) receptor; rho 3	ENSG00000183185	PAP003	105	15.2%	chr3	99194471	ENST00000329044	c.59T>C	p.F20S
GABRQ	gamma-aminobutyric acid (GABA) receptor; theta	ENSG00000147402	PAP003	108	13.0%	chrX	151570821	CCDS14707.1	c.1078C>T	p.R360C
GABRQ	gamma-aminobutyric acid (GABA) receptor; theta	ENSG00000147402	PAP003	298	12.8%	chrX	151571912	CCDS14707.1	c.1411T>C	p.F471L
GSDMB	gasdermin B	ENSG00000073605	PAP003	502	15.9%	chr17	35327067	CCDS42313.1	c.29G>T	p.R10I
GSDMC	gasdermin C	ENSG00000147697	PAP003	186	23.7%	chr8	130830072	CCDS6360.1	c.1384G>A	p.A462T
GRPR	gastrin-releasing peptide receptor	ENSG00000126010	PAP003	461	10.6%	chrX	16080608	CCDS14174.1	c.1074G>T	p.M358I
GEMIN5	gem (nuclear organelle) associated protein 5	ENSG00000082516	PAP003	142	12.0%	chr5	154296912	CCDS4330.1	c.193G>A	p.E65K
GGPS1	geranylgeranyl diphosphate synthase 1	ENSG00000152904	PAP003	102	18.6%	chr1	233565236	CCDS1604.1	c.34C>A	p.L12I
GCM1	glial cells missing homolog 1 (Drosophila)	ENSG00000137270	PAP003	150	13.3%	chr6	53118377	CCDS4950.1	c.13G>A	p.D5N
GLUD2	glutamate dehydrogenase 2	ENSG00000182890	PAP003	389	13.1%	chrX	120010118	CCDS14603.1	c.899G>T	p.R300I
GRIA4	glutamate receptor; ionotrophic; AMPA 4	ENSG00000152578	PAP003	167	12.0%	chr11	105350368	CCDS8333.1	c.2531C>T	p.A844V
GRID1	glutamate receptor; ionotropic; delta 1	ENSG00000182771	PAP003	415	17.6%	chr10	87474127	CCDS31236.1	c.1820G>A	p.S607N
GRIK5	glutamate receptor; ionotropic; kainate 5	ENSG00000105737	PAP003	72	15.3%	chr19	47198264	ENST00000301218	c.2789C>A	p.S930Y
GRIN2A	glutamate receptor; ionotropic; N-methyl D-aspartate 2A	ENSG00000183454	PAP003	179	14.5%	chr16	9842084	CCDS10539.1	c.1572C>A	p.F524L
GRM1	glutamate receptor; metabotropic 1	ENSG00000152822	PAP003	145	13.1%	chr6	146392477	CCDS5209.1	c.131A>G	p.D44G
GRM5	glutamate receptor; metabotropic 5	ENSG00000168959	PAP003	170	14.7%	chr11	87977592	CCDS8283.1	c.1336T>G	p.F446V
QSER1	glutamine and serine rich 1	ENSG00000060749	PAP003	275	13.1%	chr11	32910711	CCDS41631.1	c.944A>C	p.N315T
GPM6A	glycoprotein M6A	ENSG00000150625	PAP003	113	13.3%	chr4	176793050	CCDS3824.1	c.837A>C	p.X279Y
GAS2L1	growth arrest-specific 2 like 1	ENSG00000185340	PAP003	320	14.4%	chr22	28038377	ENST00000333679	c.1934G>A	p.R645H
GDF10	growth differentiation factor 10	ENSG00000107623	PAP003	206	17.0%	chr10	48049129	CCDS7220.1	c.763G>A	p.E255K
GNAL	guanine nucleotide binding protein (G protein); alpha activating activity polypeptide; olfactory type	ENSG00000141404	PAP003	140	15.0%	chr18	11742493	CCDS11852.1	c.61C>T	p.R21X
GNL2	guanine nucleotide binding protein-like 2 (nucleolar)	ENSG00000134697	PAP003	576	11.8%	chr1	37820520	CCDS421.1	c.800G>A	p.R267Q
GBP6	guanylate binding protein family; member 6	ENSG00000183347	PAP003	186	15.1%	chr1	89623473	CCDS723.1	c.1759A>C	p.N587H
H2BFM	H2B histone family; member M	ENSG00000101812	PAP003	110	14.5%	chrX	103181459	NM_001164416	c.260C>A	p.S87Y
HEY2	hairy/enhancer-of-split related with YRPW motif 2	ENSG00000135547	PAP003	757	13.7%	chr6	126122426	CCDS5131.1	c.799G>A	p.A267T
HEATR7B1	HEAT repeat containing 7B1	ENSG00000185038	PAP003	206	10.7%	chr2	234373605	ENST00000389758	c.1555A>C	p.K519Q
HSPA4	heat shock 70kDa protein 4	ENSG00000170606	PAP003	97	17.5%	chr5	132433987	CCDS4166.1	c.329G>A	p.R110Q
HUWE1	HECT; UBA and WWE domain containing 1	ENSG00000086758	PAP003	96	11.5%	chrX	53637128	CCDS35301.1	c.3662C>T	p.S1221L
HELLS	helicase; lymphoid-specific	ENSG00000119969	PAP003	181	16.0%	chr10	96323900	CCDS7434.1	c.671G>A	p.R224Q
HMCN2	hemicentin 2	ENSG00000148357	PAP003	161	11.8%	chr9	132266110	ENST00000277491	c.2371G>A	p.A791T
HEPN1	HEPACAM opposite strand 1	ENSG00000221932	PAP003	166	13.3%	chr11	124295089	CCDS41729.1	c.233A>C	p.Q78P
HSPG2	heparan sulfate proteoglycan 2	ENSG00000142798	PAP003	54	22.2%	chr1	22058733	CCDS30625.1	c.5206G>A	p.V1736I
HPS4	Hermansky-Pudlak syndrome 4	ENSG00000100099	PAP003	166	16.9%	chr22	25190707	CCDS13835.1	c.889G>A	p.A297T
HNRNPUL1	heterogeneous nuclear ribonucleoprotein U-like 1	ENSG00000105323	PAP003	171	15.2%	chr19	46490001	CCDS12576.1	c.1011T>G	p.C337W
HJURP	Holliday junction recognition protein	ENSG00000123485	PAP003	185	11.9%	chr2	234414862	CCDS33406.1	c.1303G>T	p.E435X
HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	ENSG00000095951	PAP003	206	15.5%	chr6	12233233	CCDS43426.1	c.5219C>T	p.S1740F
HAS2	hyaluronan synthase 2	ENSG00000170961	PAP003	308	23.1%	chr8	122696034	CCDS6335.1	c.1155C>A	p.F385L
HYDIN	hydrocephalus inducing homolog (mouse)	ENSG00000157423	PAP003	115	10.4%	chr16	69498869	CCDS42189.1	c.8420A>G	p.D2807G
HYDIN	hydrocephalus inducing homolog (mouse)	ENSG00000157423	PAP003	136	11.0%	chr16	69767039	CCDS42189.1	c.488G>A	p.R163Q
IGSF1	immunoglobulin superfamily; member 1	ENSG00000147255	PAP003	195	12.8%	chrX	130235488	CCDS14629.1	c.3974C>T	p.S1325F
IGSF1	immunoglobulin superfamily; member 1	ENSG00000147255	PAP003	120	16.7%	chrX	130244162	CCDS14629.1	c.1183C>T	p.L395F
ILDR2	immunoglobulin-like domain containing receptor 2	ENSG00000143195	PAP003	187	12.8%	chr1	165193666	CCDS1256.1	c.343G>T	p.D115Y
IMMP2L	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	ENSG00000184903	PAP003	131	13.7%	chr7	110090976	CCDS5753.1	c.446T>G	p.I149S
IRS2	insulin receptor substrate 2	ENSG00000185950	PAP003	77	14.3%	chr13	109234298	CCDS9510.1	c.6115NULL>(	p.NULL-1FsIns3bp
IRS4	insulin receptor substrate 4	ENSG00000133124	PAP003	368	15.5%	chrX	107864868	CCDS14544.1	c.1363C>T	p.R455C

ITGAE	integrin; alpha E (antigen CD103; human mucosal lymphocyte antigen 1; alpha polypeptide)	ENSG00000083457	PAP003	241	14.5%	chr17	3611164	CCDS32531.1	c.490G>T	p.E164X
ITGB7	integrin; beta 7	ENSG00000139626	PAP003	209	12.9%	chr12	51877655	CCDS8849.1	c.463T>C	p.Y155H
ILKAP	integrin-linked kinase-associated serine/threonine phosphatase 2C	ENSG00000132323	PAP003	64	18.8%	chr2	238761631	CCDS2526.1	c.305C>T	p.S102L
ITIH5L	inter-alpha (globulin) inhibitor H5-like	ENSG00000102313	PAP003	176	10.8%	chrX	54800500	CCDS14361.1	c.2732C>A	p.S911Y
IFIH1	interferon induced with helicase C domain 1	ENSG00000115267	PAP003	132	13.6%	chr2	162842363	CCDS2217.1	c.1852C>T	p.R618X
IFNA8	interferon; alpha 8	ENSG00000120242	PAP003	126	18.3%	chr9	21399308	CCDS6507.1	c.133C>T	p.R45X
IFIT5	interferon-induced protein with tetratricopeptide repeats 5	ENSG00000152778	PAP003	201	12.9%	chr10	91167744	CCDS7403.1	c.808G>A	p.E270K
IL12RB2	interleukin 12 receptor; beta 2	ENSG00000081985	PAP003	242	11.6%	chr1	67559989	CCDS638.1	c.193C>T	p.R65C
IL31RA	interleukin 31 receptor A	ENSG00000164509	PAP003	287	16.4%	chr5	55239881	CCDS3970.2	c.1386G>T	p.E462D
IRAK3	interleukin-1 receptor-associated kinase 3	ENSG00000090376	PAP003	61	21.3%	chr12	64906873	CCDS8975.1	c.757T>G	p.L253V
IMPG2	interphotoreceptor matrix proteoglycan 2	ENSG00000081148	PAP003	93	14.0%	chr3	102434501	CCDS2940.1	c.3047T>C	p.F1016S
INTU	inturned planar cell polarity effector homolog (Drosophila)	ENSG00000164066	PAP003	100	13.0%	chr4	128784245	CCDS34061.1	c.266G>A	p.R89K
IQGAP2	IQ motif containing GTPase activating protein 2	ENSG00000145703	PAP003	95	14.7%	chr5	76015429	CCDS34188.1	c.3836C>A	p.S1279Y
ICA1	islet cell autoantigen 1; 69kDa	ENSG00000003147	PAP003	79	13.9%	chr7	8227533	CCDS34602.1	c.277G>A	p.E93K
IZUMO1	izumo sperm-egg fusion 1	ENSG00000182264	PAP003	101	14.9%	chr19	53935990	CCDS12732.1	c.1040C>T	p.S347L
JAKMIP2	janus kinase and microtubule interacting protein 2	ENSG00000176049	PAP003	81	12.3%	chr5	146961528	ENST00000333010	c.2452C>A	p.L818I
KAL1	Kallmann syndrome 1 sequence	ENSG00000011201	PAP003	76	15.8%	chrX	8525122	CCDS14130.1	c.494C>T	p.S165L
KPNA3	karyopherin alpha 3 (importin alpha 4)	ENSG00000102753	PAP003	196	12.2%	chr13	49183123	CCDS9421.1	c.808A>G	p.T270A
KATNB1	katanin p80 (WD repeat containing) subunit B 1	ENSG00000140854	PAP003	402	16.2%	chr16	56342306	CCDS10788.1	c.356T>G	p.F119C
KLHL4	kelch-like 4 (Drosophila)	ENSG00000102271	PAP003	146	19.2%	chrX	86774078	CCDS14456.1	c.1537C>T	p.R513W
KLHL4	kelch-like 4 (Drosophila)	ENSG00000102271	PAP003	310	14.8%	chrX	86811000	CCDS14456.1	c.2113C>A	p.L705I
KLHL9	kelch-like 9 (Drosophila)	ENSG00000198642	PAP003	321	13.1%	chr9	21323603	CCDS6503.1	c.1256A>G	p.Y419C
KRT13	keratin 13	ENSG00000171401	PAP003	144	16.7%	chr17	36912179	CCDS11396.1	c.1217G>A	p.R406H
KRT72	keratin 72	ENSG00000170486	PAP003	98	16.3%	chr12	51266048	CCDS8833.1	c.1521A>C	p.K507N
KIAA0802	KIAA0802	ENSG00000168502	PAP003	124	16.9%	chr18	8803107	CCDS11841.1	c.2735G>A	p.R912H
KIAA1462	KIAA1462	ENSG00000165757	PAP003	270	13.7%	chr10	30358308	CCDS41500.1	c.775C>T	p.P259S
KIAA1486	KIAA1486	ENSG00000144460	PAP003	484	17.8%	chr2	226155642	NM_020864	c.1265G>A	p.R422Q
KIAA1614	KIAA1614	ENSG00000135835	PAP003	76	23.7%	chr1	179171313	CCDS41442.1	c.1645G>A	p.A549T
KIAA2018	KIAA2018	ENSG00000176542	PAP003	245	12.7%	chr3	114857494	CCDS43133.1	c.5725C>T	p.R1909X
KIF26B	kinesin family member 26B	ENSG00000162849	PAP003	303	15.5%	chr1	243597074	NM_018012	c.781G>A	p.A261T
KIF26B	kinesin family member 26B	ENSG00000162849	PAP003	274	13.1%	chr1	243916138	NM_018012	c.3230C>T	p.S1077L
KIF5B	kinesin family member 5B	ENSG00000170759	PAP003	234	12.8%	chr10	32347281	CCDS7171.1	c.2408T>G	p.F803C
KLC2	kinesin light chain 2	ENSG00000174996	PAP003	127	12.6%	chr11	65787977	CCDS8130.1	c.920G>A	p.R307Q
KNG1	kininogen 1	ENSG00000113889	PAP003	161	12.4%	chr3	187920595	CCDS43183.1	c.203C>T	p.S68F
KL	klotho	ENSG00000133116	PAP003	254	13.8%	chr13	32526327	CCDS9347.1	c.1243A>G	p.N415D
KRBA1	KRAB-A domain containing 1	ENSG00000133619	PAP003	125	10.4%	chr7	149050857	ENST00000255992	c.649G>A	p.E217K
LAMA1	laminin; alpha 1	ENSG00000101680	PAP003	150	11.3%	chr18	6946621	ENST00000344342	c.461C>T	p.S154F
LAMA4	laminin; alpha 4	ENSG00000112769	PAP003	78	15.4%	chr6	112572831	CCDS43491.1	c.-1C>A	p.IVS17-3-1SpliceAcceptor
LAMA4	laminin; alpha 4	ENSG00000112769	PAP003	95	13.7%	chr6	112629545	CCDS43491.1	c.460C>T	p.R154W
LAMB1	laminin; beta 1	ENSG00000091136	PAP003	218	11.0%	chr7	107413918	CCDS5750.1	c.550A>C	p.K184Q
LAMC1	laminin; gamma 1 (formerly LAMB2)	ENSG00000135862	PAP003	89	15.7%	chr1	181351374	CCDS1351.1	c.1307C>T	p.S436F
LSG1	large subunit GTPase 1 homolog (S. cerevisiae)	ENSG00000041802	PAP003	249	17.3%	chr3	195844115	CCDS33922.1	c.1948C>T	p.R650C
LAS1L	LAS1-like (S. cerevisiae)	ENSG00000001497	PAP003	171	13.5%	chrX	64655014	CCDS14381.1	c.1505G>A	p.R502H
LTBP4	latent transforming growth factor beta binding protein 4	ENSG00000090006	PAP003	100	12.0%	chr19	45814940	ENST00000308370	c.3238G>C	p.E1080Q
LGSN	lengsin; lens protein with glutamine synthetase domain	ENSG00000146166	PAP003	235	11.5%	chr6	64048234	CCDS4964.1	c.1181A>C	p.N394T
LRRC28	leucine rich repeat containing 28	ENSG00000168904	PAP003	106	11.3%	chr15	97719128	CCDS10380.1	c.760G>A	p.V254I
LRRC66	leucine rich repeat containing 66	ENSG00000188993	PAP003	246	11.8%	chr4	52556126	CCDS43229.1	c.1819G>T	p.G607W
LZTS2	leucine zipper; putative tumor suppressor 2	ENSG00000107816	PAP003	90	12.2%	chr10	102755336	CCDS7507.1	c.1200G>T	p.E400D
LRRK2	leucine-rich repeat kinase 2	ENSG00000188906	PAP003	131	11.5%	chr12	39044955	CCDS31774.1	c.7226C>A	p.S2409Y

LRCH2	leucine-rich repeats and calponin homology (CH) domain containing 2	ENSG00000130224	PAP003	135	13.3%	chrX	114263904	NM_020871	c.1957C>T	p.R653C
LILRB5	leukocyte immunoglobulin-like receptor; subfamily B (with TM and ITIM domains); member 5	ENSG00000105609	PAP003	108	13.0%	chr19	59451969	CCDS12885.1	c.404C>T	p.A135V
LMO7	LIM domain 7	ENSG00000136153	PAP003	70	15.7%	chr13	75313930	CCDS9454.1	c.2995G>A	p.D999N
LIMA1	LIM domain and actin binding 1	ENSG00000050405	PAP003	74	13.5%	chr12	48928738	CCDS8802.1	c.64G>T	p.E22X
LHFP	lipoma HMGIC fusion partner	ENSG00000183722	PAP003	126	14.3%	chr13	39073023	CCDS9369.1	c.331G>A	p.D111N
LRP6	low density lipoprotein receptor-related protein 6	ENSG00000070018	PAP003	219	16.9%	chr12	12225595	CCDS8647.1	c.1022G>A	p.R341H
LSM14A	LSM14A; SCD6 homolog A (S. cerevisiae)	ENSG00000105216	PAP003	67	20.9%	chr19	39377225	CCDS12435.1	c.124C>T	p.R42X
KDM3B	lysine (K)-specific demethylase 3B	ENSG00000120733	PAP003	155	13.5%	chr5	137782741	CCDS34242.1	c.3636C>A	p.C1212X
KDM5A	lysine (K)-specific demethylase 5A	ENSG00000073614	PAP003	39	25.6%	chr12	276585	CCDS41736.1	c.4117C>A	p.L1373I
KDM5A	lysine (K)-specific demethylase 5A	ENSG00000073614	PAP003	76	15.8%	chr12	302587	CCDS41736.1	c.2197A>C	p.K733Q
LPAR4	lysophosphatidic acid receptor 4	ENSG00000147145	PAP003	263	13.3%	chrX	77897456	CCDS14441.1	c.434G>A	p.R145Q
MDH1B	malate dehydrogenase 1B; NAD (soluble)	ENSG00000138400	PAP003	145	14.5%	chr2	207324033	CCDS33365.1	c.922G>A	p.V308M
MFHAS1	malignant fibrous histiocytoma amplified sequence 1	ENSG00000147324	PAP003	188	31.4%	chr8	8785241	CCDS34844.1	c.2738A>C	p.K913T
MANEA	mannosidase; endo-alpha	ENSG00000172469	PAP003	153	13.1%	chr6	96141188	CCDS5032.1	c.152G>A	p.R51Q
MGAT4C	mannosyl (alpha-1;3-)-glycoprotein beta-1;4-N-acetylglucosaminyltransferase; isozyme C (putative)	ENSG00000182050	PAP003	163	14.1%	chr12	84897506	CCDS9030.1	c.1129G>T	p.D377Y
MGAT5	mannosyl (alpha-1;6-)-glycoprotein beta-1;6-N-acetyl-glucosaminyltransferase	ENSG00000152127	PAP003	208	13.5%	chr2	134823886	CCDS2171.1	c.1153G>A	p.E385K
MMP11	matrix metallopeptidase 11 (stromelysin 3)	ENSG00000099953	PAP003	363	13.8%	chr22	22453252	CCDS13816.1	c.823G>A	p.A275T
MCF2L2	MCF.2 cell line derived transforming sequence-like 2	ENSG00000053524	PAP003	92	10.9%	chr3	184408211	CCDS3243.1	c.2591G>A	p.R864Q
MDM1	Mdm1 nuclear protein homolog (mouse)	ENSG00000111554	PAP003	152	15.1%	chr12	66993712	CCDS8983.1	c.1588G>T	p.D530Y
MDM4	Mdm4 p53 binding protein homolog (mouse)	ENSG00000198625	PAP003	209	12.0%	chr1	202785060	CCDS1447.1	c.1100C>T	p.S367L
MTOR	mechanistic target of rapamycin (serine/threonine kinase)	ENSG00000198793	PAP003	161	10.6%	chr1	11220650	CCDS127.1	c.2045G>A	p.R682H
MAGEC1	melanoma antigen family C; 1	ENSG00000155495	PAP003	428	15.2%	chrX	140823596	CCDS35417.1	c.2740G>A	p.E914K
MUM1L1	melanoma associated antigen (mutated) 1-like 1	ENSG00000157502	PAP003	159	17.0%	chrX	105337094	ENST00000372552	c.1013G>T	p.R338I
MS4A14	membrane-spanning 4-domains; subfamily A; member 14	ENSG00000166928	PAP003	340	12.9%	chr11	59939972	CCDS31569.1	c.955G>A	p.D319N
MESP2	mesoderm posterior 2 homolog (mouse)	ENSG00000188095	PAP003	158	17.7%	chr15	88122488	CCDS42078.1	c.1113G>T	p.Q371H
METRNL	meteorin; glial cell differentiation regulator-like	ENSG00000176845	PAP003	144	16.7%	chr17	78645664	CCDS32779.1	c.860G>A	p.R287H
MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type	ENSG00000151611	PAP003	90	13.3%	chr4	146795755	CCDS3766.1	c.976C>T	p.R326C
MAP6	microtubule-associated protein 6	ENSG00000171533	PAP003	571	13.1%	chr11	74975976	CCDS31641.1	c.2218C>T	p.R740C
MCART6	mitochondrial carrier triple repeat 6	ENSG00000176274	PAP003	113	13.3%	chrX	103236119	CCDS35363.1	c.478G>A	p.E160K
MAP4K1	mitogen-activated protein kinase kinase kinase kinase 1	ENSG00000104814	PAP003	126	13.5%	chr19	43779859	CCDS42564.1	c.1784A>C	p.N595T
MLXIP	MLX interacting protein	ENSG00000175727	PAP003	266	15.4%	chr12	121184086	NM_014938	c.1331C>T	p.P444L
MOCS1	molybdenum cofactor synthesis 1	ENSG00000124615	PAP003	259	10.4%	chr6	39982118	CCDS4845.1	c.1856G>T	p.R619L
MORC1	MORC family CW-type zinc finger 1	ENSG00000114487	PAP003	57	17.5%	chr3	110165021	CCDS2955.1	c.2729G>T	p.R910I
MTERFD3	MTERF domain containing 3	ENSG00000120832	PAP003	181	18.2%	chr12	105896414	CCDS9111.1	c.209T>A	p.L70H
MUC17	mucin 17; cell surface associated	ENSG00000169876	PAP003	183	14.8%	chr7	100467202	CCDS34711.1	c.5785A>G	p.T1929A
MSH4	mutS homolog 4 (E. coli)	ENSG00000057468	PAP003	89	20.2%	chr1	76151078	CCDS670.1	c.2729G>A	p.R910Q
MYCT1	myc target 1	ENSG00000120279	PAP003	215	14.9%	chr6	153084714	CCDS5239.1	c.341C>A	p.S114Y
MYBPC1	myosin binding protein C; slow type	ENSG00000196091	PAP003	232	10.8%	chr12	100598370	CCDS9083.1	c.3365G>A	p.G1122D
MYO5A	myosin VA (heavy chain 12; myoxin)	ENSG00000197535	PAP003	99	11.1%	chr15	50489827	CCDS42037.1	c.751T>G	p.F251V
MYO5C	myosin VC	ENSG00000128833	PAP003	70	14.3%	chr15	50359097	CCDS42036.1	c.205G>A	p.E69K
MYH15	myosin; heavy chain 15	ENSG00000144821	PAP003	125	15.2%	chr3	109687977	CCDS43127.1	c.1018G>T	p.E340X
MYH8	myosin; heavy chain 8; skeletal muscle; perinatal	ENSG00000133020	PAP003	133	11.3%	chr17	10240746	CCDS11153.1	c.4377G>A	p.W1459X
MTMR9	myotubularin related protein 9	ENSG00000104643	PAP003	135	13.3%	chr8	11217627	CCDS5979.1	c.1570G>T	p.E524X
NPPB	natriuretic peptide precursor B	ENSG00000120937	PAP003	315	14.3%	chr1	11840941	CCDS140.1	c.305G>A	p.R102Q
NPR2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	ENSG00000159899	PAP003	290	14.8%	chr9	35795937	CCDS6590.1	c.2158C>T	p.R720C
NKTR	natural killer-tumor recognition sequence	ENSG00000114857	PAP003	160	15.0%	chr3	42654212	CCDS2702.1	c.2012C>T	p.S671L
NEIL1	nei endonuclease VIII-like 1 (E. coli)	ENSG00000140398	PAP003	119	10.1%	chr15	73428570	CCDS10278.1	c.271G>A	p.E91K
NPHS1	nephrosis 1; congenital; Finnish type (nephrin)	ENSG00000161270	PAP003	59	16.9%	chr19	41031431	CCDS32996.1	c.1118G>A	p.R373Q
NGF	nerve growth factor (beta polypeptide)	ENSG00000134259	PAP003	199	13.6%	chr1	115630795	CCDS882.1	c.145C>T	p.R49C

NRXN3	neurexin 3	ENSG00000021645	PAP003	340	10.9%	chr14	78245612	CCDS9870.1	c.402C>A	p.F134L
NBAS	neuroblastoma amplified sequence	ENSG00000151779	PAP003	316	10.8%	chr2	15526008	CCDS1685.1	c.1826G>A	p.G609D
NEFM	neurofilament; medium polypeptide	ENSG00000104722	PAP003	191	10.5%	chr8	24829053	CCDS6046.1	c.1111C>T	p.R371W
NLGN3	neuroligin 3	ENSG00000196338	PAP003	123	17.1%	chrX	70305921	CCDS14407.1	c.1736G>A	p.R579Q
NOVA1	neuro-oncological ventral antigen 1	ENSG00000139910	PAP003	157	10.8%	chr14	26019148	CCDS32061.1	c.322G>A	p.A108T
NPBWR2	neuropeptides B/W receptor 2	ENSG00000125522	PAP003	158	16.5%	chr20	62208427	CCDS13557.1	c.202C>A	p.L68I
NKX2-2	NK2 homeobox 2	ENSG00000125820	PAP003	180	10.0%	chr20	21442281	CCDS13145.1	c.285G>NULL	p.NULL-1FsDel1bp
NLRP11	NLR family; pyrin domain containing 11	ENSG00000179873	PAP003	152	16.4%	chr19	61013476	CCDS12935.1	c.312C>A	p.F104L
NLRP4	NLR family; pyrin domain containing 4	ENSG00000160505	PAP003	275	15.3%	chr19	61061305	CCDS12936.1	c.734C>T	p.S245L
NLRP4	NLR family; pyrin domain containing 4	ENSG00000160505	PAP003	210	14.8%	chr19	61061902	CCDS12936.1	c.1331G>A	p.R444H
NLRP9	NLR family; pyrin domain containing 9	ENSG00000185792	PAP003	157	11.5%	chr19	60936095	CCDS12934.1	c.914C>T	p.S305L
NASP	nuclear autoantigenic sperm protein (histone-binding)	ENSG00000132780	PAP003	96	13.5%	chr1	45852426	CCDS526.1	c.1584G>T	p.K528N
NFATC1	nuclear factor of activated T-cells; cytoplasmic; calcineurin-dependent 1	ENSG00000131196	PAP003	194	14.9%	chr18	75328442	CCDS32850.1	c.1925C>A	p.S642Y
NCOR2	nuclear receptor co-repressor 2	ENSG00000196498	PAP003	107	11.2%	chr12	123477213	CCDS41858.1	c.1236G>T	p.M412I
NXF3	nuclear RNA export factor 3	ENSG00000147206	PAP003	268	14.2%	chrX	102221752	CCDS14503.1	c.976A>C	p.K326Q
NAP1L1	nucleosome assembly protein 1-like 1	ENSG00000187109	PAP003	87	11.5%	chr12	74730660	CCDS9013.1	c.977T>G	p.I326S
NAP1L2	nucleosome assembly protein 1-like 2	ENSG00000186462	PAP003	255	14.1%	chrX	72349810	CCDS14423.1	c.1244C>T	p.S415F
NAP1L2	nucleosome assembly protein 1-like 2	ENSG00000186462	PAP003	156	14.7%	chrX	72349978	CCDS14423.1	c.1076G>A	p.R359Q
NULL	NULL	ENSG00000178137	PAP003	138	13.0%	chr5	140222927	ENST00000319589	c.233C>T	p.S78L
NULL	NULL	ENSG00000182873	PAP003	213	14.6%	chr1	2103820	ENST00000333854	c.200G>T	p.R67I
NULL	NULL	ENSG00000189277	PAP003	133	11.3%	chr2	186381863	ENST00000343098	c.3679C>A	p.P1227T
NULL	NULL	ENSG00000198678	PAP003	175	11.4%	chr12	47239900	ENST00000328207	c.32C>A	p.S11Y
NULL	NULL	MI0006435	PAP003	122	13.1%	chr4	36104431	MI0006435	c.15G>T	p.K5N
NULL	NULL	NM_031859	PAP003	133	18.0%	chr5	140218245	NM_031859	c.2428A>G	p.N810D
ODZ3	odz; odd Oz/ten-m homolog 3 (Drosophila)	ENSG00000218336	PAP003	125	12.0%	chr4	183913088	NM_001080477	c.4574A>G	p.D1525G
OR1L8	olfactory receptor; family 1; subfamily L; member 8	ENSG00000171496	PAP003	78	20.5%	chr9	124369916	CCDS35124.1	c.662G>A	p.R221Q
OR10AB1P	olfactory receptor; family 10; subfamily AB; member 1 pseudogene	ENSG00000176716	PAP003	200	15.5%	chr11	7707141	ENST00000317359	c.650G>A	p.G217D
OR10J1	olfactory receptor; family 10; subfamily J; member 1	ENSG00000196184	PAP003	209	14.8%	chr1	157676279	CCDS1185.1	c.107T>G	p.I36S
OR10J7P	olfactory receptor; family 10; subfamily J; member 7 pseudogene	ENSG00000196184	PAP003	209	14.8%	chr1	157676279	CCDS1185.1	c.107T>G	p.I36S
OR10J8P	olfactory receptor; family 10; subfamily J; member 8 pseudogene	ENSG00000196184	PAP003	209	14.8%	chr1	157676279	CCDS1185.1	c.107T>G	p.I36S
OR10J9P	olfactory receptor; family 10; subfamily J; member 9 pseudogene	ENSG00000196184	PAP003	209	14.8%	chr1	157676279	CCDS1185.1	c.107T>G	p.I36S
OR12D3	olfactory receptor; family 12; subfamily D; member 3	ENSG00000112462	PAP003	119	13.4%	chr6	29431424	CCDS4657.1	c.528C>A	p.Y176X
OR13F1	olfactory receptor; family 13; subfamily F; member 1	ENSG00000186881	PAP003	555	10.5%	chr9	106306558	CCDS35087.1	c.194A>T	p.N65I
OR13H1	olfactory receptor; family 13; subfamily H; member 1	ENSG00000171054	PAP003	358	13.7%	chrX	130506410	CCDS35396.1	c.682C>T	p.R228C
OR14K1	olfactory receptor; family 14; subfamily K; member 1	ENSG00000153230	PAP003	196	10.7%	chr1	245969037	ENST00000283225	c.498T>G	p.F166L
OR2B2	olfactory receptor; family 2; subfamily B; member 2	ENSG00000168131	PAP003	92	18.5%	chr6	27987373	CCDS4641.1	c.704G>A	p.R235Q
OR2T6	olfactory receptor; family 2; subfamily T; member 6	ENSG00000198104	PAP003	348	15.2%	chr1	246617923	CCDS31114.1	c.391C>T	p.R131C
OR4C45	olfactory receptor; family 4; subfamily C; member 45	ENSG00000197161	PAP003	90	12.2%	chr11	48324070	ENST00000360720	c.325T>G	p.L109V
OR4F6	olfactory receptor; family 4; subfamily F; member 6	ENSG00000184140	PAP003	202	11.4%	chr15	100163929	CCDS32341.1	c.484T>G	p.F162V
OR4F6	olfactory receptor; family 4; subfamily F; member 6	ENSG00000184140	PAP003	77	19.5%	chr15	100164085	CCDS32341.1	c.640C>A	p.L214I
OR4Q3	olfactory receptor; family 4; subfamily Q; member 3	ENSG00000182652	PAP003	236	11.9%	chr14	19285956	CCDS32020.1	c.530A>C	p.N177T
OR4S1	olfactory receptor; family 4; subfamily S; member 1	ENSG00000176555	PAP003	366	14.2%	chr11	48284466	CCDS31488.1	c.116G>A	p.G39E
OR5B17	olfactory receptor; family 5; subfamily B; member 17	ENSG00000197786	PAP003	145	10.3%	chr11	57882199	CCDS31548.1	c.920A>C	p.K307T
OR5G5P	olfactory receptor; family 5; subfamily G; member 5 pseudogene	ENSG00000205025	PAP003	92	12.0%	chr11	56326583	ENST00000378368	c.264G>T	p.E88D
OR5J2	olfactory receptor; family 5; subfamily J; member 2	ENSG00000174957	PAP003	596	11.6%	chr11	55701337	CCDS31522.1	c.668T>G	p.F223C
OR5K4	olfactory receptor; family 5; subfamily K; member 4	ENSG00000196098	PAP003	204	14.7%	chr3	99555642	CCDS33802.1	c.255C>A	p.F85L
OR51B4	olfactory receptor; family 51; subfamily B; member 4	ENSG00000183251	PAP003	145	13.8%	chr11	5279093	CCDS7757.1	c.660G>T	p.K220N

OR7A5	olfactory receptor; family 7; subfamily A; member 5	ENSG00000188269	PAP003	102	15.7%	chr19	14800030	CCDS12318.1	c.24A>C	p.Q8H
OR7C1	olfactory receptor; family 7; subfamily C; member 1	ENSG00000127530	PAP003	130	12.3%	chr19	14771447	CCDS12317.1	c.502T>G	p.F168V
OR8B8	olfactory receptor; family 8; subfamily B; member 8	ENSG00000197125	PAP003	145	10.3%	chr11	123815286	CCDS8446.1	c.906G>T	p.K302N
OIT3	oncoprotein induced transcript 3	ENSG00000138315	PAP003	116	12.1%	chr10	74343230	CCDS7318.1	c.949G>A	p.D317N
OSMR	oncostatin M receptor	ENSG00000145623	PAP003	68	14.7%	chr5	38968787	CCDS3928.1	c.2424A>C	p.E808D
OTX2	orthodenticle homeobox 2	ENSG00000165588	PAP003	209	12.9%	chr14	56338737	CCDS9728.1	c.363G>T	p.K121N
ODF3L1	outer dense fiber of sperm tails 3-like 1	ENSG00000182950	PAP003	226	18.6%	chr15	73806672	CCDS10285.1	c.561G>T	p.K187N
PAPPAS	PAPPA antisense RNA (non-protein coding)	ENSG00000182752	PAP003	178	14.0%	chr9	118154933	CCDS6813.1	c.4092G>T	p.E1364D
PAPPA2	pappalysin 2	ENSG00000116183	PAP003	197	13.7%	chr1	174830652	CCDS41438.1	c.1289C>T	p.S430L
PARD6B	par-6 partitioning defective 6 homolog beta (C. elegans)	ENSG00000124171	PAP003	148	12.2%	chr20	48806677	ENST00000396039	c.338A>T	p.K113I
PNMA1	paraneoplastic antigen MA1	ENSG00000176903	PAP003	399	15.0%	chr14	73249933	CCDS9818.1	c.163T>C	p.F55L
PDZRN4	PDZ domain containing ring finger 4	ENSG00000165966	PAP003	95	15.8%	chr12	40253546	CCDS8739.1	c.1924T>C	p.Y642H
PRPH	peripherin	ENSG00000135406	PAP003	110	17.3%	chr12	47978059	CCDS8783.1	c.1319T>G	p.I440S
PXDN	peroxidasin homolog (Drosophila)	ENSG00000130508	PAP003	283	18.7%	chr2	1631569	NM_012293	c.2990G>A	p.R997H
PEX11B	peroxisomal biogenesis factor 11 beta	ENSG00000131779	PAP003	302	12.6%	chr1	144234262	CCDS917.1	c.766C>T	p.R256X
PHF12	PHD finger protein 12	ENSG00000109118	PAP003	264	12.5%	chr17	24275496	ENST00000378879	c.272C>A	p.S91Y
PHF8	PHD finger protein 8	ENSG00000172943	PAP003	137	18.2%	chrX	54057687	CCDS14355.1	c.631C>T	p.R211X
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP003	423	14.2%	chr10	89614244	CCDS31238.1	c.38A>C	p.K13T
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP003	211	12.8%	chr10	89682885	CCDS31238.1	c.389G>A	p.R130Q
PFKP	phosphofructokinase; platelet	ENSG00000067057	PAP003	143	13.3%	chr10	3114609	CCDS7059.1	c.142C>T	p.R48C
PGM2L1	phosphoglucomutase 2-like 1	ENSG00000165434	PAP003	110	10.9%	chr11	73735989	CCDS8231.1	c.791C>A	p.S264Y
PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP003	202	13.4%	chr3	180399570	CCDS43171.1	c.263G>A	p.R88Q
PIK3R1	phosphoinositide-3-kinase; regulatory subunit 1 (alpha)	ENSG00000145675	PAP003	117	12.8%	chr5	67624707	CCDS3993.1	c.1042C>T	p.R348X
PLCB4	phospholipase C; beta 4	ENSG00000101333	PAP003	230	10.4%	chr20	9299881	CCDS13104.1	c.524C>T	p.S175L
PLCB4	phospholipase C; beta 4	ENSG00000101333	PAP003	111	13.5%	chr20	9318580	CCDS13104.1	c.1213A>C	p.I405L
PLCG1	phospholipase C; gamma 1	ENSG00000124181	PAP003	221	13.1%	chr20	39228609	CCDS13313.1	c.2080C>T	p.R694W
PLCL1	phospholipase C-like 1	ENSG00000115896	PAP003	124	12.9%	chr2	198659169	CCDS2326.1	c.2389C>T	p.R797X
PHKA1	phosphorylase kinase; alpha 1 (muscle)	ENSG00000067177	PAP003	95	10.5%	chrX	71772904	CCDS14421.1	c.1517G>T	p.G506V
PYGM	phosphorylase; glycogen; muscle	ENSG00000068976	PAP003	331	13.0%	chr11	64274568	CCDS8079.1	c.2033G>A	p.G678D
PDGFRA	platelet-derived growth factor receptor; alpha polypeptide	ENSG00000134853	PAP003	59	22.0%	chr4	54834595	CCDS3495.1	c.1499G>A	p.R500Q
PDGFRB	platelet-derived growth factor receptor; beta polypeptide	ENSG00000113721	PAP003	80	16.3%	chr5	149477435	CCDS4303.1	c.3076C>T	p.P1026S
PDGFRL	platelet-derived growth factor receptor-like	ENSG00000104213	PAP003	123	30.9%	chr8	17530345	CCDS6003.1	c.575C>A	p.A192D
PHLDA1	pleckstrin homology-like domain; family A; member 1	ENSG00000139289	PAP003	367	13.1%	chr12	74711033	CCDS31861.1	c.756C>A	p.F252L
PLRG1	pleiotropic regulator 1 (PRL1 homolog; Arabidopsis)	ENSG00000171566	PAP003	83	12.0%	chr4	155677913	CCDS34083.1	c.1460A>C	p.K487T
PABPN1	poly(A) binding protein; nuclear 1	ENSG00000100836	PAP003	195	17.9%	chr14	22863200	CCDS9592.1	c.743G>A	p.R248Q
POLE	polymerase (DNA directed); epsilon	ENSG00000177084	PAP003	228	11.4%	chr12	131760362	CCDS9278.1	c.1231G>T	p.V411L
KCTD8	potassium channel tetramerisation domain containing 8	ENSG00000183783	PAP003	292	12.3%	chr4	43871656	CCDS3467.1	c.1330A>G	p.I444V
KCNN2	potassium intermediate/small conductance calcium-activated channel; subfamily N; member 2	ENSG00000080709	PAP003	91	14.3%	chr5	113726287	ENST00000389446	c.723C>A	p.H241Q
KCNJ13	potassium inwardly-rectifying channel; subfamily J; member 13	ENSG00000115474	PAP003	254	13.4%	chr2	233344192	CCDS2498.1	c.125G>A	p.R42Q
KCNA4	potassium voltage-gated channel; shaker-related subfamily; member 4	ENSG00000182255	PAP003	265	15.1%	chr11	29989463	CCDS41629.1	c.1339C>T	p.R447C
PRDM2	PR domain containing 2; with ZNF domain	ENSG00000116731	PAP003	185	15.1%	chr1	13979105	CCDS150.1	c.2228C>A	p.S743Y
PBX1	pre-B-cell leukemia homeobox 1	ENSG00000185630	PAP003	96	13.5%	chr1	163055956	CCDS1246.1	c.1021T>G	p.S341A
PAPPA	pregnancy-associated plasma protein A; pappalysin 1	ENSG00000182752	PAP003	178	14.0%	chr9	118154933	CCDS6813.1	c.4092G>T	p.E1364D
PZP	pregnancy-zone protein	ENSG00000126838	PAP003	152	17.1%	chr12	9207565	CCDS8600.1	c.2702G>T	p.R901I
PRICKLE1	prickle homolog 1 (Drosophila)	ENSG00000139174	PAP003	163	10.4%	chr12	41140239	CCDS8742.1	c.2135T>G	p.F712C
PRNT	prion protein (testis specific)	ENSG00000180259	PAP003	111	10.8%	chr20	4661069	ENST00000326539	c.254G>A	p.C85Y
PRODH2	proline dehydrogenase (oxidase) 2	ENSG00000161270	PAP003	59	16.9%	chr19	41031431	CCDS32996.1	c.1118G>A	p.R373Q
PROC	protein C (inactivator of coagulation factors Va and VIIIa)	ENSG00000115718	PAP003	119	16.0%	chr2	127902828	CCDS2145.1	c.1222G>A	p.A408T
PDIA5	protein disulfide isomerase family A; member 5	ENSG00000065485	PAP003	191	10.5%	chr3	124325666	CCDS3020.1	c.673C>T	p.R225C
PDILT	protein disulfide isomerase-like; testis expressed	ENSG00000169340	PAP003	554	13.0%	chr16	20278179	CCDS10584.1	c.1718T>C	p.V573A

PRKAG1	protein kinase; AMP-activated; gamma 1 non-catalytic subunit	ENSG00000181929	PAP003	182	13.2%	chr12	47683887	CCDS8777.1	c.623G>A	p.R208H
PRKACG	protein kinase; cAMP-dependent; catalytic; gamma	ENSG00000165059	PAP003	193	13.5%	chr9	70817987	CCDS6625.1	c.842G>A	p.R281H
POFUT2	protein O-fucosyltransferase 2	ENSG00000186866	PAP003	110	15.5%	chr21	45514305	CCDS13719.1	c.889G>T	p.D297Y
PTPDC1	protein tyrosine phosphatase domain containing 1	ENSG00000158079	PAP003	223	14.8%	chr9	95899636	CCDS6708.1	c.961C>T	p.R321C
PTPN3	protein tyrosine phosphatase; non-receptor type 3	ENSG00000070159	PAP003	84	17.9%	chr9	111183768	CCDS6776.1	c.2649G>T	p.M883I
PTPRZ1	protein tyrosine phosphatase; receptor-type; Z polypeptide 1	ENSG00000106278	PAP003	151	13.9%	chr7	121439260	CCDS34740.1	c.2924C>T	p.S975L
PLP1	proteolipid protein 1	ENSG00000123560	PAP003	64	18.8%	chrX	102927306	CCDS14513.1	c.144G>T	p.E48D
PCDH12	protocadherin 12	ENSG00000113555	PAP003	224	11.6%	chr5	141317123	CCDS4269.1	c.478C>A	p.L160I
PCDHA10	protocadherin alpha 10	ENSG00000081842	PAP003	205	11.2%	chr5	140287509	CCDS4241.1	c.848G>A	p.R283H
PCDHA10	protocadherin alpha 10	ENSG00000081842	PAP003	238	11.8%	chr5	140289003	CCDS4241.1	c.2342G>A	p.R781Q
PCDHA10	protocadherin alpha 10	ENSG00000081842	PAP003	317	11.7%	chr5	140327289	CCDS4242.1	c.754G>A	p.D252N
PCDHA10	protocadherin alpha 10	ENSG00000081842	PAP003	182	12.6%	chr5	140328322	CCDS4242.1	c.1787G>A	p.R596Q
PCDHA11	protocadherin alpha 11	ENSG00000081842	PAP003	205	11.2%	chr5	140287509	CCDS4241.1	c.848G>A	p.R283H
PCDHA11	protocadherin alpha 11	ENSG00000081842	PAP003	238	11.8%	chr5	140289003	CCDS4241.1	c.2342G>A	p.R781Q
PCDHA11	protocadherin alpha 11	ENSG00000081842	PAP003	317	11.7%	chr5	140327289	CCDS4242.1	c.754G>A	p.D252N
PCDHA11	protocadherin alpha 11	ENSG00000081842	PAP003	182	12.6%	chr5	140328322	CCDS4242.1	c.1787G>A	p.R596Q
PCDHA12	protocadherin alpha 12	ENSG00000081842	PAP003	205	11.2%	chr5	140287509	CCDS4241.1	c.848G>A	p.R283H
PCDHA12	protocadherin alpha 12	ENSG00000081842	PAP003	238	11.8%	chr5	140289003	CCDS4241.1	c.2342G>A	p.R781Q
PCDHA12	protocadherin alpha 12	ENSG00000081842	PAP003	317	11.7%	chr5	140327289	CCDS4242.1	c.754G>A	p.D252N
PCDHA12	protocadherin alpha 12	ENSG00000081842	PAP003	182	12.6%	chr5	140328322	CCDS4242.1	c.1787G>A	p.R596Q
PCDHA6	protocadherin alpha 6	ENSG00000081842	PAP003	205	11.2%	chr5	140287509	CCDS4241.1	c.848G>A	p.R283H
PCDHA6	protocadherin alpha 6	ENSG00000081842	PAP003	238	11.8%	chr5	140289003	CCDS4241.1	c.2342G>A	p.R781Q
PCDHA6	protocadherin alpha 6	ENSG00000081842	PAP003	317	11.7%	chr5	140327289	CCDS4242.1	c.754G>A	p.D252N
PCDHA6	protocadherin alpha 6	ENSG00000081842	PAP003	182	12.6%	chr5	140328322	CCDS4242.1	c.1787G>A	p.R596Q
PCDHAC1	protocadherin alpha subfamily C; 1	ENSG00000081842	PAP003	205	11.2%	chr5	140287509	CCDS4241.1	c.848G>A	p.R283H
PCDHAC1	protocadherin alpha subfamily C; 1	ENSG00000081842	PAP003	238	11.8%	chr5	140289003	CCDS4241.1	c.2342G>A	p.R781Q
PCDHAC1	protocadherin alpha subfamily C; 1	ENSG00000081842	PAP003	317	11.7%	chr5	140327289	CCDS4242.1	c.754G>A	p.D252N
PCDHAC1	protocadherin alpha subfamily C; 1	ENSG00000081842	PAP003	182	12.6%	chr5	140328322	CCDS4242.1	c.1787G>A	p.R596Q
PCDHB4	protocadherin beta 4	ENSG00000081818	PAP003	67	20.9%	chr5	140483088	CCDS4246.1	c.1324G>A	p.D442N
PCDHGA10	protocadherin gamma subfamily A; 10	ENSG00000081853	PAP003	218	15.1%	chr5	140837099	CCDS4261.1	c.1232C>T	p.T411I
PCDHGA10	protocadherin gamma subfamily A; 10	ENSG00000081853	PAP003	130	12.3%	chr5	140849038	CCDS4263.1	c.47T>G	p.L16R
PCDHGA11	protocadherin gamma subfamily A; 11	ENSG00000081853	PAP003	218	15.1%	chr5	140837099	CCDS4261.1	c.1232C>T	p.T411I
PCDHGA11	protocadherin gamma subfamily A; 11	ENSG00000081853	PAP003	130	12.3%	chr5	140849038	CCDS4263.1	c.47T>G	p.L16R
PCDHGA3	protocadherin gamma subfamily A; 3	ENSG00000081853	PAP003	218	15.1%	chr5	140837099	CCDS4261.1	c.1232C>T	p.T411I
PCDHGA3	protocadherin gamma subfamily A; 3	ENSG00000081853	PAP003	130	12.3%	chr5	140849038	CCDS4263.1	c.47T>G	p.L16R
PCDHGA8	protocadherin gamma subfamily A; 8	ENSG00000081853	PAP003	218	15.1%	chr5	140837099	CCDS4261.1	c.1232C>T	p.T411I
PCDHGA8	protocadherin gamma subfamily A; 8	ENSG00000081853	PAP003	130	12.3%	chr5	140849038	CCDS4263.1	c.47T>G	p.L16R
PCDHGB7	protocadherin gamma subfamily B; 7	ENSG00000081853	PAP003	218	15.1%	chr5	140837099	CCDS4261.1	c.1232C>T	p.T411I
PCDHGB7	protocadherin gamma subfamily B; 7	ENSG00000081853	PAP003	130	12.3%	chr5	140849038	CCDS4263.1	c.47T>G	p.L16R
PCDHGC5	protocadherin gamma subfamily C; 5	ENSG00000081853	PAP003	218	15.1%	chr5	140837099	CCDS4261.1	c.1232C>T	p.T411I
PCDHGC5	protocadherin gamma subfamily C; 5	ENSG00000081853	PAP003	130	12.3%	chr5	140849038	CCDS4263.1	c.47T>G	p.L16R
P2RY13	purinergic receptor P2Y; G-protein coupled; 13	ENSG00000181631	PAP003	92	12.0%	chr3	152529005	CCDS3158.1	c.466C>T	p.P156S
RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)	ENSG00000115839	PAP003	204	13.7%	chr2	135609829	CCDS33294.1	c.1780G>T	p.E594X
RPH3A	rabphilin 3A homolog (mouse)	ENSG00000089169	PAP003	86	17.4%	chr12	111791950	CCDS31904.1	c.602A>G	p.D201G
ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	ENSG00000129675	PAP003	84	11.9%	chrX	135623165	CCDS14660.1	c.763G>T	p.E255X
RAD51AP2	RAD51 associated protein 2	ENSG00000214842	PAP003	107	10.3%	chr2	17560404	CCDS42656.1	c.2760G>T	p.K920N
RAD51AP2	RAD51 associated protein 2	ENSG00000214842	PAP003	72	15.3%	chr2	17562494	CCDS42656.1	c.670G>T	p.E224X
RAD51L1	RAD51-like 1 (S. cerevisiae)	ENSG00000182185	PAP003	77	14.3%	chr14	67423620	CCDS9789.1	c.702C>A	p.F234L
RAD54B	RAD54 homolog B (S. cerevisiae)	ENSG00000197275	PAP003	113	12.4%	chr8	95480964	CCDS6262.1	c.1232A>C	p.E411A
REPS1	RALBP1 associated Eps domain containing 1	ENSG00000135597	PAP003	223	13.0%	chr6	139308380	CCDS5193.1	c.269G>T	p.G90V
RANBP2	RAN binding protein 2	ENSG00000153201	PAP003	268	13.4%	chr2	108746644	CCDS2079.1	c.3217G>T	p.D1073Y
RANBP2	RAN binding protein 2	ENSG00000153201	PAP003	368	14.7%	chr2	108746714	CCDS2079.1	c.3287G>A	p.R1096Q

RASA2	RAS p21 protein activator 2	ENSG00000155903	PAP003	147	14.3%	chr3	142774237	CCDS3117.1	c.1266A>C	p.L422F
REST	RE1-silencing transcription factor	ENSG00000084093	PAP003	265	12.1%	chr4	57492980	CCDS3509.1	c.3199C>T	p.R1067C
REG1B	regenerating islet-derived 1 beta	ENSG00000172023	PAP003	108	16.7%	chr2	79165877	CCDS1963.1	c.474C>A	p.F158L
RPRD1A	regulation of nuclear pre-mRNA domain containing 1A	ENSG00000141425	PAP003	305	12.1%	chr18	31860925	CCDS11917.1	c.725G>A	p.R242Q
RPRD2	regulation of nuclear pre-mRNA domain containing 2	ENSG00000163125	PAP003	205	14.1%	chr1	148710590	NM_015203	c.2542A>C	p.N848H
RTBDN	retbindin	ENSG00000132026	PAP003	119	13.4%	chr19	12797702	CCDS12283.1	c.604G>A	p.A202T
RP1	retinitis pigmentosa 1 (autosomal dominant)	ENSG00000104237	PAP003	195	23.6%	chr8	55700457	CCDS6160.1	c.1462G>T	p.E488X
RP1	retinitis pigmentosa 1 (autosomal dominant)	ENSG00000104237	PAP003	125	14.4%	chr8	55703469	CCDS6160.1	c.4474G>A	p.E1492K
RBBP6	retinoblastoma binding protein 6	ENSG00000122257	PAP003	174	14.4%	chr16	24490779	CCDS10621.1	c.4891G>T	p.E1631X
RAI14	retinoic acid induced 14	ENSG00000039560	PAP003	117	12.8%	chr5	34849467	CCDS34142.1	c.797G>T	p.R266I
RBP3	retinol binding protein 3; interstitial	ENSG00000107618	PAP003	212	17.9%	chr10	48010752	CCDS7218.1	c.132C>A	p.N44K
REV3L	REV3-like; catalytic subunit of DNA polymerase zeta (yeast)	ENSG00000009413	PAP003	222	14.0%	chr6	111800835	CCDS5091.2	c.5416G>T	p.E1806X
ARHGAP31	Rho GTPase activating protein 31	ENSG00000031081	PAP003	82	14.6%	chr3	120566897	CCDS43135.1	c.145G>A	p.G49S
ARHGAP9	Rho GTPase activating protein 9	ENSG00000123329	PAP003	147	12.2%	chr12	56153720	CCDS8941.2	c.1957G>A	p.E653K
ARHGEF4	Rho guanine nucleotide exchange factor (GEF) 4	ENSG00000136002	PAP003	68	22.1%	chr2	131390180	ENST00000409359	c.1201G>A	p.E401K
RRP9	ribosomal RNA processing 9; small subunit (SSU) processome component; homolog (yeast)	ENSG00000114767	PAP003	256	16.8%	chr3	51945387	CCDS2837.1	c.661A>G	p.K221E
RCHY1	ring finger and CHY zinc finger domain containing 1	ENSG00000163743	PAP003	83	13.3%	chr4	76626875	CCDS3567.1	c.683G>A	p.R228Q
RNF123	ring finger protein 123	ENSG00000164068	PAP003	76	17.1%	chr3	49714807	CCDS33758.1	c.1594C>T	p.R532C
RNF17	ring finger protein 17	ENSG00000132972	PAP003	147	12.2%	chr13	24247024	CCDS9308.2	c.299A>G	p.E100G
RIOK1	RIO kinase 1 (yeast)	ENSG00000124784	PAP003	62	19.4%	chr6	7347919	CCDS4500.1	c.658C>T	p.R220W
RBM24	RNA binding motif protein 24	ENSG00000112183	PAP003	119	13.4%	chr6	17400319	CCDS4538.1	c.566G>A	p.R189Q
RYR1	ryanodine receptor 1 (skeletal)	ENSG00000196218	PAP003	256	14.5%	chr19	43668362	CCDS33011.1	c.5227G>A	p.A1743T
SALL2	sal-like 2 (Drosophila)	ENSG00000165821	PAP003	221	15.4%	chr14	21060742	CCDS32045.1	c.2960C>T	p.S987L
SLFN12	schlafen family member 12	ENSG00000172123	PAP003	73	13.7%	chr17	30773368	CCDS11295.1	c.793G>A	p.E265K
SCYL1	SCY1-like 1 (S. cerevisiae)	ENSG00000142186	PAP003	193	13.5%	chr11	65060117	CCDS41672.1	c.1504G>A	p.D502N
SCRN1	secernin 1	ENSG00000136193	PAP003	207	15.0%	chr7	29975153	CCDS5422.1	c.56A>G	p.D19G
SCG3	secretogranin III	ENSG00000104112	PAP003	115	10.4%	chr15	49767776	CCDS10142.1	c.425A>G	p.D142G
SEMA5A	sema domain; seven thrombospondin repeats (type 1 and type 1-like); transmembrane domain (TM) and short cytoplasmic domain; (semaphorin) 5A	ENSG00000112902	PAP003	114	14.0%	chr5	9255170	CCDS3875.1	c.829A>G	p.N277D
SETX	senataxin	ENSG00000107290	PAP003	142	11.3%	chr9	134193141	CCDS6947.1	c.3665A>C	p.K1222T
SPINLW1	serine peptidase inhibitor-like; with Kunitz and WAP domains 1 (eppin)	ENSG00000101448	PAP003	311	10.6%	chr20	43607741	CCDS13359.1	c.174G>T	p.K58N
SERPINA10	serpin peptidase inhibitor; clade A (alpha-1 antiproteinase; antitrypsin); member 10	ENSG00000140093	PAP003	151	11.9%	chr14	93824614	CCDS9923.1	c.754G>A	p.E252K
SERPINA11	serpin peptidase inhibitor; clade A (alpha-1 antiproteinase; antitrypsin); member 11	ENSG00000186910	PAP003	170	16.5%	chr14	93984576	CCDS32149.1	c.289G>T	p.A97S
SERPINI1	serpin peptidase inhibitor; clade I (neuroserpin); member 1	ENSG00000163536	PAP003	57	22.8%	chr3	168989759	CCDS3203.1	c.149C>A	p.P50Q
SHC4	SHC (Src homology 2 domain containing) family; member 4	ENSG00000185634	PAP003	143	18.9%	chr15	46914350	CCDS10130.1	c.1645C>T	p.R549X
SHROOM2	shroom family member 2	ENSG00000146950	PAP003	261	18.4%	chrX	9872924	CCDS14135.1	c.4555T>G	p.L1519V
SGOL1	shugoshin-like 1 (S. pombe)	ENSG00000129810	PAP003	286	13.6%	chr3	20191363	CCDS33716.1	c.664G>T	p.E222X
SIGLEC8	sialic acid binding Ig-like lectin 8	ENSG00000105366	PAP003	124	14.5%	chr19	56649820	CCDS33086.1	c.1078A>G	p.T360A
SIGLEC9	sialic acid binding Ig-like lectin 9	ENSG00000129450	PAP003	103	11.7%	chr19	56322156	CCDS12825.1	c.806G>A	p.R269H
SOBP	sine oculis binding protein homolog (Drosophila)	ENSG00000112320	PAP003	158	14.6%	chr6	108063341	CCDS43488.1	c.2600G>A	p.R867Q
SLITRK4	SLIT and NTRK-like family; member 4	ENSG00000179542	PAP003	149	13.4%	chrX	142545876	CCDS14679.1	c.715G>T	p.E239X
SMEK2	SMEK homolog 2; suppressor of mek1 (Dictyostelium)	ENSG00000138041	PAP003	190	15.3%	chr2	55679390	CCDS1855.1	c.587A>C	p.E196A
SCN2A	sodium channel; voltage-gated; type II; alpha subunit	ENSG00000136531	PAP003	145	15.9%	chr2	165909315	CCDS33314.1	c.2567G>A	p.R856Q
SLC16A9	solute carrier family 16; member 9 (monocarboxylic acid transporter 9)	ENSG00000165449	PAP003	223	10.8%	chr10	61083768	CCDS7256.1	c.1022T>G	p.F341C
SLC2A13	solute carrier family 2 (facilitated glucose transporter); member 13	ENSG00000151229	PAP003	80	12.5%	chr12	38631389	CCDS8736.1	c.914G>A	p.R305Q
SLC22A3	solute carrier family 22 (extraneuronal monoamine transporter); member 3	ENSG00000146477	PAP003	88	18.2%	chr6	160751822	CCDS5277.1	c.929G>A	p.R310H

SLC22A23	solute carrier family 22; member 23	ENSG00000137266	PAP003	180	15.6%	chr6	3243363	CCDS34331.1	c.328C>T	p.R110C
SLC24A2	solute carrier family 24 (sodium/potassium/calcium exchanger); member 2	ENSG00000155886	PAP003	277	13.4%	chr9	19776146	CCDS6493.1	c.719G>A	p.R240Q
SLC25A32	solute carrier family 25; member 32	ENSG00000164933	PAP003	39	33.3%	chr8	104483454	CCDS6300.1	c.557T>G	p.F186C
SLC25A40	solute carrier family 25; member 40	ENSG00000075303	PAP003	166	13.3%	chr7	87321474	CCDS5610.1	c.245G>T	p.G82V
SLC26A1	solute carrier family 26 (sulfate transporter); member 1	ENSG00000145217	PAP003	250	11.2%	chr4	963204	CCDS33933.1	c.665G>T	p.R222I
SLC26A8	solute carrier family 26; member 8	ENSG00000112053	PAP003	175	14.3%	chr6	36030995	CCDS4813.1	c.2144C>T	p.A715V
SLC27A3	solute carrier family 27 (fatty acid transporter); member 3	ENSG00000143554	PAP003	109	14.7%	chr1	152016945	CCDS1053.1	c.1262A>G	p.Y421C
SLC33A1	solute carrier family 33 (acetyl-CoA transporter); member 1	ENSG00000169359	PAP003	97	15.5%	chr3	157030190	CCDS3173.1	c.1463G>A	p.R488Q
SLC4A4	solute carrier family 4; sodium bicarbonate cotransporter; member 4	ENSG00000080493	PAP003	218	12.4%	chr4	72482205	CCDS43236.1	c.778G>T	p.D260Y
SLC41A3	solute carrier family 41; member 3	ENSG00000114544	PAP003	76	19.7%	chr3	127224432	CCDS33843.1	c.632G>A	p.R211Q
SLC45A4	solute carrier family 45; member 4	ENSG00000022567	PAP003	288	25.7%	chr8	142297408	CCDS34948.1	c.1360C>T	p.P454S
SLC45A4	solute carrier family 45; member 4	ENSG00000022567	PAP003	198	32.3%	chr8	142297662	CCDS34948.1	c.1106G>A	p.R369H
SLC6A2	solute carrier family 6 (neurotransmitter transporter; noradrenalin); member 2	ENSG00000103546	PAP003	316	13.0%	chr16	54289940	CCDS10754.1	c.1448T>C	p.F483S
SLC9A4	solute carrier family 9 (sodium/hydrogen exchanger); member 4	ENSG00000180251	PAP003	206	15.5%	chr2	102491059	CCDS33264.1	c.1288C>T	p.R430X
SLCO1A2	solute carrier organic anion transporter family; member 1A2	ENSG00000084453	PAP003	69	20.3%	chr12	21336401	CCDS8686.1	c.1574C>A	p.S525Y
SLCO5A1	solute carrier organic anion transporter family; member 5A1	ENSG00000137571	PAP003	332	28.6%	chr8	70907153	CCDS6205.1	c.310A>G	p.T104A
SOS2	son of sevenless homolog 2 (Drosophila)	ENSG00000100485	PAP003	279	10.0%	chr14	49696381	CCDS9697.1	c.1370G>A	p.R457Q
SORL1	sortilin-related receptor; L(DLR class) A repeats-containing	ENSG00000137642	PAP003	623	13.6%	chr11	120864035	CCDS8436.1	c.613C>T	p.R205W
SNX9	sorting nexin 9	ENSG00000130340	PAP003	128	17.2%	chr6	158278505	CCDS5253.1	c.1495T>G	p.F499V
SPOCK3	sparc/osteonectin; cwcv and kazal-like domains proteoglycan (testican) 3	ENSG00000196104	PAP003	159	11.9%	chr4	167892718	CCDS34095.1	c.1231G>T	p.E411X
SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	ENSG00000151835	PAP003	182	13.7%	chr13	22811949	CCDS9300.1	c.3625C>A	p.L1209I
SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	ENSG00000151835	PAP003	153	17.0%	chr13	22813480	CCDS9300.1	c.2094A>C	p.Q698H
SYNE1	spectrin repeat containing; nuclear envelope 1	ENSG00000131018	PAP003	104	14.4%	chr6	152725102	CCDS5236.1	c.10195C>T	p.R3399X
SPAM1	sperm adhesion molecule 1 (PH-20 hyaluronidase; zona pellucida binding)	ENSG00000106304	PAP003	225	16.4%	chr7	123381211	CCDS5790.1	c.351G>T	p.K117N
SPAG17	sperm associated antigen 17	ENSG00000155761	PAP003	106	10.4%	chr1	118340603	CCDS899.1	c.4966C>T	p.R1656X
SFRS12	splicing factor; arginine/serine-rich 12	ENSG00000153914	PAP003	118	11.9%	chr5	65476007	CCDS43323.1	c.47C>T	p.T16I
SFRS15	splicing factor; arginine/serine-rich 15	ENSG00000156304	PAP003	156	17.9%	chr21	31986594	CCDS33537.1	c.1553G>T	p.R518I
SFRS7	splicing factor; arginine/serine-rich 7; 35kDa	ENSG00000115875	PAP003	103	12.6%	chr2	38829228	CCDS33183.1	c.458G>A	p.R153Q
SART3	squamous cell carcinoma antigen recognized by T cells 3	ENSG00000075856	PAP003	118	15.3%	chr12	107442333	CCDS9117.1	c.2604G>T	p.E868D
ST3GAL2	ST3 beta-galactoside alpha-2;3-sialyltransferase 2	ENSG00000157350	PAP003	99	12.1%	chr16	68974289	CCDS10890.1	c.799G>A	p.D267N
SLK	STE20-like kinase (yeast)	ENSG00000065613	PAP003	53	18.9%	chr10	105758022	CCDS7553.1	c.2702G>A	p.R901Q
SAMD3	sterile alpha motif domain containing 3	ENSG00000164483	PAP003	121	10.7%	chr6	130507585	CCDS34539.1	c.1336G>A	p.E446K
SAMD9	sterile alpha motif domain containing 9	ENSG00000205413	PAP003	190	13.7%	chr7	92569101	CCDS34680.1	c.4246C>T	p.R1416X
SAMD9L	sterile alpha motif domain containing 9-like	ENSG00000177409	PAP003	142	16.2%	chr7	92601912	CCDS34681.1	c.1309G>T	p.E437X
STON1-GTF	STON1-GTF2A1L readthrough	ENSG00000068781	PAP003	467	14.6%	chr2	48661535	CCDS1840.1	c.259G>T	p.D87Y
SULF1	sulfatase 1	ENSG00000137573	PAP003	97	20.6%	chr8	70661232	CCDS6204.1	c.499C>T	p.R167C
SOD3	superoxide dismutase 3; extracellular	ENSG00000109610	PAP003	168	13.7%	chr4	24410584	CCDS3430.1	c.343G>A	p.V115M
SUPV3L1	suppressor of var1; 3-like 1 (S. cerevisiae)	ENSG00000156502	PAP003	147	10.9%	chr10	70615790	CCDS7287.1	c.313G>T	p.E105X
SYT9	synaptotagmin IX	ENSG00000170743	PAP003	180	11.1%	chr11	7291643	CCDS7778.1	c.939C>A	p.F313L
SYTL2	synaptotagmin-like 2	ENSG00000137501	PAP003	358	14.2%	chr11	85113779	CCDS31651.1	c.1369G>A	p.D457N
SNPH	syntaphilin	ENSG00000101298	PAP003	144	11.1%	chr20	1233686	CCDS13012.1	c.473A>G	p.D158G
STX6	syntaxin 6	ENSG00000135823	PAP003	86	16.3%	chr1	179238391	CCDS1341.1	c.274A>G	p.I92V
TAF2	TAF2 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 150kDa	ENSG00000064313	PAP003	68	20.6%	chr8	120843901	CCDS34937.1	c.2493A>C	p.E831D
TAF4	TAF4 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 135kDa	ENSG00000130699	PAP003	64	18.8%	chr20	60008699	CCDS33500.1	c.2663A>C	p.K888T
TOM1	target of myb1 (chicken)	ENSG00000100284	PAP003	82	14.6%	chr22	34053319	CCDS13913.1	c.704C>T	p.S235L
TBC1D22A	TBC1 domain family; member 22A	ENSG00000054611	PAP003	123	12.2%	chr22	45811660	CCDS14078.1	c.1231G>A	p.E411K

TAL2	T-cell acute lymphocytic leukemia 2	ENSG00000186051	PAP003	205	16.1%	chr9	107464731	CCDS6767.1	c.133C>T	p.R45C
TSHZ3	teashirt zinc finger homeobox 3	ENSG00000121297	PAP003	153	10.5%	chr19	36460266	CCDS12421.2	c.2273C>T	p.A758V
TCTN1	tectonic family member 1	ENSG00000204852	PAP003	129	12.4%	chr12	109548646	CCDS41834.1	c.438T>G	p.I146M
TECTA	tectorin alpha	ENSG00000109927	PAP003	409	11.0%	chr11	120534015	CCDS8434.1	c.4561C>T	p.P1521S
TEP1	telomerase-associated protein 1	ENSG00000129566	PAP003	211	16.1%	chr14	19907699	CCDS9548.1	c.7397C>T	p.S2466L
TEP1	telomerase-associated protein 1	ENSG00000129566	PAP003	411	10.7%	chr14	19939088	CCDS9548.1	c.1444G>A	p.D482N
TNR	tenascin R (restrictin; janusin)	ENSG00000116147	PAP003	135	14.1%	chr1	173642052	CCDS1318.1	c.422T>C	p.I141T
TEX11	testis expressed 11	ENSG00000120498	PAP003	100	13.0%	chrX	69766296	CCDS35323.1	c.1543A>G	p.I515V
TSPAN12	tetraspanin 12	ENSG00000106025	PAP003	225	13.8%	chr7	120237836	CCDS5777.1	c.385G>A	p.V129I
TTC1	tetratricopeptide repeat domain 1	ENSG00000113312	PAP003	113	13.3%	chr5	159424532	CCDS4348.1	c.761T>G	p.L254R
TTC17	tetratricopeptide repeat domain 17	ENSG00000052841	PAP003	123	14.6%	chr11	43428287	CCDS31466.1	c.2866A>G	p.S956G
TTC27	tetratricopeptide repeat domain 27	ENSG00000018699	PAP003	76	14.5%	chr2	32899496	CCDS33176.1	c.2519G>A	p.R840Q
TTC39C	tetratricopeptide repeat domain 39C	ENSG00000168234	PAP003	89	21.3%	chr18	19952102	CCDS32804.1	c.911T>C	p.I304T
THSD4	thrombospondin; type I; domain containing 4	ENSG00000187720	PAP003	91	17.6%	chr15	69860161	ENST00000345002	c.494T>G	p.F165C
TYMP	thymidine phosphorylase	ENSG00000025708	PAP003	371	13.7%	chr22	49314607	CCDS14096.1	c.241C>T	p.R81W
TIGD4	tigger transposable element derived 4	ENSG00000169989	PAP003	236	11.4%	chr4	153910799	CCDS34079.1	c.808C>T	p.R270X
TLR10	toll-like receptor 10	ENSG00000174123	PAP003	224	16.1%	chr4	38452201	CCDS3445.1	c.1406G>A	p.R469Q
TLR10	toll-like receptor 10	ENSG00000174123	PAP003	153	13.1%	chr4	38452903	CCDS3445.1	c.704G>A	p.R235Q
TPX2	TPX2; microtubule-associated; homolog (Xenopus laevis)	ENSG00000088325	PAP003	103	14.6%	chr20	29821812	CCDS13190.1	c.362C>A	p.S121Y
TAAR1	trace amine associated receptor 1	ENSG00000146399	PAP003	129	10.1%	chr6	133008193	CCDS5158.1	c.643C>A	p.L215I
TCF20	transcription factor 20 (AR1)	ENSG00000100207	PAP003	375	13.3%	chr22	40939139	CCDS14033.1	c.2117G>A	p.R706H
TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	ENSG00000114126	PAP003	148	10.8%	chr3	143180053	CCDS43159.1	c.335C>T	p.S112L
TRA2A	transformer 2 alpha homolog (Drosophila)	ENSG00000164548	PAP003	129	14.0%	chr7	23513634	CCDS5383.1	c.571C>T	p.R191W
TRA2B	transformer 2 beta homolog (Drosophila)	ENSG00000136527	PAP003	79	13.9%	chr3	187118873	CCDS33905.1	c.830G>A	p.R277H
TGM5	transglutaminase 5	ENSG00000104055	PAP003	158	12.0%	chr15	41332375	CCDS32212.1	c.736T>G	p.Y246D
TRPM3	transient receptor potential cation channel; subfamily M; member 3	ENSG00000083067	PAP003	227	13.2%	chr9	72341254	CCDS43835.1	c.4559C>T	p.S1520F
TOMM34	translocase of outer mitochondrial membrane 34	ENSG00000025772	PAP003	82	12.2%	chr20	43014026	CCDS13340.1	c.412C>T	p.P138S
TMTC1	transmembrane and tetratricopeptide repeat containing 1	ENSG00000133687	PAP003	196	12.8%	chr12	29580402	ENST00000381224	c.1654G>A	p.V552I
TMBIM1	transmembrane BAX inhibitor motif containing 1	ENSG00000135926	PAP003	147	13.6%	chr2	218850632	CCDS2412.1	c.519T>G	p.F173L
TMED8	transmembrane emp24 protein transport domain containing 8	ENSG00000100580	PAP003	159	10.1%	chr14	76879880	CCDS32125.1	c.367G>A	p.V123I
TMEM126A	transmembrane protein 126A	ENSG00000171202	PAP003	123	12.2%	chr11	85042831	CCDS8268.1	c.163C>T	p.R55X
TMEM63B	transmembrane protein 63B	ENSG00000137216	PAP003	161	14.3%	chr6	44225623	CCDS34461.1	c.1463C>T	p.S488L
TMEM70	transmembrane protein 70	ENSG00000175606	PAP003	79	17.7%	chr8	75056391	CCDS6215.1	c.764G>A	p.R255Q
TRIB2	tribbles homolog 2 (Drosophila)	ENSG00000071575	PAP003	150	18.0%	chr2	12798196	CCDS1683.1	c.857G>A	p.R286Q
TRIO	triple functional domain (PTPRF interacting)	ENSG00000038382	PAP003	152	11.2%	chr5	14421959	CCDS3883.1	c.3017G>A	p.R1006H
TRMT12	tRNA methyltransferase 12 homolog (S. cerevisiae)	ENSG00000183665	PAP003	197	12.2%	chr8	125533038	CCDS6349.1	c.689C>T	p.S230L
TDO2	tryptophan 2;3-dioxygenase	ENSG00000151790	PAP003	288	12.8%	chr4	157060531	CCDS34086.1	c.1160A>C	p.K387T
TULP2	tubby like protein 2	ENSG00000104804	PAP003	174	13.8%	chr19	54083135	CCDS12739.1	c.832C>T	p.R278W
TPPP2	tubulin polymerization-promoting protein family member 2	ENSG00000179636	PAP003	74	18.9%	chr14	20568670	CCDS9566.1	c.90C>A	p.F30L
TDRKH	tudor and KH domain containing	ENSG00000182134	PAP003	104	15.4%	chr1	150018322	CCDS41394.1	c.442C>T	p.R148C
UBTD2	ubiquitin domain containing 2	ENSG00000168246	PAP003	136	12.5%	chr5	171593779	CCDS4379.2	c.259G>T	p.E87X
UIMC1	ubiquitin interaction motif containing 1	ENSG00000087206	PAP003	192	13.5%	chr5	176330408	CCDS4408.1	c.298A>C	p.N100H
USP44	ubiquitin specific peptidase 44	ENSG00000136014	PAP003	176	13.6%	chr12	94450851	CCDS9053.1	c.1313A>G	p.E438G
USP9X	ubiquitin specific peptidase 9; X-linked	ENSG00000124486	PAP003	108	18.5%	chrX	40961446	CCDS43930.1	c.6115G>T	p.E2039X
UBL3	ubiquitin-like 3	ENSG00000122042	PAP003	204	13.7%	chr13	29244297	CCDS9334.1	c.175C>T	p.R59X
UXS1	UDP-glucuronate decarboxylase 1	ENSG00000115652	PAP003	152	11.2%	chr2	106147686	ENST00000409501	c.124T>G	p.F42V
UEVLD	UEV and lactate/malate dehyrogenase domains	ENSG00000151116	PAP003	63	20.6%	chr11	18544575	CCDS41624.1	c.388G>T	p.E130X
UHRF1BP1	UHRF1 binding protein 1	ENSG00000065060	PAP003	121	13.2%	chr6	34932567	CCDS43455.1	c.1314G>T	p.K438N
UNC45B	unc-45 homolog B (C. elegans)	ENSG00000141161	PAP003	196	13.8%	chr17	30534592	CCDS11292.1	c.2413C>T	p.R805W
UMODL1	uromodulin-like 1	ENSG00000177398	PAP003	253	13.4%	chr21	42419650	CCDS42935.1	c.3658G>A	p.G1220S
USH2A	Usher syndrome 2A (autosomal recessive; mild)	ENSG00000042781	PAP003	119	19.3%	chr1	213911109	CCDS31025.1	c.13961C>A	p.S4654Y

UTP3	UTP3; small subunit (SSU) processome component; homolog (S. cerevisiae)	ENSG00000132467	PAP003	148	12.2%	chr4	71774264	CCDS3546.1	c.1006G>T	p.E336X
VPS39	vacuolar protein sorting 39 homolog (S. cerevisiae)	ENSG00000166887	PAP003	75	14.7%	chr15	40243185	CCDS10083.1	c.2060G>A	p.R687H
VCPIP1	valosin containing protein (p97)/p47 complex interacting protein 1	ENSG00000175073	PAP003	463	13.6%	chr8	67740231	CCDS6192.1	c.1517A>C	p.K506T
VCP	valosin-containing protein	ENSG00000165280	PAP003	289	18.0%	chr9	35047490	CCDS6573.1	c.2198G>A	p.R733Q
VNN2	vanin 2	ENSG00000112303	PAP003	219	10.0%	chr6	133114158	CCDS5161.1	c.1019T>G	p.F340C
VNN3	vanin 3	ENSG00000093134	PAP003	146	15.1%	chr6	133087600	ENST00000207771	c.1038T>G	p.F346L
VASN	vasorin	ENSG00000168140	PAP003	250	14.0%	chr16	4371750	CCDS10514.1	c.871C>T	p.R291W
VCAN	versican	ENSG00000038427	PAP003	203	13.3%	chr5	82871083	CCDS4060.1	c.6505G>T	p.E2169X
VGLL2	vestigial like 2 (Drosophila)	ENSG00000170162	PAP003	404	13.1%	chr6	117700322	CCDS5115.1	c.926C>A	p.S309Y
MYB	v-myb myeloblastosis viral oncogene homolog (avian)	ENSG00000118513	PAP003	183	14.2%	chr6	135559830	NM_001130173	c.1242C>A	p.F414L
WSB1	WD repeat and SOCS box-containing 1	ENSG00000109046	PAP003	220	13.2%	chr17	22645580	CCDS11220.1	c.32A>C	p.K11T
WDR48	WD repeat domain 48	ENSG00000114742	PAP003	169	17.2%	chr3	39111168	CCDS33738.1	c.1964G>A	p.R655Q
WDR64	WD repeat domain 64	ENSG00000162843	PAP003	107	15.0%	chr1	240005079	NM_144625	c.2450C>A	p.S817Y
WDR64	WD repeat domain 64	ENSG00000162843	PAP003	257	14.0%	chr1	240017803	CCDS1619.1	c.1364G>A	p.C455Y
WDSUB1	WD repeat; sterile alpha motif and U-box domain containing 1	ENSG00000196151	PAP003	219	11.4%	chr2	159847724	CCDS2208.1	c.103C>T	p.R35C
WAPAL	wings apart-like homolog (Drosophila)	ENSG00000062650	PAP003	146	13.0%	chr10	88250061	CCDS7375.1	c.919G>A	p.G307R
XDH	xanthine dehydrogenase	ENSG00000158125	PAP003	66	15.2%	chr2	31448741	CCDS1775.1	c.1713G>T	p.E571D
XIRP1	xin actin-binding repeat containing 1	ENSG00000168334	PAP003	245	18.0%	chr3	39202982	CCDS2683.1	c.2959G>A	p.A987T
ZIC4	Zic family member 4	ENSG00000174963	PAP003	162	11.1%	chr3	148591513	CCDS43160.1	c.899C>T	p.S300L
ZNRF4	zinc and ring finger 4	ENSG00000105428	PAP003	175	12.0%	chr19	5406687	CCDS42475.1	c.185G>A	p.S62N
ZFAT	zinc finger and AT hook domain containing	ENSG00000066827	PAP003	166	24.1%	chr8	135683442	CCDS43768.1	c.1666G>A	p.E556K
ZBTB38	zinc finger and BTB domain containing 38	ENSG00000177311	PAP003	181	10.5%	chr3	142645463	CCDS43157.1	c.1543C>T	p.R515X
ZSCAN4	zinc finger and SCAN domain containing 4	ENSG00000180532	PAP003	99	15.2%	chr19	62881151	CCDS12958.1	c.454G>A	p.D152N
ZC3H3	zinc finger CCCH-type containing 3	ENSG00000014164	PAP003	138	14.5%	chr8	144594336	CCDS6402.1	c.2405G>A	p.R802H
ZFHX3	zinc finger homeobox 3	ENSG00000140836	PAP003	295	12.5%	chr16	71384825	CCDS10908.1	c.14716NULL>	p.NULL-1FsIns1bp
ZFHX4	zinc finger homeobox 4	ENSG00000091656	PAP003	91	11.0%	chr8	77782365	ENST00000399468	c.2620C>T	p.L874F
ZNF10	zinc finger protein 10	ENSG00000090612	PAP003	291	12.0%	chr12	132243179	CCDS9283.1	c.1274G>A	p.R425K
ZNF217	zinc finger protein 217	ENSG00000171940	PAP003	210	15.2%	chr20	51626479	CCDS13443.1	c.2231G>A	p.R744Q
ZNF26	zinc finger protein 26	ENSG00000198393	PAP003	146	16.4%	chr12	132098043	CCDS31939.1	c.1505G>A	p.R502K
ZNF268	zinc finger protein 268	ENSG00000090612	PAP003	291	12.0%	chr12	132243179	CCDS9283.1	c.1274G>A	p.R425K
ZNF280A	zinc finger protein 280A	ENSG00000169548	PAP003	244	13.1%	chr22	21199938	CCDS13800.1	c.17T>C	p.L6S
ZNF366	zinc finger protein 366	ENSG00000178175	PAP003	157	17.8%	chr5	71792914	CCDS4015.1	c.166C>T	p.R56W
ZNF383	zinc finger protein 383	ENSG00000188283	PAP003	86	11.6%	chr19	42426122	CCDS12501.1	c.1144C>T	p.R382C
ZFP42	zinc finger protein 42 homolog (mouse)	ENSG00000179059	PAP003	224	13.8%	chr4	189161755	CCDS3849.1	c.800G>A	p.R267H
ZNF425	zinc finger protein 425	ENSG00000204947	PAP003	118	18.6%	chr7	148431698	CCDS34773.1	c.2198A>G	p.Y733C
ZNF449	zinc finger protein 449	ENSG00000173275	PAP003	168	20.8%	chrX	134309040	CCDS14649.1	c.331G>T	p.E111X
ZNF473	zinc finger protein 473	ENSG00000142528	PAP003	264	16.3%	chr19	55240864	CCDS33077.1	c.1352G>A	p.R451Q
ZNF490	zinc finger protein 490	ENSG00000188033	PAP003	136	15.4%	chr19	12552504	CCDS12272.1	c.1385G>A	p.R462Q
ZNF490	zinc finger protein 490	ENSG00000188033	PAP003	219	11.4%	chr19	12552744	CCDS12272.1	c.1145G>T	p.R382I
ZNF491	zinc finger protein 491	ENSG00000177599	PAP003	91	13.2%	chr19	11778706	CCDS12267.1	c.938C>T	p.S313L
ZNF510	zinc finger protein 510	ENSG00000081386	PAP003	136	13.2%	chr9	98561410	CCDS35074.1	c.1523G>A	p.R508K
ZNF528	zinc finger protein 528	ENSG00000167555	PAP003	138	15.9%	chr19	57611592	CCDS33091.1	c.1675C>T	p.R559X
ZNF540	zinc finger protein 540	ENSG00000171817	PAP003	148	18.9%	chr19	42795456	CCDS12506.1	c.1435C>T	p.R479C
ZNF560	zinc finger protein 560	ENSG00000198028	PAP003	174	13.8%	chr19	9438542	CCDS12214.1	c.2081G>A	p.R694Q
ZNF570	zinc finger protein 570	ENSG00000171827	PAP003	200	11.5%	chr19	42667286	CCDS12504.1	c.922C>T	p.R308X
ZNF614	zinc finger protein 614	ENSG00000142556	PAP003	180	12.8%	chr19	57211323	CCDS12847.1	c.1340G>A	p.R447Q
ZNF638	zinc finger protein 638	ENSG00000075292	PAP003	102	12.7%	chr2	71504582	CCDS1917.1	c.4430A>C	p.K1477T
ZNF648	zinc finger protein 648	ENSG00000179930	PAP003	232	14.2%	chr1	180293219	CCDS30952.1	c.550G>A	p.A184T
ZNF652	zinc finger protein 652	ENSG00000198740	PAP003	126	11.1%	chr17	44730806	CCDS32677.1	c.1789G>A	p.A597T
ZNF677	zinc finger protein 677	ENSG00000197928	PAP003	168	11.9%	chr19	58433562	CCDS12861.1	c.230T>G	p.L77X

ZNF677	zinc finger protein 677	ENSG00000197928	PAP003	285	13.0%	chr19	58438932	CCDS12861.1	c.46G>T	p.E16X
ZNF749	zinc finger protein 749	ENSG00000186230	PAP003	191	12.6%	chr19	62647385	NM_001023561	c.1057C>T	p.R353C
ZNF781	zinc finger protein 781	ENSG00000196381	PAP003	195	13.3%	chr19	42852732	CCDS12507.1	c.158G>A	p.R53Q
ZNF792	zinc finger protein 792	ENSG00000180884	PAP003	230	11.7%	chr19	40140892	NM_175872	c.1707A>C	p.K569N
ZNF792	zinc finger protein 792	ENSG00000180884	PAP003	251	11.2%	chr19	40141397	NM_175872	c.1202A>G	p.K401R
ZNF804B	zinc finger protein 804B	ENSG00000182348	PAP003	129	16.3%	chr7	88801239	CCDS5613.1	c.1007T>G	p.F336C
ZNF804B	zinc finger protein 804B	ENSG00000182348	PAP003	121	14.9%	chr7	88801262	CCDS5613.1	c.1030G>T	p.E344X
ZNF829	zinc finger protein 829	ENSG00000185869	PAP003	94	13.8%	chr19	42074754	NM_001037232	c.779G>T	p.R260I
ZNF829	zinc finger protein 829	ENSG00000185869	PAP003	247	10.5%	chr19	42090723	NM_001037232	c.267A>C	p.Q89H
ZCCHC11	zinc finger; CCHC domain containing 11	ENSG00000134744	PAP003	145	12.4%	chr1	52713217	CCDS30715.1	c.2602G>A	p.D868N
ZFYVE1	zinc finger; FYVE domain containing 1	ENSG00000165861	PAP003	580	13.1%	chr14	72560501	CCDS9811.1	c.469A>C	p.N157H
ZP3	zona pellucida glycoprotein 3 (sperm receptor)	ENSG00000188372	PAP003	58	19.0%	chr7	75900724	CCDS5586.1	c.384G>T	p.E128D
ACBD3	acyl-CoA binding domain containing 3	ENSG00000182827	PAP010	106	10.4%	chr1	224415979	CCDS1551.1	c.604G>A	p.E202K
ACAP3	ArfGAP with coiled-coil; ankyrin repeat and PH domains 3	ENSG00000131584	PAP010	46	21.7%	chr1	1221295	CCDS19.1	c.1339G>A	p.G447S
ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP010	55	41.8%	chr1	26972534	CCDS285.1	c.3826C>T	p.R1276X
ARHGEF9	Cdc42 guanine nucleotide exchange factor (GEF) 9	ENSG00000131089	PAP010	35	40.0%	chrX	62815109	CCDS35315.1	c.630A>T	p.K210N
C6orf118	chromosome 6 open reading frame 118	ENSG00000112539	PAP010	63	30.2%	chr6	165635583	CCDS5288.1	c.218C>T	p.P73L
CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	ENSG00000150938	PAP010	36	27.8%	chr2	36618119	CCDS1783.1	c.2549C>T	p.S850L
FIGLA	DAVID_folliculogenesis specific basic helix-loop-helix	NM_001004311	PAP010	46	34.8%	chr2	70866214	NM_001004311	c.450A>C	p.R150S
ND4L	DAVID_NADH-ubiquinone oxidoreductase chain 4L; NADH-ubiquinone oxidoreductase chain 4	ENSG00000198886	PAP010	622	39.1%	chrM	11033	ENST00000361381	c.273A>NULL	p.NULL-1FsDel1bp
ND4	DAVID_NADH-ubiquinone oxidoreductase chain 4L; NADH-ubiquinone oxidoreductase chain 4	ENSG00000198886	PAP010	622	39.1%	chrM	11033	ENST00000361381	c.273A>NULL	p.NULL-1FsDel1bp
ND5	DAVID_NADH-ubiquinone oxidoreductase chain 5	ENSG00000198786	PAP010	78	85.9%	chrM	12801	ENST00000361567	c.464T>C	p.I155T
FBXW7	F-box and WD repeat domain containing 7	ENSG00000109670	PAP010	53	24.5%	chr4	153466817	CCDS3777.1	c.1435C>T	p.R479X
FGF5	fibroblast growth factor 5	ENSG00000138675	PAP010	66	30.3%	chr4	81426547	CCDS34021.1	c.504A>C	p.E168D
FGFR2	fibroblast growth factor receptor 2	ENSG00000066468	PAP010	25	44.0%	chr10	123269667	CCDS7620.2	c.755C>G	p.S252W
GPR84	G protein-coupled receptor 84	ENSG00000139572	PAP010	47	31.9%	chr12	53043172	CCDS8878.1	c.731G>A	p.R244K
GRIPAP1	GRIP1 associated protein 1	ENSG00000068400	PAP010	121	10.7%	chrX	48739522	CCDS35248.1	c.186C>A	p.S62R
IL16	interleukin 16 (lymphocyte chemoattractant factor)	ENSG00000172349	PAP010	30	50.0%	chr15	79362154	CCDS42069.1	c.-1NULL>T	p.IVS8+2-1SpliceDonor
MTSS1	metastasis suppressor 1	ENSG00000170873	PAP010	53	30.2%	chr8	125634530	CCDS6353.1	c.2152G>T	p.A718S
OR5D14	olfactory receptor; family 5; subfamily D; member 14	ENSG00000186113	PAP010	110	21.8%	chr11	55320299	CCDS31508.1	c.692G>A	p.R231H
PLD2	phospholipase D2	ENSG00000129219	PAP010	69	27.5%	chr17	4665797	CCDS11057.1	c.1234A>NULL	p.NULL-1FsDel1bp
PLD2	phospholipase D2	ENSG00000129219	PAP010	69	29.0%	chr17	4665798	CCDS11057.1	c.1235A>T	p.N412I
PLXNB2	plexin B2	ENSG00000196576	PAP010	50	26.0%	chr22	49062208	CCDS43035.1	c.3436G>A	p.D1146N
P4HTM	prolyl 4-hydroxylase; transmembrane (endoplasmic reticulum)	ENSG00000178467	PAP010	47	27.7%	chr3	49013908	CCDS2781.2	c.470G>A	p.R157Q
SEBOX	SEBOX homeobox	ENSG00000109072	PAP010	54	22.2%	chr17	23718992	CCDS11229.1	c.1195G>A	p.A399T
TNS4	tensin 4	ENSG00000131746	PAP010	118	10.2%	chr17	35896945	CCDS11368.1	c.1157C>G	p.S386C
TLE1	transducin-like enhancer of split 1 (E(sp1) homolog; Drosophila)	ENSG00000196781	PAP010	90	23.3%	chr9	83392541	CCDS6661.1	c.1852G>A	p.G618R
ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	ENSG00000065361	PAP010	47	31.9%	chr12	54767927	CCDS31833.1	c.695C>T	p.A232V
VTN	vitronectin	ENSG00000109072	PAP010	54	22.2%	chr17	23718992	CCDS11229.1	c.1195G>A	p.A399T
ZNRF4	zinc and ring finger 4	ENSG00000105428	PAP010	50	22.0%	chr19	5406876	CCDS42475.1	c.374C>T	p.A125V
ZNF224	zinc finger protein 224	ENSG00000186019	PAP010	52	25.0%	chr19	49303540	CCDS33046.1	c.1387A>C	p.K463Q
PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	ENSG00000198682	PAP011	218	37.6%	chr10	89493275	CCDS7385.1	c.1373G>A	p.R458Q
HTR6	5-hydroxytryptamine (serotonin) receptor 6	ENSG00000158748	PAP011	209	12.9%	chr1	19878264	CCDS197.1	c.1139C>T	p.S380L
ACACB	acetyl-CoA carboxylase beta	ENSG00000076555	PAP011	76	14.5%	chr12	108149634	CCDS31898.1	c.3958G>A	p.V1320M
ACVRL1	activin A receptor type II-like 1	ENSG00000139567	PAP011	176	14.8%	chr12	50595419	CCDS31804.1	c.916G>A	p.A306T
ACVR2A	activin A receptor; type IIA	ENSG00000121989	PAP011	80	22.5%	chr2	148400156	CCDS33301.1	c.1303A>NULL	p.NULL-1FsDel1bp

ACBD3	acyl-CoA binding domain containing 3	ENSG00000182827	PAP011	71	29.6%	chr1	224419114	CCDS1551.1	c.708A>NULL	p.NULL-1FsDel1bp
ACSL3	acyl-CoA synthetase long-chain family member 3	ENSG00000123983	PAP011	90	34.4%	chr2	223500083	CCDS2455.1	c.1397G>A	p.C466Y
AP1G1	adaptor-related protein complex 1; gamma 1 subunit	ENSG00000166747	PAP011	36	30.6%	chr16	70360941	ENST00000393512	c.-1T>NULL	p.IVS5-1-1SpliceAcceptor
ADARB2	adenosine deaminase; RNA-specific; B2 (RED2 homolog rat)	ENSG00000185736	PAP011	243	28.8%	chr10	1395267	CCDS7058.1	c.1033C>T	p.P345S
AHCY	adenosylhomocysteinase	ENSG00000101444	PAP011	66	15.2%	chr20	32343965	CCDS13233.1	c.305G>A	p.W102X
AFF3	AF4/FMR2 family; member 3	ENSG00000144218	PAP011	107	13.1%	chr2	99576865	CCDS33258.1	c.1765C>T	p.P589S
AGRN	agrin	ENSG00000188157	PAP011	138	10.9%	chr1	966601	CCDS30551.1	c.913C>T	p.R305C
AHSA2	AHA1; activator of heat shock 90kDa protein ATPase homolog 2 (yeast)	ENSG00000173209	PAP011	119	16.0%	chr2	61259735	ENST00000389584	c.196G>NULL	p.NULL-1FsDel1bp
A1BG	alpha-1-B glycoprotein	ENSG00000121410	PAP011	111	27.0%	chr19	63550671	CCDS12976.1	c.1340G>A	p.R447H
ALPK3	alpha-kinase 3	ENSG00000136383	PAP011	373	13.4%	chr15	83201956	CCDS10333.1	c.3589G>A	p.A1197T
ABP1	amiloride binding protein 1 (amine oxidase (copper-containing))	ENSG00000002726	PAP011	350	16.3%	chr7	150189192	CCDS43679.1	c.2218C>NULI	p.NULL-1FsDel1bp
APBB1	amyloid beta (A4) precursor protein-binding; family B; member 1 (Fe65)	ENSG00000166313	PAP011	214	29.0%	chr11	6381501	CCDS31410.1	c.1024C>NULI	p.NULL-1FsDel1bp
ANAPC4	anaphase promoting complex subunit 4	ENSG00000053900	PAP011	87	27.6%	chr4	25028442	CCDS3434.1	c.2182C>T	p.R728X
AGTR2	angiotensin II receptor; type 2	ENSG00000180772	PAP011	94	12.8%	chrX	115217956	CCDS14569.1	c.395T>NULL	p.NULL-1FsDel1bp
ANK1	ankyrin 1; erythrocytic	ENSG00000029534	PAP011	158	10.1%	chr8	41692493	CCDS6119.1	c.1436G>A	p.R479H
ANK2	ankyrin 2; neuronal	ENSG00000145362	PAP011	179	27.9%	chr4	114510189	CCDS3702.1	c.11389A>G	p.T3797A
ANK3	ankyrin 3; node of Ranvier (ankyrin G)	ENSG00000151150	PAP011	50	26.0%	chr10	61500276	CCDS7258.1	c.10369C>T	p.R3457C
ANO10	anoctamin 10	ENSG00000160746	PAP011	277	10.1%	chr3	43593526	CCDS2710.2	c.824T>C	p.L275P
ANO8	anoctamin 8	ENSG00000074855	PAP011	184	11.4%	chr19	17300146	CCDS32949.1	c.2872G>NUL	p.NULL-1FsDel1bp
MKI67	antigen identified by monoclonal antibody Ki-67	ENSG00000148773	PAP011	399	11.3%	chr10	129792125	CCDS7659.1	c.7969G>A	p.V2657I
APOA4	apolipoprotein A-IV	ENSG00000110244	PAP011	448	34.4%	chr11	116197338	CCDS31681.1	c.646G>A	p.V216M
APOL6	apolipoprotein L; 6	ENSG00000221963	PAP011	95	13.7%	chr22	34385546	CCDS13919.1	c.989TG>NUL	p.NULL-1FsDel2bp
AQR	aquarius homolog (mouse)	ENSG00000021776	PAP011	81	16.0%	chr15	33027804	CCDS42013.1	c.283T>G	p.C95G
ARMCX2	armadillo repeat containing; X-linked 2	ENSG00000184867	PAP011	336	25.9%	chrX	100798557	CCDS14490.1	c.674C>T	p.T225M
ARNTL	aryl hydrocarbon receptor nuclear translocator-like	ENSG00000133794	PAP011	105	13.3%	chr11	13356501	CCDS31430.1	c.1453G>NUL	p.NULL-1FsDel1bp
ARSD	arylsulfatase D	ENSG00000006756	PAP011	105	26.7%	chrX	2853798	CCDS35196.1	c.201TT>NULI	p.NULL-1FsDel2bp
ASPM	asp (abnormal spindle) homolog; microcephaly associated (Drosophila)	ENSG00000066279	PAP011	144	16.7%	chr1	195339389	CCDS1389.1	c.10369NULL>	p.NULL-1FsIns1bp
ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP011	140	35.0%	chr1	26928876	CCDS285.1	c.1285C>T	p.R429W
ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP011	205	32.7%	chr1	26972465	CCDS285.1	c.3757NULL>A	p.NULL-1FsIns1bp
ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP011	391	12.3%	chr1	26973704	CCDS285.1	c.4399C>NULI	p.NULL-1FsDel1bp
ATG2B	ATG2 autophagy related 2 homolog B (S. cerevisiae)	ENSG00000066739	PAP011	73	13.7%	chr14	95860091	CCDS9944.2	c.-1T>NULL	p.IVS15-3-1SpliceAcceptor
AGBL5	ATP/GTP binding protein-like 5	ENSG00000084693	PAP011	190	12.1%	chr2	27129919	CCDS1732.3	c.361C>T	p.R121C
ATP6V1B1	ATPase; H+ transporting; lysosomal 56/58kDa; V1 subunit B1	ENSG00000116039	PAP011	236	25.0%	chr2	71045081	CCDS1912.1	c.1149C>NULI	p.NULL-1FsDel1bp
ABCA5	ATP-binding cassette; sub-family A (ABC1); member 5	ENSG00000154265	PAP011	80	12.5%	chr17	64817041	CCDS11685.1	c.587T>NULL	p.NULL-1FsDel1bp
ABCC1	ATP-binding cassette; sub-family C (CFTR/MRP); member 1	ENSG00000103222	PAP011	334	13.5%	chr16	16049630	CCDS42122.1	c.1349NULL>A	p.NULL-1FsIns1bp

BHLHA15	basic helix-loop-helix family; member a15	ENSG00000180535	PAP011	353	19.5%	chr7	97680073	CCDS5655.1	c.516G>T	p.Q172H
BCL9	B-cell CLL/lymphoma 9	ENSG00000116128	PAP011	230	12.2%	chr1	145558170	CCDS30833.1	c.1585G>NUL	p.NULL-1FsDel1bp
BEST4	bestrophin 4	ENSG00000142959	PAP011	56	35.7%	chr1	45022579	CCDS514.1	c.1585C>NUL	p.NULL-1FsDel1bp
BRD9	bromodomain containing 9	ENSG00000028310	PAP011	128	13.3%	chr5	942777	CCDS34127.1	c.150T>NULL	p.NULL-1FsDel1bp
BTK	Bruton agammaglobulinemia tyrosine kinase	ENSG00000010671	PAP011	84	11.9%	chrX	100498572	CCDS14482.1	c.1205T>C	p.L402P
C1QTNF4	C1q and tumor necrosis factor related protein 4	ENSG00000172247	PAP011	206	32.5%	chr11	47568763	CCDS7942.1	c.1165G>NUL	p.NULL-1FsDel1bp
CDH5	cadherin 5; type 2 (vascular endothelium)	ENSG00000179776	PAP011	155	28.4%	chr16	64981897	CCDS10804.1	c.872G>A	p.R291Q
CELSR1	cadherin; EGF LAG seven-pass G-type receptor 1 (flamingo homolog; Drosophila)	ENSG00000075275	PAP011	294	15.3%	chr22	45309891	CCDS14076.1	c.5384G>NUL	p.NULL-1FsDel1bp
CELSR2	cadherin; EGF LAG seven-pass G-type receptor 2 (flamingo homolog; Drosophila)	ENSG00000143126	PAP011	257	33.1%	chr1	109613432	CCDS796.1	c.6809T>C	p.L2270S
CABP4	calcium binding protein 4	ENSG00000175544	PAP011	176	11.4%	chr11	66979720	CCDS8166.1	c.250C>NULL	p.NULL-1FsDel1bp
CAMK2G	calcium/calmodulin-dependent protein kinase II gamma	ENSG00000148660	PAP011	362	20.2%	chr10	75244901	CCDS7338.1	c.1549G>A	p.D517N
CASR	calcium-sensing receptor	ENSG00000036828	PAP011	286	10.8%	chr3	123486321	CCDS3010.1	c.2830C>T	p.Q944X
CAMTA1	calmodulin binding transcription activator 1	ENSG00000171735	PAP011	144	14.6%	chr1	7720191	CCDS30576.1	c.3632T>A	p.V1211D
CSNK1A1L	casein kinase 1; alpha 1-like	ENSG00000180138	PAP011	302	15.9%	chr13	36577273	CCDS9363.1	c.121G>A	p.E41K
CECR1	cat eye syndrome chromosome region; candidate 1	ENSG00000093072	PAP011	240	12.5%	chr22	16070424	CCDS13742.1	c.465G>NULL	p.NULL-1FsDel1bp
CECR6	cat eye syndrome chromosome region; candidate 6	ENSG00000183307	PAP011	219	23.7%	chr22	15981399	CCDS13740.1	c.619C>G	p.L207V
CTNNB1	catenin (cadherin-associated protein); beta 1; 88kDa	ENSG00000168036	PAP011	125	33.6%	chr3	41249901	CCDS2694.1	c.1147T>C	p.W383R
CATSPER3	cation channel; sperm associated 3	ENSG00000152705	PAP011	73	13.7%	chr5	134333622	CCDS4181.1	c.193T>NULL	p.NULL-1FsDel1bp
CTCF	CCCTC-binding factor (zinc finger protein)	ENSG00000102974	PAP011	45	24.4%	chr16	66208212	CCDS10841.1	c.1016G>A	p.R339Q
CNOT6	CCR4-NOT transcription complex; subunit 6	ENSG00000113300	PAP011	52	21.2%	chr5	179924190	CCDS4455.1	c.481G>A	p.A161T
CD5L	CD5 molecule-like	ENSG00000073754	PAP011	395	13.7%	chr1	156070872	CCDS1171.1	c.667T>C	p.W223R
CEMP1	cementum protein 1	ENSG00000205923	PAP011	325	14.2%	chr16	2520867	CCDS42108.1	c.209A>G	p.H70R
CCL19	chemokine (C-C motif) ligand 19	ENSG00000172724	PAP011	316	10.1%	chr9	34680318	CCDS6570.1	c.203NULL>A	p.NULL-1FsIns1bp
CXCR4	chemokine (C-X-C motif) receptor 4	ENSG00000121966	PAP011	493	32.0%	chr2	136589439	CCDS33295.1	c.541G>A	p.V181I
CLCA1	chloride channel accessory 1	ENSG00000016490	PAP011	87	31.0%	chr1	86737071	CCDS709.1	c.2342A>G	p.D781G
CCKBR	cholecystokinin B receptor	ENSG00000110148	PAP011	291	12.0%	chr11	6249027	CCDS7761.1	c.1022T>NULL	p.NULL-1FsDel1bp
CHRM5	cholinergic receptor; muscarinic 5	ENSG00000184984	PAP011	297	31.6%	chr15	32142407	CCDS10031.1	c.197A>G	p.N66S
CHRNA9	cholinergic receptor; nicotinic; alpha 9	ENSG00000174343	PAP011	387	33.6%	chr4	40050890	CCDS3459.1	c.1036T>C	p.S346P
CHPF	chondroitin polymerizing factor	ENSG00000123989	PAP011	420	18.6%	chr2	220113998	CCDS2443.1	c.982C>T	p.R328C
CHD6	chromodomain helicase DNA binding protein 6	ENSG00000124177	PAP011	208	30.3%	chr20	39466817	CCDS13317.1	c.8872AGA>N	p.NULL-1FsDel3bp
C11orf30	chromosome 11 open reading frame 30	ENSG00000158636	PAP011	50	40.0%	chr11	75924627	CCDS8244.1	c.2235G>T	p.Q745H
C11orf57	chromosome 11 open reading frame 57	ENSG00000150776	PAP011	99	12.1%	chr11	111458499	CCDS8356.2	c.475NULL>A	p.NULL-1FsIns1bp
C12orf43	chromosome 12 open reading frame 43	ENSG00000157895	PAP011	117	15.4%	chr12	119927216	CCDS9210.1	c.425G>A	p.R142H
C12orf60	chromosome 12 open reading frame 60	ENSG00000182993	PAP011	52	19.2%	chr12	14867310	CCDS8667.1	c.174NULL>T	p.NULL-1FsIns1bp
C16orf7	chromosome 16 open reading frame 7	ENSG00000075399	PAP011	85	18.8%	chr16	88303278	CCDS42220.1	c.1663C>NUL	p.NULL-1FsDel1bp
C2orf39	chromosome 2 open reading frame 39	ENSG00000157856	PAP011	97	13.4%	chr2	26521315	CCDS1723.1	c.1391G>A	p.R464H
C2orf53	chromosome 2 open reading frame 53	ENSG00000186143	PAP011	293	30.4%	chr2	27214200	CCDS1739.1	c.502A>G	p.R168G
C2orf55	chromosome 2 open reading frame 55	ENSG00000196872	PAP011	170	35.9%	chr2	98805973	CCDS42720.1	c.1195G>A	p.A399T
C2orf69	chromosome 2 open reading frame 69	ENSG00000178074	PAP011	115	12.2%	chr2	200498780	NM_153689	c.1084G>A	p.V362M
C21orf59	chromosome 21 open reading frame 59	ENSG00000159079	PAP011	377	11.4%	chr21	32896508	CCDS13617.1	c.707G>A	p.S236N

C22orf29	chromosome 22 open reading frame 29	ENSG00000215012	PAP011	268	13.1%	chr22	18219339	CCDS13769.1	c.446G>A	p.R149Q
C22orf40	chromosome 22 open reading frame 40	ENSG00000205643	PAP011	92	21.7%	chr22	45022734	CCDS33670.1	c.112G>A	p.V38I
C22orf9	chromosome 22 open reading frame 9	ENSG00000100364	PAP011	220	14.5%	chr22	43986901	ENST00000396090	c.457T>NULL	p.NULL-1FsDel1bp
C9orf131	chromosome 9 open reading frame 131	ENSG00000174038	PAP011	322	28.6%	chr9	35033650	CCDS6572.2	c.1024C>NULL	p.NULL-1FsDel1bp
C9orf16	chromosome 9 open reading frame 16	ENSG00000171159	PAP011	214	13.1%	chr9	129965686	CCDS6893.1	c.223G>A	p.G75R
C9orf96	chromosome 9 open reading frame 96	ENSG00000198870	PAP011	22	45.5%	chr9	135257905	CCDS35169.1	c.1417A>G	p.K473E
CHURC1	churchill domain containing 1	ENSG00000125954	PAP011	262	21.0%	chr14	64589794	CCDS9769.1	c.1041G>NUL	p.NULL-1FsDel1bp
MERTK	c-mer proto-oncogene tyrosine kinase	ENSG00000153208	PAP011	146	11.6%	chr2	112439254	CCDS2094.1	c.773C>T	p.A258V
F2R	coagulation factor II (thrombin) receptor	ENSG00000181104	PAP011	234	13.7%	chr5	76064233	CCDS4032.1	c.427C>T	p.H143Y
CC2D1B	coiled-coil and C2 domain containing 1B	ENSG00000154222	PAP011	100	12.0%	chr1	52598692	CCDS30714.1	c.595G>A	p.G199S
CCDC102B	coiled-coil domain containing 102B	ENSG00000150636	PAP011	83	36.1%	chr18	64655374	CCDS11996.2	c.394A>G	p.K132E
CCDC28A	coiled-coil domain containing 28A	ENSG00000024862	PAP011	77	14.3%	chr6	139139023	CCDS5192.1	c.343A>NULL	p.NULL-1FsDel1bp
CCDC88B	coiled-coil domain containing 88B	ENSG00000168071	PAP011	72	25.0%	chr11	63866658	CCDS8072.2	c.992G>A	p.R331H
CCDC88B	coiled-coil domain containing 88B	ENSG00000168071	PAP011	283	18.4%	chr11	63881334	ENST00000359902	c.1937G>NUL	p.NULL-1FsDel1bp
CCDC92	coiled-coil domain containing 92	ENSG00000119242	PAP011	169	36.7%	chr12	122993868	CCDS9256.1	c.160C>T	p.R54W
COL4A4	collagen; type IV; alpha 4	ENSG00000081052	PAP011	157	11.5%	chr2	227615180	CCDS42828.1	c.3433G>T	p.G1145X
COL7A1	collagen; type VII; alpha 1	ENSG00000114270	PAP011	180	18.3%	chr3	48587875	CCDS2773.1	c.6281C>NULL	p.NULL-1FsDel1bp
COLEC10	collectin sub-family member 10 (C-type lectin)	ENSG00000184374	PAP011	128	20.3%	chr8	120187581	CCDS6327.1	c.804TGTC>N	p.NULL-1FsDel4bp
CSF1R	colony stimulating factor 1 receptor	ENSG00000182578	PAP011	320	15.6%	chr5	149413974	CCDS4302.1	c.2770A>G	p.T924A
C8B	complement component 8; beta polypeptide	ENSG00000021852	PAP011	159	11.3%	chr1	57192997	CCDS30730.1	c.624A>NULL	p.NULL-1FsDel1bp
CREBBP	CREB binding protein	ENSG00000005339	PAP011	253	12.6%	chr16	3759311	CCDS10509.1	c.3104C>NULL	p.NULL-1FsDel1bp
CRTC1	CREB regulated transcription coactivator 1	ENSG00000105662	PAP011	154	18.8%	chr19	18748993	CCDS42525.1	c.1754C>NULL	p.NULL-1FsDel1bp
CRB2	crumbs homolog 2 (Drosophila)	ENSG00000148204	PAP011	44	25.0%	chr9	125175239	CCDS6852.2	c.2608G>A	p.A870T
CTPS2	CTP synthase II	ENSG00000047230	PAP011	82	26.8%	chrX	16626378	CCDS14175.1	c.340G>A	p.V114I
CSMD2	CUB and Sushi multiple domains 2	ENSG00000121904	PAP011	158	10.1%	chr1	33952815	CCDS380.1	c.3433G>NUL	p.NULL-1FsDel1bp
CUL4B	cullin 4B	ENSG00000158290	PAP011	47	23.4%	chrX	119562088	CCDS35379.1	c.-1A>G	p.IVS7-2-1SpliceAcceptor
CNGA2	cyclic nucleotide gated channel alpha 2	ENSG00000183862	PAP011	220	12.3%	chrX	150663253	CCDS14701.1	c.1622G>A	p.R541H
CNNM1	cyclin M1	ENSG00000119946	PAP011	86	37.2%	chr10	101079468	NM_020348	c.334C>NULL	p.NULL-1FsDel1bp
CCNT2	cyclin T2	ENSG00000082258	PAP011	79	25.3%	chr2	135413070	CCDS2174.1	c.398T>C	p.V133A
CDK18	cyclin-dependent kinase 18	ENSG00000117266	PAP011	274	10.9%	chr1	203759313	CCDS1454.1	c.210G>NULL	p.NULL-1FsDel1bp
CYB561D1	cytochrome b-561 domain containing 1	ENSG00000174151	PAP011	235	31.5%	chr1	109839324	CCDS800.1	c.185C>T	p.A62V
CYP4F2	cytochrome P450; family 4; subfamily F; polypeptide 2	ENSG00000186115	PAP011	53	20.8%	chr19	15850696	CCDS12336.1	c.1448C>G	p.A483G
CKAP2	cytoskeleton associated protein 2	ENSG00000136108	PAP011	63	22.2%	chr13	51933368	CCDS41893.1	c.409C>T	p.P137S
DCHS1	dachsous 1 (Drosophila)	ENSG00000166341	PAP011	356	13.2%	chr11	6618718	CCDS7771.1	c.2499C>NULL	p.NULL-1FsDel1bp
Ap2a2	DAVID_adaptor-related protein complex 2: alpha 2 subunit	NM_012305	PAP011	250	19.6%	chr11	976955	NM_012305	c.-1C>T	p.IVS9+2-1SpliceDonor
ARL15	DAVID_ADP-ribosylation factor-like 15	NM_019087	PAP011	98	12.2%	chr5	53444944	NM_019087	c.515NULL>G	p.NULL-1FsIns1bp
ARL15	DAVID_ADP-ribosylation factor-like 15	NM_019087	PAP011	88	26.1%	chr5	53444965	NM_019087	c.286T>C	p.Y96H

ACAN	DAVID_aggrecan	NM_013227	PAP011	391	12.0%	chr15	87199356	NM_013227	c.2536C>NULL	p.NULL-1FsDel1bp
Ankrd24	DAVID_ankyrin repeat domain 24	NM_133475	PAP011	46	41.3%	chr19	4166981	NM_133475	c.1204C>T	p.R402W
aspG	DAVID_asparaginase homolog (S. cerevisiae)	NM_001080464	PAP011	123	34.1%	chr14	103640722	NM_001080464	c.947G>A	p.G316E
Bean	DAVID_brain expressed: associated with Nedd4	ENSG00000166546	PAP011	77	29.9%	chr16	65068972	ENST00000299694	c.268G>A	p.E90K
CDC42BPB	DAVID_CDC42 binding protein kinase beta (DMPK-like)	ENSG00000198752	PAP011	266	32.0%	chr14	102476165	CCDS9978.1	c.4562G>A	p.R1521H
Cldn25	DAVID_claudin-like	NM_001101389	PAP011	76	21.1%	chr11	113155761	NM_001101389	c.34G>NULL	p.NULL-1FsDel1bp
CCDC150	DAVID_coiled-coil domain containing 150	NM_001080539	PAP011	99	15.2%	chr2	197239764	NM_001080539	c.839A>NULL	p.NULL-1FsDel1bp
DLL4	DAVID_delta-like 4 (Drosophila)	NM_019074	PAP011	102	22.5%	chr15	39009191	NM_019074	c.33G>T	p.W11C
Ercc6	DAVID_excision repair cross-complementing rodent repair deficiency: complementation group 6	ENSG00000032514	PAP011	62	21.0%	chr10	50361417	CCDS7229.1	c.1973T>C	p.V658A
FAT3	DAVID_FAT tumor suppressor homolog 3 (Drosophila)	NM_001008781	PAP011	108	28.7%	chr11	91725695	NM_001008781	c.769G>T	p.E257X
FAT3	DAVID_FAT tumor suppressor homolog 3 (Drosophila)	NM_001008781	PAP011	121	21.5%	chr11	92173386	NM_001008781	c.7559C>T	p.A2520V
GLTSCR1	DAVID_glioma tumor suppressor candidate region gene 1	NM_015711	PAP011	142	15.5%	chr19	52889646	NM_015711	c.2746C>NULL	p.NULL-1FsDel1bp
GLTSCR1	DAVID_glioma tumor suppressor candidate region gene 1	NM_015711	PAP011	305	11.8%	chr19	52896513	NM_015711	c.3712NULL>C	p.NULL-1FsIns1bp
Gnas	DAVID_GNAS complex locus	ENSG00000213705	PAP011	370	10.0%	chr20	56848647	CCDS13471.1	c.91G>A	p.A31T
ERVFRDE1	DAVID_HERV-FRD provirus ancestral Env polyprotein	ENSG00000212121	PAP011	76	18.4%	chr6	11213049	NM_207582	c.481T>C	p.Y161H
FLJ25328	DAVID_hypothetical LOC148231	ENSG00000167459	PAP011	77	23.4%	chr19	16006569	ENST00000397365	c.68A>NULL	p.NULL-1FsDel1bp
SSC5D	DAVID_hypothetical LOC284297	NM_001144950	PAP011	101	12.9%	chr19	60694088	NM_001144950	c.724NULL>G	p.NULL-1FsIns1bp
LOC339674	DAVID_hypothetical LOC339674	ENSG00000205704	PAP011	214	18.7%	chr22	40684247	ENST00000381348	c.81G>A	p.W27X
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP011	68	22.1%	chr13	102179997	NM_001146197	c.41988T>NUL	p.NULL-1FsDel1bp
Ifrd2	DAVID_interferon-related developmental regulator 2	NM_006764	PAP011	309	14.9%	chr3	50302398	NM_006764	c.704G>A	p.S235N
C6orf174	DAVID_KIAA0408; chromosome 6 open reading frame 174	ENSG00000214338	PAP011	58	19.0%	chr6	127878476	CCDS43505.1	c.977C>T	p.A326V
KIAA0408	DAVID_KIAA0408; chromosome 6 open reading frame 174	ENSG00000214338	PAP011	58	19.0%	chr6	127878476	CCDS43505.1	c.977C>T	p.A326V
Kif13a	DAVID_kinesin family member 13A	NM_022113	PAP011	80	16.3%	chr6	17945287	NM_022113	c.1168G>NUL	p.NULL-1FsDel1bp
lmod2	DAVID_leiomodin 2 (cardiac)	NM_207163	PAP011	143	23.1%	chr7	123090306	NM_207163	c.1430A>NULL	p.NULL-1FsDel1bp
LOXHD1	DAVID_lipoxygenase homology domains 1	NM_144612	PAP011	204	17.6%	chr18	42358854	NM_144612	c.4555G>A	p.A1519T
MAGEL2	DAVID_MAGE-like 2	NM_019066	PAP011	115	18.3%	chr15	21441987	NM_019066	c.5745C>NULL	p.NULL-1FsDel1bp
HLA-DRB4	DAVID_major histocompatibility complex: class II: DR beta 4; major histocompatibility complex: class II: DR beta 1	ENSG00000196126	PAP011	67	14.9%	chr6	32659866	NM_002124	c.368G>A	p.R123Q
hla-drb1	DAVID_major histocompatibility complex: class II: DR beta 4; major histocompatibility complex: class II: DR beta 1	ENSG00000196126	PAP011	67	14.9%	chr6	32659866	NM_002124	c.368G>A	p.R123Q
HLA-DRB4	DAVID_major histocompatibility complex: class II: DR beta 4; major histocompatibility complex: class II: DR beta 1	NM_002124	PAP011	67	14.9%	chr6	32659866	NM_002124	c.368G>A	p.R123Q
hla-drb1	DAVID_major histocompatibility complex: class II: DR beta 4; major histocompatibility complex: class II: DR beta 1	NM_002124	PAP011	67	14.9%	chr6	32659866	NM_002124	c.368G>A	p.R123Q
HLA-DRB4	DAVID_major histocompatibility complex: class II: DR beta 4; major histocompatibility complex: class II: DR beta 1	NM_002124	PAP011	67	14.9%	chr6	32659866	NM_002124	c.368G>A	p.R123Q
hla-drb1	DAVID_major histocompatibility complex: class II: DR beta 4; major histocompatibility complex: class II: DR beta 1	NM_002124	PAP011	67	14.9%	chr6	32659866	NM_002124	c.368G>A	p.R123Q
MAS1L	DAVID_MAS1 oncogene-like	ENSG00000204687	PAP011	81	30.9%	chr6	29563105	CCDS4661.1	c.554G>A	p.R185H
MS4A2	DAVID_membrane-spanning 4-domains: subfamily A: member 2 (Fc fragment of IgE: high affinity I: receptor for; beta polypeptide)	NM_001142303	PAP011	112	25.9%	chr11	59617615	NM_001142303	c.545T>NULL	p.NULL-1FsDel1bp
MUC16	DAVID_mucin 16: cell surface associated	NM_024690	PAP011	124	22.6%	chr19	8923654	NM_024690	c.24792C>A	p.S8264R

MUC16	DAVID_mucin 16: cell surface associated	NM_024690	PAP011	350	13.4%	chr19	8932198	NM_024690	c.16248G>A	p.M5416I
MLL2	DAVID_myeloid/lymphoid or mixed-lineage leukemia 2	NM_003482	PAP011	275	11.6%	chr12	47712139	NM_003482	c.12616G>A	p.A4206T
MLL2	DAVID_myeloid/lymphoid or mixed-lineage leukemia 2	NM_003482	PAP011	267	12.0%	chr12	47719904	NM_003482	c.7916C>T	p.T2639I
MLL4	DAVID_myeloid/lymphoid or mixed-lineage leukemia 4	ENSG00000105663	PAP011	137	27.7%	chr19	40906238	NM_014727	c.3052NULL>A	p.NULL-1FsIns1bp
MYH14	DAVID_myosin: heavy chain 14	NM_001145809	PAP011	191	16.8%	chr19	55405816	NM_001145809	c.382C>T	p.R128W
ND4L	DAVID_NADH-ubiquinone oxidoreductase chain 4L; NADH-ubiquinone oxidoreductase chain 4	ENSG00000198868	PAP011	280	53.9%	chrM	11868	ENST00000410116	c.1108NULL>C	p.NULL-1FsIns1bp
ND4	DAVID_NADH-ubiquinone oxidoreductase chain 4L; NADH-ubiquinone oxidoreductase chain 4	ENSG00000198868	PAP011	280	53.9%	chrM	11868	ENST00000410116	c.1108NULL>C	p.NULL-1FsIns1bp
Nrk	DAVID_Nik related kinase	NM_198465	PAP011	223	23.8%	chrX	105039709	NM_198465	c.1420G>A	p.A474T
NOTCH4	DAVID_Notch homolog 4 (Drosophila)	ENSG00000204301	PAP011	339	15.0%	chr6	32276882	CCDS34420.1	c.4129C>T	p.L1377F
NOTCH4	DAVID_Notch homolog 4 (Drosophila)	ENSG00000204301	PAP011	111	19.8%	chr6	32299637	CCDS34420.1	c.117GCT>NU	p.NULL-1FsDel3bp
PNPLA6	DAVID_patatin-like phospholipase domain containing 6	NM_001166111	PAP011	184	16.8%	chr19	7506706	NM_001166111	c.59A>G	p.N20S
PHRF1	DAVID_PHD and ring finger domains 1	NM_020901	PAP011	182	13.2%	chr11	598263	NM_020901	c.2804C>NULL	p.NULL-1FsDel1bp
LPPR3	DAVID_plasticity-related gene 2	ENSG00000129951	PAP011	101	19.8%	chr19	764055	CCDS12043.1	c.1756T>C	p.S586P
Pcdhgb2	DAVID_protocadherin gamma subfamily B: 2	NM_018923	PAP011	187	26.7%	chr5	140721433	NM_018923	c.1547C>T	p.A516V
Pcdhgb7	DAVID_protocadherin gamma subfamily B: 7	NM_018927	PAP011	292	31.2%	chr5	140779586	NM_018927	c.1976C>T	p.T659M
R3HCC1	DAVID_R3H domain and coiled-coil containing 1	NM_001136108	PAP011	371	30.5%	chr8	23206828	NM_001136108	c.532T>C	p.S178P
Rgl2	DAVID_ral guanine nucleotide dissociation stimulator-like 2	ENSG00000204218	PAP011	174	16.1%	chr6	33368977	CCDS4774.1	c.1801C>A	p.L601I
RTL1	DAVID_retrotransposon-like 1	NM_001134888	PAP011	199	34.7%	chr14	100417260	NM_001134888	c.7695C>NULL	p.NULL-1FsDel1bp
RING1	DAVID_ring finger protein 1	ENSG00000204227	PAP011	110	13.6%	chr6	33286968	CCDS34424.1	c.511G>NULL	p.NULL-1FsDel1bp
SAPS1	DAVID_SAPS domain family: member 1	NM_014931	PAP011	150	32.7%	chr19	60450063	NM_014931	c.221G>A	p.R74H
SETD1B	DAVID_SET domain containing 1B	NM_015048	PAP011	49	36.7%	chr12	120727041	NM_015048	c.15C>NULL	p.NULL-1FsDel1bp
SHANK3	DAVID_SH3 and multiple ankyrin repeat domains 3	NM_001080420	PAP011	43	25.6%	chr22	49482564	NM_001080420	c.1332G>NUL	p.NULL-1FsDel1bp
smg1	DAVID_SMG1 homolog: phosphatidylinositol 3-kinase-related kinase (C. elegans)	NM_015092	PAP011	131	32.8%	chr16	18758603	NM_015092	c.6863T>C	p.M2288T
TNXB	DAVID_tenascin XB; tenascin XA pseudogene	NM_019105	PAP011	444	14.0%	chr6	32154931	NM_019105	c.4232G>T	p.G1411V
TNXA	DAVID_tenascin XB; tenascin XA pseudogene	NM_019105	PAP011	444	14.0%	chr6	32154931	NM_019105	c.4232G>T	p.G1411V
TNXB	DAVID_tenascin XB; tenascin XA pseudogene	NM_019105	PAP011	444	14.0%	chr6	32154931	NM_019105	c.4232G>T	p.G1411V
TNXA	DAVID_tenascin XB; tenascin XA pseudogene	NM_019105	PAP011	444	14.0%	chr6	32154931	NM_019105	c.4232G>T	p.G1411V
TNXB	DAVID_tenascin XB; tenascin XA pseudogene	NM_019105	PAP011	444	14.0%	chr6	32154931	NM_019105	c.4232G>T	p.G1411V
TNXA	DAVID_tenascin XB; tenascin XA pseudogene	NM_019105	PAP011	444	14.0%	chr6	32154931	NM_019105	c.4232G>T	p.G1411V
THOC1	DAVID_THO complex 1	NM_005131	PAP011	94	21.3%	chr18	215140	NM_005131	c.-1G>A	p.IVS13-1-1SpliceAcceptor
TCF19	DAVID_transcription factor 19	ENSG00000137310	PAP011	496	29.8%	chr6	31238256	CCDS43446.1	c.821A>G	p.K274R
TLE2	DAVID_transducin-like enhancer of split 2 (E(sp1) homolog: Drosophila)	NM_003260	PAP011	80	12.5%	chr19	2962087	NM_003260	c.1083C>NULL	p.NULL-1FsDel1bp
TM4SF4	DAVID_transmembrane 4 L six family member 4	NM_004617	PAP011	207	12.6%	chr3	150675453	NM_004617	c.99AA>NULL	p.NULL-1FsDel2bp
TRIM66	DAVID_tripartite motif-containing 66	NM_014818	PAP011	202	10.9%	chr11	8599397	NM_014818	c.2775G>T	p.E925D
Tnk1	DAVID_tyrosine kinase: non-receptor: 1	NM_003985	PAP011	221	18.1%	chr17	7232466	NM_003985	c.1495G>A	p.E499K
VWA5B2	DAVID_von Willebrand factor A domain containing 5B2	NM_138345	PAP011	280	11.8%	chr3	185441988	NM_138345	c.3197C>T	p.A1066V
Zc3h12b	DAVID_zinc finger CCCH-type containing 12B	NM_001010888	PAP011	207	19.3%	chrX	64638984	NM_001010888	c.1648C>T	p.H550Y
ZFHX4	DAVID_zinc finger homeobox 4	NM_024721	PAP011	112	31.3%	chr8	77928596	NM_024721	c.6749NULL>A	p.NULL-1FsIns1bp
znf292	DAVID_zinc finger protein 292	NM_015021	PAP011	141	30.5%	chr6	88023157	NM_015021	c.3091T>NULL	p.NULL-1FsDel1bp

ZNF598	DAVID_zinc finger protein 598	NM_178167	PAP011	477	16.4%	chr16	1991626	NM_178167	c.974C>T	p.A325V
Zswim6	DAVID_zinc finger: SWIM-type containing 6	NM_020928	PAP011	126	11.1%	chr5	60825941	NM_020928	c.1280G>A	p.R427Q
DCAF15	DDB1 and CUL4 associated factor 15	ENSG00000132017	PAP011	187	12.8%	chr19	13930918	CCDS32926.1	c.846C>NULL	p.NULL-1FsDel1bp
DOCK7	dedicator of cytokinesis 7	ENSG00000116641	PAP011	77	28.6%	chr1	62794156	CCDS30734.1	c.2524A>G	p.N842D
DIABLO	diablo homolog (Drosophila)	ENSG00000184047	PAP011	134	34.3%	chr12	121267008	CCDS9228.1	c.503C>T	p.A168V
DLG5	discs; large homolog 5 (Drosophila)	ENSG00000151208	PAP011	311	18.6%	chr10	79284085	CCDS7353.2	c.586G>A	p.V196M
DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	ENSG00000119772	PAP011	207	26.1%	chr2	25317071	CCDS33157.1	c.2205T>NULL	p.NULL-1FsDel1bp
DMAP1	DNA methyltransferase 1 associated protein 1	ENSG00000178028	PAP011	42	33.3%	chr1	44458567	CCDS509.1	c.1343C>T	p.S448L
DDI1	DNA-damage inducible 1 homolog 1 (S. cerevisiae)	ENSG00000170967	PAP011	215	13.0%	chr11	103413646	CCDS31660.1	c.886C>T	p.Q296X
DCT	dopachrome tautomerase (dopachrome delta-isomerase; tyrosine-related protein 2)	ENSG00000080166	PAP011	282	17.7%	chr13	93919041	CCDS9470.1	c.854T>NULL	p.NULL-1FsDel1bp
DPY19L4	dpy-19-like 4 (C. elegans)	ENSG00000156162	PAP011	62	19.4%	chr8	95816078	CCDS34924.1	c.172G>A	p.A58T
DUOX2	dual oxidase 2	ENSG00000140279	PAP011	105	12.4%	chr15	43180287	CCDS10117.1	c.2963C>A	p.P988Q
DYM	dymeclin	ENSG00000141627	PAP011	111	13.5%	chr18	44877868	CCDS11937.1	c.1762A>G	p.S588G
DNM2	dynamin 2	ENSG00000079805	PAP011	305	10.8%	chr19	10801865	CCDS32907.1	c.2342G>NUL	p.NULL-1FsDel1bp
DNAH7	dynein; axonemal; heavy chain 7	ENSG00000118997	PAP011	45	35.6%	chr2	196561069	CCDS42794.1	c.1483G>A	p.D495N
DYNC1H1	dynein; cytoplasmic 1; heavy chain 1	ENSG00000197102	PAP011	142	19.7%	chr14	101551319	CCDS9966.1	c.7139C>T	p.A2380V
EFCAB5	EF-hand calcium binding domain 5	ENSG00000176927	PAP011	60	20.0%	chr17	25405152	NM_198529	c.2054G>A	p.G685E
EFHD1	EF-hand domain family; member D1	ENSG00000115468	PAP011	234	16.7%	chr2	233235770	CCDS2497.1	c.317G>A	p.R106Q
EMILIN1	elastin microfibril interfacer 1	ENSG00000138080	PAP011	305	22.0%	chr2	27159859	CCDS1733.1	c.1916C>T	p.A639V
ERC1	ELKS/RAB6-interacting/CAST family member 1	ENSG00000082805	PAP011	167	14.4%	chr12	1007479	CCDS8508.1	c.149G>A	p.S50N
ECE2	endothelin converting enzyme 2	ENSG00000145194	PAP011	386	14.0%	chr3	185450246	CCDS3255.1	c.70G>A	p.E24K
EN1	engrailed homeobox 1	ENSG00000163064	PAP011	262	20.6%	chr2	119317184	CCDS2123.1	c.979T>C	p.Y327H
EPHA2	EPH receptor A2	ENSG00000142627	PAP011	202	24.8%	chr1	16334786	CCDS169.1	c.1494C>NULL	p.NULL-1FsDel1bp
EPHB3	EPH receptor B3	ENSG00000182580	PAP011	566	10.4%	chr3	185773418	CCDS3268.1	c.616C>T	p.R206C
EPN3	epsin 3	ENSG00000049283	PAP011	308	12.0%	chr17	45969256	CCDS11570.1	c.340C>A	p.R114S
EPN3	epsin 3	ENSG00000049283	PAP011	103	39.8%	chr17	45974456	CCDS11570.1	c.1838C>T	p.T613M
ERRFI1	ERBB receptor feedback inhibitor 1	ENSG00000116285	PAP011	161	29.2%	chr1	7996059	CCDS94.1	c.1187T>C	p.L396P
EPB41L3	erythrocyte membrane protein band 4.1-like 3	ENSG00000082397	PAP011	128	15.6%	chr18	5409724	CCDS11838.1	c.1492C>T	p.R498W
EXOC7	exocyst complex component 7	ENSG00000182473	PAP011	156	12.2%	chr17	71591377	CCDS32738.1	c.2002G>A	p.G668R
FLAD1	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	ENSG00000160688	PAP011	503	20.3%	chr1	153227251	CCDS1078.1	c.419G>A	p.R140H
FAM135A	family with sequence similarity 135; member A	ENSG00000082269	PAP011	124	34.7%	chr6	71293038	CCDS34481.1	c.2891T>C	p.I964T
FAM176B	family with sequence similarity 176; member B	ENSG00000142694	PAP011	290	14.8%	chr1	36561177	CCDS406.1	c.49G>A	p.A17T
FAM65C	family with sequence similarity 65; member C	ENSG00000042062	PAP011	70	14.3%	chr20	48659578	CCDS13431.2	c.652NULL>C	p.NULL-1FsIns1bp
FNTB	farnesyltransferase; CAAX box; beta	ENSG00000125954	PAP011	262	21.0%	chr14	64589794	CCDS9769.1	c.1041G>NUL	p.NULL-1FsDel1bp
FAT4	FAT tumor suppressor homolog 4 (Drosophila)	ENSG00000196159	PAP011	376	28.2%	chr4	126458299	CCDS3732.2	c.1283G>A	p.R428H
FERD3L	Fer3-like (Drosophila)	ENSG00000146618	PAP011	475	10.9%	chr7	19151402	CCDS5368.1	c.609G>NULL	p.NULL-1FsDel1bp
FRMPD3	FERM and PDZ domain containing 3	ENSG00000147234	PAP011	198	32.8%	chrX	106732583	ENST00000276185	c.4757G>A	p.S1586N
FDXR	ferredoxin reductase	ENSG00000161513	PAP011	315	32.4%	chr17	70371965	CCDS11707.1	c.920G>A	p.R307H
FGFR4	fibroblast growth factor receptor 4	ENSG00000160867	PAP011	330	34.2%	chr5	176450120	CCDS4410.1	c.215G>A	p.R72H
FICD	FIC domain containing	ENSG00000198855	PAP011	407	20.9%	chr12	107436963	CCDS9116.1	c.958A>G	p.I320V
FLNA	filamin A; alpha	ENSG00000196924	PAP011	200	37.5%	chrX	153247615	CCDS44021.1	c.1400G>A	p.R467H
FOXM1	forkhead box M1	ENSG00000111206	PAP011	146	15.1%	chr12	2838477	CCDS8516.1	c.1994C>T	p.T665M
FPR1	formyl peptide receptor 1	ENSG00000171051	PAP011	217	15.2%	chr19	56941681	CCDS12839.1	c.379G>A	p.V127I
FZD4	frizzled homolog 4 (Drosophila)	ENSG00000174804	PAP011	391	10.5%	chr11	86341103	CCDS8279.1	c.343G>A	p.G115S
GPER	G protein-coupled estrogen receptor 1	ENSG00000164850	PAP011	482	35.9%	chr7	1098785	CCDS5322.1	c.895C>T	p.R299C

GPR25	G protein-coupled receptor 25	ENSG00000170128	PAP011	115	38.3%	chr1	199109191	CCDS1405.1	c.403G>A	p.V135M
GPR26	G protein-coupled receptor 26	ENSG00000154478	PAP011	471	11.3%	chr10	125437476	CCDS7636.1	c.824G>NULL	p.NULL-1FsDel1bp
GPR88	G protein-coupled receptor 88	ENSG00000181656	PAP011	211	13.7%	chr1	100777411	CCDS772.1	c.301NULL>C	p.NULL-1FsIns1bp
GAL3ST3	galactose-3-O-sulfotransferase 3	ENSG00000175229	PAP011	154	35.1%	chr11	65567188	CCDS8128.1	c.662C>A	p.A221D
GJB3	gap junction protein; beta 3; 31kDa	ENSG00000188910	PAP011	402	19.2%	chr1	35023428	CCDS384.1	c.478C>T	p.R160C
GJD2	gap junction protein; delta 2; 36kDa	ENSG00000159248	PAP011	108	11.1%	chr15	32833975	CCDS10040.1	c.77G>NULL	p.NULL-1FsDel1bp
GATA3	GATA binding protein 3	ENSG00000107485	PAP011	122	23.8%	chr10	8146045	CCDS31143.1	c.862T>C	p.C288R
GATAD1	GATA zinc finger domain containing 1	ENSG00000157259	PAP011	166	12.0%	chr7	91923798	CCDS5625.1	c.796G>A	p.A266T
GDI1	GDP dissociation inhibitor 1	ENSG00000203879	PAP011	90	11.1%	chrX	153320628	CCDS35452.1	c.336G>NULL	p.NULL-1FsDel1bp
GRM2	glutamate receptor; metabotropic 2	ENSG00000164082	PAP011	276	27.5%	chr3	51721626	CCDS2834.1	c.548G>A	p.R183H
GRM5	glutamate receptor; metabotropic 5	ENSG00000168959	PAP011	103	14.6%	chr11	87940739	CCDS8283.1	c.1760C>T	p.A587V
GPC1	glypican 1	ENSG00000063660	PAP011	192	19.8%	chr2	241054334	CCDS2534.1	c.1631T>C	p.L544P
GIGYF1	GRB10 interacting GYF protein 1	ENSG00000146830	PAP011	92	10.9%	chr7	100121020	CCDS34708.1	c.1075C>G	p.L359V
GREM1	gremlin 1; cysteine knot superfamily; homolog (Xenopus laevis)	ENSG00000166923	PAP011	136	14.0%	chr15	30810374	CCDS10029.1	c.191NULL>G	p.NULL-1FsIns1bp
GAS6	growth arrest-specific 6	ENSG00000183087	PAP011	201	11.4%	chr13	113590079	NM_000820	c.2010C>NULL	p.NULL-1FsDel1bp
GDF7	growth differentiation factor 7	ENSG00000143869	PAP011	324	21.3%	chr2	20734472	CCDS1701.1	c.1159C>T	p.R387C
GIMAP8	GTPase; IMAP family member 8	ENSG00000171115	PAP011	250	27.2%	chr7	149794868	CCDS34777.1	c.149AG>NUL	p.NULL-1FsDel2bp
GNAQ	guanine nucleotide binding protein (G protein); q polypeptide	ENSG00000156052	PAP011	97	30.9%	chr9	79726936	CCDS6658.1	c.282G>A	p.M94I
HEYL	hairy/enhancer-of-split related with YRPW motif-like	ENSG00000163909	PAP011	217	34.1%	chr1	39865340	CCDS439.1	c.413C>A	p.P138H
HEATR5B	HEAT repeat containing 5B	ENSG00000008869	PAP011	101	14.9%	chr2	37062139	CCDS33181.1	c.6518T>NULL	p.NULL-1FsDel1bp
HEMGN	hemogen	ENSG00000136929	PAP011	137	10.2%	chr9	99733176	CCDS6731.1	c.1508A>NULL	p.NULL-1FsDel1bp
HHIPL2	HHIP-like 2	ENSG00000143512	PAP011	228	31.1%	chr1	220783976	CCDS1530.2	c.500G>A	p.R167H
HPCAL1	hippocalcin-like 1	ENSG00000115756	PAP011	465	11.6%	chr2	10477614	CCDS1671.1	c.280C>T	p.R94W
HDAC7	histone deacetylase 7	ENSG00000061273	PAP011	290	11.4%	chr12	46465858	CCDS41776.1	c.2539C>A	p.L847I
HKR1	HKR1; GLI-Kruppel zinc finger family member	ENSG00000181666	PAP011	93	12.9%	chr19	42517991	ENST00000392153	c.25A>NULL	p.NULL-1FsDel1bp
HRNR	hornerin	ENSG00000197915	PAP011	38	26.3%	chr1	150457647	CCDS30859.1	c.3082A>G	p.R1028G
HCFC1R1	host cell factor C1 regulator 1 (XPO1 dependent)	ENSG00000103145	PAP011	143	23.1%	chr16	3013267	CCDS10490.1	c.377C>NULL	p.NULL-1FsDel1bp
HAP1	huntingtin-associated protein 1	ENSG00000173805	PAP011	353	17.3%	chr17	37134907	CCDS11406.1	c.1432C>T	p.R478X
HAP1	huntingtin-associated protein 1	ENSG00000173805	PAP011	243	11.1%	chr17	37138110	CCDS11406.1	c.-1G>A	p.IVS6-1-1SpliceAcceptor
ILDR2	immunoglobulin-like domain containing receptor 2	ENSG00000143195	PAP011	175	32.6%	chr1	165175431	CCDS1256.1	c.500G>A	p.G167D
INO80B	INO80 complex subunit B	ENSG00000115274	PAP011	544	13.4%	chr2	74540918	CCDS1943.1	c.412C>NULL	p.NULL-1FsDel1bp
INO80E	INO80 complex subunit E	ENSG00000169592	PAP011	216	16.7%	chr16	29915166	CCDS10665.1	c.34A>NULL	p.NULL-1FsDel1bp
INPPL1	inositol polyphosphate phosphatase-like 1	ENSG00000165458	PAP011	248	12.1%	chr11	71625857	CCDS8213.1	c.2921NULL>(	p.NULL-1FsIns1bp
INTS10	integrator complex subunit 10	ENSG00000104613	PAP011	150	20.0%	chr8	19722216	CCDS6011.2	c.348A>NULL	p.NULL-1FsDel1bp
INTS10	integrator complex subunit 10	ENSG00000104613	PAP011	61	18.0%	chr8	19728222	CCDS6011.2	c.1012A>G	p.N338D
ITGA4	integrin; alpha 4 (antigen CD49D; alpha 4 subunit of VLA-4 receptor)	ENSG00000115232	PAP011	263	23.6%	chr2	182030638	CCDS42788.1	c.12A>C	p.E4D
ITGB7	integrin; beta 7	ENSG00000139626	PAP011	330	10.0%	chr12	51876731	CCDS8849.1	c.715G>A	p.A239T

IFIT3	interferon-induced protein with tetratricopeptide repeats 3	ENSG00000119917	PAP011	146	15.1%	chr10	91088683	CCDS7402.1	c.291G>A	p.W97X
IL12RB2	interleukin 12 receptor; beta 2	ENSG00000081985	PAP011	184	29.3%	chr1	67633932	CCDS638.1	c.2161C>NULL	p.NULL-1FsDel1bp
IRX4	iroquois homeobox 4	ENSG00000113430	PAP011	72	36.1%	chr5	1931496	CCDS3867.1	c.1147A>G	p.T383A
ISM1	isthmin 1 homolog (zebrafish)	ENSG00000101230	PAP011	227	10.6%	chr20	13208475	NM_080826	c.573C>NULL	p.NULL-1FsDel1bp
JAK1	Janus kinase 1	ENSG00000162434	PAP011	63	17.5%	chr1	65079585	CCDS41346.1	c.2674NULL>A	p.NULL-1FsIns1bp
JAK1	Janus kinase 1	ENSG00000162434	PAP011	63	20.6%	chr1	65079585	CCDS41346.1	c.2674A>NULL	p.NULL-1FsDel1bp
JAK1	Janus kinase 1	ENSG00000162434	PAP011	51	21.6%	chr1	65098421	CCDS41346.1	c.1446C>NULL	p.NULL-1FsDel1bp
JAKMIP1	janus kinase and microtubule interacting protein 1	ENSG00000152969	PAP011	190	36.3%	chr4	6158333	CCDS3385.1	c.392C>T	p.A131V
JUND	jun D proto-oncogene	ENSG00000130522	PAP011	234	35.9%	chr19	18252291	CCDS32959.1	c.1004G>A	p.G335D
KLHL28	kelch-like 28 (Drosophila)	ENSG00000179454	PAP011	92	27.2%	chr14	44484145	CCDS9680.1	c.737A>G	p.D246G
KRT32	keratin 32	ENSG00000108759	PAP011	366	16.4%	chr17	36876787	CCDS11393.1	c.317G>A	p.R106H
KIAA0564	KIAA0564	ENSG00000102763	PAP011	62	21.0%	chr13	41338096	CCDS41881.1	c.1289T>C	p.L430P
KIAA0753	KIAA0753	ENSG00000198920	PAP011	52	25.0%	chr17	6472162	CCDS42247.1	c.1341A>NULL	p.NULL-1FsDel1bp
KIAA0802	KIAA0802	ENSG00000168502	PAP011	138	10.1%	chr18	8774093	CCDS11841.1	c.983C>T	p.A328V
KIAA1267	KIAA1267	ENSG00000120071	PAP011	66	31.8%	chr17	41465478	CCDS11503.1	c.3124C>NULL	p.NULL-1FsDel1bp
KIAA1919	KIAA1919	ENSG00000173214	PAP011	98	26.5%	chr6	111694054	CCDS5090.1	c.596T>NULL	p.NULL-1FsDel1bp
KIRREL	kin of IRRE like (Drosophila)	ENSG00000183853	PAP011	320	17.2%	chr1	156331390	CCDS1172.1	c.1638G>T	p.Q546H
KIF12	kinesin family member 12	ENSG00000136883	PAP011	139	30.2%	chr9	115896045	CCDS6801.1	c.928C>T	p.R310X
KANK1	KN motif and ankyrin repeat domains 1	ENSG00000107104	PAP011	113	40.7%	chr9	701797	CCDS34976.1	c.1031A>G	p.E344G
KRI1	KRI1 homolog (S. cerevisiae)	ENSG00000129347	PAP011	201	16.9%	chr19	10537488	ENST00000361821	c.252NULL>G	p.NULL-1FsIns2bp
LARP1	La ribonucleoprotein domain family; member 1	ENSG00000155506	PAP011	134	24.6%	chr5	154153583	CCDS34281.1	c.899NULL>C	p.NULL-1FsIns1bp
LBX2	ladybird homeobox 2	ENSG00000179528	PAP011	500	13.8%	chr2	74578683	CCDS33228.1	c.464C>T	p.P155L
LAMC1	laminin; gamma 1 (formerly LAMB2)	ENSG00000135862	PAP011	103	14.6%	chr1	181259619	CCDS1351.1	c.145C>T	p.R49C
LZTS2	leucine zipper; putative tumor suppressor 2	ENSG00000107816	PAP011	324	32.1%	chr10	102756838	CCDS7507.1	c.1933C>T	p.R645W
LRGUK	leucine-rich repeats and guanylate kinase domain containing	ENSG00000155530	PAP011	93	10.8%	chr7	133513883	CCDS5830.1	c.1196C>T	p.P399L
LRTM2	leucine-rich repeats and transmembrane domains 2	ENSG00000166159	PAP011	182	22.0%	chr12	1813813	CCDS31726.1	c.778G>A	p.A260T
LENG9	leukocyte receptor cluster (LRC) member 9	ENSG00000182909	PAP011	264	18.6%	chr19	59665401	CCDS12895.1	c.2560C>NULL	p.NULL-1FsDel1bp
LTK	leukocyte receptor tyrosine kinase	ENSG00000062524	PAP011	215	18.1%	chr15	39583851	CCDS10077.1	c.2327G>A	p.R776H
LIG3	ligase III; DNA; ATP-dependent	ENSG00000005156	PAP011	261	22.2%	chr17	30343758	CCDS11284.2	c.1389G>T	p.K463N
LHX5	LIM homeobox 5	ENSG00000089116	PAP011	195	10.8%	chr12	112393550	CCDS9171.1	c.137G>A	p.R46H
LIPT1	lipoyltransferase 1	ENSG00000144182	PAP011	87	11.5%	chr2	99145213	CCDS2039.1	c.361A>NULL	p.NULL-1FsDel1bp
LDLRAD2	low density lipoprotein receptor class A domain containing 2	ENSG00000187942	PAP011	154	15.6%	chr1	22013774	CCDS30624.1	c.382T>C	p.S128P
KDM5A	lysine (K)-specific demethylase 5A	ENSG00000073614	PAP011	301	15.0%	chr12	368529	ENST00000382815	c.224CCCCC>	p.NULL-1FsDel5bp
KDM5B	lysine (K)-specific demethylase 5B	ENSG00000117139	PAP011	48	22.9%	chr1	200977476	CCDS30974.1	c.-1T>NULL	p.IVS18-3-1SpliceAcceptor
LOXL2	lysyl oxidase-like 2	ENSG00000134013	PAP011	108	12.0%	chr8	23211550	CCDS34864.1	c.2355A>NULL	p.NULL-1FsDel1bp
LOXL3	lysyl oxidase-like 3	ENSG00000115318	PAP011	128	10.2%	chr2	74615364	CCDS1953.1	c.1625C>T	p.A542V
HLA-C	major histocompatibility complex; class I; C	ENSG00000204525	PAP011	59	16.9%	chr6	31346949	CCDS34393.1	c.499A>T	p.T167S
MAN2C1	mannosidase; alpha; class 2C; member 1	ENSG00000140400	PAP011	129	10.1%	chr15	73436220	CCDS32298.1	c.2624C>T	p.A875V

MGAT4B	mannosyl (alpha-1;3-)-glycoprotein beta-1;4-N-acetylglucosaminyltransferase; isozyme B	ENSG00000161013	PAP011	404	12.6%	chr5	179158865	CCDS4449.1	c.1138C>A	p.L380I
MARK4	MAP/microtubule affinity-regulating kinase 4	ENSG00000007047	PAP011	57	40.4%	chr19	50466798	CCDS12658.1	c.778A>G	p.N260D
MXRA5	matrix-remodelling associated 5	ENSG00000101825	PAP011	269	31.6%	chrX	3245658	CCDS14124.1	c.6064G>A	p.V2022I
MDN1	MDN1; midasin homolog (yeast)	ENSG00000112159	PAP011	127	15.0%	chr6	90561053	CCDS5024.1	c.741GT>NUL	p.NULL-1FsDel2bp
MED25	mediator complex subunit 25	ENSG00000104973	PAP011	281	11.4%	chr19	55014244	CCDS33075.1	c.184G>NULL	p.NULL-1FsDel1bp
MRAP2	melanocortin 2 receptor accessory protein 2	ENSG00000135324	PAP011	87	11.5%	chr6	84829384	CCDS5001.1	c.181NULL>T	p.NULL-1FsIns1bp
MAGEB5	melanoma antigen family B; 5	ENSG00000188408	PAP011	120	13.3%	chrX	26145695	ENST00000379029	c.356G>A	p.G119E
MAGEF1	melanoma antigen family F; 1	ENSG00000177383	PAP011	512	12.3%	chr3	185912021	CCDS3269.1	c.1204AGA>N	p.NULL-1FsDel3bp
MTA1	metastasis associated 1	ENSG00000182979	PAP011	340	13.5%	chr14	105007282	CCDS32169.1	c.1905C>NUL	p.NULL-1FsDel1bp
MBD6	methyl-CpG binding domain protein 6	ENSG00000166987	PAP011	249	24.1%	chr12	56205964	CCDS8944.1	c.946NULL>C	p.NULL-1FsIns1bp
METTL3	methyltransferase like 3	ENSG00000165819	PAP011	262	31.7%	chr14	21041242	CCDS32044.1	c.637T>C	p.S213P
MEX3B	mex-3 homolog B (C. elegans)	ENSG00000183496	PAP011	339	10.9%	chr15	80123236	CCDS10319.1	c.1030G>A	p.A344T
MFN2	mitofusin 2	ENSG00000116688	PAP011	234	33.8%	chr1	11987545	CCDS30587.1	c.1469T>C	p.L490P
MEGF6	multiple EGF-like-domains 6	ENSG00000162591	PAP011	190	10.0%	chr1	3402314	CCDS41237.1	c.3871G>T	p.G1291C
MUTED	muted homolog (mouse)	ENSG00000188428	PAP011	230	12.6%	chr6	7828444	CCDS4505.1	c.1231C>T	p.H411Y
MSH2	mutS homolog 2; colon cancer; nonpolyposis type 1 (E. coli)	ENSG00000095002	PAP011	39	35.9%	chr2	47557015	CCDS1834.1	c.2011A>T	p.N671Y
MEF2D	myocyte enhancer factor 2D	ENSG00000116604	PAP011	206	10.7%	chr1	154705416	CCDS1143.1	c.1027G>T	p.E343X
MYRIP	myosin VIIA and Rab interacting protein	ENSG00000170011	PAP011	446	16.6%	chr3	40206383	CCDS2689.1	c.1090C>NUL	p.NULL-1FsDel1bp
MTMR7	myotubularin related protein 7	ENSG00000003987	PAP011	56	37.5%	chr8	17272959	CCDS34851.1	c.268T>C	p.C90R
MARCKS	myristoylated alanine-rich protein kinase C substrate	ENSG00000155130	PAP011	184	19.0%	chr6	114287903	CCDS5101.1	c.454A>NULL	p.NULL-1FsDel1bp
ASAH2	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2	ENSG00000188611	PAP011	174	16.7%	chr10	51673057	CCDS7239.1	c.364G>A	p.A122T
NDUFC2	NADH dehydrogenase (ubiquinone) 1; subcomplex unknown; 2; 14.5kDa	ENSG00000151366	PAP011	100	13.0%	chr11	77461795	CCDS8257.1	c.350T>NULL	p.NULL-1FsDel1bp
NAPSB	napsin B aspartic peptidase pseudogene	ENSG00000131401	PAP011	384	18.0%	chr19	55530025	ENST00000253720	c.809G>A	p.R270Q
NCKAP1L	NCK-associated protein 1-like	ENSG00000123338	PAP011	138	10.1%	chr12	53197605	CCDS31813.1	c.1117C>A	p.L373M
NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	ENSG00000070614	PAP011	162	11.7%	chr5	149881161	CCDS34277.1	c.152C>NULL	p.NULL-1FsDel1bp
NTN4	netrin 4	ENSG00000074527	PAP011	175	10.3%	chr12	94704997	CCDS9054.1	c.436C>T	p.R146C
NEDD9	neural precursor cell expressed; developmentally down-regulated 9	ENSG00000111859	PAP011	195	25.1%	chr6	11321501	CCDS4520.1	c.904A>NULL	p.NULL-1FsDel1bp
NEURL1B	neuralized homolog 1B (Drosophila)	ENSG00000214357	PAP011	111	12.6%	chr5	172029630	NM_001142651	c.269G>A	p.R90H
NRXN3	neurexin 3	ENSG00000021645	PAP011	366	11.2%	chr14	78245584	CCDS9870.1	c.374G>A	p.R125Q
NLGN4X	neuroligin 4; X-linked	ENSG00000146938	PAP011	167	12.6%	chrX	5831806	CCDS14126.1	c.913G>A	p.G305S
NIN	ninein (GSK3B interacting protein)	ENSG00000100503	PAP011	349	19.2%	chr14	50294906	CCDS41952.1	c.2592G>T	p.E864D
NIN	ninein (GSK3B interacting protein)	ENSG00000100503	PAP011	108	11.1%	chr14	50306964	CCDS41952.1	c.1499AG>NU	p.NULL-1FsDel2bp
NIN	ninein (GSK3B interacting protein)	ENSG00000100503	PAP011	103	28.2%	chr14	50306986	CCDS41952.1	c.1478A>NUL	p.NULL-1FsDel1bp
NOSIP	nitric oxide synthase interacting protein	ENSG00000142546	PAP011	245	11.4%	chr19	54754024	CCDS12772.1	c.200G>A	p.R67H
NLRX1	NLR family member X1	ENSG00000160703	PAP011	133	11.3%	chr11	118547345	CCDS8416.1	c.23C>A	p.P8H
NLRP12	NLR family; pyrin domain containing 12	ENSG00000142405	PAP011	148	22.3%	chr19	59002616	CCDS12864.1	c.2358G>NUL	p.NULL-1FsDel1bp
NONO	non-POU domain containing; octamer-binding	ENSG00000147140	PAP011	103	10.7%	chrX	70434472	CCDS14410.1	c.1090C>T	p.R364W
NOTCH2	Notch homolog 2 (Drosophila)	ENSG00000134250	PAP011	273	10.3%	chr1	120292707	CCDS908.1	c.2605C>T	p.R869W
NOTCH2NL	Notch homolog 2 (Drosophila) N-terminal like	ENSG00000213240	PAP011	163	12.9%	chr1	143920548	ENST00000362074	c.86G>C	p.R29P

NASP	nuclear autoantigenic sperm protein (histone-binding)	ENSG00000132780	PAP011	76	28.9%	chr1	45854927	CCDS526.1	c.2128T>C	p.C710R
NFATC2IP	nuclear factor of activated T-cells; cytoplasmic; calcineurin-dependent 2 interacting protein	ENSG00000176953	PAP011	183	21.3%	chr16	28882579	CCDS10645.1	c.1154C>T	p.S385L
NCOA5	nuclear receptor coactivator 5	ENSG00000124160	PAP011	187	14.4%	chr20	44125700	CCDS13392.1	c.856G>A	p.A286T
NCOR2	nuclear receptor co-repressor 2	ENSG00000196498	PAP011	128	43.0%	chr12	123405009	CCDS41858.1	c.3578T>C	p.V1193A
NRIP1	nuclear receptor interacting protein 1	ENSG00000180530	PAP011	108	19.4%	chr21	15260201	CCDS13568.1	c.5660A>NULL	p.NULL-1FsDel1bp
NULL	NULL	ENSG00000154251	PAP011	57	29.8%	chr17	63634505	ENST00000284414	c.194A>G	p.Q65R
NULL	NULL	ENSG00000206061	PAP011	114	17.5%	chr16	1602736	ENST00000293924	c.512C>NULL	p.NULL-1FsDel1bp
NULL	NULL	ENSG00000214279	PAP011	116	19.0%	chr10	135123609	ENST00000356567	c.1312G>A	p.G438R
NULL	NULL	ENSG00000214894	PAP011	160	15.0%	chr6	30890271	ENST00000399196	c.665GAA>NU	p.NULL-1FsDel3bp
NULL	NULL	MI0006384	PAP011	98	34.7%	chr22	43975500	MI0006384	c.65T>C	p.L22P
OLAH	oleoyl-ACP hydrolase	ENSG00000152463	PAP011	92	17.4%	chr10	15138979	CCDS7106.1	c.314T>NULL	p.NULL-1FsDel1bp
OR11L1	olfactory receptor; family 11; subfamily L; member 1	ENSG00000197591	PAP011	58	24.1%	chr1	246071186	CCDS31098.1	c.1604NULL>T	p.NULL-1FsIns1bp
OR14C36	olfactory receptor; family 14; subfamily C; member 36	ENSG00000177174	PAP011	207	12.6%	chr1	246578864	CCDS31112.1	c.165G>A	p.M55I
OR14I1	olfactory receptor; family 14; subfamily I; member 1	ENSG00000189181	PAP011	75	16.0%	chr1	246912020	CCDS31125.1	c.209G>C	p.C70S
OR4Q3	olfactory receptor; family 4; subfamily Q; member 3	ENSG00000182652	PAP011	65	40.0%	chr14	19285977	CCDS32020.1	c.551A>G	p.Q184R
OR5L2	olfactory receptor; family 5; subfamily L; member 2	ENSG00000205030	PAP011	71	14.1%	chr11	55352199	CCDS31511.1	c.929A>G	p.H310R
OR52B6	olfactory receptor; family 52; subfamily B; member 6	ENSG00000187747	PAP011	449	26.5%	chr11	5559122	CCDS41611.1	c.440C>NULL	p.NULL-1FsDel1bp
OS9	osteosarcoma amplified 9; endoplasmic reticulum lectin	ENSG00000135506	PAP011	92	18.5%	chr12	56400838	CCDS31843.1	c.1883C>T	p.P628L
OGDHL	oxoglutarate dehydrogenase-like	ENSG00000197444	PAP011	78	56.4%	chr10	50634838	CCDS7234.1	c.365G>A	p.R122Q
POR	P450 (cytochrome) oxidoreductase	ENSG00000127948	PAP011	232	19.0%	chr7	75448817	CCDS5579.1	c.688G>A	p.V230M
PAX4	paired box 4	ENSG00000106331	PAP011	55	21.8%	chr7	127038969	CCDS5797.1	c.-1T>NULL	p.IVS7-3-1SpliceAcceptor
PAPLN	papilin; proteoglycan-like sulfated glycoprotein	ENSG00000100767	PAP011	140	13.6%	chr14	72781180	CCDS32114.1	c.130G>T	p.G44W
PTCHD3	patched domain containing 3	ENSG00000182077	PAP011	151	23.8%	chr10	27742957	NM_001034842	c.1317C>NULL	p.NULL-1FsDel1bp
PDZD2	PDZ domain containing 2	ENSG00000133401	PAP011	307	29.6%	chr5	32126025	CCDS34137.1	c.6714C>NULL	p.NULL-1FsDel1bp
PAMR1	peptidase domain containing associated with muscle regeneration 1	ENSG00000149090	PAP011	284	18.3%	chr11	35470246	CCDS7898.1	c.430G>NULL	p.NULL-1FsDel1bp
PRX	periaxin	ENSG00000105227	PAP011	92	16.3%	chr19	45595237	CCDS33028.1	c.862G>A	p.V288M
PEX19	peroxisomal biogenesis factor 19	ENSG00000162735	PAP011	125	16.0%	chr1	158519973	CCDS1201.1	c.260C>NULL	p.NULL-1FsDel1bp
PHF16	PHD finger protein 16	ENSG00000102221	PAP011	76	26.3%	chrX	46778037	CCDS14271.1	c.758C>T	p.P253L
PHF17	PHD finger protein 17	ENSG00000077684	PAP011	227	37.9%	chr4	130002467	CCDS34062.1	c.1140G>NUL	p.NULL-1FsDel1bp
PHF23	PHD finger protein 23	ENSG00000040633	PAP011	136	17.6%	chr17	7079693	CCDS42250.1	c.1402G>NUL	p.NULL-1FsDel1bp
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP011	117	47.9%	chr10	89682872	CCDS31238.1	c.376G>NULL	p.NULL-1FsDel1bp
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP011	119	53.8%	chr10	89682873	CCDS31238.1	c.377C>T	p.A126V
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP011	116	48.3%	chr10	89682876	CCDS31238.1	c.380G>T	p.G127V
PI4KB	phosphatidylinositol 4-kinase; catalytic; beta	ENSG00000143393	PAP011	139	33.8%	chr1	149541352	CCDS993.1	c.1603C>T	p.R535X
PIGA	phosphatidylinositol glycan anchor biosynthesis; class A	ENSG00000165195	PAP011	221	18.6%	chrX	15249745	CCDS14165.1	c.1259G>A	p.C420Y
PITPNM1	phosphatidylinositol transfer protein; membrane-associated 1	ENSG00000110697	PAP011	269	31.6%	chr11	67026440	CCDS31620.1	c.314A>C	p.E105A
PIP4K2B	phosphatidylinositol-5-phosphate 4-kinase; type II; beta	ENSG00000141720	PAP011	113	31.0%	chr17	34187465	CCDS11329.1	c.-1G>A	p.IVS7+1-1SpliceDonor

PTDSS2	phosphatidylserine synthase 2	ENSG00000174915	PAP011	122	18.0%	chr11	480526	CCDS7696.1	c.1408G>A	p.E470K
PFKL	phosphofructokinase; liver	ENSG00000141959	PAP011	242	12.4%	chr21	44568867	CCDS33582.1	c.1716G>NUL	p.NULL-1FsDel1bp
PFKP	phosphofructokinase; platelet	ENSG00000067057	PAP011	53	34.0%	chr10	3166744	CCDS7059.1	c.2092A>G	p.T698A
PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	ENSG00000155629	PAP011	188	11.7%	chr10	98459327	CCDS31259.1	c.833NULL>A	p.NULL-1FsIns1bp
PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP011	130	14.6%	chr3	180399599	CCDS43171.1	c.292T>C	p.F98L
PIK3R1	phosphoinositide-3-kinase; regulatory subunit 1 (alpha)	ENSG00000145675	PAP011	153	30.1%	chr5	67624728	CCDS3993.1	c.1063NULL>T	p.NULL-1FsIns1bp
PLCB2	phospholipase C; beta 2	ENSG00000137841	PAP011	412	10.9%	chr15	38376085	CCDS42020.1	c.1529T>A	p.V510E
PABPC3	poly(A) binding protein; cytoplasmic 3	ENSG00000151846	PAP011	199	22.6%	chr13	24569588	CCDS9311.1	c.1252C>T	p.P418S
PKD1L2	polycystic kidney disease 1-like 2	ENSG00000166473	PAP011	86	24.4%	chr16	79732437	ENST00000299598	c.5615G>NUL	p.NULL-1FsDel1bp
POLR2F	polymerase (RNA) II (DNA directed) polypeptide F	ENSG00000100142	PAP011	132	34.8%	chr22	36685399	CCDS13963.1	c.191G>A	p.R64H
KCNRG	potassium channel regulator	ENSG00000198553	PAP011	229	15.7%	chr13	49487993	CCDS9424.1	c.363NULL>T	p.NULL-1FsIns1bp
KCNN4	potassium intermediate/small conductance calcium-activated channel; subfamily N; member 4	ENSG00000104783	PAP011	270	13.3%	chr19	48970391	CCDS12630.1	c.476G>A	p.R159H
KCNMA1	potassium large conductance calcium-activated channel; subfamily M; alpha member 1	ENSG00000156113	PAP011	213	11.7%	chr10	78321365	CCDS7352.1	c.3286C>NULL	p.NULL-1FsDel1bp
KCNQ3	potassium voltage-gated channel; KQT-like subfamily; member 3	ENSG00000184156	PAP011	188	13.8%	chr8	133561658	CCDS34943.1	c.304G>A	p.A102T
KCNB1	potassium voltage-gated channel; Shab-related subfamily; member 1	ENSG00000158445	PAP011	312	23.1%	chr20	47423298	CCDS13418.1	c.4215NULL>C	p.NULL-1FsIns1bp
KCNH2	potassium voltage-gated channel; subfamily H (eag-related); member 2	ENSG00000055118	PAP011	172	11.0%	chr7	150273436	CCDS5910.1	c.3579G>NUL	p.NULL-1FsDel1bp
KCNH2	potassium voltage-gated channel; subfamily H (eag-related); member 2	ENSG00000055118	PAP011	230	14.3%	chr7	150278296	CCDS5910.1	c.2291C>T	p.P764L
PCOLCE	procollagen C-endopeptidase enhancer	ENSG00000106333	PAP011	101	15.8%	chr7	100043350	CCDS5700.1	c.1167C>NULL	p.NULL-1FsDel1bp
PLOD2	procollagen-lysine; 2-oxoglutarate 5-dioxygenase 2	ENSG00000152952	PAP011	71	16.9%	chr3	147310880	CCDS3132.1	c.547A>NULL	p.NULL-1FsDel1bp
PDCD1LG2	programmed cell death 1 ligand 2	ENSG00000197646	PAP011	268	28.0%	chr9	5539526	CCDS6465.1	c.553C>NULL	p.NULL-1FsDel1bp
PDCD11	programmed cell death 11	ENSG00000148843	PAP011	128	43.8%	chr10	105190309	CCDS31276.1	c.4421G>A	p.R1474Q
PRR11	proline rich 11	ENSG00000068489	PAP011	187	10.7%	chr17	54601953	CCDS11614.1	c.58A>NULL	p.NULL-1FsDel1bp
PML	promyelocytic leukemia	ENSG00000140464	PAP011	342	30.4%	chr15	72123902	CCDS10255.1	c.2149C>T	p.R717C
PSMB11	proteasome (prosome; macropain) subunit; beta type; 11	ENSG00000222028	PAP011	247	13.0%	chr14	22582010	CCDS41923.1	c.736G>A	p.V246M
PTPRA	protein tyrosine phosphatase; receptor type; A	ENSG00000132670	PAP011	189	25.9%	chr20	2950072	CCDS13038.1	c.1159C>T	p.Q387X
PTPRE	protein tyrosine phosphatase; receptor type; E	ENSG00000132334	PAP011	182	14.8%	chr10	129756382	CCDS7657.1	c.849C>NULL	p.NULL-1FsDel1bp
PTPRS	protein tyrosine phosphatase; receptor type; S	ENSG00000105426	PAP011	277	31.8%	chr19	5165699	CCDS12140.1	c.4253G>A	p.R1418Q
PCDHA5	protocadherin alpha 5	ENSG00000204965	PAP011	65	24.6%	chr5	140182212	CCDS34250.1	c.668G>A	p.G223D
PTK2B	PTK2B protein tyrosine kinase 2 beta	ENSG00000120899	PAP011	274	27.7%	chr8	27364956	ENST00000397497	c.1673G>A	p.R558H
PPFIBP2	PTPRF interacting protein; binding protein 2 (liprin beta 2)	ENSG00000166387	PAP011	73	31.5%	chr11	7626952	CCDS31419.1	c.-1A>G	p.IVS18-2-1SpliceAcceptor
PWWP2B	PWWP domain containing 2B	ENSG00000171813	PAP011	154	27.3%	chr10	134068982	CCDS7667.2	c.988C>NULL	p.NULL-1FsDel1bp
PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	ENSG00000131828	PAP011	26	46.2%	chrX	19273785	ENST00000379815	c.68CC>NULL	p.NULL-1FsDel2bp
PKM2	pyruvate kinase; muscle	ENSG00000067225	PAP011	191	13.1%	chr15	70281958	CCDS32284.1	c.1198C>T	p.R400C
RAB11FIP5	RAB11 family interacting protein 5 (class I)	ENSG00000135631	PAP011	283	13.1%	chr2	73156173	CCDS1923.1	c.2149C>NULL	p.NULL-1FsDel1bp

RAB35	RAB35; member RAS oncogene family	ENSG00000111737	PAP011	211	13.7%	chr12	119021333	CCDS41846.1	c.236G>A	p.R79Q
RAD50	RAD50 homolog (S. cerevisiae)	ENSG00000113522	PAP011	70	38.6%	chr5	131959351	CCDS34233.1	c.2157A>NULL	p.NULL-1FsDel1bp
RANBP6	RAN binding protein 6	ENSG00000137040	PAP011	45	26.7%	chr9	6004293	CCDS6467.1	c.1315G>A	p.A439T
RADIL	Ras association and DIL domains	ENSG00000157927	PAP011	172	20.9%	chr7	4841340	CCDS43544.1	c.1472C>NULL	p.NULL-1FsDel1bp
RASIP1	Ras interacting protein 1	ENSG00000105538	PAP011	89	16.9%	chr19	53934613	CCDS12731.1	c.924G>NULL	p.NULL-1FsDel1bp
RASAL3	RAS protein activator like 3	ENSG00000105122	PAP011	114	21.1%	chr19	15436174	ENST00000343625	c.422CC>NUL	p.NULL-1FsDel2bp
RGS18	regulator of G-protein signaling 18	ENSG00000150681	PAP011	86	16.3%	chr1	190420276	CCDS1374.1	c.677A>C	p.D226A
RXFP3	relaxin/insulin-like family peptide receptor 3	ENSG00000182631	PAP011	169	10.7%	chr5	33973971	CCDS3900.1	c.1369G>NUL	p.NULL-1FsDel1bp
RP1	retinitis pigmentosa 1 (autosomal dominant)	ENSG00000104237	PAP011	107	34.6%	chr8	55702290	CCDS6160.1	c.3295C>T	p.H1099Y
RP1L1	retinitis pigmentosa 1-like 1	ENSG00000183638	PAP011	203	36.5%	chr8	10506853	CCDS43708.1	c.2165C>A	p.P722H
REXO1	REX1; RNA exonuclease 1 homolog (S. cerevisiae)	ENSG00000079313	PAP011	171	11.7%	chr19	1778970	CCDS32866.1	c.2571NULL>/	p.NULL-1FsIns1bp
ARHGAP17	Rho GTPase activating protein 17	ENSG00000140750	PAP011	216	14.8%	chr16	24849681	CCDS32409.1	c.3060C>NULL	p.NULL-1FsDel1bp
ARHGAP30	Rho GTPase activating protein 30	ENSG00000186517	PAP011	504	11.7%	chr1	159285315	CCDS30918.1	c.3738GA>NU	p.NULL-1FsDel2bp
ARHGAP5	Rho GTPase activating protein 5	ENSG00000100852	PAP011	66	18.2%	chr14	31632296	CCDS32062.1	c.2670NULL>T	p.NULL-1FsIns1bp
RTKN2	rhotekin 2	ENSG00000182010	PAP011	52	19.2%	chr10	63628155	CCDS7263.1	c.1883A>NULL	p.NULL-1FsDel1bp
RHOXF1	Rhox homeobox family; member 1	ENSG00000101883	PAP011	289	32.5%	chrX	119133716	CCDS14593.1	c.482G>NULL	p.NULL-1FsDel1bp
RPN1	ribophorin I	ENSG00000163902	PAP011	75	29.3%	chr3	129833659	CCDS3051.1	c.665G>A	p.S222N
RPS6KA1	ribosomal protein S6 kinase; 90kDa; polypeptide 1	ENSG00000117676	PAP011	289	32.2%	chr1	26756080	CCDS30649.1	c.1013T>C	p.L338P
RPS6KA3	ribosomal protein S6 kinase; 90kDa; polypeptide 3	ENSG00000177189	PAP011	102	14.7%	chrX	20084192	CCDS14197.1	c.2056C>T	p.P686S
RC3H1	ring finger and CCCH-type zinc finger domains 1	ENSG00000135870	PAP011	65	29.2%	chr1	172206342	CCDS30940.1	c.1258C>T	p.R420X
RC3H2	ring finger and CCCH-type zinc finger domains 2	ENSG00000056586	PAP011	128	16.4%	chr9	124677305	ENST00000335387	c.1684T>NULL	p.NULL-1FsDel1bp
RNF111	ring finger protein 111	ENSG00000157450	PAP011	256	30.9%	chr15	57160511	CCDS10169.1	c.2033C>T	p.P678L
RNF128	ring finger protein 128	ENSG00000133135	PAP011	255	19.6%	chrX	105856909	CCDS14521.1	c.110NULL>G	p.NULL-1FsIns1bp
RNF213	ring finger protein 213	ENSG00000173821	PAP011	460	12.4%	chr17	75928614	CCDS32761.1	c.71C>NULL	p.NULL-1FsDel1bp
RNF31	ring finger protein 31	ENSG00000092098	PAP011	319	12.5%	chr14	23688586	CCDS41931.1	c.763C>T	p.R255C
RNF43	ring finger protein 43	ENSG00000108375	PAP011	339	33.6%	chr17	53790160	CCDS11607.1	c.3331G>NUL	p.NULL-1FsDel1bp
RNF43	ring finger protein 43	ENSG00000108375	PAP011	219	30.1%	chr17	53790688	CCDS11607.1	c.1448C>T	p.T483M
RNFT2	ring finger protein; transmembrane 2	ENSG00000135119	PAP011	324	17.0%	chr12	115672058	NM_001109903	c.113C>T	p.A38V
RIOK1	RIO kinase 1 (yeast)	ENSG00000124784	PAP011	89	27.0%	chr6	7359617	CCDS4500.1	c.1591A>NULL	p.NULL-1FsDel1bp
RBM33	RNA binding motif protein 33	ENSG00000184863	PAP011	136	35.3%	chr7	155230516	NM_053043	c.2438A>G	p.Q813R
RBMXL2	RNA binding motif protein; X-linked-like 2	ENSG00000170748	PAP011	160	11.3%	chr11	7067814	CCDS7777.1	c.887G>NULL	p.NULL-1FsDel1bp
RSBN1	round spermatid basic protein 1	ENSG00000081019	PAP011	82	22.0%	chr1	114141771	CCDS862.1	c.1114G>T	p.V372F
RUNX2	runt-related transcription factor 2	ENSG00000124813	PAP011	94	12.8%	chr6	45404424	CCDS43467.1	c.187A>NULL	p.NULL-1FsDel1bp
RYR1	ryanodine receptor 1 (skeletal)	ENSG00000196218	PAP011	173	16.2%	chr19	43656008	CCDS33011.1	c.3917C>T	p.A1306V
SAC3D1	SAC3 domain containing 1	ENSG00000168061	PAP011	178	12.4%	chr11	64568762	CCDS41668.1	c.1064G>T	p.G355V
SALL1	sal-like 1 (Drosophila)	ENSG00000103449	PAP011	269	29.4%	chr16	49730212	CCDS10747.1	c.3422A>G	p.K1141R
SFMBT2	Scm-like with four mbt domains 2	ENSG00000198879	PAP011	266	10.9%	chr10	7254564	CCDS31138.1	c.2050G>A	p.G684R

SCGB3A1	secretoglobin; family 3A; member 1	ENSG00000161055	PAP011	161	18.0%	chr5	179950214	CCDS4456.1	c.283G>A	p.A95T
SCG2	secretogranin II	ENSG00000171951	PAP011	179	12.3%	chr2	224171805	CCDS2457.1	c.440T>C	p.M147T
SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	ENSG00000182199	PAP011	219	32.9%	chr12	55913344	CCDS8934.1	c.972G>NULL	p.NULL-1FsDel1bp
SPINK5	serine peptidase inhibitor; Kazal type 5	ENSG00000133710	PAP011	71	14.1%	chr5	147480068	CCDS43382.1	c.2459NULL>A	p.NULL-1FsIns1bp
STK31	serine/threonine kinase 31	ENSG00000196335	PAP011	44	25.0%	chr7	23787650	CCDS5386.1	c.2053GA>NU	p.NULL-1FsDel2bp
SRFBP1	serum response factor binding protein 1	ENSG00000151304	PAP011	113	20.4%	chr5	121384029	CCDS43354.1	c.700A>NULL	p.NULL-1FsDel1bp
SH3PXD2A	SH3 and PX domains 2A	ENSG00000107957	PAP011	257	13.2%	chr10	105352121	CCDS31278.1	c.4733C>NULL	p.NULL-1FsDel1bp
SH3BP2	SH3-domain binding protein 2	ENSG00000087266	PAP011	202	20.3%	chr4	2801566	CCDS33944.1	c.1135NULL>C	p.NULL-1FsIns1bp
SIGLEC10	sialic acid binding Ig-like lectin 10	ENSG00000142512	PAP011	214	11.2%	chr19	56612169	CCDS12832.1	c.400G>T	p.G134W
SIGLEC12	sialic acid binding Ig-like lectin 12	ENSG00000142512	PAP011	214	11.2%	chr19	56612169	CCDS12832.1	c.400G>T	p.G134W
SOBP	sine oculis binding protein homolog (Drosophila)	ENSG00000112320	PAP011	136	33.1%	chr6	108062533	CCDS43488.1	c.1792C>NULL	p.NULL-1FsDel1bp
SLC10A2	solute carrier family 10 (sodium/bile acid cotransporter family); member 2	ENSG00000125255	PAP011	75	25.3%	chr13	102499664	CCDS9506.1	c.895G>A	p.A299T
SLC12A4	solute carrier family 12 (potassium/chloride transporters); member 4	ENSG00000124067	PAP011	243	14.8%	chr16	66549328	CCDS10855.1	c.463C>A	p.L155I
SLC16A3	solute carrier family 16; member 3 (monocarboxylic acid transporter 4)	ENSG00000141526	PAP011	366	19.9%	chr17	77788629	CCDS11804.1	c.694G>A	p.A232T
SLC2A4	solute carrier family 2 (facilitated glucose transporter); member 4	ENSG00000181856	PAP011	138	10.1%	chr17	7127297	CCDS11097.1	c.43C>NULL	p.NULL-1FsDel1bp
SLC22A17	solute carrier family 22; member 17	ENSG00000092096	PAP011	170	13.5%	chr14	22891073	CCDS9593.1	c.191C>T	p.P64L
SLC5A5	solute carrier family 5 (sodium iodide symporter); member 5	ENSG00000105641	PAP011	30	43.3%	chr19	17855662	CCDS12368.1	c.1333G>A	p.V445I
SLC6A12	solute carrier family 6 (neurotransmitter transporter; betaine/GABA); member 12	ENSG00000111181	PAP011	287	15.7%	chr12	176813	CCDS8501.1	c.1066G>A	p.A356T
SLC6A16	solute carrier family 6; member 16	ENSG00000063127	PAP011	105	30.5%	chr19	54489069	CCDS42590.1	c.1445T>C	p.L482P
SLCO5A1	solute carrier organic anion transporter family; member 5A1	ENSG00000137571	PAP011	276	12.3%	chr8	70747855	CCDS6205.1	c.2806AG>NU	p.NULL-1FsDel2bp
SORBS1	sorbin and SH3 domain containing 1	ENSG00000095637	PAP011	524	29.4%	chr10	97086504	CCDS31255.1	c.4176G>NUL	p.NULL-1FsDel1bp
SNX12	sorting nexin 12	ENSG00000147164	PAP011	90	26.7%	chrX	70197598	CCDS14405.1	c.482G>A	p.R161H
SNX13	sorting nexin 13	ENSG00000071189	PAP011	123	16.3%	chr7	17800366	NM_015132	c.2702A>G	p.N901S
SNX18	sorting nexin 18	ENSG00000178996	PAP011	253	10.7%	chr5	53850713	CCDS3962.1	c.1174C>T	p.Q392X
SP4	Sp4 transcription factor	ENSG00000105866	PAP011	199	11.6%	chr7	21435976	CCDS5373.1	c.668A>G	p.N223S
SP6	Sp6 transcription factor	ENSG00000189120	PAP011	185	37.8%	chr17	43279715	CCDS11520.1	c.2210C>NULL	p.NULL-1FsDel1bp
SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	ENSG00000151835	PAP011	62	27.4%	chr13	22813430	CCDS9300.1	c.2144C>T	p.P715L
SPG11	spastic paraplegia 11 (autosomal recessive)	ENSG00000104133	PAP011	175	32.6%	chr15	42646922	CCDS10112.1	c.6746A>G	p.Q2249R
SPG21	spastic paraplegia 21 (autosomal recessive; Mast syndrome)	ENSG00000090487	PAP011	47	36.2%	chr15	63048754	CCDS10198.1	c.-1A>G	p.IVS5-2-1SpliceAcceptor
SPTBN4	spectrin; beta; non-erythrocytic 4	ENSG00000160460	PAP011	107	26.2%	chr19	45685500	CCDS12559.1	c.226G>A	p.A76T
SPATA20	spermatogenesis associated 20	ENSG00000006282	PAP011	119	11.8%	chr17	45984376	CCDS11571.1	c.1793G>A	p.R598Q
SF3B3	splicing factor 3b; subunit 3; 130kDa	ENSG00000189091	PAP011	109	11.9%	chr16	69130560	CCDS10894.1	c.1016NULL>T	p.NULL-1FsIns2bp
SFRS14	splicing factor; arginine/serine-rich 14	ENSG00000064607	PAP011	332	12.3%	chr19	18997394	CCDS12392.1	c.2370NULL>A	p.NULL-1FsIns1bp
SFRS15	splicing factor; arginine/serine-rich 15	ENSG00000156304	PAP011	71	15.5%	chr21	31982546	CCDS33537.1	c.1988C>A	p.P663H
SFRS2	splicing factor; arginine/serine-rich 2	ENSG00000161547	PAP011	66	30.3%	chr17	72244818	CCDS11749.1	c.381C>NULL	p.NULL-1FsDel1bp

SHE	Src homology 2 domain containing E	ENSG00000169291	PAP011	118	25.4%	chr1	152723343	CCDS30877.1	c.1394C>A	p.P465H
SCAF1	SR-related CTD-associated factor 1	ENSG00000126461	PAP011	265	31.7%	chr19	54849854	CCDS33074.1	c.3533C>NULL	p.NULL-1FsDel1bp
SOX11	SRY (sex determining region Y)-box 11	ENSG00000176887	PAP011	165	16.4%	chr2	5750635	CCDS1654.1	c.331G>A	p.A111T
SOX14	SRY (sex determining region Y)-box 14	ENSG00000168875	PAP011	124	17.7%	chr3	138966789	CCDS3094.1	c.473C>G	p.T158S
SOX9	SRY (sex determining region Y)-box 9	ENSG00000125398	PAP011	181	14.4%	chr17	67631312	CCDS11689.1	c.719C>NULL	p.NULL-1FsDel1bp
SOX9	SRY (sex determining region Y)-box 9	ENSG00000125398	PAP011	223	33.6%	chr17	67631362	CCDS11689.1	c.769C>T	p.R257C
STAB1	stabilin 1	ENSG00000010327	PAP011	294	22.4%	chr3	52511692	CCDS33768.1	c.492C>G	p.C164W
STARD8	StAR-related lipid transfer (START) domain containing 8	ENSG00000130052	PAP011	150	16.7%	chrX	67854667	CCDS14390.1	c.946T>C	p.W316R
SAMD9L	sterile alpha motif domain containing 9-like	ENSG00000177409	PAP011	105	10.5%	chr7	92599956	CCDS34681.1	c.3265G>A	p.A1089T
SMC2	structural maintenance of chromosomes 2	ENSG00000136824	PAP011	29	37.9%	chr9	105902243	CCDS35086.1	c.529A>NULL	p.NULL-1FsDel1bp
SUCLG1	succinate-CoA ligase; alpha subunit	ENSG00000163541	PAP011	140	25.7%	chr2	84514007	CCDS1967.2	c.653T>C	p.L218S
SULT2B1	sulfotransferase family; cytosolic; 2B; member 1	ENSG00000088002	PAP011	247	14.6%	chr19	53782360	CCDS12723.1	c.277C>T	p.R93C
SAE1	SUMO1 activating enzyme subunit 1	ENSG00000142230	PAP011	80	30.0%	chr19	52398811	CCDS12696.1	c.922G>A	p.G308R
SYNGR1	synaptogyrin 1	ENSG00000100321	PAP011	68	17.6%	chr22	38076043	CCDS13989.1	c.82C>A	p.L28M
SYNJ2	synaptojanin 2	ENSG00000078269	PAP011	359	15.0%	chr6	158427997	CCDS5254.1	c.3331C>NULL	p.NULL-1FsDel1bp
SYCP1	synaptonemal complex protein 1	ENSG00000198765	PAP011	37	27.0%	chr1	115339124	CCDS879.1	c.2892A>NULL	p.NULL-1FsDel1bp
SYT1	synaptotagmin I	ENSG00000067715	PAP011	128	14.1%	chr12	78366931	CCDS9017.1	c.1165C>T	p.R389X
SYT10	synaptotagmin X	ENSG00000110975	PAP011	103	19.4%	chr12	33426674	CCDS8732.1	c.1418A>NULL	p.NULL-1FsDel1bp
SYT14L	synaptotagmin XIV-like	ENSG00000215127	PAP011	114	28.9%	chr4	68611096	ENST00000399639	c.326G>A	p.R109H
SNPH	syntaphilin	ENSG00000101298	PAP011	226	12.8%	chr20	1229273	CCDS13012.1	c.226C>A	p.L76M
TACR2	tachykinin receptor 2	ENSG00000075073	PAP011	263	31.6%	chr10	70844750	CCDS7293.1	c.544G>A	p.V182M
TAF1	TAF1 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 250kDa	ENSG00000147133	PAP011	153	15.7%	chrX	70519725	CCDS14412.1	c.1993A>NULL	p.NULL-1FsDel1bp
TAF15	TAF15 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 68kDa	ENSG00000172660	PAP011	197	31.0%	chr17	31160688	CCDS32623.1	c.2T>C	p.M1T
TARBP1	TAR (HIV-1) RNA binding protein 1	ENSG00000059588	PAP011	153	14.4%	chr1	232631961	CCDS1601.1	c.2695C>A	p.L899M
TAS1R2	taste receptor; type 1; member 2	ENSG00000179002	PAP011	235	11.9%	chr1	19039080	CCDS187.1	c.2120G>A	p.R707H
TAS2R1	taste receptor; type 2; member 1	ENSG00000169777	PAP011	476	16.2%	chr5	9682468	CCDS3876.1	c.677C>T	p.A226V
TAF1B	TATA box binding protein (TBP)-associated factor; RNA polymerase I; B; 63kDa	ENSG00000115750	PAP011	127	19.7%	chr2	9977239	CCDS33143.1	c.1404A>NULL	p.NULL-1FsDel1bp
TBC1D24	TBC1 domain family; member 24	ENSG00000162065	PAP011	364	22.8%	chr16	2486791	CCDS42107.1	c.641G>A	p.R214H
TBX19	T-box 19	ENSG00000143178	PAP011	469	14.5%	chr1	166548794	CCDS1272.1	c.1277C>T	p.S426L
TBX4	T-box 4	ENSG00000121075	PAP011	207	13.5%	chr17	56915127	CCDS11629.1	c.1106C>NULL	p.NULL-1FsDel1bp
TIAM1	T-cell lymphoma invasion and metastasis 1	ENSG00000156299	PAP011	337	11.3%	chr21	31511757	CCDS13609.1	c.2125C>T	p.R709W
TNS1	tensin 1	ENSG00000079308	PAP011	459	33.8%	chr2	218421158	CCDS2407.1	c.1952A>G	p.Q651R
TTC28	tetratricopeptide repeat domain 28	ENSG00000100154	PAP011	287	17.8%	chr22	26740340	NM_001145418	c.4257GT>NU	p.NULL-1FsDel2bp
TTC7A	tetratricopeptide repeat domain 7A	ENSG00000068724	PAP011	103	12.6%	chr2	47104944	CCDS33193.1	c.1583C>T	p.A528V
THRAP3	thyroid hormone receptor associated protein 3	ENSG00000054118	PAP011	74	32.4%	chr1	36534919	CCDS405.1	c.2264NULL>/	p.NULL-1FsIns1bp
TOP1	topoisomerase (DNA) I	ENSG00000198900	PAP011	51	19.6%	chr20	39138334	CCDS13312.1	c.265C>T	p.R89X
TOPORS	topoisomerase I binding; arginine/serine-rich	ENSG00000197579	PAP011	158	10.1%	chr9	32534069	CCDS6527.1	c.454G>A	p.V152M
TAAR2	trace amine associated receptor 2	ENSG00000146378	PAP011	114	10.5%	chr6	132980406	CCDS34541.1	c.632C>G	p.T211S
TCEB3	transcription elongation factor B (SIII); polypeptide 3 (110kDa; elongin A)	ENSG00000011007	PAP011	143	21.0%	chr1	23950446	CCDS239.1	c.764T>C	p.V255A
TCF4	transcription factor 4	ENSG00000196628	PAP011	114	21.1%	chr18	51072784	CCDS42438.1	c.1495G>NUL	p.NULL-1FsDel1bp

TAPT1	transmembrane anterior posterior transformation 1	ENSG00000169762	PAP011	52	21.2%	chr4	15799079	NM_153365	c.-1T>NULL	p.IVS4-3-1SpliceAcceptor
TMEM108	transmembrane protein 108	ENSG00000144868	PAP011	131	16.0%	chr3	134581714	CCDS33858.1	c.469C>NULL	p.NULL-1FsDel1bp
TMEM222	transmembrane protein 222	ENSG00000186501	PAP011	269	26.4%	chr1	27521324	CCDS297.2	c.49C>NULL	p.NULL-1FsDel1bp
TMEM51	transmembrane protein 51	ENSG00000171729	PAP011	215	14.4%	chr1	15418531	CCDS154.1	c.467TC>NUL	p.NULL-1FsDel2bp
TCHH	trichohyalin	ENSG00000159450	PAP011	308	28.6%	chr1	150347333	CCDS41396.1	c.4984C>T	p.R1662C
TRIM56	tripartite motif-containing 56	ENSG00000169871	PAP011	134	14.2%	chr7	100518646	CCDS43625.1	c.1333G>A	p.E445K
TPM1	tropomyosin 1 (alpha)	ENSG00000140416	PAP011	326	13.2%	chr15	61140158	CCDS10181.1	c.530A>G	p.E177G
TUBB2C	tubulin; beta 2C	ENSG00000188229	PAP011	86	34.9%	chr9	139257429	CCDS7039.1	c.938T>C	p.V313A
TUBB6	tubulin; beta 6	ENSG00000176014	PAP011	112	33.9%	chr18	12315614	CCDS11858.1	c.826C>T	p.R276C
TUBGCP6	tubulin; gamma complex associated protein 6	ENSG00000128159	PAP011	226	23.5%	chr22	48999084	CCDS14087.1	c.5044ATG>N	p.NULL-1FsDel3bp
TDRD3	tudor domain containing 3	ENSG00000083544	PAP011	52	19.2%	chr13	60000849	CCDS9441.1	c.1210NULL>A	p.NULL-1FsIns1bp
TP53I3	tumor protein p53 inducible protein 3	ENSG00000115129	PAP011	114	22.8%	chr2	24157298	CCDS1708.1	c.514G>A	p.A172T
TPCN1	two pore segment channel 1	ENSG00000186815	PAP011	184	16.8%	chr12	112214126	CCDS31908.1	c.2093G>A	p.R698H
TIE1	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	ENSG00000066056	PAP011	339	32.4%	chr1	43543396	CCDS482.1	c.346G>A	p.V116I
UBIAD1	UbiA prenyltransferase domain containing 1	ENSG00000120942	PAP011	186	21.0%	chr1	11256275	CCDS129.1	c.100C>T	p.Q34X
UBE3B	ubiquitin protein ligase E3B	ENSG00000151148	PAP011	164	37.2%	chr12	108405828	CCDS9129.1	c.89A>G	p.E30G
USP11	ubiquitin specific peptidase 11	ENSG00000102226	PAP011	75	37.3%	chrX	46991751	CCDS14277.1	c.2654G>A	p.R885H
UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog; yeast)	ENSG00000103275	PAP011	114	14.9%	chr16	1304365	CCDS10433.1	c.137C>T	p.P46L
VAX1	ventral anterior homeobox 1	ENSG00000148704	PAP011	335	27.8%	chr10	118886127	CCDS7597.1	c.275C>A	p.P92H
ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	ENSG00000065361	PAP011	227	30.8%	chr12	54765084	CCDS31833.1	c.273G>T	p.M91I
KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	ENSG00000133703	PAP011	74	21.6%	chr12	25289551	CCDS8703.1	c.35G>C	p.G12A
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	ENSG00000136997	PAP011	87	35.6%	chr8	128819862	ENST00000259523	c.172A>G	p.T58A
WDR33	WD repeat domain 33	ENSG00000136709	PAP011	226	11.1%	chr2	128193553	CCDS2150.1	c.3604C>NULL	p.NULL-1FsDel1bp
WRNIP1	Werner helicase interacting protein 1	ENSG00000124535	PAP011	419	21.7%	chr6	2715509	CCDS4475.1	c.1171C>T	p.R391X
WTIP	Wilms tumor 1 interacting protein	ENSG00000142279	PAP011	328	13.1%	chr19	39682919	NM_001080436	c.1198C>NULL	p.NULL-1FsDel1bp
WNT3	wingless-type MMTV integration site family; member 3	ENSG00000108379	PAP011	226	14.6%	chr17	42200961	CCDS11505.1	c.962C>T	p.T321M
WSCD1	WSC domain containing 1	ENSG00000179314	PAP011	210	28.6%	chr17	5964421	CCDS32538.1	c.1444G>A	p.G482R
XKR4	XK; Kell blood group complex subunit-related family; member 4	ENSG00000206579	PAP011	297	10.1%	chr8	56598459	CCDS34893.1	c.1072C>T	p.R358W
XYLT2	xylosyltransferase II	ENSG00000015532	PAP011	105	14.3%	chr17	45790674	CCDS11563.1	c.2049C>NULL	p.NULL-1FsDel1bp
ZIC2	Zic family member 2 (odd-paired homolog; Drosophila)	ENSG00000043355	PAP011	113	10.6%	chr13	99433009	CCDS9495.1	c.690CCA>NU	p.NULL-1FsDel3bp
ZBTB46	zinc finger and BTB domain containing 46	ENSG00000130584	PAP011	148	31.8%	chr20	61854527	CCDS13538.1	c.1354G>A	p.G452R
ZFHX3	zinc finger homeobox 3	ENSG00000140836	PAP011	634	10.9%	chr16	71387723	CCDS10908.1	c.6359C>A	p.P2120H
ZNF2	zinc finger protein 2	ENSG00000163067	PAP011	129	14.7%	chr2	95210748	CCDS42712.1	c.448C>A	p.L150I
ZNF202	zinc finger protein 202	ENSG00000166261	PAP011	248	14.9%	chr11	123102391	CCDS8443.1	c.1471C>T	p.R491C
ZNF365	zinc finger protein 365	ENSG00000138311	PAP011	112	21.4%	chr10	64052918	CCDS7264.1	c.1031G>A	p.C344Y
ZNF382	zinc finger protein 382	ENSG00000161298	PAP011	206	12.1%	chr19	41810016	CCDS33004.1	c.1377G>NUL	p.NULL-1FsDel1bp
ZNF408	zinc finger protein 408	ENSG00000175213	PAP011	309	13.3%	chr11	46683277	CCDS7923.1	c.1451G>T	p.R484L
ZNF471	zinc finger protein 471	ENSG00000196263	PAP011	65	16.9%	chr19	61728320	CCDS12945.1	c.1072A>T	p.N358Y
ZNF500	zinc finger protein 500	ENSG00000103199	PAP011	211	21.8%	chr16	4755730	CCDS32383.1	c.251G>A	p.R84H
ZNF596	zinc finger protein 596	ENSG00000172748	PAP011	101	30.7%	chr8	185245	CCDS5951.2	c.398A>G	p.Y133C

ZNF610	zinc finger protein 610	ENSG00000167554	PAP011	114	15.8%	chr19	57561437	CCDS12851.1	c.994A>G	p.T332A
ZNF628	zinc finger protein 628	ENSG00000197483	PAP011	256	17.6%	chr19	60684929	NM_033113	c.545C>T	p.T182M
ZNF804B	zinc finger protein 804B	ENSG00000182348	PAP011	120	16.7%	chr7	88800672	CCDS5613.1	c.440A>G	p.Q147R
ZBED4	zinc finger; BED-type containing 4	ENSG00000100426	PAP011	274	12.4%	chr22	48663683	CCDS33677.1	c.369T>NULL	p.NULL-1FsDel1bp
ZCCHC6	zinc finger; CCHC domain containing 6	ENSG00000083223	PAP011	86	23.3%	chr9	88106071	CCDS35057.1	c.4683GTT>N	p.NULL-1FsDel3bp
ZDHHC18	zinc finger; DHHC-type containing 18	ENSG00000204160	PAP011	275	17.1%	chr1	27031687	CCDS30650.1	c.-1T>C	p.IVS2+2-1SpliceDonor
Fat1	DAVID_FAT tumor suppressor homolog 1 (Drosophila)	NM_005245	PAP024	94	12.8%	chr4	187746945	NM_005245	c.13562C>T	p.P4521L
ZNF618	DAVID_zinc finger protein 618	NM_133374	PAP024	529	13.8%	chr9	115851370	NM_133374	c.1688G>A	p.R563H
INSR	insulin receptor	ENSG00000171105	PAP024	164	11.6%	chr19	7073746	CCDS12176.1	c.3408G>A	p.M1136I
ISX	intestine-specific homeobox	ENSG00000175329	PAP024	109	11.0%	chr22	33808538	CCDS33640.1	c.257G>A	p.R86H
OR4C6	olfactory receptor; family 4; subfamily C; member 6	ENSG00000181903	PAP024	165	14.5%	chr11	55189615	CCDS31506.1	c.397A>G	p.I133V
PCDHB2	protocadherin beta 2	ENSG00000112852	PAP024	118	11.0%	chr5	140454614	CCDS4244.1	c.56T>C	p.F19S
TMEM121	transmembrane protein 121	ENSG00000184986	PAP024	44	95.5%	chr14	105067095	CCDS10006.1	c.879GCC>NU	p.NULL-1FsDel3bp
OXCT1	3-oxoacid CoA transferase 1	ENSG00000083720	PAP026	45	26.7%	chr5	41889363	CCDS3937.1	c.329G>A	p.R110H
HTR3C	5-hydroxytryptamine (serotonin) receptor 3; family member C	ENSG00000178084	PAP026	312	30.4%	chr3	185255263	CCDS3250.1	c.128C>T	p.A43V
NT5DC2	5'-nucleotidase domain containing 2	ENSG00000168268	PAP026	165	33.3%	chr3	52533883	CCDS2858.1	c.1291C>T	p.Q431X
ABHD6	abhydrolase domain containing 6	ENSG00000163686	PAP026	55	27.3%	chr3	58231819	CCDS2887.1	c.511G>A	p.V171M
AIM1L	absent in melanoma 1-like	ENSG00000176092	PAP026	62	37.1%	chr1	26523348	CCDS30648.1	c.1642G>NUL	p.NULL-1FsDel1bp
AICDA	activation-induced cytidine deaminase	ENSG00000111732	PAP026	110	12.7%	chr12	8650828	CCDS41747.1	c.56G>A	p.R19H
ACVRL1	activin A receptor type II-like 1	ENSG00000139567	PAP026	62	29.0%	chr12	50595315	CCDS31804.1	c.812C>T	p.T271M
ACADVL	acyl-CoA dehydrogenase; very long chain	ENSG00000072778	PAP026	38	28.9%	chr17	7068532	CCDS11090.1	c.1615G>A	p.A539T
ADAM17	ADAM metallopeptidase domain 17	ENSG00000151694	PAP026	79	24.1%	chr2	9548694	CCDS1665.1	c.2169CT>NU	p.NULL-1FsDel2bp
ADAM21	ADAM metallopeptidase domain 21	ENSG00000139985	PAP026	33	36.4%	chr14	69994717	CCDS9804.1	c.748G>A	p.G250S
ADAM21	ADAM metallopeptidase domain 21	ENSG00000139985	PAP026	50	24.0%	chr14	69995173	CCDS9804.1	c.1204G>A	p.E402K
ADAM21P1	ADAM metallopeptidase domain 21 pseudogene 1	ENSG00000139985	PAP026	33	36.4%	chr14	69994717	CCDS9804.1	c.748G>A	p.G250S
ADAM21P1	ADAM metallopeptidase domain 21 pseudogene 1	ENSG00000139985	PAP026	50	24.0%	chr14	69995173	CCDS9804.1	c.1204G>A	p.E402K
ADAM32	ADAM metallopeptidase domain 32	ENSG00000197140	PAP026	48	31.3%	chr8	39187924	NM_145004	c.1157A>NULL	p.NULL-1FsDel1bp
ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)	ENSG00000168615	PAP026	33	30.3%	chr8	39048052	CCDS6112.1	c.1670G>A	p.G557D
ADAMTS18	ADAM metallopeptidase with thrombospondin type 1 motif; 18	ENSG00000140873	PAP026	94	27.7%	chr16	75913812	CCDS10926.1	c.2215T>NULL	p.NULL-1FsDel1bp
ADAMTSL2	ADAMTS-like 2	ENSG00000197859	PAP026	141	29.8%	chr9	135395668	CCDS6976.1	c.540C>A	p.C180X
AP3B1	adaptor-related protein complex 3; beta 1 subunit	ENSG00000132842	PAP026	46	23.9%	chr5	77599110	CCDS4041.1	c.194G>A	p.R65Q
ADAT1	adenosine deaminase; tRNA-specific 1	ENSG00000065457	PAP026	137	30.7%	chr16	74203802	CCDS10922.1	c.883C>T	p.R295C
ADCY5	adenylate cyclase 5	ENSG00000173175	PAP026	118	24.6%	chr3	124492805	CCDS3022.1	c.3172C>T	p.R1058C
ADRA1D	adrenergic; alpha-1D-; receptor	ENSG00000171873	PAP026	170	22.9%	chr20	4150315	CCDS13079.1	c.2181G>NUL	p.NULL-1FsDel1bp
ALDH3A1	aldehyde dehydrogenase 3 family; member A1	ENSG00000108602	PAP026	83	59.0%	chr17	19582241	CCDS11212.1	c.1464C>NUL	p.NULL-1FsDel1bp
ALPK2	alpha-kinase 2	ENSG00000198796	PAP026	103	12.6%	chr18	54300124	CCDS11966.2	c.6424C>T	p.Q2142X
AMELX	amelogenin; X-linked	ENSG00000125363	PAP026	217	31.8%	chrX	11226891	CCDS14145.1	c.489G>A	p.M163I
NPEPL1	aminopeptidase-like 1	ENSG00000215440	PAP026	121	39.7%	chr20	56702281	ENST00000356091	c.229G>T	p.A77S
AMMECR1L	AMME chromosomal region gene 1-like	ENSG00000144233	PAP026	31	51.6%	chr2	128343566	CCDS2152.1	c.656T>A	p.I219N
APBA3	amyloid beta (A4) precursor protein-binding; family A; member 3	ENSG00000011132	PAP026	44	22.7%	chr19	3704848	CCDS12110.1	c.926G>A	p.R309Q
APBB1	amyloid beta (A4) precursor protein-binding; family B; member 1 (Fe65)	ENSG00000166313	PAP026	92	40.2%	chr11	6373970	CCDS31410.1	c.1718G>A	p.R573H

ANGEL2	angel homolog 2 (Drosophila)	ENSG00000174606	PAP026	46	28.3%	chr1	211247065	ENST00000310246	c.796TTTT>NU	p.NULL-1FsDel4bp
AGTR1	angiotensin II receptor; type 1	ENSG00000144891	PAP026	204	28.4%	chr3	149941930	CCDS3137.1	c.418C>T	p.R140C
ANKRD26	ankyrin repeat domain 26	ENSG00000107890	PAP026	100	19.0%	chr10	27364244	CCDS41499.1	c.3141A>T	p.K1047N
APEX2	APEX nuclease (apurinic/apyrimidinic endonuclease) 2	ENSG00000169188	PAP026	116	24.1%	chrX	55050388	CCDS14365.1	c.1352T>C	p.L451S
ALOX12	arachidonate 12-lipoxygenase	ENSG00000108839	PAP026	85	30.6%	chr17	6854153	CCDS11084.1	c.1796G>A	p.R599H
ARMCX3	armadillo repeat containing; X-linked 3	ENSG00000102401	PAP026	75	14.7%	chrX	100766789	CCDS14489.1	c.164C>A	p.A55D
AHR	aryl hydrocarbon receptor	ENSG00000106546	PAP026	79	32.9%	chr7	17346280	CCDS5366.1	c.2306T>C	p.V769A
ASGR2	asialoglycoprotein receptor 2	ENSG00000161944	PAP026	185	28.1%	chr17	6945685	CCDS32544.1	c.869A>G	p.D290G
ATR	ataxia telangiectasia and Rad3 related	ENSG00000175054	PAP026	30	36.7%	chr3	143757430	CCDS3124.1	c.2582A>NULL	p.NULL-1FsDel1bp
ATXN1	ataxin 1	ENSG00000124788	PAP026	141	16.3%	chr6	16414726	CCDS34342.1	c.2261C>T	p.A754V
ATG2B	ATG2 autophagy related 2 homolog B (S. cerevisiae)	ENSG00000066739	PAP026	183	29.0%	chr14	95821925	CCDS9944.2	c.6157G>A	p.V2053M
ATP13A5	ATPase type 13A5	ENSG00000187527	PAP026	71	25.4%	chr3	194534343	CCDS33914.1	c.1319C>NULL	p.NULL-1FsDel1bp
ATP2B2	ATPase; Ca++ transporting; plasma membrane 2	ENSG00000157087	PAP026	328	30.5%	chr3	10362773	CCDS33701.1	c.2453C>T	p.T818M
ATP2B3	ATPase; Ca++ transporting; plasma membrane 3	ENSG00000067842	PAP026	210	30.0%	chrX	152460072	CCDS35440.1	c.270C>NULL	p.NULL-1FsDel1bp
ATP10A	ATPase; class V; type 10A	ENSG00000206190	PAP026	54	27.8%	chr15	23514561	CCDS32178.1	c.1442G>A	p.R481H
ATP6V1B1	ATPase; H+ transporting; lysosomal 56/58kDa; V1 subunit B1	ENSG00000116039	PAP026	120	30.8%	chr2	71041586	CCDS1912.1	c.613G>T	p.G205W
ATP4A	ATPase; H+/K+ exchanging; alpha polypeptide	ENSG00000105675	PAP026	146	26.7%	chr19	40742683	CCDS12467.1	c.920C>T	p.A307V
ABCC3	ATP-binding cassette; sub-family C (CFTR/MRP); member 3	ENSG00000108846	PAP026	175	30.9%	chr17	46115995	CCDS32681.1	c.3833G>A	p.R1278H
ABCC5	ATP-binding cassette; sub-family C (CFTR/MRP); member 5	ENSG00000114770	PAP026	70	28.6%	chr3	185147951	CCDS43176.1	c.3455T>NULL	p.NULL-1FsDel1bp
ABCC6	ATP-binding cassette; sub-family C (CFTR/MRP); member 6	ENSG00000091262	PAP026	81	12.3%	chr16	16180172	CCDS10568.1	c.2399G>T	p.G800V
ABCC9	ATP-binding cassette; sub-family C (CFTR/MRP); member 9	ENSG00000069431	PAP026	59	37.3%	chr12	21916932	CCDS8694.1	c.-1G>T	p.IVS15-1-1SpliceAcceptor
ATRIP	ATR interacting protein	ENSG00000164053	PAP026	122	33.6%	chr3	48481346	CCDS2768.1	c.2168C>T	p.T723M
ATRNL1	attractin-like 1	ENSG00000107518	PAP026	86	23.3%	chr10	117211474	CCDS7592.1	c.3356G>A	p.S1119N
AIDA	axin interactor; dorsalization associated	ENSG00000186063	PAP026	90	23.3%	chr1	220910171	CCDS1533.1	c.868A>NULL	p.NULL-1FsDel1bp
BHLHE22	basic helix-loop-helix family; member e22	ENSG00000180828	PAP026	57	26.3%	chr8	65656698	CCDS6179.1	c.797G>A	p.R266H
BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	ENSG00000119866	PAP026	88	35.2%	chr2	60542778	CCDS1862.1	c.773G>A	p.R258H
BCL9	B-cell CLL/lymphoma 9	ENSG00000116128	PAP026	159	26.4%	chr1	145562939	CCDS30833.1	c.3836A>C	p.E1279A
BCORL1	BCL6 co-repressor-like 1	ENSG00000085185	PAP026	107	27.1%	chrX	128996201	ENST00000303743	c.3208C>T	p.R1070X
BEND3	BEN domain containing 3	ENSG00000178409	PAP026	114	43.0%	chr6	107498295	CCDS34507.1	c.3039G>NUL	p.NULL-1FsDel1bp
BEST4	bestrophin 4	ENSG00000142959	PAP026	32	46.9%	chr1	45022486	CCDS514.1	c.1405G>A	p.E469K
BOD1L	biorientation of chromosomes in cell division 1-like	ENSG00000038219	PAP026	80	12.5%	chr4	13215719	CCDS3411.2	c.8041NULL>T	p.NULL-1FsIns1bp
BMP2K	BMP2 inducible kinase	ENSG00000138756	PAP026	68	33.8%	chr4	79966242	CCDS34019.1	c.206G>A	p.R69H
BRS3	bombesin-like receptor 3	ENSG00000102239	PAP026	192	10.4%	chrX	135401868	CCDS14656.1	c.868C>A	p.L290M
BAI3	brain-specific angiogenesis inhibitor 3	ENSG00000135298	PAP026	37	32.4%	chr6	70005744	CCDS4968.1	c.2719C>T	p.R907C
BRD1	bromodomain containing 1	ENSG00000100425	PAP026	51	43.1%	chr22	48577483	CCDS14080.1	c.2072C>T	p.P691L
BRD3	bromodomain containing 3	ENSG00000169925	PAP026	101	20.8%	chr9	135908350	CCDS6980.1	c.283NULL>C	p.NULL-1FsIns1bp
BRD3	bromodomain containing 3	ENSG00000169925	PAP026	101	38.6%	chr9	135908350	CCDS6980.1	c.283C>NULL	p.NULL-1FsDel1bp
BTBD7	BTB (POZ) domain containing 7	ENSG00000011114	PAP026	25	44.0%	chr14	92782204	CCDS32146.1	c.2764C>NULL	p.NULL-1FsDel1bp
BTNL8	butyrophilin-like 8	ENSG00000113303	PAP026	104	33.7%	chr5	180307186	CCDS43413.1	c.742T>NULL	p.NULL-1FsDel1bp

CELSR1	cadherin; EGF LAG seven-pass G-type receptor 1 (flamingo homolog; Drosophila)	ENSG00000075275	PAP026	204	21.1%	chr22	45309130	CCDS14076.1	c.2602G>A	p.G868S
CELSR2	cadherin; EGF LAG seven-pass G-type receptor 2 (flamingo homolog; Drosophila)	ENSG00000143126	PAP026	47	38.3%	chr1	109605399	CCDS796.1	c.4171C>A	p.L1391M
CABP5	calcium binding protein 5	ENSG00000105507	PAP026	26	42.3%	chr19	53229347	CCDS12709.1	c.580C>NULL	p.NULL-1FsDel1bp
CACNG7	calcium channel; voltage-dependent; gamma subunit 7	ENSG00000105605	PAP026	52	25.0%	chr19	59109611	CCDS12868.1	c.242C>T	p.P81L
CALHM3	calcium homeostasis modulator 3	ENSG00000183128	PAP026	65	16.9%	chr10	105226196	NM_001129742	c.388A>G	p.S130G
CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2; beta	ENSG00000110931	PAP026	86	32.6%	chr12	120172201	CCDS9216.1	c.1181G>A	p.R394Q
CAMSAP1L1	calmodulin regulated spectrin-associated protein 1-like 1	ENSG00000118200	PAP026	127	25.2%	chr1	199093643	CCDS1404.1	c.4270A>NULL	p.NULL-1FsDel1bp
CAPN2	calpain 2; (m/II) large subunit	ENSG00000162909	PAP026	115	21.7%	chr1	222001350	CCDS31035.1	c.589G>NULL	p.NULL-1FsDel1bp
CASC3	cancer susceptibility candidate 3	ENSG00000108349	PAP026	158	31.6%	chr17	35573417	CCDS11362.1	c.943C>T	p.R315X
CAD	carbamoyl-phosphate synthetase 2; aspartate transcarbamylase; and dihydroorotase	ENSG00000084774	PAP026	60	41.7%	chr2	27310477	CCDS1742.1	c.3497C>T	p.T1166M
CPM	carboxypeptidase M	ENSG00000135678	PAP026	81	24.7%	chr12	67536573	CCDS8987.1	c.1243C>A	p.L415I
CASS4	Cas scaffolding protein family member 4	ENSG00000087589	PAP026	228	29.4%	chr20	54460798	CCDS33492.1	c.1159C>T	p.R387W
CARD11	caspase recruitment domain family; member 11	ENSG00000198286	PAP026	37	29.7%	chr7	2934849	CCDS5336.2	c.1763C>NULL	p.NULL-1FsDel1bp
CARD11	caspase recruitment domain family; member 11	ENSG00000198286	PAP026	126	35.7%	chr7	2943360	CCDS5336.2	c.1178A>G	p.Y393C
CTSF	cathepsin F	ENSG00000174080	PAP026	93	30.1%	chr11	66090349	CCDS8144.1	c.710G>T	p.S237I
CATSPER3	cation channel; sperm associated 3	ENSG00000152705	PAP026	77	27.3%	chr5	134333568	CCDS4181.1	c.139A>G	p.I47V
CATSPER3	cation channel; sperm associated 3	ENSG00000152705	PAP026	132	28.0%	chr5	134371685	CCDS4181.1	c.632G>T	p.G211V
CATSPERB	cation channel; sperm-associated; beta	ENSG00000133962	PAP026	131	23.7%	chr14	91123327	CCDS32142.1	c.3104C>A	p.T1035N
CD163L1	CD163 molecule-like 1	ENSG00000177675	PAP026	40	27.5%	chr12	7412831	CCDS8577.1	c.-1TCTC>NU	p.IVS15-3-1SpliceAcceptor
CDC20B	cell division cycle 20 homolog B (S. cerevisiae)	ENSG00000164287	PAP026	54	35.2%	chr5	54478311	CCDS3966.1	c.257C>T	p.S86F
CDC7	cell division cycle 7 homolog (S. cerevisiae)	ENSG00000097046	PAP026	64	32.8%	chr1	91739945	CCDS734.1	c.84A>NULL	p.NULL-1FsDel1bp
CEP68	centrosomal protein 68kDa	ENSG00000011523	PAP026	290	27.6%	chr2	65153194	CCDS1880.2	c.1460C>T	p.A487V
CBLN3	cerebellin 3 precursor	ENSG00000139899	PAP026	105	32.4%	chr14	23967895	CCDS32057.1	c.505C>NULL	p.NULL-1FsDel1bp
CCRL2	chemokine (C-C motif) receptor-like 2	ENSG00000121797	PAP026	40	32.5%	chr3	46424785	CCDS43079.1	c.211C>T	p.R71C
CCKAR	cholecystokinin A receptor	ENSG00000163394	PAP026	239	29.3%	chr4	26092708	CCDS3438.1	c.937C>T	p.R313C
CHRM3	cholinergic receptor; muscarinic 3	ENSG00000133019	PAP026	181	19.9%	chr1	238139067	CCDS1616.1	c.1693A>NULL	p.NULL-1FsDel1bp
CHD2	chromodomain helicase DNA binding protein 2	ENSG00000173575	PAP026	72	31.9%	chr15	91281823	CCDS10374.2	c.515A>NULL	p.NULL-1FsDel1bp
CHD3	chromodomain helicase DNA binding protein 3	ENSG00000170004	PAP026	123	29.3%	chr17	7739520	CCDS32553.1	c.1777C>T	p.R593X
C1orf112	chromosome 1 open reading frame 112	ENSG00000000460	PAP026	711	21.9%	chr1	168063596	CCDS1285.1	c.1118C>T	p.T373M
C1orf89	chromosome 1 open reading frame 89	ENSG00000132881	PAP026	87	11.5%	chr1	16432085	CCDS171.1	c.280G>A	p.V94M
C10orf71	chromosome 10 open reading frame 71	ENSG00000177354	PAP026	69	23.2%	chr10	50203329	NM_001135196	c.2733G>T	p.Q911H
C11orf53	chromosome 11 open reading frame 53	ENSG00000150750	PAP026	68	29.4%	chr11	110660209	CCDS31674.1	c.206G>A	p.R69Q
C14orf37	chromosome 14 open reading frame 37	ENSG00000139971	PAP026	149	30.2%	chr14	57633445	CCDS32089.1	c.2094CAA>N	p.NULL-1FsDel3bp
C15orf53	chromosome 15 open reading frame 53	ENSG00000175779	PAP026	92	39.1%	chr15	36777883	CCDS10048.1	c.385G>A	p.V129M
C16orf53	chromosome 16 open reading frame 53	ENSG00000185928	PAP026	85	40.0%	chr16	29738498	CCDS10655.1	c.687C>A	p.D229E
C17orf70	chromosome 17 open reading frame 70	ENSG00000185504	PAP026	156	21.2%	chr17	77128007	CCDS32765.1	c.502G>T	p.G168C
C17orf99	chromosome 17 open reading frame 99	ENSG00000187997	PAP026	131	29.8%	chr17	73668693	NM_001163075	c.133G>A	p.V45M
C19orf51	chromosome 19 open reading frame 51	ENSG00000167646	PAP026	201	34.8%	chr19	60363818	CCDS12918.2	c.-1NULL>T	p.IVS9+2-1SpliceDonor
C19orf73	chromosome 19 open reading frame 73	ENSG00000221916	PAP026	44	31.8%	chr19	54313736	CCDS42589.1	c.356T>C	p.L119P
C2orf24	chromosome 2 open reading frame 24	ENSG00000115649	PAP026	253	35.2%	chr2	219745566	CCDS2433.1	c.1219G>A	p.V407I

C2orf67	chromosome 2 open reading frame 67	ENSG00000144445	PAP026	46	30.4%	chr2	210595925	CCDS33370.1	c.3187A>NULL	p.NULL-1FsDel1bp
C20orf112	chromosome 20 open reading frame 112	ENSG00000197183	PAP026	83	25.3%	chr20	30505183	CCDS13202.1	c.430G>A	p.E144K
C20orf117	chromosome 20 open reading frame 117	ENSG00000149639	PAP026	41	41.5%	chr20	34855117	NM_080627	c.6132NULL>(	p.NULL-1FsIns1bp
C20orf186	chromosome 20 open reading frame 186	ENSG00000186191	PAP026	110	24.5%	chr20	31134875	CCDS13213.1	c.94NULL>C	p.NULL-1FsIns1bp
C20orf96	chromosome 20 open reading frame 96	ENSG00000196476	PAP026	275	17.5%	chr20	212627	CCDS12994.1	c.283C>T	p.H95Y
C3orf36	chromosome 3 open reading frame 36	ENSG00000221972	PAP026	31	58.1%	chr3	135130008	CCDS3083.1	c.827NULL>G	p.NULL-1FsIns1bp
CHURC1	churchill domain containing 1	ENSG00000125954	PAP026	196	34.2%	chr14	64580831	CCDS9769.1	c.872G>T	p.R291L
CNTFR	ciliary neurotrophic factor receptor	ENSG00000122756	PAP026	98	18.4%	chr9	34542779	CCDS6558.1	c.842C>T	p.A281V
CSTF3	cleavage stimulation factor; 3' pre-RNA; subunit 3; 77kDa	ENSG00000176102	PAP026	59	20.3%	chr11	33081279	CCDS7883.1	c.690A>NULL	p.NULL-1FsDel1bp
COTL1	coactosin-like 1 (Dictyostelium)	ENSG00000103187	PAP026	121	24.0%	chr16	83181270	CCDS10947.1	c.260G>A	p.S87N
COCH	coagulation factor C homolog; cochlin (Limulus polyphemus)	ENSG00000100473	PAP026	47	34.0%	chr14	30419649	CCDS9640.1	c.587G>T	p.G196V
F8	coagulation factor VIII; procoagulant component	ENSG00000185010	PAP026	67	17.9%	chrX	153811322	CCDS35457.1	c.3937A>G	p.T1313A
CCHCR1	coiled-coil alpha-helical rod protein 1	ENSG00000204536	PAP026	138	36.2%	chr6	31219145	CCDS43445.1	c.2192G>A	p.R731H
CCDC103	coiled-coil domain containing 103	ENSG00000167131	PAP026	76	30.3%	chr17	40335341	CCDS11490.1	c.359A>G	p.Y120C
CCDC120	coiled-coil domain containing 120	ENSG00000147144	PAP026	52	36.5%	chrX	48812506	CCDS14316.1	c.1807G>A	p.G603R
CCDC8	coiled-coil domain containing 8	ENSG00000169515	PAP026	235	11.5%	chr19	51607849	CCDS12685.1	c.59C>T	p.A20V
COL1A1	collagen; type I; alpha 1	ENSG00000108821	PAP026	36	33.3%	chr17	45621554	CCDS11561.1	c.3018NULL>A	p.NULL-1FsIns2bp
COL4A3BP	collagen; type IV; alpha 3 (Goodpasture antigen) binding protein	ENSG00000113163	PAP026	62	38.7%	chr5	74758062	CCDS4028.1	c.-1TT>NULL	p.IVS3-3-1SpliceAcceptor
COL9A3	collagen; type IX; alpha 3	ENSG00000092758	PAP026	83	28.9%	chr20	60938120	CCDS13505.1	c.1538C>T	p.P513L
COL5A1	collagen; type V; alpha 1	ENSG00000130635	PAP026	163	30.1%	chr9	136732887	CCDS6982.1	c.541C>A	p.L181I
COL5A2	collagen; type V; alpha 2	ENSG00000204262	PAP026	80	36.3%	chr2	189683253	CCDS33350.1	c.265C>A	p.P89T
CNTN6	contactin 6	ENSG00000134115	PAP026	88	15.9%	chr3	1346501	CCDS2557.1	c.1246A>NULL	p.NULL-1FsDel1bp
COPS7A	COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis)	ENSG00000111652	PAP026	53	32.1%	chr12	6707706	CCDS8558.1	c.295C>A	p.L99I
CDSN	corneodesmosin	ENSG00000204539	PAP026	119	33.6%	chr6	31192958	CCDS34389.1	c.413G>A	p.S138N
CRP	C-reactive protein; pentraxin-related	ENSG00000132693	PAP026	103	18.4%	chr1	157950335	CCDS30911.1	c.892T>NULL	p.NULL-1FsDel1bp
CKMT2	creatine kinase; mitochondrial 2 (sarcomeric)	ENSG00000131730	PAP026	106	33.0%	chr5	80597768	CCDS4053.1	c.1195AAG>N	p.NULL-1FsDel3bp
CRYGS	crystallin; gamma S	ENSG00000213139	PAP026	48	39.6%	chr3	187739888	CCDS3275.1	c.214C>T	p.R72C
CSMD3	CUB and Sushi multiple domains 3	ENSG00000164796	PAP026	41	26.8%	chr8	113419001	CCDS6315.1	c.6788C>T	p.T2263I
CSMD3	CUB and Sushi multiple domains 3	ENSG00000164796	PAP026	30	33.3%	chr8	113598490	CCDS6315.1	c.4705A>G	p.I1569V
CUL5	cullin 5	ENSG00000166266	PAP026	103	30.1%	chr11	107470765	CCDS31668.1	c.1584A>NULL	p.NULL-1FsDel1bp
CXXC4	CXXC finger 4	ENSG00000168772	PAP026	44	36.4%	chr4	105631916	ENST00000394767	c.493G>A	p.G165S
CNGA4	cyclic nucleotide gated channel alpha 4	ENSG00000132259	PAP026	174	42.0%	chr11	6218045	CCDS31408.1	c.445C>T	p.R149C
CDKL2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	ENSG00000138769	PAP026	26	38.5%	chr4	76740504	CCDS3570.1	c.1367C>T	p.P456L
CYLC1	cylicin; basic protein of sperm head cytoskeleton 1	ENSG00000183035	PAP026	60	30.0%	chrX	83016218	CCDS35341.1	c.1846C>A	p.L616I
CYLC2	cylicin; basic protein of sperm head cytoskeleton 2	ENSG00000155833	PAP026	41	29.3%	chr9	104807145	CCDS35085.1	c.411A>NULL	p.NULL-1FsDel1bp
CCBL1	cysteine conjugate-beta lyase; cytoplasmic	ENSG00000171097	PAP026	43	32.6%	chr9	130642719	ENST00000372610	c.435AAA>NU	p.NULL-1FsDel3bp
CDO1	cysteine dioxygenase; type I	ENSG00000129596	PAP026	75	36.0%	chr5	115176857	CCDS4121.1	c.-1T>NULL	p.IVS1-3-1SpliceAcceptor

CYHR1	cysteine/histidine-rich 1	ENSG00000187954	PAP026	90	34.4%	chr8	145660467	CCDS6426.1	c.914GG>NUL	p.NULL-1FsDel2bp
CSRNP2	cysteine-serine-rich nuclear protein 2	ENSG00000110925	PAP026	249	28.1%	chr12	49747997	CCDS8807.1	c.434A>G	p.E145G
CYP11B2	cytochrome P450; family 11; subfamily B; polypeptide 2	ENSG00000179142	PAP026	125	33.6%	chr8	143995515	CCDS6393.1	c.357C>A	p.Y119X
CYP27A1	cytochrome P450; family 27; subfamily A; polypeptide 1	ENSG00000135929	PAP026	184	33.7%	chr2	219385312	CCDS2423.1	c.570C>A	p.D190E
CYP4F22	cytochrome P450; family 4; subfamily F; polypeptide 22	ENSG00000171954	PAP026	52	25.0%	chr19	15512382	CCDS12331.1	c.793C>T	p.R265W
CYP4X1	cytochrome P450; family 4; subfamily X; polypeptide 1	ENSG00000186377	PAP026	98	38.8%	chr1	47271548	CCDS544.1	c.413G>A	p.R138H
CYP7B1	cytochrome P450; family 7; subfamily B; polypeptide 1	ENSG00000172817	PAP026	38	34.2%	chr8	65679864	CCDS6180.1	c.1162C>T	p.R388X
CYTSA	cytospin A	ENSG00000100014	PAP026	76	28.9%	chr22	23047441	CCDS33619.1	c.493C>T	p.R165C
DCHS2	dachsous 2 (Drosophila)	ENSG00000197410	PAP026	137	35.8%	chr4	155631054	NM_001142552	c.904C>T	p.R302C
AP1S1	DAVID_adaptor-related protein complex 1: sigma 1 subunit	NM_001283	PAP026	59	25.4%	chr7	100589125	NM_001283	c.357G>NULL	p.NULL-1FsDel1bp
Ap2a2	DAVID_adaptor-related protein complex 2: alpha 2 subunit	NM_012305	PAP026	214	27.6%	chr11	960195	NM_012305	c.163A>NULL	p.NULL-1FsDel1bp
Asb14	DAVID_ankyrin repeat and SOCS box-containing 14	NM_001142733	PAP026	123	25.2%	chr3	57292288	NM_001142733	c.689A>G	p.E230G
BEST1	DAVID_bestrophin 1	NM_001139443	PAP026	187	29.9%	chr11	61487004	NM_001139443	c.1622CT>NU	p.NULL-1FsDel2bp
BRD2	DAVID_bromodomain containing 2	ENSG00000204256	PAP026	242	21.9%	chr6	33053947	CCDS4762.1	c.1645AG>NU	p.NULL-1FsDel2bp
CDH13	DAVID_cadherin 13: H-cadherin (heart)	NM_001257	PAP026	127	31.5%	chr16	81623302	NM_001257	c.344A>G	p.K115R
Cdh23	DAVID_cadherin-like 23	NM_022124	PAP026	113	31.9%	chr10	73142517	NM_022124	c.3310C>T	p.Q1104X
CES1	DAVID_carboxylesterase 1 (monocyte/macrophage serine esterase 1)	ENSG00000196959	PAP026	100	16.0%	chr16	54402426	CCDS32450.1	c.-1TT>NULL	p.IVS9-3-1SpliceAcceptor
C14orf38	DAVID_chromosome 14 open reading frame 38	NM_001164399	PAP026	45	28.9%	chr14	59061853	NM_001164399	c.2047NULL>A	p.NULL-1FsIns1bp
C4orf47	DAVID_chromosome 4 open reading frame 47	NM_001114357	PAP026	65	38.5%	chr4	186590300	NM_001114357	c.271A>NULL	p.NULL-1FsDel1bp
C6orf103	DAVID_chromosome 6 open reading frame 103	NM_024694	PAP026	121	15.7%	chr6	146961882	NM_024694	c.13C>T	p.Q5X
COPG2	DAVID_coatomer protein complex: subunit gamma 2	NM_012133	PAP026	95	32.6%	chr7	129934783	NM_012133	c.956A>G	p.Q319R
CC2D2A	DAVID_coiled-coil and C2 domain containing 2A	NM_001080522	PAP026	118	23.7%	chr4	15174140	NM_001080522	c.3079G>T	p.G1027C
CCDC153	DAVID_coiled-coil domain containing 153	NM_001145018	PAP026	261	14.9%	chr11	118569737	NM_001145018	c.324NULL>G	p.NULL-1FsIns1bp
CCDC154	DAVID_coiled-coil domain containing 154	NM_001143980	PAP026	103	25.2%	chr16	1426005	NM_001143980	c.1571G>A	p.R524Q
Col11a2	DAVID_collagen: type XI: alpha 2	ENSG00000204248	PAP026	238	39.1%	chr6	33241379	CCDS43452.1	c.4417C>T	p.R1473W
CNTNAP5	DAVID_contactin associated protein-like 5	NM_130773	PAP026	69	34.8%	chr2	124908637	NM_130773	c.636G>A	p.M212I
Dock6	DAVID_dedicator of cytokinesis 6	NM_020812	PAP026	75	36.0%	chr19	11188672	NM_020812	c.3812G>A	p.R1271H
dock9	DAVID_dedicator of cytokinesis 9	NM_001130049	PAP026	34	29.4%	chr13	98334157	NM_001130049	c.-1T>NULL	p.IVS21-3-1SpliceAcceptor
DNA2	DAVID_DNA replication helicase 2 homolog (yeast)	NM_001080449	PAP026	36	36.1%	chr10	69862079	NM_001080449	c.-1G>A	p.IVS11-1-1SpliceAcceptor
DNAH12	DAVID_dynein: axonemal: heavy chain 12	NM_178504	PAP026	80	28.8%	chr3	57364110	NM_178504	c.6857G>T	p.S2286I
DNAH17	DAVID_dynein: axonemal: heavy chain 17	NM_173628	PAP026	55	36.4%	chr17	74002498	NM_173628	c.-1G>T	p.IVS38-1-1SpliceAcceptor
DNAH17	DAVID_dynein: axonemal: heavy chain 17	NM_173628	PAP026	66	28.8%	chr17	74065858	NM_173628	c.2105G>A	p.S702N
EPPK1	DAVID_epiplakin 1	NM_031308	PAP026	106	29.2%	chr8	145019302	NM_031308	c.7370C>NULI	p.NULL-1FsDel1bp
EHMT2	DAVID_euchromatic histone-lysine N-methyltransferase 2	ENSG00000204371	PAP026	58	51.7%	chr6	31960441	CCDS4725.1	c.2717C>NULI	p.NULL-1FsDel1bp
c2cd4c	DAVID_family with sequence similarity 148: member C; hypothetical protein LOC100133882	NM_001136263	PAP026	71	47.9%	chr19	359112	NM_001136263	c.1515C>NULI	p.NULL-1FsDel1bp

LOC100133	DAVID_family with sequence similarity 148: member C; hypothetical protein LOC100133882	NM_001136263	PAP026	71	47.9%	chr19	359112	NM_001136263	c.1515C>NULL	p.NULL-1FsDel1bp
Fam186a	DAVID_family with sequence similarity 186: member A	NM_001145475	PAP026	105	22.9%	chr12	49034288	NM_001145475	c.8513A>NULL	p.NULL-1FsDel1bp
FAT3	DAVID_FAT tumor suppressor homolog 3 (Drosophila)	NM_001008781	PAP026	94	33.0%	chr11	91726742	NM_001008781	c.1816G>A	p.D606N
Fbxo41	DAVID_F-box protein 41	NM_001080410	PAP026	102	28.4%	chr2	73341480	NM_001080410	c.2369G>A	p.R790H
LOC399715	DAVID_FLJ46311 protein	ENSG00000215244	PAP026	47	36.2%	chr10	6410294	ENST00000399868	c.574C>A	p.R192S
FNIP2	DAVID_folliculin interacting protein 2	NM_020840	PAP026	99	33.3%	chr4	160009385	NM_020840	c.2147A>C	p.K716T
FYB	DAVID_FYN binding protein (FYB-120/130)	NM_001465	PAP026	100	14.0%	chr5	39237848	NM_001465	c.2106G>NUL	p.NULL-1FsDel1bp
BAT1	DAVID_HLA-B associated transcript 1	ENSG00000198563	PAP026	101	20.8%	chr6	31612425	CCDS4697.1	c.630T>NULL	p.NULL-1FsDel1bp
BAT2	DAVID_HLA-B associated transcript 2	ENSG00000204469	PAP026	293	32.8%	chr6	31712829	CCDS4708.1	c.6179A>G	p.D2060G
LOC100129	DAVID_hypothetical protein LOC100129697	ENSG00000205018	PAP026	49	30.6%	chr16	87545136	ENST00000378347	c.1109G>A	p.R370Q
INTS2	DAVID_integrator complex subunit 2	NM_020748	PAP026	101	24.8%	chr17	57343809	NM_020748	c.832G>A	p.G278S
ITGAM	DAVID_integrin: alpha M (complement component 3 receptor 3 subunit)	NM_001145808	PAP026	213	32.9%	chr16	31244389	NM_001145808	c.2576C>T	p.A859V
KPNA7	DAVID_karyopherin alpha 7 (importin alpha 8)	NM_001145715	PAP026	76	30.3%	chr7	98609270	NM_001145715	c.1634NULL>A	p.NULL-1FsIns1bp
KIAA1239	DAVID_KIAA1239	NM_001144990	PAP026	149	30.2%	chr4	37122361	NM_001144990	c.2356C>T	p.L786F
KIAA1731	DAVID_KIAA1731	NM_033395	PAP026	147	10.2%	chr11	93072765	NM_033395	c.5039NULL>C	p.NULL-1FsIns1bp
HEATR7A	DAVID_KIAA1833-like; HEAT repeat containing 7A	NM_032450	PAP026	53	39.6%	chr8	145307399	NM_032450	c.547G>A	p.V183M
LOC377711	DAVID_KIAA1833-like; HEAT repeat containing 7A	NM_032450	PAP026	53	39.6%	chr8	145307399	NM_032450	c.547G>A	p.V183M
Kif13a	DAVID_kinesin family member 13A	NM_022113	PAP026	29	48.3%	chr6	17896002	NM_022113	c.3444A>NULL	p.NULL-1FsDel1bp
LEFTY1	DAVID_left-right determination factor 1	ENSG00000143787	PAP026	50	28.0%	chr1	224141884	CCDS1548.1	c.575G>A	p.R192Q
lrp1	DAVID_low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	ENSG00000123384	PAP026	188	26.1%	chr12	55846990	CCDS8932.1	c.2808NULL>C	p.NULL-1FsIns1bp
Kdm4dl	DAVID_lysine (K)-specific demethylase 4D-like	NM_001161630	PAP026	63	27.0%	chr11	94398401	NM_001161630	c.32C>T	p.T11M
MGAM	DAVID_maltase-glucoamylase (alpha-glucosidase)	NM_004668	PAP026	184	28.8%	chr7	141384831	NM_004668	c.2263C>T	p.H755Y
MUC16	DAVID_mucin 16: cell surface associated	NM_024690	PAP026	145	20.7%	chr19	8925310	NM_024690	c.44828C>NUL	p.NULL-1FsDel1bp
MPDZ	DAVID_multiple PDZ domain protein	NM_003829	PAP026	48	27.1%	chr9	13102042	NM_003829	c.5618C>T	p.A1873V
MYT1L	DAVID_myelin transcription factor 1-like	NM_015025	PAP026	118	32.2%	chr2	1822066	NM_015025	c.2936C>T	p.A979V
MYT1L	DAVID_myelin transcription factor 1-like	NM_015025	PAP026	165	31.5%	chr2	1905370	NM_015025	c.1178C>T	p.S393L
ND1	DAVID_NADH-ubiquinone oxidoreductase chain 1	ENSG00000198888	PAP026	519	12.9%	chrM	3726	ENST00000361390	c.419T>G	p.I140S
Naca	DAVID_nascent polypeptide-associated complex alpha subunit	NM_001113203	PAP026	38	36.8%	chr12	55396757	NM_001113203	c.10410CCT>N	p.NULL-1FsDel3bp
NEB	DAVID_nebulin	NM_001164507	PAP026	49	28.6%	chr2	152133180	NM_001164507	c.-1TT>NULL	p.IVS109-3-1SpliceAcceptor
Nedd4l	DAVID_neural precursor cell expressed: developmentally down-regulated 4-like	NM_001144967	PAP026	40	30.0%	chr18	54141495	NM_001144967	c.462A>NULL	p.NULL-1FsDel1bp
nhsl1	DAVID_NHS-like 1	NM_020464	PAP026	158	38.0%	chr6	138795479	NM_020464	c.4995C>NULL	p.NULL-1FsDel1bp
obscn	DAVID_obscurin: cytoskeletal calmodulin and titin-interacting RhoGEF	NM_001098623	PAP026	188	23.4%	chr1	226538067	NM_001098623	c.8978A>G	p.Q2993R
Odz2	DAVID_odz: odd Oz/ten-m homolog 2 (Drosophila)	NM_001122679	PAP026	34	38.2%	chr5	166644598	NM_001122679	c.178C>T	p.R60X
ptch1	DAVID_patched homolog 1 (Drosophila)	NM_001083603	PAP026	272	31.3%	chr9	97318793	NM_001083603	c.131A>G	p.E44G
PRIC285	DAVID_peroxisomal proliferator-activated receptor A interacting complex 285	ENSG00000130589	PAP026	135	36.3%	chr20	61672639	CCDS33508.1	c.305C>T	p.A102V
Pla2g4e	DAVID_phospholipase A2: group IVE	NM_001080490	PAP026	31	38.7%	chr15	40082152	NM_001080490	c.514G>A	p.V172M
Pou5f2	DAVID_POU domain class 5: transcription factor 2	NM_153216	PAP026	29	34.5%	chr5	93102190	NM_153216	c.836G>T	p.G279V

PPP4R1L	DAVID_protein phosphatase 4: regulatory subunit 1-like	ENSG00000215443	PAP026	58	36.2%	chr20	56247761	ENST00000340003	c.763T>NULL	p.NULL-1FsDel1bp
PSORS1C1	DAVID_psoriasis susceptibility 1 candidate 1	ENSG00000204540	PAP026	255	27.8%	chr6	31214480	CCDS34390.1	c.112C>NULL	p.NULL-1FsDel1bp
RAPGEF1	DAVID_Rap guanine nucleotide exchange factor (GEF) 1	NM_198679	PAP026	82	14.6%	chr9	133453012	NM_198679	c.2755A>NULL	p.NULL-1FsDel1bp
RDBP	DAVID_RD RNA binding protein	ENSG00000204356	PAP026	354	31.6%	chr6	32034185	CCDS4730.1	c.92C>NULL	p.NULL-1FsDel1bp
RGAG4	DAVID_retrotransposon gag domain containing 4	NM_001024455	PAP026	59	33.9%	chrX	71267676	NM_001024455	c.440C>T	p.P147L
ARHGAP32	DAVID_Rho GTPase-activating protein	ENSG00000134909	PAP026	85	23.5%	chr11	128346180	CCDS31718.1	c.3049G>T	p.G1017C
RICH2	DAVID_Rho-type GTPase-activating protein RICH2	NM_014859	PAP026	78	32.1%	chr17	12793198	NM_014859	c.878C>NULL	p.NULL-1FsDel1bp
RUNDC3A	DAVID_RUN domain containing 3A	NM_001144825	PAP026	65	15.4%	chr17	39746095	NM_001144825	c.321C>A	p.N107K
RYR3	DAVID_ryanodine receptor 3	NM_001036	PAP026	121	24.8%	chr15	31629741	NM_001036	c.904G>T	p.G302C
srpk1	DAVID_SFRS protein kinase 1	NM_003137	PAP026	53	28.3%	chr6	35946198	NM_003137	c.829C>T	p.R277C
SHC2	DAVID_SHC (Src homology 2 domain containing) transforming protein 2	NM_012435	PAP026	95	14.7%	chr19	373187	NM_012435	c.1579G>A	p.G527R
LOC100130	DAVID_similar to hCG1646697	NM_001162914	PAP026	100	37.0%	chr8	144862077	NM_001162914	c.191G>A	p.R64H
SLC22A24	DAVID_solute carrier family 22: member 24	NM_001136506	PAP026	72	18.1%	chr11	62607401	NM_001136506	c.1175C>T	p.A392V
SPTBN5	DAVID_spectrin: beta: non-erythrocytic 5	NM_016642	PAP026	42	47.6%	chr15	39933222	NM_016642	c.9725G>A	p.R3242Q
ttc9	DAVID_tetratricopeptide repeat domain 9	NM_015351	PAP026	74	43.2%	chr14	70178876	NM_015351	c.277C>NULL	p.NULL-1FsDel1bp
TMEM131	DAVID_transmembrane protein 131	NM_015348	PAP026	58	19.0%	chr2	97775449	NM_015348	c.4574C>NULL	p.NULL-1FsDel1bp
TMEM131	DAVID_transmembrane protein 131	NM_015348	PAP026	61	32.8%	chr2	97775500	NM_015348	c.3925C>A	p.P1309T
TNRC6B	DAVID_trinucleotide repeat containing 6B	NM_001162501	PAP026	61	34.4%	chr22	39041422	NM_001162501	c.4868G>NUL	p.NULL-1FsDel1bp
TRIM67	DAVID_tripartite motif-containing 67	NM_001004342	PAP026	56	25.0%	chr1	229406244	NM_001004342	c.1543G>A	p.V515I
TNF	DAVID_tumor necrosis factor (TNF superfamily: member 2)	ENSG00000204490	PAP026	97	27.8%	chr6	31651561	CCDS4702.1	c.64G>NULL	p.NULL-1FsDel1bp
B3gnt6	DAVID_UDP-GlcNAc:betaGal beta-1:3-N-acetylglucosaminyltransferase 6 (core 3 synthase)	NM_138706	PAP026	97	43.3%	chr11	76429073	NM_138706	c.830C>T	p.P277L
WDR19	DAVID_WD repeat domain 19	NM_025132	PAP026	40	32.5%	chr4	38931299	NM_025132	c.2868G>T	p.M956I
wdr46	DAVID_WD repeat domain 46	ENSG00000204221	PAP026	62	27.4%	chr6	33355066	CCDS4772.1	c.1798G>A	p.A600T
ZRSR1	DAVID_zinc finger (CCCH type): RNA-binding motif and serine/arginine rich 1	ENSG00000212643	PAP026	62	21.0%	chr5	112256568	ENST00000391338	c.1333C>T	p.R445C
Zc3h12b	DAVID_zinc finger CCCH-type containing 12B	NM_001010888	PAP026	38	39.5%	chrX	64635618	NM_001010888	c.730C>T	p.R244X
ZNF44	DAVID_zinc finger protein 44	NM_001164276	PAP026	46	32.6%	chr19	12265133	NM_001164276	c.61A>G	p.M21V
ZCCHC2	DAVID_zinc finger: CCHC domain containing 2	NM_017742	PAP026	162	31.5%	chr18	58393344	NM_017742	c.3050G>A	p.R1017Q
DCST1	DC-STAMP domain containing 1	ENSG00000163357	PAP026	186	19.4%	chr1	153285558	CCDS1083.1	c.1467C>A	p.H489Q
DCAF17	DDB1 and CUL4 associated factor 17	ENSG00000115827	PAP026	52	28.8%	chr2	172042784	CCDS2243.2	c.1224A>NULL	p.NULL-1FsDel1bp
DDX27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	ENSG00000124228	PAP026	94	26.6%	chr20	47291911	CCDS13416.1	c.2065A>NULL	p.NULL-1FsDel1bp
DDX59	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	ENSG00000118197	PAP026	96	14.6%	chr1	198860665	ENST00000367349	c.1876A>NULL	p.NULL-1FsDel1bp
DOCK1	dedicator of cytokinesis 1	ENSG00000150760	PAP026	65	36.9%	chr10	128707053	NM_001380	c.1228G>A	p.A410T
DEGS2	degenerative spermatocyte homolog 2; lipid desaturase (Drosophila)	ENSG00000168350	PAP026	50	34.0%	chr14	99685062	CCDS9956.1	c.821C>T	p.P274L
DCC	deleted in colorectal carcinoma	ENSG00000187323	PAP026	117	14.5%	chr18	48121157	CCDS11952.1	c.2T>C	p.M1T
DLK1	delta-like 1 homolog (Drosophila)	ENSG00000185559	PAP026	126	34.1%	chr14	100263186	CCDS9963.1	c.28G>A	p.V10I
DSG1	desmoglein 1	ENSG00000134760	PAP026	63	44.4%	chr18	27170484	CCDS11896.1	c.1175A>T	p.Y392F
DGKD	diacylglycerol kinase; delta 130kDa	ENSG00000077044	PAP026	67	26.9%	chr2	234030629	CCDS2504.1	c.2496C>NULL	p.NULL-1FsDel1bp

DGKD	diacylglycerol kinase; delta 130kDa	ENSG00000077044	PAP026	89	29.2%	chr2	234030691	CCDS2504.1	c.2558G>NUL	p.NULL-1FsDel1bp
DIS3L	DIS3 mitotic control homolog (S. cerevisiae)-like	ENSG00000166938	PAP026	41	24.4%	chr15	64405755	CCDS10214.1	c.1951C>T	p.R651W
DMRTB1	DMRT-like family B with proline-rich C-terminal; 1	ENSG00000143006	PAP026	62	29.0%	chr1	53702939	CCDS581.1	c.792GCC>NU	p.NULL-1FsDel3bp
DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	ENSG00000119772	PAP026	50	36.0%	chr2	25316707	CCDS33157.1	c.2290A>G	p.S764G
DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	ENSG00000119772	PAP026	183	29.5%	chr2	25322541	CCDS33157.1	c.1421G>A	p.R474H
DBH	dopamine beta-hydroxylase (dopamine beta-monooxygenase)	ENSG00000123454	PAP026	77	32.5%	chr9	135512126	CCDS6977.2	c.1676C>T	p.A559V
DOT1L	DOT1-like; histone H3 methyltransferase (S. cerevisiae)	ENSG00000104885	PAP026	240	31.3%	chr19	2162795	CCDS42460.1	c.1511C>NULI	p.NULL-1FsDel1bp
DARC	Duffy blood group; chemokine receptor	ENSG00000213088	PAP026	743	15.2%	chr1	157442766	CCDS1183.1	c.913G>A	p.A305T
DNMBP	dynamin binding protein	ENSG00000107554	PAP026	145	14.5%	chr10	101663762	ENST00000370423	c.62T>A	p.F21Y
DNAH7	dynein; axonemal; heavy chain 7	ENSG00000118997	PAP026	28	35.7%	chr2	196431469	CCDS42794.1	c.8041G>A	p.A2681T
DST	dystonin	ENSG00000151914	PAP026	69	42.0%	chr6	56589940	CCDS4959.1	c.6284C>A	p.T2095N
DMD	dystrophin	ENSG00000198947	PAP026	67	37.3%	chrX	31137598	CCDS14233.1	c.9501T>A	p.N3167K
EP300	E1A binding protein p300	ENSG00000100393	PAP026	171	26.9%	chr22	39904502	CCDS14010.1	c.6841C>T	p.Q2281X
EGR1	early growth response 1	ENSG00000120738	PAP026	337	32.9%	chr5	137831184	CCDS4206.1	c.1147C>T	p.L383F
EGR2	early growth response 2	ENSG00000122877	PAP026	40	27.5%	chr10	64243576	CCDS7267.1	c.2089C>NULI	p.NULL-1FsDel1bp
EML1	echinoderm microtubule associated protein like 1	ENSG00000066629	PAP026	70	30.0%	chr14	99450317	CCDS32154.1	c.1600G>A	p.D534N
ENOX2	ecto-NOX disulfide-thiol exchanger 2	ENSG00000165675	PAP026	338	28.1%	chrX	129631718	CCDS14626.1	c.683G>A	p.R228H
EVPL	envoplakin	ENSG00000167880	PAP026	138	14.5%	chr17	71514933	CCDS11737.1	c.5948C>T	p.T1983I
EPB41L3	erythrocyte membrane protein band 4.1-like 3	ENSG00000082397	PAP026	119	28.6%	chr18	5423993	CCDS11838.1	c.733T>C	p.C245R
ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	ENSG00000171320	PAP026	51	35.3%	chr8	27690496	CCDS34872.1	c.752NULL>A	p.NULL-1FsIns1bp
ESR1	estrogen receptor 1	ENSG00000091831	PAP026	176	35.8%	chr6	152461613	CCDS5234.1	c.1607T>G	p.L536R
EIF4G3	eukaryotic translation initiation factor 4 gamma; 3	ENSG00000075151	PAP026	142	29.6%	chr1	21140665	CCDS214.1	c.2239AA>NU	p.NULL-1FsDel2bp
EIF4E2	eukaryotic translation initiation factor 4E family member 2	ENSG00000135930	PAP026	261	31.0%	chr2	233139895	CCDS2496.1	c.488G>T	p.G163V
EXTL3	exostoses (multiple)-like 3	ENSG00000012232	PAP026	220	10.5%	chr8	28630061	CCDS6070.1	c.566C>A	p.P189H
EYA1	eyes absent homolog 1 (Drosophila)	ENSG00000104313	PAP026	123	24.4%	chr8	72291567	CCDS34906.1	c.1274G>A	p.R425Q
EYS	eyes shut homolog (Drosophila)	ENSG00000188107	PAP026	132	30.3%	chr6	66261626	CCDS4967.1	c.399G>A	p.M133I
FAM101A	family with sequence similarity 101; member A	ENSG00000178882	PAP026	96	36.5%	chr12	123364993	CCDS9258.1	c.377C>T	p.A126V
FAM122A	family with sequence similarity 122A	ENSG00000187866	PAP026	285	33.3%	chr9	70585607	CCDS6623.1	c.707GT>NUL	p.NULL-1FsDel2bp
FAM128B	family with sequence similarity 128; member B	ENSG00000152082	PAP026	63	28.6%	chr2	130664572	CCDS2157.1	c.380G>A	p.R127H
FAM161A	family with sequence similarity 161; member A	ENSG00000170264	PAP026	42	28.6%	chr2	61919301	ENST00000404929	c.1627C>T	p.R543W
FAM18A	family with sequence similarity 18; member A	ENSG00000166676	PAP026	97	38.1%	chr16	10819922	ENST00000299866	c.74C>T	p.P25L
FAM40B	family with sequence similarity 40; member B	ENSG00000128578	PAP026	38	36.8%	chr7	128910087	CCDS34752.1	c.2218C>T	p.R740C
FAM47C	family with sequence similarity 47; member C	ENSG00000198173	PAP026	51	23.5%	chrX	36936888	CCDS35227.1	c.484G>A	p.A162T
FAM50A	family with sequence similarity 50; member A	ENSG00000071859	PAP026	145	33.8%	chrX	153330097	CCDS14751.1	c.514C>T	p.R172C
FAM64A	family with sequence similarity 64; member A	ENSG00000129195	PAP026	138	13.8%	chr17	6291735	CCDS32541.1	c.523C>T	p.R175W
FAM70B	family with sequence similarity 70; member B	ENSG00000184497	PAP026	68	30.9%	chr13	113642788	ENST00000375348	c.47G>A	p.R16H
FAM71E1	family with sequence similarity 71; member E1	ENSG00000142530	PAP026	104	30.8%	chr19	55671417	CCDS33081.1	c.299C>NULL	p.NULL-1FsDel1bp
FAM83H	family with sequence similarity 83; member H	ENSG00000180921	PAP026	97	36.1%	chr8	144880865	CCDS6410.2	c.5556C>NULI	p.NULL-1FsDel1bp
FAM98C	family with sequence similarity 98; member C	ENSG00000130244	PAP026	39	28.2%	chr19	43591256	CCDS42562.1	c.944G>NULL	p.NULL-1FsDel1bp
FANCC	Fanconi anemia; complementation group C	ENSG00000158169	PAP026	110	35.5%	chr9	96913663	CCDS35071.1	c.1232T>A	p.L411X
FNTB	farnesyltransferase; CAAX box; beta	ENSG00000125954	PAP026	196	34.2%	chr14	64580831	CCDS9769.1	c.872G>T	p.R291L
FTO	fat mass and obesity associated	ENSG00000140718	PAP026	49	20.4%	chr16	52417276	CCDS32448.1	c.-1G>A	p.IVS2-1-1SpliceAcceptor

FBXW7	F-box and WD repeat domain containing 7	ENSG00000109670	PAP026	215	13.5%	chr4	153463606	CCDS3777.1	c.2269G>NUL	p.NULL-1FsDel1bp
FBXW9	F-box and WD repeat domain containing 9	ENSG00000132004	PAP026	60	31.7%	chr19	12661974	ENST00000380339	c.1162G>NUL	p.NULL-1FsDel1bp
FBXO39	F-box protein 39	ENSG00000177294	PAP026	45	31.1%	chr17	6624247	CCDS11082.1	c.336G>A	p.M112I
FDXR	ferredoxin reductase	ENSG00000161513	PAP026	253	15.0%	chr17	70372056	CCDS11707.1	c.829C>T	p.R277C
FRRS1	ferric-chelate reductase 1	ENSG00000156869	PAP026	36	27.8%	chr1	99950568	CCDS30780.1	c.1415A>G	p.D472G
FGF7	fibroblast growth factor 7 (keratinocyte growth factor)	ENSG00000140285	PAP026	59	30.5%	chr15	47503980	CCDS10131.1	c.194G>T	p.R65I
FNDC1	fibronectin type III domain containing 1	ENSG00000164694	PAP026	118	33.9%	chr6	159573621	NM_032532	c.2087C>T	p.P696L
FKBP10	FK506 binding protein 10; 65 kDa	ENSG00000141756	PAP026	79	36.7%	chr17	37229085	CCDS11409.1	c.825C>NULL	p.NULL-1FsDel1bp
FOLR3	folate receptor 3 (gamma)	ENSG00000110203	PAP026	55	23.6%	chr11	71524814	ENST00000325101	c.168G>T	p.Q56H
FOXP2	forkhead box P2	ENSG00000128573	PAP026	68	33.8%	chr7	114058816	CCDS43635.1	c.-1CAG>NUL	p.IVS5-1-1SpliceAcceptor
FOXP2	forkhead box P2	ENSG00000128573	PAP026	51	35.3%	chr7	114117173	CCDS43635.1	c.2179G>A	p.D727N
FOXP4	forkhead box P4	ENSG00000137166	PAP026	98	27.6%	chr6	41663164	CCDS34447.1	c.808NULL>C	p.NULL-1FsIns1bp
FOXP4	forkhead box P4	ENSG00000137166	PAP026	99	11.1%	chr6	41670628	CCDS34447.1	c.1579C>T	p.R527C
GPR113	G protein-coupled receptor 113	ENSG00000173567	PAP026	18	61.1%	chr2	26389392	CCDS33159.2	c.979A>G	p.T327A
GPR179	G protein-coupled receptor 179	ENSG00000188888	PAP026	203	34.0%	chr17	33752669	CCDS42308.1	c.530A>G	p.D177G
GABRG1	gamma-aminobutyric acid (GABA) A receptor; gamma 1	ENSG00000163285	PAP026	37	29.7%	chr4	45794097	CCDS3470.1	c.131A>G	p.D44G
GABRR2	gamma-aminobutyric acid (GABA) receptor; rho 2	ENSG00000111886	PAP026	62	33.9%	chr6	90032165	NM_002043	c.850C>T	p.R284C
GJA4	gap junction protein; alpha 4; 37kDa	ENSG00000187513	PAP026	93	10.8%	chr1	35032705	CCDS30669.1	c.304C>T	p.R102X
GFRA2	GDNF family receptor alpha 2	ENSG00000168546	PAP026	73	32.9%	chr8	21696288	NM_001495	c.424C>NULL	p.NULL-1FsDel1bp
GTF3C1	general transcription factor IIIC; polypeptide 1; alpha 220kDa	ENSG00000077235	PAP026	80	32.5%	chr16	27407099	CCDS32414.1	c.3650G>A	p.R1217Q
GTF3C4	general transcription factor IIIC; polypeptide 4; 90kDa	ENSG00000125484	PAP026	64	43.8%	chr9	134543645	CCDS6953.1	c.818G>C	p.S273T
GINS4	GINS complex subunit 4 (Sld5 homolog)	ENSG00000147536	PAP026	81	27.2%	chr8	41518519	CCDS6116.1	c.519GAGA>N	p.NULL-1FsDel4bp
GBGT1	globoside alpha-1;3-N-acetylgalactosaminyltransferase 1	ENSG00000148288	PAP026	63	33.3%	chr9	135020477	CCDS6960.1	c.268G>A	p.V90I
GRID1	glutamate receptor; ionotropic; delta 1	ENSG00000182771	PAP026	161	25.5%	chr10	87956268	CCDS31236.1	c.353G>A	p.R118H
GRIN1	glutamate receptor; ionotropic; N-methyl D-aspartate 1	ENSG00000176884	PAP026	317	26.5%	chr9	139156317	CCDS7031.1	c.290C>NULL	p.NULL-1FsDel1bp
GRIN1	glutamate receptor; ionotropic; N-methyl D-aspartate 1	ENSG00000176884	PAP026	63	42.9%	chr9	139176705	CCDS7031.1	c.1780NULL>C	p.NULL-1FsIns3bp
GRIN2C	glutamate receptor; ionotropic; N-methyl D-aspartate 2C	ENSG00000161509	PAP026	59	25.4%	chr17	70359397	CCDS32724.1	c.1027C>T	p.R343X
QRICH2	glutamine rich 2	ENSG00000129646	PAP026	72	13.9%	chr17	71799828	CCDS32741.1	c.2077C>T	p.R693C
GSTT1	glutathione S-transferase theta 1	ENSG00000184674	PAP026	32	56.3%	chr22	22706428	CCDS13822.1	c.718C>T	p.R240W
GLRA2	glycine receptor; alpha 2	ENSG00000101958	PAP026	25	40.0%	chrX	14537209	CCDS14160.1	c.891G>T	p.M297I
GSK3A	glycogen synthase kinase 3 alpha	ENSG00000105723	PAP026	43	27.9%	chr19	47428511	CCDS12599.1	c.1448C>NULL	p.NULL-1FsDel1bp
GLYR1	glyoxylate reductase 1 homolog (Arabidopsis)	ENSG00000140632	PAP026	62	29.0%	chr16	4802230	CCDS10524.1	c.1302NULL>C	p.NULL-1FsIns1bp
GPC1	glypican 1	ENSG00000063660	PAP026	60	33.3%	chr2	241053031	CCDS2534.1	c.1100G>A	p.R367Q
GBF1	golgi brefeldin A resistant guanine nucleotide exchange factor 1	ENSG00000107862	PAP026	210	29.5%	chr10	104116192	CCDS7533.1	c.2369G>A	p.R790H
GAPVD1	GTPase activating protein and VPS9 domains 1	ENSG00000165219	PAP026	61	21.3%	chr9	127109645	CCDS35138.1	c.1249C>A	p.L417M
GARNL3	GTPase activating Rap/RanGAP domain-like 3	ENSG00000136895	PAP026	35	34.3%	chr9	129144331	CCDS6869.1	c.1094A>NULL	p.NULL-1FsDel1bp
GNAZ	guanine nucleotide binding protein (G protein); alpha z polypeptide	ENSG00000128266	PAP026	88	38.6%	chr22	21768488	CCDS13804.1	c.606G>NULL	p.NULL-1FsDel1bp
GNG4	guanine nucleotide binding protein (G protein); gamma 4	ENSG00000168243	PAP026	223	22.0%	chr1	233813670	CCDS1607.1	c.92G>T	p.R31M
GUCY2D	guanylate cyclase 2D; membrane (retina-specific)	ENSG00000132518	PAP026	61	19.7%	chr17	7850626	CCDS11127.1	c.1247C>T	p.A416V

H1F0	H1 histone family; member 0	ENSG00000189060	PAP026	87	31.0%	chr22	36532071	CCDS13956.1	c.574AAG>NU	p.NULL-1FsDel3bp
HECTD1	HECT domain containing 1	ENSG00000092148	PAP026	75	32.0%	chr14	30646523	CCDS41939.1	c.-1G>A	p.IVS36+1-1SpliceDonor
HSH2D	hematopoietic SH2 domain containing	ENSG00000196684	PAP026	58	29.3%	chr19	16120673	ENST00000397369	c.113C>T	p.A38V
HEBP2	heme binding protein 2	ENSG00000051620	PAP026	63	41.3%	chr6	138775819	CCDS5191.1	c.529G>A	p.A177T
HMCN2	hemicentin 2	ENSG00000148357	PAP026	141	33.3%	chr9	132258445	ENST00000277491	c.874G>A	p.A292T
HNRNPUL1	heterogeneous nuclear ribonucleoprotein U-like 1	ENSG00000105323	PAP026	46	23.9%	chr19	46500616	CCDS12576.1	c.1894C>T	p.R632X
HGFAC	HGF activator	ENSG00000109758	PAP026	45	31.1%	chr4	3419033	CCDS3369.1	c.1372G>A	p.V458I
HRC	histidine rich calcium binding protein	ENSG00000130528	PAP026	161	17.4%	chr19	54349702	CCDS12759.1	c.2433GGA>N	p.NULL-1FsDel3bp
HDAC6	histone deacetylase 6	ENSG00000094631	PAP026	224	29.0%	chrX	48557795	CCDS14306.1	c.811C>A	p.L271I
HOXC4	homeobox C4	ENSG00000198353	PAP026	107	11.2%	chr12	52735029	CCDS8873.1	c.568G>A	p.A190T
HRNR	hornerin	ENSG00000197915	PAP026	31	38.7%	chr1	150455679	CCDS30859.1	c.5050C>T	p.R1684C
HCFC1	host cell factor C1 (VP16-accessory protein)	ENSG00000172534	PAP026	91	28.6%	chrX	152869184	CCDS44020.1	c.5708C>T	p.P1903L
HIVEP3	human immunodeficiency virus type I enhancer binding protein 3	ENSG00000127124	PAP026	104	25.0%	chr1	41820432	CCDS463.1	c.7684C>NULI	p.NULL-1FsDel1bp
HTT	huntingtin	ENSG00000197386	PAP026	81	18.5%	chr4	3152145	CCDS43206.1	c.4718C>T	p.S1573L
HUS1	HUS1 checkpoint homolog (S. pombe)	ENSG00000136273	PAP026	248	26.6%	chr7	47985608	CCDS34635.1	c.34T>C	p.C12R
HYDIN	hydrocephalus inducing homolog (mouse)	ENSG00000157423	PAP026	168	13.1%	chr16	69452115	CCDS42189.1	c.11965G>T	p.G3989C
HSD17B10	hydroxysteroid (17-beta) dehydrogenase 10	ENSG00000072506	PAP026	90	31.1%	chrX	53475993	CCDS14354.1	c.284C>T	p.A95V
HCRTR1	hypocretin (orexin) receptor 1	ENSG00000121764	PAP026	57	33.3%	chr1	31857419	CCDS344.1	c.39C>NULL	p.NULL-1FsDel1bp
HIF1A	hypoxia inducible factor 1; alpha subunit (basic helix-loop-helix transcription factor)	ENSG00000100644	PAP026	109	29.4%	chr14	61277260	CCDS9753.1	c.1694A>G	p.Y565C
IKZF1	IKAROS family zinc finger 1 (Ikaros)	ENSG00000185811	PAP026	44	31.8%	chr7	50435162	NM_006060	c.903G>T	p.K301N
IGHMBP2	immunoglobulin mu binding protein 2	ENSG00000132740	PAP026	64	39.1%	chr11	68453379	CCDS8187.1	c.1213NULL>(	p.NULL-1FsIns1bp
INHBB	inhibin; beta B	ENSG00000163083	PAP026	140	13.6%	chr2	120823252	CCDS2132.1	c.556C>T	p.P186S
INHBC	inhibin; beta C	ENSG00000175189	PAP026	139	36.0%	chr12	56115115	CCDS8938.1	c.179G>A	p.R60H
IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells; kinase epsilon	ENSG00000143466	PAP026	111	25.2%	chr1	204716222	CCDS30996.1	c.434T>C	p.V145A
ITPR2	inositol 1;4;5-triphosphate receptor; type 2	ENSG00000123104	PAP026	78	33.3%	chr12	26531313	CCDS41764.1	c.5692A>NULI	p.NULL-1FsDel1bp
IP6K2	inositol hexakisphosphate kinase 2	ENSG00000068745	PAP026	72	23.6%	chr3	48706629	CCDS33752.1	c.342T>NULL	p.NULL-1FsDel1bp
ITGB1BP2	integrin beta 1 binding protein (melusin) 2	ENSG00000147166	PAP026	114	32.5%	chrX	70439929	CCDS14411.1	c.410C>A	p.A137E
ITGA4	integrin; alpha 4 (antigen CD49D; alpha 4 subunit of VLA-4 receptor)	ENSG00000115232	PAP026	72	29.2%	chr2	182054597	CCDS42788.1	c.782G>A	p.R261Q
ITGB3	integrin; beta 3 (platelet glycoprotein IIIa; antigen CD61)	ENSG00000056345	PAP026	155	21.9%	chr17	42722595	CCDS11511.1	c.1081A>G	p.M361V
IRF2BP1	interferon regulatory factor 2 binding protein 1	ENSG00000170604	PAP026	108	35.2%	chr19	51079372	CCDS12678.1	c.3255C>NULI	p.NULL-1FsDel1bp
IL16	interleukin 16 (lymphocyte chemoattractant factor)	ENSG00000172349	PAP026	48	25.0%	chr15	79380860	CCDS42069.1	c.3270NULL>A	p.NULL-1FsIns1bp
IL2RG	interleukin 2 receptor; gamma (severe combined immunodeficiency)	ENSG00000147168	PAP026	114	25.4%	chrX	70244339	CCDS14406.1	c.1267C>NULI	p.NULL-1FsDel1bp
IL26	interleukin 26	ENSG00000111536	PAP026	56	23.2%	chr12	66905531	CCDS8981.1	c.244A>NULL	p.NULL-1FsDel1bp
IFT88	intraflagellar transport 88 homolog (Chlamydomonas)	ENSG00000032742	PAP026	38	31.6%	chr13	20103180	CCDS31944.1	c.1352A>NULI	p.NULL-1FsDel1bp
JAG2	jagged 2	ENSG00000184916	PAP026	70	31.4%	chr14	104685526	CCDS9998.1	c.2333C>NULI	p.NULL-1FsDel1bp
JARID2	jumonji; AT rich interactive domain 2	ENSG00000008083	PAP026	87	35.6%	chr6	15604958	CCDS4533.1	c.1523C>T	p.T508M
JUP	junction plakoglobin	ENSG00000173801	PAP026	136	36.8%	chr17	37172928	CCDS11407.1	c.1330C>T	p.R444C
JPH3	junctophilin 3	ENSG00000154118	PAP026	133	31.6%	chr16	86235509	CCDS10962.1	c.527C>T	p.A176V

KLK12	kallikrein-related peptidase 12	ENSG00000186474	PAP026	62	32.3%	chr19	56225921	CCDS12820.1	c.526T>C	p.Y176H
KLHDC7B	kelch domain containing 7B	ENSG00000130487	PAP026	40	32.5%	chr22	49334119	CCDS14097.1	c.361C>A	p.L121M
KLHL14	kelch-like 14 (Drosophila)	ENSG00000197705	PAP026	293	30.4%	chr18	28604512	CCDS32813.1	c.41G>A	p.S14N
KLHL28	kelch-like 28 (Drosophila)	ENSG00000179454	PAP026	69	21.7%	chr14	44484669	CCDS9680.1	c.1111A>NULI	p.NULL-1FsDel1bp
KEAP1	kelch-like ECH-associated protein 1	ENSG00000079999	PAP026	39	43.6%	chr19	10458368	CCDS12239.1	c.1835C>T	p.P612L
KRT24	keratin 24	ENSG00000167916	PAP026	220	10.9%	chr17	36109344	CCDS11372.1	c.1454GAG>N	p.NULL-1FsDel3bp
KRT85	keratin 85	ENSG00000135443	PAP026	122	26.2%	chr12	51043462	CCDS8824.1	c.-1G>T	p.IVS4-1-1SpliceAcceptor
KIAA0226	KIAA0226	ENSG00000145016	PAP026	74	28.4%	chr3	198892490	CCDS43195.1	c.2337C>A	p.D779E
KIAA0240	KIAA0240	ENSG00000112624	PAP026	100	13.0%	chr6	42940492	CCDS34451.1	c.2570C>T	p.A857V
KIAA1009	KIAA1009	ENSG00000135315	PAP026	195	22.6%	chr6	84927270	NM_014895	c.2865A>NULI	p.NULL-1FsDel1bp
KIAA1024	KIAA1024	ENSG00000169330	PAP026	122	62.3%	chr15	77537641	CCDS32306.1	c.2097A>NULI	p.NULL-1FsDel1bp
KIAA1377	KIAA1377	ENSG00000110318	PAP026	86	25.6%	chr11	101339347	CCDS31658.1	c.2371A>C	p.T791P
KIAA1614	KIAA1614	ENSG00000135835	PAP026	283	24.7%	chr1	179172184	CCDS41442.1	c.2516CT>NU	p.NULL-1FsDel2bp
KIAA1683	KIAA1683	ENSG00000130518	PAP026	102	32.4%	chr19	18237231	CCDS32958.1	c.2119G>A	p.A707T
KIAA1797	KIAA1797	ENSG00000188352	PAP026	60	16.7%	chr9	20972393	CCDS34993.1	c.4676G>A	p.C1559Y
KIAA1919	KIAA1919	ENSG00000173214	PAP026	80	28.8%	chr6	111694054	CCDS5090.1	c.596T>NULL	p.NULL-1FsDel1bp
KIAA2018	KIAA2018	ENSG00000176542	PAP026	133	11.3%	chr3	114860488	CCDS43133.1	c.2731G>T	p.D911Y
KIF6	kinesin family member 6	ENSG00000164627	PAP026	70	24.3%	chr6	39688971	CCDS4844.1	c.740T>NULL	p.NULL-1FsDel1bp
KRR1	KRR1; small subunit (SSU) processome component; homolog (yeast)	ENSG00000111615	PAP026	65	40.0%	chr12	74179860	CCDS9012.1	c.1284A>NULI	p.NULL-1FsDel1bp
LCTL	lactase-like	ENSG00000188501	PAP026	58	37.9%	chr15	64640590	CCDS10220.1	c.725CA>NUL	p.NULL-1FsDel2bp
LAD1	ladinin 1	ENSG00000159166	PAP026	245	19.6%	chr1	199622919	CCDS1410.1	c.193G>A	p.V65M
LAMA5	laminin; alpha 5	ENSG00000130702	PAP026	299	35.5%	chr20	60323267	CCDS33502.1	c.8179C>T	p.R2727W
LAMA5	laminin; alpha 5	ENSG00000130702	PAP026	219	27.4%	chr20	60339551	CCDS33502.1	c.3677GAG>N	p.NULL-1FsDel3bp
LAMA5	laminin; alpha 5	ENSG00000130702	PAP026	80	33.8%	chr20	60341910	CCDS33502.1	c.3044G>A	p.S1015N
LLGL1	lethal giant larvae homolog 1 (Drosophila)	ENSG00000131899	PAP026	67	46.3%	chr17	18086270	CCDS32586.1	c.2948CA>NU	p.NULL-1FsDel2bp
LRRC16A	leucine rich repeat containing 16A	ENSG00000079691	PAP026	54	33.3%	chr6	25560433	ENST00000332168	c.917TT>NULI	p.NULL-1FsDel2bp
LRRC4B	leucine rich repeat containing 4B	ENSG00000131409	PAP026	112	22.3%	chr19	55713208	CCDS42595.1	c.3418G>NUL	p.NULL-1FsDel1bp
LRRC4C	leucine rich repeat containing 4C	ENSG00000148948	PAP026	93	29.0%	chr11	40093389	CCDS31464.1	c.1030C>T	p.L344F
LGR4	leucine-rich repeat-containing G protein-coupled receptor 4	ENSG00000205213	PAP026	67	32.8%	chr11	27347269	CCDS31449.1	c.-1T>NULL	p.IVS17-3-1SpliceAcceptor
LARS	leucyl-tRNA synthetase	ENSG00000133706	PAP026	95	18.9%	chr5	145488876	CCDS34265.1	c.-1A>NULL	p.IVS25-2-1SpliceAcceptor
LENG1	leukocyte receptor cluster (LRC) member 1	ENSG00000105617	PAP026	38	42.1%	chr19	59351434	CCDS12881.1	c.850AG>NUL	p.NULL-1FsDel2bp
LENG8	leukocyte receptor cluster (LRC) member 8	ENSG00000167615	PAP026	113	32.7%	chr19	59659631	CCDS12894.1	c.1450G>A	p.D484N
LNX2	ligand of numb-protein X 2	ENSG00000139517	PAP026	111	28.8%	chr13	27025393	CCDS9323.1	c.1730A>G	p.Y577C
LIG3	ligase III; DNA; ATP-dependent	ENSG00000005156	PAP026	124	29.8%	chr17	30347199	CCDS11284.2	c.1615G>A	p.A539T
LGTN	ligatin	ENSG00000143486	PAP026	118	16.9%	chr1	204831789	CCDS1465.1	c.1696C>T	p.L566F

LONP2	lon peptidase 2; peroxisomal	ENSG00000102910	PAP026	51	43.1%	chr16	46854194	CCDS10734.1	c.892A>NULL	p.NULL-1FsDel1bp
LRP12	low density lipoprotein receptor-related protein 12	ENSG00000147650	PAP026	98	31.6%	chr8	105579175	CCDS6303.1	c.781C>T	p.Q261X
LYNX1	Ly6/neurotoxin 1	ENSG00000180155	PAP026	46	39.1%	chr8	143853699	CCDS6389.1	c.239C>T	p.A80V
LAG3	lymphocyte-activation gene 3	ENSG00000089692	PAP026	85	40.0%	chr12	6754046	CCDS8561.1	c.536T>C	p.L179P
LPAR1	lysophosphatidic acid receptor 1	ENSG00000198121	PAP026	119	32.8%	chr9	112744135	CCDS6777.1	c.924TTGT>N	p.NULL-1FsDel4bp
LPCAT3	lysophosphatidylcholine acyltransferase 3	ENSG00000172197	PAP026	71	42.3%	chr6	20226733	CCDS34346.1	c.925G>A	p.A309T
LYPLAL1	lysophospholipase-like 1	ENSG00000143353	PAP026	188	19.1%	chr1	217413866	CCDS1522.1	c.11C>T	p.A4V
LYST	lysosomal trafficking regulator	ENSG00000143669	PAP026	128	24.2%	chr1	233987363	CCDS31062.1	c.7074TTTG>I	p.NULL-1FsDel4bp
LYST	lysosomal trafficking regulator	ENSG00000143669	PAP026	456	20.2%	chr1	234021867	CCDS31062.1	c.4298G>A	p.R1433Q
MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	ENSG00000002822	PAP026	31	32.3%	chr7	2225604	CCDS43539.1	c.485T>C	p.L162P
MGAT3	mannosyl (beta-1;4-)-glycoprotein beta-1;4-N-acetylglucosaminyltransferase	ENSG00000128268	PAP026	46	23.9%	chr22	38213867	CCDS13994.2	c.569A>G	p.Y190C
MKKS	McKusick-Kaufman syndrome	ENSG00000125863	PAP026	68	25.0%	chr20	10342055	CCDS13111.1	c.108C>A	p.C36X
MDM4	Mdm4 p53 binding protein homolog (mouse)	ENSG00000198625	PAP026	51	21.6%	chr1	202773744	ENST00000391947	c.-1T>NULL	p.IVS1+2-1SpliceDonor
MDN1	MDN1; midasin homolog (yeast)	ENSG00000112159	PAP026	168	31.5%	chr6	90484928	CCDS5024.1	c.6461A>G	p.Y2154C
MED13	mediator complex subunit 13	ENSG00000108510	PAP026	66	36.4%	chr17	57463775	CCDS42366.1	c.821T>C	p.V274A
MAGEA4	melanoma antigen family A; 4	ENSG00000147381	PAP026	128	39.1%	chrX	150842859	CCDS14702.1	c.67C>A	p.L23M
MAGEB3	melanoma antigen family B; 3	ENSG00000198798	PAP026	78	35.9%	chrX	30164659	CCDS14220.1	c.697T>A	p.Y233N
MBOAT1	membrane bound O-acyltransferase domain containing 1	ENSG00000172197	PAP026	71	42.3%	chr6	20226733	CCDS34346.1	c.925G>A	p.A309T
MMEL1	membrane metallo-endopeptidase-like 1	ENSG00000142606	PAP026	60	30.0%	chr1	2516631	CCDS30569.1	c.1501C>T	p.H501Y
MBTPS1	membrane-bound transcription factor peptidase; site 1	ENSG00000140943	PAP026	121	14.0%	chr16	82659522	CCDS10941.1	c.1994A>G	p.Y665C
MGEA5	meningioma expressed antigen 5 (hyaluronidase)	ENSG00000198408	PAP026	62	27.4%	chr10	103543724	CCDS7520.1	c.2006C>T	p.A669V
MTSS1L	metastasis suppressor 1-like	ENSG00000132613	PAP026	168	13.1%	chr16	69255648	CCDS32476.1	c.2449C>NULI	p.NULL-1FsDel1bp
MBD6	methyl-CpG binding domain protein 6	ENSG00000166987	PAP026	96	28.1%	chr12	56207999	CCDS8944.1	c.2338G>NUL	p.NULL-1FsDel1bp
MRI1	methylthioribose-1-phosphate isomerase homolog (S. cerevisiae)	ENSG00000037757	PAP026	46	28.3%	chr19	13743968	CCDS32923.1	c.983C>NULL	p.NULL-1FsDel1bp
MEX3B	mex-3 homolog B (C. elegans)	ENSG00000183496	PAP026	123	37.4%	chr15	80123304	CCDS10319.1	c.2415C>NULI	p.NULL-1FsDel1bp
MASTL	microtubule associated serine/threonine kinase-like	ENSG00000120539	PAP026	40	37.5%	chr10	27499260	CCDS7153.1	c.1366A>NULI	p.NULL-1FsDel1bp
MACF1	microtubule-actin crosslinking factor 1	ENSG00000127603	PAP026	117	31.6%	chr1	39521719	CCDS435.1	c.875C>T	p.S292L
MCM5	minichromosome maintenance complex component 5	ENSG00000100297	PAP026	196	28.1%	chr22	34134430	CCDS13915.1	c.626T>C	p.L209S
MTG1	mitochondrial GTPase 1 homolog (S. cerevisiae)	ENSG00000148824	PAP026	220	36.4%	chr10	135083635	CCDS31320.1	c.981C>NULL	p.NULL-1FsDel1bp
MRPL15	mitochondrial ribosomal protein L15	ENSG00000137547	PAP026	53	28.3%	chr8	55210473	CCDS6158.1	c.77A>G	p.N26S
MAPKBP1	mitogen-activated protein kinase binding protein 1	ENSG00000137802	PAP026	66	34.8%	chr15	39904034	CCDS32201.1	c.4274G>A	p.R1425H
MAP2K3	mitogen-activated protein kinase kinase 3	ENSG00000034152	PAP026	158	19.6%	chr17	21142264	ENST00000316920	c.12G>T	p.Q4H
MAP3K12	mitogen-activated protein kinase kinase kinase 12	ENSG00000139625	PAP026	136	15.4%	chr12	52166147	CCDS8860.1	c.682C>T	p.H228Y
MKI67IP	MKI67 (FHA domain) interacting nucleolar phosphoprotein	ENSG00000155438	PAP026	76	26.3%	chr2	122204966	CCDS2135.1	c.748A>NULL	p.NULL-1FsDel1bp
MOSC2	MOCO sulphurase C-terminal domain containing 2	ENSG00000117791	PAP026	77	33.8%	chr1	218988511	CCDS1525.1	c.15C>A	p.S5R
MOSPD2	motile sperm domain containing 2	ENSG00000130150	PAP026	91	24.2%	chrX	14847825	CCDS14162.1	c.1530CT>NU	p.NULL-1FsDel2bp
MEGF8	multiple EGF-like-domains 8	ENSG00000105429	PAP026	129	37.2%	chr19	47559153	NM_001410	c.5971C>A	p.P1991T
MUS81	MUS81 endonuclease homolog (S. cerevisiae)	ENSG00000172732	PAP026	105	36.2%	chr11	65387253	CCDS8115.1	c.-1G>A	p.IVS7+1-1SpliceDonor
MSH3	mutS homolog 3 (E. coli)	ENSG00000113318	PAP026	47	21.3%	chr5	80006671	CCDS34195.1	c.1141A>NULI	p.NULL-1FsDel1bp

MYPOP	Myb-related transcription factor; partner of profilin	ENSG00000176182	PAP026	64	31.3%	chr19	51096462	CCDS33055.1	c.908C>NULL	p.NULL-1FsDel1bp
MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila)	ENSG00000118058	PAP026	123	22.0%	chr11	117848361	CCDS31686.1	c.1277G>A	p.R426Q
MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	ENSG00000055609	PAP026	61	41.0%	chr7	151482401	CCDS5931.1	c.12023A>G	p.E4008G
MLL5	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog; Drosophila)	ENSG00000005483	PAP026	100	32.0%	chr7	104535543	CCDS34723.1	c.3403C>T	p.R1135W
MYH9	myosin; heavy chain 9; non-muscle	ENSG00000100345	PAP026	228	29.4%	chr22	35015145	CCDS13927.1	c.4489C>T	p.R1497W
MARCKS	myristoylated alanine-rich protein kinase C substrate	ENSG00000155130	PAP026	92	26.1%	chr6	114287903	CCDS5101.1	c.454AA>NUL	p.NULL-1FsDel2bp
NAGLU	N-acetylglucosaminidase; alpha-	ENSG00000108784	PAP026	89	28.1%	chr17	37942960	CCDS11427.1	c.402TG>NUL	p.NULL-1FsDel2bp
NOX3	NADPH oxidase 3	ENSG00000074771	PAP026	116	28.4%	chr6	155785617	CCDS5250.1	c.1372TG>NU	p.NULL-1FsDel2bp
NECAP1	NECAP endocytosis associated 1	ENSG00000089818	PAP026	101	34.7%	chr12	8134160	CCDS8589.1	c.299C>G	p.T100S
N4BP2	NEDD4 binding protein 2	ENSG00000078177	PAP026	107	32.7%	chr4	39780191	CCDS3457.1	c.331G>A	p.A111T
NES	nestin	ENSG00000132688	PAP026	103	32.0%	chr1	154909428	CCDS1151.1	c.5059C>NULI	p.NULL-1FsDel1bp
NAPA	N-ethylmaleimide-sensitive factor attachment protein; alpha	ENSG00000105402	PAP026	120	10.8%	chr19	52683446	CCDS12702.1	c.799G>A	p.D267N
NTN5	netrin 5	ENSG00000142233	PAP026	86	23.3%	chr19	53859837	CCDS33068.1	c.-1G>A	p.IVS1-1-1SpliceAcceptor
NAV2	neuron navigator 2	ENSG00000166833	PAP026	39	28.2%	chr11	19847046	CCDS7851.1	c.-1G>T	p.IVS3-1-1SpliceAcceptor
NPBWR1	neuropeptides B/W receptor 1	ENSG00000183729	PAP026	261	27.6%	chr8	54015469	CCDS6151.1	c.449G>A	p.R150H
NKRF	NFKB repressing factor	ENSG00000186416	PAP026	230	30.9%	chrX	118608650	CCDS35375.1	c.766G>A	p.A256T
NCLN	nicalin homolog (zebrafish)	ENSG00000125912	PAP026	79	16.5%	chr19	3143544	CCDS32869.1	c.261G>A	p.M87I
NKX2-6	NK2 transcription factor related; locus 6 (Drosophila)	ENSG00000180053	PAP026	92	31.5%	chr8	23616160	ENST00000325017	c.655C>T	p.P219S
NLRC4	NLR family; CARD domain containing 4	ENSG00000091106	PAP026	106	32.1%	chr2	32328810	CCDS33174.1	c.1627C>T	p.Q543X
NLRP12	NLR family; pyrin domain containing 12	ENSG00000142405	PAP026	68	25.0%	chr19	59019228	CCDS12864.1	c.13G>A	p.A5T
NME7	non-metastatic cells 7; protein expressed in (nucleoside-diphosphate kinase)	ENSG00000143156	PAP026	84	46.4%	chr1	167466677	CCDS1277.1	c.893T>C	p.M298T
NUAK2	NUAK family; SNF1-like kinase; 2	ENSG00000163545	PAP026	170	10.0%	chr1	203539731	CCDS1453.1	c.2420C>NULI	p.NULL-1FsDel1bp
NCBP1	nuclear cap binding protein subunit 1; 80kDa	ENSG00000136937	PAP026	99	13.1%	chr9	99464196	CCDS6728.1	c.1652T>G	p.L551R
NUMA1	nuclear mitotic apparatus protein 1	ENSG00000137497	PAP026	94	41.5%	chr11	71392664	CCDS31633.1	c.6253C>T	p.R2085C
NR2C2	nuclear receptor subfamily 2; group C; member 2	ENSG00000177463	PAP026	90	30.0%	chr3	15059410	CCDS2621.1	c.1739T>NULI	p.NULL-1FsDel1bp
NR2F1	nuclear receptor subfamily 2; group F; member 1	ENSG00000175745	PAP026	209	13.4%	chr5	92949619	CCDS4068.1	c.704G>A	p.R235H
NOL4	nucleolar protein 4	ENSG00000101746	PAP026	22	59.1%	chr18	29777143	CCDS11907.2	c.-1T>NULL	p.IVS8-3-1SpliceAcceptor
NUP153	nucleoporin 153kDa	ENSG00000124789	PAP026	17	58.8%	chr6	17741057	CCDS4541.1	c.-1TT>NULL	p.IVS16-3-1SpliceAcceptor
NUP210	nucleoporin 210kDa	ENSG00000132182	PAP026	81	28.4%	chr3	13376823	CCDS33704.1	c.2101C>T	p.R701W
NULL	NULL	ENSG00000178404	PAP026	114	31.6%	chr17	74398405	ENST00000322630	c.1776G>C	p.Q592H
NULL	NULL	ENSG00000202582	PAP026	67	32.8%	chr12	48557804	ENST00000365712	c.1163C>T	p.T388M
NULL	NULL	ENSG00000206125	PAP026	91	31.9%	chr15	31233695	ENST00000320930	c.2579C>NULI	p.NULL-1FsDel1bp
NULL	NULL	ENSG00000214069	PAP026	117	35.0%	chr17	78379717	ENST00000397438	c.487NULL>C	p.NULL-1FsIns1bp
NULL	NULL	ENSG00000214094	PAP026	100	36.0%	chr17	77004404	ENST00000397526	c.607A>G	p.T203A
NULL	NULL	MI0006316	PAP026	83	36.1%	chr19	2185094	MI0006316	c.55C>T	p.R19W

OCRL	oculocerebrorenal syndrome of Lowe	ENSG00000122126	PAP026	199	27.1%	chrX	128531053	CCDS35393.1	c.1598T>C	p.I533T
OSR1	odd-skipped related 1 (Drosophila)	ENSG00000143867	PAP026	82	12.2%	chr2	19416911	CCDS1694.1	c.137C>T	p.A46V
ODZ1	odz; odd Oz/ten-m homolog 1(Drosophila)	ENSG00000009694	PAP026	49	36.7%	chrX	123666628	CCDS14609.1	c.931T>C	p.Y311H
OLFM2	olfactomedin 2	ENSG00000105088	PAP026	75	42.7%	chr19	9832445	CCDS12221.1	c.89G>A	p.G30D
OR10H4	olfactory receptor; family 10; subfamily H; member 4	ENSG00000176231	PAP026	200	30.0%	chr19	15921612	CCDS32941.1	c.795G>T	p.K265N
OR11G2	olfactory receptor; family 11; subfamily G; member 2	ENSG00000196832	PAP026	215	35.8%	chr14	19735747	CCDS32032.1	c.413A>G	p.Q138R
OR2A2	olfactory receptor; family 2; subfamily A; member 2	ENSG00000221989	PAP026	69	30.4%	chr7	143437903	CCDS43671.1	c.295C>T	p.Q99X
OR2G2	olfactory receptor; family 2; subfamily G; member 2	ENSG00000177489	PAP026	323	20.7%	chr1	245818442	CCDS31092.1	c.158G>A	p.R53H
OR4C15	olfactory receptor; family 4; subfamily C; member 15	ENSG00000181939	PAP026	64	35.9%	chr11	55078674	CCDS31501.1	c.316G>A	p.A106T
OR5J2	olfactory receptor; family 5; subfamily J; member 2	ENSG00000174957	PAP026	95	30.5%	chr11	55700997	CCDS31522.1	c.328A>G	p.T110A
OR51Q1	olfactory receptor; family 51; subfamily Q; member 1	ENSG00000167360	PAP026	330	13.0%	chr11	5400531	CCDS31381.1	c.525NULL>T(	p.NULL-1FsIns2bp
OR6A2	olfactory receptor; family 6; subfamily A; member 2	ENSG00000184933	PAP026	87	33.3%	chr11	6772736	CCDS7772.1	c.780T>A	p.S260R
OR6C2	olfactory receptor; family 6; subfamily C; member 2	ENSG00000179695	PAP026	87	20.7%	chr12	54133167	CCDS31824.1	c.903CT>NUL	p.NULL-1FsDel2bp
OR6C76	olfactory receptor; family 6; subfamily C; member 76	ENSG00000185821	PAP026	37	35.1%	chr12	54107226	CCDS31823.1	c.922AA>NUL	p.NULL-1FsDel2bp
ONECUT2	one cut homeobox 2	ENSG00000119547	PAP026	144	38.9%	chr18	53254999	CCDS42440.1	c.1053C>NULI	p.NULL-1FsDel1bp
OTOF	otoferlin	ENSG00000115155	PAP026	105	36.2%	chr2	26552692	CCDS1725.1	c.-1C>NULL	p.IVS22-3-1SpliceAcceptor
OTOF	otoferlin	ENSG00000115155	PAP026	88	19.3%	chr2	26554192	NM_194322	c.74G>T	p.R25M
OSBP	oxysterol binding protein	ENSG00000110048	PAP026	49	42.9%	chr11	59104308	CCDS7974.1	c.1793T>A	p.I598N
OSBPL2	oxysterol binding protein-like 2	ENSG00000130703	PAP026	187	25.1%	chr20	60287653	CCDS13495.1	c.537C>NULL	p.NULL-1FsDel1bp
PAX5	paired box 5	ENSG00000196092	PAP026	135	33.3%	chr9	37005094	CCDS6607.1	c.310C>T	p.R104C
PAPPA2	pappalysin 2	ENSG00000116183	PAP026	211	11.4%	chr1	174830632	CCDS41438.1	c.1269NULL>(	p.NULL-1FsIns1bp
PTHLH	parathyroid hormone-like hormone	ENSG00000087494	PAP026	241	38.2%	chr12	28007767	CCDS8715.1	c.305G>A	p.R102K
PNPLA7	patatin-like phospholipase domain containing 7	ENSG00000130653	PAP026	122	32.8%	chr9	139476500	CCDS7045.1	c.3674C>NULI	p.NULL-1FsDel1bp
PTCHD1	patched domain containing 1	ENSG00000165186	PAP026	149	13.4%	chrX	23307881	CCDS35215.2	c.604C>T	p.R202W
PTCH1	patched homolog 1 (Drosophila)	ENSG00000185920	PAP026	75	37.3%	chr9	97249326	CCDS6714.1	c.4033C>T	p.R1345C
PTCH2	patched homolog 2 (Drosophila)	ENSG00000117425	PAP026	132	23.5%	chr1	45070442	CCDS516.1	c.424G>A	p.A142T
PXN	paxillin	ENSG00000089159	PAP026	79	13.9%	chr12	119142145	ENST00000323871	c.985C>T	p.R329X
PCIF1	PDX1 C-terminal inhibiting factor 1	ENSG00000100982	PAP026	137	38.7%	chr20	44002940	CCDS13388.1	c.473C>T	p.T158M
PDZRN4	PDZ domain containing ring finger 4	ENSG00000165966	PAP026	84	14.3%	chr12	40253381	CCDS8739.1	c.1759G>A	p.A587T
PCNX	pecanex homolog (Drosophila)	ENSG00000100731	PAP026	148	29.7%	chr14	70444375	CCDS9806.1	c.55G>NULL	p.NULL-1FsDel1bp
PCNX	pecanex homolog (Drosophila)	ENSG00000100731	PAP026	34	38.2%	chr14	70584413	CCDS9806.1	c.4297A>G	p.M1433V
PPL	periplakin	ENSG00000118898	PAP026	292	25.0%	chr16	4875121	CCDS10526.1	c.3536G>A	p.R1179Q
PECI	peroxisomal D3;D2-enoyl-CoA isomerase	ENSG00000198721	PAP026	64	31.3%	chr6	4078935	NM_206836	c.60G>T	p.Q20H
PXMP2	peroxisomal membrane protein 2; 22kDa	ENSG00000176894	PAP026	59	25.4%	chr12	131804371	CCDS9280.1	c.499G>A	p.V167I
PPARGC1A	peroxisome proliferator-activated receptor gamma; coactivator 1 alpha	ENSG00000109819	PAP026	271	36.5%	chr4	23423590	CCDS3429.1	c.-1A>G	p.IVS9-2-1SpliceAcceptor
PPRC1	peroxisome proliferator-activated receptor gamma; coactivator-related 1	ENSG00000148840	PAP026	174	37.9%	chr10	103888982	CCDS7529.1	c.727C>T	p.R243C
PPRC1	peroxisome proliferator-activated receptor gamma; coactivator-related 1	ENSG00000148840	PAP026	84	34.5%	chr10	103898376	CCDS7529.1	c.4552T>C	p.Y1518H
PHF17	PHD finger protein 17	ENSG00000077684	PAP026	86	33.7%	chr4	130012568	CCDS34062.1	c.2230C>A	p.P744T
PHF20L1	PHD finger protein 20-like 1	ENSG00000129292	PAP026	36	36.1%	chr8	133898980	ENST00000395382	c.1512A>NULI	p.NULL-1FsDel1bp

PHF3	PHD finger protein 3	ENSG00000118482	PAP026	75	22.7%	chr6	64452056	CCDS4966.1	c.474A>NULL	p.NULL-1FsDel1bp
PREX2	phosphatidylinositol-3;4;5-trisphosphate-dependent Rac exchange factor 2	ENSG00000046889	PAP026	191	32.5%	chr8	69179946	CCDS6202.1	c.2735T>C	p.F912S
PDE4D	phosphodiesterase 4D; cAMP-specific (phosphodiesterase E3 dunce homolog; Drosophila)	ENSG00000113448	PAP026	50	20.0%	chr5	58516820	NM_001104631	c.710G>A	p.R237Q
PDE6C	phosphodiesterase 6C; cGMP-specific; cone; alpha prime	ENSG00000095464	PAP026	53	28.3%	chr10	95389842	CCDS7429.1	c.1508C>A	p.S503X
PACS1	phosphofurin acidic cluster sorting protein 1	ENSG00000175115	PAP026	69	36.2%	chr11	65765499	CCDS8129.1	c.2455G>A	p.V819M
PGAM5	phosphoglycerate mutase family member 5	ENSG00000176894	PAP026	59	25.4%	chr12	131804371	CCDS9280.1	c.499G>A	p.V167I
PIK3CB	phosphoinositide-3-kinase; catalytic; beta polypeptide	ENSG00000051382	PAP026	94	27.7%	chr3	139856988	CCDS3104.1	c.3146T>G	p.L1049R
PIK3R5	phosphoinositide-3-kinase; regulatory subunit 5	ENSG00000141506	PAP026	35	28.6%	chr17	8732405	CCDS11147.1	c.1424G>A	p.R475H
PLCB3	phospholipase C; beta 3 (phosphatidylinositol-specific)	ENSG00000149782	PAP026	48	31.3%	chr11	63791314	CCDS8064.1	c.3496C>G	p.P1166A
PHYH	phytanoyl-CoA 2-hydroxylase	ENSG00000107537	PAP026	68	16.2%	chr10	13365841	CCDS7097.1	c.832G>NULL	p.NULL-1FsDel1bp
PSD	pleckstrin and Sec7 domain containing	ENSG00000059915	PAP026	53	30.2%	chr10	104165845	CCDS31272.1	c.778C>NULL	p.NULL-1FsDel1bp
PLEKHA6	pleckstrin homology domain containing; family A member 6	ENSG00000143850	PAP026	163	24.5%	chr1	202495034	CCDS1444.1	c.1464G>NUL	p.NULL-1FsDel1bp
PLEKHN1	pleckstrin homology domain containing; family N member 1	ENSG00000187583	PAP026	252	15.9%	chr1	899110	CCDS4.1	c.1469C>T	p.T490M
PLEC	plectin	ENSG00000178209	PAP026	177	31.6%	chr8	145070909	CCDS43772.1	c.8967G>NUL	p.NULL-1FsDel1bp
PLXNB3	plexin B3	ENSG00000198753	PAP026	247	32.4%	chrX	152695968	CCDS14729.1	c.5039G>A	p.R1680H
POLQ	polymerase (DNA directed); theta	ENSG00000051341	PAP026	47	36.2%	chr3	122690545	CCDS33833.1	c.3923T>C	p.V1308A
POLR2B	polymerase (RNA) II (DNA directed) polypeptide B; 140kDa	ENSG00000047315	PAP026	56	35.7%	chr4	57591885	CCDS3511.1	c.3499A>C	p.I1167L
KCTD13	potassium channel tetramerisation domain containing 13	ENSG00000174943	PAP026	60	30.0%	chr16	29830865	CCDS10661.1	c.510A>NULL	p.NULL-1FsDel1bp
KCTD16	potassium channel tetramerisation domain containing 16	ENSG00000183775	PAP026	239	32.6%	chr5	143566923	CCDS34260.1	c.453NULL>C	p.NULL-1FsIns1bp
KCNK10	potassium channel; subfamily K; member 10	ENSG00000100433	PAP026	56	35.7%	chr14	87722143	CCDS9882.1	c.1121C>T	p.A374V
KCNJ12	potassium inwardly-rectifying channel; subfamily J; member 12	ENSG00000184185	PAP026	269	10.0%	chr17	21259635	CCDS11219.1	c.388T>G	p.F130V
KCNJ12	potassium inwardly-rectifying channel; subfamily J; member 12	ENSG00000184185	PAP026	587	10.9%	chr17	21259933	CCDS11219.1	c.686G>A	p.R229H
KCNQ1	potassium voltage-gated channel; KQT-like subfamily; member 1	ENSG00000053918	PAP026	112	43.8%	chr11	2565443	CCDS7736.1	c.1196C>NULI	p.NULL-1FsDel1bp
KCNQ2	potassium voltage-gated channel; KQT-like subfamily; member 2	ENSG00000075043	PAP026	62	38.7%	chr20	61509105	CCDS13520.1	c.2686C>NULI	p.NULL-1FsDel1bp
KCNA5	potassium voltage-gated channel; shaker-related subfamily; member 5	ENSG00000130037	PAP026	81	30.9%	chr12	5025317	CCDS8536.1	c.1743C>NULI	p.NULL-1FsDel1bp
PRDM2	PR domain containing 2; with ZNF domain	ENSG00000116731	PAP026	30	43.3%	chr1	13981336	CCDS150.1	c.4459AA>NU	p.NULL-1FsDel2bp
PRDM4	PR domain containing 4	ENSG00000110851	PAP026	151	38.4%	chr12	106664301	CCDS9115.1	c.1157C>T	p.S386L
PJA1	praja ring finger 1	ENSG00000181191	PAP026	192	12.0%	chrX	68299316	CCDS14393.1	c.491C>T	p.P164L
PTCRA	pre T-cell antigen receptor alpha	ENSG00000171611	PAP026	72	36.1%	chr6	43001111	CCDS4874.1	c.559C>A	p.R187S
PBX4	pre-B-cell leukemia homeobox 4	ENSG00000105717	PAP026	54	18.5%	chr19	19542039	CCDS12406.1	c.511C>T	p.P171S
PFDN5	prefoldin subunit 5	ENSG00000123349	PAP026	85	45.9%	chr12	51977946	CCDS8853.1	c.253G>A	p.D85N
PRNP	prion protein	ENSG00000171867	PAP026	108	25.9%	chr20	4628501	CCDS13080.1	c.635A>G	p.Q212R
PRRG1	proline rich Gla (G-carboxyglutamic acid) 1	ENSG00000130962	PAP026	287	20.2%	chrX	37197532	CCDS14239.1	c.394C>NULL	p.NULL-1FsDel1bp
PREPL	prolyl endopeptidase-like	ENSG00000138078	PAP026	38	26.3%	chr2	44404057	CCDS33190.1	c.-1T>NULL	p.IVS10-3-1SpliceAcceptor
POMC	proopiomelanocortin	ENSG00000115138	PAP026	90	33.3%	chr2	25237684	CCDS1717.1	c.574G>A	p.D192N
PCSK6	proprotein convertase subtilisin/kexin type 6	ENSG00000140479	PAP026	44	52.3%	chr15	99751082	ENST00000348070	c.1064C>T	p.S355L
PTGER4	prostaglandin E receptor 4 (subtype EP4)	ENSG00000171522	PAP026	60	38.3%	chr5	40728002	CCDS3930.1	c.1232G>A	p.G411D

PSMC4	proteasome (prosome; macropain) 26S subunit; ATPase; 4	ENSG00000013275	PAP026	72	25.0%	chr19	45172494	CCDS12547.1	c.592C>NULL	p.NULL-1FsDel1bp
PRKAA2	protein kinase; AMP-activated; alpha 2 catalytic subunit	ENSG00000162409	PAP026	63	33.3%	chr1	56944410	CCDS605.1	c.1351G>A	p.V451M
PPFIA3	protein tyrosine phosphatase; receptor type; f polypeptide (PTPRF); interacting protein (liprin); alpha 3	ENSG00000177380	PAP026	79	30.4%	chr19	54344708	CCDS12758.1	c.3447G>A	p.M1149I
PPFIA4	protein tyrosine phosphatase; receptor type; f polypeptide (PTPRF); interacting protein (liprin); alpha 4	ENSG00000143847	PAP026	91	33.0%	chr1	201304339	NM_015053	c.1766C>T	p.T589I
PTPRM	protein tyrosine phosphatase; receptor type; M	ENSG00000173482	PAP026	65	30.8%	chr18	8369288	CCDS11840.1	c.3697A>G	p.I1233V
PTPRS	protein tyrosine phosphatase; receptor type; S	ENSG00000105426	PAP026	69	33.3%	chr19	5171134	CCDS12140.1	c.3515G>A	p.R1172H
PCDHA10	protocadherin alpha 10	ENSG00000081842	PAP026	143	34.3%	chr5	140243823	CCDS4240.1	c.1786G>A	p.A596T
PCDHA11	protocadherin alpha 11	ENSG00000081842	PAP026	143	34.3%	chr5	140243823	CCDS4240.1	c.1786G>A	p.A596T
PCDHA12	protocadherin alpha 12	ENSG00000081842	PAP026	143	34.3%	chr5	140243823	CCDS4240.1	c.1786G>A	p.A596T
PCDHA6	protocadherin alpha 6	ENSG00000081842	PAP026	143	34.3%	chr5	140243823	CCDS4240.1	c.1786G>A	p.A596T
PCDHAC1	protocadherin alpha subfamily C; 1	ENSG00000081842	PAP026	143	34.3%	chr5	140243823	CCDS4240.1	c.1786G>A	p.A596T
PCDHB14	protocadherin beta 14	ENSG00000120327	PAP026	92	29.3%	chr5	140583455	CCDS4256.1	c.194NULL>G	p.NULL-1FsIns1bp
PCDHB16	protocadherin beta 16	ENSG00000196963	PAP026	91	30.8%	chr5	140543628	CCDS4251.1	c.1310T>C	p.I437T
PCDHB2	protocadherin beta 2	ENSG00000112852	PAP026	72	31.9%	chr5	140455613	CCDS4244.1	c.1055C>T	p.S352L
PRTG	protogenin homolog (Gallus gallus)	ENSG00000166450	PAP026	112	33.0%	chr15	53708452	CCDS42040.1	c.2848A>NULL	p.NULL-1FsDel1bp
PUS10	pseudouridylate synthase 10	ENSG00000162927	PAP026	68	39.7%	chr2	61028791	CCDS1865.1	c.1342G>A	p.V448I
PPFIBP2	PTPRF interacting protein; binding protein 2 (liprin beta 2)	ENSG00000166387	PAP026	89	29.2%	chr11	7627448	CCDS31419.1	c.2108G>A	p.R703Q
P2RX3	purinergic receptor P2X; ligand-gated ion channel; 3	ENSG00000109991	PAP026	61	21.3%	chr11	56872243	CCDS7953.1	c.415A>T	p.N139Y
P2RY4	pyrimidinergic receptor P2Y; G-protein coupled; 4	ENSG00000186912	PAP026	189	26.5%	chrX	69395143	CCDS14398.1	c.2154C>NULL	p.NULL-1FsDel1bp
PYCR1	pyrroline-5-carboxylate reductase 1	ENSG00000183010	PAP026	42	28.6%	chr17	77485867	CCDS11795.1	c.586G>A	p.G196R
RAB20	RAB20; member RAS oncogene family	ENSG00000139832	PAP026	136	28.7%	chr13	110011863	CCDS9512.1	c.5G>A	p.R2K
RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)	ENSG00000115839	PAP026	40	35.0%	chr2	135636788	CCDS33294.1	c.2387AA>NU	p.NULL-1FsDel2bp
RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	ENSG00000109756	PAP026	120	34.2%	chr4	160482400	CCDS43277.1	c.2286A>C	p.E762D
RSU1	Ras suppressor protein 1	ENSG00000148484	PAP026	47	29.8%	chr10	16777163	CCDS7112.1	c.-1C>NULL	p.IVS6-3-1SpliceAcceptor
RIT2	Ras-like without CAAX 2	ENSG00000152214	PAP026	89	31.5%	chr18	38757607	CCDS11921.1	c.545T>NULL	p.NULL-1FsDel1bp
RB1CC1	RB1-inducible coiled-coil 1	ENSG00000023287	PAP026	17	64.7%	chr8	53705644	CCDS34892.1	c.-1TT>NULL	p.IVS18-3-1SpliceAcceptor
RGS9BP	regulator of G protein signaling 9 binding protein	ENSG00000186326	PAP026	127	11.8%	chr19	37859616	CCDS12424.1	c.607NULL>G	p.NULL-1FsIns1bp
RXFP4	relaxin/insulin-like family peptide receptor 4	ENSG00000173080	PAP026	175	21.7%	chr1	154178869	CCDS1124.1	c.745C>T	p.R249C
RCOR3	REST corepressor 3	ENSG00000117625	PAP026	934	10.7%	chr1	209553504	CCDS31016.1	c.1259C>T	p.P420L
RET	ret proto-oncogene	ENSG00000165731	PAP026	115	35.7%	chr10	42920492	CCDS7200.1	c.712G>A	p.E238K
RBL2	retinoblastoma-like 2 (p130)	ENSG00000103479	PAP026	65	29.2%	chr16	52050952	CCDS10748.1	c.1268C>T	p.T423M
RBP3	retinol binding protein 3; interstitial	ENSG00000107618	PAP026	207	29.0%	chr10	48009254	CCDS7218.1	c.1630C>T	p.R544C
ARHGAP24	Rho GTPase activating protein 24	ENSG00000138639	PAP026	320	14.1%	chr4	87135578	CCDS34025.1	c.1747T>NULL	p.NULL-1FsDel1bp
ARHGAP27	Rho GTPase activating protein 27	ENSG00000159314	PAP026	85	29.4%	chr17	40862750	CCDS32670.1	c.679C>T	p.R227C
ARHGAP33	Rho GTPase activating protein 33	ENSG00000004777	PAP026	34	29.4%	chr19	40970342	CCDS12477.1	c.2552C>T	p.A851V
ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	ENSG00000196914	PAP026	96	22.9%	chr11	119824229	CCDS41727.1	c.1699C>T	p.H567Y
ARHGEF17	Rho guanine nucleotide exchange factor (GEF) 17	ENSG00000110237	PAP026	72	45.8%	chr11	72699175	CCDS8221.1	c.1844C>NULL	p.NULL-1FsDel1bp
RHPN1	rhophilin; Rho GTPase binding protein 1	ENSG00000158106	PAP026	120	34.2%	chr8	144534613	NM_052924	c.1444C>T	p.P482S

RTKN2	rhotekin 2	ENSG00000182010	PAP026	29	34.5%	chr10	63692589	CCDS7263.1	c.-1T>NULL	p.IVS1-3-1SpliceAcceptor
RNF123	ring finger protein 123	ENSG00000164068	PAP026	88	13.6%	chr3	49713977	CCDS33758.1	c.1327C>T	p.R443C
RNF43	ring finger protein 43	ENSG00000108375	PAP026	96	57.3%	chr17	53790160	CCDS11607.1	c.3331G>NUL	p.NULL-1FsDel1bp
RBMX2	RNA binding motif protein; X-linked 2	ENSG00000134597	PAP026	283	30.4%	chrX	129363676	ENST00000257020	c.19G>A	p.E7K
ROBLD3	roadblock domain containing 3	ENSG00000116586	PAP026	161	23.0%	chr1	154294456	CCDS1128.1	c.295G>A	p.V99M
RYR1	ryanodine receptor 1 (skeletal)	ENSG00000196218	PAP026	114	30.7%	chr19	43642995	CCDS33011.1	c.2501G>A	p.R834Q
RYR1	ryanodine receptor 1 (skeletal)	ENSG00000196218	PAP026	199	36.2%	chr19	43668406	CCDS33011.1	c.5271C>NULI	p.NULL-1FsDel1bp
SCCPDH	saccharopine dehydrogenase (putative)	ENSG00000143653	PAP026	61	26.2%	chr1	244970154	CCDS31084.1	c.442A>C	p.I148L
SCCPDH	saccharopine dehydrogenase (putative)	ENSG00000143653	PAP026	83	12.0%	chr1	244989925	CCDS31084.1	c.857T>C	p.V286A
SATB1	SATB homeobox 1	ENSG00000182568	PAP026	43	27.9%	chr3	18366081	CCDS2631.1	c.2389C>NULI	p.NULL-1FsDel1bp
SLFN12	schlafen family member 12	ENSG00000172123	PAP026	105	13.3%	chr17	30762727	CCDS11295.1	c.1480A>G	p.M494V
SCRT1	scratch homolog 1; zinc finger protein (Drosophila)	ENSG00000170616	PAP026	92	32.6%	chr8	145527843	CCDS6421.1	c.859G>A	p.D287N
SRRT	serrate RNA effector molecule homolog (Arabidopsis)	ENSG00000087087	PAP026	65	20.0%	chr7	100317268	CCDS34709.1	c.304G>NULL	p.NULL-1FsDel1bp
SETD2	SET domain containing 2	ENSG00000181555	PAP026	59	35.6%	chr3	47122501	CCDS2749.1	c.3320A>C	p.K1107T
SETDB1	SET domain; bifurcated 1	ENSG00000143379	PAP026	101	25.7%	chr1	149201814	CCDS972.1	c.3286C>T	p.P1096S
SRPK2	SFRS protein kinase 2	ENSG00000135250	PAP026	103	25.2%	chr7	104560745	CCDS34724.1	c.1586C>T	p.P529L
SHANK1	SH3 and multiple ankyrin repeat domains 1	ENSG00000161681	PAP026	65	53.8%	chr19	55898856	CCDS12799.1	c.1596G>NUL	p.NULL-1FsDel1bp
SH3PXD2B	SH3 and PX domains 2B	ENSG00000174705	PAP026	166	26.5%	chr5	171698591	CCDS34291.1	c.2123G>A	p.R708H
SH3TC1	SH3 domain and tetratricopeptide repeats 1	ENSG00000125089	PAP026	80	31.3%	chr4	8293413	CCDS3399.1	c.3842C>T	p.T1281M
SH3D20	SH3 domain containing 20	ENSG00000159314	PAP026	85	29.4%	chr17	40862750	CCDS32670.1	c.679C>T	p.R227C
SH3RF2	SH3 domain containing ring finger 2	ENSG00000156463	PAP026	60	26.7%	chr5	145419751	CCDS4280.1	c.1685C>NULI	p.NULL-1FsDel1bp
SH3BP1	SH3-domain binding protein 1	ENSG00000100092	PAP026	148	34.5%	chr22	36368876	CCDS13952.2	c.313C>T	p.Q105X
SHOX2	short stature homeobox 2	ENSG00000168779	PAP026	219	29.2%	chr3	159303336	CCDS43164.1	c.380C>T	p.A127V
STAT4	signal transducer and activator of transcription 4	ENSG00000138378	PAP026	27	37.0%	chr2	191719731	CCDS2310.1	c.-1T>NULL	p.IVS1-3-1SpliceAcceptor
STAT5B	signal transducer and activator of transcription 5B	ENSG00000173757	PAP026	52	40.4%	chr17	37623762	CCDS11423.1	c.1281C>NULI	p.NULL-1FsDel1bp
SIPA1L2	signal-induced proliferation-associated 1 like 2	ENSG00000116991	PAP026	62	25.8%	chr1	230604772	CCDS41474.1	c.5011G>A	p.D1671N
SIPA1L3	signal-induced proliferation-associated 1 like 3	ENSG00000105738	PAP026	62	32.3%	chr19	43313050	CCDS33007.1	c.2941G>A	p.V981M
SIRPA	signal-regulatory protein alpha	ENSG00000198053	PAP026	103	18.4%	chr20	1866126	CCDS13022.1	c.1427T>C	p.V476A
SSH3	slingshot homolog 3 (Drosophila)	ENSG00000172830	PAP026	73	38.4%	chr11	66831963	CCDS8157.1	c.862C>A	p.L288M
SMAP1	small ArfGAP 1	ENSG00000112305	PAP026	26	53.8%	chr6	71565091	CCDS43478.1	c.506A>NULL	p.NULL-1FsDel1bp
SMTN	smoothelin	ENSG00000183963	PAP026	347	17.3%	chr22	29817000	CCDS13887.1	c.991C>T	p.R331W
SCN2B	sodium channel; voltage-gated; type II; beta	ENSG00000149575	PAP026	241	23.2%	chr11	117542899	CCDS8390.1	c.760A>NULL	p.NULL-1FsDel1bp
SCN2B	sodium channel; voltage-gated; type II; beta	ENSG00000149575	PAP026	193	33.2%	chr11	117544608	CCDS8390.1	c.139C>T	p.R47C
SLC16A11	solute carrier family 16; member 11 (monocarboxylic acid transporter 11)	ENSG00000174326	PAP026	74	14.9%	chr17	6887547	CCDS11086.1	c.355C>NULL	p.NULL-1FsDel1bp
SLC16A13	solute carrier family 16; member 13 (monocarboxylic acid transporter 13)	ENSG00000174327	PAP026	410	25.9%	chr17	6882323	CCDS11085.1	c.472T>NULL	p.NULL-1FsDel1bp
SLC22A16	solute carrier family 22 (organic cation/carnitine transporter); member 16	ENSG00000004809	PAP026	80	31.3%	chr6	110870425	CCDS5084.1	c.898C>T	p.R300X
SLC22A23	solute carrier family 22; member 23	ENSG00000137266	PAP026	67	34.3%	chr6	3235036	CCDS34331.1	c.431G>A	p.R144Q
SLC26A9	solute carrier family 26; member 9	ENSG00000174502	PAP026	122	24.6%	chr1	204150910	CCDS30989.1	c.2688G>NUL	p.NULL-1FsDel1bp

SLC27A1	solute carrier family 27 (fatty acid transporter); member 1	ENSG00000130304	PAP026	79	25.3%	chr19	17458682	CCDS32953.1	c.478G>A	p.V160M
SLC32A1	solute carrier family 32 (GABA vesicular transporter); member 1	ENSG00000101438	PAP026	310	31.9%	chr20	36790598	CCDS13307.1	c.1480G>A	p.V494I
SLC35F1	solute carrier family 35; member F1	ENSG00000196376	PAP026	163	31.9%	chr6	118741993	CCDS34524.1	c.1112G>A	p.R371H
SLC39A3	solute carrier family 39 (zinc transporter); member 3	ENSG00000141873	PAP026	94	33.0%	chr19	2684032	CCDS12093.1	c.662G>A	p.R221Q
SLC4A3	solute carrier family 4; anion exchanger; member 3	ENSG00000114923	PAP026	42	38.1%	chr2	220202362	CCDS2446.1	c.470A>NULL	p.NULL-1FsDel1bp
SLC4A4	solute carrier family 4; sodium bicarbonate cotransporter; member 4	ENSG00000080493	PAP026	87	34.5%	chr4	72644726	CCDS43236.1	c.2990A>G	p.H997R
SLC43A2	solute carrier family 43; member 2	ENSG00000167703	PAP026	43	39.5%	chr17	1425682	CCDS11006.1	c.1676T>C	p.I559T
SLC6A5	solute carrier family 6 (neurotransmitter transporter; glycine); member 5	ENSG00000165970	PAP026	72	36.1%	chr11	20579634	CCDS7854.1	c.387G>NULL	p.NULL-1FsDel1bp
SLC7A6OS	solute carrier family 7; member 6 opposite strand	ENSG00000103061	PAP026	162	35.8%	chr16	66892699	CCDS10865.1	c.1040C>NUL	p.NULL-1FsDel1bp
SLC8A3	solute carrier family 8 (sodium/calcium exchanger); member 3	ENSG00000100678	PAP026	234	28.2%	chr14	69703430	CCDS35498.1	c.1463G>T	p.R488L
SORBS2	sorbin and SH3 domain containing 2	ENSG00000154556	PAP026	43	30.2%	chr4	186781079	CCDS3845.1	c.2486G>A	p.R829H
SORL1	sortilin-related receptor; L(DLR class) A repeats-containing	ENSG00000137642	PAP026	50	30.0%	chr11	120984030	CCDS8436.1	c.5174C>T	p.A1725V
SYNE1	spectrin repeat containing; nuclear envelope 1	ENSG00000131018	PAP026	98	23.5%	chr6	152813577	CCDS5236.1	c.3271C>T	p.R1091W
SYNE2	spectrin repeat containing; nuclear envelope 2	ENSG00000054654	PAP026	71	35.2%	chr14	63668884	CCDS9761.2	c.14489G>A	p.G4830D
SPTBN2	spectrin; beta; non-erythrocytic 2	ENSG00000173898	PAP026	62	29.0%	chr11	66224800	CCDS8150.1	c.3346C>T	p.R1116W
SPTBN4	spectrin; beta; non-erythrocytic 4	ENSG00000160460	PAP026	34	41.2%	chr19	45710434	CCDS12559.1	c.1898C>A	p.A633E
SPAG16	sperm associated antigen 16	ENSG00000144451	PAP026	46	21.7%	chr2	214062958	CCDS2396.1	c.969A>T	p.Q323H
SFRS18	splicing factor; arginine/serine-rich 18	ENSG00000132424	PAP026	102	23.5%	chr6	99956064	CCDS5043.1	c.2581A>NULI	p.NULL-1FsDel1bp
SFRS2IP	splicing factor; arginine/serine-rich 2; interacting protein	ENSG00000139218	PAP026	295	35.6%	chr12	44607088	CCDS8748.2	c.2663C>T	p.S888F
SMC1A	structural maintenance of chromosomes 1A	ENSG00000072501	PAP026	44	31.8%	chrX	53449528	CCDS14352.1	c.1631C>T	p.A544V
SULF2	sulfatase 2	ENSG00000196562	PAP026	62	32.3%	chr20	45746682	CCDS13408.1	c.788G>A	p.R263H
SENP6	SUMO1/sentrin specific peptidase 6	ENSG00000112701	PAP026	49	26.5%	chr6	76443578	CCDS43483.1	c.1713T>NULI	p.NULL-1FsDel1bp
SUSD2	sushi domain containing 2	ENSG00000099994	PAP026	221	33.9%	chr22	22912046	CCDS13824.1	c.1402C>T	p.R468C
SMARCC2	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily c; member 2	ENSG00000139613	PAP026	57	24.6%	chr12	54861802	CCDS8907.1	c.793C>A	p.P265T
SYCP2	synaptonemal complex protein 2	ENSG00000196074	PAP026	102	28.4%	chr20	57900442	CCDS13482.1	c.2798A>NULI	p.NULL-1FsDel1bp
SYNPO	synaptopodin	ENSG00000171992	PAP026	235	36.2%	chr5	150009697	CCDS4308.1	c.1667G>A	p.R556H
TAF1	TAF1 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 250kDa	ENSG00000147133	PAP026	142	33.1%	chrX	70519725	CCDS14412.1	c.1993A>NULI	p.NULL-1FsDel1bp
TAF9	TAF9 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 32kDa	ENSG00000085231	PAP026	66	15.2%	chr5	68696917	CCDS4002.1	c.1198A>NULI	p.NULL-1FsDel1bp
TAOK2	TAO kinase 2	ENSG00000149930	PAP026	133	17.3%	chr16	29910083	CCDS10662.1	c.2843G>A	p.R948H
TAPBP	TAP binding protein (tapasin)	ENSG00000112493	PAP026	60	36.7%	chr6	33389786	CCDS34426.1	c.11T>C	p.L4P
TPRN	taperin	ENSG00000176058	PAP026	94	29.8%	chr9	139206846	CCDS7035.1	c.1164GGA>N	p.NULL-1FsDel3bp
TAS1R2	taste receptor; type 1; member 2	ENSG00000179002	PAP026	78	48.7%	chr1	19038849	CCDS187.1	c.2351G>A	p.S784N
TBC1D14	TBC1 domain family; member 14	ENSG00000132405	PAP026	207	38.2%	chr4	6976198	CCDS3394.1	c.136C>A	p.L46I
TBC1D16	TBC1 domain family; member 16	ENSG00000167291	PAP026	148	28.4%	chr17	75598683	CCDS11766.1	c.650C>T	p.A217V
TBX6	T-box 6	ENSG00000149922	PAP026	143	30.8%	chr16	30007579	CCDS10670.1	c.850G>NULL	p.NULL-1FsDel1bp
TEAD2	TEA domain family member 2	ENSG00000074219	PAP026	175	18.3%	chr19	54542285	CCDS12761.1	c.1056C>NUL	p.NULL-1FsDel1bp
TEX10	testis expressed 10	ENSG00000136891	PAP026	91	34.1%	chr9	102149239	CCDS6748.1	c.451C>A	p.H151N
TET1	tet oncogene 1	ENSG00000138336	PAP026	90	26.7%	chr10	70075607	CCDS7281.1	c.3115C>T	p.P1039S
TSPAN12	tetraspanin 12	ENSG00000106025	PAP026	105	29.5%	chr7	120215903	CCDS5777.1	c.897C>A	p.H299Q
TARS	threonyl-tRNA synthetase	ENSG00000113407	PAP026	95	18.9%	chr5	33484562	CCDS3899.1	c.297A>C	p.K99N

THADA	thyroid adenoma associated	ENSG00000115970	PAP026	40	27.5%	chr2	43373821	NM_001083953	c.4852AG>NU	p.NULL-1FsDel2bp
TJP1	tight junction protein 1 (zona occludens 1)	ENSG00000104067	PAP026	59	27.1%	chr15	27807485	CCDS42007.1	c.2048A>G	p.Q683R
TRAP1	TNF receptor-associated protein 1	ENSG00000126602	PAP026	63	39.7%	chr16	3653496	CCDS10508.1	c.1774AAG>N	p.NULL-1FsDel3bp
TAAR8	trace amine associated receptor 8	ENSG00000146385	PAP026	117	10.3%	chr6	132915909	CCDS5154.1	c.385A>G	p.R129G
TANK	TRAF family member-associated NFKB activator	ENSG00000136560	PAP026	75	18.7%	chr2	161795785	CCDS2215.1	c.578T>C	p.L193P
TRAF3IP2	TRAF3 interacting protein 2	ENSG00000056972	PAP026	98	33.7%	chr6	112019744	CCDS5092.1	c.266T>C	p.V89A
TCEA2	transcription elongation factor A (SII); 2	ENSG00000171703	PAP026	94	31.9%	chr20	62172126	CCDS13553.1	c.587T>G	p.L196R
TCF23	transcription factor 23	ENSG00000163792	PAP026	79	24.1%	chr2	27226128	ENST00000407815	c.270NULL>A	p.NULL-1FsIns1bp
TTF1	transcription termination factor; RNA polymerase I	ENSG00000125482	PAP026	148	23.6%	chr9	134267209	CCDS6948.1	c.2187NULL>A	p.NULL-1FsIns1bp
TACC2	transforming; acidic coiled-coil containing protein 2	ENSG00000138162	PAP026	73	37.0%	chr10	123834089	CCDS7626.1	c.2084C>T	p.P695L
TRPC6	transient receptor potential cation channel; subfamily C; member 6	ENSG00000137672	PAP026	76	27.6%	chr11	100829023	CCDS8311.1	c.2669A>T	p.D890V
TAPT1	transmembrane anterior posterior transformation 1	ENSG00000169762	PAP026	28	60.7%	chr4	15799079	NM_153365	c.-1T>NULL	p.IVS4-3-1SpliceAcceptor
TMBIM6	transmembrane BAX inhibitor motif containing 6	ENSG00000139644	PAP026	101	14.9%	chr12	48460575	ENST00000395006	c.697AAAAA>	p.NULL-1FsDel5bp
TMBIM6	transmembrane BAX inhibitor motif containing 6	ENSG00000139644	PAP026	101	16.8%	chr12	48460575	ENST00000395006	c.697AAAA>N	p.NULL-1FsDel4bp
TMEM132E	transmembrane protein 132E	ENSG00000181291	PAP026	40	50.0%	chr17	29985951	CCDS11283.1	c.1439A>G	p.D480G
TMEM150A	transmembrane protein 150A	ENSG00000168890	PAP026	54	22.2%	chr2	85681732	CCDS33233.1	c.207AAC>NU	p.NULL-1FsDel3bp
TMEM173	transmembrane protein 173	ENSG00000184584	PAP026	116	40.5%	chr5	138840950	CCDS4215.1	c.389T>C	p.L130P
TMEM2	transmembrane protein 2	ENSG00000135048	PAP026	64	26.6%	chr9	73554880	CCDS6638.1	c.560A>NULL	p.NULL-1FsDel1bp
TMEM54	transmembrane protein 54	ENSG00000121900	PAP026	79	35.4%	chr1	33134100	CCDS371.1	c.327C>NULL	p.NULL-1FsDel1bp
TMEM57	transmembrane protein 57	ENSG00000204178	PAP026	144	37.5%	chr1	25697426	CCDS30638.1	c.1877A>G	p.Y626C
TMEM74	transmembrane protein 74	ENSG00000164841	PAP026	44	27.3%	chr8	109865857	CCDS6310.1	c.647G>A	p.R216H
TNPO2	transportin 2	ENSG00000105576	PAP026	48	33.3%	chr19	12673634	NM_001136196	c.2443G>A	p.E815K
TCHH	trichohyalin	ENSG00000159450	PAP026	125	10.4%	chr1	150348043	CCDS41396.1	c.4274G>A	p.R1425H
TCHHL1	trichohyalin-like 1	ENSG00000182898	PAP026	371	22.9%	chr1	150325434	CCDS30857.1	c.1348G>A	p.E450K
TRIM56	tripartite motif-containing 56	ENSG00000169871	PAP026	270	27.4%	chr7	100517650	CCDS43625.1	c.337G>A	p.G113R
TRIM7	tripartite motif-containing 7	ENSG00000146054	PAP026	74	31.1%	chr5	180555056	CCDS4462.1	c.1252G>A	p.V418M
TRMT61A	tRNA methyltransferase 61 homolog A (S. cerevisiae)	ENSG00000166166	PAP026	92	20.7%	chr14	103068869	CCDS41994.1	c.529G>T	p.A177S
TROVE2	TROVE domain family; member 2	ENSG00000116747	PAP026	85	15.3%	chr1	191317188	CCDS1379.1	c.1158G>T	p.L386F
TTLL10	tubulin tyrosine ligase-like family; member 10	ENSG00000162571	PAP026	57	31.6%	chr1	1108142	CCDS8.1	c.721C>T	p.P241S
TTLL2	tubulin tyrosine ligase-like family; member 2	ENSG00000120440	PAP026	82	14.6%	chr6	167674220	CCDS5301.1	c.842C>T	p.A281V
TUBGCP6	tubulin; gamma complex associated protein 6	ENSG00000128159	PAP026	104	17.3%	chr22	48999931	CCDS14087.1	c.4397C>T	p.A1466V
TNFAIP8L2	tumor necrosis factor; alpha-induced protein 8-like 2	ENSG00000163154	PAP026	162	11.7%	chr1	149398051	CCDS985.1	c.254C>A	p.A85D
TP53BP1	tumor protein p53 binding protein 1	ENSG00000067369	PAP026	30	33.3%	chr15	41517860	CCDS10096.1	c.3130C>T	p.Q1044X
TP53BP2	tumor protein p53 binding protein; 2	ENSG00000143514	PAP026	65	27.7%	chr1	222056635	CCDS1538.1	c.644C>T	p.A215V
TP53BP2	tumor protein p53 binding protein; 2	ENSG00000143514	PAP026	133	21.8%	chr1	222058554	CCDS1538.1	c.381A>NULL	p.NULL-1FsDel1bp
TP53I13	tumor protein p53 inducible protein 13	ENSG00000167543	PAP026	64	18.8%	chr17	24920201	CCDS42289.1	c.112C>T	p.P38S
UHMK1	U2AF homology motif (UHM) kinase 1	ENSG00000152332	PAP026	112	18.8%	chr1	160736534	CCDS1239.1	c.434C>A	p.A145D
UBFD1	ubiquitin family domain containing 1	ENSG00000103353	PAP026	291	30.6%	chr16	23476265	ENST00000219638	c.373A>NULL	p.NULL-1FsDel1bp
USP28	ubiquitin specific peptidase 28	ENSG00000048028	PAP026	24	45.8%	chr11	113205217	CCDS31680.1	c.971G>A	p.R324H
UBA1	ubiquitin-like modifier activating enzyme 1	ENSG00000130985	PAP026	414	37.0%	chrX	46943832	CCDS14275.1	c.355C>T	p.R119W

GALNTL4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4	ENSG00000110328	PAP026	41	41.5%	chr11	11319085	CCDS7807.1	c.1135C>T	p.R379W
ULK4	unc-51-like kinase 4 (C. elegans)	ENSG00000168038	PAP026	32	34.4%	chr3	41835989	CCDS43071.1	c.1861A>NULL	p.NULL-1FsDel1bp
UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)	ENSG00000005007	PAP026	87	33.3%	chr19	18829241	CCDS12386.1	c.2081G>A	p.R694Q
USH2A	Usher syndrome 2A (autosomal recessive; mild)	ENSG00000042781	PAP026	162	21.6%	chr1	213914392	CCDS31025.1	c.13484G>A	p.R4495H
UTP20	UTP20; small subunit (SSU) processome component; homolog (yeast)	ENSG00000120800	PAP026	97	33.0%	chr12	100204288	CCDS9081.1	c.385T>NULL	p.NULL-1FsDel1bp
VPS13C	vacuolar protein sorting 13 homolog C (S. cerevisiae)	ENSG00000129003	PAP026	55	30.9%	chr15	60070535	CCDS32257.1	c.1534A>C	p.I512L
VPS28	vacuolar protein sorting 28 homolog (S. cerevisiae)	ENSG00000160948	PAP026	138	29.7%	chr8	145620161	CCDS34967.1	c.619G>A	p.V207M
VPS39	vacuolar protein sorting 39 homolog (S. cerevisiae)	ENSG00000166887	PAP026	105	26.7%	chr15	40264117	CCDS10083.1	c.608C>T	p.A203V
VPS4B	vacuolar protein sorting 4 homolog B (S. cerevisiae)	ENSG00000119541	PAP026	138	28.3%	chr18	59215360	CCDS11983.1	c.979C>T	p.R327W
VAPB	VAMP (vesicle-associated membrane protein)-associated protein B and C	ENSG00000124164	PAP026	137	42.3%	chr20	56426736	CCDS33498.1	c.122G>A	p.C41Y
VAX2	ventral anterior homeobox 2	ENSG00000116035	PAP026	195	35.9%	chr2	71013696	CCDS1911.1	c.727C>NULL	p.NULL-1FsDel1bp
VCAN	versican	ENSG00000038427	PAP026	69	29.0%	chr5	82868746	CCDS4060.1	c.4168NULL>(	p.NULL-1FsIns3bp
VGLL2	vestigial like 2 (Drosophila)	ENSG00000170162	PAP026	196	28.6%	chr6	117698422	CCDS5115.1	c.415C>T	p.R139C
VMAC	vimentin-type intermediate filament associated coiled-coil protein	ENSG00000187650	PAP026	49	26.5%	chr19	5860058	CCDS32881.1	c.415C>NULL	p.NULL-1FsDel1bp
WIPF1	WAS/WASL interacting protein family; member 1	ENSG00000115935	PAP026	160	35.0%	chr2	175145276	CCDS2260.1	c.503G>A	p.R168Q
WDTC1	WD and tetratricopeptide repeats 1	ENSG00000142784	PAP026	65	55.4%	chr1	27493695	CCDS296.1	c.861G>NULL	p.NULL-1FsDel1bp
WDFY3	WD repeat and FYVE domain containing 3	ENSG00000163625	PAP026	127	29.1%	chr4	85876432	CCDS3609.1	c.6830G>A	p.S2277N
WDR90	WD repeat domain 90	ENSG00000161996	PAP026	112	34.8%	chr16	645111	CCDS42092.1	c.1519G>A	p.V507I
WNK3	WNK lysine deficient protein kinase 3	ENSG00000196632	PAP026	59	27.1%	chrX	54241753	CCDS14357.1	c.5132G>A	p.R1711H
WSCD2	WSC domain containing 2	ENSG00000075035	PAP026	117	34.2%	chr12	107114044	CCDS41828.1	c.305C>T	p.A102V
WAC	WW domain containing adaptor with coiled-coil	ENSG00000095787	PAP026	35	34.3%	chr10	28946655	CCDS7159.1	c.1810G>T	p.E604X
XKR5	XK; Kell blood group complex subunit-related family; member 5	ENSG00000186530	PAP026	198	30.3%	chr8	6657036	ENST00000334706	c.2292NULL>(	p.NULL-1FsIns1bp
ZBTB20	zinc finger and BTB domain containing 20	ENSG00000181722	PAP026	118	30.5%	chr3	115540693	CCDS2981.1	c.2277C>NULL	p.NULL-1FsDel1bp
ZBTB5	zinc finger and BTB domain containing 5	ENSG00000168795	PAP026	147	31.3%	chr9	37432058	CCDS6610.1	c.491G>A	p.G164D
ZSCAN29	zinc finger and SCAN domain containing 29	ENSG00000140265	PAP026	310	27.4%	chr15	41441257	CCDS10095.2	c.1865G>T	p.G622V
ZSCAN29	zinc finger and SCAN domain containing 29	ENSG00000140265	PAP026	134	32.8%	chr15	41445836	CCDS10095.2	c.986C>T	p.A329V
ZC3H13	zinc finger CCCH-type containing 13	ENSG00000123200	PAP026	94	25.5%	chr13	45441692	CCDS9400.1	c.4211NULL>/	p.NULL-1FsIns1bp
ZC3H13	zinc finger CCCH-type containing 13	ENSG00000123200	PAP026	710	26.9%	chr13	45447614	CCDS9400.1	c.2827AG>NU	p.NULL-1FsDel2bp
ZFHX3	zinc finger homeobox 3	ENSG00000140836	PAP026	88	47.7%	chr16	71549259	CCDS10908.1	c.5005G>NUL	p.NULL-1FsDel1bp
ZNF189	zinc finger protein 189	ENSG00000136870	PAP026	67	37.3%	chr9	103201274	CCDS6754.1	c.15C>NULL	p.NULL-1FsDel1bp
ZNF213	zinc finger protein 213	ENSG00000085644	PAP026	286	32.5%	chr16	3131147	CCDS10495.1	c.1178G>A	p.R393H
ZNF264	zinc finger protein 264	ENSG00000083844	PAP026	111	27.9%	chr19	62414792	CCDS33127.1	c.515G>T	p.G172V
ZNF365	zinc finger protein 365	ENSG00000138311	PAP026	43	58.1%	chr10	63829519	CCDS31209.1	c.1189A>NULL	p.NULL-1FsDel1bp
ZNF37A	zinc finger protein 37A	ENSG00000075407	PAP026	40	27.5%	chr10	38447424	CCDS31183.1	c.1339T>NULL	p.NULL-1FsDel1bp
ZNF48	zinc finger protein 48	ENSG00000180035	PAP026	103	25.2%	chr16	30316800	CCDS10679.1	c.728G>NULL	p.NULL-1FsDel1bp
ZNF521	zinc finger protein 521	ENSG00000198795	PAP026	397	29.0%	chr18	21058476	CCDS32806.1	c.6756NULL>(	p.NULL-1FsIns1bp

ZNF570	zinc finger protein 570	ENSG00000171827	PAP026	52	36.5%	chr19	42666962	CCDS12504.1	c.598A>NULL	p.NULL-1FsDel1bp
ZNF609	zinc finger protein 609	ENSG00000180357	PAP026	140	22.9%	chr15	62754300	CCDS32270.1	c.2194A>NULI	p.NULL-1FsDel1bp
ZNF638	zinc finger protein 638	ENSG00000075292	PAP026	92	15.2%	chr2	71507648	CCDS1917.1	c.5141C>T	p.T1714I
ZNF648	zinc finger protein 648	ENSG00000179930	PAP026	100	29.0%	chr1	180292948	CCDS30952.1	c.821G>C	p.G274A
ZNF649	zinc finger protein 649	ENSG00000198093	PAP026	130	31.5%	chr19	57085786	CCDS12843.1	c.1415G>A	p.S472N
ZNF649	zinc finger protein 649	ENSG00000198093	PAP026	126	20.6%	chr19	57086353	CCDS12843.1	c.848T>A	p.I283N
ZNF684	zinc finger protein 684	ENSG00000117010	PAP026	129	25.6%	chr1	40785580	CCDS454.1	c.998G>A	p.G333D
ZNF710	zinc finger protein 710	ENSG00000140548	PAP026	105	34.3%	chr15	88411712	CCDS10358.1	c.339G>T	p.K113N
ZNF81	zinc finger protein 81	ENSG00000197779	PAP026	62	30.6%	chrX	47659656	CCDS43933.1	c.667C>T	p.H223Y
ZNF828	zinc finger protein 828	ENSG00000198824	PAP026	220	35.0%	chr13	114108869	CCDS9545.1	c.1450T>NULI	p.NULL-1FsDel1bp
ZNF831	zinc finger protein 831	ENSG00000124203	PAP026	157	26.1%	chr20	57199615	CCDS42894.1	c.146NULL>C	p.NULL-1FsIns1bp
ZKSCAN1	zinc finger with KRAB and SCAN domains 1	ENSG00000106261	PAP026	89	27.0%	chr7	99469685	CCDS34698.1	c.1621AG>NU	p.NULL-1FsDel2bp
ZCCHC11	zinc finger; CCHC domain containing 11	ENSG00000134744	PAP026	73	35.6%	chr1	52713360	CCDS30715.1	c.2459C>T	p.A820V
ZDHHC3	zinc finger; DHHC-type containing 3	ENSG00000163812	PAP026	105	28.6%	chr3	44975849	CCDS2724.1	c.389C>NULL	p.NULL-1FsDel1bp
ZMYND11	zinc finger; MYND domain containing 11	ENSG00000015171	PAP026	86	14.0%	chr10	284310	CCDS7052.1	c.1142G>A	p.S381N
ZSWIM1	zinc finger; SWIM-type containing 1	ENSG00000168612	PAP026	127	34.6%	chr20	43944940	CCDS13382.2	c.302G>T	p.R101L
ZSWIM1	zinc finger; SWIM-type containing 1	ENSG00000168612	PAP026	252	33.3%	chr20	43945431	CCDS13382.2	c.793C>A	p.L265I
ZXDA	zinc finger; X-linked; duplicated A	ENSG00000198205	PAP026	83	24.1%	chrX	57953087	CCDS14376.1	c.493G>A	p.V165I
ZAN	zonadhesin	ENSG00000146839	PAP026	102	24.5%	chr7	100172170	ENST00000349350	c.235G>NULL	p.NULL-1FsDel1bp
ZAN	zonadhesin	ENSG00000146839	PAP026	53	20.8%	chr7	100199675	ENST00000349350	c.4187G>A	p.C1396Y
ALAS1	aminolevulinate; delta-; synthase 1	ENSG00000023330	PAP030	111	11.7%	chr3	52211561	CCDS2847.1	c.-1A>G	p.IVS1-2-1SpliceAcceptor
AMOTL2	angiomotin like 2	ENSG00000114019	PAP030	122	13.1%	chr3	135572905	CCDS33860.1	c.61C>T	p.R21C
ABCC10	ATP-binding cassette; sub-family C (CFTR/MRP); member 10	ENSG00000124574	PAP030	467	14.3%	chr6	43507902	CCDS4896.1	c.77G>A	p.R26Q
CHST5	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	ENSG00000135702	PAP030	143	11.2%	chr16	74120886	CCDS10919.1	c.898C>T	p.R300W
CA5A	carbonic anhydrase VA; mitochondrial	ENSG00000174990	PAP030	207	13.0%	chr16	86527463	CCDS10965.1	c.95G>A	p.R32Q
C1orf167	chromosome 1 open reading frame 167	ENSG00000215910	PAP030	141	11.3%	chr1	11767860	ENST00000312793	c.1127G>T	p.R376L
C14orf106	chromosome 14 open reading frame 106	ENSG00000129534	PAP030	135	11.1%	chr14	44781232	CCDS9684.1	c.898C>A	p.L300M
C19orf21	chromosome 19 open reading frame 21	ENSG00000099812	PAP030	82	12.2%	chr19	708898	CCDS12042.1	c.952G>A	p.D318N
CORIN	corin; serine peptidase	ENSG00000145244	PAP030	88	12.5%	chr4	47389860	CCDS3477.1	c.-1T>NULL	p.IVS5-3-1SpliceAcceptor
c19orf66	DAVID_chromosome 19 open reading frame 66	NM_018381	PAP030	121	11.6%	chr19	10062977	NM_018381	c.436AA>NUL	p.NULL-1FsDel2bp
c19orf66	DAVID_chromosome 19 open reading frame 66	NM_018381	PAP030	125	10.4%	chr19	10062979	NM_018381	c.438G>C	p.K146N
EPPK1	DAVID_epiplakin 1	NM_031308	PAP030	101	15.8%	chr8	145012800	NM_031308	c.6610C>T	p.R2204W
DKFZp686O	DAVID_hypothetical protein DKFZp686O24166	ENSG00000188211	PAP030	165	10.9%	chr11	17334944	ENST00000338965	c.241T>NULL	p.NULL-1FsDel1bp
MUC6	DAVID_mucin 6: oligomeric mucus/gel-forming	NM_005961	PAP030	122	13.1%	chr11	1010722	NM_005961	c.3602C>T	p.T1201M
PRIC285	DAVID_peroxisomal proliferator-activated receptor A interacting complex 285	ENSG00000130589	PAP030	100	17.0%	chr20	61664357	CCDS33508.1	c.6262C>A	p.L2088M
Trim31	DAVID_tripartite motif-containing 31	ENSG00000204616	PAP030	267	14.2%	chr6	30179303	CCDS34374.1	c.1267C>A	p.P423T
TRIM67	DAVID_tripartite motif-containing 67	NM_001004342	PAP030	135	17.8%	chr1	229411519	NM_001004342	c.2023G>A	p.V675M
WDR87	DAVID_WD repeat domain 87	NM_031951	PAP030	137	10.2%	chr19	43071907	NM_031951	c.9471NULL>T	p.NULL-1FsIns1bp
ZBTB34	DAVID_zinc finger and BTB domain containing 34	NM_001099270	PAP030	69	14.5%	chr9	128682070	NM_001099270	c.559A>G	p.S187G

ERF	Ets2 repressor factor	ENSG00000105722	PAP030	117	11.1%	chr19	47444644	CCDS12600.1	c.1460G>A	p.R487H
EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	ENSG00000128829	PAP030	85	11.8%	chr15	38114566	CCDS42016.1	c.4939A>C	p.I1647L
FGFBP3	fibroblast growth factor binding protein 3	ENSG00000174721	PAP030	124	11.3%	chr10	93658135	CCDS7418.1	c.572A>G	p.Q191R
GPR3	G protein-coupled receptor 3	ENSG00000181773	PAP030	146	10.3%	chr1	27592963	CCDS303.1	c.74G>C	p.G25A
INF2	inverted formin; FH2 and WH2 domain containing	ENSG00000203485	PAP030	146	13.7%	chr14	104239120	CCDS41999.1	c.373G>C	p.V125L
KIAA1614	KIAA1614	ENSG00000135835	PAP030	298	10.7%	chr1	179172042	CCDS41442.1	c.2374C>T	p.H792Y
LBR	lamin B receptor	ENSG00000143815	PAP030	121	14.0%	chr1	223676413	CCDS1545.1	c.355C>T	p.P119S
LSR	lipolysis stimulated lipoprotein receptor	ENSG00000105699	PAP030	190	12.6%	chr19	40449191	CCDS12450.1	c.1012C>NULL	p.NULL-1FsDel1bp
MTOR	mechanistic target of rapamycin (serine/threonine kinase)	ENSG00000198793	PAP030	176	17.6%	chr1	11115794	CCDS127.1	c.5294A>G	p.N1765S
NRIP1	nuclear receptor interacting protein 1	ENSG00000180530	PAP030	156	11.5%	chr21	15260383	CCDS13568.1	c.2002A>T	p.R668X
NULL	NULL	ENSG00000198938	PAP030	816	56.4%	chrM	9719	ENST00000362079	c.512T>C	p.L171P
NULL	NULL	NM_025248	PAP030	88	12.5%	chr17	33988411	NM_025248	c.182C>T	p.A61V
OPTN	optineurin	ENSG00000123240	PAP030	80	13.8%	chr10	13191198	CCDS7094.1	c.70C>NULL	p.NULL-1FsDel1bp
ODC1	ornithine decarboxylase 1	ENSG00000115758	PAP030	205	13.2%	chr2	10498320	CCDS1672.1	c.1367C>T	p.S456L
OTUD7B	OTU domain containing 7B	ENSG00000163113	PAP030	95	10.5%	chr1	148205979	CCDS41389.1	c.593G>NULL	p.NULL-1FsDel1bp
PRKDC	protein kinase; DNA-activated; catalytic polypeptide	ENSG00000121031	PAP030	80	12.5%	chr8	48937536	ENST00000314191	c.5867A>G	p.N1956S
PPM1D	protein phosphatase; Mg2+/Mn2+ dependent; 1D	ENSG00000170836	PAP030	127	18.1%	chr17	56095569	CCDS11625.1	c.1692NULL>A	p.NULL-1FsIns1bp
RNF157	ring finger protein 157	ENSG00000141576	PAP030	80	16.3%	chr17	71674203	CCDS32740.1	c.562C>T	p.L188F
RNF43	ring finger protein 43	ENSG00000108375	PAP030	158	12.7%	chr17	53790160	CCDS11607.1	c.3331G>NUL	p.NULL-1FsDel1bp
RBM33	RNA binding motif protein 33	ENSG00000184863	PAP030	187	10.7%	chr7	155223740	NM_053043	c.1619T>G	p.I540S
SNRPD2	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	ENSG00000125743	PAP030	136	10.3%	chr19	50882758	CCDS33053.1	c.250A>G	p.K84E
SLC24A2	solute carrier family 24 (sodium/potassium/calcium exchanger); member 2	ENSG00000155886	PAP030	135	14.8%	chr9	19776519	CCDS6493.1	c.346G>A	p.A116T
SLC5A12	solute carrier family 5 (sodium/glucose cotransporter); member 12	ENSG00000148942	PAP030	119	15.1%	chr11	26699722	CCDS7860.2	c.116G>A	p.R39Q
STAB1	stabilin 1	ENSG00000010327	PAP030	159	10.7%	chr3	52514162	CCDS33768.1	c.1481G>A	p.R494Q
TIAM1	T-cell lymphoma invasion and metastasis 1	ENSG00000156299	PAP030	225	12.0%	chr21	31560745	CCDS13609.1	c.415G>A	p.A139T
TRPV6	transient receptor potential cation channel; subfamily V; member 6	ENSG00000165125	PAP030	238	10.5%	chr7	142279688	CCDS5874.1	c.2072G>A	p.S691N
TMEM22	transmembrane protein 22	ENSG00000168917	PAP030	85	12.9%	chr3	138056176	CCDS3091.1	c.184A>NULL	p.NULL-1FsDel1bp
USP19	ubiquitin specific peptidase 19	ENSG00000172046	PAP030	227	17.6%	chr3	49124996	CCDS43090.1	c.2267C>G	p.T756R
AKT1	v-akt murine thymoma viral oncogene homolog 1	ENSG00000142208	PAP030	76	25.0%	chr14	104317596	CCDS9994.1	c.49G>A	p.E17K
ZFP36L2	zinc finger protein 36; C3H type-like 2	ENSG00000152518	PAP030	288	15.3%	chr2	43305878	CCDS1811.1	c.2002NULL>C	p.NULL-1FsIns1bp
HTR1B	5-hydroxytryptamine (serotonin) receptor 1B	ENSG00000135312	PAP031	86	31.4%	chr6	78229151	CCDS4986.1	c.689G>A	p.R230H
AKAP11	A kinase (PRKA) anchor protein 11	ENSG00000023516	PAP031	196	25.5%	chr13	41771588	CCDS9383.1	c.706C>G	p.L236V
AIM2	absent in melanoma 2	ENSG00000163568	PAP031	224	16.5%	chr1	157302615	CCDS1181.1	c.525G>C	p.E175D
ADAD2	adenosine deaminase domain containing 2	ENSG00000140955	PAP031	140	23.6%	chr16	82787282	CCDS10944.1	c.1577G>A	p.R526Q
ACAP3	ArfGAP with coiled-coil; ankyrin repeat and PH domains 3	ENSG00000131584	PAP031	32	43.8%	chr1	1218940	CCDS19.1	c.2147C>T	p.A716V
ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP031	64	18.8%	chr1	26979738	CCDS285.1	c.6762C>G	p.Y2254X
CSNK1D	casein kinase 1; delta	ENSG00000141551	PAP031	63	28.6%	chr17	77800005	ENST00000269361	c.908C>T	p.S303L
CTNNB1	catenin (cadherin-associated protein); beta 1; 88kDa	ENSG00000168036	PAP031	198	28.8%	chr3	41241117	CCDS2694.1	c.110C>G	p.S37C
DNAH1	DAVID_dynein: axonemal: heavy chain 1	NM_015512	PAP031	48	39.6%	chr3	52372178	NM_015512	c.5222C>G	p.S1741C
Fam186a	DAVID_family with sequence similarity 186: member A	NM_001145475	PAP031	157	24.2%	chr12	49010771	NM_001145475	c.6886G>A	p.D2296N
HIPK2	DAVID_homeodomain interacting protein kinase 2; similar to homeodomain interacting protein kinase 2	NM_022740	PAP031	28	50.0%	chr7	138908539	NM_022740	c.3271G>T	p.A1091S
LOC389333	DAVID_hypothetical protein LOC389333	NM_001161546	PAP031	98	34.7%	chr5	138756968	NM_001161546	c.1702C>G	p.R568G
LOXHD1	DAVID_lipoxygenase homology domains 1	NM_144612	PAP031	26	42.3%	chr18	42400239	NM_144612	c.2416G>C	p.E806Q
micB	DAVID_MHC class I polypeptide-related sequence B	ENSG00000204516	PAP031	136	27.9%	chr6	31582181	CCDS43449.1	c.608G>A	p.R203K

PPAN-P2RY	DAVID_PPAN-P2RY11 readthrough transcript	ENSG00000221848	PAP031	168	23.2%	chr19	10085602	CCDS42498.1	c.1573G>A	p.E525K
SCAND3	DAVID_SCAN domain containing 3	ENSG00000197202	PAP031	65	30.8%	chr6	28650753	CCDS34355.1	c.1708G>T	p.E570X
srpk1	DAVID_SFRS protein kinase 1	NM_003137	PAP031	42	28.6%	chr6	35918320	NM_003137	c.1660C>G	p.H554D
DOCK2	dedicator of cytokinesis 2	ENSG00000134516	PAP031	119	25.2%	chr5	169107024	CCDS4371.1	c.2314C>T	p.R772W
ELF1	E74-like factor 1 (ets domain transcription factor)	ENSG00000120690	PAP031	79	24.1%	chr13	40423471	CCDS9374.1	c.462NULL>A	p.NULL-1FsIns5bp
EPS8	epidermal growth factor receptor pathway substrate 8	ENSG00000151491	PAP031	71	31.0%	chr12	15665589	CCDS31753.1	c.2398C>G	p.R800G
ETV7	ets variant 7	ENSG00000010030	PAP031	152	30.3%	chr6	36442504	CCDS4819.1	c.922C>G	p.P308A
FANCM	Fanconi anemia; complementation group M	ENSG00000187790	PAP031	46	26.1%	chr14	44724172	CCDS32070.1	c.4518T>NULL	p.NULL-1FsDel1bp
QRICH1	glutamine-rich 1	ENSG00000198218	PAP031	65	26.2%	chr3	49059650	CCDS2787.1	c.1372C>T	p.Q458X
HNRNPM	heterogeneous nuclear ribonucleoprotein M	ENSG00000099783	PAP031	50	20.0%	chr19	8439713	CCDS12203.1	c.890T>C	p.L297P
MSMP	microseminoprotein; prostate associated	ENSG00000215183	PAP031	105	26.7%	chr9	35743673	NM_001044264	c.223G>A	p.V75M
MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	ENSG00000121653	PAP031	110	29.1%	chr11	45880652	CCDS7916.1	c.758C>T	p.A253V
OR5AU1	olfactory receptor; family 5; subfamily AU; member 1	ENSG00000169327	PAP031	110	27.3%	chr14	20693417	CCDS32042.1	c.608G>T	p.G203V
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP031	33	30.3%	chr10	89707676	CCDS31238.1	c.721TT>NULL	p.NULL-1FsDel2bp
PLCH1	phospholipase C; eta 1	ENSG00000114805	PAP031	61	21.3%	chr3	156750420	CCDS33881.1	c.1122C>G	p.I374M
RGS9	regulator of G-protein signaling 9	ENSG00000108370	PAP031	52	19.2%	chr17	60623758	CCDS42373.1	c.913G>A	p.E305K
RTN4RL2	reticulon 4 receptor-like 2	ENSG00000186907	PAP031	84	32.1%	chr11	57000457	CCDS7957.1	c.760G>C	p.E254Q
ARHGAP6	Rho GTPase activating protein 6	ENSG00000047648	PAP031	100	29.0%	chrX	11592362	CCDS14140.1	c.508C>T	p.P170S
SH3PXD2A	SH3 and PX domains 2A	ENSG00000107957	PAP031	47	31.9%	chr10	105474020	CCDS31278.1	c.486AA>NUL	p.NULL-1FsDel2bp
SYNE2	spectrin repeat containing; nuclear envelope 2	ENSG00000054654	PAP031	36	33.3%	chr14	63539266	CCDS9761.2	c.3862G>A	p.E1288K
SPTA1	spectrin; alpha; erythrocytic 1 (elliptocytosis 2)	ENSG00000163554	PAP031	149	16.8%	chr1	156912629	CCDS41423.1	c.1038A>T	p.E346D
STX11	syntaxin 11	ENSG00000135604	PAP031	122	32.8%	chr6	144550283	CCDS5205.1	c.826C>T	p.R276W
TOLLIP	toll interacting protein	ENSG00000078902	PAP031	100	30.0%	chr11	1268176	CCDS7723.1	c.223C>T	p.P75S
TMEM198	transmembrane protein 198	ENSG00000188760	PAP031	58	25.9%	chr2	220120646	CCDS33385.1	c.341G>A	p.R114H
TMEM2	transmembrane protein 2	ENSG00000135048	PAP031	45	33.3%	chr9	73489933	CCDS6638.1	c.4152G>C	p.X1384Y
ZNF215	zinc finger protein 215	ENSG00000149054	PAP031	49	40.8%	chr11	6933807	CCDS7775.1	c.1023C>G	p.F341L
ZNF407	zinc finger protein 407	ENSG00000215421	PAP031	62	35.5%	chr18	70476318	NM_017757	c.4355C>A	p.S1452X
ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP032	619	12.1%	chr1	26930422	CCDS285.1	c.1543C>T	p.Q515X
C9orf43	chromosome 9 open reading frame 43	ENSG00000157653	PAP032	25	44.0%	chr9	115227467	CCDS6796.1	c.888NULL>G	p.NULL-1FsIns3bp
CACNA1H	DAVID_calcium channel: voltage-dependent: T type: alpha 1H subunit	NM_021098	PAP032	331	13.6%	chr16	1210136	NM_021098	c.6203G>A	p.R2068H
SHANK3	DAVID_SH3 and multiple ankyrin repeat domains 3	NM_001080420	PAP032	83	14.5%	chr22	49516512	NM_001080420	c.5150C>T	p.A1717V
DVL2	dishevelled; dsh homolog 2 (Drosophila)	ENSG00000004975	PAP032	321	10.6%	chr17	7078188	CCDS11091.1	c.118C>T	p.L40F
EPHA8	EPH receptor A8	ENSG00000070886	PAP032	161	11.2%	chr1	22796860	CCDS225.1	c.2035C>T	p.R679W
KCNH4	potassium voltage-gated channel; subfamily H (eag-related); member 4	ENSG00000089558	PAP032	80	12.5%	chr17	37571016	CCDS11420.1	c.2062C>A	p.L688M
PRDM16	PR domain containing 16	ENSG00000142611	PAP032	191	15.2%	chr1	3319034	CCDS41236.1	c.2413C>A	p.L805M
WNT2	wingless-type MMTV integration site family member 2	ENSG00000105989	PAP032	175	10.3%	chr7	116725079	CCDS5771.1	c.676G>T	p.D226Y
ATF5	activating transcription factor 5	ENSG00000169136	PAP033	218	24.3%	chr19	55127931	CCDS12789.1	c.619C>T	p.R207X
ATF7IP	activating transcription factor 7 interacting protein	ENSG00000171681	PAP033	122	18.9%	chr12	14468555	CCDS8663.1	c.439G>A	p.G147R
ARL5B	ADP-ribosylation factor-like 5B	ENSG00000165997	PAP033	55	20.0%	chr10	19003034	CCDS7131.1	c.455G>C	p.W152S
AHR	aryl hydrocarbon receptor	ENSG00000106546	PAP033	79	19.0%	chr7	17340196	CCDS5366.1	c.841C>T	p.R281W
B3GAT1	beta-1;3-glucuronyltransferase 1 (glucuronosyltransferase P)	ENSG00000109956	PAP033	74	31.1%	chr11	133759271	CCDS8500.1	c.134G>A	p.R45H
ABL1	c-abl oncogene 1; receptor tyrosine kinase	ENSG00000097007	PAP033	40	35.0%	chr9	132728181	CCDS35165.1	c.817G>A	p.G273R
CENPM	centromere protein M	ENSG00000100162	PAP033	70	27.1%	chr22	40669621	CCDS14025.1	c.341G>T	p.R114L
CHRNA10	cholinergic receptor; nicotinic; alpha 10	ENSG00000129749	PAP033	50	20.0%	chr11	3647619	CCDS7745.1	c.190T>A	p.S64T
C11orf63	chromosome 11 open reading frame 63	ENSG00000109944	PAP033	112	25.0%	chr11	122280091	CCDS8438.1	c.593C>T	p.P198L
C5	complement component 5	ENSG00000106804	PAP033	28	35.7%	chr9	122809021	CCDS6826.1	c.2404G>A	p.V802I

C8A	complement component 8; alpha polypeptide	ENSG00000157131	PAP033	89	39.3%	chr1	57150842	CCDS606.1	c.1559G>A	p.R520H
CCND1	cyclin D1	ENSG00000110092	PAP033	50	30.0%	chr11	69175202	CCDS8191.1	c.859C>T	p.P287S
C6orf132	DAVID_chromosome 6 open reading frame 132	NM_001164446	PAP033	116	23.3%	chr6	42181262	NM_001164446	c.2366T>C	p.L789P
DNAH1	DAVID_dynein: axonemal: heavy chain 1	NM_015512	PAP033	74	17.6%	chr3	52401911	NM_015512	c.10304C>T	p.T3435M
MLL2	DAVID_myeloid/lymphoid or mixed-lineage leukemia 2	NM_003482	PAP033	92	22.8%	chr12	47712094	NM_003482	c.12661C>T	p.Q4221X
ND4L	DAVID_NADH-ubiquinone oxidoreductase chain 4L; NADH-ubiquinone oxidoreductase chain 4	ENSG00000198868	PAP033	523	17.0%	chrM	10745	ENST00000361335	c.275A>G	p.N92S
ND4	DAVID_NADH-ubiquinone oxidoreductase chain 4L; NADH-ubiquinone oxidoreductase chain 4	ENSG00000198868	PAP033	523	17.0%	chrM	10745	ENST00000361335	c.275A>G	p.N92S
SCN5A	DAVID_sodium channel: voltage-gated: type V: alpha subunit	NM_001099404	PAP033	53	24.5%	chr3	38591874	NM_001099404	c.3584G>A	p.R1195H
DTNBP1	dystrobrevin binding protein 1	ENSG00000047579	PAP033	121	19.0%	chr6	15631319	CCDS4534.1	c.922C>T	p.R308W
EPAS1	endothelial PAS domain protein 1	ENSG00000116016	PAP033	59	18.6%	chr2	46460907	CCDS1825.1	c.1592C>T	p.P531L
FAM123C	family with sequence similarity 123C	ENSG00000178171	PAP033	92	26.1%	chr2	131238201	CCDS2164.1	c.2086C>T	p.P696S
ING1	inhibitor of growth family; member 1	ENSG00000153487	PAP033	137	45.3%	chr13	110170108	CCDS9517.1	c.1097T>A	p.M366K
ITGAE	integrin; alpha E (antigen CD103; human mucosal lymphocyte antigen 1; alpha polypeptide)	ENSG00000083457	PAP033	97	23.7%	chr17	3611211	CCDS32531.1	c.443T>C	p.L148P
ITGB4	integrin; beta 4	ENSG00000132470	PAP033	254	24.4%	chr17	71247628	CCDS11727.1	c.2327C>A	p.T776K
NULL	NULL	ENSG00000222029	PAP033	61	24.6%	chr6	152530673	ENST00000409023	c.278G>A	p.R93H
NULL	NULL	MI0005565	PAP033	36	30.6%	chr14	100568107	MI0005565	c.31C>T	p.R11C
OPA3	optic atrophy 3 (autosomal recessive; with chorea and spastic paraplegia)	ENSG00000125741	PAP033	139	25.2%	chr19	50748806	CCDS12668.1	c.346C>T	p.R116C
PARP4	poly (ADP-ribose) polymerase family; member 4	ENSG00000102699	PAP033	55	25.5%	chr13	23924643	CCDS9307.1	c.2915T>G	p.I972S
KCND3	potassium voltage-gated channel; Shal-related subfamily; member 3	ENSG00000171385	PAP033	134	28.4%	chr1	112326360	CCDS843.1	c.512G>A	p.R171Q
RTN1	reticulon 1	ENSG00000139970	PAP033	97	16.5%	chr14	59263938	CCDS9740.1	c.1217C>T	p.A406V
SP140	SP140 nuclear body protein	ENSG00000079263	PAP033	57	26.3%	chr2	230882967	CCDS42831.1	c.2143G>T	p.D715Y
UBN1	ubinuclein 1	ENSG00000118900	PAP033	94	23.4%	chr16	4850971	CCDS10525.1	c.977G>T	p.G326V
B3GALT6	UDP-Gal:betaGal beta 1;3-galactosyltransferase polypeptide 6	ENSG00000176022	PAP033	109	27.5%	chr1	1158413	CCDS13.1	c.892C>T	p.R298C
WDR33	WD repeat domain 33	ENSG00000136709	PAP033	68	16.2%	chr2	128193569	CCDS2150.1	c.2500C>T	p.R834X
OASL	2'-5'-oligoadenylate synthetase-like	ENSG00000135114	PAP34	281	29.2%	chr12	119943141	CCDS9211.1	c.1151G>A	p.R384Q
ABO	ABO blood group (transferase A; alpha 1-3-N-acetylgalactosaminyltransferase; transferase B; alpha 1-3-galactosyltransferase)	ENSG00000175164	PAP34	436	29.1%	chr9	135121135	ENST00000319878	c.1491G>NUL	p.NULL-1FsDel1bp
ACACB	acetyl-CoA carboxylase beta	ENSG00000076555	PAP34	115	22.6%	chr12	108089158	CCDS31898.1	c.763G>NULL	p.NULL-1FsDel1bp
AFAP1L1	actin filament associated protein 1-like 1	ENSG00000157510	PAP34	120	33.3%	chr5	148662210	CCDS34274.1	c.364C>NULL	p.NULL-1FsDel1bp
AFAP1L2	actin filament associated protein 1-like 2	ENSG00000169129	PAP34	27	37.0%	chr10	116073001	CCDS31286.1	c.325C>T	p.R109W
ACTL6B	actin-like 6B	ENSG00000077080	PAP34	148	26.4%	chr7	100091099	CCDS5702.1	c.314G>NULL	p.NULL-1FsDel1bp
ADAM11	ADAM metallopeptidase domain 11	ENSG00000073670	PAP34	149	19.5%	chr17	40210939	CCDS11486.1	c.2164G>A	p.G722R
ADAM20	ADAM metallopeptidase domain 20	ENSG00000134007	PAP34	82	28.0%	chr14	70059609	CCDS32111.1	c.1769G>A	p.R590H
ADORA1	adenosine A1 receptor	ENSG00000163485	PAP34	799	20.4%	chr1	201401029	CCDS1434.1	c.359C>NULL	p.NULL-1FsDel1bp
ADAL	adenosine deaminase-like	ENSG00000168803	PAP34	115	29.6%	chr15	41428407	CCDS32214.1	c.644A>NULL	p.NULL-1FsDel1bp
ADCY5	adenylate cyclase 5	ENSG00000173175	PAP34	97	35.1%	chr3	124649905	CCDS3022.1	c.1311G>NUL	p.NULL-1FsDel1bp
AK5	adenylate kinase 5	ENSG00000154027	PAP34	41	34.1%	chr1	77756882	CCDS675.1	c.1193A>NULI	p.NULL-1FsDel1bp
ADSS	adenylosuccinate synthase	ENSG00000035687	PAP34	82	19.5%	chr1	242650178	CCDS1624.1	c.707A>T	p.Y236F

ALDH6A1	aldehyde dehydrogenase 6 family; member A1	ENSG00000119711	PAP34	47	72.3%	chr14	73604028	CCDS9826.1	c.-1T>NULL	p.IVS7-3-1SpliceAcceptor
ALKBH3	alkB; alkylation repair homolog 3 (E. coli)	ENSG00000166199	PAP34	117	32.5%	chr11	43879820	CCDS7906.1	c.638G>A	p.R213H
AMBN	ameloblastin (enamel matrix protein)	ENSG00000178522	PAP34	66	30.3%	chr4	71506494	CCDS3543.1	c.802G>A	p.G268R
APBA2	amyloid beta (A4) precursor protein-binding; family A; member 2	ENSG00000034053	PAP34	140	32.1%	chr15	27134011	CCDS10022.1	c.632G>A	p.R211H
ACE2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	ENSG00000130234	PAP34	61	18.0%	chrX	15499755	CCDS14169.1	c.1750C>G	p.L584V
ANK2	ankyrin 2; neuronal	ENSG00000145362	PAP34	65	29.2%	chr4	114470885	CCDS3702.1	c.2935G>T	p.G979C
ANKRD11	ankyrin repeat domain 11	ENSG00000167522	PAP34	31	38.7%	chr16	87864796	CCDS32513.1	c.7736G>A	p.R2579H
AEN	apoptosis enhancing nuclease	ENSG00000181026	PAP34	212	35.8%	chr15	86970775	CCDS10344.1	c.331G>T	p.V111L
ARAP1	ArfGAP with RhoGAP domain; ankyrin repeat and PH domain 1	ENSG00000186635	PAP34	27	37.0%	chr11	72093020	CCDS41687.1	c.1997CTT>NI	p.NULL-1FsDel3bp
AVPR1A	arginine vasopressin receptor 1A	ENSG00000166148	PAP34	41	36.6%	chr12	61827610	CCDS8965.1	c.1339T>NULI	p.NULL-1FsDel1bp
ARRDC4	arrestin domain containing 4	ENSG00000140450	PAP34	164	27.4%	chr15	96310239	CCDS10377.1	c.485T>C	p.V162A
ASTN2	astrotactin 2	ENSG00000148219	PAP34	728	26.9%	chr9	118244586	CCDS6815.1	c.3412G>A	p.A1138T
ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP34	211	29.4%	chr1	26896147	CCDS285.1	c.666C>A	p.Y222X
ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP34	310	30.6%	chr1	26973855	CCDS285.1	c.4550C>NULI	p.NULL-1FsDel1bp
ATHL1	ATH1; acid trehalase-like 1 (yeast)	ENSG00000142102	PAP34	130	31.5%	chr11	283086	ENST00000409479	c.1275C>NULI	p.NULL-1FsDel1bp
ATP6V0D2	ATPase; H+ transporting; lysosomal 38kDa; V0 subunit d2	ENSG00000147614	PAP34	309	23.0%	chr8	87180337	CCDS6241.1	c.14C>T	p.A5V
ABCG1	ATP-binding cassette; sub-family G (WHITE); member 1	ENSG00000160179	PAP34	209	32.1%	chr21	42552502	ENST00000340588	c.394G>A	p.V132M
ABCG2	ATP-binding cassette; sub-family G (WHITE); member 2	ENSG00000118777	PAP34	92	38.0%	chr4	89271295	CCDS3628.1	c.625NULL>A	p.NULL-1FsIns1bp
ATN1	atrophin 1	ENSG00000111676	PAP34	378	13.2%	chr12	6916153	CCDS31734.1	c.1462CAG>N	p.NULL-1FsDel3bp
BARHL2	BarH-like homeobox 2	ENSG00000143032	PAP34	46	30.4%	chr1	90954985	CCDS730.1	c.356A>C	p.Q119P
B4GALNT4	beta-1;4-N-acetyl-galactosaminyl transferase 4	ENSG00000182272	PAP34	117	29.1%	chr11	366772	CCDS7694.1	c.1649T>G	p.F550C
CDH15	cadherin 15; type 1; M-cadherin (myotubule)	ENSG00000129910	PAP34	82	45.1%	chr16	87785758	CCDS10976.1	c.1570A>G	p.R524G
CLIP4	CAP-GLY domain containing linker protein family; member 4	ENSG00000115295	PAP34	78	26.9%	chr2	29233729	ENST00000402240	c.1414T>NULI	p.NULL-1FsDel1bp
CA12	carbonic anhydrase XII	ENSG00000074410	PAP34	75	22.7%	chr15	61406486	CCDS10185.1	c.-1G>T	p.IVS9-1-1SpliceAcceptor
CARD14	caspase recruitment domain family; member 14	ENSG00000141527	PAP34	134	26.1%	chr17	75783660	CCDS11768.1	c.1432C>NULI	p.NULL-1FsDel1bp
CTNNA2	catenin (cadherin-associated protein); alpha 2	ENSG00000066032	PAP34	155	29.0%	chr2	79938754	CCDS42703.1	c.406C>T	p.R136C
CTNNB1	catenin (cadherin-associated protein); beta 1; 88kDa	ENSG00000168036	PAP34	200	29.0%	chr3	41241107	CCDS2694.1	c.100G>A	p.G34R
CDC42EP1	CDC42 effector protein (Rho GTPase binding) 1	ENSG00000128283	PAP34	127	33.9%	chr22	36292585	CCDS13949.1	c.283NULL>C	p.NULL-1FsIns1bp
CADM4	cell adhesion molecule 4	ENSG00000105767	PAP34	130	40.8%	chr19	48822823	CCDS12627.1	c.452G>A	p.R151H
CCPG1	cell cycle progression 1	ENSG00000214882	PAP34	49	32.7%	chr15	53439998	CCDS42039.1	c.2710A>NULI	p.NULL-1FsDel1bp
CABC1	chaperone; ABC1 activity of bc1 complex homolog (S. pombe)	ENSG00000163050	PAP34	164	12.2%	chr1	225220032	CCDS1557.1	c.626C>T	p.T209M
CHRNA4	cholinergic receptor; nicotinic; alpha 4	ENSG00000101204	PAP34	400	30.3%	chr20	61452153	CCDS13517.1	c.1054G>A	p.V352M
CHAD	chondroadherin	ENSG00000136457	PAP34	279	18.3%	chr17	45900902	CCDS11568.1	c.272C>T	p.A91V
CSGALNAC	chondroitin sulfate N-acetylgalactosaminyltransferase 1	ENSG00000147408	PAP34	252	38.1%	chr8	19407562	CCDS6010.1	c.64C>A	p.L22I
C1orf127	chromosome 1 open reading frame 127	ENSG00000175262	PAP34	145	36.6%	chr1	10931454	CCDS121.1	c.824C>T	p.P275L
C1orf172	chromosome 1 open reading frame 172	ENSG00000175707	PAP34	332	31.9%	chr1	27150992	CCDS293.1	c.467G>A	p.G156D
C1orf68	chromosome 1 open reading frame 68	ENSG00000198854	PAP34	507	23.7%	chr1	150958817	NM_001024679	c.196A>G	p.T66A
C10orf47	chromosome 10 open reading frame 47	ENSG00000148426	PAP34	117	15.4%	chr10	11951921	CCDS7085.1	c.818G>T	p.R273M
C12orf12	chromosome 12 open reading frame 12	ENSG00000197651	PAP34	47	36.2%	chr12	89872218	CCDS9036.1	c.433C>T	p.R145C

C12orf24	chromosome 12 open reading frame 24	ENSG00000204856	PAP34	124	26.6%	chr12	109408519	CCDS31899.1	c.313G>T	p.D105Y
C14orf43	chromosome 14 open reading frame 43	ENSG00000156030	PAP34	165	33.3%	chr14	73276359	CCDS9819.1	c.1554C>NULL	p.NULL-1FsDel1bp
C16orf11	chromosome 16 open reading frame 11	ENSG00000161992	PAP34	85	37.6%	chr16	554215	NM_145270	c.920C>A	p.P307Q
C17orf63	chromosome 17 open reading frame 63	ENSG00000173065	PAP34	253	26.1%	chr17	24109815	ENST00000341217	c.1286C>T	p.T429I
C19orf61	chromosome 19 open reading frame 61	ENSG00000105771	PAP34	114	35.1%	chr19	48943972	CCDS33043.2	c.223C>T	p.R75W
C2orf71	chromosome 2 open reading frame 71	ENSG00000179270	PAP34	131	26.0%	chr2	29147666	CCDS42669.1	c.6633C>NULL	p.NULL-1FsDel1bp
C7orf51	chromosome 7 open reading frame 51	ENSG00000166924	PAP34	148	31.8%	chr7	99924988	CCDS5696.1	c.1708NULL>(	p.NULL-1FsIns1bp
C9orf167	chromosome 9 open reading frame 167	ENSG00000198113	PAP34	138	29.7%	chr9	139293821	CCDS7041.1	c.859C>T	p.R287C
CPSF6	cleavage and polyadenylation specific factor 6; 68kDa	ENSG00000111605	PAP34	477	22.2%	chr12	67938748	CCDS8988.1	c.806GAG>NU	p.NULL-1FsDel3bp
CPSF6	cleavage and polyadenylation specific factor 6; 68kDa	ENSG00000111605	PAP34	1412	27.6%	chr12	67938955	CCDS8988.1	c.1013CTC>N	p.NULL-1FsDel3bp
CCDC22	coiled-coil domain containing 22	ENSG00000101997	PAP34	248	32.7%	chrX	48992111	CCDS14322.1	c.1403G>A	p.R468H
CCDC40	coiled-coil domain containing 40	ENSG00000141519	PAP34	89	21.3%	chr17	75653973	CCDS42395.1	c.1535C>T	p.A512V
COIL	coilin	ENSG00000121058	PAP34	44	27.3%	chr17	52393188	CCDS11592.1	c.436G>NULL	p.NULL-1FsDel1bp
COL24A1	collagen; type XXIV; alpha 1	ENSG00000171502	PAP34	127	18.1%	chr1	86024647	CCDS41353.1	c.4037G>T	p.S1346I
COMMD5	COMM domain containing 5	ENSG00000170619	PAP34	339	26.0%	chr8	146047344	CCDS6436.1	c.858G>NULL	p.NULL-1FsDel1bp
C1S	complement component 1; s subcomponent	ENSG00000182326	PAP34	32	34.4%	chr12	7047750	CCDS31735.1	c.1601G>T	p.R534L
CHUK	conserved helix-loop-helix ubiquitous kinase	ENSG00000213341	PAP34	115	24.3%	chr10	101943099	CCDS7488.1	c.2187C>NULL	p.NULL-1FsDel1bp
CPNE2	copine II	ENSG00000140848	PAP34	45	26.7%	chr16	55713122	CCDS10774.1	c.816GAA>NU	p.NULL-1FsDel3bp
CBFB	core-binding factor; beta subunit	ENSG00000067955	PAP34	59	20.3%	chr16	65620858	CCDS10827.1	c.47A>C	p.E16A
CRNN	cornulin	ENSG00000143536	PAP34	1684	16.9%	chr1	150649088	CCDS1010.1	c.1094C>G	p.T365S
CORO1B	coronin; actin binding protein; 1B	ENSG00000172725	PAP34	73	17.8%	chr11	66964219	CCDS8164.1	c.1098NULL>(	p.NULL-1FsIns1bp
CORO2B	coronin; actin binding protein; 2B	ENSG00000103647	PAP34	333	33.0%	chr15	66774597	CCDS10229.2	c.281A>C	p.K94T
COX18	COX18 cytochrome c oxidase assembly homolog (S. cerevisiae)	ENSG00000163626	PAP34	42	26.2%	chr4	74142845	CCDS3554.1	c.852C>A	p.C284X
CREBBP	CREB binding protein	ENSG00000005339	PAP34	115	33.9%	chr16	3730460	CCDS10509.1	c.4224T>NULL	p.NULL-1FsDel1bp
CCNT2	cyclin T2	ENSG00000082258	PAP34	64	39.1%	chr2	135410903	CCDS2174.1	c.263T>G	p.F88C
CDK12	cyclin-dependent kinase 12	ENSG00000167258	PAP34	73	20.5%	chr17	34940427	CCDS11337.1	c.3805C>NULL	p.NULL-1FsDel1bp
CDK20	cyclin-dependent kinase 20	ENSG00000156345	PAP34	181	27.1%	chr9	89772283	CCDS35060.1	c.1152C>NULL	p.NULL-1FsDel1bp
CFTR	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C; member 7)	ENSG00000001626	PAP34	245	26.9%	chr7	116962555	CCDS5773.1	c.597T>G	p.H199Q
CYTSB	cytospin B	ENSG00000128487	PAP34	83	32.5%	chr17	20048855	CCDS32590.1	c.901A>NULL	p.NULL-1FsDel1bp
BAHCC1	DAVID_BAH domain and coiled-coil containing 1	NM_001080519	PAP34	103	22.3%	chr17	77027276	NM_001080519	c.2972C>T	p.T991M
BEX2	DAVID_brain expressed X-linked 2	NM_001168399	PAP34	34	29.4%	chrX	102451990	NM_001168399	c.43G>A	p.A15T
Baz2a	DAVID_bromodomain adjacent to zinc finger domain: 2A	NM_013449	PAP34	79	30.4%	chr12	55290241	NM_013449	c.1811G>A	p.S604N
cadps2	DAVID_Ca++-dependent secretion activator 2	NM_001167940	PAP34	32	34.4%	chr7	121815997	NM_001167940	c.3207T>NULL	p.NULL-1FsDel1bp
CACNA1E	DAVID_calcium channel: voltage-dependent: R type: alpha 1E subunit	NM_000721	PAP34	267	25.8%	chr1	179719675	NM_000721	c.172G>A	p.V58I
CMYA5	DAVID_cardiomyopathy associated 5	NM_153610	PAP34	47	36.2%	chr5	79070744	NM_153610	c.10400C>A	p.A3467E
UNC80	DAVID_chromosome 2 open reading frame 21	NM_032504	PAP34	46	32.6%	chr2	210549925	NM_032504	c.8618G>A	p.R2873Q
C2	DAVID_complement component 2	ENSG00000204364	PAP34	222	29.7%	chr6	32009934	CCDS4728.1	c.728G>A	p.R243H

Dtx4	DAVID_deltex homolog 4 (Drosophila)	NM_015177	PAP34	134	11.9%	chr11	58719403	NM_015177	c.1521C>NULL	p.NULL-1FsDel1bp
DNHD1	DAVID_dynein heavy chain domain 1	NM_144666	PAP34	289	30.4%	chr11	6525260	NM_144666	c.6515A>G	p.H2172R
DNAH17	DAVID_dynein: axonemal: heavy chain 17	NM_173628	PAP34	283	26.5%	chr17	73931668	NM_173628	c.13303A>G	p.T4435A
Eml6	DAVID_echinoderm microtubule associated protein like 6	NM_001039753	PAP34	36	30.6%	chr2	55029581	NM_001039753	c.4063NULL>A	p.NULL-1FsIns1bp
EPPK1	DAVID_epiplakin 1	NM_031308	PAP34	410	31.7%	chr8	145015858	NM_031308	c.3552G>T	p.Q1184H
c2cd4c	DAVID_family with sequence similarity 148: member C; hypothetical protein LOC100133882	NM_001136263	PAP34	162	34.0%	chr19	359234	NM_001136263	c.128C>T	p.T43M
LOC100133	DAVID_family with sequence similarity 148: member C; hypothetical protein LOC100133882	NM_001136263	PAP34	162	34.0%	chr19	359234	NM_001136263	c.128C>T	p.T43M
fbxl19	DAVID_F-box and leucine-rich repeat protein 19	NM_001099784	PAP34	358	32.1%	chr16	30861202	NM_001099784	c.1531C>A	p.Q511K
FBXL7	DAVID_F-box and leucine-rich repeat protein 7	NM_012304	PAP34	950	34.6%	chr5	15989790	NM_012304	c.971C>T	p.A324V
FKBP15	DAVID_FK506 binding protein 15: 133kDa	NM_015258	PAP34	34	35.3%	chr9	114980823	NM_015258	c.2165A>NULL	p.NULL-1FsDel1bp
GABBR1	DAVID_gamma-aminobutyric acid (GABA) B receptor: 1	ENSG00000204681	PAP34	172	33.1%	chr6	29682720	CCDS4663.1	c.2150T>C	p.L717P
GRID2IP	DAVID_glutamate receptor: ionotropic: delta 2 (Grid2) interacting protein	NM_001145118	PAP34	53	43.4%	chr7	6504371	NM_001145118	c.3413C>T	p.T1138M
GRHL1	DAVID_grainyhead-like 1 (Drosophila)	NM_198182	PAP34	120	30.0%	chr2	10012541	NM_198182	c.67C>T	p.R23W
HCG9	DAVID_HLA complex group 9	ENSG00000204625	PAP34	55	29.1%	chr6	30050956	ENST00000404219	c.49C>T	p.R17W
KIAA0913	DAVID_KIAA0913	NM_015037	PAP34	218	31.7%	chr10	75230470	NM_015037	c.5093C>NULL	p.NULL-1FsDel1bp
KIAA1328	DAVID_KIAA1328	NM_020776	PAP34	83	30.1%	chr18	32901022	NM_020776	c.748G>A	p.V250I
KIAA1549	DAVID_KIAA1549	NM_001164665	PAP34	123	30.9%	chr7	138254064	NM_001164665	c.3538T>NULL	p.NULL-1FsDel1bp
LINGO1	DAVID_leucine rich repeat and Ig domain containing 1	NM_032808	PAP34	284	12.0%	chr15	75693800	NM_032808	c.1504G>A	p.A502T
lrp1	DAVID_low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	ENSG00000123384	PAP34	248	33.9%	chr12	55885517	CCDS8932.1	c.11452G>A	p.G3818S
TRANK1	DAVID_lupus brain antigen 1	NM_014831	PAP34	72	26.4%	chr3	36877587	NM_014831	c.1177G>A	p.E393K
MGAM	DAVID_maltase-glucoamylase (alpha-glucosidase)	NM_004668	PAP34	117	23.9%	chr7	141408972	NM_004668	c.-1GTAA>NU	p.IVS34+1-1SpliceDonor
MDGA1	DAVID_MAM domain containing glycosylphosphatidylinositol anchor 1	NM_153487	PAP34	119	31.9%	chr6	37730628	NM_153487	c.638C>T	p.T213I
MGA	DAVID_MAX gene associated	NM_001164273	PAP34	74	25.7%	chr15	39808734	NM_001164273	c.3738A>NULL	p.NULL-1FsDel1bp
MUC5B	DAVID_mucin 5B: oligomeric mucus/gel-forming	NM_002458	PAP34	53	30.2%	chr11	1217629	NM_002458	c.3617G>A	p.S1206N
MLL2	DAVID_myeloid/lymphoid or mixed-lineage leukemia 2	NM_003482	PAP34	116	26.7%	chr12	47726698	NM_003482	c.4560C>NULL	p.NULL-1FsDel1bp
MLL4	DAVID_myeloid/lymphoid or mixed-lineage leukemia 4	ENSG00000105663	PAP34	177	26.6%	chr19	40903739	NM_014727	c.1650C>NULL	p.NULL-1FsDel1bp
MLL4	DAVID_myeloid/lymphoid or mixed-lineage leukemia 4	ENSG00000105663	PAP34	94	42.6%	chr19	40912739	NM_014727	c.4949C>T	p.T1650M
Myo10	DAVID_myosin X	NM_012334	PAP34	215	25.1%	chr5	16735066	NM_012334	c.4103C>T	p.T1368M
nfe2l2	DAVID_nuclear factor (erythroid-derived 2)-like 2	ENSG00000222043	PAP34	124	25.8%	chr2	177805425	CCDS42782.1	c.535G>A	p.G179S
obscn	DAVID_obscurin: cytoskeletal calmodulin and titin-interacting RhoGEF	NM_001098623	PAP34	428	22.9%	chr1	226571158	NM_001098623	c.13411G>A	p.A4471T
PLCH2	DAVID_phospholipase C: eta 2	NM_014638	PAP34	308	37.7%	chr1	2401144	NM_014638	c.383G>A	p.S128N
PRR12	DAVID_proline rich 12	NM_020719	PAP34	127	33.1%	chr19	54791622	NM_020719	c.2218G>A	p.E740K
PRR12	DAVID_proline rich 12	NM_020719	PAP34	186	38.7%	chr19	54792353	NM_020719	c.2949C>NULL	p.NULL-1FsDel1bp
pelp1	DAVID_proline: glutamate and leucine rich protein 1	NM_014389	PAP34	73	24.7%	chr17	4522745	NM_014389	c.2290G>A	p.A764T
PPM1M	DAVID_protein phosphatase 1M (PP2C domain containing)	NM_144641	PAP34	215	33.5%	chr3	52257449	NM_144641	c.371G>A	p.R124Q
RIMS1	DAVID_regulating synaptic membrane exocytosis 1	NM_014989	PAP34	321	26.8%	chr6	72863414	NM_014989	c.287G>A	p.R96K
SLFN12L	DAVID_schlafen family member 12-like	NM_001145027	PAP34	113	19.5%	chr17	30830443	NM_001145027	c.986C>T	p.T329M
sspO	DAVID_SCO-spondin homolog (Bos taurus)	NM_198455	PAP34	211	27.5%	chr7	149145666	NM_198455	c.11285C>T	p.A3762V

SHANK3	DAVID_SH3 and multiple ankyrin repeat domains 3	NM_001080420	PAP34	52	26.9%	chr22	49482564	NM_001080420	c.1332G>NUL	p.NULL-1FsDel1bp
SHANK3	DAVID_SH3 and multiple ankyrin repeat domains 3	NM_001080420	PAP34	124	33.1%	chr22	49506986	NM_001080420	c.3907C>T	p.P1303S
SIGLEC12	DAVID_sialic acid binding Ig-like lectin 12	ENSG00000160296	PAP34	173	29.5%	chr19	56694676	CCDS12833.1	c.1193C>NULI	p.NULL-1FsDel1bp
C9orf172	DAVID_similar to CG15216-PA	NM_001080482	PAP34	184	31.5%	chr9	138859666	NM_001080482	c.979T>C	p.Y327H
SLC4A9	DAVID_solute carrier family 4: sodium bicarbonate cotransporter: member 9	NM_031467	PAP34	620	24.7%	chr5	139725717	NM_031467	c.1825CTC>N	p.NULL-1FsDel3bp
suds3	DAVID_suppressor of defective silencing 3 homolog (S. cerevisiae)	NM_022491	PAP34	177	32.8%	chr12	117322906	NM_022491	c.577G>A	p.V193I
SYT15	DAVID_synaptotagmin XV	NM_031912	PAP34	275	13.8%	chr10	46385008	NM_031912	c.943A>G	p.S315G
SYTL5	DAVID_synaptotagmin-like 5	NM_001163334	PAP34	60	23.3%	chrX	37847288	NM_001163334	c.1221TG>NU	p.NULL-1FsDel2bp
TTC39A	DAVID_tetratricopeptide repeat domain 39A	NM_001144832	PAP34	677	24.4%	chr1	51526496	NM_001144832	c.1667G>A	p.R556Q
Tcf7l2	DAVID_transcription factor 7-like 2 (T-cell specific: HMG-box)	NM_001146283	PAP34	93	25.8%	chr10	114839196	NM_001146283	c.531C>NULL	p.NULL-1FsDel1bp
TRIM21	DAVID_tripartite motif-containing 21	NM_003141	PAP34	278	27.3%	chr11	4363430	NM_003141	c.1656TG>NU	p.NULL-1FsDel2bp
TRIM66	DAVID_tripartite motif-containing 66	NM_014818	PAP34	167	37.7%	chr11	8618861	NM_014818	c.1202G>A	p.R401Q
TSPYL5	DAVID_TSPY-like 5	ENSG00000180543	PAP34	164	33.5%	chr8	98359163	CCDS34927.1	c.86C>T	p.P29L
Ttll11	DAVID_tubulin tyrosine ligase-like family: member 11	NM_001139442	PAP34	36	27.8%	chr9	123672611	NM_001139442	c.2240NULL>T	p.NULL-1FsIns1bp
tp53bp2	DAVID_tumor protein p53 binding protein: 2	NM_001031685	PAP34	97	15.5%	chr1	222068579	NM_001031685	c.388C>NULL	p.NULL-1FsDel1bp
UNC13A	DAVID_unc-13 homolog A (C. elegans)	NM_001080421	PAP34	420	35.2%	chr19	17620240	NM_001080421	c.2080C>T	p.R694W
shisa7	DAVID_UPF0626 protein A	NM_001145176	PAP34	63	41.3%	chr19	60645373	NM_001145176	c.670A>G	p.R224G
WDFY4	DAVID_WDFY family member 4	NM_020945	PAP34	99	25.3%	chr10	49844691	NM_020945	c.8551C>T	p.Q2851X
znf292	DAVID_zinc finger protein 292	NM_015021	PAP34	59	20.3%	chr6	88022224	NM_015021	c.2158A>NULI	p.NULL-1FsDel1bp
DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	ENSG00000151240	PAP34	162	33.3%	chr10	380822	CCDS7054.1	c.3380A>G	p.K1127R
DVL2	dishevelled; dsh homolog 2 (Drosophila)	ENSG00000004975	PAP34	823	33.9%	chr17	7070318	CCDS11091.1	c.2249G>NUL	p.NULL-1FsDel1bp
DSCAML1	Down syndrome cell adhesion molecule like 1	ENSG00000177103	PAP34	39	46.2%	chr11	117156619	CCDS8384.1	c.343G>A	p.A115T
DNHD1	dynein heavy chain domain 1	ENSG00000179532	PAP34	351	33.0%	chr11	6476481	CCDS7767.1	c.460C>T	p.R154W
ENPP7	ectonucleotide pyrophosphatase/phosphodiesterase 7	ENSG00000182156	PAP34	431	50.6%	chr17	75325549	CCDS11763.1	c.1141C>T	p.P381S
EMR3	egf-like module containing; mucin-like; hormone receptor-like 3	ENSG00000131355	PAP34	44	45.5%	chr19	14630339	CCDS12315.1	c.379G>C	p.E127Q
ELOVL1	elongation of very long chain fatty acids (FEN1/Elo2; SUR4/Elo3; yeast)-like 1	ENSG00000066322	PAP34	233	35.2%	chr1	43602174	CCDS485.1	c.840A>G	p.X280W
ENDOU	endonuclease; polyU-specific	ENSG00000111405	PAP34	322	27.3%	chr12	46393435	CCDS8754.1	c.632G>A	p.R211H
ECE2	endothelin converting enzyme 2	ENSG00000145194	PAP34	52	46.2%	chr3	185490765	CCDS43179.1	c.1718A>NULI	p.NULL-1FsDel1bp
EDC4	enhancer of mRNA decapping 4	ENSG00000038358	PAP34	175	30.3%	chr16	66468620	CCDS10849.1	c.-1G>A	p.IVS4-1-1SpliceAcceptor
EPHB6	EPH receptor B6	ENSG00000106123	PAP34	452	17.9%	chr7	142272174	CCDS5873.1	c.449NULL>C	p.NULL-1FsIns3bp
EFNA3	ephrin-A3	ENSG00000143590	PAP34	51	23.5%	chr1	153318056	CCDS1090.1	c.15NULL>GC	p.NULL-1FsIns3bp
ERO1L	ERO1-like (S. cerevisiae)	ENSG00000197930	PAP34	47	34.0%	chr14	52182644	CCDS9709.1	c.1324T>C	p.S442P
ESPNL	espin-like	ENSG00000144488	PAP34	222	32.0%	chr2	238681316	CCDS2525.1	c.818C>NULL	p.NULL-1FsDel1bp
ETV2	ets variant 2	ENSG00000105672	PAP34	134	19.4%	chr19	40825745	NM_014209	c.193T>C	p.W65R
EIF2C4	eukaryotic translation initiation factor 2C; 4	ENSG00000134698	PAP34	60	18.3%	chr1	36061103	CCDS397.1	c.239G>A	p.R80Q
EIF4G1	eukaryotic translation initiation factor 4 gamma; 1	ENSG00000114867	PAP34	161	31.7%	chr3	185531958	CCDS3259.1	c.4265T>C	p.V1422A

EIF4A1	eukaryotic translation initiation factor 4A1	ENSG00000161960	PAP34	142	38.0%	chr17	7421915	CCDS11113.1	c.953T>G	p.F318C
EXOC3L	exocyst complex component 3-like	ENSG00000179044	PAP34	200	45.0%	chr16	65778830	CCDS10832.1	c.839G>A	p.R280Q
EXOC7	exocyst complex component 7	ENSG00000182473	PAP34	52	23.1%	chr17	71591749	CCDS32738.1	c.1885C>T	p.Q629X
EXTL3	exostoses (multiple)-like 3	ENSG00000012232	PAP34	73	35.6%	chr8	28664099	CCDS6070.1	c.2557T>C	p.S853P
FAM123C	family with sequence similarity 123C	ENSG00000178171	PAP34	42	33.3%	chr2	131237778	CCDS2164.1	c.1663G>NUL	p.NULL-1FsDel1bp
FAM13B	family with sequence similarity 13; member B	ENSG00000031003	PAP34	88	27.3%	chr5	137374729	CCDS4195.1	c.557C>T	p.T186I
FAM167A	family with sequence similarity 167; member A	ENSG00000154319	PAP34	143	30.1%	chr8	11339077	CCDS5981.1	c.254T>C	p.L85P
FAM171A1	family with sequence similarity 171; member A1	ENSG00000148468	PAP34	385	13.0%	chr10	15296029	CCDS31154.1	c.1564G>A	p.A522T
FAM171A2	family with sequence similarity 171; member A2	ENSG00000161682	PAP34	751	17.4%	chr17	39788894	NM_198475	c.969C>NULL	p.NULL-1FsDel1bp
FAM47A	family with sequence similarity 47; member A	ENSG00000185448	PAP34	128	37.5%	chrX	34059328	CCDS43926.1	c.989C>T	p.P330L
FAM48A	family with sequence similarity 48; member A	ENSG00000102710	PAP34	36	41.7%	chr13	36481831	CCDS31959.1	c.2318C>T	p.T773M
FAM98B	family with sequence similarity 98; member B	ENSG00000171262	PAP34	38	28.9%	chr15	36553730	CCDS10047.2	c.668G>C	p.R223P
FAT4	FAT tumor suppressor homolog 4 (Drosophila)	ENSG00000196159	PAP34	85	35.3%	chr4	126630580	CCDS3732.2	c.12982G>A	p.A4328T
FCRLA	Fc receptor-like A	ENSG00000132185	PAP34	235	19.1%	chr1	159949534	CCDS30926.1	c.871C>A	p.P291T
FBN2	fibrillin 2	ENSG00000138829	PAP34	419	32.7%	chr5	127623149	CCDS34222.1	c.8636A>C	p.K2879T
FGFR3	fibroblast growth factor receptor 3	ENSG00000068078	PAP34	137	20.4%	chr4	1773233	CCDS3353.1	c.704G>A	p.G235D
FNDC1	fibronectin type III domain containing 1	ENSG00000164694	PAP34	318	38.4%	chr6	159574038	NM_032532	c.2504T>C	p.F835S
FILIP1L	filamin A interacting protein 1-like	ENSG00000168386	PAP34	35	37.1%	chr3	101131524	CCDS43117.1	c.465A>NULL	p.NULL-1FsDel1bp
FLNA	filamin A; alpha	ENSG00000196924	PAP34	315	38.7%	chrX	153234914	CCDS44021.1	c.5942C>T	p.P1981L
FMO5	flavin containing monooxygenase 5	ENSG00000131781	PAP34	223	19.7%	chr1	145151514	CCDS926.1	c.472C>A	p.L158M
FOXA1	forkhead box A1	ENSG00000129514	PAP34	238	35.7%	chr14	37131270	CCDS9665.1	c.470G>A	p.G157D
FOXC1	forkhead box C1	ENSG00000054598	PAP34	163	25.2%	chr6	1557017	CCDS4473.1	c.1338CGG>N	p.NULL-1FsDel3bp
FOXM1	forkhead box M1	ENSG00000111206	PAP34	136	34.6%	chr12	2838241	CCDS8516.1	c.2230G>A	p.E744K
FOXO4	forkhead box O4	ENSG00000184481	PAP34	159	33.3%	chrX	70237437	CCDS43969.1	c.632NULL>C	p.NULL-1FsIns1bp
FNBP4	formin binding protein 4	ENSG00000109920	PAP34	61	34.4%	chr11	47710740	CCDS41644.1	c.1745T>C	p.L582P
FPR1	formyl peptide receptor 1	ENSG00000171051	PAP34	163	27.0%	chr19	56941954	CCDS12839.1	c.106A>G	p.T36A
FRAS1	Fraser syndrome 1	ENSG00000138759	PAP34	142	31.0%	chr4	79547871	NM_025074	c.4160C>T	p.A1387V
FZD2	frizzled homolog 2 (Drosophila)	ENSG00000180340	PAP34	810	16.4%	chr17	39990908	CCDS11484.1	c.326C>T	p.P109L
FTSJ3	FtsJ homolog 3 (E. coli)	ENSG00000108592	PAP34	66	16.7%	chr17	59255737	CCDS11644.1	c.909G>T	p.K303N
FGD5	FYVE; RhoGEF and PH domain containing 5	ENSG00000154783	PAP34	237	10.1%	chr3	14836769	NM_152536	c.1187A>G	p.Q396R
GPR123	G protein-coupled receptor 123	ENSG00000197177	PAP34	155	34.2%	chr10	134792985	CCDS41580.1	c.1663A>NULI	p.NULL-1FsDel1bp
GPR161	G protein-coupled receptor 161	ENSG00000143147	PAP34	260	25.0%	chr1	166332578	CCDS1268.1	c.1615G>NUL	p.NULL-1FsDel1bp
GPR174	G protein-coupled receptor 174	ENSG00000147138	PAP34	99	26.3%	chrX	78313752	CCDS14443.1	c.592C>T	p.L198F
GAL3ST2	galactose-3-O-sulfotransferase 2	ENSG00000154252	PAP34	63	47.6%	chr2	242391989	CCDS33427.1	c.932G>A	p.R311H
GABRG3	gamma-aminobutyric acid (GABA) A receptor; gamma 3	ENSG00000182256	PAP34	137	27.7%	chr15	25154885	NM_033223	c.454C>T	p.R152W
GTF3C3	general transcription factor IIIC; polypeptide 3; 102kDa	ENSG00000119041	PAP34	186	24.2%	chr2	197364347	CCDS2316.1	c.494G>A	p.R165H
GFOD2	glucose-fructose oxidoreductase domain containing 2	ENSG00000141098	PAP34	396	28.5%	chr16	66267015	CCDS10845.1	c.1599GT>NU	p.NULL-1FsDel2bp
GRIK1	glutamate receptor; ionotropic; kainate 1	ENSG00000171189	PAP34	123	30.9%	chr21	29871167	CCDS42913.1	c.2118G>A	p.M706I
GRIN2A	glutamate receptor; ionotropic; N-methyl D-aspartate 2A	ENSG00000183454	PAP34	283	29.0%	chr16	9765286	CCDS10539.1	c.3616C>T	p.R1206X
GRIN2B	glutamate receptor; ionotropic; N-methyl D-aspartate 2B	ENSG00000150086	PAP34	154	27.3%	chr12	13910311	CCDS8662.1	c.509C>NULL	p.NULL-1FsDel1bp
GRM6	glutamate receptor; metabotropic 6	ENSG00000113262	PAP34	125	30.4%	chr5	178351161	CCDS4442.1	c.862NULL>G	p.NULL-1FsIns1bp
GSS	glutathione synthetase	ENSG00000100983	PAP34	61	27.9%	chr20	32988422	CCDS13245.1	c.674A>T	p.N225I
GRAMD1A	GRAM domain containing 1A	ENSG00000089351	PAP34	59	33.9%	chr19	40196088	CCDS42546.1	c.695C>NULL	p.NULL-1FsDel1bp

GRAMD1A	GRAM domain containing 1A	ENSG00000089351	PAP34	342	28.9%	chr19	40206085	CCDS42546.1	c.1959NULL>(	p.NULL-1FsIns1bp
GIGYF1	GRB10 interacting GYF protein 1	ENSG00000146830	PAP34	388	29.1%	chr7	100123106	CCDS34708.1	c.442C>NULL	p.NULL-1FsDel1bp
GDF9	growth differentiation factor 9	ENSG00000164404	PAP34	205	27.8%	chr5	132227892	CCDS4162.1	c.233G>A	p.R78K
GFI1B	growth factor independent 1B transcription repressor	ENSG00000165702	PAP34	48	27.1%	chr9	134851914	CCDS6957.1	c.28AAG>NUL	p.NULL-1FsDel3bp
GFI1B	growth factor independent 1B transcription repressor	ENSG00000165702	PAP34	138	34.1%	chr9	134856227	CCDS6957.1	c.962G>A	p.R321Q
HAX1	HCLS1 associated protein X-1	ENSG00000143575	PAP34	128	15.6%	chr1	152512981	CCDS1064.1	c.424G>NULL	p.NULL-1FsDel1bp
HSPA4	heat shock 70kDa protein 4	ENSG00000170606	PAP34	48	33.3%	chr5	132467894	CCDS4166.1	c.2390A>NULI	p.NULL-1FsDel1bp
HECW2	HECT; C2 and WW domain containing E3 ubiquitin protein ligase 2	ENSG00000138411	PAP34	78	30.8%	chr2	197006099	CCDS33354.1	c.-1T>C	p.IVS1+2-1SpliceDonor
HELZ	helicase with zinc finger	ENSG00000198265	PAP34	39	30.8%	chr17	62594270	CCDS42374.1	c.1535A>G	p.K512R
HNRNPL	heterogeneous nuclear ribonucleoprotein L	ENSG00000104824	PAP34	32	37.5%	chr19	44020998	CCDS33015.1	c.1436A>T	p.E479V
HNRPLL	heterogeneous nuclear ribonucleoprotein L-like	ENSG00000143889	PAP34	236	32.6%	chr2	38683089	CCDS1796.1	c.371TC>NUL	p.NULL-1FsDel2bp
HNF1A	HNF1 homeobox A	ENSG00000135100	PAP34	191	23.6%	chr12	119919914	ENST00000340577	c.1564G>NUL	p.NULL-1FsDel1bp
HOXA3	homeobox A3	ENSG00000105997	PAP34	41	39.0%	chr7	27114487	CCDS5404.1	c.1709C>NULI	p.NULL-1FsDel1bp
HOXB2	homeobox B2	ENSG00000173917	PAP34	44	31.8%	chr17	43976994	CCDS11527.1	c.669C>NULL	p.NULL-1FsDel1bp
HADH	hydroxyacyl-CoA dehydrogenase	ENSG00000138796	PAP34	24	45.8%	chr4	109160227	CCDS3678.1	c.502G>T	p.G168C
HIC1	hypermethylated in cancer 1	ENSG00000177374	PAP34	51	21.6%	chr17	1907855	CCDS42229.1	c.1178G>A	p.G393D
HCN1	hyperpolarization activated cyclic nucleotide-gated potassium channel 1	ENSG00000164588	PAP34	51	19.6%	chr5	45681341	CCDS3952.1	c.974CA>NUL	p.NULL-1FsDel2bp
IGHMBP2	immunoglobulin mu binding protein 2	ENSG00000132740	PAP34	304	34.2%	chr11	68457453	CCDS8187.1	c.1346T>C	p.M449T
IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells; kinase beta	ENSG00000104365	PAP34	66	22.7%	chr8	42298609	CCDS6128.1	c.1727A>NULI	p.NULL-1FsDel1bp
IPPK	inositol 1;3;4;5;6-pentakisphosphate 2-kinase	ENSG00000127080	PAP34	75	34.7%	chr9	94458602	CCDS6699.1	c.277A>NULL	p.NULL-1FsDel1bp
IRS4	insulin receptor substrate 4	ENSG00000133124	PAP34	677	27.9%	chrX	107864459	CCDS14544.1	c.5545NULL>(	p.NULL-1FsIns1bp
ITGA3	integrin; alpha 3 (antigen CD49C; alpha 3 subunit of VLA-3 receptor)	ENSG00000005884	PAP34	197	22.8%	chr17	45500645	CCDS11557.1	c.641C>NULL	p.NULL-1FsDel1bp
ITGA9	integrin; alpha 9	ENSG00000144668	PAP34	155	23.9%	chr3	37820363	CCDS2669.1	c.2935G>A	p.V979M
IRAK1	interleukin-1 receptor-associated kinase 1	ENSG00000184216	PAP34	131	29.0%	chrX	152931977	CCDS14740.1	c.1641C>A	p.Y547X
IMPG2	interphotoreceptor matrix proteoglycan 2	ENSG00000081148	PAP34	169	30.8%	chr3	102445358	CCDS2940.1	c.2507A>G	p.Q836R
IWS1	IWS1 homolog (S. cerevisiae)	ENSG00000163166	PAP34	99	33.3%	chr2	127978873	CCDS2146.1	c.2144NULL>A	p.NULL-1FsIns1bp
JPH4	junctophilin 4	ENSG00000092051	PAP34	141	11.3%	chr14	23110446	CCDS9603.1	c.1334G>T	p.G445V
KLHL10	kelch-like 10 (Drosophila)	ENSG00000161594	PAP34	175	17.1%	chr17	37254913	CCDS42340.1	c.694G>A	p.A232T
KLHL9	kelch-like 9 (Drosophila)	ENSG00000198642	PAP34	80	37.5%	chr9	21323297	CCDS6503.1	c.1562C>A	p.T521N
KRT13	keratin 13	ENSG00000171401	PAP34	45	22.2%	chr17	36914876	CCDS11396.1	c.453C>A	p.D151E
KRT35	keratin 35	ENSG00000197079	PAP34	114	20.2%	chr17	36887329	CCDS11394.2	c.1187C>T	p.T396M
KRTAP10-6	keratin associated protein 10-6	ENSG00000188155	PAP34	134	26.9%	chr21	44836125	CCDS42959.1	c.1766C>NULI	p.NULL-1FsDel1bp
KNDC1	kinase non-catalytic C-lobe domain (KIND) containing 1	ENSG00000171798	PAP34	167	17.4%	chr10	134849518	CCDS7674.1	c.676C>T	p.P226S
KIF1B	kinesin family member 1B	ENSG00000054523	PAP34	57	29.8%	chr1	10357970	CCDS111.1	c.5222T>G	p.M1741R
KIF24	kinesin family member 24	ENSG00000186638	PAP34	93	28.0%	chr9	34301062	NM_194313	c.283C>T	p.R95C
KIF6	kinesin family member 6	ENSG00000164627	PAP34	154	26.0%	chr6	39615867	CCDS4844.1	c.1535G>A	p.R512H
KLF7	Kruppel-like factor 7 (ubiquitous)	ENSG00000118263	PAP34	210	31.9%	chr2	207697151	CCDS2373.1	c.325T>C	p.C109R
L1CAM	L1 cell adhesion molecule	ENSG00000198910	PAP34	254	26.0%	chrX	152785466	CCDS14733.1	c.2263C>T	p.R755C

LBXCOR1	Lbxcor1 homolog (mouse)	ENSG00000188779	PAP34	699	23.6%	chr15	65905851	CCDS32274.1	c.604G>A	p.G202S
LRRC1	leucine rich repeat containing 1	ENSG00000137269	PAP34	123	33.3%	chr6	53768028	CCDS4953.2	c.15C>NULL	p.NULL-1FsDel1bp
LRRC16A	leucine rich repeat containing 16A	ENSG00000079691	PAP34	64	48.4%	chr6	25560433	ENST00000332168	c.917T>NULL	p.NULL-1FsDel1bp
LRRN4	leucine rich repeat neuronal 4	ENSG00000125872	PAP34	410	27.6%	chr20	5970501	CCDS13097.1	c.1390G>A	p.E464K
LRIG1	leucine-rich repeats and immunoglobulin-like domains 1	ENSG00000144749	PAP34	32	37.5%	chr3	66527296	CCDS33783.1	c.1326C>A	p.F442L
LECT1	leukocyte cell derived chemotaxin 1	ENSG00000136110	PAP34	119	16.0%	chr13	52211767	CCDS9437.1	c.142NULL>C	p.NULL-1FsIns1bp
LCN8	lipocalin 8	ENSG00000204001	PAP34	152	27.0%	chr9	138772233	ENST00000357788	c.88G>A	p.V30M
LY6E	lymphocyte antigen 6 complex; locus E	ENSG00000160932	PAP34	195	39.5%	chr8	144174556	CCDS6394.1	c.371C>T	p.P124L
KDM1A	lysine (K)-specific demethylase 1A	ENSG00000004487	PAP34	186	29.6%	chr1	23278644	CCDS30627.1	c.1995T>G	p.C665W
KDM5A	lysine (K)-specific demethylase 5A	ENSG00000073614	PAP34	40	30.0%	chr12	368529	ENST00000382815	c.224CCCCC>	p.NULL-1FsDel5bp
LPAR2	lysophosphatidic acid receptor 2	ENSG00000064547	PAP34	138	37.7%	chr19	19599044	CCDS12407.1	c.50A>G	p.Y17C
LYST	lysosomal trafficking regulator	ENSG00000143669	PAP34	96	24.0%	chr1	234039570	CCDS31062.1	c.3249GT>NU	p.NULL-1FsDel2bp
MMP14	matrix metallopeptidase 14 (membrane-inserted)	ENSG00000157227	PAP34	628	30.7%	chr14	22385063	CCDS9577.1	c.1724A>G	p.Q575R
MED4	mediator complex subunit 4	ENSG00000136146	PAP34	51	25.5%	chr13	47562558	CCDS9408.1	c.-1T>NULL	p.IVS1-3-1SpliceAcceptor
MBD6	methyl-CpG binding domain protein 6	ENSG00000166987	PAP34	286	20.3%	chr12	56205823	CCDS8944.1	c.805C>NULL	p.NULL-1FsDel1bp
MBD6	methyl-CpG binding domain protein 6	ENSG00000166987	PAP34	214	15.0%	chr12	56205827	CCDS8944.1	c.809C>T	p.P270L
MIR1279	microRNA 1279	ENSG00000111605	PAP34	477	22.2%	chr12	67938748	CCDS8988.1	c.806GAG>NU	p.NULL-1FsDel3bp
MIR1279	microRNA 1279	ENSG00000111605	PAP34	1412	27.6%	chr12	67938955	CCDS8988.1	c.1013CTC>N	p.NULL-1FsDel3bp
MAST4	microtubule associated serine/threonine kinase family member 4	ENSG00000069020	PAP34	87	39.1%	chr5	66495205	NM_001164664	c.4442A>C	p.Q1481P
MACF1	microtubule-actin crosslinking factor 1	ENSG00000127603	PAP34	96	30.2%	chr1	39507204	ENST00000372900	c.248C>NULL	p.NULL-1FsDel1bp
MAP1S	microtubule-associated protein 1S	ENSG00000130479	PAP34	264	29.9%	chr19	17705127	CCDS32954.1	c.2914C>T	p.R972C
MIDN	midnolin	ENSG00000167470	PAP34	622	22.8%	chr19	1206456	CCDS32864.1	c.892C>T	p.R298W
MCM3AP	minichromosome maintenance complex component 3 associated protein	ENSG00000160294	PAP34	117	31.6%	chr21	46505242	CCDS13734.1	c.3587A>NULI	p.NULL-1FsDel1bp
MRPL32	mitochondrial ribosomal protein L32	ENSG00000106591	PAP34	69	26.1%	chr7	42938634	CCDS5468.1	c.124C>T	p.P42S
MPV17L2	MPV17 mitochondrial membrane protein-like 2	ENSG00000127226	PAP34	378	31.2%	chr19	18166819	CCDS42522.1	c.487NULL>C	p.NULL-1FsIns1bp
MEGF11	multiple EGF-like-domains 11	ENSG00000157890	PAP34	259	10.0%	chr15	63993256	CCDS10213.1	c.2592CTC>N	p.NULL-1FsDel3bp
MPO	myeloperoxidase	ENSG00000005381	PAP34	581	25.0%	chr17	53704158	CCDS11604.1	c.2124A>NULI	p.NULL-1FsDel1bp
MYH6	myosin; heavy chain 6; cardiac muscle; alpha	ENSG00000197616	PAP34	439	28.0%	chr14	22933269	CCDS9600.1	c.2533G>A	p.A845T
NAPSB	napsin B aspartic peptidase pseudogene	ENSG00000131401	PAP34	864	24.5%	chr19	55529151	ENST00000253720	c.1055G>A	p.R352H
NCKAP1	NCK-associated protein 1	ENSG00000061676	PAP34	98	20.4%	chr2	183515139	CCDS2288.1	c.-1TT>NULL	p.IVS24-3-1SpliceAcceptor
NEBL	nebulette	ENSG00000078114	PAP34	34	29.4%	chr10	21217037	CCDS7134.1	c.364A>T	p.S122C
NCAM1	neural cell adhesion molecule 1	ENSG00000149294	PAP34	72	33.3%	chr11	112337487	ENST00000397957	c.186GG>NUL	p.NULL-1FsDel2bp
NCAM1	neural cell adhesion molecule 1	ENSG00000149294	PAP34	72	26.4%	chr11	112337487	ENST00000397957	c.186G>NULL	p.NULL-1FsDel1bp
NRXN2	neurexin 2	ENSG00000110076	PAP34	202	27.2%	chr11	64185166	CCDS8077.1	c.1820G>A	p.R607H
NF2	neurofibromin 2 (merlin)	ENSG00000186575	PAP34	169	32.0%	chr22	28404297	CCDS13861.1	c.1559A>G	p.E520G

NPAS3	neuronal PAS domain protein 3	ENSG00000151322	PAP34	100	43.0%	chr14	33339110	CCDS9645.1	c.1750C>T	p.R584C
NHLRC4	NHL repeat containing 4	ENSG00000161992	PAP34	85	37.6%	chr16	554215	NM_145270	c.920C>A	p.P307Q
NCCRP1	non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)	ENSG00000188505	PAP34	208	26.4%	chr19	44383132	CCDS12529.1	c.724C>T	p.R242C
NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	ENSG00000069275	PAP34	77	14.3%	chr1	203985770	ENST00000367142	c.361G>NULL	p.NULL-1FsDel1bp
NSD1	nuclear receptor binding SET domain protein 1	ENSG00000165671	PAP34	53	37.7%	chr5	176607875	CCDS4412.1	c.4585A>NULI	p.NULL-1FsDel1bp
NSD1	nuclear receptor binding SET domain protein 1	ENSG00000165671	PAP34	87	19.5%	chr5	176629408	CCDS4412.1	c.5503A>NULI	p.NULL-1FsDel1bp
NCOR2	nuclear receptor co-repressor 2	ENSG00000196498	PAP34	31	41.9%	chr12	123397094	CCDS41858.1	c.4349C>T	p.P1450L
NCOR2	nuclear receptor co-repressor 2	ENSG00000196498	PAP34	894	27.6%	chr12	123422790	CCDS41858.1	c.3126NULL>(	p.NULL-1FsIns1bp
NUP210L	nucleoporin 210kDa-like	ENSG00000143552	PAP34	96	22.9%	chr1	152334150	CCDS41399.1	c.2293T>NULI	p.NULL-1FsDel1bp
NUP62CL	nucleoporin 62kDa C-terminal like	ENSG00000198088	PAP34	46	30.4%	chrX	106284057	CCDS14527.1	c.270T>A	p.D90E
NUP98	nucleoporin 98kDa	ENSG00000110713	PAP34	28	42.9%	chr11	3701221	CCDS7746.1	c.1888C>T	p.Q630X
NUPL1	nucleoporin like 1	ENSG00000139496	PAP34	71	40.8%	chr13	24785024	CCDS9314.1	c.290C>T	p.T97M
NACC1	nucleus accumbens associated 1; BEN and BTB (POZ) domain containing	ENSG00000160877	PAP34	232	35.3%	chr19	13110152	CCDS12294.1	c.1516G>A	p.V506M
NULL	NULL	ENSG00000212882	PAP34	166	14.5%	chr1	156333378	ENST00000361187	c.439G>NULL	p.NULL-1FsDel1bp
NULL	NULL	ENSG00000213818	PAP34	166	34.9%	chr19	56796366	ENST00000396468	c.-1G>NULL	p.IVS3-1-1SpliceAcceptor
NULL	NULL	ENSG00000214069	PAP34	420	25.0%	chr17	78379670	ENST00000397438	c.440C>NULL	p.NULL-1FsDel1bp
NULL	NULL	NM_025248	PAP34	71	21.1%	chr17	33960968	NM_025248	c.3145C>NULI	p.NULL-1FsDel1bp
OBSCN	obscurin; cytoskeletal calmodulin and titin-interacting RhoGEF	ENSG00000154358	PAP34	166	19.3%	chr1	226614315	NM_052843	c.19099G>A	p.G6367R
OBSL1	obscurin-like 1	ENSG00000124006	PAP34	611	27.7%	chr2	220136534	NM_015311	c.2467G>A	p.E823K
OLFM1	olfactomedin 1	ENSG00000130558	PAP34	101	17.8%	chr9	137108818	ENST00000371799	c.436CA>NUL	p.NULL-1FsDel2bp
OR5C1	olfactory receptor; family 5; subfamily C; member 1	ENSG00000148215	PAP34	728	31.2%	chr9	124591181	CCDS35131.1	c.149C>T	p.A50V
OR51B4	olfactory receptor; family 51; subfamily B; member 4	ENSG00000183251	PAP34	95	21.1%	chr11	5278964	CCDS7757.1	c.789A>T	p.K263N
OR6B1	olfactory receptor; family 6; subfamily B; member 1	ENSG00000221813	PAP34	634	21.6%	chr7	143332455	CCDS43667.1	c.433G>A	p.A145T
OR6C1	olfactory receptor; family 6; subfamily C; member 1	ENSG00000205330	PAP34	46	23.9%	chr12	54001352	CCDS31818.1	c.702G>T	p.K234N
OR7C1	olfactory receptor; family 7; subfamily C; member 1	ENSG00000127530	PAP34	50	30.0%	chr19	14771414	CCDS12317.1	c.1497T>NULI	p.NULL-1FsDel1bp
OR8J1	olfactory receptor; family 8; subfamily J; member 1	ENSG00000172487	PAP34	163	16.6%	chr11	55884449	CCDS31529.1	c.151G>A	p.V51I
OS9	osteosarcoma amplified 9; endoplasmic reticulum lectin	ENSG00000135506	PAP34	55	32.7%	chr12	56398286	CCDS31843.1	c.1225C>T	p.R409W
OTOF	otoferlin	ENSG00000115155	PAP34	186	38.2%	chr2	26547078	CCDS1725.1	c.3910G>A	p.E1304K
OVGP1	oviductal glycoprotein 1; 120kDa	ENSG00000085465	PAP34	96	31.3%	chr1	111758768	CCDS834.1	c.2758C>NULI	p.NULL-1FsDel1bp
OXER1	oxoeicosanoid (OXE) receptor 1	ENSG00000162881	PAP34	65	40.0%	chr2	42844593	CCDS1810.1	c.1502NULL>(	p.NULL-1FsIns1bp
OGDHL	oxoglutarate dehydrogenase-like	ENSG00000197444	PAP34	64	37.5%	chr10	50634838	CCDS7234.1	c.365G>A	p.R122Q
PNLIPRP1	pancreatic lipase-related protein 1	ENSG00000187021	PAP34	264	25.4%	chr10	118347377	CCDS7595.1	c.622C>T	p.R208X
PXDN	peroxidasin homolog (Drosophila)	ENSG00000130508	PAP34	152	25.7%	chr2	1631731	NM_012293	c.2828G>A	p.R943Q
PEX6	peroxisomal biogenesis factor 6	ENSG00000124587	PAP34	194	17.0%	chr6	43042113	CCDS4877.1	c.2348AAG>N	p.NULL-1FsDel3bp
PXMP4	peroxisomal membrane protein 4; 24kDa	ENSG00000101417	PAP34	147	29.9%	chr20	31759330	CCDS13225.1	c.482C>T	p.A161V
PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	ENSG00000141682	PAP34	164	27.4%	chr18	55720889	CCDS11975.1	c.89G>A	p.R30K
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP34	63	31.7%	chr10	89682884	CCDS31238.1	c.388C>G	p.R130G

PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase; type I; gamma	ENSG00000186111	PAP34	69	33.3%	chr19	3612076	CCDS32872.1	c.356G>A	p.G119D
PFKL	phosphofructokinase; liver	ENSG00000141959	PAP34	104	36.5%	chr21	44568116	CCDS33582.1	c.1537C>T	p.R513C
PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP34	47	44.7%	chr3	180399630	CCDS43171.1	c.323G>A	p.R108H
PIK3R5	phosphoinositide-3-kinase; regulatory subunit 5	ENSG00000141506	PAP34	113	26.5%	chr17	8731618	CCDS11147.1	c.1886NULL>(	p.NULL-1FsIns1bp
PHKG1	phosphorylase kinase; gamma 1 (muscle)	ENSG00000164776	PAP34	148	31.1%	chr7	56118858	CCDS5525.1	c.362C>T	p.T121I
PGBD5	piggyBac transposable element derived 5	ENSG00000177614	PAP34	226	18.6%	chr1	228553380	CCDS1583.1	c.931C>T	p.R311W
PLVAP	plasmalemma vesicle associated protein	ENSG00000130300	PAP34	317	30.3%	chr19	17337643	CCDS32952.1	c.631C>T	p.R211C
PLEKHG1	pleckstrin homology domain containing; family G (with RhoGef domain) member 1	ENSG00000120278	PAP34	60	33.3%	chr6	151149270	CCDS34552.1	c.564AG>NUL	p.NULL-1FsDel2bp
PLXNA1	plexin A1	ENSG00000114554	PAP34	37	32.4%	chr3	128218081	CCDS33847.1	c.2977C>NUL	p.NULL-1FsDel1bp
PLXNA1	plexin A1	ENSG00000114554	PAP34	267	33.3%	chr3	128221785	CCDS33847.1	c.3877G>A	p.G1293S
POGZ	pogo transposable element with ZNF domain	ENSG00000143442	PAP34	72	19.4%	chr1	149647548	CCDS997.1	c.2367C>NUL	p.NULL-1FsDel1bp
POLG	polymerase (DNA directed); gamma	ENSG00000140521	PAP34	268	22.8%	chr15	87669836	CCDS10350.1	c.1798C>T	p.P600S
POLG	polymerase (DNA directed); gamma	ENSG00000140521	PAP34	154	37.0%	chr15	87677896	CCDS10350.1	c.94G>A	p.A32T
POLR1A	polymerase (RNA) I polypeptide A; 194kDa	ENSG00000068654	PAP34	63	34.9%	chr2	86133498	CCDS42706.1	c.2345C>T	p.A782V
KCTD20	potassium channel tetramerisation domain containing 20	ENSG00000112078	PAP34	140	25.0%	chr6	36545952	CCDS4821.1	c.100A>C	p.N34H
KCNK15	potassium channel; subfamily K; member 15	ENSG00000124249	PAP34	277	32.5%	chr20	42812633	CCDS13337.1	c.733C>T	p.R245C
PAQR6	progestin and adipoQ receptor family member VI	ENSG00000160781	PAP34	333	25.2%	chr1	154480566	CCDS1135.1	c.1308G>NUL	p.NULL-1FsDel1bp
PRLH	prolactin releasing hormone	ENSG00000071677	PAP34	125	30.4%	chr2	238140498	CCDS2519.1	c.205C>T	p.R69X
PRR11	proline rich 11	ENSG00000068489	PAP34	73	20.5%	chr17	54601953	CCDS11614.1	c.58A>NULL	p.NULL-1FsDel1bp
PROM2	prominin 2	ENSG00000155066	PAP34	70	22.9%	chr2	95306471	CCDS2012.1	c.707C>T	p.A236V
PCSK1N	proprotein convertase subtilisin/kexin type 1 inhibitor	ENSG00000102109	PAP34	108	38.0%	chrX	48575598	CCDS14307.1	c.212C>T	p.A71V
PTGER2	prostaglandin E receptor 2 (subtype EP2); 53kDa	ENSG00000125384	PAP34	374	36.1%	chr14	51851200	CCDS9708.1	c.184A>G	p.S62G
PTGIR	prostaglandin I2 (prostacyclin) receptor (IP)	ENSG00000160013	PAP34	279	34.8%	chr19	51816403	CCDS12686.1	c.1135G>A	p.A379T
PSMD11	proteasome (prosome; macropain) 26S subunit; non-ATPase; 11	ENSG00000108671	PAP34	71	25.4%	chr17	27795671	CCDS11272.1	c.17T>C	p.V6A
PKN3	protein kinase N3	ENSG00000160447	PAP34	78	24.4%	chr9	130517476	CCDS6908.1	c.1724T>C	p.L575P
PPP1R3F	protein phosphatase 1; regulatory (inhibitor) subunit 3F	ENSG00000049769	PAP34	66	36.4%	chrX	49029571	CCDS35254.1	c.1475A>C	p.Y492S
PPM1J	protein phosphatase; Mg2+/Mn2+ dependent; 1J	ENSG00000155367	PAP34	89	28.1%	chr1	113055471	CCDS855.2	c.986G>T	p.R329I
PPFIA3	protein tyrosine phosphatase; receptor type; f polypeptide (PTPRF); interacting protein (liprin); alpha 3	ENSG00000177380	PAP34	186	29.6%	chr19	54328375	CCDS12758.1	c.1096C>T	p.Q366X
PPFIA3	protein tyrosine phosphatase; receptor type; f polypeptide (PTPRF); interacting protein (liprin); alpha 3	ENSG00000177380	PAP34	151	22.5%	chr19	54333386	CCDS12758.1	c.1966C>NUL	p.NULL-1FsDel1bp
PTPRT	protein tyrosine phosphatase; receptor type; T	ENSG00000196090	PAP34	128	27.3%	chr20	40377801	CCDS42874.1	c.2115C>A	p.F705L
PTPRU	protein tyrosine phosphatase; receptor type; U	ENSG00000060656	PAP34	179	34.1%	chr1	29474691	CCDS334.1	c.1289G>A	p.S430N
PKM2	pyruvate kinase; muscle	ENSG00000067225	PAP34	59	25.4%	chr15	70281895	CCDS32284.1	c.1425CCT>N	p.NULL-1FsDel3bp
RILPL1	Rab interacting lysosomal protein-like 1	ENSG00000188026	PAP34	111	41.4%	chr12	122523089	NM_178314	c.1161C>A	p.H387Q
RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)	ENSG00000115839	PAP34	70	32.9%	chr2	135609779	CCDS33294.1	c.1730C>A	p.S577Y
RFTN1	raftlin; lipid raft linker 1	ENSG00000131378	PAP34	194	33.0%	chr3	16386760	CCDS33712.1	c.857C>T	p.P286L
RALGAPB	Ral GTPase activating protein; beta subunit (non-catalytic)	ENSG00000170471	PAP34	44	34.1%	chr20	36583715	CCDS13305.1	c.1579A>G	p.K527E
RASIP1	Ras interacting protein 1	ENSG00000105538	PAP34	192	25.5%	chr19	53924383	CCDS12731.1	c.1456A>G	p.M486V
RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1	ENSG00000058335	PAP34	79	32.9%	chr15	77126365	CCDS10309.1	c.656G>A	p.R219Q
RRAGA	Ras-related GTP binding A	ENSG00000155876	PAP34	305	29.8%	chr9	19040276	CCDS6488.1	c.619G>A	p.E207K
RB1CC1	RB1-inducible coiled-coil 1	ENSG00000023287	PAP34	36	30.6%	chr8	53732616	CCDS34892.1	c.2326C>T	p.R776X
RECQL4	RecQ protein-like 4	ENSG00000160957	PAP34	300	29.7%	chr8	145709669	ENST00000301323	c.2204G>A	p.R735H
RELN	reelin	ENSG00000189056	PAP34	42	31.0%	chr7	103155832	CCDS34722.1	c.715G>T	p.A239S
RARA	retinoic acid receptor; alpha	ENSG00000131759	PAP34	91	28.6%	chr17	35765928	CCDS11366.1	c.1313C>NUL	p.NULL-1FsDel1bp

ARHGAP39	Rho GTPase activating protein 39	ENSG00000147799	PAP34	232	32.8%	chr8	145744502	CCDS34971.1	c.2138C>NULL	p.NULL-1FsDel1bp
ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	ENSG00000104728	PAP34	119	36.1%	chr8	1864010	CCDS34794.1	c.2708G>A	p.C903Y
RHPN1	rhophilin; Rho GTPase binding protein 1	ENSG00000158106	PAP34	246	31.3%	chr8	144533399	NM_052924	c.1127C>T	p.T376M
RNF135	ring finger protein 135	ENSG00000181481	PAP34	279	15.4%	chr17	26349916	CCDS11262.1	c.880T>C	p.C294R
RNF39	ring finger protein 39	ENSG00000204618	PAP34	203	30.5%	chr6	30146992	CCDS4673.1	c.1138G>A	p.D380N
RIPPLY2	ripply2 homolog (zebrafish)	ENSG00000203877	PAP34	124	29.0%	chr6	84620203	CCDS34493.1	c.166G>A	p.A56T
RBM19	RNA binding motif protein 19	ENSG00000122965	PAP34	74	29.7%	chr12	112868599	CCDS9172.1	c.1472T>C	p.L491P
RUNDC1	RUN domain containing 1	ENSG00000198863	PAP34	378	15.6%	chr17	38396832	CCDS11448.1	c.1415C>T	p.P472L
SALL1	sal-like 1 (Drosophila)	ENSG00000103449	PAP34	99	36.4%	chr16	49731844	CCDS10747.1	c.5247G>NUL	p.NULL-1FsDel1bp
SALL3	sal-like 3 (Drosophila)	ENSG00000151514	PAP34	82	34.1%	chr18	74855896	CCDS12013.1	c.2917A>G	p.K973E
SALL4	sal-like 4 (Drosophila)	ENSG00000101115	PAP34	58	34.5%	chr20	49834390	CCDS13438.1	c.3402G>NUL	p.NULL-1FsDel1bp
SAP30L	SAP30-like	ENSG00000164576	PAP34	85	18.8%	chr5	153806375	CCDS4326.1	c.18GGA>NUL	p.NULL-1FsDel3bp
SEMA4F	sema domain; immunoglobulin domain (Ig); transmembrane domain (TM) and short cytoplasmic domain; (semaphorin) 4F	ENSG00000135622	PAP34	227	29.5%	chr2	74737303	CCDS1955.1	c.280NULL>G	p.NULL-1FsIns1bp
SH2D3A	SH2 domain containing 3A	ENSG00000125731	PAP34	1115	31.3%	chr19	6706180	CCDS12173.1	c.1127C>NULL	p.NULL-1FsDel1bp
SHROOM2	shroom family member 2	ENSG00000146950	PAP34	117	41.9%	chrX	9822897	CCDS14135.1	c.949C>NULL	p.NULL-1FsDel1bp
SIGLEC7	sialic acid binding Ig-like lectin 7	ENSG00000168995	PAP34	200	25.5%	chr19	56339573	CCDS12826.1	c.532A>G	p.T178A
SPN	sialophorin	ENSG00000197471	PAP34	101	25.7%	chr16	29583517	CCDS10650.1	c.967G>A	p.G323R
SIM1	single-minded homolog 1 (Drosophila)	ENSG00000112246	PAP34	196	29.1%	chr6	100948404	CCDS5045.1	c.1250C>T	p.P417L
SLC2A4RG	SLC2A4 regulator	ENSG00000125520	PAP34	98	30.6%	chr20	61844556	CCDS13537.1	c.1021G>A	p.A341T
SSH1	slingshot homolog 1 (Drosophila)	ENSG00000084112	PAP34	246	33.3%	chr12	107706444	CCDS9121.1	c.2599G>A	p.E867K
SGSM2	small G protein signaling modulator 2	ENSG00000141258	PAP34	34	35.3%	chr17	2187788	CCDS32526.1	c.56A>G	p.E19G
SGSM3	small G protein signaling modulator 3	ENSG00000100359	PAP34	458	31.4%	chr22	39132980	CCDS14002.1	c.1199G>T	p.R400M
SNRNP48	small nuclear ribonucleoprotein 48kDa (U11/U12)	ENSG00000168566	PAP34	56	37.5%	chr6	7535560	CCDS4502.1	c.71G>A	p.S24N
SNAPC4	small nuclear RNA activating complex; polypeptide 4; 190kDa	ENSG00000165684	PAP34	232	34.1%	chr9	138397838	CCDS6998.1	c.1604G>T	p.S535I
SUMO3	SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae)	ENSG00000184900	PAP34	48	43.8%	chr21	45052858	ENST00000397893	c.497T>NULL	p.NULL-1FsDel1bp
SCNN1A	sodium channel; nonvoltage-gated 1 alpha	ENSG00000111319	PAP34	117	33.3%	chr12	6341566	CCDS8543.1	c.787C>A	p.L263M
SLC16A1	solute carrier family 16; member 1 (monocarboxylic acid transporter 1)	ENSG00000155380	PAP34	145	30.3%	chr1	113258174	CCDS858.1	c.1365C>A	p.N455K
SLC16A11	solute carrier family 16; member 11 (monocarboxylic acid transporter 11)	ENSG00000174326	PAP34	131	33.6%	chr17	6886206	CCDS11086.1	c.1786G>NUL	p.NULL-1FsDel1bp
SLC16A11	solute carrier family 16; member 11 (monocarboxylic acid transporter 11)	ENSG00000174326	PAP34	68	36.8%	chr17	6887411	CCDS11086.1	c.218G>A	p.S73N
SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter); member 5	ENSG00000142583	PAP34	66	43.9%	chr1	9022454	CCDS99.1	c.877G>A	p.V293I
SLC23A2	solute carrier family 23 (nucleobase transporters); member 2	ENSG00000089057	PAP34	96	34.4%	chr20	4798569	CCDS13085.1	c.1380C>NULL	p.NULL-1FsDel1bp
SLC25A25	solute carrier family 25 (mitochondrial carrier; phosphate carrier); member 25	ENSG00000148339	PAP34	80	31.3%	chr9	129905857	CCDS35151.1	c.665G>A	p.R222K
SLC37A4	solute carrier family 37 (glucose-6-phosphate transporter); member 4	ENSG00000137700	PAP34	111	29.7%	chr11	118404280	ENST00000330775	c.215A>T	p.D72V
SLC45A4	solute carrier family 45; member 4	ENSG00000022567	PAP34	195	27.7%	chr8	142300956	CCDS34948.1	c.179G>A	p.R60Q
SLC5A8	solute carrier family 5 (iodide transporter); member 8	ENSG00000139357	PAP34	48	25.0%	chr12	100105395	CCDS9080.1	c.991TG>NUL	p.NULL-1FsDel2bp
SLC6A2	solute carrier family 6 (neurotransmitter transporter; noradrenalin); member 2	ENSG00000103546	PAP34	54	38.9%	chr16	54248360	CCDS10754.1	c.253C>A	p.L85I

SLC7A10	solute carrier family 7; (neutral amino acid transporter; y+ system) member 10	ENSG00000130876	PAP34	69	33.3%	chr19	38395634	CCDS12431.1	c.622C>NULL	p.NULL-1FsDel1bp
SP4	Sp4 transcription factor	ENSG00000105866	PAP34	200	23.5%	chr7	21435695	CCDS5373.1	c.387C>A	p.S129R
SPTBN1	spectrin; beta; non-erythrocytic 1	ENSG00000115306	PAP34	210	35.7%	chr2	54711878	CCDS33198.1	c.3190C>A	p.L1064M
SMPD3	sphingomyelin phosphodiesterase 3; neutral membrane (neutral sphingomyelinase II)	ENSG00000103056	PAP34	135	34.8%	chr16	66954966	CCDS10867.1	c.-1C>NULL	p.IVS4-3-1SpliceAcceptor
S1PR4	sphingosine-1-phosphate receptor 4	ENSG00000125910	PAP34	278	33.5%	chr19	3130245	CCDS12105.1	c.455C>T	p.A152V
SPRED2	sprouty-related; EVH1 domain containing 2	ENSG00000198369	PAP34	280	30.4%	chr2	65394633	CCDS33211.1	c.763G>A	p.A255T
SLA	Src-like-adaptor	ENSG00000155926	PAP34	126	25.4%	chr8	134132256	CCDS6370.1	c.148C>T	p.R50C
ST8SIA2	ST8 alpha-N-acetyl-neuraminide alpha-2;8-sialyltransferase 2	ENSG00000140557	PAP34	181	26.0%	chr15	90808615	CCDS10372.1	c.1124C>T	p.T375M
STAU2	staufen; RNA binding protein; homolog 2 (Drosophila)	ENSG00000040341	PAP34	93	19.4%	chr8	74496207	NM_001164380	c.1760C>NULL	p.NULL-1FsDel1bp
SAMD9L	sterile alpha motif domain containing 9-like	ENSG00000177409	PAP34	59	25.4%	chr7	92599884	CCDS34681.1	c.3337G>A	p.A1113T
SYNGAP1	synaptic Ras GTPase activating protein 1 homolog (rat)	ENSG00000197283	PAP34	84	23.8%	chr6	33519545	CCDS34434.1	c.3193G>A	p.A1065T
SYCE1	synaptonemal complex central element protein 1	ENSG00000171772	PAP34	582	33.5%	chr10	135228975	NM_001143764	c.49G>A	p.V17M
SYT1	synaptotagmin I	ENSG00000067715	PAP34	51	29.4%	chr12	78209918	CCDS9017.1	c.-1G>A	p.IVS2-1-1SpliceAcceptor
STXBP2	syntaxin binding protein 2	ENSG00000076944	PAP34	429	31.5%	chr19	7612954	CCDS12181.1	c.613G>T	p.V205F
TAS2R20	taste receptor; type 2; member 20	ENSG00000212125	PAP34	90	13.3%	chr12	11041339	CCDS8639.1	c.403G>A	p.G135R
TBC1D14	TBC1 domain family; member 14	ENSG00000132405	PAP34	154	31.2%	chr4	7077679	CCDS3394.1	c.1760G>A	p.R587H
TBC1D4	TBC1 domain family; member 4	ENSG00000136111	PAP34	45	46.7%	chr13	74834197	CCDS41901.1	c.1046C>T	p.S349L
TBX4	T-box 4	ENSG00000121075	PAP34	206	25.7%	chr17	56915127	CCDS11629.1	c.1106C>NULL	p.NULL-1FsDel1bp
TCP11	t-complex 11 homolog (mouse)	ENSG00000124678	PAP34	70	22.9%	chr6	35196700	CCDS4799.1	c.493C>T	p.R165W
TERT	telomerase reverse transcriptase	ENSG00000164362	PAP34	50	30.0%	chr5	1347903	CCDS3861.2	c.202G>A	p.A68T
TEP1	telomerase-associated protein 1	ENSG00000129566	PAP34	284	30.6%	chr14	19922487	CCDS9548.1	c.3359G>NUL	p.NULL-1FsDel1bp
TSPAN10	tetraspanin 10	ENSG00000182612	PAP34	229	27.1%	chr17	77222729	ENST00000328585	c.343C>G	p.P115A
TJP3	tight junction protein 3 (zona occludens 3)	ENSG00000105289	PAP34	178	23.0%	chr19	3701577	CCDS32873.1	c.-1C>A	p.IVS19-3-1SpliceAcceptor
TOPBP1	topoisomerase (DNA) II binding protein 1	ENSG00000163781	PAP34	144	28.5%	chr3	134819920	NM_007027	c.3639A>NULL	p.NULL-1FsDel1bp
TOPORS	topoisomerase I binding; arginine/serine-rich	ENSG00000197579	PAP34	95	30.5%	chr9	32533987	CCDS6527.1	c.536G>A	p.R179H
TFAP2E	transcription factor AP-2 epsilon (activating enhancer binding protein 2 epsilon)	ENSG00000116819	PAP34	87	12.6%	chr1	35812338	CCDS393.1	c.227A>G	p.Y76C
TRPM5	transient receptor potential cation channel; subfamily M; member 5	ENSG00000070985	PAP34	92	29.3%	chr11	2390631	CCDS31340.1	c.2542NULL>(	p.NULL-1FsIns1bp
TRPV4	transient receptor potential cation channel; subfamily V; member 4	ENSG00000111199	PAP34	214	29.9%	chr12	108710722	CCDS9134.1	c.2074C>T	p.P692S
TOMM40L	translocase of outer mitochondrial membrane 40 homolog (yeast)-like	ENSG00000158882	PAP34	331	21.8%	chr1	159464386	CCDS1227.1	c.467A>T	p.D156V
TM9SF1	transmembrane 9 superfamily member 1	ENSG00000100926	PAP34	127	29.1%	chr14	23731756	CCDS9617.1	c.1526C>NULL	p.NULL-1FsDel1bp
TMEM184C	transmembrane protein 184C	ENSG00000164168	PAP34	185	33.5%	chr4	148758601	CCDS3770.1	c.44G>T	p.R15L
TRIM55	tripartite motif-containing 55	ENSG00000147573	PAP34	95	33.7%	chr8	67229006	CCDS6184.1	c.1407A>G	p.I469M
TPP2	tripeptidyl peptidase II	ENSG00000134900	PAP34	101	26.7%	chr13	102086657	CCDS9502.1	c.1592G>A	p.R531H
TRO	trophinin	ENSG00000067445	PAP34	90	28.9%	chrX	54971801	CCDS43959.1	c.1919G>A	p.R640H
TNFAIP8L1	tumor necrosis factor; alpha-induced protein 8-like 1	ENSG00000185361	PAP34	163	35.0%	chr19	4603104	CCDS12132.1	c.223C>T	p.R75C
USP40	ubiquitin specific peptidase 40	ENSG00000085982	PAP34	41	24.4%	chr2	234058976	ENST00000251722	c.3332A>NULL	p.NULL-1FsDel1bp

UBE2R2	ubiquitin-conjugating enzyme E2R 2	ENSG00000107341	PAP34	40	35.0%	chr9	33807762	CCDS6546.1	c.7CAG>NULL	p.NULL-1FsDel3bp
UBA3	ubiquitin-like modifier activating enzyme 3	ENSG00000144744	PAP34	34	29.4%	chr3	69194845	CCDS2909.1	c.671C>T	p.T224M
GALNT14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	ENSG00000158089	PAP34	231	21.6%	chr2	31021314	CCDS1773.2	c.-1A>G	p.IVS7-2-1SpliceAcceptor
UBTF	upstream binding transcription factor; RNA polymerase I	ENSG00000108312	PAP34	88	21.6%	chr17	39643764	CCDS11480.1	c.1281G>T	p.E427D
VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	ENSG00000197969	PAP34	44	29.5%	chr9	79126463	CCDS6655.1	c.5811A>T	p.K1937N
VAT1	vesicle amine transport protein 1 homolog (T. californica)	ENSG00000108828	PAP34	162	23.5%	chr17	38423447	CCDS11451.1	c.793G>A	p.G265S
VCL	vinculin	ENSG00000035403	PAP34	67	35.8%	chr10	75513147	CCDS7341.1	c.892G>A	p.A298T
MYB	v-myb myeloblastosis viral oncogene homolog (avian)	ENSG00000118513	PAP34	290	22.1%	chr6	135560031	NM_001130173	c.1443A>NULL	p.NULL-1FsDel1bp
WDR64	WD repeat domain 64	ENSG00000162843	PAP34	105	19.0%	chr1	240020595	CCDS1619.1	c.1600T>NULL	p.NULL-1FsDel1bp
WDR66	WD repeat domain 66	ENSG00000158023	PAP34	41	46.3%	chr12	120876596	CCDS41853.1	c.1508G>A	p.G503D
WWP2	WW domain containing E3 ubiquitin protein ligase 2	ENSG00000198373	PAP34	73	34.2%	chr16	68390221	CCDS10885.1	c.206A>C	p.E69A
XDH	xanthine dehydrogenase	ENSG00000158125	PAP34	58	37.9%	chr2	31464227	CCDS1775.1	c.605C>T	p.T202M
XPC	xeroderma pigmentosum; complementation group C	ENSG00000154767	PAP34	111	10.8%	chr3	14172876	ENST00000285021	c.1984G>C	p.A662P
ZSCAN1	zinc finger and SCAN domain containing 1	ENSG00000152467	PAP34	110	25.5%	chr19	63241336	CCDS12969.1	c.320G>T	p.R107M
ZC3H7B	zinc finger CCCH-type containing 7B	ENSG00000100403	PAP34	388	30.2%	chr22	40053184	CCDS14013.1	c.314G>A	p.S105N
ZFHX2	zinc finger homeobox 2	ENSG00000136367	PAP34	142	42.3%	chr14	23063221	ENST00000258869	c.6178G>NUL	p.NULL-1FsDel1bp
ZFHX3	zinc finger homeobox 3	ENSG00000140836	PAP34	112	17.0%	chr16	71388859	CCDS10908.1	c.10682NULL>	p.NULL-1FsIns3bp
ZNF516	zinc finger protein 516	ENSG00000101493	PAP34	245	30.2%	chr18	72282902	ENST00000217537	c.1097G>A	p.R366H
ZNF687	zinc finger protein 687	ENSG00000143373	PAP34	103	17.5%	chr1	149525658	CCDS992.1	c.267TG>NUL	p.NULL-1FsDel2bp
ZNF687	zinc finger protein 687	ENSG00000143373	PAP34	1016	14.3%	chr1	149528504	CCDS992.1	c.2498AC>NU	p.NULL-1FsDel2bp
ZDHHC14	zinc finger; DHHC-type containing 14	ENSG00000175048	PAP34	160	30.0%	chr6	158014014	CCDS5252.1	c.1339C>NULL	p.NULL-1FsDel1bp
ZMYM6	zinc finger; MYM-type 6	ENSG00000163867	PAP34	53	28.3%	chr1	35245229	CCDS387.2	c.1723C>T	p.R575X
ZHX3	zinc fingers and homeoboxes 3	ENSG00000174306	PAP34	97	24.7%	chr20	39266376	CCDS13315.1	c.3454A>NULL	p.NULL-1FsDel1bp
ADNP	activity-dependent neuroprotector homeobox	ENSG00000101126	PAP43	259	19.7%	chr20	48941649	CCDS13433.1	c.3009C>G	p.S1003R
APC	adenomatous polyposis coli	ENSG00000134982	PAP43	90	11.1%	chr5	112202901	CCDS4107.1	c.3711GAGT>	p.NULL-1FsDel4bp
APC	adenomatous polyposis coli	ENSG00000134982	PAP43	90	11.1%	chr5	112202906	CCDS4107.1	c.3716G>T	p.R1239I
APC	adenomatous polyposis coli	ENSG00000134982	PAP43	135	15.6%	chr5	112203575	CCDS4107.1	c.4385AG>NU	p.NULL-1FsDel2bp
CPXM1	carboxypeptidase X (M14 family); member 1	ENSG00000088882	PAP43	211	17.5%	chr20	2722859	CCDS13033.1	c.2182C>T	p.R728W
CHGA	chromogranin A (parathyroid secretory protein 1)	ENSG00000100604	PAP43	97	15.5%	chr14	92468597	CCDS9906.1	c.938C>T	p.P313L
CBS	cystathionine-beta-synthase	ENSG00000160200	PAP43	144	11.8%	chr21	43358439	CCDS13693.1	c.679A>G	p.S227G
ANKRD6	DAVID_ankyrin repeat domain 6	NM_014942	PAP43	53	24.5%	chr6	90369522	NM_014942	c.275C>T	p.A92V
KRTAP19-6	DAVID_keratin associated protein 19-6	ENSG00000186964	PAP43	128	13.3%	chr21	30835855	CCDS13598.1	c.169T>A	p.F57I
ND1	DAVID_NADH-ubiquinone oxidoreductase chain 1	ENSG00000198888	PAP43	134	44.0%	chrM	3345	ENST00000361390	c.38T>C	p.I13T
ROBO1	DAVID_roundabout: axon guidance receptor: homolog 1 (Drosophila); similar to roundabout 1 isoform b	NM_002941	PAP43	619	18.3%	chr3	78779492	NM_002941	c.2816C>G	p.P939R
LOC642132	DAVID_roundabout: axon guidance receptor: homolog 1 (Drosophila); similar to roundabout 1 isoform b	NM_002941	PAP43	619	18.3%	chr3	78779492	NM_002941	c.2816C>G	p.P939R
GLI2	GLI family zinc finger 2	ENSG00000074047	PAP43	117	17.9%	chr2	121464266	CCDS33283.1	c.4306G>A	p.A1436T
GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	ENSG00000167588	PAP43	144	16.7%	chr12	48787665	CCDS8799.1	c.661G>A	p.D221N
ITGAE	integrin; alpha E (antigen CD103; human mucosal lymphocyte antigen 1; alpha polypeptide)	ENSG00000083457	PAP43	74	13.5%	chr17	3582440	CCDS32531.1	c.2823A>NULL	p.NULL-1FsDel1bp
NCOA6	nuclear receptor coactivator 6	ENSG00000198646	PAP43	229	18.3%	chr20	32793666	CCDS13241.1	c.4055C>T	p.P1352L

PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP43	127	18.9%	chr10	89682885	CCDS31238.1	c.389G>A	p.R130Q
PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP43	99	28.3%	chr3	180434779	CCDS43171.1	c.3140A>T	p.H1047L
PRRG3	proline rich Gla (G-carboxyglutamic acid) 3 (transmembrane)	ENSG00000130032	PAP43	83	27.7%	chrX	150619163	CCDS14699.1	c.47G>T	p.R16L
PRSS36	protease; serine; 36	ENSG00000178226	PAP43	142	18.3%	chr16	31059493	CCDS32436.1	c.1988G>A	p.R663H
PTK2	PTK2 protein tyrosine kinase 2	ENSG00000169398	PAP43	118	16.9%	chr8	141969997	CCDS6381.1	c.22C>T	p.P8S
TACC2	transforming; acidic coiled-coil containing protein 2	ENSG00000138162	PAP43	71	18.3%	chr10	123986955	CCDS7626.1	c.8183G>A	p.R2728H
TMEM178	transmembrane protein 178	ENSG00000152154	PAP43	70	15.7%	chr2	39797695	CCDS1804.1	c.694ATC>NU	p.NULL-1FsDel3bp
ZNF347	zinc finger protein 347	ENSG00000197937	PAP43	116	20.7%	chr19	58335687	CCDS33097.1	c.2206C>A	p.P736T
ZNF536	zinc finger protein 536	ENSG00000198597	PAP43	54	18.5%	chr19	35628404	CCDS32984.1	c.2095G>A	p.G699R
ZFX	zinc finger protein; X-linked	ENSG00000005889	PAP43	179	18.4%	chrX	24139353	CCDS14211.1	c.2357G>A	p.R786Q
AGPAT6	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase; zeta)	ENSG00000158669	PAP45	150	23.3%	chr8	41595427	CCDS6117.1	c.1121G>A	p.R374Q
BPGM	2;3-bisphosphoglycerate mutase	ENSG00000172331	PAP45	266	22.2%	chr7	133996967	CCDS5833.1	c.168C>A	p.F56L
HAAO	3-hydroxyanthranilate 3;4-dioxygenase	ENSG00000162882	PAP45	147	18.4%	chr2	42869187	CCDS33187.1	c.145G>A	p.E49K
HMGCLL1	3-hydroxymethyl-3-methylglutaryl-CoA lyase-like 1	ENSG00000146151	PAP45	130	30.0%	chr6	55514860	CCDS43475.1	c.236A>C	p.K79T
PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	ENSG00000138801	PAP45	113	22.1%	chr4	108772271	CCDS3676.1	c.1701G>T	p.K567N
HTR1B	5-hydroxytryptamine (serotonin) receptor 1B	ENSG00000135312	PAP45	306	24.2%	chr6	78229002	CCDS4986.1	c.838G>A	p.E280K
HTR1F	5-hydroxytryptamine (serotonin) receptor 1F	ENSG00000179097	PAP45	137	18.2%	chr3	88122929	CCDS2920.1	c.340C>A	p.L114I
HTR1F	5-hydroxytryptamine (serotonin) receptor 1F	ENSG00000179097	PAP45	101	15.8%	chr3	88123018	CCDS2920.1	c.429G>T	p.M143I
HTR2A	5-hydroxytryptamine (serotonin) receptor 2A	ENSG00000102468	PAP45	200	23.0%	chr13	46307526	CCDS9405.1	c.863C>A	p.S288Y
HTR2B	5-hydroxytryptamine (serotonin) receptor 2B	ENSG00000135914	PAP45	245	13.5%	chr2	231696614	CCDS2483.1	c.109G>T	p.E37X
HTR3B	5-hydroxytryptamine (serotonin) receptor 3B	ENSG00000149305	PAP45	198	25.8%	chr11	113322064	CCDS8364.1	c.1321G>A	p.V441M
HTR4	5-hydroxytryptamine (serotonin) receptor 4	ENSG00000164270	PAP45	66	28.8%	chr5	147880685	CCDS34273.1	c.542T>G	p.F181C
MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	ENSG00000116984	PAP45	88	13.6%	chr1	235121234	CCDS1614.1	c.3186C>A	p.F1062L
NT5DC3	5'-nucleotidase domain containing 3	ENSG00000111696	PAP45	130	23.1%	chr12	102706812	CCDS41824.1	c.1035G>T	p.M345I
NT5DC4	5'-nucleotidase domain containing 4	ENSG00000144130	PAP45	217	22.6%	chr2	113199541	ENST00000409693	c.998G>A	p.R333Q
NT5C2	5'-nucleotidase; cytosolic II	ENSG00000076685	PAP45	207	19.3%	chr10	104924621	CCDS7544.1	c.85C>T	p.R29X
NT5E	5'-nucleotidase; ecto (CD73)	ENSG00000135318	PAP45	98	19.4%	chr6	86260430	CCDS5002.1	c.1714T>G	p.L572V
PFKFB3	6-phosphofructo-2-kinase/fructose-2;6-biphosphatase 3	ENSG00000170525	PAP45	116	26.7%	chr10	6298735	CCDS7078.1	c.427G>T	p.E143X
PFKFB4	6-phosphofructo-2-kinase/fructose-2;6-biphosphatase 4	ENSG00000114268	PAP45	359	20.9%	chr3	48562376	CCDS2771.1	c.236G>A	p.R79H
PFKFB4	6-phosphofructo-2-kinase/fructose-2;6-biphosphatase 4	ENSG00000114268	PAP45	118	16.1%	chr3	48569167	CCDS2771.1	c.48G>A	p.W16X
OGG1	8-oxoguanine DNA glycosylase	ENSG00000114026	PAP45	613	25.4%	chr3	9768483	CCDS2576.1	c.415G>A	p.E139K
AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	ENSG00000127914	PAP45	103	14.6%	chr7	91468892	CCDS5622.1	c.1725T>G	p.I575M
AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	ENSG00000127914	PAP45	42	26.2%	chr7	91469067	CCDS5622.1	c.1900G>A	p.E634K
AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	ENSG00000127914	PAP45	25	44.0%	chr7	91469112	CCDS5622.1	c.1945C>T	p.R649X
AKAP1	A kinase (PRKA) anchor protein 1	ENSG00000121057	PAP45	189	23.3%	chr17	52538522	CCDS11594.1	c.698G>A	p.G233D
AKAP1	A kinase (PRKA) anchor protein 1	ENSG00000121057	PAP45	96	27.1%	chr17	52538695	CCDS11594.1	c.871G>A	p.A291T
AKAP13	A kinase (PRKA) anchor protein 13	ENSG00000170776	PAP45	257	25.3%	chr15	83924536	CCDS32320.1	c.2233G>T	p.D745Y
AKAP3	A kinase (PRKA) anchor protein 3	ENSG00000111254	PAP45	225	27.6%	chr12	4607232	CCDS8531.1	c.1097G>A	p.G366E
AKAP3	A kinase (PRKA) anchor protein 3	ENSG00000111254	PAP45	323	23.2%	chr12	4607524	CCDS8531.1	c.805C>T	p.R269X
AKAP4	A kinase (PRKA) anchor protein 4	ENSG00000147081	PAP45	514	20.6%	chrX	49844513	CCDS14329.1	c.1591G>T	p.E531X
AKAP4	A kinase (PRKA) anchor protein 4	ENSG00000147081	PAP45	339	25.4%	chrX	49844878	CCDS14329.1	c.1226G>T	p.R409I
AKAP6	A kinase (PRKA) anchor protein 6	ENSG00000151320	PAP45	331	20.2%	chr14	31972502	CCDS9644.1	c.52C>A	p.P18T
AKAP6	A kinase (PRKA) anchor protein 6	ENSG00000151320	PAP45	87	24.1%	chr14	32361664	CCDS9644.1	c.4894A>G	p.T1632A
AKAP6	A kinase (PRKA) anchor protein 6	ENSG00000151320	PAP45	143	30.8%	chr14	32362402	CCDS9644.1	c.5632A>C	p.N1878H
ABI2	abl-interactor 2	ENSG00000138443	PAP45	55	27.3%	chr2	203967805	CCDS2358.1	c.698G>A	p.R233Q
AIM2	absent in melanoma 2	ENSG00000163568	PAP45	230	16.5%	chr1	157302576	CCDS1181.1	c.564C>A	p.F188L
ACHE	acetylcholinesterase (Yt blood group)	ENSG00000087085	PAP45	365	17.8%	chr7	100329086	CCDS5710.1	c.704C>T	p.A235V
ACACB	acetyl-CoA carboxylase beta	ENSG00000076555	PAP45	43	27.9%	chr12	108098164	CCDS31898.1	c.1262G>T	p.R421I
ACACB	acetyl-CoA carboxylase beta	ENSG00000076555	PAP45	187	21.4%	chr12	108114045	CCDS31898.1	c.2306C>T	p.P769L
AAAS	achalasia; adrenocortical insufficiency; alacrimia (Allgrove; triple-A)	ENSG00000094914	PAP45	218	26.1%	chr12	51988133	CCDS8856.1	c.1301G>A	p.R434Q

ACP1	acid phosphatase 1; soluble	ENSG00000143727	PAP45	302	25.2%	chr2	261919	CCDS1639.1	c.97G>A	p.D33N
ACP6	acid phosphatase 6; lysophosphatidic	ENSG00000162836	PAP45	80	27.5%	chr1	145597756	CCDS928.1	c.502C>T	p.R168W
ACP6	acid phosphatase 6; lysophosphatidic	ENSG00000162836	PAP45	141	21.3%	chr1	145598391	CCDS928.1	c.343C>A	p.L115M
ACPL2	acid phosphatase-like 2	ENSG00000155893	PAP45	428	23.4%	chr3	142494558	CCDS3116.1	c.1264C>A	p.L422I
AFAP1L2	actin filament associated protein 1-like 2	ENSG00000169129	PAP45	60	26.7%	chr10	116054473	CCDS31286.1	c.1279C>T	p.L427F
ARPC2	actin related protein 2/3 complex; subunit 2; 34kDa	ENSG00000163466	PAP45	65	18.5%	chr2	218811721	CCDS2410.1	c.358T>G	p.C120G
ASCC3	activating signal cointegrator 1 complex subunit 3	ENSG00000112249	PAP45	63	25.4%	chr6	101201874	CCDS5046.1	c.3427G>T	p.E1143X
ATF7IP	activating transcription factor 7 interacting protein	ENSG00000171681	PAP45	116	25.0%	chr12	14501457	CCDS8663.1	c.2119G>A	p.E707K
ATF7IP	activating transcription factor 7 interacting protein	ENSG00000171681	PAP45	115	12.2%	chr12	14505248	CCDS8663.1	c.2711G>A	p.R904Q
ABR	active BCR-related gene	ENSG00000159842	PAP45	115	23.5%	chr17	908746	CCDS10999.1	c.1294C>T	p.R432W
ACAD10	acyl-CoA dehydrogenase family; member 10	ENSG00000111271	PAP45	96	27.1%	chr12	110666874	CCDS31903.1	c.1759G>A	p.E587K
ACSM2B	acyl-CoA synthetase medium-chain family member 2B	ENSG00000066813	PAP45	133	15.8%	chr16	20390421	CCDS32401.1	c.803A>G	p.N268S
ADAM10	ADAM metallopeptidase domain 10	ENSG00000137845	PAP45	123	22.0%	chr15	56720366	CCDS10167.1	c.914C>A	p.S305Y
ADAM17	ADAM metallopeptidase domain 17	ENSG00000151694	PAP45	75	18.7%	chr2	9575761	CCDS1665.1	c.1024G>T	p.D342Y
ADAM19	ADAM metallopeptidase domain 19 (meltrin beta)	ENSG00000135074	PAP45	749	24.4%	chr5	156862394	CCDS4338.1	c.1303G>T	p.E435X
ADAM19	ADAM metallopeptidase domain 19 (meltrin beta)	ENSG00000135074	PAP45	136	25.7%	chr5	156930486	CCDS4338.1	c.175G>T	p.E59X
ADAM21	ADAM metallopeptidase domain 21	ENSG00000139985	PAP45	128	12.5%	chr14	69995173	CCDS9804.1	c.1204G>A	p.E402K
ADAM21P1	ADAM metallopeptidase domain 21 pseudogene 1	ENSG00000139985	PAP45	128	12.5%	chr14	69995173	CCDS9804.1	c.1204G>A	p.E402K
ADAM23	ADAM metallopeptidase domain 23	ENSG00000114948	PAP45	87	19.5%	chr2	207130409	CCDS2369.1	c.947G>A	p.R316H
ADAM23	ADAM metallopeptidase domain 23	ENSG00000114948	PAP45	85	25.9%	chr2	207167725	CCDS2369.1	c.2098G>T	p.D700Y
ADAM29	ADAM metallopeptidase domain 29	ENSG00000168594	PAP45	103	22.3%	chr4	176133898	CCDS3823.1	c.647G>T	p.R216M
ADAM29	ADAM metallopeptidase domain 29	ENSG00000168594	PAP45	241	23.2%	chr4	176135260	CCDS3823.1	c.2009G>T	p.R670I
ADAM7	ADAM metallopeptidase domain 7	ENSG00000069206	PAP45	164	26.8%	chr8	24405428	CCDS6045.1	c.1479G>T	p.K493N
ADAMTS10	ADAM metallopeptidase with thrombospondin type 1 motif; 10	ENSG00000142303	PAP45	157	28.0%	chr19	8576511	CCDS12206.1	c.85C>A	p.Q29K
ADAMTS14	ADAM metallopeptidase with thrombospondin type 1 motif; 14	ENSG00000138316	PAP45	248	30.6%	chr10	72104392	CCDS7307.1	c.157C>A	p.L53I
ADAMTS15	ADAM metallopeptidase with thrombospondin type 1 motif; 15	ENSG00000166106	PAP45	113	21.2%	chr11	129848213	CCDS8488.1	c.2140C>T	p.R714C
ADAMTS16	ADAM metallopeptidase with thrombospondin type 1 motif; 16	ENSG00000145536	PAP45	153	20.9%	chr5	5199354	CCDS43299.1	c.287C>A	p.S96Y
ADAMTS16	ADAM metallopeptidase with thrombospondin type 1 motif; 16	ENSG00000145536	PAP45	97	17.5%	chr5	5359692	CCDS43299.1	c.3262C>T	p.R1088X
ADAMTS16	ADAM metallopeptidase with thrombospondin type 1 motif; 16	ENSG00000145536	PAP45	253	26.5%	chr5	5372206	CCDS43299.1	c.3630C>A	p.F1210L
ADAMTS17	ADAM metallopeptidase with thrombospondin type 1 motif; 17	ENSG00000140470	PAP45	340	26.5%	chr15	98510413	CCDS10383.1	c.1400G>A	p.G467D
ADAMTS18	ADAM metallopeptidase with thrombospondin type 1 motif; 18	ENSG00000140873	PAP45	186	18.8%	chr16	75912546	CCDS10926.1	c.2218G>A	p.V740I
ADAMTS18	ADAM metallopeptidase with thrombospondin type 1 motif; 18	ENSG00000140873	PAP45	87	21.8%	chr16	75945203	CCDS10926.1	c.1542T>G	p.I514M
ADAMTS19	ADAM metallopeptidase with thrombospondin type 1 motif; 19	ENSG00000145808	PAP45	104	15.4%	chr5	128889950	CCDS4146.1	c.970G>T	p.E324X
ADAMTS19	ADAM metallopeptidase with thrombospondin type 1 motif; 19	ENSG00000145808	PAP45	61	19.7%	chr5	129017948	CCDS4146.1	c.2209C>A	p.L737I
ADAMTS20	ADAM metallopeptidase with thrombospondin type 1 motif; 20	ENSG00000173157	PAP45	139	22.3%	chr12	42103793	ENST00000389417	c.4489G>T	p.D1497Y
ADAMTS3	ADAM metallopeptidase with thrombospondin type 1 motif; 3	ENSG00000156140	PAP45	165	27.3%	chr4	73367725	CCDS3553.1	c.3610G>T	p.E1204X
ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif; 5	ENSG00000154736	PAP45	164	28.0%	chr21	27224187	CCDS13579.1	c.2114G>T	p.R705I
ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif; 6	ENSG00000049192	PAP45	138	15.2%	chr5	64519770	CCDS3983.2	c.2739G>T	p.K913N
ADAMTSL1	ADAMTS-like 1	ENSG00000178031	PAP45	167	25.1%	chr9	18785425	NM_001040272	c.3708G>T	p.Q1236H
ADAMTSL1	ADAMTS-like 1	ENSG00000178031	PAP45	123	25.2%	chr9	18819885	NM_001040272	c.4159C>T	p.L1387F
ADAMTSL2	ADAMTS-like 2	ENSG00000197859	PAP45	234	23.1%	chr9	135391666	CCDS6976.1	c.11G>A	p.R4K
ADAMTSL2	ADAMTS-like 2	ENSG00000197859	PAP45	60	40.0%	chr9	135423313	CCDS6976.1	c.1972G>A	p.D658N
ADAMTSL3	ADAMTS-like 3	ENSG00000156218	PAP45	195	15.4%	chr15	82351132	CCDS10326.1	c.1259C>A	p.P420H

AP1S2	adaptor-related protein complex 1; sigma 2 subunit	ENSG00000182287	PAP45	102	24.5%	chrX	15773468	CCDS14173.1	c.381G>T	p.K127N
AP2M1	adaptor-related protein complex 2; mu 1 subunit	ENSG00000161203	PAP45	227	23.8%	chr3	185383314	CCDS43177.1	c.1137G>T	p.K379N
AP3B1	adaptor-related protein complex 3; beta 1 subunit	ENSG00000132842	PAP45	42	28.6%	chr5	77599168	CCDS4041.1	c.136G>T	p.D46Y
AP3B2	adaptor-related protein complex 3; beta 2 subunit	ENSG00000103723	PAP45	206	27.2%	chr15	81146526	ENST00000261722	c.807C>A	p.F269L
AP4B1	adaptor-related protein complex 4; beta 1 subunit	ENSG00000134262	PAP45	77	20.8%	chr1	114242883	CCDS865.1	c.1178G>A	p.R393Q
ASXL1	additional sex combs like 1 (Drosophila)	ENSG00000171456	PAP45	251	29.5%	chr20	30485334	CCDS13201.1	c.1672G>A	p.E558K
ASXL2	additional sex combs like 2 (Drosophila)	ENSG00000143970	PAP45	249	30.5%	chr2	25826239	NM_018263	c.1690G>T	p.E564X
ADD2	adducin 2 (beta)	ENSG00000075340	PAP45	201	28.4%	chr2	70744144	CCDS1906.1	c.2102C>T	p.S701F
APC2	adenomatosis polyposis coli 2	ENSG00000115266	PAP45	47	31.9%	chr19	1408978	CCDS12068.1	c.1222G>A	p.E408K
APC	adenomatous polyposis coli	ENSG00000134982	PAP45	150	14.0%	chr5	112202787	CCDS4107.1	c.3597G>T	p.K1199N
APC	adenomatous polyposis coli	ENSG00000134982	PAP45	102	25.5%	chr5	112203221	CCDS4107.1	c.4031C>A	p.S1344X
APC	adenomatous polyposis coli	ENSG00000134982	PAP45	263	16.7%	chr5	112204948	CCDS4107.1	c.5758C>T	p.R1920X
APC	adenomatous polyposis coli	ENSG00000134982	PAP45	182	23.6%	chr5	112205800	CCDS4107.1	c.6610C>T	p.R2204X
ADAD2	adenosine deaminase domain containing 2	ENSG00000140955	PAP45	246	25.2%	chr16	82787998	CCDS10944.1	c.1915C>T	p.R639C
ADARB2	adenosine deaminase; RNA-specific; B2 (RED2 homolog rat)	ENSG00000185736	PAP45	167	31.1%	chr10	1395733	CCDS7058.1	c.567C>A	p.F189L
AMPD1	adenosine monophosphate deaminase 1	ENSG00000116748	PAP45	79	26.6%	chr1	115020096	CCDS876.1	c.1440G>T	p.E480D
AMPD1	adenosine monophosphate deaminase 1	ENSG00000116748	PAP45	101	18.8%	chr1	115024473	CCDS876.1	c.697C>A	p.P233T
ADCY10	adenylate cyclase 10 (soluble)	ENSG00000143199	PAP45	305	23.9%	chr1	166081653	CCDS1265.1	c.2779C>T	p.R927X
ADCY2	adenylate cyclase 2 (brain)	ENSG00000078295	PAP45	133	23.3%	chr5	7762394	CCDS3872.2	c.1472C>T	p.S491L
ADCY6	adenylate cyclase 6	ENSG00000174233	PAP45	159	22.6%	chr12	47450915	CCDS8767.1	c.3157C>T	p.R1053C
AK3	adenylate kinase 3	ENSG00000147853	PAP45	44	25.0%	chr9	4703072	CCDS6455.1	c.588C>A	p.F196L
ADRM1	adhesion regulating molecule 1	ENSG00000130706	PAP45	58	34.5%	chr20	60316541	CCDS13496.1	c.926G>A	p.R309H
ADIPOQ	adiponectin; C1Q and collagen domain containing	ENSG00000181092	PAP45	301	20.9%	chr3	188054852	CCDS3284.1	c.400A>G	p.K134E
ADNP2	ADNP homeobox 2	ENSG00000101544	PAP45	128	18.0%	chr18	75992003	CCDS32853.1	c.135G>T	p.E45D
ARF3	ADP-ribosylation factor 3	ENSG00000134287	PAP45	162	16.0%	chr12	47619794	CCDS8774.1	c.295C>T	p.R99X
ART3	ADP-ribosyltransferase 3	ENSG00000156219	PAP45	133	26.3%	chr4	77222446	CCDS3575.1	c.515T>G	p.F172C
ART4	ADP-ribosyltransferase 4 (Dombrock blood group)	ENSG00000111339	PAP45	113	18.6%	chr12	14885339	CCDS8668.1	c.160G>A	p.D54N
ADRA1A	adrenergic; alpha-1A-; receptor	ENSG00000120907	PAP45	286	23.1%	chr8	26778292	CCDS34869.1	c.112C>A	p.L38I
ADRA1B	adrenergic; alpha-1B-; receptor	ENSG00000170214	PAP45	294	27.9%	chr5	159276860	CCDS4347.1	c.370G>A	p.V124M
ADRA1B	adrenergic; alpha-1B-; receptor	ENSG00000170214	PAP45	284	25.7%	chr5	159276914	CCDS4347.1	c.424G>A	p.D142N
ADRA2C	adrenergic; alpha-2C-; receptor	ENSG00000184160	PAP45	205	27.3%	chr4	3738522	NM_000683	c.391G>A	p.D131N
ADRBK2	adrenergic; beta; receptor kinase 2	ENSG00000100077	PAP45	83	27.7%	chr22	24429523	CCDS13832.1	c.1207G>A	p.D403N
AFF1	AF4/FMR2 family; member 1	ENSG00000172493	PAP45	91	24.2%	chr4	88186370	CCDS3616.1	c.46C>T	p.R16X
AFF3	AF4/FMR2 family; member 3	ENSG00000144218	PAP45	136	27.9%	chr2	99584341	CCDS33258.1	c.1434C>A	p.F478L
AHNAK	AHNAK nucleoprotein	ENSG00000124942	PAP45	323	23.5%	chr11	62049826	CCDS31584.1	c.8639T>C	p.V2880A
AKIRIN2	akirin 2	ENSG00000135334	PAP45	66	27.3%	chr6	88444293	CCDS5013.1	c.491G>A	p.R164Q
ADH1B	alcohol dehydrogenase 1B (class I); beta polypeptide	ENSG00000196616	PAP45	102	17.6%	chr4	100451069	CCDS34033.1	c.979G>T	p.E327X
ADH6	alcohol dehydrogenase 6 (class V)	ENSG00000172955	PAP45	108	29.6%	chr4	100345118	CCDS43255.1	c.1090A>C	p.K364Q
ADH7	alcohol dehydrogenase 7 (class IV); mu or sigma polypeptide	ENSG00000196344	PAP45	56	25.0%	chr4	100555744	CCDS34034.1	c.1050G>T	p.K350N
ALDH16A1	aldehyde dehydrogenase 16 family; member A1	ENSG00000161618	PAP45	65	23.1%	chr19	54661308	CCDS12766.1	c.1894C>T	p.R632W
ALDH18A1	aldehyde dehydrogenase 18 family; member A1	ENSG00000059573	PAP45	153	20.3%	chr10	97360036	CCDS7443.1	c.2114A>G	p.N705S
ALDH18A1	aldehyde dehydrogenase 18 family; member A1	ENSG00000059573	PAP45	75	32.0%	chr10	97370923	CCDS7443.1	c.1322G>A	p.R441Q
ALDH5A1	aldehyde dehydrogenase 5 family; member A1	ENSG00000112294	PAP45	138	17.4%	chr6	24613157	CCDS4556.1	c.691G>A	p.E231K
ALDH6A1	aldehyde dehydrogenase 6 family; member A1	ENSG00000119711	PAP45	39	41.0%	chr14	73608361	CCDS9826.1	c.418C>T	p.R140X
AKR1C3	aldo-keto reductase family 1; member C3 (3-alpha hydroxysteroid dehydrogenase; type II)	ENSG00000196139	PAP45	67	14.9%	chr10	5129726	CCDS7063.1	c.353C>T	p.S118F
ALDOB	aldolase B; fructose-bisphosphate	ENSG00000136872	PAP45	218	25.7%	chr9	103231976	CCDS6756.1	c.206C>T	p.S69F
ALPP	alkaline phosphatase; placental (Regan isozyme)	ENSG00000163283	PAP45	158	20.3%	chr2	232951960	CCDS2490.1	c.112G>A	p.A38T
ALKBH2	alkB; alkylation repair homolog 2 (E. coli)	ENSG00000189046	PAP45	256	25.0%	chr12	108014748	CCDS31897.1	c.227C>T	p.A76V
AGPS	alkylglycerone phosphate synthase	ENSG00000018510	PAP45	113	25.7%	chr2	177966018	CCDS2275.1	c.255G>T	p.K85N
AGPS	alkylglycerone phosphate synthase	ENSG00000018510	PAP45	119	26.1%	chr2	178078548	CCDS2275.1	c.1544G>A	p.R515Q
A4GNT	alpha-1;4-N-acetylglucosaminyltransferase	ENSG00000118017	PAP45	178	13.5%	chr3	139326256	CCDS3097.1	c.563G>A	p.R188Q

A2M	alpha-2-macroglobulin	ENSG00000175899	PAP45	118	22.0%	chr12	9145480	NM_000014	c.1324G>A	p.E442K
ALPK2	alpha-kinase 2	ENSG00000198796	PAP45	432	20.1%	chr18	54353335	CCDS11966.2	c.5064G>T	p.E1688D
ALPK2	alpha-kinase 2	ENSG00000198796	PAP45	171	14.0%	chr18	54353778	CCDS11966.2	c.4621C>A	p.L1541I
ALPK2	alpha-kinase 2	ENSG00000198796	PAP45	454	27.3%	chr18	54397283	CCDS11966.2	c.1705G>T	p.E569X
ALMS1	Alstrom syndrome 1	ENSG00000116127	PAP45	166	25.9%	chr2	73533836	CCDS42697.1	c.6671C>A	p.S2224Y
ALMS1	Alstrom syndrome 1	ENSG00000116127	PAP45	91	22.0%	chr2	73570600	CCDS42697.1	c.8003G>A	p.R2668Q
ALMS1	Alstrom syndrome 1	ENSG00000116127	PAP45	75	36.0%	chr2	73570671	CCDS42697.1	c.8074G>T	p.E2692X
AIMP1	aminoacyl tRNA synthetase complex-interacting multifunctional protein 1	ENSG00000164022	PAP45	96	28.1%	chr4	107472277	CCDS3674.1	c.-1G>T	p.IVS3-1-1SpliceAcceptor
AASS	aminoadipate-semialdehyde synthase	ENSG00000008311	PAP45	96	25.0%	chr7	121544018	CCDS5783.1	c.799C>T	p.R267C
AGPHD1	aminoglycoside phosphotransferase domain containing 1	ENSG00000188266	PAP45	165	25.5%	chr15	76592627	CCDS42063.1	c.142T>G	p.F48V
ALAD	aminolevulinate dehydratase	ENSG00000148218	PAP45	162	29.0%	chr9	115191888	CCDS6794.1	c.639C>A	p.F213L
ALAS2	aminolevulinate; delta-; synthase 2	ENSG00000158578	PAP45	67	22.4%	chrX	55058077	CCDS14366.1	c.1265C>A	p.S422Y
AGL	amylo-alpha-1; 6-glucosidase; 4-alpha-glucanotransferase	ENSG00000162688	PAP45	103	31.1%	chr1	100159787	CCDS759.1	c.4591G>T	p.D1531Y
APBB1IP	amyloid beta (A4) precursor protein-binding; family B; member 1 interacting protein	ENSG00000077420	PAP45	329	17.6%	chr10	26891315	CCDS31167.1	c.1424C>A	p.S475Y
APLP1	amyloid beta (A4) precursor-like protein 1	ENSG00000105290	PAP45	38	31.6%	chr19	41054417	CCDS32997.1	c.601C>T	p.R201W
APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	ENSG00000062725	PAP45	164	17.7%	chr17	55892864	CCDS32699.1	c.1003G>T	p.D335Y
ALS2	amyotrophic lateral sclerosis 2 (juvenile)	ENSG00000003393	PAP45	35	37.1%	chr2	202284060	CCDS42800.1	c.4021C>T	p.R1341C
ALS2CR4	amyotrophic lateral sclerosis 2 (juvenile) chromosome region; candidate 4	ENSG00000155755	PAP45	53	22.6%	chr2	202205127	NM_001044385	c.445G>T	p.D149Y
ANAPC2	anaphase promoting complex subunit 2	ENSG00000176248	PAP45	235	25.1%	chr9	139189522	CCDS7033.1	c.2244G>T	p.E748D
ANAPC2	anaphase promoting complex subunit 2	ENSG00000176248	PAP45	110	15.5%	chr9	139190061	CCDS7033.1	c.1940A>G	p.D647G
AR	androgen receptor	ENSG00000169083	PAP45	205	24.4%	chrX	66854077	CCDS14387.1	c.2206G>T	p.A736S
AMOT	angiomotin	ENSG00000126016	PAP45	597	21.8%	chrX	111952715	NM_001113490	c.296G>A	p.R99Q
ANGPTL4	angiopoietin-like 4	ENSG00000167772	PAP45	67	19.4%	chr19	8335487	CCDS12200.1	c.282G>T	p.E94D
AGTR2	angiotensin II receptor; type 2	ENSG00000180772	PAP45	122	26.2%	chrX	115217694	CCDS14569.1	c.133G>T	p.D45Y
ANLN	anillin; actin binding protein	ENSG00000011426	PAP45	87	25.3%	chr7	36426828	CCDS5447.1	c.2113G>T	p.E705X
ANKHD1-EIF	ANKHD1-EIF4EBP3 readthrough	ENSG00000131503	PAP45	641	25.1%	chr5	139888645	CCDS4224.1	c.5930C>A	p.S1977Y
ANK2	ankyrin 2; neuronal	ENSG00000145362	PAP45	113	23.9%	chr4	114459156	CCDS3702.1	c.2831C>A	p.S944Y
ANK2	ankyrin 2; neuronal	ENSG00000145362	PAP45	129	26.4%	chr4	114493903	CCDS3702.1	c.4680G>T	p.E1560D
ANK2	ankyrin 2; neuronal	ENSG00000145362	PAP45	173	28.9%	chr4	114499654	CCDS3702.1	c.10431C>A	p.F3477L
ANK2	ankyrin 2; neuronal	ENSG00000145362	PAP45	177	21.5%	chr4	114513887	CCDS3702.1	c.-1C>A	p.IVS44-3-1SpliceAcceptor
ANK3	ankyrin 3; node of Ranvier (ankyrin G)	ENSG00000151150	PAP45	110	18.2%	chr10	61501533	CCDS7258.1	c.9112C>A	p.L3038I
ABTB2	ankyrin repeat and BTB (POZ) domain containing 2	ENSG00000166016	PAP45	130	11.5%	chr11	34132862	CCDS7890.1	c.2170A>G	p.T724A
ANKDD1A	ankyrin repeat and death domain containing 1A	ENSG00000166839	PAP45	156	30.8%	chr15	63026753	CCDS10197.2	c.1238C>A	p.S413Y
ANKHD1	ankyrin repeat and KH domain containing 1	ENSG00000131503	PAP45	641	25.1%	chr5	139888645	CCDS4224.1	c.5930C>A	p.S1977Y
ANKLE2	ankyrin repeat and LEM domain containing 2	ENSG00000176915	PAP45	47	31.9%	chr12	131821134	CCDS41869.1	c.1801G>T	p.E601X
ANKMY2	ankyrin repeat and MYND domain containing 2	ENSG00000106524	PAP45	230	21.7%	chr7	16607022	CCDS5361.1	c.1215G>T	p.K405N
ANKMY2	ankyrin repeat and MYND domain containing 2	ENSG00000106524	PAP45	42	28.6%	chr7	16615802	CCDS5361.1	c.860G>A	p.R287Q
ASB10	ankyrin repeat and SOCS box-containing 10	ENSG00000146926	PAP45	215	11.6%	chr7	150509270	CCDS5921.1	c.793G>A	p.D265N
ASB18	ankyrin repeat and SOCS box-containing 18	ENSG00000182177	PAP45	147	17.0%	chr2	236814720	NM_212556	c.270G>T	p.E90D
ASB9	ankyrin repeat and SOCS box-containing 9	ENSG00000102048	PAP45	112	30.4%	chrX	15172640	CCDS35208.1	c.794G>T	p.R265I
ANKS4B	ankyrin repeat and sterile alpha motif domain containing 4B	ENSG00000175311	PAP45	197	20.3%	chr16	21168945	CCDS42130.1	c.557C>A	p.S186X
ANKS4B	ankyrin repeat and sterile alpha motif domain containing 4B	ENSG00000175311	PAP45	149	23.5%	chr16	21169346	CCDS42130.1	c.958G>A	p.G320R
ANKS6	ankyrin repeat and sterile alpha motif domain containing 6	ENSG00000165138	PAP45	70	15.7%	chr9	100586972	CCDS43856.1	c.870G>T	p.E290D
ANKRD12	ankyrin repeat domain 12	ENSG00000101745	PAP45	106	16.0%	chr18	9185681	CCDS11843.1	c.220C>T	p.R74X
ANKRD13C	ankyrin repeat domain 13C	ENSG00000118454	PAP45	93	18.3%	chr1	70539135	CCDS648.2	c.821G>A	p.R274Q
ANKRD17	ankyrin repeat domain 17	ENSG00000132466	PAP45	66	22.7%	chr4	74238655	CCDS34004.1	c.1040T>C	p.V347A
ANKRD22	ankyrin repeat domain 22	ENSG00000152766	PAP45	160	18.1%	chr10	90581624	CCDS7390.1	c.161G>T	p.R54I

ANKRD34B	ankyrin repeat domain 34B	ENSG00000189127	PAP45	266	26.3%	chr5	79890174	CCDS34194.1	c.1421C>T	p.S474F
ANKRD34B	ankyrin repeat domain 34B	ENSG00000189127	PAP45	152	34.2%	chr5	79890993	CCDS34194.1	c.602C>A	p.S201Y
ANKRD35	ankyrin repeat domain 35	ENSG00000198483	PAP45	248	25.8%	chr1	144278441	CCDS919.1	c.2932A>C	p.N978H
ANKRD45	ankyrin repeat domain 45	ENSG00000183831	PAP45	177	12.4%	chr1	171882730	CCDS1309.1	c.374C>A	p.T125N
ANKRD46	ankyrin repeat domain 46	ENSG00000186106	PAP45	148	20.9%	chr8	101609285	CCDS6287.1	c.434C>T	p.S145L
ANKRD49	ankyrin repeat domain 49	ENSG00000168876	PAP45	168	23.8%	chr11	93869697	CCDS8300.1	c.190C>T	p.R64X
ANKRD50	ankyrin repeat domain 50	ENSG00000151458	PAP45	226	25.2%	chr4	125810932	CCDS34060.1	c.2950C>A	p.H984N
ANKRD60	ankyrin repeat domain 60	ENSG00000124227	PAP45	170	27.1%	chr20	56229928	ENST00000371167	c.284G>A	p.R95Q
ANKRD61	ankyrin repeat domain 61	ENSG00000157999	PAP45	250	16.4%	chr7	6037621	ENST00000409061	c.89C>T	p.S30L
ANKRD62	ankyrin repeat domain 62	ENSG00000181626	PAP45	77	15.6%	chr18	12084114	ENST00000314074	c.65G>A	p.R22Q
ANO10	anoctamin 10	ENSG00000160746	PAP45	105	10.5%	chr3	43577787	CCDS2710.2	c.1405G>A	p.A469T
ANO3	anoctamin 3	ENSG00000134343	PAP45	157	26.8%	chr11	26577079	CCDS31447.1	c.1629A>C	p.K543N
APH1A	anterior pharynx defective 1 homolog A (C. elegans)	ENSG00000117362	PAP45	93	28.0%	chr1	148505580	CCDS41390.1	c.710G>A	p.R237Q
APH1B	anterior pharynx defective 1 homolog B (C. elegans)	ENSG00000138613	PAP45	92	28.3%	chr15	61366775	CCDS10184.1	c.455C>A	p.S152Y
ANTXR2	anthrax toxin receptor 2	ENSG00000163297	PAP45	212	23.6%	chr4	81117818	NM_001145794	c.1409G>A	p.R470Q
MKI67	antigen identified by monoclonal antibody Ki-67	ENSG00000148773	PAP45	267	31.5%	chr10	129794906	CCDS7659.1	c.5188G>A	p.E1730K
MKI67	antigen identified by monoclonal antibody Ki-67	ENSG00000148773	PAP45	211	26.1%	chr10	129803267	CCDS7659.1	c.1395G>T	p.E465D
AZIN1	antizyme inhibitor 1	ENSG00000155096	PAP45	188	20.7%	chr8	103915604	CCDS6295.1	c.730C>A	p.Q244K
APLNR	apelin receptor	ENSG00000134817	PAP45	301	24.9%	chr11	56759937	CCDS7950.1	c.1118G>T	p.S373I
APLNR	apelin receptor	ENSG00000134817	PAP45	104	12.5%	chr11	56760679	CCDS7950.1	c.376G>A	p.D126N
APOB	apolipoprotein B (including Ag(x) antigen)	ENSG00000084674	PAP45	161	26.1%	chr2	21081534	CCDS1703.1	c.11711A>G	p.N3904S
APOB	apolipoprotein B (including Ag(x) antigen)	ENSG00000084674	PAP45	158	32.9%	chr2	21084131	CCDS1703.1	c.9114C>A	p.F3038L
APOB	apolipoprotein B (including Ag(x) antigen)	ENSG00000084674	PAP45	183	21.9%	chr2	21089756	CCDS1703.1	c.3997C>T	p.R1333X
APOB	apolipoprotein B (including Ag(x) antigen)	ENSG00000084674	PAP45	141	17.0%	chr2	21089809	CCDS1703.1	c.3944C>T	p.T1315I
APOBEC1	apolipoprotein B mRNA editing enzyme; catalytic polypeptide 1	ENSG00000111701	PAP45	127	18.9%	chr12	7693528	CCDS8579.1	c.593G>T	p.R198I
APOBEC3F	apolipoprotein B mRNA editing enzyme; catalytic polypeptide-like 3F	ENSG00000128394	PAP45	735	24.9%	chr22	37770044	CCDS33649.1	c.182C>A	p.S61Y
APOL2	apolipoprotein L; 2	ENSG00000128335	PAP45	239	27.6%	chr22	34953647	CCDS43014.1	c.763G>T	p.E255X
APOL5	apolipoprotein L; 5	ENSG00000128313	PAP45	79	25.3%	chr22	34446593	CCDS13920.1	c.88C>T	p.R30X
AIFM1	apoptosis-inducing factor; mitochondrion-associated; 1	ENSG00000156709	PAP45	73	24.7%	chrX	129097782	CCDS14618.1	c.1224G>T	p.K408N
APITD1	apoptosis-inducing; TAF9-like domain 1	ENSG00000175279	PAP45	129	31.8%	chr1	10434175	CCDS114.1	c.431C>T	p.S144F
ALOX12	arachidonate 12-lipoxygenase	ENSG00000108839	PAP45	37	27.0%	chr17	6844378	CCDS11084.1	c.-1G>T	p.IVS6-1-1SpliceAcceptor
ALOX12B	arachidonate 12-lipoxygenase; 12R type	ENSG00000179477	PAP45	117	26.5%	chr17	7930113	CCDS11129.1	c.298C>T	p.P100S
ALOXE3	arachidonate lipoxygenase 3	ENSG00000179148	PAP45	145	24.8%	chr17	7960900	CCDS11130.1	c.271G>A	p.E91K
ARCN1	archain 1	ENSG00000095139	PAP45	144	28.5%	chr11	117949620	ENST00000359415	c.38C>A	p.S13Y
ARCN1	archain 1	ENSG00000095139	PAP45	108	30.6%	chr11	117968699	CCDS8400.1	c.1050G>T	p.E350D
AGAP2	ArfGAP with GTPase domain; ankyrin repeat and PH domain 2	ENSG00000135439	PAP45	382	27.2%	chr12	56414683	CCDS8951.1	c.266G>A	p.R89Q
ARG2	arginase; type II	ENSG00000081181	PAP45	108	24.1%	chr14	67182259	CCDS9785.1	c.509A>C	p.E170A
AVPR1A	arginine vasopressin receptor 1A	ENSG00000166148	PAP45	219	24.7%	chr12	61830142	CCDS8965.1	c.742C>T	p.R248C
AVPR1A	arginine vasopressin receptor 1A	ENSG00000166148	PAP45	131	19.8%	chr12	61830317	CCDS8965.1	c.567C>A	p.F189L
RARS	arginyl-tRNA synthetase	ENSG00000113643	PAP45	258	17.8%	chr5	167853513	CCDS4367.1	c.406G>T	p.E136X
ARIH2	ariadne homolog 2 (Drosophila)	ENSG00000177479	PAP45	218	11.9%	chr3	48991942	CCDS2780.1	c.985G>T	p.D329Y
ARMC2	armadillo repeat containing 2	ENSG00000118690	PAP45	64	28.1%	chr6	109340377	NM_032131	c.1273A>C	p.N425H
ARMC3	armadillo repeat containing 3	ENSG00000165309	PAP45	86	20.9%	chr10	23284829	CCDS7142.1	c.254G>T	p.R85I
ARMC3	armadillo repeat containing 3	ENSG00000165309	PAP45	480	27.5%	chr10	23366218	CCDS7142.1	c.2423G>T	p.R808I
ARMCX2	armadillo repeat containing; X-linked 2	ENSG00000184867	PAP45	82	25.6%	chrX	100797379	CCDS14490.1	c.1852G>T	p.D618Y
ARMCX2	armadillo repeat containing; X-linked 2	ENSG00000184867	PAP45	627	26.2%	chrX	100798425	CCDS14490.1	c.806C>A	p.P269Q
ARMCX6	armadillo repeat containing; X-linked 6	ENSG00000198960	PAP45	253	24.5%	chrX	100757980	CCDS14488.1	c.287G>A	p.R96Q
ARMCX6	armadillo repeat containing; X-linked 6	ENSG00000198960	PAP45	375	22.1%	chrX	100758076	CCDS14488.1	c.191C>A	p.T64N
ARRDC1	arrestin domain containing 1	ENSG00000197070	PAP45	129	14.0%	chr9	139627232	CCDS7049.1	c.182T>C	p.V61A

ARRDC1	arrestin domain containing 1	ENSG00000197070	PAP45	134	30.6%	chr9	139628584	CCDS7049.1	c.631A>C	p.K211Q
AADACL3	arylacetamide deacetylase-like 3	ENSG00000188984	PAP45	322	26.1%	chr1	12708188	CCDS41253.1	c.691G>T	p.E231X
ARNT2	aryl-hydrocarbon receptor nuclear translocator 2	ENSG00000172379	PAP45	134	25.4%	chr15	78673024	CCDS32307.1	c.2084C>T	p.T695I
ARSA	arylsulfatase A	ENSG00000100299	PAP45	131	27.5%	chr22	49412157	CCDS14100.1	c.649C>T	p.R217C
ARSH	arylsulfatase family; member H	ENSG00000205667	PAP45	196	26.5%	chrX	2938070	CCDS35198.1	c.-1G>T	p.IVS1-1-1SpliceAcceptor
ARSK	arylsulfatase family; member K	ENSG00000164291	PAP45	118	33.9%	chr5	94962499	CCDS4073.1	c.1289C>T	p.S430L
ARSG	arylsulfatase G	ENSG00000141337	PAP45	99	20.2%	chr17	63892910	CCDS11676.1	c.-1T>C	p.IVS8+2-1SpliceDonor
ASGR1	asialoglycoprotein receptor 1	ENSG00000141505	PAP45	134	30.6%	chr17	7018323	CCDS11089.1	c.452G>T	p.R151M
ASPM	asp (abnormal spindle) homolog; microcephaly associated (Drosophila)	ENSG00000066279	PAP45	305	24.6%	chr1	195337946	CCDS1389.1	c.7058G>A	p.R2353K
ASPM	asp (abnormal spindle) homolog; microcephaly associated (Drosophila)	ENSG00000066279	PAP45	232	25.4%	chr1	195368051	CCDS1389.1	c.2474G>A	p.R825Q
ASPM	asp (abnormal spindle) homolog; microcephaly associated (Drosophila)	ENSG00000066279	PAP45	97	22.7%	chr1	195378203	CCDS1389.1	c.1802G>T	p.R601I
ASNSD1	asparagine synthetase domain containing 1	ENSG00000138381	PAP45	98	20.4%	chr2	190240853	CCDS2300.1	c.1583G>A	p.R528Q
ALG1	asparagine-linked glycosylation 1; beta-1;4-mannosyltransferase homolog (S. cerevisiae)	ENSG00000033011	PAP45	713	25.2%	chr16	5063164	CCDS10528.1	c.296G>A	p.R99Q
DNPEP	aspartyl aminopeptidase	ENSG00000123992	PAP45	330	27.9%	chr2	219959920	CCDS42823.1	c.157C>T	p.L53F
DARS	aspartyl-tRNA synthetase	ENSG00000115866	PAP45	138	20.3%	chr2	136453337	CCDS2180.1	c.194G>T	p.R65I
ASTE1	asteroid homolog 1 (Drosophila)	ENSG00000034533	PAP45	95	10.5%	chr3	132215737	CCDS3068.1	c.2224A>NULL	p.NULL-1FsDel1bp
ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP45	335	19.4%	chr1	26973825	CCDS285.1	c.4520A>C	p.N1507T
ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP45	225	28.9%	chr1	26974093	CCDS285.1	c.4788G>T	p.E1596D
ARID1B	AT rich interactive domain 1B (SWI1-like)	ENSG00000049618	PAP45	334	27.8%	chr6	157569912	CCDS5251.1	c.5891A>G	p.H1964R
ARID2	AT rich interactive domain 2 (ARID; RFX-like)	ENSG00000189079	PAP45	358	27.4%	chr12	44530221	CCDS31783.1	c.2048G>T	p.R683I
ARID5A	AT rich interactive domain 5A (MRF1-like)	ENSG00000196843	PAP45	143	23.1%	chr2	96580730	CCDS33251.1	c.738C>A	p.F246L
ATM	ataxia telangiectasia mutated	ENSG00000149311	PAP45	99	30.3%	chr11	107620805	CCDS31669.1	c.743G>A	p.R248Q
ATM	ataxia telangiectasia mutated	ENSG00000149311	PAP45	167	16.8%	chr11	107693416	CCDS31669.1	c.6305C>T	p.A2102V
ATM	ataxia telangiectasia mutated	ENSG00000149311	PAP45	150	20.0%	chr11	107701407	CCDS31669.1	c.6733G>T	p.E2245X
ATXN2	ataxin 2	ENSG00000204842	PAP45	353	23.2%	chr12	110442193	CCDS31902.1	c.1339G>T	p.E447X
ATXN3L	ataxin 3-like	ENSG00000123594	PAP45	141	24.1%	chrX	13247260	NM_001135995	c.715G>A	p.E239K
ATXN7L2	ataxin 7-like 2	ENSG00000162650	PAP45	131	19.8%	chr1	109831820	CCDS30794.1	c.571G>T	p.E191X
ATG4A	ATG4 autophagy related 4 homolog A (S. cerevisiae)	ENSG00000101844	PAP45	216	24.5%	chrX	107268054	CCDS14538.1	c.791C>T	p.A264V
ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)	ENSG00000057663	PAP45	165	19.4%	chr6	106741231	CCDS5055.1	c.705G>T	p.K235N
ATHL1	ATH1; acid trehalase-like 1 (yeast)	ENSG00000142102	PAP45	397	24.7%	chr11	284672	CCDS31322.1	c.1606C>T	p.L536F
AKNA	AT-hook transcription factor	ENSG00000106948	PAP45	107	24.3%	chr9	116159019	CCDS6805.1	c.2791A>G	p.T931A
ACLY	ATP citrate lyase	ENSG00000131473	PAP45	72	26.4%	chr17	37314527	CCDS11412.1	c.1046A>G	p.N349S
ATPAF1	ATP synthase mitochondrial F1 complex assembly factor 1	ENSG00000123472	PAP45	138	27.5%	chr1	46903604	CCDS541.1	c.286G>T	p.E96X
ATP5G1	ATP synthase; H+ transporting; mitochondrial F0 complex; subunit C1 (subunit 9)	ENSG00000159199	PAP45	43	23.3%	chr17	44325804	CCDS11539.1	c.26T>A	p.I9N
ATP5B	ATP synthase; H+ transporting; mitochondrial F1 complex; beta polypeptide	ENSG00000110955	PAP45	158	28.5%	chr12	55324948	CCDS8924.1	c.369G>T	p.Q123H
AGTPBP1	ATP/GTP binding protein 1	ENSG00000135049	PAP45	34	41.2%	chr9	87437942	CCDS6672.1	c.1350G>T	p.K450N
AGTPBP1	ATP/GTP binding protein 1	ENSG00000135049	PAP45	87	21.8%	chr9	87477302	CCDS6672.1	c.551G>A	p.R184Q
AGBL5	ATP/GTP binding protein-like 5	ENSG00000084693	PAP45	106	27.4%	chr2	27134952	CCDS1732.3	c.1852C>T	p.R618X
ATAD2B	ATPase family; AAA domain containing 2B	ENSG00000119778	PAP45	189	20.1%	chr2	23964249	NM_017552	c.529G>T	p.E177X
ATAD5	ATPase family; AAA domain containing 5	ENSG00000176208	PAP45	81	21.0%	chr17	26244540	CCDS11260.1	c.4543C>A	p.L1515I
ATP13A3	ATPase type 13A3	ENSG00000133657	PAP45	87	25.3%	chr3	195640947	CCDS43187.1	c.1754G>A	p.R585Q
ATP8A2	ATPase; aminophospholipid transporter; class I; type 8A; member 2	ENSG00000132932	PAP45	169	16.6%	chr13	25049251	CCDS41873.1	c.1757G>A	p.R586Q
ATP8A2	ATPase; aminophospholipid transporter; class I; type 8A; member 2	ENSG00000132932	PAP45	97	21.6%	chr13	25492105	CCDS41873.1	c.3549G>T	p.K1183N

ATP8B1	ATPase; aminophospholipid transporter; class I; type 8B; member 1	ENSG00000081923	PAP45	173	22.5%	chr18	53473593	CCDS11965.1	c.2762C>T	p.S921L
ATP2A1	ATPase; Ca++ transporting; cardiac muscle; fast twitch 1	ENSG00000196296	PAP45	351	24.5%	chr16	28822198	CCDS10643.1	c.2916G>T	p.K972N
ATP2B3	ATPase; Ca++ transporting; plasma membrane 3	ENSG00000067842	PAP45	102	23.5%	chrX	152461811	CCDS35440.1	c.907G>T	p.D303Y
ATP2B3	ATPase; Ca++ transporting; plasma membrane 3	ENSG00000067842	PAP45	356	26.1%	chrX	152488375	CCDS14722.1	c.3463C>A	p.L1155I
ATP2C2	ATPase; Ca++ transporting; type 2C; member 2	ENSG00000064270	PAP45	128	21.1%	chr16	83030629	CCDS42207.1	c.1207G>A	p.E403K
ATP2C2	ATPase; Ca++ transporting; type 2C; member 2	ENSG00000064270	PAP45	213	31.9%	chr16	83052890	CCDS42207.1	c.2551C>A	p.L851I
ATP2A3	ATPase; Ca++ transporting; ubiquitous	ENSG00000074370	PAP45	103	17.5%	chr17	3780456	CCDS11042.1	c.2632G>A	p.E878K
ATP2A3	ATPase; Ca++ transporting; ubiquitous	ENSG00000074370	PAP45	174	17.8%	chr17	3787644	CCDS11042.1	c.2136G>T	p.K712N
ATP8B2	ATPase; class I; type 8B; member 2	ENSG00000143515	PAP45	191	29.8%	chr1	152582263	CCDS1066.1	c.1603G>A	p.A535T
ATP8B4	ATPase; class I; type 8B; member 4	ENSG00000104043	PAP45	47	29.8%	chr15	48126902	CCDS32238.1	c.139A>C	p.N47H
ATP9A	ATPase; class II; type 9A	ENSG00000054793	PAP45	146	29.5%	chr20	49707018	CCDS33489.1	c.1372G>A	p.E458K
ATP10A	ATPase; class V; type 10A	ENSG00000206190	PAP45	52	26.9%	chr15	23477239	CCDS32178.1	c.3568T>C	p.Y1190H
ATP11A	ATPase; class VI; type 11A	ENSG00000068650	PAP45	182	20.9%	chr13	112487565	CCDS32011.1	c.155C>T	p.S52L
ATP11A	ATPase; class VI; type 11A	ENSG00000068650	PAP45	101	20.8%	chr13	112533828	CCDS32011.1	c.1360G>A	p.D454N
ATP11B	ATPase; class VI; type 11B	ENSG00000058063	PAP45	109	15.6%	chr3	184046000	CCDS33896.1	c.765T>G	p.I255M
ATP11C	ATPase; class VI; type 11C	ENSG00000101974	PAP45	63	19.0%	chrX	138706277	CCDS14668.1	c.1036G>A	p.D346N
ATP7A	ATPase; Cu++ transporting; alpha polypeptide	ENSG00000165240	PAP45	81	24.7%	chrX	77171413	CCDS35339.1	c.2927G>T	p.R976I
ATP7A	ATPase; Cu++ transporting; alpha polypeptide	ENSG00000165240	PAP45	88	21.6%	chrX	77171425	CCDS35339.1	c.2939G>A	p.R980Q
ATP7B	ATPase; Cu++ transporting; beta polypeptide	ENSG00000123191	PAP45	307	22.8%	chr13	51446478	CCDS41892.1	c.879G>T	p.E293D
ATP6V1B1	ATPase; H+ transporting; lysosomal 56/58kDa; V1 subunit B1	ENSG00000116039	PAP45	159	13.2%	chr2	71041597	CCDS1912.1	c.624G>T	p.K208N
ATP6V1B2	ATPase; H+ transporting; lysosomal 56/58kDa; V1 subunit B2	ENSG00000147416	PAP45	136	18.4%	chr8	20114581	CCDS6014.1	c.812G>A	p.R271Q
ATP12A	ATPase; H+/K+ transporting; nongastric; alpha polypeptide	ENSG00000075673	PAP45	270	11.5%	chr13	24163224	CCDS31948.1	c.904G>T	p.E302X
ATP12A	ATPase; H+/K+ transporting; nongastric; alpha polypeptide	ENSG00000075673	PAP45	219	11.0%	chr13	24179275	CCDS31948.1	c.2284G>A	p.D762N
ATP1B3	ATPase; Na+/K+ transporting; beta 3 polypeptide	ENSG00000069849	PAP45	62	21.0%	chr3	143105241	CCDS3121.1	c.199G>T	p.D67Y
ATP1B4	ATPase; Na+/K+ transporting; beta 4 polypeptide	ENSG00000101892	PAP45	58	29.3%	chrX	119384548	CCDS14598.1	c.204G>T	p.K68N
ABCA1	ATP-binding cassette; sub-family A (ABC1); member 1	ENSG00000165029	PAP45	78	26.9%	chr9	106660656	CCDS6762.1	c.688C>T	p.R230C
ABCA12	ATP-binding cassette; sub-family A (ABC1); member 12	ENSG00000144452	PAP45	105	14.3%	chr2	215584599	CCDS33372.1	c.2141G>A	p.R714Q
ABCA13	ATP-binding cassette; sub-family A (ABC1); member 13	ENSG00000179869	PAP45	157	26.8%	chr7	48255687	ENST00000319379	c.1258G>A	p.D420N
ABCA13	ATP-binding cassette; sub-family A (ABC1); member 13	ENSG00000179869	PAP45	134	30.6%	chr7	48285042	ENST00000319379	c.5068G>T	p.D1690Y
ABCA13	ATP-binding cassette; sub-family A (ABC1); member 13	ENSG00000179869	PAP45	197	23.9%	chr7	48285445	ENST00000319379	c.5471G>A	p.R1824Q
ABCA13	ATP-binding cassette; sub-family A (ABC1); member 13	ENSG00000179869	PAP45	193	25.4%	chr7	48286097	ENST00000319379	c.6123G>T	p.K2041N
ABCA13	ATP-binding cassette; sub-family A (ABC1); member 13	ENSG00000179869	PAP45	55	21.8%	chr7	48286341	ENST00000319379	c.6367G>T	p.A2123S
ABCA13	ATP-binding cassette; sub-family A (ABC1); member 13	ENSG00000179869	PAP45	94	22.3%	chr7	48289525	ENST00000319379	c.8023G>T	p.E2675X
ABCA13	ATP-binding cassette; sub-family A (ABC1); member 13	ENSG00000179869	PAP45	46	34.8%	chr7	48437997	ENST00000319379	c.12383G>T	p.G4128V
ABCA13	ATP-binding cassette; sub-family A (ABC1); member 13	ENSG00000179869	PAP45	130	26.2%	chr7	48521244	ENST00000319379	c.13378G>A	p.V4460I
ABCA4	ATP-binding cassette; sub-family A (ABC1); member 4	ENSG00000198691	PAP45	97	23.7%	chr1	94257858	CCDS747.1	c.5064C>A	p.F1688L
ABCA6	ATP-binding cassette; sub-family A (ABC1); member 6	ENSG00000154262	PAP45	93	19.4%	chr17	64604400	CCDS11683.1	c.3258G>T	p.Q1086H
ABCA8	ATP-binding cassette; sub-family A (ABC1); member 8	ENSG00000141338	PAP45	46	23.9%	chr17	64429208	CCDS11680.1	c.1522G>A	p.E508K
ABCA9	ATP-binding cassette; sub-family A (ABC1); member 9	ENSG00000154258	PAP45	115	24.3%	chr17	64503699	CCDS11681.1	c.3487G>T	p.G1163W
ABCB1	ATP-binding cassette; sub-family B (MDR/TAP); member 1	ENSG00000085563	PAP45	111	26.1%	chr7	87013207	CCDS5608.1	c.1795G>A	p.A599T
ABCB1	ATP-binding cassette; sub-family B (MDR/TAP); member 1	ENSG00000085563	PAP45	61	21.3%	chr7	87017733	CCDS5608.1	c.1211G>A	p.R404Q
ABCB4	ATP-binding cassette; sub-family B (MDR/TAP); member 4	ENSG00000005471	PAP45	283	24.7%	chr7	86917341	CCDS5606.1	c.712C>A	p.L238I
ABCB4	ATP-binding cassette; sub-family B (MDR/TAP); member 4	ENSG00000005471	PAP45	84	20.2%	chr7	86920301	CCDS5606.1	c.431G>A	p.R144Q
ABCB5	ATP-binding cassette; sub-family B (MDR/TAP); member 5	ENSG00000004846	PAP45	157	24.8%	chr7	20649436	NM_001163941	c.419G>A	p.R140Q
ABCB7	ATP-binding cassette; sub-family B (MDR/TAP); member 7	ENSG00000131269	PAP45	221	23.5%	chrX	74196884	CCDS14428.1	c.1945C>A	p.L649I
ABCB7	ATP-binding cassette; sub-family B (MDR/TAP); member 7	ENSG00000131269	PAP45	175	18.3%	chrX	74205581	CCDS14428.1	c.1648G>A	p.G550R
ABCB9	ATP-binding cassette; sub-family B (MDR/TAP); member 9	ENSG00000150967	PAP45	63	23.8%	chr12	122000351	CCDS9241.1	c.784C>T	p.R262X
ABCC11	ATP-binding cassette; sub-family C (CFTR/MRP); member 11	ENSG00000121270	PAP45	233	19.7%	chr16	46778483	CCDS10732.1	c.2953G>A	p.G985S
ABCC2	ATP-binding cassette; sub-family C (CFTR/MRP); member 2	ENSG00000023839	PAP45	60	20.0%	chr10	101568956	CCDS7484.1	c.2560G>A	p.E854K
ABCC4	ATP-binding cassette; sub-family C (CFTR/MRP); member 4	ENSG00000125257	PAP45	115	22.6%	chr13	94684877	CCDS9474.1	c.519G>T	p.M173I

ABCC6	ATP-binding cassette; sub-family C (CFTR/MRP); member 6	ENSG00000091262	PAP45	64	28.1%	chr16	16160914	CCDS10568.1	c.3661C>T	p.R1221C
ABCC9	ATP-binding cassette; sub-family C (CFTR/MRP); member 9	ENSG00000069431	PAP45	57	21.1%	chr12	21932113	CCDS8693.1	c.1825C>A	p.L609I
ABCD3	ATP-binding cassette; sub-family D (ALD); member 3	ENSG00000117528	PAP45	30	33.3%	chr1	94736753	CCDS749.1	c.1394C>T	p.S465F
ABCG5	ATP-binding cassette; sub-family G (WHITE); member 5	ENSG00000138075	PAP45	341	25.8%	chr2	43904917	CCDS1814.1	c.1063C>A	p.P355T
ATRIP	ATR interacting protein	ENSG00000164053	PAP45	277	19.5%	chr3	48477174	CCDS2768.1	c.1717G>A	p.E573K
ATRNL1	attractin-like 1	ENSG00000107518	PAP45	236	20.8%	chr10	117694207	CCDS7592.1	c.4067C>T	p.S1356L
AMFR	autocrine motility factor receptor	ENSG00000159461	PAP45	275	25.8%	chr16	54954377	CCDS10758.1	c.1877G>A	p.R626Q
AMFR	autocrine motility factor receptor	ENSG00000159461	PAP45	93	10.8%	chr16	54980708	CCDS10758.1	c.1166G>A	p.R389H
AMBRA1	autophagy/beclin-1 regulator 1	ENSG00000110497	PAP45	185	29.7%	chr11	46520918	CCDS31475.1	c.955G>T	p.E319X
AXL	AXL receptor tyrosine kinase	ENSG00000167601	PAP45	433	24.5%	chr19	46418913	CCDS12575.1	c.331G>A	p.D111N
AXL	AXL receptor tyrosine kinase	ENSG00000167601	PAP45	97	17.5%	chr19	46457312	CCDS12575.1	c.2348C>T	p.S783L
BDP1	B double prime 1; subunit of RNA polymerase III transcription initiation factor IIIB	ENSG00000145734	PAP45	144	15.3%	chr5	70787653	CCDS43328.1	c.193G>T	p.E65X
BLK	B lymphoid tyrosine kinase	ENSG00000136573	PAP45	75	25.3%	chr8	11452949	CCDS5982.1	c.1022C>T	p.S341L
BAIAP2L2	BAI1-associated protein 2-like 2	ENSG00000128298	PAP45	70	22.9%	chr22	36833866	CCDS43018.1	c.215G>A	p.G72E
BBS10	Bardet-Biedl syndrome 10	ENSG00000179941	PAP45	69	23.2%	chr12	75265525	CCDS9014.2	c.371C>A	p.S124Y
BBS7	Bardet-Biedl syndrome 7	ENSG00000138686	PAP45	90	23.3%	chr4	122980283	CCDS3724.1	c.1324C>A	p.L442I
BBS9	Bardet-Biedl syndrome 9	ENSG00000122507	PAP45	47	27.7%	chr7	33152492	CCDS43566.1	c.103A>C	p.N35H
BBS9	Bardet-Biedl syndrome 9	ENSG00000122507	PAP45	55	23.6%	chr7	33270434	CCDS43566.1	c.625G>T	p.V209L
BCAM	basal cell adhesion molecule (Lutheran blood group)	ENSG00000187244	PAP45	69	30.4%	chr19	50009806	CCDS12644.1	c.1027G>A	p.D343N
BHLHB9	basic helix-loop-helix domain containing; class B; 9	ENSG00000198908	PAP45	106	27.4%	chrX	101891731	CCDS14502.1	c.1152G>T	p.K384N
BNC2	basonuclin 2	ENSG00000173068	PAP45	437	26.5%	chr9	16426255	CCDS6482.2	c.1937T>G	p.I646S
BCL6	B-cell CLL/lymphoma 6	ENSG00000113916	PAP45	170	26.5%	chr3	188927294	CCDS3289.1	c.1627G>T	p.D543Y
BCAP29	B-cell receptor-associated protein 29	ENSG00000075790	PAP45	94	25.5%	chr7	107041019	CCDS34730.1	c.596C>A	p.S199Y
BANK1	B-cell scaffold protein with ankyrin repeats 1	ENSG00000153064	PAP45	86	23.3%	chr4	103170347	CCDS34038.1	c.1802C>A	p.T601N
BAG4	BCL2-associated athanogene 4	ENSG00000156735	PAP45	493	15.0%	chr8	38185764	CCDS6104.1	c.710G>A	p.R237Q
BCLAF1	BCL2-associated transcription factor 1	ENSG00000029363	PAP45	336	12.5%	chr6	136640796	CCDS5177.1	c.916G>A	p.A306T
BAX	BCL2-associated X protein	ENSG00000087088	PAP45	120	22.5%	chr19	54151299	CCDS12744.1	c.266G>A	p.R89Q
BCL2L1	BCL2-like 1	ENSG00000171552	PAP45	694	24.9%	chr20	29773251	CCDS13189.1	c.432C>A	p.F144L
BCL2L15	BCL2-like 15	ENSG00000188761	PAP45	281	23.8%	chr1	114226055	CCDS30809.1	c.337C>A	p.L113M
BFSP1	beaded filament structural protein 1; filensin	ENSG00000125864	PAP45	375	10.9%	chr20	17422827	CCDS13126.1	c.1890G>T	p.K630N
BFSP1	beaded filament structural protein 1; filensin	ENSG00000125864	PAP45	465	13.8%	chr20	17423018	CCDS13126.1	c.1699G>A	p.E567K
BEND7	BEN domain containing 7	ENSG00000165626	PAP45	131	19.8%	chr10	13581852	CCDS7099.1	c.224T>G	p.F75C
BEND7	BEN domain containing 7	ENSG00000165626	PAP45	144	11.1%	chr10	13582088	ENST00000396900	c.-1A>C	p.IVS2-2-1SpliceAcceptor
BCMO1	beta-carotene 15;15'-monooxygenase 1	ENSG00000135697	PAP45	532	27.4%	chr16	79853323	CCDS10934.1	c.405C>A	p.F135L
CRYBG3	beta-gamma crystallin domain containing 3	ENSG00000080200	PAP45	137	20.4%	chr3	99088223	CCDS43113.1	c.1367T>C	p.V456A
BHMT2	betaine--homocysteine S-methyltransferase 2	ENSG00000132840	PAP45	53	18.9%	chr5	78409071	CCDS4045.1	c.46C>T	p.R16C
BHMT2	betaine--homocysteine S-methyltransferase 2	ENSG00000132840	PAP45	53	20.8%	chr5	78414494	CCDS4045.1	c.557A>G	p.D186G
BHMT2	betaine--homocysteine S-methyltransferase 2	ENSG00000132840	PAP45	136	17.6%	chr5	78420093	CCDS4045.1	c.1032G>T	p.E344D
BACE2	beta-site APP-cleaving enzyme 2	ENSG00000182240	PAP45	58	20.7%	chr21	41531423	CCDS13668.1	c.515C>A	p.S172Y
BICC1	bicaudal C homolog 1 (Drosophila)	ENSG00000122870	PAP45	103	31.1%	chr10	60216696	CCDS31206.1	c.395G>A	p.R132Q
BSPH1	binder of sperm protein homolog 1	ENSG00000188334	PAP45	292	25.3%	chr19	53171820	NM_001128326	c.360G>T	p.K120N
BSPH1	binder of sperm protein homolog 1	ENSG00000188334	PAP45	75	21.3%	chr19	53187113	NM_001128326	c.38G>A	p.R13Q
BTD	biotinidase	ENSG00000169814	PAP45	167	23.4%	chr3	15661443	CCDS2628.1	c.1076G>T	p.S359I
BMX	BMX non-receptor tyrosine kinase	ENSG00000102010	PAP45	102	24.5%	chrX	15465226	CCDS14168.1	c.1271G>A	p.G424E
BRS3	bombesin-like receptor 3	ENSG00000102239	PAP45	319	24.8%	chrX	135398225	CCDS14656.1	c.286C>A	p.L96I
BMP15	bone morphogenetic protein 15	ENSG00000130385	PAP45	163	11.0%	chrX	50675962	CCDS14334.1	c.794G>T	p.R265I
BMP4	bone morphogenetic protein 4	ENSG00000125378	PAP45	216	10.2%	chr14	53486815	CCDS9715.1	c.912G>T	p.K304N
BMPR2	bone morphogenetic protein receptor; type II (serine/threonine kinase)	ENSG00000204217	PAP45	102	16.7%	chr2	203037827	CCDS33361.1	c.127G>T	p.D43Y
BAALC	brain and acute leukemia; cytoplasmic	ENSG00000164929	PAP45	79	22.8%	chr8	104309412	CCDS6297.1	c.347G>T	p.R116I
BAI3	brain-specific angiogenesis inhibitor 3	ENSG00000135298	PAP45	72	26.4%	chr6	69780681	CCDS4968.1	c.1960G>T	p.D654Y

BAI3	brain-specific angiogenesis inhibitor 3	ENSG00000135298	PAP45	168	18.5%	chr6	70120913	CCDS4968.1	c.3527C>T	p.S1176L
BRIP1	BRCA1 interacting protein C-terminal helicase 1	ENSG00000136492	PAP45	138	26.1%	chr17	57116115	CCDS11631.1	c.3074C>A	p.S1025X
BRCA2	breast cancer 2; early onset	ENSG00000139618	PAP45	147	10.2%	chr13	31805300	CCDS9344.1	c.1685G>A	p.S562N
BRCA2	breast cancer 2; early onset	ENSG00000139618	PAP45	107	20.6%	chr13	31810207	CCDS9344.1	c.3715A>C	p.K1239Q
BRCA2	breast cancer 2; early onset	ENSG00000139618	PAP45	124	21.8%	chr13	31835348	CCDS9344.1	c.8009C>T	p.S2670L
BCAR3	breast cancer anti-estrogen resistance 3	ENSG00000137936	PAP45	362	26.0%	chr1	93820694	CCDS745.1	c.1438G>T	p.D480Y
BCAR3	breast cancer anti-estrogen resistance 3	ENSG00000137936	PAP45	168	23.2%	chr1	93852048	ENST00000370247	c.28G>A	p.A10T
BCAN	brevican	ENSG00000132692	PAP45	80	30.0%	chr1	154894551	CCDS1149.1	c.2301G>T	p.E767D
BAZ1A	bromodomain adjacent to zinc finger domain; 1A	ENSG00000198604	PAP45	131	13.7%	chr14	34313328	CCDS9651.1	c.2953G>T	p.D985Y
BAZ1B	bromodomain adjacent to zinc finger domain; 1B	ENSG00000009954	PAP45	100	32.0%	chr7	72496339	CCDS5549.1	c.3901T>C	p.S1301P
BAZ2B	bromodomain adjacent to zinc finger domain; 2B	ENSG00000123636	PAP45	181	20.4%	chr2	160003190	CCDS2209.2	c.1163C>A	p.S388Y
BRWD1	bromodomain and WD repeat domain containing 1	ENSG00000185658	PAP45	360	25.0%	chr21	39568227	CCDS13662.1	c.1187G>T	p.R396I
BRD8	bromodomain containing 8	ENSG00000112983	PAP45	105	21.0%	chr5	137534692	CCDS4198.1	c.293G>A	p.R98Q
BPTF	bromodomain PHD finger transcription factor	ENSG00000171634	PAP45	263	18.6%	chr17	63281009	CCDS11673.1	c.1105G>A	p.D369N
BRDT	bromodomain; testis-specific	ENSG00000137948	PAP45	101	21.8%	chr1	92206394	CCDS735.1	c.434G>T	p.R145I
BTBD11	BTB (POZ) domain containing 11	ENSG00000151136	PAP45	76	19.7%	chr12	106438498	CCDS31893.1	c.1240G>A	p.E414K
BTBD17	BTB (POZ) domain containing 17	ENSG00000204347	PAP45	303	10.6%	chr17	69867741	CCDS32719.1	c.324G>T	p.E108D
BTBD9	BTB (POZ) domain containing 9	ENSG00000183826	PAP45	55	29.1%	chr6	38668543	CCDS43458.1	c.397G>T	p.D133Y
BACH1	BTB and CNC homology 1; basic leucine zipper transcription factor 1	ENSG00000156273	PAP45	219	26.5%	chr21	29620548	CCDS13585.1	c.532A>C	p.N178H
BACH2	BTB and CNC homology 1; basic leucine zipper transcription factor 2	ENSG00000112182	PAP45	127	13.4%	chr6	90716756	CCDS5026.1	c.1790C>T	p.S597L
BANP	BTG3 associated nuclear protein	ENSG00000172530	PAP45	218	19.7%	chr16	86595460	ENST00000393207	c.397A>G	p.K133E
BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	ENSG00000156970	PAP45	101	31.7%	chr15	38264727	CCDS10053.1	c.821T>C	p.V274A
BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	ENSG00000156970	PAP45	209	23.4%	chr15	38297031	CCDS10053.1	c.2721G>T	p.L907F
BTNL8	butyrophilin-like 8	ENSG00000113303	PAP45	237	12.2%	chr5	180268319	CCDS43413.1	c.177G>T	p.Q59H
BCHE	butyrylcholinesterase	ENSG00000114200	PAP45	115	23.5%	chr3	167030800	CCDS3198.1	c.716C>T	p.P239L
C2CD2	C2 calcium-dependent domain containing 2	ENSG00000157617	PAP45	470	23.4%	chr21	42194906	CCDS42933.1	c.1454C>T	p.S485L
C2CD2L	C2CD2-like	ENSG00000172375	PAP45	145	20.7%	chr11	118486813	CCDS8413.1	c.617C>A	p.S206Y
CPAMD8	C3 and PZP-like; alpha-2-macroglobulin domain containing 8	ENSG00000160111	PAP45	290	24.8%	chr19	16917422	CCDS42519.1	c.2871G>T	p.E957D
CADPS	Ca++-dependent secretion activator	ENSG00000163618	PAP45	164	11.6%	chr3	62426117	CCDS2899.1	c.3484G>A	p.E1162K
CADPS	Ca++-dependent secretion activator	ENSG00000163618	PAP45	302	10.6%	chr3	62478929	CCDS2899.1	c.2328G>T	p.K776N
CDH10	cadherin 10; type 2 (T2-cadherin)	ENSG00000040731	PAP45	139	21.6%	chr5	24523759	CCDS3892.1	c.2137T>G	p.F713V
CDH10	cadherin 10; type 2 (T2-cadherin)	ENSG00000040731	PAP45	47	38.3%	chr5	24523954	CCDS3892.1	c.1942G>T	p.E648X
CDH11	cadherin 11; type 2; OB-cadherin (osteoblast)	ENSG00000140937	PAP45	144	31.3%	chr16	63573525	CCDS10803.1	c.1180G>T	p.E394X
CDH17	cadherin 17; LI cadherin (liver-intestine)	ENSG00000079112	PAP45	275	20.4%	chr8	95212348	CCDS6260.1	c.2216A>T	p.E739V
CELSR3	cadherin; EGF LAG seven-pass G-type receptor 3 (flamingo homolog; Drosophila)	ENSG00000008300	PAP45	102	22.5%	chr3	48657219	CCDS2775.1	c.8019C>A	p.F2673L
CDHR1	cadherin-related family member 1	ENSG00000148600	PAP45	187	26.2%	chr10	85947556	CCDS7372.1	c.332C>A	p.S111Y
CABIN1	calcineurin binding protein 1	ENSG00000099991	PAP45	78	26.9%	chr22	22813446	CCDS13823.1	c.3305G>A	p.R1102H
CALCOCO2	calcium binding and coiled-coil domain 2	ENSG00000136436	PAP45	103	10.7%	chr17	44284891	CCDS11538.1	c.727G>T	p.E243X
CACNA2D1	calcium channel; voltage-dependent; alpha 2/delta subunit 1	ENSG00000153956	PAP45	58	27.6%	chr7	81449876	CCDS5598.1	c.1898C>T	p.S633L
CACNA2D4	calcium channel; voltage-dependent; alpha 2/delta subunit 4	ENSG00000151062	PAP45	364	23.1%	chr12	1779851	NM_172364	c.2883C>A	p.F961L
CACNB2	calcium channel; voltage-dependent; beta 2 subunit	ENSG00000165995	PAP45	67	16.4%	chr10	18827303	CCDS7125.1	c.347C>A	p.A116E
CACNG7	calcium channel; voltage-dependent; gamma subunit 7	ENSG00000105605	PAP45	156	21.8%	chr19	59136586	CCDS12868.1	c.475G>A	p.E159K
CACNA1D	calcium channel; voltage-dependent; L type; alpha 1D subunit	ENSG00000157388	PAP45	392	18.6%	chr3	53771095	CCDS2872.1	c.3877G>T	p.D1293Y
CACNA1F	calcium channel; voltage-dependent; L type; alpha 1F subunit	ENSG00000102001	PAP45	357	28.3%	chrX	48958488	CCDS35253.1	c.-1T>C	p.IVS29+2-1SpliceDonor
CACNA1F	calcium channel; voltage-dependent; L type; alpha 1F subunit	ENSG00000102001	PAP45	167	24.0%	chrX	48958752	CCDS35253.1	c.3465G>T	p.K1155N
CACNA1I	calcium channel; voltage-dependent; T type; alpha 1I subunit	ENSG00000100346	PAP45	263	25.1%	chr22	38366917	NM_021096	c.840C>A	p.C280X

CACNA1I	calcium channel; voltage-dependent; T type; alpha 1I subunit	ENSG00000100346	PAP45	186	21.0%	chr22	38385451	NM_021096	c.2398G>A	p.D800N
CAMK2D	calcium/calmodulin-dependent protein kinase II delta	ENSG00000145349	PAP45	87	18.4%	chr4	114658222	CCDS3703.1	c.642C>A	p.F214L
CAMK4	calcium/calmodulin-dependent protein kinase IV	ENSG00000152495	PAP45	87	27.6%	chr5	110738483	CCDS4103.1	c.277C>A	p.L93I
CAMKK1	calcium/calmodulin-dependent protein kinase kinase 1; alpha	ENSG00000004660	PAP45	165	17.6%	chr17	3719615	CCDS11039.1	c.1370C>T	p.S457L
CALY	calcyon neuron-specific vesicular protein	ENSG00000130643	PAP45	30	36.7%	chr10	134992411	CCDS7678.1	c.73G>T	p.D25Y
CAPS2	calcyphosine 2	ENSG00000180881	PAP45	144	11.1%	chr12	73992962	NM_032606	c.649G>T	p.E217X
CAPS2	calcyphosine 2	ENSG00000180881	PAP45	80	28.8%	chr12	74006481	NM_032606	c.122G>T	p.R41I
CALM2	calmodulin 2 (phosphorylase kinase; delta)	ENSG00000143933	PAP45	207	24.2%	chr2	47243297	CCDS1832.1	c.43G>T	p.E15X
CAMTA1	calmodulin binding transcription activator 1	ENSG00000171735	PAP45	68	25.0%	chr1	7644504	CCDS30576.1	c.796G>A	p.G266S
CAMTA1	calmodulin binding transcription activator 1	ENSG00000171735	PAP45	168	10.7%	chr1	7720062	CCDS30576.1	c.3503G>T	p.R1168I
CAMTA1	calmodulin binding transcription activator 1	ENSG00000171735	PAP45	75	25.3%	chr1	7733916	CCDS30576.1	c.4760NULL>A	p.NULL-1FsIns1bp
CAMTA2	calmodulin binding transcription activator 2	ENSG00000108509	PAP45	470	17.2%	chr17	4814542	CCDS11063.1	c.2822C>A	p.S941X
CAMTA2	calmodulin binding transcription activator 2	ENSG00000108509	PAP45	152	26.3%	chr17	4825328	CCDS11063.1	c.616G>T	p.E206X
CAMTA2	calmodulin binding transcription activator 2	ENSG00000108509	PAP45	123	30.9%	chr17	4830003	CCDS11063.1	c.-1G>T	p.IVS1-1-1SpliceAcceptor
CAPN9	calpain 9	ENSG00000135773	PAP45	215	26.5%	chr1	228974402	CCDS1586.1	c.809G>T	p.R270I
CLSTN3	calsyntenin 3	ENSG00000139182	PAP45	144	16.0%	chr12	7180086	CCDS8575.1	c.760G>A	p.E254K
CASC3	cancer susceptibility candidate 3	ENSG00000108349	PAP45	148	29.1%	chr17	35571608	CCDS11362.1	c.374C>A	p.S125Y
CASC5	cancer susceptibility candidate 5	ENSG00000137812	PAP45	86	27.9%	chr15	38701562	CCDS42023.1	c.1886C>A	p.S629Y
CASC5	cancer susceptibility candidate 5	ENSG00000137812	PAP45	110	25.5%	chr15	38703294	CCDS42023.1	c.3618G>T	p.E1206D
CASC5	cancer susceptibility candidate 5	ENSG00000137812	PAP45	112	23.2%	chr15	38703427	CCDS42023.1	c.3751C>A	p.L1251I
CNR1	cannabinoid receptor 1 (brain)	ENSG00000118432	PAP45	286	27.6%	chr6	88910499	CCDS5015.1	c.1214G>A	p.R405Q
CLIP1	CAP-GLY domain containing linker protein 1	ENSG00000130779	PAP45	228	11.8%	chr12	121391999	CCDS9232.1	c.1672G>T	p.E558X
CLIP4	CAP-GLY domain containing linker protein family; member 4	ENSG00000115295	PAP45	111	17.1%	chr2	29221682	CCDS1770.1	c.966NULL>A	p.NULL-1FsIns1bp
CAPZA1	capping protein (actin filament) muscle Z-line; alpha 1	ENSG00000116489	PAP45	128	25.0%	chr1	112993593	CCDS30805.1	c.134T>G	p.L45R
CPS1	carbamoyl-phosphate synthase 1; mitochondrial	ENSG00000021826	PAP45	163	11.7%	chr2	211250058	CCDS2393.1	c.4357C>T	p.R1453W
CAD	carbamoyl-phosphate synthetase 2; aspartate transcarbamylase; and dihydroorotase	ENSG00000084774	PAP45	111	21.6%	chr2	27309484	CCDS1742.1	c.2963G>A	p.R988Q
CHST11	carbohydrate (chondroitin 4) sulfotransferase 11	ENSG00000171310	PAP45	228	30.7%	chr12	103675635	CCDS9099.1	c.983C>T	p.T328M
CPA3	carboxypeptidase A3 (mast cell)	ENSG00000163751	PAP45	80	26.3%	chr3	150084128	CCDS3138.1	c.817C>T	p.R273W
CPA6	carboxypeptidase A6	ENSG00000165078	PAP45	147	25.2%	chr8	68497305	CCDS6200.1	c.1302G>T	p.K434N
CPXM2	carboxypeptidase X (M14 family); member 2	ENSG00000121898	PAP45	167	24.0%	chr10	125506850	CCDS7637.1	c.1786G>A	p.D596N
CPZ	carboxypeptidase Z	ENSG00000109625	PAP45	73	17.8%	chr4	8659425	CCDS33953.1	c.968G>A	p.R323Q
CILP2	cartilage intermediate layer protein 2	ENSG00000160161	PAP45	53	32.1%	chr19	19515169	CCDS12405.1	c.1090G>T	p.E364X
CILP	cartilage intermediate layer protein; nucleotide pyrophosphohydrolase	ENSG00000138615	PAP45	559	16.8%	chr15	63276886	CCDS10203.1	c.2791G>A	p.E931K
CASS4	Cas scaffolding protein family member 4	ENSG00000087589	PAP45	333	19.2%	chr20	54460894	CCDS33492.1	c.1255G>A	p.D419N
CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	ENSG00000110395	PAP45	212	28.3%	chr11	118653697	CCDS8418.1	c.1028G>A	p.R343Q
CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	ENSG00000110395	PAP45	73	21.9%	chr11	118674389	CCDS8418.1	c.2363G>A	p.R788Q
CSNK1A1	casein kinase 1; alpha 1	ENSG00000113712	PAP45	131	22.1%	chr5	148884866	NM_001025105	c.292G>A	p.E98K
CSNK1G3	casein kinase 1; gamma 3	ENSG00000151292	PAP45	156	24.4%	chr5	122968398	CCDS43355.1	c.1264G>T	p.E422X
CSNK2A2	casein kinase 2; alpha prime polypeptide	ENSG00000070770	PAP45	112	17.9%	chr16	56788208	CCDS10794.1	c.146G>A	p.G49E
CASP5	caspase 5; apoptosis-related cysteine peptidase	ENSG00000137757	PAP45	159	23.9%	chr11	104383090	CCDS8328.1	c.315G>T	p.K105N
CASP8	caspase 8; apoptosis-related cysteine peptidase	ENSG00000064012	PAP45	56	23.2%	chr2	201839657	CCDS42798.1	c.380G>A	p.R127Q
CARD11	caspase recruitment domain family; member 11	ENSG00000198286	PAP45	80	31.3%	chr7	2916326	CCDS5336.2	c.-1G>T	p.IVS22-1-1SpliceAcceptor
CARD11	caspase recruitment domain family; member 11	ENSG00000198286	PAP45	77	33.8%	chr7	2952000	CCDS5336.2	c.337C>T	p.R113W
CARD6	caspase recruitment domain family; member 6	ENSG00000132357	PAP45	192	23.4%	chr5	40879471	CCDS3935.1	c.744G>T	p.E248D

CARD6	caspase recruitment domain family; member 6	ENSG00000132357	PAP45	128	22.7%	chr5	40879555	CCDS3935.1	c.828G>T	p.E276D
CECR2	cat eye syndrome chromosome region; candidate 2	ENSG00000099954	PAP45	580	26.2%	chr22	16402414	ENST00000400585	c.2516C>A	p.S839Y
CECR2	cat eye syndrome chromosome region; candidate 2	ENSG00000099954	PAP45	245	23.7%	chr22	16409209	ENST00000400585	c.4166G>A	p.R1389K
CTNNA3	catenin (cadherin-associated protein); alpha 3	ENSG00000183230	PAP45	118	22.0%	chr10	67350198	CCDS7269.1	c.2584G>T	p.E862X
CTNNA3	catenin (cadherin-associated protein); alpha 3	ENSG00000183230	PAP45	102	20.6%	chr10	68196072	CCDS7269.1	c.1237G>T	p.E413X
CTSE	cathepsin E	ENSG00000196188	PAP45	167	22.2%	chr1	204494157	CCDS1462.1	c.723C>A	p.F241L
CTSG	cathepsin G	ENSG00000100448	PAP45	237	26.6%	chr14	24113521	CCDS9631.1	c.364C>T	p.R122X
CTSS	cathepsin S	ENSG00000163131	PAP45	223	25.6%	chr1	148994192	CCDS968.1	c.308G>T	p.R103I
CATSPER3	cation channel; sperm associated 3	ENSG00000152705	PAP45	373	26.3%	chr5	134359870	CCDS4181.1	c.261G>T	p.E87D
CATSPERG	cation channel; sperm-associated; gamma	ENSG00000099338	PAP45	233	23.6%	chr19	43534811	NM_021185	c.896A>G	p.D299G
CITED1	Cbp/p300-interacting transactivator; with Glu/Asp-rich carboxy-terminal domain; 1	ENSG00000125931	PAP45	74	25.7%	chrX	71438768	CCDS14419.1	c.112G>T	p.D38Y
CEBPG	CCAAT/enhancer binding protein (C/EBP); gamma	ENSG00000153879	PAP45	348	14.7%	chr19	38562438	CCDS12432.1	c.453G>T	p.X151Y
CTCF	CCCTC-binding factor (zinc finger protein)	ENSG00000102974	PAP45	106	20.8%	chr16	66202255	CCDS10841.1	c.19G>A	p.E7K
CTCF	CCCTC-binding factor (zinc finger protein)	ENSG00000102974	PAP45	61	31.1%	chr16	66228147	CCDS10841.1	c.1891G>T	p.E631X
CNOT1	CCR4-NOT transcription complex; subunit 1	ENSG00000125107	PAP45	27	37.0%	chr16	57142659	CCDS10799.1	c.3220A>C	p.N1074H
CNOT10	CCR4-NOT transcription complex; subunit 10	ENSG00000182973	PAP45	48	20.8%	chr3	32749931	CCDS2655.1	c.1228G>A	p.E410K
CNOT2	CCR4-NOT transcription complex; subunit 2	ENSG00000111596	PAP45	42	33.3%	chr12	69018521	CCDS31857.1	c.932G>A	p.S311N
CNOT6	CCR4-NOT transcription complex; subunit 6	ENSG00000113300	PAP45	87	21.8%	chr5	179928862	CCDS4455.1	c.1174C>T	p.R392C
CD109	CD109 molecule	ENSG00000156535	PAP45	201	25.4%	chr6	74496850	CCDS4982.1	c.339G>T	p.E113D
CD160	CD160 molecule	ENSG00000117281	PAP45	180	29.4%	chr1	144415383	CCDS923.1	c.391C>A	p.L131I
CD163L1	CD163 molecule-like 1	ENSG00000177675	PAP45	167	22.8%	chr12	7442360	CCDS8577.1	c.1496C>A	p.T499N
CD1B	CD1b molecule	ENSG00000158485	PAP45	83	16.9%	chr1	156565832	CCDS1176.1	c.838C>T	p.R280W
CD1C	CD1c molecule	ENSG00000158481	PAP45	50	20.0%	chr1	156528692	CCDS1175.1	c.523G>T	p.E175X
CD200R1	CD200 receptor 1	ENSG00000163606	PAP45	102	11.8%	chr3	114130379	CCDS2969.1	c.743A>G	p.K248R
CD2AP	CD2-associated protein	ENSG00000198087	PAP45	77	19.5%	chr6	47688188	CCDS34472.1	c.1835G>A	p.R612Q
CD300LD	CD300 molecule-like family member d	ENSG00000204345	PAP45	483	23.2%	chr17	70096316	CCDS42379.1	c.308A>G	p.D103G
CD3D	CD3d molecule; delta (CD3-TCR complex)	ENSG00000167286	PAP45	197	22.8%	chr11	117715414	CCDS8394.1	c.412G>A	p.D138N
CD58	CD58 molecule	ENSG00000116815	PAP45	99	17.2%	chr1	116888589	CCDS888.1	c.524NULL>T	p.NULL-1FsIns1bp
CD63	CD63 molecule	ENSG00000135404	PAP45	309	25.6%	chr12	54406257	CCDS8890.1	c.482C>T	p.S161L
CD69	CD69 molecule	ENSG00000110848	PAP45	135	25.9%	chr12	9799097	CCDS8604.1	c.215A>G	p.Y72C
CD72	CD72 molecule	ENSG00000137101	PAP45	98	22.4%	chr9	35600718	CCDS6581.1	c.983T>C	p.V328A
CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	ENSG00000079335	PAP45	100	23.0%	chr1	100722585	CCDS770.1	c.1127G>A	p.R376Q
CDC5L	CDC5 cell division cycle 5-like (S. pombe)	ENSG00000096401	PAP45	118	28.0%	chr6	44479552	CCDS4912.1	c.568G>T	p.E190X
CDKN2AIP	CDKN2A interacting protein	ENSG00000168564	PAP45	211	30.3%	chr4	184605103	CCDS34110.1	c.1272C>A	p.F424L
CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	ENSG00000101290	PAP45	217	22.1%	chr20	5113538	CCDS13088.1	c.706G>T	p.D236Y
CADM2	cell adhesion molecule 2	ENSG00000175161	PAP45	100	21.0%	chr3	86067634	CCDS33792.1	c.707C>T	p.S236L
CHL1	cell adhesion molecule with homology to L1CAM (close homolog of L1)	ENSG00000134121	PAP45	35	40.0%	chr3	336524	CCDS2556.1	c.65C>A	p.S22X
CHL1	cell adhesion molecule with homology to L1CAM (close homolog of L1)	ENSG00000134121	PAP45	68	17.6%	chr3	366090	CCDS2556.1	c.897G>T	p.K299N
CHL1	cell adhesion molecule with homology to L1CAM (close homolog of L1)	ENSG00000134121	PAP45	83	32.5%	chr3	366106	CCDS2556.1	c.913G>T	p.E305X
CHL1	cell adhesion molecule with homology to L1CAM (close homolog of L1)	ENSG00000134121	PAP45	90	24.4%	chr3	379985	CCDS2556.1	c.1504G>A	p.E502K
CHL1	cell adhesion molecule with homology to L1CAM (close homolog of L1)	ENSG00000134121	PAP45	132	22.0%	chr3	406022	CCDS2556.1	c.2335G>T	p.E779X
CHL1	cell adhesion molecule with homology to L1CAM (close homolog of L1)	ENSG00000134121	PAP45	76	27.6%	chr3	411530	CCDS2556.1	c.3069G>T	p.E1023D
CCPG1	cell cycle progression 1	ENSG00000214882	PAP45	115	14.8%	chr15	53439237	CCDS42039.1	c.2026G>A	p.E676K
CCPG1	cell cycle progression 1	ENSG00000214882	PAP45	221	11.8%	chr15	53439401	CCDS42039.1	c.3307NULL>/	p.NULL-1FsIns1bp

CDC25B	cell division cycle 25 homolog B (S. pombe)	ENSG00000101224	PAP45	98	30.6%	chr20	3725285	CCDS13067.1	c.107C>A	p.S36Y
CDC6	cell division cycle 6 homolog (S. cerevisiae)	ENSG00000094804	PAP45	215	25.1%	chr17	35711739	CCDS11365.1	c.1643A>C	p.K548T
CCAR1	cell division cycle and apoptosis regulator 1	ENSG00000060339	PAP45	87	28.7%	chr10	70195694	CCDS7282.1	c.2150G>A	p.R717Q
CDCA2	cell division cycle associated 2	ENSG00000184661	PAP45	105	18.1%	chr8	25396844	CCDS6049.1	c.1045A>G	p.N349D
CDCA7	cell division cycle associated 7	ENSG00000144354	PAP45	75	22.7%	chr2	173936274	CCDS2252.1	c.459G>T	p.M153I
CWH43	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)	ENSG00000109182	PAP45	61	24.6%	chr4	48725417	CCDS3486.1	c.1281G>T	p.E427D
CNTLN	centlein; centrosomal protein	ENSG00000044459	PAP45	188	19.7%	chr9	17133340	CCDS43789.1	c.415G>A	p.D139N
CENPB	centromere protein B; 80kDa	ENSG00000125817	PAP45	324	25.6%	chr20	3713978	CCDS13064.1	c.1153C>T	p.R385C
CENPE	centromere protein E; 312kDa	ENSG00000138778	PAP45	186	26.3%	chr4	104299641	CCDS34042.1	c.2576C>T	p.S859L
CENPF	centromere protein F; 350/400ka (mitosin)	ENSG00000117724	PAP45	103	20.4%	chr1	212886404	CCDS31023.1	c.6868G>A	p.D2290N
CENPF	centromere protein F; 350/400ka (mitosin)	ENSG00000117724	PAP45	99	20.2%	chr1	212897371	CCDS31023.1	c.8958G>T	p.K2986N
CENPP	centromere protein P	ENSG00000188312	PAP45	76	22.4%	chr9	94134413	CCDS35063.1	c.248A>C	p.K83T
CENPW	centromere protein W	ENSG00000203760	PAP45	224	26.8%	chr6	126703220	CCDS34529.1	c.108G>T	p.E36D
CEP110	centrosomal protein 110kDa	ENSG00000119397	PAP45	66	27.3%	chr9	122898622	CCDS35118.1	c.581C>A	p.S194Y
CEP135	centrosomal protein 135kDa	ENSG00000174799	PAP45	194	26.3%	chr4	56518176	CCDS33986.1	c.503G>A	p.R168H
CEP152	centrosomal protein 152kDa	ENSG00000103995	PAP45	217	12.0%	chr15	46818660	CCDS42033.1	c.4043G>A	p.R1348K
CEP152	centrosomal protein 152kDa	ENSG00000103995	PAP45	192	19.3%	chr15	46835777	CCDS42033.1	c.2960G>A	p.R987Q
CEP164	centrosomal protein 164kDa	ENSG00000110274	PAP45	67	17.9%	chr11	116766949	CCDS31683.1	c.2091G>T	p.Q697H
CEP192	centrosomal protein 192kDa	ENSG00000101639	PAP45	91	31.9%	chr18	13039383	CCDS32792.1	c.805A>C	p.N269H
CEP192	centrosomal protein 192kDa	ENSG00000101639	PAP45	159	10.7%	chr18	13082456	CCDS32792.1	c.4396G>T	p.E1466X
CEP350	centrosomal protein 350kDa	ENSG00000135837	PAP45	100	16.0%	chr1	178232371	NM_014810	c.456C>A	p.Y152X
CEP55	centrosomal protein 55kDa	ENSG00000138180	PAP45	51	23.5%	chr10	95266693	CCDS7428.1	c.691G>T	p.E231X
CEP63	centrosomal protein 63kDa	ENSG00000182923	PAP45	103	15.5%	chr3	135751692	CCDS3086.1	c.1280G>A	p.R427Q
CEP63	centrosomal protein 63kDa	ENSG00000182923	PAP45	79	25.3%	chr3	135759680	CCDS3086.1	c.1474G>T	p.E492X
CEP70	centrosomal protein 70kDa	ENSG00000114107	PAP45	111	22.5%	chr3	139699614	CCDS3102.1	c.1681G>T	p.E561X
CEP76	centrosomal protein 76kDa	ENSG00000101624	PAP45	91	18.7%	chr18	12676400	CCDS11861.1	c.983G>A	p.R328Q
CEP97	centrosomal protein 97kDa	ENSG00000182504	PAP45	164	25.6%	chr3	102967008	CCDS2944.1	c.2521T>G	p.L841V
CSPP1	centrosome and spindle pole associated protein 1	ENSG00000104218	PAP45	278	24.5%	chr8	68190702	CCDS43744.1	c.-1G>A	p.IVS10-1-1SpliceAcceptor
CER1	cerberus 1; cysteine knot superfamily; homolog (Xenopus laevis)	ENSG00000147869	PAP45	355	19.4%	chr9	14712426	CCDS6476.1	c.245G>T	p.R82I
CER1	cerberus 1; cysteine knot superfamily; homolog (Xenopus laevis)	ENSG00000147869	PAP45	341	24.9%	chr9	14712585	CCDS6476.1	c.86C>T	p.S29F
CDR1	cerebellar degeneration-related protein 1; 34kDa	ENSG00000184258	PAP45	282	13.5%	chrX	139693448	CCDS14670.1	c.750G>A	p.W250X
CDR2L	cerebellar degeneration-related protein 2-like	ENSG00000109089	PAP45	52	38.5%	chr17	70511060	NM_014603	c.694C>T	p.R232C
CP	ceruloplasmin (ferroxidase)	ENSG00000047457	PAP45	85	17.6%	chr3	150409823	CCDS3141.1	c.646G>T	p.E216X
FIGF	c-fos induced growth factor (vascular endothelial growth factor D)	ENSG00000165197	PAP45	164	21.3%	chrX	15291289	CCDS14166.1	c.164G>A	p.R55Q
CGGBP1	CGG triplet repeat binding protein 1	ENSG00000163320	PAP45	84	19.0%	chr3	88187783	CCDS43111.1	c.34C>T	p.R12X
CCT3	chaperonin containing TCP1; subunit 3 (gamma)	ENSG00000163468	PAP45	111	24.3%	chr1	154555311	CCDS1140.2	c.731C>A	p.S244Y
CCT5	chaperonin containing TCP1; subunit 5 (epsilon)	ENSG00000150753	PAP45	54	18.5%	chr5	10307909	CCDS3877.1	c.290C>T	p.S97F
CCRL2	chemokine (C-C motif) receptor-like 2	ENSG00000121797	PAP45	121	27.3%	chr3	46424890	CCDS43079.1	c.316C>A	p.L106I
CXCL16	chemokine (C-X-C motif) ligand 16	ENSG00000161921	PAP45	136	22.1%	chr17	4585483	CCDS11052.1	c.428C>A	p.S143Y
CXCL2	chemokine (C-X-C motif) ligand 2	ENSG00000081041	PAP45	80	16.3%	chr4	75183198	CCDS34008.1	c.292G>A	p.E98K
CXCL5	chemokine (C-X-C motif) ligand 5	ENSG00000163735	PAP45	240	29.6%	chr4	75082664	CCDS34006.1	c.255G>T	p.K85N
CXCR1	chemokine (C-X-C motif) receptor 1	ENSG00000163464	PAP45	180	17.8%	chr2	218738104	CCDS2409.1	c.76G>T	p.D26Y
CXCR3	chemokine (C-X-C motif) receptor 3	ENSG00000186810	PAP45	258	24.8%	chrX	70754153	NM_001142797	c.35C>T	p.A12V
CLCN1	chloride channel 1; skeletal muscle	ENSG00000188037	PAP45	249	18.1%	chr7	142758893	CCDS5881.1	c.2680C>T	p.R894X
CLCN3	chloride channel 3	ENSG00000109572	PAP45	151	27.2%	chr4	170855306	CCDS34100.1	c.1409C>A	p.S470Y
CLCN5	chloride channel 5	ENSG00000171365	PAP45	180	22.2%	chrX	49741893	CCDS14328.1	c.1915G>T	p.D639Y
CHRNA1	cholinergic receptor; nicotinic; alpha 1 (muscle)	ENSG00000138435	PAP45	195	22.1%	chr2	175321706	CCDS33331.1	c.1165G>T	p.E389X
CHRNA4	cholinergic receptor; nicotinic; alpha 4	ENSG00000101204	PAP45	134	27.6%	chr20	61452717	CCDS13517.1	c.490G>A	p.D164N
CHRNA6	cholinergic receptor; nicotinic; alpha 6	ENSG00000147434	PAP45	126	27.0%	chr8	42727481	CCDS6135.1	c.1483T>G	p.X495E

CHRNA6	cholinergic receptor; nicotinic; alpha 6	ENSG00000147434	PAP45	183	23.5%	chr8	42727591	CCDS6135.1	c.1373A>G	p.Y458C
CHRNB4	cholinergic receptor; nicotinic; beta 4	ENSG00000117971	PAP45	349	23.2%	chr15	76708853	CCDS10306.1	c.849G>T	p.K283N
CHADL	chondroadherin-like	ENSG00000100399	PAP45	137	23.4%	chr22	39962541	NM_138481	c.1956G>T	p.K652N
CSPG4	chondroitin sulfate proteoglycan 4	ENSG00000173546	PAP45	70	30.0%	chr15	73768401	CCDS10284.1	c.2060C>T	p.S687L
CHSY3	chondroitin sulfate synthase 3	ENSG00000198108	PAP45	64	23.4%	chr5	129271807	CCDS34223.1	c.941G>A	p.G314D
CHRDL1	chordin-like 1	ENSG00000101938	PAP45	73	34.2%	chrX	109889602	CCDS14553.1	c.244A>C	p.N82H
CHM	choroideremia (Rab escort protein 1)	ENSG00000188419	PAP45	107	27.1%	chrX	85100542	CCDS14454.1	c.799C>T	p.R267X
CHML	choroideremia-like (Rab escort protein 2)	ENSG00000203668	PAP45	150	10.7%	chr1	239863777	CCDS31073.1	c.1915G>T	p.E639X
CHML	choroideremia-like (Rab escort protein 2)	ENSG00000203668	PAP45	139	10.1%	chr1	239864224	CCDS31073.1	c.1468C>T	p.R490W
CHAF1A	chromatin assembly factor 1; subunit A (p150)	ENSG00000167670	PAP45	220	28.6%	chr19	4383036	CCDS32875.1	c.2035C>T	p.R679C
CHD1	chromodomain helicase DNA binding protein 1	ENSG00000153922	PAP45	128	18.8%	chr5	98251780	CCDS34204.1	c.2408G>A	p.R803Q
CHD5	chromodomain helicase DNA binding protein 5	ENSG00000116254	PAP45	222	10.8%	chr1	6124782	CCDS57.1	c.2429G>A	p.R810H
CHD6	chromodomain helicase DNA binding protein 6	ENSG00000124177	PAP45	95	25.3%	chr20	39555633	CCDS13317.1	c.1273G>T	p.E425X
CHGB	chromogranin B (secretogranin 1)	ENSG00000089199	PAP45	146	15.1%	chr20	5851574	CCDS13092.1	c.784G>T	p.E262X
C1orf100	chromosome 1 open reading frame 100	ENSG00000173728	PAP45	373	20.6%	chr1	242605316	CCDS31079.1	c.76G>T	p.G26X
C1orf124	chromosome 1 open reading frame 124	ENSG00000010072	PAP45	85	24.7%	chr1	229555153	CCDS1594.1	c.893C>A	p.S298Y
C1orf129	chromosome 1 open reading frame 129	ENSG00000117501	PAP45	136	23.5%	chr1	169225643	CCDS41436.1	c.903T>G	p.I301M
C1orf14	chromosome 1 open reading frame 14	ENSG00000157060	PAP45	165	23.6%	chr1	181176205	CCDS30955.1	c.652G>T	p.D218Y
C1orf146	chromosome 1 open reading frame 146	ENSG00000203910	PAP45	168	11.9%	chr1	92480442	CCDS30772.1	c.152C>A	p.S51Y
C1orf150	chromosome 1 open reading frame 150	ENSG00000169224	PAP45	174	18.4%	chr1	245779136	CCDS1635.1	c.20G>A	p.R7Q
C1orf150	chromosome 1 open reading frame 150	ENSG00000169224	PAP45	210	21.9%	chr1	245804135	CCDS1635.1	c.236G>T	p.R79I
C1orf158	chromosome 1 open reading frame 158	ENSG00000157330	PAP45	76	23.7%	chr1	12729020	CCDS147.1	c.55G>T	p.E19X
C1orf168	chromosome 1 open reading frame 168	ENSG00000187889	PAP45	187	26.7%	chr1	57031036	CCDS30729.1	c.38G>A	p.R13Q
C1orf185	chromosome 1 open reading frame 185	ENSG00000204006	PAP45	407	26.3%	chr1	51385856	NM_001136508	c.425C>A	p.S142Y
C1orf192	chromosome 1 open reading frame 192	ENSG00000188931	PAP45	118	24.6%	chr1	159601497	CCDS30921.1	c.416G>A	p.R139Q
C1orf192	chromosome 1 open reading frame 192	ENSG00000188931	PAP45	95	15.8%	chr1	159601965	CCDS30921.1	c.323G>T	p.G108V
C1orf194	chromosome 1 open reading frame 194	ENSG00000179902	PAP45	117	33.3%	chr1	109452183	CCDS41364.1	c.-1G>T	p.IVS1-1-1SpliceAcceptor
C1orf25	chromosome 1 open reading frame 25	ENSG00000121486	PAP45	104	20.2%	chr1	183387622	CCDS1366.1	c.304T>C	p.F102L
C1orf52	chromosome 1 open reading frame 52	ENSG00000162642	PAP45	69	27.5%	chr1	85496806	CCDS703.1	c.464C>T	p.T155M
C1orf59	chromosome 1 open reading frame 59	ENSG00000162639	PAP45	95	18.9%	chr1	108995239	CCDS787.1	c.514C>A	p.P172T
C1orf87	chromosome 1 open reading frame 87	ENSG00000162598	PAP45	75	25.3%	chr1	60228985	CCDS614.1	c.1589C>T	p.S530L
C1orf88	chromosome 1 open reading frame 88	ENSG00000173947	PAP45	288	21.5%	chr1	111695426	CCDS833.1	c.530G>A	p.R177K
C1orf97	chromosome 1 open reading frame 97	ENSG00000153363	PAP45	166	22.3%	chr1	209631808	ENST00000367003	c.75G>T	p.K25N
C10orf108	chromosome 10 open reading frame 108	ENSG00000180525	PAP45	459	31.2%	chr10	686827	ENST00000316379	c.320C>A	p.S107X
C10orf118	chromosome 10 open reading frame 118	ENSG00000165813	PAP45	243	24.7%	chr10	115900903	CCDS7587.1	c.826G>A	p.D276N
C10orf12	chromosome 10 open reading frame 12	ENSG00000155640	PAP45	260	26.9%	chr10	98731564	CCDS7452.1	c.427C>T	p.R143W
C10orf120	chromosome 10 open reading frame 120	ENSG00000183559	PAP45	151	23.2%	chr10	124447397	CCDS31302.1	c.850C>T	p.L284F
C10orf137	chromosome 10 open reading frame 137	ENSG00000107938	PAP45	170	25.9%	chr10	127441942	CCDS7646.1	c.3526G>A	p.A1176T
C10orf18	chromosome 10 open reading frame 18	ENSG00000108021	PAP45	142	23.2%	chr10	5824248	CCDS41485.1	c.2510A>G	p.E837G
C10orf28	chromosome 10 open reading frame 28	ENSG00000166024	PAP45	191	32.5%	chr10	99958576	CCDS31267.1	c.715C>A	p.L239I
C10orf31	chromosome 10 open reading frame 31	ENSG00000181800	PAP45	247	23.1%	chr10	11400975	ENST00000379256	c.271G>T	p.D91Y
C10orf71	chromosome 10 open reading frame 71	ENSG00000177354	PAP45	278	27.0%	chr10	50201042	NM_001135196	c.446C>A	p.S149Y
C10orf79	chromosome 10 open reading frame 79	ENSG00000197748	PAP45	70	28.6%	chr10	105913943	CCDS31281.1	c.3145C>T	p.R1049X
C10orf81	chromosome 10 open reading frame 81	ENSG00000148735	PAP45	270	25.6%	chr10	115530433	ENST00000369309	c.752G>T	p.S251I
C11orf20	chromosome 11 open reading frame 20	ENSG00000219435	PAP45	195	12.3%	chr11	63827839	NM_001039496	c.451G>T	p.E151X
C11orf51	chromosome 11 open reading frame 51	ENSG00000110200	PAP45	242	24.8%	chr11	71498604	CCDS8210.1	c.337G>A	p.E113K
C11orf61	chromosome 11 open reading frame 61	ENSG00000120458	PAP45	81	30.9%	chr11	124142818	CCDS8454.1	c.988G>A	p.E330K
C11orf63	chromosome 11 open reading frame 63	ENSG00000109944	PAP45	240	32.1%	chr11	122310597	CCDS8438.1	c.1238C>T	p.S413L
C12orf11	chromosome 12 open reading frame 11	ENSG00000064102	PAP45	111	25.2%	chr12	26955455	CCDS8708.1	c.1868C>T	p.S623L
C12orf12	chromosome 12 open reading frame 12	ENSG00000197651	PAP45	661	27.2%	chr12	89871562	CCDS9036.1	c.1089G>T	p.M363I
C12orf12	chromosome 12 open reading frame 12	ENSG00000197651	PAP45	1166	27.9%	chr12	89871721	CCDS9036.1	c.930G>T	p.E310D
C12orf35	chromosome 12 open reading frame 35	ENSG00000174718	PAP45	153	24.2%	chr12	32026877	CCDS8725.2	c.1721A>C	p.K574T

C12orf35	chromosome 12 open reading frame 35	ENSG00000174718	PAP45	126	15.9%	chr12	32027330	CCDS8725.2	c.2174C>A	p.S725Y
C12orf4	chromosome 12 open reading frame 4	ENSG00000047621	PAP45	266	20.7%	chr12	4497601	CCDS8528.1	c.917G>A	p.R306Q
C12orf43	chromosome 12 open reading frame 43	ENSG00000157895	PAP45	283	24.4%	chr12	119926543	CCDS9210.1	c.585G>T	p.K195N
C12orf64	chromosome 12 open reading frame 64	ENSG00000165899	PAP45	66	16.7%	chr12	79276228	ENST00000298820	c.119G>A	p.S40N
C12orf66	chromosome 12 open reading frame 66	ENSG00000174206	PAP45	343	15.2%	chr12	62874706	CCDS41803.1	c.-1G>T	p.IVS2-1-1SpliceAcceptor
C13orf27	chromosome 13 open reading frame 27	ENSG00000151287	PAP45	66	19.7%	chr13	102217755	CCDS9503.1	c.250C>T	p.R84W
C14orf164	chromosome 14 open reading frame 164	ENSG00000215277	PAP45	145	26.2%	chr14	22779445	ENST00000399910	c.51C>A	p.F17L
C14orf166B	chromosome 14 open reading frame 166B	ENSG00000100565	PAP45	114	17.5%	chr14	76374041	NM_194287	c.569C>A	p.S190Y
C14orf4	chromosome 14 open reading frame 4	ENSG00000119669	PAP45	69	21.7%	chr14	76563234	CCDS9854.1	c.655T>A	p.S219T
C14orf93	chromosome 14 open reading frame 93	ENSG00000100802	PAP45	53	20.8%	chr14	22529133	CCDS9583.1	c.962G>T	p.R321I
C15orf2	chromosome 15 open reading frame 2	ENSG00000185823	PAP45	599	17.9%	chr15	22474296	CCDS10015.1	c.2189C>A	p.S730Y
C15orf23	chromosome 15 open reading frame 23	ENSG00000128944	PAP45	56	28.6%	chr15	38462389	CCDS42021.1	c.61G>T	p.E21X
C15orf55	chromosome 15 open reading frame 55	ENSG00000184507	PAP45	240	26.7%	chr15	32428060	CCDS32190.1	c.615A>C	p.K205N
C16orf87	chromosome 16 open reading frame 87	ENSG00000155330	PAP45	75	21.3%	chr16	45394393	CCDS10724.1	c.437A>C	p.K146T
C17orf46	chromosome 17 open reading frame 46	ENSG00000184361	PAP45	291	23.0%	chr17	40688382	CCDS32669.1	c.950T>C	p.F317S
C17orf70	chromosome 17 open reading frame 70	ENSG00000185504	PAP45	112	23.2%	chr17	77124898	CCDS32765.1	c.1210G>A	p.D404N
C17orf71	chromosome 17 open reading frame 71	ENSG00000167447	PAP45	180	25.0%	chr17	54643791	CCDS11615.1	c.1597C>T	p.R533X
C17orf80	chromosome 17 open reading frame 80	ENSG00000141219	PAP45	214	28.0%	chr17	68749981	CCDS11694.1	c.1517C>A	p.S506Y
C18orf25	chromosome 18 open reading frame 25	ENSG00000152242	PAP45	102	21.6%	chr18	42050552	CCDS42430.1	c.708G>T	p.E236D
C18orf8	chromosome 18 open reading frame 8	ENSG00000141452	PAP45	104	21.2%	chr18	19358394	CCDS32803.1	c.1010C>A	p.S337Y
C18orf8	chromosome 18 open reading frame 8	ENSG00000141452	PAP45	379	15.8%	chr18	19364427	CCDS32803.1	c.1747C>T	p.R583W
C19orf47	chromosome 19 open reading frame 47	ENSG00000160392	PAP45	113	23.9%	chr19	45531613	CCDS12553.1	c.196C>T	p.R66C
C2orf34	chromosome 2 open reading frame 34	ENSG00000143919	PAP45	54	24.1%	chr2	44788072	CCDS1820.1	c.523C>A	p.L175M
C2orf39	chromosome 2 open reading frame 39	ENSG00000157856	PAP45	154	32.5%	chr2	26531131	CCDS1723.1	c.2032G>A	p.D678N
C2orf42	chromosome 2 open reading frame 42	ENSG00000115998	PAP45	69	26.1%	chr2	70262608	CCDS1899.1	c.14C>A	p.S5Y
C2orf44	chromosome 2 open reading frame 44	ENSG00000163026	PAP45	236	20.8%	chr2	24114235	CCDS1705.1	c.1634G>T	p.R545I
C2orf44	chromosome 2 open reading frame 44	ENSG00000163026	PAP45	147	23.8%	chr2	24114391	CCDS1705.1	c.1478G>T	p.R493I
C2orf63	chromosome 2 open reading frame 63	ENSG00000162994	PAP45	220	20.9%	chr2	55256527	CCDS33201.1	c.1664C>A	p.S555Y
C2orf67	chromosome 2 open reading frame 67	ENSG00000144445	PAP45	86	26.7%	chr2	210617048	CCDS33370.1	c.1781T>G	p.F594C
C2orf71	chromosome 2 open reading frame 71	ENSG00000179270	PAP45	393	25.7%	chr2	29148525	CCDS42669.1	c.2107C>A	p.P703T
C2orf71	chromosome 2 open reading frame 71	ENSG00000179270	PAP45	340	25.0%	chr2	29148610	CCDS42669.1	c.2022C>A	p.F674L
C20orf132	chromosome 20 open reading frame 132	ENSG00000101353	PAP45	79	15.2%	chr20	35203080	ENST00000400441	c.1042A>G	p.T348A
C20orf152	chromosome 20 open reading frame 152	ENSG00000149646	PAP45	37	27.0%	chr20	34024016	CCDS13270.1	c.103A>C	p.M35L
C20orf194	chromosome 20 open reading frame 194	ENSG00000088854	PAP45	141	12.1%	chr20	3311145	CCDS42851.1	c.92G>A	p.R31Q
C20orf202	chromosome 20 open reading frame 202	ENSG00000215595	PAP45	93	18.3%	chr20	1132245	NM_001009612	c.85G>T	p.E29X
C20orf70	chromosome 20 open reading frame 70	ENSG00000131050	PAP45	54	22.2%	chr20	31220637	CCDS13214.1	c.25C>A	p.L9I
C20orf72	chromosome 20 open reading frame 72	ENSG00000125871	PAP45	106	24.5%	chr20	17918808	ENST00000377704	c.738A>G	p.I246M
C21orf91	chromosome 21 open reading frame 91	ENSG00000154642	PAP45	170	25.3%	chr21	18089452	CCDS42907.1	c.671C>T	p.S224L
C22orf30	chromosome 22 open reading frame 30	ENSG00000183530	PAP45	197	23.4%	chr22	30441635	NM_173566	c.2190T>G	p.C730W
C22orf33	chromosome 22 open reading frame 33	ENSG00000185264	PAP45	41	26.8%	chr22	35717208	CCDS13937.1	c.546G>T	p.E182D
C3orf38	chromosome 3 open reading frame 38	ENSG00000179021	PAP45	119	18.5%	chr3	88288110	CCDS2921.1	c.619G>T	p.E207X
C3orf48	chromosome 3 open reading frame 48	ENSG00000183977	PAP45	120	24.2%	chr3	20018240	ENST00000333083	c.376A>C	p.K126Q
C3orf59	chromosome 3 open reading frame 59	ENSG00000180611	PAP45	278	19.8%	chr3	193999626	CCDS3302.1	c.713C>A	p.S238Y
C4orf21	chromosome 4 open reading frame 21	ENSG00000138658	PAP45	188	26.6%	chr4	113758167	CCDS3700.1	c.2480C>A	p.S827Y
C4orf21	chromosome 4 open reading frame 21	ENSG00000138658	PAP45	178	23.6%	chr4	113760066	CCDS3700.1	c.581C>T	p.S194L
C4orf35	chromosome 4 open reading frame 35	ENSG00000145309	PAP45	223	11.7%	chr4	71236066	CCDS3539.1	c.721G>A	p.E241K
C4orf37	chromosome 4 open reading frame 37	ENSG00000163116	PAP45	114	29.8%	chr4	99274598	CCDS3645.1	c.145G>A	p.E49K
C4orf41	chromosome 4 open reading frame 41	ENSG00000168538	PAP45	232	27.6%	chr4	184843497	CCDS34112.1	c.1709C>A	p.S570Y
C5orf25	chromosome 5 open reading frame 25	ENSG00000170085	PAP45	109	16.5%	chr5	175684278	CCDS4398.1	c.2026G>T	p.E676X
C5orf25	chromosome 5 open reading frame 25	ENSG00000170085	PAP45	385	27.8%	chr5	175696381	CCDS4398.1	c.2167G>T	p.E723X
C5orf34	chromosome 5 open reading frame 34	ENSG00000172244	PAP45	59	35.6%	chr5	43538324	CCDS3946.1	c.1059G>T	p.E353D
C5orf41	chromosome 5 open reading frame 41	ENSG00000164463	PAP45	111	20.7%	chr5	172468302	CCDS34293.1	c.1292G>T	p.R431I

C5orf54	chromosome 5 open reading frame 54	ENSG00000221886	PAP45	160	26.3%	chr5	159754398	CCDS34283.1	c.678C>A	p.F226L
C6orf145	chromosome 6 open reading frame 145	ENSG00000168994	PAP45	147	27.9%	chr6	3684049	ENST00000380277	c.77G>A	p.S26N
C6orf170	chromosome 6 open reading frame 170	ENSG00000146350	PAP45	91	27.5%	chr6	121475417	CCDS43501.1	c.3257A>C	p.Q1086P
C6orf174	chromosome 6 open reading frame 174	ENSG00000189367	PAP45	398	27.6%	chr6	127809556	CCDS34531.1	c.1601G>A	p.R534Q
C6orf174	chromosome 6 open reading frame 174	ENSG00000189367	PAP45	185	33.5%	chr6	127810318	CCDS34531.1	c.839C>T	p.S280L
C6orf186	chromosome 6 open reading frame 186	ENSG00000053328	PAP45	193	22.8%	chr6	110673852	CCDS43489.1	c.1091G>T	p.R364I
C6orf192	chromosome 6 open reading frame 192	ENSG00000146409	PAP45	52	23.1%	chr6	133152603	CCDS5163.1	c.346C>A	p.L116I
C6orf89	chromosome 6 open reading frame 89	ENSG00000198663	PAP45	227	19.8%	chr6	36975349	CCDS4827.1	c.172NULL>C	p.NULL-1FsIns1bp
C7orf26	chromosome 7 open reading frame 26	ENSG00000146576	PAP45	129	27.1%	chr7	6606106	CCDS5353.1	c.702C>A	p.F234L
C7orf66	chromosome 7 open reading frame 66	ENSG00000205174	PAP45	91	23.1%	chr7	108311461	CCDS34735.1	c.187T>G	p.S63A
C8orf34	chromosome 8 open reading frame 34	ENSG00000165084	PAP45	78	32.1%	chr8	69890692	CCDS6203.1	c.1234C>A	p.L412I
C8orf41	chromosome 8 open reading frame 41	ENSG00000129696	PAP45	336	17.6%	chr8	33477420	CCDS6090.1	c.1390C>A	p.L464I
C8orf45	chromosome 8 open reading frame 45	ENSG00000178460	PAP45	86	15.1%	chr8	67965766	CCDS6197.1	c.1171C>A	p.Q391K
C8orf47	chromosome 8 open reading frame 47	ENSG00000177459	PAP45	89	22.5%	chr8	99170973	CCDS34929.1	c.552G>T	p.E184D
C8orf47	chromosome 8 open reading frame 47	ENSG00000177459	PAP45	88	22.7%	chr8	99171091	CCDS34929.1	c.670G>T	p.E224X
C8orf48	chromosome 8 open reading frame 48	ENSG00000164743	PAP45	217	25.8%	chr8	13468949	NM_001007090	c.78G>T	p.K26N
C8orf48	chromosome 8 open reading frame 48	ENSG00000164743	PAP45	188	25.0%	chr8	13469114	NM_001007090	c.243G>T	p.K81N
C9orf102	chromosome 9 open reading frame 102	ENSG00000182150	PAP45	72	20.8%	chr9	97683391	CCDS35072.1	c.499G>T	p.V167L
C9orf128	chromosome 9 open reading frame 128	ENSG00000204930	PAP45	264	22.3%	chr9	35815272	CCDS43799.1	c.697C>A	p.L233I
C9orf134	chromosome 9 open reading frame 134	ENSG00000205442	PAP45	244	23.4%	chr9	24534214	ENST00000380098	c.22G>T	p.G8X
C9orf30	chromosome 9 open reading frame 30	ENSG00000066697	PAP45	53	24.5%	chr9	102300942	CCDS6750.1	c.271G>T	p.D91Y
C9orf4	chromosome 9 open reading frame 4	ENSG00000136805	PAP45	172	29.7%	chr9	110943593	CCDS35098.1	c.713G>T	p.R238I
C9orf41	chromosome 9 open reading frame 41	ENSG00000156017	PAP45	107	28.0%	chr9	76788595	CCDS6649.1	c.1138G>T	p.E380X
C9orf46	chromosome 9 open reading frame 46	ENSG00000107020	PAP45	90	18.9%	chr9	5351792	CCDS6463.1	c.178T>G	p.F60V
C9orf72	chromosome 9 open reading frame 72	ENSG00000147894	PAP45	85	25.9%	chr9	27556902	CCDS6522.1	c.217C>T	p.R73X
C9orf84	chromosome 9 open reading frame 84	ENSG00000165181	PAP45	83	16.9%	chr9	113502099	CCDS6781.3	c.2947G>A	p.A983T
C9orf93	chromosome 9 open reading frame 93	ENSG00000164989	PAP45	178	23.0%	chr9	15734607	CCDS6481.1	c.2386G>T	p.G796X
CXorf21	chromosome X open reading frame 21	ENSG00000120280	PAP45	200	23.5%	chrX	30487631	CCDS14224.1	c.763C>A	p.Q255K
CXorf36	chromosome X open reading frame 36	ENSG00000147113	PAP45	196	19.4%	chrX	44898135	NM_176819	c.925G>T	p.D309Y
CXorf36	chromosome X open reading frame 36	ENSG00000147113	PAP45	51	23.5%	chrX	44944892	CCDS14266.1	c.124C>T	p.P42S
CXorf58	chromosome X open reading frame 58	ENSG00000165182	PAP45	139	19.4%	chrX	23863425	CCDS14209.1	c.747G>T	p.E249D
CXorf59	chromosome X open reading frame 59	ENSG00000176034	PAP45	146	26.7%	chrX	35974897	ENST00000397458	c.170C>A	p.S57X
CXorf59	chromosome X open reading frame 59	ENSG00000176034	PAP45	141	24.8%	chrX	36001272	CCDS14238.1	c.286C>A	p.L96I
CXorf65	chromosome X open reading frame 65	ENSG00000204165	PAP45	166	21.1%	chrX	70242704	CCDS35324.1	c.121G>A	p.D41N
CXorf67	chromosome X open reading frame 67	ENSG00000187690	PAP45	197	35.0%	chrX	51166930	CCDS14335.1	c.322G>A	p.E108K
CMA1	chymase 1; mast cell	ENSG00000092009	PAP45	47	25.5%	chr14	24047248	CCDS9630.1	c.34C>A	p.L12I
CGNL1	cingulin-like 1	ENSG00000128849	PAP45	169	34.3%	chr15	55518478	CCDS10161.1	c.989A>G	p.E330G
CMTM4	CKLF-like MARVEL transmembrane domain containing 4	ENSG00000183723	PAP45	115	22.6%	chr16	65208716	CCDS10817.1	c.670A>C	p.N224H
CMTM8	CKLF-like MARVEL transmembrane domain containing 8	ENSG00000170293	PAP45	157	25.5%	chr3	32255531	CCDS2652.1	c.63G>T	p.E21D
CLRN1	clarin 1	ENSG00000163646	PAP45	515	25.2%	chr3	152173071	CCDS3153.1	c.115C>A	p.L39I
CIITA	class II; major histocompatibility complex; transactivator	ENSG00000179583	PAP45	131	33.6%	chr16	10909029	CCDS10544.1	c.2179G>A	p.E727K
CSTF2	cleavage stimulation factor; 3' pre-RNA; subunit 2; 64kDa	ENSG00000101811	PAP45	87	25.3%	chrX	99963999	CCDS14473.1	c.241G>A	p.E81K
CLPX	ClpX caseinolytic peptidase X homolog (E. coli)	ENSG00000166855	PAP45	38	31.6%	chr15	63237193	CCDS10202.1	c.1001C>A	p.S334Y
COCH	coagulation factor C homolog; cochlin (Limulus polyphemus)	ENSG00000100473	PAP45	174	27.0%	chr14	30424385	CCDS9640.1	c.768C>A	p.F256L
F2	coagulation factor II (thrombin)	ENSG00000180210	PAP45	136	29.4%	chr11	46701547	CCDS31476.1	c.462G>T	p.E154D
F2R	coagulation factor II (thrombin) receptor	ENSG00000181104	PAP45	382	27.0%	chr5	76064596	CCDS4032.1	c.790G>A	p.E264K
F5	coagulation factor V (proaccelerin; labile factor)	ENSG00000198734	PAP45	130	23.1%	chr1	167756435	CCDS1281.1	c.6140G>A	p.R2047Q
F5	coagulation factor V (proaccelerin; labile factor)	ENSG00000198734	PAP45	99	30.3%	chr1	167756522	CCDS1281.1	c.6053T>G	p.F2018C
F11	coagulation factor XI	ENSG00000088926	PAP45	91	16.5%	chr4	187444602	CCDS3847.1	c.1520G>T	p.R507I
F13A1	coagulation factor XIII; A1 polypeptide	ENSG00000124491	PAP45	96	32.3%	chr6	6097105	CCDS4496.1	c.1985G>A	p.R662Q
F13A1	coagulation factor XIII; A1 polypeptide	ENSG00000124491	PAP45	174	25.9%	chr6	6112764	CCDS4496.1	c.1834C>T	p.R612C
F13B	coagulation factor XIII; B polypeptide	ENSG00000143278	PAP45	21	57.1%	chr1	195296122	CCDS1388.1	c.802G>A	p.E268K
COQ5	coenzyme Q5 homolog; methyltransferase (S. cerevisiae)	ENSG00000110871	PAP45	111	24.3%	chr12	119425837	ENST00000302223	c.629G>A	p.R210Q

CC2D2B	coiled-coil and C2 domain containing 2B	ENSG00000188649	PAP45	66	15.2%	chr10	97769080	CCDS41555.1	c.653G>T	p.R218I
CCDC108	coiled-coil domain containing 108	ENSG00000181378	PAP45	52	32.7%	chr2	219602399	CCDS2430.2	c.1620T>G	p.F540L
CCDC109A	coiled-coil domain containing 109A	ENSG00000156026	PAP45	129	26.4%	chr10	74314084	CCDS7317.1	c.916G>T	p.G306X
CCDC110	coiled-coil domain containing 110	ENSG00000168491	PAP45	128	18.8%	chr4	186620838	CCDS3843.1	c.190G>T	p.E64X
CCDC129	coiled-coil domain containing 129	ENSG00000180347	PAP45	117	17.1%	chr7	31580783	NM_194300	c.500G>T	p.R167I
CCDC132	coiled-coil domain containing 132	ENSG00000004766	PAP45	138	29.7%	chr7	92699733	CCDS43617.1	c.17C>A	p.S6Y
CCDC14	coiled-coil domain containing 14	ENSG00000175455	PAP45	97	23.7%	chr3	125148735	CCDS3025.1	c.470A>C	p.K157T
CCDC140	coiled-coil domain containing 140	ENSG00000163081	PAP45	223	10.3%	chr2	222877096	CCDS2452.1	c.231C>A	p.F77L
CCDC141	coiled-coil domain containing 141	ENSG00000163492	PAP45	137	24.8%	chr2	179409897	CCDS2281.1	c.2569G>T	p.V857L
CCDC141	coiled-coil domain containing 141	ENSG00000163492	PAP45	326	25.2%	chr2	179410350	CCDS2281.1	c.2116G>T	p.E706X
CCDC146	coiled-coil domain containing 146	ENSG00000135205	PAP45	149	18.8%	chr7	76729459	CCDS34671.1	c.1072G>T	p.E358X
CCDC147	coiled-coil domain containing 147	ENSG00000120051	PAP45	134	19.4%	chr10	106126575	CCDS31282.1	c.1107G>T	p.K369N
CCDC147	coiled-coil domain containing 147	ENSG00000120051	PAP45	141	26.2%	chr10	106204195	CCDS31282.1	c.2536A>G	p.N846D
CCDC148	coiled-coil domain containing 148	ENSG00000153237	PAP45	65	20.0%	chr2	158903563	CCDS33304.1	c.685C>A	p.L229I
CCDC157	coiled-coil domain containing 157	ENSG00000187860	PAP45	149	20.8%	chr22	29097695	CCDS33632.1	c.949C>T	p.R317W
CCDC24	coiled-coil domain containing 24	ENSG00000159214	PAP45	357	25.8%	chr1	44234094	CCDS507.1	c.680C>A	p.S227Y
CCDC27	coiled-coil domain containing 27	ENSG00000162592	PAP45	83	21.7%	chr1	3660596	CCDS50.1	c.373C>T	p.R125X
CCDC36	coiled-coil domain containing 36	ENSG00000173421	PAP45	94	22.3%	chr3	49268572	CCDS33755.1	c.608G>T	p.R203I
CCDC46	coiled-coil domain containing 46	ENSG00000154240	PAP45	230	25.2%	chr17	61252764	CCDS32711.1	c.116T>G	p.L39W
CCDC46	coiled-coil domain containing 46	ENSG00000154240	PAP45	174	12.6%	chr17	61522860	CCDS32710.1	c.739C>A	p.H247N
CCDC50	coiled-coil domain containing 50	ENSG00000152492	PAP45	163	22.1%	chr3	192575879	CCDS33912.1	c.783G>T	p.Q261H
CCDC63	coiled-coil domain containing 63	ENSG00000173093	PAP45	109	16.5%	chr12	109780841	CCDS9151.1	c.248C>T	p.S83L
CCDC69	coiled-coil domain containing 69	ENSG00000198624	PAP45	260	28.5%	chr5	150543135	ENST00000356749	c.280T>A	p.F94I
CCDC7	coiled-coil domain containing 7	ENSG00000216937	PAP45	204	13.2%	chr10	32780701	CCDS7173.1	c.125A>G	p.K42R
CCDC78	coiled-coil domain containing 78	ENSG00000162004	PAP45	442	26.0%	chr16	716179	ENST00000340261	c.190C>T	p.P64S
CCDC83	coiled-coil domain containing 83	ENSG00000150676	PAP45	146	19.2%	chr11	85304799	CCDS8271.1	c.1048C>A	p.L350I
CHCHD4	coiled-coil-helix-coiled-coil-helix domain containing 4	ENSG00000163528	PAP45	64	26.6%	chr3	14133016	CCDS2617.1	c.71G>A	p.R24Q
CSDA	cold shock domain protein A	ENSG00000060138	PAP45	134	17.2%	chr12	10757130	CCDS8630.1	c.520C>T	p.R174W
CSDAP1	cold shock domain protein A pseudogene 1	ENSG00000060138	PAP45	134	17.2%	chr12	10757130	CCDS8630.1	c.520C>T	p.R174W
COL4A3	collagen; type IV; alpha 3 (Goodpasture antigen)	ENSG00000169031	PAP45	201	24.9%	chr2	227880859	CCDS42829.1	c.4442G>A	p.R1481Q
COL4A4	collagen; type IV; alpha 4	ENSG00000081052	PAP45	174	20.7%	chr2	227581151	CCDS42828.1	c.4636G>A	p.A1546T
COL4A4	collagen; type IV; alpha 4	ENSG00000081052	PAP45	145	10.3%	chr2	227605156	CCDS42828.1	c.3658A>C	p.I1220L
COL4A4	collagen; type IV; alpha 4	ENSG00000081052	PAP45	64	23.4%	chr2	227672625	CCDS42828.1	c.1054C>A	p.P352T
COL4A5	collagen; type IV; alpha 5	ENSG00000188153	PAP45	122	23.8%	chrX	107822654	CCDS35366.1	c.4549C>T	p.R1517C
COL4A6	collagen; type IV; alpha 6	ENSG00000197565	PAP45	147	23.1%	chrX	107301318	CCDS14541.1	c.3235G>A	p.G1079S
COL4A6	collagen; type IV; alpha 6	ENSG00000197565	PAP45	121	26.4%	chrX	107310494	CCDS14541.1	c.2041C>T	p.R681X
COL4A6	collagen; type IV; alpha 6	ENSG00000197565	PAP45	206	28.2%	chrX	107317856	CCDS14541.1	c.1648C>A	p.L550I
COL9A1	collagen; type IX; alpha 1	ENSG00000112280	PAP45	140	11.4%	chr6	71066551	CCDS4971.1	c.215G>T	p.R72I
COL9A1	collagen; type IX; alpha 1	ENSG00000112280	PAP45	67	26.9%	chr6	71066762	CCDS4971.1	c.137A>C	p.K46T
COL5A1	collagen; type V; alpha 1	ENSG00000130635	PAP45	442	27.4%	chr9	136740647	ENST00000371814	c.557T>C	p.V186A
COL5A1	collagen; type V; alpha 1	ENSG00000130635	PAP45	190	15.8%	chr9	136763238	CCDS6982.1	c.1240G>A	p.E414K
COL5A3	collagen; type V; alpha 3	ENSG00000080573	PAP45	188	21.8%	chr19	9945984	CCDS12222.1	c.3443G>T	p.G1148V
COL6A3	collagen; type VI; alpha 3	ENSG00000163359	PAP45	316	25.6%	chr2	237942284	CCDS33412.1	c.4561G>A	p.E1521K
COL6A3	collagen; type VI; alpha 3	ENSG00000163359	PAP45	190	24.2%	chr2	237942454	CCDS33412.1	c.4391G>A	p.R1464Q
COL6A3	collagen; type VI; alpha 3	ENSG00000163359	PAP45	76	22.4%	chr2	237968388	CCDS33412.1	c.290G>A	p.R97H
COL10A1	collagen; type X; alpha 1	ENSG00000123500	PAP45	120	24.2%	chr6	116548403	CCDS5105.1	c.1569G>T	p.E523D
COL11A1	collagen; type XI; alpha 1	ENSG00000060718	PAP45	106	21.7%	chr1	103217004	CCDS779.1	c.2745G>T	p.K915N
COL11A1	collagen; type XI; alpha 1	ENSG00000060718	PAP45	146	17.8%	chr1	103260894	CCDS779.1	c.1273G>T	p.E425X
COL12A1	collagen; type XII; alpha 1	ENSG00000111799	PAP45	212	21.7%	chr6	75869107	CCDS43482.1	c.8341G>T	p.D2781Y
COL12A1	collagen; type XII; alpha 1	ENSG00000111799	PAP45	177	27.1%	chr6	75904980	CCDS43482.1	c.5134G>A	p.E1712K
COL12A1	collagen; type XII; alpha 1	ENSG00000111799	PAP45	154	24.0%	chr6	75908477	CCDS43482.1	c.4948G>T	p.E1650X
COL15A1	collagen; type XV; alpha 1	ENSG00000204291	PAP45	146	24.0%	chr9	100868998	CCDS35081.1	c.3665C>T	p.A1222V
COL16A1	collagen; type XVI; alpha 1	ENSG00000084636	PAP45	280	24.6%	chr1	31935429	CCDS41297.1	c.717C>A	p.C239X
COL17A1	collagen; type XVII; alpha 1	ENSG00000065618	PAP45	38	26.3%	chr10	105820205	CCDS7554.1	c.576G>T	p.E192D

COL21A1	collagen; type XXI; alpha 1	ENSG00000124749	PAP45	115	26.1%	chr6	56030448	NM_030820	c.2840G>T	p.R947I
COL21A1	collagen; type XXI; alpha 1	ENSG00000124749	PAP45	126	19.8%	chr6	56032939	NM_030820	c.2444G>T	p.R815I
COL21A1	collagen; type XXI; alpha 1	ENSG00000124749	PAP45	113	25.7%	chr6	56032953	NM_030820	c.2430G>T	p.Q810H
COL21A1	collagen; type XXI; alpha 1	ENSG00000124749	PAP45	83	25.3%	chr6	56033743	NM_030820	c.2257G>T	p.E753X
COL21A1	collagen; type XXI; alpha 1	ENSG00000124749	PAP45	93	19.4%	chr6	56143508	NM_030820	c.924A>C	p.Q308H
COL22A1	collagen; type XXII; alpha 1	ENSG00000169436	PAP45	80	31.3%	chr8	139959426	CCDS6376.1	c.407G>A	p.R136H
COLEC12	collectin sub-family member 12	ENSG00000158270	PAP45	217	25.3%	chr18	336439	CCDS32782.1	c.1183G>A	p.D395N
CSF3R	colony stimulating factor 3 receptor (granulocyte)	ENSG00000119535	PAP45	205	25.4%	chr1	36705833	CCDS414.1	c.1871C>T	p.S624L
COMMD3	COMM domain containing 3	ENSG00000148444	PAP45	117	17.1%	chr10	22648902	CCDS7137.1	c.557C>T	p.S186L
CR2	complement component (3d/Epstein Barr virus) receptor 2	ENSG00000117322	PAP45	183	15.3%	chr1	205710789	CCDS31007.1	c.1307A>C	p.K436T
C1S	complement component 1; s subcomponent	ENSG00000182326	PAP45	184	10.3%	chr12	7047997	CCDS31735.1	c.1848G>A	p.M616I
C3	complement component 3	ENSG00000125730	PAP45	112	28.6%	chr19	6631220	CCDS32883.1	c.4405G>T	p.V1469L
C3	complement component 3	ENSG00000125730	PAP45	323	25.7%	chr19	6632988	CCDS32883.1	c.4314C>A	p.F1438L
C3	complement component 3	ENSG00000125730	PAP45	449	26.9%	chr19	6633224	CCDS32883.1	c.4189G>A	p.D1397N
C4BPA	complement component 4 binding protein; alpha	ENSG00000123838	PAP45	62	25.8%	chr1	205353037	CCDS1477.1	c.44G>T	p.R15M
C9	complement component 9	ENSG00000113600	PAP45	59	18.6%	chr5	39342559	CCDS3929.1	c.1333C>A	p.L445I
C9	complement component 9	ENSG00000113600	PAP45	87	27.6%	chr5	39347136	CCDS3929.1	c.971A>G	p.K324R
CFI	complement factor I	ENSG00000205403	PAP45	294	23.5%	chr4	110890114	CCDS34049.1	c.1034G>A	p.R345Q
CFI	complement factor I	ENSG00000205403	PAP45	256	21.9%	chr4	110890132	CCDS34049.1	c.1016G>A	p.R339Q
CNTN6	contactin 6	ENSG00000134115	PAP45	204	23.5%	chr3	1312434	CCDS2557.1	c.604G>T	p.E202X
COPS3	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)	ENSG00000141030	PAP45	87	26.4%	chr17	17104361	CCDS11183.1	c.915G>T	p.K305N
CPNE4	copine IV	ENSG00000196353	PAP45	263	25.9%	chr3	132783155	CCDS3072.1	c.825G>T	p.K275N
CPNE6	copine VI (neuronal)	ENSG00000100884	PAP45	106	32.1%	chr14	23612014	CCDS9607.1	c.29C>A	p.P10H
CPNE7	copine VII	ENSG00000178773	PAP45	230	28.3%	chr16	88178762	CCDS10980.1	c.812C>T	p.T271M
CPNE8	copine VIII	ENSG00000139117	PAP45	52	19.2%	chr12	37350867	CCDS8733.1	c.1437G>T	p.M479I
CBFA2T2	core-binding factor; runt domain; alpha subunit 2; translocated to; 2	ENSG00000078699	PAP45	200	21.5%	chr20	31674761	CCDS13221.1	c.717G>T	p.E239D
CORIN	corin; serine peptidase	ENSG00000145244	PAP45	173	13.9%	chr4	47320459	CCDS3477.1	c.2426G>A	p.R809H
CORIN	corin; serine peptidase	ENSG00000145244	PAP45	206	10.7%	chr4	47350351	CCDS3477.1	c.1819G>A	p.D607N
CDSN	corneodesmosin	ENSG00000204539	PAP45	81	14.8%	chr6	31191797	CCDS34389.1	c.1574T>G	p.L525X
CTTNBP2	cortactin binding protein 2	ENSG00000077063	PAP45	200	18.0%	chr7	117219389	CCDS5774.1	c.1097T>C	p.I366T
CRHBP	corticotropin releasing hormone binding protein	ENSG00000145708	PAP45	91	26.4%	chr5	76285726	CCDS4034.1	c.292G>A	p.D98N
CRTC2	CREB regulated transcription coactivator 2	ENSG00000160741	PAP45	162	25.9%	chr1	152190397	CCDS30875.1	c.1367C>T	p.S456L
ROS1	c-ros oncogene 1 ; receptor tyrosine kinase	ENSG00000047936	PAP45	79	21.5%	chr6	117728962	CCDS5116.1	c.6601G>T	p.E2201X
ROS1	c-ros oncogene 1 ; receptor tyrosine kinase	ENSG00000047936	PAP45	150	16.0%	chr6	117784582	CCDS5116.1	c.4044G>T	p.E1348D
ROS1	c-ros oncogene 1 ; receptor tyrosine kinase	ENSG00000047936	PAP45	97	23.7%	chr6	117793457	CCDS5116.1	c.2953G>T	p.E985X
CRB1	crumbs homolog 1 (Drosophila)	ENSG00000134376	PAP45	107	20.6%	chr1	195580128	CCDS1390.1	c.747C>A	p.D249E
CRYAB	crystallin; alpha B	ENSG00000109846	PAP45	182	20.3%	chr11	111284748	CCDS8351.1	c.478C>T	p.P160S
CRYGB	crystallin; gamma B	ENSG00000182187	PAP45	143	21.0%	chr2	208715824	CCDS2380.1	c.311C>A	p.S104X
CTR9	Ctr9; Paf1/RNA polymerase II complex component; homolog (S. cerevisiae)	ENSG00000198730	PAP45	173	23.7%	chr11	10746101	CCDS7805.1	c.1859G>A	p.R620Q
CLEC4F	C-type lectin domain family 4; member F	ENSG00000152672	PAP45	151	31.8%	chr2	70897555	CCDS1910.1	c.466C>A	p.L156I
CSMD2	CUB and Sushi multiple domains 2	ENSG00000121904	PAP45	94	24.5%	chr1	33757779	CCDS380.1	c.10390C>T	p.R3464C
CSMD2	CUB and Sushi multiple domains 2	ENSG00000121904	PAP45	56	23.2%	chr1	33947388	CCDS380.1	c.3344C>A	p.P1115H
CSMD2	CUB and Sushi multiple domains 2	ENSG00000121904	PAP45	52	30.8%	chr1	34058675	CCDS380.1	c.1061G>T	p.R354I
CSMD3	CUB and Sushi multiple domains 3	ENSG00000164796	PAP45	78	29.5%	chr8	113345192	CCDS6315.1	c.9714G>T	p.Q3238H
CSMD3	CUB and Sushi multiple domains 3	ENSG00000164796	PAP45	61	18.0%	chr8	113374062	CCDS6315.1	c.8668G>T	p.G2890W
CSMD3	CUB and Sushi multiple domains 3	ENSG00000164796	PAP45	115	20.9%	chr8	113387496	CCDS6315.1	c.7987C>T	p.R2663X
CSMD3	CUB and Sushi multiple domains 3	ENSG00000164796	PAP45	165	24.2%	chr8	113396005	CCDS6315.1	c.7378G>T	p.E2460X
CSMD3	CUB and Sushi multiple domains 3	ENSG00000164796	PAP45	67	20.9%	chr8	113726562	CCDS6315.1	c.3262C>T	p.P1088S
CSMD3	CUB and Sushi multiple domains 3	ENSG00000164796	PAP45	63	20.6%	chr8	113767096	CCDS6315.1	c.2197C>A	p.L733I
CUZD1	CUB and zona pellucida-like domains 1	ENSG00000138161	PAP45	82	26.8%	chr10	124583214	CCDS7631.1	c.1615C>T	p.R539C
CUL3	cullin 3	ENSG00000036257	PAP45	111	18.9%	chr2	225087670	CCDS2462.1	c.442C>T	p.R148X

CUL4B	cullin 4B	ENSG00000158290	PAP45	149	23.5%	chrX	119562396	CCDS35379.1	c.1105C>T	p.R369X
CUL7	cullin 7	ENSG00000044090	PAP45	431	26.9%	chr6	43127973	CCDS4881.1	c.532C>T	p.R178C
CUL9	cullin 9	ENSG00000112659	PAP45	230	26.1%	chr6	43263024	CCDS4890.1	c.1450G>A	p.E484K
CAND1	cullin-associated and neddylation-dissociated 1	ENSG00000111530	PAP45	69	27.5%	chr12	65975111	CCDS8977.1	c.399G>T	p.K133N
CAND2	cullin-associated and neddylation-dissociated 2 (putative)	ENSG00000144712	PAP45	280	26.4%	chr3	12833166	CCDS43053.1	c.1456C>T	p.R486C
CWF19L2	CWF19-like 2; cell cycle control (S. pombe)	ENSG00000152404	PAP45	93	21.5%	chr11	106805120	CCDS8336.1	c.586G>T	p.E196X
CXXC5	CXXC finger 5	ENSG00000171604	PAP45	206	32.0%	chr5	139042662	CCDS43370.1	c.955C>T	p.R319W
CNGA1	cyclic nucleotide gated channel alpha 1	ENSG00000198515	PAP45	47	21.3%	chr4	47639993	CCDS43226.1	c.411G>T	p.K137N
CNGA2	cyclic nucleotide gated channel alpha 2	ENSG00000183862	PAP45	127	26.0%	chrX	150657618	CCDS14701.1	c.7G>A	p.E3K
CNGA3	cyclic nucleotide gated channel alpha 3	ENSG00000144191	PAP45	285	23.9%	chr2	98379294	CCDS2034.1	c.1229G>A	p.R410Q
CNGA3	cyclic nucleotide gated channel alpha 3	ENSG00000144191	PAP45	118	24.6%	chr2	98379842	CCDS2034.1	c.1777G>A	p.E593K
CNGB3	cyclic nucleotide gated channel beta 3	ENSG00000170289	PAP45	198	25.3%	chr8	87685444	CCDS6244.1	c.1774G>T	p.E592X
CCNA2	cyclin A2	ENSG00000145386	PAP45	74	17.6%	chr4	122958250	CCDS3723.1	c.1292A>C	p.N431T
CCNB2	cyclin B2	ENSG00000157456	PAP45	135	21.5%	chr15	57194012	CCDS10170.1	c.345C>A	p.C115X
CCNDBP1	cyclin D-type binding-protein 1	ENSG00000166946	PAP45	161	28.0%	chr15	41271080	CCDS10092.1	c.775C>T	p.R259W
CCNF	cyclin F	ENSG00000162063	PAP45	74	24.3%	chr16	2421180	CCDS10467.1	c.65G>T	p.R22I
CCNJ	cyclin J	ENSG00000107443	PAP45	145	17.9%	chr10	97806648	CCDS7445.1	c.481G>A	p.E161K
CNNM4	cyclin M4	ENSG00000158158	PAP45	481	23.9%	chr2	96791697	CCDS2024.2	c.1234G>A	p.E412K
CNTD1	cyclin N-terminal domain containing 1	ENSG00000176563	PAP45	177	22.6%	chr17	38204693	CCDS11440.1	c.82G>A	p.A28T
CCNT2	cyclin T2	ENSG00000082258	PAP45	34	35.3%	chr2	135393909	CCDS2174.1	c.218C>A	p.S73Y
CDK12	cyclin-dependent kinase 12	ENSG00000167258	PAP45	413	22.3%	chr17	34881115	CCDS11337.1	c.1504G>T	p.D502Y
CDK13	cyclin-dependent kinase 13	ENSG00000065883	PAP45	62	22.6%	chr7	40069160	CCDS5461.1	c.2716G>A	p.E906K
CDK14	cyclin-dependent kinase 14	ENSG00000058091	PAP45	119	29.4%	chr7	90513151	CCDS5619.1	c.991C>A	p.L331I
CDK19	cyclin-dependent kinase 19	ENSG00000155111	PAP45	118	17.8%	chr6	111095380	CCDS5085.1	c.406C>A	p.L136I
CDK7	cyclin-dependent kinase 7	ENSG00000134058	PAP45	101	24.8%	chr5	68591474	CCDS3999.1	c.482C>A	p.S161Y
CDKN3	cyclin-dependent kinase inhibitor 3	ENSG00000100526	PAP45	88	29.5%	chr14	53948155	CCDS9716.1	c.397T>C	p.Y133H
CYLC1	cylicin; basic protein of sperm head cytoskeleton 1	ENSG00000183035	PAP45	213	23.5%	chrX	83006364	ENST00000373196	c.5C>A	p.S2Y
CYLC1	cylicin; basic protein of sperm head cytoskeleton 1	ENSG00000183035	PAP45	66	15.2%	chrX	83014611	CCDS35341.1	c.239C>A	p.S80Y
CYLC1	cylicin; basic protein of sperm head cytoskeleton 1	ENSG00000183035	PAP45	37	29.7%	chrX	83015194	CCDS35341.1	c.822G>T	p.K274N
CYLC1	cylicin; basic protein of sperm head cytoskeleton 1	ENSG00000183035	PAP45	48	25.0%	chrX	83015437	CCDS35341.1	c.1065G>T	p.K355N
CDO1	cysteine dioxygenase; type I	ENSG00000129596	PAP45	77	28.6%	chr5	115174861	CCDS4121.1	c.299G>A	p.G100E
CRIPT	cysteine-rich PDZ-binding protein	ENSG00000119878	PAP45	97	24.7%	chr2	46700282	CCDS1829.1	c.95G>A	p.R32K
CSRNP1	cysteine-serine-rich nuclear protein 1	ENSG00000144655	PAP45	394	20.8%	chr3	39160481	CCDS2682.1	c.839G>A	p.G280D
CARS	cysteinyl-tRNA synthetase	ENSG00000110619	PAP45	72	29.2%	chr11	2979817	CCDS41600.1	c.2320T>G	p.F774V
CDADC1	cytidine and dCMP deaminase domain containing 1	ENSG00000102543	PAP45	91	22.0%	chr13	48740028	CCDS9415.1	c.832G>T	p.D278Y
CYBB	cytochrome b-245; beta polypeptide	ENSG00000165168	PAP45	155	23.2%	chrX	37526356	CCDS14242.1	c.117C>A	p.F39L
CYBB	cytochrome b-245; beta polypeptide	ENSG00000165168	PAP45	55	20.0%	chrX	37536186	CCDS14242.1	c.271C>T	p.R91X
COX4I1	cytochrome c oxidase subunit IV isoform 1	ENSG00000131143	PAP45	157	10.8%	chr16	84397963	CCDS10955.1	c.492G>T	p.K164N
COX4I2	cytochrome c oxidase subunit IV isoform 2 (lung)	ENSG00000131055	PAP45	91	23.1%	chr20	29696362	CCDS13187.1	c.510G>T	p.K170N
COX5A	cytochrome c oxidase subunit Va	ENSG00000178741	PAP45	146	24.0%	chr15	73006263	CCDS10273.1	c.236C>T	p.T79I
COX6C	cytochrome c oxidase subunit VIc	ENSG00000164919	PAP45	77	22.1%	chr8	100973416	CCDS6284.1	c.10G>A	p.E4K
CYP1A1	cytochrome P450; family 1; subfamily A; polypeptide 1	ENSG00000140465	PAP45	185	29.7%	chr15	72800104	CCDS10268.1	c.1318G>A	p.D440N
CYP11B1	cytochrome P450; family 11; subfamily B; polypeptide 1	ENSG00000160882	PAP45	520	11.7%	chr8	143958152	CCDS6392.1	c.80G>A	p.R27K
CYP17A1	cytochrome P450; family 17; subfamily A; polypeptide 1	ENSG00000148795	PAP45	282	25.5%	chr10	104586915	CCDS7541.1	c.194C>T	p.S65L
CYP2C18	cytochrome P450; family 2; subfamily C; polypeptide 18	ENSG00000108242	PAP45	148	19.6%	chr10	96456594	CCDS7435.1	c.706A>C	p.N236H
CYP26A1	cytochrome P450; family 26; subfamily A; polypeptide 1	ENSG00000095596	PAP45	104	17.3%	chr10	94826414	CCDS7426.1	c.1123C>T	p.R375W
CYP27A1	cytochrome P450; family 27; subfamily A; polypeptide 1	ENSG00000135929	PAP45	100	14.0%	chr2	219355356	CCDS2423.1	c.207C>A	p.F69L
CYP27A1	cytochrome P450; family 27; subfamily A; polypeptide 1	ENSG00000135929	PAP45	393	26.7%	chr2	219385920	CCDS2423.1	c.874G>T	p.D292Y
CYP27B1	cytochrome P450; family 27; subfamily B; polypeptide 1	ENSG00000111012	PAP45	203	29.6%	chr12	56444552	CCDS8954.1	c.1012G>A	p.E338K
CYP3A5	cytochrome P450; family 3; subfamily A; polypeptide 5	ENSG00000106258	PAP45	67	34.3%	chr7	99098398	CCDS5672.1	c.842C>T	p.S281L
CYP3A7	cytochrome P450; family 3; subfamily A; polypeptide 7	ENSG00000160870	PAP45	84	33.3%	chr7	99153128	CCDS5673.1	c.389G>A	p.R130Q
CYP39A1	cytochrome P450; family 39; subfamily A; polypeptide 1	ENSG00000146233	PAP45	174	25.3%	chr6	46728128	CCDS4916.1	c.151G>T	p.E51X
CYP4F2	cytochrome P450; family 4; subfamily F; polypeptide 2	ENSG00000186115	PAP45	92	20.7%	chr19	15851168	CCDS12336.1	c.1385C>T	p.S462L
CYFIP1	cytoplasmic FMR1 interacting protein 1	ENSG00000068793	PAP45	77	29.9%	chr15	20507982	CCDS10009.1	c.1778A>C	p.E593A

CKAP2	cytoskeleton associated protein 2	ENSG00000136108	PAP45	229	24.0%	chr13	51947206	CCDS41893.1	c.1981G>T	p.E661X
CKAP2L	cytoskeleton associated protein 2-like	ENSG00000169607	PAP45	120	15.8%	chr2	113230540	CCDS2100.1	c.879G>T	p.K293N
CKAP5	cytoskeleton associated protein 5	ENSG00000175216	PAP45	143	24.5%	chr11	46730779	CCDS31477.1	c.5115C>A	p.F1705L
CTLA4	cytotoxic T-lymphocyte-associated protein 4	ENSG00000163599	PAP45	98	23.5%	chr2	204445681	CCDS2362.1	c.573G>T	p.K191N
D2HGDH	D-2-hydroxyglutarate dehydrogenase	ENSG00000180902	PAP45	33	30.3%	chr2	242331863	CCDS33426.1	c.644G>A	p.R215Q
DCHS1	dachsous 1 (Drosophila)	ENSG00000166341	PAP45	158	15.8%	chr11	6601106	CCDS7771.1	c.8377C>A	p.L2793I
DCHS1	dachsous 1 (Drosophila)	ENSG00000166341	PAP45	180	24.4%	chr11	6619027	CCDS7771.1	c.394C>T	p.R132X
DCHS2	dachsous 2 (Drosophila)	ENSG00000197410	PAP45	248	24.6%	chr4	155375436	CCDS3785.1	c.8453C>A	p.S2818Y
DCHS2	dachsous 2 (Drosophila)	ENSG00000197410	PAP45	173	19.7%	chr4	155376479	CCDS3785.1	c.7410C>A	p.F2470L
DCHS2	dachsous 2 (Drosophila)	ENSG00000197410	PAP45	113	26.5%	chr4	155381145	CCDS3785.1	c.5988C>A	p.F1996L
DCHS2	dachsous 2 (Drosophila)	ENSG00000197410	PAP45	95	17.9%	chr4	155400220	CCDS3785.1	c.5351C>A	p.S1784X
DCHS2	dachsous 2 (Drosophila)	ENSG00000197410	PAP45	96	24.0%	chr4	155506908	CCDS3785.1	c.598C>A	p.L200I
DACT1	dapper; antagonist of beta-catenin; homolog 1 (Xenopus laevis)	ENSG00000165617	PAP45	40	25.0%	chr14	58174976	CCDS9736.1	c.303G>T	p.E101D
ABI3BP	DAVID_ABI family: member 3 (NESH) binding protein	NM_015429	PAP45	176	30.1%	chr3	101972294	NM_015429	c.2591T>C	p.L864P
ABLIM2	DAVID_actin binding LIM protein family: member 2	NM_001130083	PAP45	56	19.6%	chr4	8149743	NM_001130083	c.321C>A	p.F107L
arpc1a	DAVID_actin related protein 2/3 complex: subunit 1A: 41kDa	ENSG00000013455	PAP45	122	32.8%	chr7	98795225	CCDS5660.1	c.911G>A	p.R304H
ADAM22	DAVID_ADAM metallopeptidase domain 22	ENSG00000222045	PAP45	220	22.7%	chr7	87592869	CCDS43608.1	c.637A>C	p.K213Q
ASXL3	DAVID_additional sex combs like 3 (Drosophila)	NM_030632	PAP45	209	26.3%	chr18	29572969	NM_030632	c.1603G>A	p.D535N
Akd1	DAVID_adenylate kinase domain containing 1	NM_001145128	PAP45	91	17.6%	chr6	109969986	NM_001145128	c.3307C>A	p.L1103I
Arl13a	DAVID_ADP-ribosylation factor-like 13A	NM_001162490	PAP45	315	20.3%	chrX	100130036	NM_001162490	c.758G>A	p.R253K
AHNAK2	DAVID_AHNAK nucleoprotein 2	NM_138420	PAP45	213	23.0%	chr14	104475687	NM_138420	c.17146G>A	p.E5716K
AHNAK2	DAVID_AHNAK nucleoprotein 2	NM_138420	PAP45	213	27.7%	chr14	104478063	NM_138420	c.14770G>T	p.E4924X
AHNAK2	DAVID_AHNAK nucleoprotein 2	NM_138420	PAP45	84	15.5%	chr14	104494827	NM_138420	c.178G>A	p.E60K
Als2cr11	DAVID_amyotrophic lateral sclerosis 2 (juvenile) chromosome region: candidate 11	NM_001168221	PAP45	153	30.7%	chr2	202066786	NM_001168221	c.2523A>C	p.K841N
ANKRD28	DAVID_ankyrin repeat domain 28	NM_015199	PAP45	59	25.4%	chr3	15811772	NM_015199	c.73C>T	p.R25X
ANKRD31	DAVID_ankyrin repeat domain 31	NM_001164443	PAP45	319	23.2%	chr5	74436574	NM_001164443	c.4395A>C	p.E1465D
Ankrd34c	DAVID_ankyrin repeat domain 34C	NM_001146341	PAP45	233	24.5%	chr15	77372925	NM_001146341	c.244G>T	p.D82Y
ankrd52	DAVID_ankyrin repeat domain 52	NM_173595	PAP45	100	21.0%	chr12	54937073	NM_173595	c.254G>A	p.R85Q
ano2	DAVID_anoctamin 2	NM_020373	PAP45	80	35.0%	chr12	5579047	NM_020373	c.2097G>T	p.K699N
ano2	DAVID_anoctamin 2	NM_020373	PAP45	57	22.8%	chr12	5712002	NM_020373	c.1490G>T	p.S497I
ano2	DAVID_anoctamin 2	NM_020373	PAP45	140	22.1%	chr12	5786778	NM_020373	c.898G>A	p.A300T
APOBEC3D	DAVID_apolipoprotein B mRNA editing enzyme: catalytic polypeptide-like 3D	ENSG00000198904	PAP45	161	13.0%	chr22	37758259	NM_152426	c.1153C>A	p.L385I
ALG3	DAVID_asparagine-linked glycosylation 3: alpha-1:3-mannosyltransferase homolog (S. cerevisiae)	NM_001006941	PAP45	560	25.2%	chr3	185449736	NM_001006941	c.24G>T	p.E8D
Agbl1	DAVID_ATP/GTP binding protein-like 1	NM_152336	PAP45	201	19.9%	chr15	84569184	NM_152336	c.386C>A	p.S129Y
Agbl1	DAVID_ATP/GTP binding protein-like 1	NM_152336	PAP45	73	21.9%	chr15	84614302	NM_152336	c.1849G>T	p.G617W
Agbl3	DAVID_ATP/GTP binding protein-like 3	NM_178563	PAP45	106	20.8%	chr7	134368180	NM_178563	c.464G>A	p.R155Q
Agbl3	DAVID_ATP/GTP binding protein-like 3	NM_178563	PAP45	187	25.1%	chr7	134369529	NM_178563	c.647G>A	p.R216Q
Agbl3	DAVID_ATP/GTP binding protein-like 3	NM_178563	PAP45	94	26.6%	chr7	134370180	NM_178563	c.1298C>A	p.S433Y
ATP8B3	DAVID_ATPase: class I: type 8B: member 3	NM_138813	PAP45	215	25.1%	chr19	1734237	NM_138813	c.3693G>T	p.E1231D
ATP8B3	DAVID_ATPase: class I: type 8B: member 3	NM_138813	PAP45	105	24.8%	chr19	1756957	NM_138813	c.751G>A	p.A251T
abcb11	DAVID_ATP-binding cassette: sub-family B (MDR/TAP): member 11	NM_003742	PAP45	82	39.0%	chr2	169538592	NM_003742	c.1313T>G	p.L438R
abcb11	DAVID_ATP-binding cassette: sub-family B (MDR/TAP): member 11	NM_003742	PAP45	94	14.9%	chr2	169560110	NM_003742	c.606C>A	p.F202L
birc6	DAVID_baculoviral IAP repeat-containing 6	NM_016252	PAP45	96	20.8%	chr2	32686149	NM_016252	c.14194C>T	p.R4732X
Baz2a	DAVID_bromodomain adjacent to zinc finger domain: 2A	NM_013449	PAP45	264	11.7%	chr12	55294190	NM_013449	c.-1G>T	p.IVS3-1-1SpliceAcceptor
cadps2	DAVID_Ca++-dependent secretion activator 2	NM_001167940	PAP45	91	30.8%	chr7	122042543	NM_001167940	c.1151G>A	p.R384Q

CACNA2D3	DAVID_calcium channel: voltage-dependent: alpha 2/delta subunit 3	NM_018398	PAP45	113	22.1%	chr3	54578884	NM_018398	c.699G>T	p.E233D
CACNA2D3	DAVID_calcium channel: voltage-dependent: alpha 2/delta subunit 3	NM_018398	PAP45	175	26.3%	chr3	54897034	NM_018398	c.2065G>T	p.E689X
CACNB4	DAVID_calcium channel: voltage-dependent: beta 4 subunit	NM_000726	PAP45	180	24.4%	chr2	152437219	NM_000726	c.556G>T	p.E186X
Cacna1b	DAVID_calcium channel: voltage-dependent: N type: alpha 1B subunit	NM_000718	PAP45	124	19.4%	chr9	140021085	NM_000718	c.2020G>A	p.E674K
CACNA1E	DAVID_calcium channel: voltage-dependent: R type: alpha 1E subunit	NM_000721	PAP45	293	19.5%	chr1	179813590	NM_000721	c.578G>A	p.R193H
CACNA1E	DAVID_calcium channel: voltage-dependent: R type: alpha 1E subunit	NM_000721	PAP45	185	20.0%	chr1	179946748	NM_000721	c.1091G>A	p.R364Q
CACNA1E	DAVID_calcium channel: voltage-dependent: R type: alpha 1E subunit	NM_000721	PAP45	212	23.6%	chr1	180026283	NM_000721	c.5866G>A	p.D1956N
CACNA1H	DAVID_calcium channel: voltage-dependent: T type: alpha 1H subunit	NM_021098	PAP45	178	21.3%	chr16	1188770	NM_021098	c.798T>G	p.F266L
CACNA1H	DAVID_calcium channel: voltage-dependent: T type: alpha 1H subunit	NM_021098	PAP45	84	26.2%	chr16	1190279	NM_021098	c.826C>T	p.R276W
CAPN13	DAVID_calpain 13	NM_144575	PAP45	265	10.6%	chr2	30819791	NM_144575	c.1407C>A	p.F469L
CAPN13	DAVID_calpain 13	NM_144575	PAP45	73	21.9%	chr2	30863527	NM_144575	c.169C>A	p.L57I
CES1	DAVID_carboxylesterase 1 (monocyte/macrophage serine esterase 1)	ENSG00000196959	PAP45	62	35.5%	chr16	54408376	CCDS32450.1	c.-1G>T	p.IVS7-1-1SpliceAcceptor
CMYA5	DAVID_cardiomyopathy associated 5	NM_153610	PAP45	132	24.2%	chr5	79060769	NM_153610	c.425C>A	p.S142X
CMYA5	DAVID_cardiomyopathy associated 5	NM_153610	PAP45	205	21.5%	chr5	79061876	NM_153610	c.1532C>T	p.T511I
CMYA5	DAVID_cardiomyopathy associated 5	NM_153610	PAP45	452	25.9%	chr5	79062783	NM_153610	c.2439G>T	p.K813N
CMYA5	DAVID_cardiomyopathy associated 5	NM_153610	PAP45	103	20.4%	chr5	79064798	NM_153610	c.4454A>C	p.K1485T
CMYA5	DAVID_cardiomyopathy associated 5	NM_153610	PAP45	127	27.6%	chr5	79067300	NM_153610	c.6956C>A	p.S2319Y
CMYA5	DAVID_cardiomyopathy associated 5	NM_153610	PAP45	173	24.9%	chr5	79070280	NM_153610	c.9936G>T	p.E3312D
Casp8ap2	DAVID_caspase 8 associated protein 2	NM_012115	PAP45	89	20.2%	chr6	90629057	NM_012115	c.908C>T	p.S303L
chd7	DAVID_chromodomain helicase DNA binding protein 7	NM_017780	PAP45	114	12.3%	chr8	61931675	NM_017780	c.7282C>T	p.R2428X
CHD9	DAVID_chromodomain helicase DNA binding protein 9	NM_025134	PAP45	136	23.5%	chr16	51748460	NM_025134	c.958G>T	p.E320X
C1orf110	DAVID_chromosome 1 open reading frame 110	NM_178550	PAP45	100	33.0%	chr1	161092150	NM_178550	c.210C>A	p.F70L
C1orf223	DAVID_chromosome 1 open reading frame 223	NM_001145474	PAP45	374	22.5%	chr1	46911419	NM_001145474	c.325G>A	p.E109K
c10orf140	DAVID_chromosome 10 open reading frame 140	NM_207371	PAP45	47	23.4%	chr10	21844861	NM_207371	c.1897G>A	p.E633K
C10orf92	DAVID_chromosome 10 open reading frame 93; chromosome 10 open reading frame 92	ENSG00000108046	PAP45	65	18.5%	chr10	134500336	CCDS7671.1	c.994C>A	p.L332I
C10orf93	DAVID_chromosome 10 open reading frame 93; chromosome 10 open reading frame 92	ENSG00000108046	PAP45	65	18.5%	chr10	134500336	CCDS7671.1	c.994C>A	p.L332I
C11orf41	DAVID_chromosome 11 open reading frame 41	NM_012194	PAP45	207	27.1%	chr11	33521952	NM_012194	c.1376C>A	p.S459Y
C11orf41	DAVID_chromosome 11 open reading frame 41	NM_012194	PAP45	157	23.6%	chr11	33523423	NM_012194	c.2435C>T	p.S812L
C11orf80	DAVID_chromosome 11 open reading frame 80	NM_024650	PAP45	48	33.3%	chr11	66340132	NM_024650	c.1222G>A	p.E408K
c12orf51	DAVID_chromosome 12 open reading frame 51	NM_001109662	PAP45	132	22.0%	chr12	111172355	NM_001109662	c.2660G>T	p.R887I
c12orf51	DAVID_chromosome 12 open reading frame 51	NM_001109662	PAP45	86	18.6%	chr12	111205423	NM_001109662	c.220G>A	p.E74K
C12orf53	DAVID_chromosome 12 open reading frame 53	NM_153685	PAP45	166	15.7%	chr12	6675872	NM_153685	c.603C>A	p.F201L
C14orf169	DAVID_chromosome 14 open reading frame 169	NM_024644	PAP45	148	27.7%	chr14	73028984	NM_024644	c.1509G>T	p.K503N
c16orf13	DAVID_chromosome 16 open reading frame 13	NM_032366	PAP45	63	27.0%	chr16	624921	NM_032366	c.457A>G	p.N153D
C16orf73	DAVID_chromosome 16 open reading frame 73	NM_001163560	PAP45	60	23.3%	chr16	1847852	NM_001163560	c.413C>A	p.S138Y
UNC80	DAVID_chromosome 2 open reading frame 21	NM_032504	PAP45	154	27.9%	chr2	210386688	NM_032504	c.1078C>T	p.R360X
UNC80	DAVID_chromosome 2 open reading frame 21	NM_032504	PAP45	153	13.7%	chr2	210490877	NM_032504	c.4963C>T	p.R1655C
UNC80	DAVID_chromosome 2 open reading frame 21	NM_032504	PAP45	117	23.1%	chr2	210490923	NM_032504	c.5009T>G	p.F1670C
C2orf61	DAVID_chromosome 2 open reading frame 61	ENSG00000162864	PAP45	181	13.8%	chr2	47210877	CCDS1831.1	c.426C>A	p.Y142X
C20orf12	DAVID_chromosome 20 open reading frame 12	NM_001099407	PAP45	138	23.2%	chr20	18377667	NM_001099407	c.590C>T	p.T197M
ARHGAP40	DAVID_chromosome 20 open reading frame 95	NM_001164431	PAP45	366	20.2%	chr20	36690984	NM_001164431	c.556A>C	p.K186Q
C3orf55	DAVID_chromosome 3 open reading frame 55	NM_001130002	PAP45	153	26.8%	chr3	158800701	NM_001130002	c.328G>T	p.D110Y
C3orf63	DAVID_chromosome 3 open reading frame 63	NM_001112736	PAP45	89	22.5%	chr3	56680742	NM_001112736	c.496G>T	p.E166X

C3orf77	DAVID_chromosome 3 open reading frame 77	NM_001145030	PAP45	167	15.6%	chr3	44258699	NM_001145030	c.150G>T	p.R50S
poc5	DAVID_chromosome 5 open reading frame 37	NM_001099271	PAP45	293	27.0%	chr5	75034284	NM_001099271	c.415A>G	p.T139A
c5orf42	DAVID_chromosome 5 open reading frame 42	NM_023073	PAP45	124	23.4%	chr5	37260537	NM_023073	c.2354G>A	p.R785Q
c5orf42	DAVID_chromosome 5 open reading frame 42	NM_023073	PAP45	96	21.9%	chr5	37262686	NM_023073	c.1768G>T	p.E590X
C6orf103	DAVID_chromosome 6 open reading frame 103	NM_024694	PAP45	159	19.5%	chr6	147039267	NM_024694	c.1213G>T	p.D405Y
C6orf103	DAVID_chromosome 6 open reading frame 103	NM_024694	PAP45	79	25.3%	chr6	147096079	NM_024694	c.2651C>A	p.S884Y
C7orf10	DAVID_chromosome 7 open reading frame 10	NM_024728	PAP45	125	13.6%	chr7	40322931	NM_024728	c.678G>T	p.K226N
CLTCL1	DAVID_clathrin: heavy chain-like 1	NM_007098	PAP45	77	31.2%	chr22	17548288	NM_007098	c.4859G>A	p.R1620H
CLTCL1	DAVID_clathrin: heavy chain-like 1	NM_007098	PAP45	187	11.2%	chr22	17564048	NM_007098	c.3993G>T	p.K1331N
CLTCL1	DAVID_clathrin: heavy chain-like 1	NM_007098	PAP45	94	19.1%	chr22	17602116	NM_007098	c.1083G>T	p.E361D
CC2D2A	DAVID_coiled-coil and C2 domain containing 2A	NM_001080522	PAP45	92	21.7%	chr4	15113209	NM_001080522	c.307C>T	p.R103C
Ccdc136	DAVID_coiled-coil domain containing 136	NM_022742	PAP45	121	23.1%	chr7	128228532	NM_022742	c.403G>A	p.E135K
ccdc15	DAVID_coiled-coil domain containing 15	NM_025004	PAP45	58	24.1%	chr11	124414026	NM_025004	c.-1G>A	p.IVS13-1-1SpliceAcceptor
CCDC67	DAVID_coiled-coil domain containing 67	NM_181645	PAP45	88	13.6%	chr11	92758291	NM_181645	c.869G>A	p.R290Q
COL29A1	DAVID_collagen: type XXIX: alpha 1	NM_153264	PAP45	127	25.2%	chr3	131596782	NM_153264	c.3352G>T	p.D1118Y
COL29A1	DAVID_collagen: type XXIX: alpha 1	NM_153264	PAP45	107	22.4%	chr3	131602678	NM_153264	c.4105G>A	p.E1369K
CP110	DAVID_CP110 protein	ENSG00000103540	PAP45	132	16.7%	chr16	19455059	CCDS10579.1	c.567G>T	p.K189N
CKMT1A	DAVID_creatine kinase: mitochondrial 1A; creatine kinase: mitochondrial 1B	ENSG00000168775	PAP45	50	20.0%	chr15	41678414	CCDS10097.1	c.1109C>A	p.S370Y
CKMT1B	DAVID_creatine kinase: mitochondrial 1A; creatine kinase: mitochondrial 1B	ENSG00000168775	PAP45	50	20.0%	chr15	41678414	CCDS10097.1	c.1109C>A	p.S370Y
CLEC17A	DAVID_C-type lectin domain family 17: member A	NM_207390	PAP45	425	19.8%	chr19	14571952	NM_207390	c.801G>T	p.E267D
CSMD1	DAVID_CUB and Sushi multiple domains 1	NM_033225	PAP45	94	28.7%	chr8	2795190	NM_033225	c.10285C>T	p.R3429X
CNBD1	DAVID_cyclic nucleotide binding domain containing 1	NM_173538	PAP45	57	24.6%	chr8	88287458	NM_173538	c.553G>A	p.E185K
Clasp1	DAVID_cytoplasmic linker associated protein 1	NM_015282	PAP45	69	20.3%	chr2	121989805	NM_015282	c.550C>T	p.R184X
CLASP2	DAVID_cytoplasmic linker associated protein 2	NM_015097	PAP45	189	27.0%	chr3	33589748	NM_015097	c.2557C>T	p.R853X
DCP1A	DAVID_DCP1 decapping enzyme homolog A (S. cerevisiae)	NM_018403	PAP45	205	21.0%	chr3	53353973	NM_018403	c.172C>T	p.R58X
DDX60L	DAVID_DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like	NM_001012967	PAP45	111	11.7%	chr4	169542424	NM_001012967	c.4030G>T	p.G1344X
DDX60L	DAVID_DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like	NM_001012967	PAP45	260	20.8%	chr4	169579583	NM_001012967	c.2297C>A	p.P766Q
DDX60L	DAVID_DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like	NM_001012967	PAP45	156	10.3%	chr4	169599141	NM_001012967	c.1216G>T	p.E406X
Dhx16	DAVID_DEAH (Asp-Glu-Ala-His) box polypeptide 16	ENSG00000204560	PAP45	225	24.4%	chr6	30746954	CCDS4685.1	c.284G>A	p.R95Q
DOCK4	DAVID_dedicator of cytokinesis 4	NM_014705	PAP45	194	13.9%	chr7	111205629	NM_014705	c.3591G>T	p.E1197D
dock9	DAVID_dedicator of cytokinesis 9	NM_001130049	PAP45	150	20.0%	chr13	98376104	NM_001130049	c.407G>A	p.R136Q
DENND1B	DAVID_DENN/MADD domain containing 1B	ENSG00000162701	PAP45	79	17.7%	chr1	195971367	CCDS41452.1	c.24G>T	p.E8D
DENND4A	DAVID_DENN/MADD domain containing 4A	NM_001144823	PAP45	61	19.7%	chr15	63747411	NM_001144823	c.4889G>A	p.S1630N
DENND4A	DAVID_DENN/MADD domain containing 4A	NM_001144823	PAP45	80	22.5%	chr15	63817159	NM_001144823	c.980A>C	p.K327T
DNTTIP2	DAVID_deoxynucleotidyltransferase: terminal: interacting protein 2	NM_014597	PAP45	191	24.6%	chr1	94115795	NM_014597	c.284C>A	p.S95Y
LOC100271	DAVID_DH and coiled-coil domain-containing protein	NM_001145451	PAP45	89	30.3%	chr2	39046680	NM_001145451	c.2373C>A	p.F791L
DGAT2L7	DAVID_diacylglycerol O-acyltransferase 2 like protein 7	ENSG00000205267	PAP45	56	17.9%	chr7	100631845	ENST00000379421	c.647C>T	p.A216V
dip2a	DAVID_DIP2 disco-interacting protein 2 homolog A (Drosophila)	NM_015151	PAP45	241	16.6%	chr21	46741422	NM_015151	c.377C>T	p.S126L
DLG4	DAVID_discs: large homolog 4 (Drosophila)	NM_001365	PAP45	172	26.7%	chr17	7040348	NM_001365	c.1345G>A	p.D449N
Dom3z	DAVID_dom-3 homolog Z (C. elegans)	ENSG00000204348	PAP45	172	22.1%	chr6	32046689	CCDS4732.1	c.571T>G	p.F191V
DRGX	DAVID_dorsal root ganglia homeobox	NM_001080520	PAP45	62	33.9%	chr10	50268274	NM_001080520	c.160G>A	p.E54K
DNM3	DAVID_dynamin 3	NM_015569	PAP45	84	26.2%	chr1	170274100	NM_015569	c.868C>T	p.R290W
DNM3	DAVID_dynamin 3	NM_015569	PAP45	111	32.4%	chr1	170623028	NM_015569	c.2191G>T	p.E731X
DNHD1	DAVID_dynein heavy chain domain 1	NM_144666	PAP45	253	30.8%	chr11	6516267	NM_144666	c.3077G>A	p.R1026Q
DNHD1	DAVID_dynein heavy chain domain 1	NM_144666	PAP45	206	29.6%	chr11	6523913	NM_144666	c.5168G>A	p.S1723N
DNAH12	DAVID_dynein: axonemal: heavy chain 12	NM_178504	PAP45	121	24.0%	chr3	57302955	NM_178504	c.9173C>T	p.T3058M
DNAH12	DAVID_dynein: axonemal: heavy chain 12	NM_178504	PAP45	66	24.2%	chr3	57369222	NM_178504	c.6044G>T	p.R2015I
DNAH14	DAVID_dynein: axonemal: heavy chain 14	NM_001373	PAP45	72	31.9%	chr1	223557505	NM_001373	c.8377T>G	p.F2793V

DNAH14	DAVID_dynein: axonemal: heavy chain 14	NM_001373	PAP45	140	20.7%	chr1	223646728	NM_001373	c.13137C>A	p.F4379L
DYNC2H1	DAVID_dynein: cytoplasmic 2: heavy chain 1	NM_001080463	PAP45	68	16.2%	chr11	102529377	NM_001080463	c.3232NULL>/	p.NULL-1FsIns1bp
DYNC2H1	DAVID_dynein: cytoplasmic 2: heavy chain 1	NM_001080463	PAP45	77	24.7%	chr11	102550105	NM_001080463	c.5670G>T	p.Q1890H
DYNC2H1	DAVID_dynein: cytoplasmic 2: heavy chain 1	NM_001080463	PAP45	122	15.6%	chr11	102552269	NM_001080463	c.5770G>T	p.D1924Y
DYNC2H1	DAVID_dynein: cytoplasmic 2: heavy chain 1	NM_001080463	PAP45	130	26.9%	chr11	102662304	NM_001080463	c.11022G>T	p.K3674N
DST	DAVID_dystonin	NM_001144769	PAP45	245	24.5%	chr6	56623736	NM_001144769	c.1282C>A	p.L428I
DST	DAVID_dystonin	NM_001144769	PAP45	80	18.8%	chr6	56643465	NM_001144769	c.1048C>T	p.R350W
DST	DAVID_dystonin	NM_020388	PAP45	99	22.2%	chr6	56581374	NM_020388	c.4400G>T	p.R1467I
EML5	DAVID_echinoderm microtubule associated protein like 5	NM_183387	PAP45	209	24.4%	chr14	88152290	NM_183387	c.5846G>A	p.R1949Q
EML5	DAVID_echinoderm microtubule associated protein like 5	NM_183387	PAP45	108	10.2%	chr14	88272576	NM_183387	c.934G>T	p.E312X
EFCAB4B	DAVID_EF-hand calcium binding domain 4B	NM_001144958	PAP45	124	26.6%	chr12	3596455	NM_001144958	c.2037G>T	p.E679D
EFCAB8	DAVID_EF-hand calcium binding domain 8	NM_001143967	PAP45	71	21.1%	chr20	30969888	NM_001143967	c.2121G>T	p.E707D
ERN1	DAVID_endoplasmic reticulum to nucleus signaling 1	NM_001433	PAP45	90	28.9%	chr17	59529216	NM_001433	c.172G>T	p.E58X
Epha6	DAVID_EPH receptor A6	NM_001080448	PAP45	112	25.0%	chr3	98445576	NM_001080448	c.1361G>T	p.R454I
Epha6	DAVID_EPH receptor A6	NM_001080448	PAP45	136	10.3%	chr3	98445743	NM_001080448	c.1528G>T	p.E510X
Epha6	DAVID_EPH receptor A6	NM_001080448	PAP45	152	15.8%	chr3	98949025	NM_001080448	c.3197C>A	p.S1066Y
EPPK1	DAVID_epiplakin 1	NM_031308	PAP45	543	25.4%	chr8	145013901	NM_031308	c.5509G>T	p.E1837X
EPPK1	DAVID_epiplakin 1	NM_031308	PAP45	203	28.1%	chr8	145014222	NM_031308	c.5188G>A	p.D1730N
EHMT2	DAVID_euchromatic histone-lysine N-methyltransferase 2	ENSG00000204371	PAP45	106	12.3%	chr6	31960523	CCDS4725.1	c.2481C>A	p.F827L
Ercc6	DAVID_excision repair cross-complementing rodent repair deficiency: complementation group 6	ENSG00000032514	PAP45	237	24.9%	chr10	50337133	CCDS7229.1	c.4216G>T	p.E1406X
Ercc6	DAVID_excision repair cross-complementing rodent repair deficiency: complementation group 6	ENSG00000032514	PAP45	73	13.7%	chr10	50361504	CCDS7229.1	c.1886G>A	p.R629Q
Xpo5	DAVID_exportin 5	NM_020750	PAP45	45	26.7%	chr6	43600227	NM_020750	c.3437G>A	p.R1146Q
Xpo5	DAVID_exportin 5	NM_020750	PAP45	175	22.3%	chr6	43634263	NM_020750	c.1265C>A	p.S422Y
Xpo5	DAVID_exportin 5	NM_020750	PAP45	146	13.7%	chr6	43646657	NM_020750	c.353G>A	p.R118Q
eys	DAVID_eyes shut homolog (Drosophila)	NM_001142800	PAP45	265	26.0%	chr6	64489085	NM_001142800	c.8768C>A	p.S2923Y
eys	DAVID_eyes shut homolog (Drosophila)	NM_001142800	PAP45	366	28.4%	chr6	64489128	NM_001142800	c.8725C>A	p.L2909I
eys	DAVID_eyes shut homolog (Drosophila)	NM_001142800	PAP45	112	27.7%	chr6	65359883	NM_001142800	c.3725G>T	p.R1242I
FLJ46321	DAVID_FAM75-like protein FLJ46321	ENSG00000214929	PAP45	99	30.3%	chr9	83797994	NM_001001670	c.2789A>C	p.K930T
FLJ46321	DAVID_FAM75-like protein FLJ46321	ENSG00000214929	PAP45	136	16.2%	chr9	83798077	NM_001001670	c.2872G>T	p.D958Y
Fam13a	DAVID_family with sequence similarity 13: member A	ENSG00000138640	PAP45	133	30.8%	chr4	89921449	CCDS34029.1	c.1348G>A	p.E450K
C6orf94	DAVID_family with sequence similarity 164: member B	NM_001013623	PAP45	196	24.5%	chr6	144248963	NM_001013623	c.192G>T	p.K64N
Fam38b	DAVID_family with sequence similarity 38: member B	NM_022068	PAP45	106	21.7%	chr18	10692008	NM_022068	c.6081C>A	p.F2027L
Fam38b	DAVID_family with sequence similarity 38: member B	NM_022068	PAP45	90	28.9%	chr18	10748061	NM_022068	c.3754C>T	p.R1252X
Fam48b1	DAVID_family with sequence similarity 48: member B1	NM_001136234	PAP45	125	10.4%	chrX	24291756	NM_001136234	c.958G>A	p.A320T
Fat1	DAVID_FAT tumor suppressor homolog 1 (Drosophila)	NM_005245	PAP45	266	22.9%	chr4	187746790	NM_005245	c.13717G>A	p.E4573K
Fat1	DAVID_FAT tumor suppressor homolog 1 (Drosophila)	NM_005245	PAP45	153	20.3%	chr4	187779246	NM_005245	c.5488C>A	p.H1830N
Fat1	DAVID_FAT tumor suppressor homolog 1 (Drosophila)	NM_005245	PAP45	237	23.6%	chr4	187866235	NM_005245	c.1741G>T	p.D581Y
FAT3	DAVID_FAT tumor suppressor homolog 3 (Drosophila)	NM_001008781	PAP45	112	30.4%	chr11	91726626	NM_001008781	c.1700G>A	p.R567Q
FAT3	DAVID_FAT tumor suppressor homolog 3 (Drosophila)	NM_001008781	PAP45	160	28.1%	chr11	91726795	NM_001008781	c.1869C>A	p.F623L
FAT3	DAVID_FAT tumor suppressor homolog 3 (Drosophila)	NM_001008781	PAP45	245	27.3%	chr11	92173968	NM_001008781	c.8141C>T	p.S2714F
FAT3	DAVID_FAT tumor suppressor homolog 3 (Drosophila)	NM_001008781	PAP45	318	27.7%	chr11	92182804	NM_001008781	c.9395C>T	p.S3132F
FAT3	DAVID_FAT tumor suppressor homolog 3 (Drosophila)	NM_001008781	PAP45	452	24.1%	chr11	92216875	NM_001008781	c.10694T>G	p.F3565C
FAT3	DAVID_FAT tumor suppressor homolog 3 (Drosophila)	NM_001008781	PAP45	396	26.3%	chr11	92217292	NM_001008781	c.11111C>T	p.A3704V
FAT3	DAVID_FAT tumor suppressor homolog 3 (Drosophila)	NM_001008781	PAP45	85	22.4%	chr11	92255577	NM_001008781	c.12307G>T	p.E4103X
FBXL17	DAVID_F-box and leucine-rich repeat protein 17	NM_001163315	PAP45	71	14.1%	chr5	107549765	NM_001163315	c.1697A>C	p.K566T
Fbxo10	DAVID_F-box protein 10	NM_012166	PAP45	392	23.5%	chr9	37522001	NM_012166	c.1474C>T	p.R492C
Fbxo41	DAVID_F-box protein 41	NM_001080410	PAP45	85	14.1%	chr2	73343856	NM_001080410	c.2347C>A	p.H783N
Fbxo41	DAVID_F-box protein 41	NM_001080410	PAP45	121	28.1%	chr2	73351494	NM_001080410	c.58G>A	p.E20K
Fbxo45	DAVID_F-box protein 45	NM_001105573	PAP45	152	23.0%	chr3	197788802	NM_001105573	c.400C>T	p.R134X
FCAMR	DAVID_Fc receptor: IgA: IgM: high affinity	NM_001122980	PAP45	434	23.3%	chr1	205200639	NM_001122980	c.1130C>A	p.S377Y

Flvcr2	DAVID_feline leukemia virus subgroup C cellular receptor family: member 2	ENSG00000119686	PAP45	416	22.1%	chr14	75115390	CCDS9844.1	c.322A>G	p.I108V
FRMD4B	DAVID_FERM domain containing 4B	NM_015123	PAP45	62	25.8%	chr3	69434239	NM_015123	c.361C>A	p.L121I
FSIP2	DAVID_fibrous sheath interacting protein 2	ENSG00000180922	PAP45	70	18.6%	chr2	186336212	ENST00000326147	c.671G>A	p.R224K
FSIP2	DAVID_fibrous sheath interacting protein 2	ENSG00000180922	PAP45	181	29.8%	chr2	186362491	ENST00000326147	c.1756G>T	p.E586X
FSIP2	DAVID_fibrous sheath interacting protein 2	ENSG00000180922	PAP45	142	21.1%	chr2	186362879	ENST00000326147	c.2144G>T	p.R715I
FSIP2	DAVID_fibrous sheath interacting protein 2	ENSG00000180922	PAP45	73	24.7%	chr2	186363397	ENST00000326147	c.2662G>T	p.D888Y
FSIP2	DAVID_fibrous sheath interacting protein 2	ENSG00000180922	PAP45	55	18.2%	chr2	186364136	ENST00000326147	c.3401C>A	p.S1134Y
DTHD1	DAVID_FLJ16686 protein	NM_001136536	PAP45	75	22.7%	chr4	35984308	NM_001136536	c.874G>T	p.D292Y
FLJ46836	DAVID_FLJ46836 protein	ENSG00000196979	PAP45	220	13.2%	chr9	131943907	ENST00000358748	c.296C>T	p.S99L
FREM1	DAVID_FRAS1 related extracellular matrix 1	NM_144966	PAP45	255	25.1%	chr9	14727428	NM_144966	c.6506A>C	p.K2169T
FREM1	DAVID_FRAS1 related extracellular matrix 1	NM_144966	PAP45	202	26.2%	chr9	14802848	NM_144966	c.2855G>T	p.R952I
GPR126	DAVID_G protein-coupled receptor 126	NM_198569	PAP45	107	21.5%	chr6	142782870	NM_198569	c.3255C>A	p.F1085L
GLB1L3	DAVID_galactosidase: beta 1-like 3	NM_001080407	PAP45	140	26.4%	chr11	133684751	NM_001080407	c.983A>G	p.E328G
GPX5	DAVID_glutathione peroxidase 5 (epididymal androgen-related protein)	ENSG00000079782	PAP45	98	27.6%	chr6	28608170	CCDS4652.1	c.453C>A	p.F151L
GDF1	DAVID_growth differentiation factor 1; LAG1 homolog: ceramide synthase 1	NM_021267	PAP45	89	20.2%	chr19	18865320	NM_021267	c.314A>C	p.K105T
Lass1	DAVID_growth differentiation factor 1; LAG1 homolog: ceramide synthase 1	NM_021267	PAP45	89	20.2%	chr19	18865320	NM_021267	c.314A>C	p.K105T
heatr5a	DAVID_HEAT repeat containing 5A	NM_015473	PAP45	334	32.3%	chr14	30913820	NM_015473	c.935C>T	p.S312L
Heatr7b2	DAVID_HEAT repeat family member 7B2	NM_173489	PAP45	127	20.5%	chr5	41068635	NM_173489	c.2407C>T	p.R803W
Heatr7b2	DAVID_HEAT repeat family member 7B2	NM_173489	PAP45	46	26.1%	chr5	41101282	NM_173489	c.269C>T	p.S90F
HSP90B2P	DAVID_heat shock protein 90kDa beta (Grp94): member 2 (pseudogene)	ENSG00000205141	PAP45	106	13.2%	chr15	97617428	ENST00000378906	c.1003G>T	p.D335Y
HERC1	DAVID_hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	NM_003922	PAP45	151	29.1%	chr15	61802478	NM_003922	c.3698C>T	p.A1233V
HERC1	DAVID_hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	NM_003922	PAP45	433	27.5%	chr15	61854191	NM_003922	c.685C>A	p.L229I
HS3ST6	DAVID_heparan sulfate (glucosamine) 3-O-sulfotransferase 6	NM_001009606	PAP45	138	23.9%	chr16	1901725	NM_001009606	c.803G>A	p.R268H
ERVFRDE1	DAVID_HERV-FRD provirus ancestral Env polyprotein	ENSG00000212121	PAP45	262	27.5%	chr6	11212468	NM_207582	c.1062C>A	p.F354L
ERVFRDE1	DAVID_HERV-FRD provirus ancestral Env polyprotein	ENSG00000212121	PAP45	98	23.5%	chr6	11212922	NM_207582	c.608G>A	p.R203Q
HHLA2	DAVID_HERV-H LTR-associating 2	NM_007072	PAP45	272	19.5%	chr3	109559458	NM_007072	c.763G>T	p.D255Y
htatip2	DAVID_HIV-1 Tat interactive protein 2: 30kDa	NM_001098523	PAP45	155	23.2%	chr11	20345458	NM_001098523	c.358C>A	p.L120I
BAT2L1	DAVID_HLA-B associated transcript 2-like	NM_013318	PAP45	99	31.3%	chr9	133330086	NM_013318	c.1520G>A	p.R507Q
LOC151174	DAVID_hypothetical LOC151174	ENSG00000186235	PAP45	296	23.3%	chr2	238798787	ENST00000409070	c.227G>A	p.R76H
LOC389607	DAVID_hypothetical LOC389607	ENSG00000206100	PAP45	208	21.6%	chr8	597823	ENST00000382819	c.973C>A	p.L325M
LOC401286	DAVID_hypothetical LOC401286	ENSG00000203689	PAP45	158	25.3%	chr6	167813004	ENST00000366825	c.166C>A	p.L56I
LOC63930	DAVID_hypothetical LOC63930	ENSG00000203905	PAP45	109	33.0%	chr20	61181831	ENST00000370344	c.132G>T	p.E44D
CDHR3	DAVID_hypothetical protein FLJ23834	NM_152750	PAP45	223	15.2%	chr7	105422464	NM_152750	c.545G>T	p.R182I
CDHR3	DAVID_hypothetical protein FLJ23834	NM_152750	PAP45	263	27.4%	chr7	105452156	NM_152750	c.2170C>A	p.L724M
FLJ37396	DAVID_hypothetical protein FLJ37396	ENSG00000177460	PAP45	43	23.3%	chr6	109695709	ENST00000325649	c.1358C>A	p.S453Y
FLJ37543	DAVID_hypothetical protein FLJ37543	NM_173667	PAP45	450	22.9%	chr5	61035497	NM_173667	c.273G>T	p.K91N
LOC100128	DAVID_hypothetical protein LOC100128542; blocked early in transport 1 homolog (S. cerevisiae)	NM_001162367	PAP45	261	26.1%	chr7	150077802	NM_001162367	c.46G>A	p.G16R
Bet1	DAVID_hypothetical protein LOC100128542; blocked early in transport 1 homolog (S. cerevisiae)	NM_001162367	PAP45	261	26.1%	chr7	150077802	NM_001162367	c.46G>A	p.G16R
LOC100128	DAVID_hypothetical protein LOC100128788	ENSG00000205913	PAP45	108	27.8%	chr16	2730202	ENST00000382313	c.406G>T	p.E136X
LOC100128	DAVID_hypothetical protein LOC100128788	ENSG00000205913	PAP45	713	17.0%	chr16	2730520	ENST00000382313	c.88C>A	p.L30I
LOC100131	DAVID_hypothetical protein LOC100131098; calcium channel: voltage-dependent: L type: alpha 1C subunit	NM_199460	PAP45	81	17.3%	chr12	2588110	NM_199460	c.3589T>C	p.Y1197H
CACNA1C	DAVID_hypothetical protein LOC100131098; calcium channel: voltage-dependent: L type: alpha 1C subunit	NM_199460	PAP45	81	17.3%	chr12	2588110	NM_199460	c.3589T>C	p.Y1197H
LOC100132	DAVID_hypothetical protein LOC100132159	ENSG00000205488	PAP45	81	29.6%	chr10	5548081	ENST00000380330	c.154G>A	p.G52S

LOC100132	DAVID_hypothetical protein LOC100132731	ENSG00000187695	PAP45	272	27.6%	chr3	130117089	ENST00000344062	c.1328G>T	p.R443I
ZNF883	DAVID_hypothetical protein LOC169834	NM_001101338	PAP45	140	24.3%	chr9	114799927	NM_001101338	c.434G>T	p.R145I
CT62	DAVID_hypothetical protein LOC196993	NM_001102658	PAP45	35	34.3%	chr15	69191596	NM_001102658	c.80G>A	p.R27K
C9orf144	DAVID_hypothetical protein LOC259308; chromosome 9 open reading frame 144	ENSG00000215202	PAP45	104	30.8%	chr9	34827097	ENST00000378788	c.217C>A	p.Q73K
C9orf144B	DAVID_hypothetical protein LOC259308; chromosome 9 open reading frame 144	ENSG00000215202	PAP45	104	30.8%	chr9	34827097	ENST00000378788	c.217C>A	p.Q73K
C9orf144	DAVID_hypothetical protein LOC259308; chromosome 9 open reading frame 144	NM_001141917	PAP45	276	25.4%	chr9	34713431	NM_001141917	c.3806C>T	p.P1269L
C9orf144B	DAVID_hypothetical protein LOC259308; chromosome 9 open reading frame 144	NM_001141917	PAP45	276	25.4%	chr9	34713431	NM_001141917	c.3806C>T	p.P1269L
FAM200B	DAVID_hypothetical protein LOC285550	NM_001145191	PAP45	121	16.5%	chr4	15298467	NM_001145191	c.769T>G	p.F257V
FLJ44606	DAVID_hypothetical protein LOC401207	NM_001164478	PAP45	59	23.7%	chr5	126415426	NM_001164478	c.284G>A	p.R95Q
LOC642597	DAVID_hypothetical protein LOC642597	NM_001145194	PAP45	75	28.0%	chr18	5135567	NM_001145194	c.204G>T	p.K68N
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP45	108	21.3%	chr13	102179878	NM_001146197	c.21170C>A	p.S7057Y
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP45	297	15.8%	chr13	102183367	NM_001146197	c.17681A>G	p.D5894G
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP45	172	29.7%	chr13	102188152	NM_001146197	c.12896G>A	p.G4299D
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP45	205	10.7%	chr13	102191990	NM_001146197	c.9058G>T	p.E3020X
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP45	102	27.5%	chr13	102192093	NM_001146197	c.8955G>T	p.E2985D
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP45	64	23.4%	chr13	102192190	NM_001146197	c.8858G>A	p.R2953Q
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP45	46	21.7%	chr13	102196887	NM_001146197	c.4161G>T	p.K1387N
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP45	331	23.6%	chr13	102198161	NM_001146197	c.2887C>A	p.L963I
LOC729852	DAVID_hypothetical protein LOC729852	ENSG00000219545	PAP45	344	28.2%	chr7	7883530	ENST00000406829	c.145G>A	p.E49K
shisa9	DAVID_hypothetical protein LOC729993	NM_001145204	PAP45	61	34.4%	chr16	13214617	NM_001145204	c.977C>T	p.S326F
Igfn1	DAVID_immunoglobulin-like and fibronectin type III domain containing 1	NM_001164586	PAP45	136	14.0%	chr1	199448797	NM_001164586	c.8153C>A	p.S2718Y
INPP4A	DAVID_inositol polyphosphate-4-phosphatase: type I: 107kDa	NM_001134224	PAP45	126	23.0%	chr2	98548660	NM_001134224	c.2293C>T	p.R765C
INTS2	DAVID_integrator complex subunit 2	NM_020748	PAP45	108	21.3%	chr17	57353952	NM_020748	c.475G>T	p.E159X
ITIH3	DAVID_inter-alpha (globulin) inhibitor H3	NM_002217	PAP45	207	24.2%	chr3	52808097	NM_002217	c.739G>T	p.D247Y
il1rap	DAVID_interleukin 1 receptor accessory protein	NM_001167931	PAP45	443	27.1%	chr3	191856621	NM_001167931	c.1595C>A	p.S532Y
kaz	DAVID_kazrin	ENSG00000189337	PAP45	153	25.5%	chr1	15300748	NM_201628	c.1670C>A	p.S557Y
C6orf174	DAVID_KIAA0408; chromosome 6 open reading frame 174	ENSG00000214338	PAP45	204	23.0%	chr6	127839241	CCDS43505.1	c.1623G>T	p.K541N
KIAA0408	DAVID_KIAA0408; chromosome 6 open reading frame 174	ENSG00000214338	PAP45	204	23.0%	chr6	127839241	CCDS43505.1	c.1623G>T	p.K541N
Sel1l3	DAVID_KIAA0746 protein	NM_015187	PAP45	65	15.4%	chr4	25444212	NM_015187	c.938C>T	p.S313F
KIAA1210	DAVID_KIAA1210	NM_020721	PAP45	67	19.4%	chrX	118123014	NM_020721	c.1037C>T	p.A346V
KIAA1239	DAVID_KIAA1239	NM_001144990	PAP45	144	30.6%	chr4	37124759	NM_001144990	c.4754G>A	p.R1585Q
KIAA1383	DAVID_KIAA1383	NM_019090	PAP45	168	35.1%	chr1	231008980	NM_019090	c.1588C>T	p.R530X
KIAA1430	DAVID_KIAA1430	NM_020827	PAP45	136	28.7%	chr4	186348514	NM_020827	c.831A>C	p.Q277H
KIAA1549	DAVID_KIAA1549	NM_001164665	PAP45	233	19.7%	chr7	138204935	NM_001164665	c.4664C>A	p.S1555X
KIAA1549	DAVID_KIAA1549	NM_001164665	PAP45	154	25.3%	chr7	138252594	NM_001164665	c.2318G>A	p.G773D
KIAA1598	DAVID_KIAA1598	NM_001127211	PAP45	215	26.5%	chr10	118636012	NM_001127211	c.1729G>A	p.E577K
FAM190A	DAVID_KIAA1680 protein	NM_001145065	PAP45	99	10.1%	chr4	91448514	NM_001145065	c.56G>T	p.R19I
KIAA1731	DAVID_KIAA1731	NM_033395	PAP45	261	27.2%	chr11	93072068	NM_033395	c.4342C>A	p.L1448I
GREB1L	DAVID_KIAA1772	NM_001142966	PAP45	121	17.4%	chr18	17349521	NM_001142966	c.5047G>A	p.A1683T
srrm4	DAVID_KIAA1853	NM_194286	PAP45	166	23.5%	chr12	118073315	NM_194286	c.1187C>T	p.A396V
srrm4	DAVID_KIAA1853	NM_194286	PAP45	96	22.9%	chr12	118078709	NM_194286	c.1559A>G	p.Y520C
KIAA2026	DAVID_KIAA2026	NM_001017969	PAP45	144	22.2%	chr9	5958511	NM_001017969	c.1720C>T	p.R574C
KIAA2026	DAVID_KIAA2026	NM_001017969	PAP45	158	24.1%	chr9	5958850	NM_001017969	c.1381C>A	p.L461I
KSR2	DAVID_kinase suppressor of ras 2	NM_173598	PAP45	60	18.3%	chr12	116453864	NM_173598	c.1632C>A	p.F544L
Kif13b	DAVID_kinesin family member 13B	NM_015254	PAP45	309	22.0%	chr8	29093554	NM_015254	c.706G>A	p.D236N
KIF4A	DAVID_kinesin family member 4B; kinesin family member 4A	NM_001099293	PAP45	143	23.1%	chr5	154375341	NM_001099293	c.1729G>T	p.E577X
Kif4b	DAVID_kinesin family member 4B; kinesin family member 4A	NM_001099293	PAP45	143	23.1%	chr5	154375341	NM_001099293	c.1729G>T	p.E577X
KIF4A	DAVID_kinesin family member 4B; kinesin family member 4A	NM_001099293	PAP45	296	23.3%	chr5	154376459	NM_001099293	c.2847G>T	p.E949D

Kif4b	DAVID_kinesin family member 4B; kinesin family member 4A	NM_001099293	PAP45	296	23.3%	chr5	154376459	NM_001099293	c.2847G>T	p.E949D
KIF4A	DAVID_kinesin family member 4B; kinesin family member 4A	NM_001099293	PAP45	301	23.9%	chr5	154376517	NM_001099293	c.2905G>T	p.E969X
Kif4b	DAVID_kinesin family member 4B; kinesin family member 4A	NM_001099293	PAP45	301	23.9%	chr5	154376517	NM_001099293	c.2905G>T	p.E969X
AQPEP	DAVID_laeverin	ENSG00000172901	PAP45	128	13.3%	chr5	115378972	CCDS4124.1	c.2575G>T	p.A859S
LPHN3	DAVID_latrophilin 3	NM_015236	PAP45	152	28.3%	chr4	62592770	NM_015236	c.3518G>A	p.R1173Q
LMOD1	DAVID_leiomodin 1 (smooth muscle)	NM_012134	PAP45	710	27.0%	chr1	200136084	NM_012134	c.680G>A	p.R227H
LMOD3	DAVID_leiomodin 3 (fetal)	NM_198271	PAP45	193	17.1%	chr3	69251048	NM_198271	c.1148G>T	p.R383I
LRRC69	DAVID_leucine rich repeat containing 69	NM_001129890	PAP45	158	25.9%	chr8	92282176	NM_001129890	c.913C>T	p.R305X
Lrrtm2	DAVID_leucine rich repeat transmembrane neuronal 2	NM_015564	PAP45	182	19.2%	chr5	138237492	NM_015564	c.657G>T	p.K219N
LOC401387	DAVID_leucine-rich repeat and death domain-containing protein	NM_001161528	PAP45	121	27.3%	chr7	91631855	NM_001161528	c.598T>G	p.L200V
LRRIQ4	DAVID_leucine-rich repeats and IQ motif containing 4	NM_001080460	PAP45	96	19.8%	chr3	171029345	NM_001080460	c.1125G>T	p.E375D
L1TD1	DAVID_LINE-1 type transposase domain containing 1	ENSG00000162606	PAP45	55	29.1%	chr1	62445339	NM_001164835	c.451G>A	p.E151K
L1TD1	DAVID_LINE-1 type transposase domain containing 1	ENSG00000162606	PAP45	137	25.5%	chr1	62448810	NM_019079	c.1776G>T	p.K592N
LOXHD1	DAVID_lipoxygenase homology domains 1	NM_144612	PAP45	266	25.6%	chr18	42319017	NM_144612	c.5959C>A	p.L1987I
TRANK1	DAVID_lupus brain antigen 1	NM_014831	PAP45	159	25.8%	chr3	36906354	NM_014831	c.745G>A	p.A249T
lcp2	DAVID_lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	NM_005565	PAP45	90	24.4%	chr5	169657142	NM_005565	c.52G>A	p.D18N
lta	DAVID_lymphotoxin alpha (TNF superfamily: member 1)	ENSG00000204496	PAP45	415	25.5%	chr6	31649328	CCDS4701.1	c.497C>T	p.S166L
MAGEL2	DAVID_MAGE-like 2	NM_019066	PAP45	217	26.3%	chr15	21440472	NM_019066	c.3511C>T	p.R1171X
MAGEL2	DAVID_MAGE-like 2	NM_019066	PAP45	225	23.6%	chr15	21443000	NM_019066	c.983C>A	p.S328Y
MAGEL2	DAVID_MAGE-like 2	NM_019066	PAP45	217	29.5%	chr15	21443174	NM_019066	c.809A>C	p.Q270P
LOC100124(	DAVID_maltase-glucoamylase-like pseudogene	ENSG00000204987	PAP45	352	28.1%	chr7	141517594	ENST00000378229	c.17C>A	p.S6Y
LOC100124(	DAVID_maltase-glucoamylase-like pseudogene	ENSG00000204987	PAP45	65	20.0%	chr7	141532320	ENST00000378229	c.831G>T	p.K277N
LOC93432	DAVID_maltase-glucoamylase-like pseudogene	ENSG00000214088	PAP45	84	32.1%	chr7	141483805	ENST00000397504	c.951A>C	p.E317D
MDGA1	DAVID_MAM domain containing glycosylphosphatidylinositol anchor 1	NM_153487	PAP45	267	28.8%	chr6	37714016	NM_153487	c.2719G>T	p.D907Y
MAS1L	DAVID_MAS1 oncogene-like	ENSG00000204687	PAP45	210	23.3%	chr6	29563511	CCDS4661.1	c.148G>A	p.V50I
MAML2	DAVID_mastermind-like 2 (Drosophila)	NM_032427	PAP45	250	22.0%	chr11	95466030	NM_032427	c.813G>T	p.E271D
Matn2	DAVID_matrilin 2	NM_002380	PAP45	147	23.1%	chr8	99114988	NM_002380	c.2740G>A	p.D914N
MGA	DAVID_MAX gene associated	NM_001164273	PAP45	149	15.4%	chr15	39748760	NM_001164273	c.376G>T	p.D126Y
MGA	DAVID_MAX gene associated	NM_001164273	PAP45	219	24.7%	chr15	39776289	NM_001164273	c.1789G>A	p.A597T
MGA	DAVID_MAX gene associated	NM_001164273	PAP45	38	28.9%	chr15	39806703	NM_001164273	c.3464G>A	p.R1155Q
MCF2	DAVID_MCF.2 cell line derived transforming sequence	NM_001099855	PAP45	87	21.8%	chrX	138555394	NM_001099855	c.230C>T	p.S77L
MDC1	DAVID_mediator of DNA-damage checkpoint 1	ENSG00000137337	PAP45	281	23.8%	chr6	30783198	CCDS34384.1	c.3026G>T	p.C1009F
mep1b	DAVID_meprin A: beta	NM_005925	PAP45	85	17.6%	chr18	28051008	NM_005925	c.1816G>T	p.D606Y
mep1b	DAVID_meprin A: beta	NM_005925	PAP45	101	21.8%	chr18	28051904	NM_005925	c.2069G>A	p.R690Q
MCCD1	DAVID_mitochondrial coiled-coil domain 1	ENSG00000204511	PAP45	431	24.6%	chr6	31604813	CCDS34396.1	c.43C>T	p.R15C
KIAA1804	DAVID_mixed lineage kinase 4	ENSG00000143674	PAP45	218	28.9%	chr1	231556240	CCDS1598.1	c.1051G>A	p.A351T
KIAA1804	DAVID_mixed lineage kinase 4	ENSG00000143674	PAP45	408	24.5%	chr1	231581690	CCDS1598.1	c.2315G>T	p.R772I
Muc12	DAVID_mucin 12: cell surface associated; similar to mucin 11	NM_001164462	PAP45	66	21.2%	chr7	100442409	NM_001164462	c.15364G>T	p.E5122X
LOC100130(	DAVID_mucin 12: cell surface associated; similar to mucin 11	NM_001164462	PAP45	66	21.2%	chr7	100442409	NM_001164462	c.15364G>T	p.E5122X
MUC16	DAVID_mucin 16: cell surface associated	NM_024690	PAP45	139	33.8%	chr19	8917677	NM_024690	c.30769G>T	p.E10257X
MUC16	DAVID_mucin 16: cell surface associated	NM_024690	PAP45	257	25.3%	chr19	8921595	NM_024690	c.26851G>T	p.E8951X
MUC16	DAVID_mucin 16: cell surface associated	NM_024690	PAP45	134	10.4%	chr19	8929987	NM_024690	c.18459G>T	p.K6153N
muc2	DAVID_mucin 2: oligomeric mucus/gel-forming	NM_002457	PAP45	77	16.9%	chr11	1065663	NM_002457	c.89G>A	p.R30Q
muc2	DAVID_mucin 2: oligomeric mucus/gel-forming	NM_002457	PAP45	75	33.3%	chr11	1072601	NM_002457	c.1850A>C	p.D617A
MUC5B	DAVID_mucin 5B: oligomeric mucus/gel-forming	NM_002458	PAP45	132	27.3%	chr11	1214339	NM_002458	c.3037G>A	p.V1013M
MUC5B	DAVID_mucin 5B: oligomeric mucus/gel-forming	NM_002458	PAP45	86	22.1%	chr11	1219537	NM_002458	c.4860G>T	p.E1620D
MUC5B	DAVID_mucin 5B: oligomeric mucus/gel-forming	NM_002458	PAP45	168	27.4%	chr11	1219649	NM_002458	c.4972G>T	p.E1658X
MUC5B	DAVID_mucin 5B: oligomeric mucus/gel-forming	NM_002458	PAP45	36	36.1%	chr11	1220600	NM_002458	c.5923G>T	p.A1975S
MUC5B	DAVID_mucin 5B: oligomeric mucus/gel-forming	NM_002458	PAP45	88	30.7%	chr11	1237568	NM_002458	c.16729G>T	p.E5577X

MPDZ	DAVID_multiple PDZ domain protein	NM_003829	PAP45	82	23.2%	chr9	13182200	NM_003829	c.1898G>A	p.R633Q
Mog	DAVID_myelin oligodendrocyte glycoprotein	ENSG00000204655	PAP45	133	33.1%	chr6	29735146	CCDS4667.1	c.160C>T	p.R54C
Mog	DAVID_myelin oligodendrocyte glycoprotein	ENSG00000204655	PAP45	322	28.0%	chr6	29735269	CCDS4667.1	c.283C>T	p.R95W
MYT1L	DAVID_myelin transcription factor 1-like	NM_015025	PAP45	138	26.8%	chr2	1894802	NM_015025	c.1700G>T	p.R567L
MLL2	DAVID_myeloid/lymphoid or mixed-lineage leukemia 2	NM_003482	PAP45	404	25.0%	chr12	47702133	NM_003482	c.16481T>G	p.I5494S
MLL2	DAVID_myeloid/lymphoid or mixed-lineage leukemia 2	NM_003482	PAP45	437	27.5%	chr12	47707045	NM_003482	c.14971C>T	p.R4991W
MLL2	DAVID_myeloid/lymphoid or mixed-lineage leukemia 2	NM_003482	PAP45	240	11.3%	chr12	47718432	NM_003482	c.8974G>A	p.E2992K
MLL2	DAVID_myeloid/lymphoid or mixed-lineage leukemia 2	NM_003482	PAP45	146	30.1%	chr12	47718758	NM_003482	c.8648A>C	p.N2883T
Mybpc2	DAVID_myosin binding protein C: fast type	NM_004533	PAP45	75	20.0%	chr19	55636057	NM_004533	c.681G>T	p.E227D
Myo7b	DAVID_myosin VIIB	NM_001080527	PAP45	131	29.0%	chr2	128099560	NM_001080527	c.4117G>A	p.V1373I
MYO18B	DAVID_myosin XVIIIB	NM_032608	PAP45	78	20.5%	chr22	24549596	NM_032608	c.2646G>T	p.M882I
MYO18B	DAVID_myosin XVIIIB	NM_032608	PAP45	216	21.8%	chr22	24600372	NM_032608	c.4071G>T	p.K1357N
MYH13	DAVID_myosin: heavy chain 13: skeletal muscle	NM_003802	PAP45	164	27.4%	chr17	10172122	NM_003802	c.2477T>G	p.M826R
Ndufa13	DAVID_NADH dehydrogenase (ubiquinone) 1 alpha subcomplex: 13	ENSG00000130288	PAP45	380	27.4%	chr19	19499112	CCDS12404.1	c.445G>A	p.E149K
NACA2	DAVID_nascent polypeptide-associated complex alpha subunit 2	ENSG00000196861	PAP45	72	25.0%	chr17	57022905	NM_199290	c.419C>T	p.A140V
NEB	DAVID_nebulin	NM_001164507	PAP45	210	18.1%	chr2	152174755	NM_001164507	c.12144G>T	p.K4048N
NEB	DAVID_nebulin	NM_001164507	PAP45	148	24.3%	chr2	152208031	NM_001164507	c.8039G>A	p.R2680Q
NEB	DAVID_nebulin	NM_001164508	PAP45	106	22.6%	chr2	152091686	NM_001164508	c.21937G>T	p.E7313X
NEB	DAVID_nebulin	NM_001164508	PAP45	86	20.9%	chr2	152094049	NM_001164508	c.21656G>T	p.R7219I
NEB	DAVID_nebulin	NM_001164508	PAP45	121	12.4%	chr2	152261447	NM_001164508	c.1519G>T	p.D507Y
NEB	DAVID_nebulin	NM_001164508	PAP45	114	15.8%	chr2	152289711	NM_001164508	c.413G>A	p.R138Q
N4BP1	DAVID_NEDD4 binding protein 1	NM_153029	PAP45	204	26.0%	chr16	47153378	NM_153029	c.677C>A	p.S226Y
NPHP4	DAVID_nephronophthisis 4	NM_015102	PAP45	122	27.0%	chr1	5857180	NM_015102	c.3169G>A	p.E1057K
Ncam1	DAVID_neural cell adhesion molecule 1	NM_001076682	PAP45	86	22.1%	chr11	112638843	NM_001076682	c.2273C>A	p.S758Y
Ncam1	DAVID_neural cell adhesion molecule 1	NM_181351	PAP45	230	25.2%	chr11	112580421	NM_181351	c.332A>G	p.Q111R
NBEA	DAVID_neurobeachin	NM_015678	PAP45	349	21.5%	chr13	35118466	NM_015678	c.7688G>A	p.R2563Q
NBEAL1	DAVID_neurobeachin-like 1	NM_001114132	PAP45	262	17.2%	chr2	203686020	NM_001114132	c.2153G>T	p.R718I
Nrk	DAVID_Nik related kinase	NM_198465	PAP45	211	21.8%	chrX	105055566	NM_198465	c.3199C>T	p.R1067X
SGK269	DAVID_NKF3 kinase family member	ENSG00000173517	PAP45	326	28.8%	chr15	75259736	CCDS42062.1	c.1588C>T	p.R530X
SGK269	DAVID_NKF3 kinase family member	ENSG00000173517	PAP45	174	17.2%	chr15	75261222	CCDS42062.1	c.102G>T	p.E34D
Nlrp1	DAVID_NLR family: pyrin domain containing 1	ENSG00000091592	PAP45	392	24.0%	chr17	5359036	CCDS42246.1	c.4184C>T	p.S1395L
nsun6	DAVID_NOL1/NOP2/Sun domain family: member 6	ENSG00000152487	PAP45	168	25.6%	chr10	18880868	CCDS7130.1	c.961C>A	p.L321I
nfe2l2	DAVID_nuclear factor (erythroid-derived 2)-like 2	ENSG00000222043	PAP45	361	21.3%	chr2	177804130	CCDS42782.1	c.1447G>A	p.E483K
NOL8	DAVID_nucleolar protein 8	NM_017948	PAP45	178	20.2%	chr9	94117910	NM_017948	c.818C>T	p.S273F
obscn	DAVID_obscurin: cytoskeletal calmodulin and titin-interacting RhoGEF	NM_001098623	PAP45	115	28.7%	chr1	226626826	NM_001098623	c.21724G>A	p.A7242T
OR11A1	DAVID_olfactory receptor: family 11: subfamily A: member 1	ENSG00000204694	PAP45	120	30.8%	chr6	29502652	CCDS34363.1	c.746T>C	p.V249A
OR12D2	DAVID_olfactory receptor: family 12: subfamily D: member 2	ENSG00000168787	PAP45	552	26.6%	chr6	29472967	CCDS4659.1	c.512G>A	p.R171H
OR12D2	DAVID_olfactory receptor: family 12: subfamily D: member 2	ENSG00000168787	PAP45	566	25.8%	chr6	29473205	CCDS4659.1	c.750C>A	p.F250L
OR14A2	DAVID_olfactory receptor: family 14: subfamily A: member 2	ENSG00000198118	PAP45	114	22.8%	chr1	245953197	ENST00000366485	c.772C>A	p.L258I
OR2H2	DAVID_olfactory receptor: family 2: subfamily H: member 2	ENSG00000204657	PAP45	325	28.3%	chr6	29664198	CCDS34365.1	c.498C>A	p.F166L
OR2J3	DAVID_olfactory receptor: family 2: subfamily J: member 3	ENSG00000204701	PAP45	69	20.3%	chr6	29188467	CCDS43433.1	c.821G>A	p.G274D
OR4C5	DAVID_olfactory receptor: family 4: subfamily C: member 5	ENSG00000176540	PAP45	145	16.6%	chr11	48343717	ENST00000319813	c.877C>T	p.P293S
OR5K1	DAVID_olfactory receptor: family 5: subfamily K: member 1	ENSG00000185408	PAP45	151	38.4%	chr3	99671765	CCDS43115.1	c.655C>A	p.L219I
OR5M11	DAVID_olfactory receptor: family 5: subfamily M: member 11	NM_001005245	PAP45	108	24.1%	chr11	56066427	NM_001005245	c.883G>T	p.D295Y
Onecut3	DAVID_one cut homeobox 3	NM_001080488	PAP45	51	27.5%	chr19	1726215	NM_001080488	c.1256T>G	p.L419R
OPCML	DAVID_opioid binding protein/cell adhesion molecule-like	ENSG00000183715	PAP45	203	21.2%	chr11	131811291	CCDS8492.1	c.836C>A	p.S279Y

ORC5L	DAVID_origin recognition complex: subunit 5-like (yeast)	NM_181747	PAP45	109	21.1%	chr7	103596100	NM_181747	c.934G>T	p.D312Y
OC90	DAVID_otoconin 90	NM_001080399	PAP45	66	22.7%	chr8	133113332	NM_001080399	c.1009G>A	p.E337K
OTOL1	DAVID_Otolin-1	ENSG00000182447	PAP45	27	37.0%	chr3	162703701	NM_001080440	c.711G>T	p.E237D
PNMA2	DAVID_paraneoplastic antigen MA2	ENSG00000171362	PAP45	557	26.4%	chr8	26421886	NM_007257	c.303G>T	p.E101D
Pcf11	DAVID_PCF11: cleavage and polyadenylation factor subunit: homolog (S. cerevisiae)	NM_015885	PAP45	415	26.5%	chr11	82558576	NM_015885	c.3551G>A	p.R1184K
Pcf11	DAVID_PCF11: cleavage and polyadenylation factor subunit: homolog (S. cerevisiae)	NM_015885	PAP45	102	25.5%	chr11	82573573	NM_015885	c.4657G>A	p.E1553K
PXDNL	DAVID_peroxidasin homolog (Drosophila)-like	NM_144651	PAP45	182	25.3%	chr8	52421011	NM_144651	c.3951G>T	p.K1317N
PXDNL	DAVID_peroxidasin homolog (Drosophila)-like	NM_144651	PAP45	161	26.7%	chr8	52421061	NM_144651	c.-1G>T	p.IVS19-1-1SpliceAcceptor
PXDNL	DAVID_peroxidasin homolog (Drosophila)-like	NM_144651	PAP45	223	14.8%	chr8	52488278	NM_144651	c.1889G>T	p.R630I
PXDNL	DAVID_peroxidasin homolog (Drosophila)-like	NM_144651	PAP45	209	25.4%	chr8	52547408	NM_144651	c.704G>A	p.R235Q
PRIC285	DAVID_peroxisomal proliferator-activated receptor A interacting complex 285	ENSG00000130589	PAP45	123	28.5%	chr20	61665773	CCDS33508.1	c.4846G>A	p.E1616K
PXT1	DAVID_peroxisomal: testis specific 1	NM_152990	PAP45	69	18.8%	chr6	36467599	NM_152990	c.331G>T	p.D111Y
Phf1	DAVID_PHD finger protein 1	ENSG00000112511	PAP45	355	22.3%	chr6	33490068	CCDS4777.1	c.823C>T	p.R275C
ppapdc1b	DAVID_phosphatidic acid phosphatase type 2 domain containing 1B	NM_001102559	PAP45	45	33.3%	chr8	38242905	NM_001102559	c.545C>A	p.S182Y
PI4KA	DAVID_phosphatidylinositol 4-kinase: catalytic: alpha	ENSG00000133511	PAP45	54	25.9%	chr22	19518912	CCDS33603.1	c.131G>A	p.R44Q
Pde2a	DAVID_phosphodiesterase 2A: cGMP-stimulated	NM_001146209	PAP45	225	23.1%	chr11	72057012	NM_001146209	c.22G>T	p.E8X
PIK3C2G	DAVID_phosphoinositide-3-kinase: class 2: gamma polypeptide	NM_004570	PAP45	80	30.0%	chr12	18535690	NM_004570	c.2601C>A	p.F867L
PIRT	DAVID_phosphoinositide-interacting regulator of transient receptor potential channels	NM_001101387	PAP45	306	20.9%	chr17	10669317	NM_001101387	c.371C>T	p.S124L
Pla2g4e	DAVID_phospholipase A2: group IVE	NM_001080490	PAP45	53	34.0%	chr15	40063962	NM_001080490	c.2263C>T	p.L755F
PLCH2	DAVID_phospholipase C: eta 2	NM_014638	PAP45	323	24.8%	chr1	2425999	NM_014638	c.3738G>T	p.Q1246H
PCLO	DAVID_piccolo (presynaptic cytomatrix protein)	NM_033026	PAP45	238	20.2%	chr7	82417271	NM_033026	c.10569G>T	p.E3523D
PCLO	DAVID_piccolo (presynaptic cytomatrix protein)	NM_033026	PAP45	214	26.6%	chr7	82418275	NM_033026	c.9565G>T	p.E3189X
PCLO	DAVID_piccolo (presynaptic cytomatrix protein)	NM_033026	PAP45	138	21.7%	chr7	82422733	NM_033026	c.5472G>T	p.K1824N
PCLO	DAVID_piccolo (presynaptic cytomatrix protein)	NM_033026	PAP45	117	19.7%	chr7	82423983	NM_033026	c.4222G>A	p.D1408N
PCLO	DAVID_piccolo (presynaptic cytomatrix protein)	NM_033026	PAP45	315	25.4%	chr7	82622550	NM_033026	c.1343A>C	p.K448T
PITRM1	DAVID_pitrilysin metallopeptidase 1	NM_014889	PAP45	264	11.0%	chr10	3180224	NM_014889	c.2024G>A	p.R675Q
Pgcp	DAVID_plasma glutamate carboxypeptidase	ENSG00000104324	PAP45	97	15.5%	chr8	97866320	CCDS6273.1	c.19G>A	p.A7T
LPPR4	DAVID_plasticity related gene 1	ENSG00000117600	PAP45	165	24.8%	chr1	99545115	CCDS757.1	c.2253C>A	p.F751L
PLEKHB1	DAVID_pleckstrin homology domain containing: family B (evectins) member 1	NM_021200	PAP45	147	20.4%	chr11	73037741	NM_021200	c.55G>T	p.E19X
PHLDB2	DAVID_pleckstrin homology-like domain: family B: member 2; phosphatidylinositol-specific phospholipase C: X domain containing 2	NM_001134478	PAP45	136	25.7%	chr3	112922361	NM_001134478	c.968C>T	p.A323V
PLCXD2	DAVID_pleckstrin homology-like domain: family B: member 2; phosphatidylinositol-specific phospholipase C: X domain containing 2	NM_001134478	PAP45	136	25.7%	chr3	112922361	NM_001134478	c.968C>T	p.A323V
PRAM1	DAVID_PML-RARA regulated adaptor molecule 1	NM_032152	PAP45	244	15.2%	chr19	8469602	NM_032152	c.1090G>A	p.A364T
PARP14	DAVID_poly (ADP-ribose) polymerase family: member 14	NM_017554	PAP45	53	28.3%	chr3	123893849	NM_017554	c.367G>T	p.E123X
papolb	DAVID_poly(A) polymerase beta (testis specific)	NM_020144	PAP45	203	17.7%	chr7	4866407	NM_020144	c.1561G>A	p.D521N
PKHD1L1	DAVID_polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	NM_177531	PAP45	220	12.3%	chr8	110470483	NM_177531	c.-1G>T	p.IVS7-1-1SpliceAcceptor
PKHD1L1	DAVID_polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	NM_177531	PAP45	229	26.2%	chr8	110470491	NM_177531	c.631C>A	p.L211I
PKHD1L1	DAVID_polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	NM_177531	PAP45	144	19.4%	chr8	110529592	NM_177531	c.5821T>G	p.F1941V

PKHD1L1	DAVID_polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	NM_177531	PAP45	138	14.5%	chr8	110599658	NM_177531	c.11776G>T	p.G3926X
Pom121l2	DAVID_POM121 membrane glycoprotein-like 2 (rat)	NM_033482	PAP45	226	22.1%	chr6	27386740	NM_033482	c.1189C>A	p.L397I
KCNU1	DAVID_potassium channel: subfamily U: member 1	NM_001031836	PAP45	241	24.9%	chr8	36912499	NM_001031836	c.3353C>A	p.S1118Y
PRAF2	DAVID_PRA1 domain family: member 2	ENSG00000102050	PAP45	214	17.8%	chrX	48816593	CCDS14317.1	c.416C>T	p.S139L
Prox2	DAVID_prospero homeobox 2	NM_001080408	PAP45	240	27.9%	chr14	74399335	NM_001080408	c.956G>T	p.R319I
prss2	DAVID_protease: serine: 2 (trypsin 2)	NM_002770	PAP45	196	23.0%	chr7	142181103	NM_002770	c.235G>A	p.E79K
prss23	DAVID_protease: serine: 23	ENSG00000150687	PAP45	150	24.7%	chr11	86197334	CCDS8278.1	c.1001G>A	p.R334Q
Psmg4	DAVID_proteasome (prosome: macropain) assembly chaperone 4	NM_001128592	PAP45	143	26.6%	chr6	3212942	NM_001128592	c.486C>A	p.F162L
PATL1	DAVID_protein associated with topoisomerase II homolog 1 (yeast)	NM_152716	PAP45	150	22.0%	chr11	59176637	NM_152716	c.-1G>T	p.IVS10-1-1SpliceAcceptor
PPM1M	DAVID_protein phosphatase 1M (PP2C domain containing)	NM_144641	PAP45	243	28.4%	chr3	52257445	NM_144641	c.367C>T	p.R123W
PTPN13	DAVID_protein tyrosine phosphatase: non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	NM_080685	PAP45	103	19.4%	chr4	87856715	NM_080685	c.1204C>T	p.R402X
PTPN13	DAVID_protein tyrosine phosphatase: non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	NM_080685	PAP45	214	19.6%	chr4	87881867	NM_080685	c.2361G>T	p.K787N
PTPN13	DAVID_protein tyrosine phosphatase: non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	NM_080685	PAP45	66	16.7%	chr4	87898467	NM_080685	c.3254C>A	p.S1085Y
PTPN13	DAVID_protein tyrosine phosphatase: non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	NM_080685	PAP45	130	19.2%	chr4	87911361	NM_080685	c.4832C>A	p.S1611Y
PCDHA11	DAVID_protocadherin alpha 11	NM_031861	PAP45	98	21.4%	chr5	140231278	NM_031861	c.2406G>T	p.Q802H
PCDHGA10	DAVID_protocadherin gamma subfamily A: 10	NM_018913	PAP45	221	30.3%	chr5	140773360	NM_018913	c.434A>C	p.K145T
PCDHGA10	DAVID_protocadherin gamma subfamily A: 10	NM_018913	PAP45	81	14.8%	chr5	140775328	NM_018913	c.2402C>T	p.S801L
PCDHGA11	DAVID_protocadherin gamma subfamily A: 11	NM_018914	PAP45	120	18.3%	chr5	140781051	NM_018914	c.73C>T	p.R25W
PCDHGA4	DAVID_protocadherin gamma subfamily A: 4	NM_018917	PAP45	782	23.0%	chr5	140716369	NM_018917	c.1418C>A	p.S473Y
PCDHGA5	DAVID_protocadherin gamma subfamily A: 5	NM_018918	PAP45	155	25.2%	chr5	140724274	NM_018918	c.193C>A	p.R65S
PCDHGA8	DAVID_protocadherin gamma subfamily A: 8	NM_032088	PAP45	313	24.0%	chr5	140753195	NM_032088	c.631G>A	p.V211I
PCDHGA8	DAVID_protocadherin gamma subfamily A: 8	NM_032088	PAP45	196	23.5%	chr5	140754624	NM_032088	c.2060C>T	p.S687L
PCDHGA9	DAVID_protocadherin gamma subfamily A: 9	NM_018921	PAP45	123	17.9%	chr5	140763569	NM_018921	c.866C>A	p.S289Y
PCDHGB3	DAVID_protocadherin gamma subfamily B: 3	NM_018924	PAP45	138	19.6%	chr5	140730444	NM_018924	c.299C>T	p.S100L
PCDHGB3	DAVID_protocadherin gamma subfamily B: 3	NM_018924	PAP45	308	24.4%	chr5	140730612	NM_018924	c.467C>A	p.S156Y
PCDHGB4	DAVID_protocadherin gamma subfamily B: 4	NM_003736	PAP45	191	13.6%	chr5	140749556	NM_003736	c.1921C>A	p.L641M
Prpf40a	DAVID_PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	NM_017892	PAP45	71	35.2%	chr2	153224076	NM_017892	c.2363C>A	p.S788Y
PRUNE2	DAVID_prune homolog 2 (Drosophila)	NM_015225	PAP45	189	28.0%	chr9	78510572	NM_015225	c.6438T>G	p.I2146M
PSORS1C1	DAVID_psoriasis susceptibility 1 candidate 1	ENSG00000204540	PAP45	386	22.8%	chr6	31214451	CCDS34390.1	c.83A>G	p.N28S
phtf2	DAVID_putative homeodomain transcription factor 2	NM_001127357	PAP45	75	21.3%	chr7	77367984	NM_001127357	c.135G>T	p.K45N
phtf2	DAVID_putative homeodomain transcription factor 2	NM_001127357	PAP45	228	23.7%	chr7	77409963	NM_001127357	c.1781C>T	p.P594L
PDK3	DAVID_pyruvate dehydrogenase kinase: isozyme 3	NM_001142386	PAP45	224	33.0%	chrX	24467192	NM_001142386	c.1238G>T	p.R413I
RAB44	DAVID_RAB44: member RAS oncogene family	ENSG00000112090	PAP45	226	25.7%	chr6	36803361	ENST00000229824	c.275G>A	p.R92H
Rgl2	DAVID_ral guanine nucleotide dissociation stimulator-like 2	ENSG00000204218	PAP45	292	24.0%	chr6	33372045	CCDS4774.1	c.506C>T	p.S169F
RAPGEF5	DAVID_Rap guanine nucleotide exchange factor (GEF) 5	NM_012294	PAP45	141	18.4%	chr7	22226087	NM_012294	c.460G>T	p.E154X
RIN2	DAVID_Ras and Rab interactor 2	NM_018993	PAP45	316	24.7%	chr20	19929404	NM_018993	c.2512C>A	p.L838I
RASSF9	DAVID_Ras association (RalGDS/AF-6) domain family (N-terminal) member 9	NM_005447	PAP45	60	28.3%	chr12	84722634	NM_005447	c.1285G>T	p.D429Y
RASSF9	DAVID_Ras association (RalGDS/AF-6) domain family (N-terminal) member 9	NM_005447	PAP45	252	25.0%	chr12	84723567	NM_005447	c.352G>T	p.D118Y
rpe	DAVID_rcRPE; ribulose-5-phosphate-3-epimerase	NM_001143909	PAP45	444	22.7%	chr10	104995916	NM_001143909	c.173G>A	p.R58Q
LOC729020	DAVID_rcRPE; ribulose-5-phosphate-3-epimerase	NM_001143909	PAP45	444	22.7%	chr10	104995916	NM_001143909	c.173G>A	p.R58Q
RIMS1	DAVID_regulating synaptic membrane exocytosis 1	NM_014989	PAP45	184	15.2%	chr6	73002085	NM_014989	c.1790T>C	p.I597T
RIMS1	DAVID_regulating synaptic membrane exocytosis 1	NM_014989	PAP45	86	11.6%	chr6	73025475	NM_014989	c.2993G>A	p.R998Q
RPGRIP1	DAVID_retinitis pigmentosa GTPase regulator interacting protein 1	NM_020366	PAP45	714	26.5%	chr14	20864016	NM_020366	c.2554C>T	p.R852X

RPGRIP1	DAVID_retinitis pigmentosa GTPase regulator interacting protein 1	NM_020366	PAP45	81	21.0%	chr14	20866580	NM_020366	c.3053G>T	p.R1018I
RGAG1	DAVID_retrotransposon gag domain containing 1	ENSG00000181110	PAP45	160	19.4%	chrX	109584144	NM_020769	c.3643A>C	p.N1215H
RGAG1	DAVID_retrotransposon gag domain containing 1	ENSG00000181110	PAP45	83	33.7%	chrX	109585140	NM_020769	c.4102G>T	p.E1368X
RGAG4	DAVID_retrotransposon gag domain containing 4	NM_001024455	PAP45	224	29.0%	chrX	71267432	NM_001024455	c.684C>A	p.F228L
rgp1	DAVID_RGP1 retrograde golgi transport homolog (S. cerevisiae)	NM_001080496	PAP45	133	11.3%	chr9	35741662	NM_001080496	c.793A>G	p.T265A
ARHGAP32	DAVID_Rho GTPase-activating protein	ENSG00000134909	PAP45	228	13.2%	chr11	128344612	CCDS31718.1	c.4617C>A	p.F1539L
ARHGAP32	DAVID_Rho GTPase-activating protein	ENSG00000134909	PAP45	116	19.8%	chr11	128353931	CCDS31718.1	c.977G>A	p.R326Q
ARHGAP32	DAVID_Rho GTPase-activating protein	NM_001142685	PAP45	95	25.3%	chr11	128439021	NM_001142685	c.829G>A	p.E277K
Rhobtb2	DAVID_Rho-related BTB domain containing 2	NM_001160036	PAP45	91	31.9%	chr8	22908055	NM_001160036	c.14G>T	p.R5I
FLJ32810	DAVID_Rho-type GTPase-activating protein FLJ32810	NM_152432	PAP45	76	22.4%	chr11	100363528	NM_152432	c.2531C>A	p.S844Y
rnasen	DAVID_ribonuclease type III: nuclear	NM_013235	PAP45	85	11.8%	chr5	31467511	NM_013235	c.3074C>T	p.A1025V
RNF213	DAVID_ring finger protein 213	NM_020914	PAP45	55	21.8%	chr17	75916814	NM_020914	c.3606G>T	p.E1202D
LOC644006	DAVID_ring finger protein 4; hypothetical LOC644006	NM_002938	PAP45	104	24.0%	chr4	2468578	NM_002938	c.56G>A	p.R19Q
Rnf4	DAVID_ring finger protein 4; hypothetical LOC644006	NM_002938	PAP45	104	24.0%	chr4	2468578	NM_002938	c.56G>A	p.R19Q
ROBO1	DAVID_roundabout: axon guidance receptor: homolog 1 (Drosophila); similar to roundabout 1 isoform b	NM_002941	PAP45	141	24.1%	chr3	78801983	NM_002941	c.1501C>T	p.R501X
LOC642132	DAVID_roundabout: axon guidance receptor: homolog 1 (Drosophila); similar to roundabout 1 isoform b	NM_002941	PAP45	141	24.1%	chr3	78801983	NM_002941	c.1501C>T	p.R501X
RYR2	DAVID_ryanodine receptor 2 (cardiac)	NM_001035	PAP45	83	30.1%	chr1	235686641	NM_001035	c.1595C>T	p.S532F
RYR2	DAVID_ryanodine receptor 2 (cardiac)	NM_001035	PAP45	172	20.3%	chr1	235847329	NM_001035	c.5836G>A	p.E1946K
RYR2	DAVID_ryanodine receptor 2 (cardiac)	NM_001035	PAP45	79	30.4%	chr1	235890749	NM_001035	c.8315G>A	p.R2772H
RYR2	DAVID_ryanodine receptor 2 (cardiac)	NM_001035	PAP45	310	22.6%	chr1	236014071	NM_001035	c.12436G>A	p.E4146K
RYR3	DAVID_ryanodine receptor 3	NM_001036	PAP45	48	25.0%	chr15	31642341	NM_001036	c.984G>T	p.E328D
RYR3	DAVID_ryanodine receptor 3	NM_001036	PAP45	77	23.4%	chr15	31732308	NM_001036	c.4240C>A	p.L1414I
RYR3	DAVID_ryanodine receptor 3	NM_001036	PAP45	51	25.5%	chr15	31910565	NM_001036	c.11444C>A	p.S3815Y
RYR3	DAVID_ryanodine receptor 3	NM_001036	PAP45	115	20.0%	chr15	31922990	NM_001036	c.13219G>A	p.A4407T
SCAND3	DAVID_SCAN domain containing 3	ENSG00000197202	PAP45	152	32.2%	chr6	28647849	CCDS34355.1	c.3796A>G	p.K1266E
SCAND3	DAVID_SCAN domain containing 3	ENSG00000197202	PAP45	98	36.7%	chr6	28647978	CCDS34355.1	c.3667C>A	p.L1223I
SLFN12L	DAVID_schlafen family member 12-like	NM_001145027	PAP45	142	23.9%	chr17	30831043	NM_001145027	c.386C>A	p.S129Y
sspO	DAVID_SCO-spondin homolog (Bos taurus)	NM_198455	PAP45	266	10.9%	chr7	149131020	NM_198455	c.7717C>T	p.R2573W
sspO	DAVID_SCO-spondin homolog (Bos taurus)	NM_198455	PAP45	167	13.2%	chr7	149136574	NM_198455	c.9028G>A	p.A3010T
SEC16A	DAVID_SEC16 homolog A (S. cerevisiae)	NM_014866	PAP45	273	26.4%	chr9	138474035	NM_014866	c.5186C>A	p.T1729N
SEC16A	DAVID_SEC16 homolog A (S. cerevisiae)	NM_014866	PAP45	95	12.6%	chr9	138480312	NM_014866	c.4226G>A	p.R1409H
SEC16B	DAVID_SEC16 homolog B (S. cerevisiae)	NM_033127	PAP45	98	27.6%	chr1	176169039	NM_033127	c.2756G>A	p.R919Q
SELV	DAVID_selenoprotein V	ENSG00000186838	PAP45	248	23.4%	chr19	44698424	ENST00000335426	c.732G>T	p.Q244H
SIGLEC12	DAVID_sialic acid binding Ig-like lectin 12	ENSG00000160296	PAP45	180	26.1%	chr19	56686757	CCDS12833.1	c.1738G>T	p.E580X
SPPL2A	DAVID_signal peptide peptidase-like 2A	ENSG00000138600	PAP45	242	18.6%	chr15	48815648	CCDS10138.1	c.874C>A	p.L292I
LOC729195	DAVID_similar to apical early endosomal glycoprotein	ENSG00000204741	PAP45	97	21.6%	chr10	19533892	ENST00000377266	c.311C>A	p.S104Y
ZNF879	DAVID_similar to hypothetical protein 9630041N07	NM_001136116	PAP45	87	23.0%	chr5	178392126	NM_001136116	c.571C>A	p.L191I
ZNF879	DAVID_similar to hypothetical protein 9630041N07	NM_001136116	PAP45	158	21.5%	chr5	178392352	NM_001136116	c.797G>T	p.G266V
LOC100129	DAVID_similar to tudor domain containing 1	ENSG00000218819	PAP45	160	20.6%	chr2	21214858	ENST00000405799	c.1014G>T	p.K338N
ZNF605	DAVID_similar to ZNF605 protein	NM_001164715	PAP45	133	23.3%	chr12	132012384	NM_001164715	c.1667G>T	p.R556I
SLAIN2	DAVID_SLAIN motif family: member 2	NM_020846	PAP45	141	23.4%	chr4	48066739	NM_020846	c.506C>A	p.S169Y
SCN5A	DAVID_sodium channel: voltage-gated: type V: alpha subunit	NM_198056	PAP45	197	23.4%	chr3	38620541	NM_198056	c.1556C>A	p.S519Y
SLC12A1	DAVID_solute carrier family 12 (sodium/potassium/chloride transporters): member 1	NM_000338	PAP45	66	22.7%	chr15	46312314	NM_000338	c.1074C>A	p.F358L
SLC12A1	DAVID_solute carrier family 12 (sodium/potassium/chloride transporters): member 1	NM_000338	PAP45	196	21.9%	chr15	46326880	NM_000338	c.1615G>A	p.G539R
SLC12A1	DAVID_solute carrier family 12 (sodium/potassium/chloride transporters): member 1	NM_000338	PAP45	88	19.3%	chr15	46378684	NM_000338	c.3016G>T	p.D1006Y

SLC4A10	DAVID_solute carrier family 4: sodium bicarbonate transporter: member 10	NM_022058	PAP45	145	17.9%	chr2	162419791	NM_022058	c.482C>A	p.T161N
SLC4A10	DAVID_solute carrier family 4: sodium bicarbonate transporter: member 10	NM_022058	PAP45	226	26.5%	chr2	162469605	NM_022058	c.1601C>A	p.T534N
SPTBN5	DAVID_spectrin: beta: non-erythrocytic 5	NM_016642	PAP45	344	27.6%	chr15	39934887	NM_016642	c.9145C>T	p.R3049W
SPTBN5	DAVID_spectrin: beta: non-erythrocytic 5	NM_016642	PAP45	106	16.0%	chr15	39967471	NM_016642	c.501C>A	p.F167L
SGEF	DAVID_Src homology 3 domain-containing guanine nucleotide exchange factor	ENSG00000114790	PAP45	56	25.0%	chr3	155388167	ENST00000356448	c.1491C>A	p.F497L
STARD9	DAVID_StAR-related lipid transfer (START) domain containing 9	NM_020759	PAP45	165	26.1%	chr15	40766617	NM_020759	c.5549C>T	p.S1850F
ZAK	DAVID_sterile alpha motif and leucine zipper containing kinase AZK	ENSG00000091436	PAP45	102	20.6%	chr2	173839441	CCDS42777.1	c.2120G>T	p.R707I
SFTA3	DAVID_surfactant associated 3	NM_001101341	PAP45	264	20.5%	chr14	36015941	NM_001101341	c.247T>G	p.S83A
SVEP1	DAVID_sushi: von Willebrand factor type A: EGF and pentraxin domain containing 1	NM_153366	PAP45	128	33.6%	chr9	112209843	NM_153366	c.7858G>T	p.D2620Y
SNAP91	DAVID_synaptosomal-associated protein: 91kDa homolog (mouse)	NM_014841	PAP45	46	23.9%	chr6	84425526	NM_014841	c.457G>A	p.D153N
SNAP91	DAVID_synaptosomal-associated protein: 91kDa homolog (mouse)	NM_014841	PAP45	35	28.6%	chr6	84474332	NM_014841	c.34G>A	p.A12T
SYT16	DAVID_synaptotagmin XVI	NM_031914	PAP45	507	23.1%	chr14	61617732	NM_031914	c.1421G>T	p.R474I
SSX7	DAVID_synovial sarcoma: X breakpoint 7	ENSG00000204368	PAP45	67	20.9%	chrX	52694038	CCDS14343.1	c.464C>A	p.S155Y
TRAV23DV6	DAVID_T cell receptor alpha variable 23/delta variable 6	ENSG00000211803	PAP45	231	12.6%	chr14	21624894	ENST00000390451	c.180C>A	p.Y60X
TRAV38-2D	DAVID_T cell receptor alpha variable 38-2/delta variable 8	ENSG00000211817	PAP45	257	23.3%	chr14	21819306	ENST00000390465	c.184A>C	p.S62R
TRAV8-6	DAVID_T cell receptor alpha variable 8-6	ENSG00000211795	PAP45	327	25.1%	chr14	21516793	ENST00000390443	c.35NULL>T	p.NULL-1FsIns1bp
TRBV4-2	DAVID_T cell receptor beta variable 4-2	ENSG00000211708	PAP45	195	22.1%	chr7	141692266	ENST00000390355	c.322T>C	p.Y108H
Trdv3	DAVID_T cell receptor delta variable 3	ENSG00000211830	PAP45	77	24.7%	chr14	22008058	ENST00000390478	c.156C>A	p.F52L
TBC1D8	DAVID_TBC1 domain family: member 8 (with GRAM domain)	NM_001102426	PAP45	76	19.7%	chr2	101020559	NM_001102426	c.1274G>T	p.R425I
TEAD3	DAVID_TEA domain family member 3	NM_003214	PAP45	121	20.7%	chr6	35556108	NM_003214	c.289C>A	p.L97I
TNXB	DAVID_tenascin XB; tenascin XA pseudogene	NM_019105	PAP45	41	29.3%	chr6	32132374	NM_019105	c.8110C>T	p.R2704C
TNXA	DAVID_tenascin XB; tenascin XA pseudogene	NM_019105	PAP45	41	29.3%	chr6	32132374	NM_019105	c.8110C>T	p.R2704C
TNXB	DAVID_tenascin XB; tenascin XA pseudogene	NM_019105	PAP45	41	29.3%	chr6	32132374	NM_019105	c.8110C>T	p.R2704C
TNXA	DAVID_tenascin XB; tenascin XA pseudogene	NM_019105	PAP45	41	29.3%	chr6	32132374	NM_019105	c.8110C>T	p.R2704C
TNXB	DAVID_tenascin XB; tenascin XA pseudogene	NM_019105	PAP45	41	29.3%	chr6	32132374	NM_019105	c.8110C>T	p.R2704C
TNXA	DAVID_tenascin XB; tenascin XA pseudogene	NM_019105	PAP45	41	29.3%	chr6	32132374	NM_019105	c.8110C>T	p.R2704C
TSGA10IP	DAVID_testis specific: 10 interacting protein	NM_152762	PAP45	242	10.7%	chr11	65471155	NM_152762	c.-1A>G	p.IVS2-2-1SpliceAcceptor
TSGA10IP	DAVID_testis specific: 10 interacting protein	NM_152762	PAP45	290	16.9%	chr11	65471384	NM_152762	c.512C>T	p.A171V
TET2	DAVID_tet oncogene family member 2	NM_001127208	PAP45	108	29.6%	chr4	106413333	NM_001127208	c.4346C>A	p.S1449Y
TTC39A	DAVID_tetratricopeptide repeat domain 39A	NM_001144832	PAP45	235	26.0%	chr1	51551197	NM_001144832	c.165G>T	p.K55N
TANC2	DAVID_tetratricopeptide repeat: ankyrin repeat and coiled-coil containing 2	NM_025185	PAP45	222	22.5%	chr17	58669075	NM_025185	c.716T>G	p.L239R
TOP2B	DAVID_topoisomerase (DNA) II beta 180kDa	NM_001068	PAP45	240	21.3%	chr3	25615971	NM_001068	c.4654G>A	p.D1552N
TNIK	DAVID_TRAF2 and NCK interacting kinase	NM_015028	PAP45	76	18.4%	chr3	172324136	NM_015028	c.2063C>T	p.S688F
TBL1XR1	DAVID_transducin (beta)-like 1 X-linked receptor 1	NM_024665	PAP45	145	17.2%	chr3	178252034	NM_024665	c.379G>T	p.G127X
TLE3	DAVID_transducin-like enhancer of split 3 (E(sp1) homolog: Drosophila)	NM_005078	PAP45	93	20.4%	chr15	68138130	NM_005078	c.844G>T	p.D282Y
tgfbi	DAVID_transforming growth factor: beta-induced: 68kDa	NM_000358	PAP45	92	28.3%	chr5	135410902	NM_000358	c.665A>G	p.H222R
TM4SF4	DAVID_transmembrane 4 L six family member 4	NM_004617	PAP45	149	25.5%	chr3	150703170	NM_004617	c.609A>C	p.X203Y
Tmco7	DAVID_transmembrane and coiled-coil domains 7	NM_024562	PAP45	498	25.3%	chr16	67451525	NM_024562	c.332G>A	p.R111H
TMC3	DAVID_transmembrane channel-like 3	NM_001080532	PAP45	352	27.3%	chr15	79414290	NM_001080532	c.2285C>T	p.S762L
TMC3	DAVID_transmembrane channel-like 3	NM_001080532	PAP45	324	10.5%	chr15	79437835	NM_001080532	c.563C>T	p.S188L
TMEM131	DAVID_transmembrane protein 131	NM_015348	PAP45	77	14.3%	chr2	97780365	NM_015348	c.2765G>A	p.R922Q

TMEM216	DAVID_transmembrane protein 216	NM_016499	PAP45	104	19.2%	chr11	60918012	NM_016499	c.34C>T	p.R12C
TRIM15	DAVID_tripartite motif-containing 15	ENSG00000204610	PAP45	80	16.3%	chr6	30246295	CCDS4677.1	c.770C>A	p.S257Y
Trim31	DAVID_tripartite motif-containing 31	ENSG00000204616	PAP45	150	33.3%	chr6	30188168	CCDS34374.1	c.394G>A	p.E132K
TRIM75	DAVID_tripartite motif-containing 75	NM_001105575	PAP45	216	20.8%	chr4	166200678	NM_001105575	c.929C>A	p.S310Y
TRIM77	DAVID_tripartite motif-containing 77	NM_001146162	PAP45	123	11.4%	chr11	89087991	NM_001146162	c.756G>T	p.M252I
tuba4b	DAVID_tubulin: alpha 4b (pseudogene)	ENSG00000163526	PAP45	550	23.5%	chr2	219844414	ENST00000295766	c.475G>A	p.E159K
SR140	DAVID_U2-associated SR140 protein	NM_001080415	PAP45	251	20.7%	chr3	144230101	NM_001080415	c.1533C>A	p.Y511X
USP50	DAVID_ubiquitin specific peptidase 50	NM_203494	PAP45	74	23.0%	chr15	48620564	NM_203494	c.649C>A	p.P217T
B3GALT4	DAVID_UDP-Gal:betaGlcNAc beta 1:3-galactosyltransferase: polypeptide 4	ENSG00000204222	PAP45	188	20.2%	chr6	33354285	CCDS34425.1	c.1111C>T	p.R371X
UNC13A	DAVID_unc-13 homolog A (C. elegans)	NM_001080421	PAP45	308	26.9%	chr19	17604950	NM_001080421	c.3532C>A	p.L1178M
Unc13c	DAVID_unc-13 homolog C (C. elegans)	NM_001080534	PAP45	76	26.3%	chr15	52092959	NM_001080534	c.567G>T	p.K189N
Unc13c	DAVID_unc-13 homolog C (C. elegans)	NM_001080534	PAP45	121	23.1%	chr15	52093635	NM_001080534	c.1243G>T	p.E415X
Unc13c	DAVID_unc-13 homolog C (C. elegans)	NM_001080534	PAP45	171	25.1%	chr15	52094674	NM_001080534	c.2282G>A	p.R761Q
Unc13c	DAVID_unc-13 homolog C (C. elegans)	NM_001080534	PAP45	159	24.5%	chr15	52095292	NM_001080534	c.2900G>T	p.R967I
Unc13c	DAVID_unc-13 homolog C (C. elegans)	NM_001080534	PAP45	80	23.8%	chr15	52494554	NM_001080534	c.4930G>T	p.E1644X
Unc13c	DAVID_unc-13 homolog C (C. elegans)	NM_001080534	PAP45	56	17.9%	chr15	52647357	NM_001080534	c.6026C>A	p.S2009Y
Unkl	DAVID_unkempt homolog (Drosophila)-like	ENSG00000059145	PAP45	85	28.2%	chr16	1387239	ENST00000397462	c.1102G>A	p.D368N
UPK3B	DAVID_uroplakin 3B	ENSG00000135180	PAP45	58	20.7%	chr7	75982370	CCDS5588.1	c.829G>T	p.D277Y
WDR19	DAVID_WD repeat domain 19	NM_025132	PAP45	132	22.0%	chr4	38910195	NM_025132	c.2161C>A	p.L721I
DCAF8L2	DAVID_WD repeat domain 42C	NM_001136533	PAP45	138	28.3%	chrX	27675180	NM_001136533	c.247G>A	p.E83K
WDR87	DAVID_WD repeat domain 87	NM_031951	PAP45	252	26.6%	chr19	43071863	NM_031951	c.4171G>T	p.E1391X
WDR87	DAVID_WD repeat domain 87	NM_031951	PAP45	243	23.5%	chr19	43072145	NM_031951	c.3889G>A	p.E1297K
WDR87	DAVID_WD repeat domain 87	NM_031951	PAP45	237	28.7%	chr19	43072149	NM_031951	c.3885G>T	p.K1295N
YLPM1	DAVID_YLP motif containing 1	NM_019589	PAP45	91	27.5%	chr14	74348100	NM_019589	c.5253A>T	p.K1751N
YLPM1	DAVID_YLP motif containing 1	NM_019589	PAP45	88	13.6%	chr14	74353143	NM_019589	c.5682G>T	p.K1894N
ZBTB47	DAVID_zinc finger and BTB domain containing 47	NM_145166	PAP45	85	29.4%	chr3	42678067	NM_145166	c.1560C>A	p.F520L
ZSCAN12	DAVID_zinc finger and SCAN domain containing 12	NM_001163391	PAP45	162	16.0%	chr6	28467130	NM_001163391	c.916G>T	p.E306X
Zc3h12b	DAVID_zinc finger CCCH-type containing 12B	NM_001010888	PAP45	114	22.8%	chrX	64633795	NM_001010888	c.634C>A	p.L212I
Zc3h12b	DAVID_zinc finger CCCH-type containing 12B	NM_001010888	PAP45	128	18.8%	chrX	64633855	NM_001010888	c.694C>T	p.R232C
Zc3h12b	DAVID_zinc finger CCCH-type containing 12B	NM_001010888	PAP45	56	23.2%	chrX	64636542	NM_001010888	c.1005C>A	p.F335L
ZNF674	DAVID_zinc finger family member 674	NM_001039891	PAP45	184	19.6%	chrX	46244318	NM_001039891	c.1650G>T	p.E550D
ZNF674	DAVID_zinc finger family member 674	NM_001039891	PAP45	193	26.4%	chrX	46244502	NM_001039891	c.1466G>T	p.R489I
ZNF788	DAVID_zinc finger family member 788	ENSG00000188474	PAP45	103	18.4%	chr19	12083744	ENST00000339302	c.382C>T	p.R128X
ZNF788	DAVID_zinc finger family member 788	ENSG00000188474	PAP45	103	20.4%	chr19	12083856	ENST00000339302	c.494C>T	p.A165V
ZFHX4	DAVID_zinc finger homeobox 4	NM_024721	PAP45	424	25.5%	chr8	77780718	NM_024721	c.1840G>A	p.E614K
ZFHX4	DAVID_zinc finger homeobox 4	NM_024721	PAP45	100	26.0%	chr8	77925744	NM_024721	c.3897G>T	p.K1299N
ZFHX4	DAVID_zinc finger homeobox 4	NM_024721	PAP45	195	14.4%	chr8	77926378	NM_024721	c.4531C>A	p.L1511I
ZNF185	DAVID_zinc finger protein 185 (LIM domain)	NM_007150	PAP45	142	26.8%	chrX	151841949	NM_007150	c.767G>A	p.R256Q
znf292	DAVID_zinc finger protein 292	NM_015021	PAP45	187	31.0%	chr6	88023385	NM_015021	c.3319C>T	p.R1107X
ZNF311	DAVID_zinc finger protein 311	ENSG00000197935	PAP45	193	27.5%	chr6	29071887	CCDS34357.1	c.871T>G	p.S291A
ZNF432	DAVID_zinc finger protein 432	ENSG00000221897	PAP45	98	20.4%	chr19	57229986	CCDS12848.1	c.758G>T	p.R253I
ZNF432	DAVID_zinc finger protein 432	ENSG00000221897	PAP45	153	21.6%	chr19	57230056	CCDS12848.1	c.688G>T	p.E230X
ZNF564	DAVID_zinc finger protein 564	ENSG00000220949	PAP45	122	17.2%	chr19	12498936	CCDS42505.1	c.986G>T	p.R329I
ZFP57	DAVID_zinc finger protein 57 homolog (mouse)	ENSG00000204644	PAP45	511	18.8%	chr6	29748508	CCDS43436.1	c.1299G>T	p.E433D
ZNF654	DAVID_zinc finger protein 654	NM_018293	PAP45	206	25.7%	chr3	88272108	NM_018293	c.958C>A	p.Q320K
ZNF654	DAVID_zinc finger protein 654	NM_018293	PAP45	142	26.8%	chr3	88272184	NM_018293	c.1034C>A	p.S345X
ZNF766	DAVID_zinc finger protein 766	NM_001010851	PAP45	197	17.3%	chr19	57485912	NM_001010851	c.1056G>T	p.E352D
ZNF778	DAVID_zinc finger protein 778	NM_182531	PAP45	312	25.0%	chr16	87821434	NM_182531	c.1153C>T	p.R385X
ZNF780B	DAVID_zinc finger protein 780B	NM_001005851	PAP45	60	21.7%	chr19	45232907	NM_001005851	c.1699C>T	p.R567C
ZNF818P	DAVID_zinc finger protein 818 pseudogene	ENSG00000204597	PAP45	114	14.9%	chr19	58408324	ENST00000344759	c.274C>A	p.H92N
ZNF835	DAVID_zinc finger protein 835	NM_001005850	PAP45	131	26.7%	chr19	61867990	NM_001005850	c.455G>T	p.R152I
ZNF836	DAVID_zinc finger protein 836	NM_001102657	PAP45	241	16.2%	chr19	57350359	NM_001102657	c.2389C>T	p.R797W
ZNF841	DAVID_zinc finger protein 841	NM_001136499	PAP45	182	10.4%	chr19	57261937	NM_001136499	c.1010G>T	p.R337I

ZNF841	DAVID_zinc finger protein 841	NM_001136499	PAP45	207	18.8%	chr19	57262442	NM_001136499	c.505C>T	p.R169X
ZNF844	DAVID_zinc finger protein 844	NM_001136501	PAP45	102	32.4%	chr19	12047573	NM_001136501	c.638T>G	p.L213R
ZFP92	DAVID_zinc finger protein 92 homolog (mouse)	ENSG00000189420	PAP45	220	10.5%	chrX	152339442	ENST00000338647	c.413C>T	p.S138L
ZNF732	DAVID_zinc finger protein LOC654254	NM_001137608	PAP45	53	24.5%	chr4	254913	NM_001137608	c.1730A>C	p.K577T
ZDBF2	DAVID_zinc finger: DBF-type containing 2	NM_020923	PAP45	120	28.3%	chr2	206877822	NM_020923	c.325G>A	p.E109K
ZDBF2	DAVID_zinc finger: DBF-type containing 2	NM_020923	PAP45	165	13.9%	chr2	206878166	NM_020923	c.669A>C	p.K223N
ZDBF2	DAVID_zinc finger: DBF-type containing 2	NM_020923	PAP45	171	23.4%	chr2	206878521	NM_020923	c.1024G>T	p.E342X
ZDBF2	DAVID_zinc finger: DBF-type containing 2	NM_020923	PAP45	105	27.6%	chr2	206879367	NM_020923	c.1870G>T	p.A624S
ZDBF2	DAVID_zinc finger: DBF-type containing 2	NM_020923	PAP45	105	24.8%	chr2	206880426	NM_020923	c.2929G>T	p.E977X
ZDBF2	DAVID_zinc finger: DBF-type containing 2	NM_020923	PAP45	86	20.9%	chr2	206881206	NM_020923	c.3709G>T	p.E1237X
ZDBF2	DAVID_zinc finger: DBF-type containing 2	NM_020923	PAP45	159	21.4%	chr2	206882578	NM_020923	c.5081G>T	p.R1694I
ZDBF2	DAVID_zinc finger: DBF-type containing 2	NM_020923	PAP45	145	20.0%	chr2	206882673	NM_020923	c.5176NULL>/	p.NULL-1FsIns1bp
ZDBF2	DAVID_zinc finger: DBF-type containing 2	NM_020923	PAP45	86	23.3%	chr2	206883988	NM_020923	c.6491G>T	p.R2164I
zmym2	DAVID_zinc finger: MYM-type 2	NM_197968	PAP45	63	31.7%	chr13	19536647	NM_197968	c.3094G>T	p.E1032X
Zswim6	DAVID_zinc finger: SWIM-type containing 6	NM_020928	PAP45	232	21.1%	chr5	60875766	NM_020928	c.3513C>A	p.F1171L
DZIP1	DAZ interacting protein 1	ENSG00000134874	PAP45	91	18.7%	chr13	95049664	CCDS9478.1	c.1493C>T	p.S498L
DZIP1	DAZ interacting protein 1	ENSG00000134874	PAP45	92	19.6%	chr13	95083497	CCDS9478.1	c.677C>A	p.S226Y
DZIP1L	DAZ interacting protein 1-like	ENSG00000158163	PAP45	56	23.2%	chr3	139299307	CCDS3096.1	c.574G>A	p.V192M
DCUN1D5	DCN1; defective in cullin neddylation 1; domain containing 5 (S. cerevisiae)	ENSG00000137692	PAP45	182	21.4%	chr11	102465228	CCDS8325.1	c.116T>A	p.L39Q
DCP2	DCP2 decapping enzyme homolog (S. cerevisiae)	ENSG00000172795	PAP45	89	27.0%	chr5	112371631	CCDS34210.1	c.1040C>A	p.S347Y
DCAF13	DDB1 and CUL4 associated factor 13	ENSG00000164934	PAP45	86	16.3%	chr8	104517163	CCDS34934.1	c.1375C>T	p.R459X
DCAF5	DDB1 and CUL4 associated factor 5	ENSG00000139990	PAP45	170	25.9%	chr14	68591183	CCDS32106.1	c.1973G>A	p.R658Q
DCAF5	DDB1 and CUL4 associated factor 5	ENSG00000139990	PAP45	112	21.4%	chr14	68598931	CCDS32106.1	c.997C>T	p.R333X
DCAF7	DDB1 and CUL4 associated factor 7	ENSG00000136485	PAP45	103	29.1%	chr17	59014743	ENST00000310827	c.673C>T	p.R225C
DDHD2	DDHD domain containing 2	ENSG00000085788	PAP45	269	10.0%	chr8	38218986	CCDS34883.1	c.774A>C	p.E258D
DDX19A	DEAD (Asp-Glu-Ala-As) box polypeptide 19A	ENSG00000168872	PAP45	349	10.9%	chr16	68952885	CCDS10889.1	c.357G>T	p.E119D
DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	ENSG00000174243	PAP45	60	26.7%	chr12	47517999	CCDS8770.1	c.612G>T	p.K204N
DDX25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	ENSG00000109832	PAP45	98	25.5%	chr11	125286567	NM_013264	c.774C>A	p.F258L
DDX4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	ENSG00000152670	PAP45	163	43.6%	chr5	55091806	CCDS3969.1	c.149G>A	p.R50Q
DDX4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	ENSG00000152670	PAP45	165	17.6%	chr5	55091809	CCDS3969.1	c.152G>T	p.R51I
DDX4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	ENSG00000152670	PAP45	82	18.3%	chr5	55099483	CCDS3969.1	c.352G>A	p.E118K
DDX42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	ENSG00000198231	PAP45	82	28.0%	chr17	59223530	CCDS32704.1	c.248C>A	p.S83Y
DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	ENSG00000145833	PAP45	38	31.6%	chr5	134141168	CCDS34240.1	c.619G>A	p.E207K
DDX47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	ENSG00000213782	PAP45	120	25.8%	chr12	12866895	CCDS8655.1	c.595C>T	p.R199W
DDX49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	ENSG00000105671	PAP45	109	22.0%	chr19	18899798	CCDS12390.1	c.1216G>A	p.E406K
DDX5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	ENSG00000108654	PAP45	138	27.5%	chr17	59927144	CCDS11659.1	c.1426G>A	p.E476K
DDX53	DEAD (Asp-Glu-Ala-Asp) box polypeptide 53	ENSG00000184735	PAP45	192	25.5%	chrX	22928924	CCDS35214.1	c.829C>A	p.L277I
DDX56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	ENSG00000136271	PAP45	225	26.2%	chr7	44577774	CCDS5492.1	c.732A>C	p.K244N
DDX6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	ENSG00000110367	PAP45	57	24.6%	chr11	118132230	NM_004397	c.1123C>T	p.R375C
DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	ENSG00000137628	PAP45	108	21.3%	chr4	169433134	CCDS34097.1	c.2241G>T	p.L747F
DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	ENSG00000137628	PAP45	91	30.8%	chr4	169464300	CCDS34097.1	c.411G>T	p.E137D
DDX26B	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	ENSG00000165359	PAP45	118	15.3%	chrX	134534553	CCDS35401.1	c.1435G>T	p.E479X
DHX38	DEAH (Asp-Glu-Ala-His) box polypeptide 38	ENSG00000140829	PAP45	134	23.1%	chr16	70695445	CCDS10907.1	c.1924G>A	p.D642N
DHX38	DEAH (Asp-Glu-Ala-His) box polypeptide 38	ENSG00000140829	PAP45	225	24.4%	chr16	70697001	CCDS10907.1	c.2464G>A	p.D822N
DHX40	DEAH (Asp-Glu-Ala-His) box polypeptide 40	ENSG00000108406	PAP45	68	16.2%	chr17	55034756	CCDS11617.1	c.1898G>A	p.R633Q
DHX8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	ENSG00000067596	PAP45	175	19.4%	chr17	38924131	CCDS11464.1	c.380A>G	p.N127S
DHX8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	ENSG00000067596	PAP45	193	23.8%	chr17	38926601	CCDS11464.1	c.1033G>T	p.D345Y
DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	ENSG00000135829	PAP45	113	14.2%	chr1	181102289	CCDS41444.1	c.1420C>T	p.R474X
DQX1	DEAQ box RNA-dependent ATPase 1	ENSG00000144045	PAP45	375	27.2%	chr2	74604695	CCDS1949.1	c.325G>T	p.E109X
DOCK10	dedicator of cytokinesis 10	ENSG00000135905	PAP45	52	26.9%	chr2	225426082	NM_014689	c.1890T>G	p.N630K
DOCK10	dedicator of cytokinesis 10	ENSG00000135905	PAP45	116	18.1%	chr2	225519903	ENST00000409802	c.10C>T	p.R4X
DOCK11	dedicator of cytokinesis 11	ENSG00000147251	PAP45	89	20.2%	chrX	117563335	CCDS35373.1	c.414G>T	p.K138N

DOCK11	dedicator of cytokinesis 11	ENSG00000147251	PAP45	140	21.4%	chrX	117563378	CCDS35373.1	c.457G>T	p.D153Y
DOCK11	dedicator of cytokinesis 11	ENSG00000147251	PAP45	84	25.0%	chrX	117579448	CCDS35373.1	c.633G>T	p.E211D
DOCK2	dedicator of cytokinesis 2	ENSG00000134516	PAP45	191	19.4%	chr5	169400659	CCDS4371.1	c.3688C>A	p.L1230I
DOCK2	dedicator of cytokinesis 2	ENSG00000134516	PAP45	259	22.0%	chr5	169427261	CCDS4371.1	c.4637A>G	p.Y1546C
DOCK3	dedicator of cytokinesis 3	ENSG00000088538	PAP45	127	18.1%	chr3	51238233	ENST00000402669	c.1366G>T	p.E456X
DOCK3	dedicator of cytokinesis 3	ENSG00000088538	PAP45	147	12.9%	chr3	51393639	ENST00000402669	c.5702T>G	p.F1901C
DOCK5	dedicator of cytokinesis 5	ENSG00000147459	PAP45	71	25.4%	chr8	25321579	CCDS6047.1	c.5257G>A	p.D1753N
DOCK7	dedicator of cytokinesis 7	ENSG00000116641	PAP45	97	19.6%	chr1	62857017	CCDS30734.1	c.1630G>T	p.E544X
DOCK8	dedicator of cytokinesis 8	ENSG00000107099	PAP45	100	31.0%	chr9	453592	CCDS6440.1	c.5940G>T	p.K1980N
DEGS1	degenerative spermatocyte homolog 1; lipid desaturase (Drosophila)	ENSG00000143753	PAP45	172	28.5%	chr1	222444527	CCDS1540.1	c.708C>A	p.F236L
DHRS2	dehydrogenase/reductase (SDR family) member 2	ENSG00000100867	PAP45	553	24.2%	chr14	23178867	CCDS41927.1	c.343G>A	p.D115N
DHRS7	dehydrogenase/reductase (SDR family) member 7	ENSG00000100612	PAP45	150	29.3%	chr14	59690513	CCDS9743.1	c.310G>T	p.D104Y
DHRS7	dehydrogenase/reductase (SDR family) member 7	ENSG00000100612	PAP45	154	19.5%	chr14	59690519	CCDS9743.1	c.304G>T	p.E102X
DBC1	deleted in bladder cancer 1	ENSG00000078725	PAP45	149	26.8%	chr9	121051164	CCDS6822.1	c.304C>A	p.Q102K
DCC	deleted in colorectal carcinoma	ENSG00000187323	PAP45	81	14.8%	chr18	48705657	CCDS11952.1	c.904G>T	p.D302Y
DCC	deleted in colorectal carcinoma	ENSG00000187323	PAP45	48	27.1%	chr18	49086015	CCDS11952.1	c.1981C>T	p.R661X
DNER	delta/notch-like EGF repeat containing	ENSG00000187957	PAP45	351	30.8%	chr2	230164689	CCDS33390.1	c.436G>A	p.E146K
DLL1	delta-like 1 (Drosophila)	ENSG00000198719	PAP45	172	16.3%	chr6	170434410	CCDS5313.1	c.1882G>A	p.D628N
DENND1A	DENN/MADD domain containing 1A	ENSG00000119522	PAP45	121	24.0%	chr9	125681109	CCDS35133.1	c.30G>T	p.E10D
DENND2A	DENN/MADD domain containing 2A	ENSG00000146966	PAP45	47	23.4%	chr7	139906024	CCDS43659.1	c.1842C>A	p.F614L
DENND3	DENN/MADD domain containing 3	ENSG00000105339	PAP45	66	22.7%	chr8	142245478	CCDS34947.1	c.1321G>T	p.G441X
DENND3	DENN/MADD domain containing 3	ENSG00000105339	PAP45	588	20.2%	chr8	142247329	CCDS34947.1	c.1558G>A	p.E520K
DENND3	DENN/MADD domain containing 3	ENSG00000105339	PAP45	89	13.5%	chr8	142255956	CCDS34947.1	c.2380G>A	p.E794K
DSPP	dentin sialophosphoprotein	ENSG00000152591	PAP45	106	18.9%	chr4	88753983	CCDS43248.1	c.1145G>A	p.S382N
DNTTIP1	deoxynucleotidyltransferase; terminal; interacting protein 1	ENSG00000101457	PAP45	254	21.7%	chr20	43873174	CCDS13369.1	c.923G>T	p.R308I
DEPDC5	DEP domain containing 5	ENSG00000100150	PAP45	160	23.8%	chr22	30492645	CCDS43006.1	c.354G>T	p.K118N
DEPDC5	DEP domain containing 5	ENSG00000100150	PAP45	53	26.4%	chr22	30569186	CCDS43006.1	c.2594G>A	p.R865Q
DSC2	desmocollin 2	ENSG00000134755	PAP45	111	22.5%	chr18	26925075	CCDS11892.1	c.388C>A	p.L130I
DSG2	desmoglein 2	ENSG00000046604	PAP45	159	30.8%	chr18	27376803	CCDS42423.1	c.2324A>G	p.Y775C
DSG3	desmoglein 3 (pemphigus vulgaris antigen)	ENSG00000134757	PAP45	273	22.3%	chr18	27300538	CCDS11898.1	c.1459G>A	p.D487N
DSG4	desmoglein 4	ENSG00000175065	PAP45	72	29.2%	chr18	27222935	CCDS11897.1	c.473C>T	p.S158L
DSG4	desmoglein 4	ENSG00000175065	PAP45	90	17.8%	chr18	27237473	CCDS11897.1	c.1514G>A	p.C505Y
DHX58	DEXH (Asp-Glu-X-His) box polypeptide 58	ENSG00000108771	PAP45	105	21.0%	chr17	37509152	CCDS11416.1	c.1754C>T	p.S585L
DGKA	diacylglycerol kinase; alpha 80kDa	ENSG00000065357	PAP45	107	21.5%	chr12	54632852	CCDS8896.1	c.1811G>T	p.S604I
DGKB	diacylglycerol kinase; beta 90kDa	ENSG00000136267	PAP45	92	20.7%	chr7	14580469	NM_004080	c.1666G>T	p.E556X
DGKB	diacylglycerol kinase; beta 90kDa	ENSG00000136267	PAP45	70	27.1%	chr7	14724799	NM_004080	c.359G>A	p.R120Q
DGKD	diacylglycerol kinase; delta 130kDa	ENSG00000077044	PAP45	106	15.1%	chr2	234031777	CCDS2504.1	c.2689G>A	p.A897T
DGKD	diacylglycerol kinase; delta 130kDa	ENSG00000077044	PAP45	234	22.6%	chr2	234040502	CCDS2504.1	c.3338G>A	p.R1113H
DGKH	diacylglycerol kinase; eta	ENSG00000102780	PAP45	98	15.3%	chr13	41627474	CCDS9381.1	c.432G>T	p.K144N
DGKG	diacylglycerol kinase; gamma 90kDa	ENSG00000058866	PAP45	36	27.8%	chr3	187460988	CCDS3274.1	c.1358G>A	p.R453Q
DGKG	diacylglycerol kinase; gamma 90kDa	ENSG00000058866	PAP45	207	27.1%	chr3	187489276	CCDS3274.1	c.461C>T	p.S154L
DGKI	diacylglycerol kinase; iota	ENSG00000157680	PAP45	105	28.6%	chr7	136944846	CCDS5845.1	c.1043G>T	p.R348I
DGKQ	diacylglycerol kinase; theta 110kDa	ENSG00000145214	PAP45	72	30.6%	chr4	944931	CCDS3342.1	c.2633G>A	p.R878Q
DAGLB	diacylglycerol lipase; beta	ENSG00000164535	PAP45	127	33.9%	chr7	6416506	CCDS5350.1	c.1600G>A	p.E534K
DAGLB	diacylglycerol lipase; beta	ENSG00000164535	PAP45	69	23.2%	chr7	6430974	CCDS5350.1	c.1074T>G	p.F358L
DIAPH2	diaphanous homolog 2 (Drosophila)	ENSG00000147202	PAP45	68	17.6%	chrX	96072419	CCDS14467.1	c.1010T>C	p.V337A
DIAPH3	diaphanous homolog 3 (Drosophila)	ENSG00000139734	PAP45	102	26.5%	chr13	59584281	CCDS41898.1	c.254A>T	p.K85I
DMBX1	diencephalon/mesencephalon homeobox 1	ENSG00000197587	PAP45	374	25.7%	chr1	46750463	CCDS536.1	c.844G>A	p.E282K
DPCR1	diffuse panbronchiolitis critical region 1	ENSG00000168631	PAP45	150	25.3%	chr6	31028752	CCDS4692.1	c.587G>A	p.R196H
DGCR6	DiGeorge syndrome critical region gene 6	ENSG00000183628	PAP45	117	26.5%	chr22	17278448	CCDS13753.1	c.420G>T	p.K140N
DPYSL4	dihydropyrimidinase-like 4	ENSG00000151640	PAP45	97	25.8%	chr10	133866252	CCDS7665.1	c.1394C>T	p.A465V
DPYD	dihydropyrimidine dehydrogenase	ENSG00000188641	PAP45	203	29.1%	chr1	97543426	CCDS30777.1	c.2276G>A	p.R759Q

DPYD	dihydropyrimidine dehydrogenase	ENSG00000188641	PAP45	48	20.8%	chr1	97620606	CCDS30777.1	c.-1G>T	p.IVS14-1-1SpliceAcceptor
DIP2B	DIP2 disco-interacting protein 2 homolog B (Drosophila)	ENSG00000066084	PAP45	228	32.9%	chr12	49320861	CCDS31799.1	c.260G>A	p.R87Q
DIP2B	DIP2 disco-interacting protein 2 homolog B (Drosophila)	ENSG00000066084	PAP45	203	29.6%	chr12	49320896	CCDS31799.1	c.295C>T	p.R99X
DPP4	dipeptidyl-peptidase 4	ENSG00000197635	PAP45	92	21.7%	chr2	162583509	CCDS2216.1	c.1396A>G	p.K466E
DPP4	dipeptidyl-peptidase 4	ENSG00000197635	PAP45	139	21.6%	chr2	162600000	CCDS2216.1	c.694G>T	p.E232X
DPP8	dipeptidyl-peptidase 8	ENSG00000074603	PAP45	62	16.1%	chr15	63567105	CCDS10207.1	c.979G>A	p.D327N
DIRAS2	DIRAS family; GTP-binding RAS-like 2	ENSG00000165023	PAP45	348	15.8%	chr9	92415360	CCDS6687.1	c.570G>T	p.E190D
DIS3	DIS3 mitotic control homolog (S. cerevisiae)	ENSG00000083520	PAP45	124	32.3%	chr13	72244315	CCDS9447.1	c.1486G>A	p.E496K
DIS3	DIS3 mitotic control homolog (S. cerevisiae)	ENSG00000083520	PAP45	94	20.2%	chr13	72247472	CCDS9447.1	c.865G>A	p.E289K
DIS3L	DIS3 mitotic control homolog (S. cerevisiae)-like	ENSG00000166938	PAP45	217	21.7%	chr15	64405674	CCDS10214.1	c.1870C>T	p.R624C
DIS3L	DIS3 mitotic control homolog (S. cerevisiae)-like	ENSG00000166938	PAP45	44	34.1%	chr15	64412141	CCDS10214.1	c.2446G>T	p.G816C
DCBLD1	discoidin; CUB and LCCL domain containing 1	ENSG00000164465	PAP45	73	21.9%	chr6	117966681	CCDS34522.1	c.966G>T	p.K322N
DLG1	discs; large homolog 1 (Drosophila)	ENSG00000075711	PAP45	191	18.3%	chr3	198302210	CCDS3327.1	c.1730G>A	p.R577Q
DLG2	discs; large homolog 2 (Drosophila)	ENSG00000150672	PAP45	55	27.3%	chr11	84673995	NM_001142699	c.103G>A	p.E35K
DLG5	discs; large homolog 5 (Drosophila)	ENSG00000151208	PAP45	72	25.0%	chr10	79235615	CCDS7353.2	c.4978G>T	p.E1660X
DLG5	discs; large homolog 5 (Drosophila)	ENSG00000151208	PAP45	181	11.6%	chr10	79258711	CCDS7353.2	c.2224G>A	p.A742T
DISP1	dispatched homolog 1 (Drosophila)	ENSG00000154309	PAP45	323	28.8%	chr1	221244014	CCDS1536.1	c.2652G>T	p.E884D
DISC1	disrupted in schizophrenia 1	ENSG00000162946	PAP45	45	31.1%	chr1	229973312	CCDS31055.1	c.1507G>A	p.D503N
DLX5	distal-less homeobox 5	ENSG00000105880	PAP45	253	25.7%	chr7	96491760	CCDS5647.1	c.112C>T	p.P38S
DMXL1	Dmx-like 1	ENSG00000172869	PAP45	96	27.1%	chr5	118513713	CCDS4125.1	c.4292C>T	p.T1431M
DMXL1	Dmx-like 1	ENSG00000172869	PAP45	81	25.9%	chr5	118534338	CCDS4125.1	c.5953G>T	p.E1985X
DMXL2	Dmx-like 2	ENSG00000104093	PAP45	175	22.9%	chr15	49615223	CCDS10141.1	c.2365A>G	p.N789D
DNMT1	DNA (cytosine-5-)-methyltransferase 1	ENSG00000130816	PAP45	106	15.1%	chr19	10138282	CCDS12228.1	c.835G>T	p.D279Y
DNMT3B	DNA (cytosine-5-)-methyltransferase 3 beta	ENSG00000088305	PAP45	287	23.7%	chr20	30838797	CCDS13205.1	c.533A>C	p.H178P
DFFB	DNA fragmentation factor; 40kDa; beta polypeptide (caspase-activated DNase)	ENSG00000169598	PAP45	118	23.7%	chr1	3764045	CCDS52.1	c.18G>T	p.K6N
DRAM2	DNA-damage regulated autophagy modulator 2	ENSG00000156171	PAP45	98	19.4%	chr1	111462333	CCDS30801.1	c.773G>A	p.R258Q
DNAJA3	DnaJ (Hsp40) homolog; subfamily A; member 3	ENSG00000103423	PAP45	104	25.0%	chr16	4424498	CCDS10515.1	c.324G>T	p.E108D
DNAJA3	DnaJ (Hsp40) homolog; subfamily A; member 3	ENSG00000103423	PAP45	75	26.7%	chr16	4433065	CCDS10515.1	c.830G>T	p.R277I
DNAJA4	DnaJ (Hsp40) homolog; subfamily A; member 4	ENSG00000140403	PAP45	113	22.1%	chr15	76350037	CCDS10299.1	c.276C>A	p.F92L
DNAJA4	DnaJ (Hsp40) homolog; subfamily A; member 4	ENSG00000140403	PAP45	96	26.0%	chr15	76352553	CCDS10299.1	c.375G>T	p.K125N
DNAJB5	DnaJ (Hsp40) homolog; subfamily B; member 5	ENSG00000137094	PAP45	106	15.1%	chr9	34986292	CCDS35007.1	c.242G>T	p.G81V
DNAJC28	DnaJ (Hsp40) homolog; subfamily C; member 28	ENSG00000177692	PAP45	155	28.4%	chr21	33782642	CCDS13626.1	c.929G>T	p.R310L
DNAJC5B	DnaJ (Hsp40) homolog; subfamily C; member 5 beta	ENSG00000147570	PAP45	108	25.9%	chr8	67151516	CCDS6183.1	c.187G>T	p.E63X
DRD5	dopamine receptor D5	ENSG00000169676	PAP45	133	21.1%	chr4	9393946	CCDS3405.1	c.1195G>T	p.D399Y
DOPEY1	dopey family member 1	ENSG00000083097	PAP45	115	16.5%	chr6	83885402	CCDS4996.1	c.857G>A	p.R286Q
DOPEY2	dopey family member 2	ENSG00000142197	PAP45	163	23.3%	chr21	36505805	CCDS13643.1	c.766T>G	p.F256V
DOPEY2	dopey family member 2	ENSG00000142197	PAP45	91	17.6%	chr21	36517461	CCDS13643.1	c.1313C>A	p.S438Y
DOPEY2	dopey family member 2	ENSG00000142197	PAP45	44	31.8%	chr21	36575767	CCDS13643.1	c.6148C>T	p.P2050S
DOT1L	DOT1-like; histone H3 methyltransferase (S. cerevisiae)	ENSG00000104885	PAP45	65	30.8%	chr19	2177775	CCDS42460.1	c.4255G>A	p.D1419N
DCX	doublecortin	ENSG00000077279	PAP45	149	19.5%	chrX	110531141	CCDS14556.1	c.681G>A	p.W227X
DCLK1	doublecortin-like kinase 1	ENSG00000133083	PAP45	187	27.8%	chr13	35246746	ENST00000360631	c.2149G>A	p.E717K
DCLK3	doublecortin-like kinase 3	ENSG00000163673	PAP45	87	16.1%	chr3	36734577	CCDS43064.1	c.1681G>T	p.D561Y
DCLK3	doublecortin-like kinase 3	ENSG00000163673	PAP45	134	26.1%	chr3	36738147	CCDS43064.1	c.1460G>A	p.R487Q
DMRT2	doublesex and mab-3 related transcription factor 2	ENSG00000173253	PAP45	546	23.3%	chr9	1046545	CCDS6444.1	c.958G>T	p.E320X
DMRT2	doublesex and mab-3 related transcription factor 2	ENSG00000173253	PAP45	275	25.5%	chr9	1046885	CCDS6444.1	c.1298G>A	p.R433Q
DMRT2	doublesex and mab-3 related transcription factor 2	ENSG00000173253	PAP45	211	19.9%	chr9	1047076	CCDS6444.1	c.1489G>T	p.E497X
DMRT3	doublesex and mab-3 related transcription factor 3	ENSG00000064218	PAP45	304	11.5%	chr9	980705	CCDS6443.1	c.1119G>T	p.R373S
DSCAML1	Down syndrome cell adhesion molecule like 1	ENSG00000177103	PAP45	44	22.7%	chr11	116857140	CCDS8384.1	c.2795C>T	p.S932L
DYDC2	DPY30 domain containing 2	ENSG00000133665	PAP45	46	23.9%	chr10	82112252	CCDS7367.1	c.73C>T	p.R25W
DSN1	DSN1; MIND kinetochore complex component; homolog (S. cerevisiae)	ENSG00000149636	PAP45	62	16.1%	chr20	34833259	CCDS13286.1	c.17G>T	p.R6I

DSTYK	dual serine/threonine and tyrosine protein kinase	ENSG00000133059	PAP45	303	18.2%	chr1	203405428	CCDS1451.1	c.810G>T	p.K270N
DUSP21	dual specificity phosphatase 21	ENSG00000189037	PAP45	400	25.0%	chrX	44588540	CCDS14264.1	c.218T>C	p.V73A
DARC	Duffy blood group; chemokine receptor	ENSG00000213088	PAP45	337	24.6%	chr1	157441920	CCDS1183.1	c.67G>A	p.E23K
DARC	Duffy blood group; chemokine receptor	ENSG00000213088	PAP45	470	26.8%	chr1	157442549	CCDS1183.1	c.696G>T	p.K232N
DCTN4	dynactin 4 (p62)	ENSG00000132912	PAP45	323	26.0%	chr5	150070912	CCDS4310.1	c.1375C>A	p.L459I
DCTN6	dynactin 6	ENSG00000104671	PAP45	75	16.0%	chr8	30152190	CCDS6076.1	c.136G>A	p.G46R
DNM1	dynamin 1	ENSG00000106976	PAP45	477	30.8%	chr9	130024622	CCDS6895.1	c.1054G>A	p.D352N
DNMBP	dynamin binding protein	ENSG00000107554	PAP45	193	22.8%	chr10	101629595	CCDS7485.1	c.4511G>A	p.S1504N
DNMBP	dynamin binding protein	ENSG00000107554	PAP45	337	22.0%	chr10	101705201	CCDS7485.1	c.2020G>T	p.E674X
DNAH10	dynein; axonemal; heavy chain 10	ENSG00000197653	PAP45	425	24.9%	chr12	122982440	NM_207437	c.-1G>T	p.IVS74-1-1SpliceAcceptor
DNAH11	dynein; axonemal; heavy chain 11	ENSG00000105877	PAP45	126	23.0%	chr7	21696987	ENST00000409508	c.6025C>T	p.R2009X
DNAH11	dynein; axonemal; heavy chain 11	ENSG00000105877	PAP45	318	14.8%	chr7	21886969	ENST00000328843	c.12341C>A	p.P4114H
DNAH2	dynein; axonemal; heavy chain 2	ENSG00000183914	PAP45	120	26.7%	chr17	7602585	CCDS32551.1	c.2099G>A	p.R700H
DNAH2	dynein; axonemal; heavy chain 2	ENSG00000183914	PAP45	367	21.0%	chr17	7603626	CCDS32551.1	c.2610G>T	p.K870N
DNAH2	dynein; axonemal; heavy chain 2	ENSG00000183914	PAP45	492	24.4%	chr17	7668024	CCDS32551.1	c.11477C>T	p.S3826L
DNAH3	dynein; axonemal; heavy chain 3	ENSG00000158486	PAP45	142	20.4%	chr16	20938693	CCDS10594.1	c.-1G>A	p.IVS40-1-1SpliceAcceptor
DNAH3	dynein; axonemal; heavy chain 3	ENSG00000158486	PAP45	118	28.0%	chr16	21000486	CCDS10594.1	c.2941G>A	p.E981K
DNAH3	dynein; axonemal; heavy chain 3	ENSG00000158486	PAP45	188	26.6%	chr16	21005755	CCDS10594.1	c.2793G>T	p.K931N
DNAH5	dynein; axonemal; heavy chain 5	ENSG00000039139	PAP45	257	30.7%	chr5	13774196	CCDS3882.1	c.12192G>T	p.K4064N
DNAH5	dynein; axonemal; heavy chain 5	ENSG00000039139	PAP45	121	19.8%	chr5	13807448	CCDS3882.1	c.-1G>T	p.IVS61-1-1SpliceAcceptor
DNAH5	dynein; axonemal; heavy chain 5	ENSG00000039139	PAP45	177	21.5%	chr5	13876398	CCDS3882.1	c.6661G>T	p.E2221X
DNAH5	dynein; axonemal; heavy chain 5	ENSG00000039139	PAP45	121	27.3%	chr5	13924783	CCDS3882.1	c.3488G>A	p.S1163N
DNAH5	dynein; axonemal; heavy chain 5	ENSG00000039139	PAP45	270	24.4%	chr5	13976469	CCDS3882.1	c.358G>T	p.D120Y
DNAH7	dynein; axonemal; heavy chain 7	ENSG00000118997	PAP45	61	23.0%	chr2	196381759	CCDS42794.1	c.9975G>T	p.Q3325H
DNAH7	dynein; axonemal; heavy chain 7	ENSG00000118997	PAP45	269	25.3%	chr2	196437675	CCDS42794.1	c.6949C>T	p.R2317X
DNAH7	dynein; axonemal; heavy chain 7	ENSG00000118997	PAP45	138	10.1%	chr2	196445353	CCDS42794.1	c.6499C>A	p.L2167I
DNAH8	dynein; axonemal; heavy chain 8	ENSG00000124721	PAP45	52	25.0%	chr6	38867426	CCDS4838.1	c.2248G>T	p.E750X
DNAH8	dynein; axonemal; heavy chain 8	ENSG00000124721	PAP45	53	28.3%	chr6	38898603	CCDS4838.1	c.2884G>T	p.E962X
DNAH8	dynein; axonemal; heavy chain 8	ENSG00000124721	PAP45	192	26.0%	chr6	38975537	CCDS4838.1	c.8420G>A	p.R2807Q
DNAH8	dynein; axonemal; heavy chain 8	ENSG00000124721	PAP45	101	20.8%	chr6	38989629	CCDS4838.1	c.9235G>T	p.E3079X
DNAH8	dynein; axonemal; heavy chain 8	ENSG00000124721	PAP45	296	24.3%	chr6	39106046	CCDS4838.1	c.13373G>A	p.R4458Q
DNAH9	dynein; axonemal; heavy chain 9	ENSG00000007174	PAP45	121	33.9%	chr17	11452204	CCDS11160.1	c.451C>T	p.R151C
DNAH9	dynein; axonemal; heavy chain 9	ENSG00000007174	PAP45	67	28.4%	chr17	11463676	CCDS11160.1	c.1203G>T	p.L401F
DNAH9	dynein; axonemal; heavy chain 9	ENSG00000007174	PAP45	163	30.1%	chr17	11524776	CCDS11160.1	c.3588G>T	p.E1196D
DNAH9	dynein; axonemal; heavy chain 9	ENSG00000007174	PAP45	181	24.9%	chr17	11534044	CCDS11160.1	c.4180G>A	p.G1394S
DNAH9	dynein; axonemal; heavy chain 9	ENSG00000007174	PAP45	260	25.8%	chr17	11534414	CCDS11160.1	c.4550G>A	p.R1517Q
DNAH9	dynein; axonemal; heavy chain 9	ENSG00000007174	PAP45	223	26.9%	chr17	11776144	CCDS11160.1	c.12194G>A	p.R4065Q
DYSF	dysferlin; limb girdle muscular dystrophy 2B (autosomal recessive)	ENSG00000135636	PAP45	137	24.8%	chr2	71744993	CCDS1918.1	c.4974G>T	p.K1658N
DST	dystonin	ENSG00000151914	PAP45	68	38.2%	chr6	56600032	CCDS4959.1	c.3040G>A	p.E1014K
DST	dystonin	ENSG00000151914	PAP45	289	26.6%	chr6	56615481	CCDS4959.1	c.65G>A	p.R22Q
DTNA	dystrobrevin; alpha	ENSG00000134769	PAP45	200	18.5%	chr18	30646053	CCDS42425.1	c.581C>T	p.A194V
DMD	dystrophin	ENSG00000198947	PAP45	284	22.9%	chrX	31372659	CCDS14233.1	c.8944C>T	p.R2982X
DMD	dystrophin	ENSG00000198947	PAP45	83	28.9%	chrX	32144999	CCDS14233.1	c.6393A>C	p.Q2131H
DMD	dystrophin	ENSG00000198947	PAP45	100	31.0%	chrX	32270271	CCDS14233.1	c.5789G>A	p.R1930H
DMD	dystrophin	ENSG00000198947	PAP45	100	30.0%	chrX	32493752	CCDS14233.1	c.1980G>T	p.K660N
DMD	dystrophin	ENSG00000198947	PAP45	106	20.8%	chrX	32627196	CCDS14233.1	c.785A>C	p.K262T
EP400	E1A binding protein p400	ENSG00000183495	PAP45	60	21.7%	chr12	131057372	CCDS31929.1	c.3298G>A	p.E1100K

E2F1	E2F transcription factor 1	ENSG00000101412	PAP45	90	22.2%	chr20	31728201	CCDS13224.1	c.1312T>A	p.X438R
E2F6	E2F transcription factor 6	ENSG00000169016	PAP45	48	25.0%	chr2	11511315	CCDS1680.2	c.224T>G	p.F75C
ELF1	E74-like factor 1 (ets domain transcription factor)	ENSG00000120690	PAP45	141	22.7%	chr13	40415196	CCDS9374.1	c.698G>T	p.R233L
EGR1	early growth response 1	ENSG00000120738	PAP45	455	33.2%	chr5	137831646	CCDS4206.1	c.1609C>T	p.P537S
EVI5	ecotropic viral integration site 5	ENSG00000067208	PAP45	60	23.3%	chr1	92863980	CCDS30774.1	c.1579G>T	p.E527X
ENC1	ectodermal-neural cortex 1 (with BTB-like domain)	ENSG00000171617	PAP45	370	13.5%	chr5	73967112	CCDS4021.1	c.955G>T	p.E319X
ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	ENSG00000197594	PAP45	233	25.3%	chr6	132230956	CCDS5150.1	c.1114C>A	p.H372N
ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	ENSG00000197594	PAP45	74	24.3%	chr6	132247885	CCDS5150.1	c.2277G>T	p.E759D
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	ENSG00000136960	PAP45	103	21.4%	chr8	120675257	CCDS6329.1	c.1153G>A	p.D385N
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	ENSG00000136960	PAP45	217	23.0%	chr8	120719887	CCDS6329.1	c.95G>A	p.R32Q
ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	ENSG00000154269	PAP45	205	21.5%	chr6	132015429	CCDS5148.1	c.332G>A	p.S111N
EFCAB6	EF-hand calcium binding domain 6	ENSG00000186976	PAP45	106	27.4%	chr22	42335773	CCDS14049.1	c.2603G>A	p.R868Q
EFHC2	EF-hand domain (C-terminal) containing 2	ENSG00000183690	PAP45	107	22.4%	chrX	43976727	NM_025184	c.1564C>T	p.R522C
EFHC2	EF-hand domain (C-terminal) containing 2	ENSG00000183690	PAP45	115	15.7%	chrX	43993021	NM_025184	c.944C>T	p.A315V
EFHA1	EF-hand domain family; member A1	ENSG00000165487	PAP45	47	25.5%	chr13	20968279	CCDS9297.1	c.954C>A	p.F318L
EMR2	egf-like module containing; mucin-like; hormone receptor-like 2	ENSG00000127507	PAP45	404	22.3%	chr19	14737195	CCDS32935.1	c.843C>A	p.F281L
EHBP1	EH domain binding protein 1	ENSG00000115504	PAP45	159	24.5%	chr2	63036180	CCDS1872.1	c.2446G>T	p.E816X
EHBP1L1	EH domain binding protein 1-like 1	ENSG00000173442	PAP45	315	21.0%	chr11	65104290	NM_001099409	c.475C>T	p.R159W
EHD3	EH-domain containing 3	ENSG00000013016	PAP45	196	25.5%	chr2	31336945	CCDS1774.1	c.568G>A	p.D190N
ELAC1	elaC homolog 1 (E. coli)	ENSG00000141642	PAP45	219	21.5%	chr18	46764467	CCDS11949.1	c.161G>T	p.R54I
EMILIN2	elastin microfibril interfacer 2	ENSG00000132205	PAP45	127	26.0%	chr18	2880996	CCDS11828.1	c.871G>A	p.E291K
ELAVL2	ELAV (embryonic lethal; abnormal vision; Drosophila)-like 2 (Hu antigen B)	ENSG00000107105	PAP45	53	26.4%	chr9	23691431	CCDS6515.1	c.659A>C	p.Q220P
ELAVL2	ELAV (embryonic lethal; abnormal vision; Drosophila)-like 2 (Hu antigen B)	ENSG00000107105	PAP45	50	22.0%	chr9	23695025	CCDS6515.1	c.378T>G	p.N126K
ERC1	ELKS/RAB6-interacting/CAST family member 1	ENSG00000082805	PAP45	80	27.5%	chr12	1469554	CCDS8508.1	c.3248A>G	p.N1083S
EVC2	Ellis van Creveld syndrome 2	ENSG00000173040	PAP45	390	12.3%	chr4	5668103	CCDS3382.2	c.2776G>A	p.E926K
EMB	embigin homolog (mouse)	ENSG00000170571	PAP45	46	28.3%	chr5	49772718	CCDS3953.1	c.25G>A	p.E9K
ENAM	enamelin	ENSG00000132464	PAP45	149	28.2%	chr4	71727059	CCDS3544.1	c.1052G>T	p.R351I
ENAM	enamelin	ENSG00000132464	PAP45	157	22.9%	chr4	71728358	CCDS3544.1	c.2351G>T	p.R784I
ENAM	enamelin	ENSG00000132464	PAP45	114	22.8%	chr4	71729306	CCDS3544.1	c.3299C>A	p.A1100D
EDN3	endothelin 3	ENSG00000124205	PAP45	81	18.5%	chr20	57309994	CCDS13477.1	c.187G>A	p.E63K
ECE2	endothelin converting enzyme 2	ENSG00000145194	PAP45	131	23.7%	chr3	185478517	CCDS43179.1	c.727G>T	p.D243Y
ECE2	endothelin converting enzyme 2	ENSG00000145194	PAP45	160	29.4%	chr3	185485575	CCDS43179.1	c.1274G>A	p.R425H
ECE2	endothelin converting enzyme 2	ENSG00000145194	PAP45	61	16.4%	chr3	185490756	CCDS43179.1	c.1709C>A	p.S570Y
ECEL1	endothelin converting enzyme-like 1	ENSG00000171551	PAP45	109	22.0%	chr2	233056065	CCDS2493.1	c.1575G>T	p.E525D
EDC3	enhancer of mRNA decapping 3 homolog (S. cerevisiae)	ENSG00000179151	PAP45	203	15.3%	chr15	72735346	CCDS10267.1	c.601G>T	p.D201Y
EDC4	enhancer of mRNA decapping 4	ENSG00000038358	PAP45	205	25.4%	chr16	66469986	CCDS10849.1	c.1135G>A	p.E379K
EPC1	enhancer of polycomb homolog 1 (Drosophila)	ENSG00000120616	PAP45	212	24.5%	chr10	32615944	CCDS7172.1	c.1158G>T	p.L386F
EZH1	enhancer of zeste homolog 1 (Drosophila)	ENSG00000108799	PAP45	182	25.8%	chr17	38124661	CCDS32659.1	c.755A>G	p.D252G
ECHDC1	enoyl CoA hydratase domain containing 1	ENSG00000093144	PAP45	129	20.9%	chr6	127678807	ENST00000368293	c.501G>T	p.K167N
ENTHD1	ENTH domain containing 1	ENSG00000176177	PAP45	110	22.7%	chr22	38613553	CCDS13998.1	c.146C>A	p.S49Y
EPX	eosinophil peroxidase	ENSG00000121053	PAP45	92	10.9%	chr17	53631427	CCDS11602.1	c.1148A>C	p.K383T
EPX	eosinophil peroxidase	ENSG00000121053	PAP45	123	25.2%	chr17	53636653	CCDS11602.1	c.2018G>A	p.R673Q
EPHA3	EPH receptor A3	ENSG00000044524	PAP45	414	25.6%	chr3	89342167	CCDS2922.1	c.621G>T	p.K207N
EPHA4	EPH receptor A4	ENSG00000116106	PAP45	201	24.9%	chr2	222007146	CCDS2447.1	c.2456C>T	p.S819L
EPHB4	EPH receptor B4	ENSG00000196411	PAP45	310	27.4%	chr7	100240809	CCDS5706.1	c.2749C>T	p.R917W
EGF	epidermal growth factor	ENSG00000138798	PAP45	70	31.4%	chr4	111081581	CCDS3689.1	c.158G>A	p.G53E
EPM2A	epilepsy; progressive myoclonus type 2A; Lafora disease (laforin)	ENSG00000112425	PAP45	78	21.8%	chr6	146049111	CCDS5206.1	c.316C>A	p.H106N
EPS8L3	EPS8-like 3	ENSG00000198758	PAP45	103	20.4%	chr1	110095483	CCDS815.1	c.1580G>A	p.R527Q
EDEM2	ER degradation enhancer; mannosidase alpha-like 2	ENSG00000088298	PAP45	155	29.0%	chr20	33167090	CCDS13247.1	c.1544T>A	p.F515Y
ERO1LB	ERO1-like beta (S. cerevisiae)	ENSG00000086619	PAP45	135	20.0%	chr1	234456323	CCDS31064.1	c.921C>A	p.Y307X

EPB41L4A	erythrocyte membrane protein band 4.1 like 4A	ENSG00000129595	PAP45	53	28.3%	chr5	111629927	CCDS43350.1	c.-1G>T	p.IVS4-1-1SpliceAcceptor
EPB41L1	erythrocyte membrane protein band 4.1-like 1	ENSG00000088367	PAP45	99	14.1%	chr20	34226985	CCDS13271.1	c.276G>T	p.K92N
EPB41L1	erythrocyte membrane protein band 4.1-like 1	ENSG00000088367	PAP45	68	19.1%	chr20	34239753	CCDS13271.1	c.944G>T	p.R315I
EPB41L1	erythrocyte membrane protein band 4.1-like 1	ENSG00000088367	PAP45	44	38.6%	chr20	34249315	CCDS13271.1	c.1606C>T	p.R536C
EPB41L1	erythrocyte membrane protein band 4.1-like 1	ENSG00000088367	PAP45	117	17.1%	chr20	34257217	ENST00000344237	c.528G>T	p.E176D
EPB41L2	erythrocyte membrane protein band 4.1-like 2	ENSG00000079819	PAP45	138	19.6%	chr6	131239584	ENST00000257986	c.103G>A	p.D35N
EPB41L2	erythrocyte membrane protein band 4.1-like 2	ENSG00000079819	PAP45	102	18.6%	chr6	131243040	CCDS5141.1	c.-1G>T	p.IVS11-1-1SpliceAcceptor
EPB41L2	erythrocyte membrane protein band 4.1-like 2	ENSG00000079819	PAP45	148	30.4%	chr6	131318928	CCDS5141.1	c.391G>T	p.E131X
EPB41L3	erythrocyte membrane protein band 4.1-like 3	ENSG00000082397	PAP45	202	29.7%	chr18	5406299	CCDS11838.1	c.1585C>T	p.R529C
ESF1	ESF1; nucleolar pre-rRNA processing protein; homolog (S. cerevisiae)	ENSG00000089048	PAP45	73	23.3%	chr20	13711699	CCDS13117.1	c.88C>T	p.R30X
ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	ENSG00000141446	PAP45	100	33.0%	chr18	17370114	CCDS32800.1	c.2074G>T	p.D692Y
ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	ENSG00000141446	PAP45	48	20.8%	chr18	17408737	CCDS32800.1	c.66G>T	p.K22N
ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	ENSG00000171320	PAP45	93	23.7%	chr8	27701334	CCDS34872.1	c.1027G>T	p.E343X
EBAG9	estrogen receptor binding site associated; antigen; 9	ENSG00000147654	PAP45	227	29.5%	chr8	110632248	CCDS6313.1	c.19C>T	p.R7W
ETNK2	ethanolamine kinase 2	ENSG00000143845	PAP45	610	25.6%	chr1	202377091	CCDS1442.1	c.759G>T	p.K253N
EI24	etoposide induced 2.4 mRNA	ENSG00000149547	PAP45	56	21.4%	chr11	124950378	ENST00000397776	c.52G>T	p.D18Y
EIF2A	eukaryotic translation initiation factor 2A; 65kDa	ENSG00000144895	PAP45	132	10.6%	chr3	151772696	NM_032025	c.1073C>A	p.S358Y
EIF2C4	eukaryotic translation initiation factor 2C; 4	ENSG00000134698	PAP45	86	22.1%	chr1	36061102	CCDS397.1	c.238C>T	p.R80W
EIF3C	eukaryotic translation initiation factor 3; subunit C	ENSG00000184110	PAP45	140	12.1%	chr16	28642025	CCDS10638.1	c.816G>T	p.K272N
EIF3D	eukaryotic translation initiation factor 3; subunit D	ENSG00000100353	PAP45	151	20.5%	chr22	35249949	CCDS13930.1	c.331C>T	p.R111C
EIF3L	eukaryotic translation initiation factor 3; subunit L	ENSG00000100129	PAP45	92	26.1%	chr22	36600463	CCDS13960.1	c.892G>A	p.E298K
EIF4G3	eukaryotic translation initiation factor 4 gamma; 3	ENSG00000075151	PAP45	77	29.9%	chr1	21078582	CCDS214.1	c.2275C>T	p.R759X
EIF4A2	eukaryotic translation initiation factor 4A2	ENSG00000156976	PAP45	96	18.8%	chr3	187986681	CCDS3282.1	c.552A>C	p.E184D
EIF5A2	eukaryotic translation initiation factor 5A2	ENSG00000163577	PAP45	113	16.8%	chr3	172094815	CCDS3214.1	c.362A>C	p.K121T
ETAA1	Ewing tumor-associated antigen 1	ENSG00000143971	PAP45	46	23.9%	chr2	67484598	CCDS1882.1	c.1280C>T	p.T427M
ERCC1	excision repair cross-complementing rodent repair deficiency; complementation group 1 (includes overlapping antisense sequence)	ENSG00000012061	PAP45	168	26.8%	chr19	50608757	CCDS12663.1	c.861G>T	p.K287N
ERCC6L	excision repair cross-complementing rodent repair deficiency; complementation group 6-like	ENSG00000186871	PAP45	116	20.7%	chrX	71342479	CCDS35329.1	c.2863C>A	p.L955I
ERCC6L	excision repair cross-complementing rodent repair deficiency; complementation group 6-like	ENSG00000186871	PAP45	178	21.9%	chrX	71344345	CCDS35329.1	c.997G>T	p.V333L
EXOC1	exocyst complex component 1	ENSG00000090989	PAP45	87	19.5%	chr4	56419277	CCDS3502.1	c.31G>T	p.D11Y
EXOC2	exocyst complex component 2	ENSG00000112685	PAP45	100	45.0%	chr6	509894	CCDS34327.1	c.1479G>T	p.K493N
EXOC4	exocyst complex component 4	ENSG00000131558	PAP45	149	25.5%	chr7	133273260	CCDS5829.1	c.2104C>T	p.R702C
EXOC6B	exocyst complex component 6B	ENSG00000144036	PAP45	60	31.7%	chr2	72579111	NM_015189	c.1317G>T	p.K439N
EXOC8	exocyst complex component 8	ENSG00000116903	PAP45	302	20.2%	chr1	229538953	CCDS1593.1	c.1162C>T	p.R388X
EXPH5	exophilin 5	ENSG00000110723	PAP45	144	19.4%	chr11	107885927	CCDS8341.1	c.5517C>A	p.F1839L
EXPH5	exophilin 5	ENSG00000110723	PAP45	301	28.2%	chr11	107888035	CCDS8341.1	c.3409G>T	p.E1137X
EXT1	exostosin 1	ENSG00000182197	PAP45	177	20.3%	chr8	119191570	CCDS6324.1	c.897G>T	p.K299N
XPO1	exportin 1 (CRM1 homolog; yeast)	ENSG00000082898	PAP45	95	23.2%	chr2	61572976	CCDS33205.1	c.1711G>A	p.E571K
XPOT	exportin; tRNA (nuclear export receptor for tRNAs)	ENSG00000184575	PAP45	140	20.0%	chr12	63114865	CCDS31852.1	c.2594T>G	p.F865C
ESYT1	extended synaptotagmin-like protein 1	ENSG00000139641	PAP45	321	27.4%	chr12	54812575	CCDS8904.1	c.1088G>A	p.R363H
ESYT2	extended synaptotagmin-like protein 2	ENSG00000117868	PAP45	65	16.9%	chr7	158233729	CCDS34791.1	c.1642C>T	p.R548X
ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	ENSG00000135476	PAP45	135	20.7%	chr12	51956751	CCDS8852.1	c.1781C>T	p.A594V
ELFN2	extracellular leucine-rich repeat and fibronectin type III domain containing 2	ENSG00000166897	PAP45	154	22.1%	chr22	36099630	CCDS33642.1	c.1891G>A	p.V631M
ECM1	extracellular matrix protein 1	ENSG00000143369	PAP45	188	25.0%	chr1	148751863	CCDS953.1	c.1343G>A	p.R448H

ECM2	extracellular matrix protein 2; female organ and adipocyte specific	ENSG00000106823	PAP45	78	15.4%	chr9	94307752	CCDS6698.1	c.1348C>A	p.L450I
EYA4	eyes absent homolog 4 (Drosophila)	ENSG00000112319	PAP45	263	23.2%	chr6	133831479	CCDS5165.1	c.887C>T	p.S296L
FAM105B	family with sequence similarity 105; member B	ENSG00000154124	PAP45	111	13.5%	chr5	14743256	CCDS43302.1	c.703C>A	p.L235I
FAM119A	family with sequence similarity 119; member A	ENSG00000144401	PAP45	135	31.9%	chr2	208186388	CCDS2376.1	c.284G>A	p.R95Q
FAM120C	family with sequence similarity 120C	ENSG00000184083	PAP45	138	18.8%	chrX	54116216	CCDS14356.1	c.3266C>A	p.T1089N
FAM122C	family with sequence similarity 122C	ENSG00000156500	PAP45	67	26.9%	chrX	133776535	CCDS14644.1	c.179G>A	p.R60Q
FAM122C	family with sequence similarity 122C	ENSG00000156500	PAP45	145	18.6%	chrX	133814527	ENST00000370784	c.377G>T	p.R126I
FAM123A	family with sequence similarity 123A	ENSG00000165566	PAP45	575	23.5%	chr13	24641968	CCDS9312.1	c.1433G>A	p.R478Q
FAM123B	family with sequence similarity 123B	ENSG00000184675	PAP45	253	28.9%	chrX	63327143	CCDS14377.2	c.2749G>A	p.E917K
FAM123B	family with sequence similarity 123B	ENSG00000184675	PAP45	283	24.0%	chrX	63327487	CCDS14377.2	c.2405A>C	p.E802A
FAM123B	family with sequence similarity 123B	ENSG00000184675	PAP45	144	18.8%	chrX	63329877	CCDS14377.2	c.15G>T	p.K5N
FAM124A	family with sequence similarity 124A	ENSG00000150510	PAP45	290	23.4%	chr13	50723661	CCDS9427.1	c.265G>A	p.A89T
FAM126A	family with sequence similarity 126; member A	ENSG00000122591	PAP45	197	23.9%	chr7	22984505	CCDS5377.1	c.241G>A	p.E81K
FAM129C	family with sequence similarity 129; member C	ENSG00000167483	PAP45	56	23.2%	chr19	17504117	CCDS12362.1	c.325C>T	p.R109W
FAM129C	family with sequence similarity 129; member C	ENSG00000167483	PAP45	175	13.1%	chr19	17515376	CCDS12362.1	c.1583G>A	p.R528Q
FAM132B	family with sequence similarity 132; member B	ENSG00000178752	PAP45	164	21.3%	chr2	238736199	ENST00000408994	c.405G>T	p.E135D
FAM135A	family with sequence similarity 135; member A	ENSG00000082269	PAP45	75	18.7%	chr6	71252656	CCDS34481.1	c.760G>T	p.D254Y
FAM135A	family with sequence similarity 135; member A	ENSG00000082269	PAP45	34	29.4%	chr6	71304772	CCDS34481.1	c.3536G>A	p.R1179Q
FAM135A	family with sequence similarity 135; member A	ENSG00000082269	PAP45	63	38.1%	chr6	71326176	CCDS34481.1	c.3740G>A	p.R1247Q
FAM160B2	family with sequence similarity 160; member B2	ENSG00000158863	PAP45	93	24.7%	chr8	22011882	ENST00000289921	c.771G>T	p.K257N
FAM162B	family with sequence similarity 162; member B	ENSG00000183807	PAP45	78	20.5%	chr6	117189930	CCDS43497.1	c.293T>C	p.I98T
FAM162B	family with sequence similarity 162; member B	ENSG00000183807	PAP45	207	28.0%	chr6	117193030	CCDS43497.1	c.254C>A	p.S85X
FAM169A	family with sequence similarity 169; member A	ENSG00000198780	PAP45	71	35.2%	chr5	74171692	CCDS43330.1	c.195A>C	p.K65N
FAM171B	family with sequence similarity 171; member B	ENSG00000144369	PAP45	128	25.0%	chr2	187313307	CCDS33347.1	c.346G>T	p.V116L
FAM171B	family with sequence similarity 171; member B	ENSG00000144369	PAP45	73	21.9%	chr2	187334659	CCDS33347.1	c.1345G>T	p.E449X
FAM176A	family with sequence similarity 176; member A	ENSG00000115363	PAP45	130	30.0%	chr2	75574122	CCDS1959.1	c.207G>T	p.K69N
FAM184A	family with sequence similarity 184; member A	ENSG00000111879	PAP45	105	22.9%	chr6	119386882	CCDS43499.1	c.955C>T	p.L319F
FAM190B	family with sequence similarity 190; member B	ENSG00000107771	PAP45	152	25.7%	chr10	86121026	CCDS31235.1	c.238G>A	p.E80K
FAM194B	family with sequence similarity 194; member B	ENSG00000165837	PAP45	447	22.4%	chr13	45069027	NM_182542	c.115G>T	p.D39Y
FAM26D	family with sequence similarity 26; member D	ENSG00000164451	PAP45	285	18.9%	chr6	116981921	ENST00000368596	c.272G>T	p.R91I
FAM45B	family with sequence similarity 45; member B	ENSG00000221930	PAP45	401	25.9%	chrX	129457353	ENST00000408950	c.540G>T	p.K180N
FAM47A	family with sequence similarity 47; member A	ENSG00000185448	PAP45	216	35.2%	chrX	34058610	CCDS43926.1	c.1707C>A	p.F569L
FAM47A	family with sequence similarity 47; member A	ENSG00000185448	PAP45	207	24.6%	chrX	34059407	CCDS43926.1	c.910C>T	p.R304W
FAM5C	family with sequence similarity 5; member C	ENSG00000162670	PAP45	298	29.9%	chr1	188333911	CCDS1373.1	c.2161C>A	p.L721I
FAM5C	family with sequence similarity 5; member C	ENSG00000162670	PAP45	74	18.9%	chr1	188334558	CCDS1373.1	c.1514A>G	p.D505G
FAM50A	family with sequence similarity 50; member A	ENSG00000071859	PAP45	142	15.5%	chrX	153327210	CCDS14751.1	c.147C>A	p.F49L
FAM53C	family with sequence similarity 53; member C	ENSG00000120709	PAP45	302	22.8%	chr5	137704976	CCDS4204.1	c.53A>C	p.K18T
FAM57A	family with sequence similarity 57; member A	ENSG00000167695	PAP45	191	28.3%	chr17	588011	CCDS10996.1	c.382C>A	p.L128I
FAM65B	family with sequence similarity 65; member B	ENSG00000111913	PAP45	171	26.3%	chr6	24951313	NM_014722	c.1676C>T	p.S559L
FAM65B	family with sequence similarity 65; member B	ENSG00000111913	PAP45	105	18.1%	chr6	24981093	NM_014722	c.331C>T	p.R111C
FAM71A	family with sequence similarity 71; member A	ENSG00000162771	PAP45	78	34.6%	chr1	210865635	CCDS1507.1	c.793G>T	p.E265X
FAM71E1	family with sequence similarity 71; member E1	ENSG00000142530	PAP45	372	25.3%	chr19	55671367	CCDS33081.1	c.91A>C	p.K31Q
FAM71F1	family with sequence similarity 71; member F1	ENSG00000135248	PAP45	67	19.4%	chr7	128157201	CCDS5804.1	c.863C>A	p.S288Y
FAM73A	family with sequence similarity 73; member A	ENSG00000180488	PAP45	82	19.5%	chr1	78097586	CCDS681.1	c.-1G>T	p.IVS9-1-1SpliceAcceptor
FAM73B	family with sequence similarity 73; member B	ENSG00000148343	PAP45	89	21.3%	chr9	130844541	CCDS6917.1	c.234G>T	p.E78D
FAM83B	family with sequence similarity 83; member B	ENSG00000168143	PAP45	258	31.0%	chr6	54913215	CCDS34479.1	c.1487G>T	p.R496I
FAM83B	family with sequence similarity 83; member B	ENSG00000168143	PAP45	212	26.4%	chr6	54913313	CCDS34479.1	c.1585T>G	p.L529V
FAM83B	family with sequence similarity 83; member B	ENSG00000168143	PAP45	241	23.7%	chr6	54914502	CCDS34479.1	c.2774G>A	p.R925Q
FAM98A	family with sequence similarity 98; member A	ENSG00000119812	PAP45	271	25.8%	chr2	33677744	CCDS33179.1	c.49C>A	p.L17I
FANCI	Fanconi anemia; complementation group I	ENSG00000140525	PAP45	112	28.6%	chr15	87591937	CCDS10349.2	c.55G>A	p.E19K
FANCI	Fanconi anemia; complementation group I	ENSG00000140525	PAP45	94	22.3%	chr15	87648128	CCDS10349.2	c.2856G>T	p.K952N

FUBP1	far upstream element (FUSE) binding protein 1	ENSG00000162613	PAP45	64	18.8%	chr1	78201099	CCDS683.1	c.1288C>T	p.R430C
FNTA	farnesyltransferase; CAAX box; alpha	ENSG00000168522	PAP45	38	26.3%	chr8	43059481	CCDS6140.1	c.1039G>T	p.E347X
FAIM2	Fas apoptotic inhibitory molecule 2	ENSG00000135472	PAP45	221	22.6%	chr12	48578105	CCDS8791.1	c.247G>A	p.G83R
FASTKD3	FAST kinase domains 3	ENSG00000124279	PAP45	226	10.2%	chr5	7920056	CCDS3873.1	c.1141G>T	p.E381X
FASTKD3	FAST kinase domains 3	ENSG00000124279	PAP45	96	14.6%	chr5	7921106	CCDS3873.1	c.91A>C	p.N31H
FASTKD5	FAST kinase domains 5	ENSG00000215251	PAP45	342	25.4%	chr20	3076421	CCDS13048.1	c.1296G>T	p.K432N
FITM2	fat storage-inducing transmembrane protein 2	ENSG00000197296	PAP45	243	21.8%	chr20	42368963	CCDS33473.1	c.505G>T	p.E169X
FAT2	FAT tumor suppressor homolog 2 (Drosophila)	ENSG00000086570	PAP45	148	21.6%	chr5	150925557	CCDS4317.1	c.3129G>T	p.E1043D
FAT2	FAT tumor suppressor homolog 2 (Drosophila)	ENSG00000086570	PAP45	194	18.0%	chr5	150925607	CCDS4317.1	c.3079C>A	p.L1027I
FAT2	FAT tumor suppressor homolog 2 (Drosophila)	ENSG00000086570	PAP45	249	25.3%	chr5	150927454	CCDS4317.1	c.1232G>A	p.R411Q
FAT4	FAT tumor suppressor homolog 4 (Drosophila)	ENSG00000196159	PAP45	174	25.3%	chr4	126460630	CCDS3732.2	c.3614A>T	p.D1205V
FAT4	FAT tumor suppressor homolog 4 (Drosophila)	ENSG00000196159	PAP45	67	31.3%	chr4	126547539	CCDS3732.2	c.5362C>T	p.R1788C
FAT4	FAT tumor suppressor homolog 4 (Drosophila)	ENSG00000196159	PAP45	215	17.2%	chr4	126556175	CCDS3732.2	c.6607C>T	p.R2203W
FAT4	FAT tumor suppressor homolog 4 (Drosophila)	ENSG00000196159	PAP45	227	27.3%	chr4	126591102	CCDS3732.2	c.9481G>A	p.E3161K
FAT4	FAT tumor suppressor homolog 4 (Drosophila)	ENSG00000196159	PAP45	295	25.1%	chr4	126592462	CCDS3732.2	c.10841C>A	p.S3614Y
FAT4	FAT tumor suppressor homolog 4 (Drosophila)	ENSG00000196159	PAP45	306	23.9%	chr4	126592796	CCDS3732.2	c.11175C>A	p.F3725L
FAT4	FAT tumor suppressor homolog 4 (Drosophila)	ENSG00000196159	PAP45	224	22.3%	chr4	126631065	CCDS3732.2	c.13467G>T	p.K4489N
FAAH	fatty acid amide hydrolase	ENSG00000117480	PAP45	164	25.6%	chr1	46649902	CCDS535.1	c.1348G>A	p.E450K
FAAH2	fatty acid amide hydrolase 2	ENSG00000165591	PAP45	168	21.4%	chrX	57330138	CCDS14375.1	c.155C>T	p.S52L
FABP2	fatty acid binding protein 2; intestinal	ENSG00000145384	PAP45	204	25.0%	chr4	120462701	CCDS3712.1	c.5C>T	p.A2V
FABP7	fatty acid binding protein 7; brain	ENSG00000164434	PAP45	114	29.8%	chr6	123142652	CCDS5127.1	c.14T>G	p.F5C
FAR1	fatty acyl CoA reductase 1	ENSG00000197601	PAP45	84	13.1%	chr11	13688959	CCDS7813.1	c.689C>T	p.S230L
FAR2	fatty acyl CoA reductase 2	ENSG00000064763	PAP45	79	17.7%	chr12	29355246	CCDS8717.1	c.787C>T	p.R263W
FBXL3	F-box and leucine-rich repeat protein 3	ENSG00000005812	PAP45	138	26.1%	chr13	76493940	CCDS9457.1	c.57G>T	p.E19D
FBXL4	F-box and leucine-rich repeat protein 4	ENSG00000112234	PAP45	220	27.3%	chr6	99430218	CCDS5041.1	c.1496A>G	p.E499G
FBXL4	F-box and leucine-rich repeat protein 4	ENSG00000112234	PAP45	253	11.5%	chr6	99481293	CCDS5041.1	c.293G>A	p.R98Q
FBXW12	F-box and WD repeat domain containing 12	ENSG00000164049	PAP45	111	11.7%	chr3	48411115	CCDS2764.1	c.1382C>A	p.S461Y
FBXW7	F-box and WD repeat domain containing 7	ENSG00000109670	PAP45	158	29.7%	chr4	153468907	CCDS3777.1	c.1321C>T	p.R441W
FBXW8	F-box and WD repeat domain containing 8	ENSG00000174989	PAP45	80	16.3%	chr12	115850236	CCDS9182.1	c.344T>G	p.F115C
FBXO22	F-box protein 22	ENSG00000167196	PAP45	115	24.3%	chr15	73993515	CCDS10287.1	c.377G>T	p.R126I
FBXO24	F-box protein 24	ENSG00000106336	PAP45	450	19.6%	chr7	100031213	CCDS5698.1	c.1154G>T	p.R385I
FBXO30	F-box protein 30	ENSG00000118496	PAP45	229	13.5%	chr6	146167850	CCDS5208.1	c.1385C>A	p.S462X
FBXO31	F-box protein 31	ENSG00000103264	PAP45	105	23.8%	chr16	85925324	CCDS32501.1	c.1066G>A	p.D356N
FBXO32	F-box protein 32	ENSG00000156804	PAP45	77	26.0%	chr8	124613338	CCDS6345.1	c.353G>T	p.R118I
FBXO34	F-box protein 34	ENSG00000178974	PAP45	390	26.2%	chr14	54887931	CCDS32086.1	c.1070G>A	p.R357H
FBXO38	F-box protein 38	ENSG00000145868	PAP45	230	17.0%	chr5	147786995	CCDS4290.1	c.1945C>T	p.R649X
FBXO43	F-box protein 43	ENSG00000156509	PAP45	167	22.2%	chr8	101215225	CCDS43759.1	c.2006G>T	p.R669L
FBXO5	F-box protein 5	ENSG00000112029	PAP45	163	21.5%	chr6	153335106	CCDS5242.1	c.1086C>A	p.F362L
FBXO5	F-box protein 5	ENSG00000112029	PAP45	146	15.1%	chr6	153338101	CCDS5242.1	c.452C>A	p.S151Y
FBXO18	F-box protein; helicase; 18	ENSG00000134452	PAP45	63	15.9%	chr10	5985025	CCDS7073.1	c.191A>G	p.D64G
FBXO22OS	FBXO22 opposite strand (non-protein coding)	ENSG00000167196	PAP45	115	24.3%	chr15	73993515	CCDS10287.1	c.377G>T	p.R126I
FCGBP	Fc fragment of IgG binding protein	ENSG00000090920	PAP45	214	12.1%	chr19	45111877	CCDS12546.1	c.2957G>A	p.R986Q
FCRL1	Fc receptor-like 1	ENSG00000163534	PAP45	126	15.9%	chr1	156038405	CCDS1170.1	c.810T>G	p.H270Q
FCRL4	Fc receptor-like 4	ENSG00000163518	PAP45	145	29.7%	chr1	155825766	CCDS1166.1	c.159G>T	p.E53D
FEM1B	fem-1 homolog b (C. elegans)	ENSG00000169018	PAP45	180	24.4%	chr15	66369624	CCDS10228.1	c.874G>A	p.E292K
FEM1C	fem-1 homolog c (C. elegans)	ENSG00000145780	PAP45	124	21.8%	chr5	114888926	CCDS4118.1	c.832A>G	p.S278G
FER	fer (fps/fes related) tyrosine kinase	ENSG00000151422	PAP45	38	28.9%	chr5	108247015	CCDS4098.1	c.943G>T	p.E315X
FER1L6	fer-1-like 6 (C. elegans)	ENSG00000214814	PAP45	51	37.3%	chr8	125094876	CCDS43767.1	c.1846G>T	p.E616X
FER1L6	fer-1-like 6 (C. elegans)	ENSG00000214814	PAP45	112	17.9%	chr8	125103079	CCDS43767.1	c.2122C>A	p.L708I
FER1L6	fer-1-like 6 (C. elegans)	ENSG00000214814	PAP45	208	22.6%	chr8	125131038	CCDS43767.1	c.2734G>T	p.E912X
FRMPD1	FERM and PDZ domain containing 1	ENSG00000070601	PAP45	177	11.9%	chr9	37714231	CCDS6612.1	c.526C>A	p.L176M
FRMPD1	FERM and PDZ domain containing 1	ENSG00000070601	PAP45	483	28.8%	chr9	37734862	CCDS6612.1	c.2833C>T	p.R945C
FRMPD1	FERM and PDZ domain containing 1	ENSG00000070601	PAP45	404	23.5%	chr9	37735132	CCDS6612.1	c.3103A>C	p.N1035H
FRMPD1	FERM and PDZ domain containing 1	ENSG00000070601	PAP45	313	24.6%	chr9	37735496	CCDS6612.1	c.3467A>C	p.K1156T

FRMPD2	FERM and PDZ domain containing 2	ENSG00000170324	PAP45	150	28.7%	chr10	49070851	CCDS31195.1	c.2047G>A	p.E683K
FRMPD2	FERM and PDZ domain containing 2	ENSG00000170324	PAP45	116	23.3%	chr10	49110311	CCDS31195.1	c.1021C>A	p.L341I
FRMPD2	FERM and PDZ domain containing 2	ENSG00000170324	PAP45	75	25.3%	chr10	49118450	CCDS31195.1	c.659G>A	p.S220N
FRMPD3	FERM and PDZ domain containing 3	ENSG00000147234	PAP45	276	30.1%	chrX	106732037	ENST00000276185	c.4211C>T	p.S1404L
FRMD3	FERM domain containing 3	ENSG00000172159	PAP45	210	21.9%	chr9	85194364	CCDS43840.1	c.227G>A	p.R76H
FERMT3	fermitin family homolog 3 (Drosophila)	ENSG00000149781	PAP45	142	31.7%	chr11	63735481	CCDS8060.1	c.673C>T	p.L225F
FDXR	ferredoxin reductase	ENSG00000161513	PAP45	285	36.5%	chr17	70372022	CCDS11707.1	c.863G>A	p.R288Q
FATE1	fetal and adult testis expressed 1	ENSG00000147378	PAP45	125	18.4%	chrX	150640540	CCDS14700.1	c.252G>T	p.K84N
FBN1	fibrillin 1	ENSG00000166147	PAP45	142	24.6%	chr15	46490732	CCDS32232.1	c.8363C>T	p.T2788M
FBN2	fibrillin 2	ENSG00000138829	PAP45	70	25.7%	chr5	127652772	CCDS34222.1	c.6583C>T	p.R2195C
FGG	fibrinogen gamma chain	ENSG00000171557	PAP45	124	21.0%	chr4	155753154	CCDS3788.1	c.58C>A	p.L20I
FGL1	fibrinogen-like 1	ENSG00000104760	PAP45	175	18.9%	chr8	17783812	CCDS6004.1	c.220C>A	p.L74I
FGF10	fibroblast growth factor 10	ENSG00000070193	PAP45	217	10.6%	chr5	44340877	CCDS3950.1	c.604C>A	p.L202I
FGF17	fibroblast growth factor 17	ENSG00000158815	PAP45	265	28.7%	chr8	21959576	CCDS6019.1	c.78G>T	p.E26D
FGF6	fibroblast growth factor 6	ENSG00000111241	PAP45	176	22.2%	chr12	4413698	CCDS8527.1	c.571C>T	p.R191W
FGF7	fibroblast growth factor 7 (keratinocyte growth factor)	ENSG00000140285	PAP45	151	31.1%	chr15	47503811	CCDS10131.1	c.25A>G	p.I9V
FGFBP1	fibroblast growth factor binding protein 1	ENSG00000137440	PAP45	377	22.8%	chr4	15547164	CCDS3418.1	c.190G>T	p.D64Y
FGFR2	fibroblast growth factor receptor 2	ENSG00000066468	PAP45	105	27.6%	chr10	123246170	CCDS7620.2	c.1732C>T	p.R578X
FGFR2	fibroblast growth factor receptor 2	ENSG00000066468	PAP45	316	25.6%	chr10	123343306	CCDS7620.2	c.16C>T	p.R6C
FN1	fibronectin 1	ENSG00000115414	PAP45	193	25.9%	chr2	215959777	CCDS42814.1	c.4492C>T	p.P1498S
FANK1	fibronectin type III and ankyrin repeat domains 1	ENSG00000203780	PAP45	206	25.2%	chr10	127658832	CCDS31309.1	c.126G>T	p.E42D
FSCB	fibrous sheath CABYR binding protein	ENSG00000189139	PAP45	126	27.0%	chr14	44043759	CCDS9679.1	c.2182G>A	p.E728K
FSCB	fibrous sheath CABYR binding protein	ENSG00000189139	PAP45	143	28.7%	chr14	44044719	CCDS9679.1	c.1222G>A	p.A408T
FSIP1	fibrous sheath interacting protein 1	ENSG00000150667	PAP45	87	25.3%	chr15	37697668	CCDS10050.1	c.1259A>C	p.K420T
FCN1	ficolin (collagen/fibrinogen domain containing) 1	ENSG00000085265	PAP45	144	29.9%	chr9	136941227	ENST00000371807	c.693C>A	p.F231L
FCN1	ficolin (collagen/fibrinogen domain containing) 1	ENSG00000085265	PAP45	255	25.5%	chr9	136941681	CCDS6985.1	c.765C>A	p.F255L
FIGN	fidgetin	ENSG00000182263	PAP45	116	24.1%	chr2	164175644	CCDS2221.2	c.944C>A	p.S315Y
FLG	filaggrin	ENSG00000143631	PAP45	62	22.6%	chr1	150547571	CCDS30860.1	c.6415C>T	p.R2139C
FLG2	filaggrin family member 2	ENSG00000143520	PAP45	76	17.1%	chr1	150594205	CCDS30861.1	c.2681C>T	p.S894F
FLG2	filaggrin family member 2	ENSG00000143520	PAP45	97	24.7%	chr1	150594292	CCDS30861.1	c.2594C>T	p.S865L
FILIP1	filamin A interacting protein 1	ENSG00000118407	PAP45	86	30.2%	chr6	76075209	CCDS4984.1	c.3560G>A	p.R1187Q
FILIP1	filamin A interacting protein 1	ENSG00000118407	PAP45	125	21.6%	chr6	76080833	CCDS4984.1	c.1435G>T	p.E479X
FILIP1L	filamin A interacting protein 1-like	ENSG00000168386	PAP45	145	10.3%	chr3	101049938	CCDS43117.1	c.3272G>A	p.R1091Q
FILIP1L	filamin A interacting protein 1-like	ENSG00000168386	PAP45	119	16.8%	chr3	101051228	CCDS43117.1	c.1982G>A	p.R661Q
FLNB	filamin B; beta	ENSG00000136068	PAP45	48	31.3%	chr3	58042521	CCDS2885.1	c.765G>T	p.K255N
FLNB	filamin B; beta	ENSG00000136068	PAP45	83	28.9%	chr3	58084364	CCDS2885.1	c.3631G>A	p.E1211K
FMO3	flavin containing monooxygenase 3	ENSG00000007933	PAP45	140	36.4%	chr1	169353183	CCDS1292.1	c.1576G>A	p.A526T
FMO6P	flavin containing monooxygenase 6 pseudogene	ENSG00000117507	PAP45	395	25.8%	chr1	169387989	ENST00000236166	c.1144G>A	p.A382T
FMO9P	flavin containing monooxygenase 9 pseudogene	ENSG00000215834	PAP45	93	21.5%	chr1	164857761	ENST00000400978	c.202G>A	p.D68N
FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	ENSG00000102755	PAP45	157	23.6%	chr13	27775393	CCDS9330.1	c.3928G>T	p.D1310Y
FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	ENSG00000102755	PAP45	112	24.1%	chr13	27900009	CCDS9330.1	c.1156C>T	p.R386C
FLT3	fms-related tyrosine kinase 3	ENSG00000122025	PAP45	224	25.9%	chr13	27507763	CCDS31953.1	c.1466G>T	p.R489I
FOLR1	folate receptor 1 (adult)	ENSG00000110195	PAP45	111	25.2%	chr11	71584779	CCDS8211.1	c.684C>A	p.F228L
FLCN	folliculin	ENSG00000154803	PAP45	191	23.0%	chr17	17070316	CCDS32579.1	c.295G>T	p.D99Y
FNIP1	folliculin interacting protein 1	ENSG00000217128	PAP45	125	23.2%	chr5	131062528	CCDS34227.1	c.1183G>T	p.D395Y
FSTL5	follistatin-like 5	ENSG00000168843	PAP45	83	26.5%	chr4	163251880	CCDS3802.1	c.119G>A	p.R40Q
FOXA3	forkhead box A3	ENSG00000170608	PAP45	116	29.3%	chr19	51068003	CCDS12677.1	c.900C>A	p.F300L
FOXM1	forkhead box M1	ENSG00000111206	PAP45	116	29.3%	chr12	2838628	CCDS8516.1	c.1843T>C	p.F615L
FOXP1	forkhead box P1	ENSG00000114861	PAP45	109	23.9%	chr3	71104418	CCDS2914.1	c.1630C>T	p.R544X
FOXP2	forkhead box P2	ENSG00000128573	PAP45	91	15.4%	chr7	114089398	CCDS43635.1	c.1765C>T	p.R589X
FOXP3	forkhead box P3	ENSG00000049768	PAP45	313	27.2%	chrX	49000248	CCDS14323.1	c.551C>T	p.S184L
FMN1	formin 1	ENSG00000186031	PAP45	330	25.8%	chr15	31048684	NM_001103184	c.1841C>A	p.S614Y

FMN1	formin 1	ENSG00000186031	PAP45	882	19.3%	chr15	31048850	NM_001103184	c.1675G>T	p.E559X
FMN1	formin 1	ENSG00000186031	PAP45	297	26.3%	chr15	31144480	NM_001103184	c.1462G>T	p.E488X
FMNL3	formin-like 3	ENSG00000161791	PAP45	193	13.0%	chr12	48331336	CCDS41780.1	c.1526G>A	p.R509Q
FXR1	fragile X mental retardation; autosomal homolog 1	ENSG00000114416	PAP45	60	28.3%	chr3	182158336	CCDS3238.1	c.916G>T	p.E306X
FREM3	FRAS1 related extracellular matrix 3	ENSG00000183090	PAP45	304	19.4%	chr4	144836383	NM_001168235	c.4896C>A	p.F1632L
FREM3	FRAS1 related extracellular matrix 3	ENSG00000183090	PAP45	169	26.6%	chr4	144837291	NM_001168235	c.3988C>A	p.L1330I
FREM2	FRAS1 related extracellular matrix protein 2	ENSG00000150893	PAP45	211	21.8%	chr13	38162966	CCDS31960.1	c.3485G>A	p.R1162Q
FRAS1	Fraser syndrome 1	ENSG00000138759	PAP45	267	15.7%	chr4	79585742	NM_025074	c.5708C>A	p.S1903X
FZD3	frizzled homolog 3 (Drosophila)	ENSG00000104290	PAP45	216	26.4%	chr8	28476328	CCDS6069.1	c.1882C>T	p.R628W
FRYL	FRY-like	ENSG00000075539	PAP45	73	30.1%	chr4	48292428	CCDS43227.1	c.1184G>A	p.R395Q
FPGT	fucose-1-phosphate guanylyltransferase	ENSG00000116783	PAP45	304	26.6%	chr1	74677768	CCDS664.1	c.1885C>T	p.R629C
FUT4	fucosyltransferase 4 (alpha (1;3) fucosyltransferase; myeloid-specific)	ENSG00000196371	PAP45	201	12.4%	chr11	93917839	CCDS8301.1	c.892G>A	p.E298K
FUT8	fucosyltransferase 8 (alpha (1;6) fucosyltransferase)	ENSG00000033170	PAP45	234	21.8%	chr14	65205832	CCDS9775.1	c.716G>T	p.R239L
FUT8	fucosyltransferase 8 (alpha (1;6) fucosyltransferase)	ENSG00000033170	PAP45	124	24.2%	chr14	65278836	CCDS9775.1	c.1683G>T	p.K561N
FUT9	fucosyltransferase 9 (alpha (1;3) fucosyltransferase)	ENSG00000172461	PAP45	95	22.1%	chr6	96758310	CCDS5033.1	c.558G>T	p.E186D
FAHD1	fumarylacetoacetate hydrolase domain containing 1	ENSG00000180185	PAP45	231	26.4%	chr16	1817787	CCDS32367.1	c.556G>T	p.D186Y
FUNDC2P2	FUN14 domain containing 2 pseudogene 2	ENSG00000182814	PAP45	131	24.4%	chr2	84371530	ENST00000331369	c.77C>T	p.P26L
FRY	furry homolog (Drosophila)	ENSG00000073910	PAP45	182	27.5%	chr13	31726422	CCDS41875.1	c.7307C>A	p.S2436Y
FXYD2	FXYD domain containing ion transport regulator 2	ENSG00000137731	PAP45	153	22.9%	chr11	117198391	CCDS8386.1	c.79C>T	p.R27C
FXYD2	FXYD domain containing ion transport regulator 2	ENSG00000137731	PAP45	120	24.2%	chr11	117198444	NM_001127489	c.224G>T	p.R75I
FRK	fyn-related kinase	ENSG00000111816	PAP45	209	16.7%	chr6	116396526	CCDS5103.1	c.536G>A	p.R179Q
FYCO1	FYVE and coiled-coil domain containing 1	ENSG00000163820	PAP45	77	24.7%	chr3	45978812	CCDS2734.1	c.3346C>T	p.R1116C
FGD1	FYVE; RhoGEF and PH domain containing 1	ENSG00000102302	PAP45	59	20.3%	chrX	54538442	CCDS14359.1	c.149C>T	p.S50L
FGD2	FYVE; RhoGEF and PH domain containing 2	ENSG00000146192	PAP45	131	13.0%	chr6	37081592	CCDS4829.1	c.21G>T	p.E7D
FGD5	FYVE; RhoGEF and PH domain containing 5	ENSG00000154783	PAP45	176	10.2%	chr3	14835758	NM_152536	c.176C>T	p.S59L
GFM1	G elongation factor; mitochondrial 1	ENSG00000168827	PAP45	63	19.0%	chr3	159852620	CCDS33885.1	c.731C>T	p.A244V
GFM1	G elongation factor; mitochondrial 1	ENSG00000168827	PAP45	68	17.6%	chr3	159859436	CCDS33885.1	c.1115G>A	p.R372H
GFM1	G elongation factor; mitochondrial 1	ENSG00000168827	PAP45	82	17.1%	chr3	159891944	CCDS33885.1	c.2250G>T	p.K750N
GPR110	G protein-coupled receptor 110	ENSG00000153292	PAP45	244	22.5%	chr6	47085760	CCDS34471.1	c.1370C>A	p.S457Y
GPR112	G protein-coupled receptor 112	ENSG00000156920	PAP45	249	12.4%	chrX	135254736	CCDS35409.1	c.1205C>A	p.S402Y
GPR112	G protein-coupled receptor 112	ENSG00000156920	PAP45	113	27.4%	chrX	135260235	CCDS35409.1	c.6704C>T	p.S2235L
GPR112	G protein-coupled receptor 112	ENSG00000156920	PAP45	101	25.7%	chrX	135263193	CCDS35409.1	c.6854C>A	p.S2285Y
GPR114	G protein-coupled receptor 114	ENSG00000159618	PAP45	210	16.7%	chr16	56153871	CCDS10785.1	c.139C>T	p.R47C
GPR116	G protein-coupled receptor 116	ENSG00000069122	PAP45	95	24.2%	chr6	46955727	CCDS4919.1	c.823A>T	p.N275Y
GPR123	G protein-coupled receptor 123	ENSG00000197177	PAP45	137	23.4%	chr10	134736495	ENST00000368577	c.539NULL>T	p.NULL-1FsIns1bp
GPR124	G protein-coupled receptor 124	ENSG00000020181	PAP45	234	24.4%	chr8	37816858	CCDS6097.1	c.2552G>A	p.R851Q
GPR133	G protein-coupled receptor 133	ENSG00000111452	PAP45	113	18.6%	chr12	130042786	CCDS9272.1	c.862A>C	p.K288Q
GPR143	G protein-coupled receptor 143	ENSG00000101850	PAP45	112	21.4%	chrX	9653842	CCDS14134.1	c.1219G>T	p.E407X
GPR149	G protein-coupled receptor 149	ENSG00000174948	PAP45	109	23.9%	chr3	155629848	CCDS43162.1	c.251C>T	p.S84L
GPR155	G protein-coupled receptor 155	ENSG00000163328	PAP45	44	27.3%	chr2	175043386	CCDS2259.1	c.1004A>C	p.Q335P
GPR158	G protein-coupled receptor 158	ENSG00000151025	PAP45	169	23.1%	chr10	25925651	CCDS31166.1	c.2072G>A	p.R691Q
GPR158	G protein-coupled receptor 158	ENSG00000151025	PAP45	142	16.2%	chr10	25927340	CCDS31166.1	c.2779G>T	p.E927X
GPR158	G protein-coupled receptor 158	ENSG00000151025	PAP45	153	21.6%	chr10	25927379	CCDS31166.1	c.2818G>T	p.E940X
GPR179	G protein-coupled receptor 179	ENSG00000188888	PAP45	701	19.5%	chr17	33736479	CCDS42308.1	c.6499G>T	p.E2167X
GPR179	G protein-coupled receptor 179	ENSG00000188888	PAP45	416	26.9%	chr17	33738953	CCDS42308.1	c.4025G>A	p.R1342K
GPR179	G protein-coupled receptor 179	ENSG00000188888	PAP45	610	27.7%	chr17	33739516	CCDS42308.1	c.3462G>T	p.Q1154H
GPR179	G protein-coupled receptor 179	ENSG00000188888	PAP45	127	30.7%	chr17	33744543	CCDS42308.1	c.1544G>A	p.R515Q
GPR18	G protein-coupled receptor 18	ENSG00000125245	PAP45	205	22.9%	chr13	98705242	CCDS9491.1	c.886C>T	p.R296X
GPR31	G protein-coupled receptor 31	ENSG00000120436	PAP45	135	28.9%	chr6	167490430	CCDS5299.1	c.880C>T	p.R294W
GPR52	G protein-coupled receptor 52	ENSG00000203737	PAP45	446	20.9%	chr1	172684348	CCDS30941.1	c.476G>T	p.R159I
GPR55	G protein-coupled receptor 55	ENSG00000135898	PAP45	229	18.8%	chr2	231483562	CCDS2480.1	c.360C>A	p.F120L
GPR64	G protein-coupled receptor 64	ENSG00000173698	PAP45	134	23.1%	chrX	18935360	CCDS43923.1	c.1603G>A	p.V535I

GPR75	G protein-coupled receptor 75	ENSG00000119737	PAP45	57	38.6%	chr2	53934186	CCDS1849.1	c.1212G>T	p.K404N
GPR87	G protein-coupled receptor 87	ENSG00000138271	PAP45	210	24.3%	chr3	152495435	CCDS3157.1	c.289C>T	p.R97X
GPR98	G protein-coupled receptor 98	ENSG00000164199	PAP45	187	26.2%	chr5	89959186	NM_032119	c.1075C>A	p.H359N
GPR98	G protein-coupled receptor 98	ENSG00000164199	PAP45	86	18.6%	chr5	90082257	NM_032119	c.11108C>A	p.P3703H
GPR98	G protein-coupled receptor 98	ENSG00000164199	PAP45	122	28.7%	chr5	90122806	NM_032119	c.14404C>T	p.R4802X
GPRASP1	G protein-coupled receptor associated sorting protein 1	ENSG00000198932	PAP45	147	25.9%	chrX	101795622	CCDS35352.1	c.125C>T	p.T42I
GPRASP1	G protein-coupled receptor associated sorting protein 1	ENSG00000198932	PAP45	177	22.0%	chrX	101798996	CCDS35352.1	c.3499C>T	p.R1167W
GPRASP1	G protein-coupled receptor associated sorting protein 1	ENSG00000198932	PAP45	193	24.9%	chrX	101799002	CCDS35352.1	c.3505C>A	p.P1169T
GPRASP1	G protein-coupled receptor associated sorting protein 1	ENSG00000198932	PAP45	131	19.8%	chrX	101799360	CCDS35352.1	c.3863G>A	p.G1288D
GPRASP2	G protein-coupled receptor associated sorting protein 2	ENSG00000158301	PAP45	151	26.5%	chrX	101858285	CCDS14501.1	c.1832C>A	p.P611H
GPRASP2	G protein-coupled receptor associated sorting protein 2	ENSG00000158301	PAP45	162	24.7%	chrX	101858356	CCDS14501.1	c.1903C>T	p.R635X
GIT2	G protein-coupled receptor kinase interacting ArfGAP 2	ENSG00000139436	PAP45	101	20.8%	chr12	108905872	CCDS9138.1	c.416C>T	p.S139L
GPRC6A	G protein-coupled receptor; family C; group 6; member A	ENSG00000173612	PAP45	84	28.6%	chr6	117220317	CCDS5112.1	c.2462C>A	p.S821Y
GALNS	galactosamine (N-acetyl)-6-sulfate sulfatase	ENSG00000141012	PAP45	47	21.3%	chr16	87431669	CCDS10970.1	c.428T>G	p.L143R
GGNBP2	gametogenetin binding protein 2	ENSG00000005955	PAP45	120	12.5%	chr17	31987159	CCDS11314.1	c.298NULL>T	p.NULL-1FsIns1bp
GABRA1	gamma-aminobutyric acid (GABA) A receptor; alpha 1	ENSG00000022355	PAP45	287	24.4%	chr5	161256947	CCDS4357.1	c.1312T>G	p.Y438D
GABRA2	gamma-aminobutyric acid (GABA) A receptor; alpha 2	ENSG00000151834	PAP45	260	17.7%	chr4	45958851	CCDS3471.1	c.908C>A	p.S303Y
GABRB1	gamma-aminobutyric acid (GABA) A receptor; beta 1	ENSG00000163288	PAP45	267	24.7%	chr4	46729397	ENST00000381582	c.379G>A	p.G127S
GABRB1	gamma-aminobutyric acid (GABA) A receptor; beta 1	ENSG00000163288	PAP45	137	12.4%	chr4	46858230	CCDS3474.1	c.448C>A	p.L150I
GABBR2	gamma-aminobutyric acid (GABA) B receptor; 2	ENSG00000136928	PAP45	83	20.5%	chr9	100187799	CCDS6736.1	c.1606C>A	p.L536I
GGT5	gamma-glutamyltransferase 5	ENSG00000099998	PAP45	141	23.4%	chr22	22952708	CCDS42990.1	c.929C>T	p.A310V
GJA9	gap junction protein; alpha 9; 59kDa	ENSG00000131233	PAP45	653	25.4%	chr1	39113172	CCDS432.1	c.1186G>T	p.D396Y
GJA9	gap junction protein; alpha 9; 59kDa	ENSG00000131233	PAP45	187	15.0%	chr1	39113404	CCDS432.1	c.954G>T	p.E318D
GSDMB	gasdermin B	ENSG00000073605	PAP45	99	17.2%	chr17	35322205	CCDS42313.1	c.307G>T	p.E103X
GIPR	gastric inhibitory polypeptide receptor	ENSG00000010310	PAP45	116	20.7%	chr19	50868025	CCDS12671.1	c.357G>T	p.E119D
GKN2	gastrokine 2	ENSG00000183607	PAP45	137	22.6%	chr2	69027027	CCDS33215.1	c.385G>T	p.D129Y
GATA1	GATA binding protein 1 (globin transcription factor 1)	ENSG00000102145	PAP45	152	25.7%	chrX	48537187	CCDS14305.1	c.914G>A	p.R305Q
GATAD1	GATA zinc finger domain containing 1	ENSG00000157259	PAP45	62	30.6%	chr7	91917997	CCDS5625.1	c.422C>A	p.S141X
GATAD2B	GATA zinc finger domain containing 2B	ENSG00000143614	PAP45	426	16.9%	chr1	152057936	CCDS1054.1	c.552G>T	p.K184N
GFRA3	GDNF family receptor alpha 3	ENSG00000146013	PAP45	215	27.4%	chr5	137617422	CCDS4201.1	c.956G>A	p.R319Q
GDI2	GDP dissociation inhibitor 2	ENSG00000057608	PAP45	172	21.5%	chr10	5848230	CCDS7071.1	c.1171G>T	p.D391Y
GTF3C1	general transcription factor IIIC; polypeptide 1; alpha 220kDa	ENSG00000077235	PAP45	199	25.6%	chr16	27411323	CCDS32414.1	c.2988G>T	p.L996F
GTF3C2	general transcription factor IIIC; polypeptide 2; beta 110kDa	ENSG00000115207	PAP45	162	15.4%	chr2	27403082	CCDS1749.1	c.2700C>A	p.F900L
GTF3C4	general transcription factor IIIC; polypeptide 4; 90kDa	ENSG00000125484	PAP45	164	22.6%	chr9	134543467	CCDS6953.1	c.640G>T	p.E214X
GAN	gigaxonin	ENSG00000127688	PAP45	68	30.9%	chr16	79942757	CCDS10935.1	c.236C>T	p.S79L
GIPC2	GIPC PDZ domain containing family; member 2	ENSG00000137960	PAP45	146	19.9%	chr1	78319049	CCDS685.1	c.343G>A	p.E115K
GIPC3	GIPC PDZ domain containing family; member 3	ENSG00000179855	PAP45	139	26.6%	chr19	3537594	CCDS32871.1	c.327G>T	p.E109D
GLIPR1L1	GLI pathogenesis-related 1 like 1	ENSG00000173401	PAP45	125	24.8%	chr12	74050206	CCDS9009.1	c.685C>T	p.L229F
GRLF1	glucocorticoid receptor DNA binding factor 1	ENSG00000160007	PAP45	99	30.3%	chr19	52115043	NM_004491	c.1271G>A	p.R424K
GCNT2	glucosaminyl (N-acetyl) transferase 2; I-branching enzyme (I blood group)	ENSG00000111846	PAP45	516	23.1%	chr6	10637506	CCDS34338.1	c.376G>C	p.V126L
GCNT2	glucosaminyl (N-acetyl) transferase 2; I-branching enzyme (I blood group)	ENSG00000111846	PAP45	126	27.0%	chr6	10664659	CCDS4512.1	c.17G>A	p.R6H
GCNT2	glucosaminyl (N-acetyl) transferase 2; I-branching enzyme (I blood group)	ENSG00000111846	PAP45	277	24.5%	chr6	10729575	CCDS4513.1	c.931C>A	p.P311T
GCNT4	glucosaminyl (N-acetyl) transferase 4; core 2	ENSG00000176928	PAP45	169	21.3%	chr5	74360931	CCDS4026.1	c.688G>T	p.D230Y
GCNT6	glucosaminyl (N-acetyl) transferase 6	ENSG00000205318	PAP45	265	26.4%	chr6	10742224	ENST00000379591	c.12G>T	p.E4D
GCNT6	glucosaminyl (N-acetyl) transferase 6	ENSG00000205318	PAP45	284	25.4%	chr6	10742282	ENST00000379591	c.70G>A	p.V24I
GPI	glucose-6-phosphate isomerase	ENSG00000105220	PAP45	104	26.0%	chr19	39581979	CCDS12437.1	c.1297A>G	p.T433A
GFOD2	glucose-fructose oxidoreductase domain containing 2	ENSG00000141098	PAP45	332	13.3%	chr16	66266904	CCDS10845.1	c.813G>T	p.K271N
GAA	glucosidase; alpha; acid	ENSG00000171298	PAP45	254	25.6%	chr17	75705456	CCDS32760.1	c.2284G>A	p.E762K
GAD1	glutamate decarboxylase 1 (brain; 67kDa)	ENSG00000128683	PAP45	231	24.2%	chr2	171395888	CCDS2239.1	c.487G>A	p.E163K

GAD2	glutamate decarboxylase 2 (pancreatic islets and brain; 65kDa)	ENSG00000136750	PAP45	129	23.3%	chr10	26545807	CCDS7149.1	c.63G>T	p.E21D
GRIP1	glutamate receptor interacting protein 1	ENSG00000155974	PAP45	51	23.5%	chr12	65145466	CCDS41807.1	c.728C>A	p.S243Y
GRIA4	glutamate receptor; ionotrophic; AMPA 4	ENSG00000152578	PAP45	205	12.2%	chr11	105350345	CCDS8333.1	c.2508C>A	p.F836L
GRIA2	glutamate receptor; ionotropic; AMPA 2	ENSG00000120251	PAP45	98	27.6%	chr4	158453403	CCDS3797.1	c.592G>T	p.D198Y
GRID1	glutamate receptor; ionotropic; delta 1	ENSG00000182771	PAP45	128	22.7%	chr10	87477727	CCDS31236.1	c.1398C>A	p.F466L
GRID1	glutamate receptor; ionotropic; delta 1	ENSG00000182771	PAP45	76	15.8%	chr10	87888608	CCDS31236.1	c.674G>A	p.R225H
GRID2	glutamate receptor; ionotropic; delta 2	ENSG00000152208	PAP45	251	24.3%	chr4	94912599	CCDS3637.1	c.2951C>A	p.S984Y
GRIK2	glutamate receptor; ionotropic; kainate 2	ENSG00000164418	PAP45	79	27.8%	chr6	102610107	CCDS5048.1	c.2521G>T	p.E841X
GRIK4	glutamate receptor; ionotropic; kainate 4	ENSG00000149403	PAP45	119	24.4%	chr11	120343125	CCDS8433.1	c.2278C>T	p.R760W
GRINA	glutamate receptor; ionotropic; N-methyl D-aspartate-associated protein 1 (glutamate binding)	ENSG00000178719	PAP45	260	28.1%	chr8	145138402	CCDS34961.1	c.695C>T	p.S232L
GRINL1A	glutamate receptor; ionotropic; N-methyl D-aspartate-like 1A	ENSG00000137878	PAP45	72	15.3%	chr15	55719008	CCDS32247.1	c.1092G>T	p.Q364H
GRIN3A	glutamate receptor; ionotropic; N-methyl-D-aspartate 3A	ENSG00000198785	PAP45	247	23.9%	chr9	103472796	CCDS6758.1	c.1719G>T	p.K573N
GRM1	glutamate receptor; metabotropic 1	ENSG00000152822	PAP45	151	23.2%	chr6	146392526	CCDS5209.1	c.180G>T	p.E60D
GRM3	glutamate receptor; metabotropic 3	ENSG00000198822	PAP45	149	10.7%	chr7	86232542	CCDS5600.1	c.145G>A	p.E49K
GRM6	glutamate receptor; metabotropic 6	ENSG00000113262	PAP45	116	22.4%	chr5	178328360	ENST00000319065	c.3211G>T	p.E1071X
GRM8	glutamate receptor; metabotropic 8	ENSG00000179603	PAP45	371	17.8%	chr7	125961054	CCDS5794.1	c.1618C>T	p.R540C
GLS	glutaminase	ENSG00000115419	PAP45	101	15.8%	chr2	191505805	ENST00000338435	c.1769G>A	p.R590K
GLS	glutaminase	ENSG00000115419	PAP45	86	15.1%	chr2	191505824	ENST00000338435	c.1788G>T	p.E596D
QSER1	glutamine and serine rich 1	ENSG00000060749	PAP45	236	19.5%	chr11	32910485	CCDS41631.1	c.718G>A	p.D240N
QSER1	glutamine and serine rich 1	ENSG00000060749	PAP45	172	28.5%	chr11	32911741	CCDS41631.1	c.1974G>T	p.K658N
QPCT	glutaminyl-peptide cyclotransferase	ENSG00000115828	PAP45	159	32.7%	chr2	37440240	CCDS1790.1	c.281G>A	p.R94Q
EPRS	glutamyl-prolyl-tRNA synthetase	ENSG00000136628	PAP45	95	21.1%	chr1	218218545	CCDS31027.1	c.4049C>A	p.S1350Y
GLRX2	glutaredoxin 2	ENSG00000023572	PAP45	128	27.3%	chr1	191336927	CCDS1380.1	c.153G>T	p.E51D
GLRX3	glutaredoxin 3	ENSG00000108010	PAP45	294	20.7%	chr10	131849114	CCDS7661.1	c.341G>A	p.R114Q
GRXCR2	glutaredoxin; cysteine rich 2	ENSG00000204928	PAP45	85	18.8%	chr5	145226423	CCDS34263.1	c.398G>A	p.R133Q
GPX6	glutathione peroxidase 6 (olfactory)	ENSG00000198704	PAP45	50	26.0%	chr6	28582078	CCDS43432.1	c.349C>A	p.L117I
GSTM5	glutathione S-transferase mu 5	ENSG00000134201	PAP45	142	26.8%	chr1	110057832	CCDS811.1	c.286C>T	p.R96C
GPAM	glycerol-3-phosphate acyltransferase; mitochondrial	ENSG00000119927	PAP45	140	24.3%	chr10	113913450	CCDS7570.1	c.1422C>A	p.F474L
GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	ENSG00000115159	PAP45	45	31.1%	chr2	157040882	CCDS2202.1	c.19G>A	p.V7M
GDPD4	glycerophosphodiester phosphodiesterase domain containing 4	ENSG00000178795	PAP45	286	24.8%	chr11	76660012	CCDS8249.1	c.282G>T	p.W94C
GLDC	glycine dehydrogenase (decarboxylating)	ENSG00000178445	PAP45	84	33.3%	chr9	6582178	CCDS34987.1	c.1447G>A	p.D483N
GLTPD2	glycolipid transfer protein domain containing 2	ENSG00000182327	PAP45	179	18.4%	chr17	4639102	CCDS32534.1	c.56C>A	p.P19H
GP2	glycoprotein 2 (zymogen granule membrane)	ENSG00000169347	PAP45	55	30.9%	chr16	20234821	CCDS42128.1	c.1468G>A	p.D490N
GPM6A	glycoprotein M6A	ENSG00000150625	PAP45	65	20.0%	chr4	176810021	CCDS3824.1	c.499T>A	p.L167I
GPM6A	glycoprotein M6A	ENSG00000150625	PAP45	100	20.0%	chr4	176859874	CCDS3824.1	c.76C>T	p.P26S
GP5	glycoprotein V (platelet)	ENSG00000178732	PAP45	39	28.2%	chr3	195599258	CCDS3307.1	c.1043C>T	p.S348F
GP6	glycoprotein VI (platelet)	ENSG00000088053	PAP45	152	22.4%	chr19	60230903	CCDS42626.1	c.465G>T	p.K155N
GP6	glycoprotein VI (platelet)	ENSG00000088053	PAP45	182	11.5%	chr19	60235405	CCDS42626.1	c.239G>T	p.R80I
GLT25D1	glycosyltransferase 25 domain containing 1	ENSG00000130309	PAP45	79	30.4%	chr19	17531119	CCDS12363.1	c.-1G>T	p.IVS1-1-1SpliceAcceptor
GPC1	glypican 1	ENSG00000063660	PAP45	283	20.5%	chr2	241054292	CCDS2534.1	c.1589C>T	p.S530L
GPC4	glypican 4	ENSG00000076716	PAP45	254	20.5%	chrX	132266483	CCDS14637.1	c.1228G>A	p.D410N
GNAS	GNAS complex locus	ENSG00000087460	PAP45	302	23.5%	chr20	56861899	NM_080425	c.184G>A	p.E62K
GBF1	golgi brefeldin A resistant guanine nucleotide exchange factor 1	ENSG00000107862	PAP45	199	18.1%	chr10	104009803	CCDS7533.1	c.103G>T	p.E35X
GOLIM4	golgi integral membrane protein 4	ENSG00000173905	PAP45	59	25.4%	chr3	169243879	CCDS3204.1	c.499G>T	p.E167X
GOLM1	golgi membrane protein 1	ENSG00000135052	PAP45	134	19.4%	chr9	87832571	CCDS35054.1	c.1187A>C	p.K396T
GOLM1	golgi membrane protein 1	ENSG00000135052	PAP45	423	27.7%	chr9	87840349	CCDS35054.1	c.769G>T	p.E257X
GOLM1	golgi membrane protein 1	ENSG00000135052	PAP45	183	21.3%	chr9	87851286	CCDS35054.1	c.386G>T	p.R129M

GOLT1A	golgi transport 1 homolog A (S. cerevisiae)	ENSG00000174567	PAP45	111	26.1%	chr1	202435010	CCDS1443.1	c.-1G>T	p.IVS3-1-1SpliceAcceptor
GOLGA2	golgin A2	ENSG00000167110	PAP45	249	24.1%	chr9	130064696	CCDS6896.1	c.984G>T	p.K328N
GOLGA4	golgin A4	ENSG00000144674	PAP45	124	25.0%	chr3	37341996	CCDS2666.1	c.3615A>T	p.E1205D
GOLGA4	golgin A4	ENSG00000144674	PAP45	131	30.5%	chr3	37342054	CCDS2666.1	c.3673G>A	p.E1225K
GOLGA5	golgin A5	ENSG00000066455	PAP45	98	27.6%	chr14	92343023	CCDS9905.1	c.734T>G	p.M245R
GOLGB1	golgin B1	ENSG00000173230	PAP45	74	24.3%	chr3	122893661	CCDS3004.1	c.7225G>T	p.E2409X
GOLGB1	golgin B1	ENSG00000173230	PAP45	124	14.5%	chr3	122898444	CCDS3004.1	c.3601C>A	p.L1201I
GORAB	golgin; RAB6-interacting	ENSG00000120370	PAP45	204	27.0%	chr1	168775321	CCDS1289.1	c.483G>T	p.K161N
GON4L	gon-4-like (C. elegans)	ENSG00000116580	PAP45	39	28.2%	chr1	154058866	CCDS1121.1	c.723G>T	p.E241D
GNRHR	gonadotropin-releasing hormone receptor	ENSG00000109163	PAP45	151	24.5%	chr4	68292880	CCDS3517.1	c.-1G>A	p.IVS2+1-1SpliceDonor
GRHL1	grainyhead-like 1 (Drosophila)	ENSG00000134317	PAP45	81	28.4%	chr2	10021620	CCDS33144.1	c.334C>T	p.R112X
GRAMD1C	GRAM domain containing 1C	ENSG00000178075	PAP45	138	26.1%	chr3	115135163	CCDS33826.1	c.1325G>A	p.R442Q
GRAMD1C	GRAM domain containing 1C	ENSG00000178075	PAP45	115	21.7%	chr3	115137899	CCDS33826.1	c.1553G>A	p.R518Q
GIGYF1	GRB10 interacting GYF protein 1	ENSG00000146830	PAP45	432	25.2%	chr7	100118942	CCDS34708.1	c.2114G>A	p.R705Q
GAB4	GRB2-associated binding protein family; member 4	ENSG00000215568	PAP45	236	20.3%	chr22	15852804	CCDS42976.1	c.437G>A	p.S146N
GCOM1	GRINL1A complex locus	ENSG00000137878	PAP45	72	15.3%	chr15	55719008	CCDS32247.1	c.1092G>T	p.Q364H
GCC2	GRIP and coiled-coil domain containing 2	ENSG00000135968	PAP45	214	20.6%	chr2	108453733	CCDS33268.1	c.1516G>A	p.E506K
GAS2L2	growth arrest-specific 2 like 2	ENSG00000132139	PAP45	375	28.8%	chr17	31096281	CCDS11298.1	c.2348G>A	p.R783Q
GDF10	growth differentiation factor 10	ENSG00000107623	PAP45	393	28.0%	chr10	48048702	CCDS7220.1	c.1190C>T	p.P397L
GDF2	growth differentiation factor 2	ENSG00000128802	PAP45	195	15.9%	chr10	48036590	CCDS7219.1	c.110C>T	p.A37V
GRB10	growth factor receptor-bound protein 10	ENSG00000106070	PAP45	472	21.0%	chr7	50641540	CCDS43582.1	c.1260C>A	p.F420L
GHITM	growth hormone inducible transmembrane protein	ENSG00000165678	PAP45	71	25.4%	chr10	85900616	CCDS41542.1	c.953C>T	p.S318L
G3BP1	GTPase activating protein (SH3 domain) binding protein 1	ENSG00000145907	PAP45	147	27.9%	chr5	151163800	CCDS4319.1	c.1356G>T	p.Q452H
GAPVD1	GTPase activating protein and VPS9 domains 1	ENSG00000165219	PAP45	129	27.1%	chr9	127139557	CCDS35138.1	c.2824G>T	p.D942Y
GARNL3	GTPase activating Rap/RanGAP domain-like 3	ENSG00000136895	PAP45	136	27.9%	chr9	129157459	CCDS6869.1	c.1768C>T	p.R590W
GIMAP8	GTPase; IMAP family member 8	ENSG00000171115	PAP45	130	23.8%	chr7	149802062	CCDS34777.1	c.712G>A	p.G238R
GNAL	guanine nucleotide binding protein (G protein); alpha activating activity polypeptide; olfactory type	ENSG00000141404	PAP45	101	24.8%	chr18	11858638	CCDS11851.1	c.1007NULL>T	p.NULL-1FsIns1bp
GNAQ	guanine nucleotide binding protein (G protein); q polypeptide	ENSG00000156052	PAP45	232	24.6%	chr9	79727039	CCDS6658.1	c.179G>T	p.R60I
GNL3	guanine nucleotide binding protein-like 3 (nucleolar)	ENSG00000163938	PAP45	44	34.1%	chr3	52696327	CCDS2861.1	c.98G>T	p.R33I
GBP2	guanylate binding protein 2; interferon-inducible	ENSG00000162645	PAP45	73	35.6%	chr1	89355988	CCDS719.1	c.485C>A	p.S162Y
GBP2	guanylate binding protein 2; interferon-inducible	ENSG00000162645	PAP45	164	25.6%	chr1	89358548	CCDS719.1	c.330G>T	p.E110D
GBP5	guanylate binding protein 5	ENSG00000154451	PAP45	87	16.1%	chr1	89504684	CCDS722.1	c.801C>A	p.F267L
GBP7	guanylate binding protein 7	ENSG00000213512	PAP45	118	30.5%	chr1	89403102	CCDS720.1	c.218C>T	p.S73F
GBP6	guanylate binding protein family; member 6	ENSG00000183347	PAP45	118	11.0%	chr1	89620840	CCDS723.1	c.1182C>A	p.F394L
GUCY1A3	guanylate cyclase 1; soluble; alpha 3	ENSG00000164116	PAP45	198	27.3%	chr4	156837520	CCDS34085.1	c.51C>A	p.F17L
GUCY1B2	guanylate cyclase 1; soluble; beta 2	ENSG00000123201	PAP45	219	13.7%	chr13	50492775	ENST00000378172	c.913G>T	p.E305X
GUCY2F	guanylate cyclase 2F; retinal	ENSG00000101890	PAP45	48	22.9%	chrX	108525347	CCDS14545.1	c.2303C>A	p.P768H
GUCY2F	guanylate cyclase 2F; retinal	ENSG00000101890	PAP45	63	15.9%	chrX	108539040	CCDS14545.1	c.1805G>A	p.R602H
GUCY2F	guanylate cyclase 2F; retinal	ENSG00000101890	PAP45	120	25.8%	chrX	108605353	CCDS14545.1	c.469G>T	p.D157Y
GUCA1C	guanylate cyclase activator 1C	ENSG00000138472	PAP45	178	18.0%	chr3	110109705	CCDS2954.1	c.484G>T	p.D162Y
GUK1	guanylate kinase 1	ENSG00000143774	PAP45	141	22.7%	chr1	226396011	ENST00000366719	c.54C>A	p.F18L
HP	haptoglobin	ENSG00000197711	PAP45	31	32.3%	chr16	70667963	CCDS42193.1	c.529A>C	p.K177Q
HAUS3	HAUS augmin-like complex; subunit 3	ENSG00000214367	PAP45	91	27.5%	chr4	2212133	CCDS33941.1	c.339G>T	p.K113N
HEATR1	HEAT repeat containing 1	ENSG00000119285	PAP45	82	19.5%	chr1	234782027	CCDS31066.1	c.6241C>T	p.R2081X
HEATR5B	HEAT repeat containing 5B	ENSG00000008869	PAP45	188	18.1%	chr2	37089285	CCDS33181.1	c.4495G>A	p.E1499K
HEATR7B1	HEAT repeat containing 7B1	ENSG00000185038	PAP45	235	27.7%	chr2	234402419	ENST00000389758	c.4504G>A	p.D1502N
HSPH1	heat shock 105kDa/110kDa protein 1	ENSG00000120694	PAP45	237	27.4%	chr13	30610658	CCDS9340.1	c.2256G>T	p.E752D
HSPH1	heat shock 105kDa/110kDa protein 1	ENSG00000120694	PAP45	282	27.3%	chr13	30622147	CCDS9340.1	c.1081G>T	p.D361Y
HSPH1	heat shock 105kDa/110kDa protein 1	ENSG00000120694	PAP45	303	23.1%	chr13	30622191	CCDS9340.1	c.1037G>A	p.R346Q
HSPA14	heat shock 70kDa protein 14	ENSG00000187522	PAP45	76	25.0%	chr10	14937881	CCDS7103.1	c.926A>T	p.N309I

HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein; 78kDa)	ENSG00000044574	PAP45	162	27.8%	chr9	127041310	CCDS6863.1	c.727G>A	p.E243K
HSP90B3P	heat shock protein 90kDa beta (Grp94); member 3 (pseudogene)	ENSG00000203914	PAP45	99	16.2%	chr1	91881058	ENST00000370405	c.497T>C	p.L166P
HRSP12	heat-responsive protein 12	ENSG00000132541	PAP45	151	23.8%	chr8	99184259	CCDS6276.1	c.401C>T	p.T134M
HACE1	HECT domain and ankyrin repeat containing; E3 ubiquitin protein ligase 1	ENSG00000085382	PAP45	128	22.7%	chr6	105346151	CCDS5050.1	c.995G>A	p.R332Q
HERC3	hect domain and RLD 3	ENSG00000138641	PAP45	85	23.5%	chr4	89810325	CCDS34028.1	c.1810G>T	p.V604L
HERC4	hect domain and RLD 4	ENSG00000148634	PAP45	99	14.1%	chr10	69362539	CCDS41533.1	c.2683G>T	p.E895X
HERC5	hect domain and RLD 5	ENSG00000138646	PAP45	59	22.0%	chr4	89599589	CCDS3630.1	c.334C>A	p.L112I
HERC5	hect domain and RLD 5	ENSG00000138646	PAP45	70	25.7%	chr4	89616190	CCDS3630.1	c.1568C>A	p.S523Y
HECTD1	HECT domain containing 1	ENSG00000092148	PAP45	146	15.8%	chr14	30652392	CCDS41939.1	c.5906C>A	p.S1969Y
HECTD1	HECT domain containing 1	ENSG00000092148	PAP45	57	19.3%	chr14	30683880	CCDS41939.1	c.2515G>T	p.D839Y
HECW1	HECT; C2 and WW domain containing E3 ubiquitin protein ligase 1	ENSG00000002746	PAP45	163	29.4%	chr7	43444216	CCDS5469.2	c.891C>A	p.F297L
HECW2	HECT; C2 and WW domain containing E3 ubiquitin protein ligase 2	ENSG00000138411	PAP45	74	21.6%	chr2	196774307	CCDS33354.1	c.4658C>A	p.S1553Y
HECW2	HECT; C2 and WW domain containing E3 ubiquitin protein ligase 2	ENSG00000138411	PAP45	330	27.9%	chr2	196892831	CCDS33354.1	c.1028C>A	p.S343Y
HUWE1	HECT; UBA and WWE domain containing 1	ENSG00000086758	PAP45	106	14.2%	chrX	53588331	CCDS35301.1	c.11166C>A	p.F3722L
HHAT	hedgehog acyltransferase	ENSG00000054392	PAP45	114	28.1%	chr1	208863639	CCDS1495.1	c.-1T>C	p.IVS10+2-1SpliceDonor
HHATL	hedgehog acyltransferase-like	ENSG00000010282	PAP45	113	18.6%	chr3	42716257	CCDS2704.1	c.171G>T	p.K57N
HHIP	hedgehog interacting protein	ENSG00000164161	PAP45	193	18.7%	chr4	145787331	CCDS3762.1	c.54C>A	p.F18L
HELB	helicase (DNA) B	ENSG00000127311	PAP45	137	20.4%	chr12	64994100	CCDS8976.1	c.1748C>T	p.S583L
HELZ	helicase with zinc finger	ENSG00000198265	PAP45	459	25.7%	chr17	62645226	CCDS42374.1	c.157G>T	p.E53X
HELQ	helicase; POLQ-like	ENSG00000163312	PAP45	104	20.2%	chr4	84588991	CCDS3603.1	c.1160T>G	p.I387S
HLTF	helicase-like transcription factor	ENSG00000071794	PAP45	61	24.6%	chr3	150274777	CCDS33875.1	c.444G>T	p.M148I
HPGDS	hematopoietic prostaglandin D synthase	ENSG00000163106	PAP45	123	24.4%	chr4	95448900	CCDS3640.1	c.244G>T	p.E82X
HPGDS	hematopoietic prostaglandin D synthase	ENSG00000163106	PAP45	83	20.5%	chr4	95474706	CCDS3640.1	c.98G>T	p.R33I
HMCN1	hemicentin 1	ENSG00000143341	PAP45	106	31.1%	chr1	183970542	CCDS30956.1	c.8C>T	p.S3F
HMCN1	hemicentin 1	ENSG00000143341	PAP45	268	25.4%	chr1	184160880	CCDS30956.1	c.1364G>C	p.S455T
HMCN1	hemicentin 1	ENSG00000143341	PAP45	151	23.8%	chr1	184250930	CCDS30956.1	c.4647A>C	p.K1549N
HMCN1	hemicentin 1	ENSG00000143341	PAP45	79	29.1%	chr1	184410344	CCDS30956.1	c.15890G>A	p.R5297H
HEMGN	hemogen	ENSG00000136929	PAP45	115	13.9%	chr9	99732279	CCDS6731.1	c.1219G>A	p.D407N
HEPACAM2	HEPACAM family member 2	ENSG00000188175	PAP45	156	26.3%	chr7	92675948	CCDS43616.1	c.893G>A	p.R298H
HS3ST4	heparan sulfate (glucosamine) 3-O-sulfotransferase 4	ENSG00000182601	PAP45	378	24.6%	chr16	26054694	NM_006040	c.995G>A	p.R332Q
HPSE	heparanase	ENSG00000173083	PAP45	64	29.7%	chr4	84441153	CCDS3602.1	c.1456C>A	p.H486N
HNF4A	hepatocyte nuclear factor 4; alpha	ENSG00000101076	PAP45	75	30.7%	chr20	42463430	CCDS13330.1	c.4C>T	p.R2X
HPS3	Hermansky-Pudlak syndrome 3	ENSG00000163755	PAP45	202	16.8%	chr3	150340838	CCDS3140.1	c.575C>A	p.S192Y
HPS5	Hermansky-Pudlak syndrome 5	ENSG00000110756	PAP45	75	40.0%	chr11	18274984	CCDS7836.1	c.1447G>T	p.E483X
HPS5	Hermansky-Pudlak syndrome 5	ENSG00000110756	PAP45	113	24.8%	chr11	18275737	CCDS7836.1	c.1268A>C	p.K423T
HP1BP3	heterochromatin protein 1; binding protein 3	ENSG00000127483	PAP45	164	23.2%	chr1	20970114	CCDS30621.1	c.550C>T	p.R184X
HNRNPA2B	heterogeneous nuclear ribonucleoprotein A2/B1	ENSG00000122566	PAP45	159	23.9%	chr7	26203515	CCDS43557.1	c.245G>T	p.R82I
HK1	hexokinase 1	ENSG00000156515	PAP45	171	32.2%	chr10	70806847	CCDS7289.1	c.1039G>A	p.E347K
HFM1	HFM1; ATP-dependent DNA helicase homolog (S. cerevisiae)	ENSG00000162669	PAP45	66	15.2%	chr1	91557449	CCDS30769.2	c.2669G>A	p.R890Q
HDLBP	high density lipoprotein binding protein	ENSG00000115677	PAP45	79	13.9%	chr2	241843512	CCDS2547.1	c.1030C>T	p.R344X
HMGA2	high mobility group AT-hook 2	ENSG00000149948	PAP45	89	21.3%	chr12	64522230	ENST00000393577	c.299C>A	p.P100Q
HIAT1	hippocampus abundant transcript 1	ENSG00000156875	PAP45	89	14.6%	chr1	100307807	CCDS763.1	c.869G>T	p.G290V
HNMT	histamine N-methyltransferase	ENSG00000150540	PAP45	261	13.8%	chr2	138487898	CCDS2181.1	c.607G>T	p.D203Y
HAT1	histone acetyltransferase 1	ENSG00000128708	PAP45	120	26.7%	chr2	172530163	CCDS2245.1	c.368C>A	p.T123K
HIST1H2AD	histone cluster 1; H2ad	ENSG00000196866	PAP45	82	29.3%	chr6	27968721	CCDS4639.1	c.186G>T	p.E62D
HIST1H2BC	histone cluster 1; H2bc	ENSG00000180596	PAP45	153	29.4%	chr6	26231849	CCDS4584.1	c.263C>T	p.S88L

HIST1H3J	histone cluster 1; H3j	ENSG00000197153	PAP45	144	24.3%	chr6	27966258	CCDS4638.1	c.292G>A	p.E98K
HDAC2	histone deacetylase 2	ENSG00000196591	PAP45	80	20.0%	chr6	114383987	CCDS43493.1	c.662G>A	p.R221Q
HDAC5	histone deacetylase 5	ENSG00000108840	PAP45	143	26.6%	chr17	39525152	CCDS32663.1	c.949G>A	p.G317S
HDAC8	histone deacetylase 8	ENSG00000147099	PAP45	138	15.9%	chrX	71704325	ENST00000340176	c.485C>A	p.S162Y
HTATSF1	HIV-1 Tat specific factor 1	ENSG00000102241	PAP45	81	29.6%	chrX	135421254	CCDS14657.1	c.1684G>A	p.E562K
HOXB13	homeobox B13	ENSG00000159184	PAP45	102	30.4%	chr17	44160785	CCDS11536.1	c.170C>T	p.A57V
HOXB5	homeobox B5	ENSG00000120075	PAP45	218	29.4%	chr17	44026017	CCDS11530.1	c.27C>A	p.F9L
HOXB9	homeobox B9	ENSG00000170689	PAP45	214	10.7%	chr17	44055308	CCDS11534.1	c.706C>T	p.R236W
HOXD10	homeobox D10	ENSG00000128710	PAP45	328	28.0%	chr2	176690072	CCDS2266.1	c.265C>T	p.R89X
HOXD10	homeobox D10	ENSG00000128710	PAP45	270	11.9%	chr2	176690181	CCDS2266.1	c.374C>T	p.S125L
HOXD8	homeobox D8	ENSG00000175879	PAP45	67	37.3%	chr2	176704362	CCDS2268.1	c.649C>A	p.L217I
HIPK1	homeodomain interacting protein kinase 1	ENSG00000163349	PAP45	325	25.5%	chr1	114316158	CCDS868.1	c.3203G>T	p.R1068I
HIPK3	homeodomain interacting protein kinase 3	ENSG00000110422	PAP45	162	19.1%	chr11	33330290	CCDS7884.1	c.3074G>A	p.R1025Q
HIPK4	homeodomain interacting protein kinase 4	ENSG00000160396	PAP45	156	19.2%	chr19	45581819	CCDS12555.1	c.533C>T	p.S178L
HUNK	hormonally up-regulated Neu-associated kinase	ENSG00000142149	PAP45	200	15.0%	chr21	32253025	CCDS13610.1	c.-1G>T	p.IVS4-1-1SpliceAcceptor
HCFC1	host cell factor C1 (VP16-accessory protein)	ENSG00000172534	PAP45	165	24.2%	chrX	152870581	CCDS44020.1	c.5165G>A	p.S1722N
HCFC1	host cell factor C1 (VP16-accessory protein)	ENSG00000172534	PAP45	95	32.6%	chrX	152878979	CCDS44020.1	c.985G>A	p.A329T
HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	ENSG00000095951	PAP45	79	19.0%	chr6	12123855	CCDS43426.1	c.8G>A	p.R3Q
HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	ENSG00000095951	PAP45	132	22.7%	chr6	12229500	CCDS43426.1	c.1486G>T	p.E496X
HABP4	hyaluronan binding protein 4	ENSG00000130956	PAP45	70	21.4%	chr9	98260490	CCDS6719.1	c.358C>T	p.R120W
HYDIN	hydrocephalus inducing homolog (mouse)	ENSG00000157423	PAP45	101	13.9%	chr16	69483932	CCDS42189.1	c.9247T>G	p.F3083V
HAO1	hydroxyacid oxidase (glycolate oxidase) 1	ENSG00000101323	PAP45	277	23.8%	chr20	7842944	CCDS13100.1	c.412G>T	p.E138X
HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	ENSG00000164120	PAP45	213	19.2%	chr4	175679772	CCDS3821.1	c.115C>A	p.L39I
HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12	ENSG00000149084	PAP45	79	20.3%	chr11	43732189	CCDS7905.1	c.225G>T	p.M75I
HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2	ENSG00000086696	PAP45	99	25.3%	chr16	80659371	CCDS10936.1	c.361G>A	p.A121T
HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	ENSG00000025423	PAP45	124	30.6%	chr12	55464910	CCDS8925.1	c.579G>T	p.E193D
HIC2	hypermethylated in cancer 2	ENSG00000169635	PAP45	51	19.6%	chr22	20129937	CCDS13789.1	c.753G>T	p.K251N
HCRTR2	hypocretin (orexin) receptor 2	ENSG00000137252	PAP45	252	27.4%	chr6	55228113	CCDS4956.1	c.623C>T	p.T208M
IKZF3	IKAROS family zinc finger 3 (Aiolos)	ENSG00000161405	PAP45	128	20.3%	chr17	35176104	CCDS11346.1	c.995C>T	p.S332L
ITK	IL2-inducible T-cell kinase	ENSG00000113263	PAP45	56	33.9%	chr5	156568515	CCDS4336.1	c.176G>A	p.R59Q
IGHM	immunoglobulin heavy constant mu	ENSG00000211899	PAP45	149	26.2%	chr14	105393234	ENST00000390559	c.134G>T	p.R45I
IGKV5-2	immunoglobulin kappa variable 5-2	ENSG00000211599	PAP45	143	29.4%	chr2	88978207	ENST00000390244	c.137G>A	p.S46N
IGLV3-19	immunoglobulin lambda variable 3-19	ENSG00000211663	PAP45	263	27.4%	chr22	21393423	ENST00000390309	c.130G>T	p.D44Y
IGSF1	immunoglobulin superfamily; member 1	ENSG00000147255	PAP45	408	25.0%	chrX	130248292	CCDS14629.1	c.38T>C	p.L13P
IGSF10	immunoglobulin superfamily; member 10	ENSG00000152580	PAP45	275	18.2%	chr3	152647552	CCDS3160.1	c.2907C>A	p.F969L
IRG1	immunoresponsive 1 homolog (mouse)	ENSG00000102794	PAP45	350	29.1%	chr13	76429480	ENST00000377462	c.805G>A	p.V269M
IRG1	immunoresponsive 1 homolog (mouse)	ENSG00000102794	PAP45	138	19.6%	chr13	76430102	ENST00000377462	c.1427C>A	p.S476Y
IMPACT	Impact homolog (mouse)	ENSG00000154059	PAP45	58	20.7%	chr18	20262841	CCDS11886.1	c.176C>A	p.P59Q
INADL	InaD-like (Drosophila)	ENSG00000132849	PAP45	210	20.5%	chr1	62102832	CCDS617.2	c.2774G>A	p.R925K
IVNS1ABP	influenza virus NS1A binding protein	ENSG00000116679	PAP45	334	21.9%	chr1	183535548	CCDS1368.1	c.1592G>A	p.R531Q
ITPA	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	ENSG00000125877	PAP45	153	10.5%	chr20	3138222	CCDS13051.1	c.25A>C	p.K9Q
IPPK	inositol 1;3;4;5;6-pentakisphosphate 2-kinase	ENSG00000127080	PAP45	354	26.3%	chr9	94440326	CCDS6699.1	c.694G>A	p.E232K
ITPRIP	inositol 1;4;5-triphosphate receptor interacting protein	ENSG00000148841	PAP45	247	29.6%	chr10	106065138	CCDS7557.1	c.662G>A	p.R221H
ITPRIPL1	inositol 1;4;5-triphosphate receptor interacting protein-like 1	ENSG00000198885	PAP45	278	29.1%	chr2	96356768	CCDS33250.1	c.696G>T	p.E232D
ITPR1	inositol 1;4;5-triphosphate receptor; type 1	ENSG00000150995	PAP45	115	31.3%	chr3	4656078	NM_001168272	c.290A>G	p.D97G
ITPR1	inositol 1;4;5-triphosphate receptor; type 1	ENSG00000150995	PAP45	225	20.4%	chr3	4678835	NM_001168272	c.1276C>T	p.R426W
ITPKB	inositol 1;4;5-trisphosphate 3-kinase B	ENSG00000143772	PAP45	96	30.2%	chr1	224889123	CCDS1555.1	c.2713C>T	p.P905S
IP6K1	inositol hexakisphosphate kinase 1	ENSG00000176095	PAP45	155	25.2%	chr3	49760348	CCDS33760.1	c.130G>T	p.D44Y

IP6K2	inositol hexakisphosphate kinase 2	ENSG00000068745	PAP45	252	11.9%	chr3	48700967	CCDS2777.1	c.1024G>A	p.E342K
IMPAD1	inositol monophosphatase domain containing 1	ENSG00000104331	PAP45	123	18.7%	chr8	58038932	CCDS6169.1	c.1054G>T	p.D352Y
INPP4A	inositol polyphosphate-4-phosphatase; type I; 107kDa	ENSG00000040933	PAP45	70	21.4%	chr2	98564501	NM_001566	c.2715G>T	p.K905N
INPP5F	inositol polyphosphate-5-phosphatase F	ENSG00000198825	PAP45	62	25.8%	chr10	121546295	CCDS7616.1	c.748G>A	p.E250K
IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	ENSG00000141401	PAP45	75	18.7%	chr18	12020398	CCDS11855.1	c.808G>A	p.A270T
IRS4	insulin receptor substrate 4	ENSG00000133124	PAP45	84	26.2%	chrX	107862609	CCDS14544.1	c.3622G>A	p.A1208T
IRS4	insulin receptor substrate 4	ENSG00000133124	PAP45	153	38.6%	chrX	107863553	CCDS14544.1	c.2678C>A	p.S893Y
IRS4	insulin receptor substrate 4	ENSG00000133124	PAP45	171	26.9%	chrX	107863918	CCDS14544.1	c.2313G>T	p.K771N
IDE	insulin-degrading enzyme	ENSG00000119912	PAP45	172	23.8%	chr10	94213552	CCDS7421.1	c.2677C>T	p.R893X
IGF1R	insulin-like growth factor 1 receptor	ENSG00000140443	PAP45	109	23.9%	chr15	97272106	CCDS10378.1	c.1502C>T	p.S501L
IGF2R	insulin-like growth factor 2 receptor	ENSG00000197081	PAP45	93	19.4%	chr6	160388190	CCDS5273.1	c.2061G>T	p.K687N
ITM2A	integral membrane protein 2A	ENSG00000078596	PAP45	100	28.0%	chrX	78503257	CCDS14444.1	c.777G>T	p.K259N
ITM2A	integral membrane protein 2A	ENSG00000078596	PAP45	156	26.3%	chrX	78503569	CCDS14444.1	c.616C>T	p.R206C
INTS10	integrator complex subunit 10	ENSG00000104613	PAP45	234	23.9%	chr8	19753489	CCDS6011.2	c.2026C>T	p.R676C
ITGB1BP1	integrin beta 1 binding protein 1	ENSG00000119185	PAP45	88	18.2%	chr2	9469947	CCDS1662.1	c.190C>T	p.R64X
ITGA1	integrin; alpha 1	ENSG00000213949	PAP45	253	20.9%	chr5	52225355	CCDS3955.1	c.1017C>A	p.F339L
ITGA2	integrin; alpha 2 (CD49B; alpha 2 subunit of VLA-2 receptor)	ENSG00000164171	PAP45	77	14.3%	chr5	52406052	CCDS3957.1	c.2652G>T	p.K884N
ITGA7	integrin; alpha 7	ENSG00000135424	PAP45	576	26.0%	chr12	54377865	CCDS8888.1	c.1290G>T	p.E430D
ITGA8	integrin; alpha 8	ENSG00000077943	PAP45	81	29.6%	chr10	15674305	CCDS31155.1	c.2216C>T	p.S739F
ITGA8	integrin; alpha 8	ENSG00000077943	PAP45	73	24.7%	chr10	15695755	CCDS31155.1	c.1463C>A	p.T488N
ITGAD	integrin; alpha D	ENSG00000156886	PAP45	82	22.0%	chr16	31313160	CCDS32438.1	c.134C>A	p.S45Y
ITGAD	integrin; alpha D	ENSG00000156886	PAP45	125	26.4%	chr16	31344845	CCDS32438.1	c.3381C>A	p.F1127L
ITGAE	integrin; alpha E (antigen CD103; human mucosal lymphocyte antigen 1; alpha polypeptide)	ENSG00000083457	PAP45	115	22.6%	chr17	3610233	CCDS32531.1	c.696C>A	p.F232L
ITGAX	integrin; alpha X (complement component 3 receptor 4 subunit)	ENSG00000140678	PAP45	72	25.0%	chr16	31281558	CCDS10711.1	c.1342G>A	p.E448K
ITIH2	inter-alpha (globulin) inhibitor H2	ENSG00000151655	PAP45	138	20.3%	chr10	7805498	CCDS31141.1	c.946G>A	p.D316N
ITIH5	inter-alpha (globulin) inhibitor H5	ENSG00000123243	PAP45	104	12.5%	chr10	7699135	CCDS31139.1	c.769G>A	p.D257N
ITIH5L	inter-alpha (globulin) inhibitor H5-like	ENSG00000102313	PAP45	175	28.0%	chrX	54800806	CCDS14361.1	c.2426G>T	p.R809I
IFNGR2	interferon gamma receptor 2 (interferon gamma transducer 1)	ENSG00000159128	PAP45	207	29.5%	chr21	33715796	CCDS33544.1	c.346C>T	p.R116X
ISG20L2	interferon stimulated exonuclease gene 20kDa-like 2	ENSG00000143319	PAP45	164	23.8%	chr1	154963992	CCDS1153.1	c.77G>A	p.R26Q
IFNA8	interferon; alpha 8	ENSG00000120242	PAP45	89	20.2%	chr9	21399325	CCDS6507.1	c.150C>A	p.F50L
IFNB1	interferon; beta 1; fibroblast	ENSG00000171855	PAP45	143	18.2%	chr9	21067838	CCDS6495.1	c.31C>T	p.L11F
IFI44L	interferon-induced protein 44-like	ENSG00000137959	PAP45	200	27.0%	chr1	78868060	CCDS687.1	c.478C>T	p.R160C
IFIT1B	interferon-induced protein with tetratricopeptide repeats 1B	ENSG00000204010	PAP45	115	27.8%	chr10	91133714	CCDS31242.1	c.664C>A	p.L222I
IFRD1	interferon-related developmental regulator 1	ENSG00000006652	PAP45	84	28.6%	chr7	111900072	CCDS34736.1	c.1186C>T	p.R396X
IL1F8	interleukin 1 family; member 8 (eta)	ENSG00000136696	PAP45	118	20.3%	chr2	113500157	CCDS2109.1	c.385G>T	p.G129X
IL1RAPL1	interleukin 1 receptor accessory protein-like 1	ENSG00000169306	PAP45	196	19.9%	chrX	29211041	CCDS14218.1	c.148C>T	p.R50X
IL1RAPL2	interleukin 1 receptor accessory protein-like 2	ENSG00000189108	PAP45	74	31.1%	chrX	104871223	CCDS14517.1	c.931G>T	p.E311X
IL1RL2	interleukin 1 receptor-like 2	ENSG00000115598	PAP45	117	24.8%	chr2	102201956	CCDS2056.1	c.836G>A	p.R279Q
IL12RB2	interleukin 12 receptor; beta 2	ENSG00000081985	PAP45	729	26.1%	chr1	67634217	CCDS638.1	c.2446G>A	p.A816T
IL13RA2	interleukin 13 receptor; alpha 2	ENSG00000123496	PAP45	70	22.9%	chrX	114154616	CCDS14565.1	c.493C>A	p.L165I
IL17RA	interleukin 17 receptor A	ENSG00000177663	PAP45	70	24.3%	chr22	15958812	CCDS13739.1	c.289G>A	p.E97K
IL18R1	interleukin 18 receptor 1	ENSG00000115604	PAP45	118	22.0%	chr2	102379552	CCDS2060.1	c.1400G>T	p.R467I
IL18RAP	interleukin 18 receptor accessory protein	ENSG00000115607	PAP45	232	25.4%	chr2	102434919	CCDS2061.1	c.1646C>A	p.S549Y
IL2RB	interleukin 2 receptor; beta	ENSG00000100385	PAP45	215	11.2%	chr22	35854156	CCDS13942.1	c.1582C>T	p.R528C
IL20	interleukin 20	ENSG00000162891	PAP45	354	20.3%	chr1	205106489	CCDS1470.1	c.263G>T	p.R88I
IL31RA	interleukin 31 receptor A	ENSG00000164509	PAP45	86	20.9%	chr5	55200451	CCDS3970.2	c.230G>T	p.G77V
IL5RA	interleukin 5 receptor; alpha	ENSG00000091181	PAP45	279	22.9%	chr3	3086970	CCDS2559.1	c.1202T>C	p.I401T
IL5RA	interleukin 5 receptor; alpha	ENSG00000091181	PAP45	60	18.3%	chr3	3112087	CCDS2559.1	c.751G>T	p.G251X
IL6	interleukin 6 (interferon; beta 2)	ENSG00000136244	PAP45	379	22.4%	chr7	22735712	CCDS5375.1	c.379G>T	p.E127X
IL6ST	interleukin 6 signal transducer (gp130; oncostatin M receptor)	ENSG00000134352	PAP45	65	29.2%	chr5	55286399	CCDS3971.1	c.1446A>C	p.L482F

ILF2	interleukin enhancer binding factor 2; 45kDa	ENSG00000143621	PAP45	51	21.6%	chr1	151904416	CCDS1050.1	c.481G>A	p.E161K
INA	internexin neuronal intermediate filament protein; alpha	ENSG00000148798	PAP45	64	32.8%	chr10	105038381	CCDS7545.1	c.1465A>G	p.I489V
IMPG1	interphotoreceptor matrix proteoglycan 1	ENSG00000112706	PAP45	122	17.2%	chr6	76771895	CCDS4985.1	c.964C>A	p.L322I
ISX	intestine-specific homeobox	ENSG00000175329	PAP45	466	24.9%	chr22	33811525	CCDS33640.1	c.577G>C	p.A193P
IFT172	intraflagellar transport 172 homolog (Chlamydomonas)	ENSG00000138002	PAP45	199	23.6%	chr2	27537444	CCDS1755.1	c.2463G>T	p.K821N
IFT172	intraflagellar transport 172 homolog (Chlamydomonas)	ENSG00000138002	PAP45	123	24.4%	chr2	27537773	CCDS1755.1	c.2309T>C	p.I770T
IFT172	intraflagellar transport 172 homolog (Chlamydomonas)	ENSG00000138002	PAP45	73	23.3%	chr2	27559690	CCDS1755.1	c.540C>A	p.F180L
IFT52	intraflagellar transport 52 homolog (Chlamydomonas)	ENSG00000101052	PAP45	130	24.6%	chr20	41665919	CCDS33470.1	c.313G>T	p.E105X
IFT80	intraflagellar transport 80 homolog (Chlamydomonas)	ENSG00000068885	PAP45	82	25.6%	chr3	161582201	CCDS3188.1	c.43G>T	p.E15X
IFT81	intraflagellar transport 81 homolog (Chlamydomonas)	ENSG00000122970	PAP45	68	20.6%	chr12	109102634	CCDS41831.1	c.1213C>T	p.R405X
IFT88	intraflagellar transport 88 homolog (Chlamydomonas)	ENSG00000032742	PAP45	103	29.1%	chr13	20135678	CCDS31944.1	c.2137A>C	p.K713Q
INVS	inversin	ENSG00000119509	PAP45	55	23.6%	chr9	102086445	CCDS6746.1	c.1807C>T	p.R603X
IQSEC1	IQ motif and Sec7 domain 1	ENSG00000144711	PAP45	256	22.7%	chr3	12953122	CCDS33703.1	c.436C>T	p.R146C
IQSEC3	IQ motif and Sec7 domain 3	ENSG00000120645	PAP45	88	33.0%	chr12	145223	CCDS31725.1	c.1968C>A	p.F656L
IQUB	IQ motif and ubiquitin domain containing	ENSG00000164675	PAP45	95	33.7%	chr7	122892273	CCDS5787.1	c.1608A>C	p.E536D
IQCG	IQ motif containing G	ENSG00000114473	PAP45	172	23.3%	chr3	199143459	CCDS3331.1	c.627C>A	p.F209L
IQGAP1	IQ motif containing GTPase activating protein 1	ENSG00000140575	PAP45	137	30.7%	chr15	88797467	CCDS10362.1	c.1426T>C	p.W476R
IQGAP3	IQ motif containing GTPase activating protein 3	ENSG00000183856	PAP45	574	23.2%	chr1	154775406	CCDS1144.1	c.3100A>G	p.T1034A
IQCH	IQ motif containing H	ENSG00000103599	PAP45	219	27.4%	chr15	65451554	CCDS32273.1	c.805G>T	p.D269Y
IVD	isovaleryl-CoA dehydrogenase	ENSG00000128928	PAP45	325	26.2%	chr15	38491153	CCDS10057.1	c.658C>T	p.R220W
ISM2	isthmin 2 homolog (zebrafish)	ENSG00000100593	PAP45	126	31.7%	chr14	77020600	CCDS9864.1	c.446G>T	p.R149I
JAK2	Janus kinase 2	ENSG00000096968	PAP45	192	18.2%	chr9	5044606	CCDS6457.1	c.658G>T	p.D220Y
JAK3	Janus kinase 3	ENSG00000105639	PAP45	176	33.5%	chr19	17812123	CCDS12366.1	c.1170G>T	p.K390N
JAKMIP1	janus kinase and microtubule interacting protein 1	ENSG00000152969	PAP45	376	26.1%	chr4	6134370	CCDS3385.1	c.968G>A	p.R323Q
JRKL	jerky homolog-like (mouse)	ENSG00000183340	PAP45	203	23.2%	chr11	95763862	CCDS8308.1	c.401G>T	p.S134I
JHDM1D	jumonji C domain containing histone demethylase 1 homolog D (S. cerevisiae)	ENSG00000006459	PAP45	58	19.0%	chr7	139457375	CCDS43658.1	c.1417C>T	p.R473X
JMJD1C	jumonji domain containing 1C	ENSG00000171988	PAP45	151	25.2%	chr10	64622728	CCDS41532.1	c.6052C>T	p.Q2018X
JPH1	junctophilin 1	ENSG00000104369	PAP45	116	22.4%	chr8	75312035	CCDS6217.1	c.1963C>A	p.L655I
JPH3	junctophilin 3	ENSG00000154118	PAP45	164	27.4%	chr16	86194353	CCDS10962.1	c.100A>G	p.K34E
KAT2B	K(lysine) acetyltransferase 2B	ENSG00000114166	PAP45	111	27.9%	chr3	20156828	CCDS2634.1	c.1972G>T	p.E658X
KALRN	kalirin; RhoGEF kinase	ENSG00000160145	PAP45	49	20.4%	chr3	125429535	CCDS3027.1	c.76C>T	p.R26W
KALRN	kalirin; RhoGEF kinase	ENSG00000160145	PAP45	63	33.3%	chr3	125834160	CCDS3028.1	c.289C>T	p.R97C
KPNB1	karyopherin (importin) beta 1	ENSG00000108424	PAP45	122	21.3%	chr17	43113006	CCDS11513.1	c.2602G>T	p.E868X
KATNA1	katanin p60 (ATPase-containing) subunit A 1	ENSG00000186625	PAP45	107	20.6%	chr6	149966124	CCDS5217.1	c.702C>A	p.F234L
KATNAL1	katanin p60 subunit A-like 1	ENSG00000102781	PAP45	157	21.0%	chr13	29712616	CCDS31956.1	c.707G>T	p.G236V
KATNAL2	katanin p60 subunit A-like 2	ENSG00000167216	PAP45	85	23.5%	chr18	42839991	CCDS32828.1	c.301G>T	p.D101Y
KLHDC3	kelch domain containing 3	ENSG00000124702	PAP45	225	22.2%	chr6	43094141	CCDS4880.1	c.602G>A	p.R201H
KLHDC3	kelch domain containing 3	ENSG00000124702	PAP45	232	25.4%	chr6	43094188	CCDS4880.1	c.649C>T	p.R217X
KLHDC8A	kelch domain containing 8A	ENSG00000162873	PAP45	140	27.1%	chr1	203573228	CCDS30985.1	c.975G>T	p.K325N
KBTBD2	kelch repeat and BTB (POZ) domain containing 2	ENSG00000170852	PAP45	285	22.1%	chr7	32876177	CCDS34614.1	c.1177G>T	p.E393X
KBTBD2	kelch repeat and BTB (POZ) domain containing 2	ENSG00000170852	PAP45	123	20.3%	chr7	32876575	CCDS34614.1	c.779G>T	p.R260I
KBTBD8	kelch repeat and BTB (POZ) domain containing 8	ENSG00000163376	PAP45	215	19.1%	chr3	67136766	CCDS2906.1	c.607G>T	p.E203X
KLHL11	kelch-like 11 (Drosophila)	ENSG00000178502	PAP45	124	23.4%	chr17	37264849	CCDS11411.1	c.796C>A	p.L266I
KLHL15	kelch-like 15 (Drosophila)	ENSG00000174010	PAP45	305	19.0%	chrX	23916102	CCDS35217.1	c.1672G>A	p.D558N
KLHL18	kelch-like 18 (Drosophila)	ENSG00000114648	PAP45	67	22.4%	chr3	47351190	CCDS33749.1	c.775G>T	p.E259X
KLHL3	kelch-like 3 (Drosophila)	ENSG00000146021	PAP45	68	19.1%	chr5	137021823	CCDS4192.1	c.799G>T	p.D267Y
KLHL31	kelch-like 31 (Drosophila)	ENSG00000124743	PAP45	324	22.2%	chr6	53627042	CCDS34478.1	c.988A>G	p.K330E
KLHL4	kelch-like 4 (Drosophila)	ENSG00000102271	PAP45	128	18.8%	chrX	86777405	CCDS14456.1	c.1899C>A	p.C633X
KLHL7	kelch-like 7 (Drosophila)	ENSG00000122550	PAP45	103	46.6%	chr7	23150102	CCDS34609.1	c.726C>A	p.F242L
KLHL7	kelch-like 7 (Drosophila)	ENSG00000122550	PAP45	124	28.2%	chr7	23158218	CCDS34609.1	c.801G>T	p.M267I
KLHL8	kelch-like 8 (Drosophila)	ENSG00000145332	PAP45	50	20.0%	chr4	88335540	CCDS3617.1	c.176G>A	p.R59Q
KEL	Kell blood group; metallo-endopeptidase	ENSG00000197993	PAP45	190	25.3%	chr7	142351548	CCDS34766.1	c.1475G>A	p.R492Q
KEL	Kell blood group; metallo-endopeptidase	ENSG00000197993	PAP45	290	27.2%	chr7	142368200	CCDS34766.1	c.337G>T	p.E113X

KRT1	keratin 1	ENSG00000167768	PAP45	142	25.4%	chr12	51356333	CCDS8836.1	c.1468G>T	p.E490X
KRT12	keratin 12	ENSG00000187242	PAP45	336	28.3%	chr17	36276571	CCDS11378.1	c.394C>A	p.L132I
KRT23	keratin 23 (histone deacetylase inducible)	ENSG00000108244	PAP45	92	17.4%	chr17	36338385	CCDS11380.1	c.637G>T	p.E213X
KRT25	keratin 25	ENSG00000204897	PAP45	163	20.2%	chr17	36164692	CCDS11373.1	c.358C>T	p.P120S
KRT25	keratin 25	ENSG00000204897	PAP45	289	28.0%	chr17	36164964	CCDS11373.1	c.86G>T	p.S29I
KRT27	keratin 27	ENSG00000171446	PAP45	145	24.8%	chr17	36191991	CCDS11375.1	c.281G>A	p.R94H
KRT36	keratin 36	ENSG00000126337	PAP45	127	15.0%	chr17	36899201	CCDS11395.1	c.442G>A	p.E148K
KRT37	keratin 37	ENSG00000108417	PAP45	110	27.3%	chr17	36831192	CCDS32653.1	c.1194G>T	p.E398D
KRT71	keratin 71	ENSG00000139648	PAP45	104	34.6%	chr12	51226436	CCDS8831.1	c.1226C>T	p.A409V
KRT76	keratin 76	ENSG00000185069	PAP45	163	24.5%	chr12	51453657	CCDS8838.1	c.852G>T	p.E284D
KRT77	keratin 77	ENSG00000189182	PAP45	141	25.5%	chr12	51376445	CCDS8837.1	c.795G>T	p.E265D
KRT77	keratin 77	ENSG00000189182	PAP45	428	17.1%	chr12	51377738	CCDS8837.1	c.753G>T	p.K251N
KRT78	keratin 78	ENSG00000170423	PAP45	169	29.0%	chr12	51528712	CCDS8840.1	c.270G>T	p.Q90H
KRT79	keratin 79	ENSG00000185640	PAP45	365	10.4%	chr12	51510307	CCDS8839.1	c.735G>T	p.E245D
KRT82	keratin 82	ENSG00000161850	PAP45	176	27.8%	chr12	51075075	CCDS8826.1	c.1493C>A	p.S498Y
KRT86	keratin 86	ENSG00000170442	PAP45	47	36.2%	chr12	50985384	CCDS41785.1	c.829G>A	p.E277K
KRTAP10-6	keratin associated protein 10-6	ENSG00000188155	PAP45	54	24.1%	chr21	44836059	CCDS42959.1	c.735G>T	p.E245D
KRTAP12-1	keratin associated protein 12-1	ENSG00000187175	PAP45	256	22.7%	chr21	44926217	CCDS42966.1	c.250C>A	p.L84I
KRTAP12-3	keratin associated protein 12-3	ENSG00000205439	PAP45	251	19.9%	chr21	44891550	CCDS42962.1	c.747C>A	p.C249X
KRTAP13-4	keratin associated protein 13-4	ENSG00000186971	PAP45	390	30.5%	chr21	30724726	CCDS13592.1	c.262C>T	p.R88W
KPRP	keratinocyte proline-rich protein	ENSG00000203786	PAP45	436	28.4%	chr1	150999551	CCDS30862.1	c.863C>A	p.S288Y
KERA	keratocan	ENSG00000139330	PAP45	141	14.2%	chr12	89973712	CCDS9037.1	c.478G>T	p.G160W
KHDRBS1	KH domain containing; RNA binding; signal transduction associated 1	ENSG00000121774	PAP45	67	31.3%	chr1	32268552	CCDS350.1	c.449C>A	p.S150Y
KIAA0090	KIAA0090	ENSG00000127463	PAP45	103	25.2%	chr1	19434229	CCDS190.1	c.1414G>T	p.E472X
KIAA0247	KIAA0247	ENSG00000100647	PAP45	162	22.2%	chr14	69241149	CCDS9796.1	c.395T>C	p.I132T
KIAA0317	KIAA0317	ENSG00000119682	PAP45	109	31.2%	chr14	74207315	CCDS41971.1	c.1511G>A	p.G504E
KIAA0319	KIAA0319	ENSG00000137261	PAP45	43	27.9%	chr6	24680829	CCDS34348.1	c.1811C>A	p.S604Y
KIAA0319L	KIAA0319-like	ENSG00000142687	PAP45	175	27.4%	chr1	35745068	CCDS390.1	c.398A>C	p.K133T
KIAA0408	KIAA0408	ENSG00000189367	PAP45	398	27.6%	chr6	127809556	CCDS34531.1	c.1601G>A	p.R534Q
KIAA0408	KIAA0408	ENSG00000189367	PAP45	185	33.5%	chr6	127810318	CCDS34531.1	c.839C>T	p.S280L
KIAA0556	KIAA0556	ENSG00000047578	PAP45	124	31.5%	chr16	27659642	CCDS32415.1	c.2523T>G	p.F841L
KIAA0652	KIAA0652	ENSG00000175224	PAP45	135	25.2%	chr11	46622487	CCDS7921.1	c.-1G>A	p.IVS1+1-1SpliceDonor
KIAA0922	KIAA0922	ENSG00000121210	PAP45	64	18.8%	chr4	154726886	CCDS3783.1	c.943G>T	p.D315Y
KIAA1033	KIAA1033	ENSG00000136051	PAP45	105	20.0%	chr12	104029044	CCDS41826.1	c.73G>A	p.E25K
KIAA1109	KIAA1109	ENSG00000138688	PAP45	44	36.4%	chr4	123496464	CCDS43267.1	c.14369C>A	p.S4790Y
KIAA1211	KIAA1211	ENSG00000109265	PAP45	183	25.1%	chr4	56874177	CCDS43230.1	c.412G>A	p.E138K
KIAA1217	KIAA1217	ENSG00000120549	PAP45	506	22.5%	chr10	24873363	CCDS31165.1	c.5158G>T	p.E1720X
KIAA1267	KIAA1267	ENSG00000120071	PAP45	253	25.7%	chr17	41527789	CCDS11503.1	c.1385G>A	p.R462Q
KIAA1267	KIAA1267	ENSG00000120071	PAP45	145	16.6%	chr17	41605184	CCDS11503.1	c.103G>A	p.E35K
KIAA1279	KIAA1279	ENSG00000198954	PAP45	300	20.0%	chr10	70445886	CCDS7284.1	c.1574G>T	p.R525I
KIAA1328	KIAA1328	ENSG00000150477	PAP45	109	16.5%	chr18	32918153	ENST00000383055	c.1300G>T	p.E434X
KIAA1377	KIAA1377	ENSG00000110318	PAP45	148	20.9%	chr11	101339471	CCDS31658.1	c.2495T>G	p.I832S
KIAA1462	KIAA1462	ENSG00000165757	PAP45	259	30.9%	chr10	30376732	CCDS41500.1	c.16G>A	p.D6N
KIAA1486	KIAA1486	ENSG00000144460	PAP45	317	22.7%	chr2	226154967	NM_020864	c.590G>A	p.R197Q
KIAA1529	KIAA1529	ENSG00000197816	PAP45	54	18.5%	chr9	99149428	ENST00000375202	c.3059G>A	p.G1020D
KIAA1529	KIAA1529	ENSG00000197816	PAP45	67	26.9%	chr9	99172808	CCDS35077.1	c.4382C>A	p.S1461Y
KIAA1543	KIAA1543	ENSG00000076826	PAP45	167	28.7%	chr19	7579142	CCDS42489.1	c.752G>A	p.R251Q
KIAA1632	KIAA1632	ENSG00000152223	PAP45	124	25.0%	chr18	41783492	CCDS11926.2	c.1453C>T	p.R485X
KIAA1737	KIAA1737	ENSG00000198894	PAP45	319	25.7%	chr14	76649884	CCDS9855.1	c.670G>A	p.E224K
KIAA1797	KIAA1797	ENSG00000188352	PAP45	76	14.5%	chr9	20919587	CCDS34993.1	c.3309G>T	p.E1103D
KIAA2018	KIAA2018	ENSG00000176542	PAP45	170	18.8%	chr3	114856767	CCDS43133.1	c.6452G>A	p.R2151Q
KIAA2018	KIAA2018	ENSG00000176542	PAP45	260	29.6%	chr3	114857574	CCDS43133.1	c.5645C>T	p.S1882L

KIAA2018	KIAA2018	ENSG00000176542	PAP45	337	24.9%	chr3	114858491	CCDS43133.1	c.4728G>T	p.E1576D
KIRREL	kin of IRRE like (Drosophila)	ENSG00000183853	PAP45	398	24.9%	chr1	156331503	CCDS1172.1	c.1751G>A	p.R584Q
KIN	KIN; antigenic determinant of recA protein homolog (mouse)	ENSG00000151657	PAP45	38	28.9%	chr10	7851261	CCDS7080.1	c.722G>A	p.R241Q
KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	ENSG00000128052	PAP45	57	19.3%	chr4	55648647	CCDS3497.1	c.3546G>T	p.E1182D
KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	ENSG00000128052	PAP45	152	28.9%	chr4	55653545	CCDS3497.1	c.3065G>A	p.R1022Q
KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	ENSG00000128052	PAP45	123	25.2%	chr4	55675849	CCDS3497.1	c.607A>C	p.K203Q
KTN1	kinectin 1 (kinesin receptor)	ENSG00000126777	PAP45	71	26.8%	chr14	55164395	CCDS41957.1	c.976G>T	p.E326X
KIF14	kinesin family member 14	ENSG00000118193	PAP45	142	27.5%	chr1	198853957	CCDS30963.1	c.518C>A	p.S173Y
KIF16B	kinesin family member 16B	ENSG00000089177	PAP45	183	23.5%	chr20	16307714	CCDS13122.1	c.2933A>C	p.N978T
KIF16B	kinesin family member 16B	ENSG00000089177	PAP45	773	27.2%	chr20	16308177	CCDS13122.1	c.2470C>T	p.R824C
KIF16B	kinesin family member 16B	ENSG00000089177	PAP45	350	20.3%	chr20	16308622	CCDS13122.1	c.2025G>T	p.E675D
KIF1B	kinesin family member 1B	ENSG00000054523	PAP45	217	16.6%	chr1	10285997	CCDS112.1	c.2167T>G	p.L723V
KIF20A	kinesin family member 20A	ENSG00000112984	PAP45	265	22.3%	chr5	137550885	CCDS4199.1	c.2557T>G	p.L853V
KIF21B	kinesin family member 21B	ENSG00000116852	PAP45	145	24.8%	chr1	199215463	CCDS30965.1	c.3944G>A	p.R1315Q
KIF24	kinesin family member 24	ENSG00000186638	PAP45	320	19.7%	chr9	34247040	NM_194313	c.2565C>A	p.F855L
KIF26B	kinesin family member 26B	ENSG00000162849	PAP45	299	23.4%	chr1	243839283	NM_018012	c.1744G>A	p.E582K
KIF27	kinesin family member 27	ENSG00000165115	PAP45	166	12.7%	chr9	85693227	CCDS6665.1	c.2080G>T	p.E694X
KIF2B	kinesin family member 2B	ENSG00000141200	PAP45	274	21.9%	chr17	49257020	CCDS32685.1	c.1627T>G	p.L543V
KIF3A	kinesin family member 3A	ENSG00000131437	PAP45	162	18.5%	chr5	132066478	CCDS34235.1	c.1564G>T	p.E522X
KIF3A	kinesin family member 3A	ENSG00000131437	PAP45	88	22.7%	chr5	132090063	CCDS34235.1	c.307G>A	p.G103R
KIF3B	kinesin family member 3B	ENSG00000101350	PAP45	100	27.0%	chr20	30378248	CCDS13200.1	c.1762G>T	p.E588X
KIF4A	kinesin family member 4A	ENSG00000090889	PAP45	206	19.4%	chrX	69543547	CCDS14401.1	c.3152C>A	p.S1051Y
KIF6	kinesin family member 6	ENSG00000164627	PAP45	100	26.0%	chr6	39438212	CCDS4844.1	c.1922C>T	p.S641L
KIFC3	kinesin family member C3	ENSG00000140859	PAP45	107	30.8%	chr16	56361231	CCDS10789.2	c.1077G>T	p.E359D
KIF2A	kinesin heavy chain member 2A	ENSG00000068796	PAP45	149	22.8%	chr5	61704113	NM_001098511	c.1738G>A	p.D580N
KIFAP3	kinesin-associated protein 3	ENSG00000075945	PAP45	75	17.3%	chr1	168260263	CCDS1288.1	c.940C>T	p.R314W
KIFAP3	kinesin-associated protein 3	ENSG00000075945	PAP45	76	17.1%	chr1	168260317	CCDS1288.1	c.886G>A	p.E296K
KIFAP3	kinesin-associated protein 3	ENSG00000075945	PAP45	66	34.8%	chr1	168291083	CCDS1288.1	c.151G>T	p.E51X
KNG1	kininogen 1	ENSG00000113889	PAP45	123	22.0%	chr3	187932105	CCDS43183.1	c.750T>G	p.I250M
KITLG	KIT ligand	ENSG00000049130	PAP45	112	20.5%	chr12	87434305	CCDS31868.1	c.457G>T	p.D153Y
KLB	klotho beta	ENSG00000134962	PAP45	283	24.7%	chr4	39112517	CCDS3451.1	c.1118C>A	p.S373Y
KANK4	KN motif and ankyrin repeat domains 4	ENSG00000132854	PAP45	112	27.7%	chr1	62512804	CCDS620.1	c.2443NULL>A	p.NULL-1FsIns1bp
KLF17	Kruppel-like factor 17	ENSG00000171872	PAP45	181	27.6%	chr1	44367728	CCDS508.1	c.198G>T	p.E66D
L3MBTL3	l(3)mbt-like 3 (Drosophila)	ENSG00000198945	PAP45	99	18.2%	chr6	130433892	CCDS34537.1	c.1171G>T	p.A391S
LARP1	La ribonucleoprotein domain family; member 1	ENSG00000155506	PAP45	64	17.2%	chr5	154072705	CCDS4328.1	c.27G>T	p.K9N
LARP4B	La ribonucleoprotein domain family; member 4B	ENSG00000107929	PAP45	180	28.3%	chr10	850913	CCDS31131.1	c.1793G>T	p.R598L
LARP4B	La ribonucleoprotein domain family; member 4B	ENSG00000107929	PAP45	95	20.0%	chr10	865438	CCDS31131.1	c.1012G>A	p.A338T
LARP7	La ribonucleoprotein domain family; member 7	ENSG00000174720	PAP45	60	23.3%	chr4	113785317	CCDS3701.2	c.43G>T	p.E15X
LCT	lactase	ENSG00000115850	PAP45	195	25.6%	chr2	136262401	CCDS2178.1	c.5747G>A	p.R1916Q
LCTL	lactase-like	ENSG00000188501	PAP45	167	22.8%	chr15	64640665	CCDS10220.1	c.523G>A	p.A175T
LCTL	lactase-like	ENSG00000188501	PAP45	249	25.7%	chr15	64644217	CCDS10220.1	c.133G>A	p.V45M
LACE1	lactation elevated 1	ENSG00000135537	PAP45	143	17.5%	chr6	108950226	CCDS5067.1	c.1351G>T	p.E451X
LPO	lactoperoxidase	ENSG00000167419	PAP45	209	22.0%	chr17	53679998	CCDS32689.1	c.325G>T	p.D109Y
LPO	lactoperoxidase	ENSG00000167419	PAP45	140	18.6%	chr17	53699800	CCDS32689.1	c.1785G>T	p.K595N
LAMA1	laminin; alpha 1	ENSG00000101680	PAP45	220	25.5%	chr18	6954761	CCDS32787.1	c.7237G>T	p.E2413X
LAMA2	laminin; alpha 2	ENSG00000196569	PAP45	106	25.5%	chr6	129540600	CCDS5138.1	c.1363C>T	p.R455W
LAMA2	laminin; alpha 2	ENSG00000196569	PAP45	115	27.0%	chr6	129663659	CCDS5138.1	c.3123T>A	p.C1041X
LAMA2	laminin; alpha 2	ENSG00000196569	PAP45	175	22.3%	chr6	129678440	CCDS5138.1	c.3682C>A	p.L1228I
LAMA2	laminin; alpha 2	ENSG00000196569	PAP45	120	29.2%	chr6	129691137	CCDS5138.1	c.4198C>T	p.R1400X
LAMA2	laminin; alpha 2	ENSG00000196569	PAP45	273	11.0%	chr6	129819196	CCDS5138.1	c.6731C>A	p.S2244Y

LAMA3	laminin; alpha 3	ENSG00000053747	PAP45	152	24.3%	chr18	19748663	CCDS42419.1	c.7485T>G	p.I2495M
LAMA4	laminin; alpha 4	ENSG00000112769	PAP45	335	13.1%	chr6	112567059	CCDS43491.1	c.3238C>T	p.R1080X
LAMA4	laminin; alpha 4	ENSG00000112769	PAP45	381	21.8%	chr6	112600575	CCDS43491.1	c.1482G>T	p.Q494H
LAMB1	laminin; beta 1	ENSG00000091136	PAP45	132	25.8%	chr7	107381421	CCDS5750.1	c.2869G>A	p.D957N
LAMC1	laminin; gamma 1 (formerly LAMB2)	ENSG00000135862	PAP45	112	20.5%	chr1	181344073	CCDS1351.1	c.763C>T	p.R255C
LCE5A	late cornified envelope 5A	ENSG00000186207	PAP45	50	30.0%	chr1	150750870	CCDS1011.1	c.236G>A	p.R79Q
LTBP4	latent transforming growth factor beta binding protein 4	ENSG00000090006	PAP45	244	24.6%	chr19	45810829	ENST00000308370	c.2519C>T	p.S840L
LPHN1	latrophilin 1	ENSG00000072071	PAP45	260	31.5%	chr19	14124416	CCDS32928.1	c.3448C>T	p.R1150W
LEMD3	LEM domain containing 3	ENSG00000174106	PAP45	55	18.2%	chr12	63920070	CCDS8972.1	c.2016G>T	p.K672N
LGSN	lengsin; lens protein with glutamine synthetase domain	ENSG00000146166	PAP45	110	30.9%	chr6	64047983	CCDS4964.1	c.1432G>T	p.E478X
LGSN	lengsin; lens protein with glutamine synthetase domain	ENSG00000146166	PAP45	135	19.3%	chr6	64048819	CCDS4964.1	c.596G>T	p.G199V
LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	ENSG00000124831	PAP45	98	23.5%	chr2	238345524	NM_001137550	c.1571G>A	p.R524Q
LRRFIP2	leucine rich repeat (in FLII) interacting protein 2	ENSG00000093167	PAP45	195	12.3%	chr3	37125136	CCDS2664.1	c.653G>A	p.R218Q
LRRCC1	leucine rich repeat and coiled-coil domain containing 1	ENSG00000133739	PAP45	92	21.7%	chr8	86231343	CCDS43750.1	c.1863G>T	p.M621I
LINGO2	leucine rich repeat and Ig domain containing 2	ENSG00000174482	PAP45	247	24.7%	chr9	27939145	CCDS6524.1	c.1525C>A	p.L509I
LRRC15	leucine rich repeat containing 15	ENSG00000172061	PAP45	388	25.8%	chr3	195562378	CCDS3306.1	c.690G>T	p.Q230H
LRRC16B	leucine rich repeat containing 16B	ENSG00000186648	PAP45	236	27.1%	chr14	23595697	CCDS32054.1	c.892C>A	p.L298I
LRRC16B	leucine rich repeat containing 16B	ENSG00000186648	PAP45	140	27.1%	chr14	23603392	CCDS32054.1	c.3077C>A	p.S1026Y
LRRC28	leucine rich repeat containing 28	ENSG00000168904	PAP45	40	25.0%	chr15	97613695	CCDS10380.1	c.10G>A	p.E4K
LRRC3B	leucine rich repeat containing 3B	ENSG00000179796	PAP45	256	23.0%	chr3	26726413	CCDS2644.1	c.246A>C	p.E82D
LRRC4	leucine rich repeat containing 4	ENSG00000128594	PAP45	316	21.8%	chr7	127457110	CCDS5799.1	c.820G>A	p.A274T
LRRC40	leucine rich repeat containing 40	ENSG00000066557	PAP45	89	20.2%	chr1	70423157	CCDS646.1	c.436G>T	p.E146X
LRRC41	leucine rich repeat containing 41	ENSG00000132128	PAP45	135	11.1%	chr1	46517003	ENST00000254454	c.2490T>G	p.F830L
LRRC53	leucine rich repeat containing 53	ENSG00000162621	PAP45	181	26.0%	chr1	74710387	ENST00000294635	c.1507G>T	p.E503X
LRRC66	leucine rich repeat containing 66	ENSG00000188993	PAP45	435	25.5%	chr4	52555552	CCDS43229.1	c.2393G>T	p.R798I
LRRC66	leucine rich repeat containing 66	ENSG00000188993	PAP45	190	24.7%	chr4	52556327	CCDS43229.1	c.1618G>T	p.E540X
LRRC7	leucine rich repeat containing 7	ENSG00000033122	PAP45	191	20.4%	chr1	70073112	CCDS645.1	c.448C>A	p.L150I
LRRC7	leucine rich repeat containing 7	ENSG00000033122	PAP45	121	21.5%	chr1	70274880	CCDS645.1	c.2159C>A	p.S720Y
LRRC7	leucine rich repeat containing 7	ENSG00000033122	PAP45	297	10.1%	chr1	70276938	CCDS645.1	c.2729C>A	p.S910Y
LRRC8B	leucine rich repeat containing 8 family; member B	ENSG00000197147	PAP45	358	24.3%	chr1	89821072	CCDS724.1	c.275G>A	p.R92Q
LUZP2	leucine zipper protein 2	ENSG00000187398	PAP45	81	18.5%	chr11	24707379	CCDS31446.1	c.151G>T	p.E51X
LRRK2	leucine-rich repeat kinase 2	ENSG00000188906	PAP45	88	20.5%	chr12	38933023	CCDS31774.1	c.1226C>A	p.S409Y
LRRK2	leucine-rich repeat kinase 2	ENSG00000188906	PAP45	75	18.7%	chr12	39008504	CCDS31774.1	c.5732A>G	p.H1911R
LRRK2	leucine-rich repeat kinase 2	ENSG00000188906	PAP45	89	22.5%	chr12	39043476	CCDS31774.1	c.7034C>A	p.S2345Y
LGI4	leucine-rich repeat LGI family; member 4	ENSG00000153902	PAP45	168	24.4%	chr19	40314731	CCDS12444.1	c.370C>T	p.R124C
LRIG1	leucine-rich repeats and immunoglobulin-like domains 1	ENSG00000144749	PAP45	56	19.6%	chr3	66543292	CCDS33783.1	c.886G>A	p.A296T
LRIG2	leucine-rich repeats and immunoglobulin-like domains 2	ENSG00000198799	PAP45	147	20.4%	chr1	113442858	CCDS30808.1	c.1100G>T	p.R367I
LRIG3	leucine-rich repeats and immunoglobulin-like domains 3	ENSG00000139263	PAP45	164	20.7%	chr12	57563596	CCDS8960.1	c.1289T>G	p.F430C
LGI1	leucine-rich; glioma inactivated 1	ENSG00000108231	PAP45	113	11.5%	chr10	95546991	CCDS7431.1	c.1115C>A	p.S372Y
LARS	leucyl-tRNA synthetase	ENSG00000133706	PAP45	88	19.3%	chr5	145473879	CCDS34265.1	c.3514A>C	p.I1172L
LIFR	leukemia inhibitory factor receptor alpha	ENSG00000113594	PAP45	93	18.3%	chr5	38535383	CCDS3927.1	c.1660A>C	p.I554L
LECT1	leukocyte cell derived chemotaxin 1	ENSG00000136110	PAP45	53	24.5%	chr13	52211234	CCDS9437.1	c.146C>T	p.S49L
LILRB4	leukocyte immunoglobulin-like receptor; subfamily B (with TM and ITIM domains); member 4	ENSG00000186818	PAP45	68	20.6%	chr19	59867140	CCDS12902.1	c.187G>T	p.E63X
LAIR1	leukocyte-associated immunoglobulin-like receptor 1	ENSG00000167613	PAP45	264	20.5%	chr19	59564400	CCDS12891.1	c.299G>A	p.R100H
LIG4	ligase IV; DNA; ATP-dependent	ENSG00000174405	PAP45	133	13.5%	chr13	107661484	CCDS9508.1	c.134C>A	p.S45Y
LARGE	like-glycosyltransferase	ENSG00000133424	PAP45	77	32.5%	chr22	32042207	CCDS13912.1	c.1315G>A	p.E439K
LIMCH1	LIM and calponin homology domains 1	ENSG00000064042	PAP45	110	23.6%	chr4	41381184	CCDS33977.1	c.2707G>A	p.A903T
LDB3	LIM domain binding 3	ENSG00000122367	PAP45	226	23.0%	chr10	88442289	CCDS7377.1	c.877G>T	p.E293X
LDB3	LIM domain binding 3	ENSG00000122367	PAP45	170	17.6%	chr10	88456407	CCDS7377.1	c.1036G>A	p.A346T
LMO2	LIM domain only 2 (rhombotin-like 1)	ENSG00000135363	PAP45	136	21.3%	chr11	33842831	CCDS7888.1	c.150G>A	p.W50X
LMX1A	LIM homeobox transcription factor 1; alpha	ENSG00000162761	PAP45	84	23.8%	chr1	163443974	CCDS1247.1	c.767G>A	p.R256Q
LIN9	lin-9 homolog (C. elegans)	ENSG00000183814	PAP45	99	26.3%	chr1	224550251	CCDS1553.1	c.227G>A	p.R76Q
LIPA	lipase A; lysosomal acid; cholesterol esterase	ENSG00000107798	PAP45	101	14.9%	chr10	90995448	CCDS7401.1	c.194G>A	p.R65Q

LIPM	lipase; family member M	ENSG00000173239	PAP45	95	18.9%	chr10	90569975	NM_001128215	c.1009C>T	p.P337S
LIPC	lipase; hepatic	ENSG00000166035	PAP45	167	25.1%	chr15	56511554	CCDS10166.1	c.31C>A	p.L11M
LPIN3	lipin 3	ENSG00000132793	PAP45	269	13.0%	chr20	39420303	CCDS33469.1	c.2205G>T	p.E735D
LCN6	lipocalin 6	ENSG00000204003	PAP45	161	10.6%	chr9	138760160	CCDS7005.1	c.258G>T	p.M86I
LHFPL1	lipoma HMGIC fusion partner-like 1	ENSG00000182508	PAP45	254	22.4%	chrX	111790547	CCDS14562.1	c.445C>G	p.Q149E
LHFPL1	lipoma HMGIC fusion partner-like 1	ENSG00000182508	PAP45	304	31.9%	chrX	111801079	CCDS14562.1	c.196G>T	p.E66X
LIPT1	lipoyltransferase 1	ENSG00000144182	PAP45	237	22.4%	chr2	99145495	CCDS2039.1	c.643C>A	p.L215I
LIX1L	Lix1 homolog (mouse)-like	ENSG00000152022	PAP45	81	21.0%	chr1	144198725	CCDS915.1	c.357G>T	p.K119N
LONRF2	LON peptidase N-terminal domain and ring finger 2	ENSG00000170500	PAP45	52	21.2%	chr2	100267202	CCDS2046.2	c.2255G>A	p.R752K
LRP1B	low density lipoprotein receptor-related protein 1B	ENSG00000168702	PAP45	92	30.4%	chr2	140924697	CCDS2182.1	c.9967C>T	p.R3323C
LRP2	low density lipoprotein receptor-related protein 2	ENSG00000081479	PAP45	132	32.6%	chr2	169772001	CCDS2232.1	c.6475C>A	p.L2159I
LRP2	low density lipoprotein receptor-related protein 2	ENSG00000081479	PAP45	90	52.2%	chr2	169781080	CCDS2232.1	c.5755G>A	p.E1919K
LRP3	low density lipoprotein receptor-related protein 3	ENSG00000130881	PAP45	256	25.4%	chr19	38388866	CCDS12430.1	c.1350G>T	p.K450N
LRP4	low density lipoprotein receptor-related protein 4	ENSG00000134569	PAP45	140	25.0%	chr11	46877625	CCDS31478.1	c.436C>T	p.R146C
LRBA	LPS-responsive vesicle trafficking; beach and anchor containing	ENSG00000198589	PAP45	70	28.6%	chr4	151466481	CCDS3773.1	c.7415G>A	p.R2472Q
LSM1	LSM1 homolog; U6 small nuclear RNA associated (S. cerevisiae)	ENSG00000175324	PAP45	151	27.8%	chr8	38146482	CCDS6103.1	c.226G>T	p.E76X
LSM5	LSM5 homolog; U6 small nuclear RNA associated (S. cerevisiae)	ENSG00000106355	PAP45	63	34.9%	chr7	32495454	CCDS5438.1	c.74G>T	p.R25I
LTV1	LTV1 homolog (S. cerevisiae)	ENSG00000135521	PAP45	77	22.1%	chr6	144225928	CCDS5201.1	c.1129C>T	p.R377X
LUC7L2	LUC7-like 2 (S. cerevisiae)	ENSG00000146963	PAP45	86	19.8%	chr7	138733966	CCDS43656.1	c.238T>G	p.F80V
LYVE1	lymphatic vessel endothelial hyaluronan receptor 1	ENSG00000133800	PAP45	158	28.5%	chr11	10537368	CCDS7804.1	c.835G>A	p.E279K
LYVE1	lymphatic vessel endothelial hyaluronan receptor 1	ENSG00000133800	PAP45	120	39.2%	chr11	10542095	CCDS7804.1	c.365G>A	p.R122Q
LY9	lymphocyte antigen 9	ENSG00000122224	PAP45	321	28.0%	chr1	159050214	CCDS30916.1	c.619C>A	p.L207I
LRMP	lymphoid-restricted membrane protein	ENSG00000118308	PAP45	79	20.3%	chr12	25123944	CCDS8701.1	c.224C>A	p.S75Y
LRMP	lymphoid-restricted membrane protein	ENSG00000118308	PAP45	64	15.6%	chr12	25145469	CCDS8701.1	c.832G>T	p.E278X
LRMP	lymphoid-restricted membrane protein	ENSG00000118308	PAP45	53	47.2%	chr12	25145484	CCDS8701.1	c.847C>A	p.L283I
KDM1A	lysine (K)-specific demethylase 1A	ENSG00000004487	PAP45	198	21.7%	chr1	23278682	CCDS30627.1	c.2033T>G	p.F678C
KDM1B	lysine (K)-specific demethylase 1B	ENSG00000165097	PAP45	200	25.5%	chr6	18299422	ENST00000388870	c.800G>A	p.R267Q
KDM3A	lysine (K)-specific demethylase 3A	ENSG00000115548	PAP45	181	25.4%	chr2	86570205	CCDS1990.1	c.3485G>A	p.R1162Q
KDM4C	lysine (K)-specific demethylase 4C	ENSG00000107077	PAP45	52	23.1%	chr9	6974230	CCDS6471.1	c.1180G>T	p.E394X
KDM4D	lysine (K)-specific demethylase 4D	ENSG00000186280	PAP45	85	30.6%	chr11	94371068	CCDS8302.1	c.884T>C	p.F295S
KDM5B	lysine (K)-specific demethylase 5B	ENSG00000117139	PAP45	138	23.2%	chr1	201012846	CCDS30974.1	c.-1G>T	p.IVS1-1-1SpliceAcceptor
KDM6A	lysine (K)-specific demethylase 6A	ENSG00000147050	PAP45	333	25.8%	chrX	44814159	CCDS14265.1	c.2315T>G	p.L772X
LYSMD3	LysM; putative peptidoglycan-binding; domain containing 3	ENSG00000176018	PAP45	119	26.9%	chr5	89850590	CCDS43338.1	c.723A>C	p.E241D
LPAR4	lysophosphatidic acid receptor 4	ENSG00000147145	PAP45	279	25.4%	chrX	77897401	CCDS14441.1	c.379C>T	p.L127F
LYPLAL1	lysophospholipase-like 1	ENSG00000143353	PAP45	89	15.7%	chr1	217433200	CCDS1522.1	c.345G>T	p.K115N
LAPTM4A	lysosomal protein transmembrane 4 alpha	ENSG00000068697	PAP45	112	24.1%	chr2	20097608	CCDS1696.1	c.578G>A	p.R193Q
LYST	lysosomal trafficking regulator	ENSG00000143669	PAP45	44	22.7%	chr1	233946655	CCDS31062.1	c.9607C>T	p.R3203C
LYST	lysosomal trafficking regulator	ENSG00000143669	PAP45	185	22.2%	chr1	234036220	CCDS31062.1	c.2839G>T	p.E947X
LYST	lysosomal trafficking regulator	ENSG00000143669	PAP45	192	22.9%	chr1	234040065	CCDS31062.1	c.676G>T	p.E226X
LYST	lysosomal trafficking regulator	ENSG00000143669	PAP45	122	20.5%	chr1	234042954	CCDS31062.1	c.223C>A	p.L75I
KARS	lysyl-tRNA synthetase	ENSG00000065427	PAP45	101	16.8%	chr16	74227143	CCDS10923.1	c.731T>G	p.F244C
MACROD2	MACRO domain containing 2	ENSG00000172264	PAP45	187	19.3%	chr20	15915764	CCDS13120.2	c.1114C>T	p.P372S
MPEG1	macrophage expressed 1	ENSG00000197629	PAP45	529	26.5%	chr11	58734863	CCDS41650.1	c.2052G>T	p.K684N
MSR1	macrophage scavenger receptor 1	ENSG00000038945	PAP45	209	13.9%	chr8	16070597	CCDS5995.1	c.371G>T	p.R124I
MAEL	maelstrom homolog (Drosophila)	ENSG00000143194	PAP45	186	25.3%	chr1	165257556	CCDS1257.1	c.1145C>A	p.S382Y
MAEL	maelstrom homolog (Drosophila)	ENSG00000143194	PAP45	227	22.5%	chr1	165257701	CCDS1257.1	c.1290C>A	p.F430L
MFSD7	major facilitator superfamily domain containing 7	ENSG00000169026	PAP45	181	29.3%	chr4	668532	CCDS3338.1	c.699G>T	p.E233D
MVP	major vault protein	ENSG00000013364	PAP45	218	37.2%	chr16	29749824	CCDS10656.1	c.250C>T	p.R84C
MAK	male germ cell-associated kinase	ENSG00000111837	PAP45	55	30.9%	chr6	10927139	CCDS4516.1	c.122C>A	p.S41Y

MCAT	malonyl CoA:ACP acyltransferase (mitochondrial)	ENSG00000100294	PAP45	176	26.7%	chr22	41863060	CCDS33660.1	c.700G>T	p.D234Y
MDGA2	MAM domain containing glycosylphosphatidylinositol anchor 2	ENSG00000139915	PAP45	199	24.1%	chr14	46683177	NM_001113498	c.439G>T	p.E147X
MANBA	mannosidase; beta A; lysosomal	ENSG00000109323	PAP45	107	22.4%	chr4	103776083	CCDS3658.1	c.2144C>T	p.S715L
MANBA	mannosidase; beta A; lysosomal	ENSG00000109323	PAP45	230	25.2%	chr4	103811598	CCDS3658.1	c.1118G>A	p.R373Q
MKNK1	MAP kinase interacting serine/threonine kinase 1	ENSG00000079277	PAP45	192	29.2%	chr1	46821559	CCDS538.1	c.64G>A	p.A22T
MARK3	MAP/microtubule affinity-regulating kinase 3	ENSG00000075413	PAP45	123	19.5%	chr14	103028003	CCDS41993.1	c.1723G>A	p.A575T
MAP7D1	MAP7 domain containing 1	ENSG00000116871	PAP45	516	22.7%	chr1	36418435	CCDS30673.1	c.-1G>T	p.IVS16-1-1SpliceAcceptor
MAP7D3	MAP7 domain containing 3	ENSG00000129680	PAP45	137	22.6%	chrX	135141985	CCDS44004.1	c.797G>A	p.S266N
MARVELD2	MARVEL domain containing 2	ENSG00000152939	PAP45	224	29.0%	chr5	68751042	CCDS34175.1	c.74A>G	p.D25G
MRGPRF	MAS-related GPR; member F	ENSG00000172935	PAP45	77	18.2%	chr11	68529656	CCDS8188.1	c.698G>A	p.R233H
MEPE	matrix extracellular phosphoglycoprotein	ENSG00000152595	PAP45	209	21.1%	chr4	88985714	CCDS3625.1	c.670A>C	p.K224Q
MMP1	matrix metallopeptidase 1 (interstitial collagenase)	ENSG00000196611	PAP45	79	25.3%	chr11	102171143	CCDS8322.1	c.871C>T	p.R291W
MMP14	matrix metallopeptidase 14 (membrane-inserted)	ENSG00000157227	PAP45	169	34.3%	chr14	22382319	CCDS9577.1	c.702C>A	p.F234L
MMP20	matrix metallopeptidase 20	ENSG00000137674	PAP45	46	26.1%	chr11	101987710	CCDS8318.1	c.509C>A	p.S170Y
MMP25	matrix metallopeptidase 25	ENSG00000008516	PAP45	83	24.1%	chr16	3040518	CCDS10492.1	c.631G>A	p.D211N
MMP28	matrix metallopeptidase 28	ENSG00000129270	PAP45	203	26.1%	chr17	31119377	ENST00000338839	c.982G>A	p.D328N
MXRA5	matrix-remodelling associated 5	ENSG00000101825	PAP45	154	11.0%	chrX	3249527	CCDS14124.1	c.4199C>A	p.S1400Y
MXRA5	matrix-remodelling associated 5	ENSG00000101825	PAP45	230	25.7%	chrX	3250130	CCDS14124.1	c.3596C>A	p.S1199Y
MXD3	MAX dimerization protein 3	ENSG00000213347	PAP45	149	27.5%	chr5	176667543	CCDS4416.1	c.350G>A	p.R117Q
MCF2	MCF.2 cell line derived transforming sequence	ENSG00000101977	PAP45	79	26.6%	chrX	138524838	CCDS14667.1	c.1231C>T	p.R411X
MCF2L2	MCF.2 cell line derived transforming sequence-like 2	ENSG00000053524	PAP45	121	23.1%	chr3	184518693	CCDS3243.1	c.610G>A	p.E204K
MDN1	MDN1; midasin homolog (yeast)	ENSG00000112159	PAP45	218	29.4%	chr6	90445173	CCDS5024.1	c.12278C>T	p.S4093F
MTOR	mechanistic target of rapamycin (serine/threonine kinase)	ENSG00000198793	PAP45	396	26.5%	chr1	11182247	CCDS127.1	c.4045G>T	p.D1349Y
MED1	mediator complex subunit 1	ENSG00000125686	PAP45	43	39.5%	chr17	34817286	CCDS11336.1	c.4714G>T	p.D1572Y
MED12	mediator complex subunit 12	ENSG00000184634	PAP45	145	24.1%	chrX	70261416	CCDS43970.1	c.2052C>A	p.F684L
MED12L	mediator complex subunit 12-like	ENSG00000144893	PAP45	62	17.7%	chr3	152359201	CCDS33876.1	c.762G>T	p.W254C
MED13L	mediator complex subunit 13-like	ENSG00000123066	PAP45	268	24.6%	chr12	114913757	CCDS9177.1	c.3385G>T	p.D1129Y
MED13L	mediator complex subunit 13-like	ENSG00000123066	PAP45	200	22.0%	chr12	114919254	CCDS9177.1	c.2734G>T	p.E912X
MED17	mediator complex subunit 17	ENSG00000042429	PAP45	82	24.4%	chr11	93169276	CCDS8295.1	c.1065A>C	p.Q355H
MED19	mediator complex subunit 19	ENSG00000156603	PAP45	257	23.7%	chr11	57229086	CCDS7966.1	c.409C>A	p.L137I
MED6	mediator complex subunit 6	ENSG00000133997	PAP45	92	20.7%	chr14	70134158	CCDS9805.1	c.112A>C	p.N38H
MED7	mediator complex subunit 7	ENSG00000155868	PAP45	117	18.8%	chr5	156498754	CCDS4334.1	c.267C>A	p.F89L
MEIG1	meiosis expressed gene 1 homolog (mouse)	ENSG00000197889	PAP45	71	28.2%	chr10	15054614	CCDS31151.1	c.235G>T	p.E79X
MEI1	meiosis inhibitor 1	ENSG00000167077	PAP45	355	22.8%	chr22	40504726	NM_152513	c.2779G>T	p.E927X
MLANA	melan-A	ENSG00000120215	PAP45	52	30.8%	chr9	5887631	CCDS6466.1	c.152G>A	p.R51Q
MC1R	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)	ENSG00000198211	PAP45	287	29.3%	chr16	88526480	CCDS10988.1	c.58T>C	p.F20L
MAGEA11	melanoma antigen family A; 11	ENSG00000185247	PAP45	163	26.4%	chrX	148576622	NM_005366	c.637G>T	p.D213Y
MAGEA8	melanoma antigen family A; 8	ENSG00000156009	PAP45	209	26.8%	chrX	148774065	CCDS14692.1	c.361C>T	p.R121C
MAGEC1	melanoma antigen family C; 1	ENSG00000155495	PAP45	208	15.9%	chrX	140822647	CCDS35417.1	c.1791G>T	p.Q597H
MAGEC1	melanoma antigen family C; 1	ENSG00000155495	PAP45	577	21.7%	chrX	140822794	CCDS35417.1	c.1938G>T	p.E646D
MAGEC1	melanoma antigen family C; 1	ENSG00000155495	PAP45	226	25.2%	chrX	140824181	CCDS35417.1	c.3325G>T	p.D1109Y
MAGEC2	melanoma antigen family C; 2	ENSG00000046774	PAP45	206	28.6%	chrX	141118762	CCDS14678.1	c.678G>T	p.E226D
MAGEC2	melanoma antigen family C; 2	ENSG00000046774	PAP45	254	16.5%	chrX	141118963	CCDS14678.1	c.477G>T	p.E159D
MAGED1	melanoma antigen family D; 1	ENSG00000179222	PAP45	487	10.9%	chrX	51661751	CCDS35279.1	c.2490C>A	p.F830L
MAGEE1	melanoma antigen family E; 1	ENSG00000198934	PAP45	213	20.7%	chrX	75566104	CCDS14433.1	c.1377C>A	p.F459L
MAGEH1	melanoma antigen family H; 1	ENSG00000187601	PAP45	253	22.9%	chrX	55495738	CCDS14369.1	c.206C>T	p.S69L
MUM1L1	melanoma associated antigen (mutated) 1-like 1	ENSG00000157502	PAP45	83	30.1%	chrX	105336130	ENST00000372552	c.49G>A	p.A17T
MIA2	melanoma inhibitory activity 2	ENSG00000150526	PAP45	168	13.7%	chr14	38791744	CCDS9672.1	c.1609G>T	p.E537X
MAGI1	membrane associated guanylate kinase; WW and PDZ domain containing 1	ENSG00000151276	PAP45	43	37.2%	chr3	65344285	CCDS33780.1	c.2470G>T	p.G824X

MMGT1	membrane magnesium transporter 1	ENSG00000169446	PAP45	129	24.0%	chrX	134874958	CCDS14653.1	c.287G>A	p.R96H
MPP3	membrane protein; palmitoylated 3 (MAGUK p55 subfamily member 3)	ENSG00000161647	PAP45	109	36.7%	chr17	39262644	CCDS42344.1	c.482T>NULL	p.NULL-1FsDel1bp
MPP6	membrane protein; palmitoylated 6 (MAGUK p55 subfamily member 6)	ENSG00000105926	PAP45	112	25.0%	chr7	24656659	CCDS5388.1	c.454C>A	p.L152M
MPP7	membrane protein; palmitoylated 7 (MAGUK p55 subfamily member 7)	ENSG00000150054	PAP45	53	18.9%	chr10	28387480	CCDS7158.1	c.1357C>T	p.R453W
MPP7	membrane protein; palmitoylated 7 (MAGUK p55 subfamily member 7)	ENSG00000150054	PAP45	73	30.1%	chr10	28418741	CCDS7158.1	c.988G>T	p.D330Y
40247	membrane-associated ring finger (C3HC4) 10	ENSG00000173838	PAP45	379	24.8%	chr17	58167612	CCDS11635.1	c.1349C>A	p.S450Y
40241	membrane-associated ring finger (C3HC4) 4	ENSG00000144583	PAP45	180	26.1%	chr2	216856555	CCDS33376.1	c.659A>T	p.K220I
MGEA5	meningioma expressed antigen 5 (hyaluronidase)	ENSG00000198408	PAP45	87	29.9%	chr10	103536279	CCDS7520.1	c.2670T>G	p.F890L
MEP1A	meprin A; alpha (PABA peptide hydrolase)	ENSG00000112818	PAP45	171	20.5%	chr6	46869137	CCDS4918.1	c.43C>A	p.L15I
MET	met proto-oncogene (hepatocyte growth factor receptor)	ENSG00000105976	PAP45	50	20.0%	chr7	116182714	CCDS43636.1	c.1771C>T	p.R591W
MET	met proto-oncogene (hepatocyte growth factor receptor)	ENSG00000105976	PAP45	57	38.6%	chr7	116206233	CCDS43636.1	c.3508C>T	p.R1170X
MTA1	metastasis associated 1	ENSG00000182979	PAP45	84	25.0%	chr14	104991665	CCDS32169.1	c.523G>T	p.A175S
MACC1	metastasis associated in colon cancer 1	ENSG00000183742	PAP45	131	24.4%	chr7	20164931	CCDS5369.1	c.1578A>C	p.E526D
MACC1	metastasis associated in colon cancer 1	ENSG00000183742	PAP45	42	42.9%	chr7	20165215	CCDS5369.1	c.1294G>T	p.D432Y
MSRB2	methionine sulfoxide reductase B2	ENSG00000148450	PAP45	74	27.0%	chr10	23448028	ENST00000376513	c.344G>T	p.R115I
METAP1	methionyl aminopeptidase 1	ENSG00000164024	PAP45	62	24.2%	chr4	100185415	NM_015143	c.718G>T	p.E240X
MARS	methionyl-tRNA synthetase	ENSG00000166986	PAP45	98	14.3%	chr12	56192970	CCDS8942.1	c.1923G>T	p.K641N
MECP2	methyl CpG binding protein 2 (Rett syndrome)	ENSG00000169057	PAP45	349	26.9%	chrX	152950046	CCDS14741.1	c.427G>A	p.E143K
MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	ENSG00000120254	PAP45	179	26.3%	chr6	151285033	CCDS5228.1	c.-1G>T	p.IVS9-1-1SpliceAcceptor
MUT	methylmalonyl CoA mutase	ENSG00000146085	PAP45	62	22.6%	chr6	49534970	CCDS4924.1	c.169G>T	p.E57X
MEPCE	methylphosphate capping enzyme	ENSG00000146834	PAP45	251	24.7%	chr7	99866277	CCDS5693.1	c.700G>T	p.D234Y
MTAP	methylthioadenosine phosphorylase	ENSG00000099810	PAP45	474	24.9%	chr9	22019467	ENST00000404796	c.383G>T	p.R128I
METT10D	methyltransferase 10 domain containing	ENSG00000127804	PAP45	139	15.8%	chr17	2317876	CCDS42232.1	c.514G>T	p.E172X
METT5D1	methyltransferase 5 domain containing 1	ENSG00000169519	PAP45	61	27.9%	chr11	28268480	CCDS31450.1	c.559C>T	p.R187W
METTL13	methyltransferase like 13	ENSG00000010165	PAP45	140	28.6%	chr1	170027936	CCDS1299.1	c.1631G>A	p.R544Q
MCPH1	microcephalin 1	ENSG00000147316	PAP45	88	29.5%	chr8	6259794	CCDS43689.1	c.215C>T	p.S72L
MIR1248	microRNA 1248	ENSG00000156976	PAP45	96	18.8%	chr3	187986681	CCDS3282.1	c.552A>C	p.E184D
MCRS1	microspherule protein 1	ENSG00000187778	PAP45	147	17.7%	chr12	48238986	CCDS31795.1	c.1248C>A	p.F416L
MAST4	microtubule associated serine/threonine kinase family member 4	ENSG00000069020	PAP45	162	25.3%	chr5	66441733	NM_001164664	c.1408C>T	p.R470X
MASTL	microtubule associated serine/threonine kinase-like	ENSG00000120539	PAP45	107	14.0%	chr10	27499752	CCDS7153.1	c.1858C>T	p.P620S
MTUS1	microtubule associated tumor suppressor 1	ENSG00000129422	PAP45	200	14.5%	chr8	17547780	CCDS43717.1	c.3748G>A	p.A1250T
MACF1	microtubule-actin crosslinking factor 1	ENSG00000127603	PAP45	59	22.0%	chr1	39534123	CCDS435.1	c.2352G>T	p.E784D
MACF1	microtubule-actin crosslinking factor 1	ENSG00000127603	PAP45	216	26.4%	chr1	39572721	CCDS436.1	c.3194G>T	p.R1065I
MACF1	microtubule-actin crosslinking factor 1	ENSG00000127603	PAP45	80	31.3%	chr1	39679338	CCDS436.1	c.13853C>T	p.A4618V
MACF1	microtubule-actin crosslinking factor 1	ENSG00000127603	PAP45	96	17.7%	chr1	39718060	CCDS436.1	c.17222G>A	p.R5741Q
MACF1	microtubule-actin crosslinking factor 1	ENSG00000127603	PAP45	111	20.7%	chr1	39723842	CCDS436.1	c.17606G>A	p.R5869Q
MAP1A	microtubule-associated protein 1A	ENSG00000166963	PAP45	115	28.7%	chr15	41605917	CCDS42031.1	c.4954G>T	p.E1652X
MAP1A	microtubule-associated protein 1A	ENSG00000166963	PAP45	502	22.5%	chr15	41607699	CCDS42031.1	c.6736A>G	p.N2246D
MAP1B	microtubule-associated protein 1B	ENSG00000131711	PAP45	108	25.9%	chr5	71527129	CCDS4012.1	c.2191G>T	p.E731X
MAP1B	microtubule-associated protein 1B	ENSG00000131711	PAP45	581	27.0%	chr5	71528848	CCDS4012.1	c.3910G>T	p.E1304X
MAP4	microtubule-associated protein 4	ENSG00000047849	PAP45	263	12.2%	chr3	47933093	CCDS33750.1	c.1228T>G	p.L410V
MAP7	microtubule-associated protein 7	ENSG00000135525	PAP45	88	25.0%	chr6	136735405	CCDS5178.1	c.803C>T	p.S268L
MAP9	microtubule-associated protein 9	ENSG00000164114	PAP45	95	11.6%	chr4	156509122	ENST00000379248	c.555A>C	p.K185N
MIB1	mindbomb homolog 1 (Drosophila)	ENSG00000101752	PAP45	172	19.8%	chr18	17691125	CCDS11871.1	c.2702G>A	p.R901Q
MCM3	minichromosome maintenance complex component 3	ENSG00000112118	PAP45	254	27.2%	chr6	52241964	CCDS4940.1	c.1847G>A	p.R616Q
MCM6	minichromosome maintenance complex component 6	ENSG00000076003	PAP45	80	16.3%	chr2	136339153	CCDS2179.1	c.978G>T	p.K326N
MTFR1	mitochondrial fission regulator 1	ENSG00000066855	PAP45	72	20.8%	chr8	66782032	CCDS6182.1	c.751C>T	p.R251W

MTFMT	mitochondrial methionyl-tRNA formyltransferase	ENSG00000103707	PAP45	359	25.3%	chr15	63106267	NM_139242	c.374C>T	p.S125L
MRPL37	mitochondrial ribosomal protein L37	ENSG00000116221	PAP45	163	20.9%	chr1	54456465	CCDS589.1	c.1227G>T	p.E409D
MRPL51	mitochondrial ribosomal protein L51	ENSG00000111639	PAP45	134	27.6%	chr12	6471703	CCDS8547.1	c.382C>T	p.R128X
MRPS30	mitochondrial ribosomal protein S30	ENSG00000112996	PAP45	45	24.4%	chr5	44846939	CCDS3951.1	c.673C>T	p.R225X
MRPS5	mitochondrial ribosomal protein S5	ENSG00000144029	PAP45	178	22.5%	chr2	95139428	CCDS2010.1	c.363G>T	p.K121N
MFN1	mitofusin 1	ENSG00000171109	PAP45	62	27.4%	chr3	180577576	CCDS3228.1	c.1150C>T	p.R384X
MAPK14	mitogen-activated protein kinase 14	ENSG00000112062	PAP45	85	22.4%	chr6	36103953	CCDS4815.1	c.41A>G	p.N14S
MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	ENSG00000121653	PAP45	90	25.6%	chr11	45883309	CCDS7916.1	c.1996G>A	p.D666N
MAPKAP1	mitogen-activated protein kinase associated protein 1	ENSG00000119487	PAP45	97	19.6%	chr9	127459842	CCDS35140.1	c.407C>A	p.S136Y
MAP2K6	mitogen-activated protein kinase kinase 6	ENSG00000108984	PAP45	132	22.0%	chr17	65031303	CCDS11686.1	c.589G>A	p.D197N
MAP3K13	mitogen-activated protein kinase kinase kinase 13	ENSG00000073803	PAP45	56	28.6%	chr3	186629356	CCDS3270.1	c.293C>A	p.S98Y
MAP3K13	mitogen-activated protein kinase kinase kinase 13	ENSG00000073803	PAP45	323	21.4%	chr3	186673720	CCDS3270.1	c.1907C>A	p.S636Y
MAP3K4	mitogen-activated protein kinase kinase kinase 4	ENSG00000085511	PAP45	189	25.9%	chr6	161390786	CCDS34565.1	c.1492G>A	p.E498K
MAP3K4	mitogen-activated protein kinase kinase kinase 4	ENSG00000085511	PAP45	110	30.9%	chr6	161411759	CCDS34565.1	c.1837G>A	p.E613K
MAP3K4	mitogen-activated protein kinase kinase kinase 4	ENSG00000085511	PAP45	61	23.0%	chr6	161425566	CCDS34565.1	c.2299G>T	p.E767X
MAP3K4	mitogen-activated protein kinase kinase kinase 4	ENSG00000085511	PAP45	71	18.3%	chr6	161452920	CCDS34565.1	c.4459A>C	p.K1487Q
MAP3K7	mitogen-activated protein kinase kinase kinase 7	ENSG00000135341	PAP45	100	21.0%	chr6	91290150	CCDS5028.1	c.1430G>A	p.R477Q
MAP4K1	mitogen-activated protein kinase kinase kinase kinase 1	ENSG00000104814	PAP45	118	20.3%	chr19	43790613	CCDS42564.1	c.1044G>T	p.E348D
MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3	ENSG00000011566	PAP45	97	10.3%	chr2	39341416	CCDS1803.1	c.2143G>T	p.D715Y
MOCS1	molybdenum cofactor synthesis 1	ENSG00000124615	PAP45	152	18.4%	chr6	39982653	CCDS4845.1	c.1321G>A	p.A441T
MOXD1	monooxygenase; DBH-like 1	ENSG00000079931	PAP45	179	15.1%	chr6	132660620	CCDS5152.2	c.1676C>T	p.S559L
MORC1	MORC family CW-type zinc finger 1	ENSG00000114487	PAP45	147	29.3%	chr3	110206835	CCDS2955.1	c.1785G>T	p.Q595H
MORC3	MORC family CW-type zinc finger 3	ENSG00000159256	PAP45	163	18.4%	chr21	36638862	CCDS42924.1	c.872G>A	p.R291Q
MORC4	MORC family CW-type zinc finger 4	ENSG00000133131	PAP45	165	24.2%	chrX	106072864	CCDS14525.2	c.1913A>G	p.Q638R
MOSPD2	motile sperm domain containing 2	ENSG00000130150	PAP45	297	10.1%	chrX	14801783	CCDS14162.1	c.61G>A	p.E21K
MPHOSPH9	M-phase phosphoprotein 9	ENSG00000051825	PAP45	62	25.8%	chr12	122212636	CCDS9243.1	c.2656C>A	p.L886I
MPND	MPN domain containing	ENSG00000008382	PAP45	47	23.4%	chr19	4310227	CCDS42470.1	c.1304A>G	p.E435G
MUC17	mucin 17; cell surface associated	ENSG00000169876	PAP45	479	17.5%	chr7	100462685	CCDS34711.1	c.1268T>G	p.F423C
MUC21	mucin 21; cell surface associated	ENSG00000204544	PAP45	67	26.9%	chr6	31059769	CCDS34388.1	c.55G>T	p.E19X
MUC3A	mucin 3A; cell surface associated	ENSG00000169894	PAP45	950	17.4%	chr7	100387569	ENST00000379458	c.214G>A	p.E72K
MUC3A	mucin 3A; cell surface associated	ENSG00000169894	PAP45	1018	11.7%	chr7	100389245	ENST00000332750	c.933G>T	p.E311D
MUC3B	mucin 3B; cell surface associated	ENSG00000169894	PAP45	950	17.4%	chr7	100387569	ENST00000379458	c.214G>A	p.E72K
MUC3B	mucin 3B; cell surface associated	ENSG00000169894	PAP45	1018	11.7%	chr7	100389245	ENST00000332750	c.933G>T	p.E311D
MUC5AC	mucin 5AC; oligomeric mucus/gel-forming	ENSG00000215182	PAP45	101	11.9%	chr11	1173796	ENST00000358378	c.2188G>A	p.A730T
MCOLN2	mucolipin 2	ENSG00000153898	PAP45	126	20.6%	chr1	85176109	CCDS30762.1	c.1252C>A	p.L418I
MMRN2	multimerin 2	ENSG00000173269	PAP45	345	26.7%	chr10	88693251	CCDS7379.1	c.1270G>A	p.D424N
MCTP1	multiple C2 domains; transmembrane 1	ENSG00000175471	PAP45	323	26.9%	chr5	94140588	CCDS34203.1	c.2593G>T	p.D865Y
MCTP1	multiple C2 domains; transmembrane 1	ENSG00000175471	PAP45	88	23.9%	chr5	94274394	CCDS34203.1	c.1394C>T	p.S465L
MEGF10	multiple EGF-like-domains 10	ENSG00000145794	PAP45	245	23.3%	chr5	126774017	CCDS4142.1	c.955C>A	p.L319I
MEGF10	multiple EGF-like-domains 10	ENSG00000145794	PAP45	82	36.6%	chr5	126781390	CCDS4142.1	c.1292C>T	p.A431V
MEN1	multiple endocrine neoplasia I	ENSG00000133895	PAP45	192	20.8%	chr11	64333766	CCDS8083.1	c.392G>A	p.R131H
MBNL1	muscleblind-like (Drosophila)	ENSG00000152601	PAP45	90	23.3%	chr3	153633372	CCDS3165.1	c.522G>T	p.Q174H
MLH3	mutL homolog 3 (E. coli)	ENSG00000119684	PAP45	343	23.6%	chr14	74585857	CCDS32123.1	c.255G>T	p.E85D
MSH3	mutS homolog 3 (E. coli)	ENSG00000113318	PAP45	106	19.8%	chr5	79996888	CCDS34195.1	c.529G>A	p.A177T
MSH3	mutS homolog 3 (E. coli)	ENSG00000113318	PAP45	108	13.9%	chr5	80204801	CCDS34195.1	c.3241G>T	p.E1081X
MSH4	mutS homolog 4 (E. coli)	ENSG00000057468	PAP45	115	23.5%	chr1	76045284	CCDS670.1	c.458C>T	p.S153F
MSH6	mutS homolog 6 (E. coli)	ENSG00000116062	PAP45	219	22.4%	chr2	47880787	CCDS1836.1	c.2161A>T	p.R721X
MSH6	mutS homolog 6 (E. coli)	ENSG00000116062	PAP45	121	28.9%	chr2	47881665	CCDS1836.1	c.3039G>T	p.K1013N
MYBBP1A	MYB binding protein (P160) 1a	ENSG00000132382	PAP45	249	20.9%	chr17	4398643	CCDS42238.1	c.1481T>C	p.I494T
MYCBP2	MYC binding protein 2	ENSG00000005810	PAP45	64	20.3%	chr13	76549472	CCDS31994.1	c.11422G>A	p.G3808R
MYCBP2	MYC binding protein 2	ENSG00000005810	PAP45	104	25.0%	chr13	76598483	CCDS31994.1	c.7741C>A	p.L2581M
MYCBPAP	MYCBP associated protein	ENSG00000136449	PAP45	84	26.2%	chr17	45949013	CCDS32680.1	c.178G>T	p.D60Y
MAG	myelin associated glycoprotein	ENSG00000105695	PAP45	373	26.3%	chr19	40478409	CCDS12455.1	c.100G>A	p.E34K
MNDA	myeloid cell nuclear differentiation antigen	ENSG00000163563	PAP45	110	19.1%	chr1	157078815	CCDS1177.1	c.248G>A	p.R83Q

MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	ENSG00000055609	PAP45	150	20.0%	chr7	151480833	CCDS5931.1	c.12416G>A	p.R4139Q
MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	ENSG00000055609	PAP45	71	14.1%	chr7	151515399	CCDS5931.1	c.4889C>T	p.S1630L
MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	ENSG00000055609	PAP45	100	19.0%	chr7	151523970	CCDS5931.1	c.4333C>A	p.L1445I
MYADM	myeloid-associated differentiation marker	ENSG00000179820	PAP45	950	12.5%	chr19	59068993	CCDS12866.1	c.398C>T	p.S133L
MYADML2	myeloid-associated differentiation marker-like 2	ENSG00000185105	PAP45	124	10.5%	chr17	77492010	NM_001145113	c.899G>T	p.R300M
MPL	myeloproliferative leukemia virus oncogene	ENSG00000117400	PAP45	427	26.0%	chr1	43584773	CCDS483.1	c.1051C>T	p.R351C
MYOCD	myocardin	ENSG00000141052	PAP45	49	24.5%	chr17	12580290	CCDS11163.1	c.503G>A	p.R168Q
MYOCD	myocardin	ENSG00000141052	PAP45	423	22.0%	chr17	12607395	CCDS11163.1	c.2526C>A	p.F842L
MYOC	myocilin; trabecular meshwork inducible glucocorticoid response	ENSG00000034971	PAP45	458	22.1%	chr1	169871747	CCDS1297.1	c.1456C>A	p.L486I
MEF2D	myocyte enhancer factor 2D	ENSG00000116604	PAP45	116	32.8%	chr1	154717348	CCDS1143.1	c.298G>A	p.E100K
MYF6	myogenic factor 6 (herculin)	ENSG00000111046	PAP45	173	24.3%	chr12	79625889	CCDS9019.1	c.260G>T	p.R87I
MYOM2	myomesin (M-protein) 2; 165kDa	ENSG00000036448	PAP45	147	19.0%	chr8	2041721	CCDS5957.1	c.2925G>T	p.E975D
MYPN	myopalladin	ENSG00000138347	PAP45	126	19.0%	chr10	69578120	CCDS7275.1	c.1135C>T	p.Q379X
MYO1D	myosin ID	ENSG00000176658	PAP45	188	26.1%	chr17	28100089	CCDS32615.1	c.1516C>T	p.R506X
MYO3A	myosin IIIA	ENSG00000095777	PAP45	90	20.0%	chr10	26449681	CCDS7148.1	c.1847C>T	p.A616V
MYO3A	myosin IIIA	ENSG00000095777	PAP45	85	28.2%	chr10	26531929	CCDS7148.1	c.4617C>A	p.F1539L
MPRIP	myosin phosphatase Rho interacting protein	ENSG00000133030	PAP45	110	26.4%	chr17	17015856	CCDS42268.1	c.2263G>A	p.E755K
MYO5A	myosin VA (heavy chain 12; myoxin)	ENSG00000197535	PAP45	72	13.9%	chr15	50407448	CCDS42037.1	c.4528G>A	p.A1510T
MYO5A	myosin VA (heavy chain 12; myoxin)	ENSG00000197535	PAP45	118	20.3%	chr15	50495782	CCDS42037.1	c.464G>A	p.R155Q
MYO6	myosin VI	ENSG00000196586	PAP45	99	28.3%	chr6	76614846	CCDS34487.1	c.956G>T	p.R319I
MYO7B	myosin VIIB	ENSG00000169994	PAP45	221	25.3%	chr2	128101511	ENST00000272666	c.4406C>T	p.T1469M
MYO15A	myosin XVA	ENSG00000091536	PAP45	90	28.9%	chr17	17963254	CCDS42271.1	c.415A>C	p.K139Q
MYO15A	myosin XVA	ENSG00000091536	PAP45	183	30.6%	chr17	18003338	CCDS42271.1	c.9181G>A	p.E3061K
MYO16	myosin XVI	ENSG00000041515	PAP45	236	22.9%	chr13	108575520	CCDS32008.1	c.3529G>T	p.E1177X
MYH15	myosin; heavy chain 15	ENSG00000144821	PAP45	182	26.4%	chr3	109630370	CCDS43127.1	c.3421C>T	p.R1141X
MYH15	myosin; heavy chain 15	ENSG00000144821	PAP45	99	23.2%	chr3	109658397	CCDS43127.1	c.2104C>A	p.L702I
MYH4	myosin; heavy chain 4; skeletal muscle	ENSG00000141048	PAP45	94	14.9%	chr17	10310356	CCDS11154.1	c.307C>A	p.L103M
MYH8	myosin; heavy chain 8; skeletal muscle; perinatal	ENSG00000133020	PAP45	46	30.4%	chr17	10236007	CCDS11153.1	c.5581C>T	p.R1861C
MYH8	myosin; heavy chain 8; skeletal muscle; perinatal	ENSG00000133020	PAP45	112	15.2%	chr17	10245199	CCDS11153.1	c.3143G>A	p.R1048Q
MYH8	myosin; heavy chain 8; skeletal muscle; perinatal	ENSG00000133020	PAP45	160	23.1%	chr17	10245424	CCDS11153.1	c.3001G>A	p.A1001T
MYH9	myosin; heavy chain 9; non-muscle	ENSG00000100345	PAP45	533	21.4%	chr22	35014835	CCDS13927.1	c.4654G>A	p.E1552K
MTMR1	myotubularin related protein 1	ENSG00000063601	PAP45	64	29.7%	chrX	149650653	CCDS14695.1	c.771C>A	p.F257L
MTMR14	myotubularin related protein 14	ENSG00000163719	PAP45	284	31.0%	chr3	9718559	CCDS43043.1	c.1855C>T	p.R619W
MTMR15	myotubularin related protein 15	ENSG00000198690	PAP45	158	21.5%	chr15	28984444	CCDS32186.1	c.286G>T	p.D96Y
MTMR3	myotubularin related protein 3	ENSG00000100330	PAP45	228	21.5%	chr22	28746076	CCDS13870.1	c.2428C>A	p.L810I
MTMR6	myotubularin related protein 6	ENSG00000139505	PAP45	141	25.5%	chr13	24724061	CCDS9313.1	c.1408A>C	p.N470H
MYOZ3	myozenin 3	ENSG00000164591	PAP45	152	23.7%	chr5	150032170	CCDS4309.1	c.500C>A	p.P167H
MYST3	MYST histone acetyltransferase (monocytic leukemia) 3	ENSG00000083168	PAP45	307	24.4%	chr8	41933780	ENST00000396930	c.166G>T	p.E56X
MEAF6	MYST/Esa1-associated factor 6	ENSG00000163875	PAP45	65	23.1%	chr1	37747707	CCDS418.1	c.230G>A	p.R77Q
N6AMT2	N-6 adenine-specific DNA methyltransferase 2 (putative)	ENSG00000150456	PAP45	164	23.8%	chr13	20204195	CCDS9293.1	c.293C>T	p.S98L
NKAIN1	Na+/K+ transporting ATPase interacting 1	ENSG00000084628	PAP45	56	26.8%	chr1	31433618	ENST00000373736	c.58G>T	p.A20S
NAALAD2	N-acetylated alpha-linked acidic dipeptidase 2	ENSG00000077616	PAP45	116	18.1%	chr11	89536366	CCDS8288.1	c.1211G>T	p.R404I
NAT1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	ENSG00000171428	PAP45	83	24.1%	chr8	18124693	CCDS6007.1	c.857G>T	p.R286I
NAT10	N-acetyltransferase 10 (GCN5-related)	ENSG00000135372	PAP45	89	12.4%	chr11	34124309	CCDS7889.1	c.3072G>T	p.K1024N
NAT9	N-acetyltransferase 9 (GCN5-related; putative)	ENSG00000109065	PAP45	149	23.5%	chr17	70280717	CCDS11706.1	c.247G>A	p.E83K
ASAH2	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2	ENSG00000188611	PAP45	444	10.4%	chr10	51673023	CCDS7239.1	c.398G>A	p.R133Q
NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1; 75kDa (NADH-coenzyme Q reductase)	ENSG00000023228	PAP45	147	25.9%	chr2	206699735	CCDS2366.1	c.1963C>T	p.R655X
NOX1	NADPH oxidase 1	ENSG00000007952	PAP45	105	24.8%	chrX	99985678	CCDS14474.1	c.1614G>T	p.K538N
NOX1	NADPH oxidase 1	ENSG00000007952	PAP45	170	23.5%	chrX	100004433	CCDS14474.1	c.370G>T	p.D124Y
NAPSB	napsin B aspartic peptidase pseudogene	ENSG00000131401	PAP45	148	35.1%	chr19	55528972	ENST00000253720	c.1234G>A	p.E412K
NCR2	natural cytotoxicity triggering receptor 2	ENSG00000096264	PAP45	75	32.0%	chr6	41418672	ENST00000373086	c.719C>A	p.S240Y

NCKAP1L	NCK-associated protein 1-like	ENSG00000123338	PAP45	77	24.7%	chr12	53198976	CCDS31813.1	c.1432G>A	p.E478K
NCKAP5	NCK-associated protein 5	ENSG00000176771	PAP45	109	12.8%	chr2	133247919	NM_207363	c.5068A>C	p.N1690H
NCKAP5	NCK-associated protein 5	ENSG00000176771	PAP45	227	26.4%	chr2	133256252	NM_207363	c.4602G>T	p.K1534N
NCKAP5	NCK-associated protein 5	ENSG00000176771	PAP45	162	24.7%	chr2	133258672	NM_207363	c.2182G>T	p.D728Y
NCKAP5	NCK-associated protein 5	ENSG00000176771	PAP45	513	25.1%	chr2	133259074	NM_207363	c.1780G>T	p.E594X
NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	ENSG00000070614	PAP45	211	19.0%	chr5	149887640	CCDS34277.1	c.595A>C	p.S199R
NDST3	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	ENSG00000164100	PAP45	90	23.3%	chr4	119194862	CCDS3708.1	c.349C>T	p.L117F
NDST3	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	ENSG00000164100	PAP45	138	47.8%	chr4	119195120	CCDS3708.1	c.607C>T	p.R203C
NDST4	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4	ENSG00000138653	PAP45	42	26.2%	chr4	116217540	CCDS3706.1	c.102C>A	p.Y34X
NDRG3	NDRG family member 3	ENSG00000101079	PAP45	49	46.9%	chr20	34726882	CCDS13285.1	c.791C>T	p.S264L
NDN	necdin homolog (mouse)	ENSG00000182636	PAP45	113	23.9%	chr15	21482642	CCDS10014.1	c.816G>T	p.K272N
NDNL2	necdin-like 2	ENSG00000185115	PAP45	293	29.0%	chr15	27348540	CCDS10023.1	c.662A>C	p.K221T
N4BP2	NEDD4 binding protein 2	ENSG00000078177	PAP45	201	30.8%	chr4	39781159	CCDS3457.1	c.1299G>T	p.K433N
NEIL3	nei endonuclease VIII-like 3 (E. coli)	ENSG00000109674	PAP45	50	24.0%	chr4	178493894	CCDS3828.1	c.337A>C	p.N113H
NELL2	NEL-like 2 (chicken)	ENSG00000184613	PAP45	174	28.7%	chr12	43555400	CCDS8746.1	c.59G>A	p.W20X
NEO1	neogenin homolog 1 (chicken)	ENSG00000067141	PAP45	114	13.2%	chr15	71329101	CCDS10247.1	c.1880G>A	p.R627Q
NPNT	nephronectin	ENSG00000168743	PAP45	60	26.7%	chr4	107038583	CCDS34046.1	c.148C>T	p.R50C
NPHP1	nephronophthisis 1 (juvenile)	ENSG00000144061	PAP45	51	25.5%	chr2	110276552	CCDS2086.1	c.1039C>T	p.R347X
NPHP1	nephronophthisis 1 (juvenile)	ENSG00000144061	PAP45	156	10.3%	chr2	110283407	CCDS2086.1	c.535C>A	p.L179I
NPHP3	nephronophthisis 3 (adolescent)	ENSG00000113971	PAP45	36	30.6%	chr3	133902977	CCDS3078.1	c.1615C>A	p.L539I
NPHP4	nephronophthisis 4	ENSG00000131697	PAP45	69	26.1%	chr1	5862247	ENST00000378162	c.2641G>T	p.E881X
NES	nestin	ENSG00000132688	PAP45	555	26.5%	chr1	154906376	CCDS1151.1	c.4228G>A	p.D1410N
NCAM2	neural cell adhesion molecule 2	ENSG00000154654	PAP45	110	23.6%	chr21	21762900	CCDS42910.1	c.1821G>T	p.K607N
NEDD1	neural precursor cell expressed; developmentally down-regulated 1	ENSG00000139350	PAP45	76	27.6%	chr12	95858327	CCDS9063.1	c.1127G>A	p.R376Q
NEDD4	neural precursor cell expressed; developmentally down-regulated 4	ENSG00000069869	PAP45	132	18.2%	chr15	53920171	CCDS10156.1	c.2926G>A	p.E976K
NEDD9	neural precursor cell expressed; developmentally down-regulated 9	ENSG00000111859	PAP45	341	22.9%	chr6	11298509	CCDS4520.1	c.1579G>A	p.D527N
NRG1	neuregulin 1	ENSG00000157168	PAP45	104	19.2%	chr8	31617713	NM_013962	c.671G>A	p.R224Q
NRG1	neuregulin 1	ENSG00000157168	PAP45	207	25.6%	chr8	32726630	CCDS6083.1	c.701G>T	p.G234V
NRG1	neuregulin 1	ENSG00000157168	PAP45	168	16.1%	chr8	32736420	CCDS6083.1	c.1000G>T	p.E334X
NRG1	neuregulin 1	ENSG00000157168	PAP45	292	17.5%	chr8	32740977	CCDS6083.1	c.1453C>T	p.L485F
NRXN2	neurexin 2	ENSG00000110076	PAP45	272	27.9%	chr11	64191523	CCDS8077.1	c.1573G>A	p.E525K
NBEAL1	neurobeachin-like 1	ENSG00000144426	PAP45	98	23.5%	chr2	203708833	CCDS42802.1	c.45G>T	p.K15N
NBEAL1	neurobeachin-like 1	ENSG00000144426	PAP45	146	31.5%	chr2	203717670	CCDS42802.1	c.994C>A	p.L332I
NBEAL1	neurobeachin-like 1	ENSG00000144426	PAP45	126	24.6%	chr2	203740323	CCDS42802.1	c.2035A>C	p.K679Q
NCAN	neurocan	ENSG00000130287	PAP45	240	24.2%	chr19	19198360	CCDS12397.1	c.1138C>A	p.L380M
NFASC	neurofascin homolog (chicken)	ENSG00000163531	PAP45	72	19.4%	chr1	203187795	CCDS30982.1	c.125C>T	p.A42V
NF1	neurofibromin 1	ENSG00000196712	PAP45	99	40.4%	chr17	26570156	CCDS42292.1	c.1535G>T	p.R512I
NEFH	neurofilament; heavy polypeptide	ENSG00000100285	PAP45	125	15.2%	chr22	28214950	CCDS13858.1	c.1321G>A	p.E441K
NEFH	neurofilament; heavy polypeptide	ENSG00000100285	PAP45	77	14.3%	chr22	28216399	CCDS13858.1	c.2770G>T	p.E924X
NEFH	neurofilament; heavy polypeptide	ENSG00000100285	PAP45	134	10.4%	chr22	28216486	CCDS13858.1	c.2857G>A	p.E953K
NEFL	neurofilament; light polypeptide	ENSG00000104725	PAP45	544	24.1%	chr8	24868989	ENST00000221169	c.958G>A	p.E320K
NEUROD6	neurogenic differentiation 6	ENSG00000164600	PAP45	80	22.5%	chr7	31344687	CCDS5434.1	c.721G>A	p.E241K
NEUROD6	neurogenic differentiation 6	ENSG00000164600	PAP45	216	24.1%	chr7	31344903	CCDS5434.1	c.505C>A	p.L169I
NEUROG2	neurogenin 2	ENSG00000178403	PAP45	162	22.8%	chr4	113655769	CCDS3698.1	c.312G>T	p.E104D
NLGN2	neuroligin 2	ENSG00000169992	PAP45	123	22.0%	chr17	7258425	CCDS11103.1	c.547C>T	p.L183F
NENF	neuron derived neurotrophic factor	ENSG00000117691	PAP45	233	13.3%	chr1	210685936	CCDS1505.1	c.484G>T	p.D162Y
NAV1	neuron navigator 1	ENSG00000134369	PAP45	45	24.4%	chr1	200026455	CCDS1414.1	c.3259C>T	p.R1087C
NAV3	neuron navigator 3	ENSG00000067798	PAP45	34	29.4%	chr12	76939693	CCDS41815.1	c.1943C>T	p.S648L
NPY2R	neuropeptide Y receptor Y2	ENSG00000185149	PAP45	155	35.5%	chr4	156355110	CCDS3791.1	c.569C>T	p.S190L
NPY5R	neuropeptide Y receptor Y5	ENSG00000164129	PAP45	154	20.1%	chr4	164491233	CCDS3804.1	c.358C>A	p.L120I
NPBWR2	neuropeptides B/W receptor 2	ENSG00000125522	PAP45	116	22.4%	chr20	62208083	CCDS13557.1	c.546C>A	p.F182L

NPBWR2	neuropeptides B/W receptor 2	ENSG00000125522	PAP45	71	28.2%	chr20	62208136	CCDS13557.1	c.493G>A	p.V165I
NETO1	neuropilin (NRP) and tolloid (TLL)-like 1	ENSG00000166342	PAP45	47	25.5%	chr18	68683161	CCDS12000.1	c.-1G>T	p.IVS2-1-1SpliceAcceptor
NTS	neurotensin	ENSG00000133636	PAP45	85	22.4%	chr12	84800196	CCDS9029.1	c.425G>T	p.R142I
NTRK1	neurotrophic tyrosine kinase; receptor; type 1	ENSG00000198400	PAP45	122	24.6%	chr1	155108104	CCDS1161.1	c.783G>T	p.K261N
NTRK1	neurotrophic tyrosine kinase; receptor; type 1	ENSG00000198400	PAP45	96	26.0%	chr1	155112528	CCDS1161.1	c.1534C>T	p.L512F
NTRK1	neurotrophic tyrosine kinase; receptor; type 1	ENSG00000198400	PAP45	136	27.2%	chr1	155116457	CCDS1161.1	c.2089G>A	p.E697K
NTRK3	neurotrophic tyrosine kinase; receptor; type 3	ENSG00000140538	PAP45	230	10.4%	chr15	86284965	CCDS32322.1	c.1609G>T	p.D537Y
NSMAF	neutral sphingomyelinase (N-SMase) activation associated factor	ENSG00000035681	PAP45	82	14.6%	chr8	59682954	CCDS6173.1	c.-1G>T	p.IVS10-1-1SpliceAcceptor
NGLY1	N-glycanase 1	ENSG00000151092	PAP45	102	26.5%	chr3	25736122	CCDS33719.1	c.1798C>T	p.L600F
NHLRC2	NHL repeat containing 2	ENSG00000196865	PAP45	205	13.7%	chr10	115626561	CCDS7585.1	c.623A>C	p.K208T
NHLRC2	NHL repeat containing 2	ENSG00000196865	PAP45	106	16.0%	chr10	115634063	CCDS7585.1	c.973G>T	p.E325X
NHLRC3	NHL repeat containing 3	ENSG00000188811	PAP45	280	26.4%	chr13	38510861	CCDS31961.1	c.-1G>A	p.IVS1+1-1SpliceDonor
NHSL2	NHS-like 2	ENSG00000204131	PAP45	324	22.5%	chrX	71277029	CCDS35328.1	c.1808G>T	p.G603V
NBN	nibrin	ENSG00000104320	PAP45	92	17.4%	chr8	91036937	CCDS6249.1	c.1147G>T	p.E383X
NBN	nibrin	ENSG00000104320	PAP45	62	22.6%	chr8	91062298	CCDS6249.1	c.-1G>T	p.IVS3-1-1SpliceAcceptor
NMNAT1	nicotinamide nucleotide adenylyltransferase 1	ENSG00000173614	PAP45	57	31.6%	chr1	9965242	CCDS108.1	c.736G>T	p.E246X
NID1	nidogen 1	ENSG00000116962	PAP45	309	23.9%	chr1	234272124	CCDS1608.1	c.844G>A	p.G282R
NID2	nidogen 2 (osteonidogen)	ENSG00000087303	PAP45	243	24.3%	chr14	51578746	CCDS9706.1	c.1652A>G	p.D551G
NID2	nidogen 2 (osteonidogen)	ENSG00000087303	PAP45	171	27.5%	chr14	51590230	CCDS9706.1	c.1246G>T	p.E416X
NEK10	NIMA (never in mitosis gene a)- related kinase 10	ENSG00000163491	PAP45	154	16.2%	chr3	27190946	ENST00000396636	c.955G>T	p.E319X
NEK11	NIMA (never in mitosis gene a)- related kinase 11	ENSG00000114670	PAP45	119	31.1%	chr3	132281985	CCDS3069.1	c.199G>T	p.E67X
NEK11	NIMA (never in mitosis gene a)- related kinase 11	ENSG00000114670	PAP45	145	20.0%	chr3	132282094	CCDS3069.1	c.308A>C	p.N103T
NEK9	NIMA (never in mitosis gene a)- related kinase 9	ENSG00000119638	PAP45	416	20.2%	chr14	74621063	CCDS9839.1	c.2897C>T	p.S966F
NEK5	NIMA (never in mitosis gene a)-related kinase 5	ENSG00000197168	PAP45	151	26.5%	chr13	51582538	CCDS31979.1	c.406C>A	p.L136I
NEK5	NIMA (never in mitosis gene a)-related kinase 5	ENSG00000197168	PAP45	45	31.1%	chr13	51591540	CCDS31979.1	c.130G>T	p.E44X
NIN	ninein (GSK3B interacting protein)	ENSG00000100503	PAP45	55	23.6%	chr14	50309436	CCDS41952.1	c.794A>C	p.K265T
NIPAL1	NIPA-like domain containing 1	ENSG00000163293	PAP45	190	16.8%	chr4	47732652	CCDS3479.1	c.939C>A	p.F313L
NIPBL	Nipped-B homolog (Drosophila)	ENSG00000164190	PAP45	186	24.7%	chr5	37042286	CCDS3920.1	c.3926A>G	p.D1309G
NIPBL	Nipped-B homolog (Drosophila)	ENSG00000164190	PAP45	79	21.5%	chr5	37094813	CCDS3920.1	c.7474G>A	p.D2492N
NOS2	nitric oxide synthase 2; inducible	ENSG00000007171	PAP45	64	15.6%	chr17	23120240	CCDS11223.1	c.1924G>T	p.D642Y
NPRL2	nitrogen permease regulator-like 2 (S. cerevisiae)	ENSG00000114388	PAP45	249	18.1%	chr3	50361342	CCDS2826.1	c.552C>A	p.F184L
NPRL3	nitrogen permease regulator-like 3 (S. cerevisiae)	ENSG00000103148	PAP45	62	24.2%	chr16	128211	ENST00000399953	c.56G>A	p.G19D
NLRC4	NLR family; CARD domain containing 4	ENSG00000091106	PAP45	141	23.4%	chr2	32328867	CCDS33174.1	c.1570G>A	p.A524T
NLRP10	NLR family; pyrin domain containing 10	ENSG00000182261	PAP45	145	25.5%	chr11	7938157	CCDS7784.1	c.1578C>A	p.F526L
NLRP10	NLR family; pyrin domain containing 10	ENSG00000182261	PAP45	237	24.9%	chr11	7938896	CCDS7784.1	c.839G>T	p.R280I
NLRP12	NLR family; pyrin domain containing 12	ENSG00000142405	PAP45	185	22.2%	chr19	59005777	CCDS12864.1	c.948G>T	p.E316D
NLRP14	NLR family; pyrin domain containing 14	ENSG00000158077	PAP45	140	25.0%	chr11	7021679	CCDS7776.1	c.1846C>T	p.L616F
NLRP3	NLR family; pyrin domain containing 3	ENSG00000162711	PAP45	93	19.4%	chr1	245665988	CCDS1632.1	c.2592G>T	p.E864D
NLRP6	NLR family; pyrin domain containing 6	ENSG00000174885	PAP45	242	24.8%	chr11	271028	CCDS7693.1	c.1294G>A	p.V432I
NLRP7	NLR family; pyrin domain containing 7	ENSG00000167634	PAP45	256	27.7%	chr19	60143541	CCDS12912.1	c.458G>T	p.R153I
NARG2	NMDA receptor regulated 2	ENSG00000128915	PAP45	128	12.5%	chr15	58527568	CCDS10176.1	c.2188T>G	p.F730V
NMT1	N-myristoyltransferase 1	ENSG00000136448	PAP45	296	23.6%	chr17	40532347	CCDS11494.1	c.933C>A	p.F311L
NCAPD2	non-SMC condensin I complex; subunit D2	ENSG00000010292	PAP45	44	25.0%	chr12	6501318	CCDS8548.1	c.1808C>T	p.S603L
NCAPD2	non-SMC condensin I complex; subunit D2	ENSG00000010292	PAP45	74	27.0%	chr12	6502277	CCDS8548.1	c.1977C>A	p.F659L
NCAPD2	non-SMC condensin I complex; subunit D2	ENSG00000010292	PAP45	177	27.1%	chr12	6507297	CCDS8548.1	c.3001G>A	p.E1001K
NCAPD2	non-SMC condensin I complex; subunit D2	ENSG00000010292	PAP45	229	24.9%	chr12	6508131	CCDS8548.1	c.3325C>T	p.R1109W
NCAPD3	non-SMC condensin II complex; subunit D3	ENSG00000151503	PAP45	253	29.2%	chr11	133567945	CCDS31723.1	c.1894G>A	p.E632K

NSUN7	NOP2/Sun domain family; member 7	ENSG00000179299	PAP45	68	32.4%	chr4	40505182	NM_024677	c.1626G>T	p.E542D
NOTCH2	Notch homolog 2 (Drosophila)	ENSG00000134250	PAP45	133	25.6%	chr1	120309616	CCDS908.1	c.1664A>C	p.E555A
NPC1L1	NPC1 (Niemann-Pick disease; type C1; gene)-like 1	ENSG00000015520	PAP45	84	28.6%	chr7	44538286	CCDS5491.1	c.2465G>T	p.G822V
NSL1	NSL1; MIND kinetochore complex component; homolog (S. cerevisiae)	ENSG00000117697	PAP45	84	25.0%	chr1	210978610	CCDS1509.1	c.609A>C	p.Q203H
NTAN1	N-terminal asparagine amidase	ENSG00000157045	PAP45	202	29.2%	chr16	15040009	CCDS10558.1	c.676C>T	p.R226C
NTAN1	N-terminal asparagine amidase	ENSG00000157045	PAP45	202	26.7%	chr16	15040009	CCDS10558.1	c.676C>A	p.R226S
NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	ENSG00000069275	PAP45	166	20.5%	chr1	203954109	CCDS30987.1	c.654G>T	p.K218N
NFE2	nuclear factor (erythroid-derived 2); 45kDa	ENSG00000123405	PAP45	484	29.5%	chr12	52973041	CCDS8876.1	c.506G>A	p.R169H
NUMA1	nuclear mitotic apparatus protein 1	ENSG00000137497	PAP45	381	23.4%	chr11	71401847	CCDS31633.1	c.4350G>T	p.E1450D
NRBP1	nuclear receptor binding protein 1	ENSG00000115216	PAP45	97	26.8%	chr2	27513163	CCDS1753.1	c.701G>A	p.R234Q
NSD1	nuclear receptor binding SET domain protein 1	ENSG00000165671	PAP45	292	19.9%	chr5	176654594	CCDS4412.1	c.7619C>A	p.S2540Y
NCOA1	nuclear receptor coactivator 1	ENSG00000084676	PAP45	283	10.6%	chr2	24774168	CCDS1712.1	c.946G>T	p.E316X
NCOA1	nuclear receptor coactivator 1	ENSG00000084676	PAP45	538	16.9%	chr2	24805947	CCDS1712.1	c.2960G>T	p.R987I
NCOA4	nuclear receptor coactivator 4	ENSG00000138293	PAP45	318	23.9%	chr10	51252801	CCDS7237.1	c.-1G>A	p.IVS5-1-1SpliceAcceptor
NCOA6	nuclear receptor coactivator 6	ENSG00000198646	PAP45	227	14.5%	chr20	32827775	CCDS13241.1	c.373C>A	p.L125I
NCOR1	nuclear receptor co-repressor 1	ENSG00000141027	PAP45	247	22.7%	chr17	15902061	CCDS11175.1	c.6053G>A	p.R2018Q
NCOR1	nuclear receptor co-repressor 1	ENSG00000141027	PAP45	213	25.8%	chr17	15915564	CCDS11175.1	c.4036G>T	p.E1346X
NRIP2	nuclear receptor interacting protein 2	ENSG00000053702	PAP45	385	26.8%	chr12	2814357	CCDS8514.1	c.54G>T	p.E18D
NR0B1	nuclear receptor subfamily 0; group B; member 1	ENSG00000169297	PAP45	289	15.6%	chrX	30232686	CCDS14223.1	c.1344C>A	p.F448L
NR0B2	nuclear receptor subfamily 0; group B; member 2	ENSG00000131910	PAP45	163	26.4%	chr1	27110989	CCDS291.1	c.708C>A	p.F236L
NR1H4	nuclear receptor subfamily 1; group H; member 4	ENSG00000012504	PAP45	36	33.3%	chr12	99479794	CCDS9078.1	c.1067G>A	p.G356D
NR1I2	nuclear receptor subfamily 1; group I; member 2	ENSG00000144852	PAP45	101	27.7%	chr3	121016639	CCDS2995.1	c.1035C>A	p.Y345X
NR2C1	nuclear receptor subfamily 2; group C; member 1	ENSG00000120798	PAP45	44	25.0%	chr12	93976336	CCDS9051.1	c.425G>A	p.R142Q
NR3C1	nuclear receptor subfamily 3; group C; member 1 (glucocorticoid receptor)	ENSG00000113580	PAP45	59	25.4%	chr5	142669918	CCDS34258.1	c.1408C>T	p.R470X
NR3C2	nuclear receptor subfamily 3; group C; member 2	ENSG00000151623	PAP45	375	12.3%	chr4	149575799	CCDS3772.1	c.1664C>A	p.T555N
NR3C2	nuclear receptor subfamily 3; group C; member 2	ENSG00000151623	PAP45	345	28.1%	chr4	149575977	CCDS3772.1	c.1486G>T	p.E496X
NR3C2	nuclear receptor subfamily 3; group C; member 2	ENSG00000151623	PAP45	293	23.5%	chr4	149576656	CCDS3772.1	c.807A>C	p.K269N
NR4A3	nuclear receptor subfamily 4; group A; member 3	ENSG00000119508	PAP45	90	24.4%	chr9	101634793	CCDS6742.1	c.986G>T	p.R329I
NR4A3	nuclear receptor subfamily 4; group A; member 3	ENSG00000119508	PAP45	133	21.1%	chr9	101634883	CCDS6742.1	c.1076G>A	p.R359Q
NXF3	nuclear RNA export factor 3	ENSG00000147206	PAP45	289	22.8%	chrX	102221644	CCDS14503.1	c.1005C>A	p.F335L
NVL	nuclear VCP-like	ENSG00000143748	PAP45	99	21.2%	chr1	222529709	CCDS1541.1	c.2037C>A	p.F679L
NVL	nuclear VCP-like	ENSG00000143748	PAP45	66	19.7%	chr1	222580783	CCDS1541.1	c.64A>G	p.T22A
NOLC1	nucleolar and coiled-body phosphoprotein 1	ENSG00000166197	PAP45	659	22.8%	chr10	103907912	CCDS7530.1	c.558G>T	p.K186N
NUP107	nucleoporin 107kDa	ENSG00000111581	PAP45	80	21.3%	chr12	67413525	CCDS8985.1	c.2128G>T	p.E710X
NUP133	nucleoporin 133kDa	ENSG00000069248	PAP45	74	24.3%	chr1	227647300	CCDS1579.1	c.3318G>T	p.Q1106H
NUP153	nucleoporin 153kDa	ENSG00000124789	PAP45	109	31.2%	chr6	17745956	CCDS4541.1	c.1871C>A	p.S624Y
NUP210L	nucleoporin 210kDa-like	ENSG00000143552	PAP45	86	19.8%	chr1	152262284	CCDS41399.1	c.4236T>G	p.F1412L
NUP210L	nucleoporin 210kDa-like	ENSG00000143552	PAP45	88	26.1%	chr1	152293903	CCDS41399.1	c.3270G>T	p.E1090D
NUP210L	nucleoporin 210kDa-like	ENSG00000143552	PAP45	225	28.9%	chr1	152334183	CCDS41399.1	c.2039G>A	p.R680H
NUP210L	nucleoporin 210kDa-like	ENSG00000143552	PAP45	281	22.8%	chr1	152366433	CCDS41399.1	c.1163G>A	p.S388N
NUP54	nucleoporin 54kDa	ENSG00000138750	PAP45	126	19.8%	chr4	77255583	CCDS3576.1	c.1484T>C	p.L495S
NAP1L2	nucleosome assembly protein 1-like 2	ENSG00000186462	PAP45	480	25.6%	chrX	72350765	CCDS14423.1	c.289G>T	p.D97Y
NUBPL	nucleotide binding protein-like	ENSG00000151413	PAP45	46	28.3%	chr14	31212516	CCDS41940.1	c.498G>T	p.E166D
NACC1	nucleus accumbens associated 1; BEN and BTB (POZ) domain containing	ENSG00000160877	PAP45	158	17.7%	chr19	13110091	CCDS12294.1	c.1455G>T	p.E485D
NUDCD1	NudC domain containing 1	ENSG00000120526	PAP45	140	27.9%	chr8	110324572	CCDS6312.1	c.1594A>G	p.N532D
NULL	NULL	ENSG00000131152	PAP45	90	20.0%	chr16	85906085	ENST00000253461	c.323G>A	p.R108Q
NULL	NULL	ENSG00000181908	PAP45	83	25.3%	chr11	63974167	ENST00000316124	c.331G>T	p.D111Y
NULL	NULL	ENSG00000183935	PAP45	222	11.3%	chr12	13045948	ENST00000331998	c.1212A>C	p.K404N

NULL	NULL	ENSG00000188699	PAP45	91	18.7%	chr19	58419416	ENST00000340013	c.370C>T	p.R124X
NULL	NULL	ENSG00000189277	PAP45	97	13.4%	chr2	186378874	ENST00000343098	c.690T>G	p.H230Q
NULL	NULL	ENSG00000196301	PAP45	223	25.1%	chr6	32535727	ENST00000355324	c.116C>T	p.S39L
NULL	NULL	ENSG00000196478	PAP45	94	10.6%	chr9	26104423	ENST00000359978	c.262C>A	p.L88I
NULL	NULL	ENSG00000196779	PAP45	212	21.7%	chr11	57633228	ENST00000357944	c.482C>T	p.T161M
NULL	NULL	ENSG00000198678	PAP45	235	28.9%	chr12	47239900	ENST00000328207	c.32C>A	p.S11Y
NULL	NULL	ENSG00000205035	PAP45	51	27.5%	chr11	49554940	ENST00000357667	c.567G>T	p.M189I
NULL	NULL	ENSG00000205537	PAP45	301	22.9%	chr12	46581349	ENST00000380601	c.186G>T	p.L62F
NULL	NULL	ENSG00000205902	PAP45	259	25.1%	chr15	40798944	ENST00000382248	c.124G>T	p.E42X
NULL	NULL	ENSG00000206061	PAP45	172	25.0%	chr16	1600180	ENST00000293924	c.863A>C	p.E288A
NULL	NULL	ENSG00000214069	PAP45	444	24.3%	chr17	78379085	ENST00000397438	c.68G>T	p.R23I
NULL	NULL	ENSG00000214279	PAP45	169	10.1%	chr10	135128391	ENST00000356567	c.1652G>A	p.R551Q
NULL	NULL	ENSG00000215273	PAP45	60	25.0%	chr4	17485399	ENST00000399906	c.457G>T	p.E153X
NULL	NULL	ENSG00000215494	PAP45	304	27.3%	chr21	42187937	ENST00000400449	c.281C>T	p.S94L
NULL	NULL	ENSG00000217258	PAP45	308	25.6%	chr2	10513112	ENST00000404616	c.174G>T	p.K58N
NULL	NULL	ENSG00000219410	PAP45	191	19.9%	chr12	6647099	ENST00000407384	c.142G>A	p.G48R
NULL	NULL	ENSG00000220356	PAP45	169	23.1%	chr15	60323300	ENST00000304813	c.94G>A	p.E32K
NULL	NULL	MI0000480	PAP45	100	22.0%	chr14	100595856	MI0000480	c.12A>C	p.E4D
NULL	NULL	MI0003162	PAP45	58	32.8%	chr19	58908458	MI0003162	c.46C>A	p.L16I
NULL	NULL	MI0003641	PAP45	46	37.0%	chr15	40279096	MI0003641	c.61C>A	p.L21I
NULL	NULL	MI0006435	PAP45	145	24.8%	chr4	36104431	MI0006435	c.15G>T	p.K5N
NYX	nyctalopin	ENSG00000188937	PAP45	222	26.1%	chrX	41218725	CCDS14256.1	c.1075G>A	p.D359N
OBSL1	obscurin-like 1	ENSG00000124006	PAP45	210	20.5%	chr2	220132210	NM_015311	c.3207C>A	p.F1069L
OBP2B	odorant binding protein 2B	ENSG00000171102	PAP45	642	17.0%	chr9	135073054	ENST00000372033	c.377G>T	p.R126M
ODZ1	odz; odd Oz/ten-m homolog 1(Drosophila)	ENSG00000009694	PAP45	145	24.8%	chrX	123383905	CCDS14609.1	c.4348A>C	p.N1450H
ODZ3	odz; odd Oz/ten-m homolog 3 (Drosophila)	ENSG00000218336	PAP45	128	28.9%	chr4	183786969	NM_001080477	c.921G>T	p.W307C
ODZ3	odz; odd Oz/ten-m homolog 3 (Drosophila)	ENSG00000218336	PAP45	127	18.9%	chr4	183913240	NM_001080477	c.4726C>T	p.R1576X
ODZ3	odz; odd Oz/ten-m homolog 3 (Drosophila)	ENSG00000218336	PAP45	146	26.7%	chr4	183958137	NM_001080477	c.7739C>T	p.S2580L
ODZ4	odz; odd Oz/ten-m homolog 4 (Drosophila)	ENSG00000149256	PAP45	80	26.3%	chr11	78278697	NM_001098816	c.865C>T	p.P289S
OR1A1	olfactory receptor; family 1; subfamily A; member 1	ENSG00000172146	PAP45	376	10.4%	chr17	3065995	CCDS11022.1	c.331G>T	p.D111Y
OR1A1	olfactory receptor; family 1; subfamily A; member 1	ENSG00000172146	PAP45	426	28.2%	chr17	3066047	CCDS11022.1	c.383G>A	p.R128H
OR1E1	olfactory receptor; family 1; subfamily E; member 1	ENSG00000180016	PAP45	46	21.7%	chr17	3248400	CCDS11024.1	c.999NULL>A	p.NULL-1FsIns1bp
OR1G1	olfactory receptor; family 1; subfamily G; member 1	ENSG00000183024	PAP45	242	27.3%	chr17	2977043	CCDS11020.1	c.553C>A	p.L185M
OR1J2	olfactory receptor; family 1; subfamily J; member 2	ENSG00000197233	PAP45	574	16.6%	chr9	124313296	CCDS35121.1	c.395A>G	p.Y132C
OR1J2	olfactory receptor; family 1; subfamily J; member 2	ENSG00000197233	PAP45	777	23.4%	chr9	124313348	CCDS35121.1	c.447G>T	p.W149C
OR1L1	olfactory receptor; family 1; subfamily L; member 1	ENSG00000173679	PAP45	979	25.6%	chr9	124463998	CCDS35127.1	c.333C>A	p.F111L
OR1L6	olfactory receptor; family 1; subfamily L; member 6	ENSG00000171459	PAP45	77	22.1%	chr9	124552137	CCDS35130.1	c.298C>A	p.L100I
OR1N1	olfactory receptor; family 1; subfamily N; member 1	ENSG00000171505	PAP45	314	24.8%	chr9	124329061	CCDS6844.1	c.333C>A	p.F111L
OR10A7	olfactory receptor; family 10; subfamily A; member 7	ENSG00000179919	PAP45	143	21.7%	chr12	53901118	CCDS31815.1	c.43C>A	p.L15I
OR10AD1	olfactory receptor; family 10; subfamily AD; member 1	ENSG00000172640	PAP45	177	20.3%	chr12	46882640	CCDS31787.1	c.703C>T	p.R235W
OR10R2	olfactory receptor; family 10; subfamily R; member 2	ENSG00000198965	PAP45	206	26.7%	chr1	156716382	CCDS30898.1	c.91G>A	p.E31K
OR10S1	olfactory receptor; family 10; subfamily S; member 1	ENSG00000196248	PAP45	263	26.6%	chr11	123353033	CCDS31701.1	c.576C>A	p.F192L
OR10Z1	olfactory receptor; family 10; subfamily Z; member 1	ENSG00000198967	PAP45	921	25.3%	chr1	156843260	CCDS30901.1	c.408G>T	p.M136I
OR11H4	olfactory receptor; family 11; subfamily H; member 4	ENSG00000176198	PAP45	300	14.0%	chr14	19781324	CCDS32034.1	c.534C>A	p.F178L
OR12D3	olfactory receptor; family 12; subfamily D; member 3	ENSG00000112462	PAP45	120	25.8%	chr6	29431688	CCDS4657.1	c.264G>T	p.K88N
OR13C3	olfactory receptor; family 13; subfamily C; member 3	ENSG00000204246	PAP45	60	25.0%	chr9	106337943	CCDS35089.1	c.973C>A	p.L325I
OR13C4	olfactory receptor; family 13; subfamily C; member 4	ENSG00000148136	PAP45	93	21.5%	chr9	106328632	CCDS35088.1	c.680G>A	p.R227Q
OR13D1	olfactory receptor; family 13; subfamily D; member 1	ENSG00000179055	PAP45	63	23.8%	chr9	106496734	CCDS35094.1	c.211C>T	p.L71F
OR14K1	olfactory receptor; family 14; subfamily K; member 1	ENSG00000153230	PAP45	190	30.5%	chr1	245969396	ENST00000283225	c.857T>C	p.V286A
OR2A12	olfactory receptor; family 2; subfamily A; member 12	ENSG00000221858	PAP45	271	25.1%	chr7	143423590	CCDS43670.1	c.457C>T	p.L153F
OR2AT4	olfactory receptor; family 2; subfamily AT; member 4	ENSG00000171561	PAP45	320	25.6%	chr11	74477532	CCDS31639.1	c.875C>T	p.P292L
OR2B2	olfactory receptor; family 2; subfamily B; member 2	ENSG00000168131	PAP45	46	39.1%	chr6	27987040	CCDS4641.1	c.1037A>G	p.E346G
OR2G2	olfactory receptor; family 2; subfamily G; member 2	ENSG00000177489	PAP45	453	24.5%	chr1	245818752	CCDS31092.1	c.468A>G	p.I156M

OR2T1	olfactory receptor; family 2; subfamily T; member 1	ENSG00000175143	PAP45	321	14.3%	chr1	246636701	CCDS31115.1	c.783C>A	p.F261L
OR2T10	olfactory receptor; family 2; subfamily T; member 10	ENSG00000184022	PAP45	170	21.8%	chr1	246822790	CCDS31121.1	c.903G>T	p.L301F
OR2T10	olfactory receptor; family 2; subfamily T; member 10	ENSG00000184022	PAP45	113	23.0%	chr1	246823466	CCDS31121.1	c.227T>C	p.V76A
OR2W5	olfactory receptor; family 2; subfamily W; member 5	ENSG00000203664	PAP45	352	23.0%	chr1	245721124	NM_001004698	c.72G>T	p.E24D
OR2Y1	olfactory receptor; family 2; subfamily Y; member 1	ENSG00000174339	PAP45	301	18.6%	chr5	180098782	CCDS34323.1	c.883G>A	p.D295N
OR3A4	olfactory receptor; family 3; subfamily A; member 4	ENSG00000180068	PAP45	323	26.0%	chr17	3161166	ENST00000323164	c.812C>T	p.S271L
OR4A15	olfactory receptor; family 4; subfamily A; member 15	ENSG00000181958	PAP45	192	22.4%	chr11	54892227	CCDS31500.1	c.292G>T	p.D98Y
OR4A5	olfactory receptor; family 4; subfamily A; member 5	ENSG00000221840	PAP45	95	13.7%	chr11	51268692	CCDS31497.1	c.280G>T	p.G94C
OR4C3	olfactory receptor; family 4; subfamily C; member 3	ENSG00000176547	PAP45	234	18.8%	chr11	48303144	CCDS31489.1	c.76G>A	p.E26K
OR4D10	olfactory receptor; family 4; subfamily D; member 10	ENSG00000204989	PAP45	134	18.7%	chr11	59016007	ENST00000378245	c.202C>A	p.L68I
OR4D6	olfactory receptor; family 4; subfamily D; member 6	ENSG00000166884	PAP45	146	11.6%	chr11	58981100	CCDS31562.1	c.91T>G	p.F31V
OR4D8P	olfactory receptor; family 4; subfamily D; member 8 pseudogene	ENSG00000204989	PAP45	134	18.7%	chr11	59016007	ENST00000378245	c.202C>A	p.L68I
OR4H12P	olfactory receptor; family 4; subfamily H; member 12 pseudogene	ENSG00000176312	PAP45	651	13.5%	chr14	19297936	ENST00000316004	c.28C>A	p.L10I
OR4H12P	olfactory receptor; family 4; subfamily H; member 12 pseudogene	ENSG00000176312	PAP45	68	17.6%	chr14	19298589	ENST00000316004	c.681C>A	p.F227L
OR4K1	olfactory receptor; family 4; subfamily K; member 1	ENSG00000155249	PAP45	95	14.7%	chr14	19473835	CCDS32025.1	c.170C>A	p.S57Y
OR4K14	olfactory receptor; family 4; subfamily K; member 14	ENSG00000169484	PAP45	470	12.1%	chr14	19552762	CCDS32027.1	c.431G>T	p.R144M
OR4K2	olfactory receptor; family 4; subfamily K; member 2	ENSG00000165762	PAP45	242	18.6%	chr14	19415068	CCDS32023.1	c.802G>T	p.D268Y
OR4K2	olfactory receptor; family 4; subfamily K; member 2	ENSG00000165762	PAP45	220	20.5%	chr14	19415099	CCDS32023.1	c.833T>G	p.F278C
OR4K5	olfactory receptor; family 4; subfamily K; member 5	ENSG00000176281	PAP45	374	17.4%	chr14	19458955	CCDS32024.1	c.350C>T	p.S117L
OR4K5	olfactory receptor; family 4; subfamily K; member 5	ENSG00000176281	PAP45	194	16.5%	chr14	19459362	CCDS32024.1	c.757C>A	p.P253T
OR4S2	olfactory receptor; family 4; subfamily S; member 2	ENSG00000174982	PAP45	67	49.3%	chr11	55175870	CCDS31505.1	c.915C>A	p.F305L
OR5AU1	olfactory receptor; family 5; subfamily AU; member 1	ENSG00000169327	PAP45	223	23.8%	chr14	20693412	CCDS32042.1	c.613C>A	p.L205I
OR5B17	olfactory receptor; family 5; subfamily B; member 17	ENSG00000197786	PAP45	149	31.5%	chr11	57882491	CCDS31548.1	c.628C>A	p.L210I
OR5D16	olfactory receptor; family 5; subfamily D; member 16	ENSG00000205029	PAP45	153	22.9%	chr11	55363091	CCDS31512.1	c.288C>A	p.F96L
OR5D18	olfactory receptor; family 5; subfamily D; member 18	ENSG00000186119	PAP45	186	50.5%	chr11	55344562	CCDS31510.1	c.881G>T	p.R294I
OR5E1P	olfactory receptor; family 5; subfamily E; member 1 pseudogene	ENSG00000170688	PAP45	434	27.4%	chr11	7827289	ENST00000305754	c.116C>A	p.S39Y
OR5I1	olfactory receptor; family 5; subfamily I; member 1	ENSG00000167825	PAP45	199	24.6%	chr11	55460187	CCDS7949.1	c.266C>T	p.S89L
OR5J2	olfactory receptor; family 5; subfamily J; member 2	ENSG00000174957	PAP45	646	24.9%	chr11	55701275	CCDS31522.1	c.606C>A	p.F202L
OR5K3	olfactory receptor; family 5; subfamily K; member 3	ENSG00000206536	PAP45	51	27.5%	chr3	99592771	CCDS33803.1	c.572A>G	p.N191S
OR5K4	olfactory receptor; family 5; subfamily K; member 4	ENSG00000196098	PAP45	132	28.0%	chr3	99555433	CCDS33802.1	c.46G>T	p.G16X
OR5L2	olfactory receptor; family 5; subfamily L; member 2	ENSG00000205030	PAP45	536	24.3%	chr11	55351827	CCDS31511.1	c.557G>T	p.S186I
OR5P2	olfactory receptor; family 5; subfamily P; member 2	ENSG00000183303	PAP45	120	22.5%	chr11	7774747	CCDS7782.1	c.319G>A	p.E107K
OR5P3	olfactory receptor; family 5; subfamily P; member 3	ENSG00000182334	PAP45	331	23.0%	chr11	7803609	CCDS7783.1	c.487T>G	p.L163V
OR5R1	olfactory receptor; family 5; subfamily R; member 1	ENSG00000174942	PAP45	109	24.8%	chr11	55941379	CCDS31530.1	c.906G>T	p.K302N
OR5T1	olfactory receptor; family 5; subfamily T; member 1	ENSG00000181698	PAP45	109	21.1%	chr11	55800390	CCDS31525.1	c.700C>A	p.L234M
OR5T3	olfactory receptor; family 5; subfamily T; member 3	ENSG00000172489	PAP45	105	24.8%	chr11	55776341	CCDS31524.1	c.90G>T	p.R30S
OR51B2	olfactory receptor; family 51; subfamily B; member 2	ENSG00000184881	PAP45	80	18.8%	chr11	5301196	CCDS31377.1	c.908G>A	p.R303H
OR51B4	olfactory receptor; family 51; subfamily B; member 4	ENSG00000183251	PAP45	151	25.2%	chr11	5279151	CCDS7757.1	c.602C>A	p.S201Y
OR51E1	olfactory receptor; family 51; subfamily E; member 1	ENSG00000180785	PAP45	284	26.8%	chr11	4631275	CCDS31358.1	c.940G>A	p.A314T
OR51G1	olfactory receptor; family 51; subfamily G; member 1	ENSG00000176879	PAP45	134	23.1%	chr11	4901255	CCDS31366.1	c.891G>T	p.K297N
OR51J1	olfactory receptor; family 51; subfamily J; member 1 (gene/pseudogene)	ENSG00000184321	PAP45	362	18.0%	chr11	5381072	ENST00000332043	c.670C>A	p.L224I
OR52A1	olfactory receptor; family 52; subfamily A; member 1	ENSG00000182070	PAP45	228	18.0%	chr11	5130057	CCDS31374.1	c.119C>A	p.A40D
OR52E2	olfactory receptor; family 52; subfamily E; member 2	ENSG00000176787	PAP45	115	20.0%	chr11	5036767	CCDS31371.1	c.667C>A	p.L223I
OR52E4	olfactory receptor; family 52; subfamily E; member 4	ENSG00000180974	PAP45	285	15.1%	chr11	5862541	CCDS31401.1	c.443C>A	p.S148Y
OR52E4	olfactory receptor; family 52; subfamily E; member 4	ENSG00000180974	PAP45	232	30.6%	chr11	5862769	CCDS31401.1	c.671G>A	p.R224K
OR52N1	olfactory receptor; family 52; subfamily N; member 1	ENSG00000181001	PAP45	176	27.8%	chr11	5765840	CCDS31398.1	c.783C>A	p.F261L
OR52N2	olfactory receptor; family 52; subfamily N; member 2	ENSG00000180988	PAP45	151	29.8%	chr11	5798925	CCDS31399.1	c.784T>C	p.F262L
OR52N5	olfactory receptor; family 52; subfamily N; member 5	ENSG00000181009	PAP45	241	21.6%	chr11	5755637	CCDS31397.1	c.804C>A	p.F268L
OR6A2	olfactory receptor; family 6; subfamily A; member 2	ENSG00000184933	PAP45	96	34.4%	chr11	6773017	CCDS7772.1	c.499C>A	p.L167I

OR6B1	olfactory receptor; family 6; subfamily B; member 1	ENSG00000221813	PAP45	293	25.9%	chr7	143332804	CCDS43667.1	c.782G>A	p.R261Q
OR6C4	olfactory receptor; family 6; subfamily C; member 4	ENSG00000179626	PAP45	126	13.5%	chr12	54231590	CCDS31827.1	c.313C>A	p.L105I
OR6C6	olfactory receptor; family 6; subfamily C; member 6	ENSG00000188324	PAP45	118	33.9%	chr12	53974369	CCDS31817.1	c.915G>T	p.K305N
OR6C70	olfactory receptor; family 6; subfamily C; member 70	ENSG00000184954	PAP45	64	25.0%	chr12	54150184	CCDS31825.1	c.6G>T	p.K2N
OR6C75	olfactory receptor; family 6; subfamily C; member 75	ENSG00000187857	PAP45	109	25.7%	chr12	54045177	CCDS31820.1	c.16G>T	p.A6S
OR6K2	olfactory receptor; family 6; subfamily K; member 2	ENSG00000196171	PAP45	159	26.4%	chr1	156936318	CCDS30902.1	c.749C>T	p.S250L
OR6K2	olfactory receptor; family 6; subfamily K; member 2	ENSG00000196171	PAP45	165	18.8%	chr1	156936360	CCDS30902.1	c.707G>A	p.R236H
OR6K3	olfactory receptor; family 6; subfamily K; member 3	ENSG00000203757	PAP45	71	21.1%	chr1	156954431	CCDS30903.1	c.147C>A	p.F49L
OR6N2	olfactory receptor; family 6; subfamily N; member 2	ENSG00000188340	PAP45	162	27.2%	chr1	157013235	CCDS30906.1	c.815G>A	p.R272Q
OR6N2	olfactory receptor; family 6; subfamily N; member 2	ENSG00000188340	PAP45	128	24.2%	chr1	157013810	CCDS30906.1	c.240G>T	p.K80N
OR6P1	olfactory receptor; family 6; subfamily P; member 1	ENSG00000186440	PAP45	290	26.6%	chr1	156799167	ENST00000334632	c.852C>A	p.F284L
OR6Y1	olfactory receptor; family 6; subfamily Y; member 1	ENSG00000197532	PAP45	170	15.3%	chr1	156783952	CCDS30899.1	c.568C>A	p.L190I
OR7A10	olfactory receptor; family 7; subfamily A; member 10	ENSG00000127515	PAP45	214	16.4%	chr19	14813223	CCDS32936.1	c.467C>T	p.S156F
OR7C1	olfactory receptor; family 7; subfamily C; member 1	ENSG00000127530	PAP45	248	12.1%	chr19	14771766	CCDS12317.1	c.183C>A	p.F61L
OR7D2	olfactory receptor; family 7; subfamily D; member 2	ENSG00000188000	PAP45	268	18.7%	chr19	9157995	CCDS32900.1	c.538G>A	p.E180K
OR7G3	olfactory receptor; family 7; subfamily G; member 3	ENSG00000170920	PAP45	91	26.4%	chr19	9098587	CCDS32899.1	c.40C>A	p.L14I
OR8D2	olfactory receptor; family 8; subfamily D; member 2	ENSG00000197263	PAP45	146	28.8%	chr11	123695117	CCDS31707.1	c.187C>A	p.L63I
OR8I2	olfactory receptor; family 8; subfamily I; member 2	ENSG00000172154	PAP45	115	10.4%	chr11	55617517	CCDS31517.1	c.158C>A	p.S53Y
OR8K1	olfactory receptor; family 8; subfamily K; member 1	ENSG00000150261	PAP45	117	22.2%	chr11	55870714	CCDS31528.1	c.624C>A	p.F208L
OR8K3	olfactory receptor; family 8; subfamily K; member 3	ENSG00000181689	PAP45	201	24.9%	chr11	55842830	CCDS31527.1	c.472C>A	p.L158I
OR8K5	olfactory receptor; family 8; subfamily K; member 5	ENSG00000181752	PAP45	144	27.8%	chr11	55683884	CCDS31521.1	c.486G>T	p.K162N
OR9A2	olfactory receptor; family 9; subfamily A; member 2	ENSG00000179468	PAP45	186	10.2%	chr7	142434135	CCDS34767.1	c.207G>T	p.E69D
OR9G1	olfactory receptor; family 9; subfamily G; member 1	ENSG00000174914	PAP45	455	16.5%	chr11	56224977	CCDS31536.1	c.538T>G	p.L180V
OR9G9	olfactory receptor; family 9; subfamily G; member 9	ENSG00000174914	PAP45	455	16.5%	chr11	56224977	CCDS31536.1	c.538T>G	p.L180V
OR9I1	olfactory receptor; family 9; subfamily I; member 1	ENSG00000172377	PAP45	149	22.8%	chr11	57642804	CCDS31542.1	c.689C>A	p.S230Y
OR9I1	olfactory receptor; family 9; subfamily I; member 1	ENSG00000172377	PAP45	169	30.2%	chr11	57643001	CCDS31542.1	c.492C>A	p.F164L
OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	ENSG00000147162	PAP45	156	21.2%	chrX	70692646	CCDS14414.1	c.1042C>T	p.R348C
OMA1	OMA1 homolog; zinc metallopeptidase (S. cerevisiae)	ENSG00000162600	PAP45	201	36.3%	chr1	58777502	CCDS608.1	c.53G>A	p.R18Q
OOEP	oocyte expressed protein homolog (dog)	ENSG00000203907	PAP45	75	20.0%	chr6	74136138	NM_001080507	c.99G>T	p.Q33H
OPRM1	opioid receptor; mu 1	ENSG00000112038	PAP45	452	26.1%	chr6	154454077	CCDS43518.1	c.941C>A	p.T314K
OPN4	opsin 4	ENSG00000122375	PAP45	403	24.8%	chr10	88407859	CCDS31237.1	c.414C>A	p.F138L
OFD1	oral-facial-digital syndrome 1	ENSG00000046651	PAP45	156	26.9%	chrX	13664527	CCDS14157.1	c.121C>T	p.R41X
OFD1	oral-facial-digital syndrome 1	ENSG00000046651	PAP45	58	36.2%	chrX	13674903	CCDS14157.1	c.738G>T	p.Q246H
ORC3L	origin recognition complex; subunit 3-like (yeast)	ENSG00000135336	PAP45	176	14.2%	chr6	88401393	CCDS5012.1	c.1297C>T	p.R433X
OFCC1	orofacial cleft 1 candidate 1	ENSG00000181355	PAP45	216	20.4%	chr6	10016823	ENST00000316020	c.461G>T	p.G154V
OTX1	orthodenticle homeobox 1	ENSG00000115507	PAP45	54	22.2%	chr2	63134580	ENST00000405984	c.107C>A	p.S36Y
OTOF	otoferlin	ENSG00000115155	PAP45	219	23.7%	chr2	26544840	CCDS1725.1	c.4030C>T	p.R1344X
OTOF	otoferlin	ENSG00000115155	PAP45	266	12.8%	chr2	26548921	CCDS1725.1	c.3834G>T	p.K1278N
OTUD5	OTU domain containing 5	ENSG00000068308	PAP45	115	16.5%	chrX	48676788	CCDS14313.1	c.967G>A	p.E323K
OTUD7A	OTU domain containing 7A	ENSG00000169918	PAP45	181	24.9%	chr15	29564131	CCDS10026.1	c.1439C>T	p.S480L
OTUD7A	OTU domain containing 7A	ENSG00000169918	PAP45	213	24.9%	chr15	29649685	CCDS10026.1	c.159C>A	p.N53K
OVCH1	ovochymase 1	ENSG00000187950	PAP45	127	15.7%	chr12	29487591	NM_183378	c.3127G>A	p.E1043K
OVCH1	ovochymase 1	ENSG00000187950	PAP45	56	25.0%	chr12	29533945	NM_183378	c.577G>T	p.E193X
OXR1	oxidation resistance 1	ENSG00000164830	PAP45	56	25.0%	chr8	107795291	CCDS6304.1	c.1594G>T	p.E532X
OSBPL1A	oxysterol binding protein-like 1A	ENSG00000141447	PAP45	82	26.8%	chr18	19999094	CCDS11884.1	c.2683C>T	p.R895X
OSBPL6	oxysterol binding protein-like 6	ENSG00000079156	PAP45	65	20.0%	chr2	178955472	CCDS2278.1	c.1625C>A	p.S542Y
OSBPL6	oxysterol binding protein-like 6	ENSG00000079156	PAP45	117	12.8%	chr2	178956060	CCDS2278.1	c.1697C>A	p.P566H
OSBPL9	oxysterol binding protein-like 9	ENSG00000117859	PAP45	104	24.0%	chr1	52025713	CCDS41332.1	c.2101G>T	p.E701X
PAGE3	P antigen family; member 3 (prostate associated)	ENSG00000204279	PAP45	298	26.2%	chrX	55303719	CCDS35307.1	c.292C>A	p.L98M
PAK1	p21 protein (Cdc42/Rac)-activated kinase 1	ENSG00000149269	PAP45	63	30.2%	chr11	76781047	CCDS8250.1	c.167G>A	p.R56Q
PAK3	p21 protein (Cdc42/Rac)-activated kinase 3	ENSG00000077264	PAP45	73	30.1%	chrX	110277754	CCDS14554.1	c.410A>G	p.Y137C
PNLIPRP1	pancreatic lipase-related protein 1	ENSG00000187021	PAP45	107	16.8%	chr10	118347586	CCDS7595.1	c.732C>A	p.F244L

PNLIPRP1	pancreatic lipase-related protein 1	ENSG00000187021	PAP45	140	24.3%	chr10	118350672	CCDS7595.1	c.1032C>A	p.F344L
PNLIPRP3	pancreatic lipase-related protein 3	ENSG00000203837	PAP45	112	22.3%	chr10	118192576	CCDS31292.1	c.224C>T	p.S75F
PNLIPRP3	pancreatic lipase-related protein 3	ENSG00000203837	PAP45	95	21.1%	chr10	118218789	CCDS31292.1	c.1030T>G	p.L344V
PAPPAS	PAPPA antisense RNA (non-protein coding)	ENSG00000182752	PAP45	325	24.0%	chr9	118022181	CCDS6813.1	c.2063C>A	p.S688Y
PAPPAS	PAPPA antisense RNA (non-protein coding)	ENSG00000182752	PAP45	217	24.0%	chr9	118155014	CCDS6813.1	c.4173G>T	p.K1391N
PAPPAS	PAPPA antisense RNA (non-protein coding)	ENSG00000182752	PAP45	104	21.2%	chr9	118198675	CCDS6813.1	c.4843G>T	p.E1615X
PARD6B	par-6 partitioning defective 6 homolog beta (C. elegans)	ENSG00000124171	PAP45	189	22.2%	chr20	48800187	CCDS33485.1	c.874G>A	p.E292K
PACRG	PARK2 co-regulated	ENSG00000112530	PAP45	68	29.4%	chr6	163155278	CCDS5284.1	c.266C>T	p.S89L
PASD1	PAS domain containing 1	ENSG00000166049	PAP45	472	22.5%	chrX	150540077	CCDS35431.1	c.227A>C	p.K76T
PNPLA3	patatin-like phospholipase domain containing 3	ENSG00000100344	PAP45	161	18.6%	chr22	42661866	CCDS14054.1	c.744C>A	p.F248L
PNPLA7	patatin-like phospholipase domain containing 7	ENSG00000130653	PAP45	132	22.7%	chr9	139557777	CCDS7045.1	c.359C>T	p.A120V
PTCHD1	patched domain containing 1	ENSG00000165186	PAP45	242	24.8%	chrX	23321342	CCDS35215.2	c.1786C>T	p.R596W
PEG3	paternally expressed 3	ENSG00000198300	PAP45	227	23.3%	chr19	62020359	CCDS12948.1	c.1263G>T	p.E421D
PKNOX1	PBX/knotted 1 homeobox 1	ENSG00000160199	PAP45	37	27.0%	chr21	43306304	CCDS13692.1	c.409G>A	p.E137K
PCID2	PCI domain containing 2	ENSG00000126226	PAP45	69	15.9%	chr13	112898527	CCDS9532.1	c.439C>T	p.R147X
PCIF1	PDX1 C-terminal inhibiting factor 1	ENSG00000100982	PAP45	211	17.5%	chr20	44005263	CCDS13388.1	c.794G>A	p.R265H
PCIF1	PDX1 C-terminal inhibiting factor 1	ENSG00000100982	PAP45	245	24.9%	chr20	44009680	CCDS13388.1	c.1994C>T	p.A665V
PDZD2	PDZ domain containing 2	ENSG00000133401	PAP45	303	28.1%	chr5	32124311	CCDS34137.1	c.5000C>A	p.S1667X
PDZD4	PDZ domain containing 4	ENSG00000067840	PAP45	166	23.5%	chrX	152723056	CCDS14732.1	c.1256C>T	p.A419V
PDZRN4	PDZ domain containing ring finger 4	ENSG00000165966	PAP45	63	25.4%	chr12	40247952	CCDS8739.1	c.794C>A	p.A265D
PCNX	pecanex homolog (Drosophila)	ENSG00000100731	PAP45	274	23.0%	chr14	70515013	CCDS9806.1	c.2206T>G	p.L736V
PEG3AS	PEG3 antisense RNA (non-protein coding)	ENSG00000198300	PAP45	227	23.3%	chr19	62020359	CCDS12948.1	c.1263G>T	p.E421D
PELI3	pellino homolog 3 (Drosophila)	ENSG00000174516	PAP45	194	11.3%	chr11	65997305	CCDS31615.1	c.474G>T	p.E158D
PADI3	peptidyl arginine deiminase; type III	ENSG00000142619	PAP45	108	11.1%	chr1	17475915	CCDS179.1	c.1512G>T	p.Q504H
PAM	peptidylglycine alpha-amidating monooxygenase	ENSG00000145730	PAP45	150	28.7%	chr5	102230883	CCDS43348.1	c.97G>T	p.E33X
PAM	peptidylglycine alpha-amidating monooxygenase	ENSG00000145730	PAP45	161	21.7%	chr5	102277584	CCDS43348.1	c.316C>A	p.L106I
PPIL4	peptidylprolyl isomerase (cyclophilin)-like 4	ENSG00000131013	PAP45	76	26.3%	chr6	149883910	CCDS34550.1	c.961A>C	p.K321Q
PPIB	peptidylprolyl isomerase B (cyclophilin B)	ENSG00000166794	PAP45	104	31.7%	chr15	62241319	CCDS10191.1	c.223A>G	p.N75D
PPIG	peptidylprolyl isomerase G (cyclophilin G)	ENSG00000138398	PAP45	49	24.5%	chr2	170202238	CCDS2235.1	c.2224C>A	p.H742N
PTRH2	peptidyl-tRNA hydrolase 2	ENSG00000141378	PAP45	358	24.3%	chr17	55129908	CCDS11618.1	c.214C>T	p.R72X
PCM1	pericentriolar material 1	ENSG00000078674	PAP45	84	19.0%	chr8	17874230	NM_006197	c.3697G>T	p.E1233X
PLIN1	perilipin 1	ENSG00000166819	PAP45	281	27.4%	chr15	88014377	CCDS10353.1	c.436G>A	p.A146T
PXDN	peroxidasin homolog (Drosophila)	ENSG00000130508	PAP45	55	18.2%	chr2	1627488	NM_012293	c.3652G>A	p.V1218M
PXDN	peroxidasin homolog (Drosophila)	ENSG00000130508	PAP45	483	23.8%	chr2	1631216	NM_012293	c.3343G>A	p.D1115N
PXDN	peroxidasin homolog (Drosophila)	ENSG00000130508	PAP45	68	26.5%	chr2	1637197	NM_012293	c.1928G>A	p.R643Q
PEX1	peroxisomal biogenesis factor 1	ENSG00000127980	PAP45	131	14.5%	chr7	91985207	CCDS5627.1	c.558G>T	p.E186D
PEX11B	peroxisomal biogenesis factor 11 beta	ENSG00000131779	PAP45	214	21.5%	chr1	144233895	CCDS917.1	c.399G>T	p.M133I
PEX12	peroxisomal biogenesis factor 12	ENSG00000108733	PAP45	191	24.6%	chr17	30926920	CCDS11296.1	c.1074G>T	p.E358D
PEX12	peroxisomal biogenesis factor 12	ENSG00000108733	PAP45	284	21.5%	chr17	30928588	CCDS11296.1	c.262G>A	p.G88S
PPARGC1A	peroxisome proliferator-activated receptor gamma; coactivator 1 alpha	ENSG00000109819	PAP45	115	24.3%	chr4	23423799	CCDS3429.1	c.1841G>T	p.R614L
PES1	pescadillo homolog 1; containing BRCT domain (zebrafish)	ENSG00000100029	PAP45	222	27.9%	chr22	29303063	CCDS13880.1	c.1737G>T	p.E579D
PES1	pescadillo homolog 1; containing BRCT domain (zebrafish)	ENSG00000100029	PAP45	106	28.3%	chr22	29305795	CCDS13880.1	c.1297G>T	p.D433Y
PET112L	PET112-like (yeast)	ENSG00000059691	PAP45	294	28.6%	chr4	152811829	CCDS3776.1	c.1621C>T	p.R541X
PHLPP2	PH domain and leucine rich repeat protein phosphatase 2	ENSG00000040199	PAP45	281	24.6%	chr16	70282083	CCDS32479.1	c.449G>A	p.R150Q
PHF16	PHD finger protein 16	ENSG00000102221	PAP45	207	23.7%	chrX	46802761	CCDS14271.1	c.1810C>A	p.R604S
PHF20L1	PHD finger protein 20-like 1	ENSG00000129292	PAP45	197	21.3%	chr8	133913740	CCDS6367.2	c.1823C>A	p.S608Y
PHF3	PHD finger protein 3	ENSG00000118482	PAP45	145	24.8%	chr6	64453056	CCDS4966.1	c.1474A>C	p.K492Q
PHF3	PHD finger protein 3	ENSG00000118482	PAP45	135	23.7%	chr6	64480091	CCDS4966.1	c.4648A>G	p.I1550V
PHF8	PHD finger protein 8	ENSG00000172943	PAP45	159	20.8%	chrX	53983604	CCDS14355.1	c.2720G>A	p.R907H
PHF8	PHD finger protein 8	ENSG00000172943	PAP45	66	19.7%	chrX	54029060	CCDS14355.1	c.2043G>T	p.K681N
PAH	phenylalanine hydroxylase	ENSG00000171759	PAP45	137	24.8%	chr12	101773086	CCDS9092.1	c.664G>T	p.D222Y
PDC	phosducin	ENSG00000116703	PAP45	215	27.4%	chr1	184679957	CCDS1370.1	c.518C>T	p.S173L
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP45	141	29.1%	chr10	89682958	CCDS31238.1	c.462C>A	p.F154L

PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP45	44	22.7%	chr10	89707726	CCDS31238.1	c.771C>A	p.F257L
PCYT1B	phosphate cytidylyltransferase 1; choline; beta	ENSG00000102230	PAP45	59	23.7%	chrX	24507475	CCDS14213.1	c.587G>A	p.R196K
PHEX	phosphate regulating endopeptidase homolog; X-linked	ENSG00000102174	PAP45	97	26.8%	chrX	21975184	CCDS14204.1	c.283C>T	p.P95S
PIGT	phosphatidylinositol glycan anchor biosynthesis; class T	ENSG00000124155	PAP45	56	32.1%	chr20	43482189	CCDS13353.1	c.-1G>T	p.IVS5-1-1SpliceAcceptor
PREX1	phosphatidylinositol-3;4;5-trisphosphate-dependent Rac exchange factor 1	ENSG00000124126	PAP45	182	19.2%	chr20	46750732	CCDS13410.1	c.883G>A	p.D295N
PREX2	phosphatidylinositol-3;4;5-trisphosphate-dependent Rac exchange factor 2	ENSG00000046889	PAP45	156	26.3%	chr8	69221007	CCDS6201.1	c.4097T>G	p.L1366R
PIP4K2A	phosphatidylinositol-5-phosphate 4-kinase; type II; alpha	ENSG00000150867	PAP45	48	20.8%	chr10	22866170	CCDS7141.1	c.1187G>A	p.R396H
PIP4K2C	phosphatidylinositol-5-phosphate 4-kinase; type II; gamma	ENSG00000166908	PAP45	578	23.4%	chr12	56276007	CCDS8946.1	c.439C>T	p.R147W
PDE11A	phosphodiesterase 11A	ENSG00000128655	PAP45	187	25.1%	chr2	178202436	CCDS33334.1	c.2747C>A	p.S916X
PDE11A	phosphodiesterase 11A	ENSG00000128655	PAP45	159	18.9%	chr2	178242511	CCDS33334.1	c.2518G>A	p.E840K
PDE11A	phosphodiesterase 11A	ENSG00000128655	PAP45	267	24.0%	chr2	178644640	CCDS33334.1	c.771C>A	p.F257L
PDE1B	phosphodiesterase 1B; calmodulin-dependent	ENSG00000123360	PAP45	281	27.0%	chr12	53249375	CCDS8882.1	c.368G>A	p.R123Q
PDE1C	phosphodiesterase 1C; calmodulin-dependent 70kDa	ENSG00000154678	PAP45	108	22.2%	chr7	31844103	CCDS5437.1	c.988C>T	p.R330X
PDE3B	phosphodiesterase 3B; cGMP-inhibited	ENSG00000152270	PAP45	64	31.3%	chr11	14845856	CCDS7817.1	c.3115G>T	p.E1039X
PDE4DIP	phosphodiesterase 4D interacting protein	ENSG00000178104	PAP45	659	12.6%	chr1	143642599	CCDS30826.1	c.467G>A	p.G156D
PDE4D	phosphodiesterase 4D; cAMP-specific (phosphodiesterase E3 dunce homolog; Drosophila)	ENSG00000113448	PAP45	186	26.3%	chr5	58306364	NM_001104631	c.2314G>T	p.D772Y
PDE6B	phosphodiesterase 6B; cGMP-specific; rod; beta	ENSG00000133256	PAP45	228	26.8%	chr4	638624	CCDS33932.1	c.939C>A	p.F313L
PDE6B	phosphodiesterase 6B; cGMP-specific; rod; beta	ENSG00000133256	PAP45	94	19.1%	chr4	644306	CCDS33932.1	c.1518C>A	p.F506L
PDE7A	phosphodiesterase 7A	ENSG00000205268	PAP45	140	13.6%	chr8	66854560	CCDS34901.1	c.154G>T	p.E52X
PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	ENSG00000100889	PAP45	112	27.7%	chr14	23641832	CCDS9609.1	c.1265C>A	p.S422Y
PFKP	phosphofructokinase; platelet	ENSG00000067057	PAP45	187	25.1%	chr10	3133662	CCDS7059.1	c.370G>T	p.V124L
PACS1	phosphofurin acidic cluster sorting protein 1	ENSG00000175115	PAP45	260	26.9%	chr11	65763204	CCDS8129.1	c.2309C>T	p.S770F
PGK1	phosphoglycerate kinase 1	ENSG00000102144	PAP45	127	29.1%	chrX	77256240	CCDS14438.1	c.344C>A	p.S115Y
PIKFYVE	phosphoinositide kinase; FYVE finger containing	ENSG00000115020	PAP45	72	26.4%	chr2	208861781	CCDS2382.1	c.905G>A	p.R302Q
PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	ENSG00000155629	PAP45	111	11.7%	chr10	98459317	CCDS31259.1	c.427G>A	p.E143K
PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP45	239	20.5%	chr3	180399570	CCDS43171.1	c.263G>A	p.R88Q
PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP45	72	29.2%	chr3	180434712	CCDS43171.1	c.3073A>G	p.T1025A
PIK3CB	phosphoinositide-3-kinase; catalytic; beta polypeptide	ENSG00000051382	PAP45	158	21.5%	chr3	139939337	CCDS3104.1	c.703C>A	p.H235N
PIK3CB	phosphoinositide-3-kinase; catalytic; beta polypeptide	ENSG00000051382	PAP45	143	23.8%	chr3	139939386	CCDS3104.1	c.654G>T	p.M218I
PIK3C3	phosphoinositide-3-kinase; class 3	ENSG00000078142	PAP45	180	21.1%	chr18	37791570	CCDS11920.1	c.106A>C	p.K36Q
PIK3R4	phosphoinositide-3-kinase; regulatory subunit 4	ENSG00000196455	PAP45	287	20.9%	chr3	131907135	CCDS3067.1	c.2892G>T	p.M964I
PLN	phospholamban	ENSG00000198523	PAP45	170	25.3%	chr6	118986868	CCDS5120.1	c.91C>A	p.L31I
PLA1A	phospholipase A1 member A	ENSG00000144837	PAP45	126	16.7%	chr3	120810413	CCDS2991.1	c.382G>A	p.V128I
PLA1A	phospholipase A1 member A	ENSG00000144837	PAP45	461	18.4%	chr3	120826757	CCDS2991.1	c.1109C>A	p.S370Y
PLA2R1	phospholipase A2 receptor 1; 180kDa	ENSG00000153246	PAP45	103	17.5%	chr2	160512234	CCDS33309.1	c.3792T>G	p.F1264L
PLA2G4C	phospholipase A2; group IVC (cytosolic; calcium-independent)	ENSG00000105499	PAP45	86	18.6%	chr19	53257093	CCDS12710.1	c.1231G>A	p.D411N
PLA2G4C	phospholipase A2; group IVC (cytosolic; calcium-independent)	ENSG00000105499	PAP45	186	28.5%	chr19	53300507	CCDS12710.1	c.15A>C	p.E5D
PLA2G4F	phospholipase A2; group IVF	ENSG00000168907	PAP45	258	19.8%	chr15	40223503	CCDS32204.1	c.2107C>A	p.L703M
PLA2G7	phospholipase A2; group VII (platelet-activating factor acetylhydrolase; plasma)	ENSG00000146070	PAP45	121	19.0%	chr6	46786280	CCDS4917.1	c.738G>T	p.K246N
PLA2G7	phospholipase A2; group VII (platelet-activating factor acetylhydrolase; plasma)	ENSG00000146070	PAP45	92	32.6%	chr6	46787972	CCDS4917.1	c.532G>T	p.E178X
PLBD1	phospholipase B domain containing 1	ENSG00000121316	PAP45	103	30.1%	chr12	14584978	CCDS31751.1	c.545T>C	p.L182S
PLCB4	phospholipase C; beta 4	ENSG00000101333	PAP45	65	27.7%	chr20	9236525	CCDS13104.1	c.64G>A	p.V22I
PLCB4	phospholipase C; beta 4	ENSG00000101333	PAP45	296	24.7%	chr20	9312917	CCDS13104.1	c.923G>A	p.R308H
PLCB4	phospholipase C; beta 4	ENSG00000101333	PAP45	38	31.6%	chr20	9364242	CCDS13104.1	c.2524C>T	p.L842F
PLCE1	phospholipase C; epsilon 1	ENSG00000138193	PAP45	143	10.5%	chr10	95781125	CCDS41552.1	c.332G>T	p.R111I

PLCE1	phospholipase C; epsilon 1	ENSG00000138193	PAP45	174	16.7%	chr10	95781727	CCDS41552.1	c.934G>T	p.E312X
PLCH1	phospholipase C; eta 1	ENSG00000114805	PAP45	177	24.9%	chr3	156682851	CCDS33881.1	c.3568C>T	p.P1190S
PLCL1	phospholipase C-like 1	ENSG00000115896	PAP45	248	27.0%	chr2	198657342	CCDS2326.1	c.562G>T	p.E188X
PLCL1	phospholipase C-like 1	ENSG00000115896	PAP45	196	52.0%	chr2	198659035	CCDS2326.1	c.2255G>A	p.R752Q
PLCL2	phospholipase C-like 2	ENSG00000154822	PAP45	140	27.9%	chr3	17026651	CCDS33713.1	c.431C>A	p.S144Y
PRPSAP2	phosphoribosyl pyrophosphate synthetase-associated protein 2	ENSG00000141127	PAP45	64	15.6%	chr17	18726706	CCDS11200.1	c.513G>T	p.Q171H
PHKA2	phosphorylase kinase; alpha 2 (liver)	ENSG00000044446	PAP45	265	23.0%	chrX	18822407	CCDS14190.1	c.3373G>A	p.E1125K
PHKG2	phosphorylase kinase; gamma 2 (testis)	ENSG00000156873	PAP45	171	11.7%	chr16	30669963	CCDS10690.1	c.131G>A	p.R44Q
PHKG2	phosphorylase kinase; gamma 2 (testis)	ENSG00000156873	PAP45	434	23.7%	chr16	30675480	CCDS10690.1	c.870C>A	p.F290L
PYGL	phosphorylase; glycogen; liver	ENSG00000100504	PAP45	57	24.6%	chr14	50453165	CCDS32080.1	c.1037C>T	p.A346V
PSTK	phosphoseryl-tRNA kinase	ENSG00000179988	PAP45	83	18.1%	chr10	124736862	CCDS7633.1	c.900G>T	p.E300D
PION	pigeon homolog (Drosophila)	ENSG00000186088	PAP45	250	12.4%	chr7	76779183	CCDS34672.2	c.2384C>A	p.S795Y
PGBD1	piggyBac transposable element derived 1	ENSG00000137338	PAP45	131	20.6%	chr6	28377304	CCDS4648.1	c.1694G>T	p.R565I
PIM2	pim-2 oncogene	ENSG00000102096	PAP45	258	19.8%	chrX	48657589	CCDS14312.1	c.247G>A	p.E83K
PIPOX	pipecolic acid oxidase	ENSG00000179761	PAP45	441	24.5%	chr17	24405721	CCDS11248.1	c.693G>T	p.E231D
PIPOX	pipecolic acid oxidase	ENSG00000179761	PAP45	318	10.4%	chr17	24407403	CCDS11248.1	c.1127C>A	p.P376H
PIWIL1	piwi-like 1 (Drosophila)	ENSG00000125207	PAP45	65	18.5%	chr12	129406077	CCDS9268.1	c.1316G>A	p.R439Q
PIWIL1	piwi-like 1 (Drosophila)	ENSG00000125207	PAP45	199	21.1%	chr12	129411836	CCDS9268.1	c.1824G>T	p.M608I
PLAC9	placenta-specific 9	ENSG00000189129	PAP45	180	22.2%	chr10	81893967	CCDS31232.1	c.171G>T	p.E57D
PKP1	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	ENSG00000081277	PAP45	468	23.7%	chr1	199519652	CCDS30966.1	c.199C>T	p.R67X
PEAR1	platelet endothelial aggregation receptor 1	ENSG00000187800	PAP45	176	11.4%	chr1	155143284	CCDS30892.1	c.632G>T	p.R211I
PDGFRA	platelet-derived growth factor receptor; alpha polypeptide	ENSG00000134853	PAP45	179	14.0%	chr4	54828354	CCDS3495.1	c.901G>T	p.E301X
PDGFRA	platelet-derived growth factor receptor; alpha polypeptide	ENSG00000134853	PAP45	25	40.0%	chr4	54839426	CCDS3495.1	c.2143G>T	p.E715X
PDGFRB	platelet-derived growth factor receptor; beta polypeptide	ENSG00000113721	PAP45	91	27.5%	chr5	149495616	CCDS4303.1	c.59C>A	p.S20Y
PSD4	pleckstrin and Sec7 domain containing 4	ENSG00000125637	PAP45	115	33.9%	chr2	113657419	CCDS33276.1	c.915T>G	p.D305E
PLEKHA1	pleckstrin homology domain containing; family A (phosphoinositide binding specific) member 1	ENSG00000107679	PAP45	79	36.7%	chr10	124167422	CCDS7629.1	c.629G>T	p.R210I
PLEKHA6	pleckstrin homology domain containing; family A member 6	ENSG00000143850	PAP45	273	22.0%	chr1	202464738	CCDS1444.1	c.2701C>T	p.R901C
PLEKHG2	pleckstrin homology domain containing; family G (with RhoGef domain) member 2	ENSG00000090924	PAP45	176	14.2%	chr19	44607700	CCDS33022.1	c.3961C>A	p.L1321I
PLEKHG3	pleckstrin homology domain containing; family G (with RhoGef domain) member 3	ENSG00000126822	PAP45	201	20.9%	chr14	64268625	CCDS32098.1	c.1017G>T	p.E339D
PLEKHH2	pleckstrin homology domain containing; family H (with MyTH4 domain) member 2	ENSG00000152527	PAP45	436	25.7%	chr2	43780926	CCDS1812.1	c.1325G>T	p.R442M
PHLDB2	pleckstrin homology-like domain; family B; member 2	ENSG00000144824	PAP45	233	19.3%	chr3	112934200	ENST00000393934	c.911G>T	p.R304I
PTN	pleiotrophin	ENSG00000105894	PAP45	63	22.2%	chr7	136590229	CCDS5844.1	c.32G>A	p.R11Q
PLXNA2	plexin A2	ENSG00000076356	PAP45	144	27.1%	chr1	206382428	CCDS31013.1	c.1375C>T	p.R459W
PLXNA3	plexin A3	ENSG00000130827	PAP45	312	22.8%	chrX	153347578	CCDS14752.1	c.2639G>A	p.R880H
PLXNC1	plexin C1	ENSG00000136040	PAP45	55	18.2%	chr12	93104326	CCDS9049.1	c.1385C>T	p.S462L
PLXNC1	plexin C1	ENSG00000136040	PAP45	147	23.8%	chr12	93215271	CCDS9049.1	c.4015C>T	p.R1339X
PLXND1	plexin D1	ENSG00000004399	PAP45	95	23.2%	chr3	130785166	CCDS33854.1	c.2175C>A	p.F725L
PLXDC2	plexin domain containing 2	ENSG00000120594	PAP45	89	20.2%	chr10	20330797	CCDS7132.1	c.200G>T	p.R67I
PMS2CL	PMS2 C-terminal like pseudogene	ENSG00000187953	PAP45	138	17.4%	chr7	6743415	ENST00000338780	c.170G>T	p.R57I
PNMAL1	PNMA-like 1	ENSG00000182013	PAP45	321	15.9%	chr19	51665405	CCDS33059.1	c.728G>T	p.R243I
POC1A	POC1 centriolar protein homolog A (Chlamydomonas)	ENSG00000164087	PAP45	128	21.1%	chr3	52134209	CCDS2846.1	c.842G>T	p.R281I
POGK	pogo transposable element with KRAB domain	ENSG00000143157	PAP45	248	29.0%	chr1	165085311	CCDS1254.1	c.871G>A	p.E291K
POGZ	pogo transposable element with ZNF domain	ENSG00000143442	PAP45	52	21.2%	chr1	149650823	CCDS997.1	c.1828C>T	p.R610W
PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	ENSG00000130202	PAP45	97	26.8%	chr19	50083217	CCDS42576.1	c.1358G>T	p.R453L
PLK1S1	polo-like kinase 1 substrate 1	ENSG00000088970	PAP45	99	36.4%	chr20	21161417	ENST00000246027	c.1826A>C	p.K609T
PLK2	polo-like kinase 2 (Drosophila)	ENSG00000145632	PAP45	110	23.6%	chr5	57786211	CCDS3974.1	c.2014C>T	p.R672X
PLK4	polo-like kinase 4 (Drosophila)	ENSG00000142731	PAP45	118	25.4%	chr4	129027271	CCDS3735.1	c.1296C>A	p.F432L
PARP15	poly (ADP-ribose) polymerase family; member 15	ENSG00000173200	PAP45	48	31.3%	chr3	123836581	CCDS3016.1	c.895C>A	p.L299I
PARP3	poly (ADP-ribose) polymerase family; member 3	ENSG00000041880	PAP45	600	27.7%	chr3	51957504	CCDS43097.1	c.1570C>T	p.R524C

PARP4	poly (ADP-ribose) polymerase family; member 4	ENSG00000102699	PAP45	107	19.6%	chr13	23927237	CCDS9307.1	c.2676C>A	p.F892L
PARP9	poly (ADP-ribose) polymerase family; member 9	ENSG00000138496	PAP45	154	28.6%	chr3	123742309	CCDS3014.1	c.1570G>A	p.V524M
PAIP1	poly(A) binding protein interacting protein 1	ENSG00000172239	PAP45	72	20.8%	chr5	43578955	CCDS3947.1	c.642C>A	p.F214L
PABPC5	poly(A) binding protein; cytoplasmic 5	ENSG00000174740	PAP45	185	20.5%	chrX	90577565	CCDS14460.1	c.333A>T	p.K111N
PNLDC1	poly(A)-specific ribonuclease (PARN)-like domain containing 1	ENSG00000146453	PAP45	144	21.5%	chr6	160150124	CCDS5271.1	c.694C>A	p.L232I
PNLDC1	poly(A)-specific ribonuclease (PARN)-like domain containing 1	ENSG00000146453	PAP45	151	24.5%	chr6	160150127	CCDS5271.1	c.697C>A	p.L233I
PMF1	polyamine-modulated factor 1	ENSG00000160783	PAP45	816	12.1%	chr1	154479554	CCDS1134.1	c.280C>T	p.R94W
PKHD1	polycystic kidney and hepatic disease 1 (autosomal recessive)	ENSG00000170927	PAP45	114	23.7%	chr6	51591861	CCDS4935.1	c.12202G>T	p.E4068X
PKHD1	polycystic kidney and hepatic disease 1 (autosomal recessive)	ENSG00000170927	PAP45	269	15.2%	chr6	51997787	CCDS4935.1	c.4780G>T	p.E1594X
PKHD1	polycystic kidney and hepatic disease 1 (autosomal recessive)	ENSG00000170927	PAP45	162	24.7%	chr6	51997867	CCDS4935.1	c.4700G>T	p.R1567I
PKHD1	polycystic kidney and hepatic disease 1 (autosomal recessive)	ENSG00000170927	PAP45	97	33.0%	chr6	52055299	CCDS4935.1	c.131G>A	p.G44D
PKDREJ	polycystic kidney disease (polycystin) and REJ homolog (sperm receptor for egg jelly homolog; sea urchin)	ENSG00000130943	PAP45	93	30.1%	chr22	45032843	CCDS14073.1	c.5041C>T	p.R1681X
PKDREJ	polycystic kidney disease (polycystin) and REJ homolog (sperm receptor for egg jelly homolog; sea urchin)	ENSG00000130943	PAP45	410	22.9%	chr22	45034942	CCDS14073.1	c.2942C>T	p.T981M
PKD1L1	polycystic kidney disease 1 like 1	ENSG00000158683	PAP45	99	22.2%	chr7	47818121	CCDS34633.1	c.7400G>A	p.R2467H
PKD1L2	polycystic kidney disease 1-like 2	ENSG00000166473	PAP45	231	20.3%	chr16	79790074	CCDS42202.1	c.1237G>T	p.E413X
PHC1B	polyhomeotic homolog 1B (Drosophila)	ENSG00000179899	PAP45	172	26.2%	chr12	54091956	ENST00000326184	c.2832G>T	p.E944D
POLN	polymerase (DNA directed) nu	ENSG00000130997	PAP45	210	28.1%	chr4	2057175	CCDS3360.1	c.2160C>A	p.D720E
POLA1	polymerase (DNA directed); alpha 1; catalytic subunit	ENSG00000101868	PAP45	78	24.4%	chrX	24643188	CCDS14214.1	c.454G>A	p.D152N
POLA2	polymerase (DNA directed); alpha 2 (70kD subunit)	ENSG00000014138	PAP45	67	22.4%	chr11	64819589	CCDS8098.1	c.1463C>A	p.S488Y
POLE	polymerase (DNA directed); epsilon	ENSG00000177084	PAP45	137	21.2%	chr12	131729043	CCDS9278.1	c.4966C>T	p.P1656S
POLE	polymerase (DNA directed); epsilon	ENSG00000177084	PAP45	83	32.5%	chr12	131762758	CCDS9278.1	c.1015G>A	p.D339N
POLE	polymerase (DNA directed); epsilon	ENSG00000177084	PAP45	384	23.4%	chr12	131763257	CCDS9278.1	c.857C>G	p.P286R
POLE2	polymerase (DNA directed); epsilon 2 (p59 subunit)	ENSG00000100479	PAP45	79	20.3%	chr14	49192217	CCDS32073.1	c.850G>T	p.D284Y
POLG	polymerase (DNA directed); gamma	ENSG00000140521	PAP45	151	32.5%	chr15	87669782	CCDS10350.1	c.1852C>A	p.H618N
POLG2	polymerase (DNA directed); gamma 2; accessory subunit	ENSG00000136480	PAP45	85	25.9%	chr17	59912359	CCDS32706.1	c.1058C>A	p.S353Y
POLL	polymerase (DNA directed); lambda	ENSG00000166169	PAP45	388	26.3%	chr10	103337027	CCDS7513.1	c.81G>T	p.K27N
POLQ	polymerase (DNA directed); theta	ENSG00000051341	PAP45	160	32.5%	chr3	122674965	CCDS33833.1	c.6465G>T	p.K2155N
POLQ	polymerase (DNA directed); theta	ENSG00000051341	PAP45	307	14.3%	chr3	122689537	CCDS33833.1	c.4931G>T	p.R1644M
POLD3	polymerase (DNA-directed); delta 3; accessory subunit	ENSG00000077514	PAP45	105	14.3%	chr11	74014260	CCDS8233.1	c.893A>G	p.K298R
POLE4	polymerase (DNA-directed); epsilon 4 (p12 subunit)	ENSG00000115350	PAP45	149	34.2%	chr2	75040030	CCDS1957.1	c.268A>C	p.K90Q
POLR1B	polymerase (RNA) I polypeptide B; 128kDa	ENSG00000125630	PAP45	194	13.4%	chr2	113046625	CCDS2097.1	c.2090G>A	p.G697D
POLR2B	polymerase (RNA) II (DNA directed) polypeptide B; 140kDa	ENSG00000047315	PAP45	59	30.5%	chr4	57578054	CCDS3511.1	c.2044T>G	p.L682V
POLR2B	polymerase (RNA) II (DNA directed) polypeptide B; 140kDa	ENSG00000047315	PAP45	83	24.1%	chr4	57585884	CCDS3511.1	c.3040C>A	p.L1014I
POLR3B	polymerase (RNA) III (DNA directed) polypeptide B	ENSG00000013503	PAP45	167	22.2%	chr12	105345190	CCDS9105.1	c.1187G>T	p.R396I
POLR3B	polymerase (RNA) III (DNA directed) polypeptide B	ENSG00000013503	PAP45	64	28.1%	chr12	105372502	CCDS9105.1	c.2176G>T	p.E726X
POLR3C	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	ENSG00000186141	PAP45	233	18.5%	chr1	144319949	CCDS921.1	c.215T>C	p.V72A
PGAP1	post-GPI attachment to proteins 1	ENSG00000197121	PAP45	218	25.7%	chr2	197493065	CCDS2318.1	c.202C>A	p.L68I
KCTD19	potassium channel tetramerisation domain containing 19	ENSG00000168676	PAP45	415	26.0%	chr16	65886054	CCDS42179.1	c.1520C>T	p.S507F
KCTD9P2	potassium channel tetramerisation domain containing 9 pseudogene 2	ENSG00000189108	PAP45	74	31.1%	chrX	104871223	CCDS14517.1	c.931G>T	p.E311X
KCNK10	potassium channel; subfamily K; member 10	ENSG00000100433	PAP45	614	19.1%	chr14	87806846	CCDS9882.1	c.41G>A	p.R14H
KCNK18	potassium channel; subfamily K; member 18	ENSG00000186795	PAP45	449	10.7%	chr10	118959312	CCDS7598.1	c.667T>C	p.C223R
KCNT2	potassium channel; subfamily T; member 2	ENSG00000162687	PAP45	114	28.9%	chr1	194494102	CCDS1384.1	c.3056G>A	p.R1019Q
KCNJ1	potassium inwardly-rectifying channel; subfamily J; member 1	ENSG00000151704	PAP45	207	27.1%	chr11	128215252	CCDS8476.1	c.154G>T	p.E52X
KCNJ3	potassium inwardly-rectifying channel; subfamily J; member 3	ENSG00000162989	PAP45	86	17.4%	chr2	155419895	CCDS2200.1	c.1330C>A	p.P444T

KCNS3	potassium voltage-gated channel; delayed-rectifier; subfamily S; member 3	ENSG00000170745	PAP45	555	22.2%	chr2	17976652	CCDS1692.1	c.896G>A	p.R299Q
KCNQ3	potassium voltage-gated channel; KQT-like subfamily; member 3	ENSG00000184156	PAP45	199	16.1%	chr8	133256910	CCDS34943.1	c.905C>T	p.T302I
KCNQ5	potassium voltage-gated channel; KQT-like subfamily; member 5	ENSG00000185760	PAP45	128	25.8%	chr6	73843849	CCDS4976.1	c.700C>A	p.L234I
KCNQ5	potassium voltage-gated channel; KQT-like subfamily; member 5	ENSG00000185760	PAP45	133	20.3%	chr6	73843912	CCDS4976.1	c.763C>A	p.L255M
KCNQ5	potassium voltage-gated channel; KQT-like subfamily; member 5	ENSG00000185760	PAP45	46	21.7%	chr6	73896243	NM_001160133	c.1254C>A	p.F418L
KCNB2	potassium voltage-gated channel; Shab-related subfamily; member 2	ENSG00000182674	PAP45	166	30.7%	chr8	73643001	CCDS6209.1	c.478C>T	p.R160X
KCNAB1	potassium voltage-gated channel; shaker-related subfamily; beta member 1	ENSG00000169282	PAP45	124	20.2%	chr3	157343818	CCDS3175.1	c.157G>A	p.E53K
KCNAB1	potassium voltage-gated channel; shaker-related subfamily; beta member 1	ENSG00000169282	PAP45	176	14.8%	chr3	157714907	CCDS3174.1	c.719C>T	p.S240L
KCNA2	potassium voltage-gated channel; shaker-related subfamily; member 2	ENSG00000177301	PAP45	451	27.7%	chr1	110948601	CCDS827.1	c.327C>A	p.F109L
KCNA3	potassium voltage-gated channel; shaker-related subfamily; member 3	ENSG00000177272	PAP45	347	24.2%	chr1	111018503	CCDS828.2	c.452G>A	p.R151H
KCNA4	potassium voltage-gated channel; shaker-related subfamily; member 4	ENSG00000182255	PAP45	164	14.6%	chr11	29989301	CCDS41629.1	c.1501G>A	p.A501T
KCNA4	potassium voltage-gated channel; shaker-related subfamily; member 4	ENSG00000182255	PAP45	208	25.5%	chr11	29990103	CCDS41629.1	c.699T>A	p.Y233X
KCNA5	potassium voltage-gated channel; shaker-related subfamily; member 5	ENSG00000130037	PAP45	224	20.5%	chr12	5025324	CCDS8536.1	c.1750G>T	p.E584X
KCNA6	potassium voltage-gated channel; shaker-related subfamily; member 6	ENSG00000151079	PAP45	284	13.0%	chr12	4790660	CCDS8534.1	c.1192G>A	p.E398K
KCND3	potassium voltage-gated channel; Shal-related subfamily; member 3	ENSG00000171385	PAP45	41	29.3%	chr1	112124893	CCDS843.1	c.1313C>T	p.S438L
KCNG4	potassium voltage-gated channel; subfamily G; member 4	ENSG00000168418	PAP45	280	16.8%	chr16	82828238	CCDS10945.1	c.355G>A	p.A119T
KCNH3	potassium voltage-gated channel; subfamily H (eag-related); member 3	ENSG00000135519	PAP45	277	14.4%	chr12	48221720	CCDS8786.1	c.351G>T	p.K117N
KCNH8	potassium voltage-gated channel; subfamily H (eag-related); member 8	ENSG00000183960	PAP45	229	23.1%	chr3	19550546	CCDS2632.1	c.3275T>G	p.V1092G
POU2F1	POU class 2 homeobox 1	ENSG00000143190	PAP45	99	22.2%	chr1	165607785	CCDS1259.1	c.221C>A	p.S74Y
POU2F3	POU class 2 homeobox 3	ENSG00000137709	PAP45	528	25.0%	chr11	119685360	CCDS8431.1	c.923C>T	p.S308L
POU4F1	POU class 4 homeobox 1	ENSG00000152192	PAP45	310	11.9%	chr13	78073623	CCDS31996.1	c.1188G>T	p.K396N
PPPDE1	PPPDE peptidase domain containing 1	ENSG00000121644	PAP45	222	27.0%	chr1	242883898	ENST00000391840	c.41A>G	p.Y14C
PRDM2	PR domain containing 2; with ZNF domain	ENSG00000116731	PAP45	171	19.3%	chr1	13980418	CCDS150.1	c.3541C>T	p.R1181C
PRDM6	PR domain containing 6	ENSG00000061455	PAP45	488	25.6%	chr5	122534523	NM_001136239	c.1318G>T	p.E440X
PRDM8	PR domain containing 8	ENSG00000152784	PAP45	592	16.9%	chr4	81340343	CCDS43243.1	c.85G>A	p.V29I
PFDN5	prefoldin subunit 5	ENSG00000123349	PAP45	174	24.7%	chr12	51976325	CCDS8853.1	c.206C>T	p.S69F
PAPPA	pregnancy-associated plasma protein A; pappalysin 1	ENSG00000182752	PAP45	325	24.0%	chr9	118022181	CCDS6813.1	c.2063C>A	p.S688Y
PAPPA	pregnancy-associated plasma protein A; pappalysin 1	ENSG00000182752	PAP45	217	24.0%	chr9	118155014	CCDS6813.1	c.4173G>T	p.K1391N
PAPPA	pregnancy-associated plasma protein A; pappalysin 1	ENSG00000182752	PAP45	104	21.2%	chr9	118198675	CCDS6813.1	c.4843G>T	p.E1615X
POF1B	premature ovarian failure; 1B	ENSG00000124429	PAP45	158	20.3%	chrX	84521090	CCDS14452.1	c.26C>T	p.T9M
PSEN1	presenilin 1	ENSG00000080815	PAP45	68	17.6%	chr14	72729102	CCDS9812.1	c.-1C>A	p.IVS4-3-1SpliceAcceptor
PRICKLE2	prickle homolog 2 (Drosophila)	ENSG00000163637	PAP45	429	26.1%	chr3	64060486	CCDS2902.1	c.1816C>T	p.R606C
POP7	processing of precursor 7; ribonuclease P/MRP subunit (S. cerevisiae)	ENSG00000172336	PAP45	151	21.2%	chr7	100142675	CCDS5704.1	c.286T>G	p.L96V
PLOD2	procollagen-lysine; 2-oxoglutarate 5-dioxygenase 2	ENSG00000152952	PAP45	137	19.7%	chr3	147271847	CCDS3132.1	c.1902G>T	p.M634I
PLOD2	procollagen-lysine; 2-oxoglutarate 5-dioxygenase 2	ENSG00000152952	PAP45	92	23.9%	chr3	147273054	CCDS3132.1	c.1832C>T	p.S611F

PAEP	progestagen-associated endometrial protein	ENSG00000122133	PAP45	128	25.0%	chr9	137597244	ENST00000344007	c.-1G>A	p.IVS3-3-1SpliceAcceptor
PROKR2	prokineticin receptor 2	ENSG00000101292	PAP45	232	24.1%	chr20	5230830	CCDS13089.1	c.1011G>T	p.K337N
PRLR	prolactin receptor	ENSG00000113494	PAP45	200	12.0%	chr5	35106049	CCDS3909.1	c.619C>A	p.R207S
PRLR	prolactin receptor	ENSG00000113494	PAP45	197	25.4%	chr5	35108466	CCDS3909.1	c.511C>T	p.R171X
PRR10	proline rich 10	ENSG00000218109	PAP45	117	18.8%	chr11	126378837	ENST00000404882	c.285C>A	p.F95L
PRR14	proline rich 14	ENSG00000156858	PAP45	116	13.8%	chr16	30571764	CCDS10687.1	c.343G>A	p.E115K
PRR23B	proline rich 23B	ENSG00000184814	PAP45	85	21.2%	chr3	140221940	CCDS33868.1	c.254C>T	p.T85M
P4HA2	prolyl 4-hydroxylase; alpha polypeptide II	ENSG00000072682	PAP45	82	23.2%	chr5	131572858	CCDS4151.1	c.775G>T	p.E259X
PCCA	propionyl CoA carboxylase; alpha polypeptide	ENSG00000175198	PAP45	63	27.0%	chr13	99723518	CCDS9496.2	c.982A>C	p.K328Q
PCSK1	proprotein convertase subtilisin/kexin type 1	ENSG00000175426	PAP45	328	30.2%	chr5	95756478	CCDS4081.1	c.1730G>T	p.R577I
PCSK1	proprotein convertase subtilisin/kexin type 1	ENSG00000175426	PAP45	97	17.5%	chr5	95777559	CCDS4081.1	c.643G>T	p.E215X
PCSK1	proprotein convertase subtilisin/kexin type 1	ENSG00000175426	PAP45	155	23.9%	chr5	95790692	CCDS4081.1	c.266G>T	p.R89I
PCSK2	proprotein convertase subtilisin/kexin type 2	ENSG00000125851	PAP45	600	24.0%	chr20	17337959	CCDS13125.1	c.595C>T	p.R199W
PTGER3	prostaglandin E receptor 3 (subtype EP3)	ENSG00000050628	PAP45	60	23.3%	chr1	71250650	CCDS653.1	c.1003G>A	p.A335T
PRSS53	protease; serine; 53	ENSG00000151006	PAP45	102	18.6%	chr16	31005511	CCDS42153.1	c.452G>A	p.R151H
PRSS54	protease; serine; 54	ENSG00000103023	PAP45	620	29.5%	chr16	56871682	CCDS32463.1	c.1135G>A	p.E379K
PSME4	proteasome (prosome; macropain) activator subunit 4	ENSG00000068878	PAP45	59	20.3%	chr2	54006270	CCDS33197.1	c.1377G>T	p.E459D
PSMF1	proteasome (prosome; macropain) inhibitor subunit 1 (PI31)	ENSG00000125818	PAP45	106	34.9%	chr20	1063789	CCDS13010.1	c.391C>T	p.R131W
PRMT8	protein arginine methyltransferase 8	ENSG00000111218	PAP45	383	25.3%	chr12	3562616	CCDS8521.2	c.960G>T	p.K320N
PROC	protein C (inactivator of coagulation factors Va and VIIIa)	ENSG00000115718	PAP45	186	22.0%	chr2	127902769	CCDS2145.1	c.1163C>T	p.A388V
PDIA2	protein disulfide isomerase family A; member 2	ENSG00000185615	PAP45	227	22.5%	chr16	274908	CCDS42089.1	c.570C>A	p.F190L
PIAS2	protein inhibitor of activated STAT; 2	ENSG00000078043	PAP45	59	16.9%	chr18	42698167	CCDS32824.1	c.542T>G	p.F181C
PRKCE	protein kinase C; epsilon	ENSG00000171132	PAP45	172	11.0%	chr2	46225758	CCDS1824.1	c.1615C>A	p.L539I
PKN1	protein kinase N1	ENSG00000123143	PAP45	150	23.3%	chr19	14442589	CCDS42514.1	c.2569C>T	p.R857W
PRKAA1	protein kinase; AMP-activated; alpha 1 catalytic subunit	ENSG00000132356	PAP45	80	25.0%	chr5	40800945	CCDS3933.2	c.1019G>T	p.R340I
PRKAR1A	protein kinase; cAMP-dependent; regulatory; type I; alpha (tissue specific extinguisher 1)	ENSG00000108946	PAP45	207	20.8%	chr17	64038142	CCDS11678.1	c.1103G>A	p.R368Q
PRKG2	protein kinase; cGMP-dependent; type II	ENSG00000138669	PAP45	373	26.8%	chr4	82344906	CCDS3589.1	c.320G>A	p.R107Q
PRKDC	protein kinase; DNA-activated; catalytic polypeptide	ENSG00000121031	PAP45	211	10.4%	chr8	48937214	ENST00000314191	c.5944G>A	p.D1982N
PRKDC	protein kinase; DNA-activated; catalytic polypeptide	ENSG00000121031	PAP45	109	20.2%	chr8	48972294	ENST00000314191	c.3578A>C	p.K1193T
PRKDC	protein kinase; DNA-activated; catalytic polypeptide	ENSG00000121031	PAP45	85	24.7%	chr8	49004277	ENST00000314191	c.2067G>T	p.K689N
PPP1R15B	protein phosphatase 1; regulatory (inhibitor) subunit 15B	ENSG00000158615	PAP45	480	11.0%	chr1	202646067	CCDS1445.1	c.1096G>T	p.E366X
PPP1R3A	protein phosphatase 1; regulatory (inhibitor) subunit 3A	ENSG00000154415	PAP45	68	29.4%	chr7	113305660	CCDS5759.1	c.2723G>T	p.R908I
PPP1R3A	protein phosphatase 1; regulatory (inhibitor) subunit 3A	ENSG00000154415	PAP45	705	23.5%	chr7	113306586	CCDS5759.1	c.1797G>T	p.E599D
PPP1R3C	protein phosphatase 1; regulatory (inhibitor) subunit 3C	ENSG00000119938	PAP45	207	23.7%	chr10	93380485	CCDS7416.1	c.133G>T	p.E45X
PPP2R1B	protein phosphatase 2; regulatory subunit A; beta	ENSG00000137713	PAP45	122	13.9%	chr11	111123917	CCDS8348.1	c.1370C>T	p.S457F
PPP2R2D	protein phosphatase 2; regulatory subunit B; delta isoform	ENSG00000175470	PAP45	282	24.8%	chr10	133611279	CCDS41578.1	c.395C>T	p.S132L
PPP2R2C	protein phosphatase 2; regulatory subunit B; gamma	ENSG00000074211	PAP45	107	24.3%	chr4	6428530	CCDS3387.1	c.364G>A	p.E122K
PPP3CB	protein phosphatase 3; catalytic subunit; beta isozyme	ENSG00000107758	PAP45	94	20.2%	chr10	74908301	CCDS7328.1	c.373C>A	p.L125I
PPP4R1	protein phosphatase 4; regulatory subunit 1	ENSG00000154845	PAP45	55	27.3%	chr18	9567105	CCDS42412.1	c.1003G>T	p.E335X
PPM1G	protein phosphatase; Mg2+/Mn2+ dependent; 1G	ENSG00000115241	PAP45	92	26.1%	chr2	27458924	CCDS1752.1	c.1254T>G	p.I418M
PTPDC1	protein tyrosine phosphatase domain containing 1	ENSG00000158079	PAP45	235	24.3%	chr9	95899636	CCDS6708.1	c.961C>T	p.R321C
PTPN14	protein tyrosine phosphatase; non-receptor type 14	ENSG00000152104	PAP45	276	13.8%	chr1	212624261	CCDS1514.1	c.1560G>T	p.K520N
PTPN4	protein tyrosine phosphatase; non-receptor type 4 (megakaryocyte)	ENSG00000088179	PAP45	89	21.3%	chr2	120336630	CCDS2129.1	c.187G>T	p.D63Y
PTPN5	protein tyrosine phosphatase; non-receptor type 5 (striatum-enriched)	ENSG00000110786	PAP45	247	25.1%	chr11	18711412	CCDS7845.1	c.1164G>A	p.W388X
PTPN5	protein tyrosine phosphatase; non-receptor type 5 (striatum-enriched)	ENSG00000110786	PAP45	109	24.8%	chr11	18744004	CCDS7845.1	c.23G>T	p.S8I
PTPRD	protein tyrosine phosphatase; receptor type; D	ENSG00000153707	PAP45	138	18.1%	chr9	8379326	CCDS43786.1	c.4292C>A	p.S1431Y
PPFIA4	protein tyrosine phosphatase; receptor type; f polypeptide (PTPRF); interacting protein (liprin); alpha 4	ENSG00000143847	PAP45	82	18.3%	chr1	201285463	ENST00000367238	c.1393G>T	p.E465X

PTPRM	protein tyrosine phosphatase; receptor type; M	ENSG00000173482	PAP45	121	28.9%	chr18	8103519	CCDS11840.1	c.1892G>A	p.R631Q
PTPRN	protein tyrosine phosphatase; receptor type; N	ENSG00000054356	PAP45	149	26.2%	chr2	219880428	CCDS2440.1	c.262C>T	p.R88X
PTPRN2	protein tyrosine phosphatase; receptor type; N polypeptide 2	ENSG00000155093	PAP45	130	26.2%	chr7	157623795	CCDS5947.1	c.1084G>T	p.E362X
PTPRR	protein tyrosine phosphatase; receptor type; R	ENSG00000153233	PAP45	152	25.7%	chr12	69426093	CCDS8998.1	c.779G>T	p.R260I
PTPRZ1	protein tyrosine phosphatase; receptor-type; Z polypeptide 1	ENSG00000106278	PAP45	262	32.4%	chr7	121438230	CCDS34740.1	c.1894G>A	p.E632K
PTPRZ1	protein tyrosine phosphatase; receptor-type; Z polypeptide 1	ENSG00000106278	PAP45	125	19.2%	chr7	121440384	CCDS34740.1	c.4048G>T	p.A1350S
PTPRZ1	protein tyrosine phosphatase; receptor-type; Z polypeptide 1	ENSG00000106278	PAP45	107	27.1%	chr7	121441019	CCDS34740.1	c.4683G>T	p.E1561D
PTPLAD2	protein tyrosine phosphatase-like A domain containing 2	ENSG00000188921	PAP45	97	12.4%	chr9	20998089	CCDS43791.1	c.547A>G	p.K183E
POMT1	protein-O-mannosyltransferase 1	ENSG00000130714	PAP45	369	28.7%	chr9	133375132	CCDS6943.1	c.627C>A	p.F209L
PRG4	proteoglycan 4	ENSG00000116690	PAP45	123	26.0%	chr1	184539981	CCDS1369.1	c.438G>T	p.K146N
PCDH11X	protocadherin 11 X-linked	ENSG00000102290	PAP45	90	12.2%	chrX	90977251	CCDS14461.1	c.92G>A	p.R31Q
PCDH17	protocadherin 17	ENSG00000118946	PAP45	214	10.3%	chr13	57197236	CCDS31986.1	c.3287T>G	p.M1096R
PCDH19	protocadherin 19	ENSG00000165194	PAP45	87	23.0%	chrX	99438493	CCDS43976.1	c.2744G>A	p.R915Q
PCDH19	protocadherin 19	ENSG00000165194	PAP45	291	11.3%	chrX	99548385	CCDS43976.1	c.1867G>A	p.E623K
PCDH20	protocadherin 20	ENSG00000197991	PAP45	170	28.2%	chr13	60884347	CCDS9442.1	c.1805T>C	p.V602A
PCDH8	protocadherin 8	ENSG00000136099	PAP45	111	32.4%	chr13	52318595	CCDS9438.1	c.1978G>A	p.E660K
PCDH9	protocadherin 9	ENSG00000184226	PAP45	260	27.3%	chr13	66697833	CCDS9444.1	c.2741G>A	p.S914N
PCDHA1	protocadherin alpha 1	ENSG00000204970	PAP45	162	25.3%	chr5	140147096	CCDS34246.1	c.1037A>C	p.N346T
PCDHA10	protocadherin alpha 10	ENSG00000081842	PAP45	170	28.8%	chr5	140216625	CCDS34255.1	c.808G>T	p.E270X
PCDHA10	protocadherin alpha 10	ENSG00000081842	PAP45	134	20.9%	chr5	140243243	CCDS4240.1	c.1206G>T	p.K402N
PCDHA10	protocadherin alpha 10	ENSG00000081842	PAP45	241	22.0%	chr5	140287769	CCDS4241.1	c.1108G>A	p.D370N
PCDHA10	protocadherin alpha 10	ENSG00000081842	PAP45	258	22.9%	chr5	140288931	CCDS4241.1	c.2270G>A	p.R757Q
PCDHA10	protocadherin alpha 10	ENSG00000081842	PAP45	131	21.4%	chr5	140326962	CCDS4242.1	c.427G>A	p.D143N
PCDHA10	protocadherin alpha 10	ENSG00000081842	PAP45	158	15.2%	chr5	140327115	CCDS4242.1	c.580G>A	p.E194K
PCDHA10	protocadherin alpha 10	ENSG00000081842	PAP45	302	26.8%	chr5	140327447	CCDS4242.1	c.912G>T	p.E304D
PCDHA11	protocadherin alpha 11	ENSG00000081842	PAP45	170	28.8%	chr5	140216625	CCDS34255.1	c.808G>T	p.E270X
PCDHA11	protocadherin alpha 11	ENSG00000081842	PAP45	134	20.9%	chr5	140243243	CCDS4240.1	c.1206G>T	p.K402N
PCDHA11	protocadherin alpha 11	ENSG00000081842	PAP45	241	22.0%	chr5	140287769	CCDS4241.1	c.1108G>A	p.D370N
PCDHA11	protocadherin alpha 11	ENSG00000081842	PAP45	258	22.9%	chr5	140288931	CCDS4241.1	c.2270G>A	p.R757Q
PCDHA11	protocadherin alpha 11	ENSG00000081842	PAP45	131	21.4%	chr5	140326962	CCDS4242.1	c.427G>A	p.D143N
PCDHA11	protocadherin alpha 11	ENSG00000081842	PAP45	158	15.2%	chr5	140327115	CCDS4242.1	c.580G>A	p.E194K
PCDHA11	protocadherin alpha 11	ENSG00000081842	PAP45	302	26.8%	chr5	140327447	CCDS4242.1	c.912G>T	p.E304D
PCDHA12	protocadherin alpha 12	ENSG00000081842	PAP45	170	28.8%	chr5	140216625	CCDS34255.1	c.808G>T	p.E270X
PCDHA12	protocadherin alpha 12	ENSG00000081842	PAP45	134	20.9%	chr5	140243243	CCDS4240.1	c.1206G>T	p.K402N
PCDHA12	protocadherin alpha 12	ENSG00000081842	PAP45	241	22.0%	chr5	140287769	CCDS4241.1	c.1108G>A	p.D370N
PCDHA12	protocadherin alpha 12	ENSG00000081842	PAP45	258	22.9%	chr5	140288931	CCDS4241.1	c.2270G>A	p.R757Q
PCDHA12	protocadherin alpha 12	ENSG00000081842	PAP45	131	21.4%	chr5	140326962	CCDS4242.1	c.427G>A	p.D143N
PCDHA12	protocadherin alpha 12	ENSG00000081842	PAP45	158	15.2%	chr5	140327115	CCDS4242.1	c.580G>A	p.E194K
PCDHA12	protocadherin alpha 12	ENSG00000081842	PAP45	302	26.8%	chr5	140327447	CCDS4242.1	c.912G>T	p.E304D
PCDHA2	protocadherin alpha 2	ENSG00000204969	PAP45	297	23.2%	chr5	140156664	CCDS34247.1	c.1931G>A	p.R644Q
PCDHA3	protocadherin alpha 3	ENSG00000204968	PAP45	130	21.5%	chr5	140161358	CCDS34248.1	c.392C>A	p.P131Q
PCDHA6	protocadherin alpha 6	ENSG00000081842	PAP45	170	28.8%	chr5	140216625	CCDS34255.1	c.808G>T	p.E270X
PCDHA6	protocadherin alpha 6	ENSG00000081842	PAP45	134	20.9%	chr5	140243243	CCDS4240.1	c.1206G>T	p.K402N
PCDHA6	protocadherin alpha 6	ENSG00000081842	PAP45	241	22.0%	chr5	140287769	CCDS4241.1	c.1108G>A	p.D370N
PCDHA6	protocadherin alpha 6	ENSG00000081842	PAP45	258	22.9%	chr5	140288931	CCDS4241.1	c.2270G>A	p.R757Q
PCDHA6	protocadherin alpha 6	ENSG00000081842	PAP45	131	21.4%	chr5	140326962	CCDS4242.1	c.427G>A	p.D143N
PCDHA6	protocadherin alpha 6	ENSG00000081842	PAP45	158	15.2%	chr5	140327115	CCDS4242.1	c.580G>A	p.E194K
PCDHA6	protocadherin alpha 6	ENSG00000081842	PAP45	302	26.8%	chr5	140327447	CCDS4242.1	c.912G>T	p.E304D
PCDHA7	protocadherin alpha 7	ENSG00000204963	PAP45	162	13.6%	chr5	140195327	CCDS34252.1	c.1175G>A	p.R392H
PCDHA8	protocadherin alpha 8	ENSG00000204962	PAP45	168	31.0%	chr5	140203449	CCDS34253.1	c.2359G>A	p.E787K

PCDHA9	protocadherin alpha 9	ENSG00000204961	PAP45	241	27.8%	chr5	140210179	CCDS34254.1	c.1915G>A	p.E639K
PCDHAC1	protocadherin alpha subfamily C; 1	ENSG00000081842	PAP45	170	28.8%	chr5	140216625	CCDS34255.1	c.808G>T	p.E270X
PCDHAC1	protocadherin alpha subfamily C; 1	ENSG00000081842	PAP45	134	20.9%	chr5	140243243	CCDS4240.1	c.1206G>T	p.K402N
PCDHAC1	protocadherin alpha subfamily C; 1	ENSG00000081842	PAP45	241	22.0%	chr5	140287769	CCDS4241.1	c.1108G>A	p.D370N
PCDHAC1	protocadherin alpha subfamily C; 1	ENSG00000081842	PAP45	258	22.9%	chr5	140288931	CCDS4241.1	c.2270G>A	p.R757Q
PCDHAC1	protocadherin alpha subfamily C; 1	ENSG00000081842	PAP45	131	21.4%	chr5	140326962	CCDS4242.1	c.427G>A	p.D143N
PCDHAC1	protocadherin alpha subfamily C; 1	ENSG00000081842	PAP45	158	15.2%	chr5	140327115	CCDS4242.1	c.580G>A	p.E194K
PCDHAC1	protocadherin alpha subfamily C; 1	ENSG00000081842	PAP45	302	26.8%	chr5	140327447	CCDS4242.1	c.912G>T	p.E304D
PCDHB1	protocadherin beta 1	ENSG00000171815	PAP45	164	19.5%	chr5	140412596	CCDS4243.1	c.1357C>T	p.R453W
PCDHB10	protocadherin beta 10	ENSG00000120324	PAP45	206	19.4%	chr5	140552392	CCDS4252.1	c.83C>A	p.S28Y
PCDHB10	protocadherin beta 10	ENSG00000120324	PAP45	137	16.8%	chr5	140552836	CCDS4252.1	c.527C>T	p.S176F
PCDHB16	protocadherin beta 16	ENSG00000196963	PAP45	205	24.9%	chr5	140542736	CCDS4251.1	c.418C>A	p.L140I
PCDHB16	protocadherin beta 16	ENSG00000196963	PAP45	144	16.7%	chr5	140543645	CCDS4251.1	c.1327G>T	p.D443Y
PCDHB2	protocadherin beta 2	ENSG00000112852	PAP45	166	16.9%	chr5	140454736	CCDS4244.1	c.178G>T	p.E60X
PCDHB3	protocadherin beta 3	ENSG00000113205	PAP45	34	32.4%	chr5	140462767	CCDS4245.1	c.2350G>A	p.E784K
PCDHB4	protocadherin beta 4	ENSG00000081818	PAP45	407	28.7%	chr5	140482447	CCDS4246.1	c.683G>A	p.R228Q
PCDHB5	protocadherin beta 5	ENSG00000113209	PAP45	78	23.1%	chr5	140495351	CCDS4247.1	c.151G>T	p.D51Y
PCDHB6	protocadherin beta 6	ENSG00000113211	PAP45	204	22.1%	chr5	140511172	CCDS4248.1	c.1150G>T	p.E384X
PCDHB6	protocadherin beta 6	ENSG00000113211	PAP45	196	10.2%	chr5	140511210	CCDS4248.1	c.1188G>T	p.E396D
PCDHB7	protocadherin beta 7	ENSG00000113212	PAP45	166	21.1%	chr5	140533204	CCDS4249.1	c.604C>T	p.R202W
PCDHB7	protocadherin beta 7	ENSG00000113212	PAP45	65	24.6%	chr5	140533622	CCDS4249.1	c.1022A>G	p.N341S
PCDHB9	protocadherin beta 9	ENSG00000120324	PAP45	206	19.4%	chr5	140552392	CCDS4252.1	c.83C>A	p.S28Y
PCDHB9	protocadherin beta 9	ENSG00000120324	PAP45	137	16.8%	chr5	140552836	CCDS4252.1	c.527C>T	p.S176F
PCDHGA10	protocadherin gamma subfamily A; 10	ENSG00000081853	PAP45	156	30.8%	chr5	140790961	CCDS4260.1	c.451C>T	p.R151W
PCDHGA11	protocadherin gamma subfamily A; 11	ENSG00000081853	PAP45	156	30.8%	chr5	140790961	CCDS4260.1	c.451C>T	p.R151W
PCDHGA3	protocadherin gamma subfamily A; 3	ENSG00000081853	PAP45	156	30.8%	chr5	140790961	CCDS4260.1	c.451C>T	p.R151W
PCDHGA8	protocadherin gamma subfamily A; 8	ENSG00000081853	PAP45	156	30.8%	chr5	140790961	CCDS4260.1	c.451C>T	p.R151W
PCDHGB7	protocadherin gamma subfamily B; 7	ENSG00000081853	PAP45	156	30.8%	chr5	140790961	CCDS4260.1	c.451C>T	p.R151W
PCDHGC5	protocadherin gamma subfamily C; 5	ENSG00000081853	PAP45	156	30.8%	chr5	140790961	CCDS4260.1	c.451C>T	p.R151W
PCDH15	protocadherin-related 15	ENSG00000150275	PAP45	219	26.0%	chr10	55236680	ENST00000373965	c.4720C>T	p.R1574X
PCDH15	protocadherin-related 15	ENSG00000150275	PAP45	243	27.6%	chr10	55239027	ENST00000395445	c.4789G>T	p.E1597X
PCDH15	protocadherin-related 15	ENSG00000150275	PAP45	169	20.1%	chr10	55251659	CCDS7248.1	c.5833G>T	p.E1945X
PRTG	protogenin homolog (Gallus gallus)	ENSG00000166450	PAP45	128	14.8%	chr15	53718105	CCDS42040.1	c.2386C>T	p.R796X
PRPF18	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	ENSG00000165630	PAP45	83	15.7%	chr10	13698494	CCDS7100.1	c.883G>T	p.E295X
PRPF3	PRP3 pre-mRNA processing factor 3 homolog (S. cerevisiae)	ENSG00000117360	PAP45	84	25.0%	chr1	148579523	CCDS951.1	c.1228G>T	p.D410Y
PRPF3	PRP3 pre-mRNA processing factor 3 homolog (S. cerevisiae)	ENSG00000117360	PAP45	100	22.0%	chr1	148585123	CCDS951.1	c.1646G>A	p.R549Q
PRPF38B	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	ENSG00000134186	PAP45	81	16.0%	chr1	109040887	ENST00000370024	c.561C>A	p.F187L
PRPF40B	PRP40 pre-mRNA processing factor 40 homolog B (S. cerevisiae)	ENSG00000110844	PAP45	144	13.9%	chr12	48322348	CCDS31796.1	c.1882C>T	p.R628C
PUS7L	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	ENSG00000129317	PAP45	43	25.6%	chr12	42426127	CCDS8743.1	c.1252G>T	p.E418X
PPFIBP1	PTPRF interacting protein; binding protein 1 (liprin beta 1)	ENSG00000110841	PAP45	253	23.7%	chr12	27733288	CCDS8713.1	c.2570G>A	p.R857Q
PUM1	pumilio homolog 1 (Drosophila)	ENSG00000134644	PAP45	218	18.8%	chr1	31199236	CCDS338.1	c.2503G>T	p.D835Y
PUM1	pumilio homolog 1 (Drosophila)	ENSG00000134644	PAP45	470	22.8%	chr1	31210242	CCDS338.1	c.2189G>T	p.S730I
P2RX2	purinergic receptor P2X; ligand-gated ion channel; 2	ENSG00000187848	PAP45	169	27.8%	chr12	131708343	CCDS31930.1	c.1206G>T	p.K402N
P2RY12	purinergic receptor P2Y; G-protein coupled; 12	ENSG00000169313	PAP45	131	27.5%	chr3	152538877	CCDS3159.1	c.447G>A	p.W149X
P2RY14	purinergic receptor P2Y; G-protein coupled; 14	ENSG00000174944	PAP45	157	26.1%	chr3	152413907	CCDS3156.1	c.888C>A	p.F296L
PHTF1	putative homeodomain transcription factor 1	ENSG00000116793	PAP45	160	28.8%	chr1	114050096	CCDS861.1	c.1610G>T	p.R537I
PHTF1	putative homeodomain transcription factor 1	ENSG00000116793	PAP45	163	22.7%	chr1	114102838	CCDS861.1	c.11A>G	p.N4S
PYROXD2	pyridine nucleotide-disulphide oxidoreductase domain 2	ENSG00000119943	PAP45	156	25.6%	chr10	100157392	CCDS7474.1	c.252C>A	p.F84L
PDXK	pyridoxal (pyridoxine; vitamin B6) kinase	ENSG00000160209	PAP45	308	22.7%	chr21	43976831	ENST00000327574	c.145C>A	p.L49I

PYHIN1	pyrin and HIN domain family; member 1	ENSG00000163564	PAP45	65	32.3%	chr1	157173523	CCDS1178.1	c.199G>T	p.E67X
PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	ENSG00000131828	PAP45	90	27.8%	chrX	19286966	CCDS14192.1	c.911G>A	p.R304Q
PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	ENSG00000131828	PAP45	104	19.2%	chrX	19287651	CCDS14192.1	c.1132C>T	p.R378C
PDHB	pyruvate dehydrogenase (lipoamide) beta	ENSG00000168291	PAP45	160	24.4%	chr3	58392540	CCDS2890.1	c.225G>T	p.K75N
PDHX	pyruvate dehydrogenase complex; component X	ENSG00000110435	PAP45	85	17.6%	chr11	34935573	CCDS7896.1	c.409G>T	p.D137Y
QTRT1	queuine tRNA-ribosyltransferase 1	ENSG00000213339	PAP45	60	18.3%	chr19	10673354	CCDS12248.1	c.218A>C	p.N73T
R3HDM1	R3H domain containing 1	ENSG00000048991	PAP45	249	20.5%	chr2	136198325	CCDS2177.1	c.3293C>A	p.S1098Y
R3HDM2	R3H domain containing 2	ENSG00000179912	PAP45	104	22.1%	chr12	55976589	NM_014925	c.573G>T	p.K191N
RAB27A	RAB27A; member RAS oncogene family	ENSG00000069974	PAP45	224	21.9%	chr15	53303392	CCDS10153.1	c.454G>A	p.A152T
RAB39B	RAB39B; member RAS oncogene family	ENSG00000155961	PAP45	126	27.0%	chrX	154146613	CCDS14766.1	c.155T>C	p.I52T
RAB3IP	RAB3A interacting protein (rabin3)	ENSG00000127328	PAP45	331	24.5%	chr12	68435676	CCDS8993.1	c.269G>A	p.R90H
RAB8A	RAB8A; member RAS oncogene family	ENSG00000167461	PAP45	426	24.4%	chr19	16101369	CCDS12339.1	c.486T>G	p.F162L
RABEP1	rabaptin; RAB GTPase binding effector protein 1	ENSG00000029725	PAP45	57	28.1%	chr17	5179283	CCDS42243.1	c.448G>A	p.A150T
RPH3A	rabphilin 3A homolog (mouse)	ENSG00000089169	PAP45	138	20.3%	chr12	111803975	CCDS31904.1	c.1255G>A	p.D419N
ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	ENSG00000129675	PAP45	110	24.5%	chrX	135600485	CCDS14660.1	c.1135C>T	p.R379X
ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	ENSG00000129675	PAP45	87	18.4%	chrX	135616785	CCDS14660.1	c.994C>A	p.L332M
RAD18	RAD18 homolog (S. cerevisiae)	ENSG00000070950	PAP45	48	31.3%	chr3	8915615	CCDS2571.1	c.1285G>T	p.E429X
RINT1	RAD50 interactor 1	ENSG00000135249	PAP45	99	23.2%	chr7	104991465	CCDS34726.1	c.1721A>C	p.N574T
RAD51AP1	RAD51 associated protein 1	ENSG00000111247	PAP45	142	21.8%	chr12	4538383	CCDS8529.1	c.971G>A	p.R324Q
RAD51AP2	RAD51 associated protein 2	ENSG00000214842	PAP45	89	24.7%	chr2	17560058	CCDS42656.1	c.3106G>A	p.A1036T
RAD51AP2	RAD51 associated protein 2	ENSG00000214842	PAP45	59	27.1%	chr2	17560283	CCDS42656.1	c.2881G>T	p.D961Y
RAD54B	RAD54 homolog B (S. cerevisiae)	ENSG00000197275	PAP45	43	27.9%	chr8	95475260	CCDS6262.1	c.1405G>T	p.E469X
RAD54B	RAD54 homolog B (S. cerevisiae)	ENSG00000197275	PAP45	85	22.4%	chr8	95492619	CCDS6262.1	c.405G>T	p.K135N
RAD54L2	RAD54-like 2 (S. cerevisiae)	ENSG00000164080	PAP45	445	24.3%	chr3	51642778	CCDS33765.1	c.647G>A	p.R216H
RAD54L2	RAD54-like 2 (S. cerevisiae)	ENSG00000164080	PAP45	103	15.5%	chr3	51648697	CCDS33765.1	c.1759C>T	p.R587X
RSPH4A	radial spoke head 4 homolog A (Chlamydomonas)	ENSG00000111834	PAP45	211	10.9%	chr6	117055821	CCDS34521.1	c.1258G>T	p.E420X
RSPH6A	radial spoke head 6 homolog A (Chlamydomonas)	ENSG00000111834	PAP45	211	10.9%	chr6	117055821	CCDS34521.1	c.1258G>T	p.E420X
RSPH9	radial spoke head 9 homolog (Chlamydomonas)	ENSG00000172426	PAP45	52	30.8%	chr6	43726171	CCDS4905.1	c.309C>A	p.F103L
RSAD1	radical S-adenosyl methionine domain containing 1	ENSG00000136444	PAP45	186	21.0%	chr17	45914679	CCDS11569.1	c.703G>A	p.A235T
RSAD2	radical S-adenosyl methionine domain containing 2	ENSG00000134321	PAP45	73	24.7%	chr2	6940991	CCDS1656.1	c.385C>A	p.L129I
RSAD2	radical S-adenosyl methionine domain containing 2	ENSG00000134321	PAP45	138	26.1%	chr2	6953443	CCDS1656.1	c.1005C>A	p.F335L
RFTN2	raftlin family member 2	ENSG00000162944	PAP45	100	27.0%	chr2	198190872	CCDS2323.1	c.947C>A	p.S316Y
RFTN2	raftlin family member 2	ENSG00000162944	PAP45	84	27.4%	chr2	198204016	CCDS2323.1	c.892T>G	p.L298V
RFTN2	raftlin family member 2	ENSG00000162944	PAP45	120	30.0%	chr2	198217230	CCDS2323.1	c.335C>T	p.S112L
RANBP2	RAN binding protein 2	ENSG00000153201	PAP45	224	21.4%	chr2	108765701	CCDS2079.1	c.9320G>A	p.G3107D
RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	ENSG00000109756	PAP45	256	25.8%	chr4	160494549	CCDS43277.1	c.4069G>A	p.E1357K
RAPGEF3	Rap guanine nucleotide exchange factor (GEF) 3	ENSG00000079337	PAP45	78	16.7%	chr12	46428565	CCDS41775.1	c.1182G>T	p.E394D
RAPGEF4	Rap guanine nucleotide exchange factor (GEF) 4	ENSG00000091428	PAP45	138	20.3%	chr2	173368010	CCDS42775.1	c.77G>A	p.R26Q
RAPGEF4	Rap guanine nucleotide exchange factor (GEF) 4	ENSG00000091428	PAP45	250	20.8%	chr2	173624695	CCDS42775.1	c.2990G>T	p.R997I
RAPGEF5	Rap guanine nucleotide exchange factor (GEF) 5	ENSG00000136237	PAP45	103	26.2%	chr7	22324182	ENST00000405243	c.-1G>T	p.IVS1-1-1SpliceAcceptor
RIF1	RAP1 interacting factor homolog (yeast)	ENSG00000080345	PAP45	79	31.6%	chr2	152028950	CCDS2194.1	c.4670C>T	p.S1557L
RORA	RAR-related orphan receptor A	ENSG00000069667	PAP45	51	25.5%	chr15	58594166	CCDS10179.1	c.464G>T	p.R155I
RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	ENSG00000173166	PAP45	39	25.6%	chr2	204032902	CCDS2359.1	c.1065A>C	p.E355D
RASSF4	Ras association (RalGDS/AF-6) domain family member 4	ENSG00000107551	PAP45	165	20.0%	chr10	44805166	CCDS7208.1	c.676G>A	p.E226K
RADIL	Ras association and DIL domains	ENSG00000157927	PAP45	38	36.8%	chr7	4842598	CCDS43544.1	c.700G>A	p.E234K
RADIL	Ras association and DIL domains	ENSG00000157927	PAP45	288	20.5%	chr7	4883848	CCDS43544.1	c.449G>A	p.R150Q
RHOQ	ras homolog gene family; member Q	ENSG00000119729	PAP45	78	16.7%	chr2	46657284	CCDS33191.1	c.447G>T	p.Q149H
RASA1	RAS p21 protein activator (GTPase activating protein) 1	ENSG00000145715	PAP45	82	25.6%	chr5	86664903	CCDS34200.1	c.892G>T	p.E298X
RASA1	RAS p21 protein activator (GTPase activating protein) 1	ENSG00000145715	PAP45	285	25.3%	chr5	86709990	CCDS34200.1	c.2366G>A	p.R789Q
RASAL2	RAS protein activator like 2	ENSG00000075391	PAP45	354	20.9%	chr1	176693548	CCDS1321.1	c.2465C>A	p.S822Y
RASGEF1B	RasGEF domain family; member 1B	ENSG00000138670	PAP45	76	23.7%	chr4	82585932	CCDS34022.1	c.814G>T	p.E272X

RIT1	Ras-like without CAAX 1	ENSG00000143622	PAP45	220	26.4%	chr1	154146877	CCDS1123.1	c.151G>T	p.D51Y
RRAGB	Ras-related GTP binding B	ENSG00000083750	PAP45	107	24.3%	chrX	55774619	CCDS14372.1	c.475G>A	p.E159K
RRAGC	Ras-related GTP binding C	ENSG00000116954	PAP45	67	26.9%	chr1	39089905	CCDS430.1	c.868G>A	p.D290N
REST	RE1-silencing transcription factor	ENSG00000084093	PAP45	162	32.1%	chr4	57472421	CCDS3509.1	c.860G>T	p.R287I
REST	RE1-silencing transcription factor	ENSG00000084093	PAP45	106	24.5%	chr4	57492672	CCDS3509.1	c.2891C>A	p.S964X
RIPK1	receptor (TNFRSF)-interacting serine-threonine kinase 1	ENSG00000137275	PAP45	119	23.5%	chr6	3026260	CCDS4482.1	c.370G>T	p.E124X
ROR2	receptor tyrosine kinase-like orphan receptor 2	ENSG00000169071	PAP45	453	26.0%	chr9	93526590	CCDS6691.1	c.2007C>A	p.F669L
ROR2	receptor tyrosine kinase-like orphan receptor 2	ENSG00000169071	PAP45	174	20.7%	chr9	93539608	CCDS6691.1	c.508G>A	p.E170K
RAG1	recombination activating gene 1	ENSG00000166349	PAP45	343	27.1%	chr11	36551707	CCDS7902.1	c.277G>A	p.D93N
RAG1	recombination activating gene 1	ENSG00000166349	PAP45	230	10.4%	chr11	36552580	CCDS7902.1	c.1150G>T	p.E384X
RAG1	recombination activating gene 1	ENSG00000166349	PAP45	211	26.5%	chr11	36553802	CCDS7902.1	c.2372T>C	p.V791A
RAG1	recombination activating gene 1	ENSG00000166349	PAP45	210	21.9%	chr11	36554439	CCDS7902.1	c.3009G>T	p.Q1003H
RELN	reelin	ENSG00000189056	PAP45	50	32.0%	chr7	102947131	CCDS34722.1	c.7737C>A	p.F2579L
RIMS2	regulating synaptic membrane exocytosis 2	ENSG00000176406	PAP45	215	29.8%	chr8	104967226	CCDS43761.1	c.647G>A	p.R216Q
RIMS2	regulating synaptic membrane exocytosis 2	ENSG00000176406	PAP45	123	28.5%	chr8	104967530	CCDS43761.1	c.951G>T	p.Q317H
RIMS2	regulating synaptic membrane exocytosis 2	ENSG00000176406	PAP45	106	20.8%	chr8	105056852	CCDS43761.1	c.2245C>T	p.R749X
RPRD2	regulation of nuclear pre-mRNA domain containing 2	ENSG00000163125	PAP45	468	29.7%	chr1	148710416	NM_015203	c.2368C>T	p.R790X
RCBTB2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	ENSG00000136161	PAP45	120	31.7%	chr13	47987419	CCDS9411.1	c.272G>T	p.R91I
RCC1	regulator of chromosome condensation 1	ENSG00000180198	PAP45	380	20.0%	chr1	28735475	CCDS41295.1	c.1025C>A	p.S342X
RCC2	regulator of chromosome condensation 2	ENSG00000179051	PAP45	125	24.0%	chr1	17615679	CCDS181.1	c.910G>A	p.D304N
RGS18	regulator of G-protein signaling 18	ENSG00000150681	PAP45	109	24.8%	chr1	190395001	CCDS1374.1	c.148C>A	p.L50I
RGS20	regulator of G-protein signaling 20	ENSG00000147509	PAP45	131	19.8%	chr8	55021822	CCDS6155.1	c.704C>T	p.S235F
RGS20	regulator of G-protein signaling 20	ENSG00000147509	PAP45	29	34.5%	chr8	55033503	CCDS6155.1	c.1099C>T	p.R367X
RGS9	regulator of G-protein signaling 9	ENSG00000108370	PAP45	166	23.5%	chr17	60628577	CCDS42373.1	c.981G>T	p.E327D
RFX6	regulatory factor X; 6	ENSG00000185002	PAP45	158	25.3%	chr6	117356813	CCDS5113.1	c.2597G>A	p.R866Q
RFX6	regulatory factor X; 6	ENSG00000185002	PAP45	56	23.2%	chr6	117359297	CCDS5113.1	c.2722G>T	p.E908X
RXFP1	relaxin/insulin-like family peptide receptor 1	ENSG00000171509	PAP45	64	15.6%	chr4	159789229	CCDS43276.1	c.1885C>T	p.R629C
RXFP3	relaxin/insulin-like family peptide receptor 3	ENSG00000182631	PAP45	216	26.9%	chr5	33972892	CCDS3900.1	c.290C>T	p.A97V
RSF1	remodeling and spacing factor 1	ENSG00000048649	PAP45	331	10.9%	chr11	77055787	CCDS8253.1	c.4149G>T	p.L1383F
RFC1	replication factor C (activator 1) 1; 145kDa	ENSG00000035928	PAP45	123	20.3%	chr4	38994985	CCDS3450.1	c.1148G>A	p.R383Q
RFC2	replication factor C (activator 1) 2; 40kDa	ENSG00000049541	PAP45	143	24.5%	chr7	73289639	CCDS5568.1	c.829G>A	p.E277K
RERGL	RERG/RAS-like	ENSG00000111404	PAP45	121	29.8%	chr12	18125472	CCDS8679.1	c.538G>T	p.E180X
RET	ret proto-oncogene	ENSG00000165731	PAP45	221	25.8%	chr10	42916053	CCDS7200.1	c.214C>T	p.L72F
RET	ret proto-oncogene	ENSG00000165731	PAP45	103	24.3%	chr10	42924600	CCDS7200.1	c.1179C>A	p.F393L
RTN3	reticulon 3	ENSG00000133318	PAP45	130	25.4%	chr11	63243794	CCDS8050.1	c.1187C>A	p.A396D
RTN3	reticulon 3	ENSG00000133318	PAP45	167	19.2%	chr11	63282307	CCDS8048.1	c.710C>T	p.S237L
RTN4	reticulon 4	ENSG00000115310	PAP45	128	14.8%	chr2	55106668	CCDS42684.1	c.2071G>T	p.E691X
RP1	retinitis pigmentosa 1 (autosomal dominant)	ENSG00000104237	PAP45	114	28.1%	chr8	55701097	CCDS6160.1	c.2102G>T	p.R701I
RP1	retinitis pigmentosa 1 (autosomal dominant)	ENSG00000104237	PAP45	143	13.3%	chr8	55703841	CCDS6160.1	c.4846G>A	p.E1616K
RP1L1	retinitis pigmentosa 1-like 1	ENSG00000183638	PAP45	236	20.3%	chr8	10505714	CCDS43708.1	c.3304G>A	p.E1102K
RPGRIP1	retinitis pigmentosa GTPase regulator interacting protein 1	ENSG00000092200	PAP45	92	32.6%	chr14	20855642	ENST00000382933	c.25G>A	p.V9I
RBBP6	retinoblastoma binding protein 6	ENSG00000122257	PAP45	81	38.3%	chr16	24490891	CCDS10621.1	c.5003A>C	p.K1668T
RBBP9	retinoblastoma binding protein 9	ENSG00000089050	PAP45	79	35.4%	chr20	18419108	CCDS13136.1	c.265C>T	p.R89X
RBL1	retinoblastoma-like 1 (p107)	ENSG00000080839	PAP45	49	20.4%	chr20	35097140	CCDS13289.1	c.2089T>G	p.L697V
RBL2	retinoblastoma-like 2 (p130)	ENSG00000103479	PAP45	157	15.3%	chr16	52044876	CCDS10748.1	c.778G>T	p.D260Y
RBL2	retinoblastoma-like 2 (p130)	ENSG00000103479	PAP45	132	18.2%	chr16	52053200	CCDS10748.1	c.1393G>T	p.E465X
RBL2	retinoblastoma-like 2 (p130)	ENSG00000103479	PAP45	70	20.0%	chr16	52072122	CCDS10748.1	c.3024C>A	p.F1008L
RAI2	retinoic acid induced 2	ENSG00000131831	PAP45	240	20.4%	chrX	17729991	CCDS14183.1	c.61G>A	p.A21T
RARB	retinoic acid receptor; beta	ENSG00000077092	PAP45	204	24.0%	chr3	25610092	CCDS2642.1	c.881G>T	p.G294V
RBP3	retinol binding protein 3; interstitial	ENSG00000107618	PAP45	260	26.9%	chr10	48009368	CCDS7218.1	c.1516C>T	p.L506F
REV3L	REV3-like; catalytic subunit of DNA polymerase zeta (yeast)	ENSG00000009413	PAP45	46	21.7%	chr6	111739116	CCDS5091.2	c.8644G>T	p.D2882Y
REV3L	REV3-like; catalytic subunit of DNA polymerase zeta (yeast)	ENSG00000009413	PAP45	83	24.1%	chr6	111771864	CCDS5091.2	c.7495C>T	p.R2499X
REV3L	REV3-like; catalytic subunit of DNA polymerase zeta (yeast)	ENSG00000009413	PAP45	204	18.6%	chr6	111801575	CCDS5091.2	c.4676A>C	p.K1559T

REV3L	REV3-like; catalytic subunit of DNA polymerase zeta (yeast)	ENSG00000009413	PAP45	84	22.6%	chr6	111802670	CCDS5091.2	c.3581G>T	p.R1194L
RHAG	Rh-associated glycoprotein	ENSG00000112077	PAP45	49	24.5%	chr6	49682585	CCDS4927.1	c.1147C>A	p.L383I
ARHGAP11A	Rho GTPase activating protein 11A	ENSG00000198826	PAP45	121	24.8%	chr15	30716608	CCDS10028.1	c.2342G>T	p.R781I
ARHGAP19	Rho GTPase activating protein 19	ENSG00000213390	PAP45	319	21.0%	chr10	99015721	CCDS7454.2	c.208G>A	p.D70N
ARHGAP20	Rho GTPase activating protein 20	ENSG00000137727	PAP45	214	15.4%	chr11	109955683	CCDS31673.1	c.3197C>A	p.S1066Y
ARHGAP20	Rho GTPase activating protein 20	ENSG00000137727	PAP45	159	18.2%	chr11	109955914	CCDS31673.1	c.2966C>A	p.S989Y
ARHGAP20	Rho GTPase activating protein 20	ENSG00000137727	PAP45	153	24.8%	chr11	109955921	CCDS31673.1	c.2959G>T	p.D987Y
ARHGAP21	Rho GTPase activating protein 21	ENSG00000107863	PAP45	233	20.6%	chr10	24948476	CCDS7144.1	c.2351G>T	p.R784I
ARHGAP25	Rho GTPase activating protein 25	ENSG00000163219	PAP45	160	26.9%	chr2	68903433	CCDS33214.1	c.1655C>A	p.S552Y
ARHGAP26	Rho GTPase activating protein 26	ENSG00000145819	PAP45	170	26.5%	chr5	142401598	CCDS4277.1	c.1235G>A	p.R412Q
ARHGAP26	Rho GTPase activating protein 26	ENSG00000145819	PAP45	151	21.2%	chr5	142582183	CCDS4277.1	c.2424G>T	p.E808D
ARHGAP30	Rho GTPase activating protein 30	ENSG00000186517	PAP45	468	24.1%	chr1	159284167	CCDS30918.1	c.3268G>T	p.E1090X
ARHGAP31	Rho GTPase activating protein 31	ENSG00000031081	PAP45	248	21.4%	chr3	120584749	CCDS43135.1	c.668C>A	p.S223Y
ARHGAP4	Rho GTPase activating protein 4	ENSG00000089820	PAP45	172	23.8%	chrX	152826599	CCDS14736.1	c.2619G>T	p.Q873H
ARHGAP5	Rho GTPase activating protein 5	ENSG00000100852	PAP45	71	18.3%	chr14	31631325	CCDS32062.1	c.1699A>C	p.K567Q
ARHGAP5	Rho GTPase activating protein 5	ENSG00000100852	PAP45	69	27.5%	chr14	31632109	CCDS32062.1	c.2483G>A	p.R828Q
ARHGAP9	Rho GTPase activating protein 9	ENSG00000123329	PAP45	276	17.0%	chr12	56152717	CCDS8941.2	c.2046G>T	p.K682N
ARHGEF1	Rho guanine nucleotide exchange factor (GEF) 1	ENSG00000076928	PAP45	173	23.7%	chr19	47097906	CCDS12590.1	c.1342C>T	p.R448C
ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	ENSG00000104728	PAP45	179	25.7%	chr8	1892547	CCDS34794.1	c.3746C>T	p.S1249L
ARHGEF3	Rho guanine nucleotide exchange factor (GEF) 3	ENSG00000163947	PAP45	114	30.7%	chr3	56754364	CCDS2878.1	c.779G>T	p.R260I
RHBDL2	rhomboid; veinlet-like 2 (Drosophila)	ENSG00000158315	PAP45	793	25.0%	chr1	39157436	CCDS30680.1	c.36G>T	p.M12I
RHOBTB3	Rho-related BTB domain containing 3	ENSG00000164292	PAP45	89	23.6%	chr5	95145267	CCDS4077.1	c.1467C>A	p.F489L
RPP40	ribonuclease P/MRP 40kDa subunit	ENSG00000124787	PAP45	93	16.1%	chr6	4941315	CCDS34333.1	c.762T>G	p.N254K
RNASE2	ribonuclease; RNase A family; 2 (liver; eosinophil-derived neurotoxin)	ENSG00000169385	PAP45	70	25.7%	chr14	20493880	CCDS9561.1	c.110G>A	p.W37X
RNASE7	ribonuclease; RNase A family; 7	ENSG00000165799	PAP45	261	23.0%	chr14	20581080	CCDS41914.1	c.89C>T	p.P30L
RPL31	ribosomal protein L31	ENSG00000071082	PAP45	126	21.4%	chr2	101000770	ENST00000409038	c.364C>A	p.L122I
RPS3A	ribosomal protein S3A	ENSG00000145425	PAP45	34	35.3%	chr4	152244849	CCDS3775.1	c.634G>A	p.V212I
RPS5	ribosomal protein S5	ENSG00000083845	PAP45	243	21.8%	chr19	63591417	CCDS12978.1	c.101C>A	p.S34Y
RPS6KA6	ribosomal protein S6 kinase; 90kDa; polypeptide 6	ENSG00000072133	PAP45	118	19.5%	chrX	83243760	CCDS14451.1	c.1717C>T	p.R573X
RPS6KA6	ribosomal protein S6 kinase; 90kDa; polypeptide 6	ENSG00000072133	PAP45	92	28.3%	chrX	83276871	CCDS14451.1	c.505C>A	p.L169M
RRP15	ribosomal RNA processing 15 homolog (S. cerevisiae)	ENSG00000067533	PAP45	92	18.5%	chr1	216547517	CCDS1520.2	c.625G>T	p.D209Y
RPF2	ribosome production factor 2 homolog (S. cerevisiae)	ENSG00000197498	PAP45	47	34.0%	chr6	111453356	CCDS5088.1	c.799C>A	p.H267N
RC3H2	ring finger and CCCH-type zinc finger domains 2	ENSG00000056586	PAP45	138	30.4%	chr9	124653290	CCDS43874.1	c.3271G>T	p.D1091Y
RC3H2	ring finger and CCCH-type zinc finger domains 2	ENSG00000056586	PAP45	300	30.3%	chr9	124660031	CCDS43874.1	c.2446C>T	p.R816C
RSPRY1	ring finger and SPRY domain containing 1	ENSG00000159579	PAP45	104	26.9%	chr16	55830375	CCDS10775.1	c.1718C>A	p.S573Y
RNF6	ring finger protein (C3H2C3 type) 6	ENSG00000127870	PAP45	462	21.9%	chr13	25686304	CCDS9316.1	c.1715G>A	p.R572Q
RNF11	ring finger protein 11	ENSG00000123091	PAP45	61	19.7%	chr1	51509454	CCDS556.1	c.337C>T	p.R113X
RNF111	ring finger protein 111	ENSG00000157450	PAP45	157	27.4%	chr15	57131799	CCDS10169.1	c.884G>T	p.S295I
RNF139	ring finger protein 139	ENSG00000170881	PAP45	126	27.8%	chr8	125568381	CCDS6350.1	c.1310C>A	p.S437Y
RNF141	ring finger protein 141	ENSG00000110315	PAP45	183	27.3%	chr11	10512208	CCDS7803.1	c.74C>T	p.T25M
RNF160	ring finger protein 160	ENSG00000198862	PAP45	76	25.0%	chr21	29263780	CCDS33527.1	c.1190G>T	p.R397I
RNF17	ring finger protein 17	ENSG00000132972	PAP45	74	52.7%	chr13	24272666	CCDS9308.2	c.1752G>T	p.Q584H
RNF170	ring finger protein 170	ENSG00000120925	PAP45	113	13.3%	chr8	42830534	CCDS6138.1	c.702C>A	p.F234L
RNF170	ring finger protein 170	ENSG00000120925	PAP45	240	20.4%	chr8	42830641	CCDS6138.1	c.595C>T	p.R199C
RNF213	ring finger protein 213	ENSG00000173821	PAP45	256	24.2%	chr17	75933214	CCDS32761.1	c.703G>A	p.E235K
RNF219	ring finger protein 219	ENSG00000152193	PAP45	146	17.1%	chr13	78117090	CCDS31997.1	c.116C>T	p.S39L
RNF220	ring finger protein 220	ENSG00000187147	PAP45	227	27.8%	chr1	44650441	CCDS510.1	c.85G>T	p.A29S
RNF220	ring finger protein 220	ENSG00000187147	PAP45	212	18.9%	chr1	44874382	CCDS510.1	c.1087C>T	p.R363W
RNF31	ring finger protein 31	ENSG00000092098	PAP45	117	25.6%	chr14	23690212	CCDS41931.1	c.1521G>T	p.E507D
RNF39	ring finger protein 39	ENSG00000204618	PAP45	98	29.6%	chr6	30147328	CCDS4673.1	c.802G>A	p.D268N
RNF7	ring finger protein 7	ENSG00000114125	PAP45	94	18.1%	chr3	142944194	ENST00000392999	c.194G>T	p.R65L
RIOK1	RIO kinase 1 (yeast)	ENSG00000124784	PAP45	108	25.0%	chr6	7343943	CCDS4500.1	c.451G>T	p.D151Y
RBM12B	RNA binding motif protein 12B	ENSG00000183808	PAP45	287	26.1%	chr8	94817356	CCDS43755.1	c.459G>T	p.E153D

RBM16	RNA binding motif protein 16	ENSG00000213079	PAP45	56	28.6%	chr6	155173020	CCDS5247.1	c.1406C>A	p.S469Y
RBM23	RNA binding motif protein 23	ENSG00000100461	PAP45	183	22.4%	chr14	22444431	CCDS41921.1	c.527G>A	p.R176Q
RBM41	RNA binding motif protein 41	ENSG00000089682	PAP45	183	24.0%	chrX	106245271	CCDS14526.1	c.490C>T	p.R164C
RBM44	RNA binding motif protein 44	ENSG00000177483	PAP45	165	23.0%	chr2	238391659	NM_001080504	c.1361C>A	p.S454X
RBM44	RNA binding motif protein 44	ENSG00000177483	PAP45	47	27.7%	chr2	238402651	NM_001080504	c.2656G>T	p.E886X
RBM46	RNA binding motif protein 46	ENSG00000151962	PAP45	71	38.0%	chr4	155939491	CCDS3790.1	c.727T>G	p.L243V
RBM46	RNA binding motif protein 46	ENSG00000151962	PAP45	278	27.0%	chr4	155939744	CCDS3790.1	c.980C>A	p.S327Y
RBM6	RNA binding motif protein 6	ENSG00000004534	PAP45	138	26.8%	chr3	49981042	CCDS2809.1	c.1180C>A	p.L394I
RBMS3	RNA binding motif; single stranded interacting protein 3	ENSG00000144642	PAP45	47	27.7%	chr3	29451358	CCDS33724.1	c.196C>T	p.R66X
RBPMS	RNA binding protein with multiple splicing	ENSG00000157110	PAP45	81	18.5%	chr8	30456423	CCDS34876.1	c.234G>T	p.K78N
RTTN	rotatin	ENSG00000176225	PAP45	67	28.4%	chr18	65866405	CCDS42443.1	c.-1G>T	p.IVS39-1-1SpliceAcceptor
RSBN1L	round spermatid basic protein 1-like	ENSG00000187257	PAP45	106	12.3%	chr7	77246326	CCDS43607.1	c.2446G>T	p.E816X
ROBO2	roundabout; axon guidance receptor; homolog 2 (Drosophila)	ENSG00000185008	PAP45	170	14.1%	chr3	77766735	CCDS43109.1	c.3785G>T	p.R1262I
ROBO2	roundabout; axon guidance receptor; homolog 2 (Drosophila)	ENSG00000185008	PAP45	176	14.2%	chr3	77766740	CCDS43109.1	c.3790C>T	p.R1264X
RTF1	Rtf1; Paf1/RNA polymerase II complex component; homolog (S. cerevisiae)	ENSG00000137815	PAP45	148	17.6%	chr15	39555073	CCDS32200.1	c.970G>A	p.E324K
RUFY1	RUN and FYVE domain containing 1	ENSG00000176783	PAP45	74	20.3%	chr5	178945456	CCDS4445.2	c.1010C>A	p.S337X
RUFY1	RUN and FYVE domain containing 1	ENSG00000176783	PAP45	182	27.5%	chr5	178949228	CCDS4445.2	c.1102C>T	p.R368X
RUNDC1	RUN domain containing 1	ENSG00000198863	PAP45	244	23.0%	chr17	38395058	CCDS11448.1	c.832G>T	p.E278X
RUNX2	runt-related transcription factor 2	ENSG00000124813	PAP45	90	30.0%	chr6	45567696	CCDS43467.1	c.930C>A	p.F310L
SACM1L	SAC1 suppressor of actin mutations 1-like (yeast)	ENSG00000211456	PAP45	137	10.2%	chr3	45738505	CCDS33745.1	c.689C>T	p.S230L
SUN5	Sad1 and UNC84 domain containing 5	ENSG00000167098	PAP45	66	21.2%	chr20	31035361	CCDS13209.1	c.1040G>T	p.G347V
SALL3	sal-like 3 (Drosophila)	ENSG00000151514	PAP45	113	22.1%	chr18	74858197	CCDS12013.1	c.3790C>T	p.R1264C
SIK2	salt-inducible kinase 2	ENSG00000170145	PAP45	125	22.4%	chr11	111095751	CCDS8347.1	c.1309C>T	p.R437W
SAMSN1	SAM domain; SH3 domain and nuclear localization signals 1	ENSG00000155307	PAP45	41	43.9%	chr21	14780282	CCDS42906.1	c.944C>A	p.P315H
SAPS3	SAPS domain family; member 3	ENSG00000110075	PAP45	165	29.1%	chr11	68125918	CCDS8182.1	c.1964C>A	p.S655Y
SRL	sarcalumenin	ENSG00000185739	PAP45	616	29.2%	chr16	4197405	ENST00000330063	c.763G>T	p.D255Y
SAGE1	sarcoma antigen 1	ENSG00000181433	PAP45	247	24.7%	chrX	134818712	CCDS14652.1	c.1465C>T	p.R489C
SARDH	sarcosine dehydrogenase	ENSG00000123453	PAP45	99	30.3%	chr9	135518878	CCDS6978.1	c.2711A>C	p.K904T
SATB1	SATB homeobox 1	ENSG00000182568	PAP45	111	23.4%	chr3	18394806	CCDS2631.1	c.1435A>G	p.I479V
SAFB2	scaffold attachment factor B2	ENSG00000130254	PAP45	392	25.0%	chr19	5567323	CCDS32879.1	c.363G>T	p.E121D
SCARA5	scavenger receptor class A; member 5 (putative)	ENSG00000168079	PAP45	192	12.5%	chr8	27818248	CCDS6064.1	c.1119G>T	p.E373D
SLFN12	schlafen family member 12	ENSG00000172123	PAP45	227	15.4%	chr17	30762737	CCDS11295.1	c.2059NULL>A	p.NULL-1FsIns1bp
SLFN13	schlafen family member 13	ENSG00000154760	PAP45	321	22.4%	chr17	30792227	CCDS32620.1	c.2194C>T	p.R732C
SLFNL1	schlafen-like 1	ENSG00000171790	PAP45	367	24.5%	chr1	41258872	CCDS460.1	c.48C>A	p.F16L
SOSTDC1	sclerostin domain containing 1	ENSG00000171243	PAP45	302	26.2%	chr7	16468874	CCDS5360.1	c.445G>T	p.D149Y
SFMBT1	Scm-like with four mbt domains 1	ENSG00000163935	PAP45	116	20.7%	chr3	52916274	CCDS2867.1	c.2182G>T	p.E728X
SEC13	SEC13 homolog (S. cerevisiae)	ENSG00000157020	PAP45	74	25.7%	chr3	10321775	CCDS2599.1	c.650A>G	p.D217G
SEC14L3	SEC14-like 3 (S. cerevisiae)	ENSG00000100012	PAP45	150	24.0%	chr22	29196496	CCDS13877.1	c.128G>A	p.R43Q
SEC23A	Sec23 homolog A (S. cerevisiae)	ENSG00000100934	PAP45	199	18.1%	chr14	38635034	CCDS9668.1	c.40C>T	p.R14X
SEC24D	SEC24 family; member D (S. cerevisiae)	ENSG00000150961	PAP45	116	20.7%	chr4	119938398	CCDS3710.1	c.929G>A	p.R310Q
SEC31A	SEC31 homolog A (S. cerevisiae)	ENSG00000138674	PAP45	77	22.1%	chr4	83961271	CCDS3596.1	c.3426G>T	p.K1142N
SEC31B	SEC31 homolog B (S. cerevisiae)	ENSG00000075826	PAP45	81	16.0%	chr10	102240536	CCDS7495.1	c.2567C>A	p.P856H
SEC61A1	Sec61 alpha 1 subunit (S. cerevisiae)	ENSG00000058262	PAP45	80	31.3%	chr3	129269100	CCDS3046.1	c.1122C>A	p.F374L
SEC63	SEC63 homolog (S. cerevisiae)	ENSG00000025796	PAP45	36	36.1%	chr6	108336841	CCDS5061.1	c.716G>A	p.R239Q
SECISBP2L	SECIS binding protein 2-like	ENSG00000138593	PAP45	130	20.8%	chr15	47072416	CCDS32234.1	c.-1G>T	p.IVS16-1-1SpliceAcceptor
SECISBP2L	SECIS binding protein 2-like	ENSG00000138593	PAP45	195	23.6%	chr15	47075885	CCDS32234.1	c.2459C>T	p.P820L
SECISBP2L	SECIS binding protein 2-like	ENSG00000138593	PAP45	85	20.0%	chr15	47112523	CCDS32234.1	c.595G>T	p.E199X
SFRP1	secreted frizzled-related protein 1	ENSG00000104332	PAP45	154	20.1%	chr8	41280143	CCDS34886.1	c.616G>A	p.E206K

SCG2	secretogranin II	ENSG00000171951	PAP45	249	25.7%	chr2	224171446	CCDS2457.1	c.799G>A	p.D267N
SCG3	secretogranin III	ENSG00000104112	PAP45	74	28.4%	chr15	49768788	CCDS10142.1	c.621T>G	p.N207K
SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	ENSG00000071537	PAP45	122	25.4%	chr14	81040335	CCDS9876.1	c.577A>G	p.I193V
SEMA3A	sema domain; immunoglobulin domain (Ig); short basic domain; secreted; (semaphorin) 3A	ENSG00000075213	PAP45	331	22.4%	chr7	83428776	CCDS5599.1	c.2163C>A	p.F721L
SEMA3D	sema domain; immunoglobulin domain (Ig); short basic domain; secreted; (semaphorin) 3D	ENSG00000153993	PAP45	378	30.2%	chr7	84466741	CCDS34676.1	c.2285G>A	p.R762Q
SEMA3F	sema domain; immunoglobulin domain (Ig); short basic domain; secreted; (semaphorin) 3F	ENSG00000001617	PAP45	127	26.0%	chr3	50186711	CCDS2811.1	c.380G>A	p.R127Q
SEMA5A	sema domain; seven thrombospondin repeats (type 1 and type 1-like); transmembrane domain (TM) and short cytoplasmic domain; (semaphorin) 5A	ENSG00000112902	PAP45	82	24.4%	chr5	9096022	CCDS3875.1	c.3212A>G	p.Y1071C
SEMA5A	sema domain; seven thrombospondin repeats (type 1 and type 1-like); transmembrane domain (TM) and short cytoplasmic domain; (semaphorin) 5A	ENSG00000112902	PAP45	39	38.5%	chr5	9161298	CCDS3875.1	c.2027G>A	p.R676H
SEMA6D	sema domain; transmembrane domain (TM); and cytoplasmic domain; (semaphorin) 6D	ENSG00000137872	PAP45	434	26.0%	chr15	45850922	CCDS32225.1	c.2870C>A	p.S957Y
SETX	senataxin	ENSG00000107290	PAP45	262	23.3%	chr9	134192443	CCDS6947.1	c.4363G>T	p.E1455X
SETX	senataxin	ENSG00000107290	PAP45	103	25.2%	chr9	134192831	CCDS6947.1	c.3975G>T	p.K1325N
SETX	senataxin	ENSG00000107290	PAP45	132	28.0%	chr9	134192983	CCDS6947.1	c.3823C>T	p.R1275C
SNTN	sentan; cilia apical structure protein	ENSG00000188817	PAP45	141	30.5%	chr3	63613438	CCDS33779.1	c.35C>A	p.S12Y
40425	septin 4	ENSG00000108387	PAP45	280	11.4%	chr17	53954101	CCDS11610.1	c.910C>T	p.R304C
SRGN	serglycin	ENSG00000122862	PAP45	299	29.8%	chr10	70533778	CCDS7285.1	c.373G>A	p.E125K
SERINC1	serine incorporator 1	ENSG00000111897	PAP45	126	28.6%	chr6	122809975	CCDS5125.1	c.985T>G	p.F329V
SERINC3	serine incorporator 3	ENSG00000132824	PAP45	274	27.7%	chr20	42563222	CCDS13333.1	c.1189G>A	p.E397K
SPINK2	serine peptidase inhibitor; Kazal type 2 (acrosin-trypsin inhibitor)	ENSG00000128040	PAP45	90	20.0%	chr4	57372624	CCDS3508.1	c.193C>A	p.L65M
SPINK6	serine peptidase inhibitor; Kazal type 6	ENSG00000178172	PAP45	124	15.3%	chr5	147573773	CCDS34268.1	c.189G>T	p.K63N
STK39	serine threonine kinase 39 (STE20/SPS1 homolog; yeast)	ENSG00000198648	PAP45	102	25.5%	chr2	168732071	CCDS42770.1	c.414G>T	p.M138I
SRRM2	serine/arginine repetitive matrix 2	ENSG00000167978	PAP45	262	25.2%	chr16	2752314	CCDS32373.1	c.1784G>A	p.R595Q
SRRM2	serine/arginine repetitive matrix 2	ENSG00000167978	PAP45	258	24.0%	chr16	2755250	CCDS32373.1	c.4720C>T	p.R1574W
STK11IP	serine/threonine kinase 11 interacting protein	ENSG00000144589	PAP45	227	12.8%	chr2	220175041	ENST00000295641	c.430G>A	p.A144T
STK24	serine/threonine kinase 24 (STE20 homolog; yeast)	ENSG00000102572	PAP45	157	21.7%	chr13	97907535	CCDS9488.1	c.1183G>A	p.G395R
STK24	serine/threonine kinase 24 (STE20 homolog; yeast)	ENSG00000102572	PAP45	109	15.6%	chr13	97969687	CCDS9488.1	c.120G>T	p.E40D
STK3	serine/threonine kinase 3 (STE20 homolog; yeast)	ENSG00000134602	PAP45	119	26.9%	chrX	131016431	CCDS14631.1	c.134G>A	p.R45H
STK40	serine/threonine kinase 40	ENSG00000196182	PAP45	188	22.9%	chr1	36581568	CCDS407.1	c.1073C>T	p.A358V
STYXL1	serine/threonine/tyrosine interacting-like 1	ENSG00000127952	PAP45	171	26.3%	chr7	75472628	CCDS5580.1	c.484G>T	p.E162X
SERPINA12	serpin peptidase inhibitor; clade A (alpha-1 antiproteinase; antitrypsin); member 12	ENSG00000165953	PAP45	287	19.9%	chr14	94033948	CCDS9926.1	c.540T>G	p.F180L
SERPINA13	serpin peptidase inhibitor; clade A (alpha-1 antiproteinase; antitrypsin); member 13 (pseudogene)	ENSG00000187483	PAP45	265	20.4%	chr14	94177620	ENST00000338704	c.213G>T	p.E71D
SERPINA13	serpin peptidase inhibitor; clade A (alpha-1 antiproteinase; antitrypsin); member 13 (pseudogene)	ENSG00000187483	PAP45	115	32.2%	chr14	94181054	ENST00000338704	c.862G>A	p.D288N
SERPINA3	serpin peptidase inhibitor; clade A (alpha-1 antiproteinase; antitrypsin); member 3	ENSG00000196136	PAP45	175	31.4%	chr14	94151104	CCDS32150.1	c.573A>C	p.K191N
SERPINA7	serpin peptidase inhibitor; clade A (alpha-1 antiproteinase; antitrypsin); member 7	ENSG00000123561	PAP45	180	24.4%	chrX	105167190	CCDS14518.1	c.516G>T	p.E172D
SERPINB12	serpin peptidase inhibitor; clade B (ovalbumin); member 12	ENSG00000166634	PAP45	104	16.3%	chr18	59376632	CCDS11984.1	c.236A>C	p.K79T
SERPINB13	serpin peptidase inhibitor; clade B (ovalbumin); member 13	ENSG00000197641	PAP45	783	23.6%	chr18	59415485	CCDS11985.1	c.1084G>T	p.E362X
SERPINB4	serpin peptidase inhibitor; clade B (ovalbumin); member 4	ENSG00000206073	PAP45	167	19.8%	chr18	59473896	CCDS11987.1	c.1148T>C	p.F383S
SERPIND1	serpin peptidase inhibitor; clade D (heparin cofactor); member 1	ENSG00000099937	PAP45	400	26.0%	chr22	19463974	CCDS13783.1	c.374G>A	p.R125H
SERPINE1	serpin peptidase inhibitor; clade E (nexin; plasminogen activator inhibitor type 1); member 1	ENSG00000106366	PAP45	358	25.4%	chr7	100563724	CCDS5711.1	c.729C>A	p.Y243X
SRRT	serrate RNA effector molecule homolog (Arabidopsis)	ENSG00000087087	PAP45	82	24.4%	chr7	100321903	CCDS34709.1	c.1558G>T	p.D520Y

SAA4	serum amyloid A4; constitutive	ENSG00000148965	PAP45	96	24.0%	chr11	18210593	CCDS7832.1	c.155G>T	p.R52I
SBF2	SET binding factor 2	ENSG00000133812	PAP45	129	23.3%	chr11	9820781	CCDS31427.1	c.3223C>T	p.R1075C
SETBP1	SET binding protein 1	ENSG00000152217	PAP45	266	24.4%	chr18	40785155	CCDS11923.1	c.1690C>A	p.P564T
SETBP1	SET binding protein 1	ENSG00000152217	PAP45	198	22.7%	chr18	40786377	CCDS11923.1	c.2912C>A	p.T971N
SETBP1	SET binding protein 1	ENSG00000152217	PAP45	137	31.4%	chr18	40787163	CCDS11923.1	c.3698C>T	p.S1233L
SETMAR	SET domain and mariner transposase fusion gene	ENSG00000170364	PAP45	349	24.9%	chr3	4330357	CCDS2563.1	c.893C>T	p.S298L
SETD7	SET domain containing (lysine methyltransferase) 7	ENSG00000145391	PAP45	124	25.8%	chr4	140660898	CCDS3748.1	c.745C>T	p.R249X
SETD2	SET domain containing 2	ENSG00000181555	PAP45	103	27.2%	chr3	47136712	CCDS2749.1	c.2909T>C	p.F970S
SETD2	SET domain containing 2	ENSG00000181555	PAP45	137	29.2%	chr3	47136968	CCDS2749.1	c.2653G>T	p.D885Y
SETD2	SET domain containing 2	ENSG00000181555	PAP45	245	20.8%	chr3	47138139	CCDS2749.1	c.1482A>C	p.E494D
SETD5	SET domain containing 5	ENSG00000168137	PAP45	119	33.6%	chr3	9481128	NM_001080517	c.2496G>T	p.K832N
SETD5	SET domain containing 5	ENSG00000168137	PAP45	248	12.5%	chr3	9487520	NM_001080517	c.3102G>T	p.M1034I
SETDB2	SET domain; bifurcated 2	ENSG00000136169	PAP45	79	20.3%	chr13	48952457	CCDS9417.1	c.1007G>T	p.R336I
SIAH1	seven in absentia homolog 1 (Drosophila)	ENSG00000196470	PAP45	161	24.8%	chr16	46953336	CCDS32444.1	c.598G>A	p.D200N
SCML1	sex comb on midleg-like 1 (Drosophila)	ENSG00000047634	PAP45	191	31.9%	chrX	17678300	CCDS35210.1	c.669C>A	p.Y223X
SCML4	sex comb on midleg-like 4 (Drosophila)	ENSG00000146285	PAP45	70	21.4%	chr6	108177695	CCDS5060.1	c.85C>A	p.L29I
STAC2	SH3 and cysteine rich domain 2	ENSG00000141750	PAP45	237	31.6%	chr17	34622091	CCDS11335.1	c.1216G>A	p.D406N
SHANK2	SH3 and multiple ankyrin repeat domains 2	ENSG00000162105	PAP45	82	25.6%	chr11	70507649	ENST00000338508	c.285G>T	p.L95F
SH3D19	SH3 domain containing 19	ENSG00000109686	PAP45	278	23.7%	chr4	152273707	CCDS34077.1	c.1838G>A	p.R613K
SGIP1	SH3-domain GRB2-like (endophilin) interacting protein 1	ENSG00000118473	PAP45	177	14.1%	chr1	66872361	ENST00000237247	c.110A>C	p.K37T
SGIP1	SH3-domain GRB2-like (endophilin) interacting protein 1	ENSG00000118473	PAP45	176	25.0%	chr1	66920160	CCDS30744.1	c.835G>A	p.E279K
SGIP1	SH3-domain GRB2-like (endophilin) interacting protein 1	ENSG00000118473	PAP45	102	20.6%	chr1	66972032	CCDS30744.1	c.1912A>C	p.N638H
SH3KBP1	SH3-domain kinase binding protein 1	ENSG00000147010	PAP45	72	27.8%	chrX	19535991	CCDS14193.1	c.991G>A	p.E331K
SHKBP1	SH3KBP1 binding protein 1	ENSG00000160410	PAP45	436	22.7%	chr19	45775302	CCDS12560.1	c.-1G>T	p.IVS3-1-1SpliceAcceptor
SDR42E2	short chain dehydrogenase/reductase family 42E; member 2	ENSG00000183921	PAP45	468	17.3%	chr16	22089663	ENST00000330898	c.328C>T	p.R110C
SHROOM1	shroom family member 1	ENSG00000164403	PAP45	143	25.9%	chr5	132187873	CCDS4161.1	c.1379C>A	p.S460Y
SHROOM4	shroom family member 4	ENSG00000158352	PAP45	389	16.7%	chrX	50393898	CCDS35277.1	c.1915C>A	p.L639I
SGOL1	shugoshin-like 1 (S. pombe)	ENSG00000129810	PAP45	132	31.8%	chr3	20177656	CCDS33716.1	c.1631C>T	p.S544L
SIGLEC6	sialic acid binding Ig-like lectin 6	ENSG00000105492	PAP45	393	12.2%	chr19	56722844	CCDS12834.2	c.1124A>G	p.D375G
SIDT2	SID1 transmembrane family; member 2	ENSG00000149577	PAP45	142	23.2%	chr11	116569795	CCDS31682.1	c.2228G>T	p.R743M
SDK1	sidekick homolog 1; cell adhesion molecule (chicken)	ENSG00000146555	PAP45	143	18.9%	chr7	4251905	CCDS34590.1	c.6323C>T	p.A2108V
STAT1	signal transducer and activator of transcription 1; 91kDa	ENSG00000115415	PAP45	146	22.6%	chr2	191564289	CCDS2309.1	c.947C>T	p.S316L
STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	ENSG00000168610	PAP45	164	15.9%	chr17	37735112	CCDS32656.1	c.1219G>T	p.E407X
SIPA1L1	signal-induced proliferation-associated 1 like 1	ENSG00000197555	PAP45	131	21.4%	chr14	71125560	CCDS9807.1	c.1218A>C	p.K406N
SIPA1L1	signal-induced proliferation-associated 1 like 1	ENSG00000197555	PAP45	44	40.9%	chr14	71125827	CCDS9807.1	c.1485T>G	p.F495L
SIPA1L1	signal-induced proliferation-associated 1 like 1	ENSG00000197555	PAP45	104	32.7%	chr14	71155283	CCDS9807.1	c.1555C>T	p.R519X
SIPA1L1	signal-induced proliferation-associated 1 like 1	ENSG00000197555	PAP45	269	27.5%	chr14	71260262	CCDS9807.1	c.4417T>G	p.F1473V
SIPA1L2	signal-induced proliferation-associated 1 like 2	ENSG00000116991	PAP45	487	27.5%	chr1	230717224	CCDS41474.1	c.485G>T	p.S162I
SIPA1L3	signal-induced proliferation-associated 1 like 3	ENSG00000105738	PAP45	93	25.8%	chr19	43302325	CCDS33007.1	c.2831C>A	p.S944Y
SIK3	SIK family kinase 3	ENSG00000160584	PAP45	146	17.8%	chr11	116332907	CCDS8379.1	c.183G>A	p.M61I
SIN3A	SIN3 homolog A; transcription regulator (yeast)	ENSG00000169375	PAP45	98	30.6%	chr15	73475687	CCDS10279.1	c.2058G>T	p.K686N
SIN3A	SIN3 homolog A; transcription regulator (yeast)	ENSG00000169375	PAP45	66	34.8%	chr15	73492384	CCDS10279.1	c.529G>A	p.D177N
SIN3B	SIN3 homolog B; transcription regulator (yeast)	ENSG00000127511	PAP45	179	19.6%	chr19	16838350	CCDS32946.1	c.1885G>A	p.E629K
SAP130	Sin3A-associated protein; 130kDa	ENSG00000136715	PAP45	311	32.2%	chr2	128416066	CCDS2153.1	c.3131G>A	p.R1044Q
SAP18	Sin3A-associated protein; 18kDa	ENSG00000150459	PAP45	77	24.7%	chr13	20618984	CCDS9295.1	c.223G>T	p.E75X
SIM1	single-minded homolog 1 (Drosophila)	ENSG00000112246	PAP45	336	21.4%	chr6	100945271	CCDS5045.1	c.1988C>T	p.S663L
SIRT1	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	ENSG00000096717	PAP45	99	20.2%	chr10	69346123	CCDS7273.1	c.2011T>G	p.C671G
SSH1	slingshot homolog 1 (Drosophila)	ENSG00000084112	PAP45	106	22.6%	chr12	107705925	CCDS9121.1	c.3118T>G	p.L1040V
SLITRK1	SLIT and NTRK-like family; member 1	ENSG00000178235	PAP45	169	21.9%	chr13	83352384	CCDS9464.1	c.1260G>T	p.K420N
SLITRK2	SLIT and NTRK-like family; member 2	ENSG00000185985	PAP45	341	26.1%	chrX	144713219	CCDS14680.1	c.1584G>T	p.E528D

SLITRK2	SLIT and NTRK-like family; member 2	ENSG00000185985	PAP45	387	26.4%	chrX	144713298	CCDS14680.1	c.1663G>T	p.E555X
SLITRK4	SLIT and NTRK-like family; member 4	ENSG00000179542	PAP45	201	21.4%	chrX	142544304	CCDS14679.1	c.2287C>A	p.L763I
SLITRK4	SLIT and NTRK-like family; member 4	ENSG00000179542	PAP45	216	25.5%	chrX	142544768	CCDS14679.1	c.1823G>A	p.R608Q
SLITRK4	SLIT and NTRK-like family; member 4	ENSG00000179542	PAP45	115	27.8%	chrX	142545297	CCDS14679.1	c.1294C>A	p.L432I
SLITRK4	SLIT and NTRK-like family; member 4	ENSG00000179542	PAP45	62	22.6%	chrX	142546523	CCDS14679.1	c.68C>T	p.S23L
SLIT1	slit homolog 1 (Drosophila)	ENSG00000187122	PAP45	120	21.7%	chr10	98907625	CCDS7453.1	c.353G>A	p.R118Q
SLIT3	slit homolog 3 (Drosophila)	ENSG00000184347	PAP45	57	26.3%	chr5	168149146	CCDS4369.1	c.1076C>T	p.S359L
SMAD2	SMAD family member 2	ENSG00000175387	PAP45	69	21.7%	chr18	43628879	CCDS11934.1	c.962G>A	p.R321Q
SNAPC3	small nuclear RNA activating complex; polypeptide 3; 50kDa	ENSG00000164975	PAP45	117	31.6%	chr9	15437168	CCDS6478.1	c.658C>T	p.R220X
SNAPC4	small nuclear RNA activating complex; polypeptide 4; 190kDa	ENSG00000165684	PAP45	286	24.8%	chr9	138412593	CCDS6998.1	c.109C>A	p.L37I
SNAPC4	small nuclear RNA activating complex; polypeptide 4; 190kDa	ENSG00000165684	PAP45	355	23.7%	chr9	138412646	CCDS6998.1	c.56G>T	p.R19M
SNORD19B	small nucleolar RNA; C/D box 19B	ENSG00000163938	PAP45	44	34.1%	chr3	52696327	CCDS2861.1	c.98G>T	p.R33I
SNORD2	small nucleolar RNA; C/D box 2	ENSG00000156976	PAP45	96	18.8%	chr3	187986681	CCDS3282.1	c.552A>C	p.E184D
SNORA4	small nucleolar RNA; H/ACA box 4	ENSG00000156976	PAP45	96	18.8%	chr3	187986681	CCDS3282.1	c.552A>C	p.E184D
SNORA63	small nucleolar RNA; H/ACA box 63	ENSG00000156976	PAP45	96	18.8%	chr3	187986681	CCDS3282.1	c.552A>C	p.E184D
SMEK1	SMEK homolog 1; suppressor of mek1 (Dictyostelium)	ENSG00000100796	PAP45	256	25.4%	chr14	91018118	CCDS9895.1	c.470G>A	p.R157H
SHPRH	SNF2 histone linker PHD RING helicase	ENSG00000146414	PAP45	127	27.6%	chr6	146298208	CCDS43513.1	c.2632C>T	p.R878X
SRCAP	Snf2-related CREBBP activator protein	ENSG00000080603	PAP45	150	31.3%	chr16	30643864	CCDS10689.2	c.5618G>A	p.R1873Q
SNUPN	snurportin 1	ENSG00000169371	PAP45	205	26.8%	chr15	73677760	CCDS10281.1	c.1077G>T	p.E359D
SCNN1G	sodium channel; nonvoltage-gated 1; gamma	ENSG00000166828	PAP45	242	21.9%	chr16	23134232	CCDS10608.1	c.1891C>T	p.R631C
SCN1A	sodium channel; voltage-gated; type I; alpha subunit	ENSG00000144285	PAP45	89	23.6%	chr2	166638316	CCDS33316.1	c.62C>A	p.S21Y
SCN3A	sodium channel; voltage-gated; type III; alpha subunit	ENSG00000153253	PAP45	146	22.6%	chr2	165702708	CCDS33312.1	c.2318A>C	p.N773T
SCN3A	sodium channel; voltage-gated; type III; alpha subunit	ENSG00000153253	PAP45	93	23.7%	chr2	165727347	CCDS33312.1	c.932G>A	p.S311N
SCN9A	sodium channel; voltage-gated; type IX; alpha subunit	ENSG00000169432	PAP45	167	17.4%	chr2	166793512	NM_002977	c.4108C>T	p.R1370X
SCN9A	sodium channel; voltage-gated; type IX; alpha subunit	ENSG00000169432	PAP45	56	21.4%	chr2	166798152	NM_002977	c.3835C>T	p.R1279W
SCN7A	sodium channel; voltage-gated; type VII; alpha	ENSG00000136546	PAP45	72	26.4%	chr2	166970458	NM_002976	c.4927C>T	p.R1643X
SCN7A	sodium channel; voltage-gated; type VII; alpha	ENSG00000136546	PAP45	170	21.2%	chr2	166997259	NM_002976	c.2407G>T	p.D803Y
SCN10A	sodium channel; voltage-gated; type X; alpha subunit	ENSG00000185313	PAP45	165	29.1%	chr3	38714227	CCDS33736.1	c.5488A>G	p.M1830V
SCN10A	sodium channel; voltage-gated; type X; alpha subunit	ENSG00000185313	PAP45	167	26.3%	chr3	38714979	CCDS33736.1	c.4736G>A	p.R1579Q
SCN10A	sodium channel; voltage-gated; type X; alpha subunit	ENSG00000185313	PAP45	163	32.5%	chr3	38728733	CCDS33736.1	c.4012A>G	p.T1338A
SCN10A	sodium channel; voltage-gated; type X; alpha subunit	ENSG00000185313	PAP45	84	27.4%	chr3	38777194	CCDS33736.1	c.932G>A	p.G311D
SCN11A	sodium channel; voltage-gated; type XI; alpha subunit	ENSG00000168356	PAP45	178	24.2%	chr3	38863563	CCDS33737.1	c.5002C>A	p.L1668I
SCN11A	sodium channel; voltage-gated; type XI; alpha subunit	ENSG00000168356	PAP45	86	12.8%	chr3	38888088	CCDS33737.1	c.3611T>C	p.F1204S
NALCN	sodium leak channel; non-selective	ENSG00000102452	PAP45	65	27.7%	chr13	100524886	CCDS9498.1	c.4083A>T	p.K1361N
NALCN	sodium leak channel; non-selective	ENSG00000102452	PAP45	243	27.6%	chr13	100540088	CCDS9498.1	c.3416T>G	p.F1139C
SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter); member 3	ENSG00000079215	PAP45	111	18.0%	chr5	36712802	CCDS3919.1	c.619G>A	p.E207K
SLC1A7	solute carrier family 1 (glutamate transporter); member 7	ENSG00000162383	PAP45	138	26.1%	chr1	53326394	CCDS574.1	c.1558G>A	p.E520K
SLC10A1	solute carrier family 10 (sodium/bile acid cotransporter family); member 1	ENSG00000100652	PAP45	191	23.6%	chr14	69315796	CCDS9797.1	c.602C>T	p.A201V
SLC10A4	solute carrier family 10 (sodium/bile acid cotransporter family); member 4	ENSG00000145248	PAP45	130	12.3%	chr4	48185706	CCDS3482.1	c.1307C>A	p.S436Y
SLC10A5	solute carrier family 10 (sodium/bile acid cotransporter family); member 5	ENSG00000205184	PAP45	124	25.0%	chr8	82769585	CCDS34915.1	c.178C>A	p.L60I
SLC12A5	solute carrier family 12 (potassium/chloride transporter); member 5	ENSG00000124140	PAP45	112	19.6%	chr20	44117036	CCDS13391.1	c.2754G>T	p.Q918H
SLC12A4	solute carrier family 12 (potassium/chloride transporters); member 4	ENSG00000124067	PAP45	115	26.1%	chr16	66538743	CCDS10855.1	c.2064G>T	p.K688N
SLC12A3	solute carrier family 12 (sodium/chloride transporters); member 3	ENSG00000070915	PAP45	571	21.0%	chr16	55473905	CCDS10770.1	c.1664C>T	p.S555L
SLC14A1	solute carrier family 14 (urea transporter); member 1 (Kidd blood group)	ENSG00000141469	PAP45	204	27.5%	chr18	41564351	CCDS11925.1	c.68C>T	p.S23L

SLC15A2	solute carrier family 15 (H+/peptide transporter); member 2	ENSG00000163406	PAP45	113	23.0%	chr3	123130061	CCDS3007.1	c.1310C>A	p.S437Y
SLC15A1	solute carrier family 15 (oligopeptide transporter); member 1	ENSG00000088386	PAP45	95	20.0%	chr13	98135012	CCDS9489.1	c.2094C>A	p.F698L
SLC15A5	solute carrier family 15; member 5	ENSG00000188991	PAP45	79	21.5%	chr12	16268681	ENST00000344941	c.907C>T	p.P303S
SLC16A1	solute carrier family 16; member 1 (monocarboxylic acid transporter 1)	ENSG00000155380	PAP45	73	32.9%	chr1	113273318	CCDS858.1	c.136G>T	p.E46X
SLC16A2	solute carrier family 16; member 2 (monocarboxylic acid transporter 8)	ENSG00000147100	PAP45	63	19.0%	chrX	73558483	CCDS14426.1	c.508G>A	p.E170K
SLC17A6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter); member 6	ENSG00000091664	PAP45	97	20.6%	chr11	22340905	CCDS7856.1	c.706C>A	p.L236I
SLC18A1	solute carrier family 18 (vesicular monoamine); member 1	ENSG00000036565	PAP45	70	24.3%	chr8	20074913	CCDS6013.1	c.638G>A	p.G213E
SLC2A2	solute carrier family 2 (facilitated glucose transporter); member 2	ENSG00000163581	PAP45	94	21.3%	chr3	172206487	CCDS3215.1	c.714C>A	p.F238L
SLC2A6	solute carrier family 2 (facilitated glucose transporter); member 6	ENSG00000160326	PAP45	137	19.7%	chr9	135326997	CCDS6975.1	c.1491C>A	p.F497L
SLC2A9	solute carrier family 2 (facilitated glucose transporter); member 9	ENSG00000109667	PAP45	83	32.5%	chr4	9437323	CCDS3407.1	c.-1G>T	p.IVS11-1-1SpliceAcceptor
SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter); member 5	ENSG00000142583	PAP45	74	20.3%	chr1	9020242	CCDS99.1	c.1496C>T	p.S499L
SLC22A9	solute carrier family 22 (organic anion transporter); member 9	ENSG00000149742	PAP45	319	18.5%	chr11	62932773	CCDS8043.1	c.1447C>A	p.L483M
SLC22A1	solute carrier family 22 (organic cation transporter); member 1	ENSG00000175003	PAP45	162	20.4%	chr6	160477291	CCDS5274.1	c.889G>T	p.E297X
SLC22A10	solute carrier family 22; member 10	ENSG00000184999	PAP45	318	17.3%	chr11	62814493	CCDS41661.1	c.280C>T	p.P94S
SLC22A15	solute carrier family 22; member 15	ENSG00000163393	PAP45	468	28.4%	chr1	116407007	NM_018420	c.1273C>T	p.L425F
SLC22A25	solute carrier family 22; member 25	ENSG00000196600	PAP45	78	14.1%	chr11	62688613	CCDS31592.1	c.1355C>A	p.S452Y
SLC25A12	solute carrier family 25 (mitochondrial carrier; Aralar); member 12	ENSG00000115840	PAP45	101	25.7%	chr2	172457998	CCDS33327.1	c.29G>A	p.R10Q
SLC26A1	solute carrier family 26 (sulfate transporter); member 1	ENSG00000145217	PAP45	334	21.0%	chr4	973068	CCDS33934.1	c.1659C>A	p.F553L
SLC26A2	solute carrier family 26 (sulfate transporter); member 2	ENSG00000155850	PAP45	159	28.3%	chr5	149337590	CCDS4300.1	c.182A>C	p.K61T
SLC26A10	solute carrier family 26; member 10	ENSG00000135502	PAP45	151	31.8%	chr12	56301065	CCDS8949.2	c.313G>A	p.G105R
SLC26A5	solute carrier family 26; member 5 (prestin)	ENSG00000170615	PAP45	103	31.1%	chr7	102835535	CCDS5733.1	c.887C>T	p.A296V
SLC26A8	solute carrier family 26; member 8	ENSG00000112053	PAP45	183	26.8%	chr6	36031041	CCDS4813.1	c.2098G>T	p.V700L
SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport); member 2	ENSG00000168003	PAP45	136	19.9%	chr11	62405416	CCDS31587.1	c.741G>T	p.Q247H
SLC3A1	solute carrier family 3 (cystine; dibasic and neutral amino acid transporters; activator of cystine; dibasic and neutral amino acid transport); member 1	ENSG00000138079	PAP45	203	10.8%	chr2	44394477	CCDS1819.1	c.-1G>T	p.IVS8-1-1SpliceAcceptor
SLC3A1	solute carrier family 3 (cystine; dibasic and neutral amino acid transporters; activator of cystine; dibasic and neutral amino acid transport); member 1	ENSG00000138079	PAP45	169	20.7%	chr2	44401080	CCDS1819.1	c.1856G>T	p.R619I
SLC30A6	solute carrier family 30 (zinc transporter); member 6	ENSG00000152683	PAP45	119	12.6%	chr2	32299027	CCDS1780.1	c.1127C>A	p.T376N
SLC30A8	solute carrier family 30 (zinc transporter); member 8	ENSG00000164756	PAP45	136	14.7%	chr8	118252489	CCDS6322.1	c.865G>T	p.E289X
SLC32A1	solute carrier family 32 (GABA vesicular transporter); member 1	ENSG00000101438	PAP45	442	24.0%	chr20	36790154	CCDS13307.1	c.1036G>A	p.A346T
SLC34A1	solute carrier family 34 (sodium phosphate); member 1	ENSG00000131183	PAP45	217	23.5%	chr5	176757528	CCDS4418.1	c.1555C>A	p.L519I
SLC38A11	solute carrier family 38; member 11	ENSG00000169507	PAP45	109	17.4%	chr2	165476453	CCDS2224.1	c.668G>T	p.R223I
SLC38A4	solute carrier family 38; member 4	ENSG00000139209	PAP45	308	25.3%	chr12	45459714	CCDS8750.1	c.664C>A	p.L222I
SLC4A1AP	solute carrier family 4 (anion exchanger); member 1; adaptor protein	ENSG00000163798	PAP45	71	15.5%	chr2	27745719	CCDS33166.1	c.1306C>T	p.R436W
SLC4A5	solute carrier family 4; sodium bicarbonate cotransporter; member 5	ENSG00000188687	PAP45	55	21.8%	chr2	74320003	CCDS1936.1	c.2286G>T	p.K762N
SLC4A7	solute carrier family 4; sodium bicarbonate cotransporter; member 7	ENSG00000033867	PAP45	59	22.0%	chr3	27419705	CCDS33721.1	c.2223G>T	p.E741D
SLC43A1	solute carrier family 43; member 1	ENSG00000149150	PAP45	120	15.8%	chr11	57020114	CCDS7958.1	c.658G>A	p.E220K

SLC43A1	solute carrier family 43; member 1	ENSG00000149150	PAP45	72	19.4%	chr11	57021810	CCDS7958.1	c.550G>T	p.G184X
SLC44A1	solute carrier family 44; member 1	ENSG00000070214	PAP45	49	24.5%	chr9	107160457	CCDS6763.1	c.682A>G	p.I228V
SLC44A3	solute carrier family 44; member 3	ENSG00000143036	PAP45	48	27.1%	chr1	95075878	CCDS751.1	c.389G>A	p.R130Q
SLC44A5	solute carrier family 44; member 5	ENSG00000137968	PAP45	680	27.2%	chr1	75456139	CCDS667.1	c.1624C>T	p.R542C
SLC45A1	solute carrier family 45; member 1	ENSG00000162426	PAP45	122	10.7%	chr1	8313545	CCDS30577.1	c.1405G>A	p.E469K
SLC46A3	solute carrier family 46; member 3	ENSG00000139508	PAP45	150	25.3%	chr13	28185146	CCDS9332.1	c.731G>A	p.R244Q
SLC5A5	solute carrier family 5 (sodium iodide symporter); member 5	ENSG00000105641	PAP45	100	19.0%	chr19	17865531	CCDS12368.1	c.1777G>T	p.E593X
SLC5A12	solute carrier family 5 (sodium/glucose cotransporter); member 12	ENSG00000148942	PAP45	87	14.9%	chr11	26681938	CCDS7860.2	c.658G>T	p.G220X
SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter); member 3	ENSG00000198743	PAP45	367	22.3%	chr21	34389714	CCDS33549.1	c.347G>A	p.R116Q
SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter); member 3	ENSG00000198743	PAP45	148	14.9%	chr21	34391051	CCDS33549.1	c.1684G>T	p.E562X
SLC6A14	solute carrier family 6 (amino acid transporter); member 14	ENSG00000087916	PAP45	95	22.1%	chrX	115483061	CCDS14570.1	c.124A>C	p.K42Q
SLC6A1	solute carrier family 6 (neurotransmitter transporter; GABA); member 1	ENSG00000157103	PAP45	293	25.3%	chr3	11042185	CCDS2603.1	c.765C>A	p.F255L
SLC7A14	solute carrier family 7 (cationic amino acid transporter; y+ system); member 14	ENSG00000013293	PAP45	227	30.4%	chr3	171701802	CCDS33892.1	c.331C>T	p.R111X
SLC7A3	solute carrier family 7 (cationic amino acid transporter; y+ system); member 3	ENSG00000165349	PAP45	235	25.1%	chrX	70064101	CCDS14404.1	c.1141C>T	p.R381C
SLC7A7	solute carrier family 7 (cationic amino acid transporter; y+ system); member 7	ENSG00000155465	PAP45	426	26.5%	chr14	22352154	CCDS9574.1	c.294G>T	p.K98N
SLC8A3	solute carrier family 8 (sodium/calcium exchanger); member 3	ENSG00000100678	PAP45	465	16.3%	chr14	69703728	CCDS35498.1	c.1165G>A	p.D389N
SLC9A3	solute carrier family 9 (sodium/hydrogen exchanger); member 3	ENSG00000066230	PAP45	135	25.9%	chr5	536460	CCDS3855.1	c.1070C>T	p.S357L
SLC9A4	solute carrier family 9 (sodium/hydrogen exchanger); member 4	ENSG00000180251	PAP45	66	27.3%	chr2	102491822	CCDS33264.1	c.1486C>T	p.R496C
SLC9A4	solute carrier family 9 (sodium/hydrogen exchanger); member 4	ENSG00000180251	PAP45	80	35.0%	chr2	102515307	CCDS33264.1	c.2125G>T	p.E709X
SLC9A9	solute carrier family 9 (sodium/hydrogen exchanger); member 9	ENSG00000181804	PAP45	149	33.6%	chr3	144753919	CCDS33872.1	c.1064C>T	p.S355L
SOS1	son of sevenless homolog 1 (Drosophila)	ENSG00000115904	PAP45	61	23.0%	chr2	39094134	CCDS1802.1	c.2138G>A	p.R713Q
SORBS1	sorbin and SH3 domain containing 1	ENSG00000095637	PAP45	127	20.5%	chr10	97164248	CCDS31255.1	c.803C>T	p.S268L
SORBS2	sorbin and SH3 domain containing 2	ENSG00000154556	PAP45	140	21.4%	chr4	186781430	CCDS3845.1	c.2135C>T	p.S712L
SORCS1	sortilin-related VPS10 domain containing receptor 1	ENSG00000108018	PAP45	141	27.7%	chr10	108449141	CCDS31283.1	c.1234G>A	p.D412N
SORCS2	sortilin-related VPS10 domain containing receptor 2	ENSG00000184985	PAP45	121	22.3%	chr4	7766870	NM_020777	c.1993G>A	p.D665N
SNX14	sorting nexin 14	ENSG00000135317	PAP45	124	14.5%	chr6	86313793	CCDS5004.1	c.954C>A	p.F318L
SNX19	sorting nexin 19	ENSG00000120451	PAP45	128	13.3%	chr11	130285389	CCDS31721.1	c.1900G>T	p.E634X
SNX20	sorting nexin 20	ENSG00000167208	PAP45	249	22.9%	chr16	49264834	CCDS10745.1	c.935G>A	p.R312Q
SNX20	sorting nexin 20	ENSG00000167208	PAP45	166	25.9%	chr16	49264978	CCDS10745.1	c.791G>A	p.R264H
SNX31	sorting nexin 31	ENSG00000174226	PAP45	116	19.8%	chr8	101678153	CCDS6288.1	c.868C>A	p.L290I
SNX32	sorting nexin 32	ENSG00000172803	PAP45	223	31.8%	chr11	65374234	CCDS8113.2	c.290C>T	p.S97L
SNX30	sorting nexin family member 30	ENSG00000148158	PAP45	102	28.4%	chr9	114632955	CCDS43865.1	c.589G>T	p.E197X
SPOCK2	sparc/osteonectin; cwcv and kazal-like domains proteoglycan (testican) 2	ENSG00000107742	PAP45	63	28.6%	chr10	73500184	CCDS7313.1	c.366G>T	p.K122N
SPOCK2	sparc/osteonectin; cwcv and kazal-like domains proteoglycan (testican) 2	ENSG00000107742	PAP45	172	27.9%	chr10	73501977	CCDS7313.1	c.290G>A	p.R97H
SPOCK3	sparc/osteonectin; cwcv and kazal-like domains proteoglycan (testican) 3	ENSG00000196104	PAP45	45	24.4%	chr4	168220224	CCDS34095.1	c.229G>A	p.D77N
SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	ENSG00000151835	PAP45	91	16.5%	chr13	22808769	CCDS9300.1	c.6805A>C	p.I2269L
SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	ENSG00000151835	PAP45	172	30.2%	chr13	22809642	CCDS9300.1	c.5932G>T	p.D1978Y
SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	ENSG00000151835	PAP45	136	11.8%	chr13	22811178	CCDS9300.1	c.4396A>C	p.K1466Q
SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	ENSG00000151835	PAP45	106	21.7%	chr13	22811541	CCDS9300.1	c.4033G>T	p.E1345X
SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	ENSG00000151835	PAP45	111	21.6%	chr13	22813229	CCDS9300.1	c.2345G>A	p.R782H

SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	ENSG00000151835	PAP45	95	28.4%	chr13	22813297	CCDS9300.1	c.2277C>A	p.F759L
SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	ENSG00000151835	PAP45	187	27.8%	chr13	22826692	CCDS9300.1	c.1618G>T	p.D540Y
SPG21	spastic paraplegia 21 (autosomal recessive; Mast syndrome)	ENSG00000090487	PAP45	50	34.0%	chr15	63048708	CCDS10198.1	c.606G>T	p.L202F
SYNE1	spectrin repeat containing; nuclear envelope 1	ENSG00000131018	PAP45	282	14.9%	chr6	152599661	CCDS5236.1	c.20183G>A	p.R6728H
SYNE1	spectrin repeat containing; nuclear envelope 1	ENSG00000131018	PAP45	213	25.4%	chr6	152607454	CCDS5236.1	c.19603G>T	p.E6535X
SYNE1	spectrin repeat containing; nuclear envelope 1	ENSG00000131018	PAP45	71	53.5%	chr6	152739325	CCDS5236.1	c.9208C>T	p.R3070X
SYNE1	spectrin repeat containing; nuclear envelope 1	ENSG00000131018	PAP45	186	23.1%	chr6	152779770	CCDS5236.1	c.5495C>A	p.S1832Y
SYNE1	spectrin repeat containing; nuclear envelope 1	ENSG00000131018	PAP45	97	19.6%	chr6	152798868	CCDS5236.1	c.4211C>A	p.S1404X
SYNE1	spectrin repeat containing; nuclear envelope 1	ENSG00000131018	PAP45	186	28.0%	chr6	152812466	CCDS5236.1	c.3399C>A	p.F1133L
SYNE1	spectrin repeat containing; nuclear envelope 1	ENSG00000131018	PAP45	118	24.6%	chr6	152828883	CCDS5236.1	c.1656C>A	p.F552L
SYNE1	spectrin repeat containing; nuclear envelope 1	ENSG00000131018	PAP45	147	23.1%	chr6	152865540	CCDS5236.1	c.809C>A	p.S270Y
SYNE2	spectrin repeat containing; nuclear envelope 2	ENSG00000054654	PAP45	374	24.9%	chr14	63588484	CCDS9761.2	c.8100G>T	p.K2700N
SYNE2	spectrin repeat containing; nuclear envelope 2	ENSG00000054654	PAP45	110	19.1%	chr14	63589576	CCDS9761.2	c.9192A>C	p.K3064N
SYNE2	spectrin repeat containing; nuclear envelope 2	ENSG00000054654	PAP45	38	26.3%	chr14	63638428	CCDS9761.2	c.12407C>T	p.S4136L
SYNE2	spectrin repeat containing; nuclear envelope 2	ENSG00000054654	PAP45	224	28.6%	chr14	63750902	CCDS9761.2	c.19294G>A	p.E6432K
SYNE2	spectrin repeat containing; nuclear envelope 2	ENSG00000054654	PAP45	80	20.0%	chr14	63760972	CCDS9761.2	c.20423C>T	p.S6808L
SPTA1	spectrin; alpha; erythrocytic 1 (elliptocytosis 2)	ENSG00000163554	PAP45	239	13.4%	chr1	156881999	CCDS41423.1	c.3906G>T	p.Q1302H
SPTA1	spectrin; alpha; erythrocytic 1 (elliptocytosis 2)	ENSG00000163554	PAP45	295	15.3%	chr1	156910839	CCDS41423.1	c.1254G>T	p.E418D
SPTAN1	spectrin; alpha; non-erythrocytic 1 (alpha-fodrin)	ENSG00000197694	PAP45	157	20.4%	chr9	130386459	CCDS6905.1	c.2271G>T	p.K757N
SPTBN1	spectrin; beta; non-erythrocytic 1	ENSG00000115306	PAP45	79	17.7%	chr2	54736634	CCDS33198.1	c.6041G>T	p.R2014I
SPTBN4	spectrin; beta; non-erythrocytic 4	ENSG00000160460	PAP45	220	23.6%	chr19	45699693	CCDS12559.1	c.810G>T	p.E270D
SPTBN4	spectrin; beta; non-erythrocytic 4	ENSG00000160460	PAP45	79	24.1%	chr19	45701628	CCDS12559.1	c.1414G>A	p.E472K
SPTBN4	spectrin; beta; non-erythrocytic 4	ENSG00000160460	PAP45	98	25.5%	chr19	45726837	CCDS12559.1	c.3907G>T	p.D1303Y
SPTBN4	spectrin; beta; non-erythrocytic 4	ENSG00000160460	PAP45	69	29.0%	chr19	45748067	CCDS12559.1	c.4668G>T	p.K1556N
SPDYA	speedy homolog A (Xenopus laevis)	ENSG00000163806	PAP45	176	17.0%	chr2	28916626	CCDS1767.2	c.637G>T	p.D213Y
SPACA1	sperm acrosome associated 1	ENSG00000118434	PAP45	114	24.6%	chr6	88820406	CCDS5014.1	c.232G>A	p.E78K
SPAG16	sperm associated antigen 16	ENSG00000144451	PAP45	218	25.2%	chr2	214983270	CCDS2396.1	c.1882C>T	p.R628X
SPAG17	sperm associated antigen 17	ENSG00000155761	PAP45	166	23.5%	chr1	118386034	CCDS899.1	c.2969A>C	p.K990T
SPAG6	sperm associated antigen 6	ENSG00000077327	PAP45	104	11.5%	chr10	22720850	CCDS7139.1	c.1192G>T	p.V398L
SPA17	sperm autoantigenic protein 17	ENSG00000064199	PAP45	291	12.0%	chr11	124050375	CCDS8450.1	c.5C>T	p.S2L
STRBP	spermatid perinuclear RNA binding protein	ENSG00000165209	PAP45	52	34.6%	chr9	124949903	CCDS6851.1	c.1113G>T	p.K371N
SPATA18	spermatogenesis associated 18 homolog (rat)	ENSG00000163071	PAP45	184	28.3%	chr4	52612658	CCDS3489.1	c.31A>C	p.N11H
SPATA19	spermatogenesis associated 19	ENSG00000166118	PAP45	130	16.2%	chr11	133219390	CCDS8493.1	c.320T>C	p.V107A
SPATA4	spermatogenesis associated 4	ENSG00000150628	PAP45	79	30.4%	chr4	177346281	CCDS3826.1	c.788G>T	p.R263I
SPATA5L1	spermatogenesis associated 5-like 1	ENSG00000171763	PAP45	102	29.4%	chr15	43482995	CCDS10123.1	c.1076G>T	p.R359I
SAT1	spermidine/spermine N1-acetyltransferase 1	ENSG00000130066	PAP45	242	29.3%	chrX	23711916	CCDS14207.1	c.197C>T	p.P66L
SMPD3	sphingomyelin phosphodiesterase 3; neutral membrane (neutral sphingomyelinase II)	ENSG00000103056	PAP45	171	20.5%	chr16	66962883	CCDS10867.1	c.703G>A	p.D235N
SMPDL3A	sphingomyelin phosphodiesterase; acid-like 3A	ENSG00000172594	PAP45	107	24.3%	chr6	123159690	CCDS5128.1	c.349G>A	p.V117I
SGPL1	sphingosine-1-phosphate lyase 1	ENSG00000166224	PAP45	158	27.8%	chr10	72303200	CCDS31216.1	c.1146G>A	p.W382X
SGPP1	sphingosine-1-phosphate phosphatase 1	ENSG00000126821	PAP45	111	28.8%	chr14	63263767	CCDS9760.1	c.649A>C	p.I217L
SF3B3	splicing factor 3b; subunit 3; 130kDa	ENSG00000189091	PAP45	153	26.1%	chr16	69129782	CCDS10894.1	c.881A>C	p.K294T
SFRS12	splicing factor; arginine/serine-rich 12	ENSG00000153914	PAP45	82	19.5%	chr5	65510345	CCDS43323.1	c.1768G>T	p.E590X
SFRS15	splicing factor; arginine/serine-rich 15	ENSG00000156304	PAP45	875	27.4%	chr21	31965857	CCDS33537.1	c.3170G>A	p.R1057Q
SFRS15	splicing factor; arginine/serine-rich 15	ENSG00000156304	PAP45	85	27.1%	chr21	31987603	CCDS33537.1	c.1388G>A	p.R463Q
SFRS16	splicing factor; arginine/serine-rich 16	ENSG00000104859	PAP45	94	37.2%	chr19	50255665	CCDS12652.2	c.803G>A	p.R268Q
SFRS18	splicing factor; arginine/serine-rich 18	ENSG00000132424	PAP45	143	22.4%	chr6	99957218	CCDS5043.1	c.1246C>T	p.R416W
SFRS2IP	splicing factor; arginine/serine-rich 2; interacting protein	ENSG00000139218	PAP45	163	20.9%	chr12	44606701	CCDS8748.2	c.3050G>T	p.R1017I
SFRS2IP	splicing factor; arginine/serine-rich 2; interacting protein	ENSG00000139218	PAP45	229	28.4%	chr12	44606793	CCDS8748.2	c.2958G>T	p.K986N
SFRS2IP	splicing factor; arginine/serine-rich 2; interacting protein	ENSG00000139218	PAP45	168	20.8%	chr12	44608271	CCDS8748.2	c.1480A>T	p.K494X
SQLE	squalene epoxidase	ENSG00000104549	PAP45	149	28.2%	chr8	126092972	ENST00000265896	c.1117G>T	p.E373X
SRMS	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites	ENSG00000125508	PAP45	88	20.5%	chr20	61644339	CCDS13525.1	c.685G>A	p.E229K

SCAP	SREBF chaperone	ENSG00000114650	PAP45	308	29.5%	chr3	47443977	CCDS2755.2	c.595G>A	p.E199K
SOX3	SRY (sex determining region Y)-box 3	ENSG00000134595	PAP45	70	27.1%	chrX	139414878	CCDS14669.1	c.14G>A	p.R5Q
SOX5	SRY (sex determining region Y)-box 5	ENSG00000134532	PAP45	91	15.4%	chr12	23580867	CCDS8699.1	c.1775C>T	p.S592F
ST3GAL1	ST3 beta-galactoside alpha-2;3-sialyltransferase 1	ENSG00000008513	PAP45	120	10.8%	chr8	134543305	CCDS6373.1	c.844G>A	p.D282N
ST3GAL3	ST3 beta-galactoside alpha-2;3-sialyltransferase 3	ENSG00000126091	PAP45	116	25.9%	chr1	44158726	CCDS493.1	c.1015C>T	p.R339X
ST3GAL5	ST3 beta-galactoside alpha-2;3-sialyltransferase 5	ENSG00000115525	PAP45	56	19.6%	chr2	85941862	CCDS1986.2	c.271G>T	p.E91X
ST6GAL1	ST6 beta-galactosamide alpha-2;6-sialyltranferase 1	ENSG00000073849	PAP45	175	31.4%	chr3	188243786	CCDS3285.1	c.601G>T	p.E201X
ST6GAL2	ST6 beta-galactosamide alpha-2;6-sialyltranferase 2	ENSG00000144057	PAP45	257	23.3%	chr2	106789775	CCDS2073.1	c.1381C>T	p.R461W
ST7OT3	ST7 overlapping transcript 3 (non-protein coding)	ENSG00000004866	PAP45	76	18.4%	chr7	116563429	CCDS5770.1	c.769G>T	p.E257X
ST8SIA3	ST8 alpha-N-acetyl-neuraminide alpha-2;8-sialyltransferase 3	ENSG00000177511	PAP45	300	21.7%	chr18	53175566	CCDS32834.1	c.727C>A	p.L243I
ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2;8-sialyltransferase 4	ENSG00000113532	PAP45	254	16.5%	chr5	100219878	CCDS4091.1	c.625G>T	p.E209X
SND1	staphylococcal nuclease and tudor domain containing 1	ENSG00000197157	PAP45	105	37.1%	chr7	127122148	CCDS34747.1	c.259C>T	p.R87X
SND1	staphylococcal nuclease and tudor domain containing 1	ENSG00000197157	PAP45	211	21.3%	chr7	127129733	CCDS34747.1	c.598G>A	p.E200K
SND1	staphylococcal nuclease and tudor domain containing 1	ENSG00000197157	PAP45	147	25.2%	chr7	127519308	CCDS34747.1	c.2695C>T	p.R899X
STARD3NL	STARD3 N-terminal like	ENSG00000010270	PAP45	38	26.3%	chr7	38221170	CCDS5455.1	c.320G>A	p.R107Q
STARD13	StAR-related lipid transfer (START) domain containing 13	ENSG00000133121	PAP45	72	25.0%	chr13	32582190	CCDS9348.1	c.2867C>T	p.S956F
STARD4	StAR-related lipid transfer (START) domain containing 4	ENSG00000164211	PAP45	56	19.6%	chr5	110864653	CCDS4104.1	c.343G>T	p.E115X
STARD8	StAR-related lipid transfer (START) domain containing 8	ENSG00000130052	PAP45	266	26.3%	chrX	67854212	CCDS14390.1	c.491C>A	p.S164Y
STRADB	STE20-related kinase adaptor beta	ENSG00000082146	PAP45	335	32.8%	chr2	202050699	CCDS2348.1	c.661G>T	p.D221Y
SLBP	stem-loop binding protein	ENSG00000163950	PAP45	77	27.3%	chr4	1675131	CCDS3350.1	c.271G>T	p.E91X
SAMD12	sterile alpha motif domain containing 12	ENSG00000177570	PAP45	254	13.0%	chr8	119460871	CCDS6325.1	c.572G>A	p.R191K
SAMD13	sterile alpha motif domain containing 13	ENSG00000203943	PAP45	118	12.7%	chr1	84563976	CCDS30760.1	c.164G>A	p.R55Q
SAMD3	sterile alpha motif domain containing 3	ENSG00000164483	PAP45	101	22.8%	chr6	130507585	CCDS34539.1	c.1336G>A	p.E446K
SAMD3	sterile alpha motif domain containing 3	ENSG00000164483	PAP45	137	18.2%	chr6	130538804	CCDS34539.1	c.697C>T	p.R233X
SAMD3	sterile alpha motif domain containing 3	ENSG00000164483	PAP45	87	21.8%	chr6	130547435	CCDS34539.1	c.410G>T	p.R137I
STS	steroid sulfatase (microsomal); isozyme S	ENSG00000101846	PAP45	186	18.3%	chrX	7278228	CCDS14127.1	c.1678C>T	p.Q560X
STOML3	stomatin (EPB72)-like 3	ENSG00000133115	PAP45	116	22.4%	chr13	38444680	CCDS9367.1	c.281G>A	p.R94Q
STON1-GTF	STON1-GTF2A1L readthrough	ENSG00000068781	PAP45	196	21.9%	chr2	48752243	CCDS1840.1	c.3361A>C	p.N1121H
STON2	stonin 2	ENSG00000140022	PAP45	172	33.7%	chr14	80806880	CCDS9875.1	c.2500G>A	p.E834K
SBNO1	strawberry notch homolog 1 (Drosophila)	ENSG00000139697	PAP45	141	23.4%	chr12	122371089	CCDS9246.1	c.2507G>T	p.S836I
STAG1	stromal antigen 1	ENSG00000118007	PAP45	61	24.6%	chr3	137550698	CCDS3090.1	c.3263G>A	p.R1088Q
STAG1	stromal antigen 1	ENSG00000118007	PAP45	154	22.7%	chr3	137579244	CCDS3090.1	c.2410NULL>T	p.NULL-1FsIns1bp
STAG1	stromal antigen 1	ENSG00000118007	PAP45	122	27.0%	chr3	137675090	CCDS3090.1	c.1106T>C	p.L369P
STIM2	stromal interaction molecule 2	ENSG00000109689	PAP45	476	29.0%	chr4	26628656	CCDS3440.1	c.1976G>A	p.R659Q
STIM2	stromal interaction molecule 2	ENSG00000109689	PAP45	415	20.2%	chr4	26633337	CCDS3440.1	c.2123C>A	p.S708Y
SMC3	structural maintenance of chromosomes 3	ENSG00000108055	PAP45	170	18.8%	chr10	112351570	CCDS31285.1	c.2830C>T	p.R944X
SMC5	structural maintenance of chromosomes 5	ENSG00000198887	PAP45	239	19.2%	chr9	72102857	CCDS6632.1	c.1209T>G	p.I403M
SMC5	structural maintenance of chromosomes 5	ENSG00000198887	PAP45	92	31.5%	chr9	72154874	CCDS6632.1	c.2914C>T	p.R972X
STT3A	STT3; subunit of the oligosaccharyltransferase complex; homolog A (S. cerevisiae)	ENSG00000134910	PAP45	186	23.7%	chr11	124989250	CCDS8458.1	c.1613G>A	p.R538Q
SI	sucrase-isomaltase (alpha-glucosidase)	ENSG00000090402	PAP45	171	29.8%	chr3	166182756	CCDS3196.1	c.5384C>T	p.S1795L
SI	sucrase-isomaltase (alpha-glucosidase)	ENSG00000090402	PAP45	94	21.3%	chr3	166259542	CCDS3196.1	c.1301G>A	p.R434Q
SULF1	sulfatase 1	ENSG00000137573	PAP45	173	50.9%	chr8	70698781	CCDS6204.1	c.1645G>A	p.E549K
SUOX	sulfite oxidase	ENSG00000139531	PAP45	297	25.9%	chr12	54683848	CCDS8901.2	c.408C>A	p.F136L
SULT6B1	sulfotransferase family; cytosolic; 6B; member 1	ENSG00000138068	PAP45	138	31.2%	chr2	37260171	CCDS33182.1	c.349G>A	p.D117N
SULT6B1	sulfotransferase family; cytosolic; 6B; member 1	ENSG00000138068	PAP45	104	24.0%	chr2	37264160	CCDS33182.1	c.200G>T	p.R67I
SENP6	SUMO1/sentrin specific peptidase 6	ENSG00000112701	PAP45	110	11.8%	chr6	76437038	CCDS43483.1	c.1253C>A	p.S418Y
SENP7	SUMO1/sentrin specific peptidase 7	ENSG00000138468	PAP45	85	30.6%	chr3	102527530	CCDS2941.2	c.3100C>T	p.R1034X
SENP2	SUMO1/sentrin/SMT3 specific peptidase 2	ENSG00000163904	PAP45	137	22.6%	chr3	186812141	CCDS33902.1	c.731G>T	p.R244I
SVIL	supervillin	ENSG00000197321	PAP45	285	11.2%	chr10	29861738	CCDS7164.1	c.1564G>T	p.E522X

ST18	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	ENSG00000147488	PAP45	95	25.3%	chr8	53191444	CCDS6149.1	c.2947G>T	p.A983S
ST5	suppression of tumorigenicity 5	ENSG00000166444	PAP45	121	28.9%	chr11	8695999	CCDS7791.1	c.1494G>T	p.E498D
ST7	suppression of tumorigenicity 7	ENSG00000004866	PAP45	76	18.4%	chr7	116563429	CCDS5770.1	c.769G>T	p.E257X
ST7L	suppression of tumorigenicity 7 like	ENSG00000007341	PAP45	90	32.2%	chr1	112870206	CCDS848.1	c.1680G>T	p.E560D
SOCS7	suppressor of cytokine signaling 7	ENSG00000174111	PAP45	84	25.0%	chr17	33777361	CCDS32637.1	c.1262C>A	p.S421Y
SOCS7	suppressor of cytokine signaling 7	ENSG00000174111	PAP45	70	31.4%	chr17	33787093	CCDS32637.1	c.1388A>C	p.K463T
SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	ENSG00000092201	PAP45	342	19.9%	chr14	20890776	CCDS9569.1	c.3040C>T	p.R1014X
SUPT3H	suppressor of Ty 3 homolog (S. cerevisiae)	ENSG00000196284	PAP45	86	23.3%	chr6	45008409	CCDS34466.1	c.904C>T	p.R302X
SUPT5H	suppressor of Ty 5 homolog (S. cerevisiae)	ENSG00000196235	PAP45	197	20.3%	chr19	44654141	CCDS12536.1	c.1881G>T	p.K627N
SUPT5H	suppressor of Ty 5 homolog (S. cerevisiae)	ENSG00000196235	PAP45	550	15.5%	chr19	44656732	CCDS12536.1	c.2670C>A	p.F890L
SFTPB	surfactant protein B	ENSG00000168878	PAP45	34	38.2%	chr2	85744447	CCDS1983.1	c.707G>A	p.R236H
SRPX2	sushi-repeat-containing protein; X-linked 2	ENSG00000102359	PAP45	172	24.4%	chrX	99806954	CCDS14471.1	c.591G>T	p.E197D
SVOPL	SVOP-like	ENSG00000157703	PAP45	83	26.5%	chr7	137962735	CCDS5848.1	c.625A>C	p.N209H
SMARCA1	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 1	ENSG00000102038	PAP45	75	25.3%	chrX	128442742	CCDS14612.1	c.2319G>T	p.K773N
SMARCAL1	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a-like 1	ENSG00000138375	PAP45	44	34.1%	chr2	217055836	CCDS2403.1	c.2756C>T	p.S919F
SMARCC2	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily c; member 2	ENSG00000139613	PAP45	54	24.1%	chr12	54854801	CCDS8907.1	c.1397G>A	p.R466Q
SMARCAD1	SWI/SNF-related; matrix-associated actin-dependent regulator of chromatin; subfamily a; containing DEAD/H box 1	ENSG00000163104	PAP45	54	18.5%	chr4	95389856	CCDS3639.1	c.734C>A	p.S245Y
SYDE1	synapse defective 1; Rho GTPase; homolog 1 (C. elegans)	ENSG00000105137	PAP45	252	24.6%	chr19	15081143	CCDS12324.1	c.365C>A	p.P122H
SYNGAP1	synaptic Ras GTPase activating protein 1 homolog (rat)	ENSG00000197283	PAP45	157	21.0%	chr6	33514532	CCDS34434.1	c.1489G>A	p.E497K
SV2A	synaptic vesicle glycoprotein 2A	ENSG00000159164	PAP45	113	28.3%	chr1	148149096	CCDS940.1	c.861G>T	p.E287D
SV2A	synaptic vesicle glycoprotein 2A	ENSG00000159164	PAP45	526	23.6%	chr1	148151817	CCDS940.1	c.200G>A	p.R67Q
SV2C	synaptic vesicle glycoprotein 2C	ENSG00000122012	PAP45	351	25.4%	chr5	75463796	CCDS43331.1	c.465C>A	p.F155L
SV2C	synaptic vesicle glycoprotein 2C	ENSG00000122012	PAP45	102	28.4%	chr5	75541418	CCDS43331.1	c.863T>G	p.I288S
SYNGR4	synaptogyrin 4	ENSG00000105467	PAP45	47	25.5%	chr19	53560999	CCDS12717.1	c.88G>A	p.E30K
SYNJ2	synaptojanin 2	ENSG00000078269	PAP45	236	25.0%	chr6	158369954	CCDS5254.1	c.393C>A	p.F131L
SYCE1	synaptonemal complex central element protein 1	ENSG00000171772	PAP45	106	18.9%	chr10	135218569	NM_001143764	c.973C>T	p.P325S
SYCP1	synaptonemal complex protein 1	ENSG00000198765	PAP45	80	23.8%	chr1	115325634	CCDS879.1	c.2537C>A	p.T846N
SYCP2	synaptonemal complex protein 2	ENSG00000196074	PAP45	63	19.0%	chr20	57876932	CCDS13482.1	c.3919G>T	p.E1307X
SYP	synaptophysin	ENSG00000102003	PAP45	133	24.8%	chrX	48941212	CCDS14321.1	c.133G>A	p.G45S
SYNPO2	synaptopodin 2	ENSG00000172403	PAP45	219	15.5%	chr4	120167333	CCDS34054.1	c.361C>T	p.R121X
SYNPO2	synaptopodin 2	ENSG00000172403	PAP45	258	23.6%	chr4	120198431	CCDS34054.1	c.3680G>T	p.R1227I
SYNPO2L	synaptopodin 2-like	ENSG00000166317	PAP45	386	11.7%	chr10	75077056	CCDS7331.1	c.1688G>T	p.R563I
SYT3	synaptotagmin III	ENSG00000213023	PAP45	86	20.9%	chr19	55820500	CCDS12798.1	c.1536G>T	p.E512D
SYT10	synaptotagmin X	ENSG00000110975	PAP45	380	25.3%	chr12	33426647	CCDS8732.1	c.1274C>A	p.T425N
SYT14L	synaptotagmin XIV-like	ENSG00000215127	PAP45	136	26.5%	chr4	68611370	ENST00000399639	c.52C>A	p.H18N
SYTL2	synaptotagmin-like 2	ENSG00000137501	PAP45	80	25.0%	chr11	85084005	CCDS31651.1	c.3700T>G	p.W1234G
SYTL2	synaptotagmin-like 2	ENSG00000137501	PAP45	166	24.7%	chr11	85106176	CCDS31651.1	c.2627G>T	p.R876I
SYTL2	synaptotagmin-like 2	ENSG00000137501	PAP45	70	27.1%	chr11	85113395	CCDS31651.1	c.1753G>T	p.E585X
SYTL2	synaptotagmin-like 2	ENSG00000137501	PAP45	438	21.0%	chr11	85113854	CCDS31651.1	c.1294G>T	p.E432X
SYTL2	synaptotagmin-like 2	ENSG00000137501	PAP45	243	22.6%	chr11	85122954	CCDS31649.1	c.1063G>T	p.E355X
SYNM	synemin; intermediate filament protein	ENSG00000182253	PAP45	124	30.6%	chr15	97488418	ENST00000336292	c.2327C>T	p.S776L
SNPH	syntaphilin	ENSG00000101298	PAP45	55	30.9%	chr20	1166748	NM_001136566	c.536C>A	p.S179Y
SNPH	syntaphilin	ENSG00000101298	PAP45	68	32.4%	chr20	1166765	NM_001136566	c.553G>T	p.E185X
STX17	syntaxin 17	ENSG00000136874	PAP45	61	19.7%	chr9	101717462	CCDS6745.1	c.120G>T	p.E40D
STX3	syntaxin 3	ENSG00000166900	PAP45	168	19.6%	chr11	59317503	CCDS7975.1	c.615G>T	p.E205D
STXBP5L	syntaxin binding protein 5-like	ENSG00000145087	PAP45	187	26.2%	chr3	122247051	CCDS43137.1	c.449C>A	p.S150Y
STXBP5L	syntaxin binding protein 5-like	ENSG00000145087	PAP45	64	25.0%	chr3	122424558	CCDS43137.1	c.975C>A	p.F325L
STXBP5L	syntaxin binding protein 5-like	ENSG00000145087	PAP45	109	19.3%	chr3	122456577	CCDS43137.1	c.1587C>A	p.F529L

SNTB1	syntrophin; beta 1 (dystrophin-associated protein A1; 59kDa; basic component 1)	ENSG00000172164	PAP45	87	19.5%	chr8	121623405	CCDS6334.1	c.1350C>A	p.N450K
SNCAIP	synuclein; alpha interacting protein	ENSG00000064692	PAP45	182	26.4%	chr5	121815035	CCDS4131.1	c.2594G>A	p.R865Q
TIGIT	T cell immunoreceptor with Ig and ITIM domains	ENSG00000181847	PAP45	219	21.5%	chr3	115495491	ENST00000314309	c.94G>A	p.E32K
TRBV4-1	T cell receptor beta variable 4-1	ENSG00000211710	PAP45	47	25.5%	chr7	141709526	ENST00000390357	c.322T>C	p.Y108H
TRBV6-4	T cell receptor beta variable 6-4	ENSG00000211713	PAP45	70	22.9%	chr7	141749283	ENST00000390360	c.5G>T	p.R2I
TRBV9	T cell receptor beta variable 9	ENSG00000211716	PAP45	318	17.0%	chr7	141760677	ENST00000390363	c.142G>T	p.D48Y
TAF1L	TAF1 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 210kDa-like	ENSG00000122728	PAP45	437	25.4%	chr9	32621766	NM_153809	c.3812A>C	p.K1271T
TAF1L	TAF1 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 210kDa-like	ENSG00000122728	PAP45	209	23.4%	chr9	32623424	NM_153809	c.2154G>T	p.K718N
TAF1L	TAF1 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 210kDa-like	ENSG00000122728	PAP45	321	20.9%	chr9	32623905	NM_153809	c.1673G>A	p.R558Q
TAF1	TAF1 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 250kDa	ENSG00000147133	PAP45	308	17.5%	chrX	70529489	CCDS14412.1	c.3031G>T	p.G1011X
TAF3	TAF3 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 140kDa	ENSG00000165632	PAP45	182	18.1%	chr10	7906484	CCDS41487.1	c.364G>T	p.E122X
TAF3	TAF3 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 140kDa	ENSG00000165632	PAP45	98	34.7%	chr10	8047685	CCDS41487.1	c.2206G>T	p.E736X
TAF3	TAF3 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 140kDa	ENSG00000165632	PAP45	113	30.1%	chr10	8095784	CCDS41487.1	c.2653G>A	p.D885N
TAF5	TAF5 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 100kDa	ENSG00000148835	PAP45	85	17.6%	chr10	105129376	CCDS7547.1	c.1135G>T	p.E379X
TAF7	TAF7 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 55kDa	ENSG00000178913	PAP45	102	27.5%	chr5	140679793	CCDS4259.1	c.3G>T	p.M1I
TLN1	talin 1	ENSG00000137076	PAP45	321	25.2%	chr9	35700863	CCDS35009.1	c.4134G>T	p.E1378D
TNKS1BP1	tankyrase 1 binding protein 1; 182kDa	ENSG00000149115	PAP45	214	27.6%	chr11	56837041	CCDS7951.1	c.1697C>T	p.A566V
TNKS	tankyrase; TRF1-interacting ankyrin-related ADP-ribose polymerase	ENSG00000173273	PAP45	95	17.9%	chr8	9659709	CCDS5974.1	c.3446G>A	p.R1149Q
TNKS2	tankyrase; TRF1-interacting ankyrin-related ADP-ribose polymerase 2	ENSG00000107854	PAP45	158	28.5%	chr10	93605366	CCDS7417.1	c.2929C>T	p.R977X
TAPBP	TAP binding protein (tapasin)	ENSG00000112493	PAP45	102	28.4%	chr6	33380114	CCDS34426.1	c.1148G>A	p.R383Q
TARBP1	TAR (HIV-1) RNA binding protein 1	ENSG00000059588	PAP45	84	16.7%	chr1	232631507	CCDS1601.1	c.3058G>T	p.E1020X
TARDBP	TAR DNA binding protein	ENSG00000120948	PAP45	145	25.5%	chr1	10999562	CCDS122.1	c.313G>A	p.D105N
TAS1R2	taste receptor; type 1; member 2	ENSG00000179002	PAP45	151	23.2%	chr1	19054036	CCDS187.1	c.515G>A	p.R172Q
TAS2R16	taste receptor; type 2; member 16	ENSG00000128519	PAP45	415	24.6%	chr7	122422206	CCDS5785.1	c.719T>G	p.F240C
TAS2R16	taste receptor; type 2; member 16	ENSG00000128519	PAP45	84	19.0%	chr7	122422795	CCDS5785.1	c.130C>T	p.P44S
TAF1B	TATA box binding protein (TBP)-associated factor; RNA polymerase I; B; 63kDa	ENSG00000115750	PAP45	142	33.1%	chr2	9933493	CCDS33143.1	c.602G>A	p.R201Q
TMF1	TATA element modulatory factor 1	ENSG00000144747	PAP45	93	22.6%	chr3	69161748	CCDS43105.1	c.2502G>T	p.Q834H
TTBK2	tau tubulin kinase 2	ENSG00000128881	PAP45	182	26.4%	chr15	40909488	CCDS42029.1	c.372G>T	p.Q124H
TTBK2	tau tubulin kinase 2	ENSG00000128881	PAP45	222	14.9%	chr15	40952218	CCDS42029.1	c.100G>T	p.E34X
TBC1D10A	TBC1 domain family; member 10A	ENSG00000099992	PAP45	377	20.2%	chr22	29030523	CCDS13874.1	c.306A>C	p.K102N
TBC1D19	TBC1 domain family; member 19	ENSG00000109680	PAP45	103	11.7%	chr4	26359135	CCDS3439.1	c.1324C>T	p.R442C
TBC1D22A	TBC1 domain family; member 22A	ENSG00000054611	PAP45	173	22.0%	chr22	45665928	CCDS14078.1	c.811G>A	p.E271K
TBC1D4	TBC1 domain family; member 4	ENSG00000136111	PAP45	66	27.3%	chr13	74764409	CCDS41901.1	c.-1G>T	p.IVS18-1-1SpliceAcceptor
TBC1D5	TBC1 domain family; member 5	ENSG00000131374	PAP45	54	24.1%	chr3	17393037	CCDS33714.1	c.685G>T	p.E229X
TBC1D8B	TBC1 domain family; member 8B (with GRAM domain)	ENSG00000133138	PAP45	73	20.5%	chrX	105951923	CCDS14522.1	c.421C>T	p.R141X
TBC1D8B	TBC1 domain family; member 8B (with GRAM domain)	ENSG00000133138	PAP45	67	22.4%	chrX	105952073	CCDS14522.1	c.571T>G	p.L191V
TBC1D9B	TBC1 domain family; member 9B (with GRAM domain)	ENSG00000197226	PAP45	138	24.6%	chr5	179247906	CCDS43408.1	c.1057G>A	p.E353K
TBCCD1	TBCC domain containing 1	ENSG00000113838	PAP45	44	22.7%	chr3	187754883	CCDS3276.1	c.1398C>A	p.F466L
TBX10	T-box 10	ENSG00000167800	PAP45	143	17.5%	chr11	67157061	CCDS31621.1	c.639G>T	p.E213D
TBX15	T-box 15	ENSG00000092607	PAP45	104	17.3%	chr1	119235015	ENST00000344218	c.803G>A	p.R268Q

TBX19	T-box 19	ENSG00000143178	PAP45	67	16.4%	chr1	166533620	CCDS1272.1	c.638C>A	p.A213D
TBX6	T-box 6	ENSG00000149922	PAP45	291	21.0%	chr16	30007423	CCDS10670.1	c.783G>T	p.K261N
TIPARP	TCDD-inducible poly(ADP-ribose) polymerase	ENSG00000163659	PAP45	85	21.2%	chr3	157896400	CCDS3177.1	c.1139G>A	p.R380Q
TIAM1	T-cell lymphoma invasion and metastasis 1	ENSG00000156299	PAP45	232	28.4%	chr21	31435547	CCDS13609.1	c.3622G>A	p.D1208N
TCTE3	t-complex-associated-testis-expressed 3	ENSG00000184786	PAP45	365	27.4%	chr6	169893366	CCDS5310.1	c.114G>T	p.K38N
TSHZ3	teashirt zinc finger homeobox 3	ENSG00000121297	PAP45	455	24.8%	chr19	36461491	CCDS12421.2	c.1048G>A	p.D350N
TECTA	tectorin alpha	ENSG00000109927	PAP45	175	22.9%	chr11	120494483	CCDS8434.1	c.1049G>A	p.R350Q
TECTA	tectorin alpha	ENSG00000109927	PAP45	246	10.2%	chr11	120501579	CCDS8434.1	c.1562C>A	p.S521Y
TECTA	tectorin alpha	ENSG00000109927	PAP45	329	26.1%	chr11	120503899	CCDS8434.1	c.2003C>T	p.T668M
TECTA	tectorin alpha	ENSG00000109927	PAP45	137	17.5%	chr11	120505597	CCDS8434.1	c.2408C>T	p.S803L
TECTB	tectorin beta	ENSG00000119913	PAP45	114	29.8%	chr10	114043537	CCDS7571.1	c.535G>A	p.E179K
TEKT1	tektin 1	ENSG00000167858	PAP45	737	25.4%	chr17	6656995	CCDS11083.1	c.731G>A	p.R244Q
TEKT1	tektin 1	ENSG00000167858	PAP45	392	23.2%	chr17	6657080	CCDS11083.1	c.646G>A	p.D216N
TEKT1	tektin 1	ENSG00000167858	PAP45	136	22.8%	chr17	6674335	CCDS11083.1	c.85G>A	p.A29T
TNS3	tensin 3	ENSG00000136205	PAP45	42	23.8%	chr7	47352420	CCDS5506.2	c.2341G>A	p.D781N
TNS4	tensin 4	ENSG00000131746	PAP45	178	24.7%	chr17	35894324	CCDS11368.1	c.1439G>A	p.R480Q
TENC1	tensin like C1 domain containing phosphatase (tensin 2)	ENSG00000111077	PAP45	336	22.9%	chr12	51740543	CCDS8842.1	c.2735C>T	p.S912L
TEX10	testis expressed 10	ENSG00000136891	PAP45	117	28.2%	chr9	102131258	CCDS6748.1	c.1610G>T	p.R537I
TEX14	testis expressed 14	ENSG00000121101	PAP45	84	22.6%	chr17	54004391	CCDS32693.1	c.3727G>T	p.E1243X
TEX14	testis expressed 14	ENSG00000121101	PAP45	121	26.4%	chr17	54031949	CCDS32693.1	c.1756C>A	p.L586M
TEX15	testis expressed 15	ENSG00000133863	PAP45	181	24.9%	chr8	30814071	CCDS6080.1	c.8122C>A	p.L2708I
TEX15	testis expressed 15	ENSG00000133863	PAP45	47	23.4%	chr8	30819301	CCDS6080.1	c.6775C>A	p.L2259M
TEX15	testis expressed 15	ENSG00000133863	PAP45	178	21.3%	chr8	30821136	CCDS6080.1	c.4940T>G	p.F1647C
TEX15	testis expressed 15	ENSG00000133863	PAP45	78	17.9%	chr8	30821658	CCDS6080.1	c.4418C>A	p.S1473Y
TEX15	testis expressed 15	ENSG00000133863	PAP45	116	24.1%	chr8	30821772	CCDS6080.1	c.4304C>A	p.S1435Y
TEX15	testis expressed 15	ENSG00000133863	PAP45	26	46.2%	chr8	30822375	CCDS6080.1	c.3701C>T	p.S1234F
TEX2	testis expressed 2	ENSG00000136478	PAP45	79	30.4%	chr17	59582043	CCDS11658.1	c.3172C>T	p.R1058X
TSKS	testis-specific serine kinase substrate	ENSG00000126467	PAP45	120	29.2%	chr19	54957219	CCDS12780.1	c.253C>T	p.L85F
TSPAN2	tetraspanin 2	ENSG00000134198	PAP45	88	19.3%	chr1	115401725	CCDS881.1	c.472G>A	p.E158K
TSPAN5	tetraspanin 5	ENSG00000168785	PAP45	87	34.5%	chr4	99612719	CCDS3646.1	c.784G>A	p.E262K
TTC14	tetratricopeptide repeat domain 14	ENSG00000163728	PAP45	103	24.3%	chr3	181803680	CCDS3237.1	c.361C>T	p.R121X
TTC14	tetratricopeptide repeat domain 14	ENSG00000163728	PAP45	148	22.3%	chr3	181810480	CCDS3237.1	c.1769T>G	p.F590C
TTC18	tetratricopeptide repeat domain 18	ENSG00000156042	PAP45	191	31.4%	chr10	74721459	CCDS7324.1	c.2175C>A	p.F725L
TTC25	tetratricopeptide repeat domain 25	ENSG00000204815	PAP45	88	13.6%	chr17	37366959	ENST00000377543	c.1474G>T	p.E492X
TTC27	tetratricopeptide repeat domain 27	ENSG00000018699	PAP45	92	30.4%	chr2	32812400	CCDS33176.1	c.1235C>T	p.A412V
TTC28	tetratricopeptide repeat domain 28	ENSG00000100154	PAP45	391	11.0%	chr22	26724868	NM_001145418	c.4779G>T	p.E1593D
TTC3	tetratricopeptide repeat domain 3	ENSG00000182670	PAP45	158	23.4%	chr21	37459921	CCDS13651.1	c.3535A>C	p.K1179Q
TTC33	tetratricopeptide repeat domain 33	ENSG00000113638	PAP45	52	30.8%	chr5	40752350	CCDS3931.1	c.443G>A	p.R148Q
TTC35	tetratricopeptide repeat domain 35	ENSG00000104412	PAP45	269	20.8%	chr8	109551258	CCDS6309.1	c.391C>T	p.R131X
TTC3L	tetratricopeptide repeat domain 3-like	ENSG00000182670	PAP45	158	23.4%	chr21	37459921	CCDS13651.1	c.3535A>C	p.K1179Q
TTC6	tetratricopeptide repeat domain 6	ENSG00000139865	PAP45	110	25.5%	chr14	37362838	ENST00000382320	c.1092G>T	p.Q364H
TAB3	TGF-beta activated kinase 1/MAP3K7 binding protein 3	ENSG00000157625	PAP45	127	23.6%	chrX	30780918	CCDS14226.1	c.1608G>T	p.E536D
THAP9	THAP domain containing 9	ENSG00000168152	PAP45	68	25.0%	chr4	84058900	CCDS3598.1	c.2511G>T	p.K837N
THTPA	thiamine triphosphatase	ENSG00000157306	PAP45	165	25.5%	chr14	23095896	CCDS32053.1	c.90G>T	p.E30D
TXNDC12	thioredoxin domain containing 12 (endoplasmic reticulum)	ENSG00000117862	PAP45	110	16.4%	chr1	52259195	CCDS561.1	c.517T>C	p.X173Q
TXNDC6	thioredoxin domain containing 6	ENSG00000181322	PAP45	87	29.9%	chr3	139506548	CCDS3099.1	c.465G>T	p.E155D
TXNDC9	thioredoxin domain containing 9	ENSG00000115514	PAP45	111	23.4%	chr2	99304894	CCDS2044.1	c.519A>C	p.E173D
TXNIP	thioredoxin interacting protein	ENSG00000117289	PAP45	144	23.6%	chr1	144150177	CCDS913.1	c.18G>T	p.K6N
TMX2	thioredoxin-related transmembrane protein 2	ENSG00000213593	PAP45	268	24.3%	chr11	57263266	CCDS7967.1	c.702G>T	p.Q234H
THOC2	THO complex 2	ENSG00000125676	PAP45	104	29.8%	chrX	122628690	CCDS43988.1	c.1138G>A	p.A380T
THNSL1	threonine synthase-like 1 (S. cerevisiae)	ENSG00000185875	PAP45	74	16.2%	chr10	25352194	CCDS7147.1	c.36G>T	p.K12N
THNSL1	threonine synthase-like 1 (S. cerevisiae)	ENSG00000185875	PAP45	131	26.7%	chr10	25352442	CCDS7147.1	c.284G>T	p.W95L
TARS	threonyl-tRNA synthetase	ENSG00000113407	PAP45	85	15.3%	chr5	33502775	CCDS3899.1	c.1951G>T	p.D651Y
THBS4	thrombospondin 4	ENSG00000113296	PAP45	267	24.3%	chr5	79399680	CCDS4049.1	c.1323G>T	p.E441D

THSD1	thrombospondin; type I; domain containing 1	ENSG00000136114	PAP45	259	21.2%	chr13	51850103	CCDS9432.1	c.2003G>T	p.R668M
THSD7B	thrombospondin; type I; domain containing 7B	ENSG00000144229	PAP45	314	25.2%	chr2	137885708	ENST00000272643	c.2755G>T	p.E919X
THUMPD2	THUMP domain containing 2	ENSG00000138050	PAP45	57	29.8%	chr2	39835941	CCDS1805.1	c.986T>C	p.I329T
TYMS	thymidylate synthetase	ENSG00000176890	PAP45	77	19.5%	chr18	661448	CCDS11821.1	c.801T>G	p.I267M
TDG	thymine-DNA glycosylase	ENSG00000139372	PAP45	32	31.3%	chr12	102901249	CCDS9095.1	c.744G>T	p.K248N
THEMIS	thymocyte selection associated	ENSG00000172673	PAP45	146	18.5%	chr6	128176515	CCDS34534.1	c.964G>T	p.E322X
TOX	thymocyte selection-associated high mobility group box	ENSG00000198846	PAP45	147	30.6%	chr8	59890782	CCDS34897.1	c.1061C>T	p.S354L
TOX	thymocyte selection-associated high mobility group box	ENSG00000198846	PAP45	112	18.8%	chr8	59913362	CCDS34897.1	c.756G>T	p.K252N
TG	thyroglobulin	ENSG00000042832	PAP45	251	22.7%	chr8	133968721	CCDS34944.1	c.1922C>A	p.S641Y
TG	thyroglobulin	ENSG00000042832	PAP45	78	28.2%	chr8	133980249	CCDS34944.1	c.3242G>A	p.R1081Q
TG	thyroglobulin	ENSG00000042832	PAP45	271	20.7%	chr8	134022866	CCDS34944.1	c.5130C>A	p.F1710L
THADA	thyroid adenoma associated	ENSG00000115970	PAP45	410	24.9%	chr2	43373522	NM_001083953	c.4773C>A	p.F1591L
THADA	thyroid adenoma associated	ENSG00000115970	PAP45	107	15.9%	chr2	43608616	NM_022065	c.3280G>T	p.D1094Y
TRIP11	thyroid hormone receptor interactor 11	ENSG00000100815	PAP45	115	27.8%	chr14	91539946	CCDS9899.1	c.4127C>T	p.S1376L
TRIP11	thyroid hormone receptor interactor 11	ENSG00000100815	PAP45	78	25.6%	chr14	91551847	CCDS9899.1	c.769G>T	p.E257X
TRIP12	thyroid hormone receptor interactor 12	ENSG00000153827	PAP45	45	31.1%	chr2	230370667	CCDS33391.1	c.3382G>A	p.E1128K
TRIP12	thyroid hormone receptor interactor 12	ENSG00000153827	PAP45	53	32.1%	chr2	230378770	ENST00000389045	c.1535C>A	p.S512Y
THRB	thyroid hormone receptor; beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2; avian)	ENSG00000151090	PAP45	245	13.9%	chr3	24206579	CCDS2641.1	c.273G>T	p.K91N
TIGD2	tigger transposable element derived 2	ENSG00000180346	PAP45	124	31.5%	chr4	90253821	CCDS3633.1	c.673C>A	p.L225I
TIGD7	tigger transposable element derived 7	ENSG00000140993	PAP45	179	24.0%	chr16	3289068	CCDS10500.1	c.1548C>A	p.F516L
TJP2	tight junction protein 2 (zona occludens 2)	ENSG00000119139	PAP45	187	26.2%	chr9	71053019	ENST00000265384	c.2939C>T	p.S980L
TIPRL	TIP41; TOR signaling pathway regulator-like (S. cerevisiae)	ENSG00000143155	PAP45	233	19.3%	chr1	166415023	CCDS1270.1	c.84G>T	p.M28I
TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	ENSG00000003436	PAP45	91	12.1%	chr2	188069942	CCDS2294.1	c.230G>A	p.R77Q
TRAF4	TNF receptor-associated factor 4	ENSG00000076604	PAP45	183	29.5%	chr17	24099022	CCDS11243.1	c.230T>C	p.L77S
TNIP2	TNFAIP3 interacting protein 2	ENSG00000168884	PAP45	123	24.4%	chr4	2716411	CCDS3362.1	c.717G>T	p.R239S
TNNI3K	TNNI3 interacting kinase	ENSG00000116783	PAP45	304	26.6%	chr1	74677768	CCDS664.1	c.1885C>T	p.R629C
TLR5	toll-like receptor 5	ENSG00000187554	PAP45	215	20.0%	chr1	221351936	CCDS31033.1	c.1061C>T	p.S354L
TLR5	toll-like receptor 5	ENSG00000187554	PAP45	155	30.3%	chr1	221352503	CCDS31033.1	c.494C>A	p.S165X
TLR5	toll-like receptor 5	ENSG00000187554	PAP45	135	12.6%	chr1	221352531	CCDS31033.1	c.466C>A	p.Q156K
TLR8	toll-like receptor 8	ENSG00000101916	PAP45	282	29.1%	chrX	12847918	CCDS14152.1	c.838C>T	p.R280C
TLR8	toll-like receptor 8	ENSG00000101916	PAP45	378	29.1%	chrX	12849370	CCDS14152.1	c.2290T>G	p.L764V
TLL1	tolloid-like 1	ENSG00000038295	PAP45	141	27.0%	chr4	167165926	CCDS3811.1	c.1051G>T	p.E351X
TLL1	tolloid-like 1	ENSG00000038295	PAP45	113	23.9%	chr4	167200747	CCDS3811.1	c.1964G>T	p.R655I
TOP1	topoisomerase (DNA) I	ENSG00000198900	PAP45	230	20.9%	chr20	39184137	CCDS13312.1	c.2123G>A	p.R708Q
TOPORS	topoisomerase I binding; arginine/serine-rich	ENSG00000197579	PAP45	185	23.8%	chr9	32533127	CCDS6527.1	c.1396G>A	p.D466N
TOPORS	topoisomerase I binding; arginine/serine-rich	ENSG00000197579	PAP45	164	23.8%	chr9	32534158	CCDS6527.1	c.365A>C	p.K122T
TAAR6	trace amine associated receptor 6	ENSG00000146383	PAP45	475	16.8%	chr6	132933509	CCDS5155.1	c.356C>A	p.S119Y
TRAPPC10	trafficking protein particle complex 10	ENSG00000160218	PAP45	50	36.0%	chr21	44300045	CCDS13704.1	c.521G>A	p.R174Q
TRAPPC10	trafficking protein particle complex 10	ENSG00000160218	PAP45	196	27.6%	chr21	44307910	CCDS13704.1	c.854G>A	p.R285Q
TECRL	trans-2;3-enoyl-CoA reductase-like	ENSG00000205678	PAP45	140	20.0%	chr4	64957636	CCDS33990.1	c.29C>T	p.S10L
TCEAL1	transcription elongation factor A (SII)-like 1	ENSG00000172465	PAP45	174	28.2%	chrX	102771863	CCDS35358.1	c.363T>G	p.N121K
TCERG1	transcription elongation regulator 1	ENSG00000113649	PAP45	76	22.4%	chr5	145830490	CCDS4282.1	c.1498A>C	p.K500Q
TCF20	transcription factor 20 (AR1)	ENSG00000100207	PAP45	217	25.8%	chr22	40938578	CCDS14033.1	c.2678G>T	p.R893I
TFB1M	transcription factor B1; mitochondrial	ENSG00000029639	PAP45	210	20.0%	chr6	155674079	CCDS5248.1	c.220C>A	p.L74I
TFCP2	transcription factor CP2	ENSG00000135457	PAP45	261	24.9%	chr12	49783764	CCDS8808.1	c.1016G>A	p.R339Q
TTF1	transcription termination factor; RNA polymerase I	ENSG00000125482	PAP45	184	29.9%	chr9	134255941	CCDS6948.1	c.2086G>T	p.E696X
TADA2B	transcriptional adaptor 2B	ENSG00000173011	PAP45	231	28.6%	chr4	7107625	NM_152293	c.1206G>T	p.K402N
TBL1X	transducin (beta)-like 1X-linked	ENSG00000101849	PAP45	133	26.3%	chrX	9642951	CCDS14133.1	c.1615C>A	p.L539I
TLE4	transducin-like enhancer of split 4 (E(sp1) homolog; Drosophila)	ENSG00000106829	PAP45	191	23.6%	chr9	81512902	CCDS43837.1	c.986G>A	p.R329Q
TLE4	transducin-like enhancer of split 4 (E(sp1) homolog; Drosophila)	ENSG00000106829	PAP45	90	26.7%	chr9	81523479	CCDS43837.1	c.1363G>A	p.A455T

TLE4	transducin-like enhancer of split 4 (E(sp1) homolog; Drosophila)	ENSG00000106829	PAP45	241	22.4%	chr9	81526520	CCDS43837.1	c.1883C>A	p.S628Y
TLE4	transducin-like enhancer of split 4 (E(sp1) homolog; Drosophila)	ENSG00000106829	PAP45	73	21.9%	chr9	81527239	CCDS43837.1	c.2040G>T	p.E680D
TF	transferrin	ENSG00000091513	PAP45	165	17.0%	chr3	134960840	CCDS3080.1	c.1180G>T	p.E394X
TFR2	transferrin receptor 2	ENSG00000106327	PAP45	307	22.5%	chr7	100063845	CCDS34707.1	c.1411C>T	p.L471F
TBRG1	transforming growth factor beta regulator 1	ENSG00000154144	PAP45	277	21.3%	chr11	124002142	CCDS8448.1	c.271G>T	p.G91C
TGFB2	transforming growth factor; beta 2	ENSG00000092969	PAP45	146	25.3%	chr1	216674140	CCDS1521.1	c.604G>T	p.D202Y
TGFBR1	transforming growth factor; beta receptor 1	ENSG00000106799	PAP45	80	21.3%	chr9	100940083	CCDS6738.1	c.696G>T	p.K232N
TGFBR1	transforming growth factor; beta receptor 1	ENSG00000106799	PAP45	112	39.3%	chr9	100940109	CCDS6738.1	c.722C>T	p.S241L
TGFBRAP1	transforming growth factor; beta receptor associated protein 1	ENSG00000135966	PAP45	81	23.5%	chr2	105258456	CCDS2067.1	c.1658G>T	p.S553I
TGFBR3	transforming growth factor; beta receptor III	ENSG00000069702	PAP45	150	26.0%	chr1	91950577	CCDS30770.1	c.1977T>G	p.I659M
TACC1	transforming; acidic coiled-coil containing protein 1	ENSG00000147526	PAP45	92	19.6%	chr8	38823399	CCDS6109.1	c.2254C>T	p.R752X
TACC2	transforming; acidic coiled-coil containing protein 2	ENSG00000138162	PAP45	151	23.2%	chr10	123834162	CCDS7626.1	c.2157G>T	p.E719D
TRPC1	transient receptor potential cation channel; subfamily C; member 1	ENSG00000144935	PAP45	77	14.3%	chr3	143982462	CCDS3126.1	c.759C>A	p.N253K
TRPC1	transient receptor potential cation channel; subfamily C; member 1	ENSG00000144935	PAP45	83	20.5%	chr3	144003740	CCDS3126.1	c.1519C>A	p.L507I
TRPC3	transient receptor potential cation channel; subfamily C; member 3	ENSG00000138741	PAP45	108	26.9%	chr4	123048160	CCDS3725.1	c.1586G>T	p.W529L
TRPC4	transient receptor potential cation channel; subfamily C; member 4	ENSG00000133107	PAP45	84	20.2%	chr13	37123510	CCDS9365.1	c.1971C>A	p.F657L
TRPC5	transient receptor potential cation channel; subfamily C; member 5	ENSG00000072315	PAP45	86	29.1%	chrX	110906627	CCDS14561.1	c.2492C>A	p.S831X
TRPM1	transient receptor potential cation channel; subfamily M; member 1	ENSG00000134160	PAP45	172	26.7%	chr15	29126641	CCDS10024.2	c.1663C>T	p.R555W
TRPM2	transient receptor potential cation channel; subfamily M; member 2	ENSG00000142185	PAP45	147	27.9%	chr21	44635714	CCDS13710.1	c.1572G>T	p.E524D
TRPM3	transient receptor potential cation channel; subfamily M; member 3	ENSG00000083067	PAP45	109	12.8%	chr9	72395748	ENST00000396285	c.2747C>A	p.S916Y
TRPM3	transient receptor potential cation channel; subfamily M; member 3	ENSG00000083067	PAP45	218	20.6%	chr9	72588955	CCDS43835.1	c.1034C>T	p.S345L
TRPM5	transient receptor potential cation channel; subfamily M; member 5	ENSG00000070985	PAP45	216	14.4%	chr11	2392757	CCDS31340.1	c.1576G>A	p.V526M
TRPM7	transient receptor potential cation channel; subfamily M; member 7	ENSG00000092439	PAP45	150	24.0%	chr15	48716922	CCDS42035.1	c.821G>T	p.R274I
TRPV5	transient receptor potential cation channel; subfamily V; member 5	ENSG00000127412	PAP45	216	22.2%	chr7	142315976	CCDS5875.1	c.2016G>T	p.E672D
TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	ENSG00000154174	PAP45	94	30.9%	chr3	101583294	CCDS33807.1	c.739C>T	p.R247C
TPR	translocated promoter region (to activated MET oncogene)	ENSG00000047410	PAP45	123	27.6%	chr1	184591415	CCDS41446.1	c.1997T>C	p.I666T
TRAM1	translocation associated membrane protein 1	ENSG00000067167	PAP45	64	26.6%	chr8	71671052	CCDS6207.1	c.485C>T	p.T162I
TM4SF20	transmembrane 4 L six family member 20	ENSG00000168955	PAP45	40	30.0%	chr2	227939198	CCDS2466.1	c.256C>A	p.L86I
TM6SF2	transmembrane 6 superfamily member 2	ENSG00000213996	PAP45	157	28.7%	chr19	19241995	CCDS42528.1	c.388G>A	p.A130T
TM7SF3	transmembrane 7 superfamily member 3	ENSG00000064115	PAP45	219	20.5%	chr12	27039526	CCDS8710.1	c.601C>A	p.L201M
TMCO2	transmembrane and coiled-coil domains 2	ENSG00000188800	PAP45	91	15.4%	chr1	40486269	CCDS30684.1	c.17C>A	p.S6Y
TMCO2	transmembrane and coiled-coil domains 2	ENSG00000188800	PAP45	164	23.2%	chr1	40489639	CCDS30684.1	c.335G>A	p.R112Q
TMIGD1	transmembrane and immunoglobulin domain containing 1	ENSG00000182271	PAP45	204	23.0%	chr17	25676070	CCDS32605.1	c.530C>A	p.S177Y
TMTC1	transmembrane and tetratricopeptide repeat containing 1	ENSG00000133687	PAP45	85	29.4%	chr12	29551066	CCDS8718.1	c.2305C>T	p.R769X
TMTC1	transmembrane and tetratricopeptide repeat containing 1	ENSG00000133687	PAP45	66	24.2%	chr12	29551167	CCDS8718.1	c.2204G>T	p.R735I
TMTC4	transmembrane and tetratricopeptide repeat containing 4	ENSG00000125247	PAP45	33	30.3%	chr13	100106663	CCDS9497.2	c.613C>A	p.L205I
TMC5	transmembrane channel-like 5	ENSG00000103534	PAP45	308	28.9%	chr16	19409384	CCDS10577.1	c.2002A>G	p.I668V
TMPRSS11E	transmembrane protease; serine 11B	ENSG00000185873	PAP45	199	22.6%	chr4	68776297	CCDS3521.1	c.1178A>C	p.K393T
TMPRSS11L	transmembrane protease; serine 11D	ENSG00000153802	PAP45	37	32.4%	chr4	68386567	CCDS3518.1	c.393G>T	p.M131I

TMPRSS15	transmembrane protease; serine 15	ENSG00000154646	PAP45	138	21.0%	chr21	18626310	CCDS13571.1	c.1616C>A	p.S539Y
TMPRSS7	transmembrane protease; serine 7	ENSG00000176040	PAP45	198	31.3%	chr3	113263361	CCDS43129.1	c.535C>T	p.R179X
TMEM120B	transmembrane protein 120B	ENSG00000188735	PAP45	263	21.7%	chr12	120693195	CCDS41852.1	c.-1G>T	p.IVS6-1-1SpliceAcceptor
TMEM123	transmembrane protein 123	ENSG00000152558	PAP45	68	20.6%	chr11	101777595	CCDS41702.1	c.487A>G	p.K163E
TMEM126A	transmembrane protein 126A	ENSG00000171202	PAP45	129	25.6%	chr11	85042831	CCDS8268.1	c.163C>T	p.R55X
TMEM132B	transmembrane protein 132B	ENSG00000139364	PAP45	289	22.8%	chr12	124400180	CCDS41859.1	c.282G>T	p.E94D
TMEM132D	transmembrane protein 132D	ENSG00000151952	PAP45	87	24.1%	chr12	128260040	CCDS9266.1	c.1421C>T	p.S474L
TMEM14B	transmembrane protein 14B	ENSG00000137210	PAP45	156	30.1%	chr6	10857470	CCDS4515.1	c.6G>T	p.E2D
TMEM151B	transmembrane protein 151B	ENSG00000178233	PAP45	216	17.1%	chr6	44351318	NM_001137560	c.777G>T	p.E259D
TMEM168	transmembrane protein 168	ENSG00000146802	PAP45	74	28.4%	chr7	112211219	CCDS5757.1	c.898A>C	p.I300L
TMEM19	transmembrane protein 19	ENSG00000139291	PAP45	319	10.0%	chr12	70377378	CCDS9002.1	c.434A>C	p.E145A
TMEM38A	transmembrane protein 38A	ENSG00000072954	PAP45	55	40.0%	chr19	16651803	CCDS12349.1	c.133G>A	p.E45K
TMEM49	transmembrane protein 49	ENSG00000062716	PAP45	73	27.4%	chr17	55167577	CCDS11619.1	c.173C>A	p.S58Y
TMEM68	transmembrane protein 68	ENSG00000167904	PAP45	158	12.0%	chr8	56837997	CCDS6161.1	c.76G>A	p.E26K
TMEM70	transmembrane protein 70	ENSG00000175606	PAP45	101	26.7%	chr8	75053544	CCDS6215.1	c.-1G>T	p.IVS1-1-1SpliceAcceptor
TMEM71	transmembrane protein 71	ENSG00000165071	PAP45	66	22.7%	chr8	133809247	CCDS6366.1	c.598G>T	p.E200X
TMEM74	transmembrane protein 74	ENSG00000164841	PAP45	187	19.3%	chr8	109866236	CCDS6310.1	c.268A>C	p.N90H
TMEM81	transmembrane protein 81	ENSG00000174529	PAP45	195	27.2%	chr1	203319699	CCDS1450.1	c.373C>T	p.R125X
TMEM87A	transmembrane protein 87A	ENSG00000103978	PAP45	86	11.6%	chr15	40323596	CCDS32205.1	c.566G>A	p.G189D
TNPO3	transportin 3	ENSG00000064419	PAP45	52	23.1%	chr7	128424794	CCDS5809.1	c.1043G>A	p.R348Q
TREH	trehalase (brush-border membrane glycoprotein)	ENSG00000118094	PAP45	208	25.0%	chr11	118038869	ENST00000264029	c.354G>T	p.K118N
TREM1	triggering receptor expressed on myeloid cells 1	ENSG00000124731	PAP45	291	26.5%	chr6	41358222	CCDS4854.1	c.295C>T	p.R99X
TNRC6A	trinucleotide repeat containing 6A	ENSG00000090905	PAP45	123	29.3%	chr16	24709505	CCDS10624.2	c.2041C>T	p.R681C
TNRC6A	trinucleotide repeat containing 6A	ENSG00000090905	PAP45	129	24.8%	chr16	24709939	CCDS10624.2	c.2475G>T	p.E825D
TRIML2	tripartite motif family-like 2	ENSG00000179046	PAP45	453	24.1%	chr4	189249948	CCDS3850.1	c.737C>T	p.A246V
TRIM24	tripartite motif-containing 24	ENSG00000122779	PAP45	166	25.9%	chr7	137889986	CCDS5847.1	c.1265C>A	p.S422Y
TRIM3	tripartite motif-containing 3	ENSG00000110171	PAP45	230	29.1%	chr11	6434708	CCDS7764.1	c.824G>A	p.R275Q
TRIM32	tripartite motif-containing 32	ENSG00000119401	PAP45	168	23.8%	chr9	118501022	CCDS6817.1	c.1180C>T	p.R394C
TRIM36	tripartite motif-containing 36	ENSG00000152503	PAP45	85	17.6%	chr5	114490143	CCDS4115.1	c.2143G>T	p.E715X
TRIM36	tripartite motif-containing 36	ENSG00000152503	PAP45	141	30.5%	chr5	114497488	CCDS4115.1	c.1502G>T	p.R501I
TRIM36	tripartite motif-containing 36	ENSG00000152503	PAP45	74	29.7%	chr5	114527128	CCDS4115.1	c.284G>A	p.R95Q
TRIM44	tripartite motif-containing 44	ENSG00000166326	PAP45	268	26.5%	chr11	35641737	CCDS31461.1	c.502G>T	p.E168X
TRIM50	tripartite motif-containing 50	ENSG00000146755	PAP45	72	22.2%	chr7	72365026	CCDS34654.1	c.1291G>A	p.D431N
TRIM54	tripartite motif-containing 54	ENSG00000138100	PAP45	110	19.1%	chr2	27359202	CCDS1745.2	c.99C>A	p.F33L
TRIM55	tripartite motif-containing 55	ENSG00000147573	PAP45	128	25.8%	chr8	67228909	CCDS6184.1	c.1310C>T	p.A437V
TRIM6	tripartite motif-containing 6	ENSG00000121236	PAP45	420	29.0%	chr11	5589094	CCDS31389.1	c.1497T>G	p.Y499X
TRIM62	tripartite motif-containing 62	ENSG00000116525	PAP45	52	32.7%	chr1	33419320	CCDS376.1	c.301C>A	p.L101I
TRIM7	tripartite motif-containing 7	ENSG00000146054	PAP45	122	20.5%	chr5	180558333	CCDS4462.1	c.951G>T	p.K317N
TRIM8	tripartite motif-containing 8	ENSG00000171206	PAP45	62	30.6%	chr10	104394374	CCDS31274.1	c.10A>C	p.N4H
TPP1	tripeptidyl peptidase I	ENSG00000166340	PAP45	274	28.1%	chr11	6595510	CCDS7770.1	c.303A>C	p.K101N
TRIO	triple functional domain (PTPRF interacting)	ENSG00000038382	PAP45	190	22.1%	chr5	14344169	CCDS3883.1	c.885G>T	p.K295N
TRIO	triple functional domain (PTPRF interacting)	ENSG00000038382	PAP45	62	30.6%	chr5	14440901	CCDS3883.1	c.3826C>T	p.R1276X
TRIO	triple functional domain (PTPRF interacting)	ENSG00000038382	PAP45	139	15.8%	chr5	14452069	CCDS3883.1	c.4504C>T	p.R1502X
TRO	trophinin	ENSG00000067445	PAP45	176	17.6%	chrX	54966741	CCDS43959.1	c.1051C>T	p.R351W
TPM3	tropomyosin 3	ENSG00000143549	PAP45	98	22.4%	chr1	152409799	CCDS41403.1	c.655G>T	p.E219X
TNNI1	troponin I type 1 (skeletal; slow)	ENSG00000159173	PAP45	116	31.9%	chr1	199650315	CCDS1411.1	c.143G>A	p.R48H
TNNI2	troponin I type 2 (skeletal; fast)	ENSG00000130598	PAP45	121	27.3%	chr11	1818402	CCDS31333.1	c.126G>T	p.Q42H
TNNT2	troponin T type 2 (cardiac)	ENSG00000118194	PAP45	100	27.0%	chr1	199601042	CCDS30970.1	c.311G>A	p.R104H
TNNT3	troponin T type 3 (skeletal; fast)	ENSG00000130595	PAP45	173	26.0%	chr11	1912214	CCDS7727.1	c.443C>A	p.S148Y
TDO2	tryptophan 2;3-dioxygenase	ENSG00000151790	PAP45	88	20.5%	chr4	157045738	CCDS34086.1	c.211C>A	p.L71I

TPH2	tryptophan hydroxylase 2	ENSG00000139287	PAP45	73	23.3%	chr12	70702464	CCDS31859.1	c.1087G>A	p.E363K
WARS2	tryptophanyl tRNA synthetase 2; mitochondrial	ENSG00000116874	PAP45	194	30.4%	chr1	119377299	CCDS900.1	c.841G>A	p.A281T
TSC22D1	TSC22 domain family; member 1	ENSG00000102804	PAP45	148	20.9%	chr13	44047890	CCDS31966.1	c.321G>T	p.K107N
TUB	tubby homolog (mouse)	ENSG00000166402	PAP45	200	30.5%	chr11	8017038	CCDS7786.1	c.42C>A	p.F14L
TULP4	tubby like protein 4	ENSG00000130338	PAP45	180	15.0%	chr6	158655120	CCDS34561.1	c.84G>T	p.K28N
TSC1	tuberous sclerosis 1	ENSG00000165699	PAP45	129	23.3%	chr9	134767992	CCDS6956.1	c.2212G>T	p.D738Y
TSC1	tuberous sclerosis 1	ENSG00000165699	PAP45	137	29.2%	chr9	134786625	CCDS6956.1	c.683G>A	p.R228Q
TPPP2	tubulin polymerization-promoting protein family member 2	ENSG00000179636	PAP45	63	19.0%	chr14	20568664	CCDS9566.1	c.84G>T	p.K28N
TTLL11	tubulin tyrosine ligase-like family; member 11	ENSG00000175764	PAP45	437	10.1%	chr9	123791228	CCDS6834.2	c.1606C>T	p.R536C
TTLL6	tubulin tyrosine ligase-like family; member 6	ENSG00000170703	PAP45	193	20.7%	chr17	44202239	CCDS11537.1	c.1294G>A	p.E432K
TUBA4A	tubulin; alpha 4a	ENSG00000127824	PAP45	221	23.5%	chr2	219824118	CCDS2438.1	c.547G>A	p.E183K
TUBAL3	tubulin; alpha-like 3	ENSG00000178462	PAP45	211	28.0%	chr10	5426181	CCDS7066.1	c.640G>A	p.E214K
TUBAL3	tubulin; alpha-like 3	ENSG00000178462	PAP45	193	21.8%	chr10	5426270	CCDS7066.1	c.551T>C	p.I184T
TUBB2B	tubulin; beta 2B	ENSG00000137285	PAP45	147	24.5%	chr6	3171487	CCDS4485.1	c.182C>T	p.P61L
TUBB3	tubulin; beta 3	ENSG00000198211	PAP45	287	29.3%	chr16	88526480	CCDS10988.1	c.58T>C	p.F20L
TUBGCP2	tubulin; gamma complex associated protein 2	ENSG00000130640	PAP45	186	29.0%	chr10	134956042	CCDS7676.1	c.1165G>A	p.E389K
TUBGCP5	tubulin; gamma complex associated protein 5	ENSG00000153575	PAP45	70	25.7%	chr15	20387397	CCDS10008.1	c.187A>C	p.K63Q
TINAGL1	tubulointerstitial nephritis antigen-like 1	ENSG00000142910	PAP45	402	26.9%	chr1	31823138	CCDS343.1	c.771G>T	p.Q257H
TDRD6	tudor domain containing 6	ENSG00000180113	PAP45	265	23.8%	chr6	46764926	CCDS34470.1	c.1102C>T	p.R368X
TDRD6	tudor domain containing 6	ENSG00000180113	PAP45	86	23.3%	chr6	46768300	CCDS34470.1	c.4476T>G	p.I1492M
TDRD9	tudor domain containing 9	ENSG00000156414	PAP45	68	20.6%	chr14	103511512	CCDS9987.1	c.25G>A	p.E9K
TNFSF11	tumor necrosis factor (ligand) superfamily; member 11	ENSG00000120659	PAP45	199	23.1%	chr13	42072924	CCDS9384.1	c.424G>T	p.A142S
TNFSF13B	tumor necrosis factor (ligand) superfamily; member 13b	ENSG00000102524	PAP45	94	21.3%	chr13	107753664	CCDS9509.1	c.544G>T	p.E182X
TNFRSF14	tumor necrosis factor receptor superfamily; member 14 (herpesvirus entry mediator)	ENSG00000157873	PAP45	111	22.5%	chr1	2481297	NM_003820	c.561G>A	p.W187X
TPD52L1	tumor protein D52-like 1	ENSG00000111907	PAP45	105	28.6%	chr6	125592035	CCDS5130.1	c.208A>C	p.K70Q
TP53	tumor protein p53	ENSG00000141510	PAP45	233	19.3%	chr17	7519132	CCDS11118.1	c.523C>T	p.R175C
TP53BP1	tumor protein p53 binding protein 1	ENSG00000067369	PAP45	48	20.8%	chr15	41571881	CCDS10096.1	c.70G>A	p.D24N
TP63	tumor protein p63	ENSG00000073282	PAP45	385	21.0%	chr3	191094772	CCDS3293.1	c.1830C>A	p.F610L
TACSTD2	tumor-associated calcium signal transducer 2	ENSG00000184292	PAP45	151	29.1%	chr1	58814875	CCDS609.1	c.542G>A	p.R181H
TTYH1	tweety homolog 1 (Drosophila)	ENSG00000167614	PAP45	324	24.4%	chr19	59622174	CCDS33106.1	c.187G>A	p.A63T
TWISTNB	TWIST neighbor	ENSG00000105849	PAP45	344	23.0%	chr7	19706278	CCDS34606.1	c.547C>T	p.R183C
TYR	tyrosinase (oculocutaneous albinism IA)	ENSG00000077498	PAP45	97	29.9%	chr11	88564031	CCDS8284.1	c.833G>A	p.R278Q
TH	tyrosine hydroxylase	ENSG00000180176	PAP45	94	27.7%	chr11	2146419	CCDS7731.1	c.458G>A	p.R153Q
TH	tyrosine hydroxylase	ENSG00000180176	PAP45	86	29.1%	chr11	2147631	CCDS7731.1	c.230G>A	p.R77H
TYK2	tyrosine kinase 2	ENSG00000105397	PAP45	140	10.7%	chr19	10338232	CCDS12236.1	c.490G>A	p.V164M
UBAP2	ubiquitin associated protein 2	ENSG00000137073	PAP45	57	21.1%	chr9	33978974	CCDS6547.1	c.439G>T	p.E147X
UIMC1	ubiquitin interaction motif containing 1	ENSG00000087206	PAP45	330	21.8%	chr5	176328657	CCDS4408.1	c.705A>C	p.E235D
UBR2	ubiquitin protein ligase E3 component n-recognin 2	ENSG00000024048	PAP45	90	23.3%	chr6	42690847	CCDS4870.1	c.1046C>A	p.S349Y
UBR4	ubiquitin protein ligase E3 component n-recognin 4	ENSG00000127481	PAP45	635	30.9%	chr1	19280722	ENST00000375225	c.166C>A	p.L56I
UBR4	ubiquitin protein ligase E3 component n-recognin 4	ENSG00000127481	PAP45	176	27.3%	chr1	19397071	CCDS189.1	c.708G>T	p.K236N
UBR5	ubiquitin protein ligase E3 component n-recognin 5	ENSG00000104517	PAP45	173	24.9%	chr8	103380349	CCDS34933.1	c.3229G>T	p.E1077X
UBR5	ubiquitin protein ligase E3 component n-recognin 5	ENSG00000104517	PAP45	313	27.5%	chr8	103395255	CCDS34933.1	c.1960C>T	p.R654W
UBE3A	ubiquitin protein ligase E3A	ENSG00000114062	PAP45	168	19.6%	chr15	23167153	CCDS32177.1	c.1201C>T	p.R401X
UBE3A	ubiquitin protein ligase E3A	ENSG00000114062	PAP45	113	15.9%	chr15	23171719	CCDS32177.1	c.287G>T	p.R96I
USP13	ubiquitin specific peptidase 13 (isopeptidase T-3)	ENSG00000058056	PAP45	112	23.2%	chr3	180922000	CCDS3235.1	c.1017G>T	p.K339N
USP16	ubiquitin specific peptidase 16	ENSG00000156256	PAP45	84	22.6%	chr21	29324915	CCDS13583.1	c.190G>T	p.E64X
USP16	ubiquitin specific peptidase 16	ENSG00000156256	PAP45	178	11.2%	chr21	29341441	CCDS13583.1	c.1939C>T	p.R647X
USP26	ubiquitin specific peptidase 26	ENSG00000134588	PAP45	82	26.8%	chrX	131987818	CCDS14635.1	c.2097G>T	p.K699N
USP26	ubiquitin specific peptidase 26	ENSG00000134588	PAP45	199	18.6%	chrX	131989249	CCDS14635.1	c.666G>T	p.L222F
USP28	ubiquitin specific peptidase 28	ENSG00000048028	PAP45	64	21.9%	chr11	113230201	CCDS31680.1	c.124G>T	p.E42X
USP29	ubiquitin specific peptidase 29	ENSG00000131864	PAP45	199	29.1%	chr19	62334017	CCDS33124.1	c.2162A>G	p.N721S
USP32	ubiquitin specific peptidase 32	ENSG00000170832	PAP45	69	23.2%	chr17	55654629	CCDS32697.1	c.1672G>T	p.D558Y
USP34	ubiquitin specific peptidase 34	ENSG00000115464	PAP45	302	26.2%	chr2	61269117	CCDS42686.1	c.10265C>T	p.S3422L

USP47	ubiquitin specific peptidase 47	ENSG00000170242	PAP45	146	28.8%	chr11	11862652	CCDS41619.1	c.102G>T	p.K34N
USP49	ubiquitin specific peptidase 49	ENSG00000164663	PAP45	86	22.1%	chr6	41879698	CCDS4861.1	c.1385C>A	p.S462Y
USP51	ubiquitin specific peptidase 51	ENSG00000185295	PAP45	120	19.2%	chrX	55529992	NM_201286	c.2106C>A	p.F702L
USP51	ubiquitin specific peptidase 51	ENSG00000185295	PAP45	198	28.3%	chrX	55530278	NM_201286	c.1820G>A	p.R607Q
USP53	ubiquitin specific peptidase 53	ENSG00000145390	PAP45	200	32.5%	chr4	120433095	CCDS43265.1	c.2503A>C	p.N835H
USP53	ubiquitin specific peptidase 53	ENSG00000145390	PAP45	299	14.4%	chr4	120433268	CCDS43265.1	c.2676G>T	p.E892D
USP54	ubiquitin specific peptidase 54	ENSG00000166348	PAP45	163	11.0%	chr10	74971469	CCDS7329.2	c.606G>T	p.E202D
USP7	ubiquitin specific peptidase 7 (herpes virus-associated)	ENSG00000187555	PAP45	218	11.0%	chr16	8899761	CCDS32385.1	c.2675G>A	p.R892Q
USP9X	ubiquitin specific peptidase 9; X-linked	ENSG00000124486	PAP45	56	19.6%	chrX	40887578	CCDS43930.1	c.1252C>T	p.R418C
USPL1	ubiquitin specific peptidase like 1	ENSG00000132952	PAP45	132	27.3%	chr13	30125412	CCDS9336.1	c.1366C>A	p.H456N
UBE4A	ubiquitination factor E4A (UFD2 homolog; yeast)	ENSG00000110344	PAP45	263	10.6%	chr11	117748502	CCDS8396.1	c.632G>A	p.R211Q
UBE4A	ubiquitination factor E4A (UFD2 homolog; yeast)	ENSG00000110344	PAP45	36	33.3%	chr11	117752541	CCDS8396.1	c.1514C>T	p.P505L
UBE2E1	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog; yeast)	ENSG00000170142	PAP45	57	17.5%	chr3	23904153	CCDS2638.1	c.295G>A	p.D99N
UBL3	ubiquitin-like 3	ENSG00000122042	PAP45	184	27.2%	chr13	29244273	CCDS9334.1	c.199C>A	p.L67I
UBLCP1	ubiquitin-like domain containing CTD phosphatase 1	ENSG00000164332	PAP45	120	25.0%	chr5	158637874	CCDS4345.1	c.735G>T	p.K245N
UBA6	ubiquitin-like modifier activating enzyme 6	ENSG00000033178	PAP45	122	13.1%	chr4	68172503	CCDS3516.1	c.2776C>A	p.L926I
UHRF2	ubiquitin-like with PHD and ring finger domains 2	ENSG00000147854	PAP45	151	19.2%	chr9	6424047	CCDS6469.1	c.518G>T	p.R173M
UBXN4	UBX domain protein 4	ENSG00000144224	PAP45	109	17.4%	chr2	136244746	CCDS42761.1	c.793C>T	p.R265X
UBXN7	UBX domain protein 7	ENSG00000163960	PAP45	229	10.0%	chr3	197568044	CCDS43191.1	c.1379G>A	p.R460Q
UGT1A6	UDP glucuronosyltransferase 1 family; polypeptide A6	ENSG00000167165	PAP45	256	23.8%	chr2	234266803	CCDS2507.1	c.414C>A	p.F138L
UGT3A1	UDP glycosyltransferase 3 family; polypeptide A1	ENSG00000145626	PAP45	129	24.8%	chr5	36001410	CCDS3913.1	c.678G>T	p.K226N
B3GALT1	UDP-Gal:betaGlcNAc beta 1;3-galactosyltransferase; polypeptide 1	ENSG00000172318	PAP45	86	23.3%	chr2	168434058	CCDS2227.1	c.263A>G	p.H88R
B3GNT7	UDP-GlcNAc:betaGal beta-1;3-N-acetylglucosaminyltransferase 7	ENSG00000156966	PAP45	79	24.1%	chr2	231971856	NM_145236	c.1182C>A	p.C394X
UGDH	UDP-glucose 6-dehydrogenase	ENSG00000109814	PAP45	150	20.0%	chr4	39187807	CCDS3455.1	c.779G>T	p.R260I
UGDH	UDP-glucose 6-dehydrogenase	ENSG00000109814	PAP45	235	25.5%	chr4	39188792	CCDS3455.1	c.349G>T	p.V117L
UGDH	UDP-glucose 6-dehydrogenase	ENSG00000109814	PAP45	115	13.0%	chr4	39199388	CCDS3455.1	c.140C>A	p.S47Y
UGGT1	UDP-glucose glycoprotein glucosyltransferase 1	ENSG00000136731	PAP45	74	13.5%	chr2	128607252	CCDS2154.1	c.1445G>A	p.R482Q
UGP2	UDP-glucose pyrophosphorylase 2	ENSG00000169764	PAP45	59	23.7%	chr2	63967109	CCDS1875.1	c.1004C>T	p.S335F
GALNT13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)	ENSG00000144278	PAP45	48	27.1%	chr2	154807510	CCDS2199.1	c.532A>C	p.K178Q
GALNT13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)	ENSG00000144278	PAP45	124	24.2%	chr2	154810701	CCDS2199.1	c.817G>T	p.E273X
GALNT3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)	ENSG00000115339	PAP45	66	37.9%	chr2	166319794	CCDS2226.1	c.1418G>T	p.R473I
GALNT5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5)	ENSG00000136542	PAP45	93	25.8%	chr2	157823699	CCDS2203.1	c.859C>T	p.R287C
GALNT5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5)	ENSG00000136542	PAP45	81	19.8%	chr2	157861149	CCDS2203.1	c.-1T>G	p.IVS4-3-1SpliceAcceptor
GALNT7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)	ENSG00000109586	PAP45	50	32.0%	chr4	174453185	CCDS3815.1	c.818G>A	p.R273Q
GALNT8	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8)	ENSG00000130035	PAP45	164	26.2%	chr12	4700135	CCDS8533.1	c.31C>A	p.L11I
GALNTL6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 6	ENSG00000174473	PAP45	156	28.8%	chr4	173469468	CCDS34104.1	c.376C>A	p.R126S
UAP1	UDP-N-acteylglucosamine pyrophosphorylase 1	ENSG00000117143	PAP45	84	21.4%	chr1	160825216	CCDS1240.1	c.1138A>C	p.K380Q
UHRF1BP1L	UHRF1 binding protein 1-like	ENSG00000111647	PAP45	36	30.6%	chr12	98976130	CCDS31882.1	c.3056T>G	p.I1019R
UNC13B	unc-13 homolog B (C. elegans)	ENSG00000198722	PAP45	164	24.4%	chr9	35367584	CCDS6579.1	c.1708C>T	p.R570W
UNC5A	unc-5 homolog A (C. elegans)	ENSG00000113763	PAP45	187	28.3%	chr5	176238195	CCDS34299.1	c.2133G>A	p.W711X
UNC5D	unc-5 homolog D (C. elegans)	ENSG00000156687	PAP45	76	32.9%	chr8	35708117	CCDS6093.1	c.1712C>A	p.S571Y
UCP2	uncoupling protein 2 (mitochondrial; proton carrier)	ENSG00000175567	PAP45	204	27.0%	chr11	73366598	CCDS8228.1	c.318C>A	p.F106L
UNG	uracil-DNA glycosylase	ENSG00000076248	PAP45	96	20.8%	chr12	108024141	CCDS9124.1	c.487C>A	p.H163N

URB1	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	ENSG00000142207	PAP45	135	23.0%	chr21	32619552	NM_014825	c.4979G>A	p.R1660Q
URB2	URB2 ribosome biogenesis 2 homolog (S. cerevisiae)	ENSG00000135763	PAP45	113	29.2%	chr1	227839025	CCDS31052.1	c.2042A>C	p.K681T
UPB1	ureidopropionase; beta	ENSG00000100024	PAP45	489	11.5%	chr22	23228307	ENST00000382760	c.367C>A	p.L123I
UROC1	urocanase domain containing 1	ENSG00000159650	PAP45	195	24.6%	chr3	127699626	CCDS3038.1	c.1396G>A	p.E466K
UROD	uroporphyrinogen decarboxylase	ENSG00000126088	PAP45	177	10.2%	chr1	45251440	CCDS518.1	c.179G>A	p.R60H
UTS2D	urotensin 2 domain containing	ENSG00000188958	PAP45	95	22.1%	chr3	192477301	CCDS3300.1	c.229G>T	p.E77X
USHBP1	Usher syndrome 1C binding protein 1	ENSG00000130307	PAP45	500	27.0%	chr19	17234555	CCDS12353.1	c.448G>A	p.E150K
USH1G	Usher syndrome 1G (autosomal recessive)	ENSG00000182040	PAP45	241	10.8%	chr17	70427872	CCDS32725.1	c.654G>T	p.K218N
USH2A	Usher syndrome 2A (autosomal recessive; mild)	ENSG00000042781	PAP45	328	24.7%	chr1	213915302	CCDS31025.1	c.12574C>T	p.R4192C
USH2A	Usher syndrome 2A (autosomal recessive; mild)	ENSG00000042781	PAP45	132	27.3%	chr1	214118768	CCDS31025.1	c.8519C>A	p.S2840Y
USH2A	Usher syndrome 2A (autosomal recessive; mild)	ENSG00000042781	PAP45	214	27.6%	chr1	214128468	CCDS31025.1	c.8146G>T	p.E2716X
USH2A	Usher syndrome 2A (autosomal recessive; mild)	ENSG00000042781	PAP45	57	19.3%	chr1	214286494	CCDS31025.1	c.6227A>G	p.N2076S
USH2A	Usher syndrome 2A (autosomal recessive; mild)	ENSG00000042781	PAP45	243	23.9%	chr1	214486786	CCDS31025.1	c.2573C>A	p.S858Y
USO1	USO1 vesicle docking protein homolog (yeast)	ENSG00000138768	PAP45	48	20.8%	chr4	76911050	ENST00000264904	c.403T>G	p.L135V
USO1	USO1 vesicle docking protein homolog (yeast)	ENSG00000138768	PAP45	219	17.4%	chr4	76944378	ENST00000264904	c.2009C>T	p.T670M
UTP20	UTP20; small subunit (SSU) processome component; homolog (yeast)	ENSG00000120800	PAP45	42	35.7%	chr12	100220457	CCDS9081.1	c.1776A>C	p.L592F
UTRN	utrophin	ENSG00000152818	PAP45	103	24.3%	chr6	144810534	CCDS34547.1	c.1826A>C	p.K609T
UTRN	utrophin	ENSG00000152818	PAP45	165	25.5%	chr6	144902175	CCDS34547.1	c.6422G>T	p.R2141I
UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats	ENSG00000137831	PAP45	99	23.2%	chr15	68747645	CCDS10235.1	c.2432A>C	p.K811T
ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg; Abelson-related gene)	ENSG00000143322	PAP45	142	23.2%	chr1	177345046	CCDS30947.1	c.1979G>T	p.R660I
VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	ENSG00000197969	PAP45	80	23.8%	chr9	79161522	CCDS6655.1	c.7725G>T	p.E2575D
VPS13B	vacuolar protein sorting 13 homolog B (yeast)	ENSG00000132549	PAP45	119	21.0%	chr8	100216518	CCDS6280.1	c.1402G>A	p.E468K
VPS13B	vacuolar protein sorting 13 homolog B (yeast)	ENSG00000132549	PAP45	182	29.1%	chr8	100657116	CCDS6280.1	c.5079T>G	p.F1693L
VPS13B	vacuolar protein sorting 13 homolog B (yeast)	ENSG00000132549	PAP45	76	21.1%	chr8	100781004	CCDS6280.1	c.6197T>A	p.F2066Y
VPS13B	vacuolar protein sorting 13 homolog B (yeast)	ENSG00000132549	PAP45	102	23.5%	chr8	100935212	CCDS6280.1	c.10494G>T	p.K3498N
VPS13C	vacuolar protein sorting 13 homolog C (S. cerevisiae)	ENSG00000129003	PAP45	50	22.0%	chr15	59991455	CCDS32257.1	c.8591G>A	p.R2864Q
VPS13C	vacuolar protein sorting 13 homolog C (S. cerevisiae)	ENSG00000129003	PAP45	65	26.2%	chr15	60053785	CCDS32257.1	c.2532G>T	p.E844D
VPS16	vacuolar protein sorting 16 homolog (S. cerevisiae)	ENSG00000215305	PAP45	357	24.1%	chr20	2789453	CCDS13036.1	c.574C>A	p.L192I
VPS18	vacuolar protein sorting 18 homolog (S. cerevisiae)	ENSG00000104142	PAP45	185	28.6%	chr15	38978685	CCDS10069.1	c.377G>A	p.R126Q
VPS33A	vacuolar protein sorting 33 homolog A (S. cerevisiae)	ENSG00000139719	PAP45	131	19.8%	chr12	121311838	CCDS9231.1	c.406C>A	p.H136N
VPS33B	vacuolar protein sorting 33 homolog B (yeast)	ENSG00000184056	PAP45	213	26.3%	chr15	89352173	CCDS10369.1	c.429C>A	p.F143L
VCPIP1	valosin containing protein (p97)/p47 complex interacting protein 1	ENSG00000175073	PAP45	155	23.2%	chr8	67726328	CCDS6192.1	c.2716G>A	p.D906N
VCPIP1	valosin containing protein (p97)/p47 complex interacting protein 1	ENSG00000175073	PAP45	498	15.5%	chr8	67740163	CCDS6192.1	c.1585G>A	p.D529N
VNN1	vanin 1	ENSG00000112299	PAP45	142	32.4%	chr6	133056853	CCDS5159.1	c.503C>A	p.S168Y
VEGFC	vascular endothelial growth factor C	ENSG00000150630	PAP45	115	11.3%	chr4	177845555	CCDS43285.1	c.925G>T	p.E309X
VAV1	vav 1 guanine nucleotide exchange factor	ENSG00000141968	PAP45	52	21.2%	chr19	6771722	CCDS12174.1	c.214C>A	p.L72I
VENTX	VENT homeobox homolog (Xenopus laevis)	ENSG00000151650	PAP45	334	26.9%	chr10	134903447	CCDS7675.1	c.424C>T	p.R142C
ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	ENSG00000178568	PAP45	399	27.1%	chr2	211956688	CCDS2394.1	c.3824G>A	p.R1275Q
ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	ENSG00000178568	PAP45	187	18.2%	chr2	211959840	CCDS2394.1	c.3464G>A	p.R1155Q
ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	ENSG00000178568	PAP45	47	29.8%	chr2	212203444	CCDS2394.1	c.2067C>A	p.F689L
ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	ENSG00000178568	PAP45	88	31.8%	chr2	212275070	CCDS2394.1	c.1356A>C	p.E452D
ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	ENSG00000065361	PAP45	124	28.2%	chr12	54782099	CCDS31833.1	c.4022G>T	p.R1341I
VCAN	versican	ENSG00000038427	PAP45	197	23.4%	chr5	82851011	CCDS4060.1	c.1130G>T	p.R377I
VCAN	versican	ENSG00000038427	PAP45	278	13.3%	chr5	82853469	CCDS4060.1	c.3588T>G	p.F1196L

VCAN	versican	ENSG00000038427	PAP45	206	19.4%	chr5	82869859	CCDS4060.1	c.5281G>T	p.V1761L
VCAN	versican	ENSG00000038427	PAP45	110	25.5%	chr5	82870903	CCDS4060.1	c.6325G>T	p.E2109X
VCAN	versican	ENSG00000038427	PAP45	49	26.5%	chr5	82885005	CCDS4060.1	c.9560G>A	p.R3187Q
VLDLR	very low density lipoprotein receptor	ENSG00000147852	PAP45	122	23.0%	chr9	2641470	CCDS6446.1	c.2307T>G	p.I769M
VIM	vimentin	ENSG00000026025	PAP45	121	27.3%	chr10	17311808	CCDS7120.1	c.381G>T	p.Q127H
VCL	vinculin	ENSG00000035403	PAP45	143	27.3%	chr10	75504620	CCDS7341.1	c.736C>T	p.R246C
VIT	vitrin	ENSG00000205221	PAP45	221	31.2%	chr2	36886116	CCDS33180.1	c.1194C>A	p.F398L
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	ENSG00000178573	PAP45	124	20.2%	chr16	78185914	CCDS10928.1	c.1156T>C	p.Y386H
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	ENSG00000178573	PAP45	367	16.6%	chr16	78190363	CCDS10928.1	c.938G>T	p.R313I
VWF	von Willebrand factor	ENSG00000110799	PAP45	97	11.3%	chr12	6089972	CCDS8539.1	c.361G>T	p.E121X
VWF	von Willebrand factor	ENSG00000110799	PAP45	329	26.1%	chr12	6102284	ENST00000321023	c.34G>T	p.D12Y
VWA3B	von Willebrand factor A domain containing 3B	ENSG00000168658	PAP45	88	18.2%	chr2	98116753	CCDS42718.1	c.907G>T	p.E303X
VWA3B	von Willebrand factor A domain containing 3B	ENSG00000168658	PAP45	130	36.2%	chr2	98219570	CCDS42718.1	c.2618G>A	p.S873N
VIPAR	VPS33B interacting protein; apical-basolateral polarity regulator	ENSG00000151445	PAP45	94	13.8%	chr14	76978731	CCDS9862.1	c.659G>A	p.R220Q
RELA	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	ENSG00000173039	PAP45	228	20.6%	chr11	65186102	CCDS31609.1	c.68T>G	p.I23S
VSIG4	V-set and immunoglobulin domain containing 4	ENSG00000155659	PAP45	210	11.9%	chrX	65169227	CCDS14383.1	c.502C>T	p.R168W
WFDC8	WAP four-disulfide core domain 8	ENSG00000158901	PAP45	300	21.3%	chr20	43614174	CCDS13361.1	c.631A>G	p.I211V
WFDC8	WAP four-disulfide core domain 8	ENSG00000158901	PAP45	169	23.7%	chr20	43620995	CCDS13361.1	c.187C>A	p.P63T
WFIKKN2	WAP; follistatin/kazal; immunoglobulin; kunitz and netrin domain containing 2	ENSG00000173714	PAP45	123	26.0%	chr17	46273320	CCDS11575.1	c.1672C>T	p.R558C
WASF1	WAS protein family; member 1	ENSG00000112290	PAP45	73	32.9%	chr6	110529799	CCDS5080.1	c.1207G>T	p.A403S
WDFY3	WD repeat and FYVE domain containing 3	ENSG00000163625	PAP45	268	14.6%	chr4	85813127	CCDS3609.1	c.10499C>A	p.S3500X
WDFY3	WD repeat and FYVE domain containing 3	ENSG00000163625	PAP45	100	16.0%	chr4	85969296	CCDS3609.1	c.841G>A	p.E281K
WDR13	WD repeat domain 13	ENSG00000101940	PAP45	94	21.3%	chrX	48341175	ENST00000344046	c.319C>T	p.R107C
WDR16	WD repeat domain 16	ENSG00000166596	PAP45	146	19.9%	chr17	9430828	CCDS11149.2	c.359C>A	p.S120Y
WDR26	WD repeat domain 26	ENSG00000162923	PAP45	140	27.1%	chr1	222665821	CCDS31037.1	c.648C>A	p.F216L
WDR35	WD repeat domain 35	ENSG00000118965	PAP45	320	25.3%	chr2	19976848	CCDS33152.1	c.3498A>C	p.E1166D
WDR35	WD repeat domain 35	ENSG00000118965	PAP45	97	27.8%	chr2	20001099	CCDS33152.1	c.2186A>C	p.K729T
WDR43	WD repeat domain 43	ENSG00000163811	PAP45	85	23.5%	chr2	29004032	NM_015131	c.1267G>A	p.E423K
WDR43	WD repeat domain 43	ENSG00000163811	PAP45	82	20.7%	chr2	29004045	NM_015131	c.1280G>A	p.S427N
WDR45	WD repeat domain 45	ENSG00000196998	PAP45	99	32.3%	chrX	48820034	CCDS14318.1	c.763G>A	p.A255T
WDR49	WD repeat domain 49	ENSG00000174776	PAP45	90	18.9%	chr3	168755281	CCDS3201.1	c.-1G>T	p.IVS4-1-1SpliceAcceptor
WDR5	WD repeat domain 5	ENSG00000196363	PAP45	149	16.1%	chr9	136003268	CCDS6981.1	c.566G>T	p.S189I
WDR52	WD repeat domain 52	ENSG00000206530	PAP45	39	33.3%	chr3	114564840	CCDS2972.1	c.2776G>A	p.E926K
WDR53	WD repeat domain 53	ENSG00000185798	PAP45	224	24.6%	chr3	197765892	CCDS3318.1	c.664C>T	p.R222X
WDR55	WD repeat domain 55	ENSG00000120314	PAP45	226	22.6%	chr5	140028225	CCDS4235.1	c.334G>T	p.D112Y
WDR5B	WD repeat domain 5B	ENSG00000196981	PAP45	208	18.8%	chr3	123616384	CCDS3012.1	c.682G>A	p.A228T
WDR6	WD repeat domain 6	ENSG00000178252	PAP45	265	14.3%	chr3	49025802	CCDS2782.1	c.1831C>T	p.R611X
WDR63	WD repeat domain 63	ENSG00000162643	PAP45	103	23.3%	chr1	85324218	CCDS702.1	c.657A>C	p.K219N
WDR64	WD repeat domain 64	ENSG00000162843	PAP45	120	21.7%	chr1	239987325	CCDS1619.1	c.1018G>A	p.A340T
WDR66	WD repeat domain 66	ENSG00000158023	PAP45	211	21.3%	chr12	120856603	CCDS41853.1	c.956A>G	p.K319R
WDR66	WD repeat domain 66	ENSG00000158023	PAP45	72	29.2%	chr12	120897617	CCDS41853.1	c.2856C>A	p.F952L
WDR67	WD repeat domain 67	ENSG00000156787	PAP45	86	24.4%	chr8	124165679	CCDS6338.1	c.437C>A	p.S146Y
WDR69	WD repeat domain 69	ENSG00000123977	PAP45	132	25.0%	chr2	228462878	CCDS2470.1	c.176G>A	p.R59Q
WDR7	WD repeat domain 7	ENSG00000091157	PAP45	117	26.5%	chr18	52839034	CCDS11962.1	c.4225C>A	p.L1409I
WDR78	WD repeat domain 78	ENSG00000152763	PAP45	120	20.8%	chr1	67078859	CCDS635.1	c.1375G>T	p.E459X
WDR91	WD repeat domain 91	ENSG00000105875	PAP45	166	28.9%	chr7	134521598	CCDS34758.1	c.2089G>A	p.D697N
WDR93	WD repeat domain 93	ENSG00000140527	PAP45	56	37.5%	chr15	88046276	CCDS32326.1	c.295G>T	p.E99X
WRN	Werner syndrome; RecQ helicase-like	ENSG00000165392	PAP45	108	19.4%	chr8	31067946	CCDS6082.1	c.1775G>A	p.G592D

WIZ	widely interspaced zinc finger motifs	ENSG00000011451	PAP45	375	28.3%	chr19	15411880	ENST00000389282	c.532G>A	p.D178N
WT1	Wilms tumor 1	ENSG00000184937	PAP45	91	18.7%	chr11	32378152	ENST00000379079	c.380A>G	p.Y127C
WNT10B	wingless-type MMTV integration site family; member 10B	ENSG00000169884	PAP45	152	27.6%	chr12	47648361	CCDS8775.1	c.346G>T	p.E116X
WNT3	wingless-type MMTV integration site family; member 3	ENSG00000108379	PAP45	173	26.0%	chr17	42200964	CCDS11505.1	c.959A>C	p.N320T
WAPAL	wings apart-like homolog (Drosophila)	ENSG00000062650	PAP45	214	21.0%	chr10	88267422	CCDS7375.1	c.385G>A	p.V129I
WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	ENSG00000015285	PAP45	142	29.6%	chrX	48427246	CCDS14303.1	c.60G>T	p.Q20H
WNK3	WNK lysine deficient protein kinase 3	ENSG00000196632	PAP45	184	31.5%	chrX	54292069	CCDS14357.1	c.3437C>A	p.S1146Y
WNK3	WNK lysine deficient protein kinase 3	ENSG00000196632	PAP45	143	16.8%	chrX	54337948	CCDS14357.1	c.1456G>A	p.D486N
WBP4	WW domain binding protein 4 (formin binding protein 21)	ENSG00000120688	PAP45	67	14.9%	chr13	40548203	CCDS9375.1	c.586G>T	p.D196Y
WWOX	WW domain containing oxidoreductase	ENSG00000186153	PAP45	264	18.6%	chr16	77016296	CCDS42196.1	c.634G>T	p.A212S
XPC	xeroderma pigmentosum; complementation group C	ENSG00000154767	PAP45	352	18.2%	chr3	14174692	ENST00000285021	c.1687C>A	p.P563T
XAF1	XIAP associated factor 1	ENSG00000132530	PAP45	197	26.4%	chr17	6614830	CCDS11080.1	c.652A>C	p.N218H
XIRP2	xin actin-binding repeat containing 2	ENSG00000163092	PAP45	271	28.0%	chr2	167468306	CCDS42769.1	c.68G>T	p.R23I
XIRP2	xin actin-binding repeat containing 2	ENSG00000163092	PAP45	164	17.1%	chr2	167468560	CCDS42769.1	c.322G>A	p.E108K
XIRP2	xin actin-binding repeat containing 2	ENSG00000163092	PAP45	195	21.0%	chr2	167783001	CCDS42769.1	c.803C>A	p.S268Y
XIRP2	xin actin-binding repeat containing 2	ENSG00000163092	PAP45	717	25.5%	chr2	167807499	CCDS42769.1	c.1351G>A	p.E451K
XIRP2	xin actin-binding repeat containing 2	ENSG00000163092	PAP45	156	33.3%	chr2	167808312	CCDS42769.1	c.2164C>T	p.L722F
XIRP2	xin actin-binding repeat containing 2	ENSG00000163092	PAP45	122	22.1%	chr2	167808391	CCDS42769.1	c.2243C>T	p.S748L
XIRP2	xin actin-binding repeat containing 2	ENSG00000163092	PAP45	163	20.9%	chr2	167810226	CCDS42769.1	c.4078G>T	p.D1360Y
XIRP2	xin actin-binding repeat containing 2	ENSG00000163092	PAP45	83	37.3%	chr2	167811900	CCDS42769.1	c.5752C>A	p.L1918I
XIRP2	xin actin-binding repeat containing 2	ENSG00000163092	PAP45	129	23.3%	chr2	167814840	CCDS42769.1	c.8692T>G	p.C2898G
XIRP2	xin actin-binding repeat containing 2	ENSG00000163092	PAP45	110	33.6%	chr2	167814926	CCDS42769.1	c.8778C>A	p.F2926L
XKRX	XK; Kell blood group complex subunit-related; X-linked	ENSG00000182489	PAP45	61	19.7%	chrX	100069954	CCDS14476.1	c.35C>T	p.S12L
XIAP	X-linked inhibitor of apoptosis	ENSG00000101966	PAP45	155	24.5%	chrX	122847906	CCDS14606.1	c.713G>A	p.R238Q
XRRA1	X-ray radiation resistance associated 1	ENSG00000166435	PAP45	77	18.2%	chr11	74329493	NM_182969	c.79C>T	p.R27C
XRCC1	X-ray repair complementing defective repair in Chinese hamster cells 1	ENSG00000073050	PAP45	159	22.6%	chr19	48741904	CCDS12624.1	c.1527G>T	p.E509D
YIPF1	Yip1 domain family; member 1	ENSG00000058799	PAP45	207	19.8%	chr1	54109645	CCDS584.1	c.469G>A	p.E157K
YPEL5	yippee-like 5 (Drosophila)	ENSG00000119801	PAP45	194	19.1%	chr2	30235052	CCDS1771.1	c.205C>T	p.R69X
YSK4	YSK4 Sps1/Ste20-related kinase homolog (S. cerevisiae)	ENSG00000176601	PAP45	52	21.2%	chr2	135457350	ENST00000392915	c.3295A>C	p.N1099H
YSK4	YSK4 Sps1/Ste20-related kinase homolog (S. cerevisiae)	ENSG00000176601	PAP45	213	27.7%	chr2	135460958	CCDS2176.2	c.1954G>T	p.E652X
YSK4	YSK4 Sps1/Ste20-related kinase homolog (S. cerevisiae)	ENSG00000176601	PAP45	198	24.2%	chr2	135461203	CCDS2176.2	c.1709A>C	p.K570T
YSK4	YSK4 Sps1/Ste20-related kinase homolog (S. cerevisiae)	ENSG00000176601	PAP45	99	25.3%	chr2	135461910	CCDS2176.2	c.1002G>T	p.E334D
YY1	YY1 transcription factor	ENSG00000100811	PAP45	142	28.2%	chr14	99812579	CCDS9957.1	c.-1G>A	p.IVS3-1-1SpliceAcceptor
ZIC1	Zic family member 1 (odd-paired homolog; Drosophila)	ENSG00000152977	PAP45	138	31.2%	chr3	148610762	CCDS3136.1	c.173C>T	p.S58L
ZBTB1	zinc finger and BTB domain containing 1	ENSG00000126804	PAP45	139	21.6%	chr14	64059082	CCDS32097.1	c.1107T>G	p.F369L
ZBTB33	zinc finger and BTB domain containing 33	ENSG00000177485	PAP45	178	21.3%	chrX	119271446	CCDS14596.1	c.148C>A	p.L50I
ZBTB37	zinc finger and BTB domain containing 37	ENSG00000185278	PAP45	229	26.6%	chr1	172106062	CCDS1312.1	c.76C>T	p.R26C
ZBTB4	zinc finger and BTB domain containing 4	ENSG00000174282	PAP45	193	21.8%	chr17	7309850	CCDS11107.1	c.995C>T	p.S332L
ZBTB41	zinc finger and BTB domain containing 41	ENSG00000177888	PAP45	50	24.0%	chr1	195395183	CCDS30960.1	c.2659C>A	p.L887I
ZBTB41	zinc finger and BTB domain containing 41	ENSG00000177888	PAP45	73	27.4%	chr1	195435380	CCDS30960.1	c.847G>A	p.E283K
ZBTB44	zinc finger and BTB domain containing 44	ENSG00000196323	PAP45	183	35.5%	chr11	129612021	ENST00000397753	c.1445G>A	p.R482H
ZBTB46	zinc finger and BTB domain containing 46	ENSG00000130584	PAP45	164	17.7%	chr20	61891794	CCDS13538.1	c.761C>A	p.S254Y
ZBTB6	zinc finger and BTB domain containing 6	ENSG00000186130	PAP45	227	26.4%	chr9	124713635	CCDS6846.1	c.538G>T	p.E180X
ZBTB9	zinc finger and BTB domain containing 9	ENSG00000213588	PAP45	252	34.1%	chr6	33531704	CCDS4780.1	c.849C>A	p.F283L
ZSCAN16	zinc finger and SCAN domain containing 16	ENSG00000196812	PAP45	251	30.3%	chr6	28205364	CCDS4644.1	c.704G>A	p.R235Q
ZSCAN4	zinc finger and SCAN domain containing 4	ENSG00000180532	PAP45	526	20.9%	chr19	62881946	CCDS12958.1	c.1163G>T	p.R388I
ZSCAN5A	zinc finger and SCAN domain containing 5A	ENSG00000131848	PAP45	80	17.5%	chr19	61428061	CCDS12941.1	c.167C>T	p.S56L
ZC3H13	zinc finger CCCH-type containing 13	ENSG00000123200	PAP45	355	21.7%	chr13	45457795	CCDS9400.1	c.1358G>A	p.R453Q
ZC3H13	zinc finger CCCH-type containing 13	ENSG00000123200	PAP45	159	25.2%	chr13	45517579	CCDS9400.1	c.65G>T	p.R22L
ZC3H14	zinc finger CCCH-type containing 14	ENSG00000100722	PAP45	151	25.8%	chr14	88108295	CCDS32133.1	c.404C>T	p.S135L
ZC3H18	zinc finger CCCH-type containing 18	ENSG00000158545	PAP45	365	21.1%	chr16	87217884	CCDS10967.1	c.1811C>T	p.S604L

ZC3H7A	zinc finger CCCH-type containing 7A	ENSG00000122299	PAP45	143	46.9%	chr16	11769723	CCDS10550.1	c.1309G>A	p.E437K
ZC3HAV1	zinc finger CCCH-type; antiviral 1	ENSG00000105939	PAP45	67	29.9%	chr7	138389257	CCDS5851.1	c.2312T>G	p.F771C
ZC3HAV1	zinc finger CCCH-type; antiviral 1	ENSG00000105939	PAP45	402	22.9%	chr7	138414861	CCDS5851.1	c.1366G>T	p.E456X
ZEB1	zinc finger E-box binding homeobox 1	ENSG00000148516	PAP45	161	24.8%	chr10	31850466	CCDS7169.1	c.2197G>T	p.E733X
ZFHX3	zinc finger homeobox 3	ENSG00000140836	PAP45	346	23.1%	chr16	71550322	CCDS10908.1	c.1224C>A	p.S408R
ZFHX3	zinc finger homeobox 3	ENSG00000140836	PAP45	500	26.2%	chr16	71550738	CCDS10908.1	c.808G>A	p.D270N
ZFP1	zinc finger protein 1 homolog (mouse)	ENSG00000184517	PAP45	143	23.8%	chr16	73761220	CCDS10914.2	c.711G>T	p.E237D
ZNF10	zinc finger protein 10	ENSG00000090612	PAP45	87	28.7%	chr12	132243408	CCDS9283.1	c.1503G>T	p.K501N
ZFP106	zinc finger protein 106 homolog (mouse)	ENSG00000103994	PAP45	188	14.4%	chr15	40530471	CCDS32208.1	c.1222G>T	p.E408X
ZNF124	zinc finger protein 124	ENSG00000196418	PAP45	82	23.2%	chr1	245386504	CCDS31089.1	c.857G>T	p.C286F
ZNF140	zinc finger protein 140	ENSG00000196387	PAP45	187	17.1%	chr12	132192749	CCDS9282.1	c.813A>C	p.K271N
ZNF157	zinc finger protein 157	ENSG00000147117	PAP45	159	23.3%	chrX	47157381	CCDS14278.1	c.965G>T	p.R322I
ZNF157	zinc finger protein 157	ENSG00000147117	PAP45	171	33.3%	chrX	47157434	CCDS14278.1	c.1018C>T	p.R340X
ZFP161	zinc finger protein 161 homolog (mouse)	ENSG00000198081	PAP45	180	31.1%	chr18	5281672	CCDS11837.1	c.535G>T	p.E179X
ZNF165	zinc finger protein 165	ENSG00000197279	PAP45	99	26.3%	chr6	28164437	CCDS4643.1	c.668C>T	p.S223F
ZNF167	zinc finger protein 167	ENSG00000196345	PAP45	107	29.0%	chr3	44587654	CCDS2715.1	c.2048G>T	p.R683I
ZNF174	zinc finger protein 174	ENSG00000103343	PAP45	255	22.4%	chr16	3398580	CCDS10504.1	c.884G>T	p.R295I
ZNF175	zinc finger protein 175	ENSG00000105497	PAP45	134	21.6%	chr19	56783083	CCDS12837.1	c.1687G>T	p.E563X
ZNF180	zinc finger protein 180	ENSG00000167384	PAP45	91	27.5%	chr19	49673084	CCDS12639.1	c.1454G>T	p.R485I
ZNF180	zinc finger protein 180	ENSG00000167384	PAP45	175	18.9%	chr19	49673504	CCDS12639.1	c.1034G>T	p.R345I
ZNF181	zinc finger protein 181	ENSG00000197841	PAP45	93	24.7%	chr19	39923708	CCDS32990.1	c.390A>C	p.K130N
ZNF182	zinc finger protein 182	ENSG00000147118	PAP45	229	28.8%	chrX	47721669	CCDS35236.1	c.761G>A	p.R254K
ZNF182	zinc finger protein 182	ENSG00000147118	PAP45	229	22.7%	chrX	47721673	CCDS35236.1	c.757T>C	p.W253R
ZNF182	zinc finger protein 182	ENSG00000147118	PAP45	128	17.2%	chrX	47722090	CCDS35236.1	c.340G>T	p.D114Y
ZNF182	zinc finger protein 182	ENSG00000147118	PAP45	115	20.9%	chrX	47727323	CCDS35236.1	c.259G>T	p.E87X
ZNF184	zinc finger protein 184	ENSG00000096654	PAP45	138	21.7%	chr6	27528340	CCDS4624.1	c.977G>T	p.R326I
ZNF189	zinc finger protein 189	ENSG00000136870	PAP45	129	25.6%	chr9	103210431	CCDS6754.1	c.560G>A	p.R187H
ZNF189	zinc finger protein 189	ENSG00000136870	PAP45	207	26.1%	chr9	103211130	CCDS6754.1	c.1259G>T	p.R420I
ZNF189	zinc finger protein 189	ENSG00000136870	PAP45	177	31.6%	chr9	103211230	CCDS6754.1	c.1359G>T	p.E453D
ZNF192	zinc finger protein 192	ENSG00000198315	PAP45	127	22.0%	chr6	28228057	CCDS4645.1	c.691C>T	p.R231X
ZNF192	zinc finger protein 192	ENSG00000198315	PAP45	187	25.1%	chr6	28229650	CCDS4645.1	c.1613G>T	p.R538I
ZNF197	zinc finger protein 197	ENSG00000186448	PAP45	162	20.4%	chr3	44659356	CCDS2717.1	c.1730G>A	p.R577Q
ZNF197	zinc finger protein 197	ENSG00000186448	PAP45	160	20.6%	chr3	44659399	CCDS2717.1	c.1773G>T	p.K591N
ZNF2	zinc finger protein 2	ENSG00000163067	PAP45	141	24.1%	chr2	95210688	CCDS42712.1	c.388C>T	p.P130S
ZNF202	zinc finger protein 202	ENSG00000166261	PAP45	151	29.8%	chr11	123106410	CCDS8443.1	c.397C>T	p.R133W
ZNF214	zinc finger protein 214	ENSG00000149050	PAP45	111	27.0%	chr11	6977781	CCDS31418.1	c.1709G>A	p.R570Q
ZNF217	zinc finger protein 217	ENSG00000171940	PAP45	298	20.1%	chr20	51632410	CCDS13443.1	c.363G>T	p.K121N
ZNF223	zinc finger protein 223	ENSG00000178386	PAP45	181	21.5%	chr19	49262660	CCDS12635.1	c.839G>T	p.R280I
ZNF224	zinc finger protein 224	ENSG00000186019	PAP45	154	18.2%	chr19	49302672	CCDS33046.1	c.519G>T	p.E173D
ZNF229	zinc finger protein 229	ENSG00000167383	PAP45	366	22.7%	chr19	49625633	CCDS42574.1	c.1163G>A	p.R388Q
ZNF233	zinc finger protein 233	ENSG00000159915	PAP45	138	31.9%	chr19	49469092	CCDS33047.1	c.439G>T	p.E147X
ZNF233	zinc finger protein 233	ENSG00000159915	PAP45	123	30.9%	chr19	49470068	CCDS33047.1	c.1415G>T	p.R472I
ZNF235	zinc finger protein 235	ENSG00000159917	PAP45	257	22.2%	chr19	49484476	CCDS33048.1	c.952C>T	p.R318C
ZNF236	zinc finger protein 236	ENSG00000130856	PAP45	43	27.9%	chr18	72692726	CCDS42447.1	c.200G>A	p.R67Q
ZNF263	zinc finger protein 263	ENSG00000006194	PAP45	296	27.0%	chr16	3280459	CCDS10499.1	c.1952G>T	p.R651I
ZNF264	zinc finger protein 264	ENSG00000083844	PAP45	164	22.6%	chr19	62416033	CCDS33127.1	c.1756C>T	p.R586X
ZNF267	zinc finger protein 267	ENSG00000185947	PAP45	132	24.2%	chr16	31834495	CCDS32440.1	c.1424G>A	p.R475H
ZNF268	zinc finger protein 268	ENSG00000090612	PAP45	87	28.7%	chr12	132243408	CCDS9283.1	c.1503G>T	p.K501N
ZNF271	zinc finger protein 271	ENSG00000118267	PAP45	182	28.6%	chr18	31141047	ENST00000317475	c.461T>C	p.F154S
ZNF280B	zinc finger protein 280B	ENSG00000198477	PAP45	300	21.7%	chr22	21172325	CCDS13799.1	c.1399C>A	p.L467I
ZNF280C	zinc finger protein 280C	ENSG00000056277	PAP45	33	45.5%	chrX	129167012	CCDS14622.1	c.2101C>T	p.R701C
ZNF280D	zinc finger protein 280D	ENSG00000137871	PAP45	92	23.9%	chr15	54746466	CCDS32245.1	c.1556G>A	p.R519Q
ZNF282	zinc finger protein 282	ENSG00000170265	PAP45	66	34.8%	chr7	148540472	CCDS5895.1	c.1042G>T	p.D348Y
ZNF286A	zinc finger protein 286A	ENSG00000187607	PAP45	58	29.3%	chr17	15560542	CCDS11172.1	c.779G>A	p.R260Q

ZNF287	zinc finger protein 287	ENSG00000141040	PAP45	120	25.8%	chr17	16396703	CCDS11179.1	c.1457C>A	p.S486X
ZNF287	zinc finger protein 287	ENSG00000141040	PAP45	224	29.9%	chr17	16411581	CCDS11179.1	c.169C>T	p.R57X
ZNF295	zinc finger protein 295	ENSG00000173276	PAP45	326	24.8%	chr21	42284579	CCDS13678.1	c.2695G>T	p.E899X
ZNF3	zinc finger protein 3	ENSG00000166526	PAP45	427	29.0%	chr7	99506964	CCDS43619.1	c.1079G>T	p.R360I
ZFP30	zinc finger protein 30 homolog (mouse)	ENSG00000120784	PAP45	171	31.6%	chr19	42818749	CCDS33005.1	c.533G>T	p.R178I
ZNF300	zinc finger protein 300	ENSG00000145908	PAP45	112	19.6%	chr5	150255540	CCDS4311.1	c.1454G>T	p.R485I
ZNF300	zinc finger protein 300	ENSG00000145908	PAP45	114	25.4%	chr5	150255572	CCDS4311.1	c.1422C>A	p.F474L
ZNF304	zinc finger protein 304	ENSG00000131845	PAP45	162	25.3%	chr19	62560617	CCDS12950.1	c.1568G>T	p.R523I
ZNF331	zinc finger protein 331	ENSG00000130844	PAP45	297	25.6%	chr19	58772399	CCDS33102.1	c.773T>G	p.L258R
ZNF335	zinc finger protein 335	ENSG00000198026	PAP45	242	23.1%	chr20	44022285	CCDS13389.1	c.1989C>A	p.F663L
ZNF33B	zinc finger protein 33B	ENSG00000196693	PAP45	34	32.4%	chr10	42409841	CCDS7198.1	c.563G>A	p.R188Q
ZNF345	zinc finger protein 345	ENSG00000167637	PAP45	51	31.4%	chr19	42061019	CCDS12497.1	c.1447G>A	p.E483K
ZNF347	zinc finger protein 347	ENSG00000197937	PAP45	108	31.5%	chr19	58337610	CCDS33097.1	c.283G>A	p.E95K
ZNF350	zinc finger protein 350	ENSG00000197619	PAP45	123	13.0%	chr19	57189050	CCDS12846.1	c.1091G>A	p.R364Q
ZNF365	zinc finger protein 365	ENSG00000138311	PAP45	176	22.7%	chr10	63806458	CCDS7264.1	c.500G>A	p.R167Q
ZFP37	zinc finger protein 37 homolog (mouse)	ENSG00000136866	PAP45	80	15.0%	chr9	114845109	CCDS6787.1	c.1610G>T	p.R537I
ZFP37	zinc finger protein 37 homolog (mouse)	ENSG00000136866	PAP45	60	21.7%	chr9	114846131	CCDS6787.1	c.588C>A	p.N196K
ZNF382	zinc finger protein 382	ENSG00000161298	PAP45	153	13.1%	chr19	41809705	CCDS33004.1	c.1066G>A	p.D356N
ZNF382	zinc finger protein 382	ENSG00000161298	PAP45	455	28.1%	chr19	41809922	CCDS33004.1	c.1283G>T	p.R428I
ZNF383	zinc finger protein 383	ENSG00000188283	PAP45	125	18.4%	chr19	42425451	CCDS12501.1	c.473C>A	p.T158N
ZNF383	zinc finger protein 383	ENSG00000188283	PAP45	82	20.7%	chr19	42426219	CCDS12501.1	c.1241G>T	p.R414I
ZNF394	zinc finger protein 394	ENSG00000160908	PAP45	213	27.7%	chr7	98930141	CCDS5666.1	c.633T>G	p.I211M
ZNF396	zinc finger protein 396	ENSG00000186496	PAP45	193	26.9%	chr18	31203316	CCDS11913.1	c.869G>A	p.R290Q
ZNF407	zinc finger protein 407	ENSG00000215421	PAP45	125	23.2%	chr18	70473252	NM_017757	c.1289G>A	p.R430Q
ZNF407	zinc finger protein 407	ENSG00000215421	PAP45	111	25.2%	chr18	70474102	NM_017757	c.2139A>C	p.K713N
ZNF407	zinc finger protein 407	ENSG00000215421	PAP45	183	23.5%	chr18	70475013	NM_017757	c.3050A>C	p.N1017T
ZNF415	zinc finger protein 415	ENSG00000170954	PAP45	52	23.1%	chr19	58303819	CCDS12860.1	c.1291C>T	p.R431W
ZNF415	zinc finger protein 415	ENSG00000170954	PAP45	134	20.1%	chr19	58304062	CCDS12860.1	c.1048C>A	p.H350N
ZNF416	zinc finger protein 416	ENSG00000083817	PAP45	103	18.4%	chr19	62779023	CCDS12954.1	c.163G>A	p.D55N
ZNF418	zinc finger protein 418	ENSG00000196724	PAP45	225	20.0%	chr19	63129670	CCDS42642.1	c.1691G>A	p.R564K
ZNF423	zinc finger protein 423	ENSG00000102935	PAP45	291	15.5%	chr16	48228285	CCDS32445.1	c.2279G>A	p.R760H
ZNF425	zinc finger protein 425	ENSG00000204947	PAP45	268	22.8%	chr7	148433352	CCDS34773.1	c.544G>T	p.E182X
ZNF425	zinc finger protein 425	ENSG00000204947	PAP45	130	16.9%	chr7	148440272	CCDS34773.1	c.194G>T	p.R65I
ZNF429	zinc finger protein 429	ENSG00000197013	PAP45	67	23.9%	chr19	21510972	CCDS42537.1	c.277G>T	p.D93Y
ZNF432	zinc finger protein 432	ENSG00000197619	PAP45	123	13.0%	chr19	57189050	CCDS12846.1	c.1091G>A	p.R364Q
ZNF441	zinc finger protein 441	ENSG00000197044	PAP45	76	22.4%	chr19	11753194	CCDS12266.1	c.1354C>T	p.R452X
ZNF442	zinc finger protein 442	ENSG00000198342	PAP45	90	17.8%	chr19	12322473	CCDS12271.1	c.926G>A	p.R309Q
ZNF45	zinc finger protein 45	ENSG00000124459	PAP45	231	33.8%	chr19	49109892	CCDS12632.1	c.1536C>A	p.F512L
ZNF451	zinc finger protein 451	ENSG00000112200	PAP45	93	34.4%	chr6	57114751	CCDS43477.1	c.903G>T	p.K301N
ZNF451	zinc finger protein 451	ENSG00000112200	PAP45	98	11.2%	chr6	57120382	CCDS43477.1	c.1540C>T	p.R514C
ZNF470	zinc finger protein 470	ENSG00000197016	PAP45	149	22.1%	chr19	61780943	CCDS33122.1	c.1334G>T	p.R445I
ZNF471	zinc finger protein 471	ENSG00000196263	PAP45	108	28.7%	chr19	61728177	CCDS12945.1	c.929G>T	p.R310I
ZNF471	zinc finger protein 471	ENSG00000196263	PAP45	83	21.7%	chr19	61728936	CCDS12945.1	c.1688G>T	p.R563I
ZNF473	zinc finger protein 473	ENSG00000142528	PAP45	191	18.3%	chr19	55241775	CCDS33077.1	c.2263G>T	p.E755X
ZNF480	zinc finger protein 480	ENSG00000198464	PAP45	53	28.3%	chr19	57517466	CCDS12850.1	c.1094C>T	p.S365L
ZNF483	zinc finger protein 483	ENSG00000173258	PAP45	265	20.8%	chr9	113345248	CCDS35106.1	c.2212C>T	p.R738W
ZNF484	zinc finger protein 484	ENSG00000127081	PAP45	116	22.4%	chr9	94650341	CCDS35066.1	c.549G>T	p.K183N
ZNF493	zinc finger protein 493	ENSG00000196268	PAP45	123	13.8%	chr19	21398182	CCDS42536.1	c.881A>C	p.K294T
ZNF500	zinc finger protein 500	ENSG00000103199	PAP45	60	20.0%	chr16	4752650	CCDS32383.1	c.523C>T	p.R175X
ZNF502	zinc finger protein 502	ENSG00000196653	PAP45	104	27.9%	chr3	44738005	CCDS2719.1	c.692G>T	p.R231I
ZNF514	zinc finger protein 514	ENSG00000144026	PAP45	138	24.6%	chr2	95178782	CCDS2011.1	c.1175G>T	p.R392I
ZNF514	zinc finger protein 514	ENSG00000144026	PAP45	194	21.6%	chr2	95178887	CCDS2011.1	c.1070C>A	p.S357X
ZNF518A	zinc finger protein 518A	ENSG00000177853	PAP45	77	19.5%	chr10	97908312	ENST00000371192	c.2243C>A	p.S748Y
ZNF518A	zinc finger protein 518A	ENSG00000177853	PAP45	144	19.4%	chr10	97909242	ENST00000371192	c.3173C>A	p.S1058Y

ZNF519	zinc finger protein 519	ENSG00000175322	PAP45	32	34.4%	chr18	14095184	CCDS32797.1	c.1355G>T	p.R452I
ZNF530	zinc finger protein 530	ENSG00000183647	PAP45	104	20.2%	chr19	62809697	CCDS12955.1	c.992C>A	p.S331Y
ZNF532	zinc finger protein 532	ENSG00000074657	PAP45	48	25.0%	chr18	54737463	CCDS11969.1	c.964G>A	p.D322N
ZNF540	zinc finger protein 540	ENSG00000171817	PAP45	45	24.4%	chr19	42794725	CCDS12506.1	c.704G>T	p.R235I
ZNF543	zinc finger protein 543	ENSG00000178229	PAP45	259	24.7%	chr19	62531603	CCDS33130.1	c.961C>T	p.R321X
ZNF544	zinc finger protein 544	ENSG00000198131	PAP45	97	22.7%	chr19	63464197	CCDS12973.1	c.413A>G	p.N138S
ZNF546	zinc finger protein 546	ENSG00000187187	PAP45	150	14.0%	chr19	45196110	CCDS12548.1	c.37G>T	p.D13Y
ZNF546	zinc finger protein 546	ENSG00000187187	PAP45	87	14.9%	chr19	45212992	CCDS12548.1	c.1975C>A	p.H659N
ZNF546	zinc finger protein 546	ENSG00000187187	PAP45	90	18.9%	chr19	45213442	CCDS12548.1	c.2425G>T	p.E809X
ZNF546	zinc finger protein 546	ENSG00000187187	PAP45	65	16.9%	chr19	45213568	ENST00000392042	c.1321G>T	p.E441X
ZNF551	zinc finger protein 551	ENSG00000204519	PAP45	184	28.3%	chr19	62890845	CCDS12959.1	c.1342C>T	p.R448X
ZNF554	zinc finger protein 554	ENSG00000172006	PAP45	406	10.1%	chr19	2785041	CCDS42462.1	c.808C>T	p.R270W
ZNF554	zinc finger protein 554	ENSG00000172006	PAP45	129	15.5%	chr19	2785837	CCDS42462.1	c.1604T>G	p.L535R
ZNF556	zinc finger protein 556	ENSG00000172000	PAP45	305	21.6%	chr19	2828779	CCDS12097.1	c.823C>T	p.R275X
ZNF560	zinc finger protein 560	ENSG00000198028	PAP45	65	16.9%	chr19	9439875	CCDS12214.1	c.748G>T	p.D250Y
ZNF560	zinc finger protein 560	ENSG00000198028	PAP45	196	10.2%	chr19	9442093	CCDS12214.1	c.423G>T	p.E141D
ZNF560	zinc finger protein 560	ENSG00000198028	PAP45	227	21.6%	chr19	9442121	CCDS12214.1	c.395G>T	p.R132I
ZNF560	zinc finger protein 560	ENSG00000198028	PAP45	96	27.1%	chr19	9444864	CCDS12214.1	c.229G>T	p.V77F
ZNF563	zinc finger protein 563	ENSG00000188868	PAP45	40	27.5%	chr19	12291285	CCDS12270.1	c.554G>A	p.R185Q
ZNF564	zinc finger protein 564	ENSG00000196826	PAP45	89	15.7%	chr19	12437054	CCDS42504.1	c.682G>T	p.E228X
ZNF567	zinc finger protein 567	ENSG00000189042	PAP45	135	29.6%	chr19	41902983	CCDS12495.1	c.1424A>T	p.E475V
ZNF571	zinc finger protein 571	ENSG00000180479	PAP45	140	29.3%	chr19	42747689	CCDS12505.1	c.1481G>T	p.R494I
ZNF573	zinc finger protein 573	ENSG00000189144	PAP45	108	15.7%	chr19	42921867	CCDS12508.1	c.1190G>T	p.R397I
ZNF583	zinc finger protein 583	ENSG00000198440	PAP45	99	27.3%	chr19	61627374	CCDS12943.1	c.1535G>T	p.R512I
ZNF585A	zinc finger protein 585A	ENSG00000196967	PAP45	67	19.4%	chr19	42335436	CCDS12499.1	c.1040G>T	p.R347I
ZNF585B	zinc finger protein 585B	ENSG00000197800	PAP45	106	11.3%	chr19	42369158	CCDS12500.1	c.1121G>T	p.R374I
ZNF594	zinc finger protein 594	ENSG00000180626	PAP45	174	26.4%	chr17	5025072	ENST00000381752	c.839G>A	p.S280N
ZNF594	zinc finger protein 594	ENSG00000180626	PAP45	58	24.1%	chr17	5026753	CCDS42241.1	c.1523G>T	p.R508I
ZNF594	zinc finger protein 594	ENSG00000180626	PAP45	275	24.0%	chr17	5027752	CCDS42241.1	c.524G>T	p.R175I
ZNF597	zinc finger protein 597	ENSG00000167981	PAP45	179	12.3%	chr16	3426641	CCDS10505.1	c.1059C>A	p.F353L
ZNF606	zinc finger protein 606	ENSG00000166704	PAP45	95	14.7%	chr19	63183018	CCDS12968.1	c.842G>T	p.R281I
ZNF606	zinc finger protein 606	ENSG00000166704	PAP45	243	25.9%	chr19	63183372	CCDS12968.1	c.488G>T	p.R163I
ZNF606	zinc finger protein 606	ENSG00000166704	PAP45	177	19.8%	chr19	63183450	CCDS12968.1	c.410G>T	p.R137I
ZNF607	zinc finger protein 607	ENSG00000198182	PAP45	192	13.0%	chr19	42881104	CCDS33006.1	c.1768G>T	p.E590X
ZNF608	zinc finger protein 608	ENSG00000168916	PAP45	208	27.4%	chr5	124011326	CCDS34219.1	c.2650G>T	p.D884Y
ZNF608	zinc finger protein 608	ENSG00000168916	PAP45	236	26.7%	chr5	124012288	CCDS34219.1	c.4142NULL>A	p.NULL-1FsIns1bp
ZNF608	zinc finger protein 608	ENSG00000168916	PAP45	259	22.4%	chr5	124108229	CCDS34219.1	c.353C>A	p.S118Y
ZNF610	zinc finger protein 610	ENSG00000167554	PAP45	96	18.8%	chr19	57561198	CCDS12851.1	c.755G>A	p.R252K
ZNF613	zinc finger protein 613	ENSG00000176024	PAP45	46	26.1%	chr19	57140681	CCDS33089.1	c.1733C>T	p.S578F
ZNF615	zinc finger protein 615	ENSG00000197619	PAP45	123	13.0%	chr19	57189050	CCDS12846.1	c.1091G>A	p.R364Q
ZNF619	zinc finger protein 619	ENSG00000177873	PAP45	169	21.9%	chr3	40504264	CCDS2692.1	c.1211G>T	p.R404I
ZNF619	zinc finger protein 619	ENSG00000177873	PAP45	189	29.1%	chr3	40504290	CCDS2692.1	c.1237G>T	p.E413X
ZNF622	zinc finger protein 622	ENSG00000173545	PAP45	344	23.3%	chr5	16516254	CCDS3886.1	c.1012G>A	p.D338N
ZNF623	zinc finger protein 623	ENSG00000183309	PAP45	88	18.2%	chr8	144804668	CCDS34957.1	c.1483G>T	p.D495Y
ZNF627	zinc finger protein 627	ENSG00000198551	PAP45	139	23.0%	chr19	11588697	CCDS42502.1	c.379G>T	p.E127X
ZNF638	zinc finger protein 638	ENSG00000075292	PAP45	249	12.0%	chr2	71430468	CCDS1917.1	c.876G>T	p.K292N
ZNF643	zinc finger protein 643	ENSG00000187801	PAP45	188	26.6%	chr1	40701559	CCDS452.1	c.1010G>T	p.R337I
ZNF643	zinc finger protein 643	ENSG00000187801	PAP45	192	28.6%	chr1	40701573	CCDS452.1	c.1024G>T	p.E342X
ZNF644	zinc finger protein 644	ENSG00000122482	PAP45	180	22.2%	chr1	91175790	CCDS731.1	c.3528A>C	p.K1176N
ZNF644	zinc finger protein 644	ENSG00000122482	PAP45	143	11.9%	chr1	91178180	CCDS731.1	c.1319G>A	p.R440H
ZNF645	zinc finger protein 645	ENSG00000175809	PAP45	168	26.8%	chrX	22201489	CCDS14205.1	c.460C>T	p.R154C
ZNF649	zinc finger protein 649	ENSG00000198093	PAP45	222	27.0%	chr19	57085852	CCDS12843.1	c.1349G>A	p.R450K
ZNF655	zinc finger protein 655	ENSG00000197343	PAP45	43	27.9%	chr7	99007960	CCDS5669.1	c.293G>T	p.R98I

ZNF662	zinc finger protein 662	ENSG00000182983	PAP45	98	31.6%	chr3	42931264	CCDS2708.1	c.695G>A	p.R232Q
ZNF664	zinc finger protein 664	ENSG00000179195	PAP45	145	14.5%	chr12	123062696	CCDS9257.1	c.52C>A	p.L18I
ZNF667	zinc finger protein 667	ENSG00000198046	PAP45	121	18.2%	chr19	61644462	CCDS12944.1	c.1714C>T	p.R572X
ZNF667	zinc finger protein 667	ENSG00000198046	PAP45	157	24.2%	chr19	61645601	CCDS12944.1	c.575G>T	p.R192I
ZNF692	zinc finger protein 692	ENSG00000171163	PAP45	183	20.8%	chr1	247118097	CCDS31127.1	c.434G>T	p.R145I
ZNF7	zinc finger protein 7	ENSG00000147789	PAP45	225	19.6%	chr8	146038846	CCDS6435.1	c.1550G>T	p.R517I
ZNF707	zinc finger protein 707	ENSG00000181135	PAP45	93	14.0%	chr8	144847838	NM_001100599	c.266A>C	p.K89T
ZNF71	zinc finger protein 71	ENSG00000197951	PAP45	439	20.5%	chr19	61825116	CCDS12947.1	c.649G>A	p.D217N
ZNF711	zinc finger protein 711	ENSG00000147180	PAP45	183	26.8%	chrX	84413310	CCDS35344.1	c.2106G>T	p.K702N
ZNF724P	zinc finger protein 724 (pseudogene)	ENSG00000196081	PAP45	59	16.9%	chr19	23198318	ENST00000397097	c.569G>T	p.R190I
ZNF74	zinc finger protein 74	ENSG00000185252	PAP45	171	28.1%	chr22	19090245	CCDS42982.1	c.922G>T	p.E308X
ZNF75D	zinc finger protein 75D	ENSG00000186376	PAP45	87	26.4%	chrX	134249243	CCDS14648.1	c.1025C>A	p.A342E
ZNF776	zinc finger protein 776	ENSG00000152443	PAP45	104	33.7%	chr19	62957209	CCDS12962.1	c.773C>T	p.S258F
ZNF782	zinc finger protein 782	ENSG00000196597	PAP45	368	22.6%	chr9	98620636	NM_001001662	c.1490G>A	p.R497Q
ZNF790	zinc finger protein 790	ENSG00000197863	PAP45	332	27.1%	chr19	42001519	CCDS12496.1	c.1567C>T	p.R523X
ZNF792	zinc finger protein 792	ENSG00000180884	PAP45	443	26.9%	chr19	40142049	NM_175872	c.550G>A	p.V184I
ZNF800	zinc finger protein 800	ENSG00000048405	PAP45	117	26.5%	chr7	126801129	CCDS5795.1	c.1497G>T	p.Q499H
ZNF800	zinc finger protein 800	ENSG00000048405	PAP45	138	18.1%	chr7	126801822	CCDS5795.1	c.804G>T	p.K268N
ZNF804A	zinc finger protein 804A	ENSG00000170396	PAP45	210	26.2%	chr2	185509559	CCDS2291.1	c.1191G>T	p.E397D
ZNF804A	zinc finger protein 804A	ENSG00000170396	PAP45	198	16.2%	chr2	185510867	CCDS2291.1	c.2499T>A	p.D833E
ZNF829	zinc finger protein 829	ENSG00000185869	PAP45	47	29.8%	chr19	42074352	NM_001037232	c.1181A>C	p.N394T
ZNF831	zinc finger protein 831	ENSG00000124203	PAP45	67	19.4%	chr20	57215425	CCDS42894.1	c.3946C>T	p.R1316X
ZNF84	zinc finger protein 84	ENSG00000198040	PAP45	177	26.6%	chr12	132144526	CCDS31940.1	c.1152C>A	p.F384L
ZNF84	zinc finger protein 84	ENSG00000198040	PAP45	133	27.8%	chr12	132145230	CCDS31940.1	c.1856G>T	p.R619I
ZNF84	zinc finger protein 84	ENSG00000198040	PAP45	128	24.2%	chr12	132145244	CCDS31940.1	c.1870G>T	p.E624X
ZFP90	zinc finger protein 90 homolog (mouse)	ENSG00000184939	PAP45	332	27.7%	chr16	67155180	CCDS42183.1	c.989G>A	p.R330Q
ZFPM2	zinc finger protein; multitype 2	ENSG00000169946	PAP45	191	25.1%	chr8	106884527	NM_012082	c.3041C>T	p.S1014F
ZFR	zinc finger RNA binding protein	ENSG00000056097	PAP45	64	25.0%	chr5	32436012	CCDS34139.1	c.1570G>A	p.E524K
ZKSCAN2	zinc finger with KRAB and SCAN domains 2	ENSG00000155592	PAP45	185	30.3%	chr16	25165827	CCDS32410.1	c.1191C>A	p.F397L
ZKSCAN3	zinc finger with KRAB and SCAN domains 3	ENSG00000189298	PAP45	207	24.2%	chr6	28441469	CCDS4650.1	c.1045A>G	p.K349E
ZFC3H1	zinc finger; C3H1-type containing	ENSG00000133858	PAP45	93	24.7%	chr12	70290495	CCDS41813.1	c.5950A>G	p.T1984A
ZFC3H1	zinc finger; C3H1-type containing	ENSG00000133858	PAP45	93	17.2%	chr12	70303525	CCDS41813.1	c.4626T>G	p.F1542L
ZCCHC6	zinc finger; CCHC domain containing 6	ENSG00000083223	PAP45	95	18.9%	chr9	88127137	CCDS35057.1	c.2951G>T	p.R984I
ZIM2	zinc finger; imprinted 2	ENSG00000198300	PAP45	227	23.3%	chr19	62020359	CCDS12948.1	c.1263G>T	p.E421D
ZIM3	zinc finger; imprinted 3	ENSG00000141946	PAP45	266	23.7%	chr19	62338964	CCDS33125.1	c.553C>A	p.H185N
ZMYM6	zinc finger; MYM-type 6	ENSG00000163867	PAP45	118	25.4%	chr1	35225447	CCDS387.2	c.3823T>G	p.L1275V
ZMYND11	zinc finger; MYND domain containing 11	ENSG00000015171	PAP45	62	24.2%	chr10	276037	CCDS7052.1	c.619G>T	p.D207Y
ZMYND8	zinc finger; MYND-type containing 8	ENSG00000101040	PAP45	75	20.0%	chr20	45345787	CCDS13405.1	c.817G>A	p.E273K
ZRANB2	zinc finger; RAN-binding domain containing 2	ENSG00000132485	PAP45	129	24.8%	chr1	71309126	CCDS659.1	c.655T>C	p.S219P
ZSWIM2	zinc finger; SWIM-type containing 2	ENSG00000163012	PAP45	95	23.2%	chr2	187406923	CCDS33348.1	c.823C>T	p.R275C
ZSWIM3	zinc finger; SWIM-type containing 3	ENSG00000132801	PAP45	327	23.5%	chr20	43939343	CCDS13381.1	c.739C>T	p.R247X
ZZEF1	zinc finger; ZZ-type with EF-hand domain 1	ENSG00000074755	PAP45	105	25.7%	chr17	3863543	CCDS11043.1	c.8528G>A	p.R2843Q
ZHX1	zinc fingers and homeoboxes 1	ENSG00000165156	PAP45	224	29.0%	chr8	124335465	CCDS6342.1	c.1903A>C	p.S635R
ZHX1	zinc fingers and homeoboxes 1	ENSG00000165156	PAP45	96	27.1%	chr8	124336735	CCDS6342.1	c.633G>T	p.E211D
ZMPSTE24	zinc metallopeptidase (STE24 homolog; S. cerevisiae)	ENSG00000084073	PAP45	97	27.8%	chr1	40519659	CCDS449.1	c.827G>A	p.R276Q
ZP1	zona pellucida glycoprotein 1 (sperm receptor)	ENSG00000149506	PAP45	219	28.8%	chr11	60393281	CCDS31572.1	c.284C>T	p.S95L
ZP4	zona pellucida glycoprotein 4	ENSG00000116996	PAP45	109	30.3%	chr1	236112457	CCDS1615.1	c.1511C>T	p.S504L
ZAN	zonadhesin	ENSG00000146839	PAP45	138	20.3%	chr7	100187429	ENST00000349350	c.1765G>T	p.E589X
ZYG11A	zyg-11 homolog A (C. elegans)	ENSG00000203995	PAP45	64	18.8%	chr1	53119752	NM_001004339	c.1771G>T	p.E591X
ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif; 9	ENSG00000163638	PAP46	191	35.6%	chr3	64608730	CCDS2903.1	c.1636G>A	p.V546I
AGBL4	ATP/GTP binding protein-like 4	ENSG00000186094	PAP46	36	30.6%	chr1	49283930	NM_032785	c.507T>A	p.Y169X
ATP2B2	ATPase; Ca++ transporting; plasma membrane 2	ENSG00000157087	PAP46	135	45.2%	chr3	10362241	CCDS33701.1	c.2530G>A	p.V844M
BEGAIN	brain-enriched guanylate kinase-associated homolog (rat)	ENSG00000183092	PAP46	63	46.0%	chr14	100075014	CCDS9962.1	c.827C>A	p.A276E
CLIP4	CAP-GLY domain containing linker protein family; member 4	ENSG00000115295	PAP46	213	36.6%	chr2	29220292	CCDS1770.1	c.862C>T	p.R288C

CTNNB1	catenin (cadherin-associated protein); beta 1; 88kDa	ENSG00000168036	PAP46	183	33.9%	chr3	41241102	CCDS2694.1	c.95A>G	p.D32G
CCT8L2	chaperonin containing TCP1; subunit 8 (theta)-like 2	ENSG00000198445	PAP46	100	30.0%	chr22	15452972	CCDS13738.1	c.469C>A	p.P157T
C7orf51	chromosome 7 open reading frame 51	ENSG00000166924	PAP46	93	30.1%	chr7	99922721	CCDS5696.1	c.410C>T	p.T137M
CLEC4D	C-type lectin domain family 4; member D	ENSG00000166527	PAP46	61	26.2%	chr12	8563107	ENST00000382064	c.408TCTG>N	p.NULL-1FsDel4bp
LOC100129	DAVID_similar to tudor domain containing 1	ENSG00000218819	PAP46	44	25.0%	chr2	21213909	ENST00000405799	c.65G>A	p.C22Y
DHDH	dihydrodiol dehydrogenase (dimeric)	ENSG00000104808	PAP46	166	12.7%	chr19	54134674	CCDS12741.1	c.523C>G	p.L175V
DAB2	disabled homolog 2; mitogen-responsive phosphoprotein (Drosophila)	ENSG00000153071	PAP46	208	33.7%	chr5	39419018	CCDS34149.1	c.800G>A	p.R267Q
DMXL2	Dmx-like 2	ENSG00000104093	PAP46	44	25.0%	chr15	49655673	CCDS10141.1	c.-1TT>NULL	p.IVS1-3-1SpliceAcceptor
ESR1	estrogen receptor 1	ENSG00000091831	PAP46	301	39.2%	chr6	152461613	CCDS5234.1	c.1607T>C	p.L536P
XPO6	exportin 6	ENSG00000169180	PAP46	102	44.1%	chr16	28030744	CCDS42135.1	c.2236G>A	p.V746M
FAM40B	family with sequence similarity 40; member B	ENSG00000128578	PAP46	110	15.5%	chr7	128910033	CCDS34752.1	c.2164C>T	p.R722C
G6PD	glucose-6-phosphate dehydrogenase	ENSG00000160211	PAP46	153	45.8%	chrX	153415471	CCDS14756.2	c.958G>NULL	p.NULL-1FsDel1bp
QRICH2	glutamine rich 2	ENSG00000129646	PAP46	285	33.0%	chr17	71800191	CCDS32741.1	c.1714C>T	p.R572C
GRB7	growth factor receptor-bound protein 7	ENSG00000141738	PAP46	60	38.3%	chr17	35155523	CCDS11345.1	c.1226G>A	p.R409H
KIAA1486	KIAA1486	ENSG00000144460	PAP46	180	36.1%	chr2	226155107	NM_020864	c.730G>A	p.V244M
MFSD2A	major facilitator superfamily domain containing 2A	ENSG00000168389	PAP46	342	34.2%	chr1	40206841	CCDS446.1	c.1366C>A	p.Q456K
MARS	methionyl-tRNA synthetase	ENSG00000166986	PAP46	137	19.0%	chr12	56169975	CCDS8942.1	c.444G>C	p.L148F
MAP3K1	mitogen-activated protein kinase kinase kinase 1	ENSG00000095015	PAP46	113	31.0%	chr5	56216368	CCDS43318.1	c.3940NULL>T	p.NULL-1FsIns1bp
MMRN1	multimerin 1	ENSG00000138722	PAP46	134	26.1%	chr4	91075980	CCDS3635.1	c.2126G>A	p.R709H
NFASC	neurofascin homolog (chicken)	ENSG00000163531	PAP46	154	35.1%	chr1	203189952	CCDS30982.1	c.211C>T	p.R71X
NULL	NULL	ENSG00000212950	PAP46	95	20.0%	chr10	97105593	ENST00000371228	c.1234G>A	p.D412N
PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP46	76	31.6%	chr3	180418776	CCDS43171.1	c.1624G>A	p.E542K
PLEC	plectin	ENSG00000178209	PAP46	241	36.5%	chr8	145064201	CCDS43772.1	c.12187C>T	p.Q4063X
POLR3K	polymerase (RNA) III (DNA directed) polypeptide K; 12.3 kDa	ENSG00000161980	PAP46	186	41.4%	chr16	37503	CCDS10395.1	c.254G>A	p.R85H
PCDHA2	protocadherin alpha 2	ENSG00000204969	PAP46	46	34.8%	chr5	140156357	CCDS34247.1	c.1624G>A	p.V542M
RAPGEFL1	Rap guanine nucleotide exchange factor (GEF)-like 1	ENSG00000108352	PAP46	65	38.5%	chr17	35594035	CCDS11363.1	c.25C>T	p.R9W
ROBO2	roundabout; axon guidance receptor; homolog 2 (Drosophila)	ENSG00000185008	PAP46	215	27.0%	chr3	77682756	CCDS43109.1	c.1157C>T	p.A386V
SLC44A5	solute carrier family 44; member 5	ENSG00000137968	PAP46	69	24.6%	chr1	75779714	CCDS667.1	c.7G>T	p.D3Y
SLC6A1	solute carrier family 6 (neurotransmitter transporter; GABA); member 1	ENSG00000157103	PAP46	134	41.8%	chr3	11034013	CCDS2603.1	c.116C>A	p.A39E
SCAF1	SR-related CTD-associated factor 1	ENSG00000126461	PAP46	126	27.0%	chr19	54841897	CCDS33074.1	c.476C>T	p.T159M
TGM4	transglutaminase 4 (prostate)	ENSG00000163810	PAP46	178	33.1%	chr3	44904291	CCDS2723.1	c.300G>T	p.E100D
TMEM8B	transmembrane protein 8B	ENSG00000137103	PAP46	122	39.3%	chr9	35843587	CCDS43800.1	c.1169C>A	p.A390E
MYCN	v-myc myelocytomatosis viral related oncogene; neuroblastoma derived (avian)	ENSG00000134323	PAP46	247	36.4%	chr2	15999768	CCDS1687.1	c.131C>T	p.P44L
ZBP1	Z-DNA binding protein 1	ENSG00000124256	PAP46	250	36.4%	chr20	55618744	CCDS13461.1	c.960G>T	p.Q320H
ZNF774	zinc finger protein 774	ENSG00000196391	PAP46	269	33.5%	chr15	88705139	CCDS32330.1	c.1072C>G	p.Q358E
AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	ENSG00000138678	PAP47	190	31.6%	chr4	84744901	CCDS3606.1	c.1262A>C	p.K421T
HACL1	2-hydroxyacyl-CoA lyase 1	ENSG00000131373	PAP47	165	25.5%	chr3	15585023	CCDS2627.1	c.1170A>C	p.R390S
BDH1	3-hydroxybutyrate dehydrogenase; type 1	ENSG00000161267	PAP47	48	22.9%	chr3	198757663	CCDS3328.1	c.131NULL>A	p.NULL-1FsIns1bp
ABAT	4-aminobutyrate aminotransferase	ENSG00000183044	PAP47	108	10.2%	chr16	8774162	CCDS10534.1	c.841C>T	p.R281W
HTR1E	5-hydroxytryptamine (serotonin) receptor 1E	ENSG00000168830	PAP47	391	10.2%	chr6	87781959	CCDS5006.1	c.188C>A	p.S63Y
NT5C1A	5'-nucleotidase; cytosolic IA	ENSG00000116981	PAP47	273	10.6%	chr1	39899517	CCDS440.1	c.562G>A	p.A188T
NT5C2	5'-nucleotidase; cytosolic II	ENSG00000076685	PAP47	71	28.2%	chr10	104847048	CCDS7544.1	c.761A>C	p.K254T
PFKFB1	6-phosphofructo-2-kinase/fructose-2;6-biphosphatase 1	ENSG00000158571	PAP47	120	25.8%	chrX	55006529	CCDS14364.1	c.234C>NULL	p.NULL-1FsDel1bp

AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	ENSG00000127914	PAP47	78	12.8%	chr7	91469878	CCDS5622.1	c.2711G>T	p.R904I
AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	ENSG00000127914	PAP47	170	26.5%	chr7	91520132	CCDS5622.1	c.5525T>G	p.L1842R
AKAP1	A kinase (PRKA) anchor protein 1	ENSG00000121057	PAP47	87	21.8%	chr17	52538707	CCDS11594.1	c.883G>A	p.A295T
AKAP13	A kinase (PRKA) anchor protein 13	ENSG00000170776	PAP47	192	14.1%	chr15	84066272	CCDS32320.1	c.6311T>G	p.F2104C
AKAP14	A kinase (PRKA) anchor protein 14	ENSG00000186471	PAP47	133	27.8%	chrX	118921373	CCDS14591.1	c.159G>T	p.K53N
ABHD5	abhydrolase domain containing 5	ENSG00000011198	PAP47	157	31.2%	chr3	43718781	CCDS2711.1	c.204C>A	p.F68L
AIM2	absent in melanoma 2	ENSG00000163568	PAP47	202	19.8%	chr1	157302617	CCDS1181.1	c.523G>A	p.E175K
AIM2	absent in melanoma 2	ENSG00000163568	PAP47	159	28.3%	chr1	157309833	CCDS1181.1	c.81C>A	p.F27L
ACACA	acetyl-CoA carboxylase alpha	ENSG00000132142	PAP47	376	26.1%	chr17	32528903	CCDS42302.1	c.6695G>A	p.R2232Q
ACPP	acid phosphatase; prostate	ENSG00000014257	PAP47	148	23.6%	chr3	133533736	CCDS3073.1	c.314G>A	p.R105Q
ANP32D	acidic (leucine-rich) nuclear phosphoprotein 32 family; member D	ENSG00000139223	PAP47	40	25.0%	chr12	47152775	CCDS31788.1	c.61G>T	p.E21X
ANP32D	acidic (leucine-rich) nuclear phosphoprotein 32 family; member D	ENSG00000139223	PAP47	87	29.9%	chr12	47152997	CCDS31788.1	c.283T>G	p.L95V
ACN9	ACN9 homolog (S. cerevisiae)	ENSG00000196636	PAP47	116	26.7%	chr7	96648456	CCDS5648.1	c.371A>T	p.K124I
ABLIM1	actin binding LIM protein 1	ENSG00000099204	PAP47	350	27.4%	chr10	116407849	CCDS7590.1	c.101G>T	p.R34I
ASCC3	activating signal cointegrator 1 complex subunit 3	ENSG00000112249	PAP47	142	28.2%	chr6	101280281	CCDS5046.1	c.1757A>C	p.E586A
ATF6B	activating transcription factor 6 beta	ENSG00000213676	PAP47	116	22.4%	chr6	32201911	CCDS4737.1	c.439G>A	p.V147I
ATF7IP	activating transcription factor 7 interacting protein	ENSG00000171681	PAP47	69	34.8%	chr12	14480373	CCDS8663.1	c.1712G>A	p.R571Q
ABR	active BCR-related gene	ENSG00000159842	PAP47	359	27.9%	chr17	975308	CCDS10999.1	c.206A>G	p.D69G
ACVR2B	activin A receptor; type IIB	ENSG00000114739	PAP47	249	36.1%	chr3	38494752	CCDS2679.1	c.487C>T	p.R163C
ACSL4	acyl-CoA synthetase long-chain family member 4	ENSG00000068366	PAP47	108	34.3%	chrX	108810887	CCDS14548.1	c.774A>C	p.E258D
ACOT6	acyl-CoA thioesterase 6	ENSG00000205669	PAP47	213	29.6%	chr14	73155952	CCDS32118.1	c.280C>A	p.L94I
AWAT2	acyl-CoA wax alcohol acyltransferase 2	ENSG00000147160	PAP47	104	27.9%	chrX	69178506	NM_001002254	c.879G>T	p.E293D
AOAH	acyloxyacyl hydrolase (neutrophil)	ENSG00000136250	PAP47	71	35.2%	chr7	36622590	CCDS5448.1	c.767G>A	p.G256E
ADAM23	ADAM metallopeptidase domain 23	ENSG00000114948	PAP47	225	25.8%	chr2	207132923	CCDS2369.1	c.-1G>T	p.IVS10-1-1SpliceAcceptor
ADAMTS15	ADAM metallopeptidase with thrombospondin type 1 motif; 15	ENSG00000166106	PAP47	303	31.4%	chr11	129824300	CCDS8488.1	c.222C>A	p.F74L
ADAMTS18	ADAM metallopeptidase with thrombospondin type 1 motif; 18	ENSG00000140873	PAP47	180	27.2%	chr16	76022826	CCDS10926.1	c.362A>C	p.H121P
ADAMTS4	ADAM metallopeptidase with thrombospondin type 1 motif; 4	ENSG00000158859	PAP47	176	30.1%	chr1	159433294	CCDS1223.1	c.634C>T	p.R212C
ADAMTSL4	ADAMTS-like 4	ENSG00000143382	PAP47	209	33.0%	chr1	148792275	CCDS955.1	c.356G>A	p.R119Q
AP2B1	adaptor-related protein complex 2; beta 1 subunit	ENSG00000006125	PAP47	32	31.3%	chr17	30949408	CCDS32621.1	c.84A>C	p.E28D
APCDD1L	adenomatosis polyposis coli down-regulated 1-like	ENSG00000198768	PAP47	125	30.4%	chr20	56469639	CCDS13467.1	c.1119C>A	p.F373L
APC	adenomatous polyposis coli	ENSG00000134982	PAP47	132	29.5%	chr5	112202781	CCDS4107.1	c.3591C>A	p.F1197L
ADORA3	adenosine A3 receptor	ENSG00000121933	PAP47	188	26.6%	chr1	111844374	CCDS839.1	c.678C>A	p.F226L
AMPD1	adenosine monophosphate deaminase 1	ENSG00000116748	PAP47	59	22.0%	chr1	115020129	CCDS876.1	c.1407G>T	p.K469N
ADCY10	adenylate cyclase 10 (soluble)	ENSG00000143199	PAP47	254	27.2%	chr1	166081653	CCDS1265.1	c.2779C>T	p.R927X
ADCY2	adenylate cyclase 2 (brain)	ENSG00000078295	PAP47	161	37.3%	chr5	7870001	CCDS3872.2	c.2906A>G	p.H969R
ADCY3	adenylate cyclase 3	ENSG00000138031	PAP47	174	29.9%	chr2	24897217	CCDS1715.1	c.3132G>T	p.M1044I
ADCY5	adenylate cyclase 5	ENSG00000173175	PAP47	130	26.9%	chr3	124488304	CCDS3022.1	c.3575G>A	p.R1192Q
ADCY9	adenylate cyclase 9	ENSG00000162104	PAP47	231	28.1%	chr16	3956580	CCDS32382.1	c.3259G>A	p.E1087K
ARFGAP2	ADP-ribosylation factor GTPase activating protein 2	ENSG00000149182	PAP47	404	29.0%	chr11	47146249	CCDS7926.1	c.-1G>T	p.IVS11+1-1SpliceDonor
ARFGEF2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	ENSG00000124198	PAP47	51	19.6%	chr20	47003515	CCDS13411.1	c.619G>T	p.E207X
ARFIP2	ADP-ribosylation factor interacting protein 2	ENSG00000132254	PAP47	247	30.8%	chr11	6456732	CCDS7765.1	c.349C>T	p.R117X
AEBP1	AE binding protein 1	ENSG00000106624	PAP47	97	34.0%	chr7	44112718	CCDS5476.1	c.302A>C	p.K101T
AFM	afamin	ENSG00000079557	PAP47	40	27.5%	chr4	74573282	CCDS3557.1	c.785T>G	p.V262G
AHNAK	AHNAK nucleoprotein	ENSG00000124942	PAP47	162	30.2%	chr11	62043311	CCDS31584.1	c.15154G>T	p.D5052Y
AHNAK	AHNAK nucleoprotein	ENSG00000124942	PAP47	132	27.3%	chr11	62049658	CCDS31584.1	c.8807A>C	p.D2936A

ALDH1L2	aldehyde dehydrogenase 1 family; member L2	ENSG00000136010	PAP47	77	26.0%	chr12	103986625	CCDS31891.1	c.-1T>C	p.IVS4+2-1SpliceDonor
ALDH18A1	aldehyde dehydrogenase 18 family; member A1	ENSG00000059573	PAP47	279	30.5%	chr10	97363896	CCDS7443.1	c.1618G>T	p.E540X
ALPL	alkaline phosphatase; liver/bone/kidney	ENSG00000162551	PAP47	409	26.4%	chr1	21762263	CCDS217.1	c.371A>C	p.N124T
ALKBH3	alkB; alkylation repair homolog 3 (E. coli)	ENSG00000166199	PAP47	114	11.4%	chr11	43875401	ENST00000378840	c.448C>T	p.R150C
ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog; S. cerevisiae)	ENSG00000085224	PAP47	42	31.0%	chrX	76798731	CCDS14434.1	c.4189G>A	p.E1397K
ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog; S. cerevisiae)	ENSG00000085224	PAP47	126	27.0%	chrX	76823760	CCDS14434.1	c.3644C>A	p.S1215Y
ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog; S. cerevisiae)	ENSG00000085224	PAP47	78	38.5%	chrX	76824334	CCDS14434.1	c.3070G>T	p.E1024X
AMBP	alpha-1-microglobulin/bikunin precursor	ENSG00000106927	PAP47	50	36.0%	chr9	115864785	CCDS6800.1	c.678G>T	p.K226N
A2M	alpha-2-macroglobulin	ENSG00000175899	PAP47	54	24.1%	chr12	9123987	NM_000014	c.2824G>T	p.E942X
A2ML1	alpha-2-macroglobulin-like 1	ENSG00000166535	PAP47	143	33.6%	chr12	8907659	CCDS8596.2	c.3505G>T	p.E1169X
ALPK2	alpha-kinase 2	ENSG00000198796	PAP47	247	32.4%	chr18	54354069	CCDS11966.2	c.4330G>A	p.E1444K
ALPK2	alpha-kinase 2	ENSG00000198796	PAP47	66	21.2%	chr18	54398695	CCDS11966.2	c.293G>T	p.C98F
ALMS1	Alstrom syndrome 1	ENSG00000116127	PAP47	473	26.6%	chr2	73531602	CCDS42697.1	c.4437G>T	p.E1479D
ACCN5	amiloride-sensitive cation channel 5; intestinal	ENSG00000023843	PAP47	133	28.6%	chr4	157004292	CCDS3793.1	c.105G>T	p.K35N
AOC2	amine oxidase; copper containing 2 (retina-specific)	ENSG00000131480	PAP47	250	30.0%	chr17	38250889	CCDS11443.1	c.720G>T	p.E240D
AGL	amylo-alpha-1; 6-glucosidase; 4-alpha-glucanotransferase	ENSG00000162688	PAP47	117	21.4%	chr1	100099791	CCDS759.1	c.227A>G	p.D76G
APBA1	amyloid beta (A4) precursor protein-binding; family A; member 1	ENSG00000107282	PAP47	73	32.9%	chr9	71236131	CCDS6630.1	c.2446C>A	p.H816N
APBB2	amyloid beta (A4) precursor protein-binding; family B; member 2	ENSG00000163697	PAP47	93	31.2%	chr4	40631261	CCDS43224.1	c.1157C>T	p.S386F
AR	androgen receptor	ENSG00000169083	PAP47	94	16.0%	chrX	66682866	CCDS14387.1	c.1153G>A	p.A385T
AMOT	angiomotin	ENSG00000126016	PAP47	63	28.6%	chrX	111921726	CCDS14563.1	c.689G>T	p.R230I
AMOT	angiomotin	ENSG00000126016	PAP47	297	25.9%	chrX	111952941	NM_001113490	c.70C>T	p.R24C
ANLN	anillin; actin binding protein	ENSG00000011426	PAP47	57	35.1%	chr7	36428814	CCDS5447.1	c.2347G>A	p.E783K
ANKHD1-EIF	ANKHD1-EIF4EBP3 readthrough	ENSG00000131503	PAP47	232	22.4%	chr5	139824517	CCDS4224.1	c.1754A>G	p.D585G
ANK2	ankyrin 2; neuronal	ENSG00000145362	PAP47	69	23.2%	chr4	114337064	CCDS3702.1	c.278C>T	p.A93V
ANKHD1	ankyrin repeat and KH domain containing 1	ENSG00000131503	PAP47	232	22.4%	chr5	139824517	CCDS4224.1	c.1754A>G	p.D585G
ANKMY1	ankyrin repeat and MYND domain containing 1	ENSG00000144504	PAP47	233	29.2%	chr2	241100942	CCDS2536.1	c.1828G>A	p.D610N
ANKMY2	ankyrin repeat and MYND domain containing 2	ENSG00000106524	PAP47	94	21.3%	chr7	16622012	CCDS5361.1	c.413G>A	p.R138Q
ANKRD27	ankyrin repeat domain 27 (VPS9 domain)	ENSG00000105186	PAP47	136	22.8%	chr19	37787152	CCDS32986.1	c.2512G>A	p.A838T
ANKRD5	ankyrin repeat domain 5	ENSG00000132623	PAP47	91	28.6%	chr20	9978754	CCDS13108.1	c.1537G>T	p.E513X
ANO4	anoctamin 4	ENSG00000151572	PAP47	77	35.1%	chr12	100034629	CCDS31884.1	c.2387G>A	p.R796Q
AQR	aquarius homolog (mouse)	ENSG00000021776	PAP47	80	35.0%	chr15	32999845	CCDS42013.1	c.1201G>T	p.E401X
ALOX5	arachidonate 5-lipoxygenase	ENSG00000012779	PAP47	184	29.9%	chr10	45261081	CCDS7212.1	c.1965G>T	p.K655N
AGFG2	ArfGAP with FG repeats 2	ENSG00000106351	PAP47	301	30.2%	chr7	99998506	CCDS5697.1	c.-1G>T	p.IVS9+1-1SpliceDonor
AGAP2	ArfGAP with GTPase domain; ankyrin repeat and PH domain 2	ENSG00000135439	PAP47	251	26.7%	chr12	56411519	CCDS8951.1	c.1034G>A	p.S345N
ASAP3	ArfGAP with SH3 domain; ankyrin repeat and PH domain 3	ENSG00000088280	PAP47	123	30.9%	chr1	23635725	CCDS235.1	c.1486A>C	p.N496H
RSRC2	arginine/serine-rich coiled-coil 2	ENSG00000111011	PAP47	145	30.3%	chr12	121556133	CCDS31920.1	c.1199T>C	p.F400S
ARMC2	armadillo repeat containing 2	ENSG00000118690	PAP47	109	28.4%	chr6	109304120	NM_032131	c.545C>A	p.S182X
ARMCX5	armadillo repeat containing; X-linked 5	ENSG00000125962	PAP47	156	18.6%	chrX	101743823	CCDS14500.1	c.98A>C	p.K33T
ARMCX5	armadillo repeat containing; X-linked 5	ENSG00000125962	PAP47	144	32.6%	chrX	101745127	CCDS14500.1	c.1402G>T	p.E468X
ACTR5	ARP5 actin-related protein 5 homolog (yeast)	ENSG00000101442	PAP47	93	28.0%	chr20	36828344	CCDS13308.1	c.1343G>T	p.R448I
ARRDC3	arrestin domain containing 3	ENSG00000113369	PAP47	264	27.7%	chr5	90714529	CCDS34202.1	c.137C>A	p.S46Y
ARSF	arylsulfatase F	ENSG00000062096	PAP47	473	32.6%	chrX	3040299	CCDS14123.1	c.1475G>C	p.R492T
ASPM	asp (abnormal spindle) homolog; microcephaly associated (Drosophila)	ENSG00000066279	PAP47	61	29.5%	chr1	195324115	CCDS1389.1	c.10055T>C	p.I3352T
ALG2	asparagine-linked glycosylation 2; alpha-1;3-mannosyltransferase homolog (S. cerevisiae)	ENSG00000119523	PAP47	264	31.1%	chr9	101020251	CCDS6739.1	c.1037C>T	p.S346L

ASPH	aspartate beta-hydroxylase	ENSG00000198363	PAP47	91	28.6%	chr8	62740546	CCDS34900.1	c.496G>T	p.E166X
DARS	aspartyl-tRNA synthetase	ENSG00000115866	PAP47	95	28.4%	chr2	136386533	CCDS2180.1	c.1223G>T	p.R408I
ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP47	332	28.6%	chr1	26978941	CCDS285.1	c.5965C>T	p.R1989X
ARID4A	AT rich interactive domain 4A (RBP1-like)	ENSG00000032219	PAP47	77	33.8%	chr14	57900961	CCDS9732.1	c.2401G>T	p.D801Y
ARID5B	AT rich interactive domain 5B (MRF1-like)	ENSG00000150347	PAP47	31	45.2%	chr10	63515633	CCDS31208.1	c.1366G>T	p.E456X
ATXN1	ataxin 1	ENSG00000124788	PAP47	189	12.7%	chr6	16414936	CCDS34342.1	c.2051C>T	p.S684L
ATMIN	ATM interactor	ENSG00000166454	PAP47	139	22.3%	chr16	79635527	CCDS32494.1	c.1923C>A	p.F641L
ATP5B	ATP synthase; H+ transporting; mitochondrial F1 complex; beta polypeptide	ENSG00000110955	PAP47	48	27.1%	chr12	55319313	CCDS8924.1	c.1333G>T	p.E445X
ATP5SL	ATP5S-like	ENSG00000105341	PAP47	313	27.2%	chr19	46631329	CCDS33032.1	c.386T>C	p.V129A
ATAD5	ATPase family; AAA domain containing 5	ENSG00000176208	PAP47	35	34.3%	chr17	26220446	CCDS11260.1	c.3368G>A	p.R1123H
ATP13A3	ATPase type 13A3	ENSG00000133657	PAP47	265	24.9%	chr3	195639362	CCDS43187.1	c.1966G>A	p.E656K
ATP13A3	ATPase type 13A3	ENSG00000133657	PAP47	93	34.4%	chr3	195640947	CCDS43187.1	c.1754G>A	p.R585Q
ATP8B1	ATPase; aminophospholipid transporter; class I; type 8B; member 1	ENSG00000081923	PAP47	65	21.5%	chr18	53470876	CCDS11965.1	c.3099C>A	p.F1033L
ATP2B1	ATPase; Ca++ transporting; plasma membrane 1	ENSG00000070961	PAP47	139	25.9%	chr12	88529154	CCDS9035.1	c.2194C>A	p.L732M
ATP2B2	ATPase; Ca++ transporting; plasma membrane 2	ENSG00000157087	PAP47	161	13.7%	chr3	10345751	CCDS33701.1	c.3479C>T	p.S1160F
ATP2B2	ATPase; Ca++ transporting; plasma membrane 2	ENSG00000157087	PAP47	86	30.2%	chr3	10352920	ENST00000342354	c.3485C>T	p.S1162L
ATP8B4	ATPase; class I; type 8B; member 4	ENSG00000104043	PAP47	78	20.5%	chr15	48186430	CCDS32238.1	c.26G>A	p.R9H
ATP10B	ATPase; class V; type 10B	ENSG00000118322	PAP47	175	28.6%	chr5	159993813	ENST00000326831	c.1423C>T	p.L475F
ATP11C	ATPase; class VI; type 11C	ENSG00000101974	PAP47	86	37.2%	chrX	138647874	CCDS14668.1	c.3164G>T	p.R1055I
ATP6V1E1	ATPase; H+ transporting; lysosomal 31kDa; V1 subunit E1	ENSG00000131100	PAP47	102	11.8%	chr22	16457351	CCDS13745.1	c.562C>T	p.R188C
ATP6V1A	ATPase; H+ transporting; lysosomal 70kDa; V1 subunit A	ENSG00000114573	PAP47	106	21.7%	chr3	114982670	CCDS2976.1	c.166C>T	p.R56X
ATP1A4	ATPase; Na+/K+ transporting; alpha 4 polypeptide	ENSG00000132681	PAP47	141	26.2%	chr1	158413958	CCDS1197.1	c.2616C>A	p.F872L
ABCA12	ATP-binding cassette; sub-family A (ABC1); member 12	ENSG00000144452	PAP47	58	22.4%	chr2	215551317	CCDS33372.1	c.5096C>A	p.S1699Y
ABCA12	ATP-binding cassette; sub-family A (ABC1); member 12	ENSG00000144452	PAP47	82	19.5%	chr2	215584474	CCDS33372.1	c.2266G>T	p.D756Y
ABCA12	ATP-binding cassette; sub-family A (ABC1); member 12	ENSG00000144452	PAP47	98	28.6%	chr2	215592609	CCDS33372.1	c.1444G>A	p.E482K
ABCA13	ATP-binding cassette; sub-family A (ABC1); member 13	ENSG00000179869	PAP47	86	24.4%	chr7	48286328	ENST00000319379	c.6354A>C	p.K2118N
ABCA13	ATP-binding cassette; sub-family A (ABC1); member 13	ENSG00000179869	PAP47	56	32.1%	chr7	48286593	ENST00000319379	c.6619G>T	p.D2207Y
ABCA13	ATP-binding cassette; sub-family A (ABC1); member 13	ENSG00000179869	PAP47	58	22.4%	chr7	48481676	ENST00000319379	c.12744G>T	p.K4248N
ABCA4	ATP-binding cassette; sub-family A (ABC1); member 4	ENSG00000198691	PAP47	235	27.2%	chr1	94315971	CCDS747.1	c.1417A>T	p.I473F
ABCB1	ATP-binding cassette; sub-family B (MDR/TAP); member 1	ENSG00000085563	PAP47	150	22.7%	chr7	86988128	CCDS5608.1	c.2686A>G	p.I896V
ABCB6	ATP-binding cassette; sub-family B (MDR/TAP); member 6	ENSG00000115657	PAP47	66	22.7%	chr2	219789767	CCDS2436.1	c.719G>A	p.R240Q
ABCB7	ATP-binding cassette; sub-family B (MDR/TAP); member 7	ENSG00000131269	PAP47	117	12.0%	chrX	74208227	CCDS14428.1	c.1052G>T	p.R351I
ABCC12	ATP-binding cassette; sub-family C (CFTR/MRP); member 12	ENSG00000140798	PAP47	178	21.9%	chr16	46703280	CCDS10730.1	c.2032G>T	p.E678X
ABCC2	ATP-binding cassette; sub-family C (CFTR/MRP); member 2	ENSG00000023839	PAP47	156	24.4%	chr10	101557897	CCDS7484.1	c.1736C>T	p.A579V
ABCD1	ATP-binding cassette; sub-family D (ALD); member 1	ENSG00000101986	PAP47	37	45.9%	chrX	152644046	CCDS14728.1	c.131G>A	p.R44K
ABCD2	ATP-binding cassette; sub-family D (ALD); member 2	ENSG00000173208	PAP47	111	25.2%	chr12	38298772	CCDS8734.1	c.913G>T	p.E305X
ATRNL1	attractin-like 1	ENSG00000107518	PAP47	50	22.0%	chr10	117218821	CCDS7592.1	c.3646A>C	p.K1216Q
AMBRA1	autophagy/beclin-1 regulator 1	ENSG00000110497	PAP47	58	29.3%	chr11	46412981	CCDS31475.1	c.2545C>T	p.R849X
AXIN2	axin 2	ENSG00000168646	PAP47	127	18.9%	chr17	60963929	CCDS11662.1	c.1687G>A	p.E563K
BIRC7	baculoviral IAP repeat-containing 7	ENSG00000101197	PAP47	122	32.0%	chr20	61341196	CCDS13513.1	c.691C>A	p.L231I
BAIAP3	BAI1-associated protein 3	ENSG00000007516	PAP47	307	33.6%	chr16	1338006	CCDS10434.1	c.3241G>A	p.E1081K
BCL10	B-cell CLL/lymphoma 10	ENSG00000142867	PAP47	117	24.8%	chr1	85505936	CCDS704.1	c.664T>C	p.F222L
BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	ENSG00000127152	PAP47	47	34.0%	chr14	98711235	CCDS9950.1	c.1691G>A	p.R564H
BCL9	B-cell CLL/lymphoma 9	ENSG00000116128	PAP47	167	28.1%	chr1	145551445	CCDS30833.1	c.193G>T	p.D65Y
BCL9	B-cell CLL/lymphoma 9	ENSG00000116128	PAP47	240	32.9%	chr1	145562864	CCDS30833.1	c.3761G>A	p.R1254Q
BCLAF1	BCL2-associated transcription factor 1	ENSG00000029363	PAP47	701	22.7%	chr6	136641534	CCDS5177.1	c.178G>A	p.D60N
B3GAT3	beta-1;3-glucuronyltransferase 3 (glucuronosyltransferase I)	ENSG00000149541	PAP47	50	20.0%	chr11	62144585	CCDS8025.1	c.217G>A	p.A73T
BAAT	bile acid CoA: amino acid N-acyltransferase (glycine N-choloyltransferase)	ENSG00000136881	PAP47	240	17.1%	chr9	103164898	CCDS6752.1	c.890G>A	p.R297H
BMPER	BMP binding endothelial regulator	ENSG00000164619	PAP47	86	31.4%	chr7	34061402	CCDS5442.1	c.889G>T	p.D297Y
BMP15	bone morphogenetic protein 15	ENSG00000130385	PAP47	140	30.0%	chrX	50676156	CCDS14334.1	c.988G>A	p.D330N

BMP4	bone morphogenetic protein 4	ENSG00000125378	PAP47	168	24.4%	chr14	53486639	CCDS9715.1	c.1088C>A	p.S363Y
BMPR2	bone morphogenetic protein receptor; type II (serine/threonine kinase)	ENSG00000204217	PAP47	219	34.7%	chr2	203128384	CCDS33361.1	c.1751G>A	p.R584Q
BRSK1	BR serine/threonine kinase 1	ENSG00000160469	PAP47	101	27.7%	chr19	60506002	CCDS12921.1	c.983G>A	p.C328Y
BRSK1	BR serine/threonine kinase 1	ENSG00000160469	PAP47	107	28.0%	chr19	60506028	CCDS12921.1	c.1009C>T	p.R337C
BDNF	brain-derived neurotrophic factor	ENSG00000176697	PAP47	313	20.8%	chr11	27636456	CCDS41628.1	c.277C>T	p.R93W
BAI1	brain-specific angiogenesis inhibitor 1	ENSG00000181790	PAP47	225	25.8%	chr8	143555813	NM_001702	c.1288C>T	p.R430W
BAI3	brain-specific angiogenesis inhibitor 3	ENSG00000135298	PAP47	66	19.7%	chr6	69405702	CCDS4968.1	c.414C>A	p.F138L
BAI3	brain-specific angiogenesis inhibitor 3	ENSG00000135298	PAP47	88	11.4%	chr6	69741477	CCDS4968.1	c.1627G>T	p.G543C
BAI3	brain-specific angiogenesis inhibitor 3	ENSG00000135298	PAP47	225	27.1%	chr6	70127545	CCDS4968.1	c.3659C>T	p.S1220F
BRCC3	BRCA1/BRCA2-containing complex; subunit 3	ENSG00000185515	PAP47	179	12.3%	chrX	153958684	NM_024332	c.241C>T	p.R81X
BRCA1	breast cancer 1; early onset	ENSG00000012048	PAP47	93	20.4%	chr17	38509699	CCDS11453.1	c.407G>T	p.R136I
BAHD1	bromo adjacent homology domain containing 1	ENSG00000140320	PAP47	204	28.4%	chr15	38538374	CCDS10058.1	c.419T>C	p.L140P
BAZ1B	bromodomain adjacent to zinc finger domain; 1B	ENSG00000009954	PAP47	171	30.4%	chr7	72530363	CCDS5549.1	c.1364G>A	p.R455Q
BRD8	bromodomain containing 8	ENSG00000112983	PAP47	213	26.8%	chr5	137514491	CCDS4198.1	c.2962G>A	p.E988K
BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	ENSG00000169679	PAP47	115	23.5%	chr2	111115699	CCDS33273.1	c.2617A>G	p.T873A
BCHE	butyrylcholinesterase	ENSG00000114200	PAP47	99	32.3%	chr3	167031097	CCDS3198.1	c.419G>T	p.W140L
C1GALT1C1	C1GALT1-specific chaperone 1	ENSG00000171155	PAP47	192	30.2%	chrX	119644815	CCDS14602.1	c.235G>T	p.D79Y
CADPS	Ca++-dependent secretion activator	ENSG00000163618	PAP47	411	11.7%	chr3	62360224	CCDS2899.1	c.3842A>G	p.N1281S
ABL1	c-abl oncogene 1; receptor tyrosine kinase	ENSG00000097007	PAP47	72	38.9%	chr9	132720257	CCDS35165.1	c.559G>A	p.E187K
CDH10	cadherin 10; type 2 (T2-cadherin)	ENSG00000040731	PAP47	93	29.0%	chr5	24545643	CCDS3892.1	c.1045G>A	p.E349K
CDH2	cadherin 2; type 1; N-cadherin (neuronal)	ENSG00000170558	PAP47	69	34.8%	chr18	23847871	CCDS11891.1	c.173T>G	p.V58G
CDH2	cadherin 2; type 1; N-cadherin (neuronal)	ENSG00000170558	PAP47	172	20.3%	chr18	23870443	ENST00000399380	c.68T>C	p.V23A
CDH20	cadherin 20; type 2	ENSG00000101542	PAP47	69	18.8%	chr18	57321181	CCDS11977.1	c.677C>T	p.A226V
CDH22	cadherin 22; type 2	ENSG00000149654	PAP47	57	28.1%	chr20	44313134	CCDS13395.1	c.207C>A	p.F69L
CDH7	cadherin 7; type 2	ENSG00000081138	PAP47	167	29.9%	chr18	61698767	CCDS11993.1	c.2015G>T	p.R672I
CELSR2	cadherin; EGF LAG seven-pass G-type receptor 2 (flamingo homolog; Drosophila)	ENSG00000143126	PAP47	277	27.4%	chr1	109596999	CCDS796.1	c.2775G>T	p.E925D
CELSR3	cadherin; EGF LAG seven-pass G-type receptor 3 (flamingo homolog; Drosophila)	ENSG00000008300	PAP47	178	33.7%	chr3	48645995	CCDS43087.1	c.101C>T	p.P34L
CDHR1	cadherin-related family member 1	ENSG00000148600	PAP47	140	33.6%	chr10	85954318	CCDS7372.1	c.839G>A	p.R280Q
CDHR1	cadherin-related family member 1	ENSG00000148600	PAP47	232	26.7%	chr10	85964090	CCDS7372.1	c.2313G>T	p.E771D
CIB4	calcium and integrin binding family member 4	ENSG00000157884	PAP47	184	20.1%	chr2	26717636	CCDS33160.1	c.51C>A	p.Y17X
CACNA2D1	calcium channel; voltage-dependent; alpha 2/delta subunit 1	ENSG00000153956	PAP47	196	23.5%	chr7	81437928	CCDS5598.1	c.2203G>T	p.E735X
CACNA1S	calcium channel; voltage-dependent; L type; alpha 1S subunit	ENSG00000081248	PAP47	350	29.1%	chr1	199321272	CCDS1407.1	c.1065G>T	p.E355D
CALHM1	calcium homeostasis modulator 1	ENSG00000185933	PAP47	114	21.1%	chr10	105208284	CCDS7550.1	c.215A>G	p.N72S
CAMKK1	calcium/calmodulin-dependent protein kinase kinase 1; alpha	ENSG00000004660	PAP47	152	32.2%	chr17	3735403	CCDS11039.1	c.328G>A	p.E110K
CAPN6	calpain 6	ENSG00000077274	PAP47	143	27.3%	chrX	110382241	CCDS14555.1	c.649G>T	p.E217X
CLIP4	CAP-GLY domain containing linker protein family; member 4	ENSG00000115295	PAP47	176	22.7%	chr2	29208567	CCDS1770.1	c.319G>T	p.D107Y
CAD	carbamoyl-phosphate synthetase 2; aspartate transcarbamylase; and dihydroorotase	ENSG00000084774	PAP47	317	31.2%	chr2	27307894	CCDS1742.1	c.2342G>A	p.R781H
CHST15	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15	ENSG00000182022	PAP47	212	35.4%	chr10	125795583	CCDS7638.1	c.136C>T	p.R46C
CA13	carbonic anhydrase XIII	ENSG00000185015	PAP47	174	28.7%	chr8	86350295	CCDS6236.1	c.112G>T	p.E38X
CPVL	carboxypeptidase; vitellogenic-like	ENSG00000106066	PAP47	116	28.4%	chr7	29102248	CCDS5419.1	c.399G>T	p.M133I
CEACAM20	carcinoembryonic antigen-related cell adhesion molecule 20	ENSG00000176395	PAP47	93	23.7%	chr19	49720065	ENST00000316962	c.266A>G	p.Y89C
CEACAM5	carcinoembryonic antigen-related cell adhesion molecule 5	ENSG00000105388	PAP47	383	31.3%	chr19	46911462	CCDS12584.1	c.757G>A	p.E253K
CRTAP	cartilage associated protein	ENSG00000170275	PAP47	79	24.1%	chr3	33136898	CCDS2657.1	c.530A>G	p.D177G
CASD1	CAS1 domain containing 1	ENSG00000127995	PAP47	115	40.0%	chr7	94012845	CCDS5636.1	c.1529G>A	p.R510Q
CASD1	CAS1 domain containing 1	ENSG00000127995	PAP47	199	22.6%	chr7	94022923	CCDS5636.1	c.2311C>A	p.L771I
CASP5	caspase 5; apoptosis-related cysteine peptidase	ENSG00000137757	PAP47	182	25.3%	chr11	104376311	CCDS8328.1	c.1025NULL>/	p.NULL-1Fsins1bp
CTNNB1	catenin (cadherin-associated protein); beta 1; 88kDa	ENSG00000168036	PAP47	73	24.7%	chr3	41252295	CCDS2694.1	c.1760G>A	p.R587Q

CTNND2	catenin (cadherin-associated protein); delta 2 (neural plakophilin-related arm-repeat protein)	ENSG00000169862	PAP47	156	21.2%	chr5	11026780	CCDS3881.1	c.3463G>A	p.E1155K
CTSL2	cathepsin L2	ENSG00000136943	PAP47	263	23.6%	chr9	98840034	CCDS6723.1	c.113G>T	p.R38I
CATSPER1	cation channel; sperm associated 1	ENSG00000175294	PAP47	108	25.0%	chr11	65546958	CCDS8127.1	c.1367T>G	p.V456G
CATSPER4	cation channel; sperm associated 4	ENSG00000188782	PAP47	114	28.9%	chr1	26399120	CCDS30645.1	c.971G>A	p.R324Q
CDX1	caudal type homeobox 1	ENSG00000113722	PAP47	98	18.4%	chr5	149542588	CCDS4304.1	c.510G>T	p.E170D
CAV3	caveolin 3	ENSG00000182533	PAP47	396	32.3%	chr3	8762402	CCDS2569.1	c.305C>T	p.A102V
CTCF	CCCTC-binding factor (zinc finger protein)	ENSG00000102974	PAP47	217	25.3%	chr16	66202633	CCDS10841.1	c.397G>T	p.E133X
CTCF	CCCTC-binding factor (zinc finger protein)	ENSG00000102974	PAP47	214	28.0%	chr16	66219954	CCDS10841.1	c.1699C>T	p.R567W
CTCFL	CCCTC-binding factor (zinc finger protein)-like	ENSG00000124092	PAP47	104	16.3%	chr20	55531553	CCDS13459.1	c.731C>A	p.T244K
CD101	CD101 molecule	ENSG00000134256	PAP47	134	29.1%	chr1	117365958	CCDS891.1	c.2258C>T	p.T753I
CD163	CD163 molecule	ENSG00000177575	PAP47	104	20.2%	chr12	7523814	CCDS8578.1	c.3389C>A	p.S1130Y
CD2	CD2 molecule	ENSG00000116824	PAP47	167	28.1%	chr1	117098792	CCDS889.1	c.78G>T	p.E26D
CD22	CD22 molecule	ENSG00000012124	PAP47	176	23.9%	chr19	40529345	CCDS12457.1	c.2449G>T	p.D817Y
CD40	CD40 molecule; TNF receptor superfamily member 5	ENSG00000101017	PAP47	268	25.0%	chr20	44185198	CCDS13393.1	c.430G>A	p.E144K
CD93	CD93 molecule	ENSG00000125810	PAP47	218	27.1%	chr20	23013005	CCDS13149.1	c.1825C>T	p.R609W
CDC5L	CDC5 cell division cycle 5-like (S. pombe)	ENSG00000096401	PAP47	107	28.0%	chr6	44500224	CCDS4912.1	c.1495G>A	p.E499K
CDKAL1	CDK5 regulatory subunit associated protein 1-like 1	ENSG00000145996	PAP47	53	22.6%	chr6	20656835	CCDS4546.1	c.206G>A	p.R69Q
CADM3	cell adhesion molecule 3	ENSG00000162706	PAP47	48	22.9%	chr1	157432855	CCDS1182.1	c.871C>T	p.R291C
CHL1	cell adhesion molecule with homology to L1CAM (close homolog of L1)	ENSG00000134121	PAP47	97	40.2%	chr3	407720	CCDS2556.1	c.2669G>T	p.R890I
CDC25C	cell division cycle 25 homolog C (S. pombe)	ENSG00000158402	PAP47	90	20.0%	chr5	137655663	CCDS4202.1	c.657G>T	p.E219D
CDC7	cell division cycle 7 homolog (S. cerevisiae)	ENSG00000097046	PAP47	81	27.2%	chr1	91752139	CCDS734.1	c.869G>T	p.R290I
CDC73	cell division cycle 73; Paf1/RNA polymerase II complex component; homolog (S. cerevisiae)	ENSG00000134371	PAP47	138	18.1%	chr1	191365961	CCDS1382.1	c.272G>A	p.R91Q
CENPF	centromere protein F; 350/400ka (mitosin)	ENSG00000117724	PAP47	48	29.2%	chr1	212881902	CCDS31023.1	c.3598G>T	p.E1200X
CENPF	centromere protein F; 350/400ka (mitosin)	ENSG00000117724	PAP47	119	23.5%	chr1	212886979	CCDS31023.1	c.7443G>T	p.E2481D
CENPJ	centromere protein J	ENSG00000151849	PAP47	205	32.2%	chr13	24377748	CCDS9310.1	c.2428G>T	p.D810Y
CENPP	centromere protein P	ENSG00000188312	PAP47	77	13.0%	chr9	94181901	CCDS35063.1	c.503G>A	p.R168Q
CEP135	centrosomal protein 135kDa	ENSG00000174799	PAP47	32	31.3%	chr4	56541133	CCDS33986.1	c.1541G>T	p.R514I
CEP350	centrosomal protein 350kDa	ENSG00000135837	PAP47	133	25.6%	chr1	178329865	NM_014810	c.8002G>T	p.D2668Y
CERKL	ceramide kinase-like	ENSG00000188452	PAP47	67	22.4%	chr2	182121560	CCDS42789.1	c.1168A>C	p.I390L
CBLN4	cerebellin 4 precursor	ENSG00000054803	PAP47	135	29.6%	chr20	54007076	CCDS13448.1	c.550T>G	p.L184V
CCRL2	chemokine (C-C motif) receptor-like 2	ENSG00000121797	PAP47	169	24.9%	chr3	46425601	CCDS43079.1	c.1027G>A	p.E343K
CXCL11	chemokine (C-X-C motif) ligand 11	ENSG00000169248	PAP47	104	26.9%	chr4	77175431	CCDS3574.1	c.150A>G	p.I50M
CXCR2	chemokine (C-X-C motif) receptor 2	ENSG00000180871	PAP47	346	28.0%	chr2	218708631	CCDS2408.1	c.862C>T	p.R288C
CLCN5	chloride channel 5	ENSG00000171365	PAP47	318	27.4%	chrX	49742075	CCDS14328.1	c.1942C>T	p.R648X
CLCA1	chloride channel accessory 1	ENSG00000016490	PAP47	62	38.7%	chr1	86727393	CCDS709.1	c.1309T>G	p.L437V
CLCA4	chloride channel accessory 4	ENSG00000016602	PAP47	209	34.4%	chr1	86804268	CCDS41355.1	c.931C>A	p.L311I
CLCA4	chloride channel accessory 4	ENSG00000016602	PAP47	382	24.6%	chr1	86818425	CCDS41355.1	c.2569G>T	p.V857L
CETP	cholesteryl ester transfer protein; plasma	ENSG00000087237	PAP47	299	28.1%	chr16	55572606	CCDS10772.1	c.1182G>T	p.K394N
CHRNA10	cholinergic receptor; nicotinic; alpha 10	ENSG00000129749	PAP47	268	28.4%	chr11	3644025	CCDS7745.1	c.1241G>A	p.R414H
CHSY3	chondroitin sulfate synthase 3	ENSG00000198108	PAP47	188	27.1%	chr5	129548469	CCDS34223.1	c.1735G>T	p.D579Y
C1orf101	chromosome 1 open reading frame 101	ENSG00000179397	PAP47	89	25.8%	chr1	242869932	NM_001130957	c.2782C>T	p.R928W
C1orf105	chromosome 1 open reading frame 105	ENSG00000180999	PAP47	506	29.4%	chr1	170692241	CCDS1301.1	c.262G>T	p.E88X
C1orf125	chromosome 1 open reading frame 125	ENSG00000162779	PAP47	34	29.4%	chr1	177680962	CCDS30948.1	c.1798G>T	p.G600C
C1orf125	chromosome 1 open reading frame 125	ENSG00000162779	PAP47	63	38.1%	chr1	177761104	CCDS30948.1	c.2509G>T	p.E837X
C1orf127	chromosome 1 open reading frame 127	ENSG00000175262	PAP47	138	35.5%	chr1	10937802	CCDS121.1	c.306A>C	p.L102F
C1orf129	chromosome 1 open reading frame 129	ENSG00000117501	PAP47	106	33.0%	chr1	169234143	CCDS41436.1	c.1700C>A	p.S567Y
C1orf173	chromosome 1 open reading frame 173	ENSG00000178965	PAP47	72	31.9%	chr1	74844912	CCDS30755.1	c.1450G>T	p.E484X
C1orf220	chromosome 1 open reading frame 220	ENSG00000213057	PAP47	305	21.3%	chr1	176781308	CCDS1324.1	c.71G>T	p.R24I
C1orf25	chromosome 1 open reading frame 25	ENSG00000121486	PAP47	65	18.5%	chr1	183379662	CCDS1366.1	c.778C>T	p.R260W
C1orf26	chromosome 1 open reading frame 26	ENSG00000116668	PAP47	114	33.3%	chr1	183410525	CCDS1367.1	c.623G>T	p.R208I
C1orf57	chromosome 1 open reading frame 57	ENSG00000135778	PAP47	58	36.2%	chr1	231172320	CCDS1597.1	c.337G>A	p.D113N

C1orf66	chromosome 1 open reading frame 66	ENSG00000143303	PAP47	183	31.7%	chr1	154970798	CCDS1154.1	c.1010G>A	p.R337Q
C10orf68	chromosome 10 open reading frame 68	ENSG00000150076	PAP47	78	20.5%	chr10	33023839	CCDS31177.1	c.292C>A	p.L98I
C10orf71	chromosome 10 open reading frame 71	ENSG00000177354	PAP47	139	28.8%	chr10	50201656	NM_001135196	c.1060C>A	p.P354T
C10orf81	chromosome 10 open reading frame 81	ENSG00000148735	PAP47	43	30.2%	chr10	115524649	CCDS7583.1	c.854A>G	p.D285G
C10orf82	chromosome 10 open reading frame 82	ENSG00000165863	PAP47	181	30.4%	chr10	118413690	ENST00000388884	c.544G>A	p.D182N
C10orf90	chromosome 10 open reading frame 90	ENSG00000154493	PAP47	44	34.1%	chr10	128108355	CCDS31310.1	c.1952G>A	p.R651Q
C13orf33	chromosome 13 open reading frame 33	ENSG00000102802	PAP47	41	39.0%	chr13	30393808	CCDS9338.1	c.612C>A	p.F204L
C14orf4	chromosome 14 open reading frame 4	ENSG00000119669	PAP47	99	32.3%	chr14	76563799	CCDS9854.1	c.90C>A	p.F30L
C15orf27	chromosome 15 open reading frame 27	ENSG00000169758	PAP47	48	29.2%	chr15	74249254	CCDS10289.2	c.499G>A	p.E167K
C15orf33	chromosome 15 open reading frame 33	ENSG00000166262	PAP47	299	26.1%	chr15	47447029	CCDS32237.1	c.1179G>T	p.L393F
C16orf89	chromosome 16 open reading frame 89	ENSG00000153446	PAP47	125	26.4%	chr16	5037883	CCDS42116.1	c.1066C>T	p.P356S
C17orf104	chromosome 17 open reading frame 104	ENSG00000180336	PAP47	233	37.8%	chr17	40100469	NM_001145080	c.1664G>T	p.R555I
C17orf80	chromosome 17 open reading frame 80	ENSG00000141219	PAP47	174	23.0%	chr17	68743653	CCDS11694.1	c.437C>T	p.T146I
C19orf57	chromosome 19 open reading frame 57	ENSG00000132016	PAP47	195	23.1%	chr19	13861441	CCDS12299.1	c.1228G>T	p.D410Y
C2orf56	chromosome 2 open reading frame 56	ENSG00000003509	PAP47	43	25.6%	chr2	37312779	CCDS1788.1	c.82T>C	p.Y28H
C2orf85	chromosome 2 open reading frame 85	ENSG00000188011	PAP47	174	25.9%	chr2	242463818	CCDS42843.1	c.1438G>A	p.D480N
C20orf26	chromosome 20 open reading frame 26	ENSG00000089101	PAP47	47	34.0%	chr20	20180373	CCDS33447.1	c.2294A>G	p.D765G
C20orf29	chromosome 20 open reading frame 29	ENSG00000125843	PAP47	274	26.6%	chr20	3752642	CCDS13070.1	c.301G>A	p.A101T
C21orf91	chromosome 21 open reading frame 91	ENSG00000154642	PAP47	190	28.9%	chr21	18089452	CCDS42907.1	c.671C>T	p.S224L
C4orf17	chromosome 4 open reading frame 17	ENSG00000138813	PAP47	146	23.3%	chr4	100682236	CCDS3649.1	c.1027G>T	p.E343X
C4orf49	chromosome 4 open reading frame 49	ENSG00000137463	PAP47	66	31.8%	chr4	140409316	CCDS43269.1	c.240T>G	p.N80K
C5orf4	chromosome 5 open reading frame 4	ENSG00000170271	PAP47	127	26.8%	chr5	154183306	CCDS43390.1	c.406C>A	p.L136I
C5orf41	chromosome 5 open reading frame 41	ENSG00000164463	PAP47	69	27.5%	chr5	172450354	CCDS34293.1	c.566A>C	p.K189T
C6orf114	chromosome 6 open reading frame 114	ENSG00000187461	PAP47	169	34.9%	chr6	13578317	CCDS4525.1	c.175G>A	p.G59S
C6orf127	chromosome 6 open reading frame 127	ENSG00000204140	PAP47	407	19.7%	chr6	35863697	CCDS43456.1	c.298C>T	p.L100F
C6orf70	chromosome 6 open reading frame 70	ENSG00000130023	PAP47	64	25.0%	chr6	169923480	CCDS34576.1	c.1983G>T	p.K661N
C6orf72	chromosome 6 open reading frame 72	ENSG00000055211	PAP47	87	27.6%	chr6	149945302	CCDS5216.1	c.751G>T	p.D251Y
C7orf25	chromosome 7 open reading frame 25	ENSG00000136197	PAP47	451	31.3%	chr7	42916588	CCDS5466.1	c.437C>T	p.A146V
C7orf31	chromosome 7 open reading frame 31	ENSG00000153790	PAP47	54	33.3%	chr7	25148804	CCDS5394.1	c.839C>T	p.S280L
C9orf11	chromosome 9 open reading frame 11	ENSG00000120160	PAP47	159	28.3%	chr9	27274831	CCDS35001.1	c.775G>T	p.D259Y
C9orf119	chromosome 9 open reading frame 119	ENSG00000175854	PAP47	82	30.5%	chr9	130078319	CCDS43883.1	c.74C>A	p.P25H
C9orf96	chromosome 9 open reading frame 96	ENSG00000198870	PAP47	123	25.2%	chr9	135241243	CCDS35169.1	c.241C>T	p.R81W
C9orf98	chromosome 9 open reading frame 98	ENSG00000165695	PAP47	29	34.5%	chr9	134728939	CCDS6954.1	c.267G>T	p.E89D
CXorf22	chromosome X open reading frame 22	ENSG00000165164	PAP47	99	31.3%	chrX	35879212	CCDS14237.2	c.700G>A	p.A234T
CXorf22	chromosome X open reading frame 22	ENSG00000165164	PAP47	56	28.6%	chrX	35881755	CCDS14237.2	c.1172A>G	p.K391R
CXorf23	chromosome X open reading frame 23	ENSG00000173681	PAP47	244	30.3%	chrX	19894344	CCDS14194.2	c.386C>A	p.S129Y
CLRN1	clarin 1	ENSG00000163646	PAP47	381	20.2%	chr3	152173158	CCDS3153.1	c.28T>G	p.F10V
CLRN3	clarin 3	ENSG00000180745	PAP47	73	31.5%	chr10	129580945	CCDS7656.1	c.94G>T	p.A32S
F8	coagulation factor VIII; procoagulant component	ENSG00000185010	PAP47	90	30.0%	chrX	153829280	CCDS35457.1	c.2000T>C	p.F667S
CCDC130	coiled-coil domain containing 130	ENSG00000104957	PAP47	94	23.4%	chr19	13729605	CCDS12296.1	c.202C>T	p.R68C
CCDC147	coiled-coil domain containing 147	ENSG00000120051	PAP47	137	23.4%	chr10	106129806	CCDS31282.1	c.1203G>T	p.Q401H
CCDC30	coiled-coil domain containing 30	ENSG00000186409	PAP47	48	41.7%	chr1	42794572	CCDS30690.1	c.584T>G	p.I195S
CCDC41	coiled-coil domain containing 41	ENSG00000173588	PAP47	211	31.3%	chr12	93296861	CCDS41820.1	c.638T>A	p.L213H
CCDC68	coiled-coil domain containing 68	ENSG00000166510	PAP47	123	25.2%	chr18	50755075	CCDS11959.1	c.458A>C	p.K153T
CCDC88A	coiled-coil domain containing 88A	ENSG00000115355	PAP47	106	31.1%	chr2	55426844	CCDS33203.1	c.1012G>T	p.D338Y
CCDC90A	coiled-coil domain containing 90A	ENSG00000050393	PAP47	126	17.5%	chr6	13900188	CCDS35495.1	c.925C>T	p.R309W
CTHRC1	collagen triple helix repeat containing 1	ENSG00000164932	PAP47	191	25.1%	chr8	104459584	CCDS6299.1	c.526A>C	p.I176L
COL5A1	collagen; type V; alpha 1	ENSG00000130635	PAP47	195	28.7%	chr9	136844339	CCDS6982.1	c.3812C>A	p.P1271H
COL12A1	collagen; type XII; alpha 1	ENSG00000111799	PAP47	117	23.9%	chr6	75920924	CCDS43482.1	c.3493G>T	p.E1165X
COL14A1	collagen; type XIV; alpha 1	ENSG00000187955	PAP47	144	27.8%	chr8	121285212	CCDS34938.1	c.961G>A	p.D321N
COL14A1	collagen; type XIV; alpha 1	ENSG00000187955	PAP47	161	30.4%	chr8	121297870	CCDS34938.1	c.1697G>A	p.R566Q
COL18A1	collagen; type XVIII; alpha 1	ENSG00000182871	PAP47	119	28.6%	chr21	45739714	CCDS42972.1	c.2988G>T	p.M996I
COL22A1	collagen; type XXII; alpha 1	ENSG00000169436	PAP47	282	27.7%	chr8	139902800	CCDS6376.1	c.1006G>A	p.E336K
COL25A1	collagen; type XXV; alpha 1	ENSG00000188517	PAP47	58	22.4%	chr4	110441224	CCDS43258.1	c.331G>A	p.A111T

COMMD10	COMM domain containing 10	ENSG00000145781	PAP47	91	22.0%	chr5	115456188	CCDS34215.1	c.291G>T	p.E97D
C4BPA	complement component 4 binding protein; alpha	ENSG00000123838	PAP47	78	30.8%	chr1	205384677	CCDS1477.1	c.1786G>T	p.E596X
C9	complement component 9	ENSG00000113600	PAP47	153	27.5%	chr5	39377134	CCDS3929.1	c.347G>A	p.R116Q
CFB	complement factor B	ENSG00000204359	PAP47	213	26.3%	chr6	32022786	CCDS4729.1	c.322G>A	p.D108N
CFHR3	complement factor H-related 3	ENSG00000116785	PAP47	114	28.9%	chr1	195015583	CCDS30958.1	c.287A>G	p.Y96C
CFHR5	complement factor H-related 5	ENSG00000134389	PAP47	34	38.2%	chr1	195238369	CCDS1387.1	c.1282G>T	p.E428X
COG2	component of oligomeric golgi complex 2	ENSG00000135775	PAP47	69	15.9%	chr1	228865540	CCDS1584.1	c.331C>T	p.R111W
COG2	component of oligomeric golgi complex 2	ENSG00000135775	PAP47	182	25.8%	chr1	228873922	CCDS1584.1	c.812G>A	p.G271D
COG6	component of oligomeric golgi complex 6	ENSG00000133103	PAP47	83	21.7%	chr13	39149644	CCDS9370.1	c.468C>A	p.F156L
CNTN1	contactin 1	ENSG00000018236	PAP47	75	28.0%	chr12	39602353	CCDS8737.1	c.256C>T	p.L86F
CNTNAP2	contactin associated protein-like 2	ENSG00000174469	PAP47	123	30.1%	chr7	146460286	CCDS5889.1	c.1100C>A	p.S367Y
CPNE4	copine IV	ENSG00000196353	PAP47	42	33.3%	chr3	132887453	CCDS3072.1	c.547C>T	p.R183C
CRB1	crumbs homolog 1 (Drosophila)	ENSG00000134376	PAP47	317	22.4%	chr1	195657028	CCDS1390.1	c.1447G>A	p.A483T
CSE1L	CSE1 chromosome segregation 1-like (yeast)	ENSG00000124207	PAP47	118	28.8%	chr20	47118757	CCDS13412.1	c.666A>C	p.L222F
CTR9	Ctr9; Paf1/RNA polymerase II complex component; homolog (S. cerevisiae)	ENSG00000198730	PAP47	117	26.5%	chr11	10740067	CCDS7805.1	c.-1T>G	p.IVS6-3-1SpliceAcceptor
CLEC9A	C-type lectin domain family 9; member A	ENSG00000197992	PAP47	48	25.0%	chr12	10106930	CCDS8611.1	c.329G>T	p.S110I
CLECL1	C-type lectin-like 1	ENSG00000184293	PAP47	39	38.5%	chr12	9777113	CCDS8603.1	c.15C>A	p.F5L
CSMD3	CUB and Sushi multiple domains 3	ENSG00000164796	PAP47	84	14.3%	chr8	113395377	CCDS6315.1	c.7630G>T	p.E2544X
CSMD3	CUB and Sushi multiple domains 3	ENSG00000164796	PAP47	152	28.3%	chr8	113464995	CCDS6315.1	c.6008C>A	p.A2003D
CSMD3	CUB and Sushi multiple domains 3	ENSG00000164796	PAP47	51	29.4%	chr8	114036100	CCDS6315.1	c.1409A>C	p.K470T
CUZD1	CUB and zona pellucida-like domains 1	ENSG00000138161	PAP47	95	27.4%	chr10	124584330	CCDS7631.1	c.1264C>A	p.L422I
CUBN	cubilin (intrinsic factor-cobalamin receptor)	ENSG00000107611	PAP47	94	34.0%	chr10	17170278	CCDS7113.1	c.1838G>T	p.G613V
CUL1	cullin 1	ENSG00000055130	PAP47	72	26.4%	chr7	148085090	CCDS34772.1	c.398T>G	p.L133R
CUL2	cullin 2	ENSG00000108094	PAP47	90	14.4%	chr10	35373798	CCDS7179.1	c.511C>T	p.R171C
CUL5	cullin 5	ENSG00000166266	PAP47	116	21.6%	chr11	107425865	CCDS31668.1	c.273A>C	p.K91N
CUL9	cullin 9	ENSG00000112659	PAP47	264	28.0%	chr6	43260300	CCDS4890.1	c.274G>A	p.E92K
CNGA1	cyclic nucleotide gated channel alpha 1	ENSG00000198515	PAP47	86	26.7%	chr4	47640043	CCDS43226.1	c.361G>A	p.E121K
CNGA2	cyclic nucleotide gated channel alpha 2	ENSG00000183862	PAP47	121	27.3%	chrX	150657625	CCDS14701.1	c.14C>A	p.T5N
CNGB3	cyclic nucleotide gated channel beta 3	ENSG00000170289	PAP47	142	26.8%	chr8	87657165	CCDS6244.1	c.2413G>T	p.E805X
CCNE1	cyclin E1	ENSG00000105173	PAP47	223	31.8%	chr19	35000268	CCDS12419.1	c.442C>A	p.L148I
CCNG1	cyclin G1	ENSG00000113328	PAP47	123	26.8%	chr5	162800765	CCDS4360.1	c.368G>A	p.R123Q
CCNT2	cyclin T2	ENSG00000082258	PAP47	185	36.2%	chr2	135427524	CCDS2174.1	c.1029C>A	p.Y343X
CCNYL3	cyclin Y-like 3	ENSG00000216671	PAP47	45	35.6%	chr16	34147992	ENST00000407030	c.501C>A	p.F167L
CDK13	cyclin-dependent kinase 13	ENSG00000065883	PAP47	603	18.1%	chr7	40099271	CCDS5461.1	c.3598G>T	p.D1200Y
CDK14	cyclin-dependent kinase 14	ENSG00000058091	PAP47	60	25.0%	chr7	90546688	CCDS5619.1	c.1057T>G	p.F353V
CSRP3	cysteine and glycine-rich protein 3 (cardiac LIM protein)	ENSG00000129170	PAP47	207	25.6%	chr11	19164418	CCDS7848.1	c.335C>T	p.A112V
CYSLTR1	cysteinyl leukotriene receptor 1	ENSG00000173198	PAP47	117	29.9%	chrX	77415425	CCDS14439.1	c.475C>A	p.L159I
CFTR	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C; member 7)	ENSG00000001626	PAP47	97	26.8%	chr7	117092787	CCDS5773.1	c.4175T>G	p.F1392C
CYBRD1	cytochrome b reductase 1	ENSG00000071967	PAP47	125	32.8%	chr2	172119399	CCDS2244.1	c.677G>A	p.R226H
CYP2A7P1	cytochrome P450; family 2; subfamily A; polypeptide 7 pseudogene 1	ENSG00000213908	PAP47	151	20.5%	chr19	46222020	ENST00000301171	c.811C>T	p.R271C
CYP2C8	cytochrome P450; family 2; subfamily C; polypeptide 8	ENSG00000138115	PAP47	112	31.3%	chr10	96808179	CCDS7438.1	c.722G>A	p.R241Q
CYP27B1	cytochrome P450; family 27; subfamily B; polypeptide 1	ENSG00000111012	PAP47	211	34.6%	chr12	56444552	CCDS8954.1	c.1012G>A	p.E338K
CYP4A11	cytochrome P450; family 4; subfamily A; polypeptide 11	ENSG00000187048	PAP47	100	27.0%	chr1	47176275	CCDS543.1	c.317A>C	p.K106T
CYP4F2	cytochrome P450; family 4; subfamily F; polypeptide 2	ENSG00000186115	PAP47	33	30.3%	chr19	15850713	CCDS12336.1	c.1431G>T	p.E477D
CYP4V2	cytochrome P450; family 4; subfamily V; polypeptide 2	ENSG00000145476	PAP47	143	30.1%	chr4	187367091	CCDS34119.1	c.1169G>A	p.R390H
CYP4V2	cytochrome P450; family 4; subfamily V; polypeptide 2	ENSG00000145476	PAP47	111	28.8%	chr4	187368682	CCDS34119.1	c.1471G>T	p.E491X
CYP8B1	cytochrome P450; family 8; subfamily B; polypeptide 1	ENSG00000180432	PAP47	209	31.1%	chr3	42890981	CCDS2707.1	c.1332C>A	p.F444L
DPF1	D4; zinc and double PHD fingers family 1	ENSG00000011332	PAP47	102	26.5%	chr19	43398872	CCDS33008.1	c.607G>T	p.E203X
DCHS2	dachsous 2 (Drosophila)	ENSG00000197410	PAP47	77	32.5%	chr4	155410560	CCDS3785.1	c.5154G>T	p.M1718I
ASXL3	DAVID_additional sex combs like 3 (Drosophila)	NM_030632	PAP47	203	35.5%	chr18	29572978	NM_030632	c.1612G>T	p.E538X

ASXL3	DAVID_additional sex combs like 3 (Drosophila)	NM_030632	PAP47	168	31.0%	chr18	29577173	NM_030632	c.3363C>A	p.F1121L
AHNAK2	DAVID_AHNAK nucleoprotein 2	NM_138420	PAP47	830	20.8%	chr14	104491091	NM_138420	c.1742G>T	p.R581I
Als2cr11	DAVID_amyotrophic lateral sclerosis 2 (juvenile) chromosome region: candidate 11	NM_001168221	PAP47	141	26.2%	chr2	202064201	NM_001168221	c.5108G>T	p.R1703I
Als2cr11	DAVID_amyotrophic lateral sclerosis 2 (juvenile) chromosome region: candidate 11	NM_001168221	PAP47	50	24.0%	chr2	202064951	NM_001168221	c.4358C>T	p.S1453F
ANKIB1	DAVID_ankyrin repeat and IBR domain containing 1	NM_019004	PAP47	126	38.1%	chr7	91795141	NM_019004	c.778C>T	p.R260X
Ankrd24	DAVID_ankyrin repeat domain 24	NM_133475	PAP47	34	35.3%	chr19	4167949	NM_133475	c.1792G>T	p.E598X
ano2	DAVID_anoctamin 2	NM_020373	PAP47	130	32.3%	chr12	5542818	NM_020373	c.2905C>T	p.R969X
APOC2	DAVID_apolipoprotein C-II	ENSG00000213044	PAP47	355	29.9%	chr19	50143906	CCDS12650.1	c.164C>T	p.A55V
aspdh	DAVID_aspartate dehydrogenase domain containing	NM_001114598	PAP47	90	24.4%	chr19	55708395	NM_001114598	c.143C>T	p.A48V
Agbl3	DAVID_ATP/GTP binding protein-like 3	NM_178563	PAP47	149	24.8%	chr7	134381108	NM_178563	c.1747G>T	p.E583X
Agbl3	DAVID_ATP/GTP binding protein-like 3	NM_178563	PAP47	142	27.5%	chr7	134470141	NM_178563	c.2351C>T	p.P784L
abcb11	DAVID_ATP-binding cassette: sub-family B (MDR/TAP): member 11	NM_003742	PAP47	70	27.1%	chr2	169495546	NM_003742	c.3286C>A	p.L1096M
birc6	DAVID_baculoviral IAP repeat-containing 6	NM_016252	PAP47	33	36.4%	chr2	32554839	NM_016252	c.6775G>T	p.E2259X
BTNL2	DAVID_butyrophilin-like 2 (MHC class II associated)	ENSG00000204290	PAP47	88	33.0%	chr6	32472138	NM_019602	c.734C>A	p.S245Y
BTNL2	DAVID_butyrophilin-like 2 (MHC class II associated)	NM_019602	PAP47	88	33.0%	chr6	32472138	NM_019602	c.734C>A	p.S245Y
BTNL2	DAVID_butyrophilin-like 2 (MHC class II associated)	NM_019602	PAP47	88	33.0%	chr6	32472138	NM_019602	c.734C>A	p.S245Y
cadps2	DAVID_Ca++-dependent secretion activator 2	NM_001167940	PAP47	58	25.9%	chr7	122048977	NM_001167940	c.898G>T	p.D300Y
CDH13	DAVID_cadherin 13: H-cadherin (heart)	NM_001257	PAP47	216	22.2%	chr16	81623212	NM_001257	c.254G>T	p.R85I
Cdh23	DAVID_cadherin-like 23	NM_022124	PAP47	90	22.2%	chr10	73131856	NM_022124	c.2469C>A	p.F823L
CDHR4	DAVID_cadherin-like 29	NM_001007540	PAP47	62	27.4%	chr3	49804932	NM_001007540	c.2111G>A	p.G704D
chp2	DAVID_calcineurin B homologous protein 2	ENSG00000166869	PAP47	102	27.5%	chr16	23674722	CCDS10617.1	c.194G>A	p.R65Q
CACNA2D3	DAVID_calcium channel: voltage-dependent: alpha 2/delta subunit 3	NM_018398	PAP47	178	28.1%	chr3	54773325	NM_018398	c.1287G>T	p.E429D
CACNA1H	DAVID_calcium channel: voltage-dependent: T type: alpha 1H subunit	NM_021098	PAP47	107	24.3%	chr16	1201243	NM_021098	c.4298T>G	p.I1433S
CMYA5	DAVID_cardiomyopathy associated 5	NM_153610	PAP47	112	28.6%	chr5	79061056	NM_153610	c.712G>T	p.E238X
CMYA5	DAVID_cardiomyopathy associated 5	NM_153610	PAP47	171	25.1%	chr5	79066883	NM_153610	c.6539C>T	p.S2180L
CENPC1	DAVID_centromere protein C 1	NM_001812	PAP47	48	27.1%	chr4	68062734	NM_001812	c.1097A>C	p.K366T
Chd8	DAVID_chromodomain helicase DNA binding protein 8	NM_020920	PAP47	91	34.1%	chr14	20946409	NM_020920	c.1795T>G	p.F599V
Chd8	DAVID_chromodomain helicase DNA binding protein 8	NM_020920	PAP47	69	24.6%	chr14	20952957	NM_020920	c.1167C>A	p.F389L
C12orf55	DAVID_chromosome 12 open reading frame 55	ENSG00000165990	PAP47	70	31.4%	chr12	95407819	ENST00000298953	c.301G>A	p.E101K
C12orf55	DAVID_chromosome 12 open reading frame 55	ENSG00000165990	PAP47	97	22.7%	chr12	95456311	ENST00000298953	c.1810G>T	p.E604X
C14orf176	DAVID_chromosome 14 open reading frame 176	NM_001146683	PAP47	82	22.0%	chr14	20640109	NM_001146683	c.266G>A	p.R89H
ARHGAP40	DAVID_chromosome 20 open reading frame 95	NM_001164431	PAP47	135	25.9%	chr20	36705923	NM_001164431	c.1522G>A	p.E508K
Fam198a	DAVID_chromosome 3 open reading frame 41; hypothetical protein LOC729085	NM_001129908	PAP47	65	21.5%	chr3	43071964	NM_001129908	c.1450G>A	p.D484N
LOC26172	DAVID_chromosome 3 open reading frame 41; hypothetical protein LOC729085	NM_001129908	PAP47	65	21.5%	chr3	43071964	NM_001129908	c.1450G>A	p.D484N
C3orf55	DAVID_chromosome 3 open reading frame 55	NM_001130002	PAP47	42	28.6%	chr3	158753810	NM_001130002	c.70A>C	p.T24P
C5orf36	DAVID_chromosome 5 open reading frame 36	NM_001145678	PAP47	126	29.4%	chr5	93757733	NM_001145678	c.3125G>T	p.R1042I
c5orf42	DAVID_chromosome 5 open reading frame 42	NM_023073	PAP47	103	24.3%	chr5	37278891	NM_023073	c.658A>C	p.N220H
C6orf103	DAVID_chromosome 6 open reading frame 103	NM_024694	PAP47	91	27.5%	chr6	147039159	NM_024694	c.1105G>T	p.D369Y
C6orf27	DAVID_chromosome 6 open reading frame 27	ENSG00000204396	PAP47	81	37.0%	chr6	31842271	CCDS4721.2	c.2132G>A	p.R711H
c8orf79	DAVID_chromosome 8 open reading frame 79	NM_020844	PAP47	127	22.8%	chr8	12923296	NM_020844	c.737C>T	p.S246L
c8orf79	DAVID_chromosome 8 open reading frame 79	NM_020844	PAP47	185	19.5%	chr8	12923874	NM_020844	c.1315G>T	p.D439Y
Ccdc155	DAVID_coiled-coil domain containing 155	NM_144688	PAP47	43	27.9%	chr19	54601988	NM_144688	c.832A>G	p.K278E
COL6A6	DAVID_collagen type VI alpha 6	NM_001102608	PAP47	150	36.0%	chr3	131772576	NM_001102608	c.2626C>T	p.L876F
Col11a2	DAVID_collagen: type XI: alpha 2	ENSG00000204248	PAP47	316	23.1%	chr6	33248319	CCDS43452.1	c.2606G>T	p.G869V
Col11a2	DAVID_collagen: type XI: alpha 2	ENSG00000204248	PAP47	367	15.5%	chr6	33254219	CCDS43452.1	c.1486C>T	p.P496S
CR1	DAVID_complement component (3b/4b) receptor 1 (Knops blood group)	NM_000651	PAP47	164	28.0%	chr1	205820355	NM_000651	c.5084A>G	p.D1695G

CFHR2	DAVID_complement factor H-related 2	ENSG00000134391	PAP47	54	35.2%	chr1	195194825	CCDS30959.1	c.805G>T	p.E269X
CSMD1	DAVID_CUB and Sushi multiple domains 1	NM_033225	PAP47	92	18.5%	chr8	2845050	NM_033225	c.8041C>T	p.R2681W
ARPP21	DAVID_cyclic AMP-regulated phosphoprotein: 21 kD	ENSG00000172995	PAP47	83	24.1%	chr3	35699372	CCDS2661.1	c.158G>T	p.R53I
CYFIP2	DAVID_cytoplasmic FMR1 interacting protein 2	NM_001037332	PAP47	83	26.5%	chr5	156667417	NM_001037332	c.866G>T	p.R289I
Dock6	DAVID_dedicator of cytokinesis 6	NM_020812	PAP47	82	14.6%	chr19	11180606	NM_020812	c.4925T>C	p.V1642A
Dock6	DAVID_dedicator of cytokinesis 6	NM_020812	PAP47	92	12.0%	chr19	11180607	NM_020812	c.4924G>A	p.V1642M
DENND4A	DAVID_DENN/MADD domain containing 4A	NM_001144823	PAP47	49	28.6%	chr15	63776695	NM_001144823	c.2911G>T	p.E971X
DENND4A	DAVID_DENN/MADD domain containing 4A	NM_001144823	PAP47	111	27.0%	chr15	63781222	NM_001144823	c.2491C>T	p.R831X
DNHD1	DAVID_dynein heavy chain domain 1	NM_144666	PAP47	591	25.5%	chr11	6522644	NM_144666	c.3899G>A	p.R1300H
DNAH1	DAVID_dynein: axonemal: heavy chain 1	NM_015512	PAP47	157	28.7%	chr3	52392956	NM_015512	c.8191C>T	p.P2731S
DNAH6	DAVID_dynein: axonemal: heavy chain 6	NM_001370	PAP47	117	36.8%	chr2	84715206	NM_001370	c.4583G>A	p.R1528Q
DST	DAVID_dystonin	NM_020388	PAP47	102	18.6%	chr6	56581575	NM_020388	c.4199G>T	p.R1400I
Epha6	DAVID_EPH receptor A6	NM_001080448	PAP47	94	26.6%	chr3	98650211	NM_001080448	c.1841C>T	p.A614V
ephb1	DAVID_EPH receptor B1	NM_004441	PAP47	203	22.7%	chr3	136394152	NM_004441	c.1927A>G	p.K643E
ephb1	DAVID_EPH receptor B1	NM_004441	PAP47	108	24.1%	chr3	136449893	NM_004441	c.2542G>T	p.D848Y
ETV5	DAVID_ets variant 5	ENSG00000171656	PAP47	98	28.6%	chr3	187305787	CCDS33906.1	c.-1G>A	p.IVS4+1-1SpliceDonor
eys	DAVID_eyes shut homolog (Drosophila)	NM_001142800	PAP47	126	10.3%	chr6	65357700	NM_001142800	c.4781C>A	p.A1594D
eys	DAVID_eyes shut homolog (Drosophila)	NM_001142800	PAP47	262	30.2%	chr6	65358360	NM_001142800	c.4121G>A	p.R1374Q
Fam13a	DAVID_family with sequence similarity 13: member A	ENSG00000138640	PAP47	162	32.7%	chr4	90078355	CCDS34029.1	c.666A>C	p.K222N
FAM38A	DAVID_family with sequence similarity 38: member A	NM_001142864	PAP47	103	25.2%	chr16	87326268	NM_001142864	c.2967C>A	p.F989L
Fam38b	DAVID_family with sequence similarity 38: member B	NM_022068	PAP47	90	20.0%	chr18	10692008	NM_022068	c.6081C>A	p.F2027L
FAM81A	DAVID_family with sequence similarity 81: member A	NM_152450	PAP47	422	26.3%	chr15	57539539	NM_152450	c.136G>A	p.A46T
FAT3	DAVID_FAT tumor suppressor homolog 3 (Drosophila)	NM_001008781	PAP47	218	25.2%	chr11	91726979	NM_001008781	c.2053G>T	p.E685X
FAT3	DAVID_FAT tumor suppressor homolog 3 (Drosophila)	NM_001008781	PAP47	224	33.0%	chr11	92174699	NM_001008781	c.8872C>T	p.R2958C
Fbxo46	DAVID_F-box protein 46	NM_001080469	PAP47	111	35.1%	chr19	50907699	NM_001080469	c.895C>T	p.R299X
FER1L5	DAVID_fer-1-like 5 (C. elegans)	NM_001113382	PAP47	251	28.7%	chr2	96729120	NM_001113382	c.4798G>A	p.D1600N
Fdxacb1	DAVID_ferredoxin-fold anticodon binding domain containing 1	NM_138378	PAP47	202	25.7%	chr11	111251644	NM_138378	c.1087G>A	p.D363N
fgf13	DAVID_fibroblast growth factor 13	NM_001139500	PAP47	81	25.9%	chrX	137767397	NM_001139500	c.160G>A	p.E54K
FSIP2	DAVID_fibrous sheath interacting protein 2	ENSG00000180922	PAP47	104	19.2%	chr2	186364559	ENST00000326147	c.3824C>A	p.S1275Y
flj41603	DAVID_FLJ41603 protein	ENSG00000183111	PAP47	164	30.5%	chr5	148981754	CCDS43385.1	c.1271T>C	p.F424S
FREM1	DAVID_FRAS1 related extracellular matrix 1	NM_144966	PAP47	94	23.4%	chr9	14791734	NM_144966	c.3610G>T	p.D1204Y
FREM1	DAVID_FRAS1 related extracellular matrix 1	NM_144966	PAP47	212	25.9%	chr9	14841530	NM_144966	c.904G>A	p.V302M
GPR137C	DAVID_G protein-coupled receptor 137C	NM_001099652	PAP47	124	25.8%	chr14	52136702	NM_001099652	c.610C>T	p.R204X
GVIN1	DAVID_GTPase: very large interferon inducible 1	ENSG00000187878	PAP47	112	24.1%	chr11	6696496	ENST00000339980	c.662C>A	p.S221Y
gucy1b3	DAVID_guanylate cyclase 1: soluble: beta 3	NM_000857	PAP47	165	31.5%	chr4	156918233	NM_000857	c.286G>T	p.E96X
heatr5a	DAVID_HEAT repeat containing 5A	NM_015473	PAP47	246	28.5%	chr14	30897717	NM_015473	c.1409C>T	p.S470L
HGSNAT	DAVID_heparan-alpha-glucosaminide N-acetyltransferase	NM_152419	PAP47	76	28.9%	chr8	43133242	NM_152419	c.391G>T	p.E131X
HHLA2	DAVID_HERV-H LTR-associating 2	NM_007072	PAP47	202	32.7%	chr3	109559657	NM_007072	c.962C>T	p.S321L
homez	DAVID_homeobox and leucine zipper encoding	NM_020834	PAP47	261	36.4%	chr14	22815472	NM_020834	c.805A>C	p.I269L
SGK223	DAVID_homolog of rat pragma of Rnd2	ENSG00000182319	PAP47	111	27.9%	chr8	8276575	CCDS43706.1	c.93G>T	p.K31N
FLJ10357	DAVID_hypothetical protein FLJ10357	ENSG00000165801	PAP47	185	29.2%	chr14	20613340	CCDS32041.1	c.1460G>A	p.G487D
VSIG10L	DAVID_hypothetical protein LOC147645	NM_001163922	PAP47	116	34.5%	chr19	56536723	NM_001163922	c.391G>T	p.D131Y
C9orf144	DAVID_hypothetical protein LOC259308; chromosome 9 open reading frame 144	NM_001141917	PAP47	204	30.9%	chr9	34716848	NM_001141917	c.389C>T	p.S130L
C9orf144B	DAVID_hypothetical protein LOC259308; chromosome 9 open reading frame 144	NM_001141917	PAP47	204	30.9%	chr9	34716848	NM_001141917	c.389C>T	p.S130L
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP47	160	25.6%	chr13	102185041	NM_001146197	c.16007G>T	p.R5336I
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP47	150	24.0%	chr13	102185056	NM_001146197	c.15992G>T	p.R5331I
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP47	138	26.8%	chr13	102191809	NM_001146197	c.9239T>C	p.V3080A
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP47	71	25.4%	chr13	102192148	NM_001146197	c.8900G>T	p.R2967I
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP47	202	33.7%	chr13	102193337	NM_001146197	c.7711A>C	p.K2571Q
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP47	89	29.2%	chr13	102194142	NM_001146197	c.6906G>T	p.K2302N

LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP47	132	34.8%	chr13	102197819	NM_001146197	c.3229T>G	p.L1077V
LOC729173	DAVID_hypothetical protein LOC729173	ENSG00000176984	PAP47	471	29.5%	chr11	119546248	ENST00000319763	c.521C>T	p.S174F
IGSF9B	DAVID_immunoglobulin superfamily: member 9B	NM_014987	PAP47	294	29.3%	chr11	133300906	NM_014987	c.1972G>A	p.E658K
INTS2	DAVID_integrator complex subunit 2	NM_020748	PAP47	139	36.0%	chr17	57344119	NM_020748	c.768G>T	p.M256I
IL12RB1	DAVID_interleukin 12 receptor: beta 1	NM_005535	PAP47	94	25.5%	chr19	18040261	NM_005535	c.1265C>T	p.A422V
papL	DAVID_iron/zinc purple acid phosphatase-like protein	ENSG00000183760	PAP47	176	37.5%	chr19	44283226	CCDS33018.1	c.700C>A	p.L234M
KRTAP25-1	DAVID_keratin associated protein 25-1	NM_001128598	PAP47	84	26.2%	chr21	30583424	NM_001128598	c.256G>A	p.A86T
KIAA0947	DAVID_KIAA0947	NM_015325	PAP47	114	26.3%	chr5	5518224	NM_015325	c.5777C>A	p.S1926Y
KIAA1107	DAVID_KIAA1107	NM_015237	PAP47	92	37.0%	chr1	92419875	NM_015237	c.2733T>G	p.I911M
KIAA1239	DAVID_KIAA1239	NM_001144990	PAP47	219	36.5%	chr4	37123347	NM_001144990	c.3342C>A	p.F1114L
KIAA1383	DAVID_KIAA1383	NM_019090	PAP47	125	30.4%	chr1	231009644	NM_019090	c.2252G>T	p.R751I
KIAA1383	DAVID_KIAA1383	NM_019090	PAP47	150	28.7%	chr1	231009724	NM_019090	c.2332C>A	p.L778M
KIAA1731	DAVID_KIAA1731	NM_033395	PAP47	102	31.4%	chr11	93072983	NM_033395	c.5257T>G	p.F1753V
KIRREL3	DAVID_kin of IRRE like 3 (Drosophila)	NM_032531	PAP47	201	27.4%	chr11	125838403	NM_032531	c.601C>T	p.R201W
KSR1	DAVID_kinase suppressor of ras 1	NM_014238	PAP47	185	30.3%	chr17	22948433	NM_014238	c.901G>A	p.A301T
Kif13a	DAVID_kinesin family member 13A	NM_022113	PAP47	78	29.5%	chr6	17896031	NM_022113	c.3316C>T	p.R1106X
KIF26A	DAVID_kinesin family member 26A	NM_015656	PAP47	116	29.3%	chr14	103703040	NM_015656	c.1015G>A	p.D339N
KNTC1	DAVID_kinetochore associated 1	NM_014708	PAP47	55	18.2%	chr12	121648403	NM_014708	c.4528G>T	p.D1510Y
LPHN3	DAVID_latrophilin 3	NM_015236	PAP47	117	17.1%	chr4	62586147	NM_015236	c.3491G>A	p.G1164E
LRRC70	DAVID_leucine rich repeat containing 70	NM_181506	PAP47	102	35.3%	chr5	61911947	NM_181506	c.925G>T	p.E309X
lrtomt	DAVID_leucine rich transmembrane and 0-methyltransferase domain containing	NM_001145308	PAP47	63	33.3%	chr11	71494746	NM_001145308	c.200G>A	p.R67Q
LILRA2	DAVID_leukocyte immunoglobulin-like receptor: subfamily A (with TM domain): member 2	ENSG00000187095	PAP47	44	22.7%	chr19	59778132	CCDS12900.1	c.475G>T	p.E159X
L1TD1	DAVID_LINE-1 type transposase domain containing 1	ENSG00000162606	PAP47	55	18.2%	chr1	62445808	NM_019079	c.920C>A	p.S307Y
lcp2	DAVID_lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	NM_005565	PAP47	103	11.7%	chr5	169626452	NM_005565	c.710G>T	p.R237I
MAGIX	DAVID_MAGI family member: X-linked	NM_024859	PAP47	168	32.1%	chrX	48908580	NM_024859	c.616C>T	p.R206C
HLA-G	DAVID_major histocompatibility complex: class I: G	ENSG00000204632	PAP47	159	17.0%	chr6	29903994	CCDS4668.1	c.265C>T	p.R89W
MGA	DAVID_MAX gene associated	NM_001164273	PAP47	107	28.0%	chr15	39829969	NM_001164273	c.6872G>T	p.R2291I
MUC16	DAVID_mucin 16: cell surface associated	NM_024690	PAP47	110	26.4%	chr19	8834573	NM_024690	c.42743G>A	p.R14248H
myom1	DAVID_myomesin 1: 185kDa	NM_003803	PAP47	64	34.4%	chr18	3141785	NM_003803	c.1750G>T	p.V584F
MYH13	DAVID_myosin: heavy chain 13: skeletal muscle	NM_003802	PAP47	310	31.3%	chr17	10153587	NM_003802	c.4942C>T	p.R1648C
NEB	DAVID_nebulin	NM_001164507	PAP47	61	37.7%	chr2	152081311	NM_001164507	c.22813G>A	p.E7605K
NEB	DAVID_nebulin	NM_001164507	PAP47	62	25.8%	chr2	152113096	NM_001164507	c.20129T>C	p.V6710A
NEB	DAVID_nebulin	NM_001164507	PAP47	153	31.4%	chr2	152262190	NM_001164507	c.1285G>T	p.D429Y
NEB	DAVID_nebulin	NM_001164508	PAP47	140	30.0%	chr2	152249725	NM_001164508	c.2648G>A	p.R883Q
NEB	DAVID_nebulin	NM_001164508	PAP47	245	31.0%	chr2	152256662	NM_001164508	c.2173G>T	p.E725X
NRXN1	DAVID_neurexin 1	NM_001135659	PAP47	190	24.7%	chr2	51107011	NM_001135659	c.-1T>G	p.IVS2+2-1SpliceDonor
NAV2	DAVID_neuron navigator 2	NM_001111018	PAP47	135	25.9%	chr11	19329083	NM_001111018	c.8C>T	p.S3L
GPR109B	DAVID_niacin receptor 2; niacin receptor 1	NM_006018	PAP47	267	23.2%	chr12	121766118	NM_006018	c.1120G>A	p.E374K
GPR109A	DAVID_niacin receptor 2; niacin receptor 1	NM_006018	PAP47	267	23.2%	chr12	121766118	NM_006018	c.1120G>A	p.E374K
NEK10	DAVID_NIMA (never in mitosis gene a)- related kinase 10	NM_199347	PAP47	161	32.3%	chr3	27318325	NM_199347	c.1034G>T	p.R345I
NCRNA0017	DAVID_non-protein coding RNA 171; HLA complex P5 pseudogene 10	ENSG00000196299	PAP47	68	26.5%	chr6	30133173	ENST00000354576	c.112G>T	p.E38X
HCP5P10	DAVID_non-protein coding RNA 171; HLA complex P5 pseudogene 10	ENSG00000196299	PAP47	68	26.5%	chr6	30133173	ENST00000354576	c.112G>T	p.E38X
NOL7	DAVID_nucleolar protein 7: 27kDa	ENSG00000137420	PAP47	61	27.9%	chr6	13725987	CCDS4528.1	c.393G>T	p.K131N
obscn	DAVID_obscurin: cytoskeletal calmodulin and titin-interacting RhoGEF	NM_001098623	PAP47	209	33.5%	chr1	226576386	NM_001098623	c.15221G>A	p.R5074H
Odz2	DAVID_odz: odd Oz/ten-m homolog 2 (Drosophila)	NM_001122679	PAP47	91	33.0%	chr5	166644569	NM_001122679	c.149A>G	p.D50G
OR1J4	DAVID_olfactory receptor: family 1: subfamily J: member 4	ENSG00000213457	PAP47	548	11.3%	chr9	124321601	CCDS35122.1	c.361G>A	p.D121N

OR10D3P	DAVID_olfactory receptor: family 10: subfamily D: member 3 pseudogene	ENSG00000197309	PAP47	562	26.0%	chr11	123561806	ENST00000318666	c.620C>A	p.S207Y
OR10G4	DAVID_olfactory receptor: family 10: subfamily G: member 4	ENSG00000181457	PAP47	68	16.2%	chr11	123392192	CCDS31702.1	c.701G>A	p.R234H
OR4D1	DAVID_olfactory receptor: family 4: subfamily D: member 1	ENSG00000141194	PAP47	426	29.8%	chr17	53587813	CCDS42365.1	c.300G>T	p.Q100H
OR4D10	DAVID_olfactory receptor: family 4: subfamily D: member 10	NM_001004705	PAP47	428	20.8%	chr11	59001697	NM_001004705	c.219C>A	p.F73L
OR5K2	DAVID_olfactory receptor: family 5: subfamily K: member 2	ENSG00000181828	PAP47	41	29.3%	chr3	99700127	CCDS33804.1	c.913C>A	p.L305M
OR8G2	DAVID_olfactory receptor: family 8: subfamily G: member 2	NM_001007249	PAP47	218	24.8%	chr11	123600666	NM_001007249	c.59C>T	p.S20F
OTOL1	DAVID_Otolin-1	ENSG00000182447	PAP47	132	39.4%	chr3	162697470	NM_001080440	c.181G>T	p.E61X
Ovch2	DAVID_ovochymase 2	NM_198185	PAP47	131	29.8%	chr11	7680344	NM_198185	c.399C>A	p.F133L
PISD	DAVID_phosphatidylserine decarboxylase	ENSG00000100141	PAP47	179	30.2%	chr22	30376684	ENST00000397508	c.-1G>A	p.IVS2+1-1SpliceDonor
PIK3C2G	DAVID_phosphoinositide-3-kinase: class 2: gamma polypeptide	NM_004570	PAP47	61	23.0%	chr12	18607611	NM_004570	c.3691G>A	p.E1231K
Prps1l1	DAVID_phosphoribosyl pyrophosphate synthetase 1; phosphoribosyl pyrophosphate synthetase 1-like 1	NM_175886	PAP47	273	26.7%	chr7	18033153	NM_175886	c.778C>T	p.R260C
PRPS1	DAVID_phosphoribosyl pyrophosphate synthetase 1; phosphoribosyl pyrophosphate synthetase 1-like 1	NM_175886	PAP47	273	26.7%	chr7	18033153	NM_175886	c.778C>T	p.R260C
PCLO	DAVID_piccolo (presynaptic cytomatrix protein)	NM_033026	PAP47	147	28.6%	chr7	82227952	NM_033026	c.15227G>A	p.R5076Q
PCLO	DAVID_piccolo (presynaptic cytomatrix protein)	NM_033026	PAP47	190	32.6%	chr7	82383897	NM_033026	c.11341C>T	p.R3781X
LPPR4	DAVID_plasticity related gene 1	ENSG00000117600	PAP47	181	34.3%	chr1	99543967	CCDS757.1	c.1105A>C	p.I369L
PRAM1	DAVID_PML-RARA regulated adaptor molecule 1	NM_032152	PAP47	142	35.9%	chr19	8469570	NM_032152	c.1122C>A	p.F374L
PARP14	DAVID_poly (ADP-ribose) polymerase family: member 14	NM_017554	PAP47	169	31.4%	chr3	123902161	NM_017554	c.2070G>T	p.K690N
PKHD1L1	DAVID_polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	NM_177531	PAP47	162	18.5%	chr8	110568184	NM_177531	c.9838G>A	p.V3280I
prss23	DAVID_protease: serine: 23	ENSG00000150687	PAP47	338	29.3%	chr11	86196499	CCDS8278.1	c.166G>A	p.E56K
PTPN13	DAVID_protein tyrosine phosphatase: non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	NM_080685	PAP47	113	25.7%	chr4	87856715	NM_080685	c.1204C>T	p.R402X
PTPN13	DAVID_protein tyrosine phosphatase: non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	NM_080685	PAP47	116	30.2%	chr4	87874493	NM_080685	c.1872C>A	p.F624L
PTPN13	DAVID_protein tyrosine phosphatase: non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	NM_080685	PAP47	95	26.3%	chr4	87911624	NM_080685	c.5095C>A	p.H1699N
PTPRB	DAVID_protein tyrosine phosphatase: receptor type: B	NM_001109754	PAP47	69	26.1%	chr12	69224711	NM_001109754	c.-1G>T	p.IVS21-1-1SpliceAcceptor
PTPRB	DAVID_protein tyrosine phosphatase: receptor type: B	NM_001109754	PAP47	88	34.1%	chr12	69232902	NM_001109754	c.5309T>C	p.M1770T
ptprq	DAVID_protein tyrosine phosphatase: receptor type: Q	NM_001145026	PAP47	164	10.4%	chr12	79506179	NM_001145026	c.3910G>T	p.E1304X
PCDHA8	DAVID_protocadherin alpha 8; protocadherin alpha 6	ENSG00000204964	PAP47	131	26.7%	chr5	140188587	CCDS34251.1	c.727G>A	p.E243K
PCDHA6	DAVID_protocadherin alpha 8; protocadherin alpha 6	ENSG00000204964	PAP47	131	26.7%	chr5	140188587	CCDS34251.1	c.727G>A	p.E243K
PCDHGA11	DAVID_protocadherin gamma subfamily A: 11	NM_018914	PAP47	314	19.7%	chr5	140781666	NM_018914	c.688C>T	p.R230C
PCDHGA5	DAVID_protocadherin gamma subfamily A: 5	NM_018918	PAP47	339	30.4%	chr5	140724840	NM_018918	c.759G>T	p.E253D
Pcdhga7	DAVID_protocadherin gamma subfamily A: 7	NM_018920	PAP47	104	26.9%	chr5	140743049	NM_018920	c.399C>A	p.F133L
Pcdhgb2	DAVID_protocadherin gamma subfamily B: 2	NM_018923	PAP47	205	21.5%	chr5	140720571	NM_018923	c.685C>T	p.R229X
Pcdhgb7	DAVID_protocadherin gamma subfamily B: 7	NM_018927	PAP47	216	28.7%	chr5	140778620	NM_018927	c.1010T>G	p.V337G
PRUNE2	DAVID_prune homolog 2 (Drosophila)	NM_015225	PAP47	310	33.5%	chr9	78509985	NM_015225	c.7025T>C	p.I2342T
phtf2	DAVID_putative homeodomain transcription factor 2	NM_001127357	PAP47	48	27.1%	chr7	77367984	NM_001127357	c.135G>T	p.K45N
RSPH6A	DAVID_radial spokehead-like 1	ENSG00000104941	PAP47	378	11.1%	chr19	50999645	CCDS12675.1	c.1358G>A	p.R453Q
RASGRP4	DAVID_RAS guanyl releasing protein 4	NM_170604	PAP47	134	20.1%	chr19	43593469	NM_170604	c.1862A>G	p.E621G
RFX7	DAVID_regulatory factor X: 7	NM_022841	PAP47	333	29.4%	chr15	54175682	NM_022841	c.1536G>T	p.K512N
RPGRIP1	DAVID_retinitis pigmentosa GTPase regulator interacting protein 1	NM_020366	PAP47	88	26.1%	chr14	20865767	NM_020366	c.2856G>T	p.K952N
RYR2	DAVID_ryanodine receptor 2 (cardiac)	NM_001035	PAP47	102	29.4%	chr1	235699018	NM_001035	c.1616C>T	p.A539V
RYR2	DAVID_ryanodine receptor 2 (cardiac)	NM_001035	PAP47	87	14.9%	chr1	235884290	NM_001035	c.7918T>G	p.L2640V
RYR2	DAVID_ryanodine receptor 2 (cardiac)	NM_001035	PAP47	155	20.6%	chr1	236036099	NM_001035	c.14191C>A	p.L4731I

Slfn14	DAVID_schlafen family member 14	NM_001129820	PAP47	454	28.4%	chr17	30904410	NM_001129820	c.1356G>T	p.Q452H
MGC42105	DAVID_serine/threonine-protein kinase NIM1	ENSG00000177453	PAP47	230	15.7%	chr5	43316130	CCDS3943.1	c.853G>A	p.E285K
srpk1	DAVID_SFRS protein kinase 1	NM_003137	PAP47	50	30.0%	chr6	35946045	NM_003137	c.982G>T	p.E328X
SIGLEC12	DAVID_sialic acid binding Ig-like lectin 12	ENSG00000160296	PAP47	69	18.8%	chr19	56693203	CCDS12833.1	c.1286G>T	p.G429V
SPCS3	DAVID_signal peptidase complex subunit 3 homolog (S. cerevisiae)	NM_021928	PAP47	31	35.5%	chr4	177480374	NM_021928	c.203T>G	p.F68C
LOC100133	DAVID_similar to hypoxia-inducible protein 2; EF-hand calcium binding domain 3	ENSG00000172421	PAP47	125	23.2%	chr17	57826175	CCDS11632.1	c.382A>G	p.T128A
EFCAB3	DAVID_similar to hypoxia-inducible protein 2; EF-hand calcium binding domain 3	ENSG00000172421	PAP47	125	23.2%	chr17	57826175	CCDS11632.1	c.382A>G	p.T128A
Tmem233	DAVID_similar to mCG53783	NM_001136534	PAP47	416	32.7%	chr12	118516172	NM_001136534	c.136T>C	p.F46L
LOC100129	DAVID_similar to tudor domain containing 1	ENSG00000218819	PAP47	44	27.3%	chr2	21216859	ENST00000405799	c.3015A>C	p.Q1005H
ZNF605	DAVID_similar to ZNF605 protein	NM_001164715	PAP47	243	28.8%	chr12	132013161	NM_001164715	c.890C>T	p.S297L
SMTNL1	DAVID_smoothelin-like 1	NM_001105565	PAP47	143	21.7%	chr11	57074155	NM_001105565	c.1533G>T	p.K511N
SCN5A	DAVID_sodium channel: voltage-gated: type V: alpha subunit	NM_001099404	PAP47	329	27.7%	chr3	38646914	NM_001099404	c.284T>C	p.V95A
SLC12A1	DAVID_solute carrier family 12 (sodium/potassium/chloride transporters): member 1	NM_000338	PAP47	114	29.8%	chr15	46287531	NM_000338	c.323C>T	p.A108V
SLC12A1	DAVID_solute carrier family 12 (sodium/potassium/chloride transporters): member 1	NM_000338	PAP47	40	27.5%	chr15	46347056	NM_000338	c.2161C>T	p.R721C
SLC4A10	DAVID_solute carrier family 4: sodium bicarbonate transporter: member 10	NM_022058	PAP47	126	21.4%	chr2	162528969	NM_022058	c.2851C>T	p.R951X
LOC284379	DAVID_solute carrier family 7 (cationic amino acid transporter: y+ system): member 3 pseudogene	ENSG00000188666	PAP47	249	27.3%	chr19	58798549	ENST00000342791	c.8C>A	p.S3Y
SPTBN5	DAVID_spectrin: beta: non-erythrocytic 5	NM_016642	PAP47	287	23.7%	chr15	39953065	NM_016642	c.4819G>A	p.V1607M
SOHLH1	DAVID_spermatogenesis and oogenesis specific basic helix-loop-helix 1	NM_001101677	PAP47	165	29.7%	chr9	137725454	NM_001101677	c.974G>A	p.G325D
SOHLH2	DAVID_spermatogenesis and oogenesis specific basic helix-loop-helix 2	ENSG00000083622	PAP47	81	27.2%	chr13	35674231	CCDS9355.1	c.-1G>T	p.IVS1-1-1SpliceAcceptor
scaper	DAVID_S-phase cyclin A-associated protein in the ER	NM_020843	PAP47	89	37.1%	chr15	74782382	NM_020843	c.2264G>A	p.R755Q
STMN3	DAVID_stathmin-like 3	ENSG00000213603	PAP47	78	34.6%	chr20	61745557	CCDS13529.1	c.287G>T	p.R96M
SENP1	DAVID_SUMO1/sentrin specific peptidase 1	NM_014554	PAP47	185	28.6%	chr12	46729149	NM_014554	c.1441C>T	p.R481X
SVEP1	DAVID_sushi: von Willebrand factor type A: EGF and pentraxin domain containing 1	NM_153366	PAP47	235	30.2%	chr9	112315096	NM_153366	c.1234C>A	p.L412I
SYT16	DAVID_synaptotagmin XVI	NM_031914	PAP47	142	28.2%	chr14	61637048	NM_031914	c.1808G>A	p.R603H
TRAV6	DAVID_T cell receptor alpha variable 6	ENSG00000211780	PAP47	71	28.2%	chr14	21306889	ENST00000390428	c.69G>T	p.K23N
TRAV8-3	DAVID_T cell receptor alpha variable 8-3	ENSG00000211787	PAP47	129	36.4%	chr14	21390841	ENST00000390435	c.159C>A	p.F53L
TRBV4-1	DAVID_T cell receptor beta variable 4-1	ENSG00000211704	PAP47	309	28.2%	chr7	141659756	ENST00000390351	c.116C>A	p.S39Y
TSGA10IP	DAVID_testis specific: 10 interacting protein	NM_152762	PAP47	184	16.3%	chr11	65482946	NM_152762	c.1339C>T	p.R447C
THSD7A	DAVID_thrombospondin: type I: domain containing 7A	NM_015204	PAP47	111	35.1%	chr7	11413100	NM_015204	c.4024C>T	p.R1342W
TOP2B	DAVID_topoisomerase (DNA) II beta 180kDa	NM_001068	PAP47	50	26.0%	chr3	25635284	NM_001068	c.3109G>A	p.E1037K
tceanc	DAVID_transcription elongation factor A (SII) N-terminal and central domain containing	NM_152634	PAP47	172	26.7%	chrX	13590610	NM_152634	c.152G>T	p.R51M
TBL1XR1	DAVID_transducin (beta)-like 1 X-linked receptor 1	NM_024665	PAP47	60	21.7%	chr3	178250535	NM_024665	c.646C>T	p.R216X
TBL1XR1	DAVID_transducin (beta)-like 1 X-linked receptor 1	NM_024665	PAP47	60	40.0%	chr3	178250593	NM_024665	c.588G>A	p.W196X
TLE6	DAVID_transducin-like enhancer of split 6 (E(sp1) homolog: Drosophila)	NM_001143986	PAP47	142	26.1%	chr19	2929250	NM_001143986	c.19C>T	p.P7S
tgfbi	DAVID_transforming growth factor: beta-induced: 68kDa	NM_000358	PAP47	174	27.0%	chr5	135416525	NM_000358	c.944C>T	p.A315V
tgfbi	DAVID_transforming growth factor: beta-induced: 68kDa	NM_000358	PAP47	84	34.5%	chr5	135417657	NM_000358	c.1253C>A	p.S418Y
TRPC7	DAVID_transient receptor potential cation channel: subfamily C: member 7	NM_020389	PAP47	551	32.3%	chr5	135720772	NM_020389	c.203C>T	p.T68I
TRIM15	DAVID_tripartite motif-containing 15	ENSG00000204610	PAP47	110	34.5%	chr6	30248351	ENST00000376689	c.337C>T	p.R113W
SR140	DAVID_U2-associated SR140 protein	NM_001080415	PAP47	105	28.6%	chr3	144218405	NM_001080415	c.468A>C	p.K156N

B3GNT2	DAVID_UDP-GlcNAc:betaGal beta-1:3-N-acetylglucosaminyltransferase 1; UDP-GlcNAc:betaGal beta-1:3-N-acetylglucosaminyltransferase 2	ENSG00000174684	PAP47	197	28.9%	chr11	65870794	CCDS8136.1	c.799C>T	p.R267C
b3gnt1	DAVID_UDP-GlcNAc:betaGal beta-1:3-N-acetylglucosaminyltransferase 1; UDP-GlcNAc:betaGal beta-1:3-N-acetylglucosaminyltransferase 2	ENSG00000174684	PAP47	197	28.9%	chr11	65870794	CCDS8136.1	c.799C>T	p.R267C
VWDE	DAVID_von Willebrand factor D and EGF domains	NM_001135924	PAP47	144	30.6%	chr7	12375780	NM_001135924	c.2677T>G	p.L893V
DCAF8L2	DAVID_WD repeat domain 42C	NM_001136533	PAP47	109	28.4%	chrX	27675180	NM_001136533	c.247G>A	p.E83K
DCAF8L2	DAVID_WD repeat domain 42C	NM_001136533	PAP47	154	30.5%	chrX	27676756	NM_001136533	c.1823C>T	p.S608L
WDR87	DAVID_WD repeat domain 87	NM_031951	PAP47	175	27.4%	chr19	43074179	NM_031951	c.3130G>A	p.D1044N
WNT5A	DAVID_wingless-type MMTV integration site family: member 5A	NM_003392	PAP47	27	37.0%	chr3	55489859	NM_003392	c.134C>A	p.S45Y
YY2	DAVID_YY2 transcription factor	ENSG00000198767	PAP47	130	36.2%	chrX	21784544	CCDS14202.1	c.21C>A	p.F7L
YY2	DAVID_YY2 transcription factor	ENSG00000198767	PAP47	204	29.4%	chrX	21784753	CCDS14202.1	c.230A>C	p.E77A
Zfat	DAVID_zinc finger and AT hook domain containing	NM_020863	PAP47	87	37.9%	chr8	135671774	NM_020863	c.2569NULL>/	p.NULL-1FsIns1bp
ZNF788	DAVID_zinc finger family member 788	ENSG00000188474	PAP47	120	27.5%	chr19	12084994	ENST00000339302	c.1632C>A	p.F544L
ZFHX4	DAVID_zinc finger homeobox 4	NM_024721	PAP47	461	27.8%	chr8	77779219	NM_024721	c.341G>A	p.S114N
ZFHX4	DAVID_zinc finger homeobox 4	NM_024721	PAP47	137	29.2%	chr8	77930011	NM_024721	c.8164C>A	p.L2722I
ZNF20	DAVID_zinc finger protein 20	NM_021143	PAP47	206	33.0%	chr19	12105377	NM_021143	c.624C>A	p.F208L
ZNF226	DAVID_zinc finger protein 226	NM_001032372	PAP47	146	21.2%	chr19	49372211	NM_001032372	c.956G>A	p.G319D
znf292	DAVID_zinc finger protein 292	NM_015021	PAP47	254	30.3%	chr6	88021845	NM_015021	c.1779A>C	p.K593N
ZNF350	DAVID_zinc finger protein 350	ENSG00000171032	PAP47	118	26.3%	chr19	57160589	CCDS12845.1	c.929G>A	p.R310Q
ZNF469	DAVID_zinc finger protein 469	NM_001127464	PAP47	118	23.7%	chr16	87028538	NM_001127464	c.7075C>T	p.R2359C
ZNF548	DAVID_zinc finger protein 548	NM_152909	PAP47	334	31.4%	chr19	62602060	NM_152909	c.593A>G	p.K198R
ZFP62	DAVID_zinc finger protein 62 homolog (mouse)	NM_152283	PAP47	259	25.9%	chr5	180209446	NM_152283	c.1475A>C	p.K492T
ZFP62	DAVID_zinc finger protein 62 homolog (mouse)	NM_152283	PAP47	259	25.9%	chr5	180209446	NM_152283	c.1475A>C	p.K492T
ZNF716	DAVID_zinc finger protein 716	NM_001159279	PAP47	79	25.3%	chr7	57532498	NM_001159279	c.389A>C	p.K130T
ZNF717	DAVID_zinc finger protein 717	NM_001128223	PAP47	243	22.2%	chr3	75869773	NM_001128223	c.1691A>C	p.E564A
ZNF836	DAVID_zinc finger protein 836	NM_001102657	PAP47	189	31.7%	chr19	57350187	NM_001102657	c.2561G>T	p.R854I
Zswim6	DAVID_zinc finger: SWIM-type containing 6	NM_020928	PAP47	112	25.0%	chr5	60852923	NM_020928	c.1410G>T	p.K470N
DCAF16	DDB1 and CUL4 associated factor 16	ENSG00000163257	PAP47	157	24.8%	chr4	17414634	CCDS3423.1	c.229C>T	p.H77Y
DDX20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	ENSG00000064703	PAP47	163	30.7%	chr1	112104912	CCDS842.1	c.742G>A	p.E248K
DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	ENSG00000145833	PAP47	63	28.6%	chr5	134174922	CCDS34240.1	c.2261G>A	p.S754N
DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	ENSG00000107201	PAP47	86	31.4%	chr9	32479366	CCDS6526.1	c.775A>C	p.N259H
DDX26B	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	ENSG00000165359	PAP47	183	25.7%	chrX	134535624	CCDS35401.1	c.1601C>T	p.T534M
DFNA5	deafness; autosomal dominant 5	ENSG00000105928	PAP47	97	26.8%	chr7	24714340	CCDS5389.1	c.921G>T	p.Q307H
DFNB31	deafness; autosomal recessive 31	ENSG00000095397	PAP47	178	27.5%	chr9	116208915	CCDS6806.1	c.1777G>A	p.D593N
DFNB59	deafness; autosomal recessive 59	ENSG00000204311	PAP47	136	22.1%	chr2	179026560	CCDS42787.1	c.178G>T	p.D60Y
DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	ENSG00000135829	PAP47	105	25.7%	chr1	181111955	CCDS41444.1	c.1963G>T	p.V655F
DOCK10	dedicator of cytokinesis 10	ENSG00000135905	PAP47	93	25.8%	chr2	225360032	NM_014689	c.5606C>T	p.S1869L
DOCK2	dedicator of cytokinesis 2	ENSG00000134516	PAP47	103	18.4%	chr5	169030176	CCDS4371.1	c.221G>T	p.R74I
DOCK2	dedicator of cytokinesis 2	ENSG00000134516	PAP47	134	27.6%	chr5	169071776	CCDS4371.1	c.1630G>A	p.D544N
DOCK2	dedicator of cytokinesis 2	ENSG00000134516	PAP47	122	29.5%	chr5	169073974	CCDS4371.1	c.1876A>G	p.K626E
DOCK3	dedicator of cytokinesis 3	ENSG00000088538	PAP47	147	28.6%	chr3	51248864	ENST00000402669	c.1966A>G	p.T656A
DHRS7	dehydrogenase/reductase (SDR family) member 7	ENSG00000100612	PAP47	164	28.7%	chr14	59690519	CCDS9743.1	c.304G>T	p.E102X
DCC	deleted in colorectal carcinoma	ENSG00000187323	PAP47	61	18.0%	chr18	49085971	CCDS11952.1	c.1937C>A	p.P646H
DLEC1	deleted in lung and esophageal cancer 1	ENSG00000008226	PAP47	146	28.1%	chr3	38125974	CCDS2672.2	c.3177G>T	p.K1059N
DNER	delta/notch-like EGF repeat containing	ENSG00000187957	PAP47	264	23.9%	chr2	230164622	CCDS33390.1	c.503G>A	p.R168H
DLK1	delta-like 1 homolog (Drosophila)	ENSG00000185559	PAP47	124	26.6%	chr14	100270586	CCDS9963.1	c.752G>A	p.S251N
DENND3	DENN/MADD domain containing 3	ENSG00000105339	PAP47	140	28.6%	chr8	142254519	CCDS34947.1	c.2074T>G	p.F692V
DMP1	dentin matrix acidic phosphoprotein 1	ENSG00000152592	PAP47	147	33.3%	chr4	88803050	CCDS3623.1	c.1096G>T	p.D366Y
DEPDC7	DEP domain containing 7	ENSG00000121690	PAP47	106	28.3%	chr11	33009537	CCDS41632.1	c.820G>T	p.E274X

DEPDC7	DEP domain containing 7	ENSG00000121690	PAP47	78	26.9%	chr11	33011091	CCDS41632.1	c.-1T>C	p.IVS8+2-1SpliceDonor
DSEL	dermatan sulfate epimerase-like	ENSG00000171451	PAP47	203	26.6%	chr18	63331114	CCDS11995.1	c.1742G>A	p.R581H
DSEL	dermatan sulfate epimerase-like	ENSG00000171451	PAP47	96	27.1%	chr18	63332769	CCDS11995.1	c.87C>A	p.F29L
DSP	desmoplakin	ENSG00000096696	PAP47	106	31.1%	chr6	7525061	CCDS4501.1	c.3639G>T	p.E1213D
DPPA4	developmental pluripotency associated 4	ENSG00000121570	PAP47	148	21.6%	chr3	110535506	CCDS33814.1	c.79G>T	p.E27X
DRG2	developmentally regulated GTP binding protein 2	ENSG00000108591	PAP47	116	33.6%	chr17	17945588	CCDS11191.1	c.688G>A	p.D230N
DGKK	diacylglycerol kinase; kappa	ENSG00000204466	PAP47	42	28.6%	chrX	50147388	ENST00000376025	c.2022C>A	p.F674L
DGKK	diacylglycerol kinase; kappa	ENSG00000204466	PAP47	56	30.4%	chrX	50153065	ENST00000376025	c.1420G>T	p.V474L
DLD	dihydrolipoamide dehydrogenase	ENSG00000091140	PAP47	116	14.7%	chr7	107346874	CCDS5749.1	c.-1G>T	p.IVS13-1-1SpliceAcceptor
DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	ENSG00000151240	PAP47	175	31.4%	chr10	405568	CCDS7054.1	c.1997C>T	p.T666M
DPP10	dipeptidyl-peptidase 10 (non-functional)	ENSG00000175497	PAP47	55	29.1%	chr2	115783370	CCDS33278.1	c.125T>C	p.I42T
DLG2	discs; large homolog 2 (Drosophila)	ENSG00000150672	PAP47	186	28.0%	chr11	82921406	CCDS41696.1	c.1871C>T	p.S624L
DAAM1	dishevelled associated activator of morphogenesis 1	ENSG00000100592	PAP47	86	19.8%	chr14	58876603	CCDS9737.1	c.2057C>T	p.S686L
DAAM1	dishevelled associated activator of morphogenesis 1	ENSG00000100592	PAP47	72	19.4%	chr14	58903954	CCDS9737.1	c.2911G>T	p.E971X
DVL3	dishevelled; dsh homolog 3 (Drosophila)	ENSG00000161202	PAP47	54	38.9%	chr3	185366621	CCDS3253.1	c.777C>A	p.F259L
DLX4	distal-less homeobox 4	ENSG00000108813	PAP47	113	31.0%	chr17	45405478	CCDS11555.1	c.326G>A	p.R109H
DMRTC2	DMRT-like family C2	ENSG00000142025	PAP47	597	31.8%	chr19	47044764	CCDS33034.1	c.509C>T	p.P170L
DNMT1	DNA (cytosine-5-)-methyltransferase 1	ENSG00000130816	PAP47	189	31.7%	chr19	10152206	CCDS12228.1	c.265G>T	p.D89Y
DNAJB14	DnaJ (Hsp40) homolog; subfamily B; member 14	ENSG00000164031	PAP47	45	22.2%	chr4	101041237	CCDS34035.1	c.1111C>T	p.R371W
DNAJC10	DnaJ (Hsp40) homolog; subfamily C; member 10	ENSG00000077232	PAP47	56	37.5%	chr2	183324748	CCDS33345.1	c.1425C>A	p.F475L
DNAJC13	DnaJ (Hsp40) homolog; subfamily C; member 13	ENSG00000138246	PAP47	59	22.0%	chr3	133679621	CCDS33857.1	c.2656G>A	p.E886K
DNLZ	DNL-type zinc finger	ENSG00000213221	PAP47	130	26.2%	chr9	138376441	CCDS35179.1	c.381G>T	p.E127D
DOK6	docking protein 6	ENSG00000206052	PAP47	49	24.5%	chr18	65557288	CCDS32841.1	c.707G>T	p.R236I
DRD3	dopamine receptor D3	ENSG00000151577	PAP47	145	27.6%	chr3	115332750	CCDS2978.1	c.911G>A	p.G304D
DCX	doublecortin	ENSG00000077279	PAP47	68	19.1%	chrX	110540292	CCDS14556.1	c.234C>A	p.F78L
DCLK1	doublecortin-like kinase 1	ENSG00000133083	PAP47	148	29.1%	chr13	35598087	CCDS9354.1	c.188G>T	p.R63L
DSCAM	Down syndrome cell adhesion molecule	ENSG00000171587	PAP47	53	26.4%	chr21	40662955	CCDS42929.1	c.596C>T	p.T199M
DSCR3	Down syndrome critical region gene 3	ENSG00000157538	PAP47	37	27.0%	chr21	37521954	CCDS33553.1	c.682G>A	p.D228N
DSTYK	dual serine/threonine and tyrosine protein kinase	ENSG00000133059	PAP47	177	31.6%	chr1	203405044	CCDS1451.1	c.1194G>T	p.E398D
DUSP9	dual specificity phosphatase 9	ENSG00000130829	PAP47	264	27.7%	chrX	152568240	CCDS14724.1	c.733G>A	p.E245K
DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	ENSG00000157540	PAP47	91	28.6%	chr21	37772435	CCDS42925.1	c.290C>A	p.S97Y
DYRK4	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	ENSG00000010219	PAP47	199	28.1%	chr12	4572472	CCDS8530.1	c.162A>C	p.Q54H
DNAH10	dynein; axonemal; heavy chain 10	ENSG00000197653	PAP47	282	23.4%	chr12	122889092	NM_207437	c.4685G>A	p.R1562K
DNAH11	dynein; axonemal; heavy chain 11	ENSG00000105877	PAP47	126	31.7%	chr7	21612651	ENST00000328843	c.3731T>C	p.V1244A
DNAH11	dynein; axonemal; heavy chain 11	ENSG00000105877	PAP47	370	29.7%	chr7	21898650	ENST00000328843	c.12611A>G	p.E4204G
DNAH2	dynein; axonemal; heavy chain 2	ENSG00000183914	PAP47	496	31.5%	chr17	7587241	ENST00000082259	c.2206G>T	p.E736X
DNAH7	dynein; axonemal; heavy chain 7	ENSG00000118997	PAP47	153	29.4%	chr2	196507636	CCDS42794.1	c.3395C>A	p.S1132X
DNAH7	dynein; axonemal; heavy chain 7	ENSG00000118997	PAP47	250	32.4%	chr2	196533464	CCDS42794.1	c.2656G>T	p.D886Y
DNAH8	dynein; axonemal; heavy chain 8	ENSG00000124721	PAP47	50	24.0%	chr6	38883409	CCDS4838.1	c.2545A>C	p.S849R
DNAH8	dynein; axonemal; heavy chain 8	ENSG00000124721	PAP47	186	30.6%	chr6	38975621	CCDS4838.1	c.8504T>G	p.F2835C
DNAH8	dynein; axonemal; heavy chain 8	ENSG00000124721	PAP47	47	25.5%	chr6	39058142	CCDS4838.1	c.12226G>A	p.E4076K
DNAI1	dynein; axonemal; intermediate chain 1	ENSG00000122735	PAP47	35	40.0%	chr9	34483227	CCDS6557.1	c.717G>T	p.E239D
DYNC1H1	dynein; cytoplasmic 1; heavy chain 1	ENSG00000197102	PAP47	110	32.7%	chr14	101540709	CCDS9966.1	c.4985C>T	p.S1662L
DYNC1I2	dynein; cytoplasmic 1; intermediate chain 2	ENSG00000077380	PAP47	60	26.7%	chr2	172271301	NM_001378	c.-1A>C	p.IVS2-2-1SpliceAcceptor
DYSF	dysferlin; limb girdle muscular dystrophy 2B (autosomal recessive)	ENSG00000135636	PAP47	114	30.7%	chr2	71651298	CCDS1918.1	c.3093G>T	p.E1031D

DYSF	dysferlin; limb girdle muscular dystrophy 2B (autosomal recessive)	ENSG00000135636	PAP47	144	25.0%	chr2	71745020	CCDS1918.1	c.5001G>T	p.E1667D
DST	dystonin	ENSG00000151914	PAP47	140	23.6%	chr6	56576374	ENST00000370769	c.10255G>T	p.E3419X
DMD	dystrophin	ENSG00000198947	PAP47	57	22.8%	chrX	32238185	CCDS14233.1	c.6052C>A	p.L2018I
DMD	dystrophin	ENSG00000198947	PAP47	65	26.2%	chrX	32419321	CCDS14233.1	c.2616T>G	p.I872M
DMD	dystrophin	ENSG00000198947	PAP47	71	25.4%	chrX	32419437	CCDS14233.1	c.2500G>A	p.A834T
DMD	dystrophin	ENSG00000198947	PAP47	221	27.6%	chrX	32501830	CCDS14233.1	c.1657C>A	p.L553I
DMD	dystrophin	ENSG00000198947	PAP47	110	31.8%	chrX	32772840	CCDS14233.1	c.245G>A	p.R82Q
E2F8	E2F transcription factor 8	ENSG00000129173	PAP47	151	29.1%	chr11	19207891	CCDS7849.1	c.1579C>T	p.P527S
EML3	echinoderm microtubule associated protein like 3	ENSG00000149499	PAP47	330	32.7%	chr11	62130007	CCDS8023.2	c.1678G>A	p.V560M
EFCAB6	EF-hand calcium binding domain 6	ENSG00000186976	PAP47	96	27.1%	chr22	42405307	CCDS14049.1	c.1321G>A	p.D441N
EFCAB9	EF-hand calcium binding domain 9	ENSG00000214360	PAP47	60	25.0%	chr5	171560251	ENST00000398186	c.362G>T	p.R121I
ELAVL2	ELAV (embryonic lethal; abnormal vision; Drosophila)-like 2 (Hu antigen B)	ENSG00000107105	PAP47	69	27.5%	chr9	23691443	CCDS6515.1	c.647C>A	p.S216Y
EAF2	ELL associated factor 2	ENSG00000145088	PAP47	142	31.7%	chr3	123058565	CCDS3006.1	c.356A>C	p.K119T
EVC2	Ellis van Creveld syndrome 2	ENSG00000173040	PAP47	99	30.3%	chr4	5678394	CCDS3382.2	c.2029C>T	p.R677X
ELOVL5	ELOVL family member 5; elongation of long chain fatty acids (FEN1/Elo2; SUR4/Elo3-like; yeast)	ENSG00000012660	PAP47	68	35.3%	chr6	53247976	CCDS4951.1	c.367G>T	p.E123X
ENAM	enamelin	ENSG00000132464	PAP47	159	32.1%	chr4	71727340	CCDS3544.1	c.1333G>T	p.E445X
ENAM	enamelin	ENSG00000132464	PAP47	135	26.7%	chr4	71727467	CCDS3544.1	c.1460C>A	p.S487Y
ENGASE	endo-beta-N-acetylglucosaminidase	ENSG00000167280	PAP47	120	28.3%	chr17	74588731	CCDS42394.1	c.853G>A	p.E285K
ERP44	endoplasmic reticulum protein 44	ENSG00000023318	PAP47	123	29.3%	chr9	101824276	CCDS35082.1	c.340C>T	p.R114C
EDN1	endothelin 1	ENSG00000078401	PAP47	221	19.5%	chr6	12402308	CCDS4522.1	c.382G>T	p.E128X
ELMO3	engulfment and cell motility 3	ENSG00000102890	PAP47	313	27.5%	chr16	65793801	CCDS10833.2	c.1421G>T	p.C474F
ENO3	enolase 3 (beta; muscle)	ENSG00000108515	PAP47	168	25.6%	chr17	4797336	CCDS11062.1	c.264A>C	p.E88D
EPHA3	EPH receptor A3	ENSG00000044524	PAP47	117	23.9%	chr3	89604411	CCDS2922.1	c.2798C>T	p.T933M
EFNA5	ephrin-A5	ENSG00000184349	PAP47	400	26.3%	chr5	106790832	CCDS4097.1	c.403G>T	p.E135X
EPS8L3	EPS8-like 3	ENSG00000198758	PAP47	100	26.0%	chr1	110094894	CCDS815.1	c.1684C>T	p.R562C
ERMAP	erythroblast membrane-associated protein (Scianna blood group)	ENSG00000164010	PAP47	431	34.8%	chr1	43080981	CCDS475.1	c.919C>A	p.L307I
EPB41L4A	erythrocyte membrane protein band 4.1 like 4A	ENSG00000129595	PAP47	178	33.7%	chr5	111532657	CCDS43350.1	c.1784G>A	p.R595Q
ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	ENSG00000141446	PAP47	68	39.7%	chr18	17407434	CCDS32800.1	c.1369G>T	p.E457X
ETV3	ets variant 3	ENSG00000117036	PAP47	130	29.2%	chr1	155370599	CCDS1164.1	c.329G>T	p.R110I
ETV3L	ets variant 3-like	ENSG00000172018	PAP47	58	22.4%	chr1	155329361	NM_001004341	c.790G>A	p.A264T
EIF2C3	eukaryotic translation initiation factor 2C; 3	ENSG00000126070	PAP47	91	31.9%	chr1	36278522	CCDS399.1	c.2065C>T	p.R689X
EIF2C3	eukaryotic translation initiation factor 2C; 3	ENSG00000126070	PAP47	43	34.9%	chr1	36293304	CCDS399.1	c.2445A>C	p.R815S
EIF4G1	eukaryotic translation initiation factor 4 gamma; 1	ENSG00000114867	PAP47	80	28.8%	chr3	185524805	CCDS3259.1	c.2595A>C	p.Q865H
EIF4H	eukaryotic translation initiation factor 4H	ENSG00000106682	PAP47	44	34.1%	chr7	73240056	CCDS5564.1	c.239A>C	p.K80T
ETF1	eukaryotic translation termination factor 1	ENSG00000120705	PAP47	103	14.6%	chr5	137874712	CCDS4207.1	c.939A>C	p.E313D
ERCC5	excision repair cross-complementing rodent repair deficiency; complementation group 5	ENSG00000134899	PAP47	112	26.8%	chr13	102325936	CCDS32004.1	c.3243G>T	p.K1081N
ERCC6L	excision repair cross-complementing rodent repair deficiency; complementation group 6-like	ENSG00000186871	PAP47	181	30.9%	chrX	71343387	CCDS35329.1	c.1955C>A	p.S652Y
EXOC2	exocyst complex component 2	ENSG00000112685	PAP47	110	21.8%	chr6	537478	CCDS34327.1	c.1183G>T	p.D395Y
ESYT1	extended synaptotagmin-like protein 1	ENSG00000139641	PAP47	194	20.6%	chr12	54813713	CCDS8904.1	c.1368G>T	p.E456D
ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	ENSG00000135476	PAP47	102	30.4%	chr12	51957630	CCDS8852.1	c.2195A>G	p.N732S
FAM118B	family with sequence similarity 118; member B	ENSG00000197798	PAP47	97	34.0%	chr11	125631693	CCDS8470.1	c.718G>A	p.E240K
FAM129A	family with sequence similarity 129; member A	ENSG00000135842	PAP47	261	21.1%	chr1	183054472	CCDS1364.1	c.1096C>T	p.R366C
FAM149A	family with sequence similarity 149; member A	ENSG00000109794	PAP47	76	26.3%	chr4	187325345	CCDS34117.1	c.1310G>A	p.R437Q
FAM155B	family with sequence similarity 155; member B	ENSG00000130054	PAP47	197	32.5%	chrX	68642322	CCDS35317.1	c.472G>A	p.E158K
FAM164C	family with sequence similarity 164; member C	ENSG00000119703	PAP47	156	28.8%	chr14	74607574	CCDS41972.1	c.545A>G	p.N182S
FAM170A	family with sequence similarity 170; member A	ENSG00000164334	PAP47	45	40.0%	chr5	118993370	CCDS43353.1	c.8G>A	p.R3Q
FAM173B	family with sequence similarity 173; member B	ENSG00000150756	PAP47	115	32.2%	chr5	10292316	CCDS43301.1	c.169C>T	p.P57S
FAM178A	family with sequence similarity 178; member A	ENSG00000119906	PAP47	143	22.4%	chr10	102666607	CCDS7500.1	c.475A>G	p.K159E

FAM47B	family with sequence similarity 47; member B	ENSG00000189132	PAP47	214	23.4%	chrX	34871611	CCDS14236.1	c.742C>T	p.R248C
FAM5C	family with sequence similarity 5; member C	ENSG00000162670	PAP47	59	32.2%	chr1	188334624	CCDS1373.1	c.1448A>G	p.D483G
FAM5C	family with sequence similarity 5; member C	ENSG00000162670	PAP47	60	28.3%	chr1	188500724	CCDS1373.1	c.512C>T	p.S171L
FAM50A	family with sequence similarity 50; member A	ENSG00000071859	PAP47	139	26.6%	chrX	153327186	CCDS14751.1	c.123G>T	p.M41I
FAM54A	family with sequence similarity 54; member A	ENSG00000146410	PAP47	45	24.4%	chr6	136596259	CCDS5176.1	c.941C>A	p.S314Y
FAM65B	family with sequence similarity 65; member B	ENSG00000111913	PAP47	89	24.7%	chr6	24977323	NM_014722	c.392G>A	p.R131H
FANCM	Fanconi anemia; complementation group M	ENSG00000187790	PAP47	43	23.3%	chr14	44687881	CCDS32070.1	c.851G>T	p.R284I
FASTKD1	FAST kinase domains 1	ENSG00000138399	PAP47	101	23.8%	chr2	170136737	CCDS33318.1	c.49C>T	p.R17C
FAT2	FAT tumor suppressor homolog 2 (Drosophila)	ENSG00000086570	PAP47	107	31.8%	chr5	150877462	CCDS4317.1	c.11375G>A	p.R3792Q
FAT2	FAT tumor suppressor homolog 2 (Drosophila)	ENSG00000086570	PAP47	259	24.7%	chr5	150926458	CCDS4317.1	c.2228A>G	p.D743G
FAT4	FAT tumor suppressor homolog 4 (Drosophila)	ENSG00000196159	PAP47	65	21.5%	chr4	126549344	CCDS3732.2	c.5865G>T	p.E1955D
FAT4	FAT tumor suppressor homolog 4 (Drosophila)	ENSG00000196159	PAP47	50	28.0%	chr4	126627978	CCDS3732.2	c.12674C>T	p.S4225F
FAT4	FAT tumor suppressor homolog 4 (Drosophila)	ENSG00000196159	PAP47	247	26.7%	chr4	126631765	CCDS3732.2	c.14167G>T	p.E4723X
FBXL21	F-box and leucine-rich repeat protein 21 (gene/pseudogene)	ENSG00000164616	PAP47	119	25.2%	chr5	135304739	ENST00000297158	c.311G>A	p.R104Q
FBXL4	F-box and leucine-rich repeat protein 4	ENSG00000112234	PAP47	245	33.9%	chr6	99481293	CCDS5041.1	c.293G>A	p.R98Q
FBXO3	F-box protein 3	ENSG00000110429	PAP47	122	21.3%	chr11	33736642	CCDS7887.1	c.440G>A	p.R147Q
FBXO34	F-box protein 34	ENSG00000178974	PAP47	271	19.6%	chr14	54888066	CCDS32086.1	c.1205G>A	p.R402K
FBXO40	F-box protein 40	ENSG00000163833	PAP47	254	25.2%	chr3	122824676	CCDS33835.1	c.1710G>T	p.Q570H
FCRL2	Fc receptor-like 2	ENSG00000132704	PAP47	211	25.1%	chr1	156006431	CCDS1168.1	c.444A>C	p.E148D
FRMPD1	FERM and PDZ domain containing 1	ENSG00000070601	PAP47	252	28.2%	chr9	37719762	CCDS6612.1	c.650G>A	p.R217Q
FRMPD1	FERM and PDZ domain containing 1	ENSG00000070601	PAP47	401	28.7%	chr9	37735036	CCDS6612.1	c.3007G>T	p.E1003X
FRMPD1	FERM and PDZ domain containing 1	ENSG00000070601	PAP47	295	31.5%	chr9	37736338	CCDS6612.1	c.4309G>T	p.E1437X
FRMPD3	FERM and PDZ domain containing 3	ENSG00000147234	PAP47	165	31.5%	chrX	106732601	ENST00000276185	c.4775G>A	p.R1592H
FRMPD3	FERM and PDZ domain containing 3	ENSG00000147234	PAP47	438	28.3%	chrX	106733207	ENST00000276185	c.5381C>T	p.S1794L
FERMT3	fermitin family homolog 3 (Drosophila)	ENSG00000149781	PAP47	73	28.8%	chr11	63735781	CCDS8060.1	c.772G>A	p.D258N
FGGY	FGGY carbohydrate kinase domain containing	ENSG00000172456	PAP47	67	28.4%	chr1	59695223	CCDS611.1	c.221C>A	p.S74Y
FBN1	fibrillin 1	ENSG00000166147	PAP47	116	26.7%	chr15	46490720	CCDS32232.1	c.8375G>T	p.R2792I
FGB	fibrinogen beta chain	ENSG00000171564	PAP47	93	21.5%	chr4	155709892	CCDS3786.1	c.941A>C	p.N314T
FGL1	fibrinogen-like 1	ENSG00000104760	PAP47	202	24.3%	chr8	17775834	CCDS6004.1	c.476A>C	p.K159T
FGF12	fibroblast growth factor 12	ENSG00000114279	PAP47	102	23.5%	chr3	193560926	CCDS3301.1	c.295G>A	p.E99K
FGF14	fibroblast growth factor 14	ENSG00000102466	PAP47	125	11.2%	chr13	101852001	CCDS9500.1	c.29G>T	p.R10I
FGF2	fibroblast growth factor 2 (basic)	ENSG00000138685	PAP47	198	22.7%	chr4	124016989	ENST00000394350	c.242G>A	p.R81H
FGFR2	fibroblast growth factor receptor 2	ENSG00000066468	PAP47	126	24.6%	chr10	123237506	CCDS7620.2	c.1978A>G	p.K660E
FN1	fibronectin 1	ENSG00000115414	PAP47	89	24.7%	chr2	215987909	CCDS42814.1	c.1837G>A	p.E613K
FNDC3A	fibronectin type III domain containing 3A	ENSG00000102531	PAP47	190	32.6%	chr13	48670504	CCDS41886.1	c.2780G>A	p.R927Q
FSCB	fibrous sheath CABYR binding protein	ENSG00000189139	PAP47	238	28.2%	chr14	44045374	CCDS9679.1	c.567G>T	p.K189N
FBLN2	fibulin 2	ENSG00000163520	PAP47	103	30.1%	chr3	13587435	ENST00000295761	c.580G>A	p.E194K
FCN2	ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin)	ENSG00000160339	PAP47	179	33.0%	chr9	136919024	CCDS6983.1	c.884C>T	p.S295L
FIGN	fidgetin	ENSG00000182263	PAP47	175	12.0%	chr2	164174817	CCDS2221.2	c.1771C>A	p.L591I
FILIP1L	filamin A interacting protein 1-like	ENSG00000168386	PAP47	133	22.6%	chr3	101051349	CCDS43117.1	c.1861G>T	p.E621X
FLNA	filamin A; alpha	ENSG00000196924	PAP47	230	26.1%	chrX	153233967	CCDS44021.1	c.6521C>T	p.S2174L
FMO6P	flavin containing monooxygenase 6 pseudogene	ENSG00000117507	PAP47	124	35.5%	chr1	169379099	ENST00000236166	c.298C>A	p.L100I
FLT3LG	fms-related tyrosine kinase 3 ligand	ENSG00000090554	PAP47	81	42.0%	chr19	54675514	CCDS12767.1	c.629C>T	p.T210M
FSHR	follicle stimulating hormone receptor	ENSG00000170820	PAP47	74	41.9%	chr2	49043558	CCDS1843.1	c.1906G>T	p.D636Y
FSHR	follicle stimulating hormone receptor	ENSG00000170820	PAP47	115	27.8%	chr2	49049485	CCDS1843.1	c.710G>A	p.G237D
FOXG1	forkhead box G1	ENSG00000176165	PAP47	81	30.9%	chr14	28306875	CCDS9636.1	c.639G>T	p.K213N
FOXO1	forkhead box O1	ENSG00000150907	PAP47	328	26.5%	chr13	40031770	CCDS9371.1	c.1858A>G	p.N620D
FOXR1	forkhead box R1	ENSG00000176302	PAP47	145	27.6%	chr11	118354942	CCDS31688.1	c.202C>A	p.L68M
FOXR1	forkhead box R1	ENSG00000176302	PAP47	285	29.5%	chr11	118356480	CCDS31688.1	c.682C>T	p.R228X
FMN2	formin 2	ENSG00000155816	PAP47	85	42.4%	chr1	238702366	CCDS31069.1	c.5561A>G	p.D1854G
FMR1	fragile X mental retardation 1	ENSG00000102081	PAP47	98	20.4%	chrX	146832391	CCDS14682.1	c.1324C>T	p.R442X
FREM3	FRAS1 related extracellular matrix 3	ENSG00000183090	PAP47	105	32.4%	chr4	144764808	NM_001168235	c.5556G>T	p.E1852D
FUT10	fucosyltransferase 10 (alpha (1;3) fucosyltransferase)	ENSG00000172728	PAP47	182	25.3%	chr8	33366538	CCDS6088.1	c.697G>A	p.E233K

FUT11	fucosyltransferase 11 (alpha (1;3) fucosyltransferase)	ENSG00000196968	PAP47	142	28.2%	chr10	75203369	CCDS7333.1	c.1124T>C	p.V375A
GPR112	G protein-coupled receptor 112	ENSG00000156920	PAP47	451	34.6%	chrX	135258922	CCDS35409.1	c.5391G>T	p.K1797N
GPR119	G protein-coupled receptor 119	ENSG00000147262	PAP47	287	28.9%	chrX	129346855	CCDS14625.1	c.248C>T	p.A83V
GPR146	G protein-coupled receptor 146	ENSG00000164849	PAP47	85	40.0%	chr7	1064239	CCDS5321.1	c.562G>A	p.D188N
GPR156	G protein-coupled receptor 156	ENSG00000175697	PAP47	203	30.5%	chr3	121368925	CCDS2997.1	c.2089C>T	p.R697C
GPR172B	G protein-coupled receptor 172B	ENSG00000132517	PAP47	194	30.4%	chr17	4877181	CCDS11066.1	c.1142C>T	p.S381L
GPR174	G protein-coupled receptor 174	ENSG00000147138	PAP47	147	30.6%	chrX	78313998	CCDS14443.1	c.838C>A	p.L280I
GPR179	G protein-coupled receptor 179	ENSG00000188888	PAP47	298	34.9%	chr17	33737157	CCDS42308.1	c.5821G>T	p.E1941X
GPR19	G protein-coupled receptor 19	ENSG00000183150	PAP47	242	24.0%	chr12	12706158	CCDS8652.1	c.492C>A	p.F164L
GPR31	G protein-coupled receptor 31	ENSG00000120436	PAP47	94	33.0%	chr6	167490780	CCDS5299.1	c.530G>T	p.W177L
GPR32	G protein-coupled receptor 32	ENSG00000142511	PAP47	210	19.5%	chr19	55966582	CCDS12801.1	c.913G>T	p.G305C
GPR63	G protein-coupled receptor 63	ENSG00000112218	PAP47	216	30.6%	chr6	97353374	CCDS5036.1	c.955C>A	p.L319I
GPR78	G protein-coupled receptor 78	ENSG00000155269	PAP47	243	25.9%	chr4	8635196	CCDS3403.1	c.707G>A	p.R236H
GPR82	G protein-coupled receptor 82	ENSG00000171657	PAP47	191	19.4%	chrX	41471927	CCDS14259.1	c.704C>T	p.T235M
GPRASP2	G protein-coupled receptor associated sorting protein 2	ENSG00000158301	PAP47	144	30.6%	chrX	101858356	CCDS14501.1	c.1903C>T	p.R635X
GPRC5C	G protein-coupled receptor; family C; group 5; member C	ENSG00000170412	PAP47	887	17.0%	chr17	69947664	CCDS11699.1	c.289G>A	p.V97I
GABARAP	GABA(A) receptor-associated protein	ENSG00000170296	PAP47	327	26.9%	chr17	7085672	CCDS11092.1	c.141G>T	p.K47N
GLB1L	galactosidase; beta 1-like	ENSG00000163521	PAP47	425	28.5%	chr2	219812591	CCDS2437.1	c.838C>T	p.R280W
GLB1L	galactosidase; beta 1-like	ENSG00000163521	PAP47	348	33.6%	chr2	219812976	CCDS2437.1	c.631G>T	p.E211X
GABRB2	gamma-aminobutyric acid (GABA) A receptor; beta 2	ENSG00000145864	PAP47	241	11.6%	chr5	160653797	CCDS4355.1	c.1408C>T	p.R470C
GABRG2	gamma-aminobutyric acid (GABA) A receptor; gamma 2	ENSG00000113327	PAP47	177	27.1%	chr5	161512837	CCDS4359.1	c.1313G>T	p.R438I
GABBR2	gamma-aminobutyric acid (GABA) B receptor; 2	ENSG00000136928	PAP47	93	34.4%	chr9	100275438	CCDS6736.1	c.810G>T	p.E270D
GDAP2	ganglioside induced differentiation associated protein 2	ENSG00000196505	PAP47	185	25.9%	chr1	118262817	CCDS897.1	c.241G>A	p.D81N
GATAD1	GATA zinc finger domain containing 1	ENSG00000157259	PAP47	33	36.4%	chr7	91915042	CCDS5625.1	c.63G>T	p.K21N
GDI1	GDP dissociation inhibitor 1	ENSG00000203879	PAP47	222	32.0%	chrX	153320304	CCDS35452.1	c.-1G>T	p.IVS2-1-1SpliceAcceptor
GTF3C1	general transcription factor IIIC; polypeptide 1; alpha 220kDa	ENSG00000077235	PAP47	302	31.1%	chr16	27425951	CCDS32414.1	c.1270C>T	p.R424X
GMCL1	germ cell-less homolog 1 (Drosophila)	ENSG00000087338	PAP47	32	50.0%	chr2	69920132	CCDS1895.1	c.424G>T	p.E142X
GHDC	GH3 domain containing	ENSG00000167925	PAP47	163	35.0%	chr17	37598187	CCDS11422.1	c.487C>T	p.P163S
GLI1	GLI family zinc finger 1	ENSG00000111087	PAP47	102	35.3%	chr12	56144127	CCDS8940.1	c.179A>C	p.N60T
GCNT7	glucosaminyl (N-acetyl) transferase family member 7	ENSG00000124091	PAP47	116	22.4%	chr20	54505324	ENST00000243913	c.382G>A	p.E128K
GANAB	glucosidase; alpha; neutral AB	ENSG00000089597	PAP47	328	32.3%	chr11	62157498	CCDS41656.1	c.691G>A	p.D231N
GRIA2	glutamate receptor; ionotropic; AMPA 2	ENSG00000120251	PAP47	105	27.6%	chr4	158444216	CCDS43274.1	c.292A>C	p.N98H
GRID2	glutamate receptor; ionotropic; delta 2	ENSG00000152208	PAP47	76	21.1%	chr4	94563056	CCDS3637.1	c.1459G>A	p.E487K
GRID2	glutamate receptor; ionotropic; delta 2	ENSG00000152208	PAP47	86	31.4%	chr4	94595938	CCDS3637.1	c.1648C>T	p.R550X
GRM4	glutamate receptor; metabotropic 4	ENSG00000124493	PAP47	191	30.9%	chr6	34111838	CCDS4787.1	c.2027G>A	p.R676H
GRM5	glutamate receptor; metabotropic 5	ENSG00000168959	PAP47	211	30.3%	chr11	87940320	CCDS8283.1	c.2179C>T	p.R727X
GRM6	glutamate receptor; metabotropic 6	ENSG00000113262	PAP47	68	22.1%	chr5	178348950	CCDS4442.1	c.1075G>A	p.E359K
GOT1	glutamic-oxaloacetic transaminase 1; soluble (aspartate aminotransferase 1)	ENSG00000120053	PAP47	171	27.5%	chr10	101153511	CCDS7479.1	c.753C>A	p.F251L
GSTM4	glutathione S-transferase mu 4	ENSG00000168765	PAP47	374	25.7%	chr1	110003262	ENST00000369833	c.451C>T	p.P151S
GPAM	glycerol-3-phosphate acyltransferase; mitochondrial	ENSG00000119927	PAP47	54	24.1%	chr10	113923452	CCDS7570.1	c.555G>T	p.M185I
GDPD4	glycerophosphodiester phosphodiesterase domain containing 4	ENSG00000178795	PAP47	149	25.5%	chr11	76634102	CCDS8249.1	c.958C>A	p.L320I
GDPD4	glycerophosphodiester phosphodiesterase domain containing 4	ENSG00000178795	PAP47	36	36.1%	chr11	76647116	CCDS8249.1	c.827C>T	p.S276L
GLRA2	glycine receptor; alpha 2	ENSG00000101958	PAP47	95	27.4%	chrX	14537123	CCDS14160.1	c.805G>A	p.V269I
GLRA4	glycine receptor; alpha 4	ENSG00000188828	PAP47	262	26.0%	chrX	102865825	CCDS43980.1	c.208G>T	p.E70X
GP2	glycoprotein 2 (zymogen granule membrane)	ENSG00000169347	PAP47	44	29.5%	chr16	20236058	CCDS42128.1	c.1403C>A	p.S468Y
GML	glycosylphosphatidylinositol anchored molecule like protein	ENSG00000104499	PAP47	66	19.7%	chr8	143924822	CCDS6391.1	c.191C>A	p.S64Y
GLO1	glyoxalase I	ENSG00000124767	PAP47	59	35.6%	chr6	38762724	CCDS4837.1	c.89T>G	p.F30C
GPC5	glypican 5	ENSG00000179399	PAP47	227	22.0%	chr13	91143784	CCDS9468.1	c.668G>A	p.R223H

GORAB	golgin; RAB6-interacting	ENSG00000120370	PAP47	208	38.5%	chr1	168788078	CCDS1289.1	c.1036G>T	p.E346X
GPRIN3	GPRIN family member 3	ENSG00000185477	PAP47	293	27.6%	chr4	90390098	CCDS34030.1	c.187G>A	p.E63K
GRAMD1C	GRAM domain containing 1C	ENSG00000178075	PAP47	74	25.7%	chr3	115110631	CCDS33826.1	c.926G>T	p.S309I
GIGYF2	GRB10 interacting GYF protein 2	ENSG00000204120	PAP47	98	26.5%	chr2	233382693	CCDS33401.1	c.1826G>A	p.R609Q
GRB10	growth factor receptor-bound protein 10	ENSG00000106070	PAP47	72	36.1%	chr7	50653331	CCDS43582.1	c.-1G>T	p.IVS6-1-1SpliceAcceptor
GNAO1	guanine nucleotide binding protein (G protein); alpha activating activity polypeptide O	ENSG00000087258	PAP47	207	24.6%	chr16	54932371	CCDS10757.1	c.848C>T	p.P283L
GNAT2	guanine nucleotide binding protein (G protein); alpha transducing activity polypeptide 2	ENSG00000134183	PAP47	80	22.5%	chr1	109950561	CCDS803.1	c.482G>A	p.R161Q
GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	ENSG00000130119	PAP47	189	32.8%	chrX	54586115	CCDS14360.1	c.309G>T	p.E103D
GUCY1A2	guanylate cyclase 1; soluble; alpha 2	ENSG00000152402	PAP47	82	30.5%	chr11	106063646	CCDS8335.1	c.2038G>T	p.E680X
GUCY1A3	guanylate cyclase 1; soluble; alpha 3	ENSG00000164116	PAP47	216	31.9%	chr4	156837509	CCDS34085.1	c.40G>A	p.E14K
GUCY2C	guanylate cyclase 2C (heat stable enterotoxin receptor)	ENSG00000070019	PAP47	89	16.9%	chr12	14696171	CCDS8664.1	c.1594G>T	p.E532X
GUCY2F	guanylate cyclase 2F; retinal	ENSG00000101890	PAP47	74	32.4%	chrX	108578046	CCDS14545.1	c.1477C>T	p.R493C
HDHD2	haloacid dehalogenase-like hydrolase domain containing 2	ENSG00000167220	PAP47	52	25.0%	chr18	42916727	CCDS32829.1	c.82G>A	p.A28T
HBS1L	HBS1-like (S. cerevisiae)	ENSG00000112339	PAP47	56	32.1%	chr6	135348219	CCDS5173.1	c.1445G>A	p.R482Q
HEATR1	HEAT repeat containing 1	ENSG00000119285	PAP47	57	19.3%	chr1	234786141	CCDS31066.1	c.5396C>T	p.A1799V
HEATR5B	HEAT repeat containing 5B	ENSG00000008869	PAP47	57	36.8%	chr2	37121931	CCDS33181.1	c.2705C>T	p.S902L
HEATR5B	HEAT repeat containing 5B	ENSG00000008869	PAP47	71	26.8%	chr2	37151014	CCDS33181.1	c.790C>T	p.R264X
HEATR6	HEAT repeat containing 6	ENSG00000068097	PAP47	157	35.0%	chr17	55483041	CCDS11623.1	c.2369C>T	p.A790V
HSP90AA1	heat shock protein 90kDa alpha (cytosolic); class A member 1	ENSG00000080824	PAP47	46	30.4%	chr14	101619760	CCDS32160.1	c.1728A>C	p.Q576H
HACE1	HECT domain and ankyrin repeat containing; E3 ubiquitin protein ligase 1	ENSG00000085382	PAP47	162	16.0%	chr6	105346151	CCDS5050.1	c.995G>A	p.R332Q
HHIP	hedgehog interacting protein	ENSG00000164161	PAP47	69	27.5%	chr4	145854943	CCDS3762.1	c.1540C>T	p.R514C
HELB	helicase (DNA) B	ENSG00000127311	PAP47	250	27.2%	chr12	64990116	CCDS8976.1	c.1141G>A	p.D381N
HBA2	hemoglobin; alpha 2	ENSG00000188536	PAP47	248	23.0%	chr16	163556	CCDS10398.1	c.386T>A	p.F129Y
HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	ENSG00000019991	PAP47	118	26.3%	chr7	81188091	CCDS5597.1	c.1177C>T	p.R393C
HNRNPH2	heterogeneous nuclear ribonucleoprotein H2 (H')	ENSG00000126945	PAP47	142	26.8%	chrX	100554446	CCDS14485.1	c.814T>C	p.S272P
HFM1	HFM1; ATP-dependent DNA helicase homolog (S. cerevisiae)	ENSG00000162669	PAP47	102	32.4%	chr1	91616211	CCDS30769.2	c.1354C>T	p.R452X
HIST1H3D	histone cluster 1; H3d	ENSG00000197409	PAP47	83	26.5%	chr6	26307345	CCDS4591.1	c.106C>T	p.R36C
HDAC4	histone deacetylase 4	ENSG00000068024	PAP47	132	35.6%	chr2	239674210	CCDS2529.1	c.2411C>T	p.A804V
HDAC8	histone deacetylase 8	ENSG00000147099	PAP47	88	23.9%	chrX	71601302	CCDS14420.1	c.742C>A	p.L248I
HTATSF1	HIV-1 Tat specific factor 1	ENSG00000102241	PAP47	94	30.9%	chrX	135421434	CCDS14657.1	c.1864G>A	p.E622K
HBP1	HMG-box transcription factor 1	ENSG00000105856	PAP47	93	26.9%	chr7	106607662	CCDS5741.1	c.88G>T	p.D30Y
HLCS	holocarboxylase synthetase (biotin-(proprionyl-CoA-carboxylase (ATP-hydrolysing)) ligase)	ENSG00000159267	PAP47	55	23.6%	chr21	37233009	CCDS13647.1	c.45G>T	p.K15N
HCCS	holocytochrome c synthase	ENSG00000004961	PAP47	119	27.7%	chrX	11045431	CCDS14139.1	c.376T>C	p.F126L
HOXA1	homeobox A1	ENSG00000105991	PAP47	182	25.3%	chr7	27100737	CCDS5401.1	c.855G>T	p.K285N
HIPK1	homeodomain interacting protein kinase 1	ENSG00000163349	PAP47	114	21.9%	chr1	114300881	CCDS867.1	c.1517G>T	p.R506I
HCFC1	host cell factor C1 (VP16-accessory protein)	ENSG00000172534	PAP47	137	30.7%	chrX	152871360	CCDS44020.1	c.4741G>A	p.E1581K
HIVEP3	human immunodeficiency virus type I enhancer binding protein 3	ENSG00000127124	PAP47	46	26.1%	chr1	41813810	CCDS463.1	c.5199C>A	p.F1733L
HYDIN	hydrocephalus inducing homolog (mouse)	ENSG00000157423	PAP47	193	14.0%	chr16	69475357	CCDS42189.1	c.9943C>A	p.L3315I
HYDIN	hydrocephalus inducing homolog (mouse)	ENSG00000157423	PAP47	211	12.8%	chr16	69728649	CCDS42189.1	c.949C>T	p.R317X
HAO2	hydroxyacid oxidase 2 (long chain)	ENSG00000116882	PAP47	93	33.3%	chr1	119737940	CCDS901.1	c.1010C>T	p.S337L
HSD17B3	hydroxysteroid (17-beta) dehydrogenase 3	ENSG00000130948	PAP47	92	22.8%	chr9	98042968	CCDS6716.1	c.715C>A	p.L239I
HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	ENSG00000025423	PAP47	104	31.7%	chr12	55467272	CCDS8925.1	c.833G>A	p.R278Q
HCRTR2	hypocretin (orexin) receptor 2	ENSG00000137252	PAP47	63	22.2%	chr6	55250165	CCDS4956.1	c.791G>T	p.R264I
ICT1	immature colon carcinoma transcript 1	ENSG00000167862	PAP47	53	39.6%	chr17	70520531	CCDS11711.1	c.155C>T	p.S52F

IGHV1-24	immunoglobulin heavy variable 1-24	ENSG00000211950	PAP47	122	26.2%	chr14	105804326	ENST00000390610	c.214C>A	p.P72T
IGKV5-2	immunoglobulin kappa variable 5-2	ENSG00000211599	PAP47	144	28.5%	chr2	88978212	ENST00000390244	c.142G>T	p.D48Y
ISLR2	immunoglobulin superfamily containing leucine-rich repeat 2	ENSG00000167178	PAP47	250	30.8%	chr15	72213070	CCDS10259.1	c.922T>G	p.L308V
IGSF10	immunoglobulin superfamily; member 10	ENSG00000152580	PAP47	176	30.1%	chr3	152637757	CCDS3160.1	c.7282A>G	p.I2428V
IHH	Indian hedgehog homolog (Drosophila)	ENSG00000163501	PAP47	175	26.3%	chr2	219630650	CCDS33380.1	c.326A>G	p.D109G
IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	ENSG00000005700	PAP47	98	30.6%	chr6	82981092	CCDS34490.1	c.1775T>C	p.L592S
INO80E	INO80 complex subunit E	ENSG00000169592	PAP47	66	34.8%	chr16	29915175	CCDS10665.1	c.43T>C	p.Y15H
ITPR2	inositol 1;4;5-triphosphate receptor; type 2	ENSG00000123104	PAP47	150	19.3%	chr12	26384523	CCDS41764.1	c.7863G>T	p.K2621N
ITPR2	inositol 1;4;5-triphosphate receptor; type 2	ENSG00000123104	PAP47	211	30.3%	chr12	26463264	CCDS41764.1	c.7095C>A	p.F2365L
ITPR2	inositol 1;4;5-triphosphate receptor; type 2	ENSG00000123104	PAP47	209	23.9%	chr12	26487804	CCDS41764.1	c.6389C>T	p.S2130L
ITPR2	inositol 1;4;5-triphosphate receptor; type 2	ENSG00000123104	PAP47	88	26.1%	chr12	26703446	CCDS41764.1	c.1753A>C	p.I585L
IP6K2	inositol hexakisphosphate kinase 2	ENSG00000068745	PAP47	243	30.5%	chr3	48700967	CCDS2777.1	c.1024G>A	p.E342K
INPP5F	inositol polyphosphate-5-phosphatase F	ENSG00000198825	PAP47	220	27.3%	chr10	121576189	CCDS7616.1	c.2306C>A	p.S769Y
IRS4	insulin receptor substrate 4	ENSG00000133124	PAP47	183	26.8%	chrX	107862864	CCDS14544.1	c.3367G>A	p.A1123T
IRS4	insulin receptor substrate 4	ENSG00000133124	PAP47	168	17.9%	chrX	107863706	CCDS14544.1	c.2525A>G	p.D842G
IGF2BP1	insulin-like growth factor 2 mRNA binding protein 1	ENSG00000159217	PAP47	236	25.8%	chr17	44474703	CCDS11543.1	c.1042C>T	p.R348W
ITFG1	integrin alpha FG-GAP repeat containing 1	ENSG00000129636	PAP47	71	32.4%	chr16	45753205	CCDS10728.1	c.1618T>C	p.S540P
ITGA9	integrin; alpha 9	ENSG00000144668	PAP47	164	10.4%	chr3	37511019	CCDS2669.1	c.568G>A	p.E190K
ITGAE	integrin; alpha E (antigen CD103; human mucosal lymphocyte antigen 1; alpha polypeptide)	ENSG00000083457	PAP47	147	28.6%	chr17	3564914	CCDS32531.1	c.3516G>T	p.E1172D
ITGAE	integrin; alpha E (antigen CD103; human mucosal lymphocyte antigen 1; alpha polypeptide)	ENSG00000083457	PAP47	80	13.8%	chr17	3570436	CCDS32531.1	c.3247G>T	p.D1083Y
ITGB8	integrin; beta 8	ENSG00000105855	PAP47	152	32.2%	chr7	20410832	CCDS5370.1	c.1744C>T	p.R582X
IPCEF1	interaction protein for cytohesin exchange factors 1	ENSG00000074706	PAP47	37	29.7%	chr6	154586064	CCDS5245.1	c.249G>T	p.E83D
ITIH1	inter-alpha (globulin) inhibitor H1	ENSG00000055957	PAP47	84	31.0%	chr3	52793490	CCDS2864.1	c.1364C>T	p.A455V
ITIH5	inter-alpha (globulin) inhibitor H5	ENSG00000123243	PAP47	175	28.0%	chr10	7658796	CCDS31139.1	c.1604G>A	p.S535N
ITIH5L	inter-alpha (globulin) inhibitor H5-like	ENSG00000102313	PAP47	103	28.2%	chrX	54803086	CCDS14361.1	c.-1G>T	p.IVS6-1-1SpliceAcceptor
IRF2	interferon regulatory factor 2	ENSG00000168310	PAP47	49	36.7%	chr4	185566413	CCDS3835.1	c.422T>G	p.V141G
IFI30	interferon; gamma-inducible protein 30	ENSG00000216490	PAP47	68	38.2%	chr19	18148978	NM_006332	c.512C>T	p.S171L
IFIT1B	interferon-induced protein with tetratricopeptide repeats 1B	ENSG00000204010	PAP47	104	28.8%	chr10	91133147	CCDS31242.1	c.97C>T	p.P33S
IFIT1B	interferon-induced protein with tetratricopeptide repeats 1B	ENSG00000204010	PAP47	134	13.4%	chr10	91134319	CCDS31242.1	c.1269G>T	p.E423D
IL1RAPL1	interleukin 1 receptor accessory protein-like 1	ENSG00000169306	PAP47	139	30.2%	chrX	29848102	CCDS14218.1	c.1027C>T	p.R343X
IL12RB2	interleukin 12 receptor; beta 2	ENSG00000081985	PAP47	266	24.4%	chr1	67560056	CCDS638.1	c.260C>A	p.S87Y
IL12RB2	interleukin 12 receptor; beta 2	ENSG00000081985	PAP47	197	36.5%	chr1	67618370	CCDS638.1	c.1831A>C	p.N611H
IL17F	interleukin 17F	ENSG00000112116	PAP47	140	29.3%	chr6	52209894	CCDS4938.1	c.286G>A	p.E96K
IL2RA	interleukin 2 receptor; alpha	ENSG00000134460	PAP47	283	31.1%	chr10	6103617	CCDS7076.1	c.413G>A	p.R138K
IL2RG	interleukin 2 receptor; gamma (severe combined immunodeficiency)	ENSG00000147168	PAP47	168	26.2%	chrX	70244910	CCDS14406.1	c.866G>A	p.R289Q
IL6ST	interleukin 6 signal transducer (gp130; oncostatin M receptor)	ENSG00000134352	PAP47	64	28.1%	chr5	55286492	CCDS3971.1	c.1353G>T	p.K451N
IRAK1BP1	interleukin-1 receptor-associated kinase 1 binding protein 1	ENSG00000146243	PAP47	185	34.1%	chr6	79664394	CCDS34488.1	c.511C>T	p.R171X
IMPG2	interphotoreceptor matrix proteoglycan 2	ENSG00000081148	PAP47	41	29.3%	chr3	102521875	CCDS2940.1	c.32C>A	p.S11Y
IQUB	IQ motif and ubiquitin domain containing	ENSG00000164675	PAP47	195	25.1%	chr7	122880099	CCDS5787.1	c.2310G>T	p.E770D
IQGAP3	IQ motif containing GTPase activating protein 3	ENSG00000183856	PAP47	143	27.3%	chr1	154805873	CCDS1144.1	c.44G>A	p.R15H
IQCK	IQ motif containing K	ENSG00000174628	PAP47	103	18.4%	chr16	19682894	CCDS10580.1	c.564A>T	p.E188D
IRX6	iroquois homeobox 6	ENSG00000159387	PAP47	113	42.5%	chr16	53920289	CCDS32449.1	c.898C>T	p.R300X
ICA1	islet cell autoantigen 1; 69kDa	ENSG00000003147	PAP47	47	38.3%	chr7	8227533	CCDS34602.1	c.277G>A	p.E93K
IDH2	isocitrate dehydrogenase 2 (NADP+); mitochondrial	ENSG00000182054	PAP47	249	32.5%	chr15	88431480	CCDS10359.1	c.835G>A	p.D279N
JAK3	Janus kinase 3	ENSG00000105639	PAP47	40	27.5%	chr19	17809024	CCDS12366.1	c.-1A>C	p.IVS11-2-1SpliceAcceptor
JMJD7-PLA2	JMJD7-PLA2G4B readthrough	ENSG00000168970	PAP47	152	21.1%	chr15	39926171	CCDS32202.1	c.2486A>G	p.D829G

JARID2	jumonji; AT rich interactive domain 2	ENSG00000008083	PAP47	169	33.1%	chr6	15615461	CCDS4533.1	c.2657C>T	p.S886L
KALRN	kalirin; RhoGEF kinase	ENSG00000160145	PAP47	253	11.5%	chr3	125694319	CCDS3027.1	c.4726C>T	p.R1576X
KBTBD4	kelch repeat and BTB (POZ) domain containing 4	ENSG00000123444	PAP47	234	29.9%	chr11	47555906	CCDS7940.1	c.222C>A	p.F74L
KLHL11	kelch-like 11 (Drosophila)	ENSG00000178502	PAP47	177	29.4%	chr17	37264977	CCDS11411.1	c.668A>C	p.K223T
KRT20	keratin 20	ENSG00000171431	PAP47	46	23.9%	chr17	36290462	CCDS11379.1	c.560A>C	p.K187T
KRT74	keratin 74	ENSG00000170484	PAP47	82	23.2%	chr12	51250764	CCDS8832.1	c.964G>A	p.A322T
KRT77	keratin 77	ENSG00000189182	PAP47	171	11.1%	chr12	51374751	CCDS8837.1	c.1006G>A	p.D336N
KERA	keratocan	ENSG00000139330	PAP47	174	28.7%	chr12	89974114	CCDS9037.1	c.76G>A	p.V26I
KIAA0146	KIAA0146	ENSG00000164808	PAP47	290	30.3%	chr8	48471622	CCDS43737.1	c.659T>G	p.M220R
KIAA0232	KIAA0232	ENSG00000170871	PAP47	92	31.5%	chr4	6916164	CCDS43209.1	c.3154C>A	p.L1052I
KIAA0232	KIAA0232	ENSG00000170871	PAP47	158	24.1%	chr4	6916336	CCDS43209.1	c.3326G>A	p.R1109H
KIAA0467	KIAA0467	ENSG00000198198	PAP47	58	25.9%	chr1	43641499	CCDS30693.1	c.92G>A	p.R31H
KIAA0494	KIAA0494	ENSG00000159658	PAP47	68	32.4%	chr1	46921643	CCDS30706.1	c.1228A>C	p.K410Q
KIAA0528	KIAA0528	ENSG00000111731	PAP47	224	28.6%	chr12	22567748	CCDS31758.1	c.679G>A	p.D227N
KIAA0892	KIAA0892	ENSG00000129933	PAP47	241	29.0%	chr19	19339943	ENST00000262816	c.1772C>A	p.S591Y
KIAA1109	KIAA1109	ENSG00000138688	PAP47	51	41.2%	chr4	123390215	CCDS43267.1	c.5638C>T	p.R1880X
KIAA1211	KIAA1211	ENSG00000109265	PAP47	167	19.8%	chr4	56876106	CCDS43230.1	c.1681G>A	p.A561T
KIAA1244	KIAA1244	ENSG00000112379	PAP47	317	33.8%	chr6	138699257	NM_020340	c.6475C>T	p.R2159C
KIAA1462	KIAA1462	ENSG00000165757	PAP47	274	31.8%	chr10	30356998	CCDS41500.1	c.2085C>A	p.F695L
KIAA1529	KIAA1529	ENSG00000197816	PAP47	73	31.5%	chr9	99111569	CCDS35077.1	c.671C>A	p.S224Y
KIAA1529	KIAA1529	ENSG00000197816	PAP47	155	29.7%	chr9	99157068	CCDS35077.1	c.3266T>G	p.I1089S
KIAA1586	KIAA1586	ENSG00000168116	PAP47	64	23.4%	chr6	57026643	CCDS34480.1	c.1387G>T	p.G463X
KIAA1598	KIAA1598	ENSG00000187164	PAP47	201	25.9%	chr10	118664934	CCDS31293.1	c.1247G>T	p.R416I
KIAA1704	KIAA1704	ENSG00000133114	PAP47	111	26.1%	chr13	44476505	CCDS9394.1	c.154G>A	p.D52N
KIAA1826	KIAA1826	ENSG00000170903	PAP47	186	28.5%	chr11	105385500	CCDS31663.1	c.1010G>A	p.R337Q
KIAA2022	KIAA2022	ENSG00000050030	PAP47	96	21.9%	chrX	73879235	CCDS35337.1	c.1882C>T	p.R628X
KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	ENSG00000128052	PAP47	141	32.6%	chr4	55663367	CCDS3497.1	c.2053G>A	p.E685K
KIF14	kinesin family member 14	ENSG00000118193	PAP47	148	18.9%	chr1	198834082	CCDS30963.1	c.2455A>G	p.M819V
KIF26B	kinesin family member 26B	ENSG00000162849	PAP47	57	28.1%	chr1	243918205	NM_018012	c.5297C>T	p.A1766V
KIF5A	kinesin family member 5A	ENSG00000155980	PAP47	140	29.3%	chr12	56252762	CCDS8945.1	c.1702G>A	p.G568R
KL	klotho	ENSG00000133116	PAP47	104	11.5%	chr13	32527359	CCDS9347.1	c.1506G>T	p.E502D
KLB	klotho beta	ENSG00000134962	PAP47	282	28.0%	chr4	39112570	CCDS3451.1	c.1171A>C	p.N391H
KRR1	KRR1; small subunit (SSU) processome component; homolog (yeast)	ENSG00000111615	PAP47	81	28.4%	chr12	74179877	CCDS9012.1	c.1125G>T	p.K375N
KCNIP1	Kv channel interacting protein 1	ENSG00000182132	PAP47	183	32.8%	chr5	169864183	CCDS34286.1	c.29C>A	p.S10Y
L3MBTL	l(3)mbt-like (Drosophila)	ENSG00000185513	PAP47	155	26.5%	chr20	41592890	CCDS13319.1	c.961C>T	p.R321C
LACE1	lactation elevated 1	ENSG00000135537	PAP47	210	26.7%	chr6	108751820	CCDS5067.1	c.238G>T	p.D80Y
LTF	lactotransferrin	ENSG00000012223	PAP47	177	28.8%	chr3	46472466	CCDS33747.1	c.323G>A	p.R108Q
LAMA1	laminin; alpha 1	ENSG00000101680	PAP47	139	30.9%	chr18	6932125	CCDS32787.1	c.9181G>T	p.E3061X
LAMA3	laminin; alpha 3	ENSG00000053747	PAP47	106	27.4%	chr18	19584918	CCDS42419.1	c.723A>C	p.K241N
LAMA5	laminin; alpha 5	ENSG00000130702	PAP47	280	18.9%	chr20	60319430	CCDS33502.1	c.10204G>A	p.V3402I
LAMB2	laminin; beta 2 (laminin S)	ENSG00000172037	PAP47	234	26.9%	chr3	49133775	CCDS2789.1	c.5285A>C	p.N1762T
LAS1L	LAS1-like (S. cerevisiae)	ENSG00000001497	PAP47	296	31.8%	chrX	64666250	CCDS14381.1	c.748G>A	p.E250K
LMAN2	lectin; mannose-binding 2	ENSG00000169223	PAP47	42	26.2%	chr5	176710803	CCDS4417.1	c.292G>A	p.E98K
LEPREL1	leprecan-like 1	ENSG00000090530	PAP47	128	22.7%	chr3	191194700	CCDS3294.1	c.700G>A	p.E234K
LRRCC1	leucine rich repeat and coiled-coil domain containing 1	ENSG00000133739	PAP47	34	41.2%	chr8	86224286	CCDS43750.1	c.1132C>T	p.R378C
LRFN5	leucine rich repeat and fibronectin type III domain containing 5	ENSG00000165379	PAP47	136	33.1%	chr14	41426416	CCDS9678.1	c.838G>T	p.E280X
LRFN5	leucine rich repeat and fibronectin type III domain containing 5	ENSG00000165379	PAP47	165	34.5%	chr14	41426792	CCDS9678.1	c.1214C>A	p.S405Y
LRRC16A	leucine rich repeat containing 16A	ENSG00000079691	PAP47	78	15.4%	chr6	25590513	NM_017640	c.924G>T	p.K308N
LRRC16A	leucine rich repeat containing 16A	ENSG00000079691	PAP47	206	23.8%	chr6	25708744	NM_017640	c.3343G>A	p.E1115K
LRRC23	leucine rich repeat containing 23	ENSG00000010626	PAP47	106	31.1%	chr12	6892411	CCDS8569.1	c.1015G>A	p.E339K

LRRC43	leucine rich repeat containing 43	ENSG00000158113	PAP47	225	30.2%	chr12	121243317	CCDS41854.1	c.607G>A	p.E203K
LRRC66	leucine rich repeat containing 66	ENSG00000188993	PAP47	125	23.2%	chr4	52564153	CCDS43229.1	c.659A>C	p.K220T
LRRC8D	leucine rich repeat containing 8 family; member D	ENSG00000171492	PAP47	160	30.6%	chr1	90172097	CCDS726.1	c.882C>G	p.F294L
LRRN1	leucine rich repeat neuronal 1	ENSG00000175928	PAP47	282	31.6%	chr3	3862126	CCDS33685.1	c.801C>A	p.F267L
LRRN3	leucine rich repeat neuronal 3	ENSG00000173114	PAP47	137	25.5%	chr7	110551706	CCDS5754.1	c.1642C>A	p.L548I
LRRTM3	leucine rich repeat transmembrane neuronal 3	ENSG00000198739	PAP47	86	34.9%	chr10	68358197	CCDS7270.1	c.1517C>A	p.S506X
LUZP4	leucine zipper protein 4	ENSG00000102021	PAP47	223	28.3%	chrX	114447189	CCDS14567.1	c.506C>A	p.S169Y
LUZP4	leucine zipper protein 4	ENSG00000102021	PAP47	186	30.6%	chrX	114447210	CCDS14567.1	c.527C>A	p.S176Y
LZTS1	leucine zipper; putative tumor suppressor 1	ENSG00000061337	PAP47	229	30.6%	chr8	20151560	CCDS6015.1	c.1744G>T	p.E582X
LRPPRC	leucine-rich PPR-motif containing	ENSG00000138095	PAP47	42	26.2%	chr2	44062931	CCDS33189.1	c.296G>A	p.R99H
LRGUK	leucine-rich repeats and guanylate kinase domain containing	ENSG00000155530	PAP47	82	26.8%	chr7	133582854	CCDS5830.1	c.1990G>T	p.D664Y
LRRIQ1	leucine-rich repeats and IQ motif containing 1	ENSG00000133640	PAP47	217	21.7%	chr12	84042182	CCDS41816.1	c.3761G>A	p.R1254H
LARS	leucyl-tRNA synthetase	ENSG00000133706	PAP47	127	29.1%	chr5	145488752	CCDS34265.1	c.2751G>T	p.M917I
LILRB2	leukocyte immunoglobulin-like receptor; subfamily B (with TM and ITIM domains); member 2	ENSG00000131042	PAP47	68	23.5%	chr19	59474676	CCDS12886.1	c.758G>T	p.R253I
LIG4	ligase IV; DNA; ATP-dependent	ENSG00000174405	PAP47	125	32.8%	chr13	107659364	CCDS9508.1	c.2254G>T	p.E752X
LDB1	LIM domain binding 1	ENSG00000198728	PAP47	595	29.2%	chr10	103860677	CCDS7528.1	c.183C>A	p.F61L
LDB3	LIM domain binding 3	ENSG00000122367	PAP47	203	18.2%	chr10	88467744	CCDS7377.1	c.1720G>T	p.E574X
LIN7C	lin-7 homolog C (C. elegans)	ENSG00000148943	PAP47	57	19.3%	chr11	27480039	CCDS7864.1	c.42T>G	p.I14M
LIPG	lipase; endothelial	ENSG00000101670	PAP47	80	26.3%	chr18	45364058	CCDS11938.1	c.1292G>A	p.R431H
LIPK	lipase; family member K	ENSG00000204021	PAP47	73	28.8%	chr10	90482178	NM_001080518	c.559G>T	p.E187X
LIPC	lipase; hepatic	ENSG00000166035	PAP47	178	23.6%	chr15	56511554	CCDS10166.1	c.31C>A	p.L11M
LPIN2	lipin 2	ENSG00000101577	PAP47	99	30.3%	chr18	2941174	CCDS11829.1	c.469C>T	p.R157X
LRP1B	low density lipoprotein receptor-related protein 1B	ENSG00000168702	PAP47	72	29.2%	chr2	141008069	CCDS2182.1	c.7753G>T	p.D2585Y
LRP1B	low density lipoprotein receptor-related protein 1B	ENSG00000168702	PAP47	57	31.6%	chr2	141075679	CCDS2182.1	c.-1G>T	p.IVS41-1-1SpliceAcceptor
LRP4	low density lipoprotein receptor-related protein 4	ENSG00000134569	PAP47	64	31.3%	chr11	46859911	CCDS31478.1	c.2732A>G	p.D911G
LRP4	low density lipoprotein receptor-related protein 4	ENSG00000134569	PAP47	105	34.3%	chr11	46864615	CCDS31478.1	c.2261G>A	p.R754Q
KDM3A	lysine (K)-specific demethylase 3A	ENSG00000115548	PAP47	107	20.6%	chr2	86571554	CCDS1990.1	c.3613G>A	p.D1205N
LYSMD4	LysM; putative peptidoglycan-binding; domain containing 4	ENSG00000183060	PAP47	238	28.2%	chr15	98087390	CCDS10381.1	c.355A>C	p.I119L
LPAR4	lysophosphatidic acid receptor 4	ENSG00000147145	PAP47	77	33.8%	chrX	77897820	CCDS14441.1	c.798C>A	p.N266K
LAMP2	lysosomal-associated membrane protein 2	ENSG00000005893	PAP47	154	32.5%	chrX	119473303	CCDS14599.1	c.334G>T	p.D112Y
ME1	malic enzyme 1; NADP(+)-dependent; cytosolic	ENSG00000065833	PAP47	42	23.8%	chr6	83983034	CCDS34492.1	c.1450G>A	p.V484I
ME3	malic enzyme 3; NADP(+)-dependent; mitochondrial	ENSG00000151376	PAP47	107	29.9%	chr11	85853859	CCDS8277.1	c.841G>A	p.D281N
MARVELD3	MARVEL domain containing 3	ENSG00000140832	PAP47	188	24.5%	chr16	70232192	CCDS32478.1	c.994G>A	p.D332N
MELK	maternal embryonic leucine zipper kinase	ENSG00000165304	PAP47	176	22.2%	chr9	36641740	CCDS6606.1	c.-1T>G	p.IVS10-3-1SpliceAcceptor
MCF2L2	MCF.2 cell line derived transforming sequence-like 2	ENSG00000053524	PAP47	48	33.3%	chr3	184430170	CCDS3243.1	c.2023G>A	p.E675K
MKKS	McKusick-Kaufman syndrome	ENSG00000125863	PAP47	115	25.2%	chr20	10337304	CCDS13111.1	c.1133G>T	p.R378I
MDM4	Mdm4 p53 binding protein homolog (mouse)	ENSG00000198625	PAP47	54	22.2%	chr1	202778552	CCDS1447.1	c.529A>C	p.N177H
MED1	mediator complex subunit 1	ENSG00000125686	PAP47	237	25.3%	chr17	34818647	CCDS11336.1	c.3353A>C	p.K1118T
MED12	mediator complex subunit 12	ENSG00000184634	PAP47	325	32.9%	chrX	70262015	CCDS43970.1	c.2316G>T	p.K772N
MED13L	mediator complex subunit 13-like	ENSG00000123066	PAP47	47	36.2%	chr12	114909297	CCDS9177.1	c.4114G>A	p.G1372S
MEFV	Mediterranean fever	ENSG00000103313	PAP47	111	22.5%	chr16	3244311	CCDS10498.1	c.758C>T	p.A253V
MKL1	megakaryoblastic leukemia (translocation) 1	ENSG00000196588	PAP47	72	27.8%	chr22	39149599	CCDS14003.1	c.514G>T	p.E172X
MATK	megakaryocyte-associated tyrosine kinase	ENSG00000007264	PAP47	120	25.8%	chr19	3730379	CCDS12113.1	c.1001C>A	p.S334Y
MAGEB10	melanoma antigen family B; 10	ENSG00000177689	PAP47	195	25.1%	chrX	27749382	CCDS35221.1	c.38NULL>A	p.NULL-1FsIns1bp
MAGED1	melanoma antigen family D; 1	ENSG00000179222	PAP47	135	28.1%	chrX	51661388	CCDS35279.1	c.-1G>T	p.IVS11-1-1SpliceAcceptor
MAGEE1	melanoma antigen family E; 1	ENSG00000198934	PAP47	233	26.2%	chrX	75566766	CCDS14433.1	c.2039C>A	p.P680H

MAGEE1	melanoma antigen family E; 1	ENSG00000198934	PAP47	267	20.6%	chrX	75566782	CCDS14433.1	c.2055G>T	p.E685D
MAGEE2	melanoma antigen family E; 2	ENSG00000186675	PAP47	262	26.0%	chrX	74920523	CCDS14431.1	c.1089C>A	p.F363L
MUM1L1	melanoma associated antigen (mutated) 1-like 1	ENSG00000157502	PAP47	132	25.8%	chrX	105337207	ENST00000372552	c.1126G>A	p.E376K
MUM1L1	melanoma associated antigen (mutated) 1-like 1	ENSG00000157502	PAP47	133	26.3%	chrX	105337413	ENST00000357175	c.1332G>T	p.K444N
MCAM	melanoma cell adhesion molecule	ENSG00000076706	PAP47	90	18.9%	chr11	118685820	CCDS31690.1	c.1927G>A	p.D643N
MLPH	melanophilin	ENSG00000115648	PAP47	113	31.0%	chr2	238100762	CCDS2518.1	c.884C>T	p.S295L
MAGI2	membrane associated guanylate kinase; WW and PDZ domain containing 2	ENSG00000187391	PAP47	189	31.2%	chr7	77602307	CCDS5594.1	c.2998C>A	p.L1000I
MPP6	membrane protein; palmitoylated 6 (MAGUK p55 subfamily member 6)	ENSG00000105926	PAP47	145	28.3%	chr7	24671808	CCDS5388.1	c.860T>G	p.V287G
40241	membrane-associated ring finger (C3HC4) 4	ENSG00000144583	PAP47	291	26.1%	chr2	216850697	CCDS33376.1	c.808G>T	p.D270Y
MBD5	methyl-CpG binding domain protein 5	ENSG00000204406	PAP47	395	30.1%	chr2	148957218	CCDS33302.1	c.2588C>A	p.S863Y
MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1; methenyltetrahydrofolate cyclohydrolase; formyltetrahydrofolate synthetase	ENSG00000100714	PAP47	56	26.8%	chr14	63962238	CCDS9763.1	c.893T>G	p.F298C
MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2; methenyltetrahydrofolate cyclohydrolase	ENSG00000065911	PAP47	82	29.3%	chr2	74288399	CCDS1935.2	c.347T>G	p.L116X
MCEE	methylmalonyl CoA epimerase	ENSG00000124370	PAP47	110	10.0%	chr2	71190660	CCDS1915.1	c.479T>A	p.F160Y
MACF1	microtubule-actin crosslinking factor 1	ENSG00000127603	PAP47	47	40.4%	chr1	39692098	CCDS436.1	c.16204C>T	p.R5402C
MACF1	microtubule-actin crosslinking factor 1	ENSG00000127603	PAP47	90	23.3%	chr1	39718059	CCDS436.1	c.17221C>T	p.R5741X
MAP2	microtubule-associated protein 2	ENSG00000078018	PAP47	197	29.9%	chr2	210267130	CCDS2384.1	c.1991C>T	p.P664L
MAP2	microtubule-associated protein 2	ENSG00000078018	PAP47	179	17.9%	chr2	210268308	CCDS2384.1	c.3169G>A	p.A1057T
MAPT	microtubule-associated protein tau	ENSG00000186868	PAP47	79	24.1%	chr17	41416419	CCDS11501.1	c.412C>T	p.R138X
MDK	midkine (neurite growth-promoting factor 2)	ENSG00000110492	PAP47	326	29.1%	chr11	46361879	ENST00000405098	c.446A>G	p.Q149R
MCM8	minichromosome maintenance complex component 8	ENSG00000125885	PAP47	95	22.1%	chr20	5891981	CCDS13094.1	c.851T>C	p.V284A
MIOS	missing oocyte; meiosis regulator; homolog (Drosophila)	ENSG00000164654	PAP47	153	20.9%	chr7	7579388	CCDS43554.1	c.757C>A	p.L253I
MCART6	mitochondrial carrier triple repeat 6	ENSG00000176274	PAP47	131	15.3%	chrX	103235710	CCDS35363.1	c.887G>T	p.R296M
MCART6	mitochondrial carrier triple repeat 6	ENSG00000176274	PAP47	126	27.0%	chrX	103236109	CCDS35363.1	c.488C>T	p.S163F
MIPEP	mitochondrial intermediate peptidase	ENSG00000027001	PAP47	37	32.4%	chr13	23358630	CCDS9303.1	c.205C>A	p.P69T
MRPL19	mitochondrial ribosomal protein L19	ENSG00000115364	PAP47	55	29.1%	chr2	75732841	CCDS1960.2	c.287G>T	p.R96I
MRPL35	mitochondrial ribosomal protein L35	ENSG00000132313	PAP47	39	25.6%	chr2	86287929	CCDS1988.1	c.346C>T	p.R116X
MRPS14	mitochondrial ribosomal protein S14	ENSG00000120333	PAP47	354	26.6%	chr1	173254259	CCDS1316.1	c.122G>A	p.R41Q
MRPS9	mitochondrial ribosomal protein S9	ENSG00000135972	PAP47	83	25.3%	chr2	105075306	CCDS2065.1	c.667C>T	p.R223W
MAP3K1	mitogen-activated protein kinase kinase kinase 1	ENSG00000095015	PAP47	252	28.2%	chr5	56213852	CCDS43318.1	c.3068G>A	p.R1023H
MORC2	MORC family CW-type zinc finger 2	ENSG00000133422	PAP47	46	34.8%	chr22	29684670	ENST00000397641	c.79G>A	p.E27K
MUC19	mucin 19; oligomeric	ENSG00000205592	PAP47	173	32.9%	chr12	39225459	ENST00000380816	c.407C>A	p.S136Y
MMRN1	multimerin 1	ENSG00000138722	PAP47	143	29.4%	chr4	91035222	CCDS3635.1	c.77C>A	p.S26Y
MEN1	multiple endocrine neoplasia I	ENSG00000133895	PAP47	203	33.0%	chr11	64333791	CCDS8083.1	c.367G>A	p.D123N
MINPP1	multiple inositol-polyphosphate phosphatase 1	ENSG00000107789	PAP47	217	27.6%	chr10	89302135	CCDS7384.1	c.1384T>C	p.Y462H
MSI2	musashi homolog 2 (Drosophila)	ENSG00000153944	PAP47	265	29.8%	chr17	53059607	CCDS11596.1	c.671C>T	p.A224V
MLH3	mutL homolog 3 (E. coli)	ENSG00000119684	PAP47	134	31.3%	chr14	74553629	CCDS32123.1	c.4271A>C	p.K1424T
MSH2	mutS homolog 2; colon cancer; nonpolyposis type 1 (E. coli)	ENSG00000095002	PAP47	37	32.4%	chr2	47555881	CCDS1834.1	c.1973NULL>A	p.NULL-1FsIns1bp
MSH6	mutS homolog 6 (E. coli)	ENSG00000116062	PAP47	111	35.1%	chr2	47887257	CCDS1836.1	c.3964G>T	p.E1322X
MYSM1	Myb-like; SWIRM and MPN domains 1	ENSG00000162601	PAP47	207	21.7%	chr1	58915216	CCDS41343.1	c.1360G>A	p.E454K
MYT1	myelin transcription factor 1	ENSG00000196132	PAP47	83	33.7%	chr20	62309669	CCDS13558.1	c.676G>A	p.E226K
MYT1	myelin transcription factor 1	ENSG00000196132	PAP47	247	28.7%	chr20	62333999	CCDS13558.1	c.2714G>A	p.S905N
MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	ENSG00000143384	PAP47	150	24.7%	chr1	148817471	CCDS957.1	c.809T>G	p.F270C
MNDA	myeloid cell nuclear differentiation antigen	ENSG00000163563	PAP47	180	32.2%	chr1	157080526	CCDS1177.1	c.560C>T	p.S187L
MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila); translocated to; 3	ENSG00000171843	PAP47	84	20.2%	chr9	20353529	CCDS6494.1	c.1276G>A	p.D426N
MPL	myeloproliferative leukemia virus oncogene	ENSG00000117400	PAP47	72	16.7%	chr1	43578316	CCDS483.1	c.785G>A	p.G262E
MYOF	myoferlin	ENSG00000138119	PAP47	160	34.4%	chr10	95085732	CCDS41551.1	c.4499C>T	p.T1500M
MYPN	myopalladin	ENSG00000138347	PAP47	205	26.3%	chr10	69551643	CCDS7275.1	c.442A>T	p.K148X

MYO1E	myosin IE	ENSG00000157483	PAP47	33	30.3%	chr15	57242697	CCDS32254.1	c.2578C>T	p.R860C
MYO3A	myosin IIIA	ENSG00000095777	PAP47	29	34.5%	chr10	26474387	CCDS7148.1	c.2423T>G	p.F808C
MYO3A	myosin IIIA	ENSG00000095777	PAP47	60	18.3%	chr10	26502868	CCDS7148.1	c.3669G>T	p.E1223D
MYLK	myosin light chain kinase	ENSG00000065534	PAP47	84	26.2%	chr3	124923711	CCDS3023.1	c.1758G>T	p.E586D
MYLK4	myosin light chain kinase family; member 4	ENSG00000145949	PAP47	340	30.0%	chr6	2694405	CCDS34330.1	c.123T>G	p.N41K
MYO5A	myosin VA (heavy chain 12; myoxin)	ENSG00000197535	PAP47	40	32.5%	chr15	50487554	CCDS42037.1	c.832C>T	p.R278X
MYH3	myosin; heavy chain 3; skeletal muscle; embryonic	ENSG00000109063	PAP47	47	27.7%	chr17	10479568	CCDS11157.1	c.4013G>A	p.R1338H
MYH3	myosin; heavy chain 3; skeletal muscle; embryonic	ENSG00000109063	PAP47	316	29.4%	chr17	10484438	CCDS11157.1	c.2363G>A	p.R788Q
MYH4	myosin; heavy chain 4; skeletal muscle	ENSG00000141048	PAP47	141	35.5%	chr17	10300566	CCDS11154.1	c.1929G>T	p.K643N
MTM1	myotubularin 1	ENSG00000171100	PAP47	122	24.6%	chrX	149515627	CCDS14694.1	c.71G>A	p.R24Q
MTM1	myotubularin 1	ENSG00000171100	PAP47	60	36.7%	chrX	149582615	CCDS14694.1	c.1519G>T	p.E507X
MTMR1	myotubularin related protein 1	ENSG00000063601	PAP47	105	29.5%	chrX	149637812	CCDS14695.1	c.310G>T	p.E104X
MTMR15	myotubularin related protein 15	ENSG00000198690	PAP47	133	32.3%	chr15	29001767	CCDS32186.1	c.2090G>T	p.R697I
MTMR4	myotubularin related protein 4	ENSG00000108389	PAP47	179	34.1%	chr17	53936718	CCDS11608.1	c.1430T>C	p.V477A
MTMR8	myotubularin related protein 8	ENSG00000102043	PAP47	318	31.4%	chrX	63405473	CCDS14379.1	c.1784G>A	p.R595Q
NAA25	N(alpha)-acetyltransferase 25; NatB auxiliary subunit	ENSG00000111300	PAP47	104	24.0%	chr12	110994114	CCDS9159.1	c.1004G>A	p.R335Q
NAA25	N(alpha)-acetyltransferase 25; NatB auxiliary subunit	ENSG00000111300	PAP47	75	28.0%	chr12	110994181	CCDS9159.1	c.937G>T	p.E313X
NAA35	N(alpha)-acetyltransferase 35; NatC auxiliary subunit	ENSG00000135040	PAP47	137	31.4%	chr9	87817823	CCDS6673.1	c.1333C>T	p.R445X
NHEDC2	Na+/H+ exchanger domain containing 2	ENSG00000164038	PAP47	90	28.9%	chr4	104207053	CCDS3662.1	c.151C>A	p.L51I
NAALAD2	N-acetylated alpha-linked acidic dipeptidase 2	ENSG00000077616	PAP47	129	27.9%	chr11	89536398	CCDS8288.1	c.1243G>T	p.E415X
NAALAD2	N-acetylated alpha-linked acidic dipeptidase 2	ENSG00000077616	PAP47	67	34.3%	chr11	89550734	CCDS8288.1	c.1659G>T	p.E553D
NAALADL1	N-acetylated alpha-linked acidic dipeptidase-like 1	ENSG00000168060	PAP47	292	27.7%	chr11	64578699	CCDS31604.1	c.691G>A	p.E231K
NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 5; 13kDa	ENSG00000128609	PAP47	97	28.9%	chr7	122984154	ENST00000340034	c.604C>A	p.L202I
NOX5	NADPH oxidase; EF-hand calcium binding domain 5	ENSG00000137808	PAP47	165	12.1%	chr15	67115209	CCDS32276.1	c.1013C>T	p.T338M
NHS	Nance-Horan syndrome (congenital cataracts and dental anomalies)	ENSG00000188158	PAP47	67	28.4%	chrX	17654845	CCDS14181.1	c.2635C>T	p.R879X
NHS	Nance-Horan syndrome (congenital cataracts and dental anomalies)	ENSG00000188158	PAP47	126	34.9%	chrX	17655052	CCDS14181.1	c.2842G>A	p.A948T
NPPB	natriuretic peptide precursor B	ENSG00000120937	PAP47	154	19.5%	chr1	11841468	CCDS140.1	c.10C>A	p.Q4K
NDST4	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4	ENSG00000138653	PAP47	68	27.9%	chr4	115986516	CCDS3706.1	c.2027C>T	p.A676V
NRAP	nebulin-related anchoring protein	ENSG00000197893	PAP47	58	24.1%	chr10	115403873	CCDS7579.1	c.362G>T	p.R121I
NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	ENSG00000166681	PAP47	108	37.0%	chrX	102519217	CCDS14508.1	c.142C>T	p.R48X
NCAM1	neural cell adhesion molecule 1	ENSG00000149294	PAP47	149	29.5%	chr11	112611031	ENST00000404693	c.1376C>T	p.A459V
NCAM2	neural cell adhesion molecule 2	ENSG00000154654	PAP47	78	24.4%	chr21	21712739	CCDS42910.1	c.1459G>T	p.E487X
NEDD4	neural precursor cell expressed; developmentally down-regulated 4	ENSG00000069869	PAP47	255	25.9%	chr15	53994961	CCDS10156.1	c.1361G>A	p.R454Q
NEDD4	neural precursor cell expressed; developmentally down-regulated 4	ENSG00000069869	PAP47	107	32.7%	chr15	53995142	CCDS10156.1	c.1180A>C	p.N394H
NRXN2	neurexin 2	ENSG00000110076	PAP47	177	22.6%	chr11	64185166	CCDS8077.1	c.1820G>A	p.R607H
NRXN2	neurexin 2	ENSG00000110076	PAP47	167	28.7%	chr11	64209698	CCDS8077.1	c.1148G>A	p.R383H
NBEAL1	neurobeachin-like 1	ENSG00000144426	PAP47	118	36.4%	chr2	203753446	CCDS42802.1	c.2604C>A	p.F868L
NBEAL1	neurobeachin-like 1	ENSG00000144426	PAP47	55	29.1%	chr2	203790243	CCDS42802.1	c.4136G>A	p.R1379Q
NBAS	neuroblastoma amplified sequence	ENSG00000151779	PAP47	188	34.0%	chr2	15334575	CCDS1685.1	c.5240T>G	p.I1747S
NF1	neurofibromin 1	ENSG00000196712	PAP47	211	29.4%	chr17	26677275	CCDS42292.1	c.5147C>T	p.A1716V
NEUROD1	neurogenic differentiation 1	ENSG00000162992	PAP47	196	26.5%	chr2	182251703	CCDS2283.1	c.130G>A	p.E44K
NAV3	neuron navigator 3	ENSG00000067798	PAP47	144	30.6%	chr12	77095555	ENST00000228327	c.5322G>T	p.K1774N
NPAS4	neuronal PAS domain protein 4	ENSG00000174576	PAP47	425	32.0%	chr11	65948673	CCDS8138.1	c.1736G>A	p.S579N
NPSR1	neuropeptide S receptor 1	ENSG00000187258	PAP47	163	22.1%	chr7	34840544	CCDS5443.1	c.704G>A	p.R235Q
NPSR1	neuropeptide S receptor 1	ENSG00000187258	PAP47	276	19.6%	chr7	34884245	CCDS5443.1	c.1058C>T	p.A353V
NPY5R	neuropeptide Y receptor Y5	ENSG00000164129	PAP47	313	28.4%	chr4	164491748	CCDS3804.1	c.873G>T	p.K291N
NTS	neurotensin	ENSG00000133636	PAP47	112	27.7%	chr12	84800232	CCDS9029.1	c.461A>C	p.E154A
NKIRAS1	NFKB inhibitor interacting Ras-like 1	ENSG00000197885	PAP47	184	27.7%	chr3	23917535	CCDS33717.1	c.104A>C	p.D35A

NEK4	NIMA (never in mitosis gene a)-related kinase 4	ENSG00000114904	PAP47	66	36.4%	chr3	52774981	CCDS2863.1	c.628G>T	p.D210Y
NINL	ninein-like	ENSG00000101004	PAP47	216	26.9%	chr20	25405555	CCDS33452.1	c.2372C>T	p.A791V
NIPBL	Nipped-B homolog (Drosophila)	ENSG00000164190	PAP47	97	26.8%	chr5	37094942	CCDS3920.1	c.7603G>A	p.E2535K
NLRC4	NLR family; CARD domain containing 4	ENSG00000091106	PAP47	279	26.9%	chr2	32316862	CCDS33174.1	c.2364A>C	p.K788N
NLRC4	NLR family; CARD domain containing 4	ENSG00000091106	PAP47	95	23.2%	chr2	32328909	CCDS33174.1	c.1528G>A	p.A510T
NLRC4	NLR family; CARD domain containing 4	ENSG00000091106	PAP47	174	33.9%	chr2	32329212	CCDS33174.1	c.1225G>A	p.E409K
NOTCH2	Notch homolog 2 (Drosophila)	ENSG00000134250	PAP47	100	30.0%	chr1	120273215	CCDS908.1	c.3799G>A	p.E1267K
NPC1L1	NPC1 (Niemann-Pick disease; type C1; gene)-like 1	ENSG00000015520	PAP47	68	33.8%	chr7	44538337	CCDS5491.1	c.2414C>T	p.S805F
NCBP1	nuclear cap binding protein subunit 1; 80kDa	ENSG00000136937	PAP47	145	30.3%	chr9	99471870	ENST00000375130	c.379A>C	p.K127Q
NFIL3	nuclear factor; interleukin 3 regulated	ENSG00000165030	PAP47	530	28.9%	chr9	93212281	CCDS6690.1	c.557C>T	p.S186L
NCOA3	nuclear receptor coactivator 3	ENSG00000124151	PAP47	149	29.5%	chr20	45698358	CCDS13407.1	c.1821G>T	p.E607D
NR1I2	nuclear receptor subfamily 1; group I; member 2	ENSG00000144852	PAP47	393	27.0%	chr3	120984368	CCDS2995.1	c.74C>T	p.A25V
NR1I2	nuclear receptor subfamily 1; group I; member 2	ENSG00000144852	PAP47	70	28.6%	chr3	121004465	ENST00000393719	c.11C>T	p.S4F
NUCB1	nucleobindin 1	ENSG00000104805	PAP47	62	46.8%	chr19	54108137	CCDS12740.1	c.538G>A	p.E180K
NOL4	nucleolar protein 4	ENSG00000101746	PAP47	178	23.6%	chr18	29939046	CCDS11907.2	c.491G>T	p.R164I
NUP153	nucleoporin 153kDa	ENSG00000124789	PAP47	101	25.7%	chr6	17783216	CCDS4541.1	c.751A>C	p.T251P
NUP160	nucleoporin 160kDa	ENSG00000030066	PAP47	75	40.0%	chr11	47771027	CCDS31484.1	c.3337C>T	p.R1113X
NUP210	nucleoporin 210kDa	ENSG00000132182	PAP47	215	31.6%	chr3	13352006	CCDS33704.1	c.3791C>T	p.S1264L
NUP210L	nucleoporin 210kDa-like	ENSG00000143552	PAP47	88	33.0%	chr1	152377300	CCDS41399.1	c.756G>T	p.E252D
NUP214	nucleoporin 214kDa	ENSG00000126883	PAP47	161	32.3%	chr9	133057488	CCDS6940.1	c.3647T>G	p.F1216C
NUP62CL	nucleoporin 62kDa C-terminal like	ENSG00000198088	PAP47	152	23.0%	chrX	106283146	CCDS14527.1	c.442G>T	p.E148X
NUP98	nucleoporin 98kDa	ENSG00000110713	PAP47	97	27.8%	chr11	3703013	CCDS7746.1	c.1743G>T	p.K581N
NACC1	nucleus accumbens associated 1; BEN and BTB (POZ) domain containing	ENSG00000160877	PAP47	264	32.6%	chr19	13107233	CCDS12294.1	c.212C>T	p.A71V
NDEL1	nudE nuclear distribution gene E homolog (A. nidulans)-like 1	ENSG00000166579	PAP47	49	28.6%	chr17	8289803	CCDS11143.1	c.136G>T	p.E46X
NULL	NULL	ENSG00000122339	PAP47	127	33.9%	chr6	157634006	CCDS43519.1	c.341G>A	p.R114Q
NULL	NULL	ENSG00000154251	PAP47	71	18.3%	chr17	63635809	ENST00000284414	c.171C>A	p.F57L
NULL	NULL	ENSG00000174093	PAP47	166	10.2%	chr17	33612834	ENST00000312412	c.-1G>T	p.IVS5-1-1SpliceAcceptor
NULL	NULL	ENSG00000174450	PAP47	28	35.7%	chr15	21236451	ENST00000312015	c.1633G>A	p.E545K
NULL	NULL	ENSG00000197735	PAP47	171	28.7%	chr10	134094131	ENST00000354756	c.25A>G	p.T9A
NULL	NULL	ENSG00000197825	PAP47	65	33.8%	chr8	27260501	ENST00000355177	c.59C>A	p.S20Y
NULL	NULL	ENSG00000202582	PAP47	80	26.3%	chr12	48557999	ENST00000365712	c.968G>A	p.R323H
NULL	NULL	ENSG00000204913	PAP47	614	30.5%	chr17	35354085	ENST00000377924	c.349G>A	p.D117N
NULL	NULL	ENSG00000211723	PAP47	56	30.4%	chr7	141831953	ENST00000390370	c.249C>A	p.F83L
NULL	NULL	ENSG00000211821	PAP47	194	33.0%	chr14	21961801	ENST00000390469	c.273G>T	p.K91N
NULL	NULL	ENSG00000214094	PAP47	202	22.3%	chr17	77004401	ENST00000397526	c.610C>T	p.R204C
NULL	NULL	ENSG00000214279	PAP47	123	19.5%	chr10	135129712	ENST00000368526	c.402G>T	p.K134N
NULL	NULL	ENSG00000214894	PAP47	181	24.3%	chr6	30890023	ENST00000399196	c.430G>A	p.E144K
NULL	NULL	ENSG00000215474	PAP47	158	29.1%	chr18	43029303	ENST00000400404	c.250C>T	p.R84C
NULL	NULL	ENSG00000215490	PAP47	117	29.1%	chr18	31118621	ENST00000400443	c.431T>C	p.V144A
NULL	NULL	ENSG00000215518	PAP47	86	25.6%	chr21	35344226	ENST00000400501	c.101G>T	p.R34I
NULL	NULL	ENSG00000218758	PAP47	72	29.2%	chr19	12219683	ENST00000393337	c.753G>T	p.Q251H
NULL	NULL	MI0000440	PAP47	97	24.7%	chr9	96887602	MI0000440	c.55G>A	p.A19T
OCA2	oculocutaneous albinism II	ENSG00000104044	PAP47	122	29.5%	chr15	25946720	CCDS10020.1	c.407G>A	p.R136Q
OSR2	odd-skipped related 2 (Drosophila)	ENSG00000164920	PAP47	192	34.4%	chr8	100032927	NM_001142462	c.761C>T	p.S254F
ODZ3	odz; odd Oz/ten-m homolog 3 (Drosophila)	ENSG00000218336	PAP47	209	19.6%	chr4	183913016	NM_001080477	c.4502A>G	p.N1501S
OLFM1	olfactomedin 1	ENSG00000130558	PAP47	52	32.7%	chr9	137130007	CCDS6986.1	c.457T>C	p.Y153H
OLFM4	olfactomedin 4	ENSG00000102837	PAP47	215	29.3%	chr13	52522720	CCDS9440.1	c.1346G>T	p.R449I
OLFML2A	olfactomedin-like 2A	ENSG00000185585	PAP47	177	30.5%	chr9	126612033	CCDS6857.2	c.1480C>T	p.R494C
OR10AG1	olfactory receptor; family 10; subfamily AG; member 1	ENSG00000174970	PAP47	98	23.5%	chr11	55491920	CCDS31514.1	c.596C>T	p.T199M
OR14A16	olfactory receptor; family 14; subfamily A; member 16	ENSG00000196772	PAP47	131	32.8%	chr1	246045407	CCDS31097.1	c.248C>A	p.S83Y
OR2A14	olfactory receptor; family 2; subfamily A; member 14	ENSG00000221938	PAP47	246	26.4%	chr7	143457228	CCDS43672.1	c.90C>A	p.F30L

OR2B2	olfactory receptor; family 2; subfamily B; member 2	ENSG00000168131	PAP47	149	20.8%	chr6	27987718	CCDS4641.1	c.359T>C	p.F120S
OR2C3	olfactory receptor; family 2; subfamily C; member 3	ENSG00000196242	PAP47	161	31.7%	chr1	245762335	CCDS1634.1	c.99T>G	p.S33R
OR2L5	olfactory receptor; family 2; subfamily L; member 5	ENSG00000197454	PAP47	49	20.4%	chr1	246252666	ENST00000355281	c.794G>A	p.R265Q
OR4B1	olfactory receptor; family 4; subfamily B; member 1	ENSG00000175619	PAP47	314	32.2%	chr11	48195264	CCDS31485.1	c.327G>T	p.E109D
OR4C15	olfactory receptor; family 4; subfamily C; member 15	ENSG00000181939	PAP47	92	27.2%	chr11	55078380	CCDS31501.1	c.22G>A	p.A8T
OR4C6	olfactory receptor; family 4; subfamily C; member 6	ENSG00000181903	PAP47	242	27.3%	chr11	55189928	CCDS31506.1	c.710C>T	p.T237I
OR4F15	olfactory receptor; family 4; subfamily F; member 15	ENSG00000182854	PAP47	203	31.5%	chr15	100176532	CCDS32342.1	c.620C>A	p.S207Y
OR4F6	olfactory receptor; family 4; subfamily F; member 6	ENSG00000184140	PAP47	48	33.3%	chr15	100164370	CCDS32341.1	c.925A>G	p.S309G
OR4M1	olfactory receptor; family 4; subfamily M; member 1	ENSG00000176299	PAP47	260	12.7%	chr14	19318650	CCDS32021.1	c.329C>T	p.S110L
OR5D14	olfactory receptor; family 5; subfamily D; member 14	ENSG00000186113	PAP47	238	34.5%	chr11	55319952	CCDS31508.1	c.345C>A	p.F115L
OR5D14	olfactory receptor; family 5; subfamily D; member 14	ENSG00000186113	PAP47	346	23.7%	chr11	55320117	CCDS31508.1	c.510C>A	p.F170L
OR5D16	olfactory receptor; family 5; subfamily D; member 16	ENSG00000205029	PAP47	196	20.9%	chr11	55363045	CCDS31512.1	c.242C>T	p.P81L
OR5H2	olfactory receptor; family 5; subfamily H; member 2	ENSG00000197938	PAP47	128	25.0%	chr3	99484714	CCDS33801.1	c.293C>A	p.S98Y
OR5I1	olfactory receptor; family 5; subfamily I; member 1	ENSG00000167825	PAP47	164	29.9%	chr11	55460192	CCDS7949.1	c.261C>A	p.F87L
OR5T2	olfactory receptor; family 5; subfamily T; member 2	ENSG00000181718	PAP47	169	32.0%	chr11	55756864	CCDS31523.1	c.374C>T	p.T125M
OR5T3	olfactory receptor; family 5; subfamily T; member 3	ENSG00000172489	PAP47	101	38.6%	chr11	55776295	CCDS31524.1	c.44T>C	p.V15A
OR51B2	olfactory receptor; family 51; subfamily B; member 2	ENSG00000184881	PAP47	190	26.3%	chr11	5301787	CCDS31377.1	c.317C>A	p.S106Y
OR51F1	olfactory receptor; family 51; subfamily F; member 1	ENSG00000188069	PAP47	149	10.7%	chr11	4746859	CCDS31359.1	c.865C>T	p.L289F
OR52A5	olfactory receptor; family 52; subfamily A; member 5	ENSG00000171944	PAP47	129	30.2%	chr11	5109705	CCDS31373.1	c.744T>G	p.I248M
OR52M1	olfactory receptor; family 52; subfamily M; member 1	ENSG00000197790	PAP47	316	18.4%	chr11	4523160	CCDS31353.1	c.164G>A	p.R55H
OR52N4	olfactory receptor; family 52; subfamily N; member 4	ENSG00000181074	PAP47	260	29.2%	chr11	5732655	NM_001005175	c.109T>C	p.Y37H
OR6C76	olfactory receptor; family 6; subfamily C; member 76	ENSG00000185821	PAP47	219	29.7%	chr12	54106811	CCDS31823.1	c.507T>G	p.N169K
OR6F1	olfactory receptor; family 6; subfamily F; member 1	ENSG00000169214	PAP47	41	24.4%	chr1	245942644	CCDS31095.1	c.37C>A	p.L13I
OR7G1	olfactory receptor; family 7; subfamily G; member 1	ENSG00000161807	PAP47	117	24.8%	chr19	9086792	CCDS32898.1	c.648C>A	p.F216L
OR8B12	olfactory receptor; family 8; subfamily B; member 12	ENSG00000170953	PAP47	108	26.9%	chr11	123918556	CCDS31711.1	c.205G>T	p.D69Y
OR8J1	olfactory receptor; family 8; subfamily J; member 1	ENSG00000172487	PAP47	125	28.0%	chr11	55885106	CCDS31529.1	c.808A>G	p.T270A
OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	ENSG00000147162	PAP47	83	28.9%	chrX	70698437	CCDS14414.1	c.1939C>T	p.R647X
OPRM1	opioid receptor; mu 1	ENSG00000112038	PAP47	503	34.2%	chr6	154454241	CCDS43518.1	c.1105C>T	p.R369C
OPA1	optic atrophy 1 (autosomal dominant)	ENSG00000198836	PAP47	41	31.7%	chr3	194843488	CCDS33917.1	c.1207C>T	p.R403X
OTUD5	OTU domain containing 5	ENSG00000068308	PAP47	98	30.6%	chrX	48665949	CCDS14313.1	c.1499C>T	p.S500L
OXR1	oxidation resistance 1	ENSG00000164830	PAP47	141	29.8%	chr8	107788290	CCDS6304.1	c.1101G>T	p.E367D
OSGIN2	oxidative stress induced growth inhibitor family member 2	ENSG00000164823	PAP47	133	29.3%	chr8	91002570	CCDS6248.1	c.485G>A	p.R162Q
OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	ENSG00000105953	PAP47	59	25.4%	chr7	44680575	CCDS34627.1	c.829C>T	p.R277C
OSBPL10	oxysterol binding protein-like 10	ENSG00000144645	PAP47	96	27.1%	chr3	31685310	CCDS2651.1	c.1924G>T	p.E642X
OSBPL6	oxysterol binding protein-like 6	ENSG00000079156	PAP47	175	30.9%	chr2	178946987	CCDS2278.1	c.1532C>T	p.S511L
PAK7	p21 protein (Cdc42/Rac)-activated kinase 7	ENSG00000101349	PAP47	430	32.8%	chr20	9509352	CCDS13107.1	c.430G>A	p.E144K
PAX5	paired box 5	ENSG00000196092	PAP47	160	28.8%	chr9	37010640	CCDS6607.1	c.205C>A	p.L69I
PNLIPRP2	pancreatic lipase-related protein 2	ENSG00000165862	PAP47	198	32.3%	chr10	118376455	ENST00000298771	c.421C>T	p.R141W
PRCC	papillary renal cell carcinoma (translocation-associated)	ENSG00000143294	PAP47	206	29.1%	chr1	155004624	CCDS1157.1	c.437A>G	p.K146R
PTH	parathyroid hormone	ENSG00000152266	PAP47	220	28.2%	chr11	13470911	CCDS7812.1	c.68C>T	p.S23L
PDS5A	PDS5; regulator of cohesion maintenance; homolog A (S. cerevisiae)	ENSG00000121892	PAP47	83	27.7%	chr4	39591653	NM_001100399	c.965G>A	p.R322H
PDZD8	PDZ domain containing 8	ENSG00000165650	PAP47	217	31.3%	chr10	119123896	CCDS7600.1	c.833T>C	p.I278T
PDZRN3	PDZ domain containing ring finger 3	ENSG00000121440	PAP47	65	30.8%	chr3	73540068	ENST00000308537	c.952C>T	p.P318S
PDZRN4	PDZ domain containing ring finger 4	ENSG00000165966	PAP47	146	32.9%	chr12	40253568	CCDS8739.1	c.1946G>A	p.R649Q
PTX4	pentraxin 4; long	ENSG00000167957	PAP47	128	24.2%	chr16	1477777	CCDS32362.1	c.322C>T	p.R108C
PGLYRP4	peptidoglycan recognition protein 4	ENSG00000163218	PAP47	66	37.9%	chr1	151580750	CCDS30871.1	c.602G>A	p.R201Q
PPIL5	peptidylprolyl isomerase (cyclophilin)-like 5	ENSG00000165501	PAP47	177	36.2%	chr14	49144341	CCDS9686.1	c.756G>T	p.K252N
PPIB	peptidylprolyl isomerase B (cyclophilin B)	ENSG00000166794	PAP47	128	27.3%	chr15	62236141	CCDS10191.1	c.364C>T	p.R122C
PLIN2	perilipin 2	ENSG00000147872	PAP47	193	14.0%	chr9	19116113	CCDS6490.1	c.225A>C	p.Q75H
PMP2	peripheral myelin protein 2	ENSG00000147588	PAP47	37	37.8%	chr8	82519636	CCDS6229.1	c.217G>T	p.E73X

PMP2	peripheral myelin protein 2	ENSG00000147588	PAP47	111	30.6%	chr8	82522122	CCDS6229.1	c.55G>A	p.D19N
PEX1	peroxisomal biogenesis factor 1	ENSG00000127980	PAP47	148	22.3%	chr7	91984546	CCDS5627.1	c.1219C>A	p.L407I
PHF20L1	PHD finger protein 20-like 1	ENSG00000129292	PAP47	111	28.8%	chr8	133920837	CCDS6367.2	c.2215C>T	p.R739C
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP47	150	30.0%	chr10	89682772	CCDS31238.1	c.276C>A	p.D92E
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP47	53	24.5%	chr10	89707652	CCDS31238.1	c.697C>T	p.R233X
PIGC	phosphatidylinositol glycan anchor biosynthesis; class C	ENSG00000135845	PAP47	253	26.5%	chr1	170677818	CCDS1302.1	c.568G>A	p.A190T
PIGG	phosphatidylinositol glycan anchor biosynthesis; class G	ENSG00000174227	PAP47	128	13.3%	chr4	523119	CCDS3336.1	c.2889C>A	p.F963L
PREX2	phosphatidylinositol-3;4;5-trisphosphate-dependent Rac exchange factor 2	ENSG00000046889	PAP47	167	10.8%	chr8	69143897	CCDS6201.1	c.1415G>T	p.R472I
PREX2	phosphatidylinositol-3;4;5-trisphosphate-dependent Rac exchange factor 2	ENSG00000046889	PAP47	155	31.6%	chr8	69152204	CCDS6201.1	c.1588G>T	p.E530X
PDE1A	phosphodiesterase 1A; calmodulin-dependent	ENSG00000115252	PAP47	65	27.7%	chr2	182813150	CCDS2285.1	c.330G>T	p.K110N
PDE3B	phosphodiesterase 3B; cGMP-inhibited	ENSG00000152270	PAP47	181	32.6%	chr11	14796388	CCDS7817.1	c.1606G>T	p.E536X
PDE3B	phosphodiesterase 3B; cGMP-inhibited	ENSG00000152270	PAP47	99	23.2%	chr11	14821994	CCDS7817.1	c.2366C>T	p.S789L
PDE6C	phosphodiesterase 6C; cGMP-specific; cone; alpha prime	ENSG00000095464	PAP47	55	29.1%	chr10	95385292	CCDS7429.1	c.1318G>A	p.D440N
PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	ENSG00000124253	PAP47	92	25.0%	chr20	55573034	CCDS13460.1	c.1277T>G	p.V426G
PGM5	phosphoglucomutase 5	ENSG00000154330	PAP47	191	27.2%	chr9	70269883	CCDS6622.2	c.1098C>A	p.F366L
PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP47	198	21.2%	chr3	180399570	CCDS43171.1	c.263G>A	p.R88Q
PLA1A	phospholipase A1 member A	ENSG00000144837	PAP47	439	31.0%	chr3	120826761	CCDS2991.1	c.1113G>T	p.K371N
PLCB4	phospholipase C; beta 4	ENSG00000101333	PAP47	47	36.2%	chr20	9349975	CCDS13104.1	c.2150A>C	p.K717T
PLCL2	phospholipase C-like 2	ENSG00000154822	PAP47	169	22.5%	chr3	17027674	CCDS33713.1	c.1454G>A	p.R485Q
PLD4	phospholipase D family; member 4	ENSG00000166428	PAP47	46	28.3%	chr14	104466785	CCDS9995.2	c.565G>A	p.D189N
PLSCR1	phospholipid scramblase 1	ENSG00000188313	PAP47	200	26.5%	chr3	147722434	CCDS3135.1	c.452G>A	p.R151Q
PLSCR4	phospholipid scramblase 4	ENSG00000114698	PAP47	122	23.0%	chr3	147407165	CCDS3133.1	c.192G>T	p.Q64H
PHKG1	phosphorylase kinase; gamma 1 (muscle)	ENSG00000164776	PAP47	73	30.1%	chr7	56122177	CCDS5525.1	c.297C>A	p.F99L
PGBD1	piggyBac transposable element derived 1	ENSG00000137338	PAP47	197	30.5%	chr6	28376744	CCDS4648.1	c.1134G>T	p.K378N
PIPOX	pipecolic acid oxidase	ENSG00000179761	PAP47	360	18.1%	chr17	24396022	CCDS11248.1	c.134G>A	p.R45Q
PIWIL1	piwi-like 1 (Drosophila)	ENSG00000125207	PAP47	72	25.0%	chr12	129396364	CCDS9268.1	c.304G>T	p.E102X
PIWIL1	piwi-like 1 (Drosophila)	ENSG00000125207	PAP47	77	29.9%	chr12	129400451	CCDS9268.1	c.1030G>A	p.E344K
PIWIL4	piwi-like 4 (Drosophila)	ENSG00000134627	PAP47	74	18.9%	chr11	93947911	CCDS31656.1	c.265G>T	p.E89X
PIWIL4	piwi-like 4 (Drosophila)	ENSG00000134627	PAP47	103	21.4%	chr11	93950212	CCDS31656.1	c.419G>A	p.R140K
PLAUR	plasminogen activator; urokinase receptor	ENSG00000011422	PAP47	59	22.0%	chr19	48848225	CCDS12628.1	c.746G>A	p.G249D
PLEK	pleckstrin	ENSG00000115956	PAP47	103	25.2%	chr2	68461483	CCDS1887.1	c.323A>G	p.K108R
PLEK	pleckstrin	ENSG00000115956	PAP47	91	29.7%	chr2	68461495	CCDS1887.1	c.335A>C	p.K112T
PLEKHA6	pleckstrin homology domain containing; family A member 6	ENSG00000143850	PAP47	175	24.6%	chr1	202500709	CCDS1444.1	c.365G>A	p.R122Q
PLEKHA7	pleckstrin homology domain containing; family A member 7	ENSG00000166689	PAP47	53	30.2%	chr11	16830454	CCDS31434.1	c.547A>G	p.K183E
PLEKHA7	pleckstrin homology domain containing; family A member 7	ENSG00000166689	PAP47	105	30.5%	chr11	16834020	CCDS31434.1	c.323C>T	p.S108L
PLXNA3	plexin A3	ENSG00000130827	PAP47	170	21.8%	chrX	153348914	CCDS14752.1	c.3347G>A	p.R1116H
PLXND1	plexin D1	ENSG00000004399	PAP47	148	31.8%	chr3	130772639	CCDS33854.1	c.3534C>A	p.F1178L
PABPC1	poly(A) binding protein; cytoplasmic 1	ENSG00000070756	PAP47	39	28.2%	chr8	101799631	CCDS6289.1	c.247C>T	p.R83C
PAPOLA	poly(A) polymerase alpha	ENSG00000090060	PAP47	27	37.0%	chr14	96063565	CCDS9946.1	c.377G>A	p.R126Q
PNLDC1	poly(A)-specific ribonuclease (PARN)-like domain containing 1	ENSG00000146453	PAP47	327	29.4%	chr6	160159999	CCDS5271.1	c.1256G>A	p.R419Q
PKHD1	polycystic kidney and hepatic disease 1 (autosomal recessive)	ENSG00000170927	PAP47	64	29.7%	chr6	51605336	CCDS4935.1	c.11651G>T	p.R3884I
PKDREJ	polycystic kidney disease (polycystin) and REJ homolog (sperm receptor for egg jelly homolog; sea urchin)	ENSG00000130943	PAP47	87	36.8%	chr22	45032177	CCDS14073.1	c.5707G>T	p.E1903X
PKD1L3	polycystic kidney disease 1-like 3	ENSG00000187008	PAP47	67	41.8%	chr16	70589733	ENST00000335106	c.357C>A	p.F119L
PKD2L1	polycystic kidney disease 2-like 1	ENSG00000107593	PAP47	269	31.6%	chr10	102040153	CCDS7492.1	c.2121C>A	p.F707L
POLN	polymerase (DNA directed) nu	ENSG00000130997	PAP47	85	35.3%	chr4	2128338	CCDS3360.1	c.1706C>T	p.T569I
POLA1	polymerase (DNA directed); alpha 1; catalytic subunit	ENSG00000101868	PAP47	303	30.7%	chrX	24816139	CCDS14214.1	c.4125G>T	p.M1375I
POLE	polymerase (DNA directed); epsilon	ENSG00000177084	PAP47	99	28.3%	chr12	131759920	CCDS9278.1	c.1376C>T	p.S459F
POLQ	polymerase (DNA directed); theta	ENSG00000051341	PAP47	127	21.3%	chr3	122641578	CCDS33833.1	c.7340G>A	p.R2447H
PTBP1	polypyrimidine tract binding protein 1	ENSG00000011304	PAP47	123	32.5%	chr19	755125	CCDS42456.1	c.205G>A	p.D69N

KCTD14	potassium channel tetramerisation domain containing 14	ENSG00000151364	PAP47	123	30.1%	chr11	77405396	CCDS8255.2	c.659A>G	p.D220G
KCTD3	potassium channel tetramerisation domain containing 3	ENSG00000136636	PAP47	110	26.4%	chr1	213814067	CCDS1515.1	c.166C>T	p.R56X
KCNJ3	potassium inwardly-rectifying channel; subfamily J; member 3	ENSG00000162989	PAP47	121	24.0%	chr2	155263547	CCDS2200.1	c.14G>A	p.R5Q
KCNQ3	potassium voltage-gated channel; KQT-like subfamily; member 3	ENSG00000184156	PAP47	106	33.0%	chr8	133251799	CCDS34943.1	c.1199G>A	p.R400K
KCNB2	potassium voltage-gated channel; Shab-related subfamily; member 2	ENSG00000182674	PAP47	227	25.6%	chr8	73642787	CCDS6209.1	c.264C>A	p.F88L
KCNB2	potassium voltage-gated channel; Shab-related subfamily; member 2	ENSG00000182674	PAP47	136	13.2%	chr8	73643002	CCDS6209.1	c.479G>A	p.R160Q
KCNA3	potassium voltage-gated channel; shaker-related subfamily; member 3	ENSG00000177272	PAP47	217	10.6%	chr1	111017375	CCDS828.2	c.1580C>T	p.S527L
KCNG2	potassium voltage-gated channel; subfamily G; member 2	ENSG00000178342	PAP47	47	40.4%	chr18	75760679	CCDS12019.1	c.1276G>A	p.E426K
KCNH3	potassium voltage-gated channel; subfamily H (eag-related); member 3	ENSG00000135519	PAP47	94	25.5%	chr12	48229191	CCDS8786.1	c.1436A>C	p.K479T
POU4F1	POU class 4 homeobox 1	ENSG00000152192	PAP47	31	32.3%	chr13	78075400	CCDS31996.1	c.63G>T	p.K21N
PRELID2	PRELI domain containing 2	ENSG00000186314	PAP47	87	27.6%	chr5	145156239	CCDS34262.1	c.469G>T	p.E157X
PSENEN	presenilin enhancer 2 homolog (C. elegans)	ENSG00000205155	PAP47	254	26.0%	chr19	40929183	CCDS12474.1	c.85C>A	p.L29I
PRICKLE1	prickle homolog 1 (Drosophila)	ENSG00000139174	PAP47	302	30.5%	chr12	41145045	CCDS8742.1	c.1058C>T	p.S353L
POP5	processing of precursor 5; ribonuclease P/MRP subunit (S. cerevisiae)	ENSG00000167272	PAP47	86	25.6%	chr12	119502106	CCDS9202.1	c.167G>A	p.R56Q
PCOLCE2	procollagen C-endopeptidase enhancer 2	ENSG00000163710	PAP47	249	28.1%	chr3	144049998	CCDS3127.1	c.199G>A	p.E67K
PENK	proenkephalin	ENSG00000181195	PAP47	64	31.3%	chr8	57520975	CCDS6168.1	c.92C>T	p.A31V
PDCD10	programmed cell death 10	ENSG00000114209	PAP47	150	27.3%	chr3	168896160	CCDS3202.1	c.313G>A	p.E105K
PDCD11	programmed cell death 11	ENSG00000148843	PAP47	80	28.8%	chr10	105150207	CCDS31276.1	c.166A>C	p.K56Q
PDCD11	programmed cell death 11	ENSG00000148843	PAP47	82	15.9%	chr10	105155826	CCDS31276.1	c.659C>T	p.A220V
PRRT1	proline-rich transmembrane protein 1	ENSG00000204314	PAP47	85	29.4%	chr6	32224599	ENST00000375149	c.1420C>T	p.R474W
P4HA3	prolyl 4-hydroxylase; alpha polypeptide III	ENSG00000149380	PAP47	45	33.3%	chr11	73677810	CCDS8230.1	c.731C>T	p.S244L
PROP1	PROP paired-like homeobox 1	ENSG00000175325	PAP47	95	20.0%	chr5	177352639	CCDS4430.1	c.358C>T	p.R120C
PCSK9	proprotein convertase subtilisin/kexin type 9	ENSG00000169174	PAP47	103	25.2%	chr1	55282174	CCDS603.1	c.278G>A	p.R93H
PSAP	prosaposin	ENSG00000197746	PAP47	63	38.1%	chr10	73264239	CCDS7311.1	c.70G>T	p.E24X
PRSS27	protease; serine 27	ENSG00000172382	PAP47	183	17.5%	chr16	2702674	CCDS10476.1	c.821G>A	p.R274Q
PRKG1	protein kinase; cGMP-dependent; type I	ENSG00000185532	PAP47	59	25.4%	chr10	53234384	CCDS7244.1	c.626G>A	p.R209Q
PRKG2	protein kinase; cGMP-dependent; type II	ENSG00000138669	PAP47	25	40.0%	chr4	82275368	CCDS3589.1	c.1741A>C	p.N581H
PPP1R12B	protein phosphatase 1; regulatory (inhibitor) subunit 12B	ENSG00000077157	PAP47	155	29.7%	chr1	200798662	CCDS30973.1	c.2641G>T	p.D881Y
PPP1R3A	protein phosphatase 1; regulatory (inhibitor) subunit 3A	ENSG00000154415	PAP47	608	28.6%	chr7	113306638	CCDS5759.1	c.1745C>A	p.S582Y
PPP1R3A	protein phosphatase 1; regulatory (inhibitor) subunit 3A	ENSG00000154415	PAP47	154	31.2%	chr7	113346053	CCDS5759.1	c.235G>T	p.E79X
PPP1R3F	protein phosphatase 1; regulatory (inhibitor) subunit 3F	ENSG00000049769	PAP47	97	20.6%	chrX	49014124	CCDS35254.1	c.848T>G	p.V283G
PPP1R9A	protein phosphatase 1; regulatory (inhibitor) subunit 9A	ENSG00000158528	PAP47	131	12.2%	chr7	94378182	CCDS34683.1	c.821G>T	p.S274I
PPP1R9B	protein phosphatase 1; regulatory (inhibitor) subunit 9B	ENSG00000108819	PAP47	237	28.3%	chr17	45577572	ENST00000316878	c.1400G>A	p.R467H
PPP2R1B	protein phosphatase 2; regulatory subunit A; beta	ENSG00000137713	PAP47	215	29.8%	chr11	111113453	CCDS8348.1	c.1840G>T	p.E614X
PPP2R2B	protein phosphatase 2; regulatory subunit B; beta	ENSG00000156475	PAP47	309	28.8%	chr5	145949935	CCDS4283.1	c.1109G>T	p.R370I
PPP2R2D	protein phosphatase 2; regulatory subunit B; delta isoform	ENSG00000175470	PAP47	148	30.4%	chr10	133611077	CCDS41578.1	c.193T>C	p.S65P
PPP3CA	protein phosphatase 3; catalytic subunit; alpha isozyme	ENSG00000138814	PAP47	131	29.0%	chr4	102166163	CCDS34037.1	c.1448T>C	p.M483T
PPP3CA	protein phosphatase 3; catalytic subunit; alpha isozyme	ENSG00000138814	PAP47	127	32.3%	chr4	102201303	CCDS34037.1	c.1120G>T	p.D374Y
PPM1D	protein phosphatase; Mg2+/Mn2+ dependent; 1D	ENSG00000170836	PAP47	165	28.5%	chr17	56032932	CCDS11625.1	c.375G>T	p.K125N
PRC1	protein regulator of cytokinesis 1	ENSG00000198901	PAP47	175	28.0%	chr15	89313709	CCDS32334.1	c.1721C>A	p.S574Y
PTPRD	protein tyrosine phosphatase; receptor type; D	ENSG00000153707	PAP47	262	10.7%	chr9	8508111	CCDS43786.1	c.1280G>A	p.R427Q
PTPRD	protein tyrosine phosphatase; receptor type; D	ENSG00000153707	PAP47	176	29.5%	chr9	8508412	CCDS43786.1	c.979G>T	p.G327X
PTPRH	protein tyrosine phosphatase; receptor type; H	ENSG00000080031	PAP47	188	33.0%	chr19	60394857	CCDS33110.1	c.2322C>A	p.F774L
PTPRZ1	protein tyrosine phosphatase; receptor-type; Z polypeptide 1	ENSG00000106278	PAP47	130	29.2%	chr7	121404133	CCDS34740.1	c.611G>A	p.S204N
PCMTD2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	ENSG00000203880	PAP47	101	21.8%	chr20	62375158	CCDS13559.1	c.847C>T	p.R283C

POMT1	protein-O-mannosyltransferase 1	ENSG00000130714	PAP47	114	21.1%	chr9	133372659	CCDS6943.1	c.364A>G	p.I122V
PRG3	proteoglycan 3	ENSG00000156575	PAP47	101	28.7%	chr11	56901773	CCDS7954.1	c.-1G>A	p.IVS4+1-1SpliceDonor
PCDH10	protocadherin 10	ENSG00000138650	PAP47	266	28.6%	chr4	134290989	CCDS34063.1	c.244G>A	p.E82K
PCDH11X	protocadherin 11 X-linked	ENSG00000102290	PAP47	66	27.3%	chrX	90977265	CCDS14461.1	c.106G>T	p.E36X
PCDH19	protocadherin 19	ENSG00000165194	PAP47	115	27.0%	chrX	99492345	CCDS43976.1	c.2489C>A	p.S830Y
PCDH9	protocadherin 9	ENSG00000184226	PAP47	200	26.0%	chr13	66698782	CCDS9444.1	c.1792G>T	p.D598Y
PCDHA5	protocadherin alpha 5	ENSG00000204965	PAP47	137	29.9%	chr5	140182747	CCDS34250.1	c.1203G>T	p.K401N
PCDHB15	protocadherin beta 15	ENSG00000113248	PAP47	170	35.3%	chr5	140605594	CCDS4257.1	c.264G>T	p.E88D
PCDHB15	protocadherin beta 15	ENSG00000113248	PAP47	179	25.1%	chr5	140606404	CCDS4257.1	c.1074G>T	p.E358D
PCDHB16	protocadherin beta 16	ENSG00000196963	PAP47	194	27.8%	chr5	140543222	CCDS4251.1	c.904C>T	p.R302X
PCDHB8	protocadherin beta 8	ENSG00000120322	PAP47	359	12.8%	chr5	140538881	CCDS4250.1	c.1082C>T	p.A361V
PCDHGA10	protocadherin gamma subfamily A; 10	ENSG00000081853	PAP47	123	23.6%	chr5	140792920	CCDS4260.1	c.2410C>A	p.H804N
PCDHGA11	protocadherin gamma subfamily A; 11	ENSG00000081853	PAP47	123	23.6%	chr5	140792920	CCDS4260.1	c.2410C>A	p.H804N
PCDHGA3	protocadherin gamma subfamily A; 3	ENSG00000081853	PAP47	123	23.6%	chr5	140792920	CCDS4260.1	c.2410C>A	p.H804N
PCDHGA8	protocadherin gamma subfamily A; 8	ENSG00000081853	PAP47	123	23.6%	chr5	140792920	CCDS4260.1	c.2410C>A	p.H804N
PCDHGB7	protocadherin gamma subfamily B; 7	ENSG00000081853	PAP47	123	23.6%	chr5	140792920	CCDS4260.1	c.2410C>A	p.H804N
PCDHGC5	protocadherin gamma subfamily C; 5	ENSG00000081853	PAP47	123	23.6%	chr5	140792920	CCDS4260.1	c.2410C>A	p.H804N
PRTG	protogenin homolog (Gallus gallus)	ENSG00000166450	PAP47	54	25.9%	chr15	53759995	CCDS42040.1	c.800C>A	p.S267Y
PRPF18	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	ENSG00000165630	PAP47	76	19.7%	chr10	13698452	CCDS7100.1	c.841A>G	p.I281V
PRPF3	PRP3 pre-mRNA processing factor 3 homolog (S. cerevisiae)	ENSG00000117360	PAP47	101	33.7%	chr1	148582471	CCDS951.1	c.1345C>T	p.R449W
PRPF38B	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	ENSG00000134186	PAP47	58	31.0%	chr1	109040191	CCDS788.1	c.349C>T	p.R117X
PRPF38B	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	ENSG00000134186	PAP47	52	26.9%	chr1	109042959	CCDS788.1	c.769C>T	p.R257C
PRPF39	PRP39 pre-mRNA processing factor 39 homolog (S. cerevisiae)	ENSG00000185246	PAP47	131	26.7%	chr14	44635158	NM_017922	c.427G>A	p.D143N
PTK6	PTK6 protein tyrosine kinase 6	ENSG00000101213	PAP47	162	34.6%	chr20	61635353	CCDS13524.1	c.665C>A	p.S222Y
PUM2	pumilio homolog 2 (Drosophila)	ENSG00000055917	PAP47	144	33.3%	chr2	20381821	CCDS1698.1	c.118C>A	p.L40I
PDXDC1	pyridoxal-dependent decarboxylase domain containing 1	ENSG00000179889	PAP47	140	12.9%	chr16	15031408	CCDS32393.1	c.1393G>A	p.A465T
P2RY4	pyrimidinergic receptor P2Y; G-protein coupled; 4	ENSG00000186912	PAP47	200	20.5%	chrX	69395481	CCDS14398.1	c.719G>A	p.R240H
PDP1	pyruvate dehyrogenase phosphatase catalytic subunit 1	ENSG00000164951	PAP47	251	29.5%	chr8	95004695	CCDS6259.1	c.1232A>C	p.K411T
PDP2	pyruvate dehyrogenase phosphatase catalytic subunit 2	ENSG00000172840	PAP47	85	25.9%	chr16	65475948	CCDS10822.1	c.260G>A	p.R87Q
R3HDM2	R3H domain containing 2	ENSG00000179912	PAP47	262	23.3%	chr12	55934879	CCDS8937.1	c.1858C>T	p.R620X
RAB32	RAB32; member RAS oncogene family	ENSG00000118508	PAP47	83	39.8%	chr6	146917333	CCDS5210.1	c.577C>T	p.L193F
RAB7L1	RAB7; member RAS oncogene family-like 1	ENSG00000117280	PAP47	81	42.0%	chr1	204006181	CCDS1459.1	c.524G>T	p.R175I
RAB9A	RAB9A; member RAS oncogene family	ENSG00000123595	PAP47	388	30.4%	chrX	13637160	CCDS14156.1	c.374A>T	p.K125M
RAD50	RAD50 homolog (S. cerevisiae)	ENSG00000113522	PAP47	98	24.5%	chr5	131943053	CCDS34233.1	c.511G>A	p.A171T
RAD51AP2	RAD51 associated protein 2	ENSG00000214842	PAP47	85	24.7%	chr2	17562069	CCDS42656.1	c.1095G>T	p.K365N
RGL1	ral guanine nucleotide dissociation stimulator-like 1	ENSG00000143344	PAP47	114	28.9%	chr1	182041059	ENST00000360851	c.5A>C	p.K2T
REPS1	RALBP1 associated Eps domain containing 1	ENSG00000135597	PAP47	121	32.2%	chr6	139280407	CCDS5193.1	c.1420G>A	p.G474R
RANBP6	RAN binding protein 6	ENSG00000137040	PAP47	189	29.1%	chr9	6004946	CCDS6467.1	c.662A>C	p.D221A
RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	ENSG00000158987	PAP47	96	21.9%	chr5	130825382	CCDS34225.1	c.2779C>T	p.R927X
RASSF7	Ras association (RalGDS/AF-6) domain family (N-terminal) member 7	ENSG00000099849	PAP47	59	22.0%	chr11	552702	CCDS7702.1	c.748C>T	p.R250W
RASSF4	Ras association (RalGDS/AF-6) domain family member 4	ENSG00000107551	PAP47	154	27.9%	chr10	44787145	ENST00000374411	c.254A>C	p.E85A
RASGRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	ENSG00000152689	PAP47	118	27.1%	chr2	33636839	NM_170672	c.1637G>T	p.R546I
RASA1	RAS p21 protein activator (GTPase activating protein) 1	ENSG00000145715	PAP47	85	27.1%	chr5	86664897	CCDS34200.1	c.886A>G	p.T296A
RRAD	Ras-related associated with diabetes	ENSG00000166592	PAP47	313	29.4%	chr16	65513485	CCDS10824.1	c.922C>A	p.L308I
RB1CC1	RB1-inducible coiled-coil 1	ENSG00000023287	PAP47	138	27.5%	chr8	53732877	CCDS34892.1	c.2065G>A	p.E689K
RB1CC1	RB1-inducible coiled-coil 1	ENSG00000023287	PAP47	144	29.2%	chr8	53732945	CCDS34892.1	c.1997C>T	p.T666I
RAG1	recombination activating gene 1	ENSG00000166349	PAP47	155	28.4%	chr11	36554348	CCDS7902.1	c.2918G>A	p.R973H

RELN	reelin	ENSG00000189056	PAP47	60	21.7%	chr7	102919684	CCDS34722.1	c.9395C>A	p.S3132Y
RELN	reelin	ENSG00000189056	PAP47	66	33.3%	chr7	103128598	CCDS34722.1	c.897A>C	p.K299N
RGS12	regulator of G-protein signaling 12	ENSG00000159788	PAP47	50	30.0%	chr4	3386304	CCDS3366.1	c.2218G>T	p.E740X
RGS2	regulator of G-protein signaling 2; 24kDa	ENSG00000116741	PAP47	51	25.5%	chr1	191046795	CCDS1377.1	c.336C>A	p.F112L
RSF1	remodeling and spacing factor 1	ENSG00000048649	PAP47	28	39.3%	chr11	77073853	CCDS8253.1	c.-1G>T	p.IVS9-1-1SpliceAcceptor
RSF1	remodeling and spacing factor 1	ENSG00000048649	PAP47	52	34.6%	chr11	77090535	CCDS8253.1	c.1387A>G	p.K463E
RFC2	replication factor C (activator 1) 2; 40kDa	ENSG00000049541	PAP47	116	17.2%	chr7	73302033	CCDS5568.1	c.197A>G	p.E66G
RLBP1	retinaldehyde binding protein 1	ENSG00000140522	PAP47	244	31.1%	chr15	87561409	CCDS32324.1	c.292C>T	p.R98C
RP1	retinitis pigmentosa 1 (autosomal dominant)	ENSG00000104237	PAP47	152	24.3%	chr8	55704133	CCDS6160.1	c.5138A>C	p.Y1713S
RB1	retinoblastoma 1	ENSG00000139687	PAP47	38	28.9%	chr13	47840687	CCDS31973.1	c.1073G>A	p.R358Q
RS1	retinoschisin 1	ENSG00000102104	PAP47	103	31.1%	chrX	18600094	CCDS14187.1	c.16G>T	p.E6X
REV1	REV1 homolog (S. cerevisiae)	ENSG00000135945	PAP47	142	23.9%	chr2	99385960	CCDS2045.1	c.3208G>A	p.E1070K
RHAG	Rh-associated glycoprotein	ENSG00000112077	PAP47	151	28.5%	chr6	49712415	CCDS4927.1	c.70G>T	p.V24F
ARHGAP15	Rho GTPase activating protein 15	ENSG00000075884	PAP47	128	23.4%	chr2	144177497	CCDS2184.1	c.1178C>A	p.S393Y
ARHGAP31	Rho GTPase activating protein 31	ENSG00000031081	PAP47	209	23.0%	chr3	120615471	CCDS43135.1	c.2005C>A	p.L669I
ARHGAP5	Rho GTPase activating protein 5	ENSG00000100852	PAP47	103	27.2%	chr14	31630913	CCDS32062.1	c.1287A>C	p.E429D
ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	ENSG00000196914	PAP47	94	27.7%	chr11	119783707	CCDS41727.1	c.107T>G	p.V36G
ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	ENSG00000196914	PAP47	327	27.5%	chr11	119856098	CCDS41727.1	c.3986G>A	p.R1329Q
ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	ENSG00000102606	PAP47	44	38.6%	chr13	110604278	CCDS32009.1	c.191G>A	p.S64N
ROCK2	Rho-associated; coiled-coil containing protein kinase 2	ENSG00000134318	PAP47	125	27.2%	chr2	11272452	CCDS42654.1	c.1901G>A	p.R634Q
RHBDL3	rhomboid; veinlet-like 3 (Drosophila)	ENSG00000141314	PAP47	212	29.7%	chr17	27672347	CCDS32613.1	c.1201C>T	p.P401S
RHOBTB3	Rho-related BTB domain containing 3	ENSG00000164292	PAP47	251	15.1%	chr5	95116993	CCDS4077.1	c.820C>A	p.L274I
RNASE2	ribonuclease; RNase A family; 2 (liver; eosinophil-derived neurotoxin)	ENSG00000169385	PAP47	113	21.2%	chr14	20494044	CCDS9561.1	c.274A>G	p.N92D
RPL10L	ribosomal protein L10-like	ENSG00000165496	PAP47	274	27.4%	chr14	46190233	CCDS32071.1	c.457C>T	p.R153C
RPL10L	ribosomal protein L10-like	ENSG00000165496	PAP47	114	19.3%	chr14	46190422	CCDS32071.1	c.268C>T	p.R90W
RPS21	ribosomal protein S21	ENSG00000171858	PAP47	338	10.4%	chr20	60396310	CCDS13497.1	c.131G>A	p.G44D
RPS6KA5	ribosomal protein S6 kinase; 90kDa; polypeptide 5	ENSG00000100784	PAP47	119	27.7%	chr14	90439005	CCDS9893.1	c.1019G>A	p.R340Q
RPS6KA6	ribosomal protein S6 kinase; 90kDa; polypeptide 6	ENSG00000072133	PAP47	84	16.7%	chrX	83305999	CCDS14451.1	c.134C>A	p.S45Y
RNF113A	ring finger protein 113A	ENSG00000125352	PAP47	353	26.6%	chrX	118889460	CCDS14589.1	c.145G>A	p.E49K
RNF128	ring finger protein 128	ENSG00000133135	PAP47	66	60.6%	chrX	105903008	CCDS14521.1	c.694C>T	p.R232X
RNF26	ring finger protein 26	ENSG00000173456	PAP47	158	32.9%	chr11	118711908	CCDS8419.1	c.866G>A	p.R289Q
RMI1	RMI1; RecQ mediated genome instability 1; homolog (S. cerevisiae)	ENSG00000178966	PAP47	52	19.2%	chr9	85806978	CCDS6669.1	c.1257G>T	p.K419N
RBM10	RNA binding motif protein 10	ENSG00000182872	PAP47	176	36.4%	chrX	46915462	CCDS14274.1	c.293G>A	p.R98Q
RBM11	RNA binding motif protein 11	ENSG00000185272	PAP47	62	19.4%	chr21	14515288	NM_144770	c.-1G>T	p.IVS2-1-1SpliceAcceptor
RBM12B	RNA binding motif protein 12B	ENSG00000183808	PAP47	106	25.5%	chr8	94816958	CCDS43755.1	c.857T>C	p.V286A
RBM15	RNA binding motif protein 15	ENSG00000162775	PAP47	232	20.3%	chr1	110684884	CCDS822.1	c.1334A>C	p.K445T
RBM26	RNA binding motif protein 26	ENSG00000139746	PAP47	414	31.2%	chr13	78843167	CCDS9462.1	c.548G>A	p.R183Q
RPAIN	RPA interacting protein	ENSG00000129197	PAP47	95	31.6%	chr17	5265341	CCDS32536.1	c.83G>A	p.R28K
RUFY1	RUN and FYVE domain containing 1	ENSG00000176783	PAP47	150	25.3%	chr5	178949228	CCDS4445.2	c.1102C>T	p.R368X
RUSC2	RUN and SH3 domain containing 2	ENSG00000198853	PAP47	141	11.3%	chr9	35538205	CCDS35008.1	c.1687C>T	p.R563C
S100Z	S100 calcium binding protein Z	ENSG00000171643	PAP47	112	28.6%	chr5	76209401	CCDS43333.1	c.288G>T	p.K96N
SALL1	sal-like 1 (Drosophila)	ENSG00000103449	PAP47	375	30.7%	chr16	49731182	CCDS10747.1	c.2452T>G	p.F818V
SAV1	salvador homolog 1 (Drosophila)	ENSG00000151748	PAP47	48	35.4%	chr14	50201976	CCDS9701.1	c.206G>T	p.R69I
SASH1	SAM and SH3 domain containing 1	ENSG00000111961	PAP47	73	28.8%	chr6	148803061	CCDS5212.1	c.334G>A	p.E112K
SGCG	sarcoglycan; gamma (35kDa dystrophin-associated glycoprotein)	ENSG00000102683	PAP47	64	21.9%	chr13	22751608	CCDS9299.1	c.496C>T	p.R166X
SAGE1	sarcoma antigen 1	ENSG00000181433	PAP47	298	28.2%	chrX	134815882	CCDS14652.1	c.488G>T	p.R163I
SAGE1	sarcoma antigen 1	ENSG00000181433	PAP47	142	31.7%	chrX	134821611	CCDS14652.1	c.2354C>T	p.A785V

SCARA5	scavenger receptor class A; member 5 (putative)	ENSG00000168079	PAP47	129	25.6%	chr8	27820586	CCDS6064.1	c.1094A>G	p.K365R
SLFN5	schlafen family member 5	ENSG00000166750	PAP47	157	15.9%	chr17	30612190	CCDS32619.1	c.1100C>T	p.S367L
SCEL	sciellin	ENSG00000136155	PAP47	122	26.2%	chr13	77039832	CCDS9459.1	c.307G>T	p.D103Y
SCIN	scinderin	ENSG00000006747	PAP47	70	25.7%	chr7	12610669	NM_001112706	c.522T>G	p.I174M
STIL	SCL/TAL1 interrupting locus	ENSG00000123473	PAP47	63	23.8%	chr1	47525827	CCDS41329.1	c.1116G>T	p.K372N
SFMBT2	Scm-like with four mbt domains 2	ENSG00000198879	PAP47	101	36.6%	chr10	7279520	CCDS31138.1	c.1694A>C	p.K565T
SESTD1	SEC14 and spectrin domains 1	ENSG00000187231	PAP47	140	30.7%	chr2	179697410	CCDS33338.1	c.1093C>T	p.R365X
SEC23IP	SEC23 interacting protein	ENSG00000107651	PAP47	54	18.5%	chr10	121681634	CCDS7618.1	c.-1G>T	p.IVS15-1-1SpliceAcceptor
SCRN3	secernin 3	ENSG00000144306	PAP47	151	27.2%	chr2	174995894	CCDS2258.1	c.790C>T	p.R264X
SEMA3D	sema domain; immunoglobulin domain (Ig); short basic domain; secreted; (semaphorin) 3D	ENSG00000153993	PAP47	141	21.3%	chr7	84467068	CCDS34676.1	c.1958G>A	p.R653Q
SEMA6D	sema domain; transmembrane domain (TM); and cytoplasmic domain; (semaphorin) 6D	ENSG00000137872	PAP47	212	32.5%	chr15	45850793	CCDS32225.1	c.2741C>T	p.S914L
40427	septin 6	ENSG00000125354	PAP47	163	27.6%	chrX	118670964	CCDS14584.1	c.409C>T	p.R137X
40427	septin 6	ENSG00000125354	PAP47	70	28.6%	chrX	118681521	CCDS14584.1	c.293C>T	p.T98M
SRGN	serglycin	ENSG00000122862	PAP47	155	27.7%	chr10	70533659	CCDS7285.1	c.254G>A	p.R85H
SRRM2	serine/arginine repetitive matrix 2	ENSG00000167978	PAP47	371	27.8%	chr16	2752526	CCDS32373.1	c.1996C>T	p.R666C
STK11IP	serine/threonine kinase 11 interacting protein	ENSG00000144589	PAP47	209	31.1%	chr2	220188181	ENST00000295641	c.2991G>T	p.E997D
SERPINA13	serpin peptidase inhibitor; clade A (alpha-1 antiproteinase; antitrypsin); member 13 (pseudogene)	ENSG00000187483	PAP47	103	33.0%	chr14	94181048	ENST00000338704	c.856G>T	p.E286X
SERPINB4	serpin peptidase inhibitor; clade B (ovalbumin); member 4	ENSG00000206073	PAP47	144	22.2%	chr18	59473883	CCDS11987.1	c.1161C>A	p.F387L
SERPINC1	serpin peptidase inhibitor; clade C (antithrombin); member 1	ENSG00000117601	PAP47	55	32.7%	chr1	172147600	CCDS1313.1	c.584A>G	p.E195G
SERPINF1	serpin peptidase inhibitor; clade F (alpha-2 antiplasmin; pigment epithelium derived factor); member 1	ENSG00000132386	PAP47	180	29.4%	chr17	1627257	CCDS11012.1	c.1024G>A	p.D342N
SERPINI1	serpin peptidase inhibitor; clade I (neuroserpin); member 1	ENSG00000163536	PAP47	94	26.6%	chr3	169025797	CCDS3203.1	c.1225G>A	p.E409K
SCML1	sex comb on midleg-like 1 (Drosophila)	ENSG00000047634	PAP47	194	26.3%	chrX	17681338	CCDS35210.1	c.895G>A	p.V299M
SFI1	Sfi1 homolog; spindle assembly associated (yeast)	ENSG00000198089	PAP47	100	26.0%	chr22	30299134	CCDS43004.1	c.856A>G	p.K286E
SH2D3C	SH2 domain containing 3C	ENSG00000095370	PAP47	79	30.4%	chr9	129553398	CCDS6877.1	c.558C>A	p.F186L
SH2B1	SH2B adaptor protein 1	ENSG00000178188	PAP47	166	32.5%	chr16	28790683	CCDS32424.1	c.1391C>T	p.S464L
SH3BP5	SH3-domain binding protein 5 (BTK-associated)	ENSG00000131370	PAP47	160	31.3%	chr3	15275453	CCDS2625.2	c.778C>T	p.R260W
SH3KBP1	SH3-domain kinase binding protein 1	ENSG00000147010	PAP47	289	32.2%	chrX	19516751	CCDS14193.1	c.1229C>A	p.S410Y
SHROOM3	shroom family member 3	ENSG00000138771	PAP47	172	27.3%	chr4	77879527	CCDS3579.1	c.1174G>A	p.A392T
SHROOM4	shroom family member 4	ENSG00000158352	PAP47	358	10.9%	chrX	50393880	CCDS35277.1	c.1933A>C	p.K645Q
SFXN2	sideroflexin 2	ENSG00000156398	PAP47	173	30.6%	chr10	104485651	CCDS7539.1	c.864G>T	p.Q288H
SIPA1L1	signal-induced proliferation-associated 1 like 1	ENSG00000197555	PAP47	156	28.8%	chr14	71221896	CCDS9807.1	c.3169G>A	p.E1057K
SIPA1L2	signal-induced proliferation-associated 1 like 2	ENSG00000116991	PAP47	260	24.6%	chr1	230667637	CCDS41474.1	c.2392C>T	p.R798X
SOBP	sine oculis binding protein homolog (Drosophila)	ENSG00000112320	PAP47	101	26.7%	chr6	108061447	CCDS43488.1	c.706G>T	p.E236X
SOBP	sine oculis binding protein homolog (Drosophila)	ENSG00000112320	PAP47	221	26.7%	chr6	108063177	CCDS43488.1	c.2436G>T	p.E812D
SIX5	SIX homeobox 5	ENSG00000177045	PAP47	57	28.1%	chr19	50961638	CCDS12673.1	c.1419G>T	p.L473F
SLAMF7	SLAM family member 7	ENSG00000026751	PAP47	151	25.8%	chr1	158989550	CCDS1209.1	c.967C>T	p.P323S
SSH1	slingshot homolog 1 (Drosophila)	ENSG00000084112	PAP47	308	28.6%	chr12	107734981	CCDS9121.1	c.363G>T	p.E121D
SLITRK1	SLIT and NTRK-like family; member 1	ENSG00000178235	PAP47	118	30.5%	chr13	83352472	CCDS9464.1	c.1172G>A	p.R391Q
SLITRK4	SLIT and NTRK-like family; member 4	ENSG00000179542	PAP47	206	24.3%	chrX	142544304	CCDS14679.1	c.2287C>A	p.L763I
SLITRK4	SLIT and NTRK-like family; member 4	ENSG00000179542	PAP47	145	35.9%	chrX	142544529	CCDS14679.1	c.2062C>T	p.P688S
SLITRK6	SLIT and NTRK-like family; member 6	ENSG00000184564	PAP47	170	27.1%	chr13	85266952	CCDS41903.1	c.1693C>A	p.L565I
SNRNP200	small nuclear ribonucleoprotein 200kDa (U5)	ENSG00000144028	PAP47	92	33.7%	chr2	96322555	CCDS2020.1	c.2042G>A	p.R681H
SMCR8	Smith-Magenis syndrome chromosome region; candidate 8	ENSG00000176994	PAP47	190	34.7%	chr17	18160489	CCDS11195.2	c.661G>A	p.D221N
SHPRH	SNF2 histone linker PHD RING helicase	ENSG00000146414	PAP47	337	32.3%	chr6	146305980	CCDS43513.1	c.2230C>T	p.R744X
SCNN1B	sodium channel; nonvoltage-gated 1; beta	ENSG00000168447	PAP47	124	24.2%	chr16	23222913	ENST00000307331	c.92A>C	p.K31T
SCN1A	sodium channel; voltage-gated; type I; alpha subunit	ENSG00000144285	PAP47	79	29.1%	chr2	166556297	CCDS33316.1	c.5701C>T	p.R1901X
SCN3A	sodium channel; voltage-gated; type III; alpha subunit	ENSG00000153253	PAP47	89	31.5%	chr2	165655820	CCDS33312.1	c.5089A>G	p.N1697D
SCN9A	sodium channel; voltage-gated; type IX; alpha subunit	ENSG00000169432	PAP47	102	31.4%	chr2	166845293	NM_002977	c.2130C>A	p.F710L

SCN7A	sodium channel; voltage-gated; type VII; alpha	ENSG00000136546	PAP47	88	18.2%	chr2	166970412	NM_002976	c.4973G>A	p.R1658K
SCN11A	sodium channel; voltage-gated; type XI; alpha subunit	ENSG00000168356	PAP47	157	29.9%	chr3	38863980	CCDS33737.1	c.4585G>A	p.D1529N
SCN11A	sodium channel; voltage-gated; type XI; alpha subunit	ENSG00000168356	PAP47	311	26.4%	chr3	38911228	CCDS33737.1	c.2635G>T	p.D879Y
SLC10A6	solute carrier family 10 (sodium/bile acid cotransporter family); member 6	ENSG00000145283	PAP47	50	38.0%	chr4	87964054	CCDS3614.1	c.945G>T	p.L315F
SLC15A1	solute carrier family 15 (oligopeptide transporter); member 1	ENSG00000088386	PAP47	127	29.9%	chr13	98176626	CCDS9489.1	c.100C>T	p.R34X
SLC15A4	solute carrier family 15; member 4	ENSG00000139370	PAP47	124	22.6%	chr12	127860472	CCDS9264.1	c.980C>T	p.A327V
SLC16A1	solute carrier family 16; member 1 (monocarboxylic acid transporter 1)	ENSG00000155380	PAP47	147	11.6%	chr1	113258308	CCDS858.1	c.1231C>T	p.R411W
SLC2A13	solute carrier family 2 (facilitated glucose transporter); member 13	ENSG00000151229	PAP47	98	30.6%	chr12	38544943	CCDS8736.1	c.1150G>A	p.V384I
SLC22A2	solute carrier family 22 (organic cation transporter); member 2	ENSG00000112499	PAP47	47	21.3%	chr6	160588261	CCDS5276.1	c.902G>T	p.R301I
SLC22A16	solute carrier family 22 (organic cation/carnitine transporter); member 16	ENSG00000004809	PAP47	165	29.7%	chr6	110870184	CCDS5084.1	c.1139C>A	p.S380Y
SLC22A4	solute carrier family 22 (organic cation/ergothioneine transporter); member 4	ENSG00000197208	PAP47	56	32.1%	chr5	131690988	CCDS4153.1	c.944C>A	p.S315Y
SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchanger); member 1	ENSG00000074621	PAP47	134	33.6%	chr15	63703665	ENST00000261892	c.194G>A	p.R65Q
SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchanger); member 1	ENSG00000074621	PAP47	106	31.1%	chr15	63717564	ENST00000261892	c.1932G>T	p.K644N
SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger); member 3	ENSG00000185052	PAP47	106	30.2%	chr20	19602253	CCDS13140.1	c.722C>A	p.S241Y
SLC25A14	solute carrier family 25 (mitochondrial carrier; brain); member 14	ENSG00000102078	PAP47	158	24.7%	chrX	129301989	CCDS14623.1	c.56C>T	p.A19V
SLC25A2	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 2	ENSG00000120329	PAP47	54	29.6%	chr5	140662755	CCDS4258.1	c.862G>A	p.E288K
SLC25A37	solute carrier family 25; member 37	ENSG00000147454	PAP47	235	27.2%	chr8	23485243	NM_016612	c.947C>A	p.S316Y
SLC38A10	solute carrier family 38; member 10	ENSG00000157637	PAP47	85	24.7%	chr17	76834061	CCDS42397.1	c.3250G>A	p.D1084N
SLC4A2	solute carrier family 4; anion exchanger; member 2 (erythrocyte membrane protein band 3-like 1)	ENSG00000164889	PAP47	175	36.0%	chr7	150399212	CCDS5917.1	c.1870C>T	p.R624C
SLC44A1	solute carrier family 44; member 1	ENSG00000070214	PAP47	75	17.3%	chr9	107111886	CCDS6763.1	c.187G>A	p.D63N
SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter); member 3	ENSG00000198743	PAP47	175	33.1%	chr21	34389501	CCDS33549.1	c.134C>G	p.S45C
SLC6A14	solute carrier family 6 (amino acid transporter); member 14	ENSG00000087916	PAP47	153	28.1%	chrX	115488973	CCDS14570.1	c.643G>T	p.E215X
SLC6A12	solute carrier family 6 (neurotransmitter transporter; betaine/GABA); member 12	ENSG00000111181	PAP47	72	31.9%	chr12	178357	CCDS8501.1	c.713T>G	p.V238G
SLC6A3	solute carrier family 6 (neurotransmitter transporter; dopamine); member 3	ENSG00000142319	PAP47	96	31.3%	chr5	1485744	CCDS3863.1	c.488C>T	p.A163V
SLC6A13	solute carrier family 6 (neurotransmitter transporter; GABA); member 13	ENSG00000010379	PAP47	92	29.3%	chr12	203491	CCDS8502.1	c.1239G>T	p.K413N
SLC6A7	solute carrier family 6 (neurotransmitter transporter; L-proline); member 7	ENSG00000011083	PAP47	233	28.3%	chr5	149562195	CCDS4305.1	c.951G>T	p.Q317H
SLC6A4	solute carrier family 6 (neurotransmitter transporter; serotonin); member 4	ENSG00000108576	PAP47	257	33.5%	chr17	25569986	CCDS11256.1	c.433A>C	p.N145H
SLC6A15	solute carrier family 6 (neutral amino acid transporter); member 15	ENSG00000072041	PAP47	154	31.2%	chr12	83801688	CCDS9027.1	c.837C>A	p.F279L
SLC8A3	solute carrier family 8 (sodium/calcium exchanger); member 3	ENSG00000100678	PAP47	94	26.6%	chr14	69597358	CCDS35498.1	c.1836G>T	p.E612D
SLC9A7	solute carrier family 9 (sodium/hydrogen exchanger); member 7	ENSG00000065923	PAP47	168	30.4%	chrX	46426786	CCDS14269.1	c.454G>A	p.E152K
SON	SON DNA binding protein	ENSG00000159140	PAP47	47	23.4%	chr21	33853427	CCDS13629.1	c.6343A>G	p.S2115G
SORCS1	sortilin-related VPS10 domain containing receptor 1	ENSG00000108018	PAP47	207	23.2%	chr10	108402173	CCDS31283.1	c.2432C>T	p.A811V
SORCS3	sortilin-related VPS10 domain containing receptor 3	ENSG00000156395	PAP47	95	21.1%	chr10	106966765	CCDS7558.1	c.2629G>T	p.D877Y
SNX13	sorting nexin 13	ENSG00000071189	PAP47	105	21.0%	chr7	17851776	NM_015132	c.1132C>T	p.L378F

SPARCL1	SPARC-like 1 (hevin)	ENSG00000152583	PAP47	263	33.1%	chr4	88634198	CCDS3622.1	c.778G>T	p.E260X
SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	ENSG00000151835	PAP47	111	27.9%	chr13	22806936	CCDS9300.1	c.8638T>G	p.F2880V
SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	ENSG00000151835	PAP47	204	25.5%	chr13	22808454	CCDS9300.1	c.7120G>T	p.E2374X
SYNE1	spectrin repeat containing; nuclear envelope 1	ENSG00000131018	PAP47	116	14.7%	chr6	152543110	CCDS5236.1	c.23314C>T	p.R7772W
SYNE1	spectrin repeat containing; nuclear envelope 1	ENSG00000131018	PAP47	107	18.7%	chr6	152679714	CCDS5236.1	c.16673C>A	p.S5558Y
SYNE1	spectrin repeat containing; nuclear envelope 1	ENSG00000131018	PAP47	182	24.2%	chr6	152689187	CCDS5236.1	c.15230C>A	p.S5077Y
SYNE2	spectrin repeat containing; nuclear envelope 2	ENSG00000054654	PAP47	147	29.9%	chr14	63564130	CCDS9761.2	c.6580G>T	p.D2194Y
SPTA1	spectrin; alpha; erythrocytic 1 (elliptocytosis 2)	ENSG00000163554	PAP47	94	28.7%	chr1	156894025	CCDS41423.1	c.2671C>T	p.R891X
SPEN	spen homolog; transcriptional regulator (Drosophila)	ENSG00000065526	PAP47	150	17.3%	chr1	16129620	CCDS164.1	c.4298C>A	p.S1433Y
SPATA21	spermatogenesis associated 21	ENSG00000187144	PAP47	258	33.7%	chr1	16608930	CCDS172.1	c.340C>T	p.P114S
SPZ1	spermatogenic leucine zipper 1	ENSG00000164299	PAP47	371	26.7%	chr5	79651866	CCDS43336.1	c.76G>T	p.E26X
SPZ1	spermatogenic leucine zipper 1	ENSG00000164299	PAP47	113	14.2%	chr5	79652415	CCDS43336.1	c.625G>T	p.D209Y
SPHKAP	SPHK1 interactor; AKAP domain containing	ENSG00000153820	PAP47	211	31.3%	chr2	228590364	CCDS33389.1	c.3450C>A	p.Y1150X
SF3B1	splicing factor 3b; subunit 1; 155kDa	ENSG00000115524	PAP47	116	35.3%	chr2	197993347	ENST00000409915	c.465A>C	p.X155Y
SFRS15	splicing factor; arginine/serine-rich 15	ENSG00000156304	PAP47	91	23.1%	chr21	31996482	CCDS33537.1	c.403G>A	p.A135T
SPON1	spondin 1; extracellular matrix protein	ENSG00000152268	PAP47	105	26.7%	chr11	14241001	ENST00000310358	c.2161C>T	p.R721X
SCAP	SREBF chaperone	ENSG00000114650	PAP47	228	27.2%	chr3	47430422	CCDS2755.2	c.3766G>A	p.A1256T
SOX2	SRY (sex determining region Y)-box 2	ENSG00000181449	PAP47	298	10.1%	chr3	182913567	CCDS3239.1	c.725C>T	p.S242L
SOX5	SRY (sex determining region Y)-box 5	ENSG00000134532	PAP47	260	30.8%	chr12	23890312	CCDS8699.1	c.353G>A	p.R118Q
ST7OT3	ST7 overlapping transcript 3 (non-protein coding)	ENSG00000004866	PAP47	58	31.0%	chr7	116646379	CCDS5770.1	c.1411C>T	p.R471W
ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2;8-sialyltransferase 4	ENSG00000113532	PAP47	176	30.7%	chr5	100250006	CCDS4091.1	c.443C>A	p.S148Y
STAB2	stabilin 2	ENSG00000136011	PAP47	195	26.2%	chr12	102578245	CCDS31888.1	c.1741C>T	p.R581W
STARD13	StAR-related lipid transfer (START) domain containing 13	ENSG00000133121	PAP47	141	27.0%	chr13	32582837	CCDS9348.1	c.2815C>A	p.L939I
SAMD13	sterile alpha motif domain containing 13	ENSG00000203943	PAP47	56	25.0%	chr1	84587936	CCDS30760.1	c.242G>T	p.R81I
SAMD7	sterile alpha motif domain containing 7	ENSG00000187033	PAP47	109	32.1%	chr3	171138837	CCDS3209.1	c.1190C>A	p.T397N
SAMD9L	sterile alpha motif domain containing 9-like	ENSG00000177409	PAP47	142	33.8%	chr7	92599281	CCDS34681.1	c.3940C>A	p.L1314I
SCP2	sterol carrier protein 2	ENSG00000116171	PAP47	76	31.6%	chr1	53226349	CCDS572.1	c.1034A>C	p.N345T
STON2	stonin 2	ENSG00000140022	PAP47	148	33.1%	chr14	80814456	CCDS9875.1	c.952G>T	p.E318X
SMC3	structural maintenance of chromosomes 3	ENSG00000108055	PAP47	107	23.4%	chr10	112352727	CCDS31285.1	c.3452C>T	p.A1151V
STT3A	STT3; subunit of the oligosaccharyltransferase complex; homolog A (S. cerevisiae)	ENSG00000134910	PAP47	101	38.6%	chr11	124988265	CCDS8458.1	c.1537C>T	p.R513C
SUCNR1	succinate receptor 1	ENSG00000198829	PAP47	114	11.4%	chr3	153081365	CCDS3162.1	c.344T>G	p.F115C
SI	sucrase-isomaltase (alpha-glucosidase)	ENSG00000090402	PAP47	191	30.4%	chr3	166182762	CCDS3196.1	c.5378A>C	p.K1793T
SI	sucrase-isomaltase (alpha-glucosidase)	ENSG00000090402	PAP47	61	34.4%	chr3	166220199	CCDS3196.1	c.3308C>T	p.S1103L
SI	sucrase-isomaltase (alpha-glucosidase)	ENSG00000090402	PAP47	194	24.7%	chr3	166247387	CCDS3196.1	c.1823C>A	p.S608X
SUOX	sulfite oxidase	ENSG00000139531	PAP47	204	29.9%	chr12	54683781	CCDS8901.2	c.341T>G	p.F114C
SKIV2L2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	ENSG00000039123	PAP47	151	24.5%	chr5	54676195	CCDS3967.1	c.995T>C	p.V332A
SKIV2L2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	ENSG00000039123	PAP47	42	35.7%	chr5	54682587	CCDS3967.1	c.1404A>C	p.E468D
ST7	suppression of tumorigenicity 7	ENSG00000004866	PAP47	58	31.0%	chr7	116646379	CCDS5770.1	c.1411C>T	p.R471W
SUPV3L1	suppressor of var1; 3-like 1 (S. cerevisiae)	ENSG00000156502	PAP47	62	35.5%	chr10	70619180	CCDS7287.1	c.724G>A	p.E242K
SUSD2	sushi domain containing 2	ENSG00000099994	PAP47	116	35.3%	chr22	22911636	CCDS13824.1	c.1078T>C	p.Y360H
SMARCA1	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 1	ENSG00000102038	PAP47	74	31.1%	chrX	128469721	CCDS14612.1	c.844G>T	p.E282X
SMARCA1	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 1	ENSG00000102038	PAP47	102	37.3%	chrX	128478156	CCDS14612.1	c.-1G>T	p.IVS2-1-1SpliceAcceptor
SYN1	synapsin I	ENSG00000008056	PAP47	125	26.4%	chrX	47351371	CCDS14280.1	c.444C>A	p.F148L
SYN3	synapsin III	ENSG00000185666	PAP47	248	26.2%	chr22	31239688	CCDS13908.1	c.1734C>A	p.F578L
SYCP2	synaptonemal complex protein 2	ENSG00000196074	PAP47	31	38.7%	chr20	57923636	CCDS13482.1	c.613G>T	p.E205X
SYNPO	synaptopodin	ENSG00000171992	PAP47	359	33.4%	chr5	150008551	CCDS4308.1	c.521C>A	p.A174D
SYNPO2L	synaptopodin 2-like	ENSG00000166317	PAP47	101	31.7%	chr10	75078512	CCDS7331.1	c.232C>T	p.R78W
SYT14	synaptotagmin XIV	ENSG00000143469	PAP47	95	31.6%	chr1	208261027	CCDS31014.1	c.247G>T	p.D83Y
SYNM	synemin; intermediate filament protein	ENSG00000182253	PAP47	239	27.6%	chr15	97489509	ENST00000336292	c.3418T>C	p.S1140P

STX16	syntaxin 16	ENSG00000124222	PAP47	101	33.7%	chr20	56699677	ENST00000371137	c.1004C>A	p.S335Y
STXBP1	syntaxin binding protein 1	ENSG00000136854	PAP47	55	36.4%	chr9	129455884	CCDS6874.1	c.157G>A	p.E53K
STXBP1	syntaxin binding protein 1	ENSG00000136854	PAP47	140	32.1%	chr9	129486521	CCDS6874.1	c.1756G>A	p.D586N
SNCAIP	synuclein; alpha interacting protein	ENSG00000064692	PAP47	239	31.0%	chr5	121814294	CCDS4131.1	c.1853A>C	p.K618T
TRBV25-1	T cell receptor beta variable 25-1	ENSG00000211751	PAP47	99	11.1%	chr7	142058637	ENST00000390398	c.342A>T	p.E114D
TAF1L	TAF1 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 210kDa-like	ENSG00000122728	PAP47	491	36.7%	chr9	32622872	NM_153809	c.2706G>T	p.E902D
TAF1	TAF1 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 250kDa	ENSG00000147133	PAP47	189	22.2%	chrX	70519383	CCDS14412.1	c.1773T>G	p.D591E
TAF1	TAF1 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 250kDa	ENSG00000147133	PAP47	282	25.9%	chrX	70524955	CCDS14412.1	c.-1T>C	p.IVS16+2-1SpliceDonor
TAF5L	TAF5-like RNA polymerase II; p300/CBP-associated factor (PCAF)-associated factor; 65kDa	ENSG00000135801	PAP47	139	25.9%	chr1	227796839	CCDS1581.1	c.1598C>T	p.S533L
TLN2	talin 2	ENSG00000171914	PAP47	104	35.6%	chr15	60735540	CCDS32261.1	c.623C>T	p.S208L
TNKS	tankyrase; TRF1-interacting ankyrin-related ADP-ribose polymerase	ENSG00000173273	PAP47	62	32.3%	chr8	9604933	CCDS5974.1	c.1637G>T	p.R546I
TARBP1	TAR (HIV-1) RNA binding protein 1	ENSG00000059588	PAP47	32	34.4%	chr1	232620535	CCDS1601.1	c.3623A>C	p.K1208T
TAS2R40	taste receptor; type 2; member 40	ENSG00000221937	PAP47	164	31.7%	chr7	142629670	CCDS43662.1	c.377T>G	p.F126C
TATDN1	TatD DNase domain containing 1	ENSG00000147687	PAP47	92	21.7%	chr8	125575371	CCDS6351.1	c.675G>A	p.W225X
TTBK1	tau tubulin kinase 1	ENSG00000146216	PAP47	49	26.5%	chr6	43359938	CCDS34455.1	c.3482G>T	p.G1161V
TBC1D8B	TBC1 domain family; member 8B (with GRAM domain)	ENSG00000133138	PAP47	186	32.3%	chrX	105948566	CCDS14522.1	c.148C>A	p.L50I
TBC1D8B	TBC1 domain family; member 8B (with GRAM domain)	ENSG00000133138	PAP47	112	30.4%	chrX	105983487	CCDS14522.1	c.2204C>A	p.T735N
TEC	tec protein tyrosine kinase	ENSG00000135605	PAP47	171	23.4%	chr4	47864595	CCDS3481.1	c.628G>T	p.E210X
TECTB	tectorin beta	ENSG00000119913	PAP47	104	29.8%	chr10	114043485	CCDS7571.1	c.-1G>T	p.IVS4-1-1SpliceAcceptor
TEK	TEK tyrosine kinase; endothelial	ENSG00000120156	PAP47	219	33.8%	chr9	27099505	ENST00000406359	c.16A>C	p.K6Q
TEKT3	tektin 3	ENSG00000125409	PAP47	58	24.1%	chr17	15152824	CCDS11169.1	c.1138G>T	p.E380X
TNC	tenascin C	ENSG00000041982	PAP47	71	31.0%	chr9	116859390	CCDS6811.1	c.4442C>A	p.T1481N
TNS4	tensin 4	ENSG00000131746	PAP47	139	33.8%	chr17	35898495	CCDS11368.1	c.692T>A	p.I231N
TENC1	tensin like C1 domain containing phosphatase (tensin 2)	ENSG00000111077	PAP47	104	27.9%	chr12	51738130	CCDS8842.1	c.1102C>T	p.L368F
TEX15	testis expressed 15	ENSG00000133863	PAP47	76	32.9%	chr8	30823506	CCDS6080.1	c.2570C>A	p.S857Y
TEX15	testis expressed 15	ENSG00000133863	PAP47	247	27.5%	chr8	30824899	CCDS6080.1	c.1177G>T	p.E393X
TESK2	testis-specific kinase 2	ENSG00000070759	PAP47	583	27.4%	chr1	45586184	CCDS41323.1	c.616G>A	p.D206N
TET1	tet oncogene 1	ENSG00000138336	PAP47	361	21.6%	chr10	70003468	CCDS7281.1	c.1367T>C	p.V456A
TET2	tet oncogene family member 2	ENSG00000168769	PAP47	66	43.9%	chr4	106377858	CCDS3666.1	c.3310T>G	p.F1104V
TSPAN12	tetraspanin 12	ENSG00000106025	PAP47	113	24.8%	chr7	120233893	CCDS5777.1	c.558C>A	p.F186L
TTC13	tetratricopeptide repeat domain 13	ENSG00000143643	PAP47	130	36.9%	chr1	229127949	CCDS1588.1	c.1525C>T	p.R509C
TTC29	tetratricopeptide repeat domain 29	ENSG00000137473	PAP47	64	31.3%	chr4	148044323	NM_031956	c.409G>A	p.E137K
TTC4P1	tetratricopeptide repeat domain 4 pseudogene 1	ENSG00000221971	PAP47	103	37.9%	chr1	54966608	CCDS596.1	c.596G>A	p.R199Q
TAB2	TGF-beta activated kinase 1/MAP3K7 binding protein 2	ENSG00000055208	PAP47	62	22.6%	chr6	149760435	CCDS5214.1	c.1606C>T	p.L536F
THAP9	THAP domain containing 9	ENSG00000168152	PAP47	230	29.1%	chr4	84058527	CCDS3598.1	c.2138G>A	p.R713Q
THEG	Theg homolog (mouse)	ENSG00000105549	PAP47	207	12.6%	chr19	313317	CCDS12025.1	c.1023G>T	p.K341N
TXNDC16	thioredoxin domain containing 16	ENSG00000087301	PAP47	65	35.4%	chr14	52073191	CCDS32083.1	c.388C>A	p.L130I
THOC2	THO complex 2	ENSG00000125676	PAP47	49	20.4%	chrX	122575035	CCDS43988.1	c.4573G>T	p.E1525X
THOC2	THO complex 2	ENSG00000125676	PAP47	61	32.8%	chrX	122593381	CCDS43988.1	c.2320C>A	p.H774N
THSD7B	thrombospondin; type I; domain containing 7B	ENSG00000144229	PAP47	241	35.7%	chr2	137531251	ENST00000272643	c.931G>T	p.G311X
TRIP11	thyroid hormone receptor interactor 11	ENSG00000100815	PAP47	99	27.3%	chr14	91539761	CCDS9899.1	c.4312G>A	p.E1438K
TRIP12	thyroid hormone receptor interactor 12	ENSG00000153827	PAP47	68	22.1%	chr2	230376534	CCDS33391.1	c.2770G>T	p.E924X
TIGD7	tigger transposable element derived 7	ENSG00000140993	PAP47	112	34.8%	chr16	3289565	CCDS10500.1	c.1051C>A	p.L351I
TIPRL	TIP41; TOR signaling pathway regulator-like (S. cerevisiae)	ENSG00000143155	PAP47	73	20.5%	chr1	166420699	CCDS1270.1	c.343G>T	p.D115Y
TNIP3	TNFAIP3 interacting protein 3	ENSG00000050730	PAP47	56	35.7%	chr4	122301771	CCDS3718.1	c.117G>T	p.K39N
TLR7	toll-like receptor 7	ENSG00000196664	PAP47	258	26.4%	chrX	12815726	CCDS14151.1	c.2178G>T	p.K726N
TLL1	tolloid-like 1	ENSG00000038295	PAP47	120	26.7%	chr4	167148580	CCDS3811.1	c.847G>T	p.E283X

TOP2A	topoisomerase (DNA) II alpha 170kDa	ENSG00000131747	PAP47	50	38.0%	chr17	35821394	ENST00000357601	c.993G>T	p.M331I
TOR2A	torsin family 2; member A	ENSG00000160404	PAP47	101	26.7%	chr9	129535597	CCDS43879.1	c.481G>A	p.D161N
TRAK2	trafficking protein; kinesin binding 2	ENSG00000115993	PAP47	189	28.0%	chr2	201960740	CCDS2347.1	c.1627G>A	p.D543N
TFAP2B	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)	ENSG00000008196	PAP47	53	24.5%	chr6	50911862	CCDS4934.2	c.731C>T	p.S244L
TFAP2E	transcription factor AP-2 epsilon (activating enhancer binding protein 2 epsilon)	ENSG00000116819	PAP47	175	21.7%	chr1	35813176	CCDS393.1	c.526G>A	p.V176M
TTF2	transcription termination factor; RNA polymerase II	ENSG00000116830	PAP47	112	20.5%	chr1	117445601	CCDS892.1	c.3421C>A	p.L1141I
TLE1	transducin-like enhancer of split 1 (E(sp1) homolog; Drosophila)	ENSG00000196781	PAP47	49	24.5%	chr9	83388947	CCDS6661.1	c.2299G>T	p.E767X
TLE4	transducin-like enhancer of split 4 (E(sp1) homolog; Drosophila)	ENSG00000106829	PAP47	281	23.5%	chr9	81511623	CCDS43837.1	c.925G>T	p.E309X
TF	transferrin	ENSG00000091513	PAP47	196	25.5%	chr3	134950029	CCDS3080.1	c.127G>A	p.D43N
TRRAP	transformation/transcription domain-associated protein	ENSG00000196367	PAP47	83	13.3%	chr7	98367102	CCDS5659.1	c.3730G>A	p.D1244N
TRPM2	transient receptor potential cation channel; subfamily M; member 2	ENSG00000142185	PAP47	343	28.6%	chr21	44646056	CCDS13710.1	c.2386G>A	p.V796M
TRPM5	transient receptor potential cation channel; subfamily M; member 5	ENSG00000070985	PAP47	146	21.2%	chr11	2385623	CCDS31340.1	c.2878G>A	p.V960I
TRPM8	transient receptor potential cation channel; subfamily M; member 8	ENSG00000144481	PAP47	136	30.1%	chr2	234519385	CCDS33407.1	c.846G>T	p.E282D
TRPM8	transient receptor potential cation channel; subfamily M; member 8	ENSG00000144481	PAP47	173	26.0%	chr2	234543791	CCDS33407.1	c.2337C>A	p.F779L
TRPM8	transient receptor potential cation channel; subfamily M; member 8	ENSG00000144481	PAP47	168	31.5%	chr2	234556551	CCDS33407.1	c.2705C>T	p.S902L
TRPV5	transient receptor potential cation channel; subfamily V; member 5	ENSG00000127412	PAP47	222	28.4%	chr7	142337659	CCDS5875.1	c.133C>A	p.L45I
TRPV5	transient receptor potential cation channel; subfamily V; member 5	ENSG00000127412	PAP47	152	36.2%	chr7	142340556	CCDS5875.1	c.123G>T	p.Q41H
TRPV6	transient receptor potential cation channel; subfamily V; member 6	ENSG00000165125	PAP47	370	31.6%	chr7	142279703	CCDS5874.1	c.2057G>A	p.R686Q
TRPV6	transient receptor potential cation channel; subfamily V; member 6	ENSG00000165125	PAP47	313	24.9%	chr7	142279776	CCDS5874.1	c.1984G>T	p.D662Y
TSNAX	translin-associated factor X	ENSG00000116918	PAP47	83	24.1%	chr1	229731655	CCDS1596.1	c.48C>A	p.D16E
TSNAXIP1	translin-associated factor X interacting protein 1	ENSG00000102904	PAP47	56	32.1%	chr16	66416165	CCDS10846.2	c.498G>T	p.K166N
TM9SF2	transmembrane 9 superfamily member 2	ENSG00000125304	PAP47	71	43.7%	chr13	99009780	CCDS9493.1	c.1915C>A	p.L639I
TMCO2	transmembrane and coiled-coil domains 2	ENSG00000188800	PAP47	169	27.8%	chr1	40489685	CCDS30684.1	c.381G>T	p.E127D
TMCO3	transmembrane and coiled-coil domains 3	ENSG00000150403	PAP47	64	34.4%	chr13	113236377	CCDS9537.1	c.1360C>A	p.L454I
TMTC3	transmembrane and tetratricopeptide repeat containing 3	ENSG00000139324	PAP47	62	32.3%	chr12	87078114	CCDS9032.1	c.601T>C	p.Y201H
TMC1	transmembrane channel-like 1	ENSG00000165091	PAP47	76	21.1%	chr9	74620891	CCDS6643.1	c.1708G>A	p.E570K
TMC4	transmembrane channel-like 4	ENSG00000167608	PAP47	224	25.9%	chr19	59355913	CCDS12882.1	c.2063A>C	p.N688T
TMC5	transmembrane channel-like 5	ENSG00000103534	PAP47	128	34.4%	chr16	19379076	CCDS42126.1	c.1067C>A	p.S356Y
TMEM106C	transmembrane protein 106C	ENSG00000134291	PAP47	345	27.2%	chr12	46646010	CCDS8758.1	c.374T>G	p.F125C
TMEM117	transmembrane protein 117	ENSG00000139173	PAP47	85	22.4%	chr12	42823627	CCDS8745.1	c.443G>A	p.R148Q
TMEM132D	transmembrane protein 132D	ENSG00000151952	PAP47	129	27.9%	chr12	128124822	CCDS9266.1	c.2851C>A	p.P951T
TMEM163	transmembrane protein 163	ENSG00000152128	PAP47	176	26.1%	chr2	135187324	CCDS2172.1	c.238G>A	p.E80K
TMEM168	transmembrane protein 168	ENSG00000146802	PAP47	117	26.5%	chr7	112194978	CCDS5757.1	c.1604C>T	p.S535F
TMEM176B	transmembrane protein 176B	ENSG00000106565	PAP47	386	22.5%	chr7	150121167	CCDS5908.1	c.542G>T	p.R181L
TMEM182	transmembrane protein 182	ENSG00000170417	PAP47	115	21.7%	chr2	102797711	CCDS2064.1	c.542G>A	p.R181Q
TMEM187	transmembrane protein 187	ENSG00000177854	PAP47	211	28.4%	chrX	152900840	CCDS14739.1	c.133G>A	p.V45M
TMEM212	transmembrane protein 212	ENSG00000186329	PAP47	455	35.2%	chr3	173054118	NM_001164436	c.327T>G	p.F109L
TMEM217	transmembrane protein 217	ENSG00000172738	PAP47	117	30.8%	chr6	37294231	CCDS4831.1	c.554C>T	p.S185L
TMEM43	transmembrane protein 43	ENSG00000170876	PAP47	78	33.3%	chr3	14155732	CCDS2618.1	c.934C>T	p.R312W
TMEM45B	transmembrane protein 45B	ENSG00000151715	PAP47	228	27.6%	chr11	129229791	CCDS8482.1	c.255G>T	p.M85I
TMEM70	transmembrane protein 70	ENSG00000175606	PAP47	165	29.1%	chr8	75056132	CCDS6215.1	c.505C>T	p.R169X
TMEM82	transmembrane protein 82	ENSG00000162460	PAP47	208	28.4%	chr1	15946096	CCDS30608.1	c.905T>C	p.L302P

TCHH	trichohyalin	ENSG00000159450	PAP47	145	26.9%	chr1	150347264	CCDS41396.1	c.5053C>T	p.R1685C
TREM1	triggering receptor expressed on myeloid cells 1	ENSG00000124731	PAP47	237	27.0%	chr6	41358462	CCDS4854.1	c.55C>T	p.R19X
TRIOBP	TRIO and F-actin binding protein	ENSG00000100106	PAP47	545	31.4%	chr22	36451478	CCDS43015.1	c.2969G>A	p.R990Q
TRIM3	tripartite motif-containing 3	ENSG00000110171	PAP47	185	28.6%	chr11	6428228	ENST00000379914	c.1584T>G	p.I528M
TRIM38	tripartite motif-containing 38	ENSG00000112343	PAP47	208	25.0%	chr6	26091666	CCDS4568.1	c.1170G>T	p.K390N
TRIM59	tripartite motif-containing 59	ENSG00000213186	PAP47	122	13.1%	chr3	161639272	CCDS3190.1	c.394G>A	p.D132N
TRIM6	tripartite motif-containing 6	ENSG00000121236	PAP47	119	31.1%	chr11	5583342	CCDS31388.1	c.803G>A	p.R268Q
WARS	tryptophanyl-tRNA synthetase	ENSG00000140105	PAP47	114	22.8%	chr14	99890640	CCDS9960.1	c.439C>A	p.L147I
TUB	tubby homolog (mouse)	ENSG00000166402	PAP47	59	25.4%	chr11	8017142	CCDS7786.1	c.146G>A	p.R49Q
TULP1	tubby like protein 1	ENSG00000112041	PAP47	190	30.0%	chr6	35581578	CCDS4807.1	c.1030C>T	p.R344W
TTLL11	tubulin tyrosine ligase-like family; member 11	ENSG00000175764	PAP47	388	32.2%	chr9	123791228	CCDS6834.2	c.1606C>T	p.R536C
TDRD1	tudor domain containing 1	ENSG00000095627	PAP47	103	32.0%	chr10	115975815	CCDS7588.1	c.3025C>T	p.R1009C
TFIP11	tuftelin interacting protein 11	ENSG00000100109	PAP47	107	27.1%	chr22	25232803	CCDS13838.1	c.301G>A	p.E101K
TNFSF13	tumor necrosis factor (ligand) superfamily; member 13	ENSG00000161955	PAP47	364	31.6%	chr17	7403888	CCDS11108.1	c.579G>T	p.K193N
TNFRSF12A	tumor necrosis factor receptor superfamily; member 12A	ENSG00000006327	PAP47	203	31.5%	chr16	3011781	CCDS10489.1	c.343G>T	p.E115X
TNFRSF19	tumor necrosis factor receptor superfamily; member 19	ENSG00000127863	PAP47	117	24.8%	chr13	23141175	CCDS9302.1	c.1184G>T	p.R395I
TNFRSF21	tumor necrosis factor receptor superfamily; member 21	ENSG00000146072	PAP47	214	28.0%	chr6	47308536	CCDS4921.1	c.1892T>G	p.I631S
TP53BP2	tumor protein p53 binding protein; 2	ENSG00000143514	PAP47	195	28.2%	chr1	222050714	CCDS1538.1	c.1763G>A	p.R588Q
TP63	tumor protein p63	ENSG00000073282	PAP47	307	27.0%	chr3	191094772	CCDS3293.1	c.1830C>A	p.F610L
TUSC3	tumor suppressor candidate 3	ENSG00000104723	PAP47	77	23.4%	chr8	15645466	CCDS5994.1	c.911C>T	p.S304L
TTYH2	tweety homolog 2 (Drosophila)	ENSG00000141540	PAP47	502	17.1%	chr17	69760036	CCDS32717.1	c.1185C>A	p.F395L
TPCN1	two pore segment channel 1	ENSG00000186815	PAP47	131	25.2%	chr12	112199503	CCDS31908.1	c.1135C>T	p.R379C
TDP2	tyrosyl-DNA phosphodiesterase 2	ENSG00000111802	PAP47	114	32.5%	chr6	24759135	CCDS4557.1	c.949C>T	p.R317X
YARS2	tyrosyl-tRNA synthetase 2; mitochondrial	ENSG00000139131	PAP47	41	34.1%	chr12	32798151	CCDS31770.1	c.915C>A	p.F305L
UBQLN2	ubiquilin 2	ENSG00000188021	PAP47	163	33.7%	chrX	56607618	CCDS14374.1	c.587C>T	p.S196L
UBR3	ubiquitin protein ligase E3 component n-recognin 3 (putative)	ENSG00000144357	PAP47	126	22.2%	chr2	170645337	CCDS2238.1	c.2005C>A	p.L669I
UBR4	ubiquitin protein ligase E3 component n-recognin 4	ENSG00000127481	PAP47	89	25.8%	chr1	19352406	CCDS189.1	c.6808C>T	p.R2270X
UBR5	ubiquitin protein ligase E3 component n-recognin 5	ENSG00000104517	PAP47	122	25.4%	chr8	103376439	CCDS34933.1	c.4135C>T	p.R1379W
USP22	ubiquitin specific peptidase 22	ENSG00000124422	PAP47	198	28.3%	chr17	20861908	CCDS42285.1	c.629G>A	p.R210H
USP26	ubiquitin specific peptidase 26	ENSG00000134588	PAP47	158	27.2%	chrX	131988186	CCDS14635.1	c.1729C>T	p.R577X
USP29	ubiquitin specific peptidase 29	ENSG00000131864	PAP47	94	28.7%	chr19	62332006	CCDS33124.1	c.151T>G	p.F51V
USP51	ubiquitin specific peptidase 51	ENSG00000185295	PAP47	69	21.7%	chrX	55531231	NM_201286	c.867G>T	p.K289N
USP51	ubiquitin specific peptidase 51	ENSG00000185295	PAP47	263	27.4%	chrX	55532085	NM_201286	c.13C>T	p.R5X
USP7	ubiquitin specific peptidase 7 (herpes virus-associated)	ENSG00000187555	PAP47	43	44.2%	chr16	8903753	CCDS32385.1	c.1927G>A	p.D643N
USP9X	ubiquitin specific peptidase 9; X-linked	ENSG00000124486	PAP47	116	27.6%	chrX	40928816	CCDS43930.1	c.3502C>T	p.R1168X
UBA3	ubiquitin-like modifier activating enzyme 3	ENSG00000144744	PAP47	220	34.1%	chr3	69209696	CCDS2909.1	c.126G>T	p.K42N
UBA5	ubiquitin-like modifier activating enzyme 5	ENSG00000081307	PAP47	104	26.9%	chr3	133870389	CCDS3076.1	c.335A>C	p.N112T
UGDH	UDP-glucose 6-dehydrogenase	ENSG00000109814	PAP47	165	23.0%	chr4	39199388	CCDS3455.1	c.140C>A	p.S47Y
UGP2	UDP-glucose pyrophosphorylase 2	ENSG00000169764	PAP47	96	26.0%	chr2	63938494	CCDS1875.1	c.175C>T	p.R59W
UEVLD	UEV and lactate/malate dehyrogenase domains	ENSG00000151116	PAP47	109	22.9%	chr11	18543104	CCDS41624.1	c.523G>A	p.A175T
UNC5CL	unc-5 homolog C (C. elegans)-like	ENSG00000124602	PAP47	298	31.5%	chr6	41110460	CCDS4847.1	c.332G>A	p.R111H
UBTF	upstream binding transcription factor; RNA polymerase I	ENSG00000108312	PAP47	168	13.1%	chr17	39640594	CCDS11480.1	c.2024C>T	p.S675L
URB1	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	ENSG00000142207	PAP47	182	25.8%	chr21	32614757	NM_014825	c.5549G>A	p.R1850Q
UCN	urocortin	ENSG00000163794	PAP47	76	17.1%	chr2	27383910	CCDS1747.1	c.358G>A	p.D120N
UMODL1	uromodulin-like 1	ENSG00000177398	PAP47	45	31.1%	chr21	42412395	CCDS42935.1	c.2965T>G	p.L989V
USH2A	Usher syndrome 2A (autosomal recessive; mild)	ENSG00000042781	PAP47	160	33.1%	chr1	213915533	CCDS31025.1	c.12343C>T	p.R4115C
USH2A	Usher syndrome 2A (autosomal recessive; mild)	ENSG00000042781	PAP47	57	26.3%	chr1	214532295	CCDS31025.1	c.1685G>A	p.R562H
VPS13C	vacuolar protein sorting 13 homolog C (S. cerevisiae)	ENSG00000129003	PAP47	48	31.3%	chr15	60103323	CCDS32257.1	c.462A>C	p.K154N
VPS72	vacuolar protein sorting 72 homolog (S. cerevisiae)	ENSG00000163159	PAP47	133	17.3%	chr1	149415974	CCDS989.1	c.865C>T	p.R289C
VCPIP1	valosin containing protein (p97)/p47 complex interacting protein 1	ENSG00000175073	PAP47	266	24.4%	chr8	67709712	CCDS6192.1	c.3247C>T	p.R1083X
VCP	valosin-containing protein	ENSG00000165280	PAP47	122	27.0%	chr9	35049495	CCDS6573.1	c.1999G>A	p.A667T
VASH2	vasohibin 2	ENSG00000143494	PAP47	76	27.6%	chr1	211214030	CCDS1511.1	c.858G>T	p.E286D
VEPH1	ventricular zone expressed PH domain homolog 1 (zebrafish)	ENSG00000197415	PAP47	251	27.9%	chr3	158461792	CCDS3179.1	c.2327C>T	p.A776V

VILL	villin-like	ENSG00000136059	PAP47	72	13.9%	chr3	38014119	CCDS2670.2	c.703C>T	p.R235C
MOS	v-mos Moloney murine sarcoma viral oncogene homolog	ENSG00000172680	PAP47	450	36.0%	chr8	57188722	CCDS6164.1	c.374C>T	p.T125M
MYCL1	v-myc myelocytomatosis viral oncogene homolog 1; lung carcinoma derived (avian)	ENSG00000116990	PAP47	122	36.9%	chr1	40139659	CCDS30682.1	c.35A>C	p.D12A
VN1R1	vomeronasal 1 receptor 1	ENSG00000178201	PAP47	106	35.8%	chr19	62659494	CCDS12951.1	c.173T>C	p.V58A
REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	ENSG00000162924	PAP47	181	30.9%	chr2	61002674	CCDS1864.1	c.1360G>T	p.D454Y
WASF3	WAS protein family; member 3	ENSG00000132970	PAP47	109	22.0%	chr13	26137234	CCDS9318.1	c.203C>A	p.S68Y
WDR17	WD repeat domain 17	ENSG00000150627	PAP47	90	26.7%	chr4	177319108	CCDS3825.1	c.2783C>T	p.A928V
WDR43	WD repeat domain 43	ENSG00000163811	PAP47	96	20.8%	chr2	29017890	NM_015131	c.1680A>C	p.K560N
WDR64	WD repeat domain 64	ENSG00000162843	PAP47	241	22.8%	chr1	240017820	CCDS1619.1	c.1381C>T	p.R461X
WDR66	WD repeat domain 66	ENSG00000158023	PAP47	78	29.5%	chr12	120843898	CCDS41853.1	c.304G>T	p.E102X
WDR66	WD repeat domain 66	ENSG00000158023	PAP47	38	28.9%	chr12	120926009	CCDS41853.1	c.3406C>A	p.L1136I
WDR74	WD repeat domain 74	ENSG00000133316	PAP47	116	22.4%	chr11	62363226	NM_018093	c.229T>G	p.F77V
WDR93	WD repeat domain 93	ENSG00000140527	PAP47	73	35.6%	chr15	88066294	CCDS32326.1	c.800C>A	p.A267E
WIPI2	WD repeat domain; phosphoinositide interacting 2	ENSG00000157954	PAP47	108	29.6%	chr7	5224097	CCDS5339.1	c.595C>T	p.P199S
WBSCR28	Williams-Beuren syndrome chromosome region 28	ENSG00000175877	PAP47	352	32.1%	chr7	72918134	CCDS43597.1	c.793G>T	p.E265X
WNT2B	wingless-type MMTV integration site family; member 2B	ENSG00000134245	PAP47	106	27.4%	chr1	112853573	CCDS847.1	c.166G>A	p.V56I
WNT2B	wingless-type MMTV integration site family; member 2B	ENSG00000134245	PAP47	100	21.0%	chr1	112861384	CCDS847.1	c.800G>A	p.R267Q
WNK3	WNK lysine deficient protein kinase 3	ENSG00000196632	PAP47	232	26.7%	chrX	54294718	CCDS14357.1	c.2495C>A	p.S832Y
WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	ENSG00000147548	PAP47	104	36.5%	chr8	38308159	CCDS43729.1	c.1012G>T	p.E338X
XIRP1	xin actin-binding repeat containing 1	ENSG00000168334	PAP47	108	22.2%	chr3	39202067	CCDS2683.1	c.3874C>A	p.L1292I
XIRP2	xin actin-binding repeat containing 2	ENSG00000163092	PAP47	103	31.1%	chr2	167809356	CCDS42769.1	c.3208T>C	p.F1070L
XIRP2	xin actin-binding repeat containing 2	ENSG00000163092	PAP47	126	31.0%	chr2	167814926	CCDS42769.1	c.8778C>A	p.F2926L
XIRP2	xin actin-binding repeat containing 2	ENSG00000163092	PAP47	67	28.4%	chr2	167823760	CCDS42768.1	c.2458C>A	p.L820I
XKRX	XK; Kell blood group complex subunit-related; X-linked	ENSG00000182489	PAP47	98	14.3%	chrX	100069833	CCDS14476.1	c.156C>A	p.F52L
XPNPEP2	X-prolyl aminopeptidase (aminopeptidase P) 2; membrane-bound	ENSG00000122121	PAP47	89	31.5%	chrX	128729986	CCDS14613.1	c.1869G>T	p.E623D
XRRA1	X-ray radiation resistance associated 1	ENSG00000166435	PAP47	120	36.7%	chr11	74309983	NM_182969	c.556C>A	p.L186M
YEATS2	YEATS domain containing 2	ENSG00000163872	PAP47	137	32.1%	chr3	184922506	CCDS43175.1	c.425C>A	p.S142Y
YIPF4	Yip1 domain family; member 4	ENSG00000119820	PAP47	48	22.9%	chr2	32384180	CCDS1781.1	c.716C>T	p.S239L
YSK4	YSK4 Sps1/Ste20-related kinase homolog (S. cerevisiae)	ENSG00000176601	PAP47	155	35.5%	chr2	135460518	CCDS2176.2	c.2394G>T	p.Q798H
YSK4	YSK4 Sps1/Ste20-related kinase homolog (S. cerevisiae)	ENSG00000176601	PAP47	233	29.2%	chr2	135460690	CCDS2176.2	c.2222C>A	p.S741Y
ZBP1	Z-DNA binding protein 1	ENSG00000124256	PAP47	376	31.4%	chr20	55618727	CCDS13461.1	c.977C>T	p.S326L
ZIC3	Zic family member 3 (odd-paired homolog; Drosophila)	ENSG00000156925	PAP47	148	26.4%	chrX	136477246	CCDS14663.1	c.730C>T	p.R244W
ZBTB16	zinc finger and BTB domain containing 16	ENSG00000109906	PAP47	234	35.5%	chr11	113439809	CCDS8367.1	c.577C>A	p.L193I
ZBTB2	zinc finger and BTB domain containing 2	ENSG00000181472	PAP47	259	30.9%	chr6	151728456	CCDS5231.1	c.1438G>A	p.E480K
ZBTB38	zinc finger and BTB domain containing 38	ENSG00000177311	PAP47	234	31.6%	chr3	142644744	CCDS43157.1	c.824C>T	p.S275L
ZBTB48	zinc finger and BTB domain containing 48	ENSG00000204859	PAP47	120	28.3%	chr1	6569915	CCDS84.1	c.1201C>A	p.H401N
ZBTB48	zinc finger and BTB domain containing 48	ENSG00000204859	PAP47	301	24.9%	chr1	6570835	CCDS84.1	c.1508G>A	p.R503Q
ZSCAN20	zinc finger and SCAN domain containing 20	ENSG00000121903	PAP47	180	32.2%	chr1	33717531	CCDS41300.1	c.55G>T	p.E19X
ZSCAN23	zinc finger and SCAN domain containing 23	ENSG00000187987	PAP47	292	30.5%	chr6	28511910	NM_001012455	c.113G>T	p.R38I
ZC3H13	zinc finger CCCH-type containing 13	ENSG00000123200	PAP47	707	29.3%	chr13	45447714	CCDS9400.1	c.2173C>T	p.R725C
ZC3H6	zinc finger CCCH-type containing 6	ENSG00000188177	PAP47	287	26.8%	chr2	112805869	NM_198581	c.2903A>T	p.N968I
ZEB1	zinc finger E-box binding homeobox 1	ENSG00000148516	PAP47	164	27.4%	chr10	31850180	CCDS7169.1	c.1911T>G	p.I637M
ZEB1	zinc finger E-box binding homeobox 1	ENSG00000148516	PAP47	69	27.5%	chr10	31852979	CCDS7169.1	c.2714C>A	p.A905D
ZFHX3	zinc finger homeobox 3	ENSG00000140836	PAP47	157	19.7%	chr16	71385081	CCDS10908.1	c.9001G>T	p.E3001X
ZFHX3	zinc finger homeobox 3	ENSG00000140836	PAP47	75	25.3%	chr16	71481223	CCDS10908.1	c.3356G>A	p.R1119Q
ZNF107	zinc finger protein 107	ENSG00000196247	PAP47	115	30.4%	chr7	63804281	CCDS5527.1	c.164C>T	p.T55M
ZNF136	zinc finger protein 136	ENSG00000196646	PAP47	54	33.3%	chr19	12158875	CCDS32916.1	c.682G>A	p.E228K
ZNF154	zinc finger protein 154	ENSG00000179909	PAP47	233	27.5%	chr19	62905087	CCDS42639.1	c.1042C>T	p.R348W
ZNF182	zinc finger protein 182	ENSG00000147118	PAP47	138	23.2%	chrX	47721265	CCDS35236.1	c.1165C>A	p.L389I
ZNF184	zinc finger protein 184	ENSG00000096654	PAP47	180	29.4%	chr6	27543636	CCDS4624.1	c.50A>C	p.N17T
ZNF197	zinc finger protein 197	ENSG00000186448	PAP47	152	23.0%	chr3	44659476	CCDS2717.1	c.1850G>A	p.S617N
ZFP2	zinc finger protein 2 homolog (mouse)	ENSG00000198939	PAP47	112	25.0%	chr5	178291228	CCDS4440.1	c.308A>C	p.E103A

ZNF211	zinc finger protein 211	ENSG00000121417	PAP47	142	33.1%	chr19	62844314	CCDS12956.1	c.687C>A	p.N229K
ZNF250	zinc finger protein 250	ENSG00000196150	PAP47	140	32.1%	chr8	146078647	NM_021061	c.740G>T	p.R247I
ZNF267	zinc finger protein 267	ENSG00000185947	PAP47	65	35.4%	chr16	31803421	CCDS32440.1	c.105A>C	p.E35D
ZNF280C	zinc finger protein 280C	ENSG00000056277	PAP47	36	33.3%	chrX	129177452	CCDS14622.1	c.1832A>G	p.N611S
ZNF281	zinc finger protein 281	ENSG00000162702	PAP47	150	30.0%	chr1	198644265	CCDS1402.1	c.1192A>C	p.N398H
ZNF3	zinc finger protein 3	ENSG00000166526	PAP47	348	20.7%	chr7	99507309	CCDS43619.1	c.734A>G	p.Q245R
ZNF304	zinc finger protein 304	ENSG00000131845	PAP47	228	26.8%	chr19	62560701	CCDS12950.1	c.1652G>T	p.R551I
ZNF354C	zinc finger protein 354C	ENSG00000177932	PAP47	203	30.5%	chr5	178438998	CCDS4443.1	c.959G>T	p.R320I
ZNF397OS	zinc finger protein 397 opposite strand	ENSG00000186814	PAP47	200	22.5%	chr18	31087851	CCDS42427.1	c.1046G>T	p.R349I
ZNF407	zinc finger protein 407	ENSG00000215421	PAP47	94	33.0%	chr18	70475622	NM_017757	c.3659C>T	p.S1220L
ZNF416	zinc finger protein 416	ENSG00000083817	PAP47	182	28.0%	chr19	62775963	CCDS12954.1	c.1121G>T	p.R374I
ZNF420	zinc finger protein 420	ENSG00000197050	PAP47	100	23.0%	chr19	42310599	CCDS12498.1	c.866C>T	p.T289I
ZNF420	zinc finger protein 420	ENSG00000197050	PAP47	55	34.5%	chr19	42311385	CCDS12498.1	c.1652G>T	p.R551I
ZNF442	zinc finger protein 442	ENSG00000198342	PAP47	59	25.4%	chr19	12322221	CCDS12271.1	c.1178G>A	p.R393Q
ZNF442	zinc finger protein 442	ENSG00000198342	PAP47	107	30.8%	chr19	12322713	CCDS12271.1	c.686G>T	p.R229I
ZNF445	zinc finger protein 445	ENSG00000185219	PAP47	182	11.0%	chr3	44464878	CCDS2713.1	c.1289A>G	p.Y430C
ZNF449	zinc finger protein 449	ENSG00000173275	PAP47	293	29.4%	chrX	134309198	ENST00000370761	c.489C>A	p.F163L
ZNF449	zinc finger protein 449	ENSG00000173275	PAP47	106	34.9%	chrX	134321831	CCDS14649.1	c.721A>C	p.K241Q
ZNF451	zinc finger protein 451	ENSG00000112200	PAP47	137	32.8%	chr6	57121102	CCDS43477.1	c.2260C>T	p.R754C
ZNF471	zinc finger protein 471	ENSG00000196263	PAP47	118	14.4%	chr19	61728616	CCDS12945.1	c.1368G>T	p.E456D
ZNF484	zinc finger protein 484	ENSG00000127081	PAP47	114	29.8%	chr9	94650243	CCDS35066.1	c.647C>A	p.S216Y
ZNF500	zinc finger protein 500	ENSG00000103199	PAP47	188	25.5%	chr16	4755918	CCDS32383.1	c.63G>T	p.E21D
ZNF521	zinc finger protein 521	ENSG00000198795	PAP47	93	23.7%	chr18	21060430	CCDS32806.1	c.1450G>A	p.E484K
ZNF527	zinc finger protein 527	ENSG00000189164	PAP47	94	21.3%	chr19	42571348	CCDS42559.1	c.557C>T	p.T186I
ZNF528	zinc finger protein 528	ENSG00000167555	PAP47	66	39.4%	chr19	57633017	ENST00000332323	c.528A>C	p.R176S
ZNF536	zinc finger protein 536	ENSG00000198597	PAP47	170	24.7%	chr19	35626679	CCDS32984.1	c.370G>A	p.A124T
ZNF536	zinc finger protein 536	ENSG00000198597	PAP47	151	20.5%	chr19	35627515	CCDS32984.1	c.1206G>T	p.K402N
ZNF546	zinc finger protein 546	ENSG00000187187	PAP47	105	21.0%	chr19	45212903	CCDS12548.1	c.1886G>T	p.R629I
ZNF559	zinc finger protein 559	ENSG00000188321	PAP47	108	28.7%	chr19	9314040	CCDS12211.1	c.913G>T	p.E305X
ZNF564	zinc finger protein 564	ENSG00000196826	PAP47	63	38.1%	chr19	12436849	CCDS42504.1	c.887G>A	p.R296Q
ZNF569	zinc finger protein 569	ENSG00000196437	PAP47	92	21.7%	chr19	42595873	CCDS12503.1	c.1527C>A	p.F509L
ZNF570	zinc finger protein 570	ENSG00000171827	PAP47	182	36.3%	chr19	42667472	CCDS12504.1	c.1108C>T	p.R370C
ZNF585B	zinc finger protein 585B	ENSG00000197800	PAP47	104	14.4%	chr19	42369226	CCDS12500.1	c.1053G>T	p.E351D
ZNF597	zinc finger protein 597	ENSG00000167981	PAP47	180	23.9%	chr16	3426641	CCDS10505.1	c.1059C>A	p.F353L
ZNF597	zinc finger protein 597	ENSG00000167981	PAP47	253	24.1%	chr16	3426744	CCDS10505.1	c.956A>G	p.D319G
ZNF609	zinc finger protein 609	ENSG00000180357	PAP47	534	29.4%	chr15	62753814	CCDS32270.1	c.1708C>T	p.R570X
ZNF649	zinc finger protein 649	ENSG00000198093	PAP47	137	20.4%	chr19	57086272	CCDS12843.1	c.929G>A	p.R310Q
ZNF684	zinc finger protein 684	ENSG00000117010	PAP47	257	24.9%	chr1	40785538	CCDS454.1	c.956G>T	p.R319I
ZNF689	zinc finger protein 689	ENSG00000156853	PAP47	166	12.7%	chr16	30524071	CCDS10686.1	c.518T>C	p.L173P
ZNF699	zinc finger protein 699	ENSG00000196110	PAP47	237	30.0%	chr19	9267748	CCDS42495.1	c.1332G>T	p.E444D
ZNF7	zinc finger protein 7	ENSG00000147789	PAP47	136	24.3%	chr8	146038105	CCDS6435.1	c.809G>T	p.R270I
ZNF7	zinc finger protein 7	ENSG00000147789	PAP47	113	14.2%	chr8	146038357	CCDS6435.1	c.1061G>T	p.R354I
ZNF700	zinc finger protein 700	ENSG00000196757	PAP47	112	25.9%	chr19	11921910	CCDS32915.1	c.2071C>T	p.L691F
ZNF77	zinc finger protein 77	ENSG00000175691	PAP47	211	30.8%	chr19	2885086	CCDS12099.1	c.1039A>C	p.S347R
ZNF782	zinc finger protein 782	ENSG00000196597	PAP47	34	29.4%	chr9	98629201	NM_001001662	c.226C>A	p.L76I
ZNF792	zinc finger protein 792	ENSG00000180884	PAP47	660	30.2%	chr19	40142172	NM_175872	c.427G>T	p.D143Y
ZNF804A	zinc finger protein 804A	ENSG00000170396	PAP47	140	30.7%	chr2	185509017	CCDS2291.1	c.649G>A	p.A217T
ZNF804A	zinc finger protein 804A	ENSG00000170396	PAP47	179	28.5%	chr2	185510803	CCDS2291.1	c.2435G>A	p.R812Q
ZNF846	zinc finger protein 846	ENSG00000196605	PAP47	86	30.2%	chr19	9729260	CCDS42496.1	c.1493G>A	p.R498Q
ZNF859P	zinc finger protein 859 (pseudogene)	ENSG00000215887	PAP47	103	31.1%	chr1	50083478	ENST00000401053	c.479G>T	p.R160I
ZFP90	zinc finger protein 90 homolog (mouse)	ENSG00000184939	PAP47	298	33.9%	chr16	67155207	CCDS42183.1	c.1016G>A	p.R339Q
ZKSCAN1	zinc finger with KRAB and SCAN domains 1	ENSG00000106261	PAP47	100	38.0%	chr7	99459864	CCDS34698.1	c.578G>A	p.R193Q
ZC4H2	zinc finger; C4H2 domain containing	ENSG00000126970	PAP47	89	27.0%	chrX	64112967	CCDS14380.1	c.16G>T	p.E6X
ZCCHC11	zinc finger; CCHC domain containing 11	ENSG00000134744	PAP47	188	29.8%	chr1	52703399	CCDS30715.1	c.3000G>T	p.K1000N

ZCCHC11	zinc finger; CCHC domain containing 11	ENSG00000134744	PAP47	153	28.8%	chr1	52719877	CCDS30715.1	c.1654A>G	p.K552E
ZFYVE26	zinc finger; FYVE domain containing 26	ENSG00000072121	PAP47	126	27.8%	chr14	67342025	CCDS9788.1	c.1081G>T	p.E361X
ZMYM4	zinc finger; MYM-type 4	ENSG00000146463	PAP47	102	23.5%	chr1	35653686	CCDS389.1	c.4093T>G	p.L1365V
ZMYM5	zinc finger; MYM-type 5	ENSG00000132950	PAP47	80	30.0%	chr13	19324082	CCDS31942.1	c.239G>T	p.R80I
ZAN	zonadhesin	ENSG00000146839	PAP47	138	36.2%	chr7	100186330	ENST00000349350	c.1396G>A	p.E466K
ZAN	zonadhesin	ENSG00000146839	PAP47	375	12.8%	chr7	100188092	ENST00000349350	c.2428A>C	p.I810L
ACTN2	actinin; alpha 2	ENSG00000077522	PAP48	46	45.7%	chr1	234947820	CCDS1613.1	c.166G>A	p.G56S
ACVR1B	activin A receptor; type IB	ENSG00000135503	PAP48	94	11.7%	chr12	50666913	CCDS8816.1	c.1181A>G	p.H394R
ACSM5	acyl-CoA synthetase medium-chain family member 5	ENSG00000183549	PAP48	113	15.0%	chr16	20330387	CCDS10585.1	c.80C>T	p.A27V
ADAMTSL1	ADAMTS-like 1	ENSG00000178031	PAP48	170	27.1%	chr9	18767687	NM_001040272	c.3460G>NUL	p.NULL-1FsDel1bp
ADA	adenosine deaminase	ENSG00000196839	PAP48	159	19.5%	chr20	42686350	CCDS13335.1	c.638AAG>NU	p.NULL-1FsDel3bp
ARFGAP2	ADP-ribosylation factor GTPase activating protein 2	ENSG00000149182	PAP48	126	12.7%	chr11	47153429	CCDS7926.1	c.407T>NULL	p.NULL-1FsDel1bp
ALDH3B1	aldehyde dehydrogenase 3 family; member B1	ENSG00000006534	PAP48	124	10.5%	chr11	67542636	ENST00000007633	c.226A>G	p.R76G
ALPK3	alpha-kinase 3	ENSG00000136383	PAP48	116	44.0%	chr15	83201271	CCDS10333.1	c.2904A>NULI	p.NULL-1FsDel1bp
ANGPT2	angiopoietin 2	ENSG00000091879	PAP48	158	24.1%	chr8	6366206	CCDS5958.1	c.932A>NULL	p.NULL-1FsDel1bp
ANKH	ankylosis; progressive homolog (mouse)	ENSG00000154122	PAP48	60	23.3%	chr5	14804249	CCDS3885.1	c.616A>G	p.T206A
MKI67	antigen identified by monoclonal antibody Ki-67	ENSG00000148773	PAP48	465	10.1%	chr10	129795102	CCDS7659.1	c.11836NULL>	p.NULL-1FsIns2bp
APLN	apelin	ENSG00000171388	PAP48	61	26.2%	chrX	128609407	ENST00000307484	c.296G>A	p.G99D
ARAP3	ArfGAP with RhoGAP domain; ankyrin repeat and PH domain 3	ENSG00000120318	PAP48	95	24.2%	chr5	141021863	CCDS4266.1	c.2944C>T	p.R982C
RARS2	arginyl-tRNA synthetase 2; mitochondrial	ENSG00000146282	PAP48	45	22.2%	chr6	88351154	ENST00000392851	c.17T>C	p.L6P
ARMC3	armadillo repeat containing 3	ENSG00000165309	PAP48	165	17.0%	chr10	23310411	CCDS7142.1	c.1053T>NULI	p.NULL-1FsDel1bp
ARSH	arylsulfatase family; member H	ENSG00000205667	PAP48	69	26.1%	chrX	2946600	CCDS35198.1	c.790T>NULL	p.NULL-1FsDel1bp
ARSJ	arylsulfatase family; member J	ENSG00000180801	PAP48	102	23.5%	chr4	115042943	CCDS43264.1	c.3137A>NULI	p.NULL-1FsDel1bp
ASGR1	asialoglycoprotein receptor 1	ENSG00000141505	PAP48	142	24.6%	chr17	7022479	ENST00000380920	c.583C>NULL	p.NULL-1FsDel1bp
ATXN10	ataxin 10	ENSG00000130638	PAP48	116	17.2%	chr22	44513305	CCDS14070.1	c.925G>A	p.V309I
ATG9A	ATG9 autophagy related 9 homolog A (S. cerevisiae)	ENSG00000198925	PAP48	130	36.9%	chr2	219794190	CCDS42820.1	c.2224G>A	p.A742T
ATL3	atlastin GTPase 3	ENSG00000184743	PAP48	67	14.9%	chr11	63176626	CCDS41663.1	c.-1T>NULL	p.IVS3-3-1SpliceAcceptor
ATP7B	ATPase; Cu++ transporting; beta polypeptide	ENSG00000123191	PAP48	95	22.1%	chr13	51483423	CCDS41892.1	c.-1G>A	p.IVS1+1-1SpliceDonor
ABCC10	ATP-binding cassette; sub-family C (CFTR/MRP); member 10	ENSG00000124574	PAP48	578	23.9%	chr6	43521346	CCDS4896.1	c.2978C>T	p.T993M
ABCC5	ATP-binding cassette; sub-family C (CFTR/MRP); member 5	ENSG00000114770	PAP48	72	13.9%	chr3	185147951	CCDS43176.1	c.3455NULL>T	p.NULL-1FsIns1bp
ABCC5	ATP-binding cassette; sub-family C (CFTR/MRP); member 5	ENSG00000114770	PAP48	114	13.2%	chr3	185188341	CCDS43176.1	c.502C>T	p.R168X
BHLHA15	basic helix-loop-helix family; member a15	ENSG00000180535	PAP48	85	32.9%	chr7	97679863	CCDS5655.1	c.306C>NULL	p.NULL-1FsDel1bp
BAX	BCL2-associated X protein	ENSG00000087088	PAP48	69	18.8%	chr19	54150783	CCDS12744.1	c.114G>NULL	p.NULL-1FsDel1bp
B4GALNT4	beta-1;4-N-acetyl-galactosaminyl transferase 4	ENSG00000182272	PAP48	165	23.6%	chr11	365700	CCDS7694.1	c.912G>NULL	p.NULL-1FsDel1bp
BLM	Bloom syndrome; RecQ helicase-like	ENSG00000197299	PAP48	39	28.2%	chr15	89109548	CCDS10363.1	c.2093G>A	p.C698Y
BMP2K	BMP2 inducible kinase	ENSG00000138756	PAP48	75	32.0%	chr4	79966238	CCDS34019.1	c.202G>T	p.V68L

BRSK1	BR serine/threonine kinase 1	ENSG00000160469	PAP48	140	28.6%	chr19	60497508	CCDS12921.1	c.-1G>T	p.IVS6-1-1SpliceAccept or
BRWD3	bromodomain and WD repeat domain containing 3	ENSG00000165288	PAP48	163	25.2%	chrX	79835195	CCDS14447.1	c.3163C>T	p.R1055C
BTBD10	BTB (POZ) domain containing 10	ENSG00000148925	PAP48	203	11.3%	chr11	13367220	CCDS7811.1	c.1162C>T	p.R388C
CPAMD8	C3 and PZP-like; alpha-2-macroglobulin domain containing 8	ENSG00000160111	PAP48	93	12.9%	chr19	16980514	ENST00000388925	c.515T>NULL	p.NULL-1FsDel1bp
CDH10	cadherin 10; type 2 (T2-cadherin)	ENSG00000040731	PAP48	72	38.9%	chr5	24573450	CCDS3892.1	c.616A>NULL	p.NULL-1FsDel1bp
CELSR3	cadherin; EGF LAG seven-pass G-type receptor 3 (flamingo homolog; Drosophila)	ENSG00000008300	PAP48	142	77.5%	chr3	48672842	CCDS2775.1	c.2230G>A	p.V744M
CABYR	calcium binding tyrosine-(Y)-phosphorylation regulated	ENSG00000154040	PAP48	90	17.8%	chr18	19993919	CCDS42420.1	c.1027A>NULI	p.NULL-1FsDel1bp
CACNA1I	calcium channel; voltage-dependent; T type; alpha 1I subunit	ENSG00000100346	PAP48	155	21.3%	chr22	38390791	NM_021096	c.3768NULL>(	p.NULL-1FsIns1bp
CALHM1	calcium homeostasis modulator 1	ENSG00000185933	PAP48	221	12.2%	chr10	105208351	CCDS7550.1	c.148G>A	p.A50T
CAD	carbamoyl-phosphate synthetase 2; aspartate transcarbamylase; and dihydroorotase	ENSG00000084774	PAP48	318	39.9%	chr2	27301429	CCDS1742.1	c.1434C>NULI	p.NULL-1FsDel1bp
CAD	carbamoyl-phosphate synthetase 2; aspartate transcarbamylase; and dihydroorotase	ENSG00000084774	PAP48	92	29.3%	chr2	27319643	CCDS1742.1	c.6554T>C	p.M2185T
CPA1	carboxypeptidase A1 (pancreatic)	ENSG00000091704	PAP48	344	32.8%	chr7	129810817	CCDS5820.1	c.642C>A	p.D214E
CPZ	carboxypeptidase Z	ENSG00000109625	PAP48	50	20.0%	chr4	8667056	CCDS33953.1	c.1434NULL>(	p.NULL-1FsIns1bp
CASKIN1	CASK interacting protein 1	ENSG00000167971	PAP48	126	30.2%	chr16	2177063	CCDS42103.1	c.847G>A	p.A283T
CARD11	caspase recruitment domain family; member 11	ENSG00000198286	PAP48	42	45.2%	chr7	2925539	CCDS5336.2	c.2503T>C	p.Y835H
CDX4	caudal type homeobox 4	ENSG00000131264	PAP48	159	47.8%	chrX	72584029	CCDS14424.1	c.215G>T	p.W72L
CAV3	caveolin 3	ENSG00000182533	PAP48	51	27.5%	chr3	8750569	CCDS2569.1	c.7G>A	p.A3T
CENPI	centromere protein I	ENSG00000102384	PAP48	115	22.6%	chrX	100286783	CCDS14479.1	c.1640C>T	p.A547V
CEP135	centrosomal protein 135kDa	ENSG00000174799	PAP48	56	37.5%	chr4	56572380	CCDS33986.1	c.2551A>G	p.M851V
CHML	choroideremia-like (Rab escort protein 2)	ENSG00000203668	PAP48	139	20.9%	chr1	239864116	CCDS31073.1	c.1576G>A	p.V526M
CHMP4A	chromatin modifying protein 4A	ENSG00000100931	PAP48	293	20.5%	chr14	23752531	CCDS9619.1	c.243NULL>A/	p.NULL-1FsIns2bp
CHD4	chromodomain helicase DNA binding protein 4	ENSG00000111642	PAP48	102	32.4%	chr12	6570953	CCDS8552.1	c.3280G>A	p.E1094K
C1orf183	chromosome 1 open reading frame 183	ENSG00000197852	PAP48	235	32.8%	chr1	112071448	CCDS841.1	c.1395G>NUL	p.NULL-1FsDel1bp
C10orf136	chromosome 10 open reading frame 136	ENSG00000204187	PAP48	157	16.6%	chr10	43660842	ENST00000409928	c.76C>NULL	p.NULL-1FsDel1bp
C11orf46	chromosome 11 open reading frame 46	ENSG00000152219	PAP48	101	20.8%	chr11	30309330	CCDS7869.1	c.259NULL>A	p.NULL-1FsIns1bp
C11orf68	chromosome 11 open reading frame 68	ENSG00000175573	PAP48	168	29.8%	chr11	65441978	CCDS8122.1	c.284G>A	p.G95D
C14orf43	chromosome 14 open reading frame 43	ENSG00000156030	PAP48	265	21.1%	chr14	73275842	CCDS9819.1	c.2071NULL>(	p.NULL-1FsIns1bp
C17orf70	chromosome 17 open reading frame 70	ENSG00000185504	PAP48	65	30.8%	chr17	77124568	CCDS32765.1	c.2309G>NUL	p.NULL-1FsDel1bp
C19orf50	chromosome 19 open reading frame 50	ENSG00000105700	PAP48	79	36.7%	chr19	18533906	CCDS12381.1	c.40C>T	p.R14C
C2orf16	chromosome 2 open reading frame 16	ENSG00000221843	PAP48	319	31.7%	chr2	27657741	CCDS42666.1	c.4798A>G	p.S1600G
C2orf18	chromosome 2 open reading frame 18	ENSG00000213699	PAP48	38	28.9%	chr2	26851971	CCDS1728.1	c.458C>T	p.A153V
C2orf39	chromosome 2 open reading frame 39	ENSG00000157856	PAP48	175	36.0%	chr2	26529777	CCDS1723.1	c.1775C>T	p.T592M
C21orf59	chromosome 21 open reading frame 59	ENSG00000159079	PAP48	83	19.3%	chr21	32897406	CCDS13617.1	c.602C>T	p.T201M
C3orf49	chromosome 3 open reading frame 49	ENSG00000163632	PAP48	109	28.4%	chr3	63784202	ENST00000295896	c.362C>T	p.T121M
C5orf42	chromosome 5 open reading frame 42	ENSG00000197603	PAP48	98	11.2%	chr5	37144304	CCDS34146.1	c.5959C>T	p.Q1987X
C9orf131	chromosome 9 open reading frame 131	ENSG00000174038	PAP48	372	15.9%	chr9	35033650	CCDS6572.2	c.1024C>NULI	p.NULL-1FsDel1bp
C9orf84	chromosome 9 open reading frame 84	ENSG00000165181	PAP48	89	11.2%	chr9	113516626	CCDS6781.3	c.2143A>G	p.K715E

C9orf86	chromosome 9 open reading frame 86	ENSG00000196642	PAP48	81	12.3%	chr9	138855006	NM_017995	c.1328NULL>(	p.NULL-1FsIns1bp
CELA1	chymotrypsin-like elastase family; member 1	ENSG00000139610	PAP48	57	19.3%	chr12	50022665	CCDS8812.1	c.287T>C	p.V96A
CPSF4	cleavage and polyadenylation specific factor 4; 30kDa	ENSG00000160917	PAP48	118	26.3%	chr7	98887962	CCDS5664.1	c.533A>T	p.Q178L
COPG	coatomer protein complex; subunit gamma	ENSG00000181789	PAP48	69	30.4%	chr3	130470136	CCDS33851.1	c.1757T>C	p.M586T
CCDC129	coiled-coil domain containing 129	ENSG00000180347	PAP48	99	18.2%	chr7	31584151	NM_194300	c.748C>T	p.R250X
CCDC148	coiled-coil domain containing 148	ENSG00000153237	PAP48	100	26.0%	chr2	158743662	CCDS33304.1	c.1463G>A	p.R488Q
CCDC40	coiled-coil domain containing 40	ENSG00000141519	PAP48	55	50.9%	chr17	75683735	CCDS42395.1	c.2911G>A	p.V971I
CCDC73	coiled-coil domain containing 73	ENSG00000186714	PAP48	49	20.4%	chr11	32592527	CCDS41630.1	c.3433A>NULI	p.NULL-1FsDel1bp
CCDC85A	coiled-coil domain containing 85A	ENSG00000055813	PAP48	52	25.0%	chr2	56273449	NM_001080433	c.610G>A	p.V204M
COL6A2	collagen; type VI; alpha 2	ENSG00000142173	PAP48	170	29.4%	chr21	46369860	CCDS13728.1	c.1870G>A	p.E624K
COL24A1	collagen; type XXIV; alpha 1	ENSG00000171502	PAP48	135	21.5%	chr1	86080612	CCDS41353.1	c.3515G>T	p.R1172M
CR2	complement component (3d/Epstein Barr virus) receptor 2	ENSG00000117322	PAP48	316	24.7%	chr1	205708667	CCDS31007.1	c.618C>NULL	p.NULL-1FsDel1bp
COBL	cordon-bleu homolog (mouse)	ENSG00000106078	PAP48	332	23.2%	chr7	51063595	CCDS34637.1	c.2692G>T	p.G898C
CBFA2T3	core-binding factor; runt domain; alpha subunit 2; translocated to; 3	ENSG00000129993	PAP48	37	27.0%	chr16	87495496	CCDS10972.1	c.221G>A	p.R74Q
CELF3	CUGBP; Elav-like family member 3	ENSG00000159409	PAP48	164	22.0%	chr1	149948406	CCDS1002.1	c.320C>T	p.T107I
CAND2	cullin-associated and neddylation-dissociated 2 (putative)	ENSG00000144712	PAP48	330	71.8%	chr3	12850440	CCDS43053.1	c.3319T>C	p.S1107P
CWC22	CWC22 spliceosome-associated protein homolog (S. cerevisiae)	ENSG00000163510	PAP48	85	17.6%	chr2	180543538	NM_020943	c.-1T>NULL	p.IVS9-3-1SpliceAcceptor
CNGB1	cyclic nucleotide gated channel beta 1	ENSG00000070729	PAP48	65	43.1%	chr16	56504384	CCDS42169.1	c.2320G>A	p.E774K
CDK7	cyclin-dependent kinase 7	ENSG00000134058	PAP48	185	21.6%	chr5	68604623	CCDS3999.1	c.863A>G	p.Q288R
CDO1	cysteine dioxygenase; type I	ENSG00000129596	PAP48	79	15.2%	chr5	115176857	CCDS4121.1	c.-1T>NULL	p.IVS1-3-1SpliceAcceptor
Ankrd24	DAVID_ankyrin repeat domain 24	NM_133475	PAP48	33	30.3%	chr19	4153920	NM_133475	c.463G>A	p.A155T
ANXA6	DAVID_annexin A6	NM_001155	PAP48	144	33.3%	chr5	150494189	NM_001155	c.538G>C	p.D180H
ATCAY	DAVID_ataxia: cerebellar: Cayman type	NM_033064	PAP48	222	39.6%	chr19	3858798	NM_033064	c.425C>T	p.T142M
CCDC88C	DAVID_coiled-coil domain containing 88C	NM_001080414	PAP48	139	23.0%	chr14	90809256	NM_001080414	c.6581C>NULI	p.NULL-1FsDel1bp
C2	DAVID_complement component 2	ENSG00000204364	PAP48	176	29.5%	chr6	32004490	CCDS4728.1	c.259G>A	p.V87M
CYP4F3	DAVID_cytochrome P450: family 4: subfamily F: polypeptide 3	ENSG00000186529	PAP48	75	36.0%	chr19	15613248	CCDS12332.1	c.23C>T	p.S8L
DNHD1	DAVID_dynein heavy chain domain 1	NM_144666	PAP48	104	33.7%	chr11	6524363	NM_144666	c.5618G>A	p.R1873H
ephb1	DAVID_EPH receptor B1	NM_004441	PAP48	109	33.0%	chr3	136355756	NM_004441	c.1370C>T	p.P457L
FAM38A	DAVID_family with sequence similarity 38: member A	NM_001142864	PAP48	78	19.2%	chr16	87326261	NM_001142864	c.3172TCT>NI	p.NULL-1FsDel3bp
FAT3	DAVID_FAT tumor suppressor homolog 3 (Drosophila)	NM_001008781	PAP48	139	33.8%	chr11	92255812	NM_001008781	c.12542G>A	p.R4181H
FIGNL2	DAVID_fidgetin-like 2	NM_001013690	PAP48	87	24.1%	chr12	50502140	NM_001013690	c.325G>A	p.A109T
GLTSCR1	DAVID_glioma tumor suppressor candidate region gene 1	NM_015711	PAP48	92	44.6%	chr19	52889703	NM_015711	c.2803C>NULI	p.NULL-1FsDel1bp
Grsf1	DAVID_G-rich RNA sequence binding factor 1	NM_002092	PAP48	160	22.5%	chr4	71910802	NM_002092	c.1281NULL>A	p.NULL-1FsIns1bp
Heatr7b2	DAVID_HEAT repeat family member 7B2	NM_173489	PAP48	157	29.3%	chr5	41040285	NM_173489	c.4296A>NULI	p.NULL-1FsDel1bp
LOC388282	DAVID_hypothetical LOC388282	ENSG00000187185	PAP48	71	19.7%	chr16	56408051	ENST00000335616	c.469G>A	p.A157T
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP48	135	25.2%	chr13	102197820	NM_001146197	c.24165A>NUI	p.NULL-1FsDel1bp
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP48	88	20.5%	chr13	102199553	NM_001146197	c.22432A>NUI	p.NULL-1FsDel1bp
kiaa0284	DAVID_KIAA0284	NM_001112726	PAP48	123	10.6%	chr14	104424545	NM_001112726	c.2924C>NULI	p.NULL-1FsDel1bp

KIAA0913	DAVID_KIAA0913	NM_015037	PAP48	65	23.1%	chr10	75221997	NM_015037	c.1694G>A	p.R565H
KIAA0913	DAVID_KIAA0913	NM_015037	PAP48	185	22.2%	chr10	75223472	NM_015037	c.2434C>NULL	p.NULL-1FsDel1bp
MS4A2	DAVID_membrane-spanning 4-domains: subfamily A: member 2 (Fc fragment of IgE: high affinity I: receptor for; beta polypeptide)	NM_001142303	PAP48	123	26.0%	chr11	59617615	NM_001142303	c.545T>NULL	p.NULL-1FsDel1bp
MTP18	DAVID_mitochondrial protein 18 kDa	ENSG00000100010	PAP48	599	22.2%	chr22	29153280	CCDS33635.1	c.318NULL>C	p.NULL-1FsIns2bp
Myo10	DAVID_myosin X	NM_012334	PAP48	49	34.7%	chr5	16728070	NM_012334	c.4856A>G	p.H1619R
ND5	DAVID_NADH-ubiquinone oxidoreductase chain 5	ENSG00000198786	PAP48	273	86.8%	chrM	13028	ENST00000361567	c.691C>T	p.P231S
npffr1	DAVID_neuropeptide FF receptor 1	NM_022146	PAP48	95	11.6%	chr10	71695898	NM_022146	c.257G>A	p.S86N
GPR109B	DAVID_niacin receptor 2; niacin receptor 1	NM_006018	PAP48	136	20.6%	chr12	121766982	NM_006018	c.256T>A	p.Y86N
GPR109A	DAVID_niacin receptor 2; niacin receptor 1	NM_006018	PAP48	136	20.6%	chr12	121766982	NM_006018	c.256T>A	p.Y86N
GPR109B	DAVID_niacin receptor 2; niacin receptor 1	NM_006018	PAP48	112	19.6%	chr12	121766991	NM_006018	c.247G>C	p.V83L
GPR109A	DAVID_niacin receptor 2; niacin receptor 1	NM_006018	PAP48	112	19.6%	chr12	121766991	NM_006018	c.247G>C	p.V83L
nsun6	DAVID_NOL1/NOP2/Sun domain family: member 6	ENSG00000152487	PAP48	55	23.6%	chr10	18980107	CCDS7130.1	c.32C>A	p.P11H
obscn	DAVID_obscurin: cytoskeletal calmodulin and titin-interacting RhoGEF	NM_001098623	PAP48	190	21.6%	chr1	226626073	NM_001098623	c.20971G>NU	p.NULL-1FsDel1bp
OR14J1	DAVID_olfactory receptor: family 14: subfamily J: member 1	ENSG00000204695	PAP48	208	24.5%	chr6	29382572	CCDS34362.1	c.127A>G	p.I43V
LST-3TM12	DAVID_organic anion transporter LST-3b	NM_001009562	PAP48	82	17.1%	chr12	21067119	NM_001009562	c.409G>NULL	p.NULL-1FsDel1bp
PKHD1L1	DAVID_polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	NM_177531	PAP48	49	20.4%	chr8	110486048	NM_177531	c.1463AACA>I	p.NULL-1FsDel4bp
PATL1	DAVID_protein associated with topoisomerase II homolog 1 (yeast)	NM_152716	PAP48	64	26.6%	chr11	59180631	NM_152716	c.741G>NULL	p.NULL-1FsDel1bp
PIAS1	DAVID_protein inhibitor of activated STAT: 1	NM_016166	PAP48	102	24.5%	chr15	66267145	NM_016166	c.1874A>G	p.H625R
PPP1R10	DAVID_protein phosphatase 1: regulatory (inhibitor) subunit 10	ENSG00000204569	PAP48	206	34.0%	chr6	30677840	CCDS4681.1	c.3320G>NUL	p.NULL-1FsDel1bp
PCDHGA4	DAVID_protocadherin gamma subfamily A: 4	NM_018917	PAP48	129	10.9%	chr5	140715505	NM_018917	c.554G>A	p.G185E
PCDHGB1	DAVID_protocadherin gamma subfamily B: 1	NM_018922	PAP48	295	28.1%	chr5	140712116	NM_018922	c.2105C>T	p.A702V
FLJ32810	DAVID_Rho-type GTPase-activating protein FLJ32810	NM_152432	PAP48	42	33.3%	chr11	100350491	NM_152432	c.1802C>T	p.T601I
RBM20	DAVID_RNA binding motif protein 20	NM_001134363	PAP48	241	22.4%	chr10	112531574	NM_001134363	c.1217C>NULL	p.NULL-1FsDel1bp
RYR2	DAVID_ryanodine receptor 2 (cardiac)	NM_001035	PAP48	180	30.6%	chr1	235796490	NM_001035	c.3215C>A	p.A1072E
SLFN12L	DAVID_schlafen family member 12-like	NM_001145027	PAP48	137	13.9%	chr17	30826295	NM_001145027	c.2176A>NULL	p.NULL-1FsDel1bp
SHANK2	DAVID_SH3 and multiple ankyrin repeat domains 2	NM_133266	PAP48	227	23.8%	chr11	70009951	NM_133266	c.4737C>NULL	p.NULL-1FsDel1bp
pabpn1l	DAVID_similar to poly(A)binding protein nuclear-like 1	NM_001080487	PAP48	271	22.9%	chr16	87460488	NM_001080487	c.281CT>NUL	p.NULL-1FsDel2bp
SLC8A1	DAVID_solute carrier family 8 (sodium/calcium exchanger): member 1	NM_001112801	PAP48	164	23.8%	chr2	40258395	NM_001112801	c.-1G>A	p.IVS2+1-1SpliceDonor
scaper	DAVID_S-phase cyclin A-associated protein in the ER	NM_020843	PAP48	41	24.4%	chr15	74879690	NM_020843	c.565G>A	p.D189N
TBKBP1	DAVID_TBK1 binding protein 1	NM_014726	PAP48	45	26.7%	chr17	43131772	NM_014726	c.722G>NULL	p.NULL-1FsDel1bp
TNIK	DAVID_TRAF2 and NCK interacting kinase	NM_015028	PAP48	185	37.8%	chr3	172326412	NM_015028	c.1996G>T	p.E666X
TRIM21	DAVID_tripartite motif-containing 21	NM_003141	PAP48	336	26.8%	chr11	4363410	NM_003141	c.1677T>NULL	p.NULL-1FsDel1bp
UNC13A	DAVID_unc-13 homolog A (C. elegans)	NM_001080421	PAP48	159	13.8%	chr19	17620243	NM_001080421	c.2077C>T	p.Q693X
ZNF788	DAVID_zinc finger family member 788	ENSG00000188474	PAP48	115	33.0%	chr19	12085319	ENST00000397757	c.709TTCTC>I	p.NULL-1FsDel5bp
ZFHX4	DAVID_zinc finger homeobox 4	NM_024721	PAP48	400	27.3%	chr8	77779221	NM_024721	c.343G>A	p.E115K
ZNF548	DAVID_zinc finger protein 548	NM_152909	PAP48	69	14.5%	chr19	62602500	NM_152909	c.1033T>NULL	p.NULL-1FsDel1bp

DCP1B	DCP1 decapping enzyme homolog B (S. cerevisiae)	ENSG00000151065	PAP48	197	10.2%	chr12	1932612	CCDS31727.1	c.1627NULL>(	p.NULL-1FsIns3bp
DOCK3	dedicator of cytokinesis 3	ENSG00000088538	PAP48	58	58.6%	chr3	51392644	ENST00000402669	c.5549C>NULI	p.NULL-1FsDel1bp
DEPDC4	DEP domain containing 4	ENSG00000166153	PAP48	273	11.0%	chr12	99181637	CCDS9075.1	c.323C>T	p.T108M
DES	desmin	ENSG00000175084	PAP48	118	22.9%	chr2	219993906	CCDS33383.1	c.1010C>T	p.A337V
DPYSL5	dihydropyrimidinase-like 5	ENSG00000157851	PAP48	44	56.8%	chr2	27008034	CCDS1730.1	c.692G>A	p.R231H
DLG3	discs; large homolog 3 (Drosophila)	ENSG00000082458	PAP48	61	19.7%	chrX	69581965	CCDS14403.1	c.189G>NULL	p.NULL-1FsDel1bp
DISP2	dispatched homolog 2 (Drosophila)	ENSG00000140323	PAP48	319	11.6%	chr15	38446749	CCDS10056.1	c.1144C>T	p.P382S
DSCAML1	Down syndrome cell adhesion molecule like 1	ENSG00000177103	PAP48	49	30.6%	chr11	116894657	CCDS8384.1	c.1424G>A	p.S475N
DUSP13	dual specificity phosphatase 13	ENSG00000079393	PAP48	144	18.1%	chr10	76524461	CCDS31225.1	c.1057G>NUL	p.NULL-1FsDel1bp
DYRK1B	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	ENSG00000105204	PAP48	44	22.7%	chr19	45008452	CCDS12543.1	c.2004C>NULI	p.NULL-1FsDel1bp
DNAH7	dynein; axonemal; heavy chain 7	ENSG00000118997	PAP48	83	12.0%	chr2	196470737	CCDS42794.1	c.-1TTT>NULL	p.IVS28-3-1SpliceAcceptor
EP400	E1A binding protein p400	ENSG00000183495	PAP48	74	24.3%	chr12	131095840	CCDS31929.1	c.6805C>T	p.R2269C
EBF3	early B-cell factor 3	ENSG00000108001	PAP48	34	29.4%	chr10	131529253	CCDS31314.1	c.1379C>T	p.P460L
EML4	echinoderm microtubule associated protein like 4	ENSG00000143924	PAP48	120	10.0%	chr2	42396682	CCDS1807.1	c.2044C>T	p.R682C
EFCAB9	EF-hand calcium binding domain 9	ENSG00000214360	PAP48	86	15.1%	chr5	171562936	ENST00000398186	c.576A>NULL	p.NULL-1FsDel1bp
EGFL6	EGF-like-domain; multiple 6	ENSG00000198759	PAP48	137	40.1%	chrX	13545880	CCDS14155.1	c.889A>T	p.K297X
EGF	epidermal growth factor	ENSG00000138798	PAP48	87	21.8%	chr4	111124121	CCDS3689.1	c.2466G>A	p.M822I
EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog; avian)	ENSG00000146648	PAP48	236	20.8%	chr7	55208228	CCDS5514.1	c.1978G>A	p.V660M
EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	ENSG00000095203	PAP48	145	33.1%	chr9	110978794	CCDS43859.1	c.2491G>T	p.D831Y
EPB41L1	erythrocyte membrane protein band 4.1-like 1	ENSG00000088367	PAP48	114	29.8%	chr20	34261068	CCDS13271.1	c.1913G>A	p.R638H
ETV7	ets variant 7	ENSG00000010030	PAP48	192	11.5%	chr6	36447121	CCDS4819.1	c.628G>A	p.A210T
ETV7	ets variant 7	ENSG00000010030	PAP48	195	23.1%	chr6	36451745	CCDS4819.1	c.188T>C	p.L63P
EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	ENSG00000172071	PAP48	158	17.1%	chr2	88655384	CCDS33241.1	c.3511AG>NU	p.NULL-1FsDel2bp
ERCC4	excision repair cross-complementing rodent repair deficiency; complementation group 4	ENSG00000175595	PAP48	141	13.5%	chr16	13949690	CCDS32390.1	c.2736NULL>A	p.NULL-1FsIns1bp
EYA2	eyes absent homolog 2 (Drosophila)	ENSG00000064655	PAP48	313	10.9%	chr20	45063489	CCDS13403.1	c.125C>NULL	p.NULL-1FsDel1bp
FAM111B	family with sequence similarity 111; member B	ENSG00000189057	PAP48	59	18.6%	chr11	58648953	CCDS7972.1	c.807A>NULL	p.NULL-1FsDel1bp
FAM113B	family with sequence similarity 113; member B	ENSG00000179715	PAP48	151	29.8%	chr12	45915265	CCDS8752.1	c.152G>NULL	p.NULL-1FsDel1bp
FBXO30	F-box protein 30	ENSG00000118496	PAP48	142	21.1%	chr6	146167596	CCDS5208.1	c.1639C>G	p.L547V
FSCB	fibrous sheath CABYR binding protein	ENSG00000189139	PAP48	88	13.6%	chr14	44043786	CCDS9679.1	c.2155C>T	p.P719S
FREM3	FRAS1 related extracellular matrix 3	ENSG00000183090	PAP48	159	28.9%	chr4	144836730	NM_001168235	c.4549G>A	p.G1517S
FRYL	FRY-like	ENSG00000075539	PAP48	78	25.6%	chr4	48331192	ENST00000302806	c.345A>NULL	p.NULL-1FsDel1bp
FPGT	fucose-1-phosphate guanylyltransferase	ENSG00000116783	PAP48	206	24.3%	chr1	74677867	CCDS664.1	c.1984G>A	p.E662K
FXYD7	FXYD domain containing ion transport regulator 7	ENSG00000221946	PAP48	503	37.0%	chr19	40334044	CCDS12446.1	c.109T>C	p.F37L
GPR108	G protein-coupled receptor 108	ENSG00000125734	PAP48	197	24.4%	chr19	6682908	CCDS42479.1	c.1294G>A	p.G432R
GPR109A	G protein-coupled receptor 109A	ENSG00000182782	PAP48	141	12.1%	chr12	121753266	CCDS9235.1	c.518G>C	p.G173A
GPR109A	G protein-coupled receptor 109A	ENSG00000182782	PAP48	150	11.3%	chr12	121753267	CCDS9235.1	c.517G>C	p.G173R
GPR109B	G protein-coupled receptor 109B	ENSG00000182782	PAP48	141	12.1%	chr12	121753266	CCDS9235.1	c.518G>C	p.G173A
GPR109B	G protein-coupled receptor 109B	ENSG00000182782	PAP48	150	11.3%	chr12	121753267	CCDS9235.1	c.517G>C	p.G173R
GPR119	G protein-coupled receptor 119	ENSG00000147262	PAP48	183	13.1%	chrX	129346916	CCDS14625.1	c.187A>G	p.T63A
GPR123	G protein-coupled receptor 123	ENSG00000197177	PAP48	113	30.1%	chr10	134746067	ENST00000368577	c.1163G>A	p.R388H

GPR142	G protein-coupled receptor 142	ENSG00000196169	PAP48	42	26.2%	chr17	69862970	NM_153209	c.2921G>A	p.R974Q
GPR144	G protein-coupled receptor 144	ENSG00000180264	PAP48	81	27.2%	chr9	126254735	ENST00000334810	c.250C>NULL	p.NULL-1FsDel1bp
GRK5	G protein-coupled receptor kinase 5	ENSG00000198873	PAP48	146	17.1%	chr10	121174550	CCDS7612.1	c.496T>NULL	p.NULL-1FsDel1bp
GABRG2	gamma-aminobutyric acid (GABA) A receptor; gamma 2	ENSG00000113327	PAP48	103	21.4%	chr5	161460882	CCDS4359.1	c.612NULL>C	p.NULL-1FsIns1bp
GRLF1	glucocorticoid receptor DNA binding factor 1	ENSG00000160007	PAP48	173	26.0%	chr19	52116681	NM_004491	c.2909C>NULL	p.NULL-1FsDel1bp
G6PD	glucose-6-phosphate dehydrogenase	ENSG00000160211	PAP48	104	19.2%	chrX	153414996	CCDS14756.2	c.943C>T	p.R315C
GFOD1	glucose-fructose oxidoreductase domain containing 1	ENSG00000145990	PAP48	68	32.4%	chr6	13473357	CCDS4524.1	c.770G>A	p.R257H
GAA	glucosidase; alpha; acid	ENSG00000171298	PAP48	245	28.2%	chr17	75693232	CCDS32760.1	c.252C>NULL	p.NULL-1FsDel1bp
GCDH	glutaryl-CoA dehydrogenase	ENSG00000105607	PAP48	99	19.2%	chr19	12869601	CCDS12286.1	c.1167G>NUL	p.NULL-1FsDel1bp
GPC4	glypican 4	ENSG00000076716	PAP48	76	15.8%	chrX	132267589	CCDS14637.1	c.1178C>NULL	p.NULL-1FsDel1bp
GOLGB1	golgin B1	ENSG00000173230	PAP48	186	30.6%	chr3	122895489	CCDS3004.1	c.6556C>A	p.Q2186K
GOLGB1	golgin B1	ENSG00000173230	PAP48	168	34.5%	chr3	122899811	CCDS3004.1	c.2234A>G	p.E745G
GIGYF1	GRB10 interacting GYF protein 1	ENSG00000146830	PAP48	87	12.6%	chr7	100123649	CCDS34708.1	c.185G>NULL	p.NULL-1FsDel1bp
GFI1B	growth factor independent 1B transcription repressor	ENSG00000165702	PAP48	226	27.0%	chr9	134855113	CCDS6957.1	c.812C>G	p.T271R
GIMAP1	GTPase; IMAP family member 1	ENSG00000213203	PAP48	85	20.0%	chr7	150048893	CCDS5906.1	c.868G>T	p.V290L
HEATR5B	HEAT repeat containing 5B	ENSG00000008869	PAP48	41	29.3%	chr2	37121907	CCDS33181.1	c.2729C>T	p.T910I
HSPB7	heat shock 27kDa protein family; member 7 (cardiovascular)	ENSG00000173641	PAP48	75	14.7%	chr1	16217132	ENST00000311890	c.178G>T	p.A60S
HNRNPM	heterogeneous nuclear ribonucleoprotein M	ENSG00000099783	PAP48	73	37.0%	chr19	8437219	CCDS12203.1	c.731G>A	p.R244H
HRASLS2	HRAS-like suppressor 2	ENSG00000133328	PAP48	255	28.2%	chr11	63082667	CCDS8046.1	c.160C>A	p.L54M
INHA	inhibin; alpha	ENSG00000123999	PAP48	396	29.8%	chr2	220148086	CCDS2444.1	c.695G>A	p.R232H
INPPL1	inositol polyphosphate phosphatase-like 1	ENSG00000165458	PAP48	198	24.2%	chr11	71618368	CCDS8213.1	c.767C>T	p.T256I
ITGA10	integrin; alpha 10	ENSG00000143127	PAP48	130	10.8%	chr1	144249092	CCDS918.1	c.-1AG>NULL	p.IVS20-1-1SpliceAcceptor
IFNGR1	interferon gamma receptor 1	ENSG00000027697	PAP48	108	11.1%	chr6	137561198	CCDS5185.1	c.1740AG>NU	p.NULL-1FsDel2bp
IFIT1	interferon-induced protein with tetratricopeptide repeats 1	ENSG00000185745	PAP48	190	16.3%	chr10	91152597	CCDS31243.1	c.585A>NULL	p.NULL-1FsDel1bp
IQSEC3	IQ motif and Sec7 domain 3	ENSG00000120645	PAP48	52	21.2%	chr12	136999	CCDS31725.1	c.1412A>G	p.H471R
IQGAP3	IQ motif containing GTPase activating protein 3	ENSG00000183856	PAP48	84	27.4%	chr1	154769396	CCDS1144.1	c.4103G>A	p.S1368N
KLHDC3	kelch domain containing 3	ENSG00000124702	PAP48	283	18.7%	chr6	43093279	CCDS4880.1	c.199C>T	p.R67C
KRT73	keratin 73	ENSG00000186049	PAP48	105	12.4%	chr12	51295367	CCDS8834.1	c.686G>A	p.R229H
KIAA0182	KIAA0182	ENSG00000131149	PAP48	33	30.3%	chr16	84239791	CCDS10952.1	c.359C>NULL	p.NULL-1FsDel1bp
KIAA1462	KIAA1462	ENSG00000165757	PAP48	388	21.1%	chr10	30355995	CCDS41500.1	c.6851G>NUL	p.NULL-1FsDel1bp
KIAA1958	KIAA1958	ENSG00000165185	PAP48	135	25.9%	chr9	114376923	CCDS35108.1	c.742G>T	p.G248W
KIF19	kinesin family member 19	ENSG00000196169	PAP48	42	26.2%	chr17	69862970	NM_153209	c.2921G>A	p.R974Q
LAMB3	laminin; beta 3	ENSG00000196878	PAP48	148	10.1%	chr1	207890906	CCDS1487.1	c.7C>T	p.P3S
LANCL3	LanC lantibiotic synthetase component C-like 3 (bacterial)	ENSG00000147036	PAP48	80	25.0%	chrX	37399882	CCDS14240.1	c.596A>G	p.K199R
LRRC7	leucine rich repeat containing 7	ENSG00000033122	PAP48	143	50.3%	chr1	70277281	CCDS645.1	c.3072A>NULL	p.NULL-1FsDel1bp
LENG8	leukocyte receptor cluster (LRC) member 8	ENSG00000167615	PAP48	377	23.6%	chr19	59664614	ENST00000376526	c.2246T>NULL	p.NULL-1FsDel1bp
LOR	loricrin	ENSG00000203782	PAP48	85	21.2%	chr1	151500976	CCDS30870.1	c.927G>T	p.W309C
KDM5A	lysine (K)-specific demethylase 5A	ENSG00000073614	PAP48	26	46.2%	chr12	368529	ENST00000382815	c.225CCCC>N	p.NULL-1FsDel4bp

MED12L	mediator complex subunit 12-like	ENSG00000144893	PAP48	93	25.8%	chr3	152565617	CCDS33876.1	c.3013G>A	p.A1005T
MCHR2	melanin-concentrating hormone receptor 2	ENSG00000152034	PAP48	83	24.1%	chr6	100489079	CCDS5044.1	c.742T>NULL	p.NULL-1FsDel1bp
MAGEA4	melanoma antigen family A; 4	ENSG00000147381	PAP48	103	17.5%	chrX	150843228	CCDS14702.1	c.436C>T	p.R146C
MAGEB1	melanoma antigen family B; 1	ENSG00000214107	PAP48	103	13.6%	chrX	30178880	CCDS14222.1	c.349C>T	p.H117Y
MAGEH1	melanoma antigen family H; 1	ENSG00000187601	PAP48	81	34.6%	chrX	55495591	CCDS14369.1	c.59G>A	p.R20H
MBOAT2	membrane bound O-acyltransferase domain containing 2	ENSG00000143797	PAP48	133	28.6%	chr2	8940137	CCDS1660.1	c.461G>A	p.R154Q
MS4A3	membrane-spanning 4-domains; subfamily A; member 3 (hematopoietic cell-specific)	ENSG00000149516	PAP48	199	21.6%	chr11	59586607	CCDS31567.1	c.247T>NULL	p.NULL-1FsDel1bp
MACF1	microtubule-actin crosslinking factor 1	ENSG00000127603	PAP48	328	10.4%	chr1	39507755	ENST00000372900	c.799C>NULL	p.NULL-1FsDel1bp
MAP3K1	mitogen-activated protein kinase kinase kinase 1	ENSG00000095015	PAP48	77	16.9%	chr5	56219814	CCDS43318.1	c.4262T>C	p.L1421P
MMS19	MMS19 nucleotide excision repair homolog (S. cerevisiae)	ENSG00000155229	PAP48	98	20.4%	chr10	99220527	NM_022362	c.766G>A	p.A256T
MUC5AC	mucin 5AC; oligomeric mucus/gel-forming	ENSG00000215182	PAP48	495	16.0%	chr11	1170057	ENST00000358378	c.728G>A	p.R243Q
MMRN2	multimerin 2	ENSG00000173269	PAP48	375	13.3%	chr10	88693999	CCDS7379.1	c.655G>A	p.E219K
MEGF8	multiple EGF-like-domains 8	ENSG00000105429	PAP48	52	21.2%	chr19	47539543	NM_001410	c.1588G>NUL	p.NULL-1FsDel1bp
MEN1	multiple endocrine neoplasia I	ENSG00000133895	PAP48	166	21.1%	chr11	64328669	CCDS8083.1	c.2043C>NULI	p.NULL-1FsDel1bp
MYSM1	Myb-like; SWIRM and MPN domains 1	ENSG00000162601	PAP48	94	10.6%	chr1	58903833	CCDS41343.1	c.2090G>A	p.R697Q
MYH3	myosin; heavy chain 3; skeletal muscle; embryonic	ENSG00000109063	PAP48	256	22.7%	chr17	10478968	CCDS11157.1	c.4270G>T	p.G1424X
MYH3	myosin; heavy chain 3; skeletal muscle; embryonic	ENSG00000109063	PAP48	228	31.6%	chr17	10482213	CCDS11157.1	c.3601G>A	p.V1201M
NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7; 20kDa (NADH-coenzyme Q reductase)	ENSG00000115286	PAP48	162	22.8%	chr19	1340116	ENST00000382445	c.407C>NULL	p.NULL-1FsDel1bp
NDN	necdin homolog (mouse)	ENSG00000182636	PAP48	226	41.2%	chr15	21482545	CCDS10014.1	c.913C>T	p.R305W
NTNG2	netrin G2	ENSG00000196358	PAP48	164	29.9%	chr9	134063432	CCDS6946.1	c.472G>A	p.G158R
NCALD	neurocalcin delta	ENSG00000104490	PAP48	232	27.2%	chr8	102800684	CCDS6292.1	c.350G>A	p.S117N
NPAS4	neuronal PAS domain protein 4	ENSG00000174576	PAP48	290	26.2%	chr11	65947956	CCDS8138.1	c.1019C>T	p.P340L
NRP1	neuropilin 1	ENSG00000099250	PAP48	90	22.2%	chr10	33515365	CCDS7177.1	c.2120G>A	p.R707H
NTF3	neurotrophin 3	ENSG00000185652	PAP48	162	28.4%	chr12	5474053	CCDS8538.1	c.412C>T	p.R138W
NAB1	NGFI-A binding protein 1 (EGR1 binding protein 1)	ENSG00000138386	PAP48	51	27.5%	chr2	191232288	CCDS2307.1	c.141G>T	p.E47D
NAB2	NGFI-A binding protein 2 (EGR1 binding protein 2)	ENSG00000166886	PAP48	48	25.0%	chr12	55771745	CCDS8930.1	c.654G>NULL	p.NULL-1FsDel1bp
NOP56	NOP56 ribonucleoprotein homolog (yeast)	ENSG00000101361	PAP48	72	23.6%	chr20	2583981	CCDS13030.1	c.580G>A	p.G194R
NOTCH3	Notch homolog 3 (Drosophila)	ENSG00000074181	PAP48	152	22.4%	chr19	15164200	CCDS12326.1	c.470C>NULL	p.NULL-1FsDel1bp
NR2C1	nuclear receptor subfamily 2; group C; member 1	ENSG00000120798	PAP48	43	25.6%	chr12	93948742	NM_001127362	c.1432C>G	p.R478G
NOL4	nucleolar protein 4	ENSG00000101746	PAP48	67	29.9%	chr18	29963928	CCDS11907.2	c.319G>A	p.D107N
NULL	NULL	ENSG00000186261	PAP48	175	21.7%	chr16	10533561	ENST00000320378	c.604NULL>C	p.NULL-1FsIns1bp
NULL	NULL	ENSG00000214820	PAP48	126	10.3%	chr3	44596472	ENST00000399045	c.2087C>NULI	p.NULL-1FsDel1bp
NULL	NULL	NM_033486	PAP48	106	33.0%	chr1	1562217	NM_033486	c.1699G>A	p.G567R
ODZ4	odz; odd Oz/ten-m homolog 4 (Drosophila)	ENSG00000149256	PAP48	161	40.4%	chr11	78090319	NM_001098816	c.4987G>T	p.V1663L
ODZ4	odz; odd Oz/ten-m homolog 4 (Drosophila)	ENSG00000149256	PAP48	91	40.7%	chr11	78097152	NM_001098816	c.4111C>T	p.R1371C
OR10G3	olfactory receptor; family 10; subfamily G; member 3	ENSG00000169208	PAP48	132	28.0%	chr14	21107842	CCDS32046.1	c.874C>T	p.R292W
OR4A16	olfactory receptor; family 4; subfamily A; member 16	ENSG00000181961	PAP48	75	26.7%	chr11	54867653	CCDS31499.1	c.401T>C	p.M134T
OR52N5	olfactory receptor; family 52; subfamily N; member 5	ENSG00000181009	PAP48	33	78.8%	chr11	5756228	CCDS31397.1	c.1187T>NULI	p.NULL-1FsDel1bp
OR8B12	olfactory receptor; family 8; subfamily B; member 12	ENSG00000170953	PAP48	97	23.7%	chr11	123918130	CCDS31711.1	c.631G>A	p.V211I
OR8D4	olfactory receptor; family 8; subfamily D; member 4	ENSG00000181518	PAP48	115	18.3%	chr11	123282652	CCDS31698.1	c.304NULL>T	p.NULL-1FsIns1bp
OSM	oncostatin M	ENSG00000099985	PAP48	89	22.5%	chr22	28991061	CCDS13873.1	c.107G>A	p.R36H
OSGIN2	oxidative stress induced growth inhibitor family member 2	ENSG00000164823	PAP48	81	24.7%	chr8	91006562	CCDS6248.1	c.1145G>A	p.R382H

PAX6	paired box 6	ENSG00000007372	PAP48	71	26.8%	chr11	31768893	CCDS31452.1	c.1316C>NULL	p.NULL-1FsDel1bp
PALMD	palmdelphin	ENSG00000099260	PAP48	81	21.0%	chr1	99927796	CCDS758.1	c.1392C>NULL	p.NULL-1FsDel1bp
PTH1R	parathyroid hormone 1 receptor	ENSG00000160801	PAP48	55	29.1%	chr3	46918342	CCDS2747.1	c.1199G>A	p.R400Q
PTHLH	parathyroid hormone-like hormone	ENSG00000087494	PAP48	290	11.0%	chr12	28007776	CCDS8715.1	c.296A>C	p.D99A
PNPLA6	patatin-like phospholipase domain containing 6	ENSG00000032444	PAP48	71	15.5%	chr19	7521191	CCDS32891.1	c.1705C>T	p.R569C
PCNXL2	pecanex-like 2 (Drosophila)	ENSG00000135749	PAP48	118	16.1%	chr1	231454749	NM_014801	c.2102C>T	p.A701V
PAMR1	peptidase domain containing associated with muscle regeneration 1	ENSG00000149090	PAP48	291	19.2%	chr11	35470246	CCDS7898.1	c.430G>NULL	p.NULL-1FsDel1bp
PLIN2	perilipin 2	ENSG00000147872	PAP48	105	24.8%	chr9	19116227	CCDS6490.1	c.111G>T	p.K37N
PPARGC1A	peroxisome proliferator-activated receptor gamma; coactivator 1 alpha	ENSG00000109819	PAP48	169	27.8%	chr4	23424598	CCDS3429.1	c.1606G>A	p.V536M
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP48	247	21.9%	chr10	89682884	CCDS31238.1	c.388C>G	p.R130G
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP48	57	57.9%	chr10	89707667	CCDS31238.1	c.712NULL>T	p.NULL-1FsIns1bp
PIGO	phosphatidylinositol glycan anchor biosynthesis; class O	ENSG00000165282	PAP48	112	25.0%	chr9	35081693	CCDS6575.1	c.3718C>NULL	p.NULL-1FsDel1bp
PIGW	phosphatidylinositol glycan anchor biosynthesis; class W	ENSG00000184886	PAP48	98	27.6%	chr17	31967947	CCDS11313.1	c.884G>T	p.R295L
PIGZ	phosphatidylinositol glycan anchor biosynthesis; class Z	ENSG00000119227	PAP48	91	36.3%	chr3	198158757	CCDS3324.1	c.2936C>NULL	p.NULL-1FsDel1bp
PDE3A	phosphodiesterase 3A; cGMP-inhibited	ENSG00000172572	PAP48	70	30.0%	chr12	20413990	CCDS31754.1	c.505G>NULL	p.NULL-1FsDel1bp
PDE4DIP	phosphodiesterase 4D interacting protein	ENSG00000178104	PAP48	165	16.4%	chr1	143633881	CCDS30824.1	c.883C>T	p.R295C
PFKP	phosphofructokinase; platelet	ENSG00000067057	PAP48	82	19.5%	chr10	3162106	CCDS7059.1	c.1779G>NUL	p.NULL-1FsDel1bp
PACS2	phosphofurin acidic cluster sorting protein 2	ENSG00000179364	PAP48	39	48.7%	chr14	104889799	CCDS32168.1	c.247NULL>C	p.NULL-1FsIns1bp
PACS2	phosphofurin acidic cluster sorting protein 2	ENSG00000179364	PAP48	139	23.7%	chr14	104919873	CCDS32168.1	c.1416TG>NU	p.NULL-1FsDel2bp
PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP48	89	23.6%	chr3	180434779	CCDS43171.1	c.3140A>T	p.H1047L
PLEKHA6	pleckstrin homology domain containing; family A member 6	ENSG00000143850	PAP48	129	10.1%	chr1	202495034	CCDS1444.1	c.1464G>NUL	p.NULL-1FsDel1bp
PLAG1	pleiomorphic adenoma gene 1	ENSG00000181690	PAP48	45	26.7%	chr8	57243380	CCDS6165.1	c.3G>T	p.M1I
PLXNA3	plexin A3	ENSG00000130827	PAP48	112	34.8%	chrX	153351535	CCDS14752.1	c.4817G>A	p.S1606N
PVRL1	poliovirus receptor-related 1 (herpesvirus entry mediator C)	ENSG00000110400	PAP48	187	25.7%	chr11	119040977	CCDS8426.1	c.1794A>NULL	p.NULL-1FsDel1bp
PHC1	polyhomeotic homolog 1 (Drosophila)	ENSG00000111752	PAP48	119	19.3%	chr12	8961595	CCDS8597.1	c.55G>NULL	p.NULL-1FsDel1bp
POLR2B	polymerase (RNA) II (DNA directed) polypeptide B; 140kDa	ENSG00000047315	PAP48	88	25.0%	chr4	57556252	CCDS3511.1	c.655G>A	p.G219R
PTBP1	polypyrimidine tract binding protein 1	ENSG00000011304	PAP48	105	27.6%	chr19	755646	CCDS42456.1	c.550C>G	p.L184V
KCND1	potassium voltage-gated channel; Shal-related subfamily; member 1	ENSG00000102057	PAP48	308	36.7%	chrX	48711208	CCDS14314.1	c.415C>T	p.R139X
KCND1	potassium voltage-gated channel; Shal-related subfamily; member 1	ENSG00000102057	PAP48	43	25.6%	chrX	48711566	CCDS14314.1	c.57G>A	p.W19X
KCNH8	potassium voltage-gated channel; subfamily H (eag-related); member 8	ENSG00000183960	PAP48	177	24.9%	chr3	19467665	CCDS2632.1	c.1590T>A	p.F530L
PRR11	proline rich 11	ENSG00000068489	PAP48	169	33.1%	chr17	54601953	CCDS11614.1	c.58A>NULL	p.NULL-1FsDel1bp
PTGER4	prostaglandin E receptor 4 (subtype EP4)	ENSG00000171522	PAP48	182	24.7%	chr5	40727680	CCDS3930.1	c.910C>T	p.R304X
PTOV1	prostate tumor overexpressed 1	ENSG00000104960	PAP48	72	23.6%	chr19	55055339	CCDS12782.1	c.1242G>NUL	p.NULL-1FsDel1bp
POMGNT1	protein O-linked mannose beta1;2-N-acetylglucosaminyltransferase	ENSG00000085998	PAP48	223	24.2%	chr1	46431466	CCDS531.1	c.1119G>T	p.K373N
PPP1R16A	protein phosphatase 1; regulatory (inhibitor) subunit 16A	ENSG00000160972	PAP48	59	33.9%	chr8	145693470	CCDS6429.1	c.85C>T	p.R29W

PTPN23	protein tyrosine phosphatase; non-receptor type 23	ENSG00000076201	PAP48	65	24.6%	chr3	47429482	CCDS2754.1	c.4714C>NULL	p.NULL-1FsDel1bp
PCDH17	protocadherin 17	ENSG00000118946	PAP48	234	23.1%	chr13	57105298	CCDS31986.1	c.617A>G	p.Q206R
PCDH15	protocadherin-related 15	ENSG00000150275	PAP48	450	22.0%	chr10	55583031	CCDS7248.1	c.1619C>T	p.S540L
PPFIBP2	PTPRF interacting protein; binding protein 2 (liprin beta 2)	ENSG00000166387	PAP48	100	19.0%	chr11	7626647	CCDS31419.1	c.1838T>NULL	p.NULL-1FsDel1bp
RAB11FIP3	RAB11 family interacting protein 3 (class II)	ENSG00000090565	PAP48	64	18.8%	chr16	510136	CCDS32351.1	c.1874T>C	p.L625P
RAD50	RAD50 homolog (S. cerevisiae)	ENSG00000113522	PAP48	44	29.5%	chr5	131959351	CCDS34233.1	c.2157A>NULL	p.NULL-1FsDel1bp
REPS1	RALBP1 associated Eps domain containing 1	ENSG00000135597	PAP48	137	31.4%	chr6	139308074	CCDS5193.1	c.447G>C	p.W149C
RIMS2	regulating synaptic membrane exocytosis 2	ENSG00000176406	PAP48	97	12.4%	chr8	104967418	CCDS43761.1	c.839A>NULL	p.NULL-1FsDel1bp
RGS12	regulator of G-protein signaling 12	ENSG00000159788	PAP48	68	32.4%	chr4	3400197	CCDS3366.1	c.3526A>NULL	p.NULL-1FsDel1bp
RXFP4	relaxin/insulin-like family peptide receptor 4	ENSG00000173080	PAP48	202	31.2%	chr1	154179249	CCDS1124.1	c.1125A>NULL	p.NULL-1FsDel1bp
RARRES1	retinoic acid receptor responder (tazarotene induced) 1	ENSG00000118849	PAP48	70	28.6%	chr3	159898164	CCDS3184.1	c.882C>A	p.F294L
RXRA	retinoid X receptor; alpha	ENSG00000186350	PAP48	42	35.7%	chr9	136439861	CCDS35172.1	c.325C>NULL	p.NULL-1FsDel1bp
REV3L	REV3-like; catalytic subunit of DNA polymerase zeta (yeast)	ENSG00000009413	PAP48	122	19.7%	chr6	111795710	CCDS5091.2	c.6887A>NULL	p.NULL-1FsDel1bp
ARHGEF5	Rho guanine nucleotide exchange factor (GEF) 5	ENSG00000050327	PAP48	318	24.8%	chr7	143706791	CCDS34771.1	c.4535C>NULL	p.NULL-1FsDel1bp
RRBP1	ribosome binding protein 1 homolog 180kDa (dog)	ENSG00000125844	PAP48	574	23.0%	chr20	17587549	ENST00000246043	c.1604A>G	p.N535S
RPUSD2	RNA pseudouridylate synthase domain containing 2	ENSG00000166133	PAP48	155	20.0%	chr15	38651230	CCDS10061.1	c.742C>T	p.R248C
RUFY1	RUN and FYVE domain containing 1	ENSG00000176783	PAP48	162	21.6%	chr5	178949216	CCDS4445.2	c.1090A>C	p.N364H
SALL1	sal-like 1 (Drosophila)	ENSG00000103449	PAP48	120	10.8%	chr16	49733162	CCDS10747.1	c.472A>G	p.S158G
SLFN12	schlafen family member 12	ENSG00000172123	PAP48	81	27.2%	chr17	30773368	CCDS11295.1	c.793G>A	p.E265K
SCFD2	sec1 family domain containing 2	ENSG00000184178	PAP48	137	11.7%	chr4	53834832	CCDS33984.1	c.1229G>A	p.G410E
SEC14L1	SEC14-like 1 (S. cerevisiae)	ENSG00000129657	PAP48	74	25.7%	chr17	72651307	CCDS42385.1	c.34T>C	p.Y12H
SEC31A	SEC31 homolog A (S. cerevisiae)	ENSG00000138674	PAP48	51	23.5%	chr4	84004589	CCDS3596.1	c.1620A>NULL	p.NULL-1FsDel1bp
SEMA6D	sema domain; transmembrane domain (TM); and cytoplasmic domain; (semaphorin) 6D	ENSG00000137872	PAP48	141	32.6%	chr15	45840880	CCDS32225.1	c.407G>A	p.C136Y
SERPINA10	serpin peptidase inhibitor; clade A (alpha-1 antiproteinase; antitrypsin); member 10	ENSG00000140093	PAP48	231	35.1%	chr14	93826431	CCDS9923.1	c.253A>G	p.S85G
SH3PXD2B	SH3 and PX domains 2B	ENSG00000174705	PAP48	279	26.9%	chr5	171698436	CCDS34291.1	c.2278C>T	p.R760C
SHC1	SHC (Src homology 2 domain containing) transforming protein 1	ENSG00000160691	PAP48	73	16.4%	chr1	153205514	CCDS30881.1	c.1285NULL>(	p.NULL-1FsIns1bp
STAT5B	signal transducer and activator of transcription 5B	ENSG00000173757	PAP48	145	15.9%	chr17	37628985	CCDS11423.1	c.665A>NULL	p.NULL-1FsDel1bp
SLAMF6	SLAM family member 6	ENSG00000162739	PAP48	195	31.8%	chr1	158732658	CCDS1205.1	c.199C>T	p.P67S
SLC25A30	solute carrier family 25; member 30	ENSG00000174032	PAP48	138	16.7%	chr13	44874462	CCDS31967.1	c.437T>C	p.I146T
SLC4A11	solute carrier family 4; sodium borate transporter; member 11	ENSG00000088836	PAP48	130	26.9%	chr20	3157313	CCDS13052.1	c.2281G>A	p.A761T
SLC4A11	solute carrier family 4; sodium borate transporter; member 11	ENSG00000088836	PAP48	180	23.9%	chr20	3163425	CCDS13052.1	c.404T>NULL	p.NULL-1FsDel1bp
SLC45A1	solute carrier family 45; member 1	ENSG00000162426	PAP48	170	18.2%	chr1	8308515	CCDS30577.1	c.541G>A	p.A181T
SP100	SP100 nuclear antigen	ENSG00000067066	PAP48	41	24.4%	chr2	231042740	ENST00000341950	c.1350A>NULL	p.NULL-1FsDel1bp
SYNE1	spectrin repeat containing; nuclear envelope 1	ENSG00000131018	PAP48	269	10.8%	chr6	152687998	CCDS5236.1	c.15571C>T	p.R5191C
SYNE2	spectrin repeat containing; nuclear envelope 2	ENSG00000054654	PAP48	88	11.4%	chr14	63754978	CCDS9761.2	c.19652A>G	p.Q6551R
SPATA16	spermatogenesis associated 16	ENSG00000144962	PAP48	89	18.0%	chr3	174157309	CCDS3221.1	c.-1G>T	p.IVS4-1-1SpliceAcceptor

SPATA18	spermatogenesis associated 18 homolog (rat)	ENSG00000163071	PAP48	190	22.6%	chr4	52637910	CCDS3489.1	c.967C>T	p.R323C
SPTY2D1	SPT2; Suppressor of Ty; domain containing 1 (S. cerevisiae)	ENSG00000179119	PAP48	109	21.1%	chr11	18592943	CCDS31441.1	c.2989C>NULL	p.NULL-1FsDel1bp
SOX14	SRY (sex determining region Y)-box 14	ENSG00000168875	PAP48	181	10.5%	chr3	138966936	CCDS3094.1	c.620G>T	p.W207L
STAB1	stabilin 1	ENSG00000010327	PAP48	148	26.4%	chr3	52521441	CCDS33768.1	c.2928C>NULL	p.NULL-1FsDel1bp
SAMD9	sterile alpha motif domain containing 9	ENSG00000205413	PAP48	221	20.8%	chr7	92572658	CCDS34680.1	c.689G>A	p.R230H
STS	steroid sulfatase (microsomal); isozyme S	ENSG00000101846	PAP48	300	27.3%	chrX	7187556	CCDS14127.1	c.564C>NULL	p.NULL-1FsDel1bp
STAG2	stromal antigen 2	ENSG00000101972	PAP48	84	27.4%	chrX	123042995	CCDS43990.1	c.2860C>T	p.R954C
ST18	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	ENSG00000147488	PAP48	244	21.7%	chr8	53247051	CCDS6149.1	c.923A>C	p.Q308P
SYNGAP1	synaptic Ras GTPase activating protein 1 homolog (rat)	ENSG00000197283	PAP48	250	17.2%	chr6	33519224	CCDS34434.1	c.2872G>NUL	p.NULL-1FsDel1bp
TAS1R2	taste receptor; type 1; member 2	ENSG00000179002	PAP48	110	44.5%	chr1	19038880	CCDS187.1	c.2320G>A	p.V774I
TAS2R60	taste receptor; type 2; member 60	ENSG00000185899	PAP48	143	10.5%	chr7	142851370	CCDS5885.1	c.703C>T	p.R235X
TLX1	T-cell leukemia homeobox 1	ENSG00000107807	PAP48	80	26.3%	chr10	102884081	CCDS7510.1	c.728C>T	p.A243V
TSHZ3	teashirt zinc finger homeobox 3	ENSG00000121297	PAP48	247	13.4%	chr19	36459712	CCDS12421.2	c.2827A>G	p.M943V
TEP1	telomerase-associated protein 1	ENSG00000129566	PAP48	160	26.3%	chr14	19921554	CCDS9548.1	c.3800G>A	p.G1267E
TEX19	testis expressed 19	ENSG00000182459	PAP48	119	40.3%	chr17	77913601	CCDS11809.1	c.286G>A	p.E96K
TTC15	tetratricopeptide repeat domain 15	ENSG00000171853	PAP48	289	26.3%	chr2	3371438	CCDS1652.1	c.1037A>G	p.D346G
TXNL4A	thioredoxin-like 4A	ENSG00000141759	PAP48	93	19.4%	chr18	75834786	CCDS32852.1	c.316A>G	p.M106V
THNSL1	threonine synthase-like 1 (S. cerevisiae)	ENSG00000185875	PAP48	142	52.1%	chr10	25352628	CCDS7147.1	c.470C>T	p.P157L
TPO	thyroid peroxidase	ENSG00000115705	PAP48	76	26.3%	chr2	1523419	CCDS1643.1	c.2665G>A	p.G889R
TRAF1	TNF receptor-associated factor 1	ENSG00000056558	PAP48	87	40.2%	chr9	122707161	CCDS6825.1	c.1209C>G	p.D403E
TNNI3K	TNNI3 interacting kinase	ENSG00000116783	PAP48	206	24.3%	chr1	74677867	CCDS664.1	c.1984G>A	p.E662K
TCERG1	transcription elongation regulator 1	ENSG00000113649	PAP48	115	24.3%	chr5	145863698	CCDS4282.1	c.2666GA>NU	p.NULL-1FsDel2bp
TCF25	transcription factor 25 (basic helix-loop-helix)	ENSG00000141002	PAP48	187	22.5%	chr16	88487662	CCDS10987.1	c.723A>NULL	p.NULL-1FsDel1bp
TCF4	transcription factor 4	ENSG00000196628	PAP48	67	22.4%	chr18	51075621	CCDS42438.1	c.-1G>A	p.IVS12-1-1SpliceAcceptor
TMEM50A	transmembrane protein 50A	ENSG00000183726	PAP48	165	22.4%	chr1	25539611	CCDS264.1	c.47G>NULL	p.NULL-1FsDel1bp
TRIT1	tRNA isopentenyltransferase 1	ENSG00000043514	PAP48	70	27.1%	chr1	40121687	CCDS30681.1	c.64A>G	p.T22A
TUB	tubby homolog (mouse)	ENSG00000166402	PAP48	27	44.4%	chr11	8073707	CCDS7786.1	c.649G>T	p.A217S
TTLL2	tubulin tyrosine ligase-like family; member 2	ENSG00000120440	PAP48	155	32.9%	chr6	167674147	CCDS5301.1	c.769C>T	p.R257C
TNFRSF10C	tumor necrosis factor receptor superfamily; member 10c; decoy without an intracellular domain	ENSG00000173535	PAP48	151	10.6%	chr8	23025264	CCDS6037.1	c.147G>NULL	p.NULL-1FsDel1bp
TP73	tumor protein p73	ENSG00000078900	PAP48	119	28.6%	chr1	3635825	CCDS49.1	c.1149G>T	p.Q383H
UBQLN2	ubiquilin 2	ENSG00000188021	PAP48	75	25.3%	chrX	56608477	CCDS14374.1	c.1446G>NUL	p.NULL-1FsDel1bp
USP34	ubiquitin specific peptidase 34	ENSG00000115464	PAP48	211	26.1%	chr2	61428600	CCDS42686.1	c.2804NULL>C	p.NULL-1FsIns1bp
UGT1A6	UDP glucuronosyltransferase 1 family; polypeptide A6	ENSG00000167165	PAP48	104	20.2%	chr2	234191244	CCDS33402.1	c.152G>A	p.R51K
B3GALT1	UDP-Gal:betaGlcNAc beta 1;3-galactosyltransferase; polypeptide 1	ENSG00000172318	PAP48	196	24.5%	chr2	168434310	CCDS2227.1	c.515A>G	p.Y172C
UNC5B	unc-5 homolog B (C. elegans)	ENSG00000107731	PAP48	411	58.9%	chr10	72723274	CCDS7309.1	c.1879G>A	p.E627K
USF2	upstream transcription factor 2; c-fos interacting	ENSG00000105698	PAP48	287	10.5%	chr19	40453524	CCDS12452.1	c.644C>NULL	p.NULL-1FsDel1bp
USH2A	Usher syndrome 2A (autosomal recessive; mild)	ENSG00000042781	PAP48	184	12.5%	chr1	214313102	CCDS31025.1	c.5939A>NULL	p.NULL-1FsDel1bp
VANGL1	vang-like 1 (van gogh; Drosophila)	ENSG00000173218	PAP48	307	20.5%	chr1	116008109	CCDS883.1	c.509T>NULL	p.NULL-1FsDel1bp

ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2; neuro/glioblastoma derived oncogene homolog (avian)	ENSG00000141736	PAP48	90	24.4%	chr17	35136682	CCDS32642.1	c.3059C>T	p.A1020V
VGLL4	vestigial like 4 (Drosophila)	ENSG00000144560	PAP48	47	66.0%	chr3	11581325	CCDS2606.1	c.645NULL>C	p.NULL-1FsIns1bp
WDR62	WD repeat domain 62	ENSG00000075702	PAP48	144	12.5%	chr19	41287332	CCDS33001.1	c.4211C>A	p.P1404Q
WFS1	Wolfram syndrome 1 (wolframin)	ENSG00000109501	PAP48	89	27.0%	chr4	6354803	CCDS3386.1	c.2380GAG>N	p.NULL-1FsDel3bp
XPR1	xenotropic and polytropic retrovirus receptor 1	ENSG00000143324	PAP48	100	19.0%	chr1	179060614	CCDS1340.1	c.866C>T	p.T289M
XKR5	XK; Kell blood group complex subunit-related family; member 5	ENSG00000186530	PAP48	39	33.3%	chr8	6677783	NM_207411	c.291NULL>G	p.NULL-1FsIns1bp
XRCC3	X-ray repair complementing defective repair in Chinese hamster cells 3	ENSG00000126215	PAP48	36	38.9%	chr14	103234998	CCDS9984.1	c.931C>A	p.P311T
XYLT2	xylosyltransferase II	ENSG00000015532	PAP48	97	14.4%	chr17	45786333	CCDS11563.1	c.479C>A	p.P160H
ZBTB5	zinc finger and BTB domain containing 5	ENSG00000168795	PAP48	223	23.3%	chr9	37431765	CCDS6610.1	c.784C>G	p.Q262E
ZEB2	zinc finger E-box binding homeobox 2	ENSG00000169554	PAP48	124	21.0%	chr2	144873340	CCDS2186.1	c.3853T>NULL	p.NULL-1FsDel1bp
ZNF143	zinc finger protein 143	ENSG00000166478	PAP48	66	22.7%	chr11	9479391	CCDS7799.2	c.1145C>T	p.T382I
ZNF223	zinc finger protein 223	ENSG00000178386	PAP48	82	37.8%	chr19	49256533	CCDS12635.1	c.101G>A	p.R34Q
ZNF365	zinc finger protein 365	ENSG00000138311	PAP48	88	19.3%	chr10	63829519	CCDS31209.1	c.1189A>NULL	p.NULL-1FsDel1bp
ZNF490	zinc finger protein 490	ENSG00000188033	PAP48	80	23.8%	chr19	12553077	CCDS12272.1	c.2051A>NULL	p.NULL-1FsDel1bp
ZNF500	zinc finger protein 500	ENSG00000103199	PAP48	91	37.4%	chr16	4755733	CCDS32383.1	c.248T>C	p.L83P
ZNF670	zinc finger protein 670	ENSG00000135747	PAP48	95	34.7%	chr1	245267753	CCDS31087.1	c.791G>A	p.R264H
ZNF749	zinc finger protein 749	ENSG00000186230	PAP48	130	10.8%	chr19	62647482	NM_001023561	c.1154G>A	p.S385N
ZNF804B	zinc finger protein 804B	ENSG00000182348	PAP48	126	38.9%	chr7	88800659	CCDS5613.1	c.427G>A	p.E143K
ZNF831	zinc finger protein 831	ENSG00000124203	PAP48	158	26.6%	chr20	57200090	CCDS42894.1	c.621G>NULL	p.NULL-1FsDel1bp
ZFPM2	zinc finger protein; multitype 2	ENSG00000169946	PAP48	47	25.5%	chr8	106642805	NM_012082	c.340ATT>NU	p.NULL-1FsDel3bp
ZFPM2	zinc finger protein; multitype 2	ENSG00000169946	PAP48	48	25.0%	chr8	106642808	NM_012082	c.343C>T	p.Q115X
ZMIZ1	zinc finger; MIZ-type containing 1	ENSG00000108175	PAP48	254	15.7%	chr10	80742452	CCDS7357.1	c.3144C>NULL	p.NULL-1FsDel1bp
ZMYM1	zinc finger; MYM-type 1	ENSG00000197056	PAP48	82	31.7%	chr1	35351528	CCDS41302.1	c.1510A>NULL	p.NULL-1FsDel1bp
ZMYND8	zinc finger; MYND-type containing 8	ENSG00000101040	PAP48	91	12.1%	chr20	45372209	CCDS13405.1	c.232C>A	p.Q78K
CDH7	cadherin 7; type 2	ENSG00000081138	PAP49	93	19.4%	chr18	61698793	CCDS11993.1	c.2041A>G	p.K681E
CASZ1	castor zinc finger 1	ENSG00000130940	PAP49	55	21.8%	chr1	10636176	CCDS41246.1	c.2525C>A	p.S842X
CD1A	CD1a molecule	ENSG00000158477	PAP49	57	22.8%	chr1	156493413	CCDS1174.1	c.818C>A	p.A273E
KIAA1239	DAVID_KIAA1239	NM_001144990	PAP49	126	25.4%	chr4	37124011	NM_001144990	c.4006G>A	p.G1336R
MAML3	DAVID_mastermind-like 3 (Drosophila)	NM_018717	PAP49	89	21.3%	chr4	141030833	NM_018717	c.1207G>A	p.A403T
GRIA3	glutamate receptor; ionotrophic; AMPA 3	ENSG00000125675	PAP49	48	20.8%	chrX	122287719	CCDS14604.1	c.670G>A	p.E224K
HYDIN	hydrocephalus inducing homolog (mouse)	ENSG00000157423	PAP49	481	10.8%	chr16	69512297	CCDS42189.1	c.7480G>A	p.D2494N
INSRR	insulin receptor-related receptor	ENSG00000027644	PAP49	92	19.6%	chr1	155088471	CCDS1160.1	c.774C>A	p.C258X
ITM2A	integral membrane protein 2A	ENSG00000078596	PAP49	131	21.4%	chrX	78503514	CCDS14444.1	c.671C>T	p.S224F
ITGAD	integrin; alpha D	ENSG00000156886	PAP49	200	22.0%	chr16	31333769	CCDS32438.1	c.2239C>T	p.R747C
KIAA0196	KIAA0196	ENSG00000164961	PAP49	93	18.3%	chr8	126160320	CCDS6355.1	c.553G>A	p.D185N
KLRG2	killer cell lectin-like receptor subfamily G; member 2	ENSG00000188883	PAP49	62	25.8%	chr7	138815432	CCDS5854.1	c.859G>A	p.G287R
MCM7	minichromosome maintenance complex component 7	ENSG00000166508	PAP49	91	35.2%	chr7	99534157	CCDS5683.1	c.700G>A	p.E234K
NULL	NULL	NM_025248	PAP49	98	24.5%	chr17	33970120	NM_025248	c.1768C>T	p.R590X
PUS7	pseudouridylate synthase 7 homolog (S. cerevisiae)	ENSG00000091127	PAP49	68	17.6%	chr7	104933691	CCDS34725.1	c.532C>T	p.R178X
RNF128	ring finger protein 128	ENSG00000133135	PAP49	60	20.0%	chrX	105856906	CCDS14521.1	c.107C>G	p.S36C
RYR1	ryanodine receptor 1 (skeletal)	ENSG00000196218	PAP49	47	23.4%	chr19	43665839	CCDS33011.1	c.4777C>T	p.R1593W
TOX3	TOX high mobility group box family member 3	ENSG00000103460	PAP49	95	20.0%	chr16	51031143	NM_001080430	c.1226C>T	p.S409L
USH2A	Usher syndrome 2A (autosomal recessive; mild)	ENSG00000042781	PAP49	80	18.8%	chr1	214563472	CCDS31025.1	c.1517A>T	p.Y506F

WBSCR28	Williams-Beuren syndrome chromosome region 28	ENSG00000175877	PAP49	278	18.7%	chr7	72918081	CCDS43597.1	c.740C>T	p.A247V
AKR1A1	aldo-keto reductase family 1; member A1 (aldehyde reductase)	ENSG00000117448	PAP50	179	31.8%	chr1	45800082	CCDS523.1	c.29C>A	p.T10N
ARAP3	ArfGAP with RhoGAP domain; ankyrin repeat and PH domain 3	ENSG00000120318	PAP50	122	42.6%	chr5	141039970	CCDS4266.1	c.268C>A	p.Q90K
ATP2B3	ATPase; Ca++ transporting; plasma membrane 3	ENSG00000067842	PAP50	299	30.1%	chrX	152479490	CCDS35440.1	c.3002T>A	p.F1001Y
ATP2B3	ATPase; Ca++ transporting; plasma membrane 3	ENSG00000067842	PAP50	297	31.6%	chrX	152479491	CCDS35440.1	c.3003C>A	p.F1001L
BMP5	bone morphogenetic protein 5	ENSG00000112175	PAP50	360	29.2%	chr6	55847321	CCDS4958.1	c.302T>C	p.V101A
BCR	breakpoint cluster region	ENSG00000186716	PAP50	66	21.2%	chr22	21967272	CCDS13806.1	c.2942ACA>N	p.NULL-1FsDel3bp
CHGB	chromogranin B (secretogranin 1)	ENSG00000089199	PAP50	66	36.4%	chr20	5851270	CCDS13092.1	c.480C>NULL	p.NULL-1FsDel1bp
C20orf106	chromosome 20 open reading frame 106	ENSG00000124103	PAP50	139	22.3%	chr20	54534496	CCDS33493.1	c.479C>T	p.T160M
COG1	component of oligomeric golgi complex 1	ENSG00000166685	PAP50	438	34.9%	chr17	68709295	CCDS11692.1	c.1734C>G	p.I578M
CRX	cone-rod homeobox	ENSG00000105392	PAP50	69	30.4%	chr19	53031330	CCDS12706.1	c.119G>A	p.R40Q
ANKRD36	DAVID_ankyrin repeat domain 36; similar to ankyrin repeat domain 36	NM_001164315	PAP50	56	21.4%	chr2	97187572	NM_001164315	c.1262A>C	p.N421T
LOC652726	DAVID_ankyrin repeat domain 36; similar to ankyrin repeat domain 36	NM_001164315	PAP50	56	21.4%	chr2	97187572	NM_001164315	c.1262A>C	p.N421T
C6orf138	DAVID_chromosome 6 open reading frame 138	NM_001013732	PAP50	228	32.5%	chr6	47955476	NM_001013732	c.1063G>T	p.A355S
CNTNAP5	DAVID_contactin associated protein-like 5	NM_130773	PAP50	151	32.5%	chr2	124920940	NM_130773	c.874T>G	p.F292V
EFCAB4B	DAVID_EF-hand calcium binding domain 4B	NM_001144958	PAP50	99	25.3%	chr12	3613102	NM_001144958	c.1664C>T	p.A555V
LPHN3	DAVID_latrophilin 3	NM_015236	PAP50	87	19.5%	chr4	62483293	NM_015236	c.2049C>A	p.N683K
ND2	DAVID_NADH-ubiquinone oxidoreductase chain 2	ENSG00000198763	PAP50	121	89.3%	chrM	4564	ENST00000361453	c.94G>A	p.G32S
PROM1	DAVID_prominin 1	NM_006017	PAP50	182	30.8%	chr4	15604766	NM_006017	c.1793NULL>A	p.NULL-1FsIns1bp
PCDHA12	DAVID_protocadherin alpha 12	NM_018903	PAP50	134	35.1%	chr5	140237111	NM_018903	c.1870G>A	p.V624M
shisa7	DAVID_UPF0626 protein A	NM_001145176	PAP50	43	41.9%	chr19	60636349	NM_001145176	c.1603G>A	p.E535K
DSC2	desmocollin 2	ENSG00000134755	PAP50	288	32.3%	chr18	26903031	CCDS11892.1	c.2335G>A	p.G779R
DGAT1	diacylglycerol O-acyltransferase homolog 1 (mouse)	ENSG00000185000	PAP50	53	41.5%	chr8	145513018	CCDS6420.1	c.488C>T	p.A163V
FBN1	fibrillin 1	ENSG00000166147	PAP50	147	29.9%	chr15	46495236	CCDS32232.1	c.7840G>A	p.A2614T
GMPR	guanosine monophosphate reductase	ENSG00000137198	PAP50	347	21.0%	chr6	16358563	CCDS4537.1	c.277C>T	p.P93S
GUCY1A3	guanylate cyclase 1; soluble; alpha 3	ENSG00000164116	PAP50	187	30.5%	chr4	156851599	CCDS34085.1	c.832C>T	p.P278S
IGF2AS	insulin-like growth factor 2 antisense	ENSG00000099869	PAP50	84	26.2%	chr11	2124179	CCDS41597.1	c.433G>A	p.A145T
LTBP2	latent transforming growth factor beta binding protein 2	ENSG00000119681	PAP50	75	28.0%	chr14	74039927	CCDS9831.1	c.4718C>T	p.T1573M
MAP3K3	mitogen-activated protein kinase kinase kinase 3	ENSG00000198909	PAP50	179	33.0%	chr17	59120719	CCDS32701.1	c.1048G>A	p.G350S
MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila)	ENSG00000118058	PAP50	106	30.2%	chr11	117874409	CCDS31686.1	c.5908NULL>A	p.NULL-1FsIns1bp
NLRP2	NLR family; pyrin domain containing 2	ENSG00000022556	PAP50	57	33.3%	chr19	60185375	CCDS12913.1	c.497C>T	p.T166M
NULL	NULL	ENSG00000188314	PAP50	489	14.9%	chr19	9207280	ENST00000344049	c.146G>T	p.W49L
NULL	NULL	ENSG00000198938	PAP50	265	88.3%	chrM	9646	ENST00000362079	c.439G>A	p.A147T
PTH2R	parathyroid hormone 2 receptor	ENSG00000144407	PAP50	128	31.3%	chr2	209066384	CCDS2383.1	c.1408C>T	p.R470C
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP50	300	72.3%	chr10	89682884	CCDS31238.1	c.388C>G	p.R130G
PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP50	68	27.9%	chr3	180418788	CCDS43171.1	c.1636C>A	p.Q546K
PLXNA3	plexin A3	ENSG00000130827	PAP50	81	14.8%	chrX	153341759	CCDS14752.1	c.42NULL>G	p.NULL-1FsIns1bp
POLR2D	polymerase (RNA) II (DNA directed) polypeptide D	ENSG00000144231	PAP50	180	22.8%	chr2	128322168	CCDS2151.1	c.412C>T	p.R138C
PCSK1	proprotein convertase subtilisin/kexin type 1	ENSG00000175426	PAP50	78	32.1%	chr5	95769701	CCDS4081.1	c.1178C>G	p.A393G
PPM1E	protein phosphatase; Mg2+/Mn2+ dependent; 1E	ENSG00000175175	PAP50	176	21.0%	chr17	54188369	CCDS11613.1	c.12C>A	p.C4X
RNF41	ring finger protein 41	ENSG00000181852	PAP50	346	33.2%	chr12	54886512	CCDS8909.1	c.940G>A	p.V314M
SHROOM4	shroom family member 4	ENSG00000158352	PAP50	372	32.5%	chrX	50394168	CCDS35277.1	c.1645G>A	p.G549S
SLC27A3	solute carrier family 27 (fatty acid transporter); member 3	ENSG00000143554	PAP50	74	36.5%	chr1	152015795	CCDS1053.1	c.986C>T	p.T329M
SPHK2	sphingosine kinase 2	ENSG00000063176	PAP50	34	41.2%	chr19	53824630	CCDS12727.1	c.1753T>G	p.L585V
SPHKAP	SPHK1 interactor; AKAP domain containing	ENSG00000153820	PAP50	155	32.3%	chr2	228589415	CCDS33389.1	c.4399G>C	p.D1467H

TNFSF15	tumor necrosis factor (ligand) superfamily; member 15	ENSG00000181634	PAP50	206	27.2%	chr9	116592857	CCDS6809.1	c.452C>A	p.S151Y
UNC5CL	unc-5 homolog C (C. elegans)-like	ENSG00000124602	PAP50	104	24.0%	chr6	41109653	CCDS4847.1	c.631C>T	p.R211W
KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	ENSG00000133703	PAP50	186	22.6%	chr12	25289551	CCDS8703.1	c.35G>C	p.G12A
WBSCR22	Williams Beuren syndrome chromosome region 22	ENSG00000071462	PAP50	328	27.4%	chr7	72739136	CCDS5557.1	c.235G>T	p.V79L
WBSCR17	Williams-Beuren syndrome chromosome region 17	ENSG00000185274	PAP50	96	22.9%	chr7	70518909	CCDS5540.1	c.688C>T	p.R230C
ZNF121	zinc finger protein 121	ENSG00000197961	PAP50	151	25.2%	chr19	9537854	CCDS32902.1	c.935A>C	p.Y312S
MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	ENSG00000116984	PAP52	85	12.9%	chr1	235091097	CCDS1614.1	c.2093A>NULI	p.NULL-1FsDel1bp
ACAD10	acyl-CoA dehydrogenase family; member 10	ENSG00000111271	PAP52	140	19.3%	chr12	110628114	CCDS31903.1	c.526G>C	p.D176H
ADAM30	ADAM metallopeptidase domain 30	ENSG00000134249	PAP52	90	11.1%	chr1	120238689	CCDS907.1	c.1794G>A	p.M598I
ALPL	alkaline phosphatase; liver/bone/kidney	ENSG00000162551	PAP52	283	13.4%	chr1	21762227	CCDS217.1	c.335G>C	p.G112A
ANGEL2	angel homolog 2 (Drosophila)	ENSG00000174606	PAP52	91	12.1%	chr1	211247065	ENST00000310246	c.796TTTT>NU	p.NULL-1FsDel4bp
ANK3	ankyrin 3; node of Ranvier (ankyrin G)	ENSG00000151150	PAP52	204	20.1%	chr10	61505923	CCDS7258.1	c.12533NULL>	p.NULL-1FsIns1bp
ANKRD50	ankyrin repeat domain 50	ENSG00000151458	PAP52	113	16.8%	chr4	125811673	CCDS34060.1	c.2209C>T	p.R737X
ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP52	85	15.3%	chr1	26961269	CCDS285.1	c.2291C>NULI	p.NULL-1FsDel1bp
ARID5B	AT rich interactive domain 5B (MRF1-like)	ENSG00000150347	PAP52	98	19.4%	chr10	63520971	CCDS31208.1	c.1743T>NULI	p.NULL-1FsDel1bp
ATP10B	ATPase; class V; type 10B	ENSG00000118322	PAP52	102	14.7%	chr5	160044462	ENST00000326831	c.344C>T	p.S115L
ABCA4	ATP-binding cassette; sub-family A (ABC1); member 4	ENSG00000198691	PAP52	125	20.0%	chr1	94252689	CCDS747.1	c.5458C>T	p.R1820W
BEND3	BEN domain containing 3	ENSG00000178409	PAP52	62	24.2%	chr6	107498295	CCDS34507.1	c.3039G>NUL	p.NULL-1FsDel1bp
CDH1	cadherin 1; type 1; E-cadherin (epithelial)	ENSG00000039068	PAP52	181	16.0%	chr16	67393098	CCDS10869.1	c.188G>A	p.R63Q
CAPN10	calpain 10	ENSG00000142330	PAP52	112	12.5%	chr2	241184961	CCDS42838.1	c.1672C>T	p.R558C
CREB3L3	cAMP responsive element binding protein 3-like 3	ENSG00000060566	PAP52	191	10.5%	chr19	4107993	CCDS12121.1	c.158A>G	p.Q53R
CASP5	caspase 5; apoptosis-related cysteine peptidase	ENSG00000137757	PAP52	309	13.9%	chr11	104378062	CCDS8328.1	c.572C>A	p.P191H
CD207	CD207 molecule; langerin	ENSG00000116031	PAP52	84	17.9%	chr2	70911747	NM_015717	c.1079NULL>(	p.NULL-1FsIns1bp
CD37	CD37 molecule	ENSG00000104894	PAP52	209	20.6%	chr19	54532058	CCDS12760.1	c.223G>T	p.G75C
CDK5RAP3	CDK5 regulatory subunit associated protein 3	ENSG00000108465	PAP52	99	12.1%	chr17	43407993	CCDS42356.1	c.628G>A	p.A210T
CENPB	centromere protein B; 80kDa	ENSG00000125817	PAP52	401	10.5%	chr20	3713819	CCDS13064.1	c.3111G>NUL	p.NULL-1FsDel1bp
CENPE	centromere protein E; 312kDa	ENSG00000138778	PAP52	177	12.4%	chr4	104302058	CCDS34042.1	c.1848C>G	p.S616R
CERK	ceramide kinase	ENSG00000100422	PAP52	86	17.4%	chr22	45464666	CCDS14077.1	c.1636G>NUL	p.NULL-1FsDel1bp
CCT7	chaperonin containing TCP1; subunit 7 (eta)	ENSG00000135624	PAP52	99	13.1%	chr2	73333370	CCDS42696.1	c.893C>T	p.A298V
C11orf82	chromosome 11 open reading frame 82	ENSG00000165490	PAP52	99	12.1%	chr11	82321624	CCDS8263.1	c.1596T>NULI	p.NULL-1FsDel1bp
C16orf7	chromosome 16 open reading frame 7	ENSG00000075399	PAP52	52	23.1%	chr16	88306434	CCDS42220.1	c.-1C>NULL	p.IVS5-3-1SpliceAccept or
C17orf39	chromosome 17 open reading frame 39	ENSG00000141034	PAP52	144	13.2%	chr17	17909232	CCDS11190.1	c.853A>G	p.N285D
C17orf74	chromosome 17 open reading frame 74	ENSG00000184560	PAP52	139	23.0%	chr17	7270441	CCDS42255.1	c.407G>A	p.R136H
C22orf29	chromosome 22 open reading frame 29	ENSG00000215012	PAP52	117	14.5%	chr22	18219298	CCDS13769.1	c.487C>T	p.P163S
CCDC107	coiled-coil domain containing 107	ENSG00000159884	PAP52	267	20.6%	chr9	35650484	ENST00000378405	c.345G>T	p.W115C
COL24A1	collagen; type XXIV; alpha 1	ENSG00000171502	PAP52	149	14.1%	chr1	86363720	CCDS41353.1	c.2256A>NULI	p.NULL-1FsDel1bp
CWC22	CWC22 spliceosome-associated protein homolog (S. cerevisiae)	ENSG00000163510	PAP52	94	12.8%	chr2	180543538	NM_020943	c.-1T>NULL	p.IVS9-3-1SpliceAccept or
DAB2IP	DAB2 interacting protein	ENSG00000136848	PAP52	72	13.9%	chr9	123576458	CCDS6833.2	c.2982C>NULI	p.NULL-1FsDel1bp
CDH13	DAVID_cadherin 13: H-cadherin (heart)	NM_001257	PAP52	137	16.1%	chr16	82077691	NM_001257	c.890A>G	p.N297S

COL6A6	DAVID_collagen type VI alpha 6	NM_001102608	PAP52	175	13.1%	chr3	131772759	NM_001102608	c.2809C>T	p.R937W
Fam184b	DAVID_family with sequence similarity 184: member B	NM_015688	PAP52	268	11.6%	chr4	17318440	NM_015688	c.1095NULL>A	p.NULL-1FsIns1bp
GLTSCR1	DAVID_glioma tumor suppressor candidate region gene 1	NM_015711	PAP52	130	16.2%	chr19	52890002	NM_015711	c.2929G>NUL	p.NULL-1FsDel1bp
Heatr7b2	DAVID_HEAT repeat family member 7B2	NM_173489	PAP52	72	18.1%	chr5	41068665	NM_173489	c.2377G>A	p.E793K
HERC1	DAVID_hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	NM_003922	PAP52	114	14.0%	chr15	61729009	NM_003922	c.10715G>A	p.R3572H
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP52	133	10.5%	chr13	102179997	NM_001146197	c.41988T>NUL	p.NULL-1FsDel1bp
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP52	128	15.6%	chr13	102197820	NM_001146197	c.24165NULL>	p.NULL-1FsIns1bp
INPP4A	DAVID_inositol polyphosphate-4-phosphatase: type I: 107kDa	NM_001134224	PAP52	93	16.1%	chr2	98548645	NM_001134224	c.2278G>A	p.V760I
LPHN3	DAVID_latrophilin 3	NM_015236	PAP52	118	23.7%	chr4	62531767	NM_015236	c.2883G>NUL	p.NULL-1FsDel1bp
Lrrtm2	DAVID_leucine rich repeat transmembrane neuronal 2	NM_015564	PAP52	46	23.9%	chr5	138236663	NM_015564	c.1486A>G	p.I496V
MFRP	DAVID_membrane frizzled-related protein	ENSG00000184824	PAP52	54	24.1%	chr11	118721465	CCDS8421.1	c.516G>A	p.W172X
MLL4	DAVID_myeloid/lymphoid or mixed-lineage leukemia 4	ENSG00000105663	PAP52	410	14.1%	chr19	40913083	NM_014727	c.5077G>T	p.E1693X
ND4L	DAVID_NADH-ubiquinone oxidoreductase chain 4L; NADH-ubiquinone oxidoreductase chain 4	ENSG00000198886	PAP52	102	51.0%	chrM	11712	ENST00000361381	c.952G>A	p.A318T
ND4	DAVID_NADH-ubiquinone oxidoreductase chain 4L; NADH-ubiquinone oxidoreductase chain 4	ENSG00000198886	PAP52	102	51.0%	chrM	11712	ENST00000361381	c.952G>A	p.A318T
ND5	DAVID_NADH-ubiquinone oxidoreductase chain 5	ENSG00000198786	PAP52	102	61.8%	chrM	13629	ENST00000361567	c.1292T>C	p.L431P
nfe2l2	DAVID_nuclear factor (erythroid-derived 2)-like 2	ENSG00000222043	PAP52	210	31.4%	chr2	177807049	CCDS42782.1	c.242G>A	p.G81D
PCLO	DAVID_piccolo (presynaptic cytomatrix protein)	NM_033026	PAP52	188	11.7%	chr7	82268797	NM_033026	c.15053G>NU	p.NULL-1FsDel1bp
RAPGEF5	DAVID_Rap guanine nucleotide exchange factor (GEF) 5	NM_012294	PAP52	67	29.9%	chr7	22297388	NM_012294	c.-1TT>NULL	p.IVS2-3-1SpliceAcceptor
STK11	DAVID_serine/threonine kinase 11	NM_000455	PAP52	49	26.5%	chr19	1172966	NM_000455	c.881C>T	p.P294L
Ik	DAVID_similar to CG18005; IK cytokine: down-regulator of HLA II	NM_006083	PAP52	361	11.6%	chr5	140011524	NM_006083	c.125C>NULL	p.NULL-1FsDel1bp
LOC644456	DAVID_similar to CG18005; IK cytokine: down-regulator of HLA II	NM_006083	PAP52	361	11.6%	chr5	140011524	NM_006083	c.125C>NULL	p.NULL-1FsDel1bp
TBC1D9	DAVID_TBC1 domain family: member 9 (with GRAM domain)	NM_015130	PAP52	123	12.2%	chr4	141817639	NM_015130	c.1125A>NULI	p.NULL-1FsDel1bp
znf292	DAVID_zinc finger protein 292	NM_015021	PAP52	97	20.6%	chr6	88026203	NM_015021	c.6137A>NULI	p.NULL-1FsDel1bp
DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	ENSG00000132153	PAP52	128	13.3%	chr3	47866126	CCDS2759.1	c.3194A>G	p.E1065G
DISP1	dispatched homolog 1 (Drosophila)	ENSG00000154309	PAP52	116	13.8%	chr1	221244535	CCDS1536.1	c.3173T>C	p.V1058A
DNAJB4	DnaJ (Hsp40) homolog; subfamily B; member 4	ENSG00000162616	PAP52	111	10.8%	chr1	78251608	CCDS684.1	c.497T>C	p.V166A
DNAH10	dynein; axonemal; heavy chain 10	ENSG00000197653	PAP52	93	11.8%	chr12	122969393	NM_207437	c.11096G>A	p.R3699H
EP400	E1A binding protein p400	ENSG00000183495	PAP52	193	11.9%	chr12	131088462	CCDS31929.1	c.6072G>T	p.Q2024H
EPN2	epsin 2	ENSG00000072134	PAP52	135	22.2%	chr17	19173543	CCDS11203.1	c.1401A>NULI	p.NULL-1FsDel1bp
EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	ENSG00000187840	PAP52	130	13.1%	chr8	38036601	CCDS6100.1	c.348G>A	p.M116I
FAM82A1	family with sequence similarity 82; member A1	ENSG00000115841	PAP52	151	17.2%	chr2	38032287	CCDS1792.1	c.425T>NULL	p.NULL-1FsDel1bp
FAT2	FAT tumor suppressor homolog 2 (Drosophila)	ENSG00000086570	PAP52	120	17.5%	chr5	150905053	CCDS4317.1	c.5828C>A	p.A1943D
FAT4	FAT tumor suppressor homolog 4 (Drosophila)	ENSG00000196159	PAP52	77	28.6%	chr4	126630661	CCDS3732.2	c.13063G>T	p.D4355Y
FGFR1OP	FGFR1 oncogene partner	ENSG00000213066	PAP52	108	11.1%	chr6	167358312	CCDS5296.1	c.859C>NULL	p.NULL-1FsDel1bp
FNIP1	folliculin interacting protein 1	ENSG00000217128	PAP52	236	12.3%	chr5	131034056	CCDS34227.1	c.3107A>G	p.Q1036R
FUT9	fucosyltransferase 9 (alpha (1;3) fucosyltransferase)	ENSG00000172461	PAP52	126	14.3%	chr6	96757856	CCDS5033.1	c.104G>A	p.S35N

FRY	furry homolog (Drosophila)	ENSG00000073910	PAP52	102	15.7%	chr13	31711960	CCDS41875.1	c.6629G>A	p.R2210Q
GFM2	G elongation factor; mitochondrial 2	ENSG00000164347	PAP52	91	18.7%	chr5	74057306	CCDS4023.1	c.1943T>C	p.V648A
GPR149	G protein-coupled receptor 149	ENSG00000174948	PAP52	90	15.6%	chr3	155629987	CCDS43162.1	c.1092T>NULI	p.NULL-1FsDel1bp
GPR50	G protein-coupled receptor 50	ENSG00000102195	PAP52	227	13.2%	chrX	150098946	CCDS44012.1	c.233C>T	p.A78V
GAL3ST4	galactose-3-O-sulfotransferase 4	ENSG00000197093	PAP52	73	13.7%	chr7	99596377	CCDS5688.1	c.571A>G	p.N191D
GRIN2B	glutamate receptor; ionotropic; N-methyl D-aspartate 2B	ENSG00000150086	PAP52	79	17.7%	chr12	13608678	CCDS8662.1	c.2761G>A	p.A921T
GREB1	growth regulation by estrogen in breast cancer 1	ENSG00000196208	PAP52	67	17.9%	chr2	11652909	CCDS42655.1	c.1778C>T	p.T593M
HIRIP3	HIRA interacting protein 3	ENSG00000149929	PAP52	176	13.1%	chr16	29914180	CCDS10664.1	c.289GAG>NU	p.NULL-1FsDel3bp
HIST1H4A	histone cluster 1; H4a	ENSG00000196176	PAP52	103	18.4%	chr6	26130087	CCDS4571.1	c.202C>A	p.R68S
HTATSF1	HIV-1 Tat specific factor 1	ENSG00000102241	PAP52	70	15.7%	chrX	135421297	CCDS14657.1	c.1727A>T	p.E576V
HOXA11	homeobox A11	ENSG00000005073	PAP52	151	12.6%	chr7	27188987	CCDS5411.1	c.1127A>NULI	p.NULL-1FsDel1bp
HCFC1	host cell factor C1 (VP16-accessory protein)	ENSG00000172534	PAP52	138	23.2%	chrX	152877224	CCDS44020.1	c.1793C>T	p.S598L
ITPKB	inositol 1;4;5-trisphosphate 3-kinase B	ENSG00000143772	PAP52	156	23.1%	chr1	224991065	CCDS1555.1	c.718C>T	p.R240W
ICA1	islet cell autoantigen 1; 69kDa	ENSG00000003147	PAP52	91	28.6%	chr7	8164776	CCDS34602.1	c.736A>NULL	p.NULL-1FsDel1bp
JAK1	Janus kinase 1	ENSG00000162434	PAP52	38	26.3%	chr1	65079585	CCDS41346.1	c.2674A>NULI	p.NULL-1FsDel1bp
KIAA1244	KIAA1244	ENSG00000112379	PAP52	159	13.2%	chr6	138697077	NM_020340	c.5401G>A	p.G1801R
KIAA1919	KIAA1919	ENSG00000173214	PAP52	117	11.1%	chr6	111694054	CCDS5090.1	c.596T>NULL	p.NULL-1FsDel1bp
KIAA2018	KIAA2018	ENSG00000176542	PAP52	98	10.2%	chr3	114858801	CCDS43133.1	c.10899NULL>	p.NULL-1FsIns3bp
KIR3DP1	killer cell immunoglobulin-like receptor; three domains; pseudogene 1	ENSG00000215765	PAP52	30	33.3%	chr19	59991501	NM_001015070	c.395C>G	p.P132R
KIF21A	kinesin family member 21A	ENSG00000139116	PAP52	189	11.6%	chr12	38006398	ENST00000361418	c.3417NULL>T	p.NULL-1FsIns1bp
LARP1	La ribonucleoprotein domain family; member 1	ENSG00000155506	PAP52	227	15.0%	chr5	154163392	CCDS34281.1	c.2333G>A	p.R778H
LAMA1	laminin; alpha 1	ENSG00000101680	PAP52	102	20.6%	chr18	7003887	CCDS32787.1	c.3290C>T	p.T1097M
LELP1	late cornified envelope-like proline-rich 1	ENSG00000203784	PAP52	462	14.9%	chr1	151443985	CCDS30869.1	c.178C>T	p.P60S
LRRC16A	leucine rich repeat containing 16A	ENSG00000079691	PAP52	84	25.0%	chr6	25560433	ENST00000332168	c.917TT>NULI	p.NULL-1FsDel2bp
LRRC3B	leucine rich repeat containing 3B	ENSG00000179796	PAP52	170	12.9%	chr3	26726207	CCDS2644.1	c.40A>G	p.M14V
LRRK2	leucine-rich repeat kinase 2	ENSG00000188906	PAP52	108	15.7%	chr12	38984225	ENST00000343742	c.3799A>NULI	p.NULL-1FsDel1bp
LPCAT2	lysophosphatidylcholine acyltransferase 2	ENSG00000087253	PAP52	122	13.1%	chr16	54128995	CCDS10753.1	c.802C>T	p.Q268X
MED8	mediator complex subunit 8	ENSG00000159479	PAP52	138	11.6%	chr1	43622730	NM_052877	c.986A>NULL	p.NULL-1FsDel1bp
MBD4	methyl-CpG binding domain protein 4	ENSG00000129071	PAP52	118	13.6%	chr3	130638238	CCDS3058.1	c.1804A>NULI	p.NULL-1FsDel1bp
MACF1	microtubule-actin crosslinking factor 1	ENSG00000127603	PAP52	145	11.7%	chr1	39578795	CCDS436.1	c.5570T>C	p.L1857S
MCM3AP	minichromosome maintenance complex component 3 associated protein	ENSG00000160294	PAP52	120	19.2%	chr21	46529188	CCDS13734.1	c.441A>C	p.K147N
MPRIP	myosin phosphatase Rho interacting protein	ENSG00000133030	PAP52	165	14.5%	chr17	16987644	CCDS42268.1	c.1085C>NULI	p.NULL-1FsDel1bp
MYO15A	myosin XVA	ENSG00000091536	PAP52	302	16.2%	chr17	17964018	CCDS42271.1	c.1179NULL>(	p.NULL-1FsIns1bp
MYH10	myosin; heavy chain 10; non-muscle	ENSG00000133026	PAP52	78	23.1%	chr17	8467130	CCDS11144.1	c.160C>T	p.R54W
NDUFC2	NADH dehydrogenase (ubiquinone) 1; subcomplex unknown; 2; 14.5kDa	ENSG00000151366	PAP52	101	13.9%	chr11	77461795	CCDS8257.1	c.349TT>NULI	p.NULL-1FsDel2bp
NRAP	nebulin-related anchoring protein	ENSG00000197893	PAP52	92	16.3%	chr10	115362156	CCDS7579.1	c.3325C>G	p.H1109D
NPHS1	nephrosis 1; congenital; Finnish type (nephrin)	ENSG00000161270	PAP52	85	11.8%	chr19	41028184	CCDS32996.1	c.1856A>G	p.Q619R

NFASC	neurofascin homolog (chicken)	ENSG00000163531	PAP52	101	10.9%	chr1	203190656	CCDS30982.1	c.471C>NULL	p.NULL-1FsDel1bp
NUDT17	nudix (nucleoside diphosphate linked moiety X)-type motif 17	ENSG00000186364	PAP52	38	31.6%	chr1	144298838	CCDS30830.1	c.599G>T	p.R200L
NULL	NULL	NM_001015070	PAP52	30	33.3%	chr19	59991501	NM_001015070	c.395C>G	p.P132R
OLFM2	olfactomedin 2	ENSG00000105088	PAP52	101	14.9%	chr19	9826091	CCDS12221.1	c.1136T>C	p.V379A
OR13A1	olfactory receptor; family 13; subfamily A; member 1	ENSG00000172678	PAP52	75	26.7%	chr10	45118928	CCDS31188.1	c.949G>T	p.A317S
OR6M1	olfactory receptor; family 6; subfamily M; member 1	ENSG00000196099	PAP52	240	12.1%	chr11	123182038	CCDS31696.1	c.1171NULL>(	p.NULL-1FsIns1bp
OR8H2	olfactory receptor; family 8; subfamily H; member 2	ENSG00000181767	PAP52	15	73.3%	chr11	55629233	CCDS31518.1	c.139A>C	p.I47L
OLR1	oxidized low density lipoprotein (lectin-like) receptor 1	ENSG00000173391	PAP52	95	14.7%	chr12	10204671	CCDS8618.1	c.545T>A	p.I182N
PITX2	paired-like homeodomain 2	ENSG00000164093	PAP52	99	13.1%	chr4	111758875	CCDS3694.1	c.830C>T	p.P277L
PDZD2	PDZ domain containing 2	ENSG00000133401	PAP52	223	20.6%	chr5	32125169	CCDS34137.1	c.5858C>NULI	p.NULL-1FsDel1bp
PLIN5	perilipin 5	ENSG00000214456	PAP52	125	11.2%	chr19	4474694	CCDS42473.1	c.1238C>T	p.P413L
PHF3	PHD finger protein 3	ENSG00000118482	PAP52	98	13.3%	chr6	64473912	CCDS4966.1	c.3402A>NULI	p.NULL-1FsDel1bp
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP52	181	12.2%	chr10	89682897	CCDS31238.1	c.401T>A	p.M134K
PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP52	86	11.6%	chr3	180418776	CCDS43171.1	c.1624G>A	p.E542K
PBRM1	polybromo 1	ENSG00000163939	PAP52	93	10.8%	chr3	52626466	CCDS2859.1	c.1574A>G	p.D525G
PBRM1	polybromo 1	ENSG00000163939	PAP52	87	17.2%	chr3	52651104	CCDS2859.1	c.-1GT>NULL	p.IVS8-3-1SpliceAcceptor
KCNE1	potassium voltage-gated channel; Isk-related family; member 1	ENSG00000180509	PAP52	89	15.7%	chr21	34743417	CCDS13636.1	c.775NULL>C	p.NULL-1FsIns1bp
KCNQ3	potassium voltage-gated channel; KQT-like subfamily; member 3	ENSG00000184156	PAP52	44	22.7%	chr8	133219386	CCDS34943.1	c.1628T>C	p.V543A
PRODH2	proline dehydrogenase (oxidase) 2	ENSG00000161270	PAP52	85	11.8%	chr19	41028184	CCDS32996.1	c.1856A>G	p.Q619R
PRR15L	proline rich 15-like	ENSG00000167183	PAP52	177	16.4%	chr17	43385329	CCDS11523.1	c.271A>G	p.N91D
P4HA1	prolyl 4-hydroxylase; alpha polypeptide I	ENSG00000122884	PAP52	56	23.2%	chr10	74483330	CCDS41537.1	c.488C>T	p.T163M
PCSK5	proprotein convertase subtilisin/kexin type 5	ENSG00000099139	PAP52	115	18.3%	chr9	77998074	CCDS6652.1	c.2728A>G	p.T910A
PSME4	proteasome (prosome; macropain) activator subunit 4	ENSG00000068878	PAP52	71	18.3%	chr2	54020644	CCDS33197.1	c.-1C>NULL	p.IVS2-3-1SpliceAcceptor
PRKCB	protein kinase C; beta	ENSG00000166501	PAP52	117	17.1%	chr16	24103969	CCDS10619.1	c.1570T>C	p.W524R
PTPN3	protein tyrosine phosphatase; non-receptor type 3	ENSG00000070159	PAP52	177	18.1%	chr9	111212416	CCDS6776.1	c.1414G>A	p.G472S
P2RY4	pyrimidinergic receptor P2Y; G-protein coupled; 4	ENSG00000186912	PAP52	76	22.4%	chrX	69395809	CCDS14398.1	c.391G>A	p.V131M
PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	ENSG00000131828	PAP52	39	38.5%	chrX	19273785	ENST00000379815	c.68CCC>NUL	p.NULL-1FsDel3bp
RANBP2	RAN binding protein 2	ENSG00000153201	PAP52	121	10.7%	chr2	108746561	CCDS2079.1	c.3134C>T	p.T1045M
RTP3	receptor (chemosensory) transporter protein 3	ENSG00000163825	PAP52	262	12.2%	chr3	46517207	CCDS2740.1	c.513C>NULL	p.NULL-1FsDel1bp
RRAS2	related RAS viral (r-ras) oncogene homolog 2	ENSG00000133818	PAP52	153	32.7%	chr11	14272966	CCDS7814.1	c.215A>T	p.Q72L
ARHGEF1	Rho guanine nucleotide exchange factor (GEF) 1	ENSG00000076928	PAP52	52	19.2%	chr19	47092299	CCDS12590.1	c.1070C>NULI	p.NULL-1FsDel1bp
RNF43	ring finger protein 43	ENSG00000108375	PAP52	92	20.7%	chr17	53790160	CCDS11607.1	c.3331G>NUL	p.NULL-1FsDel1bp
RBM23	RNA binding motif protein 23	ENSG00000100461	PAP52	142	19.0%	chr14	22440863	CCDS41921.1	c.1316T>C	p.M439T
SEC31A	SEC31 homolog A (S. cerevisiae)	ENSG00000138674	PAP52	76	21.1%	chr4	83997923	CCDS3596.1	c.1645G>T	p.E549X
SEC31A	SEC31 homolog A (S. cerevisiae)	ENSG00000138674	PAP52	82	18.3%	chr4	84010567	CCDS3596.1	c.817C>A	p.P273T
SELP	selectin P (granule membrane protein 140kDa; antigen CD62)	ENSG00000174175	PAP52	171	14.6%	chr1	167845449	CCDS1282.1	c.1250C>T	p.A417V
SRP72	signal recognition particle 72kDa	ENSG00000174780	PAP52	57	22.8%	chr4	57028577	CCDS3506.1	c.19G>NULL	p.NULL-1FsDel1bp
SIN3A	SIN3 homolog A; transcription regulator (yeast)	ENSG00000169375	PAP52	48	22.9%	chr15	73480186	CCDS10279.1	c.1675C>T	p.R559X

SLC26A1	solute carrier family 26 (sulfate transporter); member 1	ENSG00000145217	PAP52	198	18.2%	chr4	972997	CCDS33934.1	c.3259G>NUL	p.NULL-1FsDel1bp
SPEG	SPEG complex locus	ENSG00000072195	PAP52	92	13.0%	chr2	220034912	CCDS42824.1	c.2505G>T	p.E835D
SND1	staphylococcal nuclease and tudor domain containing 1	ENSG00000197157	PAP52	141	13.5%	chr7	127132172	CCDS34747.1	c.884G>A	p.R295H
SMC4	structural maintenance of chromosomes 4	ENSG00000113810	PAP52	91	13.2%	chr3	161604838	CCDS3189.1	c.539A>G	p.N180S
SMARCA4	SWI/SNF related; matrix associated; actin dependent regulator of chromatin; subfamily a; member 4	ENSG00000127616	PAP52	75	16.0%	chr19	10993428	CCDS12253.1	c.2644G>A	p.E882K
SYCP1	synaptonemal complex protein 1	ENSG00000198765	PAP52	63	27.0%	chr1	115339124	CCDS879.1	c.2892A>NULL	p.NULL-1FsDel1bp
SYT14L	synaptotagmin XIV-like	ENSG00000215127	PAP52	163	15.3%	chr4	68611142	ENST00000399639	c.280C>T	p.R94W
TECTA	tectorin alpha	ENSG00000109927	PAP52	61	19.7%	chr11	120501719	CCDS8434.1	c.1702A>T	p.I568F
TRPV4	transient receptor potential cation channel; subfamily V; member 4	ENSG00000111199	PAP52	98	10.2%	chr12	108705943	CCDS9134.1	c.2639C>NULL	p.NULL-1FsDel1bp
TMEM120A	transmembrane protein 120A	ENSG00000189077	PAP52	131	17.6%	chr7	75455575	ENST00000338761	c.236A>G	p.N79S
TCHH	trichohyalin	ENSG00000159450	PAP52	271	14.0%	chr1	150350928	CCDS41396.1	c.7080GAG>N	p.NULL-1FsDel3bp
USP38	ubiquitin specific peptidase 38	ENSG00000170185	PAP52	227	15.4%	chr4	144354719	CCDS3758.1	c.2140A>G	p.T714A
URGCP	upregulator of cell proliferation	ENSG00000106608	PAP52	164	18.9%	chr7	43884025	CCDS43572.1	c.4026C>NULL	p.NULL-1FsDel1bp
VPS13D	vacuolar protein sorting 13 homolog D (S. cerevisiae)	ENSG00000048707	PAP52	118	11.0%	chr1	12291126	CCDS30588.1	c.6491A>G	p.D2164G
WDTC1	WD and tetratricopeptide repeats 1	ENSG00000142784	PAP52	62	32.3%	chr1	27493695	CCDS296.1	c.861G>NULL	p.NULL-1FsDel1bp
WEE2	WEE1 homolog 2 (S. pombe)	ENSG00000214102	PAP52	139	15.1%	chr7	141060631	CCDS43660.1	c.496T>A	p.L166I
WNT1	wingless-type MMTV integration site family; member 1	ENSG00000125084	PAP52	101	15.8%	chr12	47660615	CCDS8776.1	c.500G>NULL	p.NULL-1FsDel1bp
ZNF484	zinc finger protein 484	ENSG00000127081	PAP52	277	11.2%	chr9	94650028	CCDS35066.1	c.862T>C	p.F288L
ZMIZ1	zinc finger; MIZ-type containing 1	ENSG00000108175	PAP52	118	23.7%	chr10	80742452	CCDS7357.1	c.3144C>NULL	p.NULL-1FsDel1bp
ZAR1	zygote arrest 1	ENSG00000182223	PAP52	99	10.1%	chr4	48189760	CCDS3483.1	c.1105T>C	p.Y369H
CNP	2';3'-cyclic nucleotide 3' phosphodiesterase	ENSG00000173786	PAP53	229	13.1%	chr17	37379105	CCDS11414.2	c.903G>T	p.E301D
HMGCLL1	3-hydroxymethyl-3-methylglutaryl-CoA lyase-like 1	ENSG00000146151	PAP53	177	23.7%	chr6	55551757	CCDS43475.1	c.56G>A	p.R19Q
XRN1	5'-3' exoribonuclease 1	ENSG00000114127	PAP53	70	15.7%	chr3	143622580	CCDS3123.1	c.1276AAG>N	p.NULL-1FsDel3bp
XRN2	5'-3' exoribonuclease 2	ENSG00000088930	PAP53	169	18.3%	chr20	21259324	CCDS13144.1	c.557C>A	p.P186H
AZI1	5-azacytidine induced 1	ENSG00000141577	PAP53	341	12.9%	chr17	76779684	CCDS32764.1	c.2561G>A	p.R854Q
HTR3C	5-hydroxytryptamine (serotonin) receptor 3; family member C	ENSG00000178084	PAP53	94	22.3%	chr3	185256672	CCDS3250.1	c.293C>T	p.P98L
HTR6	5-hydroxytryptamine (serotonin) receptor 6	ENSG00000158748	PAP53	86	25.6%	chr1	19878093	CCDS197.1	c.968T>C	p.F323S
NT5C1B	5'-nucleotidase; cytosolic IB	ENSG00000185013	PAP53	51	21.6%	chr2	18621555	CCDS33150.1	c.1289C>T	p.A430V
OPLAH	5-oxoprolinase (ATP-hydrolysing)	ENSG00000178814	PAP53	210	26.7%	chr8	145181469	ENST00000360660	c.2843G>NUL	p.NULL-1FsDel1bp
AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	ENSG00000127914	PAP53	70	14.3%	chr7	91469032	CCDS5622.1	c.1865T>C	p.L622S
AKAP13	A kinase (PRKA) anchor protein 13	ENSG00000170776	PAP53	248	21.0%	chr15	83923384	CCDS32320.1	c.1081GAG>N	p.NULL-1FsDel3bp
ABHD15	abhydrolase domain containing 15	ENSG00000168792	PAP53	264	28.4%	chr17	24913793	CCDS32602.1	c.1319G>A	p.R440H
ACACB	acetyl-CoA carboxylase beta	ENSG00000076555	PAP53	75	21.3%	chr12	108187347	CCDS31898.1	c.6992G>A	p.R2331H
ACTL6B	actin-like 6B	ENSG00000077080	PAP53	59	25.4%	chr7	100078846	CCDS5702.1	c.1240G>T	p.E414X
ACTL9	actin-like 9	ENSG00000181786	PAP53	137	20.4%	chr19	8669138	CCDS12207.1	c.2164C>NULL	p.NULL-1FsDel1bp
ABR	active BCR-related gene	ENSG00000159842	PAP53	60	20.0%	chr17	863117	CCDS10999.1	c.1829C>T	p.T610M
ACVR2B	activin A receptor; type IIB	ENSG00000114739	PAP53	98	29.6%	chr3	38493862	CCDS2679.1	c.133G>A	p.G45S
ACADSB	acyl-CoA dehydrogenase; short/branched chain	ENSG00000196177	PAP53	77	23.4%	chr10	124800579	CCDS7634.1	c.1015G>A	p.V339M
ACOX3	acyl-CoA oxidase 3; pristanoyl	ENSG00000087008	PAP53	140	35.0%	chr4	8458608	CCDS3401.1	c.838A>NULL	p.NULL-1FsDel1bp
ACSS3	acyl-CoA synthetase short-chain family member 3	ENSG00000111058	PAP53	104	27.9%	chr12	80057098	CCDS9022.1	c.703G>A	p.V235I

ACOT2	acyl-CoA thioesterase 2	ENSG00000119673	PAP53	169	10.1%	chr14	73110021	CCDS9816.1	c.820A>G	p.M274V
ADAM11	ADAM metallopeptidase domain 11	ENSG00000073670	PAP53	72	22.2%	chr17	40192652	CCDS11486.1	c.98G>NULL	p.NULL-1FsDel1bp
ADAM15	ADAM metallopeptidase domain 15	ENSG00000143537	PAP53	337	24.6%	chr1	153295297	CCDS1087.1	c.862C>T	p.R288C
ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif; 1	ENSG00000154734	PAP53	197	19.8%	chr21	27132654	CCDS33524.1	c.2354A>NULL	p.NULL-1FsDel1bp
ADAMTS13	ADAM metallopeptidase with thrombospondin type 1 motif; 13	ENSG00000160323	PAP53	101	26.7%	chr9	135291812	CCDS6970.1	c.1351G>A	p.A451T
ADAMTS13	ADAM metallopeptidase with thrombospondin type 1 motif; 13	ENSG00000160323	PAP53	38	34.2%	chr9	135298397	CCDS6970.1	c.2314G>A	p.A772T
ADAMTS15	ADAM metallopeptidase with thrombospondin type 1 motif; 15	ENSG00000166106	PAP53	37	40.5%	chr11	129848640	CCDS8488.1	c.2567G>A	p.G856D
ADAMTS5	ADAM metallopeptidase with thrombospondin type 1 motif; 5	ENSG00000154736	PAP53	242	26.4%	chr21	27218499	CCDS13579.1	c.2537G>A	p.R846H
ADAMTSL4	ADAMTS-like 4	ENSG00000143382	PAP53	85	36.5%	chr1	148797130	CCDS955.1	c.2263G>NUL	p.NULL-1FsDel1bp
AP1G2	adaptor-related protein complex 1; gamma 2 subunit	ENSG00000213983	PAP53	242	23.1%	chr14	23103612	CCDS9602.1	c.920G>A	p.R307Q
AP3B2	adaptor-related protein complex 3; beta 2 subunit	ENSG00000103723	PAP53	67	26.9%	chr15	81145561	ENST00000261722	c.1156G>A	p.D386N
AP3D1	adaptor-related protein complex 3; delta 1 subunit	ENSG00000065000	PAP53	117	25.6%	chr19	2080381	CCDS42459.1	c.668C>T	p.P223L
ASXL1	additional sex combs like 1 (Drosophila)	ENSG00000171456	PAP53	49	26.5%	chr20	30486103	CCDS13201.1	c.1927G>NUL	p.NULL-1FsDel1bp
ADD1	adducin 1 (alpha)	ENSG00000087274	PAP53	312	20.2%	chr4	2900028	CCDS3363.1	c.2287AAG>N	p.NULL-1FsDel3bp
AMPD1	adenosine monophosphate deaminase 1	ENSG00000116748	PAP53	49	34.7%	chr1	115017827	CCDS876.1	c.2041G>A	p.E681K
ADCY9	adenylate cyclase 9	ENSG00000162104	PAP53	123	38.2%	chr16	4104547	CCDS32382.1	c.898G>A	p.V300I
ARF1	ADP-ribosylation factor 1	ENSG00000143761	PAP53	138	21.0%	chr1	226351494	CCDS1565.1	c.56G>A	p.R19H
ADRBK1	adrenergic; beta; receptor kinase 1	ENSG00000173020	PAP53	61	29.5%	chr11	66806339	CCDS8156.1	c.979G>A	p.E327K
AEBP1	AE binding protein 1	ENSG00000106624	PAP53	225	26.7%	chr7	44120063	CCDS5476.1	c.3155C>T	p.T1052M
AFF3	AF4/FMR2 family; member 3	ENSG00000144218	PAP53	115	25.2%	chr2	99551798	CCDS33258.1	c.3005C>T	p.A1002V
ADH6	alcohol dehydrogenase 6 (class V)	ENSG00000172955	PAP53	313	23.6%	chr4	100347749	CCDS43255.1	c.841G>A	p.A281T
ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	ENSG00000111275	PAP53	83	27.7%	chr12	110722171	CCDS9155.1	c.1327G>A	p.G443R
AHSG	alpha-2-HS-glycoprotein	ENSG00000145192	PAP53	433	13.9%	chr3	187821252	CCDS3278.1	c.943G>A	p.D315N
AHSG	alpha-2-HS-glycoprotein	ENSG00000145192	PAP53	400	20.5%	chr3	187821327	CCDS3278.1	c.1018C>T	p.R340C
ACCN2	amiloride-sensitive cation channel 2; neuronal	ENSG00000110881	PAP53	145	29.0%	chr12	48738853	CCDS8796.1	c.37G>A	p.V13I
ALK	anaplastic lymphoma receptor tyrosine kinase	ENSG00000171094	PAP53	207	26.6%	chr2	29270150	CCDS33172.1	c.4307G>A	p.R1436H
ANGEL2	angel homolog 2 (Drosophila)	ENSG00000174606	PAP53	133	20.3%	chr1	211248264	CCDS1512.1	c.808TC>NUL	p.NULL-1FsDel2bp
AMOTL2	angiomotin like 2	ENSG00000114019	PAP53	138	21.7%	chr3	135572263	CCDS33860.1	c.703G>A	p.G235S
ANK2	ankyrin 2; neuronal	ENSG00000145362	PAP53	120	25.0%	chr4	114499584	CCDS3702.1	c.10361G>NU	p.NULL-1FsDel1bp
ANKRD26	ankyrin repeat domain 26	ENSG00000107890	PAP53	155	23.2%	chr10	27324053	ENST00000342931	c.802AT>NULL	p.NULL-1FsDel2bp
ANKRD54	ankyrin repeat domain 54	ENSG00000100124	PAP53	50	30.0%	chr22	36558640	CCDS13959.1	c.778C>T	p.R260C
ANXA11	annexin A11	ENSG00000122359	PAP53	160	20.6%	chr10	81916983	CCDS7364.1	c.628C>T	p.R210W
ANO7	anoctamin 7	ENSG00000146205	PAP53	239	23.4%	chr2	241788267	CCDS33423.1	c.670C>NULL	p.NULL-1FsDel1bp
AQP5	aquaporin 5	ENSG00000161798	PAP53	344	25.9%	chr12	48644176	CCDS8793.1	c.563G>A	p.R188H
AGAP3	ArfGAP with GTPase domain; ankyrin repeat and PH domain 3	ENSG00000133612	PAP53	79	34.2%	chr7	150468010	CCDS43681.1	c.1678G>A	p.A560T
AGAP3	ArfGAP with GTPase domain; ankyrin repeat and PH domain 3	ENSG00000133612	PAP53	146	26.7%	chr7	150470564	CCDS43681.1	c.2183C>T	p.A728V
ARAP2	ArfGAP with RhoGAP domain; ankyrin repeat and PH domain 2	ENSG00000047365	PAP53	111	17.1%	chr4	35826487	CCDS3441.1	c.2935C>T	p.R979C
ARMC9	armadillo repeat containing 9	ENSG00000135931	PAP53	311	24.1%	chr2	231829559	CCDS2484.1	c.896G>A	p.R299Q
ACTR1A	ARP1 actin-related protein 1 homolog A; centractin alpha (yeast)	ENSG00000138107	PAP53	75	28.0%	chr10	104234007	CCDS7536.1	c.557C>T	p.A186V

ARSA	arylsulfatase A	ENSG00000100299	PAP53	133	27.8%	chr22	49412623	CCDS14100.1	c.536G>NULL	p.NULL-1FsDel1bp
ASH1L	ash1 (absent; small; or homeotic)-like (Drosophila)	ENSG00000116539	PAP53	225	19.1%	chr1	153674986	CCDS1113.2	c.5584G>A	p.V1862I
ALG12	asparagine-linked glycosylation 12; alpha-1;6-mannosyltransferase homolog (S. cerevisiae)	ENSG00000182858	PAP53	85	32.9%	chr22	48683006	ENST00000332276	c.1624C>NULL	p.NULL-1FsDel1bp
ASPH	aspartate beta-hydroxylase	ENSG00000198363	PAP53	88	15.9%	chr8	62637921	CCDS34898.1	c.1509A>NULL	p.NULL-1FsDel1bp
ASTE1	asteroid homolog 1 (Drosophila)	ENSG00000034533	PAP53	92	23.9%	chr3	132215737	CCDS3068.1	c.2223AA>NU	p.NULL-1FsDel2bp
ASTN2	astrotactin 2	ENSG00000148219	PAP53	279	20.8%	chr9	118227955	CCDS6815.1	c.3863G>A	p.R1288Q
ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP53	273	26.4%	chr1	26978509	CCDS285.1	c.5533C>T	p.R1845W
ARID1B	AT rich interactive domain 1B (SWI1-like)	ENSG00000049618	PAP53	142	21.1%	chr6	157569390	CCDS5251.1	c.5369G>A	p.R1790H
ARID5B	AT rich interactive domain 5B (MRF1-like)	ENSG00000150347	PAP53	67	35.8%	chr10	63520711	CCDS31208.1	c.1483A>NULL	p.NULL-1FsDel1bp
ATM	ataxia telangiectasia mutated	ENSG00000149311	PAP53	103	22.3%	chr11	107711858	CCDS31669.1	c.8228C>T	p.T2743M
ATXN2L	ataxin 2-like	ENSG00000168488	PAP53	52	23.1%	chr16	28754851	CCDS10640.1	c.2992G>NUL	p.NULL-1FsDel1bp
ATG16L1	ATG16 autophagy related 16-like 1 (S. cerevisiae)	ENSG00000085978	PAP53	77	22.1%	chr2	233856106	CCDS2503.2	c.1171C>T	p.R391X
ATP2B1	ATPase; Ca++ transporting; plasma membrane 1	ENSG00000070961	PAP53	471	23.4%	chr12	88553007	CCDS9035.1	c.559C>T	p.R187X
ATP2B3	ATPase; Ca++ transporting; plasma membrane 3	ENSG00000067842	PAP53	303	30.0%	chrX	152460155	CCDS35440.1	c.353C>T	p.A118V
ATP9A	ATPase; class II; type 9A	ENSG00000054793	PAP53	175	26.3%	chr20	49746048	CCDS33489.1	c.538G>T	p.E180X
ABCA3	ATP-binding cassette; sub-family A (ABC1); member 3	ENSG00000167972	PAP53	172	18.6%	chr16	2268037	CCDS10466.1	c.4753G>A	p.A1585T
ABCB8	ATP-binding cassette; sub-family B (MDR/TAP); member 8	ENSG00000197150	PAP53	57	22.8%	chr7	150356832	ENST00000356058	c.107G>A	p.R36H
ABCB9	ATP-binding cassette; sub-family B (MDR/TAP); member 9	ENSG00000150967	PAP53	98	16.3%	chr12	121980563	CCDS9241.1	c.2149C>T	p.R717C
ABCC1	ATP-binding cassette; sub-family C (CFTR/MRP); member 1	ENSG00000103222	PAP53	350	17.1%	chr16	16049621	CCDS42122.1	c.1340C>NULL	p.NULL-1FsDel1bp
ABCC12	ATP-binding cassette; sub-family C (CFTR/MRP); member 12	ENSG00000140798	PAP53	164	22.0%	chr16	46696676	CCDS10730.1	c.2548G>A	p.V850M
ABCE1	ATP-binding cassette; sub-family E (OABP); member 1	ENSG00000164163	PAP53	46	28.3%	chr4	146252908	CCDS34071.1	c.778C>T	p.R260X
AXIN2	axin 2	ENSG00000168646	PAP53	102	33.3%	chr17	60963047	CCDS11662.1	c.2227G>NUL	p.NULL-1FsDel1bp
BPIL1	bactericidal/permeability-increasing protein-like 1	ENSG00000078898	PAP53	84	26.2%	chr20	31065332	CCDS13210.1	c.364G>A	p.V122M
BBS7	Bardet-Biedl syndrome 7	ENSG00000138686	PAP53	395	22.3%	chr4	122993577	CCDS3724.1	c.833T>C	p.V278A
BCAM	basal cell adhesion molecule (Lutheran blood group)	ENSG00000187244	PAP53	47	29.8%	chr19	50015881	CCDS12644.1	c.1843G>A	p.G615R
BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	ENSG00000119866	PAP53	284	20.8%	chr2	60542758	CCDS1862.1	c.2813C>NULL	p.NULL-1FsDel1bp
BCL6	B-cell CLL/lymphoma 6	ENSG00000113916	PAP53	105	13.3%	chr3	188922986	CCDS3289.1	c.2075G>A	p.R692H
BCAP31	B-cell receptor-associated protein 31	ENSG00000185825	PAP53	77	26.0%	chrX	152634296	CCDS14727.1	c.383A>NULL	p.NULL-1FsDel1bp
BNIP1	BCL2/adenovirus E1B 19kDa interacting protein 1	ENSG00000113734	PAP53	78	24.4%	chr5	172511217	CCDS4385.1	c.220T>NULL	p.NULL-1FsDel1bp
BAX	BCL2-associated X protein	ENSG00000087088	PAP53	82	22.0%	chr19	54150783	CCDS12744.1	c.114G>NULL	p.NULL-1FsDel1bp
BCOR	BCL6 co-repressor	ENSG00000183337	PAP53	106	24.5%	chrX	39798197	CCDS14250.1	c.4916C>NULL	p.NULL-1FsDel1bp
BCORL1	BCL6 co-repressor-like 1	ENSG00000085185	PAP53	252	26.2%	chrX	129017692	CCDS14616.1	c.5036C>NULL	p.NULL-1FsDel1bp
BEND2	BEN domain containing 2	ENSG00000177324	PAP53	143	28.7%	chrX	18102265	CCDS14184.1	c.1787G>A	p.R596H
B3GAT1	beta-1;3-glucuronyltransferase 1 (glucuronosyltransferase P)	ENSG00000109956	PAP53	50	22.0%	chr11	133759072	CCDS8500.1	c.841C>NULL	p.NULL-1FsDel1bp
B4GALNT1	beta-1;4-N-acetyl-galactosaminyl transferase 1	ENSG00000135454	PAP53	150	20.7%	chr12	56311370	CCDS8950.1	c.427NULL>G	p.NULL-1FsIns1bp
B4GALNT4	beta-1;4-N-acetyl-galactosaminyl transferase 4	ENSG00000182272	PAP53	197	14.7%	chr11	365700	CCDS7694.1	c.912G>NULL	p.NULL-1FsDel1bp
BLVRB	biliverdin reductase B (flavin reductase (NADPH))	ENSG00000090013	PAP53	61	26.2%	chr19	45645698	CCDS33029.1	c.559C>T	p.R187C

BOD1L	biorientation of chromosomes in cell division 1-like	ENSG00000038219	PAP53	65	32.3%	chr4	13191779	CCDS3411.2	c.-1T>NULL	p.IVS20-3-1SpliceAcceptor
BOD1L	biorientation of chromosomes in cell division 1-like	ENSG00000038219	PAP53	232	24.6%	chr4	13214949	CCDS3411.2	c.2673G>T	p.E891D
BAI2	brain-specific angiogenesis inhibitor 2	ENSG00000121753	PAP53	159	27.7%	chr1	31982448	CCDS346.2	c.1184C>NULL	p.NULL-1FsDel1bp
BCR	breakpoint cluster region	ENSG00000186716	PAP53	60	25.0%	chr22	21870462	ENST00000334149	c.25G>A	p.V9I
BRD1	bromodomain containing 1	ENSG00000100425	PAP53	60	28.3%	chr22	48557388	CCDS14080.1	c.2542C>T	p.R848X
BRD3	bromodomain containing 3	ENSG00000169925	PAP53	286	14.7%	chr9	135896839	CCDS6980.1	c.1271C>T	p.A424V
CADPS	Ca++-dependent secretion activator	ENSG00000163618	PAP53	51	25.5%	chr3	62453124	CCDS2899.1	c.2795C>T	p.A932V
CDH11	cadherin 11; type 2; OB-cadherin (osteoblast)	ENSG00000140937	PAP53	409	24.7%	chr16	63579601	CCDS10803.1	c.959C>T	p.T320M
CDH2	cadherin 2; type 1; N-cadherin (neuronal)	ENSG00000170558	PAP53	213	37.6%	chr18	23786234	CCDS11891.1	c.2602G>T	p.G868W
CDH26	cadherin 26	ENSG00000124215	PAP53	195	25.6%	chr20	58042016	ENST00000244047	c.2557C>T	p.R853X
CELSR3	cadherin; EGF LAG seven-pass G-type receptor 3 (flamingo homolog; Drosophila)	ENSG00000008300	PAP53	125	20.0%	chr3	48644385	CCDS43087.1	c.682G>A	p.V228I
CDHR5	cadherin-related family member 5	ENSG00000099834	PAP53	77	24.7%	chr11	609794	CCDS7707.1	c.1266C>NULL	p.NULL-1FsDel1bp
CPPED1	calcineurin-like phosphoesterase domain containing 1	ENSG00000103381	PAP53	35	40.0%	chr16	12706383	CCDS42120.1	c.314C>T	p.T105M
CHERP	calcium homeostasis endoplasmic reticulum protein	ENSG00000085872	PAP53	50	24.0%	chr19	16497432	CCDS42518.1	c.1797C>NULL	p.NULL-1FsDel1bp
CASR	calcium-sensing receptor	ENSG00000036828	PAP53	141	23.4%	chr3	123486120	CCDS3010.1	c.2629G>A	p.A877T
CALD1	caldesmon 1	ENSG00000122786	PAP53	67	17.9%	chr7	134268356	CCDS5835.1	c.296G>A	p.R99H
CALML4	calmodulin-like 4	ENSG00000129007	PAP53	104	24.0%	chr15	66273418	CCDS10226.2	c.580C>T	p.R194W
CALML4	calmodulin-like 4	ENSG00000129007	PAP53	99	24.2%	chr15	66278953	CCDS10226.2	c.284A>T	p.H95L
CASC5	cancer susceptibility candidate 5	ENSG00000137812	PAP53	215	14.9%	chr15	38701054	CCDS42023.1	c.1378A>G	p.N460D
CHST6	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	ENSG00000183196	PAP53	207	22.7%	chr16	74070284	CCDS10918.1	c.944G>A	p.R315H
CHST10	carbohydrate sulfotransferase 10	ENSG00000115526	PAP53	302	24.5%	chr2	100376416	CCDS2047.1	c.794C>T	p.T265M
CA12	carbonic anhydrase XII	ENSG00000074410	PAP53	86	26.7%	chr15	61420019	CCDS10185.1	c.542C>T	p.P181L
CPA6	carboxypeptidase A6	ENSG00000165078	PAP53	109	20.2%	chr8	68502875	CCDS6200.1	c.1087G>A	p.G363R
CILP2	cartilage intermediate layer protein 2	ENSG00000160161	PAP53	174	23.0%	chr19	19515610	CCDS12405.1	c.1256G>A	p.R419H
CASS4	Cas scaffolding protein family member 4	ENSG00000087589	PAP53	372	19.1%	chr20	54460799	CCDS33492.1	c.1160G>A	p.R387Q
CBLL1	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1	ENSG00000105879	PAP53	566	28.4%	chr7	107185979	CCDS5747.1	c.596G>A	p.R199H
CARD10	caspase recruitment domain family; member 10	ENSG00000100065	PAP53	118	16.9%	chr22	36220068	CCDS13948.1	c.2447C>T	p.P816L
CARD14	caspase recruitment domain family; member 14	ENSG00000141527	PAP53	243	28.4%	chr17	75779749	CCDS11768.1	c.1122G>T	p.E374D
CARD9	caspase recruitment domain family; member 9	ENSG00000187796	PAP53	103	28.2%	chr9	138379471	CCDS6997.1	c.1453G>NUL	p.NULL-1FsDel1bp
CASZ1	castor zinc finger 1	ENSG00000130940	PAP53	226	22.6%	chr1	10636686	CCDS41246.1	c.2015G>A	p.R672H
CAT	catalase	ENSG00000121691	PAP53	65	20.0%	chr11	34427388	CCDS7891.1	c.140G>A	p.R47H
CATSPER1	cation channel; sperm associated 1	ENSG00000175294	PAP53	226	17.3%	chr11	65545667	CCDS8127.1	c.1567G>A	p.V523M
CDX2	caudal type homeobox 2	ENSG00000165556	PAP53	111	21.6%	chr13	27435412	CCDS9328.1	c.782C>A	p.P261H
CCRN4L	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	ENSG00000151014	PAP53	140	20.0%	chr4	140186014	CCDS3743.1	c.1232C>A	p.P411H
CNOT1	CCR4-NOT transcription complex; subunit 1	ENSG00000125107	PAP53	31	32.3%	chr16	57142680	CCDS10799.1	c.-1T>NULL	p.IVS22-3-1SpliceAcceptor
CD163L1	CD163 molecule-like 1	ENSG00000177675	PAP53	260	23.8%	chr12	7440200	CCDS8577.1	c.1808G>A	p.R603Q
CD1B	CD1b molecule	ENSG00000158485	PAP53	355	17.7%	chr1	156567228	CCDS1176.1	c.310G>A	p.G104S
CD3G	CD3g molecule; gamma (CD3-TCR complex)	ENSG00000160654	PAP53	134	17.9%	chr11	117725793	CCDS8395.1	c.205A>NULL	p.NULL-1FsDel1bp
CD3G	CD3g molecule; gamma (CD3-TCR complex)	ENSG00000160654	PAP53	134	22.4%	chr11	117725793	CCDS8395.1	c.205NULL>A	p.NULL-1FsIns1bp
CD5L	CD5 molecule-like	ENSG00000073754	PAP53	164	27.4%	chr1	156069705	CCDS1171.1	c.940C>T	p.R314C
CD82	CD82 molecule	ENSG00000085117	PAP53	45	22.2%	chr11	44596378	CCDS7909.1	c.529G>A	p.E177K
CD97	CD97 molecule	ENSG00000123146	PAP53	295	10.2%	chr19	14378314	CCDS32929.1	c.1993C>T	p.L665F

CNTLN	centlein; centrosomal protein	ENSG00000044459	PAP53	135	15.6%	chr9	17125271	CCDS43789.1	c.208G>NULL	p.NULL-1FsDel1bp
CENPF	centromere protein F; 350/400ka (mitosin)	ENSG00000117724	PAP53	90	25.6%	chr1	212888707	CCDS31023.1	c.7897G>A	p.A2633T
CXCL12	chemokine (C-X-C motif) ligand 12	ENSG00000107562	PAP53	76	35.5%	chr10	44196290	CCDS31186.1	c.106G>A	p.E36K
CHIA	chitinase; acidic	ENSG00000134216	PAP53	39	28.2%	chr1	111663505	CCDS41368.1	c.1069G>A	p.A357T
CHMP7	CHMP family; member 7	ENSG00000147457	PAP53	192	25.0%	chr8	23173712	CCDS6040.1	c.1231G>A	p.V411M
CSH2	chorionic somatomammotropin hormone 2	ENSG00000213218	PAP53	75	13.3%	chr17	59304306	CCDS42369.1	c.136G>A	p.A46T
CSHL1	chorionic somatomammotropin hormone-like 1	ENSG00000204414	PAP53	44	25.0%	chr17	59341511	CCDS11652.1	c.-1G>A	p.IVS3+1-1SpliceDonor
CHD4	chromodomain helicase DNA binding protein 4	ENSG00000111642	PAP53	694	22.2%	chr12	6574774	CCDS8552.1	c.2108C>T	p.T703M
CHD5	chromodomain helicase DNA binding protein 5	ENSG00000116254	PAP53	49	34.7%	chr1	6089106	CCDS57.1	c.5793C>A	p.F1931L
CHD5	chromodomain helicase DNA binding protein 5	ENSG00000116254	PAP53	315	23.5%	chr1	6135117	CCDS57.1	c.812C>T	p.T271M
CHD6	chromodomain helicase DNA binding protein 6	ENSG00000124177	PAP53	80	21.3%	chr20	39483906	CCDS13317.1	c.4783C>T	p.R1595C
CHGA	chromogranin A (parathyroid secretory protein 1)	ENSG00000100604	PAP53	104	23.1%	chr14	92468569	CCDS9906.1	c.910GAG>NU	p.NULL-1FsDel3bp
C1orf14	chromosome 1 open reading frame 14	ENSG00000157060	PAP53	115	25.2%	chr1	181174993	CCDS30955.1	c.1235A>NULI	p.NULL-1FsDel1bp
C1orf173	chromosome 1 open reading frame 173	ENSG00000178965	PAP53	131	13.0%	chr1	74844917	CCDS30755.1	c.1445G>A	p.G482E
C1orf192	chromosome 1 open reading frame 192	ENSG00000188931	PAP53	56	23.2%	chr1	159602061	CCDS30921.1	c.403C>NULL	p.NULL-1FsDel1bp
C1orf201	chromosome 1 open reading frame 201	ENSG00000001460	PAP53	194	26.8%	chr1	24556731	ENST00000399974	c.736G>A	p.A246T
C1orf222	chromosome 1 open reading frame 222	ENSG00000142609	PAP53	58	17.2%	chr1	1893287	NM_001080484	c.880G>A	p.A294T
C1orf50	chromosome 1 open reading frame 50	ENSG00000164008	PAP53	197	16.8%	chr1	43011845	CCDS473.1	c.220G>A	p.A74T
C1orf57	chromosome 1 open reading frame 57	ENSG00000135778	PAP53	55	23.6%	chr1	231172372	CCDS1597.1	c.389G>A	p.R130H
C10orf76	chromosome 10 open reading frame 76	ENSG00000120029	PAP53	163	13.5%	chr10	103783058	CCDS41563.1	c.131G>A	p.R44Q
C12orf4	chromosome 12 open reading frame 4	ENSG00000047621	PAP53	106	16.0%	chr12	4504989	CCDS8528.1	c.626AA>NUL	p.NULL-1FsDel2bp
C12orf50	chromosome 12 open reading frame 50	ENSG00000165805	PAP53	104	11.5%	chr12	86913593	ENST00000378568	c.-1G>A	p.IVS5-1-1SpliceAcceptor
C13orf23	chromosome 13 open reading frame 23	ENSG00000120685	PAP53	128	22.7%	chr13	38483518	CCDS9368.2	c.2819A>G	p.Q940R
C14orf1	chromosome 14 open reading frame 1	ENSG00000133935	PAP53	74	32.4%	chr14	75187891	CCDS9845.1	c.319G>A	p.V107I
C14orf106	chromosome 14 open reading frame 106	ENSG00000129534	PAP53	263	19.0%	chr14	44763472	CCDS9684.1	c.2896NULL>/	p.NULL-1FsIns1bp
C15orf55	chromosome 15 open reading frame 55	ENSG00000184507	PAP53	62	22.6%	chr15	32430208	CCDS32190.1	c.737G>A	p.R246H
C16orf62	chromosome 16 open reading frame 62	ENSG00000103544	PAP53	113	26.5%	chr16	19601174	CCDS32397.1	c.2488G>A	p.A830T
C16orf80	chromosome 16 open reading frame 80	ENSG00000070761	PAP53	117	19.7%	chr16	56707519	CCDS10793.1	c.203C>T	p.T68M
C17orf74	chromosome 17 open reading frame 74	ENSG00000184560	PAP53	268	30.6%	chr17	7271221	CCDS42255.1	c.1187G>A	p.R396H
C17orf99	chromosome 17 open reading frame 99	ENSG00000187997	PAP53	192	27.6%	chr17	73671989	NM_001163075	c.589G>A	p.A197T
C19orf33	chromosome 19 open reading frame 33	ENSG00000167644	PAP53	274	20.8%	chr19	43487421	CCDS12511.1	c.298AAG>NU	p.NULL-1FsDel3bp
C2orf55	chromosome 2 open reading frame 55	ENSG00000196872	PAP53	151	30.5%	chr2	98804977	CCDS42720.1	c.2191G>A	p.G731R
C2orf67	chromosome 2 open reading frame 67	ENSG00000144445	PAP53	149	12.1%	chr2	210595925	CCDS33370.1	c.3187A>NULI	p.NULL-1FsDel1bp
C2orf73	chromosome 2 open reading frame 73	ENSG00000177994	PAP53	242	22.7%	chr2	54441126	NM_001100396	c.787G>A	p.A263T
C20orf117	chromosome 20 open reading frame 117	ENSG00000149639	PAP53	263	30.8%	chr20	34877719	NM_080627	c.1540C>T	p.R514X
C20orf134	chromosome 20 open reading frame 134	ENSG00000182584	PAP53	48	35.4%	chr20	31719053	CCDS33463.1	c.89C>T	p.T30M
C20orf151	chromosome 20 open reading frame 151	ENSG00000130701	PAP53	62	24.2%	chr20	60426875	CCDS13498.1	c.103C>T	p.R35W
C20orf186	chromosome 20 open reading frame 186	ENSG00000186191	PAP53	172	30.8%	chr20	31134875	CCDS13213.1	c.94C>NULL	p.NULL-1FsDel1bp
C3orf34	chromosome 3 open reading frame 34	ENSG00000174007	PAP53	289	46.7%	chr3	197918869	CCDS43193.1	c.442G>A	p.D148N
C6orf203	chromosome 6 open reading frame 203	ENSG00000130349	PAP53	67	20.9%	chr6	107479074	CCDS5058.1	c.664AG>NUL	p.NULL-1FsDel2bp
C9orf4	chromosome 9 open reading frame 4	ENSG00000136805	PAP53	203	20.2%	chr9	110943549	CCDS35098.1	c.757G>A	p.V253I
CGN	cingulin	ENSG00000143375	PAP53	108	16.7%	chr1	149763789	CCDS999.1	c.1417C>T	p.R473W

CMTM4	CKLF-like MARVEL transmembrane domain containing 4	ENSG00000183723	PAP53	38	28.9%	chr16	65213490	CCDS10817.1	c.599G>A	p.R200H
CMTM5	CKLF-like MARVEL transmembrane domain containing 5	ENSG00000166091	PAP53	241	14.9%	chr14	22917808	ENST00000339180	c.370A>C	p.T124P
CMTM5	CKLF-like MARVEL transmembrane domain containing 5	ENSG00000166091	PAP53	462	19.3%	chr14	22917809	ENST00000339180	c.371NULL>C	p.NULL-1FsIns1bp
CIITA	class II; major histocompatibility complex; transactivator	ENSG00000179583	PAP53	52	28.8%	chr16	10896726	CCDS10544.1	c.139C>A	p.L47I
CLDN4	claudin 4	ENSG00000189143	PAP53	338	34.6%	chr7	72883999	CCDS5560.1	c.532G>NULL	p.NULL-1FsDel1bp
CLU	clusterin	ENSG00000120885	PAP53	137	12.4%	chr8	27512051	CCDS6061.1	c.1339G>A	p.D447N
COPB1	coatomer protein complex; subunit beta 1	ENSG00000129083	PAP53	45	24.4%	chr11	14466709	CCDS7815.1	c.-1T>NULL	p.IVS4-3-1SpliceAcceptor
CCDC107	coiled-coil domain containing 107	ENSG00000159884	PAP53	80	13.8%	chr9	35650894	CCDS6583.1	c.562AA>NUL	p.NULL-1FsDel2bp
CCDC21	coiled-coil domain containing 21	ENSG00000130695	PAP53	292	25.7%	chr1	26454299	CCDS277.1	c.259G>A	p.V87I
CCDC42	coiled-coil domain containing 42	ENSG00000161973	PAP53	125	20.8%	chr17	8579468	CCDS11145.1	c.679C>T	p.R227C
CCDC85A	coiled-coil domain containing 85A	ENSG00000055813	PAP53	131	22.1%	chr2	56273647	NM_001080433	c.808C>T	p.R270C
CCDC88B	coiled-coil domain containing 88B	ENSG00000168071	PAP53	213	33.3%	chr11	63873086	ENST00000359902	c.58C>T	p.R20C
CCDC97	coiled-coil domain containing 97	ENSG00000142039	PAP53	162	28.4%	chr19	46514302	CCDS12578.1	c.220C>T	p.R74C
COL1A2	collagen; type I; alpha 2	ENSG00000164692	PAP53	58	22.4%	chr7	93888269	CCDS34682.1	c.2308C>NULL	p.NULL-1FsDel1bp
COL4A1	collagen; type IV; alpha 1	ENSG00000187498	PAP53	78	15.4%	chr13	109620924	CCDS9511.1	c.3713G>A	p.R1238H
COL4A2	collagen; type IV; alpha 2	ENSG00000134871	PAP53	200	27.5%	chr13	109880971	ENST00000257309	c.664C>T	p.Q222X
COL4A3BP	collagen; type IV; alpha 3 (Goodpasture antigen) binding protein	ENSG00000113163	PAP53	161	22.4%	chr5	74758062	CCDS4028.1	c.-1T>NULL	p.IVS3-3-1SpliceAcceptor
COL5A1	collagen; type V; alpha 1	ENSG00000130635	PAP53	179	29.1%	chr9	136844311	CCDS6982.1	c.3784G>T	p.A1262S
COL7A1	collagen; type VII; alpha 1	ENSG00000114270	PAP53	130	20.0%	chr3	48594929	CCDS2773.1	c.4585C>T	p.R1529C
COL10A1	collagen; type X; alpha 1	ENSG00000123500	PAP53	127	26.8%	chr6	116548638	CCDS5105.1	c.3222C>NULL	p.NULL-1FsDel1bp
C3	complement component 3	ENSG00000125730	PAP53	116	33.6%	chr19	6630423	CCDS32883.1	c.4541C>T	p.A1514V
C7	complement component 7	ENSG00000112936	PAP53	149	14.1%	chr5	40983649	NM_000587	c.927AGG>NU	p.NULL-1FsDel3bp
CNTN4	contactin 4	ENSG00000144619	PAP53	127	22.0%	chr3	3042806	CCDS43041.1	c.1507C>NULL	p.NULL-1FsDel1bp
CNTNAP1	contactin associated protein 1	ENSG00000108797	PAP53	63	19.0%	chr17	38104258	CCDS11436.1	c.3959C>A	p.P1320H
CPNE7	copine VII	ENSG00000178773	PAP53	115	20.0%	chr16	88189471	CCDS10980.1	c.1723C>T	p.R575W
CORIN	corin; serine peptidase	ENSG00000145244	PAP53	233	25.3%	chr4	47389860	CCDS3477.1	c.-1T>NULL	p.IVS5-3-1SpliceAcceptor
CORO1C	coronin; actin binding protein; 1C	ENSG00000110880	PAP53	97	33.0%	chr12	107596200	CCDS9120.1	c.295G>A	p.G99S
CORO2B	coronin; actin binding protein; 2B	ENSG00000103647	PAP53	55	40.0%	chr15	66790194	CCDS10229.2	c.403G>A	p.G135R
CREBBP	CREB binding protein	ENSG00000005339	PAP53	201	16.4%	chr16	3840704	CCDS10509.1	c.1105NULL>C	p.NULL-1FsIns1bp
CSRP2BP	CSRP2 binding protein	ENSG00000149474	PAP53	112	25.0%	chr20	18110409	CCDS13133.1	c.1727G>A	p.R576H
CTDSPL2	CTD (carboxy-terminal domain; RNA polymerase II; polypeptide A) small phosphatase like 2	ENSG00000137770	PAP53	110	25.5%	chr15	42566068	CCDS10110.1	c.353A>C	p.Q118P
CHTF8	CTF8; chromosome transmission fidelity factor 8 homolog (S. cerevisiae)	ENSG00000168802	PAP53	177	21.5%	chr16	67711802	ENST00000306585	c.31C>T	p.R11W
CLEC10A	C-type lectin domain family 10; member A	ENSG00000132514	PAP53	186	15.6%	chr17	6919457	CCDS11087.1	c.728A>G	p.D243G
CLEC2B	C-type lectin domain family 2; member B	ENSG00000110852	PAP53	171	23.4%	chr12	9898337	CCDS8605.1	c.251G>A	p.R84Q
CLEC3A	C-type lectin domain family 3; member A	ENSG00000166509	PAP53	581	23.8%	chr16	76622112	CCDS10927.1	c.467G>A	p.R156H
CUL2	cullin 2	ENSG00000108094	PAP53	41	39.0%	chr10	35360253	CCDS7179.1	c.1367C>T	p.A456V
CUL4B	cullin 4B	ENSG00000158290	PAP53	79	17.7%	chrX	119559559	CCDS35379.1	c.1423C>T	p.L475F
CUL4B	cullin 4B	ENSG00000158290	PAP53	79	19.0%	chrX	119559566	CCDS35379.1	c.1416T>G	p.D472E

CUX1	cut-like homeobox 1	ENSG00000160967	PAP53	155	18.7%	chr7	101545205	CCDS5721.1	c.-1A>G	p.IVS7-2-1SpliceAcceptor
CNGA2	cyclic nucleotide gated channel alpha 2	ENSG00000183862	PAP53	154	35.1%	chrX	150662961	CCDS14701.1	c.1330G>A	p.V444I
CNGA4	cyclic nucleotide gated channel alpha 4	ENSG00000132259	PAP53	633	19.7%	chr11	6217515	CCDS31408.1	c.190G>A	p.G64S
CNGB1	cyclic nucleotide gated channel beta 1	ENSG00000070729	PAP53	75	30.7%	chr16	56508852	CCDS42169.1	c.1987G>A	p.V663M
CYP26B1	cytochrome P450; family 26; subfamily B; polypeptide 1	ENSG00000003137	PAP53	57	29.8%	chr2	72213827	CCDS1919.1	c.979C>T	p.R327W
CPEB3	cytoplasmic polyadenylation element binding protein 3	ENSG00000107864	PAP53	124	29.0%	chr10	93841582	CCDS31246.1	c.1672C>T	p.R558X
CKAP2	cytoskeleton associated protein 2	ENSG00000136108	PAP53	293	18.1%	chr13	51933588	CCDS41893.1	c.629C>T	p.A210V
AP2A1	DAVID_adaptor-related protein complex 2: alpha 1 subunit	NM_014203	PAP53	227	25.1%	chr19	54990799	NM_014203	c.806C>T	p.P269L
Ankrd24	DAVID_ankyrin repeat domain 24	NM_133475	PAP53	214	25.2%	chr19	4161118	NM_133475	c.934G>A	p.A312T
ankrd52	DAVID_ankyrin repeat domain 52	NM_173595	PAP53	106	21.7%	chr12	54924832	NM_173595	c.2593G>A	p.A865T
ano2	DAVID_anoctamin 2	NM_020373	PAP53	112	26.8%	chr12	5545049	NM_020373	c.2663A>G	p.Y888C
CARNS1	DAVID_ATP-grasp domain containing 1	NM_001166222	PAP53	73	16.4%	chr11	66941577	NM_001166222	c.127C>T	p.R43C
BAHCC1	DAVID_BAH domain and coiled-coil containing 1	NM_001080519	PAP53	86	20.9%	chr17	77038062	NM_001080519	c.4549G>NUL	p.NULL-1FsDel1bp
BRI3P1	DAVID_brain protein I3; brain protein I3 pseudogene 1	NM_001159491	PAP53	174	24.7%	chr7	97759913	NM_001159491	c.272C>T	p.T91M
Bri3	DAVID_brain protein I3; brain protein I3 pseudogene 1	NM_001159491	PAP53	174	24.7%	chr7	97759913	NM_001159491	c.272C>T	p.T91M
Cdh23	DAVID_cadherin-like 23	NM_022124	PAP53	125	19.2%	chr10	73164034	NM_022124	c.4136G>A	p.R1379H
Cacna1a	DAVID_calcium channel: voltage-dependent: P/Q type: alpha 1A subunit	NM_001127222	PAP53	95	17.9%	chr19	13477854	NM_001127222	c.185A>G	p.Y62C
CACNA1E	DAVID_calcium channel: voltage-dependent: R type: alpha 1E subunit	NM_000721	PAP53	560	23.8%	chr1	179746247	NM_000721	c.278A>G	p.Y93C
CACNA1G	DAVID_calcium channel: voltage-dependent: T type: alpha 1G subunit	NM_018896	PAP53	220	30.0%	chr17	46051097	NM_018896	c.5510C>T	p.T1837M
CAPN13	DAVID_calpain 13	NM_144575	PAP53	145	27.6%	chr2	30829477	NM_144575	c.1033G>A	p.E345K
Cd177	DAVID_CD177 molecule	NM_020406	PAP53	270	25.9%	chr19	48558251	NM_020406	c.1253G>NUL	p.NULL-1FsDel1bp
C1orf49	DAVID_chromosome 1 open reading frame 49	ENSG00000184909	PAP53	223	28.7%	chr1	176756633	CCDS1323.1	c.-1G>A	p.IVS7+1-1SpliceDonor
C16orf85	DAVID_chromosome 16 open reading frame 85	ENSG00000205036	PAP53	146	27.4%	chr16	87147871	ENST00000378416	c.260G>A	p.G87D
C3orf77	DAVID_chromosome 3 open reading frame 77	NM_001145030	PAP53	78	16.7%	chr3	44285784	NM_001145030	c.3233A>NULI	p.NULL-1FsDel1bp
C5orf36	DAVID_chromosome 5 open reading frame 36	NM_001145678	PAP53	93	16.1%	chr5	93747732	NM_001145678	c.3590C>T	p.A1197V
poc5	DAVID_chromosome 5 open reading frame 37	NM_001099271	PAP53	187	24.6%	chr5	75006122	NM_001099271	c.1622G>A	p.R541Q
C6orf103	DAVID_chromosome 6 open reading frame 103	NM_024694	PAP53	98	16.3%	chr6	147048595	NM_024694	c.1249G>A	p.V417I
C6orf47	DAVID_chromosome 6 open reading frame 47	ENSG00000204439	PAP53	1019	22.2%	chr6	31734825	CCDS34399.1	c.1763G>NUL	p.NULL-1FsDel1bp
C6orf47	DAVID_chromosome 6 open reading frame 47	ENSG00000204439	PAP53	163	25.8%	chr6	31735253	CCDS34399.1	c.451C>T	p.R151C
C7orf54	DAVID_chromosome 7 open reading frame 54	ENSG00000221922	PAP53	629	27.3%	chr7	127425014	ENST00000408904	c.32C>T	p.S11L
C8orf80	DAVID_chromosome 8 open reading frame 80	NM_001010906	PAP53	486	23.3%	chr8	27944695	NM_001010906	c.2030A>NULI	p.NULL-1FsDel1bp
Cldn25	DAVID_claudin-like	NM_001101389	PAP53	199	23.6%	chr11	113155851	NM_001101389	c.124G>A	p.E42K
ccdc15	DAVID_coiled-coil domain containing 15	NM_025004	PAP53	133	24.8%	chr11	124415704	NM_025004	c.2743C>T	p.R915W
COL29A1	DAVID_collagen: type XXIX: alpha 1	NM_153264	PAP53	224	17.4%	chr3	131670719	NM_153264	c.7181T>C	p.I2394T
Chtf18	DAVID_CTF18: chromosome transmission fidelity factor 18 homolog (S. cerevisiae)	NM_022092	PAP53	41	31.7%	chr16	779070	NM_022092	c.230G>A	p.G77D
CSMD1	DAVID_CUB and Sushi multiple domains 1	NM_033225	PAP53	109	22.0%	chr8	3034890	NM_033225	c.5350C>T	p.R1784C
CLASP2	DAVID_cytoplasmic linker associated protein 2	NM_015097	PAP53	94	27.7%	chr3	33551783	NM_015097	c.3733A>G	p.K1245E
Dock6	DAVID_dedicator of cytokinesis 6	NM_020812	PAP53	51	31.4%	chr19	11174384	NM_020812	c.5237G>A	p.R1746H
DENND1C	DAVID_DENN/MADD domain containing 1C	NM_024898	PAP53	162	11.1%	chr19	6418555	NM_024898	c.2366G>A	p.R789Q
dennd4b	DAVID_DENN/MADD domain containing 4B	NM_014856	PAP53	100	18.0%	chr1	152172797	NM_014856	c.3116G>A	p.R1039Q
DPP9	DAVID_dipeptidyl-peptidase 9	NM_139159	PAP53	100	25.0%	chr19	4633739	NM_139159	c.2443G>A	p.V815M
DNHD1	DAVID_dynein heavy chain domain 1	NM_144666	PAP53	137	21.2%	chr11	6524009	NM_144666	c.5264G>A	p.R1755H
DNHD1	DAVID_dynein heavy chain domain 1	NM_144666	PAP53	575	25.6%	chr11	6549478	NM_144666	c.13948G>A	p.G4650R

DNAH12	DAVID_dynein: axonemal: heavy chain 12	NM_178504	PAP53	154	19.5%	chr3	57389416	NM_178504	c.-1G>A	p.IVS33+1-1SpliceDonor
DST	DAVID_dystonin	NM_001144769	PAP53	303	10.9%	chr6	56618638	NM_001144769	c.1664G>A	p.R555H
EML5	DAVID_echinoderm microtubule associated protein like 5	NM_183387	PAP53	106	13.2%	chr14	88241062	NM_183387	c.2062AGA>N	p.NULL-1FsDel3bp
Eml6	DAVID_echinoderm microtubule associated protein like 6	NM_001039753	PAP53	59	16.9%	chr2	54908239	NM_001039753	c.558NULL>A	p.NULL-1FsIns1bp
Epha6	DAVID_EPH receptor A6	NM_001080448	PAP53	95	45.3%	chr3	98016340	NM_001080448	c.183G>T	p.E61D
epn1	DAVID_epsin 1	NM_001130071	PAP53	288	20.5%	chr19	60881764	NM_001130071	c.292C>T	p.R98C
EHMT2	DAVID_euchromatic histone-lysine N-methyltransferase 2	ENSG00000204371	PAP53	91	24.2%	chr6	31960540	CCDS4725.1	c.2464C>A	p.L822M
EIF2C2	DAVID_eukaryotic translation initiation factor 2C: 2	ENSG00000123908	PAP53	62	21.0%	chr8	141630648	CCDS6380.1	c.1339G>A	p.E447K
FBRSL1	DAVID_fibrosin-like 1	NM_001142641	PAP53	67	32.8%	chr12	131661109	NM_001142641	c.1716G>NUL	p.NULL-1FsDel1bp
FKSG83	DAVID_FKSG83	NM_032030	PAP53	222	28.8%	chr6	27401362	NM_032030	c.322G>A	p.V108M
FMNL2	DAVID_formin-like 2	NM_052905	PAP53	200	28.0%	chr2	153107532	NM_052905	c.235T>C	p.Y79H
GEMIN4	DAVID_gem (nuclear organelle) associated protein 4	NM_015721	PAP53	279	24.0%	chr17	595670	NM_015721	c.2363C>T	p.A788V
gli4	DAVID_GLI family zinc finger 4	ENSG00000221850	PAP53	354	27.1%	chr8	144428543	ENST00000344692	c.188G>A	p.R63Q
GRIP2	DAVID_glutamate receptor interacting protein 2	NM_001080423	PAP53	54	37.0%	chr3	14511456	NM_001080423	c.3163G>A	p.V1055I
HERC1	DAVID_hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	NM_003922	PAP53	525	20.8%	chr15	61854104	NM_003922	c.772C>T	p.R258X
BAT4	DAVID_HLA-B associated transcript 4	ENSG00000204438	PAP53	348	14.1%	chr6	31740012	CCDS4711.1	c.846GAA>NU	p.NULL-1FsDel3bp
TARM1	DAVID_hypothetical LOC441864	NM_001135686	PAP53	136	20.6%	chr19	59269933	NM_001135686	c.606C>NULL	p.NULL-1FsDel1bp
LOC100131(	DAVID_hypothetical protein LOC100131098; calcium channel: voltage-dependent: L type: alpha 1C subunit	NM_199460	PAP53	124	26.6%	chr12	2465684	NM_199460	c.911T>C	p.I304T
CACNA1C	DAVID_hypothetical protein LOC100131098; calcium channel: voltage-dependent: L type: alpha 1C subunit	NM_199460	PAP53	124	26.6%	chr12	2465684	NM_199460	c.911T>C	p.I304T
LOC113230	DAVID_hypothetical protein LOC113230	ENSG00000141854	PAP53	97	35.1%	chr19	14046241	ENST00000269720	c.908C>A	p.P303H
C9orf144	DAVID_hypothetical protein LOC259308; chromosome 9 open reading frame 144	NM_001141917	PAP53	107	20.6%	chr9	34713857	NM_001141917	c.3380G>A	p.R1127Q
C9orf144B	DAVID_hypothetical protein LOC259308; chromosome 9 open reading frame 144	NM_001141917	PAP53	107	20.6%	chr9	34713857	NM_001141917	c.3380G>A	p.R1127Q
LOC389333	DAVID_hypothetical protein LOC389333	NM_001161546	PAP53	73	16.4%	chr5	138756502	NM_001161546	c.2168G>A	p.S723N
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP53	143	21.0%	chr13	102194488	NM_001146197	c.6560G>A	p.R2187H
shisa9	DAVID_hypothetical protein LOC729993	NM_001145204	PAP53	163	19.0%	chr16	13236543	NM_001145204	c.1174C>T	p.R392C
IGSF22	DAVID_immunoglobulin superfamily: member 22	NM_173588	PAP53	782	28.1%	chr11	18690264	NM_173588	c.2339A>G	p.N780S
Igfn1	DAVID_immunoglobulin-like and fibronectin type III domain containing 1	NM_001164586	PAP53	137	19.0%	chr1	199435386	NM_001164586	c.439C>T	p.R147W
Igfn1	DAVID_immunoglobulin-like and fibronectin type III domain containing 1	NM_001164586	PAP53	31	32.3%	chr1	199446771	NM_001164586	c.6127A>G	p.R2043G
INTS2	DAVID_integrator complex subunit 2	NM_020748	PAP53	194	17.0%	chr17	57353942	NM_020748	c.587T>NULL	p.NULL-1FsDel1bp
KRTAP10-7	DAVID_keratin associated protein 10-7	NM_198689	PAP53	237	22.4%	chr21	44846016	NM_198689	c.1052G>A	p.R351H
Sel1l3	DAVID_KIAA0746 protein	NM_015187	PAP53	63	27.0%	chr4	25415274	NM_015187	c.1763G>A	p.R588Q
Sel1l3	DAVID_KIAA0746 protein	NM_015187	PAP53	49	34.7%	chr4	25444270	NM_015187	c.880C>G	p.L294V
Nynrin	DAVID_KIAA1305	NM_025081	PAP53	192	24.5%	chr14	23948210	NM_025081	c.1370C>T	p.T457M
KIAA1549	DAVID_KIAA1549	NM_001164665	PAP53	204	18.6%	chr7	138254083	NM_001164665	c.829G>A	p.V277M
NCKAP5L	DAVID_KIAA1602	NM_001037806	PAP53	280	23.9%	chr12	48475059	NM_001037806	c.2851C>T	p.R951W
FAM190A	DAVID_KIAA1680 protein	NM_001145065	PAP53	310	27.7%	chr4	92738977	NM_001145065	c.2449G>A	p.V817I
KSR1	DAVID_kinase suppressor of ras 1	NM_014238	PAP53	242	24.0%	chr17	22943678	NM_014238	c.787C>T	p.R263W
Kif13b	DAVID_kinesin family member 13B	NM_015254	PAP53	62	19.4%	chr8	29099911	NM_015254	c.-1T>NULL	p.IVS5-3-1SpliceAcceptor
KIF26A	DAVID_kinesin family member 26A	NM_015656	PAP53	158	23.4%	chr14	103688519	NM_015656	c.703C>T	p.R235W

KIF26A	DAVID_kinesin family member 26A	NM_015656	PAP53	59	37.3%	chr14	103707963	NM_015656	c.1264G>A	p.A422T
MGAM	DAVID_maltase-glucoamylase (alpha-glucosidase)	NM_004668	PAP53	284	21.1%	chr7	141441050	NM_004668	c.4688C>T	p.A1563V
MFRP	DAVID_membrane frizzled-related protein	ENSG00000184824	PAP53	54	18.5%	chr11	118718898	CCDS8421.1	c.1280C>NULL	p.NULL-1FsDel1bp
manf	DAVID_mesencephalic astrocyte-derived neurotrophic factor	NM_006010	PAP53	226	11.9%	chr3	51401496	NM_006010	c.494G>A	p.R165Q
MINK1	DAVID_misshapen-like kinase 1 (zebrafish)	NM_153827	PAP53	140	27.9%	chr17	4735772	NM_153827	c.1739C>T	p.T580M
Muc12	DAVID_mucin 12: cell surface associated; similar to mucin 11	NM_001164462	PAP53	122	26.2%	chr7	100438655	NM_001164462	c.15079G>A	p.A5027T
LOC100130	DAVID_mucin 12: cell surface associated; similar to mucin 11	NM_001164462	PAP53	122	26.2%	chr7	100438655	NM_001164462	c.15079G>A	p.A5027T
MUC16	DAVID_mucin 16: cell surface associated	NM_024690	PAP53	183	25.7%	chr19	8857435	NM_024690	c.41137C>A	p.P13713T
muc2	DAVID_mucin 2: oligomeric mucus/gel-forming	NM_002457	PAP53	102	16.7%	chr11	1067671	NM_002457	c.421G>A	p.A141T
Muc5ac	DAVID_mucin 5AC: oligomeric mucus/gel-forming; similar to hCG1778310	ENSG00000196292	PAP53	132	22.7%	chr11	1145595	ENST00000406844	c.283G>A	p.D95N
MUC5B	DAVID_mucin 5B: oligomeric mucus/gel-forming	NM_002458	PAP53	112	25.9%	chr11	1223712	NM_002458	c.9035C>T	p.T3012M
MRVI1	DAVID_murine retrovirus integration site 1 homolog	NM_001098579	PAP53	135	19.3%	chr11	10554519	NM_001098579	c.2648C>T	p.S883L
MUSK	DAVID_muscle: skeletal: receptor tyrosine kinase	NM_005592	PAP53	271	25.8%	chr9	112602658	NM_005592	c.2179G>A	p.A727T
MYT1L	DAVID_myelin transcription factor 1-like	NM_015025	PAP53	121	28.1%	chr2	1961984	NM_015025	c.112G>A	p.G38S
MOBP	DAVID_myelin-associated oligodendrocyte basic protein	ENSG00000214905	PAP53	79	26.6%	chr3	39530101	ENST00000383754	c.163G>T	p.G55C
MLL2	DAVID_myeloid/lymphoid or mixed-lineage leukemia 2	NM_003482	PAP53	96	21.9%	chr12	47720759	NM_003482	c.8872C>NULL	p.NULL-1FsDel1bp
MLL2	DAVID_myeloid/lymphoid or mixed-lineage leukemia 2	NM_003482	PAP53	295	14.9%	chr12	47731497	NM_003482	c.2236C>T	p.R746W
MLL4	DAVID_myeloid/lymphoid or mixed-lineage leukemia 4	ENSG00000105663	PAP53	177	22.0%	chr19	40902604	NM_014727	c.515C>NULL	p.NULL-1FsDel1bp
MLL4	DAVID_myeloid/lymphoid or mixed-lineage leukemia 4	ENSG00000105663	PAP53	88	14.8%	chr19	40905830	NM_014727	c.2816C>T	p.T939I
MLL4	DAVID_myeloid/lymphoid or mixed-lineage leukemia 4	ENSG00000105663	PAP53	159	31.4%	chr19	40908534	NM_014727	c.3860G>A	p.R1287Q
MYH13	DAVID_myosin: heavy chain 13: skeletal muscle	NM_003802	PAP53	128	21.9%	chr17	10156668	NM_003802	c.4313G>A	p.R1438H
ND1	DAVID_NADH-ubiquinone oxidoreductase chain 1	ENSG00000198888	PAP53	127	20.5%	chrM	3974	ENST00000361390	c.667T>C	p.F223L
ND5	DAVID_NADH-ubiquinone oxidoreductase chain 5	ENSG00000198786	PAP53	118	78.8%	chrM	12614	ENST00000361567	c.277G>A	p.A93T
ND5	DAVID_NADH-ubiquinone oxidoreductase chain 5	ENSG00000198786	PAP53	102	64.7%	chrM	12864	ENST00000361567	c.527G>A	p.R176H
NEB	DAVID_nebulin	NM_001164507	PAP53	145	10.3%	chr2	152133180	NM_001164507	c.-1TT>NULL	p.IVS109-3-1SpliceAcceptor
NEB	DAVID_nebulin	NM_001164508	PAP53	695	25.5%	chr2	152090762	NM_001164508	c.22117C>T	p.R7373W
NPHP4	DAVID_nephronophthisis 4	NM_015102	PAP53	36	33.3%	chr1	5857732	NM_015102	c.2833C>T	p.R945C
NRXN1	DAVID_neurexin 1	NM_001135659	PAP53	119	35.3%	chr2	51108593	NM_001135659	c.323C>T	p.P108L
NBEAL1	DAVID_neurobeachin-like 1	NM_001114132	PAP53	51	23.5%	chr2	203630303	NM_001114132	c.397A>NULL	p.NULL-1FsDel1bp
NBEAL2	DAVID_neurobeachin-like 2	NM_015175	PAP53	25	48.0%	chr3	47017534	NM_015175	c.4345G>A	p.V1449M
NECAB1	DAVID_N-terminal EF-hand calcium binding protein 1	NM_022351	PAP53	174	23.0%	chr8	91962523	NM_022351	c.346A>NULL	p.NULL-1FsDel1bp
Nploc4	DAVID_nuclear protein localization 4 homolog (S. cerevisiae)	NM_017921	PAP53	84	29.8%	chr17	77136877	NM_017921	c.1679G>A	p.G560D
NOL8	DAVID_nucleolar protein 8	NM_017948	PAP53	109	20.2%	chr9	94121449	NM_017948	c.292G>T	p.E98X
obscn	DAVID_obscurin: cytoskeletal calmodulin and titin-interacting RhoGEF	NM_001098623	PAP53	54	20.4%	chr1	226467917	NM_001098623	c.1141GAG>N	p.NULL-1FsDel3bp
obscn	DAVID_obscurin: cytoskeletal calmodulin and titin-interacting RhoGEF	NM_001098623	PAP53	263	19.0%	chr1	226595537	NM_001098623	c.17816G>A	p.R5939H
obscn	DAVID_obscurin: cytoskeletal calmodulin and titin-interacting RhoGEF	NM_001098623	PAP53	227	28.2%	chr1	226626080	NM_001098623	c.20978C>G	p.A6993G
Odz2	DAVID_odz: odd Oz/ten-m homolog 2 (Drosophila)	NM_001122679	PAP53	176	26.1%	chr5	166734928	NM_001122679	c.374C>T	p.P125L
Odz2	DAVID_odz: odd Oz/ten-m homolog 2 (Drosophila)	NM_001122679	PAP53	339	23.6%	chr5	167578543	NM_001122679	c.5042C>T	p.A1681V
PALM3	DAVID_Paralemmin-3	NM_001145028	PAP53	165	26.1%	chr19	14030967	NM_001145028	c.5C>T	p.A2V
PRIC285	DAVID_peroxisomal proliferator-activated receptor A interacting complex 285	ENSG00000130589	PAP53	58	22.4%	chr20	61665028	CCDS33508.1	c.5591G>T	p.R1864L
PHACTR1	DAVID_phosphatase and actin regulator 1	NM_030948	PAP53	150	24.0%	chr6	13314115	NM_030948	c.754G>T	p.G252W

PIGB	DAVID_phosphatidylinositol glycan anchor biosynthesis: class B	NM_004855	PAP53	95	26.3%	chr15	53398776	NM_004855	c.36G>NULL	p.NULL-1FsDel1bp
Pla2g4e	DAVID_phospholipase A2: group IVE	NM_001080490	PAP53	87	11.5%	chr15	40063269	NM_001080490	c.2495G>A	p.R832H
PLCH2	DAVID_phospholipase C: eta 2	NM_014638	PAP53	71	23.9%	chr1	2399849	NM_014638	c.199C>T	p.R67C
PCLO	DAVID_piccolo (presynaptic cytomatrix protein)	NM_033026	PAP53	51	31.4%	chr7	82420880	NM_033026	c.12404A>NUI	p.NULL-1FsDel1bp
PATL1	DAVID_protein associated with topoisomerase II homolog 1 (yeast)	NM_152716	PAP53	89	12.4%	chr11	59163417	NM_152716	c.2065C>T	p.L689F
PPP1R12B	DAVID_protein phosphatase 1: regulatory (inhibitor) subunit 12B	NM_001167857	PAP53	72	27.8%	chr1	200673813	NM_001167857	c.1496T>NULI	p.NULL-1FsDel1bp
PCDHA11	DAVID_protocadherin alpha 11	NM_018902	PAP53	116	30.2%	chr5	140230872	NM_018902	c.2000C>T	p.S667L
PCDHA12	DAVID_protocadherin alpha 12	NM_018903	PAP53	249	26.9%	chr5	140236100	NM_018903	c.859G>C	p.V287L
PCDHGA3	DAVID_protocadherin gamma subfamily A: 3	NM_018916	PAP53	55	30.9%	chr5	140705537	NM_018916	c.1753G>A	p.G585S
Pcdhga7	DAVID_protocadherin gamma subfamily A: 7	NM_018920	PAP53	85	22.4%	chr5	140742865	NM_018920	c.215C>T	p.T72M
Pcdhga7	DAVID_protocadherin gamma subfamily A: 7	NM_018920	PAP53	108	19.4%	chr5	140744499	NM_018920	c.1849TT>NUI	p.NULL-1FsDel2bp
Pcdhgb2	DAVID_protocadherin gamma subfamily B: 2	NM_018923	PAP53	103	28.2%	chr5	140721466	NM_018923	c.1580C>T	p.A527V
RIMS1	DAVID_regulating synaptic membrane exocytosis 1	NM_014989	PAP53	153	17.0%	chr6	73016865	NM_014989	c.2353T>A	p.Y785N
RGSL1	DAVID_regulator of G-protein signaling like 1	NM_001137669	PAP53	103	23.3%	chr1	180776104	NM_001137669	c.2594G>A	p.R865H
RTN4RL1	DAVID_reticulon 4 receptor-like 1	NM_178568	PAP53	148	23.6%	chr17	1787691	NM_178568	c.175G>A	p.V59I
sspO	DAVID_SCO-spondin homolog (Bos taurus)	NM_198455	PAP53	43	23.3%	chr7	149104412	NM_198455	c.95T>C	p.V32A
SIGLEC12	DAVID_sialic acid binding Ig-like lectin 12	ENSG00000160296	PAP53	109	24.8%	chr19	56695284	CCDS12833.1	c.890C>NULL	p.NULL-1FsDel1bp
LOC100130:	DAVID_similar to hCG1646697	NM_001162914	PAP53	31	35.5%	chr8	144861211	NM_001162914	c.1835C>NULI	p.NULL-1FsDel1bp
SLC44A4	DAVID_solute carrier family 44: member 4	ENSG00000204385	PAP53	92	23.9%	chr6	31941763	CCDS4724.2	c.1353C>A	p.F451L
SENP1	DAVID_SUMO1/sentrin specific peptidase 1	NM_014554	PAP53	99	52.5%	chr12	46745163	NM_014554	c.1382A>NULI	p.NULL-1FsDel1bp
SYT16	DAVID_synaptotagmin XVI	NM_031914	PAP53	200	25.0%	chr14	61620847	NM_031914	c.1615C>G	p.R539G
TRBV6-3	DAVID_T cell receptor beta variable 6-3	ENSG00000211711	PAP53	42	26.2%	chr7	141717497	ENST00000390358	c.73C>T	p.Q25X
TBC1D9	DAVID_TBC1 domain family: member 9 (with GRAM domain)	NM_015130	PAP53	185	24.9%	chr4	141763092	NM_015130	c.3508G>A	p.A1170T
TM2D1	DAVID_TM2 domain containing 1	NM_032027	PAP53	447	31.8%	chr1	61963278	NM_032027	c.268NULL>G	p.NULL-1FsIns1bp
Tmco7	DAVID_transmembrane and coiled-coil domains 7	NM_024562	PAP53	117	42.7%	chr16	67519119	NM_024562	c.2275G>A	p.V759I
TRDN	DAVID_triadin	NM_006073	PAP53	221	23.5%	chr6	123933914	NM_006073	c.85G>A	p.G29R
TRIM26	DAVID_tripartite motif-containing 26	ENSG00000137313	PAP53	330	23.9%	chr6	30261848	CCDS4678.1	c.2084TCC>N	p.NULL-1FsDel3bp
TRIM27	DAVID_tripartite motif-containing 27	ENSG00000204713	PAP53	249	19.7%	chr6	28995976	CCDS4654.1	c.539A>G	p.E180G
GALNT4	DAVID_UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4)	NM_003774	PAP53	239	28.9%	chr12	88441725	NM_003774	c.733G>T	p.G245W
alg11	DAVID_UTP14: U3 small nucleolar ribonucleoprotein: homolog C (yeast); asparagine-linked glycosylation 11: alpha-1:2-mannosyltransferase homolog (yeast)	ENSG00000136112	PAP53	77	24.7%	chr13	51491259	CCDS31977.1	c.254C>T	p.A85V
UTP14C	DAVID_UTP14: U3 small nucleolar ribonucleoprotein: homolog C (yeast); asparagine-linked glycosylation 11: alpha-1:2-mannosyltransferase homolog (yeast)	ENSG00000136112	PAP53	77	24.7%	chr13	51491259	CCDS31977.1	c.254C>T	p.A85V
YLPM1	DAVID_YLP motif containing 1	NM_019589	PAP53	366	26.0%	chr14	74346031	NM_019589	c.4717C>T	p.R1573X
ZBTB8B	DAVID_zinc finger and BTB domain containing 8B	NM_001145720	PAP53	162	22.8%	chr1	32709468	NM_001145720	c.656A>T	p.N219I
ZFHX4	DAVID_zinc finger homeobox 4	NM_024721	PAP53	286	22.7%	chr8	77853108	NM_024721	c.3125C>T	p.S1042L
ZFHX4	DAVID_zinc finger homeobox 4	NM_024721	PAP53	184	26.1%	chr8	77925887	NM_024721	c.4040G>A	p.R1347H
ZFP62	DAVID_zinc finger protein 62 homolog (mouse)	NM_152283	PAP53	341	24.9%	chr5	180210748	NM_152283	c.173G>A	p.R58H
ZFP62	DAVID_zinc finger protein 62 homolog (mouse)	NM_152283	PAP53	341	24.9%	chr5	180210748	NM_152283	c.173G>A	p.R58H
ZNF654	DAVID_zinc finger protein 654	NM_018293	PAP53	237	24.9%	chr3	88272684	NM_018293	c.1534C>T	p.R512W
ZNF763	DAVID_zinc finger protein 763	NM_001012753	PAP53	75	26.7%	chr19	11950703	NM_001012753	c.973C>T	p.R325C

ZNF835	DAVID_zinc finger protein 835	NM_001005850	PAP53	103	29.1%	chr19	61867217	NM_001005850	c.1228C>T	p.R410W
ZNF880	DAVID_zinc finger protein LOC400713	NM_001145434	PAP53	143	17.5%	chr19	57580250	NM_001145434	c.1605NULL>A	p.NULL-1FsIns1bp
DCAF15	DDB1 and CUL4 associated factor 15	ENSG00000132017	PAP53	163	22.7%	chr19	13931066	CCDS32926.1	c.994AA>NUL	p.NULL-1FsDel2bp
DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	ENSG00000100201	PAP53	99	21.2%	chr22	37227157	ENST00000396821	c.275A>NULL	p.NULL-1FsDel1bp
DDX59	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	ENSG00000118197	PAP53	132	17.4%	chr1	198860665	ENST00000367349	c.1876A>NULL	p.NULL-1FsDel1bp
DIDO1	death inducer-obliterator 1	ENSG00000101191	PAP53	271	23.6%	chr20	61007795	CCDS33506.1	c.1477G>A	p.G493R
DOCK3	dedicator of cytokinesis 3	ENSG00000088538	PAP53	76	25.0%	chr3	51392644	ENST00000402669	c.5549C>NULL	p.NULL-1FsDel1bp
DEFB116	defensin; beta 116	ENSG00000215545	PAP53	217	21.2%	chr20	29354814	CCDS42860.1	c.412NULL>A	p.NULL-1FsIns1bp
DEAF1	deformed epidermal autoregulatory factor 1 (Drosophila)	ENSG00000177030	PAP53	96	17.7%	chr11	676985	CCDS31327.1	c.677G>T	p.R226L
DHTKD1	dehydrogenase E1 and transketolase domain containing 1	ENSG00000181192	PAP53	139	20.1%	chr10	12176147	CCDS7087.1	c.1229G>A	p.R410Q
DCC	deleted in colorectal carcinoma	ENSG00000187323	PAP53	222	32.4%	chr18	49172149	CCDS11952.1	c.2582G>T	p.R861M
DLL3	delta-like 3 (Drosophila)	ENSG00000090932	PAP53	222	26.1%	chr19	44686686	CCDS12538.1	c.788C>T	p.P263L
DENND5A	DENN/MADD domain containing 5A	ENSG00000184014	PAP53	184	27.2%	chr11	9148001	CCDS31423.1	c.2129G>T	p.R710L
DNASE1	deoxyribonuclease I	ENSG00000213918	PAP53	325	12.6%	chr16	3647002	CCDS10507.1	c.438G>T	p.E146D
DNASE2	deoxyribonuclease II; lysosomal	ENSG00000105612	PAP53	214	15.0%	chr19	12847962	CCDS12284.1	c.925G>A	p.V309M
DSP	desmoplakin	ENSG00000096696	PAP53	87	26.4%	chr6	7516658	CCDS4501.1	c.1745A>G	p.D582G
DGKB	diacylglycerol kinase; beta 90kDa	ENSG00000136267	PAP53	117	25.6%	chr7	14847399	NM_004080	c.15A>C	p.E5D
DGAT1	diacylglycerol O-acyltransferase homolog 1 (mouse)	ENSG00000185000	PAP53	61	32.8%	chr8	145513324	CCDS6420.1	c.397G>A	p.A133T
DICER1	dicer 1; ribonuclease type III	ENSG00000100697	PAP53	167	15.6%	chr14	94640088	CCDS9931.1	c.3398C>T	p.A1133V
DKK1	dickkopf homolog 1 (Xenopus laevis)	ENSG00000107984	PAP53	42	23.8%	chr10	53744795	CCDS7246.1	c.350G>A	p.R117H
DEF6	differentially expressed in FDCP 6 homolog (mouse)	ENSG00000023892	PAP53	124	25.8%	chr6	35388222	CCDS4802.1	c.589G>A	p.V197M
DLAT	dihydrolipoamide S-acetyltransferase	ENSG00000150768	PAP53	94	14.9%	chr11	111402187	CCDS8354.1	c.335A>NULL	p.NULL-1FsDel1bp
DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	ENSG00000119689	PAP53	89	28.1%	chr14	74437589	CCDS9833.1	c.1127T>NULL	p.NULL-1FsDel1bp
PPIP5K1	diphosphoinositol pentakisphosphate kinase 1	ENSG00000168781	PAP53	151	24.5%	chr15	41618981	CCDS32215.1	c.3403C>T	p.R1135C
DLG1	discs; large homolog 1 (Drosophila)	ENSG00000075711	PAP53	98	40.8%	chr3	198327325	CCDS3327.1	c.1412G>A	p.R471H
DMXL2	Dmx-like 2	ENSG00000104093	PAP53	55	20.0%	chr15	49655673	CCDS10141.1	c.-1TTTT>NUL	p.IVS1-3-1SpliceAcceptor
DCLRE1A	DNA cross-link repair 1A (PSO2 homolog; S. cerevisiae)	ENSG00000198924	PAP53	139	26.6%	chr10	115602871	CCDS7584.1	c.61C>T	p.R21X
DFFA	DNA fragmentation factor; 45kDa; alpha polypeptide	ENSG00000160049	PAP53	562	23.5%	chr1	10449887	CCDS118.1	c.388C>T	p.Q130X
DNAJC10	DnaJ (Hsp40) homolog; subfamily C; member 10	ENSG00000077232	PAP53	130	20.8%	chr2	183335694	CCDS33345.1	c.2186A>G	p.Q729R
DOK7	docking protein 7	ENSG00000175920	PAP53	79	19.0%	chr4	3461238	CCDS3370.2	c.689G>A	p.R230H
DOPEY2	dopey family member 2	ENSG00000142197	PAP53	277	25.3%	chr21	36587627	CCDS13643.1	c.6785C>T	p.A2262V
DOT1L	DOT1-like; histone H3 methyltransferase (S. cerevisiae)	ENSG00000104885	PAP53	112	28.6%	chr19	2142024	CCDS42460.1	c.278C>T	p.T93M
DCLK2	doublecortin-like kinase 2	ENSG00000170390	PAP53	117	18.8%	chr4	151388912	CCDS34076.1	c.1881AATC>N	p.NULL-1FsDel4bp
DUSP18	dual specificity phosphatase 18	ENSG00000167065	PAP53	263	24.3%	chr22	29389578	CCDS13883.1	c.413G>A	p.R138Q
DCTN2	dynactin 2 (p50)	ENSG00000175203	PAP53	99	18.2%	chr12	56214073	ENST00000354743	c.758C>NULL	p.NULL-1FsDel1bp
DNAH10	dynein; axonemal; heavy chain 10	ENSG00000197653	PAP53	138	30.4%	chr12	122921978	NM_207437	c.7307G>A	p.R2436Q
DNAH10	dynein; axonemal; heavy chain 10	ENSG00000197653	PAP53	116	23.3%	chr12	122928402	NM_207437	c.8012C>T	p.P2671L
DNAH7	dynein; axonemal; heavy chain 7	ENSG00000118997	PAP53	165	20.6%	chr2	196470737	CCDS42794.1	c.-1TTT>NULL	p.IVS28-3-1SpliceAcceptor
DNAH9	dynein; axonemal; heavy chain 9	ENSG00000007174	PAP53	466	15.5%	chr17	11698448	CCDS11160.1	c.9911C>T	p.A3304V
DYSF	dysferlin; limb girdle muscular dystrophy 2B (autosomal recessive)	ENSG00000135636	PAP53	379	21.9%	chr2	71619799	CCDS1918.1	c.1402C>T	p.R468C

E2F8	E2F transcription factor 8	ENSG00000129173	PAP53	54	22.2%	chr11	19203953	CCDS7849.1	c.1928C>T	p.T643M
EDAR	ectodysplasin A receptor	ENSG00000135960	PAP53	68	17.6%	chr2	108913123	CCDS2081.1	c.180CT>NUL	p.NULL-1FsDel2bp
ENPP7	ectonucleotide pyrophosphatase/phosphodiesterase 7	ENSG00000182156	PAP53	135	27.4%	chr17	75323716	CCDS11763.1	c.679C>T	p.R227W
EGFLAM	EGF-like; fibronectin type III and laminin G domains	ENSG00000164318	PAP53	228	21.9%	chr5	38453950	CCDS3924.1	c.1520G>A	p.R507Q
EHD3	EH-domain containing 3	ENSG00000013016	PAP53	184	23.9%	chr2	31337252	CCDS1774.1	c.875G>A	p.R292H
ERC1	ELKS/RAB6-interacting/CAST family member 1	ENSG00000082805	PAP53	54	20.4%	chr12	1169335	CCDS8508.1	c.2207G>A	p.R736Q
EVC2	Ellis van Creveld syndrome 2	ENSG00000173040	PAP53	98	30.6%	chr4	5675606	CCDS3382.2	c.2060G>A	p.R687H
EBPL	emopamil binding protein-like	ENSG00000123179	PAP53	200	24.5%	chr13	49133210	CCDS9420.1	c.756T>NULL	p.NULL-1FsDel1bp
ERMP1	endoplasmic reticulum metallopeptidase 1	ENSG00000099219	PAP53	130	27.7%	chr9	5777254	CCDS34983.1	c.2605C>G	p.L869V
EDNRA	endothelin receptor type A	ENSG00000151617	PAP53	171	32.2%	chr4	148683140	CCDS3769.1	c.1204G>A	p.G402R
EPC2	enhancer of polycomb homolog 2 (Drosophila)	ENSG00000135999	PAP53	118	25.4%	chr2	149164299	NM_015630	c.200A>NULL	p.NULL-1FsDel1bp
EOMES	eomesodermin homolog (Xenopus laevis)	ENSG00000163508	PAP53	99	13.1%	chr3	27736707	CCDS2646.1	c.1149G>NUL	p.NULL-1FsDel1bp
EPHA2	EPH receptor A2	ENSG00000142627	PAP53	101	17.8%	chr1	16334786	CCDS169.1	c.1494C>NUL	p.NULL-1FsDel1bp
EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog; avian)	ENSG00000146648	PAP53	406	17.0%	chr7	55205573	CCDS5515.1	c.1960G>A	p.V654M
EDEM3	ER degradation enhancer; mannosidase alpha-like 3	ENSG00000116406	PAP53	130	24.6%	chr1	182944005	CCDS1363.1	c.1813C>T	p.R605X
ERGIC3	ERGIC and golgi 3	ENSG00000125991	PAP53	99	26.3%	chr20	33599981	CCDS13258.1	c.634G>A	p.G212R
EPB49	erythrocyte membrane protein band 4.9 (dematin)	ENSG00000158856	PAP53	172	22.1%	chr8	21995769	ENST00000381455	c.1572C>NUL	p.NULL-1FsDel1bp
EIF4G1	eukaryotic translation initiation factor 4 gamma; 1	ENSG00000114867	PAP53	169	14.2%	chr3	185527930	CCDS3259.1	c.3661G>A	p.V1221M
EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	ENSG00000187840	PAP53	194	27.3%	chr8	38036581	CCDS6100.1	c.328G>A	p.E110K
EVX1	even-skipped homeobox 1	ENSG00000106038	PAP53	150	24.7%	chr7	27251227	CCDS5413.1	c.463G>A	p.G155R
EWSR1	Ewing sarcoma breakpoint region 1	ENSG00000182944	PAP53	64	45.3%	chr22	28025771	CCDS13851.1	c.1861C>G	p.P621A
ERCC4	excision repair cross-complementing rodent repair deficiency; complementation group 4	ENSG00000175595	PAP53	216	24.1%	chr16	13949418	CCDS32390.1	c.2464C>T	p.Q822X
EXOC3L2	exocyst complex component 3-like 2	ENSG00000130201	PAP53	81	23.5%	chr19	50408327	CCDS12657.1	c.1070G>A	p.R357H
EXOC8	exocyst complex component 8	ENSG00000116903	PAP53	196	22.4%	chr1	229538596	CCDS1593.1	c.1519C>T	p.Q507X
ESYT2	extended synaptotagmin-like protein 2	ENSG00000117868	PAP53	125	38.4%	chr7	158229040	CCDS34791.1	c.1816C>T	p.R606C
ELFN2	extracellular leucine-rich repeat and fibronectin type III domain containing 2	ENSG00000166897	PAP53	195	19.0%	chr22	36100155	CCDS33642.1	c.1366G>A	p.A456T
FAM134C	family with sequence similarity 134; member C	ENSG00000141699	PAP53	115	17.4%	chr17	37990673	CCDS11432.1	c.859GA>NUL	p.NULL-1FsDel2bp
FAM154B	family with sequence similarity 154; member B	ENSG00000188659	PAP53	135	25.2%	chr15	80351137	CCDS32310.1	c.192A>G	p.I64M
FAM190B	family with sequence similarity 190; member B	ENSG00000107771	PAP53	150	25.3%	chr10	86263272	CCDS31235.1	c.2498C>T	p.P833L
FAM190B	family with sequence similarity 190; member B	ENSG00000107771	PAP53	350	23.7%	chr10	86263805	ENST00000372088	c.945C>NULL	p.NULL-1FsDel1bp
FAM193A	family with sequence similarity 193; member A	ENSG00000125386	PAP53	110	21.8%	chr4	2671322	CCDS33943.1	c.2752A>G	p.K918E
FAM59A	family with sequence similarity 59; member A	ENSG00000141441	PAP53	69	24.6%	chr18	28104241	CCDS11905.1	c.1670C>T	p.A557V
FAM65A	family with sequence similarity 65; member A	ENSG00000039523	PAP53	404	10.6%	chr16	66130123	CCDS10840.1	c.152C>T	p.A51V
FAM70B	family with sequence similarity 70; member B	ENSG00000184497	PAP53	119	25.2%	chr13	113599098	NM_182614	c.1117C>NUL	p.NULL-1FsDel1bp
FASN	fatty acid synthase	ENSG00000169710	PAP53	197	27.4%	chr17	77640307	CCDS11801.1	c.2131C>T	p.R711C
FOS	FBJ murine osteosarcoma viral oncogene homolog	ENSG00000170345	PAP53	237	20.3%	chr14	74816498	CCDS9841.1	c.307G>A	p.A103T
FBXW7	F-box and WD repeat domain containing 7	ENSG00000109670	PAP53	263	24.0%	chr4	153463541	CCDS3777.1	c.2066G>A	p.R689Q
FBXO34	F-box protein 34	ENSG00000178974	PAP53	341	23.5%	chr14	54888308	CCDS32086.1	c.1447T>NULL	p.NULL-1FsDel1bp
FBXO18	F-box protein; helicase; 18	ENSG00000134452	PAP53	258	24.4%	chr10	5999476	CCDS7073.1	c.2029G>A	p.G677S
FRMD3	FERM domain containing 3	ENSG00000172159	PAP53	130	26.9%	chr9	85052759	CCDS43840.1	c.1688G>A	p.R563H
FRMD4A	FERM domain containing 4A	ENSG00000151474	PAP53	117	22.2%	chr10	13736458	CCDS7101.1	c.3110C>NUL	p.NULL-1FsDel1bp

FRMD8	FERM domain containing 8	ENSG00000126391	PAP53	158	13.9%	chr11	64911135	CCDS8102.1	c.52C>A	p.H18N
FEZF2	FEZ family zinc finger 2	ENSG00000153266	PAP53	151	15.9%	chr3	62332757	CCDS2897.1	c.1678A>NULL	p.NULL-1FsDel1bp
FGGY	FGGY carbohydrate kinase domain containing	ENSG00000172456	PAP53	71	19.7%	chr1	59996234	CCDS611.1	c.1220C>T	p.P407L
FGF3	fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog)	ENSG00000186895	PAP53	92	32.6%	chr11	69334529	CCDS8195.1	c.445G>A	p.A149T
FLRT3	fibronectin leucine rich transmembrane protein 3	ENSG00000125848	PAP53	260	21.5%	chr20	14255684	CCDS13121.1	c.469C>T	p.R157X
FSIP2	fibrous sheath interacting protein 2	ENSG00000188738	PAP53	320	13.1%	chr2	186370348	ENST00000344648	c.2092A>NULL	p.NULL-1FsDel1bp
FLNA	filamin A; alpha	ENSG00000196924	PAP53	175	30.3%	chrX	153249259	CCDS44021.1	c.664G>A	p.V222I
FLNB	filamin B; beta	ENSG00000136068	PAP53	315	29.2%	chr3	58093677	CCDS2885.1	c.4493C>T	p.A1498V
FLNC	filamin C; gamma	ENSG00000128591	PAP53	118	17.8%	chr7	128262699	CCDS43644.1	c.436C>T	p.P146S
FOXA2	forkhead box A2	ENSG00000125798	PAP53	226	31.4%	chr20	22510560	CCDS13147.1	c.1302C>G	p.D434E
FOXA3	forkhead box A3	ENSG00000170608	PAP53	219	24.2%	chr19	51067318	CCDS12677.1	c.215C>NULL	p.NULL-1FsDel1bp
FOXM1	forkhead box M1	ENSG00000111206	PAP53	68	17.6%	chr12	2844152	CCDS8516.1	c.1048C>T	p.R350C
FOXP1	forkhead box P1	ENSG00000114861	PAP53	155	24.5%	chr3	71132830	CCDS2914.1	c.1045C>T	p.Q349X
FMNL1	formin-like 1	ENSG00000184922	PAP53	74	31.1%	chr17	40674685	CCDS11497.1	c.1486G>T	p.G496W
FREM3	FRAS1 related extracellular matrix 3	ENSG00000183090	PAP53	56	26.8%	chr4	144833808	NM_001168235	c.-1T>NULL	p.IVS1-3-1SpliceAcceptor
FRAS1	Fraser syndrome 1	ENSG00000138759	PAP53	73	30.1%	chr4	79503805	NM_025074	c.2537G>A	p.C846Y
FUK	fucokinase	ENSG00000157353	PAP53	152	25.7%	chr16	69064413	CCDS10891.2	c.1433C>T	p.T478M
FKRP	fukutin related protein	ENSG00000181027	PAP53	241	31.1%	chr19	51951862	CCDS12691.1	c.1315G>A	p.V439M
FGD5	FYVE; RhoGEF and PH domain containing 5	ENSG00000154783	PAP53	185	23.8%	chr3	14880731	NM_152536	c.2618A>C	p.E873A
GPR123	G protein-coupled receptor 123	ENSG00000197177	PAP53	37	27.0%	chr10	134792638	CCDS41580.1	c.1316A>G	p.H439R
GPR128	G protein-coupled receptor 128	ENSG00000144820	PAP53	111	13.5%	chr3	101857517	CCDS2938.1	c.1811G>A	p.R604Q
GPR153	G protein-coupled receptor 153	ENSG00000158292	PAP53	78	34.6%	chr1	6236688	CCDS64.1	c.463C>T	p.R155C
GPR22	G protein-coupled receptor 22	ENSG00000172209	PAP53	125	20.0%	chr7	106902794	CCDS5744.1	c.1053T>NULL	p.NULL-1FsDel1bp
GPR64	G protein-coupled receptor 64	ENSG00000173698	PAP53	56	30.4%	chrX	18936040	CCDS43923.1	c.1688T>NULL	p.NULL-1FsDel1bp
GPR83	G protein-coupled receptor 83	ENSG00000123901	PAP53	73	26.0%	chr11	93753382	CCDS8297.1	c.853C>T	p.R285C
GJB5	gap junction protein; beta 5; 31.1kDa	ENSG00000189280	PAP53	394	22.1%	chr1	34996278	CCDS382.1	c.760G>T	p.D254Y
GATAD2B	GATA zinc finger domain containing 2B	ENSG00000143614	PAP53	167	25.7%	chr1	152055606	CCDS1054.1	c.983C>T	p.T328M
GFRA3	GDNF family receptor alpha 3	ENSG00000146013	PAP53	46	32.6%	chr5	137621323	CCDS4201.1	c.689G>A	p.R230H
GTF3C2	general transcription factor IIIC; polypeptide 2; beta 110kDa	ENSG00000115207	PAP53	101	13.9%	chr2	27405850	CCDS1749.1	c.1777C>T	p.R593W
GLI2	GLI family zinc finger 2	ENSG00000074047	PAP53	141	18.4%	chr2	121463636	CCDS33283.1	c.3676C>T	p.R1226X
GLI4	GLI family zinc finger 4	ENSG00000181638	PAP53	252	22.2%	chr8	144403623	CCDS6397.1	c.235A>G	p.I79V
GRLF1	glucocorticoid receptor DNA binding factor 1	ENSG00000160007	PAP53	177	20.3%	chr19	52116916	NM_004491	c.3144T>NULL	p.NULL-1FsDel1bp
GRLF1	glucocorticoid receptor DNA binding factor 1	ENSG00000160007	PAP53	336	20.8%	chr19	52195615	NM_004491	c.4330NULL>C	p.NULL-1FsIns1bp
GCNT2	glucosaminyl (N-acetyl) transferase 2; I-branching enzyme (I blood group)	ENSG00000111846	PAP53	168	22.6%	chr6	10665391	CCDS4512.1	c.749C>T	p.P250L
GBA2	glucosidase; beta (bile acid) 2	ENSG00000070610	PAP53	120	26.7%	chr9	35734657	CCDS6589.1	c.406C>A	p.P136T
GRIP1	glutamate receptor interacting protein 1	ENSG00000155974	PAP53	109	22.0%	chr12	65197954	CCDS41807.1	c.572C>T	p.A191V
GRIA3	glutamate receptor; ionotrophic; AMPA 3	ENSG00000125675	PAP53	109	11.0%	chrX	122146070	CCDS14604.1	c.2T>A	p.M1K
GRIA2	glutamate receptor; ionotropic; AMPA 2	ENSG00000120251	PAP53	189	19.0%	chr4	158477029	CCDS3797.1	c.1524G>T	p.E508D
GRIK1	glutamate receptor; ionotropic; kainate 1	ENSG00000171189	PAP53	125	23.2%	chr21	29881651	CCDS42913.1	c.1699G>A	p.V567I
GRIK2	glutamate receptor; ionotropic; kainate 2	ENSG00000164418	PAP53	65	18.5%	chr6	102610125	CCDS5048.1	c.2539A>NULL	p.NULL-1FsDel1bp
ERICH1	glutamate-rich 1	ENSG00000104714	PAP53	499	19.6%	chr8	613820	CCDS5955.1	c.532G>A	p.G178S
GPC3	glypican 3	ENSG00000147257	PAP53	100	24.0%	chrX	132715195	CCDS14638.1	c.1012G>A	p.A338T
GPC6	glypican 6	ENSG00000183098	PAP53	306	19.6%	chr13	93280602	CCDS9469.1	c.514A>T	p.M172L

GNAS	GNAS complex locus	ENSG00000087460	PAP53	238	23.9%	chr20	56862463	NM_080425	c.748G>A	p.D250N
GOLGB1	golgin B1	ENSG00000173230	PAP53	276	22.1%	chr3	122896056	CCDS3004.1	c.5989G>A	p.A1997T
GSC	goosecoid homeobox	ENSG00000133937	PAP53	64	18.8%	chr14	94305079	CCDS9930.1	c.584G>A	p.R195Q
GIGYF1	GRB10 interacting GYF protein 1	ENSG00000146830	PAP53	154	29.9%	chr7	100123106	CCDS34708.1	c.442C>NULL	p.NULL-1FsDel1bp
GCC2	GRIP and coiled-coil domain containing 2	ENSG00000135968	PAP53	99	15.2%	chr2	108454316	CCDS33268.1	c.2099A>NULI	p.NULL-1FsDel1bp
GDF6	growth differentiation factor 6	ENSG00000156466	PAP53	175	26.3%	chr8	97226161	CCDS34926.1	c.1174C>T	p.R392C
GDF7	growth differentiation factor 7	ENSG00000143869	PAP53	90	26.7%	chr2	20733732	CCDS1701.1	c.419G>A	p.S140N
GNAT1	guanine nucleotide binding protein (G protein); alpha transducing activity polypeptide 1	ENSG00000114349	PAP53	56	17.9%	chr3	50206222	CCDS2812.1	c.482C>T	p.P161L
GNL3	guanine nucleotide binding protein-like 3 (nucleolar)	ENSG00000163938	PAP53	53	30.2%	chr3	52695876	CCDS2861.1	c.65A>NULL	p.NULL-1FsDel1bp
GBP6	guanylate binding protein family; member 6	ENSG00000183347	PAP53	57	21.1%	chr1	89618695	CCDS723.1	c.788AACA>N	p.NULL-1FsDel4bp
GUK1	guanylate kinase 1	ENSG00000143774	PAP53	299	13.7%	chr1	226403084	ENST00000366719	c.769C>NULL	p.NULL-1FsDel1bp
HBS1L	HBS1-like (S. cerevisiae)	ENSG00000112339	PAP53	88	26.1%	chr6	135341568	CCDS5173.1	c.1739G>A	p.R580H
HEATR1	HEAT repeat containing 1	ENSG00000119285	PAP53	86	24.4%	chr1	234796688	CCDS31066.1	c.4189C>A	p.P1397T
HSPA4	heat shock 70kDa protein 4	ENSG00000170606	PAP53	67	34.3%	chr5	132467894	CCDS4166.1	c.2390A>NULI	p.NULL-1FsDel1bp
HERC2	hect domain and RLD 2	ENSG00000128731	PAP53	91	18.7%	chr15	26034253	CCDS10021.1	c.13639G>A	p.G4547R
HEG1	HEG homolog 1 (zebrafish)	ENSG00000173706	PAP53	208	14.4%	chr3	126215125	NM_020733	c.3353CTC>N	p.NULL-1FsDel3bp
HMCN1	hemicentin 1	ENSG00000143341	PAP53	217	27.2%	chr1	184291318	CCDS30956.1	c.7033G>T	p.G2345C
HSPG2	heparan sulfate proteoglycan 2	ENSG00000142798	PAP53	316	23.7%	chr1	22047154	CCDS30625.1	c.7757G>A	p.R2586Q
HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	ENSG00000019991	PAP53	187	26.7%	chr7	81174543	CCDS5597.1	c.1615C>T	p.R539X
HPS1	Hermansky-Pudlak syndrome 1	ENSG00000107521	PAP53	67	23.9%	chr10	100185038	CCDS7475.1	c.379G>T	p.G127C
HPS6	Hermansky-Pudlak syndrome 6	ENSG00000166189	PAP53	253	24.5%	chr10	103816242	CCDS7527.1	c.1021C>T	p.Q341X
HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	ENSG00000092199	PAP53	281	19.9%	chr14	20749250	CCDS41915.1	c.975GA>NUL	p.NULL-1FsDel2bp
HKDC1	hexokinase domain containing 1	ENSG00000156510	PAP53	71	19.7%	chr10	70695454	CCDS7288.1	c.2480G>A	p.R827Q
HEXDC	hexosaminidase (glycosyl hydrolase family 20; catalytic domain) containing	ENSG00000169660	PAP53	223	26.0%	chr17	77992350	CCDS42402.1	c.1171C>A	p.L391M
HIRIP3	HIRA interacting protein 3	ENSG00000149929	PAP53	280	31.1%	chr16	29912177	CCDS10664.1	c.1523G>A	p.R508H
HDAC11	histone deacetylase 11	ENSG00000163517	PAP53	140	21.4%	chr3	13520999	CCDS2615.1	c.860G>A	p.R287Q
HDAC7	histone deacetylase 7	ENSG00000061273	PAP53	56	19.6%	chr12	46475778	CCDS41776.1	c.835C>T	p.R279W
HDAC8	histone deacetylase 8	ENSG00000147099	PAP53	112	24.1%	chrX	71631782	CCDS14420.1	c.499C>T	p.R167W
HOXA3	homeobox A3	ENSG00000105997	PAP53	176	32.4%	chr7	27114663	CCDS5404.1	c.728G>A	p.R243H
HOXA6	homeobox A6	ENSG00000106006	PAP53	132	23.5%	chr7	27151956	CCDS5407.1	c.548G>A	p.R183H
HOMER3	homer homolog 3 (Drosophila)	ENSG00000051128	PAP53	67	26.9%	chr19	18910562	CCDS12391.1	c.146G>A	p.R49H
HIP1	huntingtin interacting protein 1	ENSG00000127946	PAP53	282	21.3%	chr7	75024928	CCDS34669.1	c.1547C>T	p.S516L
HIP1R	huntingtin interacting protein 1 related	ENSG00000130787	PAP53	220	28.6%	chr12	121900703	ENST00000376938	c.187G>A	p.A63T
HCN1	hyperpolarization activated cyclic nucleotide-gated potassium channel 1	ENSG00000164588	PAP53	245	28.6%	chr5	45297998	CCDS3952.1	c.2455G>A	p.V819M
IDUA	iduronidase; alpha-L-	ENSG00000127415	PAP53	136	29.4%	chr4	984437	CCDS3343.1	c.337C>T	p.H113Y
IDUA	iduronidase; alpha-L-	ENSG00000127415	PAP53	156	26.9%	chr4	986158	CCDS3343.1	c.1074C>NULI	p.NULL-1FsDel1bp
IRGQ	immunity-related GTPase family; Q	ENSG00000167378	PAP53	453	27.2%	chr19	48788893	CCDS33040.1	c.997G>A	p.G333S
IGLV11-55	immunoglobulin lambda variable 11-55 (non-functional)	ENSG00000211641	PAP53	210	20.0%	chr22	20886082	ENST00000390286	c.14CT>NULL	p.NULL-1FsDel2bp
IGFN1	immunoglobulin-like and fibronectin type III domain containing 1	ENSG00000163395	PAP53	126	24.6%	chr1	199453185	CCDS1409.1	c.1223C>T	p.T408M
INADL	InaD-like (Drosophila)	ENSG00000132849	PAP53	68	16.2%	chr1	62228595	CCDS617.2	c.3838C>T	p.R1280X
INHA	inhibin; alpha	ENSG00000123999	PAP53	359	30.6%	chr2	220148379	CCDS2444.1	c.988G>A	p.A330T

ITPR1	inositol 1;4;5-triphosphate receptor; type 1	ENSG00000150995	PAP53	85	24.7%	chr3	4700478	NM_001168272	c.3449C>T	p.T1150M
ITPR3	inositol 1;4;5-triphosphate receptor; type 3	ENSG00000096433	PAP53	154	11.0%	chr6	33763281	CCDS4783.1	c.6226C>T	p.R2076C
ITPKC	inositol 1;4;5-trisphosphate 3-kinase C	ENSG00000086544	PAP53	147	25.9%	chr19	45923176	CCDS12563.1	c.1247G>T	p.G416V
INPP5B	inositol polyphosphate-5-phosphatase; 75kDa	ENSG00000204084	PAP53	81	23.5%	chr1	38125251	CCDS41306.1	c.1027C>T	p.R343X
INSRR	insulin receptor-related receptor	ENSG00000027644	PAP53	108	28.7%	chr1	155078169	CCDS1160.1	c.3439C>T	p.R1147C
IGF1R	insulin-like growth factor 1 receptor	ENSG00000140443	PAP53	260	26.2%	chr15	97252157	CCDS10378.1	c.721G>A	p.A241T
INTS5	integrator complex subunit 5	ENSG00000185085	PAP53	168	28.6%	chr11	62173668	CCDS8027.1	c.460C>A	p.Q154K
ITGA3	integrin; alpha 3 (antigen CD49C; alpha 3 subunit of VLA-3 receptor)	ENSG00000005884	PAP53	419	14.8%	chr17	45511829	CCDS11557.1	c.2615G>A	p.R872H
ITGB4	integrin; beta 4	ENSG00000132470	PAP53	236	32.2%	chr17	71243761	CCDS11727.1	c.1692T>A	p.C564X
ITGB5	integrin; beta 5	ENSG00000082781	PAP53	73	24.7%	chr3	126043048	CCDS3030.1	c.652C>T	p.R218C
ITLN1	intelectin 1 (galactofuranose binding)	ENSG00000179914	PAP53	65	24.6%	chr1	159113119	CCDS1211.1	c.901C>T	p.R301C
ITIH5L	inter-alpha (globulin) inhibitor H5-like	ENSG00000102313	PAP53	176	26.7%	chrX	54794322	CCDS14361.1	c.3569A>G	p.Y1190C
IL1RL1	interleukin 1 receptor-like 1	ENSG00000115602	PAP53	177	18.1%	chr2	102334775	CCDS2057.1	c.1633G>T	p.A545S
IL1RL2	interleukin 1 receptor-like 2	ENSG00000115598	PAP53	56	28.6%	chr2	102202870	CCDS2056.1	c.952G>A	p.A318T
ILF3	interleukin enhancer binding factor 3; 90kDa	ENSG00000129351	PAP53	84	27.4%	chr19	10650366	CCDS12246.1	c.637G>A	p.A213T
INF2	inverted formin; FH2 and WH2 domain containing	ENSG00000203485	PAP53	204	19.6%	chr14	104240707	CCDS41999.1	c.538A>G	p.I180V
IQSEC2	IQ motif and Sec7 domain 2	ENSG00000124313	PAP53	112	29.5%	chrX	53301852	CCDS35298.1	c.500C>NULL	p.NULL-1FsDel1bp
IQCD	IQ motif containing D	ENSG00000166578	PAP53	632	25.8%	chr12	112117917	CCDS9167.1	c.890G>A	p.R297H
IQGAP2	IQ motif containing GTPase activating protein 2	ENSG00000145703	PAP53	110	19.1%	chr5	76005103	CCDS34188.1	c.3142ATT>NU	p.NULL-1FsDel3bp
JAG1	jagged 1 (Alagille syndrome)	ENSG00000101384	PAP53	97	25.8%	chr20	10578248	CCDS13112.1	c.1270G>A	p.A424T
JPH3	junctophilin 3	ENSG00000154118	PAP53	135	31.1%	chr16	86235443	CCDS10962.1	c.461C>T	p.A154V
KLK4	kallikrein-related peptidase 4	ENSG00000167749	PAP53	72	16.7%	chr19	56102140	CCDS12809.1	c.779G>NULL	p.NULL-1FsDel1bp
KAZALD1	Kazal-type serine peptidase inhibitor domain 1	ENSG00000107821	PAP53	29	37.9%	chr10	102812403	CCDS7509.1	c.64G>A	p.V22M
KBTBD4	kelch repeat and BTB (POZ) domain containing 4	ENSG00000123444	PAP53	438	13.2%	chr11	47551459	CCDS7940.1	c.2016G>NUL	p.NULL-1FsDel1bp
KLHL36	kelch-like 36 (Drosophila)	ENSG00000135686	PAP53	135	24.4%	chr16	83248303	CCDS10948.1	c.389C>T	p.T130M
KRTAP10-3	keratin associated protein 10-3	ENSG00000212935	PAP53	98	17.3%	chr21	44802393	CCDS42956.1	c.634G>A	p.G212S
KIAA0100	KIAA0100	ENSG00000007202	PAP53	192	19.3%	chr17	23966217	CCDS32595.1	c.6700C>T	p.R2234C
KIAA0247	KIAA0247	ENSG00000100647	PAP53	124	29.8%	chr14	69239911	CCDS9796.1	c.168C>NULL	p.NULL-1FsDel1bp
KIAA0467	KIAA0467	ENSG00000198198	PAP53	133	25.6%	chr1	43659073	ENST00000406439	c.1328C>T	p.A443V
KIAA0556	KIAA0556	ENSG00000047578	PAP53	84	27.4%	chr16	27658998	CCDS32415.1	c.1879G>A	p.E627K
KIAA1267	KIAA1267	ENSG00000120071	PAP53	50	24.0%	chr17	41465448	CCDS11503.1	c.3154C>NUL	p.NULL-1FsDel1bp
KIAA1522	KIAA1522	ENSG00000162522	PAP53	159	17.0%	chr1	33008487	CCDS41298.1	c.1120C>A	p.L374M
KIAA1529	KIAA1529	ENSG00000197816	PAP53	231	26.8%	chr9	99116767	CCDS35077.1	c.1184G>A	p.R395Q
KIAA1529	KIAA1529	ENSG00000197816	PAP53	76	17.1%	chr9	99176654	CCDS35077.1	c.4576C>NUL	p.NULL-1FsDel1bp
KIAA1543	KIAA1543	ENSG00000076826	PAP53	221	22.2%	chr19	7582671	CCDS42489.1	c.1292G>A	p.S431N
KIAA1751	KIAA1751	ENSG00000142609	PAP53	58	17.2%	chr1	1893287	NM_001080484	c.880G>A	p.A294T
KLRK1	killer cell lectin-like receptor subfamily K; member 1	ENSG00000213809	PAP53	77	22.1%	chr12	10417028	CCDS8623.1	c.603A>C	p.E201D
KIRREL2	kin of IRRE like 2 (Drosophila)	ENSG00000126259	PAP53	237	10.1%	chr19	41043728	CCDS12481.1	c.1006C>T	p.R336C
KIF15	kinesin family member 15	ENSG00000163808	PAP53	93	18.3%	chr3	44816886	CCDS33744.1	c.1175C>T	p.A392V
KIF16B	kinesin family member 16B	ENSG00000089177	PAP53	787	24.0%	chr20	16308332	CCDS13122.1	c.2315A>G	p.K772R
KIF1A	kinesin family member 1A	ENSG00000130294	PAP53	183	15.8%	chr2	241338587	NM_004321	c.2606G>A	p.R869H
KIF1B	kinesin family member 1B	ENSG00000054523	PAP53	131	31.3%	chr1	10287245	CCDS112.1	c.3415C>T	p.Q1139X
KIF6	kinesin family member 6	ENSG00000164627	PAP53	142	19.7%	chr6	39688971	CCDS4844.1	c.740T>NULL	p.NULL-1FsDel1bp
KLC2	kinesin light chain 2	ENSG00000174996	PAP53	220	21.8%	chr11	65786921	CCDS8130.1	c.590G>A	p.R197Q
KLC3	kinesin light chain 3	ENSG00000104892	PAP53	94	29.8%	chr19	50543799	CCDS12660.2	c.835C>T	p.R279W

KLRAQ1	KLRAQ motif containing 1	ENSG00000162869	PAP53	104	21.2%	chr2	48588014	CCDS1839.1	c.2038C>T	p.H680Y
KANK1	KN motif and ankyrin repeat domains 1	ENSG00000107104	PAP53	76	19.7%	chr9	703437	CCDS34976.1	c.2671C>T	p.Q891X
KANK2	KN motif and ankyrin repeat domains 2	ENSG00000197256	PAP53	289	15.2%	chr19	11141590	CCDS12255.1	c.2465C>T	p.A822V
KRBA2	KRAB-A domain containing 2	ENSG00000184619	PAP53	204	23.0%	chr17	8214212	CCDS11141.1	c.1696A>NULL	p.NULL-1FsDel1bp
LARP7	La ribonucleoprotein domain family; member 7	ENSG00000174720	PAP53	70	22.9%	chr4	113797932	CCDS3701.2	c.1749A>NULL	p.NULL-1FsDel1bp
LMNB2	lamin B2	ENSG00000176619	PAP53	78	15.4%	chr19	2382862	CCDS12090.1	c.1688NULL>C	p.NULL-1FsIns1bp
LAMA2	laminin; alpha 2	ENSG00000196569	PAP53	67	23.9%	chr6	129615012	CCDS5138.1	c.1975T>A	p.S659T
LAMB1	laminin; beta 1	ENSG00000091136	PAP53	217	19.8%	chr7	107426085	CCDS5750.1	c.302C>A	p.T101N
LAMB2	laminin; beta 2 (laminin S)	ENSG00000172037	PAP53	63	23.8%	chr3	49142670	CCDS2789.1	c.1223G>A	p.R408H
LTBP1	latent transforming growth factor beta binding protein 1	ENSG00000049323	PAP53	178	20.8%	chr2	33442045	CCDS33177.1	c.4358G>A	p.C1453Y
LGALS3BP	lectin; galactoside-binding; soluble; 3 binding protein	ENSG00000108679	PAP53	149	22.1%	chr17	74480824	CCDS11759.1	c.452G>A	p.R151Q
LMTK3	lemur tyrosine kinase 3	ENSG00000142235	PAP53	186	28.5%	chr19	53696204	NM_001080434	c.1248G>NUL	p.NULL-1FsDel1bp
LINGO4	leucine rich repeat and Ig domain containing 4	ENSG00000213171	PAP53	152	22.4%	chr1	150040904	CCDS30855.1	c.901C>T	p.R301W
LRRC16B	leucine rich repeat containing 16B	ENSG00000186648	PAP53	108	14.8%	chr14	23603370	CCDS32054.1	c.3055C>T	p.R1019X
LRRC25	leucine rich repeat containing 25	ENSG00000175489	PAP53	219	20.5%	chr19	18368292	CCDS12377.1	c.482T>C	p.L161P
LRCH1	leucine-rich repeats and calponin homology (CH) domain containing 1	ENSG00000136141	PAP53	173	21.4%	chr13	46177259	CCDS31972.1	c.1456G>A	p.A486T
LARS2	leucyl-tRNA synthetase 2; mitochondrial	ENSG00000011376	PAP53	164	18.9%	chr3	45512803	CCDS2728.1	c.1556C>T	p.T519M
LIMS2	LIM and senescent cell antigen-like domains 2	ENSG00000072163	PAP53	90	20.0%	chr2	128116173	CCDS2147.1	c.653G>A	p.G218D
LIMS2	LIM and senescent cell antigen-like domains 2	ENSG00000072163	PAP53	66	24.2%	chr2	128131494	CCDS2147.1	c.196G>A	p.V66M
LHX8	LIM homeobox 8	ENSG00000162624	PAP53	57	24.6%	chr1	75386945	CCDS30756.1	c.800G>A	p.R267H
LIPI	lipase; member I	ENSG00000188992	PAP53	99	29.3%	chr21	14483509	CCDS13564.1	c.212G>A	p.R71K
LRP10	low density lipoprotein receptor-related protein 10	ENSG00000197324	PAP53	172	23.8%	chr14	22415006	CCDS9578.1	c.1009C>T	p.R337C
LRRN4CL	LRRN4 C-terminal like	ENSG00000177363	PAP53	240	18.8%	chr11	62212236	CCDS8030.1	c.1037NULL>C	p.NULL-1FsIns1bp
LYPD3	LY6/PLAUR domain containing 3	ENSG00000124466	PAP53	188	18.6%	chr19	48657659	CCDS12620.1	c.725C>T	p.P242L
KDM4B	lysine (K)-specific demethylase 4B	ENSG00000127663	PAP53	70	20.0%	chr19	5089034	CCDS12138.1	c.2503C>T	p.R835C
KDM5A	lysine (K)-specific demethylase 5A	ENSG00000073614	PAP53	263	22.4%	chr12	290362	CCDS41736.1	c.3166C>T	p.R1056W
KDM5A	lysine (K)-specific demethylase 5A	ENSG00000073614	PAP53	57	35.1%	chr12	368529	ENST00000382815	c.224CCCCC>	p.NULL-1FsDel5bp
LPAR3	lysophosphatidic acid receptor 3	ENSG00000171517	PAP53	171	25.7%	chr1	85103727	CCDS700.1	c.665C>T	p.P222L
LYST	lysosomal trafficking regulator	ENSG00000143669	PAP53	197	28.4%	chr1	233964433	CCDS31062.1	c.8684A>NULL	p.NULL-1FsDel1bp
LYST	lysosomal trafficking regulator	ENSG00000143669	PAP53	109	22.0%	chr1	234005012	CCDS31062.1	c.-1T>NULL	p.IVS15-3-1SpliceAcceptor
MR1	major histocompatibility complex; class I-related	ENSG00000153029	PAP53	57	33.3%	chr1	179284973	CCDS1342.1	c.230C>T	p.A77V
MIP	major intrinsic protein of lens fiber	ENSG00000135517	PAP53	338	11.2%	chr12	55133169	CCDS8919.1	c.560G>A	p.R187H
MDH1	malate dehydrogenase 1; NAD (soluble)	ENSG00000014641	PAP53	187	27.8%	chr2	63679901	CCDS1874.1	c.469C>T	p.R157C
MASP1	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	ENSG00000127241	PAP53	301	21.3%	chr3	188420614	CCDS33907.1	c.2039T>C	p.V680A
MAN1C1	mannosidase; alpha; class 1C; member 1	ENSG00000117643	PAP53	115	25.2%	chr1	25817039	CCDS265.1	c.164C>NULL	p.NULL-1FsDel1bp
MGAT2	mannosyl (alpha-1;6-)-glycoprotein beta-1;2-N-acetylglucosaminyltransferase	ENSG00000168282	PAP53	344	14.8%	chr14	49158121	CCDS9690.1	c.385G>A	p.E129K
MEG3	maternally expressed 3 (non-protein coding)	ENSG00000214548	PAP53	93	19.4%	chr14	100381572	ENST00000398518	c.164C>T	p.T55M
MMP10	matrix metallopeptidase 10 (stromelysin 2)	ENSG00000166670	PAP53	47	29.8%	chr11	102154603	CCDS8321.1	c.584A>G	p.H195R
MMP11	matrix metallopeptidase 11 (stromelysin 3)	ENSG00000099953	PAP53	152	25.7%	chr22	22452593	CCDS13816.1	c.386C>T	p.T129M
MXRA8	matrix-remodelling associated 8	ENSG00000162576	PAP53	47	38.3%	chr1	1279973	CCDS24.1	c.1371C>NULL	p.NULL-1FsDel1bp
MTCP1	mature T-cell proliferation 1	ENSG00000214827	PAP53	87	23.0%	chrX	153947449	CCDS44027.1	c.31G>A	p.D11N

MLX	MAX-like protein X	ENSG00000108788	PAP53	115	16.5%	chr17	37975623	CCDS11430.1	c.736A>G	p.M246V
MTOR	mechanistic target of rapamycin (serine/threonine kinase)	ENSG00000198793	PAP53	101	25.7%	chr1	11193505	CCDS127.1	c.3607C>T	p.R1203X
MED12L	mediator complex subunit 12-like	ENSG00000144893	PAP53	135	21.5%	chr3	152391194	CCDS33876.1	c.1754C>T	p.S585L
MED13L	mediator complex subunit 13-like	ENSG00000123066	PAP53	98	21.4%	chr12	114929627	CCDS9177.1	c.2210C>T	p.T737M
MED15	mediator complex subunit 15	ENSG00000099917	PAP53	69	27.5%	chr22	19266976	CCDS33602.1	c.1351C>NULL	p.NULL-1FsDel1bp
MED25	mediator complex subunit 25	ENSG00000104973	PAP53	205	25.9%	chr19	55024925	CCDS33075.1	c.596C>NULL	p.NULL-1FsDel1bp
MGEA5	meningioma expressed antigen 5 (hyaluronidase)	ENSG00000198408	PAP53	80	30.0%	chr10	103543739	CCDS7520.1	c.1991G>A	p.R664H
MTA2	metastasis associated 1 family; member 2	ENSG00000149480	PAP53	54	24.1%	chr11	62119095	CCDS8022.1	c.1507G>A	p.A503T
MBD4	methyl-CpG binding domain protein 4	ENSG00000129071	PAP53	228	11.0%	chr3	130638238	CCDS3058.1	c.1804A>NULL	p.NULL-1FsDel1bp
MRI1	methylthioribose-1-phosphate isomerase homolog (S. cerevisiae)	ENSG00000037757	PAP53	590	23.7%	chr19	13740698	CCDS32923.1	c.785C>T	p.T262I
METT11D1	methyltransferase 11 domain containing 1	ENSG00000165792	PAP53	90	31.1%	chr14	20532881	CCDS41913.1	c.857G>A	p.R286H
METTL1	methyltransferase like 1	ENSG00000037897	PAP53	117	24.8%	chr12	56449057	CCDS8955.2	c.895C>T	p.P299S
MASTL	microtubule associated serine/threonine kinase-like	ENSG00000120539	PAP53	125	20.0%	chr10	27499062	CCDS7153.1	c.1168A>NULL	p.NULL-1FsDel1bp
MACF1	microtubule-actin crosslinking factor 1	ENSG00000127603	PAP53	275	25.8%	chr1	39697434	CCDS436.1	c.16615C>T	p.R5539C
MAP1S	microtubule-associated protein 1S	ENSG00000130479	PAP53	77	33.8%	chr19	17699081	CCDS32954.1	c.1888G>A	p.A630T
MAPT	microtubule-associated protein tau	ENSG00000186868	PAP53	147	25.9%	chr17	41429670	CCDS11501.1	c.1576C>T	p.R526C
MCM6	minichromosome maintenance complex component 6	ENSG00000076003	PAP53	231	23.8%	chr2	136342838	CCDS2179.1	c.428G>A	p.R143Q
MCART6	mitochondrial carrier triple repeat 6	ENSG00000176274	PAP53	55	29.1%	chrX	103236248	CCDS35363.1	c.349C>T	p.R117C
MRPS15	mitochondrial ribosomal protein S15	ENSG00000116898	PAP53	70	20.0%	chr1	36694013	CCDS411.1	c.737C>T	p.A246V
MT-CO2	mitochondrially encoded cytochrome c oxidase II	ENSG00000198712	PAP53	100	80.0%	chrM	7851	ENST00000361739	c.265G>A	p.E89K
MAPK9	mitogen-activated protein kinase 9	ENSG00000050748	PAP53	89	22.5%	chr5	179621429	CCDS4453.1	c.-1G>T	p.IVS3-1-1SpliceAcceptor
MAPKBP1	mitogen-activated protein kinase binding protein 1	ENSG00000137802	PAP53	147	20.4%	chr15	39895195	CCDS32201.1	c.1399G>A	p.A467T
MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	ENSG00000162889	PAP53	88	23.9%	chr1	204970022	CCDS31001.1	c.647G>A	p.S216N
MLST8	MTOR associated protein; LST8 homolog (S. cerevisiae)	ENSG00000167965	PAP53	70	21.4%	chr16	2198625	ENST00000301724	c.872G>A	p.R291H
MCOLN1	mucolipin 1	ENSG00000090674	PAP53	142	17.6%	chr19	7498442	CCDS12180.1	c.608C>T	p.P203L
MSH2	mutS homolog 2; colon cancer; nonpolyposis type 1 (E. coli)	ENSG00000095002	PAP53	27	37.0%	chr2	47489073	CCDS1834.1	c.241AG>NUL	p.NULL-1FsDel2bp
MSH2	mutS homolog 2; colon cancer; nonpolyposis type 1 (E. coli)	ENSG00000095002	PAP53	112	18.8%	chr2	47543752	CCDS1834.1	c.1465G>T	p.E489X
MYCBP2	MYC binding protein 2	ENSG00000005810	PAP53	69	23.2%	chr13	76742150	CCDS31994.1	c.1195A>NULL	p.NULL-1FsDel1bp
MINA	MYC induced nuclear antigen	ENSG00000170854	PAP53	127	12.6%	chr3	99151442	CCDS43114.1	c.1165AAG>N	p.NULL-1FsDel3bp
MYD88	myeloid differentiation primary response gene (88)	ENSG00000172936	PAP53	499	19.4%	chr3	38157752	CCDS2674.1	c.862C>T	p.R288C
MLLT6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog; Drosophila); translocated to; 6	ENSG00000108292	PAP53	136	11.0%	chr17	34129618	CCDS11327.1	c.2099C>T	p.T700M
MYOF	myoferlin	ENSG00000138119	PAP53	107	22.4%	chr10	95231924	CCDS41551.1	c.104TG>NUL	p.NULL-1FsDel2bp
MYOM3	myomesin family; member 3	ENSG00000142661	PAP53	88	17.0%	chr1	24297006	CCDS41281.1	c.739G>A	p.V247I
MYLK3	myosin light chain kinase 3	ENSG00000140795	PAP53	106	32.1%	chr16	45322075	CCDS10723.2	c.1499G>A	p.R500Q
MYO6	myosin VI	ENSG00000196586	PAP53	123	26.8%	chr6	76680538	CCDS34487.1	c.3478C>T	p.R1160W
MYO6	myosin VI	ENSG00000196586	PAP53	143	23.1%	chr6	76680590	CCDS34487.1	c.3530G>A	p.R1177H
MYH15	myosin; heavy chain 15	ENSG00000144821	PAP53	260	42.7%	chr3	109646198	CCDS43127.1	c.2694C>A	p.D898E
MYH7B	myosin; heavy chain 7B; cardiac muscle; beta	ENSG00000078814	PAP53	82	29.3%	chr20	33048125	CCDS42869.1	c.3295C>T	p.R1099W
MYH7B	myosin; heavy chain 7B; cardiac muscle; beta	ENSG00000078814	PAP53	92	15.2%	chr20	33051071	CCDS42869.1	c.4703G>A	p.S1568N
MTMR11	myotubularin related protein 11	ENSG00000014914	PAP53	53	20.8%	chr1	148171965	CCDS942.1	c.727G>A	p.V243I
NACC2	NACC family member 2; BEN and BTB (POZ) domain containing	ENSG00000148411	PAP53	58	36.2%	chr9	138043509	CCDS6993.1	c.1438G>A	p.D480N
NAGS	N-acetylglutamate synthase	ENSG00000161653	PAP53	106	16.0%	chr17	39438931	CCDS11473.1	c.715G>A	p.V239I

NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 10; 42kDa	ENSG00000130414	PAP53	95	27.4%	chr2	240602894	CCDS2531.1	c.725C>NULL	p.NULL-1FsDel1bp
NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex; 9; 39kDa	ENSG00000139180	PAP53	63	19.0%	chr12	4666494	CCDS8532.1	c.1093G>A	p.E365K
NKTR	natural killer-tumor recognition sequence	ENSG00000114857	PAP53	50	26.0%	chr3	42649247	CCDS2702.1	c.701G>A	p.R234H
NKTR	natural killer-tumor recognition sequence	ENSG00000114857	PAP53	87	23.0%	chr3	42651170	CCDS2702.1	c.991C>T	p.R331W
NCKAP5	NCK-associated protein 5	ENSG00000176771	PAP53	171	22.2%	chr2	133604111	NM_207363	c.380TTAC>N	p.NULL-1FsDel4bp
NELL1	NEL-like 1 (chicken)	ENSG00000165973	PAP53	131	20.6%	chr11	20896338	CCDS7855.1	c.638C>T	p.P213L
NPHP1	nephronophthisis 1 (juvenile)	ENSG00000144061	PAP53	74	21.6%	chr2	110262885	CCDS2086.1	c.1334G>A	p.R445H
NPHP1	nephronophthisis 1 (juvenile)	ENSG00000144061	PAP53	72	26.4%	chr2	110262889	CCDS2086.1	c.1330A>G	p.T444A
NCAM1	neural cell adhesion molecule 1	ENSG00000149294	PAP53	122	12.3%	chr11	112337487	ENST00000397957	c.186GG>NUL	p.NULL-1FsDel2bp
NEDD9	neural precursor cell expressed; developmentally down-regulated 9	ENSG00000111859	PAP53	476	15.3%	chr6	11299081	CCDS4520.1	c.1007C>T	p.A336V
NRG2	neuregulin 2	ENSG00000158458	PAP53	53	22.6%	chr5	139240642	CCDS4217.1	c.974G>A	p.R325Q
NFASC	neurofascin homolog (chicken)	ENSG00000163531	PAP53	143	18.2%	chr1	203190656	CCDS30982.1	c.471C>NULL	p.NULL-1FsDel1bp
NFASC	neurofascin homolog (chicken)	ENSG00000163531	PAP53	144	18.1%	chr1	203204664	CCDS30982.1	c.967G>A	p.G323R
NIPBL	Nipped-B homolog (Drosophila)	ENSG00000164190	PAP53	78	17.9%	chr5	37100656	CCDS3920.1	c.8320A>NULL	p.NULL-1FsDel1bp
NKX2-3	NK2 transcription factor related; locus 3 (Drosophila)	ENSG00000119919	PAP53	74	25.7%	chr10	101283053	CCDS41558.1	c.175G>T	p.G59W
NMT2	N-myristoyltransferase 2	ENSG00000152465	PAP53	289	24.6%	chr10	15215116	CCDS7109.1	c.544T>G	p.Y182D
NCAPD2	non-SMC condensin I complex; subunit D2	ENSG00000010292	PAP53	286	17.8%	chr12	6505734	CCDS8548.1	c.2502C>NULL	p.NULL-1FsDel1bp
NCCRP1	non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)	ENSG00000188505	PAP53	158	22.8%	chr19	44381657	CCDS12529.1	c.460G>T	p.V154L
NSUN4	NOP2/Sun domain family; member 4	ENSG00000117481	PAP53	44	29.5%	chr1	46599088	CCDS534.1	c.-1G>A	p.IVS5+1-1SpliceDonor
NOTCH2	Notch homolog 2 (Drosophila)	ENSG00000134250	PAP53	181	16.0%	chr1	120309672	CCDS908.1	c.1720GT>NU	p.NULL-1FsDel2bp
NECAB2	N-terminal EF-hand calcium binding protein 2	ENSG00000103154	PAP53	109	28.4%	chr16	82588347	CCDS10940.1	c.821G>A	p.R274H
NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor; zeta	ENSG00000144802	PAP53	158	15.8%	chr3	103058623	CCDS2946.1	c.1841G>A	p.R614H
NUMA1	nuclear mitotic apparatus protein 1	ENSG00000137497	PAP53	131	22.9%	chr11	71396080	CCDS31633.1	c.5266G>A	p.A1756T
NCOA7	nuclear receptor coactivator 7	ENSG00000111912	PAP53	139	13.7%	chr6	126241209	CCDS5132.1	c.459G>T	p.Q153H
NCOR2	nuclear receptor co-repressor 2	ENSG00000196498	PAP53	60	25.0%	chr12	123414181	CCDS41858.1	c.3045C>NULL	p.NULL-1FsDel1bp
NRIP1	nuclear receptor interacting protein 1	ENSG00000180530	PAP53	154	20.1%	chr21	15260201	CCDS13568.1	c.5660A>NULL	p.NULL-1FsDel1bp
NRIP1	nuclear receptor interacting protein 1	ENSG00000180530	PAP53	262	21.0%	chr21	15260874	CCDS13568.1	c.1511T>A	p.L504Q
NR0B1	nuclear receptor subfamily 0; group B; member 1	ENSG00000169297	PAP53	105	19.0%	chrX	30236906	CCDS14223.1	c.496C>T	p.R166W
NRF1	nuclear respiratory factor 1	ENSG00000106459	PAP53	98	22.4%	chr7	129137483	CCDS5813.2	c.799NULL>A	p.NULL-1FsIns1bp
NUP153	nucleoporin 153kDa	ENSG00000124789	PAP53	277	21.7%	chr6	17769927	CCDS4541.1	c.1457G>NUL	p.NULL-1FsDel1bp
NUBPL	nucleotide binding protein-like	ENSG00000151413	PAP53	71	18.3%	chr14	31365589	CCDS41940.1	c.611C>T	p.A204V
NUDT7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	ENSG00000140876	PAP53	187	21.9%	chr16	76333245	CCDS42195.1	c.614A>NULL	p.NULL-1FsDel1bp
NULL	NULL	ENSG00000184334	PAP53	82	28.0%	chr8	142514997	ENST00000355850	c.394C>T	p.R132W
NULL	NULL	ENSG00000206083	PAP53	280	23.2%	chr14	23071657	ENST00000382785	c.2518G>A	p.A840T
NULL	NULL	ENSG00000214279	PAP53	118	39.0%	chr10	135128303	ENST00000356567	c.1564C>T	p.R522C
NULL	NULL	ENSG00000214473	PAP53	294	26.2%	chr9	136453523	ENST00000398385	c.47G>A	p.R16H
NULL	NULL	ENSG00000215099	PAP53	42	23.8%	chr17	5275529	ENST00000399576	c.388AA>NUL	p.NULL-1FsDel2bp

NULL	NULL	ENSG00000222037	PAP53	69	26.1%	chr22	21560424	ENST00000410090	c.191G>A	p.R64Q
NULL	NULL	MI0002470	PAP53	100	12.0%	chr8	41637119	MI0002470	c.65A>T	p.D22V
NULL	NULL	MI0002470	PAP53	98	11.2%	chr8	41637120	MI0002470	c.64G>A	p.D22N
NULL	NULL	MI0006370	PAP53	40	25.0%	chr5	154045563	MI0006370	c.35T>NULL	p.NULL-1FsDel1bp
NUMB	numb homolog (Drosophila)	ENSG00000133961	PAP53	119	26.1%	chr14	72892119	CCDS32116.1	c.94G>A	p.V32I
OSR2	odd-skipped related 2 (Drosophila)	ENSG00000164920	PAP53	90	21.1%	chr8	100030970	NM_001142462	c.614G>A	p.C205Y
ODZ1	odz; odd Oz/ten-m homolog 1(Drosophila)	ENSG00000009694	PAP53	154	11.0%	chrX	123345420	CCDS14609.1	c.7021C>G	p.P2341A
ODZ1	odz; odd Oz/ten-m homolog 1(Drosophila)	ENSG00000009694	PAP53	281	30.2%	chrX	123857709	CCDS14609.1	c.280G>A	p.V94I
ODZ4	odz; odd Oz/ten-m homolog 4 (Drosophila)	ENSG00000149256	PAP53	654	17.7%	chr11	78046864	NM_001098816	c.8197C>T	p.R2733W
OR10A6	olfactory receptor; family 10; subfamily A; member 6	ENSG00000175393	PAP53	208	28.4%	chr11	7906422	CCDS31420.1	c.364C>T	p.R122X
OR10G3	olfactory receptor; family 10; subfamily G; member 3	ENSG00000169208	PAP53	222	16.7%	chr14	21107985	CCDS32046.1	c.731C>T	p.A244V
OR13C8	olfactory receptor; family 13; subfamily C; member 8	ENSG00000186943	PAP53	188	20.7%	chr9	106371346	CCDS35090.1	c.77T>C	p.V26A
OR4D9	olfactory receptor; family 4; subfamily D; member 9	ENSG00000172742	PAP53	259	25.1%	chr11	59039152	CCDS31564.1	c.191G>A	p.R64H
OR4E2	olfactory receptor; family 4; subfamily E; member 2	ENSG00000221977	PAP53	273	16.1%	chr14	21203586	CCDS41916.1	c.450G>NULL	p.NULL-1FsDel1bp
OR8J1	olfactory receptor; family 8; subfamily J; member 1	ENSG00000172487	PAP53	92	19.6%	chr11	55884909	CCDS31529.1	c.611C>A	p.A204E
OPRD1	opioid receptor; delta 1	ENSG00000116329	PAP53	177	26.0%	chr1	29058127	CCDS329.1	c.302C>T	p.T101M
OPN4	opsin 4	ENSG00000122375	PAP53	164	29.9%	chr10	88409771	CCDS31237.1	c.973G>A	p.A325T
OAZ1	ornithine decarboxylase antizyme 1	ENSG00000104904	PAP53	125	28.0%	chr19	2223983	ENST00000322297	c.560G>A	p.R187Q
OTOF	otoferlin	ENSG00000115155	PAP53	75	22.7%	chr2	26537394	CCDS1725.1	c.5542G>A	p.E1848K
OXER1	oxoeicosanoid (OXE) receptor 1	ENSG00000162881	PAP53	225	13.8%	chr2	42844673	CCDS1810.1	c.151T>C	p.S51P
OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	ENSG00000105953	PAP53	131	14.5%	chr7	44714086	CCDS34627.1	c.3035C>T	p.T1012M
PTHLH	parathyroid hormone-like hormone	ENSG00000087494	PAP53	70	24.3%	chr12	28006165	ENST00000354417	c.660AAA>NU	p.NULL-1FsDel3bp
PNPLA7	patatin-like phospholipase domain containing 7	ENSG00000130653	PAP53	131	28.2%	chr9	139520021	CCDS7045.1	c.1264G>A	p.V422M
PTCH1	patched homolog 1 (Drosophila)	ENSG00000185920	PAP53	208	25.0%	chr9	97251370	CCDS6714.1	c.3860C>NULI	p.NULL-1FsDel1bp
PDS5A	PDS5; regulator of cohesion maintenance; homolog A (S. cerevisiae)	ENSG00000121892	PAP53	112	31.3%	chr4	39586514	NM_001100399	c.1129C>T	p.R377C
PDZD7	PDZ domain containing 7	ENSG00000186862	PAP53	79	22.8%	chr10	102759023	ENST00000238965	c.875G>NULL	p.NULL-1FsDel1bp
PEF1	penta-EF-hand domain containing 1	ENSG00000162517	PAP53	118	20.3%	chr1	31870800	CCDS345.1	c.508C>T	p.R170C
PPIL1	peptidylprolyl isomerase (cyclophilin)-like 1	ENSG00000137168	PAP53	131	26.7%	chr6	36931698	CCDS4826.1	c.370G>A	p.G124S
PCNT	pericentrin	ENSG00000160299	PAP53	153	25.5%	chr21	46660846	CCDS33592.1	c.6586G>A	p.V2196I
PLIN1	perilipin 1	ENSG00000166819	PAP53	88	25.0%	chr15	88015724	CCDS10353.1	c.408C>NULL	p.NULL-1FsDel1bp
PLIN3	perilipin 3	ENSG00000105355	PAP53	55	23.6%	chr19	4798894	CCDS12137.1	c.643G>A	p.A215T
PER2	period homolog 2 (Drosophila)	ENSG00000132326	PAP53	90	20.0%	chr2	238824997	CCDS2528.1	c.3256G>A	p.A1086T
PER2	period homolog 2 (Drosophila)	ENSG00000132326	PAP53	85	12.9%	chr2	238833347	CCDS2528.1	c.-1T>G	p.IVS13+2-1SpliceDonor
PER2	period homolog 2 (Drosophila)	ENSG00000132326	PAP53	90	11.1%	chr2	238833349	CCDS2528.1	c.1627G>A	p.E543K
PEX6	peroxisomal biogenesis factor 6	ENSG00000124587	PAP53	55	29.1%	chr6	43040070	CCDS4877.1	c.2924G>A	p.R975H
PEX6	peroxisomal biogenesis factor 6	ENSG00000124587	PAP53	540	28.9%	chr6	43042339	CCDS4877.1	c.2128NULL>(	p.NULL-1FsIns1bp
PPRC1	peroxisome proliferator-activated receptor gamma; coactivator-related 1	ENSG00000148840	PAP53	92	25.0%	chr10	103888400	CCDS7529.1	c.377C>T	p.S126L
FARSA	phenylalanyl-tRNA synthetase; alpha subunit	ENSG00000179115	PAP53	82	34.1%	chr19	12894566	CCDS12287.1	c.1523C>T	p.A508V
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP53	63	25.4%	chr10	89707750	CCDS31238.1	c.795A>NULL	p.NULL-1FsDel1bp
PITPNM1	phosphatidylinositol transfer protein; membrane-associated 1	ENSG00000110697	PAP53	130	26.2%	chr11	67023985	CCDS31620.1	c.1039G>A	p.E347K
PREX1	phosphatidylinositol-3;4;5-trisphosphate-dependent Rac exchange factor 1	ENSG00000124126	PAP53	345	16.2%	chr20	46699332	CCDS13410.1	c.3218G>A	p.R1073H

PDE11A	phosphodiesterase 11A	ENSG00000128655	PAP53	190	24.7%	chr2	178202449	CCDS33334.1	c.2734C>T	p.R912X
PDE3A	phosphodiesterase 3A; cGMP-inhibited	ENSG00000172572	PAP53	98	24.5%	chr12	20413990	CCDS31754.1	c.505G>NULL	p.NULL-1FsDel1bp
PDE7B	phosphodiesterase 7B	ENSG00000171408	PAP53	57	21.1%	chr6	136510272	CCDS5175.1	c.257G>A	p.R86H
PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	ENSG00000124253	PAP53	50	20.0%	chr20	55570037	CCDS13460.1	c.164G>A	p.R55Q
PGM2L1	phosphoglucomutase 2-like 1	ENSG00000165434	PAP53	132	18.2%	chr11	73735904	CCDS8231.1	c.1065A>NULL	p.NULL-1FsDel1bp
PIK3CB	phosphoinositide-3-kinase; catalytic; beta polypeptide	ENSG00000051382	PAP53	232	15.5%	chr3	139883499	CCDS3104.1	c.2504G>A	p.R835Q
PLCB1	phospholipase C; beta 1 (phosphoinositide-specific)	ENSG00000182621	PAP53	105	10.5%	chr20	8651013	CCDS13102.1	c.1526C>T	p.T509M
PYGB	phosphorylase; glycogen; brain	ENSG00000100994	PAP53	88	27.3%	chr20	25219180	CCDS13171.1	c.1891G>A	p.V631I
PKP4	plakophilin 4	ENSG00000144283	PAP53	214	19.2%	chr2	159196633	CCDS33305.1	c.1276C>T	p.R426C
PLAT	plasminogen activator; tissue	ENSG00000104368	PAP53	108	25.0%	chr8	42161803	CCDS6126.1	c.584C>T	p.A195V
PDGFD	platelet derived growth factor D	ENSG00000170962	PAP53	49	24.5%	chr11	103319560	CCDS41703.1	c.602C>T	p.T201M
PLEKHA6	pleckstrin homology domain containing; family A member 6	ENSG00000143850	PAP53	79	30.4%	chr1	202493223	CCDS1444.1	c.1405C>T	p.R469C
PLEKHG2	pleckstrin homology domain containing; family G (with RhoGef domain) member 2	ENSG00000090924	PAP53	113	26.5%	chr19	44603294	CCDS33022.1	c.1235G>T	p.R412L
PLEKHG3	pleckstrin homology domain containing; family G (with RhoGef domain) member 3	ENSG00000126822	PAP53	274	28.1%	chr14	64277798	CCDS32098.1	c.1642G>A	p.V548I
PLEKHO1	pleckstrin homology domain containing; family O member 1	ENSG00000023902	PAP53	252	25.8%	chr1	148398017	CCDS945.1	c.905C>T	p.P302L
PHLDB2	pleckstrin homology-like domain; family B; member 2	ENSG00000144824	PAP53	95	11.6%	chr3	113146853	CCDS2962.1	c.2317G>NUL	p.NULL-1FsDel1bp
PLEC	plectin	ENSG00000178209	PAP53	258	24.8%	chr8	145067164	CCDS43772.1	c.9224G>A	p.R3075Q
PLXNA2	plexin A2	ENSG00000076356	PAP53	89	27.0%	chr1	206284533	CCDS31013.1	c.3817C>T	p.R1273W
PLXNA3	plexin A3	ENSG00000130827	PAP53	78	20.5%	chrX	153341759	CCDS14752.1	c.42G>NULL	p.NULL-1FsDel1bp
PLXNA3	plexin A3	ENSG00000130827	PAP53	162	32.1%	chrX	153349922	CCDS14752.1	c.4046C>T	p.T1349M
PLXNA4	plexin A4	ENSG00000221866	PAP53	277	23.8%	chr7	131843863	CCDS43646.1	c.130C>T	p.R44X
PNMAL2	PNMA-like 2	ENSG00000204851	PAP53	85	27.1%	chr19	51687250	ENST00000377655	c.769G>A	p.G257R
PODNL1	podocan-like 1	ENSG00000132000	PAP53	63	23.8%	chr19	13909771	CCDS12300.1	c.73G>A	p.A25T
PMFBP1	polyamine modulated factor 1 binding protein 1	ENSG00000118557	PAP53	155	12.3%	chr16	70716175	CCDS32483.1	c.2581G>A	p.D861N
PBRM1	polybromo 1	ENSG00000163939	PAP53	120	33.3%	chr3	52596533	CCDS2859.1	c.2903G>A	p.R968Q
PKD1L2	polycystic kidney disease 1-like 2	ENSG00000166473	PAP53	101	25.7%	chr16	79748086	ENST00000299598	c.4004C>A	p.A1335D
POLD1	polymerase (DNA directed); delta 1; catalytic subunit 125kDa	ENSG00000062822	PAP53	133	25.6%	chr19	55603946	CCDS12795.1	c.1868G>A	p.R623Q
POLH	polymerase (DNA directed); eta	ENSG00000170734	PAP53	108	12.0%	chr6	43663079	CCDS4902.1	c.365C>T	p.T122I
POLH	polymerase (DNA directed); eta	ENSG00000170734	PAP53	75	22.7%	chr6	43690249	CCDS4902.1	c.2119T>NULL	p.NULL-1FsDel1bp
POLR2A	polymerase (RNA) II (DNA directed) polypeptide A; 220kDa	ENSG00000181222	PAP53	120	30.0%	chr17	7347769	CCDS32548.1	c.3175C>T	p.R1059W
KCNS1	potassium voltage-gated channel; delayed-rectifier; subfamily S; member 1	ENSG00000124134	PAP53	270	23.3%	chr20	43157076	CCDS13342.1	c.1430G>T	p.S477I
KCNQ2	potassium voltage-gated channel; KQT-like subfamily; member 2	ENSG00000075043	PAP53	83	13.3%	chr20	61509057	CCDS13520.1	c.2003C>T	p.P668L
KCNB1	potassium voltage-gated channel; Shab-related subfamily; member 1	ENSG00000158445	PAP53	488	26.4%	chr20	47424267	CCDS13418.1	c.1237G>A	p.V413I
KCNA6	potassium voltage-gated channel; shaker-related subfamily; member 6	ENSG00000151079	PAP53	168	20.2%	chr12	4789941	CCDS8534.1	c.473G>A	p.R158H
PRDM14	PR domain containing 14	ENSG00000147596	PAP53	147	27.2%	chr8	71144168	CCDS6206.1	c.482C>A	p.P161H
POP1	processing of precursor 1; ribonuclease P/MRP subunit (S. cerevisiae)	ENSG00000104356	PAP53	170	31.2%	chr8	99239373	CCDS6277.1	c.2773C>T	p.R925C
PRRG2	proline rich Gla (G-carboxyglutamic acid) 2	ENSG00000126460	PAP53	219	27.9%	chr19	54783677	CCDS12773.1	c.413G>A	p.R138Q
PARS2	prolyl-tRNA synthetase 2; mitochondrial (putative)	ENSG00000162396	PAP53	172	27.9%	chr1	54996329	CCDS597.1	c.1094G>A	p.S365N
PCSK5	proprotein convertase subtilisin/kexin type 5	ENSG00000099139	PAP53	143	23.8%	chr9	77872752	CCDS6652.1	c.694G>A	p.G232R
PMEPA1	prostate transmembrane protein; androgen induced 1	ENSG00000124225	PAP53	67	28.4%	chr20	55660755	CCDS13463.1	c.1169C>NULL	p.NULL-1FsDel1bp
PMEPA1	prostate transmembrane protein; androgen induced 1	ENSG00000124225	PAP53	47	31.9%	chr20	55660939	CCDS13463.1	c.440C>T	p.P147L

PRSS27	protease; serine 27	ENSG00000172382	PAP53	244	21.7%	chr16	2704327	CCDS10476.1	c.248C>T	p.T83M
PRSS38	protease; serine; 38	ENSG00000185888	PAP53	56	23.2%	chr1	226070462	CCDS1563.1	c.197C>T	p.A66V
PSME4	proteasome (prosome; macropain) activator subunit 4	ENSG00000068878	PAP53	62	16.1%	chr2	54020644	CCDS33197.1	c.-1C>NULL	p.IVS2-3-1SpliceAcceptor
POT1	protection of telomeres 1 homolog (S. pombe)	ENSG00000128513	PAP53	112	19.6%	chr7	124290908	CCDS5793.1	c.278C>A	p.T93N
PRKCDBP	protein kinase C; delta binding protein	ENSG00000170955	PAP53	146	28.1%	chr11	6297216	CCDS7762.1	c.539G>A	p.R180H
PKN3	protein kinase N3	ENSG00000160447	PAP53	147	25.2%	chr9	130516177	CCDS6908.1	c.1268G>A	p.R423Q
PPP1R13B	protein phosphatase 1; regulatory (inhibitor) subunit 13B	ENSG00000088808	PAP53	51	31.4%	chr14	103290301	CCDS41997.1	c.490C>T	p.R164C
PPP1R15A	protein phosphatase 1; regulatory (inhibitor) subunit 15A	ENSG00000087074	PAP53	159	18.2%	chr19	54068676	CCDS12738.1	c.374G>A	p.S125N
PPP1R15B	protein phosphatase 1; regulatory (inhibitor) subunit 15B	ENSG00000158615	PAP53	576	15.1%	chr1	202646192	CCDS1445.1	c.971G>A	p.S324N
PPP2R1A	protein phosphatase 2; regulatory subunit A; alpha	ENSG00000105568	PAP53	92	19.6%	chr19	57407794	CCDS12849.1	c.547C>T	p.R183W
PPP4C	protein phosphatase 4; catalytic subunit	ENSG00000149923	PAP53	198	28.8%	chr16	30001611	CCDS10669.1	c.245A>C	p.D82A
PTPN9	protein tyrosine phosphatase; non-receptor type 9	ENSG00000169410	PAP53	111	20.7%	chr15	73606543	CCDS10280.1	c.178C>T	p.R60C
PTPRM	protein tyrosine phosphatase; receptor type; M	ENSG00000173482	PAP53	107	30.8%	chr18	8103537	CCDS11840.1	c.1910C>T	p.T637I
PTPRN	protein tyrosine phosphatase; receptor type; N	ENSG00000054356	PAP53	155	22.6%	chr2	219872319	CCDS2440.1	c.1555C>T	p.R519W
PTPLA	protein tyrosine phosphatase-like (proline instead of catalytic arginine); member A	ENSG00000165996	PAP53	56	39.3%	chr10	17686055	CCDS7121.1	c.-1T>NULL	p.IVS1-3-1SpliceAcceptor
PCDH10	protocadherin 10	ENSG00000138650	PAP53	234	23.9%	chr4	134291047	CCDS34063.1	c.302A>G	p.N101S
PCDH12	protocadherin 12	ENSG00000113555	PAP53	289	13.5%	chr5	141314902	CCDS4269.1	c.5578NULL>(	p.NULL-1FsIns1bp
PCDH20	protocadherin 20	ENSG00000197991	PAP53	267	25.5%	chr13	60885344	CCDS9442.1	c.808T>C	p.S270P
PCDHA1	protocadherin alpha 1	ENSG00000204970	PAP53	47	38.3%	chr5	140146198	CCDS34246.1	c.139C>T	p.R47C
PCDHA10	protocadherin alpha 10	ENSG00000081842	PAP53	237	24.5%	chr5	140288975	CCDS4241.1	c.2314C>T	p.R772C
PCDHA11	protocadherin alpha 11	ENSG00000081842	PAP53	237	24.5%	chr5	140288975	CCDS4241.1	c.2314C>T	p.R772C
PCDHA12	protocadherin alpha 12	ENSG00000081842	PAP53	237	24.5%	chr5	140288975	CCDS4241.1	c.2314C>T	p.R772C
PCDHA6	protocadherin alpha 6	ENSG00000081842	PAP53	237	24.5%	chr5	140288975	CCDS4241.1	c.2314C>T	p.R772C
PCDHAC1	protocadherin alpha subfamily C; 1	ENSG00000081842	PAP53	237	24.5%	chr5	140288975	CCDS4241.1	c.2314C>T	p.R772C
PCDHB8	protocadherin beta 8	ENSG00000120322	PAP53	210	15.2%	chr5	140538355	CCDS4250.1	c.556C>T	p.R186C
PCDHGA10	protocadherin gamma subfamily A; 10	ENSG00000081853	PAP53	130	23.8%	chr5	140790979	CCDS4260.1	c.469G>A	p.A157T
PCDHGA11	protocadherin gamma subfamily A; 11	ENSG00000081853	PAP53	130	23.8%	chr5	140790979	CCDS4260.1	c.469G>A	p.A157T
PCDHGA3	protocadherin gamma subfamily A; 3	ENSG00000081853	PAP53	130	23.8%	chr5	140790979	CCDS4260.1	c.469G>A	p.A157T
PCDHGA8	protocadherin gamma subfamily A; 8	ENSG00000081853	PAP53	130	23.8%	chr5	140790979	CCDS4260.1	c.469G>A	p.A157T
PCDHGB7	protocadherin gamma subfamily B; 7	ENSG00000081853	PAP53	130	23.8%	chr5	140790979	CCDS4260.1	c.469G>A	p.A157T
PCDHGC5	protocadherin gamma subfamily C; 5	ENSG00000081853	PAP53	130	23.8%	chr5	140790979	CCDS4260.1	c.469G>A	p.A157T
PCDH15	protocadherin-related 15	ENSG00000150275	PAP53	210	24.3%	chr10	55239234	ENST00000395445	c.4582G>A	p.E1528K
PRPF6	PRP6 pre-mRNA processing factor 6 homolog (S. cerevisiae)	ENSG00000101161	PAP53	65	29.2%	chr20	62095239	CCDS13550.1	c.395G>A	p.R132H
P2RX2	purinergic receptor P2X; ligand-gated ion channel; 2	ENSG00000187848	PAP53	202	29.7%	chr12	131708405	CCDS31930.1	c.1268G>A	p.R423H
PYROXD2	pyridine nucleotide-disulphide oxidoreductase domain 2	ENSG00000119943	PAP53	146	32.9%	chr10	100157384	CCDS7474.1	c.260C>T	p.A87V
P2RY6	pyrimidinergic receptor P2Y; G-protein coupled; 6	ENSG00000171631	PAP53	382	19.4%	chr11	72685324	CCDS8220.1	c.113C>T	p.A38V
QRFPR	pyroglutamylated RFamide peptide receptor	ENSG00000186867	PAP53	67	28.4%	chr4	122521165	CCDS3719.1	c.88C>T	p.R30W
RABEP2	rabaptin; RAB GTPase binding effector protein 2	ENSG00000177548	PAP53	92	23.9%	chr16	28823821	CCDS42140.1	c.1654C>T	p.R552C
RABEP2	rabaptin; RAB GTPase binding effector protein 2	ENSG00000177548	PAP53	124	22.6%	chr16	28824915	CCDS42140.1	c.1349G>T	p.R450L
ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	ENSG00000129675	PAP53	159	16.4%	chrX	135591769	CCDS14660.1	c.1504G>T	p.V502L
RINT1	RAD50 interactor 1	ENSG00000135249	PAP53	109	30.3%	chr7	104993013	CCDS34726.1	c.1940C>T	p.S647L
REPS2	RALBP1 associated Eps domain containing 2	ENSG00000169891	PAP53	50	22.0%	chrX	16996477	CCDS14180.2	c.1241C>A	p.P414H
RANBP10	RAN binding protein 10	ENSG00000141084	PAP53	181	22.7%	chr16	66319914	CCDS32469.1	c.1354G>A	p.D452N
RANGRF	RAN guanine nucleotide release factor	ENSG00000108961	PAP53	224	23.7%	chr17	8133006	CCDS11137.1	c.85C>T	p.R29X
RIF1	RAP1 interacting factor homolog (yeast)	ENSG00000080345	PAP53	61	37.7%	chr2	152016447	CCDS2194.1	c.2326T>C	p.Y776H
RIF1	RAP1 interacting factor homolog (yeast)	ENSG00000080345	PAP53	127	24.4%	chr2	152028787	CCDS2194.1	c.4507A>NULI	p.NULL-1FsDel1bp

RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	ENSG00000173166	PAP53	248	10.9%	chr2	204068236	CCDS2359.1	c.86G>A	p.G29E
RASSF4	Ras association (RalGDS/AF-6) domain family member 4	ENSG00000107551	PAP53	60	18.3%	chr10	44800383	CCDS7208.1	c.490C>T	p.R164X
RASA3	RAS p21 protein activator 3	ENSG00000185989	PAP53	52	25.0%	chr13	113801707	CCDS32016.1	c.1066G>A	p.A356T
RASAL3	RAS protein activator like 3	ENSG00000105122	PAP53	63	31.7%	chr19	15436174	ENST00000343625	c.421CCC>NU	p.NULL-1FsDel3bp
RASAL3	RAS protein activator like 3	ENSG00000105122	PAP53	63	23.8%	chr19	15436174	ENST00000343625	c.422CC>NUL	p.NULL-1FsDel2bp
RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1	ENSG00000058335	PAP53	117	23.1%	chr15	77085647	CCDS10309.1	c.2050G>A	p.A684T
RGS20	regulator of G-protein signaling 20	ENSG00000147509	PAP53	49	24.5%	chr8	55033398	CCDS6155.1	c.994C>T	p.R332W
RTEL1	regulator of telomere elongation helicase 1	ENSG00000026036	PAP53	196	31.1%	chr20	61799293	CCDS13532.1	c.593G>A	p.G198D
RXFP2	relaxin/insulin-like family peptide receptor 2	ENSG00000133105	PAP53	71	26.8%	chr13	31269553	CCDS9342.1	c.2002C>T	p.P668S
RP1L1	retinitis pigmentosa 1-like 1	ENSG00000183638	PAP53	178	30.3%	chr8	10504441	CCDS43708.1	c.4577C>T	p.T1526M
RPGRIP1	retinitis pigmentosa GTPase regulator interacting protein 1	ENSG00000092200	PAP53	68	30.9%	chr14	20855642	ENST00000382933	c.25G>A	p.V9I
RBL2	retinoblastoma-like 2 (p130)	ENSG00000103479	PAP53	100	21.0%	chr16	52034255	CCDS10748.1	c.556C>T	p.R186X
RAI1	retinoic acid induced 1	ENSG00000108557	PAP53	61	23.0%	chr17	17637354	CCDS11188.1	c.367G>C	p.A123P
RAI1	retinoic acid induced 1	ENSG00000108557	PAP53	294	17.3%	chr17	17637819	CCDS11188.1	c.832NULL>C/	p.NULL-1FsIns3bp
RAI2	retinoic acid induced 2	ENSG00000131831	PAP53	247	24.7%	chrX	17728959	CCDS14183.1	c.1093G>C	p.A365P
RND2	Rho family GTPase 2	ENSG00000108830	PAP53	126	19.0%	chr17	38432746	CCDS11452.1	c.211G>A	p.V71I
ARHGAP1	Rho GTPase activating protein 1	ENSG00000175220	PAP53	258	13.2%	chr11	46666368	CCDS7922.1	c.248G>A	p.R83Q
ARHGAP6	Rho GTPase activating protein 6	ENSG00000047648	PAP53	317	23.3%	chrX	11071997	CCDS14142.1	c.2200C>T	p.R734C
ARHGEF17	Rho guanine nucleotide exchange factor (GEF) 17	ENSG00000110237	PAP53	177	31.6%	chr11	72698766	CCDS8221.1	c.1435C>T	p.R479C
ARHGEF3	Rho guanine nucleotide exchange factor (GEF) 3	ENSG00000163947	PAP53	399	24.6%	chr3	56891415	NM_001128615	c.137G>A	p.R46Q
RHOBTB1	Rho-related BTB domain containing 1	ENSG00000072422	PAP53	342	12.3%	chr10	62318492	CCDS7261.1	c.940G>C	p.E314Q
RPS27L	ribosomal protein S27-like	ENSG00000185088	PAP53	70	25.7%	chr15	61234986	CCDS42048.1	c.-1TTT>NULL	p.IVS2-3-1SpliceAcceptor
RC3H2	ring finger and CCCH-type zinc finger domains 2	ENSG00000056586	PAP53	122	18.0%	chr9	124692528	CCDS43874.1	c.467G>A	p.R156H
RNF113B	ring finger protein 113B	ENSG00000139797	PAP53	76	25.0%	chr13	97627313	CCDS9486.1	c.179C>T	p.P60L
RBM19	RNA binding motif protein 19	ENSG00000122965	PAP53	63	20.6%	chr12	112781014	CCDS9172.1	c.2629G>A	p.G877S
RBM23	RNA binding motif protein 23	ENSG00000100461	PAP53	393	18.3%	chr14	22441096	CCDS41921.1	c.1296GCC>N	p.NULL-1FsDel3bp
RPUSD2	RNA pseudouridylate synthase domain containing 2	ENSG00000166133	PAP53	150	25.3%	chr15	38653111	CCDS10061.1	c.997G>NULL	p.NULL-1FsDel1bp
RYR1	ryanodine receptor 1 (skeletal)	ENSG00000196218	PAP53	291	19.2%	chr19	43642923	CCDS33011.1	c.2429G>A	p.C810Y
RYR1	ryanodine receptor 1 (skeletal)	ENSG00000196218	PAP53	626	26.4%	chr19	43651599	CCDS33011.1	c.3535C>T	p.R1179W
RYR1	ryanodine receptor 1 (skeletal)	ENSG00000196218	PAP53	153	26.1%	chr19	43673132	CCDS33011.1	c.6047C>T	p.T2016I
SALL4	sal-like 4 (Drosophila)	ENSG00000101115	PAP53	218	22.9%	chr20	49840676	CCDS13438.1	c.1753T>C	p.Y585H
SAMHD1	SAM domain and HD domain 1	ENSG00000101347	PAP53	268	23.1%	chr20	34954843	CCDS13288.1	c.1921A>NULI	p.NULL-1FsDel1bp
SAMHD1	SAM domain and HD domain 1	ENSG00000101347	PAP53	192	23.4%	chr20	34996927	CCDS13288.1	c.428G>A	p.R143H
SRL	sarcalumenin	ENSG00000185739	PAP53	71	19.7%	chr16	4193251	CCDS42113.1	c.176G>A	p.R59Q
SCARA5	scavenger receptor class A; member 5 (putative)	ENSG00000168079	PAP53	54	20.4%	chr8	27785480	CCDS6064.1	c.1378G>A	p.V460I
SCHIP1	schwannomin interacting protein 1	ENSG00000151967	PAP53	150	13.3%	chr3	160964968	CCDS3186.1	c.106A>G	p.S36G
SCRIB	scribbled homolog (Drosophila)	ENSG00000180900	PAP53	127	25.2%	chr8	144965494	CCDS6412.1	c.916C>T	p.R306C
SCYL1	SCY1-like 1 (S. cerevisiae)	ENSG00000142186	PAP53	70	25.7%	chr11	65061099	CCDS41672.1	c.1883AGG>N	p.NULL-1FsDel3bp
SEC31A	SEC31 homolog A (S. cerevisiae)	ENSG00000138674	PAP53	60	40.0%	chr4	84004589	CCDS3596.1	c.1620A>NULI	p.NULL-1FsDel1bp
SECISBP2	SECIS binding protein 2	ENSG00000187742	PAP53	88	21.6%	chr9	91139340	CCDS6683.1	c.964A>G	p.M322V
40429	septin 8	ENSG00000164402	PAP53	110	29.1%	chr5	132125127	CCDS43358.1	c.884G>A	p.R295Q
SPINK5	serine peptidase inhibitor; Kazal type 5	ENSG00000133710	PAP53	72	16.7%	chr5	147471563	CCDS43382.1	c.1732C>T	p.R578X
STK25	serine/threonine kinase 25 (STE20 homolog; yeast)	ENSG00000115694	PAP53	50	26.0%	chr2	242084589	CCDS2549.1	c.1138G>A	p.V380M

STK35	serine/threonine kinase 35	ENSG00000125834	PAP53	111	18.0%	chr20	2031892	CCDS13024.1	c.374A>G	p.H125R
SBF1	SET binding factor 1	ENSG00000100241	PAP53	87	28.7%	chr22	49233693	CCDS14091.1	c.5120G>A	p.R1707H
SFRS12IP1	SFRS12-interacting protein 1	ENSG00000153006	PAP53	70	17.1%	chr5	64056054	CCDS34171.1	c.570A>NULL	p.NULL-1FsDel1bp
SH2B1	SH2B adaptor protein 1	ENSG00000178188	PAP53	188	30.3%	chr16	28785486	CCDS32424.1	c.570C>NULL	p.NULL-1FsDel1bp
SH3PXD2B	SH3 and PX domains 2B	ENSG00000174705	PAP53	324	25.9%	chr5	171698768	CCDS34291.1	c.1946C>T	p.S649F
SBK2	SH3-binding domain kinase family; member 2	ENSG00000187550	PAP53	71	16.9%	chr19	60734462	CCDS42631.1	c.316G>A	p.E106K
SGIP1	SH3-domain GRB2-like (endophilin) interacting protein 1	ENSG00000118473	PAP53	138	15.2%	chr1	66872357	ENST00000237247	c.106A>NULL	p.NULL-1FsDel1bp
SH3KBP1	SH3-domain kinase binding protein 1	ENSG00000147010	PAP53	104	19.2%	chrX	19635014	CCDS14193.1	c.296G>A	p.R99Q
SIGLEC10	sialic acid binding Ig-like lectin 10	ENSG00000142512	PAP53	106	20.8%	chr19	56610417	CCDS12832.1	c.1417C>NULL	p.NULL-1FsDel1bp
SIGLEC12	sialic acid binding Ig-like lectin 12	ENSG00000142512	PAP53	106	20.8%	chr19	56610417	CCDS12832.1	c.1417C>NULL	p.NULL-1FsDel1bp
NEU4	sialidase 4	ENSG00000204099	PAP53	110	27.3%	chr2	242406167	CCDS2553.1	c.611G>A	p.R204Q
SRP72	signal recognition particle 72kDa	ENSG00000174780	PAP53	91	29.7%	chr4	57028577	CCDS3506.1	c.19G>NULL	p.NULL-1FsDel1bp
SRP72	signal recognition particle 72kDa	ENSG00000174780	PAP53	79	34.2%	chr4	57028590	CCDS3506.1	c.32T>A	p.V11E
STAT2	signal transducer and activator of transcription 2; 113kDa	ENSG00000170581	PAP53	131	15.3%	chr12	55029084	CCDS8917.1	c.1602NULL>C	p.NULL-1FsIns1bp
SIK3	SIK family kinase 3	ENSG00000160584	PAP53	79	27.8%	chr11	116222327	CCDS8379.1	c.3787G>A	p.V1263M
SILV	silver homolog (mouse)	ENSG00000185664	PAP53	58	19.0%	chr12	54634335	CCDS8897.1	c.1916G>A	p.R639H
SIX6	SIX homeobox 6	ENSG00000184302	PAP53	151	19.9%	chr14	60046419	CCDS9747.1	c.550C>T	p.R184X
SLAMF8	SLAM family member 8	ENSG00000158714	PAP53	379	23.2%	chr1	158069415	CCDS1188.1	c.493C>T	p.R165X
SLIT3	slit homolog 3 (Drosophila)	ENSG00000184347	PAP53	202	19.8%	chr5	168045338	CCDS4369.1	c.3487G>A	p.V1163M
SGSM1	small G protein signaling modulator 1	ENSG00000167037	PAP53	138	21.7%	chr22	23602613	NM_001039948	c.1526C>A	p.S509Y
SNAPC2	small nuclear RNA activating complex; polypeptide 2; 45kDa	ENSG00000104976	PAP53	179	26.3%	chr19	7893428	CCDS12190.1	c.784C>T	p.R262C
SNAPC3	small nuclear RNA activating complex; polypeptide 3; 50kDa	ENSG00000164975	PAP53	246	22.8%	chr9	15449725	CCDS6478.1	c.1097C>T	p.T366M
SNORD19B	small nucleolar RNA; C/D box 19B	ENSG00000163938	PAP53	53	30.2%	chr3	52695876	CCDS2861.1	c.65A>NULL	p.NULL-1FsDel1bp
SHPRH	SNF2 histone linker PHD RING helicase	ENSG00000146414	PAP53	191	25.7%	chr6	146306452	CCDS43513.1	c.2417A>NULL	p.NULL-1FsDel1bp
SCN9A	sodium channel; voltage-gated; type IX; alpha subunit	ENSG00000169432	PAP53	170	22.4%	chr2	166846567	NM_002977	c.-1TT>NULL	p.IVS11-3-1SpliceAcceptor
SLC10A3	solute carrier family 10 (sodium/bile acid cotransporter family); member 3	ENSG00000126903	PAP53	185	14.6%	chrX	153369359	CCDS14755.1	c.1115G>A	p.R372H
SLC12A4	solute carrier family 12 (potassium/chloride transporters); member 4	ENSG00000124067	PAP53	81	19.8%	chr16	66538508	CCDS10855.1	c.2074C>T	p.P692S
SLC12A8	solute carrier family 12 (potassium/chloride transporters); member 8	ENSG00000221955	PAP53	188	14.4%	chr3	126322193	CCDS43143.1	c.851G>NULL	p.NULL-1FsDel1bp
SLC17A9	solute carrier family 17; member 9	ENSG00000101194	PAP53	84	21.4%	chr20	61067500	CCDS42901.1	c.1039G>A	p.G347S
SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter); member 5	ENSG00000142583	PAP53	119	26.9%	chr1	9022553	CCDS99.1	c.778G>A	p.A260T
SLC22A10	solute carrier family 22; member 10	ENSG00000184999	PAP53	297	26.9%	chr11	62828813	CCDS41661.1	c.1474T>NULL	p.NULL-1FsDel1bp
SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchanger); member 1	ENSG00000074621	PAP53	238	26.1%	chr15	63704072	ENST00000261892	c.601G>A	p.V201M
SLC35A4	solute carrier family 35; member A4	ENSG00000176087	PAP53	485	15.1%	chr5	139927252	CCDS4231.1	c.314A>G	p.Y105C
SLC35E1	solute carrier family 35; member E1	ENSG00000127526	PAP53	65	15.4%	chr19	16539932	CCDS12346.1	c.109G>A	p.V37I
SLC4A2	solute carrier family 4; anion exchanger; member 2 (erythrocyte membrane protein band 3-like 1)	ENSG00000164889	PAP53	147	21.8%	chr7	150392697	CCDS5917.1	c.369G>NULL	p.NULL-1FsDel1bp
SLC46A2	solute carrier family 46; member 2	ENSG00000119457	PAP53	146	24.0%	chr9	114692188	CCDS6786.1	c.595G>A	p.A199T

SLC5A6	solute carrier family 5 (sodium-dependent vitamin transporter); member 6	ENSG00000138074	PAP53	70	21.4%	chr2	27276938	CCDS1740.1	c.1778C>T	p.T593I
SLC6A19	solute carrier family 6 (neutral amino acid transporter); member 19	ENSG00000174358	PAP53	137	20.4%	chr5	1254802	CCDS34130.1	c.37G>A	p.A13T
SLC7A2	solute carrier family 7 (cationic amino acid transporter; y+ system); member 2	ENSG00000003989	PAP53	154	30.5%	chr8	17450719	CCDS6002.2	c.806C>A	p.S269X
SLC8A3	solute carrier family 8 (sodium/calcium exchanger); member 3	ENSG00000100678	PAP53	325	27.4%	chr14	69703233	CCDS35498.1	c.1660C>T	p.R554W
SLC9A6	solute carrier family 9 (sodium/hydrogen exchanger); member 6	ENSG00000198689	PAP53	212	24.1%	chrX	134912028	CCDS44003.1	c.889G>A	p.V297M
SORBS2	sorbin and SH3 domain containing 2	ENSG00000154556	PAP53	98	16.3%	chr4	186781433	CCDS3845.1	c.3712A>NULL	p.NULL-1FsDel1bp
SNX17	sorting nexin 17	ENSG00000115234	PAP53	320	27.5%	chr2	27452336	CCDS1750.1	c.1098C>NULL	p.NULL-1FsDel1bp
SP100	SP100 nuclear antigen	ENSG00000067066	PAP53	49	24.5%	chr2	231042740	ENST00000341950	c.1350AA>NU	p.NULL-1FsDel2bp
SPOP	speckle-type POZ protein	ENSG00000121067	PAP53	93	23.7%	chr17	45054361	CCDS11551.1	c.146G>T	p.G49V
SYNE1	spectrin repeat containing; nuclear envelope 1	ENSG00000131018	PAP53	43	25.6%	chr6	152569037	CCDS5236.1	c.22978C>T	p.R7660W
SPTB	spectrin; beta; erythrocytic	ENSG00000070182	PAP53	457	25.6%	chr14	64329799	CCDS32099.1	c.2335C>T	p.R779W
SPEN	spen homolog; transcriptional regulator (Drosophila)	ENSG00000065526	PAP53	186	27.4%	chr1	16127706	CCDS164.1	c.2384G>A	p.R795Q
SAT1	spermidine/spermine N1-acetyltransferase 1	ENSG00000130066	PAP53	175	20.0%	chrX	23712068	ENST00000379251	c.439AA>NUL	p.NULL-1FsDel2bp
SPHK1	sphingosine kinase 1	ENSG00000176170	PAP53	65	29.2%	chr17	71893914	CCDS11744.1	c.439C>T	p.R147W
SPIRE2	spire homolog 2 (Drosophila)	ENSG00000204991	PAP53	203	27.1%	chr16	88464114	CCDS32516.1	c.2078C>T	p.T693M
SF3B2	splicing factor 3b; subunit 2; 145kDa	ENSG00000087365	PAP53	178	23.6%	chr11	65592722	CCDS31612.1	c.2618A>NULL	p.NULL-1FsDel1bp
SRMS	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites	ENSG00000125508	PAP53	152	23.0%	chr20	61643328	CCDS13525.1	c.1036G>A	p.V346I
SCAP	SREBF chaperone	ENSG00000114650	PAP53	186	28.0%	chr3	47435858	CCDS2755.2	c.1904C>T	p.T635M
STAB1	stabilin 1	ENSG00000010327	PAP53	149	16.8%	chr3	52521441	CCDS33768.1	c.2928C>NULL	p.NULL-1FsDel1bp
STAB1	stabilin 1	ENSG00000010327	PAP53	157	24.2%	chr3	52528579	CCDS33768.1	c.5194G>A	p.A1732T
STARD8	StAR-related lipid transfer (START) domain containing 8	ENSG00000130052	PAP53	120	24.2%	chrX	67854008	CCDS14390.1	c.287G>A	p.G96D
SAMD4B	sterile alpha motif domain containing 4B	ENSG00000179134	PAP53	176	21.6%	chr19	44560124	CCDS33020.1	c.1264G>NUL	p.NULL-1FsDel1bp
SAMD9L	sterile alpha motif domain containing 9-like	ENSG00000177409	PAP53	263	22.4%	chr7	92600264	CCDS34681.1	c.2957G>A	p.R986H
STRA6	stimulated by retinoic acid gene 6 homolog (mouse)	ENSG00000137868	PAP53	96	24.0%	chr15	72281646	CCDS10261.1	c.16G>A	p.A6T
SDF4	stromal cell derived factor 4	ENSG00000078808	PAP53	160	26.3%	chr1	1153861	CCDS30553.1	c.501C>NULL	p.NULL-1FsDel1bp
SVIL	supervillin	ENSG00000197321	PAP53	521	23.8%	chr10	29852512	CCDS7164.1	c.3613G>NUL	p.NULL-1FsDel1bp
SVIL	supervillin	ENSG00000197321	PAP53	325	23.4%	chr10	29862181	CCDS7164.1	c.1121G>A	p.G374D
ST18	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	ENSG00000147488	PAP53	322	25.5%	chr8	53247010	CCDS6149.1	c.964A>G	p.N322D
SUPV3L1	suppressor of var1; 3-like 1 (S. cerevisiae)	ENSG00000156502	PAP53	254	17.7%	chr10	70638691	CCDS7287.1	c.2255AA>NU	p.NULL-1FsDel2bp
SUSD2	sushi domain containing 2	ENSG00000099994	PAP53	176	21.0%	chr22	22913990	CCDS13824.1	c.2228C>T	p.A743V
SYMPK	symplekin	ENSG00000125755	PAP53	138	24.6%	chr19	51018544	CCDS12676.2	c.2626C>T	p.R876W
SYN3	synapsin III	ENSG00000185666	PAP53	107	16.8%	chr22	31732512	CCDS13908.1	c.446C>NULL	p.NULL-1FsDel1bp
SYNJ2	synaptojanin 2	ENSG00000078269	PAP53	132	27.3%	chr6	158374621	CCDS5254.1	c.632G>A	p.C211Y
SDC1	syndecan 1	ENSG00000115884	PAP53	131	28.2%	chr2	20267333	CCDS1697.1	c.349C>T	p.R117W
SYNRG	synergin; gamma	ENSG00000006114	PAP53	106	17.9%	chr17	33013401	ENST00000394379	c.931G>A	p.V311I
SNPH	syntaphilin	ENSG00000101298	PAP53	98	19.4%	chr20	1234559	CCDS13012.1	c.1346G>A	p.R449H
TRBV6-7	T cell receptor beta variable 6-7 (non-functional)	ENSG00000211726	PAP53	219	22.8%	chr7	141856587	ENST00000390373	c.163C>T	p.R55X

TAF1	TAF1 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 250kDa	ENSG00000147133	PAP53	338	18.9%	chrX	70519725	CCDS14412.1	c.1993A>NULL	p.NULL-1FsDel1bp
TAS2R3	taste receptor; type 2; member 3	ENSG00000127362	PAP53	276	13.8%	chr7	141111141	CCDS5867.1	c.714CTT>NU	p.NULL-1FsDel3bp
TXLNG	taxilin gamma	ENSG00000086712	PAP53	198	26.8%	chrX	16769626	CCDS14178.1	c.1403C>T	p.A468V
TBC1D10B	TBC1 domain family; member 10B	ENSG00000169221	PAP53	377	20.2%	chr16	30277314	CCDS10676.1	c.1683G>NUL	p.NULL-1FsDel1bp
TBC1D16	TBC1 domain family; member 16	ENSG00000167291	PAP53	127	33.1%	chr17	75598941	CCDS11766.1	c.392G>A	p.R131Q
TBC1D19	TBC1 domain family; member 19	ENSG00000109680	PAP53	99	18.2%	chr4	26350653	CCDS3439.1	c.1187G>A	p.R396H
TIAM1	T-cell lymphoma invasion and metastasis 1	ENSG00000156299	PAP53	68	27.9%	chr21	31448470	CCDS13609.1	c.3137G>A	p.C1046Y
TIAM1	T-cell lymphoma invasion and metastasis 1	ENSG00000156299	PAP53	118	27.1%	chr21	31504267	CCDS13609.1	c.2353G>A	p.D785N
TEP1	telomerase-associated protein 1	ENSG00000129566	PAP53	537	25.3%	chr14	19939084	CCDS9548.1	c.1448C>A	p.S483Y
TESK1	testis-specific kinase 1	ENSG00000107140	PAP53	204	27.9%	chr9	35597340	CCDS6580.1	c.554G>T	p.R185L
TSSK1B	testis-specific serine kinase 1B	ENSG00000212122	PAP53	239	21.3%	chr5	112797361	CCDS4112.1	c.2178C>NULL	p.NULL-1FsDel1bp
TSKS	testis-specific serine kinase substrate	ENSG00000126467	PAP53	225	32.0%	chr19	54941663	CCDS12780.1	c.868G>A	p.D290N
TTC16	tetratricopeptide repeat domain 16	ENSG00000167094	PAP53	183	32.2%	chr9	129519499	CCDS6875.1	c.257G>A	p.R86H
THAP10	THAP domain containing 10	ENSG00000129028	PAP53	144	12.5%	chr15	68962271	CCDS10237.1	c.460C>T	p.Q154X
TMX4	thioredoxin-related transmembrane protein 4	ENSG00000125827	PAP53	114	20.2%	chr20	7928479	CCDS13101.1	c.367C>T	p.R123C
TARS2	threonyl-tRNA synthetase 2; mitochondrial (putative)	ENSG00000143374	PAP53	95	24.2%	chr1	148737712	CCDS952.1	c.1349G>A	p.R450Q
THBS4	thrombospondin 4	ENSG00000113296	PAP53	103	27.2%	chr5	79410782	CCDS4049.1	c.2456C>T	p.T819I
TJP2	tight junction protein 2 (zona occludens 2)	ENSG00000119139	PAP53	165	24.2%	chr9	71032731	CCDS6627.1	c.1334C>T	p.T445M
TICAM1	toll-like receptor adaptor molecule 1	ENSG00000127666	PAP53	56	25.0%	chr19	4767465	CCDS12136.1	c.4063C>NULL	p.NULL-1FsDel1bp
TOPBP1	topoisomerase (DNA) II binding protein 1	ENSG00000163781	PAP53	83	27.7%	chr3	134862632	NM_007027	c.113T>NULL	p.NULL-1FsDel1bp
TLK2	tousled-like kinase 2	ENSG00000146872	PAP53	74	21.6%	chr17	57996113	CCDS11633.1	c.851C>T	p.A284V
TRAK1	trafficking protein; kinesin binding 1	ENSG00000182606	PAP53	79	26.6%	chr3	42204628	CCDS43072.1	c.568G>A	p.V190I
TCEB3	transcription elongation factor B (SIII); polypeptide 3 (110kDa; elongin A)	ENSG00000011007	PAP53	70	24.3%	chr1	23950991	CCDS239.1	c.1309A>NULL	p.NULL-1FsDel1bp
TFAM	transcription factor A; mitochondrial	ENSG00000108064	PAP53	31	32.3%	chr10	59818576	CCDS7253.1	c.432AA>NUL	p.NULL-1FsDel2bp
TTF1	transcription termination factor; RNA polymerase I	ENSG00000125482	PAP53	99	22.2%	chr9	134257349	CCDS6948.1	c.1922C>T	p.T641M
TBL2	transducin (beta)-like 2	ENSG00000106638	PAP53	122	23.8%	chr7	72623030	CCDS5551.1	c.1087G>A	p.E363K
TLE1	transducin-like enhancer of split 1 (E(sp1) homolog; Drosophila)	ENSG00000196781	PAP53	92	26.1%	chr9	83395748	CCDS6661.1	c.1621G>A	p.D541N
TFRC	transferrin receptor (p90; CD71)	ENSG00000072274	PAP53	20	50.0%	chr3	197286571	CCDS3312.1	c.94G>A	p.D32N
TRRAP	transformation/transcription domain-associated protein	ENSG00000196367	PAP53	81	29.6%	chr7	98388768	CCDS5659.1	c.5431C>T	p.R1811W
TRRAP	transformation/transcription domain-associated protein	ENSG00000196367	PAP53	138	26.1%	chr7	98429203	CCDS5659.1	c.9825G>A	p.M3275I
TGM7	transglutaminase 7	ENSG00000159495	PAP53	162	16.0%	chr15	41356420	CCDS32213.1	c.1905G>A	p.M635I
TMTC4	transmembrane and tetratricopeptide repeat containing 4	ENSG00000125247	PAP53	127	27.6%	chr13	100092473	CCDS9497.2	c.734C>T	p.T245I
TAPT1	transmembrane anterior posterior transformation 1	ENSG00000169762	PAP53	92	15.2%	chr4	15799079	NM_153365	c.-1T>NULL	p.IVS4-3-1SpliceAcceptor
TMC6	transmembrane channel-like 6	ENSG00000141524	PAP53	251	33.9%	chr17	73634247	CCDS32748.1	c.134C>T	p.T45M
TMED6	transmembrane emp24 protein transport domain containing 6	ENSG00000157315	PAP53	71	29.6%	chr16	67941025	CCDS10878.1	c.244C>T	p.R82W
TMEM108	transmembrane protein 108	ENSG00000144868	PAP53	186	46.8%	chr3	134581843	CCDS33858.1	c.598C>T	p.R200X
TMEM129	transmembrane protein 129	ENSG00000168936	PAP53	63	22.2%	chr4	1689975	CCDS3351.1	c.382C>A	p.L128M
TMEM139	transmembrane protein 139	ENSG00000178826	PAP53	384	26.0%	chr7	142693967	CCDS5878.1	c.574C>NULL	p.NULL-1FsDel1bp
TMEM143	transmembrane protein 143	ENSG00000161558	PAP53	96	25.0%	chr19	53558360	CCDS12716.1	c.264G>T	p.Q88H
TMEM175	transmembrane protein 175	ENSG00000127419	PAP53	301	25.2%	chr4	931630	CCDS3341.1	c.103C>T	p.R35C
TMEM177	transmembrane protein 177	ENSG00000144120	PAP53	127	28.3%	chr2	120155752	CCDS2128.1	c.853C>T	p.R285X
TMEM204	transmembrane protein 204	ENSG00000131634	PAP53	222	26.1%	chr16	1544978	CCDS42098.1	c.631G>A	p.A211T

TMEM63B	transmembrane protein 63B	ENSG00000137216	PAP53	69	21.7%	chr6	44230090	CCDS34461.1	c.2237C>T	p.T746M
TMEM8A	transmembrane protein 8A	ENSG00000129925	PAP53	78	37.2%	chr16	362071	CCDS10407.1	c.2233G>A	p.E745K
TAP1	transporter 1; ATP-binding cassette; sub-family B (MDR/TAP)	ENSG00000168394	PAP53	170	20.6%	chr6	32929172	CCDS4758.1	c.400G>A	p.G134R
TRIB3	tribbles homolog 3 (Drosophila)	ENSG00000101255	PAP53	352	22.2%	chr20	316745	CCDS12997.1	c.91G>A	p.V31I
TRIOBP	TRIO and F-actin binding protein	ENSG00000100106	PAP53	598	23.7%	chr22	36451460	CCDS43015.1	c.2951G>A	p.G984D
TRIM42	tripartite motif-containing 42	ENSG00000155890	PAP53	212	18.9%	chr3	141884622	CCDS3113.1	c.970A>G	p.I324V
TRIM55	tripartite motif-containing 55	ENSG00000147573	PAP53	142	23.2%	chr8	67202064	CCDS6184.1	c.7G>A	p.A3T
TRIM7	tripartite motif-containing 7	ENSG00000146054	PAP53	55	18.2%	chr5	180555259	CCDS4462.1	c.1049C>T	p.T350M
TRMU	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	ENSG00000100416	PAP53	85	20.0%	chr22	45130556	CCDS14075.1	c.1024T>C	p.C342R
TSEN54	tRNA splicing endonuclease 54 homolog (S. cerevisiae)	ENSG00000182173	PAP53	121	25.6%	chr17	71026677	CCDS11724.1	c.475A>G	p.S159G
TPM3	tropomyosin 3	ENSG00000143549	PAP53	231	17.3%	chr1	152411516	ENST00000368545	c.584A>NULL	p.NULL-1FsDel1bp
TUBB4	tubulin; beta 4	ENSG00000104833	PAP53	223	13.9%	chr19	6447082	CCDS12168.1	c.428C>T	p.T143M
TUBGCP3	tubulin; gamma complex associated protein 3	ENSG00000126216	PAP53	131	14.5%	chr13	112218844	CCDS9525.1	c.1997T>C	p.F666S
TUBGCP6	tubulin; gamma complex associated protein 6	ENSG00000128159	PAP53	95	28.4%	chr22	49007611	CCDS14087.1	c.1435G>A	p.V479I
TNFSF8	tumor necrosis factor (ligand) superfamily; member 8	ENSG00000106952	PAP53	277	27.1%	chr9	116732364	CCDS6810.1	c.41C>T	p.P14L
TNFAIP1	tumor necrosis factor; alpha-induced protein 1 (endothelial)	ENSG00000109079	PAP53	266	29.3%	chr17	23691549	CCDS11227.1	c.293G>A	p.R98Q
TTYH2	tweety homolog 2 (Drosophila)	ENSG00000141540	PAP53	103	26.2%	chr17	69730369	CCDS32717.1	c.280G>A	p.V94M
TH	tyrosine hydroxylase	ENSG00000180176	PAP53	209	24.9%	chr11	2143828	CCDS7731.1	c.1177G>T	p.E393X
U2AF2	U2 small nuclear RNA auxiliary factor 2	ENSG00000063244	PAP53	35	31.4%	chr19	60864367	CCDS12933.1	c.486G>T	p.E162D
U2AF2	U2 small nuclear RNA auxiliary factor 2	ENSG00000063244	PAP53	83	14.5%	chr19	60872625	CCDS12933.1	c.1048A>G	p.T350A
UBAC1	UBA domain containing 1	ENSG00000130560	PAP53	93	24.7%	chr9	137977977	CCDS35177.1	c.503C>T	p.A168V
UBQLN3	ubiquilin 3	ENSG00000175520	PAP53	135	20.7%	chr11	5485401	CCDS7758.1	c.1964C>T	p.S655L
UQCRC1	ubiquinol-cytochrome c reductase core protein I	ENSG00000010256	PAP53	107	22.4%	chr3	48613805	CCDS2774.1	c.806G>A	p.R269H
UBR4	ubiquitin protein ligase E3 component n-recognin 4	ENSG00000127481	PAP53	168	18.5%	chr1	19360158	CCDS189.1	c.5246C>A	p.P1749H
USP16	ubiquitin specific peptidase 16	ENSG00000156256	PAP53	195	25.1%	chr21	29348135	CCDS13583.1	c.2335G>A	p.G779S
USP18	ubiquitin specific peptidase 18	ENSG00000184979	PAP53	196	17.9%	chr22	17020441	CCDS13752.1	c.11C>T	p.A4V
USP26	ubiquitin specific peptidase 26	ENSG00000134588	PAP53	169	28.4%	chrX	131989034	CCDS14635.1	c.881G>A	p.C294Y
USP28	ubiquitin specific peptidase 28	ENSG00000048028	PAP53	194	21.1%	chr11	113179140	CCDS31680.1	c.2812C>T	p.R938W
USP35	ubiquitin specific peptidase 35	ENSG00000118369	PAP53	220	20.9%	chr11	77588857	CCDS41693.1	c.967C>T	p.R323W
USP47	ubiquitin specific peptidase 47	ENSG00000170242	PAP53	100	25.0%	chr11	11926202	CCDS41619.1	c.3022C>T	p.R1008W
UGCG	UDP-glucose ceramide glucosyltransferase	ENSG00000148154	PAP53	226	20.4%	chr9	113734979	CCDS6782.1	c.1066C>T	p.R356C
UNC45B	unc-45 homolog B (C. elegans)	ENSG00000141161	PAP53	90	31.1%	chr17	30528727	CCDS11292.1	c.2246G>A	p.R749Q
UPF3A	UPF3 regulator of nonsense transcripts homolog A (yeast)	ENSG00000169062	PAP53	24	54.2%	chr13	114075313	CCDS9543.1	c.790A>NULL	p.NULL-1FsDel1bp
URGCP	upregulator of cell proliferation	ENSG00000106608	PAP53	427	26.9%	chr7	43888040	CCDS43572.1	c.25C>T	p.R9C
USF2	upstream transcription factor 2; c-fos interacting	ENSG00000105698	PAP53	145	31.0%	chr19	40453296	CCDS12452.1	c.536C>T	p.T179M
URB1	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	ENSG00000142207	PAP53	78	15.4%	chr21	32628405	NM_014825	c.4795C>T	p.R1599W
UPB1	ureidopropionase; beta	ENSG00000100024	PAP53	98	24.5%	chr22	23249647	CCDS13827.1	c.977G>A	p.R326Q
USH2A	Usher syndrome 2A (autosomal recessive; mild)	ENSG00000042781	PAP53	99	24.2%	chr1	214439726	CCDS31025.1	c.3677G>A	p.G1226E
UTP20	UTP20; small subunit (SSU) processome component; homolog (yeast)	ENSG00000120800	PAP53	216	24.1%	chr12	100204288	CCDS9081.1	c.385T>NULL	p.NULL-1FsDel1bp
VPS13C	vacuolar protein sorting 13 homolog C (S. cerevisiae)	ENSG00000129003	PAP53	307	21.5%	chr15	60031342	CCDS32257.1	c.4585A>NULI	p.NULL-1FsDel1bp
VPS37D	vacuolar protein sorting 37 homolog D (S. cerevisiae)	ENSG00000176428	PAP53	31	35.5%	chr7	72723293	CCDS43596.1	c.407A>T	p.Q136L
VPS54	vacuolar protein sorting 54 homolog (S. cerevisiae)	ENSG00000143952	PAP53	151	14.6%	chr2	63997563	CCDS33208.1	c.2203G>A	p.E735K
VEZF1	vascular endothelial zinc finger 1	ENSG00000136451	PAP53	150	14.7%	chr17	53411604	CCDS32687.1	c.1205GCA>N	p.NULL-1FsDel3bp
VCAN	versican	ENSG00000038427	PAP53	287	24.7%	chr5	82871207	CCDS4060.1	c.6629C>A	p.A2210E
VIL1	villin 1	ENSG00000127831	PAP53	94	11.7%	chr2	219010128	CCDS2417.1	c.2009AGA>N	p.NULL-1FsDel3bp
VILL	villin-like	ENSG00000136059	PAP53	63	28.6%	chr3	38019682	CCDS2670.2	c.1679G>A	p.R560H
VSX1	visual system homeobox 1	ENSG00000100987	PAP53	194	27.3%	chr20	25007386	CCDS13169.1	c.706G>A	p.V236I

ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	ENSG00000078061	PAP53	272	15.8%	chrX	47311038	CCDS35232.1	c.614C>NULL	p.NULL-1FsDel1bp
WDHD1	WD repeat and HMG-box DNA binding protein 1	ENSG00000198554	PAP53	66	27.3%	chr14	54503818	CCDS9721.1	c.2108G>A	p.R703H
WDR24	WD repeat domain 24	ENSG00000127580	PAP53	88	22.7%	chr16	675472	CCDS10420.1	c.1805C>T	p.A602V
WDR33	WD repeat domain 33	ENSG00000136709	PAP53	145	24.1%	chr2	128187645	CCDS2150.1	c.3290G>A	p.R1097Q
WDR6	WD repeat domain 6	ENSG00000178252	PAP53	169	29.6%	chr3	49025475	CCDS2782.1	c.1504C>A	p.P502T
WDR67	WD repeat domain 67	ENSG00000156787	PAP53	94	20.2%	chr8	124158617	CCDS6338.1	c.163G>A	p.D55N
WDR78	WD repeat domain 78	ENSG00000152763	PAP53	506	18.6%	chr1	67163014	CCDS635.1	c.258A>NULL	p.NULL-1FsDel1bp
WDR93	WD repeat domain 93	ENSG00000140527	PAP53	51	21.6%	chr15	88046258	CCDS32326.1	c.277G>A	p.V93I
WIPI2	WD repeat domain; phosphoinositide interacting 2	ENSG00000157954	PAP53	142	27.5%	chr7	5220531	ENST00000315176	c.37NULL>C	p.NULL-1FsIns1bp
WBSCR27	Williams Beuren syndrome chromosome region 27	ENSG00000165171	PAP53	76	28.9%	chr7	72892727	CCDS5561.1	c.341G>A	p.R114H
WNT7B	wingless-type MMTV integration site family; member 7B	ENSG00000188064	PAP53	193	21.8%	chr22	44697659	CCDS33667.1	c.791T>C	p.M264T
WNK1	WNK lysine deficient protein kinase 1	ENSG00000060237	PAP53	353	24.1%	chr12	733739	CCDS8506.1	c.747G>A	p.W249X
WNK2	WNK lysine deficient protein kinase 2	ENSG00000165238	PAP53	311	28.3%	chr9	95120145	ENST00000349097	c.6643C>T	p.R2215C
WNK3	WNK lysine deficient protein kinase 3	ENSG00000196632	PAP53	68	20.6%	chrX	54376803	CCDS14357.1	c.29G>A	p.S10N
WNK4	WNK lysine deficient protein kinase 4	ENSG00000126562	PAP53	570	28.4%	chr17	38201192	CCDS11439.1	c.3046C>T	p.R1016C
WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	ENSG00000147548	PAP53	154	24.7%	chr8	38308232	CCDS43729.1	c.1093T>NULL	p.NULL-1FsDel1bp
XIRP1	xin actin-binding repeat containing 1	ENSG00000168334	PAP53	183	21.9%	chr3	39201020	CCDS2683.1	c.4921G>A	p.A1641T
XKR6	XK; Kell blood group complex subunit-related family; member 6	ENSG00000171044	PAP53	143	25.2%	chr8	10793086	CCDS5978.2	c.2676C>NULL	p.NULL-1FsDel1bp
XRRA1	X-ray radiation resistance associated 1	ENSG00000166435	PAP53	92	27.2%	chr11	74309971	NM_182969	c.568C>T	p.R190C
B4GALT7	xylosylprotein beta 1;4-galactosyltransferase; polypeptide 7 (galactosyltransferase I)	ENSG00000027847	PAP53	115	20.0%	chr5	176964046	CCDS4429.1	c.311G>A	p.R104H
YTHDC2	YTH domain containing 2	ENSG00000047188	PAP53	133	14.3%	chr5	112930849	CCDS4113.1	c.3004C>T	p.R1002X
YTHDC2	YTH domain containing 2	ENSG00000047188	PAP53	105	18.1%	chr5	112945064	CCDS4113.1	c.3406C>T	p.R1136C
ZIC3	Zic family member 3 (odd-paired homolog; Drosophila)	ENSG00000156925	PAP53	323	22.3%	chrX	136476760	CCDS14663.1	c.244G>A	p.A82T
ZNRF4	zinc and ring finger 4	ENSG00000105428	PAP53	186	26.3%	chr19	5406986	CCDS42475.1	c.484C>T	p.R162C
ZBTB2	zinc finger and BTB domain containing 2	ENSG00000181472	PAP53	270	17.8%	chr6	151729043	CCDS5231.1	c.851G>A	p.S284N
ZBTB39	zinc finger and BTB domain containing 39	ENSG00000166860	PAP53	112	21.4%	chr12	55682903	CCDS31839.1	c.4204C>NULL	p.NULL-1FsDel1bp
ZSCAN5B	zinc finger and SCAN domain containing 5B	ENSG00000197213	PAP53	156	26.9%	chr19	61393331	NM_001080456	c.1165C>T	p.R389W
ZC3H14	zinc finger CCCH-type containing 14	ENSG00000100722	PAP53	111	22.5%	chr14	88145429	CCDS32133.1	c.1934C>T	p.A645V
ZC3H3	zinc finger CCCH-type containing 3	ENSG00000014164	PAP53	207	17.4%	chr8	144692378	CCDS6402.1	c.1619G>NUL	p.NULL-1FsDel1bp
ZC3H7B	zinc finger CCCH-type containing 7B	ENSG00000100403	PAP53	258	15.5%	chr22	40065889	CCDS14013.1	c.940A>C	p.S314R
ZFHX3	zinc finger homeobox 3	ENSG00000140836	PAP53	225	23.6%	chr16	71390020	CCDS10908.1	c.9520TG>NU	p.NULL-1FsDel2bp
ZNF124	zinc finger protein 124	ENSG00000196418	PAP53	160	25.6%	chr1	245386631	CCDS31089.1	c.730C>T	p.R244C
ZNF180	zinc finger protein 180	ENSG00000167384	PAP53	120	26.7%	chr19	49673706	CCDS12639.1	c.832C>T	p.R278C
ZNF250	zinc finger protein 250	ENSG00000196150	PAP53	99	29.3%	chr8	146078147	NM_021061	c.1240G>A	p.E414K
ZNF324	zinc finger protein 324	ENSG00000083812	PAP53	107	15.0%	chr19	63672443	CCDS12981.1	c.79C>T	p.R27C
ZNF341	zinc finger protein 341	ENSG00000131061	PAP53	99	19.2%	chr20	31842655	CCDS13227.1	c.2215NULL>(	p.NULL-1FsIns1bp
ZNF350	zinc finger protein 350	ENSG00000197619	PAP53	123	30.9%	chr19	57189847	CCDS12846.1	c.294G>C	p.Q98H
ZNF365	zinc finger protein 365	ENSG00000138311	PAP53	162	26.5%	chr10	63806430	CCDS7264.1	c.472G>A	p.E158K
ZNF365	zinc finger protein 365	ENSG00000138311	PAP53	107	21.5%	chr10	63829519	CCDS31209.1	c.1189A>NULL	p.NULL-1FsDel1bp
ZFP41	zinc finger protein 41 homolog (mouse)	ENSG00000181638	PAP53	252	22.2%	chr8	144403623	CCDS6397.1	c.235A>G	p.I79V
ZNF43	zinc finger protein 43	ENSG00000198521	PAP53	65	26.2%	chr19	21793866	CCDS12413.2	c.-1T>NULL	p.IVS1-3-1SpliceAcceptor
ZNF432	zinc finger protein 432	ENSG00000197619	PAP53	123	30.9%	chr19	57189847	CCDS12846.1	c.294G>C	p.Q98H

ZNF45	zinc finger protein 45	ENSG00000124459	PAP53	213	28.6%	chr19	49110481	CCDS12632.1	c.947G>A	p.R316H
ZNF560	zinc finger protein 560	ENSG00000198028	PAP53	192	13.5%	chr19	9438561	CCDS12214.1	c.2062G>A	p.A688T
ZNF566	zinc finger protein 566	ENSG00000186017	PAP53	151	21.9%	chr19	41632000	CCDS12494.1	c.976C>T	p.L326F
ZNF607	zinc finger protein 607	ENSG00000198182	PAP53	308	14.9%	chr19	42882213	CCDS33006.1	c.659A>G	p.Y220C
ZNF608	zinc finger protein 608	ENSG00000168916	PAP53	632	21.4%	chr5	124012583	CCDS34219.1	c.3847G>NUL	p.NULL-1FsDel1bp
ZNF615	zinc finger protein 615	ENSG00000197619	PAP53	123	30.9%	chr19	57189847	CCDS12846.1	c.294G>C	p.Q98H
ZNF630	zinc finger protein 630	ENSG00000221994	PAP53	179	22.3%	chrX	47803205	CCDS35237.1	c.1198T>G	p.F400V
ZNF710	zinc finger protein 710	ENSG00000140548	PAP53	153	16.3%	chr15	88411394	CCDS10358.1	c.21AG>NULL	p.NULL-1FsDel2bp
ZNF785	zinc finger protein 785	ENSG00000197162	PAP53	322	21.4%	chr16	30502220	CCDS10685.1	c.380C>T	p.P127L
ZNF843	zinc finger protein 843	ENSG00000176723	PAP53	72	20.8%	chr16	31354687	NM_001136509	c.985G>A	p.A329T
ZIK1	zinc finger protein interacting with K protein 1 homolog (mouse)	ENSG00000171649	PAP53	205	21.0%	chr19	62794004	CCDS33135.1	c.1013T>C	p.L338P
ZFC3H1	zinc finger; C3H1-type containing	ENSG00000133858	PAP53	52	26.9%	chr12	70314875	CCDS41813.1	c.-1TTT>NULL	p.IVS10-3-1SpliceAcceptor
ZCCHC18	zinc finger; CCHC domain containing 18	ENSG00000166707	PAP53	88	14.8%	chrX	103246501	NM_001143978	c.1043G>A	p.R348H
ZIM3	zinc finger; imprinted 3	ENSG00000141946	PAP53	324	14.2%	chr19	62338367	CCDS33125.1	c.2327NULL>A	p.NULL-1FsIns1bp
ZMYM1	zinc finger; MYM-type 1	ENSG00000197056	PAP53	98	30.6%	chr1	35353257	CCDS41302.1	c.3239C>T	p.S1080L
ZSWIM2	zinc finger; SWIM-type containing 2	ENSG00000163012	PAP53	83	21.7%	chr2	187406929	CCDS33348.1	c.817A>G	p.T273A
ZAN	zonadhesin	ENSG00000146839	PAP53	149	19.5%	chr7	100211027	ENST00000349350	c.5918C>T	p.A1973V
PFKFB1	6-phosphofructo-2-kinase/fructose-2;6-biphosphatase 1	ENSG00000158571	PAP54	331	13.6%	chrX	54992277	CCDS14364.1	c.949G>T	p.G317C
ACTA2	actin; alpha 2; smooth muscle; aorta	ENSG00000107796	PAP54	136	31.6%	chr10	90691047	CCDS7392.1	c.535C>T	p.R179C
ACTRT1	actin-related protein T1	ENSG00000123165	PAP54	177	11.9%	chrX	127013561	CCDS14611.1	c.306C>G	p.S102R
ALCAM	activated leukocyte cell adhesion molecule	ENSG00000170017	PAP54	78	20.5%	chr3	106743260	CCDS33810.1	c.952A>NULL	p.NULL-1FsDel1bp
ACBD3	acyl-CoA binding domain containing 3	ENSG00000182827	PAP54	86	15.1%	chr1	224419114	CCDS1551.1	c.708A>NULL	p.NULL-1FsDel1bp
AP4E1	adaptor-related protein complex 4; epsilon 1 subunit	ENSG00000081014	PAP54	69	18.8%	chr15	49077346	CCDS32240.1	c.2878G>A	p.E960K
ALPP	alkaline phosphatase; placental (Regan isozyme)	ENSG00000163283	PAP54	170	15.9%	chr2	232951773	CCDS2490.1	c.17NULL>TG	p.NULL-1FsIns3bp
ALPK2	alpha-kinase 2	ENSG00000198796	PAP54	86	19.8%	chr18	54355442	CCDS11966.2	c.2957G>A	p.W986X
AASDH	aminoadipate-semialdehyde dehydrogenase	ENSG00000157426	PAP54	128	19.5%	chr4	56915026	CCDS3504.1	c.1491T>NULL	p.NULL-1FsDel1bp
ALS2CR8	amyotrophic lateral sclerosis 2 (juvenile) chromosome region; candidate 8	ENSG00000138380	PAP54	104	29.8%	chr2	203540004	CCDS42801.1	c.891NULL>A	p.NULL-1FsIns1bp
ANGEL2	angel homolog 2 (Drosophila)	ENSG00000174606	PAP54	64	17.2%	chr1	211247065	ENST00000310246	c.797TTT>NUL	p.NULL-1FsDel3bp
ANGPTL3	angiopoietin-like 3	ENSG00000132855	PAP54	109	33.9%	chr1	62836958	CCDS622.1	c.499T>C	p.F167L
ANKMY2	ankyrin repeat and MYND domain containing 2	ENSG00000106524	PAP54	36	30.6%	chr7	16642608	CCDS5361.1	c.-1TTT>NULL	p.IVS1-3-1SpliceAcceptor
ANKRD12	ankyrin repeat domain 12	ENSG00000101745	PAP54	269	14.5%	chr18	9248337	CCDS11843.1	c.5072NULL>T	p.NULL-1FsIns1bp
AATK	apoptosis-associated tyrosine kinase	ENSG00000181409	PAP54	167	11.4%	chr17	76709605	NM_001080395	c.2726C>T	p.P909L
AGAP3	ArfGAP with GTPase domain; ankyrin repeat and PH domain 3	ENSG00000133612	PAP54	191	24.1%	chr7	150448062	CCDS43681.1	c.1025C>NULL	p.NULL-1FsDel1bp
ARSJ	arylsulfatase family; member J	ENSG00000180801	PAP54	133	17.3%	chr4	115042943	CCDS43264.1	c.3137A>NULL	p.NULL-1FsDel1bp
ASH1L	ash1 (absent; small; or homeotic)-like (Drosophila)	ENSG00000116539	PAP54	178	33.1%	chr1	153574570	CCDS1113.2	c.8737C>T	p.H2913Y
ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP54	226	21.2%	chr1	26978518	CCDS285.1	c.5542G>NUL	p.NULL-1FsDel1bp
ARID5B	AT rich interactive domain 5B (MRF1-like)	ENSG00000150347	PAP54	310	12.3%	chr10	63522257	CCDS31208.1	c.3029G>A	p.R1010Q

ATXN3	ataxin 3	ENSG00000066427	PAP54	57	31.6%	chr14	91619358	CCDS9900.1	c.-1T>NULL	p.IVS6-3-1SpliceAcceptor
ABCB6	ATP-binding cassette; sub-family B (MDR/TAP); member 6	ENSG00000115657	PAP54	92	18.5%	chr2	219783377	CCDS2436.1	c.2321C>T	p.A774V
ABCB9	ATP-binding cassette; sub-family B (MDR/TAP); member 9	ENSG00000150967	PAP54	41	26.8%	chr12	121990672	CCDS9241.1	c.1855G>NUL	p.NULL-1FsDel1bp
BCAS1	breast carcinoma amplified sequence 1	ENSG00000064787	PAP54	152	17.8%	chr20	52016934	CCDS13444.1	c.1268C>T	p.A423V
BRD8	bromodomain containing 8	ENSG00000112983	PAP54	128	10.9%	chr5	137523145	CCDS4198.1	c.2619NULL>(	p.NULL-1FsIns2bp
BTBD11	BTB (POZ) domain containing 11	ENSG00000151136	PAP54	240	18.3%	chr12	106575567	CCDS31893.1	c.3257C>T	p.T1086M
CDH12	cadherin 12; type 2 (N-cadherin 2)	ENSG00000154162	PAP54	63	36.5%	chr5	21791507	CCDS3890.1	c.1835T>G	p.L612R
CANT1	calcium activated nucleotidase 1	ENSG00000171302	PAP54	175	19.4%	chr17	74501343	CCDS11760.1	c.1090G>A	p.E364K
CACNB3	calcium channel; voltage-dependent; beta 3 subunit	ENSG00000167535	PAP54	122	29.5%	chr12	47505214	CCDS8769.1	c.494C>T	p.A165V
CLMN	calmin (calponin-like; transmembrane)	ENSG00000165959	PAP54	107	30.8%	chr14	94732702	CCDS9933.1	c.2790A>NULI	p.NULL-1FsDel1bp
CANX	calnexin	ENSG00000127022	PAP54	77	36.4%	chr5	179083273	CCDS4447.1	c.1405G>A	p.V469I
CHST6	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	ENSG00000183196	PAP54	99	13.1%	chr16	74070975	CCDS10918.1	c.253G>A	p.A85T
CARD10	caspase recruitment domain family; member 10	ENSG00000100065	PAP54	158	30.4%	chr22	36230195	CCDS13948.1	c.1693C>NULI	p.NULL-1FsDel1bp
CARD6	caspase recruitment domain family; member 6	ENSG00000132357	PAP54	163	33.1%	chr5	40888851	CCDS3935.1	c.1660T>NULI	p.NULL-1FsDel1bp
CTNNA3	catenin (cadherin-associated protein); alpha 3	ENSG00000183230	PAP54	149	14.8%	chr10	67350105	CCDS7269.1	c.2677C>T	p.Q893X
CTNNB1	catenin (cadherin-associated protein); beta 1; 88kDa	ENSG00000168036	PAP54	163	18.4%	chr3	41241117	CCDS2694.1	c.110C>A	p.S37Y
CD34	CD34 molecule	ENSG00000174059	PAP54	106	13.2%	chr1	206129724	ENST00000367036	c.204T>NULL	p.NULL-1FsDel1bp
CDS1	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	ENSG00000163624	PAP54	80	12.5%	chr4	85775499	CCDS3608.1	c.781T>NULL	p.NULL-1FsDel1bp
CHPT1	choline phosphotransferase 1	ENSG00000111666	PAP54	162	32.7%	chr12	100632469	CCDS9086.1	c.478T>NULL	p.NULL-1FsDel1bp
C10orf71	chromosome 10 open reading frame 71	ENSG00000177354	PAP54	123	13.8%	chr10	50201844	NM_001135196	c.1248C>NULI	p.NULL-1FsDel1bp
C10orf79	chromosome 10 open reading frame 79	ENSG00000197748	PAP54	117	16.2%	chr10	105895302	CCDS31281.1	c.3866G>A	p.R1289H
C12orf32	chromosome 12 open reading frame 32	ENSG00000171792	PAP54	215	38.1%	chr12	2867465	ENST00000303648	c.296C>T	p.P99L
C13orf23	chromosome 13 open reading frame 23	ENSG00000120685	PAP54	60	16.7%	chr13	38506336	CCDS9368.2	c.-1TT>NULL	p.IVS1-3-1SpliceAcceptor
C14orf102	chromosome 14 open reading frame 102	ENSG00000119720	PAP54	200	36.0%	chr14	89839130	CCDS9890.1	c.1501AAG>N	p.NULL-1FsDel3bp
C14orf109	chromosome 14 open reading frame 109	ENSG00000153485	PAP54	73	45.2%	chr14	92722685	CCDS41980.1	c.312A>G	p.I104M
C14orf43	chromosome 14 open reading frame 43	ENSG00000156030	PAP54	176	19.9%	chr14	73275526	CCDS9819.1	c.2387C>NULI	p.NULL-1FsDel1bp
C16orf70	chromosome 16 open reading frame 70	ENSG00000125149	PAP54	238	14.7%	chr16	65725630	CCDS10828.1	c.509G>A	p.R170Q
C19orf40	chromosome 19 open reading frame 40	ENSG00000131944	PAP54	99	11.1%	chr19	38156021	CCDS12426.1	c.79G>T	p.G27W
C19orf62	chromosome 19 open reading frame 62	ENSG00000105393	PAP54	163	35.0%	chr19	17250949	ENST00000300965	c.1087G>NUL	p.NULL-1FsDel1bp
C2orf85	chromosome 2 open reading frame 85	ENSG00000188011	PAP54	251	19.9%	chr2	242463048	CCDS42843.1	c.668NULL>C	p.NULL-1FsIns1bp
C21orf56	chromosome 21 open reading frame 56	ENSG00000160284	PAP54	104	18.3%	chr21	46412968	NM_001142854	c.226G>A	p.D76N
C4orf26	chromosome 4 open reading frame 26	ENSG00000174792	PAP54	337	19.0%	chr4	76708346	CCDS3569.1	c.-1A>G	p.IVS1-2-1SpliceAcceptor
C4orf26	chromosome 4 open reading frame 26	ENSG00000174792	PAP54	361	31.0%	chr4	76708398	CCDS3569.1	c.118G>A	p.A40T
C6orf89	chromosome 6 open reading frame 89	ENSG00000198663	PAP54	138	12.3%	chr6	36975349	CCDS4827.1	c.172NULL>C	p.NULL-1FsIns1bp

C8orf41	chromosome 8 open reading frame 41	ENSG00000129696	PAP54	84	20.2%	chr8	33486853	CCDS6090.1	c.972GA>NUL	p.NULL-1FsDel2bp
C8orf46	chromosome 8 open reading frame 46	ENSG00000169085	PAP54	179	16.2%	chr8	67590749	CCDS6191.1	c.505C>T	p.P169S
CLOCK	clock homolog (mouse)	ENSG00000134852	PAP54	64	17.2%	chr4	56031711	CCDS3500.1	c.457T>NULL	p.NULL-1FsDel1bp
CCDC110	coiled-coil domain containing 110	ENSG00000168491	PAP54	81	14.8%	chr4	186616487	CCDS3843.1	c.2248G>A	p.V750I
COL5A3	collagen; type V; alpha 3	ENSG00000080573	PAP54	112	12.5%	chr19	9977768	CCDS12222.1	c.386C>NULL	p.NULL-1FsDel1bp
COL8A2	collagen; type VIII; alpha 2	ENSG00000171812	PAP54	123	21.1%	chr1	36337153	CCDS403.1	c.716C>A	p.P239H
COL22A1	collagen; type XXII; alpha 1	ENSG00000169436	PAP54	54	42.6%	chr8	139672860	CCDS6376.1	c.4759C>NUL	p.NULL-1FsDel1bp
CNTNAP1	contactin associated protein 1	ENSG00000108797	PAP54	220	34.5%	chr17	38090811	CCDS11436.1	c.562C>T	p.P188S
CORO2A	coronin; actin binding protein; 2A	ENSG00000106789	PAP54	216	14.4%	chr9	99928752	CCDS6735.1	c.1346T>C	p.M449T
CLEC12A	C-type lectin domain family 12; member A	ENSG00000172322	PAP54	82	19.5%	chr12	10062324	NM_001129998	c.808G>A	p.V270M
CLEC12B	C-type lectin domain family 12; member B	ENSG00000172322	PAP54	82	19.5%	chr12	10062324	NM_001129998	c.808G>A	p.V270M
CELF6	CUGBP; Elav-like family member 6	ENSG00000140488	PAP54	123	10.6%	chr15	70367807	CCDS10242.1	c.1214A>G	p.Q405R
CWF19L2	CWF19-like 2; cell cycle control (S. pombe)	ENSG00000152404	PAP54	94	29.8%	chr11	106710844	CCDS8336.1	c.2027AGAT>I	p.NULL-1FsDel4bp
CYLC1	cylicin; basic protein of sperm head cytoskeleton 1	ENSG00000183035	PAP54	128	14.1%	chrX	83016272	CCDS35341.1	c.1900C>A	p.P634T
CYTH4	cytohesin 4	ENSG00000100055	PAP54	118	37.3%	chr22	36026174	ENST00000405206	c.469G>T	p.G157W
DAB2IP	DAB2 interacting protein	ENSG00000136848	PAP54	112	15.2%	chr9	123576458	CCDS6833.2	c.2982C>NUL	p.NULL-1FsDel1bp
DCHS1	dachsous 1 (Drosophila)	ENSG00000166341	PAP54	193	14.5%	chr11	6618469	CCDS7771.1	c.952C>T	p.R318W
actn3	DAVID_actinin: alpha 3	NM_001104	PAP54	289	31.1%	chr11	66079237	NM_001104	c.618C>G	p.D206E
Ceacam16	DAVID_carcinoembryonic antigen-related cell adhesion molecule 16	NM_001039213	PAP54	98	11.2%	chr19	49899343	NM_001039213	c.775C>T	p.Q259X
Fam198a	DAVID_chromosome 3 open reading frame 41; hypothetical protein LOC729085	NM_001129908	PAP54	63	38.1%	chr3	43049229	NM_001129908	c.470G>A	p.G157D
LOC26172	DAVID_chromosome 3 open reading frame 41; hypothetical protein LOC729085	NM_001129908	PAP54	63	38.1%	chr3	43049229	NM_001129908	c.470G>A	p.G157D
C3orf77	DAVID_chromosome 3 open reading frame 77	NM_001145030	PAP54	144	34.7%	chr3	44260887	NM_001145030	c.1885A>NULI	p.NULL-1FsDel1bp
C6orf103	DAVID_chromosome 6 open reading frame 103	NM_024694	PAP54	128	10.9%	chr6	146961918	NM_024694	c.49G>A	p.A17T
CCDC150	DAVID_coiled-coil domain containing 150	NM_001080539	PAP54	115	16.5%	chr2	197239764	NM_001080539	c.839AA>NUL	p.NULL-1FsDel2bp
Col11a2	DAVID_collagen: type XI: alpha 2	ENSG00000204248	PAP54	187	16.0%	chr6	33256738	CCDS43452.1	c.985C>NULL	p.NULL-1FsDel1bp
DENND1B	DAVID_DENN/MADD domain containing 1B	NM_001142795	PAP54	96	17.7%	chr1	195746638	NM_001142795	c.1843G>T	p.D615Y
DRGX	DAVID_dorsal root ganglia homeobox	NM_001080520	PAP54	294	33.3%	chr10	50264805	NM_001080520	c.355G>A	p.V119M
Fat1	DAVID_FAT tumor suppressor homolog 1 (Drosophila)	NM_005245	PAP54	384	31.8%	chr4	187758447	NM_005245	c.12163GT>NI	p.NULL-1FsDel2bp
BAT4	DAVID_HLA-B associated transcript 4	ENSG00000204438	PAP54	157	16.6%	chr6	31738396	CCDS4711.1	c.697T>G	p.S233A
FLJ44790	DAVID_hypothetical FLJ44790	ENSG00000203951	PAP54	70	14.3%	chr20	60241422	ENST00000370795	c.137G>A	p.R46H
LOC100130!	DAVID_hypothetical LOC100130557	ENSG00000181295	PAP54	81	18.5%	chr1	40930178	ENST00000325093	c.477C>NULL	p.NULL-1FsDel1bp
LOC388588	DAVID_hypothetical LOC388588	NM_001163724	PAP54	43	46.5%	chr1	3682256	NM_001163724	c.148G>A	p.A50T
TMEM232	DAVID_hypothetical protein LOC642987	NM_001039763	PAP54	142	32.4%	chr5	109932100	NM_001039763	c.1402A>G	p.T468A
kiaa0284	DAVID_KIAA0284	NM_001112726	PAP54	84	40.5%	chr14	104424190	NM_001112726	c.2569G>T	p.D857Y
KIAA0913	DAVID_KIAA0913	NM_015037	PAP54	156	38.5%	chr10	75230470	NM_015037	c.5093C>NUL	p.NULL-1FsDel1bp
Kif7	DAVID_kinesin family member 7	NM_198525	PAP54	290	19.7%	chr15	87991935	NM_198525	c.1572G>NUL	p.NULL-1FsDel1bp
HLA-DOA	DAVID_major histocompatibility complex: class II: DO alpha	ENSG00000204252	PAP54	94	17.0%	chr6	33083257	CCDS4763.1	c.703C>NULL	p.NULL-1FsDel1bp

MLL2	DAVID_myeloid/lymphoid or mixed-lineage leukemia 2	NM_003482	PAP54	149	12.1%	chr12	47729934	NM_003482	c.4812G>NUL	p.NULL-1FsDel1bp
MLL4	DAVID_myeloid/lymphoid or mixed-lineage leukemia 4	ENSG00000105663	PAP54	295	13.9%	chr19	40914777	NM_014727	c.5566G>A	p.A1856T
ND2	DAVID_NADH-ubiquinone oxidoreductase chain 2	ENSG00000198763	PAP54	51	98.0%	chrM	4625	ENST00000361453	c.155C>T	p.S52F
Naca	DAVID_nascent polypeptide-associated complex alpha subunit	NM_001113203	PAP54	293	18.1%	chr12	55396386	NM_001113203	c.5195C>T	p.T1732I
NPHP4	DAVID_nephronophthisis 4	NM_015102	PAP54	118	27.1%	chr1	5930799	NM_015102	c.910G>A	p.V304I
NOBOX	DAVID_NOBOX oogenesis homeobox	NM_001080413	PAP54	43	60.5%	chr7	143727123	NM_001080413	c.1199C>NULI	p.NULL-1FsDel1bp
obscn	DAVID_obscurin: cytoskeletal calmodulin and titin-interacting RhoGEF	NM_001098623	PAP54	259	19.3%	chr1	226470877	NM_001098623	c.2228G>A	p.G743D
PCLO	DAVID_piccolo (presynaptic cytomatrix protein)	NM_033026	PAP54	112	17.0%	chr7	82382769	NM_033026	c.12469C>T	p.H4157Y
PCLO	DAVID_piccolo (presynaptic cytomatrix protein)	NM_033026	PAP54	119	18.5%	chr7	82622004	NM_033026	c.1889C>T	p.T630M
PRSS8	DAVID_protease: serine: 8	NM_002773	PAP54	135	34.1%	chr16	31051611	NM_002773	c.431T>A	p.I144N
PPP1R12B	DAVID_protein phosphatase 1: regulatory (inhibitor) subunit 12B	NM_001167857	PAP54	79	12.7%	chr1	200673813	NM_001167857	c.1496T>NULI	p.NULL-1FsDel1bp
ptprq	DAVID_protein tyrosine phosphatase: receptor type: Q	NM_001145026	PAP54	61	21.3%	chr12	79537452	NM_001145026	c.4873G>A	p.A1625T
PCDHGA8	DAVID_protocadherin gamma subfamily A: 8	NM_032088	PAP54	94	17.0%	chr5	140754722	NM_032088	c.2158C>T	p.H720Y
RGAG4	DAVID_retrotransposon gag domain containing 4	NM_001024455	PAP54	31	45.2%	chrX	71267774	NM_001024455	c.2051C>NULI	p.NULL-1FsDel1bp
ROBO1	DAVID_roundabout: axon guidance receptor: homolog 1 (Drosophila); similar to roundabout 1 isoform b	NM_002941	PAP54	170	15.3%	chr3	78771685	NM_002941	c.2936C>T	p.T979M
LOC642132	DAVID_roundabout: axon guidance receptor: homolog 1 (Drosophila); similar to roundabout 1 isoform b	NM_002941	PAP54	170	15.3%	chr3	78771685	NM_002941	c.2936C>T	p.T979M
RYR2	DAVID_ryanodine receptor 2 (cardiac)	NM_001035	PAP54	171	16.4%	chr1	235699050	NM_001035	c.1648C>A	p.Q550K
RYR2	DAVID_ryanodine receptor 2 (cardiac)	NM_001035	PAP54	42	28.6%	chr1	236015918	NM_001035	c.13287G>T	p.K4429N
SEZ6	DAVID_seizure related 6 homolog (mouse)	NM_178860	PAP54	113	38.1%	chr17	24321040	NM_178860	c.1110G>NUL	p.NULL-1FsDel1bp
Spint2	DAVID_serine peptidase inhibitor: Kunitz type: 2	ENSG00000167642	PAP54	57	21.1%	chr19	43472635	CCDS12510.1	c.428G>T	p.R143L
Ik	DAVID_similar to CG18005; IK cytokine: down-regulator of HLA II	NM_006083	PAP54	74	31.1%	chr5	140012777	NM_006083	c.268GA>NUL	p.NULL-1FsDel2bp
LOC644456	DAVID_similar to CG18005; IK cytokine: down-regulator of HLA II	NM_006083	PAP54	74	31.1%	chr5	140012777	NM_006083	c.268GA>NUL	p.NULL-1FsDel2bp
SCN5A	DAVID_sodium channel: voltage-gated: type V: alpha subunit	NM_001099404	PAP54	132	18.9%	chr3	38567193	NM_001099404	c.5674A>G	p.I1892V
tgfbi	DAVID_transforming growth factor: beta-induced: 68kDa	NM_000358	PAP54	89	16.9%	chr5	135419353	NM_000358	c.1496C>NULI	p.NULL-1FsDel1bp
Trim17	DAVID_tripartite motif-containing 17	NM_001134855	PAP54	132	13.6%	chr1	226663402	NM_001134855	c.1229NULL>(	p.NULL-1FsIns1bp
SR140	DAVID_U2-associated SR140 protein	NM_001080415	PAP54	93	14.0%	chr3	144225538	NM_001080415	c.1262T>A	p.I421N
B3gnt6	DAVID_UDP-GlcNAc:betaGal beta-1:3-N-acetylglucosaminyltransferase 6 (core 3 synthase)	NM_138706	PAP54	100	23.0%	chr11	76428908	NM_138706	c.665A>G	p.D222G
VWA5B2	DAVID_von Willebrand factor A domain containing 5B2	NM_138345	PAP54	196	32.7%	chr3	185437799	NM_138345	c.1625C>NULI	p.NULL-1FsDel1bp
WDR87	DAVID_WD repeat domain 87	NM_031951	PAP54	140	12.9%	chr19	43067875	NM_031951	c.13503A>NUI	p.NULL-1FsDel1bp
ZNF629	DAVID_zinc finger protein 629	NM_001080417	PAP54	108	20.4%	chr16	30703061	NM_001080417	c.2625A>NULI	p.NULL-1FsDel1bp
ZNF793	DAVID_zinc finger protein 793	NM_001013659	PAP54	123	16.3%	chr19	42720356	NM_001013659	c.956C>T	p.S319L
ZNF99	DAVID_zinc finger protein 99	NM_001080409	PAP54	43	39.5%	chr19	22734165	NM_001080409	c.449C>G	p.A150G
ZDBF2	DAVID_zinc finger: DBF-type containing 2	NM_020923	PAP54	97	11.3%	chr2	206882673	NM_020923	c.5176A>NULI	p.NULL-1FsDel1bp
DCAF8L2	DDB1 and CUL4 associated factor 8-like 2	ENSG00000189186	PAP54	324	18.2%	chrX	27907716	CCDS35222.1	c.1657C>T	p.R553C
DDX51	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	ENSG00000185163	PAP54	218	13.8%	chr12	131191330	CCDS41865.1	c.1439C>T	p.T480M
DFNB31	deafness; autosomal recessive 31	ENSG00000095397	PAP54	68	26.5%	chr9	116208809	CCDS6806.1	c.1883G>A	p.S628N

DEK	DEK oncogene	ENSG00000124795	PAP54	147	32.7%	chr6	18358028	CCDS34344.1	c.783A>NULL	p.NULL-1FsDel1bp
DEPDC5	DEP domain containing 5	ENSG00000100150	PAP54	93	12.9%	chr22	30548752	CCDS43006.1	c.2080G>A	p.G694S
DHX58	DEXH (Asp-Glu-X-His) box polypeptide 58	ENSG00000108771	PAP54	57	17.5%	chr17	37509252	CCDS11416.1	c.1654G>A	p.V552M
DRD1	dopamine receptor D1	ENSG00000184845	PAP54	94	35.1%	chr5	174802320	CCDS4393.1	c.389G>A	p.R130Q
DYRK4	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	ENSG00000010219	PAP54	101	28.7%	chr12	4576122	CCDS8530.1	c.526C>T	p.R176C
DCTN1	dynactin 1 (p150; glued homolog; Drosophila)	ENSG00000204843	PAP54	270	15.2%	chr2	74449751	CCDS1939.1	c.1683G>T	p.E561D
DNAH10	dynein; axonemal; heavy chain 10	ENSG00000197653	PAP54	52	28.8%	chr12	122969278	NM_207437	c.10981G>A	p.V3661I
EMR1	egf-like module containing; mucin-like; hormone receptor-like 1	ENSG00000174837	PAP54	229	25.3%	chr19	6848531	CCDS12175.1	c.487T>A	p.F163I
ERN2	endoplasmic reticulum to nucleus signaling 2	ENSG00000134398	PAP54	192	13.0%	chr16	23619430	CCDS32407.1	c.1765G>NUL	p.NULL-1FsDel1bp
ENO3	enolase 3 (beta; muscle)	ENSG00000108515	PAP54	173	28.9%	chr17	4797321	CCDS11062.1	c.249C>A	p.S83R
EPHB3	EPH receptor B3	ENSG00000182580	PAP54	109	10.1%	chr3	185777893	CCDS3268.1	c.1423C>NULI	p.NULL-1FsDel1bp
EGF	epidermal growth factor	ENSG00000138798	PAP54	212	25.0%	chr4	111121511	CCDS3689.1	c.2302C>T	p.R768C
EPS8	epidermal growth factor receptor pathway substrate 8	ENSG00000151491	PAP54	60	45.0%	chr12	15667491	CCDS31753.1	c.-1TT>NULL	p.IVS18-3-1SpliceAcceptor
EPN3	epsin 3	ENSG00000049283	PAP54	237	13.5%	chr17	45974257	CCDS11570.1	c.1639C>T	p.P547S
EIF3K	eukaryotic translation initiation factor 3; subunit K	ENSG00000178982	PAP54	88	26.1%	chr19	43802894	CCDS12517.1	c.137C>T	p.A46V
EIF4H	eukaryotic translation initiation factor 4H	ENSG00000106682	PAP54	71	33.8%	chr7	73242130	CCDS5564.1	c.355A>G	p.R119G
XPO1	exportin 1 (CRM1 homolog; yeast)	ENSG00000082898	PAP54	176	32.4%	chr2	61559547	CCDS33205.1	c.3128G>A	p.R1043Q
EYA4	eyes absent homolog 4 (Drosophila)	ENSG00000112319	PAP54	206	36.9%	chr6	133825205	CCDS5166.1	c.477NULL>A	p.NULL-1FsIns1bp
FAM120A	family with sequence similarity 120A	ENSG00000048828	PAP54	129	14.7%	chr9	95360755	CCDS6706.1	c.2740G>A	p.A914T
FAM122B	family with sequence similarity 122B	ENSG00000156504	PAP54	117	10.3%	chrX	133733901	CCDS14643.1	c.824AG>NUL	p.NULL-1FsDel2bp
FANCM	Fanconi anemia; complementation group M	ENSG00000187790	PAP54	110	17.3%	chr14	44735341	CCDS32070.1	c.5557TG>NU	p.NULL-1FsDel2bp
FAT4	FAT tumor suppressor homolog 4 (Drosophila)	ENSG00000196159	PAP54	393	12.2%	chr4	126459847	CCDS3732.2	c.2831A>NULI	p.NULL-1FsDel1bp
FBXL5	F-box and leucine-rich repeat protein 5	ENSG00000118564	PAP54	134	28.4%	chr4	15255299	CCDS3415.1	c.215G>A	p.R72H
FGA	fibrinogen alpha chain	ENSG00000171560	PAP54	179	27.4%	chr4	155725438	CCDS3787.1	c.-1T>NULL	p.IVS5-3-1SpliceAcceptor
FN1	fibronectin 1	ENSG00000115414	PAP54	73	37.0%	chr2	215964737	CCDS42814.1	c.4115A>C	p.D1372A
FLRT2	fibronectin leucine rich transmembrane protein 2	ENSG00000185070	PAP54	200	33.5%	chr14	85157773	CCDS9877.1	c.162G>T	p.L54F
FSIP2	fibrous sheath interacting protein 2	ENSG00000188738	PAP54	284	11.6%	chr2	186370348	ENST00000344648	c.2092NULL>A	p.NULL-1FsIns1bp
FUT4	fucosyltransferase 4 (alpha (1;3) fucosyltransferase; myeloid-specific)	ENSG00000196371	PAP54	602	13.0%	chr11	93918377	CCDS8301.1	c.1430G>A	p.R477H
GPS1	G protein pathway suppressor 1	ENSG00000169727	PAP54	82	12.2%	chr17	77603447	ENST00000320548	c.60G>NULL	p.NULL-1FsDel1bp
GPR182	G protein-coupled receptor 182	ENSG00000166856	PAP54	396	12.1%	chr12	55675736	CCDS8927.1	c.476C>NULL	p.NULL-1FsDel1bp
GPR39	G protein-coupled receptor 39	ENSG00000183840	PAP54	282	13.5%	chr2	132891135	CCDS2170.1	c.50A>G	p.H17R
GRK4	G protein-coupled receptor kinase 4	ENSG00000125388	PAP54	119	16.0%	chr4	2960308	CCDS33946.1	c.205C>T	p.Q69X
GABRE	gamma-aminobutyric acid (GABA) A receptor; epsilon	ENSG00000102287	PAP54	244	17.2%	chrX	150874588	CCDS14703.1	c.1045G>A	p.V349I
GABBR2	gamma-aminobutyric acid (GABA) B receptor; 2	ENSG00000136928	PAP54	67	32.8%	chr9	100344127	CCDS6736.1	c.479C>T	p.T160M
GJB7	gap junction protein; beta 7; 25kDa	ENSG00000164411	PAP54	116	16.4%	chr6	88050820	CCDS5008.1	c.530C>T	p.T177M
GINS1	GINS complex subunit 1 (Psf1 homolog)	ENSG00000101003	PAP54	189	15.9%	chr20	25370397	CCDS33451.1	c.507A>NULL	p.NULL-1FsDel1bp
GLI4	GLI family zinc finger 4	ENSG00000181638	PAP54	262	13.0%	chr8	144403782	CCDS6397.1	c.394A>G	p.K132E

GRLF1	glucocorticoid receptor DNA binding factor 1	ENSG00000160007	PAP54	184	34.2%	chr19	52116493	NM_004491	c.2721G>NUL	p.NULL-1FsDel1bp
GCNT2	glucosaminyl (N-acetyl) transferase 2; I-branching enzyme (I blood group)	ENSG00000111846	PAP54	343	21.3%	chr6	10694911	CCDS4513.1	c.703G>T	p.E235X
GXYLT1	glucoside xylosyltransferase 1	ENSG00000151233	PAP54	103	21.4%	chr12	40778043	CCDS41772.1	c.1047A>NULI	p.NULL-1FsDel1bp
QRICH1	glutamine-rich 1	ENSG00000198218	PAP54	321	15.0%	chr3	49070152	CCDS2787.1	c.485C>T	p.S162L
GLYATL2	glycine-N-acyltransferase-like 2	ENSG00000156689	PAP54	149	30.9%	chr11	58362408	CCDS41649.1	c.88G>A	p.A30T
GYLTL1B	glycosyltransferase-like 1B	ENSG00000165905	PAP54	117	17.9%	chr11	45904949	CCDS31473.1	c.1276C>NULI	p.NULL-1FsDel1bp
GIGYF2	GRB10 interacting GYF protein 2	ENSG00000204120	PAP54	100	27.0%	chr2	233423241	CCDS33401.1	c.3710G>A	p.S1237N
GFI1	growth factor independent 1 transcription repressor	ENSG00000162676	PAP54	131	39.7%	chr1	92714280	CCDS30773.1	c.1163G>A	p.R388H
GRB14	growth factor receptor-bound protein 14	ENSG00000115290	PAP54	151	12.6%	chr2	165073534	CCDS2222.1	c.1001A>NULI	p.NULL-1FsDel1bp
GNAZ	guanine nucleotide binding protein (G protein); alpha z polypeptide	ENSG00000128266	PAP54	168	18.5%	chr22	21768488	CCDS13804.1	c.606G>NULL	p.NULL-1FsDel1bp
HP1BP3	heterochromatin protein 1; binding protein 3	ENSG00000127483	PAP54	145	45.5%	chr1	20944119	CCDS30621.1	c.1420C>T	p.Q474X
HKDC1	hexokinase domain containing 1	ENSG00000156510	PAP54	140	35.0%	chr10	70678196	CCDS7288.1	c.1276C>T	p.R426C
H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	ENSG00000049239	PAP54	119	16.8%	chr1	9246891	CCDS101.1	c.1752G>C	p.Q584H
HIST1H2BA	histone cluster 1; H2ba	ENSG00000146047	PAP54	79	20.3%	chr6	25835342	CCDS4563.1	c.227C>T	p.A76V
HDAC4	histone deacetylase 4	ENSG00000068024	PAP54	106	12.3%	chr2	239640190	CCDS2529.1	c.3118C>T	p.R1040C
HOXB3	homeobox B3	ENSG00000120093	PAP54	96	17.7%	chr17	43984736	CCDS11528.1	c.547C>NULL	p.NULL-1FsDel1bp
HORMAD1	HORMA domain containing 1	ENSG00000143452	PAP54	38	28.9%	chr1	148953224	CCDS967.1	c.-1T>NULL	p.IVS3-3-1SpliceAcceptor
HCFC1	host cell factor C1 (VP16-accessory protein)	ENSG00000172534	PAP54	126	12.7%	chrX	152877374	CCDS44020.1	c.1643C>T	p.A548V
HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	ENSG00000010818	PAP54	240	16.3%	chr6	143134228	CCDS43510.1	c.3341G>A	p.G1114D
HIVEP3	human immunodeficiency virus type I enhancer binding protein 3	ENSG00000127124	PAP54	80	15.0%	chr1	41821455	CCDS463.1	c.6661C>NULI	p.NULL-1FsDel1bp
IGLV1-50	immunoglobulin lambda variable 1-50 (non-functional)	ENSG00000211645	PAP54	54	46.3%	chr22	21011718	ENST00000390291	c.10TCT>NUL	p.NULL-1FsDel3bp
IGDCC4	immunoglobulin superfamily; DCC subclass; member 4	ENSG00000103742	PAP54	100	15.0%	chr15	63463677	CCDS10206.1	c.3476T>C	p.L1159P
IGSF8	immunoglobulin superfamily; member 8	ENSG00000162729	PAP54	206	30.1%	chr1	158329583	CCDS1195.1	c.1067G>A	p.G356D
ITFG3	integrin alpha FG-GAP repeat containing 3	ENSG00000167930	PAP54	77	24.7%	chr16	244500	CCDS10402.1	c.87A>NULL	p.NULL-1FsDel1bp
ITGB4	integrin; beta 4	ENSG00000132470	PAP54	98	23.5%	chr17	71256689	CCDS11727.1	c.3284C>T	p.P1095L
IRF7	interferon regulatory factor 7	ENSG00000185507	PAP54	201	10.9%	chr11	604275	CCDS7705.1	c.617C>T	p.A206V
IFT88	intraflagellar transport 88 homolog (Chlamydomonas)	ENSG00000032742	PAP54	117	42.7%	chr13	20135725	CCDS31944.1	c.2184G>T	p.M728I
IQCB1	IQ motif containing B1	ENSG00000173226	PAP54	18	55.6%	chr3	122983389	CCDS33837.1	c.1301G>A	p.C434Y
IVD	isovaleryl-CoA dehydrogenase	ENSG00000128928	PAP54	140	14.3%	chr15	38487177	CCDS10057.1	c.193G>A	p.A65T
KLHDC8A	kelch domain containing 8A	ENSG00000162873	PAP54	106	17.0%	chr1	203574967	CCDS30985.1	c.735G>T	p.M245I
KRT26	keratin 26	ENSG00000186393	PAP54	113	27.4%	chr17	36180042	CCDS11374.1	c.826A>NULL	p.NULL-1FsDel1bp
KIAA1324L	KIAA1324-like	ENSG00000164659	PAP54	115	30.4%	chr7	86380459	CCDS34677.1	c.-1T>NULL	p.IVS9-3-1SpliceAcceptor
KIAA1407	KIAA1407	ENSG00000163617	PAP54	53	37.7%	chr3	115204007	CCDS2977.1	c.2047G>C	p.E683Q
KIAA1543	KIAA1543	ENSG00000076826	PAP54	62	43.5%	chr19	7588941	CCDS42489.1	c.3748T>G	p.X1250E
KIAA1614	KIAA1614	ENSG00000135835	PAP54	90	17.8%	chr1	179176992	CCDS41442.1	c.3107C>T	p.P1036L
KIAA1919	KIAA1919	ENSG00000173214	PAP54	158	17.1%	chr6	111694054	CCDS5090.1	c.596T>NULL	p.NULL-1FsDel1bp
KIF24	kinesin family member 24	ENSG00000186638	PAP54	300	19.7%	chr9	34247482	NM_194313	c.2123C>T	p.T708I

KIF5A	kinesin family member 5A	ENSG00000155980	PAP54	97	17.5%	chr12	56261163	CCDS8945.1	c.2696G>A	p.R899H
KIF7	kinesin family member 7	ENSG00000166813	PAP54	202	35.1%	chr15	87972908	CCDS32325.1	c.2606C>NULL	p.NULL-1FsDel1bp
LATS2	LATS; large tumor suppressor; homolog 2 (Drosophila)	ENSG00000150457	PAP54	232	14.7%	chr13	20461349	CCDS9294.1	c.1993C>NULL	p.NULL-1FsDel1bp
LRRC16A	leucine rich repeat containing 16A	ENSG00000079691	PAP54	84	40.5%	chr6	25560433	ENST00000332168	c.917T>NULL	p.NULL-1FsDel1bp
LRRC16A	leucine rich repeat containing 16A	ENSG00000079691	PAP54	84	15.5%	chr6	25560433	ENST00000332168	c.917TT>NULL	p.NULL-1FsDel2bp
LRRC41	leucine rich repeat containing 41	ENSG00000132128	PAP54	119	36.1%	chr1	46524082	CCDS533.1	c.2171C>NULL	p.NULL-1FsDel1bp
LRRC8D	leucine rich repeat containing 8 family; member D	ENSG00000171492	PAP54	77	14.3%	chr1	90172514	CCDS726.1	c.1299T>NULL	p.NULL-1FsDel1bp
LRRN1	leucine rich repeat neuronal 1	ENSG00000175928	PAP54	243	11.9%	chr3	3862104	CCDS33685.1	c.779A>NULL	p.NULL-1FsDel1bp
LRRTM1	leucine rich repeat transmembrane neuronal 1	ENSG00000162951	PAP54	172	15.7%	chr2	80383003	CCDS1966.1	c.1453G>A	p.A485T
LGR4	leucine-rich repeat-containing G protein-coupled receptor 4	ENSG00000205213	PAP54	81	18.5%	chr11	27347269	CCDS31449.1	c.-1T>NULL	p.IVS17-3-1SpliceAcceptor
LENG8	leukocyte receptor cluster (LRC) member 8	ENSG00000167615	PAP54	451	30.4%	chr19	59664614	ENST00000376526	c.2246T>NULL	p.NULL-1FsDel1bp
LAT2	linker for activation of T cells family; member 2	ENSG00000086730	PAP54	69	37.7%	chr7	73273937	CCDS5566.2	c.367C>T	p.R123W
LONP1	lon peptidase 1; mitochondrial	ENSG00000196365	PAP54	71	39.4%	chr19	5644310	CCDS12148.1	c.2702C>T	p.A901V
LRP1B	low density lipoprotein receptor-related protein 1B	ENSG00000168702	PAP54	59	32.2%	chr2	141075625	CCDS2182.1	c.6853T>C	p.W2285R
LHCGR	luteinizing hormone/choriogonadotropin receptor	ENSG00000138039	PAP54	79	12.7%	chr2	48769415	CCDS1842.1	c.1025G>A	p.R342Q
KDM5A	lysine (K)-specific demethylase 5A	ENSG00000073614	PAP54	45	40.0%	chr12	368529	ENST00000382815	c.224CCCCC>	p.NULL-1FsDel5bp
MFHAS1	malignant fibrous histiocytoma amplified sequence 1	ENSG00000147324	PAP54	77	40.3%	chr8	8785338	CCDS34844.1	c.2641C>T	p.Q881X
MRC2	mannose receptor; C type 2	ENSG00000011028	PAP54	129	11.6%	chr17	58112213	CCDS11634.1	c.2693G>A	p.G898E
MAN2A2	mannosidase; alpha; class 2A; member 2	ENSG00000196547	PAP54	1072	15.7%	chr15	89262473	CCDS32332.1	c.3040C>A	p.L1014M
MARK3	MAP/microtubule affinity-regulating kinase 3	ENSG00000075413	PAP54	81	18.5%	chr14	103028019	CCDS41993.1	c.1739C>A	p.P580H
MAS1	MAS1 oncogene	ENSG00000130368	PAP54	284	36.3%	chr6	160248519	CCDS5272.1	c.542G>A	p.R181Q
MMP10	matrix metallopeptidase 10 (stromelysin 2)	ENSG00000166670	PAP54	219	11.4%	chr11	102155605	CCDS8321.1	c.428A>NULL	p.NULL-1FsDel1bp
MMP15	matrix metallopeptidase 15 (membrane-inserted)	ENSG00000102996	PAP54	252	35.3%	chr16	56629750	CCDS10792.1	c.391C>T	p.R131C
MMP24	matrix metallopeptidase 24 (membrane-inserted)	ENSG00000125966	PAP54	121	40.5%	chr20	33318548	NM_006690	c.947G>A	p.R316Q
MCF2L	MCF.2 cell line derived transforming sequence-like	ENSG00000126217	PAP54	137	11.7%	chr13	112726983	CCDS9527.1	c.182C>A	p.P61Q
MDM4	Mdm4 p53 binding protein homolog (mouse)	ENSG00000198625	PAP54	113	11.5%	chr1	202773726	ENST00000391947	c.62T>C	p.F21S
MED12	mediator complex subunit 12	ENSG00000184634	PAP54	81	44.4%	chrX	70255394	CCDS43970.1	c.65C>A	p.P22H
MED24	mediator complex subunit 24	ENSG00000008838	PAP54	40	47.5%	chr17	35430093	CCDS11359.1	c.2663T>A	p.L888H
MAGEB3	melanoma antigen family B; 3	ENSG00000198798	PAP54	139	28.1%	chrX	30164068	CCDS14220.1	c.106A>NULL	p.NULL-1FsDel1bp
MAGEB6	melanoma antigen family B; 6	ENSG00000176746	PAP54	162	13.0%	chrX	26122176	CCDS14217.1	c.292C>T	p.R98C
MTDH	metadherin	ENSG00000147649	PAP54	36	30.6%	chr8	98772587	CCDS6274.1	c.1043G>A	p.G348D
MCPH1	microcephalin 1	ENSG00000147316	PAP54	42	35.7%	chr8	6276507	CCDS43689.1	c.313AA>NUL	p.NULL-1FsDel2bp
MCM10	minichromosome maintenance complex component 10	ENSG00000065328	PAP54	102	34.3%	chr10	13279747	CCDS7096.1	c.2096A>NULL	p.NULL-1FsDel1bp
MRPL27	mitochondrial ribosomal protein L27	ENSG00000108826	PAP54	91	13.2%	chr17	45802454	CCDS11564.1	c.178T>C	p.Y60H
MRPS18A	mitochondrial ribosomal protein S18A	ENSG00000096080	PAP54	54	48.1%	chr6	43750996	ENST00000372118	c.589C>T	p.R197C
MAP3K6	mitogen-activated protein kinase kinase kinase 6	ENSG00000142733	PAP54	130	22.3%	chr1	27558965	CCDS299.1	c.2290G>A	p.D764N
MOBKL1A	MOB1; Mps One Binder kinase activator-like 1A (yeast)	ENSG00000173542	PAP54	73	13.7%	chr4	72063736	CCDS34002.1	c.437C>T	p.S146F
MSH3	mutS homolog 3 (E. coli)	ENSG00000113318	PAP54	106	14.2%	chr5	80006671	CCDS34195.1	c.1141A>NULL	p.NULL-1FsDel1bp
MSH3	mutS homolog 3 (E. coli)	ENSG00000113318	PAP54	94	29.8%	chr5	80207363	CCDS34195.1	c.3340C>T	p.H1114Y

MSH5	mutS homolog 5 (E. coli)	ENSG00000204410	PAP54	123	15.4%	chr6	31834334	CCDS34409.1	c.1225C>T	p.R409C
MPRIP	myosin phosphatase Rho interacting protein	ENSG00000133030	PAP54	185	18.9%	chr17	16987611	CCDS42268.1	c.1052C>NULL	p.NULL-1FsDel1bp
MPRIP	myosin phosphatase Rho interacting protein	ENSG00000133030	PAP54	170	10.6%	chr17	17010414	ENST00000313485	c.1715A>G	p.H572R
N6AMT2	N-6 adenine-specific DNA methyltransferase 2 (putative)	ENSG00000150456	PAP54	124	14.5%	chr13	20204160	CCDS9293.1	c.328A>G	p.M110V
NDOR1	NADPH dependent diflavin oxidoreductase 1	ENSG00000188566	PAP54	197	18.3%	chr9	139228120	CCDS7036.1	c.379G>A	p.V127M
NPAS3	neuronal PAS domain protein 3	ENSG00000151322	PAP54	89	19.1%	chr14	33339729	CCDS9645.1	c.2369G>T	p.R790M
NIPBL	Nipped-B homolog (Drosophila)	ENSG00000164190	PAP54	139	33.8%	chr5	37056462	CCDS3920.1	c.5155C>T	p.R1719X
NCAPD3	non-SMC condensin II complex; subunit D3	ENSG00000151503	PAP54	62	17.7%	chr11	133553796	CCDS31723.1	c.2832C>NULL	p.NULL-1FsDel1bp
NFATC2	nuclear factor of activated T-cells; cytoplasmic; calcineurin-dependent 2	ENSG00000101096	PAP54	335	33.1%	chr20	49523960	CCDS13437.1	c.1672G>A	p.V558I
NSD1	nuclear receptor binding SET domain protein 1	ENSG00000165671	PAP54	156	17.9%	chr5	176653595	CCDS4412.1	c.6620C>T	p.P2207L
NCOR2	nuclear receptor co-repressor 2	ENSG00000196498	PAP54	51	31.4%	chr12	123385701	CCDS41858.1	c.6365C>T	p.P2122L
NULL	NULL	ENSG00000198938	PAP54	99	84.8%	chrM	9599	ENST00000362079	c.392T>C	p.L131P
NULL	NULL	ENSG00000205301	PAP54	56	19.6%	chr4	141597275	ENST00000388762	c.253T>NULL	p.NULL-1FsDel1bp
NULL	NULL	ENSG00000214820	PAP54	128	18.0%	chr3	44596472	ENST00000399045	c.2087C>NULL	p.NULL-1FsDel1bp
NULL	NULL	ENSG00000215916	PAP54	69	58.0%	chr1	1007870	ENST00000379325	c.429G>NULL	p.NULL-1FsDel1bp
OR10S1	olfactory receptor; family 10; subfamily S; member 1	ENSG00000196248	PAP54	164	11.0%	chr11	123353019	CCDS31701.1	c.1585C>NULL	p.NULL-1FsDel1bp
OR10Z1	olfactory receptor; family 10; subfamily Z; member 1	ENSG00000198967	PAP54	402	12.7%	chr1	156842853	CCDS30901.1	c.1A>G	p.M1V
OR13G1	olfactory receptor; family 13; subfamily G; member 1	ENSG00000197437	PAP54	88	15.9%	chr1	245902684	CCDS31094.1	c.283A>G	p.M95V
OR2AJ1	olfactory receptor; family 2; subfamily AJ; member 1	ENSG00000177275	PAP54	184	21.7%	chr1	246164211	ENST00000318244	c.518C>T	p.A173V
OR2AJ1	olfactory receptor; family 2; subfamily AJ; member 1	ENSG00000177275	PAP54	234	12.8%	chr1	246164460	ENST00000318244	c.767T>NULL	p.NULL-1FsDel1bp
OR5B2	olfactory receptor; family 5; subfamily B; member 2	ENSG00000172365	PAP54	121	14.0%	chr11	57946690	CCDS31550.1	c.1550NULL>T	p.NULL-1FsIns1bp
OR51E1	olfactory receptor; family 51; subfamily E; member 1	ENSG00000180785	PAP54	177	16.9%	chr11	4630793	CCDS31358.1	c.458G>NULL	p.NULL-1FsDel1bp
OR52K2	olfactory receptor; family 52; subfamily K; member 2	ENSG00000181963	PAP54	304	14.8%	chr11	4427185	CCDS31351.1	c.40T>C	p.F14L
OR52M1	olfactory receptor; family 52; subfamily M; member 1	ENSG00000197790	PAP54	277	35.4%	chr11	4523406	CCDS31353.1	c.410T>C	p.V137A
OMA1	OMA1 homolog; zinc metallopeptidase (S. cerevisiae)	ENSG00000162600	PAP54	121	21.5%	chr1	58765590	CCDS608.1	c.1146G>A	p.M382I
OTOR	otoraplin	ENSG00000125879	PAP54	208	11.5%	chr20	16677140	CCDS13124.1	c.94T>C	p.C32R
PAX4	paired box 4	ENSG00000106331	PAP54	26	38.5%	chr7	127038969	CCDS5797.1	c.-1T>NULL	p.IVS7-3-1SpliceAcceptor
PLDN	pallidin homolog (mouse)	ENSG00000104164	PAP54	75	14.7%	chr15	43685985	CCDS10126.1	c.500G>A	p.R167K
PALMD	palmdelphin	ENSG00000099260	PAP54	83	12.0%	chr1	99927752	CCDS758.1	c.1348GAG>N	p.NULL-1FsDel3bp
PDZD4	PDZ domain containing 4	ENSG00000067840	PAP54	29	44.8%	chrX	152722819	CCDS14732.1	c.1493G>A	p.G498D
PCNXL2	pecanex-like 2 (Drosophila)	ENSG00000135749	PAP54	43	27.9%	chr1	231404571	ENST00000324142	c.909A>NULL	p.NULL-1FsDel1bp
PER3	period homolog 3 (Drosophila)	ENSG00000049246	PAP54	592	34.6%	chr1	7810149	CCDS89.1	c.2549NULL>T	p.NULL-1FsIns1bp
PXDN	peroxidasin homolog (Drosophila)	ENSG00000130508	PAP54	354	15.0%	chr2	1631174	NM_012293	c.3385C>T	p.R1129C
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP54	41	39.0%	chr10	89643821	CCDS31238.1	c.139A>G	p.R47G
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP54	217	30.0%	chr10	89682884	CCDS31238.1	c.388C>G	p.R130G
PDE4A	phosphodiesterase 4A; cAMP-specific (phosphodiesterase E2 dunce homolog; Drosophila)	ENSG00000065989	PAP54	108	13.9%	chr19	10433638	CCDS12238.1	c.989G>T	p.G330V
PDE6A	phosphodiesterase 6A; cGMP-specific; rod; alpha	ENSG00000132915	PAP54	131	13.7%	chr5	149290873	CCDS4299.1	c.769C>T	p.R257X
PIKFYVE	phosphoinositide kinase; FYVE finger containing	ENSG00000115020	PAP54	140	32.9%	chr2	208898893	CCDS2382.1	c.3113G>A	p.R1038Q
PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP54	255	22.4%	chr3	180399570	CCDS43171.1	c.263G>A	p.R88Q

PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP54	99	40.4%	chr3	180434701	CCDS43171.1	c.3062A>G	p.Y1021C
PLD3	phospholipase D family; member 3	ENSG00000105223	PAP54	93	36.6%	chr19	45574384	CCDS33027.1	c.1048C>T	p.R350W
PGBD1	piggyBac transposable element derived 1	ENSG00000137338	PAP54	129	17.8%	chr6	28376787	CCDS4648.1	c.1177A>G	p.R393G
PGBD5	piggyBac transposable element derived 5	ENSG00000177614	PAP54	123	28.5%	chr1	228553380	CCDS1583.1	c.931C>T	p.R311W
PIWIL1	piwi-like 1 (Drosophila)	ENSG00000125207	PAP54	59	28.8%	chr12	129411703	CCDS9268.1	c.1691G>A	p.R564Q
PEAR1	platelet endothelial aggregation receptor 1	ENSG00000187800	PAP54	279	21.9%	chr1	155151107	CCDS30892.1	c.3007C>NULL	p.NULL-1FsDel1bp
PLEKHG4	pleckstrin homology domain containing; family G (with RhoGef domain) member 4	ENSG00000196155	PAP54	461	35.4%	chr16	65872361	CCDS32466.1	c.671G>A	p.S224N
PLEKHG5	pleckstrin homology domain containing; family G (with RhoGef domain) member 5	ENSG00000171680	PAP54	184	28.3%	chr1	6455256	CCDS41240.1	c.1229G>A	p.R410Q
PKHD1	polycystic kidney and hepatic disease 1 (autosomal recessive)	ENSG00000170927	PAP54	115	31.3%	chr6	51820627	CCDS4935.1	c.8012G>A	p.R2671Q
POLG2	polymerase (DNA directed); gamma 2; accessory subunit	ENSG00000136480	PAP54	403	15.9%	chr17	59923296	CCDS32706.1	c.253C>T	p.Q85X
POLR1D	polymerase (RNA) I polypeptide D; 16kDa	ENSG00000186184	PAP54	139	20.1%	chr13	27094146	CCDS9325.1	c.26G>T	p.R9I
KCTD16	potassium channel tetramerisation domain containing 16	ENSG00000183775	PAP54	88	11.4%	chr5	143833724	CCDS34260.1	c.1141A>NULL	p.NULL-1FsDel1bp
KCNK7	potassium channel; subfamily K; member 7	ENSG00000173338	PAP54	222	39.6%	chr11	65117431	CCDS8106.1	c.-1G>T	p.IVS2-1-1SpliceAcceptor
KCNK7	potassium channel; subfamily K; member 7	ENSG00000173338	PAP54	67	20.9%	chr11	65117615	CCDS31608.1	c.626C>T	p.S209L
PRDM14	PR domain containing 14	ENSG00000147596	PAP54	105	16.2%	chr8	71144446	CCDS6206.1	c.903C>NULL	p.NULL-1FsDel1bp
PRDM4	PR domain containing 4	ENSG00000110851	PAP54	519	39.1%	chr12	106669975	CCDS9115.1	c.473T>C	p.L158S
PRICKLE1	prickle homolog 1 (Drosophila)	ENSG00000139174	PAP54	197	28.4%	chr12	41144616	CCDS8742.1	c.2348AAG>N	p.NULL-1FsDel3bp
PRRG3	proline rich Gla (G-carboxyglutamic acid) 3 (transmembrane)	ENSG00000130032	PAP54	148	16.2%	chrX	150619887	CCDS14699.1	c.422G>A	p.S141N
PREPL	prolyl endopeptidase-like	ENSG00000138078	PAP54	59	23.7%	chr2	44404057	CCDS33190.1	c.-1T>NULL	p.IVS10-3-1SpliceAcceptor
PSMC2	proteasome (prosome; macropain) 26S subunit; ATPase; 2	ENSG00000161057	PAP54	88	39.8%	chr7	102795403	CCDS5731.1	c.1055C>T	p.T352I
PSME4	proteasome (prosome; macropain) activator subunit 4	ENSG00000068878	PAP54	141	12.1%	chr2	53967929	CCDS33197.1	c.4358G>A	p.R1453Q
PRKAA2	protein kinase; AMP-activated; alpha 2 catalytic subunit	ENSG00000162409	PAP54	236	14.0%	chr1	56945929	CCDS605.1	c.1614NULL>T	p.NULL-1FsIns1bp
PTPN5	protein tyrosine phosphatase; non-receptor type 5 (striatum-enriched)	ENSG00000110786	PAP54	159	40.9%	chr11	18707631	CCDS7845.1	c.1549C>T	p.R517W
PTPLA	protein tyrosine phosphatase-like (proline instead of catalytic arginine); member A	ENSG00000165996	PAP54	49	26.5%	chr10	17686055	CCDS7121.1	c.-1T>NULL	p.IVS1-3-1SpliceAcceptor
PCDHA2	protocadherin alpha 2	ENSG00000204969	PAP54	93	10.8%	chr5	140157022	CCDS34247.1	c.2289C>NULL	p.NULL-1FsDel1bp
PCDHB7	protocadherin beta 7	ENSG00000113212	PAP54	75	34.7%	chr5	140533930	CCDS4249.1	c.1330G>A	p.V444I
P2RY10	purinergic receptor P2Y; G-protein coupled; 10	ENSG00000078589	PAP54	219	11.0%	chrX	78103316	CCDS14442.1	c.643G>A	p.A215T
P2RY13	purinergic receptor P2Y; G-protein coupled; 13	ENSG00000181631	PAP54	39	28.2%	chr3	152528832	CCDS3158.1	c.1640A>NULL	p.NULL-1FsDel1bp
PYGO1	pygopus homolog 1 (Drosophila)	ENSG00000171016	PAP54	158	13.3%	chr15	53628488	CCDS10155.1	c.-1T>NULL	p.IVS1-3-1SpliceAcceptor
PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	ENSG00000131828	PAP54	26	42.3%	chrX	19273785	ENST00000379815	c.68CC>NULL	p.NULL-1FsDel2bp
RALGAPB	Ral GTPase activating protein; beta subunit (non-catalytic)	ENSG00000170471	PAP54	261	33.7%	chr20	36579647	CCDS13305.1	c.1136C>NULL	p.NULL-1FsDel1bp
RANBP3	RAN binding protein 3	ENSG00000031823	PAP54	84	29.8%	chr19	5882462	CCDS42478.1	c.646G>A	p.A216T
RINL	Ras and Rab interactor-like	ENSG00000187994	PAP54	54	18.5%	chr19	44052521	CCDS12522.1	c.902C>T	p.A301V

RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	ENSG00000173166	PAP54	72	13.9%	chr2	204013270	CCDS2359.1	c.2888C>T	p.T963M
RB1CC1	RB1-inducible coiled-coil 1	ENSG00000023287	PAP54	37	45.9%	chr8	53705644	CCDS34892.1	c.-1T>NULL	p.IVS18-3-1SpliceAcceptor
RPTOR	regulatory associated protein of MTOR; complex 1	ENSG00000141564	PAP54	244	38.1%	chr17	76511138	CCDS11773.1	c.2540C>T	p.P847L
RXFP2	relaxin/insulin-like family peptide receptor 2	ENSG00000133105	PAP54	92	28.3%	chr13	31274429	CCDS9342.1	c.2152NULL>A	p.NULL-1FsIns1bp
RXFP4	relaxin/insulin-like family peptide receptor 4	ENSG00000173080	PAP54	158	28.5%	chr1	154179178	CCDS1124.1	c.1054G>T	p.V352F
RLBP1	retinaldehyde binding protein 1	ENSG00000140522	PAP54	355	16.1%	chr15	87561451	CCDS32324.1	c.250G>A	p.V84M
RP1	retinitis pigmentosa 1 (autosomal dominant)	ENSG00000104237	PAP54	145	33.8%	chr8	55696347	CCDS6160.1	c.268C>T	p.H90Y
RXRB	retinoid X receptor; beta	ENSG00000204231	PAP54	269	13.4%	chr6	33272274	CCDS4768.1	c.908G>T	p.R303M
RBP3	retinol binding protein 3; interstitial	ENSG00000107618	PAP54	117	11.1%	chr10	48002068	CCDS7218.1	c.3587G>A	p.R1196H
RHBDL1	rhomboid; veinlet-like 1 (Drosophila)	ENSG00000103269	PAP54	100	15.0%	chr16	666685	CCDS10418.1	c.409C>T	p.R137C
RNF20	ring finger protein 20	ENSG00000155827	PAP54	44	29.5%	chr9	103354666	CCDS35084.1	c.1711C>T	p.R571X
RNF43	ring finger protein 43	ENSG00000108375	PAP54	172	54.7%	chr17	53790160	CCDS11607.1	c.3331G>NUL	p.NULL-1FsDel1bp
SLFN5	schlafen family member 5	ENSG00000166750	PAP54	72	27.8%	chr17	30609925	CCDS32619.1	c.103C>A	p.L35M
SECISBP2L	SECIS binding protein 2-like	ENSG00000138593	PAP54	141	15.6%	chr15	47096342	CCDS32234.1	c.1279T>A	p.L427I
SDCCAG1	serologically defined colon cancer antigen 1	ENSG00000165525	PAP54	83	13.3%	chr14	49338993	CCDS9694.1	c.2023G>A	p.V675I
SETD2	SET domain containing 2	ENSG00000181555	PAP54	153	14.4%	chr3	47118001	CCDS2749.1	c.3457G>T	p.V1153F
SETD5	SET domain containing 5	ENSG00000168137	PAP54	80	23.8%	chr3	9491132	NM_001080517	c.-1G>T	p.IVS18-1-1SpliceAcceptor
SETDB1	SET domain; bifurcated 1	ENSG00000143379	PAP54	212	33.5%	chr1	149184248	ENST00000368962	c.1180NULL>C	p.NULL-1FsIns1bp
SHROOM2	shroom family member 2	ENSG00000146950	PAP54	77	44.2%	chrX	9823762	CCDS14135.1	c.1814G>A	p.S605N
STAT4	signal transducer and activator of transcription 4	ENSG00000138378	PAP54	40	32.5%	chr2	191719731	CCDS2310.1	c.-1TT>NULL	p.IVS1-3-1SpliceAcceptor
SLAMF1	signaling lymphocytic activation molecule family member 1	ENSG00000117090	PAP54	141	14.2%	chr1	158856225	CCDS1207.1	c.902A>NULL	p.NULL-1FsDel1bp
SIN3B	SIN3 homolog B; transcription regulator (yeast)	ENSG00000127511	PAP54	130	16.9%	chr19	16847975	CCDS32946.1	c.2798C>T	p.A933V
SSBP2	single-stranded DNA binding protein 2	ENSG00000145687	PAP54	43	32.6%	chr5	80805348	CCDS4056.1	c.-1T>NULL	p.IVS7-3-1SpliceAcceptor
SIX5	SIX homeobox 5	ENSG00000177045	PAP54	127	40.9%	chr19	50963339	CCDS12673.1	c.604G>A	p.E202K
SGSM2	small G protein signaling modulator 2	ENSG00000141258	PAP54	120	15.0%	chr17	2223021	CCDS32526.1	c.1813C>T	p.R605W
SGSM3	small G protein signaling modulator 3	ENSG00000100359	PAP54	231	15.2%	chr22	39133400	CCDS14002.1	c.1406G>A	p.R469Q
SMCR7L	Smith-Magenis syndrome chromosome region; candidate 7-like	ENSG00000100335	PAP54	193	34.2%	chr22	38240121	CCDS13995.1	c.1239G>T	p.R413S
SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters); member 2	ENSG00000064651	PAP54	169	14.8%	chr5	127516383	CCDS4144.1	c.2350G>A	p.V784M
SLC2A11	solute carrier family 2 (facilitated glucose transporter); member 11	ENSG00000133460	PAP54	198	15.7%	chr22	22556083	ENST00000407566	c.260G>NULL	p.NULL-1FsDel1bp
SLC39A14	solute carrier family 39 (zinc transporter); member 14	ENSG00000104635	PAP54	203	14.8%	chr8	22318214	CCDS6030.1	c.46C>G	p.L16V
SLC43A1	solute carrier family 43; member 1	ENSG00000149150	PAP54	106	31.1%	chr11	57025217	CCDS7958.1	c.316G>A	p.V106M
SLC45A4	solute carrier family 45; member 4	ENSG00000022567	PAP54	309	35.9%	chr8	142297456	CCDS34948.1	c.2330G>NUL	p.NULL-1FsDel1bp
SLC8A1	solute carrier family 8 (sodium/calcium exchanger); member 1	ENSG00000183023	PAP54	127	16.5%	chr2	40509706	CCDS1806.1	c.1219A>G	p.S407G
SLC9A9	solute carrier family 9 (sodium/hydrogen exchanger); member 9	ENSG00000181804	PAP54	60	21.7%	chr3	145033756	CCDS33872.1	c.-1T>NULL	p.IVS1-3-1SpliceAcceptor

SNX1	sorting nexin 1	ENSG00000028528	PAP54	165	28.5%	chr15	62205354	CCDS32266.1	c.534CAAA>N	p.NULL-1FsDel4bp
SP2	Sp2 transcription factor	ENSG00000167182	PAP54	215	40.5%	chr17	43348948	CCDS11521.2	c.512C>T	p.P171L
SPTB	spectrin; beta; erythrocytic	ENSG00000070182	PAP54	192	33.9%	chr14	64285923	CCDS32099.1	c.6841C>T	p.Q2281X
SPAG9	sperm associated antigen 9	ENSG00000008294	PAP54	67	26.9%	chr17	46511976	CCDS11577.1	c.392T>G	p.L131R
SPATC1	spermatogenesis and centriole associated 1	ENSG00000186583	PAP54	246	21.1%	chr8	145166928	CCDS6413.1	c.69G>A	p.M23I
SPATS2L	spermatogenesis associated; serine-rich 2-like	ENSG00000196141	PAP54	147	34.0%	chr2	201050634	NM_001100423	c.1312A>G	p.N438D
SMPD2	sphingomyelin phosphodiesterase 2; neutral membrane (neutral sphingomyelinase)	ENSG00000135587	PAP54	224	10.7%	chr6	109871233	CCDS5075.1	c.800C>NULL	p.NULL-1FsDel1bp
SF3A2	splicing factor 3a; subunit 2; 66kDa	ENSG00000104897	PAP54	37	43.2%	chr19	2199142	CCDS12084.1	c.992C>A	p.P331H
SART3	squamous cell carcinoma antigen recognized by T cells 3	ENSG00000075856	PAP54	87	23.0%	chr12	107463181	CCDS9117.1	c.593G>C	p.G198A
ST8SIA5	ST8 alpha-N-acetyl-neuraminide alpha-2;8-sialyltransferase 5	ENSG00000101638	PAP54	167	17.4%	chr18	42514353	CCDS11930.1	c.781G>A	p.V261I
SMC5	structural maintenance of chromosomes 5	ENSG00000198887	PAP54	44	29.5%	chr9	72087288	CCDS6632.1	c.950G>A	p.R317H
SNED1	sushi; nidogen and EGF-like domains 1	ENSG00000162804	PAP54	213	34.3%	chr2	241661465	ENST00000401884	c.3929C>T	p.A1310V
TAF1L	TAF1 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 210kDa-like	ENSG00000122728	PAP54	753	18.5%	chr9	32620413	NM_153809	c.5165G>T	p.G1722V
TBC1D10C	TBC1 domain family; member 10C	ENSG00000175463	PAP54	160	58.1%	chr11	66933747	CCDS8162.1	c.1287NULL>T	p.NULL-1FsIns1bp
TBC1D4	TBC1 domain family; member 4	ENSG00000136111	PAP54	78	15.4%	chr13	74784934	CCDS41901.1	c.2324G>A	p.R775H
TIMD4	T-cell immunoglobulin and mucin domain containing 4	ENSG00000145850	PAP54	157	12.1%	chr5	156314309	CCDS4332.1	c.436NULL>T	p.NULL-1FsIns1bp
TTC29	tetratricopeptide repeat domain 29	ENSG00000137473	PAP54	33	48.5%	chr4	147848156	NM_031956	c.-1T>NULL	p.IVS9-3-1SpliceAcceptor
TRIP12	thyroid hormone receptor interactor 12	ENSG00000153827	PAP54	210	11.4%	chr2	230384157	CCDS33391.1	c.1918A>NULL	p.NULL-1FsDel1bp
TIGD7	tigger transposable element derived 7	ENSG00000140993	PAP54	203	11.3%	chr16	3290473	CCDS10500.1	c.1792A>NULL	p.NULL-1FsDel1bp
TOR1B	torsin family 1; member B (torsin B)	ENSG00000136816	PAP54	123	17.9%	chr9	131611594	CCDS6929.1	c.922G>A	p.A308T
TRERF1	transcriptional regulating factor 1	ENSG00000124496	PAP54	191	13.6%	chr6	42312084	CCDS4867.1	c.3109NULL>C	p.NULL-1FsIns3bp
TRRAP	transformation/transcription domain-associated protein	ENSG00000196367	PAP54	98	40.8%	chr7	98347738	CCDS5659.1	c.2165C>T	p.S722F
TBRG1	transforming growth factor beta regulator 1	ENSG00000154144	PAP54	116	12.1%	chr11	124000892	CCDS8448.1	c.21G>T	p.W7C
TRPM2	transient receptor potential cation channel; subfamily M; member 2	ENSG00000142185	PAP54	252	29.8%	chr21	44662359	CCDS13710.1	c.3268C>A	p.L1090M
TAPT1	transmembrane anterior posterior transformation 1	ENSG00000169762	PAP54	56	57.1%	chr4	15799079	NM_153365	c.-1T>NULL	p.IVS4-3-1SpliceAcceptor
TREM1	triggering receptor expressed on myeloid cells 1	ENSG00000124731	PAP54	387	13.7%	chr6	41358311	CCDS4854.1	c.206G>A	p.C69Y
TRIM17	tripartite motif-containing 17	ENSG00000162931	PAP54	118	39.0%	chr1	226669265	CCDS1571.1	c.132G>A	p.W44X
TRIM41	tripartite motif-containing 41	ENSG00000146063	PAP54	75	21.3%	chr5	180594034	CCDS4466.1	c.1546G>NUL	p.NULL-1FsDel1bp
TULP4	tubby like protein 4	ENSG00000130338	PAP54	108	24.1%	chr6	158820945	CCDS34561.1	c.1201C>NULL	p.NULL-1FsDel1bp
TNFRSF9	tumor necrosis factor receptor superfamily; member 9	ENSG00000049249	PAP54	232	10.3%	chr1	7903573	CCDS92.1	c.-1T>NULL	p.IVS6-3-1SpliceAcceptor
TPD52	tumor protein D52	ENSG00000076554	PAP54	112	13.4%	chr8	81126332	CCDS34912.1	c.592A>NULL	p.NULL-1FsDel1bp
TPCN2	two pore segment channel 2	ENSG00000162341	PAP54	77	27.3%	chr11	68594539	CCDS8189.1	c.895G>T	p.G299X
UBR5	ubiquitin protein ligase E3 component n-recognin 5	ENSG00000104517	PAP54	38	26.3%	chr8	103424028	CCDS34933.1	c.947G>A	p.R316H
USP28	ubiquitin specific peptidase 28	ENSG00000048028	PAP54	113	12.4%	chr11	113210239	CCDS31680.1	c.563G>T	p.R188I
UBE4B	ubiquitination factor E4B (UFD2 homolog; yeast)	ENSG00000130939	PAP54	185	38.9%	chr1	10088326	CCDS41245.1	c.746C>G	p.S249C

UBXN4	UBX domain protein 4	ENSG00000144224	PAP54	40	25.0%	chr2	136250288	CCDS42761.1	c.-1G>A	p.IVS9-1-1SpliceAcceptor
UHRF1BP1	UHRF1 binding protein 1	ENSG00000065060	PAP54	67	22.4%	chr6	34932656	CCDS43455.1	c.1403T>C	p.V468A
USH2A	Usher syndrome 2A (autosomal recessive; mild)	ENSG00000042781	PAP54	166	13.9%	chr1	214128435	CCDS31025.1	c.8807G>NUL	p.NULL-1FsDel1bp
VPS13C	vacuolar protein sorting 13 homolog C (S. cerevisiae)	ENSG00000129003	PAP54	50	32.0%	chr15	60103311	CCDS32257.1	c.539A>NULL	p.NULL-1FsDel1bp
WDFY1	WD repeat and FYVE domain containing 1	ENSG00000085449	PAP54	98	15.3%	chr2	224468499	CCDS33387.1	c.691A>G	p.R231G
WDHD1	WD repeat and HMG-box DNA binding protein 1	ENSG00000198554	PAP54	290	32.1%	chr14	54523718	CCDS9721.1	c.1664G>A	p.R555Q
WDR37	WD repeat domain 37	ENSG00000047056	PAP54	138	13.0%	chr10	1108109	CCDS7057.1	c.14G>A	p.S5N
WDR5	WD repeat domain 5	ENSG00000196363	PAP54	397	17.1%	chr9	136009419	CCDS6981.1	c.642C>NULL	p.NULL-1FsDel1bp
WDR55	WD repeat domain 55	ENSG00000120314	PAP54	158	15.2%	chr5	140029286	CCDS4235.1	c.1015A>NULI	p.NULL-1FsDel1bp
WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	ENSG00000015285	PAP54	87	11.5%	chrX	48429284	CCDS14303.1	c.469C>T	p.R157C
WWC3	WWC family member 3	ENSG00000047644	PAP54	116	37.9%	chrX	10066900	CCDS14136.1	c.3008G>A	p.R1003H
XPC	xeroderma pigmentosum; complementation group C	ENSG00000154767	PAP54	102	13.7%	chr3	14172873	ENST00000285021	c.1987A>T	p.I663F
XPC	xeroderma pigmentosum; complementation group C	ENSG00000154767	PAP54	108	15.7%	chr3	14172876	ENST00000285021	c.1984G>C	p.A662P
ZNRF1	zinc and ring finger 1	ENSG00000186187	PAP54	70	14.3%	chr16	73591263	CCDS10912.1	c.193G>NULL	p.NULL-1FsDel1bp
ZBTB4	zinc finger and BTB domain containing 4	ENSG00000174282	PAP54	168	33.9%	chr17	7307508	CCDS11107.1	c.1517C>T	p.S506L
ZBTB7C	zinc finger and BTB domain containing 7C	ENSG00000184828	PAP54	346	14.7%	chr18	43821083	CCDS32830.1	c.1601G>NUL	p.NULL-1FsDel1bp
ZC3H13	zinc finger CCCH-type containing 13	ENSG00000123200	PAP54	651	10.6%	chr13	45447904	CCDS9400.1	c.2537AG>NU	p.NULL-1FsDel2bp
ZFHX3	zinc finger homeobox 3	ENSG00000140836	PAP54	261	12.3%	chr16	71387490	CCDS10908.1	c.12050CT>NU	p.NULL-1FsDel2bp
ZFP106	zinc finger protein 106 homolog (mouse)	ENSG00000103994	PAP54	187	38.5%	chr15	40503516	CCDS32208.1	c.5156A>C	p.D1719A
ZNF205	zinc finger protein 205	ENSG00000122386	PAP54	56	32.1%	chr16	3110293	CCDS10494.2	c.1631G>C	p.G544A
ZNF280C	zinc finger protein 280C	ENSG00000056277	PAP54	91	18.7%	chrX	129198224	CCDS14622.1	c.734NULL>A	p.NULL-1FsIns1bp
ZFP36L2	zinc finger protein 36; C3H type-like 2	ENSG00000152518	PAP54	61	37.7%	chr2	43305764	CCDS1811.1	c.2116G>NUL	p.NULL-1FsDel1bp
ZFP36L2	zinc finger protein 36; C3H type-like 2	ENSG00000152518	PAP54	53	35.8%	chr2	43306127	CCDS1811.1	c.1753G>NUL	p.NULL-1FsDel1bp
ZFP37	zinc finger protein 37 homolog (mouse)	ENSG00000136866	PAP54	110	35.5%	chr9	114846237	CCDS6787.1	c.2025A>NULI	p.NULL-1FsDel1bp
ZNF391	zinc finger protein 391	ENSG00000124613	PAP54	145	13.1%	chr6	27476795	CCDS43429.1	c.667T>G	p.C223G
ZFP41	zinc finger protein 41 homolog (mouse)	ENSG00000181638	PAP54	262	13.0%	chr8	144403782	CCDS6397.1	c.394A>G	p.K132E
ZNF423	zinc finger protein 423	ENSG00000102935	PAP54	213	21.6%	chr16	48229879	CCDS32445.1	c.685C>T	p.R229C
ZKSCAN5	zinc finger with KRAB and SCAN domains 5	ENSG00000196652	PAP54	118	30.5%	chr7	98961834	CCDS5667.1	c.1235G>A	p.R412Q
ZDHHC5	zinc finger; DHHC-type containing 5	ENSG00000156599	PAP54	123	11.4%	chr11	57220061	CCDS7965.1	c.979C>T	p.R327X
ZFYVE21	zinc finger; FYVE domain containing 21	ENSG00000100711	PAP54	120	39.2%	chr14	103269097	CCDS9985.1	c.694C>T	p.R232W
ZSWIM5	zinc finger; SWIM-type containing 5	ENSG00000162415	PAP54	51	49.0%	chr1	45273956	CCDS41319.1	c.2282G>A	p.R761H
ZSWIM5	zinc finger; SWIM-type containing 5	ENSG00000162415	PAP54	127	24.4%	chr1	45326219	CCDS41319.1	c.873C>A	p.H291Q
OASL	2'-5'-oligoadenylate synthetase-like	ENSG00000135114	PAP55	46	26.1%	chr12	119949889	CCDS9211.1	c.772G>A	p.E258K
NT5C1B	5'-nucleotidase; cytosolic IB	ENSG00000185013	PAP55	134	29.1%	chr2	18631799	CCDS33150.1	c.242G>A	p.R81H
NT5E	5'-nucleotidase; ecto (CD73)	ENSG00000135318	PAP55	148	19.6%	chr6	86237753	CCDS5002.1	c.642A>C	p.K214N
AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	ENSG00000127914	PAP55	99	26.3%	chr7	91546693	CCDS5622.1	c.7310G>A	p.R2437H
AKAP10	A kinase (PRKA) anchor protein 10	ENSG00000108599	PAP55	182	28.0%	chr17	19802318	CCDS11214.1	c.478A>C	p.S160R
AKAP11	A kinase (PRKA) anchor protein 11	ENSG00000023516	PAP55	124	26.6%	chr13	41771781	CCDS9383.1	c.899C>T	p.S300L
ACP5	acid phosphatase 5; tartrate resistant	ENSG00000102575	PAP55	193	28.0%	chr19	11548638	CCDS12265.1	c.282C>A	p.F94L
ANP32D	acidic (leucine-rich) nuclear phosphoprotein 32 family; member D	ENSG00000139223	PAP55	35	45.7%	chr12	47152736	CCDS31788.1	c.22C>T	p.H8Y

ACTA1	actin; alpha 1; skeletal muscle	ENSG00000143632	PAP55	92	33.7%	chr1	227634120	CCDS1578.1	c.961G>A	p.A321T
ATF7IP	activating transcription factor 7 interacting protein	ENSG00000171681	PAP55	37	27.0%	chr12	14469537	CCDS8663.1	c.1421C>A	p.S474Y
ATF7IP	activating transcription factor 7 interacting protein	ENSG00000171681	PAP55	232	27.2%	chr12	14522523	CCDS8663.1	c.2947A>G	p.K983E
ADAM7	ADAM metallopeptidase domain 7	ENSG00000069206	PAP55	98	30.6%	chr8	24404273	CCDS6045.1	c.1338A>C	p.E446D
ADAMTSL1	ADAMTS-like 1	ENSG00000178031	PAP55	103	28.2%	chr9	18612388	ENST00000380570	c.622C>T	p.R208X
APPL2	adaptor protein; phosphotyrosine interaction; PH domain and leucine zipper containing 2	ENSG00000136044	PAP55	118	22.0%	chr12	104108029	CCDS9101.1	c.1276A>C	p.N426H
AP1G1	adaptor-related protein complex 1; gamma 1 subunit	ENSG00000166747	PAP55	42	28.6%	chr16	70324505	CCDS32480.1	c.2426A>C	p.D809A
AP1G2	adaptor-related protein complex 1; gamma 2 subunit	ENSG00000213983	PAP55	248	30.2%	chr14	23101458	CCDS9602.1	c.1507G>A	p.E503K
AP2B1	adaptor-related protein complex 2; beta 1 subunit	ENSG00000006125	PAP55	139	29.5%	chr17	30975706	CCDS32621.1	c.703C>T	p.R235W
ADD3	adducin 3 (gamma)	ENSG00000148700	PAP55	65	26.2%	chr10	111883348	CCDS7561.1	c.2103G>T	p.K701N
APC	adenomatous polyposis coli	ENSG00000134982	PAP55	219	31.1%	chr5	112202530	CCDS4107.1	c.3340C>T	p.R1114X
AHCYL1	adenosylhomocysteinase-like 1	ENSG00000168710	PAP55	159	25.8%	chr1	110353237	CCDS818.1	c.179G>A	p.R60Q
ADSS	adenylosuccinate synthase	ENSG00000035687	PAP55	148	32.4%	chr1	242650205	CCDS1624.1	c.680T>G	p.I227S
ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	ENSG00000066777	PAP55	107	25.2%	chr8	68366741	CCDS6199.1	c.811G>T	p.D271Y
ADRB2	adrenergic; beta-2-; receptor; surface	ENSG00000169252	PAP55	102	26.5%	chr5	148187614	CCDS4292.1	c.1027C>T	p.R343C
AFF3	AF4/FMR2 family; member 3	ENSG00000144218	PAP55	130	30.0%	chr2	99548516	CCDS33258.1	c.3059T>C	p.V1020A
AGMAT	agmatine ureohydrolase (agmatinase)	ENSG00000116771	PAP55	32	37.5%	chr1	15778087	CCDS160.1	c.574G>A	p.D192N
AHNAK	AHNAK nucleoprotein	ENSG00000124942	PAP55	108	24.1%	chr11	62044844	CCDS31584.1	c.13621G>A	p.V4541I
AKNAD1	AKNA domain containing 1	ENSG00000162641	PAP55	102	30.4%	chr1	109193120	CCDS791.2	c.1119G>T	p.K373N
AOX1	aldehyde oxidase 1	ENSG00000138356	PAP55	37	27.0%	chr2	201211199	CCDS33360.1	c.2497C>T	p.R833C
AKR1E2	aldo-keto reductase family 1; member E2	ENSG00000165568	PAP55	139	27.3%	chr10	4874623	CCDS31134.1	c.764G>A	p.R255Q
ALPK1	alpha-kinase 1	ENSG00000073331	PAP55	189	28.6%	chr4	113572274	CCDS3697.1	c.2122A>C	p.N708H
ALPK2	alpha-kinase 2	ENSG00000198796	PAP55	64	42.2%	chr18	54398661	CCDS11966.2	c.327G>T	p.E109D
ALMS1	Alstrom syndrome 1	ENSG00000116127	PAP55	193	31.1%	chr2	73530953	CCDS42697.1	c.3788A>C	p.K1263T
AMELX	amelogenin; X-linked	ENSG00000125363	PAP55	311	14.5%	chrX	11226923	CCDS14145.1	c.521C>T	p.P174L
ALAS2	aminolevulinate; delta-; synthase 2	ENSG00000158578	PAP55	81	29.6%	chrX	55056653	CCDS14366.1	c.1591G>T	p.D531Y
ANGEL1	angel homolog 1 (Drosophila)	ENSG00000013523	PAP55	197	25.9%	chr14	76345501	CCDS9852.1	c.303G>T	p.E101D
AAMP	angio-associated; migratory cell protein	ENSG00000127837	PAP55	586	30.2%	chr2	218842438	CCDS33378.1	c.185A>G	p.E62G
AGTR1	angiotensin II receptor; type 1	ENSG00000144891	PAP55	78	33.3%	chr3	149942193	CCDS3137.1	c.681A>C	p.E227D
ANK1	ankyrin 1; erythrocytic	ENSG00000029534	PAP55	97	29.9%	chr8	41699868	CCDS6119.1	c.841C>T	p.R281X
ANK2	ankyrin 2; neuronal	ENSG00000145362	PAP55	186	26.3%	chr4	114496610	CCDS3702.1	c.7387T>G	p.S2463A
ANK3	ankyrin 3; node of Ranvier (ankyrin G)	ENSG00000151150	PAP55	275	27.6%	chr10	61499753	CCDS7258.1	c.10892T>G	p.F3631C
ANKAR	ankyrin and armadillo repeat containing	ENSG00000151687	PAP55	33	33.3%	chr2	190317757	CCDS33351.1	c.3842G>T	p.R1281I
ANKRD26	ankyrin repeat domain 26	ENSG00000107890	PAP55	155	34.2%	chr10	27364300	CCDS41499.1	c.3085G>T	p.E1029X
ANKRD26	ankyrin repeat domain 26	ENSG00000107890	PAP55	44	38.6%	chr10	27364565	CCDS41499.1	c.2820G>T	p.K940N
ANO3	anoctamin 3	ENSG00000134343	PAP55	37	32.4%	chr11	26520139	CCDS31447.1	c.1102C>T	p.R368C
ANO5	anoctamin 5	ENSG00000171714	PAP55	61	24.6%	chr11	22204118	CCDS31444.1	c.307G>T	p.E103X
MKI67	antigen identified by monoclonal antibody Ki-67	ENSG00000148773	PAP55	194	26.3%	chr10	129795761	CCDS7659.1	c.4333G>A	p.A1445T
APOBEC2	apolipoprotein B mRNA editing enzyme; catalytic polypeptide-like 2	ENSG00000124701	PAP55	238	26.5%	chr6	41137281	CCDS4848.1	c.368T>C	p.V123A
API5	apoptosis inhibitor 5	ENSG00000166181	PAP55	77	37.7%	chr11	43308137	CCDS31465.1	c.1174C>T	p.R392C
ACIN1	apoptotic chromatin condensation inducer 1	ENSG00000100813	PAP55	76	25.0%	chr14	22602100	CCDS9587.1	c.2935C>T	p.R979X
APAF1	apoptotic peptidase activating factor 1	ENSG00000120868	PAP55	59	16.9%	chr12	97577115	CCDS9069.1	c.573C>A	p.D191E
AQP4	aquaporin 4	ENSG00000171885	PAP55	299	30.4%	chr18	22690364	CCDS11889.1	c.781C>T	p.R261C
ARCN1	archain 1	ENSG00000095139	PAP55	82	26.8%	chr11	117966387	CCDS8400.1	c.940C>T	p.R314C
ARAP2	ArfGAP with RhoGAP domain; ankyrin repeat and PH domain 2	ENSG00000047365	PAP55	75	24.0%	chr4	35811333	CCDS3441.1	c.3337A>G	p.T1113A
RARS2	arginyl-tRNA synthetase 2; mitochondrial	ENSG00000146282	PAP55	117	35.9%	chr6	88321908	CCDS5011.1	c.332A>T	p.K111I
ARMCX5	armadillo repeat containing; X-linked 5	ENSG00000125962	PAP55	149	43.0%	chrX	101744023	CCDS14500.1	c.298C>T	p.R100C
ACTR1A	ARP1 actin-related protein 1 homolog A; centractin alpha (yeast)	ENSG00000138107	PAP55	116	31.0%	chr10	104238863	CCDS7536.1	c.136C>T	p.R46C
ALG14	asparagine-linked glycosylation 14 homolog (S. cerevisiae)	ENSG00000172339	PAP55	135	27.4%	chr1	95221245	CCDS752.1	c.626C>T	p.S209L

AHDC1	AT hook; DNA binding motif; containing 1	ENSG00000126705	PAP55	30	36.7%	chr1	27747915	CCDS30652.1	c.3299G>A	p.R1100Q
ARID2	AT rich interactive domain 2 (ARID; RFX-like)	ENSG00000189079	PAP55	83	24.1%	chr12	44528977	CCDS31783.1	c.1672C>T	p.R558C
ATG4C	ATG4 autophagy related 4 homolog C (S. cerevisiae)	ENSG00000125703	PAP55	50	36.0%	chr1	63079763	CCDS623.1	c.1166G>A	p.R389Q
AGBL2	ATP/GTP binding protein-like 2	ENSG00000165923	PAP55	61	23.0%	chr11	47664155	CCDS7944.1	c.1654C>A	p.L552M
AGBL5	ATP/GTP binding protein-like 5	ENSG00000084693	PAP55	53	37.7%	chr2	27129542	CCDS1732.3	c.212A>G	p.N71S
ATP13A3	ATPase type 13A3	ENSG00000133657	PAP55	61	37.7%	chr3	195646758	CCDS43187.1	c.1544G>A	p.R515Q
ATP8B1	ATPase; aminophospholipid transporter; class I; type 8B; member 1	ENSG00000081923	PAP55	102	32.4%	chr18	53489738	CCDS11965.1	c.1892G>A	p.R631Q
ATP2B3	ATPase; Ca++ transporting; plasma membrane 3	ENSG00000067842	PAP55	88	25.0%	chrX	152461773	CCDS35440.1	c.869C>T	p.T290M
ATP8B4	ATPase; class I; type 8B; member 4	ENSG00000104043	PAP55	105	28.6%	chr15	48076233	CCDS32238.1	c.522A>C	p.K174N
ATP10A	ATPase; class V; type 10A	ENSG00000206190	PAP55	101	24.8%	chr15	23577390	CCDS32178.1	c.523G>A	p.E175K
ATP6V0B	ATPase; H+ transporting; lysosomal 21kDa; V0 subunit b	ENSG00000117410	PAP55	160	35.6%	chr1	44215464	CCDS505.1	c.580G>A	p.A194T
ATP6V1H	ATPase; H+ transporting; lysosomal 50/57kDa; V1 subunit H	ENSG00000047249	PAP55	45	33.3%	chr8	54847154	CCDS6153.1	c.997G>A	p.E333K
ABCA4	ATP-binding cassette; sub-family A (ABC1); member 4	ENSG00000198691	PAP55	99	27.3%	chr1	94341274	CCDS747.1	c.455G>A	p.R152Q
ABCA5	ATP-binding cassette; sub-family A (ABC1); member 5	ENSG00000154265	PAP55	112	25.0%	chr17	64810580	CCDS11685.1	c.993A>C	p.E331D
ABCB4	ATP-binding cassette; sub-family B (MDR/TAP); member 4	ENSG00000005471	PAP55	64	28.1%	chr7	86920288	CCDS5606.1	c.444A>C	p.K148N
ABCB5	ATP-binding cassette; sub-family B (MDR/TAP); member 5	ENSG00000004846	PAP55	113	31.0%	chr7	20649436	NM_001163941	c.419G>A	p.R140Q
ABCC9	ATP-binding cassette; sub-family C (CFTR/MRP); member 9	ENSG00000069431	PAP55	51	39.2%	chr12	21960039	CCDS8693.1	c.646C>T	p.L216F
ABCD3	ATP-binding cassette; sub-family D (ALD); member 3	ENSG00000117528	PAP55	91	29.7%	chr1	94737726	CCDS749.1	c.1708G>A	p.V570I
ABCG4	ATP-binding cassette; sub-family G (WHITE); member 4	ENSG00000172350	PAP55	132	32.6%	chr11	118536952	CCDS8415.1	c.1867T>G	p.L623V
ATRN	attractin	ENSG00000088812	PAP55	70	25.7%	chr20	3491087	CCDS13053.1	c.1612G>T	p.D538Y
BCS1L	BCS1-like (yeast)	ENSG00000074582	PAP55	117	21.4%	chr2	219234893	CCDS2419.1	c.628G>A	p.D210N
BEND6	BEN domain containing 6	ENSG00000151917	PAP55	40	25.0%	chr6	56990089	CCDS43476.1	c.645A>C	p.K215N
B3GALTL	beta 1;3-galactosyltransferase-like	ENSG00000187676	PAP55	383	28.2%	chr13	30801792	CCDS9341.1	c.1484G>A	p.R495Q
BCO2	beta-carotene oxygenase 2	ENSG00000197580	PAP55	61	23.0%	chr11	111575762	CCDS8358.2	c.-1T>C	p.IVS6+2-1SpliceDonor
CRYBG3	beta-gamma crystallin domain containing 3	ENSG00000080200	PAP55	65	24.6%	chr3	99094511	CCDS43113.1	c.1714C>T	p.R572C
BOD1L	biorientation of chromosomes in cell division 1-like	ENSG00000038219	PAP55	91	28.6%	chr4	13221748	CCDS3411.2	c.1399C>T	p.R467W
BBX	bobby sox homolog (Drosophila)	ENSG00000114439	PAP55	51	25.5%	chr3	108975090	CCDS2950.1	c.1832C>T	p.S611F
BEX5	brain expressed; X-linked 5	ENSG00000184515	PAP55	350	26.6%	chrX	101295830	CCDS35350.1	c.64G>A	p.A22T
BRCA1	breast cancer 1; early onset	ENSG00000012048	PAP55	100	25.0%	chr17	38499213	CCDS11453.1	c.1861C>A	p.H621N
BRCA2	breast cancer 2; early onset	ENSG00000139618	PAP55	107	28.0%	chr13	31810163	CCDS9344.1	c.3671G>T	p.G1224V
BAZ1B	bromodomain adjacent to zinc finger domain; 1B	ENSG00000009954	PAP55	121	41.3%	chr7	72530372	CCDS5549.1	c.1355G>A	p.R452Q
BRPF3	bromodomain and PHD finger containing; 3	ENSG00000096070	PAP55	106	25.5%	chr6	36276403	CCDS34437.1	c.326G>A	p.G109D
BRWD3	bromodomain and WD repeat domain containing 3	ENSG00000165288	PAP55	133	35.3%	chrX	79819384	CCDS14447.1	c.4789G>T	p.E1597X
BRWD3	bromodomain and WD repeat domain containing 3	ENSG00000165288	PAP55	93	28.0%	chrX	79832132	CCDS14447.1	c.3718C>T	p.R1240X
BPTF	bromodomain PHD finger transcription factor	ENSG00000171634	PAP55	138	33.3%	chr17	63280665	CCDS11673.1	c.761G>A	p.R254Q
BTBD12	BTB (POZ) domain containing 12	ENSG00000188827	PAP55	120	34.2%	chr16	3587686	CCDS10506.2	c.1378C>T	p.R460C
BACH1	BTB and CNC homology 1; basic leucine zipper transcription factor 1	ENSG00000156273	PAP55	198	30.3%	chr21	29620857	CCDS13585.1	c.841G>A	p.E281K
BACH2	BTB and CNC homology 1; basic leucine zipper transcription factor 2	ENSG00000112182	PAP55	239	27.2%	chr6	90717206	CCDS5026.1	c.1340C>A	p.S447Y
BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	ENSG00000156970	PAP55	56	26.8%	chr15	38276225	CCDS10053.1	c.1246C>T	p.R416W
C1GALT1C1	C1GALT1-specific chaperone 1	ENSG00000171155	PAP55	249	26.1%	chrX	119644144	CCDS14602.1	c.906T>G	p.I302M
CDH5	cadherin 5; type 2 (vascular endothelium)	ENSG00000179776	PAP55	113	24.8%	chr16	64992283	CCDS10804.1	c.1700G>A	p.G567D
CALB2	calbindin 2	ENSG00000172137	PAP55	105	25.7%	chr16	69981219	CCDS10899.1	c.766C>T	p.L256F
CACNG1	calcium channel; voltage-dependent; gamma subunit 1	ENSG00000108878	PAP55	78	19.2%	chr17	62480631	CCDS11668.1	c.287A>G	p.E96G
CAMK1D	calcium/calmodulin-dependent protein kinase ID	ENSG00000183049	PAP55	209	29.7%	chr10	12873219	CCDS7091.1	c.622G>A	p.G208R
CAMSAP1L1	calmodulin regulated spectrin-associated protein 1-like 1	ENSG00000118200	PAP55	228	22.8%	chr1	198975700	CCDS1404.1	c.122C>T	p.A41V
CAPN5	calpain 5	ENSG00000149260	PAP55	333	30.9%	chr11	76510632	CCDS8248.1	c.1492C>A	p.L498M
CAPNS1	calpain; small subunit 1	ENSG00000126247	PAP55	185	25.9%	chr19	41325847	CCDS12489.1	c.433C>T	p.R145C
CASC5	cancer susceptibility candidate 5	ENSG00000137812	PAP55	44	25.0%	chr15	38700463	CCDS42023.1	c.787G>T	p.E263X
CLIP1	CAP-GLY domain containing linker protein 1	ENSG00000130779	PAP55	160	29.4%	chr12	121391422	CCDS9232.1	c.2249A>C	p.N750T

CHST15	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15	ENSG00000182022	PAP55	55	21.8%	chr10	125794245	CCDS7638.1	c.727G>A	p.A243T
CHST6	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	ENSG00000183196	PAP55	79	25.3%	chr16	74071035	CCDS10918.1	c.193G>A	p.D65N
CPXM1	carboxypeptidase X (M14 family); member 1	ENSG00000088882	PAP55	143	32.9%	chr20	2726919	CCDS13033.1	c.469G>A	p.D157N
CPXM2	carboxypeptidase X (M14 family); member 2	ENSG00000121898	PAP55	126	25.4%	chr10	125511610	CCDS7637.1	c.1545C>G	p.N515K
CPVL	carboxypeptidase; vitellogenic-like	ENSG00000106066	PAP55	100	20.0%	chr7	29036845	CCDS5419.1	c.1193G>A	p.R398H
CEACAM21	carcinoembryonic antigen-related cell adhesion molecule 21	ENSG00000007129	PAP55	76	30.3%	chr19	46783643	NM_001098506	c.805G>A	p.D269N
CNDP1	carnosine dipeptidase 1 (metallopeptidase M20 family)	ENSG00000150656	PAP55	104	30.8%	chr18	70389413	CCDS12007.1	c.769G>T	p.D257Y
CASS4	Cas scaffolding protein family member 4	ENSG00000087589	PAP55	98	24.5%	chr20	54461102	CCDS33492.1	c.1463A>C	p.E488A
CASP4	caspase 4; apoptosis-related cysteine peptidase	ENSG00000196954	PAP55	127	27.6%	chr11	104325582	CCDS8327.1	c.679G>A	p.D227N
CTCF	CCCTC-binding factor (zinc finger protein)	ENSG00000102974	PAP55	35	28.6%	chr16	66208211	CCDS10841.1	c.1015C>T	p.R339W
CNOT1	CCR4-NOT transcription complex; subunit 1	ENSG00000125107	PAP55	84	20.2%	chr16	57128599	CCDS10799.1	c.5441G>A	p.R1814Q
CNOT10	CCR4-NOT transcription complex; subunit 10	ENSG00000182973	PAP55	76	22.4%	chr3	32780968	CCDS2655.1	c.1858A>C	p.N620H
CD163	CD163 molecule	ENSG00000177575	PAP55	176	31.3%	chr12	7530445	CCDS8578.1	c.2375A>G	p.E792G
CD1A	CD1a molecule	ENSG00000158477	PAP55	37	35.1%	chr1	156493346	CCDS1174.1	c.751G>A	p.D251N
CD70	CD70 molecule	ENSG00000125726	PAP55	125	29.6%	chr19	6537275	CCDS12170.1	c.338C>T	p.A113V
CD79B	CD79b molecule; immunoglobulin-associated beta	ENSG00000007312	PAP55	184	35.9%	chr17	59361292	CCDS42372.1	c.307G>A	p.E103K
CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	ENSG00000143776	PAP55	84	33.3%	chr1	225283485	CCDS1558.1	c.3823C>T	p.R1275C
ARHGEF9	Cdc42 guanine nucleotide exchange factor (GEF) 9	ENSG00000131089	PAP55	136	32.4%	chrX	62861226	CCDS35315.1	c.100G>A	p.V34I
CDON	Cdon homolog (mouse)	ENSG00000064309	PAP55	41	29.3%	chr11	125393518	CCDS8468.1	c.557A>C	p.K186T
CDC37L1	cell division cycle 37 homolog (S. cerevisiae)-like 1	ENSG00000106993	PAP55	34	29.4%	chr9	4675150	CCDS6454.1	c.406T>C	p.F136L
CCAR1	cell division cycle and apoptosis regulator 1	ENSG00000060339	PAP55	53	22.6%	chr10	70179396	CCDS7282.1	c.1066C>T	p.R356X
CDCA8	cell division cycle associated 8	ENSG00000134690	PAP55	94	27.7%	chr1	37945243	CCDS424.1	c.718C>T	p.R240X
CENPM	centromere protein M	ENSG00000100162	PAP55	107	22.4%	chr22	40671222	CCDS14025.1	c.263T>C	p.V88A
CEP164	centrosomal protein 164kDa	ENSG00000110274	PAP55	48	25.0%	chr11	116770847	CCDS31683.1	c.2762A>G	p.E921G
CSPP1	centrosome and spindle pole associated protein 1	ENSG00000104218	PAP55	59	32.2%	chr8	68233308	CCDS43744.1	c.2299C>T	p.R767W
CDNF	cerebral dopamine neurotrophic factor	ENSG00000185267	PAP55	88	33.0%	chr10	14919882	CCDS31148.1	c.70A>G	p.T24A
CCT6B	chaperonin containing TCP1; subunit 6B (zeta 2)	ENSG00000132141	PAP55	45	33.3%	chr17	30305634	CCDS32617.1	c.434G>T	p.R145I
C1orf111	chromosome 1 open reading frame 111	ENSG00000171722	PAP55	117	32.5%	chr1	160610829	CCDS1238.1	c.419C>T	p.S140L
C1orf175	chromosome 1 open reading frame 175	ENSG00000184313	PAP55	124	29.8%	chr1	54944763	CCDS41342.1	c.3623G>A	p.R1208Q
C1orf175	chromosome 1 open reading frame 175	ENSG00000184313	PAP55	117	28.2%	chr1	54948392	CCDS41342.1	c.3907C>T	p.R1303W
C1orf26	chromosome 1 open reading frame 26	ENSG00000116668	PAP55	65	24.6%	chr1	183438475	CCDS1367.1	c.1590G>T	p.L530F
C10orf111	chromosome 10 open reading frame 111	ENSG00000176236	PAP55	196	24.5%	chr10	15178645	CCDS7107.1	c.185G>A	p.G62D
C10orf18	chromosome 10 open reading frame 18	ENSG00000108021	PAP55	75	34.7%	chr10	5802639	CCDS41485.1	c.-1T>C	p.IVS1+2-1SpliceDonor
C10orf27	chromosome 10 open reading frame 27	ENSG00000166220	PAP55	69	26.1%	chr10	72204977	CCDS7308.1	c.746T>C	p.F249S
C12orf4	chromosome 12 open reading frame 4	ENSG00000047621	PAP55	56	28.6%	chr12	4470613	CCDS8528.1	c.1489T>C	p.C497R
C13orf27	chromosome 13 open reading frame 27	ENSG00000151287	PAP55	135	24.4%	chr13	102216817	CCDS9503.1	c.496G>T	p.E166X
C14orf145	chromosome 14 open reading frame 145	ENSG00000100629	PAP55	82	12.2%	chr14	80321575	CCDS32130.1	c.1628G>A	p.R543Q
C14orf28	chromosome 14 open reading frame 28	ENSG00000179476	PAP55	135	38.5%	chr14	44439446	CCDS32069.1	c.58C>T	p.R20X
C15orf55	chromosome 15 open reading frame 55	ENSG00000184507	PAP55	84	32.1%	chr15	32434574	CCDS32190.1	c.1339G>A	p.D447N
C17orf104	chromosome 17 open reading frame 104	ENSG00000180336	PAP55	303	25.7%	chr17	40100417	NM_001145080	c.1612G>T	p.E538X
C18orf8	chromosome 18 open reading frame 8	ENSG00000141452	PAP55	29	48.3%	chr18	19338370	CCDS32803.1	c.140T>C	p.V47A
C2orf16	chromosome 2 open reading frame 16	ENSG00000221843	PAP55	185	35.7%	chr2	27657411	CCDS42666.1	c.4468T>G	p.F1490V
C2orf63	chromosome 2 open reading frame 63	ENSG00000162994	PAP55	231	29.9%	chr2	55258329	CCDS33201.1	c.1477T>G	p.F493V
C20orf186	chromosome 20 open reading frame 186	ENSG00000186191	PAP55	121	23.1%	chr20	31134862	CCDS13213.1	c.81C>A	p.F27L
C20orf94	chromosome 20 open reading frame 94	ENSG00000149346	PAP55	61	19.7%	chr20	10551348	CCDS33439.1	c.548C>T	p.S183L
C4orf39	chromosome 4 open reading frame 39	ENSG00000221891	PAP55	81	27.2%	chr4	166098004	CCDS3807.1	c.380G>T	p.R127I
C5orf42	chromosome 5 open reading frame 42	ENSG00000197603	PAP55	117	29.1%	chr5	37204930	CCDS34146.1	c.3593A>G	p.D1198G
C5orf42	chromosome 5 open reading frame 42	ENSG00000197603	PAP55	71	21.1%	chr5	37218714	CCDS34146.1	c.1969C>T	p.R657C
C6orf136	chromosome 6 open reading frame 136	ENSG00000204564	PAP55	153	23.5%	chr6	30728462	CCDS43443.1	c.823C>T	p.R275C
C6orf167	chromosome 6 open reading frame 167	ENSG00000146263	PAP55	71	35.2%	chr6	97835852	CCDS5039.1	c.272A>T	p.E91V
C6orf170	chromosome 6 open reading frame 170	ENSG00000146350	PAP55	93	30.1%	chr6	121680510	CCDS43501.1	c.325G>T	p.E109X
C6orf174	chromosome 6 open reading frame 174	ENSG00000189367	PAP55	128	18.0%	chr6	127813070	CCDS34531.1	c.256G>A	p.D86N

C6orf225	chromosome 6 open reading frame 225	ENSG00000203778	PAP55	76	25.0%	chr6	112528643	CCDS34513.1	c.203A>C	p.K68T
C7orf42	chromosome 7 open reading frame 42	ENSG00000106609	PAP55	143	31.5%	chr7	66047485	CCDS5536.1	c.247A>C	p.T83P
C7orf44	chromosome 7 open reading frame 44	ENSG00000106603	PAP55	83	28.9%	chr7	43651410	CCDS5471.1	c.229G>A	p.D77N
C7orf58	chromosome 7 open reading frame 58	ENSG00000106034	PAP55	70	17.1%	chr7	120568205	CCDS34739.1	c.1788T>G	p.Y596X
C9orf56	chromosome 9 open reading frame 56	ENSG00000182981	PAP55	444	28.8%	chr9	125068278	ENST00000328281	c.92C>T	p.A31V
C9orf79	chromosome 9 open reading frame 79	ENSG00000177992	PAP55	104	25.0%	chr9	89691921	CCDS6676.1	c.2699A>C	p.Q900P
CXorf22	chromosome X open reading frame 22	ENSG00000165164	PAP55	52	34.6%	chrX	35898912	CCDS14237.2	c.1921T>C	p.Y641H
CXorf26	chromosome X open reading frame 26	ENSG00000102390	PAP55	120	34.2%	chrX	75309874	CCDS14432.1	c.83C>T	p.S28L
CXorf57	chromosome X open reading frame 57	ENSG00000147231	PAP55	89	27.0%	chrX	105742355	CCDS14519.1	c.389G>T	p.R130I
CGN	cingulin	ENSG00000143375	PAP55	173	30.6%	chr1	149759516	CCDS999.1	c.977G>A	p.S326N
CLSPN	claspin homolog (Xenopus laevis)	ENSG00000092853	PAP55	94	31.9%	chr1	35999329	CCDS396.1	c.959G>A	p.R320H
CLPX	ClpX caseinolytic peptidase X homolog (E. coli)	ENSG00000166855	PAP55	142	35.2%	chr15	63235244	CCDS10202.1	c.1150T>G	p.L384V
CNKSR3	CNKSR family member 3	ENSG00000153721	PAP55	115	27.8%	chr6	154773838	CCDS5246.1	c.1201G>A	p.D401N
COBLL1	COBL-like 1	ENSG00000082438	PAP55	123	26.8%	chr2	165260443	CCDS2223.2	c.1819G>T	p.E607X
CCDC102B	coiled-coil domain containing 102B	ENSG00000150636	PAP55	61	18.0%	chr18	64657127	CCDS11996.2	c.811T>G	p.L271V
CCDC125	coiled-coil domain containing 125	ENSG00000183323	PAP55	97	26.8%	chr5	68639551	CCDS4000.1	c.514A>C	p.N172H
CCDC151	coiled-coil domain containing 151	ENSG00000198003	PAP55	179	27.4%	chr19	11398327	CCDS42501.1	c.779A>T	p.H260L
CCDC157	coiled-coil domain containing 157	ENSG00000187860	PAP55	37	32.4%	chr22	29099605	CCDS33632.1	c.1202G>A	p.R401Q
CCDC158	coiled-coil domain containing 158	ENSG00000163749	PAP55	39	35.9%	chr4	77519535	CCDS43242.1	c.961G>A	p.D321N
CCDC30	coiled-coil domain containing 30	ENSG00000186409	PAP55	73	30.1%	chr1	42892202	CCDS30690.1	c.2268G>T	p.Q756H
CCDC47	coiled-coil domain containing 47	ENSG00000108588	PAP55	97	27.8%	chr17	59178009	CCDS11643.1	c.1416A>C	p.Q472H
CCDC81	coiled-coil domain containing 81	ENSG00000149201	PAP55	35	34.3%	chr11	85796851	CCDS8276.1	c.734G>A	p.R245Q
CCDC88A	coiled-coil domain containing 88A	ENSG00000115355	PAP55	89	23.6%	chr2	55393150	CCDS33203.1	c.4003A>T	p.M1335L
COL20A1	collagen; type XX; alpha 1	ENSG00000101203	PAP55	98	34.7%	chr20	61412238	ENST00000326996	c.1345T>A	p.Y449N
COL24A1	collagen; type XXIV; alpha 1	ENSG00000171502	PAP55	61	23.0%	chr1	86208524	CCDS41353.1	c.2437G>A	p.G813R
CSF1R	colony stimulating factor 1 receptor	ENSG00000182578	PAP55	69	24.6%	chr5	149420725	CCDS4302.1	c.1862C>T	p.T621M
CSF3R	colony stimulating factor 3 receptor (granulocyte)	ENSG00000119535	PAP55	73	26.0%	chr1	36710298	CCDS414.1	c.1027C>T	p.R343W
COMMD8	COMM domain containing 8	ENSG00000169019	PAP55	53	30.2%	chr4	47153404	CCDS3475.1	c.322G>A	p.E108K
CR2	complement component (3d/Epstein Barr virus) receptor 2	ENSG00000117322	PAP55	38	34.2%	chr1	205709962	CCDS31007.1	c.1117G>A	p.D373N
C8A	complement component 8; alpha polypeptide	ENSG00000157131	PAP55	153	28.1%	chr1	57114418	CCDS606.1	c.412G>A	p.E138K
CFP	complement factor properdin	ENSG00000126759	PAP55	157	29.9%	chrX	47371591	CCDS14282.1	c.659G>A	p.R220Q
COG3	component of oligomeric golgi complex 3	ENSG00000136152	PAP55	24	45.8%	chr13	44975383	CCDS9398.1	c.1492A>C	p.I498L
CNIH3	cornichon homolog 3 (Drosophila)	ENSG00000143786	PAP55	53	41.5%	chr1	222984828	CCDS1544.1	c.240T>G	p.I80M
COX18	COX18 cytochrome c oxidase assembly homolog (S. cerevisiae)	ENSG00000163626	PAP55	32	43.8%	chr4	74153924	CCDS3554.1	c.307G>A	p.A103T
ROS1	c-ros oncogene 1 ; receptor tyrosine kinase	ENSG00000047936	PAP55	167	29.9%	chr6	117749188	CCDS5116.1	c.5704G>A	p.E1902K
CHTF8	CTF8; chromosome transmission fidelity factor 8 homolog (S. cerevisiae)	ENSG00000168802	PAP55	70	30.0%	chr16	67710694	ENST00000306585	c.1139C>T	p.S380L
CTTNBP2NL	CTTNBP2 N-terminal like	ENSG00000143079	PAP55	210	30.0%	chr1	112801024	CCDS845.1	c.1387C>T	p.R463C
CSMD2	CUB and Sushi multiple domains 2	ENSG00000121904	PAP55	187	27.8%	chr1	33839082	CCDS380.1	c.6832A>G	p.T2278A
CSMD2	CUB and Sushi multiple domains 2	ENSG00000121904	PAP55	31	35.5%	chr1	34043063	ENST00000338325	c.141A>G	p.I47M
CSMD3	CUB and Sushi multiple domains 3	ENSG00000164796	PAP55	88	38.6%	chr8	113654980	CCDS6315.1	c.3968C>A	p.T1323N
CUL4B	cullin 4B	ENSG00000158290	PAP55	137	26.3%	chrX	119562396	CCDS35379.1	c.1105C>T	p.R369X
CNGA2	cyclic nucleotide gated channel alpha 2	ENSG00000183862	PAP55	125	23.2%	chrX	150663291	CCDS14701.1	c.1660G>A	p.D554N
CNNM2	cyclin M2	ENSG00000148842	PAP55	253	29.6%	chr10	104669835	CCDS7543.1	c.1608A>C	p.E536D
CYLD	cylindromatosis (turban tumor syndrome)	ENSG00000083799	PAP55	81	29.6%	chr16	49385708	CCDS42164.1	c.2545G>A	p.G849S
CRISPLD1	cysteine-rich secretory protein LCCL domain containing 1	ENSG00000121005	PAP55	51	29.4%	chr8	76092137	CCDS6219.1	c.1024C>A	p.H342N
CYSLTR2	cysteinyl leukotriene receptor 2	ENSG00000152207	PAP55	177	28.8%	chr13	48178968	CCDS9412.1	c.14T>G	p.F5C
CFTR	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette sub-family C; member 7)	ENSG00000001626	PAP55	75	36.0%	chr7	117038927	CCDS5773.1	c.3196C>T	p.R1066C
CTNS	cystinosis; nephropathic	ENSG00000040531	PAP55	71	18.3%	chr17	3500274	ENST00000399306	c.283C>T	p.Q95X
CYP4F12	cytochrome P450; family 4; subfamily F; polypeptide 12	ENSG00000186204	PAP55	38	28.9%	chr19	15656947	CCDS42517.1	c.1055A>G	p.E352G
CYP7B1	cytochrome P450; family 7; subfamily B; polypeptide 1	ENSG00000172817	PAP55	77	22.1%	chr8	65690862	CCDS6180.1	c.790T>G	p.F264V
CYTIP	cytohesin 1 interacting protein	ENSG00000115165	PAP55	181	27.1%	chr2	157980553	CCDS2204.1	c.962T>C	p.L321S

CKAP5	cytoskeleton associated protein 5	ENSG00000175216	PAP55	233	21.5%	chr11	46728469	CCDS31477.1	c.5635T>G	p.Y1879D
DCHS1	dachsous 1 (Drosophila)	ENSG00000166341	PAP55	46	54.3%	chr11	6619080	CCDS7771.1	c.341G>A	p.R114H
DCHS2	dachsous 2 (Drosophila)	ENSG00000197410	PAP55	69	29.0%	chr4	155461670	CCDS3785.1	c.2966T>C	p.V989A
DCHS2	dachsous 2 (Drosophila)	ENSG00000197410	PAP55	58	25.9%	chr4	155473289	CCDS3785.1	c.2024G>A	p.S675N
ABI3BP	DAVID_ABI family: member 3 (NESH) binding protein	NM_015429	PAP55	68	32.4%	chr3	101976172	NM_015429	c.2365G>T	p.E789X
ADAM22	DAVID_ADAM metallopeptidase domain 22	ENSG00000222045	PAP55	51	27.5%	chr7	87635466	CCDS43608.1	c.2270C>T	p.A757V
ASXL3	DAVID_additional sex combs like 3 (Drosophila)	NM_030632	PAP55	113	36.3%	chr18	29573030	NM_030632	c.1664A>G	p.D555G
ASXL3	DAVID_additional sex combs like 3 (Drosophila)	NM_030632	PAP55	212	29.2%	chr18	29580470	NM_030632	c.6660G>T	p.M2220I
AHNAK2	DAVID_AHNAK nucleoprotein 2	NM_138420	PAP55	147	21.8%	chr14	104475687	NM_138420	c.17146G>A	p.E5716K
ANKK1	DAVID_ankyrin repeat and kinase domain containing 1	NM_178510	PAP55	127	25.2%	chr11	112775842	NM_178510	c.1941G>C	p.Q647H
Ankrd24	DAVID_ankyrin repeat domain 24	NM_133475	PAP55	37	29.7%	chr19	4175455	NM_133475	c.3394C>A	p.L1132I
ANKRD31	DAVID_ankyrin repeat domain 31	NM_001164443	PAP55	134	21.6%	chr5	74477815	NM_001164443	c.3177G>T	p.K1059N
armc8	DAVID_armadillo repeat containing 8	NM_015396	PAP55	88	33.0%	chr3	139492124	NM_015396	c.1899T>G	p.D633E
abcb11	DAVID_ATP-binding cassette: sub-family B (MDR/TAP): member 11	NM_003742	PAP55	84	27.4%	chr2	169522807	NM_003742	c.2256G>A	p.W752X
cadps2	DAVID_Ca++-dependent secretion activator 2	NM_001167940	PAP55	57	17.5%	chr7	122164328	NM_001167940	c.370G>T	p.E124X
CACNA2D3	DAVID_calcium channel: voltage-dependent: alpha 2/delta subunit 3	NM_018398	PAP55	38	36.8%	chr3	54846292	NM_018398	c.1465G>A	p.E489K
CACNA2D3	DAVID_calcium channel: voltage-dependent: alpha 2/delta subunit 3	NM_018398	PAP55	160	20.6%	chr3	54894591	NM_018398	c.1994G>A	p.R665H
Cacna1b	DAVID_calcium channel: voltage-dependent: N type: alpha 1B subunit	NM_000718	PAP55	121	20.7%	chr9	140000786	NM_000718	c.1870G>A	p.A624T
Cacna1b	DAVID_calcium channel: voltage-dependent: N type: alpha 1B subunit	NM_000718	PAP55	123	29.3%	chr9	140001083	NM_000718	c.1930A>G	p.T644A
Cacna1a	DAVID_calcium channel: voltage-dependent: P/Q type: alpha 1A subunit	NM_001127222	PAP55	52	30.8%	chr19	13196586	NM_001127222	c.5626C>T	p.R1876W
CACNA1E	DAVID_calcium channel: voltage-dependent: R type: alpha 1E subunit	NM_000721	PAP55	80	28.8%	chr1	179953921	NM_000721	c.1633T>A	p.F545I
cnot1	DAVID_CCR4-NOT transcription complex: subunit 1	NM_206999	PAP55	48	29.2%	chr16	57134828	NM_206999	c.4618T>G	p.F1540V
C1orf49	DAVID_chromosome 1 open reading frame 49	ENSG00000184909	PAP55	99	25.3%	chr1	176752412	CCDS1323.1	c.256G>A	p.E86K
c10orf140	DAVID_chromosome 10 open reading frame 140	NM_207371	PAP55	152	32.9%	chr10	21844449	NM_207371	c.2309A>G	p.E770G
C17orf75	DAVID_chromosome 17 open reading frame 75	NM_022344	PAP55	159	33.3%	chr17	27684584	NM_022344	c.940C>A	p.L314I
C20orf123	DAVID_chromosome 20 open reading frame 123	NM_080721	PAP55	81	35.8%	chr20	44607669	NM_080721	c.751G>T	p.D251Y
C3orf63	DAVID_chromosome 3 open reading frame 63	NM_001112736	PAP55	82	25.6%	chr3	56682667	NM_001112736	c.458A>C	p.N153T
C3orf77	DAVID_chromosome 3 open reading frame 77	NM_001145030	PAP55	77	31.2%	chr3	44326438	NM_001145030	c.4258A>T	p.I1420F
C3orf77	DAVID_chromosome 3 open reading frame 77	NM_001145030	PAP55	97	28.9%	chr3	44348307	NM_001145030	c.4879C>T	p.R1627W
c5orf42	DAVID_chromosome 5 open reading frame 42	NM_023073	PAP55	108	28.7%	chr5	37262680	NM_023073	c.1774A>C	p.N592H
C6orf103	DAVID_chromosome 6 open reading frame 103	NM_024694	PAP55	80	17.5%	chr6	147087015	NM_024694	c.2096C>T	p.A699V
C6orf103	DAVID_chromosome 6 open reading frame 103	NM_024694	PAP55	50	26.0%	chr6	147088977	NM_024694	c.2303T>C	p.V768A
C6orf103	DAVID_chromosome 6 open reading frame 103	NM_024694	PAP55	131	32.1%	chr6	147108931	NM_024694	c.3358T>G	p.L1120V
C7orf10	DAVID_chromosome 7 open reading frame 10	NM_024728	PAP55	49	22.4%	chr7	40194694	NM_024728	c.323G>A	p.R108Q
Fam188b	DAVID_chromosome 7 open reading frame 67	ENSG00000106121	PAP55	113	24.8%	chr7	30797494	CCDS43565.1	c.852A>C	p.K284N
COL6A6	DAVID_collagen type VI alpha 6	NM_001102608	PAP55	205	28.3%	chr3	131866627	NM_001102608	c.6593G>A	p.R2198Q
Clnk	DAVID_cytokine-dependent hematopoietic cell linker	NM_052964	PAP55	109	22.0%	chr4	10118743	NM_052964	c.922G>T	p.E308X
Clasp1	DAVID_cytoplasmic linker associated protein 1	NM_015282	PAP55	121	32.2%	chr2	121999931	NM_015282	c.506T>G	p.V169G
DOCK4	DAVID_dedicator of cytokinesis 4	NM_014705	PAP55	48	39.6%	chr7	111327823	NM_014705	c.1323T>G	p.F441L
Dtx4	DAVID_deltex homolog 4 (Drosophila)	NM_015177	PAP55	61	32.8%	chr11	58715162	NM_015177	c.-1G>A	p.IVS4-1-1SpliceAcceptor
DENND5B	DAVID_DENN/MADD domain containing 5B	NM_144973	PAP55	37	32.4%	chr12	31496664	NM_144973	c.1106T>C	p.F369S
DNHD1	DAVID_dynein heavy chain domain 1	NM_144666	PAP55	154	30.5%	chr11	6545511	NM_144666	c.12196C>T	p.R4066W
DNAH14	DAVID_dynein: axonemal: heavy chain 14	NM_001373	PAP55	108	19.4%	chr1	223587730	NM_001373	c.9700C>T	p.R3234C
DNAH14	DAVID_dynein: axonemal: heavy chain 14	NM_001373	PAP55	44	25.0%	chr1	223600649	NM_001373	c.10762C>T	p.L3588F
DNAH14	DAVID_dynein: axonemal: heavy chain 14	NM_001373	PAP55	73	28.8%	chr1	223615191	NM_001373	c.11683C>T	p.P3895S

DST	DAVID_dystonin	NM_001144769	PAP55	197	22.3%	chr6	56525530	NM_001144769	c.9662T>C	p.V3221A
DST	DAVID_dystonin	NM_001144769	PAP55	78	23.1%	chr6	56551578	NM_001144769	c.6663A>C	p.K2221N
DST	DAVID_dystonin	NM_020388	PAP55	129	26.4%	chr6	56578792	NM_020388	c.6982A>C	p.S2328R
Fam13a	DAVID_family with sequence similarity 13: member A	ENSG00000138640	PAP55	129	31.0%	chr4	90131157	CCDS34029.1	c.595A>C	p.N199H
FSCN2	DAVID_fascin homolog 2: actin-bundling protein: retinal (Strongylocentrotus purpuratus)	NM_001077182	PAP55	61	32.8%	chr17	77110207	NM_001077182	c.55G>A	p.D19N
Fat1	DAVID_FAT tumor suppressor homolog 1 (Drosophila)	NM_005245	PAP55	167	26.3%	chr4	187777685	NM_005245	c.7049A>G	p.Y2350C
FAT3	DAVID_FAT tumor suppressor homolog 3 (Drosophila)	NM_001008781	PAP55	94	25.5%	chr11	92171885	NM_001008781	c.6058T>G	p.L2020V
FBRS	DAVID_fibrosin	NM_001105079	PAP55	54	25.9%	chr16	30585781	NM_001105079	c.284A>G	p.Y95C
FIGNL2	DAVID_fidgetin-like 2	NM_001013690	PAP55	134	32.1%	chr12	50502320	NM_001013690	c.145G>A	p.D49N
FMNL3	DAVID_formin-like 3	NM_175736	PAP55	42	33.3%	chr12	48338645	NM_175736	c.-1G>T	p.IVS5-1-1SpliceAcceptor
FREM1	DAVID_FRAS1 related extracellular matrix 1	NM_144966	PAP55	156	36.5%	chr9	14849471	NM_144966	c.341G>T	p.R114I
GPR126	DAVID_G protein-coupled receptor 126	NM_198569	PAP55	80	31.3%	chr6	142782678	NM_198569	c.3063T>G	p.F1021L
GEMIN4	DAVID_gem (nuclear organelle) associated protein 4	NM_015721	PAP55	206	19.9%	chr17	596208	NM_015721	c.1825G>T	p.E609X
LOC200726	DAVID_hCG1657980	NM_001102659	PAP55	91	31.9%	chr2	207217468	NM_001102659	c.263G>A	p.G88E
HERC1	DAVID_hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	NM_003922	PAP55	350	28.9%	chr15	61691561	NM_003922	c.14342G>A	p.R4781Q
HERC1	DAVID_hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	NM_003922	PAP55	42	31.0%	chr15	61703525	NM_003922	c.13330C>T	p.R4444W
Hephl1	DAVID_hephaestin-like 1	NM_001098672	PAP55	36	30.6%	chr11	93458896	NM_001098672	c.1973G>A	p.G658E
Hephl1	DAVID_hephaestin-like 1	NM_001098672	PAP55	54	24.1%	chr11	93475787	NM_001098672	c.2635C>T	p.P879S
LOC360030	DAVID_homeobox C14	ENSG00000205857	PAP55	39	35.9%	chr12	7814344	NM_001145465	c.478G>T	p.E160X
HIPK2	DAVID_homeodomain interacting protein kinase 2; similar to homeodomain interacting protein kinase 2	NM_022740	PAP55	84	33.3%	chr7	139063224	NM_022740	c.96A>C	p.K32N
C9orf144	DAVID_hypothetical protein LOC259308; chromosome 9 open reading frame 144	ENSG00000215202	PAP55	71	22.5%	chr9	34825944	ENST00000378788	c.353G>A	p.R118Q
C9orf144B	DAVID_hypothetical protein LOC259308; chromosome 9 open reading frame 144	ENSG00000215202	PAP55	71	22.5%	chr9	34825944	ENST00000378788	c.353G>A	p.R118Q
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP55	123	25.2%	chr13	102187171	NM_001146197	c.13877G>T	p.R4626I
LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP55	98	27.6%	chr13	102197186	NM_001146197	c.3862A>C	p.K1288Q
LOC729852	DAVID_hypothetical protein LOC729852	ENSG00000219545	PAP55	49	22.4%	chr7	7807871	ENST00000406829	c.23C>T	p.S8L
LOC729852	DAVID_hypothetical protein LOC729852	ENSG00000219545	PAP55	243	28.0%	chr7	7883680	ENST00000406829	c.295C>T	p.L99F
Igfn1	DAVID_immunoglobulin-like and fibronectin type III domain containing 1	NM_001164586	PAP55	48	31.3%	chr1	199445304	NM_001164586	c.4660G>A	p.G1554S
ITGA11	DAVID_integrin: alpha 11	NM_001004439	PAP55	66	30.3%	chr15	66411373	NM_001004439	c.1648C>T	p.R550X
IFFO2	DAVID_intermediate filament family orphan 2	NM_001136265	PAP55	183	27.9%	chr1	19115999	NM_001136265	c.1088G>A	p.R363H
KIAA0748	DAVID_KIAA0748	NM_001136030	PAP55	136	30.1%	chr12	53642768	NM_001136030	c.1181C>A	p.S394Y
KIAA0913	DAVID_KIAA0913	NM_015037	PAP55	167	31.1%	chr10	75219188	NM_015037	c.515A>G	p.Y172C
KIAA1210	DAVID_KIAA1210	NM_020721	PAP55	149	28.2%	chrX	118107615	NM_020721	c.1606A>T	p.R536X
KIAA1239	DAVID_KIAA1239	NM_001144990	PAP55	68	36.8%	chr4	37116898	NM_001144990	c.787A>G	p.I263V
KIAA1239	DAVID_KIAA1239	NM_001144990	PAP55	138	29.0%	chr4	37121893	NM_001144990	c.1888G>A	p.D630N
GREB1L	DAVID_KIAA1772	NM_001142966	PAP55	35	28.6%	chr18	17354774	NM_001142966	c.5600T>G	p.F1867C
KIFC1	DAVID_kinesin family member C1	ENSG00000204197	PAP55	38	31.6%	chr6	33473817	CCDS34430.1	c.46G>T	p.E16X
Irrc48	DAVID_leucine rich repeat containing 48	NM_031294	PAP55	123	24.4%	chr17	17860151	NM_031294	c.1375G>A	p.D459N
LRRC70	DAVID_leucine rich repeat containing 70	NM_181506	PAP55	69	33.3%	chr5	61911953	NM_181506	c.931G>T	p.E311X
LOXHD1	DAVID_lipoxygenase homology domains 1	NM_144612	PAP55	126	31.7%	chr18	42438121	NM_144612	c.829G>A	p.E277K
TRANK1	DAVID_lupus brain antigen 1	NM_014831	PAP55	66	27.3%	chr3	36854995	NM_014831	c.5257A>C	p.K1753Q
LY6G6D	DAVID_lymphocyte antigen 6 complex: locus G6F; lymphocyte antigen 6 complex: locus G6D	ENSG00000204424	PAP55	54	29.6%	chr6	31791125	CCDS34404.1	c.14T>G	p.F5C
LY6G6F	DAVID_lymphocyte antigen 6 complex: locus G6F; lymphocyte antigen 6 complex: locus G6D	ENSG00000204424	PAP55	54	29.6%	chr6	31791125	CCDS34404.1	c.14T>G	p.F5C
MUC16	DAVID_mucin 16: cell surface associated	NM_024690	PAP55	565	27.8%	chr19	8926602	NM_024690	c.21844G>A	p.E7282K

MUC16	DAVID_mucin 16: cell surface associated	NM_024690	PAP55	103	25.2%	chr19	8933384	NM_024690	c.15062G>T	p.R5021I
MUC16	DAVID_mucin 16: cell surface associated	NM_024690	PAP55	346	28.0%	chr19	8934267	NM_024690	c.14179G>T	p.D4727Y
MUC16	DAVID_mucin 16: cell surface associated	NM_024690	PAP55	127	29.9%	chr19	8936303	NM_024690	c.12143G>T	p.R4048I
MUC16	DAVID_mucin 16: cell surface associated	NM_024690	PAP55	99	30.3%	chr19	8949807	NM_024690	c.3008C>A	p.S1003Y
Mybpc2	DAVID_myosin binding protein C: fast type	NM_004533	PAP55	233	30.9%	chr19	55650222	NM_004533	c.2060A>C	p.K687T
ND4L	DAVID_NADH-ubiquinone oxidoreductase chain 4L; NADH-ubiquinone oxidoreductase chain 4	ENSG00000198868	PAP55	92	85.9%	chrM	12012	ENST00000410116	c.1252T>C	p.S418P
ND4	DAVID_NADH-ubiquinone oxidoreductase chain 4L; NADH-ubiquinone oxidoreductase chain 4	ENSG00000198868	PAP55	92	85.9%	chrM	12012	ENST00000410116	c.1252T>C	p.S418P
NEB	DAVID_nebulin	NM_001164507	PAP55	170	21.2%	chr2	152209325	NM_001164507	c.7547G>A	p.R2516Q
NEB	DAVID_nebulin	NM_001164507	PAP55	152	23.0%	chr2	152232585	NM_001164507	c.4698T>G	p.S1566R
NBEAL1	DAVID_neurobeachin-like 1	NM_001114132	PAP55	181	27.6%	chr2	203680709	NM_001114132	c.1415G>T	p.R472I
Nrk	DAVID_Nik related kinase	NM_198465	PAP55	47	38.3%	chrX	105077068	NM_198465	c.4309G>A	p.D1437N
nek1	DAVID_NIMA (never in mitosis gene a)-related kinase 1	NM_012224	PAP55	76	26.3%	chr4	170666009	NM_012224	c.1714C>T	p.R572C
Ncoa2	DAVID_nuclear receptor coactivator 2	NM_006540	PAP55	152	30.3%	chr8	71230917	NM_006540	c.2237G>A	p.R746H
nfyc	DAVID_nuclear transcription factor Y: gamma	NM_001142588	PAP55	80	30.0%	chr1	41005184	NM_001142588	c.836G>T	p.R279I
obscn	DAVID_obscurin: cytoskeletal calmodulin and titin-interacting RhoGEF	NM_001098623	PAP55	40	37.5%	chr1	226531004	NM_001098623	c.6451G>A	p.E2151K
Odz2	DAVID_odz: odd Oz/ten-m homolog 2 (Drosophila)	NM_001122679	PAP55	161	29.2%	chr5	167587486	NM_001122679	c.5266C>T	p.R1756W
OR10C1	DAVID_olfactory receptor: family 10: subfamily C: member 1	ENSG00000206474	PAP55	341	26.1%	chr6	29516645	CCDS34364.1	c.874C>T	p.R292W
OR52E6	DAVID_olfactory receptor: family 52: subfamily E: member 6	NM_001005167	PAP55	70	38.6%	chr11	5819231	NM_001005167	c.473T>C	p.V158A
oxr1	DAVID_oxidation resistance 1	NM_018002	PAP55	72	22.2%	chr8	107600519	NM_018002	c.196G>A	p.E66K
PYY3	DAVID_peptide YY: 3	ENSG00000204474	PAP55	54	31.5%	chrX	49807658	ENST00000376079	c.112G>A	p.E38K
PXDNL	DAVID_peroxidasin homolog (Drosophila)-like	NM_144651	PAP55	90	35.6%	chr8	52395923	NM_144651	c.4234G>T	p.E1412X
PXDNL	DAVID_peroxidasin homolog (Drosophila)-like	NM_144651	PAP55	153	32.0%	chr8	52547408	NM_144651	c.704G>A	p.R235Q
PHACTR1	DAVID_phosphatase and actin regulator 1	NM_030948	PAP55	27	40.7%	chr6	12827017	NM_030948	c.55T>G	p.L19V
PIGB	DAVID_phosphatidylinositol glycan anchor biosynthesis: class B	NM_004855	PAP55	137	25.5%	chr15	53430263	NM_004855	c.1198G>A	p.A400T
PISD	DAVID_phosphatidylserine decarboxylase	ENSG00000100141	PAP55	31	41.9%	chr22	30349678	CCDS13899.1	c.211G>A	p.V71I
Pla2g4e	DAVID_phospholipase A2: group IVE	NM_001080490	PAP55	80	27.5%	chr15	40064074	NM_001080490	c.2151G>T	p.Q717H
PCLO	DAVID_piccolo (presynaptic cytomatrix protein)	NM_033026	PAP55	189	32.8%	chr7	82419632	NM_033026	c.8573G>A	p.G2858D
Lppr1	DAVID_plasticity related gene 3	ENSG00000148123	PAP55	113	24.8%	chr9	103072025	CCDS6751.1	c.106G>A	p.E36K
PARP14	DAVID_poly (ADP-ribose) polymerase family: member 14	NM_017554	PAP55	89	34.8%	chr3	123902067	NM_017554	c.1976A>C	p.K659T
papolb	DAVID_poly(A) polymerase beta (testis specific)	NM_020144	PAP55	53	34.0%	chr7	4867631	NM_020144	c.337G>A	p.A113T
PRODH2	DAVID_proline dehydrogenase (oxidase) 2	ENSG00000221873	PAP55	94	27.7%	chr19	40994898	CCDS12478.1	c.716C>T	p.A239V
prss23	DAVID_protease: serine: 23	ENSG00000150687	PAP55	147	30.6%	chr11	86196868	CCDS8278.1	c.535G>A	p.D179N
psmb8	DAVID_proteasome (prosome: macropain) subunit: beta type: 8 (large multifunctional peptidase 7)	ENSG00000204264	PAP55	57	31.6%	chr6	32917342	CCDS4757.1	c.686G>A	p.R229H
PTPRB	DAVID_protein tyrosine phosphatase: receptor type: B	NM_001109754	PAP55	109	27.5%	chr12	69252015	NM_001109754	c.2962A>C	p.N988H
PPFIA2	DAVID_protein tyrosine phosphatase: receptor type: f polypeptide (PTPRF): interacting protein (liprin): alpha 2	NM_003625	PAP55	85	34.1%	chr12	80265540	NM_003625	c.2135C>T	p.S712L
PCDHGA4	DAVID_protocadherin gamma subfamily A: 4	NM_018917	PAP55	55	29.1%	chr5	140717284	NM_018917	c.2333C>T	p.T778M
PCDHGA5	DAVID_protocadherin gamma subfamily A: 5	NM_018918	PAP55	151	25.2%	chr5	140726020	NM_018918	c.1939G>A	p.E647K
PCDHGB1	DAVID_protocadherin gamma subfamily B: 1	NM_018922	PAP55	177	28.8%	chr5	140710897	NM_018922	c.886G>A	p.D296N
phtf2	DAVID_putative homeodomain transcription factor 2	NM_001127357	PAP55	38	39.5%	chr7	77405003	NM_001127357	c.1277NULL>/	p.NULL-1Fslns1bp
RGAG4	DAVID_retrotransposon gag domain containing 4	NM_001024455	PAP55	331	32.0%	chrX	71267072	NM_001024455	c.1044A>C	p.E348D
RGAG4	DAVID_retrotransposon gag domain containing 4	NM_001024455	PAP55	123	32.5%	chrX	71267321	NM_001024455	c.795G>C	p.L265F
RLTPR	DAVID_RGD motif: leucine rich repeats: tropomodulin domain and proline-rich containing	NM_001013838	PAP55	84	19.0%	chr16	66243326	NM_001013838	c.2590G>A	p.D864N
RBMXL3	DAVID_RNA binding motif protein: X-linked-like 3	NM_001145346	PAP55	95	23.2%	chrX	114332815	NM_001145346	c.2555G>T	p.S852I
RYR2	DAVID_ryanodine receptor 2 (cardiac)	NM_001035	PAP55	126	23.0%	chr1	235699047	NM_001035	c.1645G>C	p.A549P

RYR2	DAVID_ryanodine receptor 2 (cardiac)	NM_001035	PAP55	165	24.2%	chr1	236014044	NM_001035	c.12409G>A	p.E4137K
RYR3	DAVID_ryanodine receptor 3	NM_001036	PAP55	203	28.6%	chr15	31927856	NM_001036	c.13570G>A	p.E4524K
SCAND3	DAVID_SCAN domain containing 3	ENSG00000197202	PAP55	102	29.4%	chr6	28650583	CCDS34355.1	c.1878T>G	p.I626M
sspO	DAVID_SCO-spondin homolog (Bos taurus)	NM_198455	PAP55	114	28.9%	chr7	149128396	NM_198455	c.7225G>A	p.A2409T
stk19	DAVID_serine/threonine kinase 19	ENSG00000204344	PAP55	170	34.7%	chr6	32055248	CCDS4733.1	c.754G>A	p.D252N
SERPINE3	DAVID_serpin peptidase inhibitor: clade E (nexin: plasminogen activator inhibitor type 1): member 3	NM_001101320	PAP55	73	27.4%	chr13	50827224	NM_001101320	c.944C>A	p.S315Y
SERPINE3	DAVID_serpin peptidase inhibitor: clade E (nexin: plasminogen activator inhibitor type 1): member 3	NM_001101320	PAP55	242	29.8%	chr13	50834065	NM_001101320	c.1206T>G	p.I402M
SIGLEC12	DAVID_sialic acid binding Ig-like lectin 12	ENSG00000160296	PAP55	114	13.2%	chr19	56696597	CCDS12833.1	c.203A>G	p.D68G
LOC285141	DAVID_similar to CG14853-PB	ENSG00000204334	PAP55	129	26.4%	chr2	171362853	ENST00000375280	c.1168G>T	p.E390X
ZNF879	DAVID_similar to hypothetical protein 9630041N07	NM_001136116	PAP55	96	14.6%	chr5	178392457	NM_001136116	c.902C>A	p.S301X
ZNF605	DAVID_similar to ZNF605 protein	NM_001164715	PAP55	120	27.5%	chr12	132012993	NM_001164715	c.1058C>T	p.S353L
SLC12A1	DAVID_solute carrier family 12 (sodium/potassium/chloride transporters): member 1	NM_000338	PAP55	142	25.4%	chr15	46306054	NM_000338	c.718C>T	p.R240C
SLC12A1	DAVID_solute carrier family 12 (sodium/potassium/chloride transporters): member 1	NM_000338	PAP55	92	27.2%	chr15	46382249	NM_000338	c.3175G>A	p.V1059M
SLC4A10	DAVID_solute carrier family 4: sodium bicarbonate transporter: member 10	NM_022058	PAP55	87	43.7%	chr2	162513907	NM_022058	c.2179C>T	p.R727X
STARD9	DAVID_StAR-related lipid transfer (START) domain containing 9	NM_020759	PAP55	188	27.7%	chr15	40770913	NM_020759	c.9845A>G	p.Q3282R
SMCHD1	DAVID_structural maintenance of chromosomes flexible hinge domain containing 1	NM_015295	PAP55	65	46.2%	chr18	2729443	NM_015295	c.3439G>A	p.E1147K
SMCHD1	DAVID_structural maintenance of chromosomes flexible hinge domain containing 1	NM_015295	PAP55	32	31.3%	chr18	2765864	NM_015295	c.5308C>T	p.R1770C
SVEP1	DAVID_sushi: von Willebrand factor type A: EGF and pentraxin domain containing 1	NM_153366	PAP55	72	23.6%	chr9	112209515	NM_153366	c.8186G>A	p.R2729H
SVEP1	DAVID_sushi: von Willebrand factor type A: EGF and pentraxin domain containing 1	NM_153366	PAP55	194	30.4%	chr9	112210988	NM_153366	c.6713T>C	p.V2238A
SVEP1	DAVID_sushi: von Willebrand factor type A: EGF and pentraxin domain containing 1	NM_153366	PAP55	188	30.3%	chr9	112213266	NM_153366	c.6546G>T	p.K2182N
SNAP91	DAVID_synaptosomal-associated protein: 91kDa homolog (mouse)	NM_014841	PAP55	74	27.0%	chr6	84407605	NM_014841	c.694G>T	p.D232Y
TRBV4-2	DAVID_T cell receptor beta variable 4-2	ENSG00000211708	PAP55	79	30.4%	chr7	141691860	ENST00000390355	c.26C>T	p.A9V
ttc9	DAVID_tetratricopeptide repeat domain 9	NM_015351	PAP55	160	22.5%	chr14	70204162	NM_015351	c.535G>A	p.D179N
TNP2	DAVID_transition protein 2 (during histone to protamine replacement)	NM_005425	PAP55	111	31.5%	chr16	11270269	NM_005425	c.352A>G	p.M118V
TRIM66	DAVID_tripartite motif-containing 66	NM_014818	PAP55	90	23.3%	chr11	8627953	NM_014818	c.67C>T	p.R23C
ttll6	DAVID_tubulin tyrosine ligase-like family: member 6	NM_001130918	PAP55	400	31.8%	chr17	44237214	NM_001130918	c.242C>T	p.A81V
C7orf72	DAVID_Uncharacterized protein LOC340228	NM_001161834	PAP55	192	33.9%	chr7	50106529	NM_001161834	c.302T>C	p.V101A
CCDC160	DAVID_UPF0625 coiled-coil domain-containing protein ENSP00000359845	NM_001101357	PAP55	36	36.1%	chrX	133206727	NM_001101357	c.231A>C	p.Q77H
Vprbp	DAVID_Vpr (HIV-1) binding protein	NM_014703	PAP55	39	33.3%	chr3	51426527	NM_014703	c.3689G>A	p.R1230Q
DCAF8L2	DAVID_WD repeat domain 42C	NM_001136533	PAP55	94	26.6%	chrX	27675600	NM_001136533	c.667C>A	p.R223S
DCAF8L2	DAVID_WD repeat domain 42C	NM_001136533	PAP55	86	27.9%	chrX	27676135	NM_001136533	c.1202A>C	p.K401T
WDR87	DAVID_WD repeat domain 87	NM_031951	PAP55	294	32.7%	chr19	43069176	NM_031951	c.6858G>T	p.E2286D
WDR87	DAVID_WD repeat domain 87	NM_031951	PAP55	234	24.8%	chr19	43072056	NM_031951	c.3978G>T	p.E1326D
ZBTB34	DAVID_zinc finger and BTB domain containing 34	NM_001099270	PAP55	219	32.0%	chr9	128681536	NM_001099270	c.25T>G	p.F9V
ZFHX4	DAVID_zinc finger homeobox 4	NM_024721	PAP55	195	30.3%	chr8	77779045	NM_024721	c.167G>A	p.R56H
ZFHX4	DAVID_zinc finger homeobox 4	NM_024721	PAP55	227	27.3%	chr8	77928266	NM_024721	c.6419G>A	p.R2140Q
ZNF252	DAVID_zinc finger protein 252	ENSG00000196922	PAP55	98	22.4%	chr8	146174086	ENST00000355436	c.656G>A	p.R219K
ZNF268	DAVID_zinc finger protein 268	ENSG00000151963	PAP55	101	31.7%	chr12	132289130	ENST00000228289	c.785C>T	p.S262L
ZNF283	DAVID_zinc finger protein 283	NM_181845	PAP55	130	38.5%	chr19	49044381	NM_181845	c.1788G>T	p.E596D
ZNF284	DAVID_zinc finger protein 284	NM_001037813	PAP55	53	30.2%	chr19	49282966	NM_001037813	c.1495C>T	p.R499C
znf292	DAVID_zinc finger protein 292	NM_015021	PAP55	101	33.7%	chr6	88021964	NM_015021	c.1898G>A	p.R633Q

znf292	DAVID_zinc finger protein 292	NM_015021	PAP55	104	33.7%	chr6	88023398	NM_015021	c.3332C>A	p.S1111Y
ZNF323	DAVID_zinc finger protein 323	ENSG00000197657	PAP55	195	29.2%	chr6	28402520	CCDS4649.1	c.623G>T	p.R208I
ZNF432	DAVID_zinc finger protein 432	ENSG00000221897	PAP55	50	38.0%	chr19	57229566	CCDS12848.1	c.1178G>A	p.R393Q
ZNF818P	DAVID_zinc finger protein 818 pseudogene	ENSG00000204597	PAP55	67	43.3%	chr19	58408292	ENST00000344759	c.242G>T	p.R81I
ZNF99	DAVID_zinc finger protein 99	NM_001080409	PAP55	52	23.1%	chr19	22743906	NM_001080409	c.127G>A	p.D43N
ZNF880	DAVID_zinc finger protein LOC400713	NM_001145434	PAP55	103	32.0%	chr19	57580273	NM_001145434	c.1628C>T	p.T543I
ZMYM5	DAVID_zinc finger: MYM-type 5	NM_001142684	PAP55	149	22.8%	chr13	19297236	NM_001142684	c.1391A>G	p.E464G
DZIP1	DAZ interacting protein 1	ENSG00000134874	PAP55	166	39.2%	chr13	95091566	CCDS9478.1	c.581A>C	p.K194T
DCAF8L2	DDB1 and CUL4 associated factor 8-like 2	ENSG00000189186	PAP55	392	31.4%	chrX	27909135	CCDS35222.1	c.238G>A	p.E80K
DDX53	DEAD (Asp-Glu-Ala-Asp) box polypeptide 53	ENSG00000184735	PAP55	94	21.3%	chrX	22929476	CCDS35214.1	c.1381G>A	p.V461I
DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	ENSG00000137628	PAP55	33	36.4%	chr4	169444926	CCDS34097.1	c.1187T>C	p.L396P
DDX26B	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	ENSG00000165359	PAP55	52	26.9%	chrX	134507984	CCDS35401.1	c.353T>G	p.F118C
DDX26B	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	ENSG00000165359	PAP55	141	27.0%	chrX	134508341	CCDS35401.1	c.478G>T	p.E160X
DQX1	DEAQ box RNA-dependent ATPase 1	ENSG00000144045	PAP55	378	27.8%	chr2	74600310	CCDS1949.1	c.1333C>T	p.R445W
DOCK11	dedicator of cytokinesis 11	ENSG00000147251	PAP55	38	26.3%	chrX	117626238	CCDS35373.1	c.2768A>C	p.E923A
DOCK2	dedicator of cytokinesis 2	ENSG00000134516	PAP55	104	26.9%	chr5	169041421	CCDS4371.1	c.566A>G	p.E189G
DOCK7	dedicator of cytokinesis 7	ENSG00000116641	PAP55	53	34.0%	chr1	62791074	CCDS30734.1	c.2683C>T	p.R895X
DEFB125	defensin; beta 125	ENSG00000178591	PAP55	221	31.2%	chr20	24787	CCDS12989.2	c.200G>A	p.R67Q
DENND1A	DENN/MADD domain containing 1A	ENSG00000119522	PAP55	385	26.2%	chr9	125185937	CCDS35133.1	c.1654C>T	p.R552W
DENND2C	DENN/MADD domain containing 2C	ENSG00000175984	PAP55	145	24.8%	chr1	114967729	CCDS875.1	c.865C>T	p.R289C
DENND2C	DENN/MADD domain containing 2C	ENSG00000175984	PAP55	119	20.2%	chr1	114969489	CCDS875.1	c.640C>T	p.R214C
DENND3	DENN/MADD domain containing 3	ENSG00000105339	PAP55	190	30.5%	chr8	142247537	CCDS34947.1	c.1766G>A	p.R589Q
DEPDC1	DEP domain containing 1	ENSG00000024526	PAP55	20	50.0%	chr1	68727844	CCDS644.1	c.350G>A	p.R117Q
DGKI	diacylglycerol kinase; iota	ENSG00000157680	PAP55	62	24.2%	chr7	136920503	CCDS5845.1	c.1555G>A	p.V519I
DGKK	diacylglycerol kinase; kappa	ENSG00000204466	PAP55	64	32.8%	chrX	50184009	ENST00000376025	c.733C>T	p.L245F
DIAPH2	diaphanous homolog 2 (Drosophila)	ENSG00000147202	PAP55	88	33.0%	chrX	95899827	CCDS14467.1	c.361G>A	p.E121K
DIAPH3	diaphanous homolog 3 (Drosophila)	ENSG00000139734	PAP55	64	32.8%	chr13	59584314	CCDS41898.1	c.221A>C	p.K74T
DAB2	disabled homolog 2; mitogen-responsive phosphoprotein (Drosophila)	ENSG00000153071	PAP55	117	28.2%	chr5	39418751	CCDS34149.1	c.1067A>C	p.K356T
DLGAP3	discs; large (Drosophila) homolog-associated protein 3	ENSG00000116544	PAP55	49	30.6%	chr1	35143274	CCDS30670.1	c.298G>A	p.D100N
DLG2	discs; large homolog 2 (Drosophila)	ENSG00000150672	PAP55	69	27.5%	chr11	82861448	CCDS41696.1	c.1999C>A	p.L667I
DLG3	discs; large homolog 3 (Drosophila)	ENSG00000082458	PAP55	51	27.5%	chrX	69636560	CCDS14403.1	c.2081C>T	p.A694V
DVL2	dishevelled; dsh homolog 2 (Drosophila)	ENSG00000004975	PAP55	48	35.4%	chr17	7074446	CCDS11091.1	c.292G>A	p.E98K
DMRTA1	DMRT-like family A1	ENSG00000176399	PAP55	88	27.3%	chr9	22441420	CCDS6514.1	c.1025G>A	p.R342H
DMXL1	Dmx-like 1	ENSG00000172869	PAP55	82	23.2%	chr5	118510869	CCDS4125.1	c.2716G>A	p.E906K
DNAJA3	DnaJ (Hsp40) homolog; subfamily A; member 3	ENSG00000103423	PAP55	143	28.0%	chr16	4434711	CCDS10515.1	c.977A>G	p.E326G
DNAJC2	DnaJ (Hsp40) homolog; subfamily C; member 2	ENSG00000105821	PAP55	72	16.7%	chr7	102749737	CCDS43628.1	c.961C>T	p.R321W
DNAJC24	DnaJ (Hsp40) homolog; subfamily C; member 24	ENSG00000170946	PAP55	49	24.5%	chr11	31393003	CCDS7873.2	c.181G>A	p.E61K
DNM1P17	DNM1 pseudogene 17	ENSG00000107951	PAP55	81	19.8%	chr10	30651384	CCDS7165.1	c.1387NULL>T	p.NULL-1FsIns1bp
DOPEY2	dopey family member 2	ENSG00000142197	PAP55	152	32.9%	chr21	36524691	CCDS13643.1	c.1739C>T	p.S580L
DSCAM	Down syndrome cell adhesion molecule	ENSG00000171587	PAP55	167	33.5%	chr21	40345838	CCDS42929.1	c.5102C>T	p.T1701M
DSCAML1	Down syndrome cell adhesion molecule like 1	ENSG00000177103	PAP55	100	19.0%	chr11	116815803	CCDS8384.1	c.4102C>T	p.R1368W
DYRK4	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	ENSG00000010219	PAP55	103	21.4%	chr12	4576122	CCDS8530.1	c.526C>T	p.R176C
DNAH2	dynein; axonemal; heavy chain 2	ENSG00000183914	PAP55	31	35.5%	chr17	7624226	CCDS32551.1	c.5749G>A	p.E1917K
DNAH3	dynein; axonemal; heavy chain 3	ENSG00000158486	PAP55	124	27.4%	chr16	20904489	CCDS10594.1	c.7076G>A	p.R2359Q
DNAH5	dynein; axonemal; heavy chain 5	ENSG00000039139	PAP55	67	32.8%	chr5	13873548	CCDS3882.1	c.6748G>A	p.E2250K
DNAH5	dynein; axonemal; heavy chain 5	ENSG00000039139	PAP55	74	28.4%	chr5	13954576	CCDS3882.1	c.1837G>A	p.D613N
DNAH9	dynein; axonemal; heavy chain 9	ENSG00000007174	PAP55	76	23.7%	chr17	11563468	CCDS11160.1	c.5645A>G	p.D1882G
DNAI1	dynein; axonemal; intermediate chain 1	ENSG00000122735	PAP55	125	27.2%	chr9	34507334	CCDS6557.1	c.1870C>T	p.P624S
DYNC1H1	dynein; cytoplasmic 1; heavy chain 1	ENSG00000197102	PAP55	102	31.4%	chr14	101565987	CCDS9966.1	c.9721A>G	p.K3241E
DYSF	dysferlin; limb girdle muscular dystrophy 2B (autosomal recessive)	ENSG00000135636	PAP55	76	32.9%	chr2	71692161	CCDS1918.1	c.4064C>A	p.P1355H

DYX1C1	dyslexia susceptibility 1 candidate 1	ENSG00000128845	PAP55	75	30.7%	chr15	53510211	CCDS10154.1	c.1212T>G	p.I404M
DMD	dystrophin	ENSG00000198947	PAP55	49	26.5%	chrX	31586182	CCDS14233.1	c.7873C>T	p.Q2625X
DMD	dystrophin	ENSG00000198947	PAP55	66	24.2%	chrX	32751368	CCDS14233.1	c.322C>A	p.L108I
EP400	E1A binding protein p400	ENSG00000183495	PAP55	78	29.5%	chr12	131078576	CCDS31929.1	c.5168G>A	p.R1723H
ENTPD7	ectonucleoside triphosphate diphosphohydrolase 7	ENSG00000198018	PAP55	107	29.9%	chr10	101448316	CCDS7480.1	c.1046A>G	p.N349S
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	ENSG00000136960	PAP55	98	29.6%	chr8	120700678	CCDS6329.1	c.466G>A	p.E156K
EFCAB6	EF-hand calcium binding domain 6	ENSG00000186976	PAP55	46	32.6%	chr22	42353784	CCDS14049.1	c.2341G>A	p.E781K
ELK1	ELK1; member of ETS oncogene family	ENSG00000126767	PAP55	73	30.1%	chrX	47382503	CCDS14283.1	c.677C>T	p.A226V
ERAP1	endoplasmic reticulum aminopeptidase 1	ENSG00000164307	PAP55	45	42.2%	chr5	96145413	CCDS4085.1	c.2071G>T	p.D691Y
ECE2	endothelin converting enzyme 2	ENSG00000145194	PAP55	72	25.0%	chr3	185485575	CCDS43179.1	c.1274G>A	p.R425H
ELMO1	engulfment and cell motility 1	ENSG00000155849	PAP55	36	33.3%	chr7	36861840	CCDS5449.1	c.2025G>T	p.K675N
EPC2	enhancer of polycomb homolog 2 (Drosophila)	ENSG00000135999	PAP55	51	37.3%	chr2	149257730	NM_015630	c.1952G>A	p.R651H
EVPLL	envoplakin-like	ENSG00000214860	PAP55	93	23.7%	chr17	18225658	NM_001145127	c.235G>A	p.E79K
EPHA3	EPH receptor A3	ENSG00000044524	PAP55	66	31.8%	chr3	89473778	CCDS2922.1	c.1154G>A	p.R385Q
EPHA4	EPH receptor A4	ENSG00000116106	PAP55	314	33.1%	chr2	222009527	CCDS2447.1	c.2182C>T	p.R728C
EPHA5	EPH receptor A5	ENSG00000145242	PAP55	98	29.6%	chr4	66150479	CCDS3513.1	c.385G>T	p.E129X
EGF	epidermal growth factor	ENSG00000138798	PAP55	109	37.6%	chr4	111140310	CCDS3689.1	c.3032G>A	p.R1011Q
EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog; avian)	ENSG00000146648	PAP55	44	34.1%	chr7	55192921	CCDS5514.1	c.1279C>T	p.R427C
EPYC	epiphycan	ENSG00000083782	PAP55	64	21.9%	chr12	89889830	CCDS31870.1	c.580C>T	p.R194X
EMP1	epithelial membrane protein 1	ENSG00000134531	PAP55	274	29.9%	chr12	13258863	CCDS8660.1	c.445G>A	p.V149I
EPHX4	epoxide hydrolase 4	ENSG00000172031	PAP55	59	27.1%	chr1	92290791	CCDS736.1	c.845G>A	p.R282Q
EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	ENSG00000095203	PAP55	117	34.2%	chr9	111057926	CCDS43859.1	c.948G>T	p.M316I
EME1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	ENSG00000154920	PAP55	65	32.3%	chr17	45807695	CCDS11565.1	c.127A>G	p.K43E
ETV1	ets variant 1	ENSG00000006468	PAP55	88	29.5%	chr7	13992273	NM_001163150	c.54A>C	p.R18S
EEF2K	eukaryotic elongation factor-2 kinase	ENSG00000103319	PAP55	53	32.1%	chr16	22183676	CCDS10604.1	c.1414G>A	p.E472K
EIF3A	eukaryotic translation initiation factor 3; subunit A	ENSG00000107581	PAP55	198	29.8%	chr10	120799464	CCDS7608.1	c.2497G>A	p.E833K
EVX1	even-skipped homeobox 1	ENSG00000106038	PAP55	52	30.8%	chr7	27249524	CCDS5413.1	c.350C>T	p.S117L
ERCC5	excision repair cross-complementing rodent repair deficiency; complementation group 5	ENSG00000134899	PAP55	70	21.4%	chr13	102302591	CCDS32004.1	c.211C>T	p.R71C
ERCC6L	excision repair cross-complementing rodent repair deficiency; complementation group 6-like	ENSG00000186871	PAP55	110	11.8%	chrX	71342235	CCDS35329.1	c.3107C>A	p.S1036Y
EXOC1	exocyst complex component 1	ENSG00000090989	PAP55	98	38.8%	chr4	56454512	CCDS3502.1	c.1762C>T	p.R588C
EXOC1	exocyst complex component 1	ENSG00000090989	PAP55	56	30.4%	chr4	56463304	CCDS3502.1	c.2375G>A	p.G792D
EXO1	exonuclease 1	ENSG00000174371	PAP55	145	27.6%	chr1	240091383	CCDS1620.1	c.997A>C	p.N333H
EXO1	exonuclease 1	ENSG00000174371	PAP55	102	30.4%	chr1	240109099	CCDS1620.1	c.1940A>C	p.N647T
EXPH5	exophilin 5	ENSG00000110723	PAP55	56	35.7%	chr11	107887652	CCDS8341.1	c.3792C>A	p.F1264L
EYA3	eyes absent homolog 3 (Drosophila)	ENSG00000158161	PAP55	173	33.5%	chr1	28192646	CCDS316.1	c.1155C>A	p.F385L
FOXRED1	FAD-dependent oxidoreductase domain containing 1	ENSG00000110074	PAP55	106	31.1%	chr11	125646584	CCDS8471.1	c.128C>T	p.S43L
FAM104B	family with sequence similarity 104; member B	ENSG00000182518	PAP55	104	17.3%	chrX	55202321	CCDS35305.1	c.86G>T	p.R29I
FAM107B	family with sequence similarity 107; member B	ENSG00000065809	PAP55	302	25.5%	chr10	14603894	CCDS7102.1	c.784C>T	p.R262W
FAM123C	family with sequence similarity 123C	ENSG00000178171	PAP55	184	30.4%	chr2	131236527	CCDS2164.1	c.412T>G	p.F138V
FAM135A	family with sequence similarity 135; member A	ENSG00000082269	PAP55	164	28.7%	chr6	71291378	CCDS34481.1	c.1231G>A	p.D411N
FAM160B2	family with sequence similarity 160; member B2	ENSG00000158863	PAP55	81	27.2%	chr8	22014415	ENST00000289921	c.1600G>A	p.E534K
FAM187B	family with sequence similarity 187; member B	ENSG00000177558	PAP55	357	32.5%	chr19	40407741	CCDS12448.1	c.937G>A	p.D313N
FAM194B	family with sequence similarity 194; member B	ENSG00000165837	PAP55	302	20.5%	chr13	45068694	NM_182542	c.448G>A	p.D150N
FAM49A	family with sequence similarity 49; member A	ENSG00000197872	PAP55	45	31.1%	chr2	16604237	CCDS1688.1	c.809G>A	p.G270E
FAM78A	family with sequence similarity 78; member A	ENSG00000126882	PAP55	189	28.6%	chr9	133126278	CCDS6941.2	c.604G>T	p.D202Y
FAM89A	family with sequence similarity 89; member A	ENSG00000182118	PAP55	164	28.7%	chr1	229222360	CCDS1590.1	c.427G>A	p.D143N
FASTKD2	FAST kinase domains 2	ENSG00000118246	PAP55	176	26.7%	chr2	207340152	CCDS2371.1	c.490A>C	p.N164H
FBXL3	F-box and leucine-rich repeat protein 3	ENSG00000005812	PAP55	150	29.3%	chr13	76493915	CCDS9457.1	c.82A>G	p.N28D
FBXW7	F-box and WD repeat domain containing 7	ENSG00000109670	PAP55	185	35.7%	chr4	153493081	CCDS3778.1	c.252T>G	p.I84M
FBXW8	F-box and WD repeat domain containing 8	ENSG00000174989	PAP55	122	30.3%	chr12	115907406	CCDS9182.1	c.848T>C	p.I283T
FBXO38	F-box protein 38	ENSG00000145868	PAP55	66	27.3%	chr5	147800218	CCDS4290.1	c.3209G>A	p.R1070Q

FBXO40	F-box protein 40	ENSG00000163833	PAP55	190	27.9%	chr3	122824185	CCDS33835.1	c.1219G>T	p.E407X
FEM1C	fem-1 homolog c (C. elegans)	ENSG00000145780	PAP55	73	31.5%	chr5	114888263	CCDS4118.1	c.1495C>T	p.R499W
FRMPD3	FERM and PDZ domain containing 3	ENSG00000147234	PAP55	76	27.6%	chrX	106684313	ENST00000276185	c.784C>T	p.R262X
FETUB	fetuin B	ENSG00000090512	PAP55	208	33.7%	chr3	187852944	CCDS3279.1	c.979C>G	p.H327D
FN1	fibronectin 1	ENSG00000115414	PAP55	92	23.9%	chr2	215982642	CCDS42814.1	c.2188G>A	p.E730K
FNDC1	fibronectin type III domain containing 1	ENSG00000164694	PAP55	38	36.8%	chr6	159567528	NM_032532	c.1108C>A	p.P370T
FBLN2	fibulin 2	ENSG00000163520	PAP55	101	29.7%	chr3	13587870	ENST00000295761	c.1011G>T	p.E337D
FILIP1	filamin A interacting protein 1	ENSG00000118407	PAP55	156	28.2%	chr6	76080888	CCDS4984.1	c.1380G>T	p.K460N
FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	ENSG00000102755	PAP55	206	37.4%	chr13	27862097	CCDS9330.1	c.1805A>C	p.Y602S
FLT4	fms-related tyrosine kinase 4	ENSG00000037280	PAP55	54	37.0%	chr5	179985577	CCDS4457.1	c.1319G>A	p.R440H
FSHR	follicle stimulating hormone receptor	ENSG00000170820	PAP55	109	51.4%	chr2	49069653	CCDS1843.1	c.491C>A	p.S164Y
FOXJ3	forkhead box J3	ENSG00000198815	PAP55	107	29.9%	chr1	42427121	CCDS30689.1	c.1519G>A	p.D507N
FOXO1	forkhead box O1	ENSG00000150907	PAP55	61	19.7%	chr13	40032988	CCDS9371.1	c.640C>T	p.R214C
FMN1	formin 1	ENSG00000186031	PAP55	363	31.1%	chr15	31048710	NM_001103184	c.1815A>C	p.L605F
FHOD1	formin homology 2 domain containing 1	ENSG00000135723	PAP55	129	30.2%	chr16	65828488	CCDS10834.1	c.1024G>A	p.E342K
FHL5	four and a half LIM domains 5	ENSG00000112214	PAP55	40	25.0%	chr6	97165313	CCDS5035.1	c.649C>A	p.L217I
FHIT	fragile histidine triad gene	ENSG00000189283	PAP55	54	25.9%	chr3	60497666	CCDS2894.1	c.70G>A	p.A24T
FXR1	fragile X mental retardation; autosomal homolog 1	ENSG00000114416	PAP55	58	32.8%	chr3	182149773	CCDS3238.1	c.578G>A	p.R193H
FZD5	frizzled homolog 5 (Drosophila)	ENSG00000163251	PAP55	57	29.8%	chr2	208340328	CCDS33366.1	c.1381G>A	p.A461T
FRY	furry homolog (Drosophila)	ENSG00000073910	PAP55	46	34.8%	chr13	31619488	CCDS41875.1	c.1249C>T	p.R417X
FYCO1	FYVE and coiled-coil domain containing 1	ENSG00000163820	PAP55	131	34.4%	chr3	45983744	CCDS2734.1	c.2086G>T	p.A696S
GPATCH8	G patch domain containing 8	ENSG00000186566	PAP55	45	35.6%	chr17	39897377	CCDS32666.1	c.182A>C	p.K61T
GPR143	G protein-coupled receptor 143	ENSG00000101850	PAP55	98	24.5%	chrX	9674147	CCDS14134.1	c.655T>C	p.Y219H
GPR149	G protein-coupled receptor 149	ENSG00000174948	PAP55	81	30.9%	chr3	155629792	CCDS43162.1	c.307T>G	p.F103V
GPR15	G protein-coupled receptor 15	ENSG00000154165	PAP55	97	25.8%	chr3	99734496	CCDS2931.1	c.929G>A	p.R310H
GPR155	G protein-coupled receptor 155	ENSG00000163328	PAP55	92	34.8%	chr2	175046075	CCDS2259.1	c.724G>A	p.E242K
GPR174	G protein-coupled receptor 174	ENSG00000147138	PAP55	218	27.5%	chrX	78313518	CCDS14443.1	c.358C>T	p.L120F
GPR180	G protein-coupled receptor 180	ENSG00000152749	PAP55	94	31.9%	chr13	94062462	CCDS9472.1	c.322G>A	p.E108K
GPR50	G protein-coupled receptor 50	ENSG00000102195	PAP55	259	36.7%	chrX	150100382	CCDS44012.1	c.1669G>A	p.D557N
GPR6	G protein-coupled receptor 6	ENSG00000146360	PAP55	181	32.6%	chr6	110408071	CCDS5079.1	c.1063C>T	p.R355C
GPR87	G protein-coupled receptor 87	ENSG00000138271	PAP55	238	28.6%	chr3	152495110	CCDS3157.1	c.614C>T	p.T205M
GPR98	G protein-coupled receptor 98	ENSG00000164199	PAP55	73	27.4%	chr5	90085313	NM_032119	c.11288C>T	p.S3763F
GPRC5C	G protein-coupled receptor; family C; group 5; member C	ENSG00000170412	PAP55	81	25.9%	chr17	69948322	CCDS11699.1	c.947A>G	p.N316S
GTSE1	G-2 and S-phase expressed 1	ENSG00000075218	PAP55	153	22.9%	chr22	45082933	CCDS14074.1	c.134NULL>AA	p.NULL-1FsIns5bp
GAL3ST1	galactose-3-O-sulfotransferase 1	ENSG00000128242	PAP55	144	34.0%	chr22	29280960	CCDS13879.1	c.1252C>T	p.R418C
GABRR1	gamma-aminobutyric acid (GABA) receptor; rho 1	ENSG00000146276	PAP55	102	28.4%	chr6	89945458	CCDS5019.1	c.1172T>C	p.L391P
GGT5	gamma-glutamyltransferase 5	ENSG00000099998	PAP55	81	29.6%	chr22	22951320	CCDS42990.1	c.1399C>T	p.R467C
GDAP1	ganglioside-induced differentiation-associated protein 1	ENSG00000104381	PAP55	45	24.4%	chr8	75437781	CCDS34911.1	c.632A>G	p.E211G
GJA10	gap junction protein; alpha 10; 62kDa	ENSG00000135355	PAP55	111	36.0%	chr6	90661702	CCDS5025.1	c.794C>A	p.S265Y
GJC1	gap junction protein; gamma 1; 45kDa	ENSG00000182963	PAP55	485	27.6%	chr17	40238156	CCDS11487.1	c.556G>A	p.V186M
GBX1	gastrulation brain homeobox 1	ENSG00000164900	PAP55	364	31.3%	chr7	150477094	CCDS43682.1	c.607G>A	p.E203K
GPHN	gephyrin	ENSG00000171723	PAP55	159	18.2%	chr14	66459173	CCDS9777.1	c.494C>T	p.A165V
GLUD2	glutamate dehydrogenase 2	ENSG00000182890	PAP55	129	27.9%	chrX	120010652	CCDS14603.1	c.1433T>G	p.F478C
GRIP1	glutamate receptor interacting protein 1	ENSG00000155974	PAP55	78	26.9%	chr12	65195762	CCDS41807.1	c.628C>T	p.R210W
GRIN2B	glutamate receptor; ionotropic; N-methyl D-aspartate 2B	ENSG00000150086	PAP55	204	28.9%	chr12	13608438	CCDS8662.1	c.3001G>A	p.D1001N
GRIN2B	glutamate receptor; ionotropic; N-methyl D-aspartate 2B	ENSG00000150086	PAP55	74	28.4%	chr12	13797641	CCDS8662.1	c.887G>T	p.G296V
GRM2	glutamate receptor; metabotropic 2	ENSG00000164082	PAP55	240	27.1%	chr3	51721710	CCDS2834.1	c.632C>T	p.A211V
GCLC	glutamate-cysteine ligase; catalytic subunit	ENSG00000001084	PAP55	75	28.0%	chr6	53473041	CCDS4952.1	c.1544A>G	p.Y515C
GSTCD	glutathione S-transferase; C-terminal domain containing	ENSG00000138780	PAP55	51	33.3%	chr4	106858350	CCDS43257.1	c.131A>C	p.K44T
GSTZ1	glutathione transferase zeta 1	ENSG00000100577	PAP55	106	28.3%	chr14	76861012	CCDS9858.1	c.62G>A	p.R21Q
GPC6	glypican 6	ENSG00000183098	PAP55	104	21.2%	chr13	93756374	CCDS9469.1	c.1148G>A	p.R383Q
GNAS	GNAS complex locus	ENSG00000087460	PAP55	46	26.1%	chr20	56863507	NM_080425	c.1792C>T	p.R598C

GRHL1	grainyhead-like 1 (Drosophila)	ENSG00000134317	PAP55	84	34.5%	chr2	10043738	CCDS33144.1	c.579C>A	p.F193L
GIGYF2	GRB10 interacting GYF protein 2	ENSG00000204120	PAP55	58	34.5%	chr2	233363688	CCDS33401.1	c.749A>G	p.E250G
GAB3	GRB2-associated binding protein 3	ENSG00000160219	PAP55	234	23.1%	chrX	153594773	CCDS14760.1	c.496G>A	p.V166I
GAS2L2	growth arrest-specific 2 like 2	ENSG00000132139	PAP55	123	30.9%	chr17	31097338	CCDS11298.1	c.1291G>A	p.D431N
GAS6	growth arrest-specific 6	ENSG00000183087	PAP55	66	27.3%	chr13	113587491	NM_000820	c.1549G>A	p.A517T
GDF10	growth differentiation factor 10	ENSG00000107623	PAP55	45	26.7%	chr10	48049544	CCDS7220.1	c.348C>A	p.F116L
GRB14	growth factor receptor-bound protein 14	ENSG00000115290	PAP55	75	30.7%	chr2	165073581	CCDS2222.1	c.844G>A	p.E282K
GNAI3	guanine nucleotide binding protein (G protein); alpha inhibiting activity polypeptide 3	ENSG00000065135	PAP55	138	30.4%	chr1	109926646	CCDS802.1	c.526C>T	p.R176W
GUCY1A2	guanylate cyclase 1; soluble; alpha 2	ENSG00000152402	PAP55	128	20.3%	chr11	106315509	CCDS8335.1	c.1093G>A	p.E365K
GUCY1A3	guanylate cyclase 1; soluble; alpha 3	ENSG00000164116	PAP55	88	26.1%	chr4	156851605	CCDS34085.1	c.838T>C	p.S280P
GUCY2C	guanylate cyclase 2C (heat stable enterotoxin receptor)	ENSG00000070019	PAP55	96	28.1%	chr12	14657435	CCDS8664.1	c.3105G>T	p.Q1035H
GUCY2D	guanylate cyclase 2D; membrane (retina-specific)	ENSG00000132518	PAP55	225	32.9%	chr17	7848008	CCDS11127.1	c.835G>A	p.D279N
GUCA1A	guanylate cyclase activator 1A (retina)	ENSG00000048545	PAP55	131	35.9%	chr6	42254586	CCDS4864.1	c.420C>A	p.F140L
H2AFZ	H2A histone family; member Z	ENSG00000164032	PAP55	74	31.1%	chr4	101089075	CCDS3654.1	c.241C>T	p.R81C
HR	hairless homolog (mouse)	ENSG00000168453	PAP55	63	31.7%	chr8	22039100	CCDS6022.1	c.1496G>T	p.S499I
HAUS2	HAUS augmin-like complex; subunit 2	ENSG00000137814	PAP55	110	34.5%	chr15	40646153	CCDS10090.1	c.555G>T	p.E185D
HBS1L	HBS1-like (S. cerevisiae)	ENSG00000112339	PAP55	62	19.4%	chr6	135332096	CCDS5173.1	c.1871C>T	p.T624M
HBS1L	HBS1-like (S. cerevisiae)	ENSG00000112339	PAP55	66	30.3%	chr6	135341556	CCDS5173.1	c.1751G>A	p.R584Q
HSF4	heat shock transcription factor 4	ENSG00000102878	PAP55	83	25.3%	chr16	65758955	CCDS42175.1	c.806C>T	p.S269F
HERC2	hect domain and RLD 2	ENSG00000128731	PAP55	43	25.6%	chr15	26167352	CCDS10021.1	c.3176G>A	p.R1059H
HMCN1	hemicentin 1	ENSG00000143341	PAP55	176	29.0%	chr1	184233192	CCDS30956.1	c.3787A>C	p.T1263P
HS3ST5	heparan sulfate (glucosamine) 3-O-sulfotransferase 5	ENSG00000175818	PAP55	77	19.5%	chr6	114485814	CCDS34517.1	c.341C>T	p.P114L
HERPUD2	HERPUD family member 2	ENSG00000122557	PAP55	78	26.9%	chr7	35640497	CCDS5446.1	c.1009G>A	p.E337K
HNRNPM	heterogeneous nuclear ribonucleoprotein M	ENSG00000099783	PAP55	58	20.7%	chr19	8437135	CCDS12203.1	c.647G>T	p.G216V
HDLBP	high density lipoprotein binding protein	ENSG00000115677	PAP55	67	31.3%	chr2	241826830	CCDS2547.1	c.2656C>T	p.R886X
HDX	highly divergent homeobox	ENSG00000165259	PAP55	199	21.6%	chrX	83610437	CCDS35342.1	c.950G>T	p.R317I
HNMT	histamine N-methyltransferase	ENSG00000150540	PAP55	35	28.6%	chr2	138444221	CCDS2181.1	c.154T>C	p.S52P
HIST1H3E	histone cluster 1; H3e	ENSG00000196966	PAP55	86	25.6%	chr6	26333578	CCDS4596.1	c.217C>T	p.R73X
HDAC6	histone deacetylase 6	ENSG00000094631	PAP55	121	32.2%	chrX	48551479	CCDS14306.1	c.728G>A	p.R243H
HDAC8	histone deacetylase 8	ENSG00000147099	PAP55	54	25.9%	chrX	71625574	CCDS14420.1	c.671A>G	p.Y224C
HTATSF1	HIV-1 Tat specific factor 1	ENSG00000102241	PAP55	58	34.5%	chrX	135421281	CCDS14657.1	c.1711G>A	p.E571K
BAT2L2	HLA-B associated transcript 2-like 2	ENSG00000117523	PAP55	210	29.5%	chr1	169819861	ENST00000392080	c.7546A>G	p.T2516A
HOXA6	homeobox A6	ENSG00000106006	PAP55	84	22.6%	chr7	27151939	CCDS5407.1	c.565G>A	p.A189T
HMBOX1	homeobox containing 1	ENSG00000147421	PAP55	143	25.2%	chr8	28964575	CCDS6071.1	c.1247C>T	p.A416V
HIPK1	homeodomain interacting protein kinase 1	ENSG00000163349	PAP55	120	26.7%	chr1	114285510	CCDS867.1	c.982C>T	p.R328C
HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	ENSG00000095951	PAP55	119	11.8%	chr6	12233368	CCDS43426.1	c.5354C>T	p.S1785L
IDS	iduronate 2-sulfatase	ENSG00000010404	PAP55	37	29.7%	chrX	148393728	CCDS14685.1	c.-1G>T	p.IVS1-1-1SpliceAcceptor
ILVBL	ilvB (bacterial acetolactate synthase)-like	ENSG00000105135	PAP55	74	27.0%	chr19	15087687	CCDS12325.1	c.1588G>A	p.E530K
IGDCC4	immunoglobulin superfamily; DCC subclass; member 4	ENSG00000103742	PAP55	63	23.8%	chr15	63467909	CCDS10206.1	c.2776C>T	p.R926C
IGSF10	immunoglobulin superfamily; member 10	ENSG00000152580	PAP55	196	34.2%	chr3	152637621	CCDS3160.1	c.7418T>C	p.V2473A
IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells; kinase beta	ENSG00000104365	PAP55	48	22.9%	chr8	42281922	CCDS6128.1	c.449A>C	p.N150T
IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells; kinase gamma	ENSG00000073009	PAP55	242	26.9%	chrX	153423806	NM_001099856	c.134G>T	p.R45I
IRS4	insulin receptor substrate 4	ENSG00000133124	PAP55	177	31.1%	chrX	107864873	CCDS14544.1	c.1358G>A	p.G453E
IGF1R	insulin-like growth factor 1 receptor	ENSG00000140443	PAP55	158	24.1%	chr15	97260304	CCDS10378.1	c.1178C>A	p.S393Y
IGF2R	insulin-like growth factor 2 receptor	ENSG00000197081	PAP55	44	29.5%	chr6	160414837	CCDS5273.1	c.5006G>A	p.R1669H
INTS7	integrator complex subunit 7	ENSG00000143493	PAP55	83	24.1%	chr1	210260141	CCDS1501.1	c.317G>T	p.R106I
ITFG1	integrin alpha FG-GAP repeat containing 1	ENSG00000129636	PAP55	43	34.9%	chr16	45902682	CCDS10728.1	c.1040C>T	p.A347V
ITGA9	integrin; alpha 9	ENSG00000144668	PAP55	59	25.4%	chr3	37700422	CCDS2669.1	c.1979C>A	p.S660Y

ITGAX	integrin; alpha X (complement component 3 receptor 4 subunit)	ENSG00000140678	PAP55	30	33.3%	chr16	31281558	CCDS10711.1	c.1342G>A	p.E448K
IFNA6	interferon; alpha 6	ENSG00000120235	PAP55	30	33.3%	chr9	21340744	CCDS6504.1	c.143C>A	p.S48Y
IL1RAPL2	interleukin 1 receptor accessory protein-like 2	ENSG00000189108	PAP55	116	22.4%	chrX	104898258	CCDS14517.1	c.2009C>A	p.S670Y
IL17RC	interleukin 17 receptor C	ENSG00000163702	PAP55	61	37.7%	chr3	9934009	CCDS2590.1	c.10C>T	p.P4S
IVL	involucrin	ENSG00000163207	PAP55	382	27.2%	chr1	151148999	CCDS1030.1	c.102G>T	p.M34I
IQGAP1	IQ motif containing GTPase activating protein 1	ENSG00000140575	PAP55	139	27.3%	chr15	88821417	CCDS10362.1	c.3055G>A	p.E1019K
JAK1	Janus kinase 1	ENSG00000162434	PAP55	36	36.1%	chr1	65111728	CCDS41346.1	c.396G>T	p.K132N
JUB	jub; ajuba homolog (Xenopus laevis)	ENSG00000129474	PAP55	255	30.2%	chr14	22521213	CCDS9581.1	c.103A>G	p.K35E
JMJD1C	jumonji domain containing 1C	ENSG00000171988	PAP55	211	28.4%	chr10	64638364	CCDS41532.1	c.3071G>A	p.R1024Q
KPNA3	karyopherin alpha 3 (importin alpha 4)	ENSG00000102753	PAP55	159	29.6%	chr13	49183108	CCDS9421.1	c.823G>T	p.E275X
KBTBD12	kelch repeat and BTB (POZ) domain containing 12	ENSG00000187715	PAP55	97	34.0%	chr3	129124842	NM_207335	c.248C>A	p.S83X
KBTBD5	kelch repeat and BTB (POZ) domain containing 5	ENSG00000157119	PAP55	59	47.5%	chr3	42702307	CCDS2703.1	c.193G>A	p.E65K
KLHL23	kelch-like 23 (Drosophila)	ENSG00000213160	PAP55	84	28.6%	chr2	170299904	CCDS2236.1	c.134G>A	p.G45D
KLHL31	kelch-like 31 (Drosophila)	ENSG00000124743	PAP55	115	26.1%	chr6	53627879	CCDS34478.1	c.151A>G	p.T51A
KLHL9	kelch-like 9 (Drosophila)	ENSG00000198642	PAP55	109	21.1%	chr9	21323187	CCDS6503.1	c.1672C>T	p.R558C
KRT23	keratin 23 (histone deacetylase inducible)	ENSG00000108244	PAP55	122	32.0%	chr17	36338072	CCDS11380.1	c.865G>A	p.E289K
KRT80	keratin 80	ENSG00000167767	PAP55	330	30.3%	chr12	50865436	CCDS8821.2	c.503G>A	p.R168Q
KRTAP10-3	keratin associated protein 10-3	ENSG00000212935	PAP55	68	25.0%	chr21	44802460	CCDS42956.1	c.567C>A	p.C189X
KRTAP24-1	keratin associated protein 24-1	ENSG00000188694	PAP55	47	21.3%	chr21	30576581	CCDS42915.1	c.541C>A	p.P181T
KIAA0368	KIAA0368	ENSG00000136813	PAP55	119	29.4%	chr9	113286831	NM_001080398	c.16A>G	p.K6E
KIAA0408	KIAA0408	ENSG00000189367	PAP55	128	18.0%	chr6	127813070	CCDS34531.1	c.256G>A	p.D86N
KIAA0430	KIAA0430	ENSG00000166783	PAP55	52	25.0%	chr16	15632789	CCDS10562.2	c.1301G>A	p.R434H
KIAA0564	KIAA0564	ENSG00000102763	PAP55	105	25.7%	chr13	41363566	CCDS41881.1	c.641A>C	p.K214T
KIAA0776	KIAA0776	ENSG00000014123	PAP55	44	31.8%	chr6	97083229	CCDS5034.1	c.596G>A	p.R199Q
KIAA1267	KIAA1267	ENSG00000120071	PAP55	374	18.4%	chr17	41604758	CCDS11503.1	c.529A>G	p.N177D
KIAA1432	KIAA1432	ENSG00000107036	PAP55	72	30.6%	chr9	5762740	CCDS34982.1	c.3556C>T	p.R1186W
KIAA1586	KIAA1586	ENSG00000168116	PAP55	96	24.0%	chr6	57027561	CCDS34480.1	c.2305C>T	p.R769W
KIAA1755	KIAA1755	ENSG00000149633	PAP55	47	42.6%	chr20	36303646	CCDS33467.1	c.301C>T	p.R101C
KIAA2013	KIAA2013	ENSG00000116685	PAP55	68	19.1%	chr1	11906007	CCDS141.1	c.1160G>A	p.R387Q
KLRD1	killer cell lectin-like receptor subfamily D; member 1	ENSG00000134539	PAP55	93	28.0%	chr12	10353302	CCDS8621.1	c.56T>C	p.I19T
KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	ENSG00000128052	PAP55	97	35.1%	chr4	55675845	CCDS3497.1	c.611T>A	p.I204N
KIF12	kinesin family member 12	ENSG00000136883	PAP55	162	34.0%	chr9	115897400	CCDS6801.1	c.515G>A	p.R172Q
KIF20B	kinesin family member 20B	ENSG00000138182	PAP55	92	28.3%	chr10	91487706	CCDS7407.1	c.3008G>A	p.R1003Q
KIF24	kinesin family member 24	ENSG00000186638	PAP55	202	31.7%	chr9	34246886	NM_194313	c.2719G>A	p.D907N
KIF5A	kinesin family member 5A	ENSG00000155980	PAP55	45	28.9%	chr12	56251379	CCDS8945.1	c.1302A>C	p.E434D
KLB	klotho beta	ENSG00000134962	PAP55	178	27.0%	chr4	39124483	CCDS3451.1	c.1742A>G	p.N581S
KANK1	KN motif and ankyrin repeat domains 1	ENSG00000107104	PAP55	72	29.2%	chr9	721188	CCDS34976.1	c.2927C>T	p.S976F
KLF17	Kruppel-like factor 17	ENSG00000171872	PAP55	62	17.7%	chr1	44368390	CCDS508.1	c.860A>G	p.Y287C
L1CAM	L1 cell adhesion molecule	ENSG00000198910	PAP55	73	26.0%	chrX	152783300	CCDS14733.1	c.3100G>A	p.V1034I
L2HGDH	L-2-hydroxyglutarate dehydrogenase	ENSG00000087299	PAP55	45	28.9%	chr14	49783621	CCDS9698.1	c.1297C>A	p.L433I
LACTBL1	lactamase; beta-like 1	ENSG00000215906	PAP55	171	30.4%	chr1	23157921	ENST00000401081	c.352G>T	p.D118Y
LCT	lactase	ENSG00000115850	PAP55	206	30.6%	chr2	136283503	CCDS2178.1	c.2884G>A	p.D962N
LASS5	LAG1 homolog; ceramide synthase 5	ENSG00000139624	PAP55	81	25.9%	chr12	48810740	CCDS8801.1	c.1034C>T	p.S345L
LBR	lamin B receptor	ENSG00000143815	PAP55	71	22.5%	chr1	223665720	CCDS1545.1	c.1130G>A	p.R377Q
LAMA3	laminin; alpha 3	ENSG00000053747	PAP55	74	33.8%	chr18	19681440	CCDS42419.1	c.3946C>T	p.R1316W
LGALS13	lectin; galactoside-binding; soluble; 13	ENSG00000105198	PAP55	35	31.4%	chr19	44789782	CCDS33024.1	c.383G>T	p.R128I
LRFN5	leucine rich repeat and fibronectin type III domain containing 5	ENSG00000165379	PAP55	63	31.7%	chr14	41430606	CCDS9678.1	c.1789G>A	p.E597K
LRRC52	leucine rich repeat containing 52	ENSG00000162763	PAP55	158	18.4%	chr1	163780263	CCDS30930.1	c.106G>T	p.E36X
LRRC7	leucine rich repeat containing 7	ENSG00000033122	PAP55	202	29.7%	chr1	70276524	CCDS645.1	c.2315C>T	p.S772L
LRRC8B	leucine rich repeat containing 8 family; member B	ENSG00000197147	PAP55	158	24.7%	chr1	89822050	CCDS724.1	c.1253C>T	p.A418V
LRRTM4	leucine rich repeat transmembrane neuronal 4	ENSG00000176204	PAP55	103	31.1%	chr2	77599922	NM_001134745	c.581G>A	p.R194Q

LZTS1	leucine zipper; putative tumor suppressor 1	ENSG00000061337	PAP55	110	25.5%	chr8	20156778	CCDS6015.1	c.195C>A	p.F65L
LRG1	leucine-rich alpha-2-glycoprotein 1	ENSG00000171236	PAP55	79	25.3%	chr19	4489710	CCDS12130.1	c.286G>T	p.E96X
LRPPRC	leucine-rich PPR-motif containing	ENSG00000138095	PAP55	28	35.7%	chr2	43980197	CCDS33189.1	c.3621G>T	p.E1207D
LRRK2	leucine-rich repeat kinase 2	ENSG00000188906	PAP55	132	21.2%	chr12	38958327	CCDS31774.1	c.2238T>G	p.C746W
LRRK2	leucine-rich repeat kinase 2	ENSG00000188906	PAP55	94	27.7%	chr12	38967463	CCDS31774.1	c.2544G>T	p.M848I
LRIT2	leucine-rich repeat; immunoglobulin-like and transmembrane domains 2	ENSG00000204033	PAP55	78	24.4%	chr10	85974768	CCDS31234.1	c.193T>G	p.S65A
LRTM1	leucine-rich repeats and transmembrane domains 1	ENSG00000144771	PAP55	122	29.5%	chr3	54933802	CCDS2876.1	c.488G>A	p.R163Q
LECT1	leukocyte cell derived chemotaxin 1	ENSG00000136110	PAP55	56	28.6%	chr13	52196162	CCDS9437.1	c.439G>A	p.V147M
LIMCH1	LIM and calponin homology domains 1	ENSG00000064042	PAP55	76	19.7%	chr4	41382582	CCDS33977.1	c.2914G>A	p.E972K
LPIN2	lipin 2	ENSG00000101577	PAP55	99	24.2%	chr18	2950688	CCDS11829.1	c.151C>T	p.R51W
LRP1B	low density lipoprotein receptor-related protein 1B	ENSG00000168702	PAP55	187	27.8%	chr2	141456288	CCDS2182.1	c.2798C>A	p.S933Y
LRP2	low density lipoprotein receptor-related protein 2	ENSG00000081479	PAP55	27	40.7%	chr2	169774236	CCDS2232.1	c.6442C>T	p.R2148W
LRP2BP	LRP2 binding protein	ENSG00000109771	PAP55	82	30.5%	chr4	186528910	CCDS3840.1	c.856G>A	p.D286N
LSM11	LSM11; U7 small nuclear RNA associated	ENSG00000155858	PAP55	105	27.6%	chr5	157114807	CCDS4342.1	c.1040T>G	p.F347C
LHCGR	luteinizing hormone/choriogonadotropin receptor	ENSG00000138039	PAP55	105	25.7%	chr2	48769005	CCDS1842.1	c.1435C>T	p.R479X
LY6K	lymphocyte antigen 6 complex; locus K	ENSG00000160886	PAP55	94	34.0%	chr8	143781648	CCDS6385.1	c.529C>T	p.R177C
LYRM7	Lyrm7 homolog (mouse)	ENSG00000186687	PAP55	92	16.3%	chr5	130563166	CCDS4148.1	c.288T>G	p.Y96X
KDM4C	lysine (K)-specific demethylase 4C	ENSG00000107077	PAP55	89	25.8%	chr9	6839645	CCDS6471.1	c.574G>A	p.E192K
LPAR4	lysophosphatidic acid receptor 4	ENSG00000147145	PAP55	183	28.4%	chrX	77897456	CCDS14441.1	c.434G>A	p.R145Q
LAPTM4A	lysosomal protein transmembrane 4 alpha	ENSG00000068697	PAP55	105	32.4%	chr2	20097608	CCDS1696.1	c.578G>A	p.R193Q
LYST	lysosomal trafficking regulator	ENSG00000143669	PAP55	77	24.7%	chr1	234034486	CCDS31062.1	c.3496C>T	p.R1166X
LYZL2	lysozyme-like 2	ENSG00000151033	PAP55	126	30.2%	chr10	30941771	CCDS7167.2	c.501A>C	p.Q167H
MST1R	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	ENSG00000164078	PAP55	141	32.6%	chr3	49915818	CCDS2807.1	c.229C>T	p.R77C
MAEL	maelstrom homolog (Drosophila)	ENSG00000143194	PAP55	82	18.3%	chr1	165241183	CCDS1257.1	c.770T>G	p.F257C
MDGA2	MAM domain containing glycosylphosphatidylinositol anchor 2	ENSG00000139915	PAP55	42	23.8%	chr14	46380891	CCDS41948.1	c.2177G>A	p.R726Q
MGAT4C	mannosyl (alpha-1;3-)-glycoprotein beta-1;4-N-acetylglucosaminyltransferase; isozyme C (putative)	ENSG00000182050	PAP55	126	32.5%	chr12	84898130	CCDS9030.1	c.505T>G	p.L169V
MMP1	matrix metallopeptidase 1 (interstitial collagenase)	ENSG00000196611	PAP55	93	29.0%	chr11	102173437	CCDS8322.1	c.110A>G	p.Y37C
MMP27	matrix metallopeptidase 27	ENSG00000137675	PAP55	117	22.2%	chr11	102080629	CCDS8319.1	c.190C>T	p.R64W
MXRA5	matrix-remodelling associated 5	ENSG00000101825	PAP55	215	26.0%	chrX	3251613	CCDS14124.1	c.2113G>A	p.G705R
MCF2	MCF.2 cell line derived transforming sequence	ENSG00000101977	PAP55	66	27.3%	chrX	138506530	CCDS14667.1	c.2121G>T	p.K707N
MCF2L2	MCF.2 cell line derived transforming sequence-like 2	ENSG00000053524	PAP55	55	40.0%	chr3	184428835	CCDS3243.1	c.2059G>T	p.E687X
MTOR	mechanistic target of rapamycin (serine/threonine kinase)	ENSG00000198793	PAP55	89	22.5%	chr1	11223166	CCDS127.1	c.1567G>A	p.D523N
MED1	mediator complex subunit 1	ENSG00000125686	PAP55	54	20.4%	chr17	34829513	CCDS11336.1	c.1280G>T	p.R427I
MED14	mediator complex subunit 14	ENSG00000180182	PAP55	113	29.2%	chrX	40416101	CCDS14254.1	c.3089G>A	p.S1030N
MAGEB16	melanoma antigen family B; 16	ENSG00000189023	PAP55	182	26.4%	chrX	35730569	CCDS43927.1	c.335C>T	p.A112V
MAGED1	melanoma antigen family D; 1	ENSG00000179222	PAP55	255	26.7%	chrX	51661751	CCDS35279.1	c.2490C>A	p.F830L
MBOAT2	membrane bound O-acyltransferase domain containing 2	ENSG00000143797	PAP55	86	30.2%	chr2	8926124	CCDS1660.1	c.890C>T	p.A297V
40241	membrane-associated ring finger (C3HC4) 4	ENSG00000144583	PAP55	178	28.7%	chr2	216850703	CCDS33376.1	c.802C>T	p.R268C
MS4A12	membrane-spanning 4-domains; subfamily A; member 12	ENSG00000071203	PAP55	40	32.5%	chr11	60025169	CCDS7988.1	c.352G>T	p.E118X
MS4A2	membrane-spanning 4-domains; subfamily A; member 2 (Fc fragment of IgE; high affinity I; receptor for; beta polypeptide)	ENSG00000149534	PAP55	179	29.1%	chr11	59619680	CCDS7980.1	c.710A>G	p.E237G
MS4A7	membrane-spanning 4-domains; subfamily A; member 7	ENSG00000166927	PAP55	93	17.2%	chr11	59917891	CCDS7985.1	c.704C>A	p.S235Y
MEOX2	mesenchyme homeobox 2	ENSG00000106511	PAP55	81	22.2%	chr7	15632931	CCDS34605.1	c.655G>A	p.E219K
MACC1	metastasis associated in colon cancer 1	ENSG00000183742	PAP55	82	26.8%	chr7	20165105	CCDS5369.1	c.1404A>C	p.Q468H
MAP1B	microtubule-associated protein 1B	ENSG00000131711	PAP55	37	35.1%	chr5	71527772	CCDS4012.1	c.2834A>C	p.K945T
MAP4	microtubule-associated protein 4	ENSG00000047849	PAP55	163	29.4%	chr3	47926366	NM_030884	c.370G>A	p.E124K
MAP9	microtubule-associated protein 9	ENSG00000164114	PAP55	81	35.8%	chr4	156509125	ENST00000379248	c.552G>T	p.M184I
MTPAP	mitochondrial poly(A) polymerase	ENSG00000107951	PAP55	81	19.8%	chr10	30651384	CCDS7165.1	c.1387NULL>T	p.NULL-1FsIns1bp

MRPL47	mitochondrial ribosomal protein L47	ENSG00000136522	PAP55	67	22.4%	chr3	180789434	CCDS3232.1	c.673A>C	p.N225H
MRPL49	mitochondrial ribosomal protein L49	ENSG00000149792	PAP55	21	47.6%	chr11	64649608	CCDS8096.1	c.302C>T	p.T101M
MAP3K3	mitogen-activated protein kinase kinase kinase 3	ENSG00000198909	PAP55	118	27.1%	chr17	59098125	CCDS32701.1	c.568G>A	p.E190K
MAP3K3	mitogen-activated protein kinase kinase kinase 3	ENSG00000198909	PAP55	108	31.5%	chr17	59116636	CCDS32701.1	c.757A>C	p.N253H
MAP4K1	mitogen-activated protein kinase kinase kinase kinase 1	ENSG00000104814	PAP55	149	28.9%	chr19	43800065	CCDS42564.1	c.140T>C	p.M47T
MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	ENSG00000114738	PAP55	202	32.7%	chr3	50652916	CCDS2832.1	c.335G>A	p.R112H
MUC4	mucin 4; cell surface associated	ENSG00000145113	PAP55	71	19.7%	chr3	196979234	CCDS3310.1	c.881G>A	p.R294H
MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	ENSG00000172175	PAP55	33	30.3%	chr18	54551743	CCDS11967.1	c.1357G>T	p.E453X
MMRN1	multimerin 1	ENSG00000138722	PAP55	185	31.9%	chr4	91076610	CCDS3635.1	c.2756C>T	p.S919L
MEGF11	multiple EGF-like-domains 11	ENSG00000157890	PAP55	60	43.3%	chr15	63995591	CCDS10213.1	c.2068A>G	p.S690G
MSH2	mutS homolog 2; colon cancer; nonpolyposis type 1 (E. coli)	ENSG00000095002	PAP55	175	26.3%	chr2	47558976	CCDS1834.1	c.2272G>A	p.D758N
MYCBP2	MYC binding protein 2	ENSG00000005810	PAP55	141	31.2%	chr13	76570322	CCDS31994.1	c.8854C>T	p.R2952X
MPZL3	myelin protein zero-like 3	ENSG00000160588	PAP55	61	29.5%	chr11	117613102	CCDS8392.1	c.324A>C	p.K108N
MYT1	myelin transcription factor 1	ENSG00000196132	PAP55	60	31.7%	chr20	62307487	CCDS13558.1	c.287A>C	p.D96A
MYOCD	myocardin	ENSG00000141052	PAP55	155	24.5%	chr17	12596481	CCDS11163.1	c.1151G>A	p.R384Q
MYO1E	myosin IE	ENSG00000157483	PAP55	63	44.4%	chr15	57274986	CCDS32254.1	c.1771G>A	p.E591K
MYO9A	myosin IXA	ENSG00000066933	PAP55	113	22.1%	chr15	70125459	CCDS10239.1	c.500G>A	p.R167Q
MYLK4	myosin light chain kinase family; member 4	ENSG00000145949	PAP55	61	31.1%	chr6	2624546	CCDS34330.1	c.854A>G	p.D285G
MYO6	myosin VI	ENSG00000196586	PAP55	51	31.4%	chr6	76653319	CCDS34487.1	c.2546G>A	p.R849Q
MYO16	myosin XVI	ENSG00000041515	PAP55	55	18.2%	chr13	108459309	CCDS32008.1	c.2440G>A	p.E814K
MYH1	myosin; heavy chain 1; skeletal muscle; adult	ENSG00000109061	PAP55	63	27.0%	chr17	10344773	CCDS11155.1	c.3760C>T	p.R1254C
MYH4	myosin; heavy chain 4; skeletal muscle	ENSG00000141048	PAP55	49	24.5%	chr17	10289329	CCDS11154.1	c.5245G>A	p.V1749I
MYH4	myosin; heavy chain 4; skeletal muscle	ENSG00000141048	PAP55	63	30.2%	chr17	10299861	CCDS11154.1	c.2051C>T	p.T684I
MYH7	myosin; heavy chain 7; cardiac muscle; beta	ENSG00000092054	PAP55	110	25.5%	chr14	22963819	CCDS9601.1	c.2678C>T	p.A893V
MTMR11	myotubularin related protein 11	ENSG00000014914	PAP55	61	26.2%	chr1	148170798	CCDS942.1	c.818G>A	p.R273Q
MTMR15	myotubularin related protein 15	ENSG00000198690	PAP55	50	40.0%	chr15	29001767	CCDS32186.1	c.2090G>T	p.R697I
MTMR2	myotubularin related protein 2	ENSG00000087053	PAP55	202	34.2%	chr11	95222595	CCDS8305.1	c.884G>A	p.R295Q
MTMR6	myotubularin related protein 6	ENSG00000139505	PAP55	149	30.9%	chr13	24721488	CCDS9313.1	c.1748G>A	p.R583Q
NAA15	N(alpha)-acetyltransferase 15; NatA auxiliary subunit	ENSG00000164134	PAP55	29	44.8%	chr4	140483534	CCDS43270.1	c.507G>T	p.K169N
NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2; 24kDa	ENSG00000178127	PAP55	77	31.2%	chr18	9112581	CCDS11842.1	c.371G>A	p.R124Q
NCKAP1L	NCK-associated protein 1-like	ENSG00000123338	PAP55	152	33.6%	chr12	53203904	CCDS31813.1	c.2053G>T	p.E685X
NCKAP5	NCK-associated protein 5	ENSG00000176771	PAP55	48	37.5%	chr2	133352904	NM_207363	c.635G>A	p.R212Q
NEBL	nebulette	ENSG00000078114	PAP55	64	20.3%	chr10	21169718	CCDS7134.1	c.1294C>A	p.L432I
NRAP	nebulin-related anchoring protein	ENSG00000197893	PAP55	77	24.7%	chr10	115403811	CCDS7579.1	c.424G>A	p.E142K
NDNL2	necdin-like 2	ENSG00000185115	PAP55	267	30.3%	chr15	27348415	CCDS10023.1	c.787G>A	p.V263I
N4BP2	NEDD4 binding protein 2	ENSG00000078177	PAP55	287	33.1%	chr4	39780797	CCDS3457.1	c.937C>T	p.R313W
N4BP2	NEDD4 binding protein 2	ENSG00000078177	PAP55	84	27.4%	chr4	39798530	CCDS3457.1	c.2404A>C	p.K802Q
NLK	nemo-like kinase	ENSG00000087095	PAP55	53	26.4%	chr17	23519773	NM_016231	c.1010G>A	p.R337Q
NPHP3	nephronophthisis 3 (adolescent)	ENSG00000113971	PAP55	59	23.7%	chr3	133901932	CCDS3078.1	c.1679T>G	p.F560C
NPHS1	nephrosis 1; congenital; Finnish type (nephrin)	ENSG00000161270	PAP55	32	43.8%	chr19	41032055	CCDS32996.1	c.763G>A	p.V255M
NRG3	neuregulin 3	ENSG00000185737	PAP55	45	31.1%	chr10	84488382	CCDS31233.1	c.1023T>G	p.D341E
NRG3	neuregulin 3	ENSG00000185737	PAP55	104	30.8%	chr10	84735201	CCDS31233.1	c.1951G>A	p.E651K
NRXN2	neurexin 2	ENSG00000110076	PAP55	28	39.3%	chr11	64192649	CCDS8077.1	c.1201A>G	p.T401A
NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	ENSG00000213281	PAP55	124	22.6%	chr1	115060271	CCDS877.1	c.34G>T	p.G12C
NEUROG1	neurogenin 1	ENSG00000181965	PAP55	54	35.2%	chr5	134898960	CCDS4187.1	c.320A>G	p.N107S
NMUR1	neuromedin U receptor 1	ENSG00000171596	PAP55	98	31.6%	chr2	232098254	CCDS2486.1	c.1025G>A	p.G342D
NAV2	neuron navigator 2	ENSG00000166833	PAP55	89	29.2%	chr11	19962285	CCDS7851.1	c.2753G>A	p.R918H
NAV2	neuron navigator 2	ENSG00000166833	PAP55	65	30.8%	chr11	20023191	CCDS7851.1	c.3370G>A	p.E1124K
NPAS4	neuronal PAS domain protein 4	ENSG00000174576	PAP55	240	23.3%	chr11	65947988	CCDS8138.1	c.1051C>A	p.L351I
NPSR1	neuropeptide S receptor 1	ENSG00000187258	PAP55	137	33.6%	chr7	34840544	CCDS5443.1	c.704G>A	p.R235Q
NSMAF	neutral sphingomyelinase (N-SMase) activation associated factor	ENSG00000035681	PAP55	83	28.9%	chr8	59661107	CCDS6173.1	c.2453G>A	p.R818H
NKAP	NFKB activating protein	ENSG00000101882	PAP55	80	35.0%	chrX	118943356	CCDS14592.1	c.1103G>A	p.R368Q

NID1	nidogen 1	ENSG00000116962	PAP55	45	44.4%	chr1	234241963	CCDS1608.1	c.2408T>C	p.V803A
NID2	nidogen 2 (osteonidogen)	ENSG00000087303	PAP55	89	31.5%	chr14	51604564	CCDS9706.1	c.296T>C	p.F99S
NEK10	NIMA (never in mitosis gene a)- related kinase 10	ENSG00000163491	PAP55	135	25.2%	chr3	27178995	ENST00000396636	c.1162A>T	p.S388C
NIN	ninein (GSK3B interacting protein)	ENSG00000100503	PAP55	51	31.4%	chr14	50280818	CCDS41952.1	c.5080G>A	p.D1694N
NOS3	nitric oxide synthase 3 (endothelial cell)	ENSG00000164867	PAP55	92	33.7%	chr7	150334983	CCDS5912.1	c.1894G>A	p.E632K
NOSTRIN	nitric oxide synthase trafficker	ENSG00000163072	PAP55	32	31.3%	chr2	169429615	CCDS42771.1	c.1410A>C	p.K470N
NLRC5	NLR family; CARD domain containing 5	ENSG00000140853	PAP55	67	28.4%	chr16	55638995	CCDS10773.1	c.3376C>T	p.R1126C
NLRP2	NLR family; pyrin domain containing 2	ENSG00000022556	PAP55	76	31.6%	chr19	60193749	CCDS12913.1	c.2605G>A	p.E869K
NLRP4	NLR family; pyrin domain containing 4	ENSG00000160505	PAP55	38	34.2%	chr19	61055346	CCDS12936.1	c.88C>A	p.L30I
NLRP4	NLR family; pyrin domain containing 4	ENSG00000160505	PAP55	175	25.7%	chr19	61061415	CCDS12936.1	c.844G>A	p.V282M
NLRP5	NLR family; pyrin domain containing 5	ENSG00000171487	PAP55	77	31.2%	chr19	61207131	NM_153447	c.300A>T	p.E100D
NLRP9	NLR family; pyrin domain containing 9	ENSG00000185792	PAP55	86	20.9%	chr19	60936089	CCDS12934.1	c.920T>G	p.F307C
NOTCH2	Notch homolog 2 (Drosophila)	ENSG00000134250	PAP55	113	29.2%	chr1	120259826	CCDS908.1	c.7042T>G	p.L2348V
NOTCH2	Notch homolog 2 (Drosophila)	ENSG00000134250	PAP55	36	36.1%	chr1	120267834	CCDS908.1	c.4808A>C	p.Q1603P
NFIA	nuclear factor I/A	ENSG00000162599	PAP55	124	32.3%	chr1	61326907	CCDS615.1	c.526G>A	p.D176N
NSD1	nuclear receptor binding SET domain protein 1	ENSG00000165671	PAP55	192	31.3%	chr5	176495191	CCDS4412.1	c.481G>A	p.D161N
NR6A1	nuclear receptor subfamily 6; group A; member 1	ENSG00000148200	PAP55	49	26.5%	chr9	126340286	CCDS35137.1	c.730C>T	p.R244C
NOC3L	nucleolar complex associated 3 homolog (S. cerevisiae)	ENSG00000173145	PAP55	125	28.0%	chr10	96104715	CCDS7433.1	c.691A>C	p.N231H
NUP153	nucleoporin 153kDa	ENSG00000124789	PAP55	102	25.5%	chr6	17773528	CCDS4541.1	c.1136G>A	p.R379Q
NUP210	nucleoporin 210kDa	ENSG00000132182	PAP55	118	28.8%	chr3	13392924	CCDS33704.1	c.1160G>A	p.R387Q
NUP214	nucleoporin 214kDa	ENSG00000126883	PAP55	374	22.2%	chr9	133062824	CCDS6940.1	c.4122T>G	p.F1374L
NUDCD3	NudC domain containing 3	ENSG00000015676	PAP55	207	32.4%	chr7	44491354	CCDS5490.2	c.247G>A	p.E83K
NULL	NULL	ENSG00000189277	PAP55	96	37.5%	chr2	186380875	ENST00000343098	c.2691A>C	p.K897N
NULL	NULL	ENSG00000202582	PAP55	79	32.9%	chr12	48559463	ENST00000365712	c.766A>G	p.M256V
NULL	NULL	ENSG00000215490	PAP55	37	27.0%	chr18	31118807	ENST00000400443	c.245C>A	p.S82Y
NULL	NULL	MI0003150	PAP55	95	31.6%	chr19	58889511	MI0003150	c.53A>G	p.K18R
NULL	NULL	NM_018901	PAP55	75	33.3%	chr5	140217682	NM_018901	c.1865G>A	p.R622H
OBSL1	obscurin-like 1	ENSG00000124006	PAP55	51	27.5%	chr2	220139876	NM_015311	c.2054C>T	p.A685V
OCRL	oculocerebrorenal syndrome of Lowe	ENSG00000122126	PAP55	40	42.5%	chrX	128528920	CCDS35393.1	c.1365T>G	p.I455M
ODZ1	odz; odd Oz/ten-m homolog 1(Drosophila)	ENSG00000009694	PAP55	63	20.6%	chrX	123353875	CCDS14609.1	c.5375A>G	p.H1792R
OLFML2A	olfactomedin-like 2A	ENSG00000185585	PAP55	49	26.5%	chr9	126589322	CCDS6857.2	c.338C>T	p.A113V
OR1S2	olfactory receptor; family 1; subfamily S; member 2	ENSG00000197887	PAP55	71	32.4%	chr11	57727884	CCDS31545.1	c.346T>C	p.F116L
OR10H3	olfactory receptor; family 10; subfamily H; member 3	ENSG00000171936	PAP55	630	14.1%	chr19	15713363	CCDS12334.1	c.161G>A	p.R54H
OR10H5	olfactory receptor; family 10; subfamily H; member 5	ENSG00000172519	PAP55	80	33.8%	chr19	15766389	CCDS32940.1	c.531C>A	p.F177L
OR10J5	olfactory receptor; family 10; subfamily J; member 5	ENSG00000184155	PAP55	99	20.2%	chr1	157772400	CCDS30910.1	c.22G>T	p.E8X
OR11H6	olfactory receptor; family 11; subfamily H; member 6	ENSG00000176219	PAP55	57	29.8%	chr14	19762639	CCDS32033.1	c.931C>T	p.R311X
OR14A16	olfactory receptor; family 14; subfamily A; member 16	ENSG00000196772	PAP55	110	28.2%	chr1	246045101	CCDS31097.1	c.554T>G	p.I185S
OR14C36	olfactory receptor; family 14; subfamily C; member 36	ENSG00000177174	PAP55	248	25.4%	chr1	246579006	CCDS31112.1	c.307G>T	p.V103F
OR4A15	olfactory receptor; family 4; subfamily A; member 15	ENSG00000181958	PAP55	225	28.0%	chr11	54892750	CCDS31500.1	c.815T>C	p.V272A
OR4C15	olfactory receptor; family 4; subfamily C; member 15	ENSG00000181939	PAP55	105	36.2%	chr11	55078835	CCDS31501.1	c.477C>A	p.F159L
OR4K5	olfactory receptor; family 4; subfamily K; member 5	ENSG00000176281	PAP55	287	28.6%	chr14	19459180	CCDS32024.1	c.575C>A	p.S192Y
OR5AN1	olfactory receptor; family 5; subfamily AN; member 1	ENSG00000176495	PAP55	217	37.3%	chr11	58889142	CCDS31559.1	c.635C>T	p.A212V
OR5M9	olfactory receptor; family 5; subfamily M; member 9	ENSG00000150269	PAP55	47	23.4%	chr11	55986653	CCDS31531.1	c.801G>T	p.E267D
OR51B4	olfactory receptor; family 51; subfamily B; member 4	ENSG00000183251	PAP55	143	27.3%	chr11	5279724	CCDS7757.1	c.29T>G	p.F10C
OR51D1	olfactory receptor; family 51; subfamily D; member 1	ENSG00000197428	PAP55	180	26.7%	chr11	4617912	CCDS31357.1	c.316G>A	p.E106K
OR51I2	olfactory receptor; family 51; subfamily I; member 2	ENSG00000187918	PAP55	290	24.5%	chr11	5431602	CCDS31383.1	c.308T>G	p.L103R
OR52A5	olfactory receptor; family 52; subfamily A; member 5	ENSG00000171944	PAP55	321	27.1%	chr11	5110163	CCDS31373.1	c.286T>G	p.F96V
OR52E4	olfactory receptor; family 52; subfamily E; member 4	ENSG00000180974	PAP55	178	28.1%	chr11	5862583	CCDS31401.1	c.485T>C	p.V162A
OR6C2	olfactory receptor; family 6; subfamily C; member 2	ENSG00000179695	PAP55	105	24.8%	chr12	54132694	CCDS31824.1	c.430C>T	p.L144F
OR6T1	olfactory receptor; family 6; subfamily T; member 1	ENSG00000181499	PAP55	100	20.0%	chr11	123318922	CCDS31700.1	c.834C>A	p.S278R
OR9G4	olfactory receptor; family 9; subfamily G; member 4	ENSG00000172457	PAP55	59	44.1%	chr11	56267670	CCDS31537.1	c.194G>A	p.R65Q
OR9Q1	olfactory receptor; family 9; subfamily Q; member 1	ENSG00000186509	PAP55	163	25.2%	chr11	57704026	CCDS31543.1	c.534C>A	p.F178L

OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	ENSG00000147162	PAP55	57	24.6%	chrX	70693678	CCDS14414.1	c.1318A>G	p.K440E
OSMR	oncostatin M receptor	ENSG00000145623	PAP55	106	28.3%	chr5	38957642	CCDS3928.1	c.1754T>C	p.V585A
OTUD5	OTU domain containing 5	ENSG00000068308	PAP55	43	27.9%	chrX	48676814	CCDS14313.1	c.941T>G	p.F314C
OSGIN2	oxidative stress induced growth inhibitor family member 2	ENSG00000164823	PAP55	84	29.8%	chr8	91006822	CCDS6248.1	c.1405A>T	p.N469Y
OSBPL9	oxysterol binding protein-like 9	ENSG00000117859	PAP55	148	24.3%	chr1	52019453	CCDS41332.1	c.1286G>A	p.R429Q
PNMA3	paraneoplastic antigen MA3	ENSG00000183837	PAP55	86	37.2%	chrX	151976834	CCDS35435.2	c.766G>A	p.A256T
PTH	parathyroid hormone	ENSG00000152266	PAP55	191	25.1%	chr11	13470911	CCDS7812.1	c.68C>T	p.S23L
PASD1	PAS domain containing 1	ENSG00000166049	PAP55	54	33.3%	chrX	150567831	CCDS35431.1	c.-1G>A	p.IVS8+1-1SpliceDonor
PTCHD1	patched domain containing 1	ENSG00000165186	PAP55	240	23.3%	chrX	23321839	CCDS35215.2	c.2283T>G	p.I761M
PTCHD3	patched domain containing 3	ENSG00000182077	PAP55	89	27.0%	chr10	27727600	NM_001034842	c.1933G>A	p.V645I
PEG3	paternally expressed 3	ENSG00000198300	PAP55	217	23.0%	chr19	62018856	CCDS12948.1	c.2766C>A	p.F922L
PEG3AS	PEG3 antisense RNA (non-protein coding)	ENSG00000198300	PAP55	217	23.0%	chr19	62018856	CCDS12948.1	c.2766C>A	p.F922L
PPIL6	peptidylprolyl isomerase (cyclophilin)-like 6	ENSG00000185250	PAP55	56	23.2%	chr6	109859232	CCDS5074.1	c.241A>C	p.N81H
PTRH2	peptidyl-tRNA hydrolase 2	ENSG00000141378	PAP55	226	30.5%	chr17	55129907	CCDS11618.1	c.215G>A	p.R72Q
PER3	period homolog 3 (Drosophila)	ENSG00000049246	PAP55	104	23.1%	chr1	7786491	CCDS89.1	c.1129C>T	p.R377X
PHF3	PHD finger protein 3	ENSG00000118482	PAP55	82	32.9%	chr6	64453171	CCDS4966.1	c.1589G>A	p.R530Q
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP55	130	33.1%	chr10	89682885	CCDS31238.1	c.389G>A	p.R130Q
PIGG	phosphatidylinositol glycan anchor biosynthesis; class G	ENSG00000174227	PAP55	185	25.9%	chr4	505705	CCDS3336.1	c.1565T>G	p.L522R
PDE8A	phosphodiesterase 8A	ENSG00000073417	PAP55	76	32.9%	chr15	83411373	CCDS10336.1	c.368A>C	p.K123T
PDE8A	phosphodiesterase 8A	ENSG00000073417	PAP55	216	27.8%	chr15	83461930	CCDS10336.1	c.1590C>A	p.F530L
PFKM	phosphofructokinase; muscle	ENSG00000152556	PAP55	63	27.0%	chr12	46787450	NM_001166686	c.27A>C	p.K9N
PACS1	phosphofurin acidic cluster sorting protein 1	ENSG00000175115	PAP55	126	21.4%	chr11	65740791	CCDS8129.1	c.947G>T	p.R316M
PGM2L1	phosphoglucomutase 2-like 1	ENSG00000165434	PAP55	113	30.1%	chr11	73735468	CCDS8231.1	c.994G>A	p.D332N
PGM2L1	phosphoglucomutase 2-like 1	ENSG00000165434	PAP55	105	27.6%	chr11	73763214	CCDS8231.1	c.173G>A	p.R58Q
PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP55	188	25.0%	chr3	180399570	CCDS43171.1	c.263G>A	p.R88Q
PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP55	211	27.5%	chr3	180399585	CCDS43171.1	c.278G>A	p.R93Q
PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP55	48	20.8%	chr3	180418787	CCDS43171.1	c.1635G>T	p.E545D
PLCB2	phospholipase C; beta 2	ENSG00000137841	PAP55	98	21.4%	chr15	38375796	CCDS42020.1	c.1689C>A	p.F563L
PLCL1	phospholipase C-like 1	ENSG00000115896	PAP55	271	25.1%	chr2	198657145	CCDS2326.1	c.365A>G	p.Y122C
PLSCR1	phospholipid scramblase 1	ENSG00000188313	PAP55	114	26.3%	chr3	147716529	CCDS3135.1	c.950T>C	p.V317A
PLSCR4	phospholipid scramblase 4	ENSG00000114698	PAP55	85	27.1%	chr3	147421381	CCDS3133.1	c.29A>C	p.E10A
PLEK	pleckstrin	ENSG00000115956	PAP55	107	23.4%	chr2	68469080	CCDS1887.1	c.715G>T	p.E239X
PSD	pleckstrin and Sec7 domain containing	ENSG00000059915	PAP55	192	22.9%	chr10	104162203	CCDS31272.1	c.1673C>T	p.A558V
PSD2	pleckstrin and Sec7 domain containing 2	ENSG00000146005	PAP55	31	35.5%	chr5	139173181	CCDS4216.1	c.475G>A	p.D159N
PLEKHH2	pleckstrin homology domain containing; family H (with MyTH4 domain) member 2	ENSG00000152527	PAP55	100	31.0%	chr2	43784640	CCDS1812.1	c.1667C>T	p.A556V
PHIP	pleckstrin homology domain interacting protein	ENSG00000146247	PAP55	164	23.8%	chr6	79714169	CCDS4987.1	c.4096G>A	p.V1366I
PHLDB2	pleckstrin homology-like domain; family B; member 2	ENSG00000144824	PAP55	24	45.8%	chr3	113175350	CCDS2962.1	c.3488A>C	p.N1163T
PTN	pleiotrophin	ENSG00000105894	PAP55	41	29.3%	chr7	136590202	CCDS5844.1	c.59T>G	p.F20C
PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	ENSG00000064933	PAP55	78	30.8%	chr2	190417053	CCDS2302.1	c.-1T>C	p.IVS5+2-1SpliceDonor
PVRL3	poliovirus receptor-related 3	ENSG00000177707	PAP55	80	21.3%	chr3	112320418	CCDS2957.1	c.728G>A	p.R243Q
PARP8	poly (ADP-ribose) polymerase family; member 8	ENSG00000151883	PAP55	144	27.1%	chr5	50159595	CCDS3954.1	c.2038G>T	p.E680X
PABPC3	poly(A) binding protein; cytoplasmic 3	ENSG00000151846	PAP55	79	32.9%	chr13	24568648	CCDS9311.1	c.312A>C	p.K104N
PCBP2	poly(rC) binding protein 2	ENSG00000197111	PAP55	79	26.6%	chr12	52134886	CCDS8859.1	c.35T>C	p.V12A
PKHD1	polycystic kidney and hepatic disease 1 (autosomal recessive)	ENSG00000170927	PAP55	47	25.5%	chr6	51717247	CCDS4935.1	c.10051A>C	p.K3351Q
PKD1L1	polycystic kidney disease 1 like 1	ENSG00000158683	PAP55	114	26.3%	chr7	47894269	CCDS34633.1	c.2680G>A	p.V894I
POLN	polymerase (DNA directed) nu	ENSG00000130997	PAP55	72	18.1%	chr4	2142673	CCDS3360.1	c.1408T>G	p.F470V
POLE	polymerase (DNA directed); epsilon	ENSG00000177084	PAP55	144	27.1%	chr12	131760362	CCDS9278.1	c.1231G>T	p.V411L
POLG2	polymerase (DNA directed); gamma 2; accessory subunit	ENSG00000136480	PAP55	144	33.3%	chr17	59917416	CCDS32706.1	c.928G>A	p.E310K

POLQ	polymerase (DNA directed); theta	ENSG00000051341	PAP55	36	33.3%	chr3	122713552	CCDS33833.1	c.1483A>C	p.I495L
POLR1D	polymerase (RNA) I polypeptide D; 16kDa	ENSG00000186184	PAP55	72	27.8%	chr13	27138007	CCDS9324.1	c.286C>T	p.R96C
POLR1E	polymerase (RNA) I polypeptide E; 53kDa	ENSG00000137054	PAP55	495	36.0%	chr9	37476442	ENST00000377792	c.5A>G	p.Y2C
PTBP2	polypyrimidine tract binding protein 2	ENSG00000117569	PAP55	77	22.1%	chr1	97050900	CCDS754.1	c.1216C>T	p.R406C
POPDC3	popeye domain containing 3	ENSG00000132429	PAP55	62	24.2%	chr6	105714365	CCDS5052.1	c.508G>A	p.E170K
PGAP1	post-GPI attachment to proteins 1	ENSG00000197121	PAP55	44	31.8%	chr2	197420138	CCDS2318.1	c.1984T>G	p.L662V
KCTD3	potassium channel tetramerisation domain containing 3	ENSG00000136636	PAP55	87	26.4%	chr1	213819893	CCDS1515.1	c.554G>A	p.R185Q
KCTD9P2	potassium channel tetramerisation domain containing 9 pseudogene 2	ENSG00000189108	PAP55	116	22.4%	chrX	104898258	CCDS14517.1	c.2009C>A	p.S670Y
KCNK18	potassium channel; subfamily K; member 18	ENSG00000186795	PAP55	313	30.4%	chr10	118959138	CCDS7598.1	c.493C>T	p.R165W
KCNB2	potassium voltage-gated channel; Shab-related subfamily; member 2	ENSG00000182674	PAP55	98	19.4%	chr8	73642876	CCDS6209.1	c.353C>T	p.S118L
KCNA3	potassium voltage-gated channel; shaker-related subfamily; member 3	ENSG00000177272	PAP55	118	28.8%	chr1	111017961	CCDS828.2	c.994G>A	p.D332N
KCND3	potassium voltage-gated channel; Shal-related subfamily; member 3	ENSG00000171385	PAP55	121	19.8%	chr1	112325902	CCDS843.1	c.970C>T	p.L324F
KCNH6	potassium voltage-gated channel; subfamily H (eag-related); member 6	ENSG00000173826	PAP55	67	22.4%	chr17	58975447	CCDS11638.1	c.2447A>G	p.D816G
PRDM4	PR domain containing 4	ENSG00000110851	PAP55	352	30.4%	chr12	106652247	CCDS9115.1	c.2276C>T	p.S759L
PRDM9	PR domain containing 9	ENSG00000164256	PAP55	85	23.5%	chr5	23563479	CCDS43307.1	c.2525G>A	p.R842H
PBX3	pre-B-cell leukemia homeobox 3	ENSG00000167081	PAP55	121	24.0%	chr9	127737679	CCDS6865.1	c.815C>T	p.A272V
PBX4	pre-B-cell leukemia homeobox 4	ENSG00000105717	PAP55	71	22.5%	chr19	19542616	CCDS12406.1	c.220G>A	p.E74K
PRODH2	proline dehydrogenase (oxidase) 2	ENSG00000161270	PAP55	32	43.8%	chr19	41032055	CCDS32996.1	c.763G>A	p.V255M
PRR9	proline rich 9	ENSG00000203783	PAP55	143	30.1%	chr1	151457404	ENST00000368744	c.160C>A	p.L54I
P4HTM	prolyl 4-hydroxylase; transmembrane (endoplasmic reticulum)	ENSG00000178467	PAP55	77	32.5%	chr3	49014952	CCDS2781.2	c.643C>A	p.R215S
PRSS55	protease; serine; 55	ENSG00000184647	PAP55	62	33.9%	chr8	10433682	CCDS5976.1	c.1028C>T	p.S343F
PSMC5	proteasome (prosome; macropain) 26S subunit; ATPase; 5	ENSG00000087191	PAP55	126	31.0%	chr17	59261268	CCDS11645.1	c.308T>G	p.I103S
PSMC5	proteasome (prosome; macropain) 26S subunit; ATPase; 5	ENSG00000087191	PAP55	84	36.9%	chr17	59262622	CCDS11645.1	c.994C>A	p.H332N
PRMT8	protein arginine methyltransferase 8	ENSG00000111218	PAP55	44	31.8%	chr12	3572596	CCDS8521.2	c.1172A>G	p.Y391C
PRKCG	protein kinase C; gamma	ENSG00000126583	PAP55	152	28.3%	chr19	59093133	CCDS12867.1	c.1048G>A	p.D350N
PRKAA2	protein kinase; AMP-activated; alpha 2 catalytic subunit	ENSG00000162409	PAP55	308	31.5%	chr1	56942596	CCDS605.1	c.1153G>A	p.D385N
PRKAA2	protein kinase; AMP-activated; alpha 2 catalytic subunit	ENSG00000162409	PAP55	230	31.7%	chr1	56945842	CCDS605.1	c.1527C>A	p.S509R
PRKAB1	protein kinase; AMP-activated; beta 1 non-catalytic subunit	ENSG00000111725	PAP55	40	35.0%	chr12	118594576	CCDS9191.1	c.247C>T	p.R83X
PRKDC	protein kinase; DNA-activated; catalytic polypeptide	ENSG00000121031	PAP55	41	31.7%	chr8	48896740	ENST00000314191	c.9086T>G	p.I3029S
PPP2R1A	protein phosphatase 2; regulatory subunit A; alpha	ENSG00000105568	PAP55	194	23.7%	chr19	57408029	CCDS12849.1	c.661C>T	p.R221W
PPP4R4	protein phosphatase 4; regulatory subunit 4	ENSG00000119698	PAP55	97	26.8%	chr14	93769810	CCDS9921.1	c.584A>C	p.K195T
PRC1	protein regulator of cytokinesis 1	ENSG00000198901	PAP55	96	38.5%	chr15	89313709	CCDS32334.1	c.1721C>A	p.S574Y
PTPDC1	protein tyrosine phosphatase domain containing 1	ENSG00000158079	PAP55	124	25.8%	chr9	95899636	CCDS6708.1	c.961C>T	p.R321C
PTPN1	protein tyrosine phosphatase; non-receptor type 1	ENSG00000196396	PAP55	177	32.8%	chr20	48631258	CCDS13430.1	c.1138C>T	p.R380X
PTPN12	protein tyrosine phosphatase; non-receptor type 12	ENSG00000127947	PAP55	129	30.2%	chr7	77094227	CCDS5592.1	c.1295G>A	p.R432Q
PTPN21	protein tyrosine phosphatase; non-receptor type 21	ENSG00000070778	PAP55	49	28.6%	chr14	88009892	CCDS9884.1	c.2519A>C	p.K840T
PTPRD	protein tyrosine phosphatase; receptor type; D	ENSG00000153707	PAP55	89	27.0%	chr9	8331129	CCDS43786.1	c.5087G>A	p.G1696E
PTPRG	protein tyrosine phosphatase; receptor type; G	ENSG00000144724	PAP55	94	34.0%	chr3	61709625	CCDS2895.1	c.119A>G	p.E40G
PTPRG	protein tyrosine phosphatase; receptor type; G	ENSG00000144724	PAP55	136	28.7%	chr3	62215860	CCDS2895.1	c.2489T>C	p.V830A
PTPRG	protein tyrosine phosphatase; receptor type; G	ENSG00000144724	PAP55	121	24.0%	chr3	62215905	CCDS2895.1	c.2534A>C	p.Q845P
PTPRZ1	protein tyrosine phosphatase; receptor-type; Z polypeptide 1	ENSG00000106278	PAP55	39	41.0%	chr7	121410994	CCDS34740.1	c.659T>G	p.L220R
PTPRZ1	protein tyrosine phosphatase; receptor-type; Z polypeptide 1	ENSG00000106278	PAP55	60	25.0%	chr7	121411027	CCDS34740.1	c.692A>G	p.Y231C
PTPRZ1	protein tyrosine phosphatase; receptor-type; Z polypeptide 1	ENSG00000106278	PAP55	248	20.2%	chr7	121438455	CCDS34740.1	c.2119G>T	p.D707Y
PCMTD2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	ENSG00000203880	PAP55	57	26.3%	chr20	62375158	CCDS13559.1	c.847C>T	p.R283C

PCDH17	protocadherin 17	ENSG00000118946	PAP55	169	16.6%	chr13	57196858	CCDS31986.1	c.2909G>A	p.R970H
PCDHA3	protocadherin alpha 3	ENSG00000204968	PAP55	74	31.1%	chr5	140161380	CCDS34248.1	c.414G>T	p.K138N
PCDHA3	protocadherin alpha 3	ENSG00000204968	PAP55	91	25.3%	chr5	140161517	CCDS34248.1	c.551G>T	p.R184I
PCDHA7	protocadherin alpha 7	ENSG00000204963	PAP55	65	30.8%	chr5	140196083	CCDS34252.1	c.1931G>A	p.R644H
PCDHB12	protocadherin beta 12	ENSG00000120328	PAP55	65	21.5%	chr5	140571013	CCDS4254.1	c.2350G>A	p.E784K
PCDHB5	protocadherin beta 5	ENSG00000113209	PAP55	166	29.5%	chr5	140496053	CCDS4247.1	c.853G>A	p.D285N
PCDHB6	protocadherin beta 6	ENSG00000113211	PAP55	93	25.8%	chr5	140510283	CCDS4248.1	c.261A>C	p.E87D
PCDHB7	protocadherin beta 7	ENSG00000113212	PAP55	90	11.1%	chr5	140533009	CCDS4249.1	c.409G>T	p.E137X
PCDHB8	protocadherin beta 8	ENSG00000120322	PAP55	225	16.4%	chr5	140538734	CCDS4250.1	c.935A>T	p.K312I
PCDHGA1	protocadherin gamma subfamily A; 1	ENSG00000204956	PAP55	226	26.1%	chr5	140692011	CCDS34256.1	c.1576C>T	p.R526W
PCDHGA10	protocadherin gamma subfamily A; 10	ENSG00000081853	PAP55	130	22.3%	chr5	140845085	CCDS4262.1	c.161T>G	p.L54R
PCDHGA11	protocadherin gamma subfamily A; 11	ENSG00000081853	PAP55	130	22.3%	chr5	140845085	CCDS4262.1	c.161T>G	p.L54R
PCDHGA3	protocadherin gamma subfamily A; 3	ENSG00000081853	PAP55	130	22.3%	chr5	140845085	CCDS4262.1	c.161T>G	p.L54R
PCDHGA8	protocadherin gamma subfamily A; 8	ENSG00000081853	PAP55	130	22.3%	chr5	140845085	CCDS4262.1	c.161T>G	p.L54R
PCDHGB7	protocadherin gamma subfamily B; 7	ENSG00000081853	PAP55	130	22.3%	chr5	140845085	CCDS4262.1	c.161T>G	p.L54R
PCDHGC5	protocadherin gamma subfamily C; 5	ENSG00000081853	PAP55	130	22.3%	chr5	140845085	CCDS4262.1	c.161T>G	p.L54R
PCDH15	protocadherin-related 15	ENSG00000150275	PAP55	91	36.3%	chr10	55251821	CCDS7248.1	c.5671G>T	p.E1891X
PCDH15	protocadherin-related 15	ENSG00000150275	PAP55	35	31.4%	chr10	55252313	CCDS7248.1	c.5179G>A	p.E1727K
PCDH15	protocadherin-related 15	ENSG00000150275	PAP55	238	29.0%	chr10	55252858	CCDS7248.1	c.4634G>T	p.R1545I
PCDH15	protocadherin-related 15	ENSG00000150275	PAP55	51	25.5%	chr10	55808640	CCDS7248.1	c.226T>C	p.S76P
PRPF38B	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	ENSG00000134186	PAP55	68	23.5%	chr1	109040326	CCDS788.1	c.484T>G	p.F162V
PTK7	PTK7 protein tyrosine kinase 7	ENSG00000112655	PAP55	107	21.5%	chr6	43235556	CCDS4884.1	c.2926G>A	p.E976K
PUM1	pumilio homolog 1 (Drosophila)	ENSG00000134644	PAP55	98	23.5%	chr1	31211698	CCDS338.1	c.1804G>A	p.A602T
QRFPR	pyroglutamylated RFamide peptide receptor	ENSG00000186867	PAP55	133	35.3%	chr4	122470103	CCDS3719.1	c.1112G>A	p.R371Q
RABGGTB	Rab geranylgeranyltransferase; beta subunit	ENSG00000137955	PAP55	46	34.8%	chr1	76025869	CCDS669.1	c.103G>A	p.D35N
RAB11FIP2	RAB11 family interacting protein 2 (class I)	ENSG00000107560	PAP55	183	32.2%	chr10	119789782	CCDS7602.1	c.638A>C	p.K213T
RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)	ENSG00000115839	PAP55	120	29.2%	chr2	135609800	CCDS33294.1	c.1751A>C	p.E584A
RAB3B	RAB3B; member RAS oncogene family	ENSG00000169213	PAP55	110	22.7%	chr1	52171687	CCDS560.1	c.363G>T	p.K121N
RAB9B	RAB9B; member RAS oncogene family	ENSG00000123570	PAP55	124	29.0%	chrX	102966778	CCDS14515.1	c.593C>T	p.S198F
ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	ENSG00000129675	PAP55	73	38.4%	chrX	135597797	CCDS14660.1	c.1205A>G	p.Q402R
RAD51AP2	RAD51 associated protein 2	ENSG00000214842	PAP55	82	31.7%	chr2	17561771	CCDS42656.1	c.1393G>T	p.E465X
RAD51AP2	RAD51 associated protein 2	ENSG00000214842	PAP55	63	23.8%	chr2	17562085	CCDS42656.1	c.1079T>C	p.V360A
RALGAPB	Ral GTPase activating protein; beta subunit (non-catalytic)	ENSG00000170471	PAP55	52	23.1%	chr20	36594821	CCDS13305.1	c.2150G>A	p.R717H
REPS2	RALBP1 associated Eps domain containing 2	ENSG00000169891	PAP55	66	28.8%	chrX	17075473	CCDS14180.2	c.1931G>A	p.R644Q
RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	ENSG00000173166	PAP55	93	24.7%	chr2	204021731	CCDS2359.1	c.1487G>A	p.W496X
RASGRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	ENSG00000152689	PAP55	88	27.3%	chr2	33634130	NM_170672	c.1571A>G	p.K524R
RASAL1	RAS protein activator like 1 (GAP1 like)	ENSG00000111344	PAP55	214	26.6%	chr12	112050054	CCDS9165.1	c.244G>A	p.D82N
RERG	RAS-like; estrogen-regulated; growth inhibitor	ENSG00000134533	PAP55	38	36.8%	chr12	15155589	CCDS8673.1	c.148G>A	p.D50N
RB1CC1	RB1-inducible coiled-coil 1	ENSG00000023287	PAP55	100	27.0%	chr8	53717672	CCDS34892.1	c.4129C>T	p.R1377C
RGS6	regulator of G-protein signaling 6	ENSG00000182732	PAP55	63	20.6%	chr14	72011109	CCDS9808.1	c.642A>C	p.E214D
RIC3	resistance to inhibitors of cholinesterase 3 homolog (C. elegans)	ENSG00000166405	PAP55	230	31.3%	chr11	8088901	CCDS7788.1	c.1027G>T	p.D343Y
RCOR2	REST corepressor 2	ENSG00000167771	PAP55	329	28.0%	chr11	63436732	CCDS8052.1	c.1019C>T	p.A340V
RTN2	reticulon 2	ENSG00000125744	PAP55	103	28.2%	chr19	50689654	CCDS12665.1	c.529A>G	p.N177D
RB1	retinoblastoma 1	ENSG00000139687	PAP55	36	27.8%	chr13	47853540	CCDS31973.1	c.1655G>A	p.R552Q
RARRES3	retinoic acid receptor responder (tazarotene induced) 3	ENSG00000133321	PAP55	56	28.6%	chr11	63063603	CCDS41662.1	c.49T>G	p.F17V
REV1	REV1 homolog (S. cerevisiae)	ENSG00000135945	PAP55	109	28.4%	chr2	99404492	CCDS2045.1	c.1732G>A	p.E578K
REV1	REV1 homolog (S. cerevisiae)	ENSG00000135945	PAP55	38	26.3%	chr2	99417301	CCDS2045.1	c.1363G>A	p.A455T
RFPL3S	RFPL3 antisense RNA (non-protein coding)	ENSG00000205853	PAP55	87	21.8%	chr22	31088945	ENST00000382086	c.225T>G	p.I75M
ARHGAP17	Rho GTPase activating protein 17	ENSG00000140750	PAP55	75	17.3%	chr16	24849807	CCDS32409.1	c.2314A>G	p.S772G
ARHGAP36	Rho GTPase activating protein 36	ENSG00000147256	PAP55	63	27.0%	chrX	130047614	CCDS14628.1	c.1151G>A	p.G384E
ARHGAP4	Rho GTPase activating protein 4	ENSG00000089820	PAP55	175	26.3%	chrX	152827764	CCDS14736.1	c.2561G>A	p.R854H

RHBDF1	rhomboid 5 homolog 1 (Drosophila)	ENSG00000007384	PAP55	37	29.7%	chr16	54358	ENST00000338527	c.329G>A	p.R110H
RNASE3	ribonuclease; RNase A family; 3	ENSG00000169397	PAP55	62	21.0%	chr14	20429716	CCDS9560.1	c.31T>C	p.C11R
RNASE6	ribonuclease; RNase A family; k6	ENSG00000169413	PAP55	45	28.9%	chr14	20319724	CCDS9558.1	c.26T>C	p.L9S
RPL31	ribosomal protein L31	ENSG00000071082	PAP55	66	30.3%	chr2	100988932	CCDS2049.1	c.313T>G	p.L105V
RPS20	ribosomal protein S20	ENSG00000008988	PAP55	45	33.3%	chr8	57149493	CCDS6163.1	c.-1G>A	p.IVS1+1-1SpliceDonor
RPS6KC1	ribosomal protein S6 kinase; 52kDa; polypeptide 1	ENSG00000136643	PAP55	41	24.4%	chr1	211472171	CCDS1513.1	c.1175A>C	p.K392T
RPS6KA3	ribosomal protein S6 kinase; 90kDa; polypeptide 3	ENSG00000177189	PAP55	230	30.4%	chrX	20115961	CCDS14197.1	c.680C>A	p.S227Y
RPS6KA6	ribosomal protein S6 kinase; 90kDa; polypeptide 6	ENSG00000072133	PAP55	98	25.5%	chrX	83261598	CCDS14451.1	c.740G>T	p.R247M
RPF1	ribosome production factor 1 homolog (S. cerevisiae)	ENSG00000117133	PAP55	125	24.8%	chr1	84728642	CCDS695.1	c.515T>C	p.V172A
RNF113A	ring finger protein 113A	ENSG00000125352	PAP55	220	32.3%	chrX	118889431	CCDS14589.1	c.174G>T	p.K58N
RNF157	ring finger protein 157	ENSG00000141576	PAP55	68	26.5%	chr17	71667074	CCDS32740.1	c.1241C>T	p.S414L
RNF165	ring finger protein 165	ENSG00000141622	PAP55	114	34.2%	chr18	42269284	CCDS32823.1	c.412C>T	p.R138C
RNF19A	ring finger protein 19A	ENSG00000034677	PAP55	67	25.4%	chr8	101369388	CCDS6286.1	c.191G>T	p.R64I
RNF213	ring finger protein 213	ENSG00000173821	PAP55	52	26.9%	chr17	75960953	CCDS32761.1	c.6794A>C	p.N2265T
RNF214	ring finger protein 214	ENSG00000167257	PAP55	368	23.9%	chr11	116657929	CCDS41720.1	c.1445G>A	p.R482H
RNF43	ring finger protein 43	ENSG00000108375	PAP55	175	35.4%	chr17	53847702	CCDS11607.1	c.236A>G	p.E79G
RBM12B	RNA binding motif protein 12B	ENSG00000183808	PAP55	49	22.4%	chr8	94814885	CCDS43755.1	c.2930A>C	p.N977T
RBM12B	RNA binding motif protein 12B	ENSG00000183808	PAP55	247	30.8%	chr8	94816562	CCDS43755.1	c.1253A>C	p.K418T
RBM16	RNA binding motif protein 16	ENSG00000213079	PAP55	61	31.1%	chr6	155178598	CCDS5247.1	c.1477T>G	p.L493V
RBM22	RNA binding motif protein 22	ENSG00000086589	PAP55	73	27.4%	chr5	150056629	CCDS34278.1	c.289C>T	p.R97C
RBMXL2	RNA binding motif protein; X-linked-like 2	ENSG00000170748	PAP55	55	18.2%	chr11	7067000	CCDS7777.1	c.73G>A	p.E25K
SALL3	sal-like 3 (Drosophila)	ENSG00000151514	PAP55	165	32.1%	chr18	74854301	CCDS12013.1	c.1322C>T	p.S441L
SAPS3	SAPS domain family; member 3	ENSG00000110075	PAP55	89	31.5%	chr11	68114754	CCDS8182.1	c.1541A>G	p.E514G
SCARB1	scavenger receptor class B; member 1	ENSG00000073060	PAP55	40	32.5%	chr12	123850733	CCDS9259.1	c.1018T>G	p.L340V
SCEL	sciellin	ENSG00000136155	PAP55	25	40.0%	chr13	77075219	CCDS9459.1	c.1045G>A	p.D349N
SLURP1	secreted LY6/PLAUR domain containing 1	ENSG00000126233	PAP55	45	35.6%	chr8	143820796	CCDS6387.1	c.10C>T	p.R4C
SEMA3D	sema domain; immunoglobulin domain (Ig); short basic domain; secreted; (semaphorin) 3D	ENSG00000153993	PAP55	300	30.7%	chr7	84466742	CCDS34676.1	c.2284C>T	p.R762X
SDS	serine dehydratase	ENSG00000135094	PAP55	56	33.9%	chr12	112315206	CCDS9169.1	c.910G>A	p.G304R
STK17A	serine/threonine kinase 17a	ENSG00000164543	PAP55	90	22.2%	chr7	43625778	CCDS5470.1	c.622T>G	p.F208V
SERPINA3	serpin peptidase inhibitor; clade A (alpha-1 antiproteinase; antitrypsin); member 3	ENSG00000196136	PAP55	105	24.8%	chr14	94158432	CCDS32150.1	c.919G>A	p.E307K
SERPINH1	serpin peptidase inhibitor; clade H (heat shock protein 47); member 1; (collagen binding protein 1)	ENSG00000149257	PAP55	156	30.8%	chr11	74957652	CCDS8239.1	c.742G>A	p.D248N
SRRT	serrate RNA effector molecule homolog (Arabidopsis)	ENSG00000087087	PAP55	76	36.8%	chr7	100319632	CCDS34709.1	c.593G>A	p.R198Q
SETDB2	SET domain; bifurcated 2	ENSG00000136169	PAP55	71	38.0%	chr13	48948870	CCDS9417.1	c.599G>A	p.R200Q
SH3BGRL	SH3 domain binding glutamic acid-rich protein like	ENSG00000131171	PAP55	45	28.9%	chrX	80419244	CCDS14449.1	c.151G>T	p.E51X
SGIP1	SH3-domain GRB2-like (endophilin) interacting protein 1	ENSG00000118473	PAP55	108	35.2%	chr1	66957607	CCDS30744.1	c.1673A>G	p.D558G
SH3KBP1	SH3-domain kinase binding protein 1	ENSG00000147010	PAP55	147	24.5%	chrX	19497162	CCDS14193.1	c.1364C>T	p.S455L
SDR16C5	short chain dehydrogenase/reductase family 16C; member 5	ENSG00000170786	PAP55	52	28.8%	chr8	57381891	CCDS6167.1	c.608C>A	p.S203Y
SDK1	sidekick homolog 1; cell adhesion molecule (chicken)	ENSG00000146555	PAP55	259	21.6%	chr7	4180452	CCDS34590.1	c.4873G>A	p.A1625T
SIM1	single-minded homolog 1 (Drosophila)	ENSG00000112246	PAP55	126	27.8%	chr6	100948335	CCDS5045.1	c.1319C>T	p.S440L
SLITRK1	SLIT and NTRK-like family; member 1	ENSG00000178235	PAP55	203	28.1%	chr13	83353279	CCDS9464.1	c.365G>A	p.R122Q
SNRNP200	small nuclear ribonucleoprotein 200kDa (U5)	ENSG00000144028	PAP55	37	32.4%	chr2	96308971	CCDS2020.1	c.5078G>A	p.R1693H
SNRNP48	small nuclear ribonucleoprotein 48kDa (U11/U12)	ENSG00000168566	PAP55	73	27.4%	chr6	7538990	CCDS4502.1	c.181G>A	p.D61N
SNAPC4	small nuclear RNA activating complex; polypeptide 4; 190kDa	ENSG00000165684	PAP55	71	21.1%	chr9	138392372	CCDS6998.1	c.3728G>A	p.R1243H
SNAPC4	small nuclear RNA activating complex; polypeptide 4; 190kDa	ENSG00000165684	PAP55	63	28.6%	chr9	138396189	CCDS6998.1	c.2225G>A	p.R742H
SHOC2	soc-2 suppressor of clear homolog (C. elegans)	ENSG00000108061	PAP55	39	28.2%	chr10	112714132	CCDS7568.1	c.26A>C	p.K9T
SCN1A	sodium channel; voltage-gated; type I; alpha subunit	ENSG00000144285	PAP55	87	18.4%	chr2	166638245	CCDS33316.1	c.133G>A	p.D45N
SCN4B	sodium channel; voltage-gated; type IV; beta	ENSG00000177098	PAP55	78	35.9%	chr11	117513032	CCDS8389.1	c.607G>A	p.V203M
SCN10A	sodium channel; voltage-gated; type X; alpha subunit	ENSG00000185313	PAP55	48	35.4%	chr3	38730509	CCDS33736.1	c.3748C>T	p.R1250X

SCN11A	sodium channel; voltage-gated; type XI; alpha subunit	ENSG00000168356	PAP55	48	20.8%	chr3	38888128	CCDS33737.1	c.3571G>A	p.V1191I
SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter); member 2	ENSG00000110436	PAP55	96	34.4%	chr11	35290359	CCDS31459.1	c.523C>A	p.L175I
SLC14A1	solute carrier family 14 (urea transporter); member 1 (Kidd blood group)	ENSG00000141469	PAP55	136	25.0%	chr18	41564387	CCDS11925.1	c.104T>G	p.L35R
SLC17A6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter); member 6	ENSG00000091664	PAP55	75	22.7%	chr11	22337597	CCDS7856.1	c.521G>T	p.R174I
SLC19A2	solute carrier family 19 (thiamine transporter); member 2	ENSG00000117479	PAP55	77	42.9%	chr1	167704505	CCDS1280.1	c.-1G>A	p.IVS4+1-1SpliceDonor
SLC2A13	solute carrier family 2 (facilitated glucose transporter); member 13	ENSG00000151229	PAP55	55	25.5%	chr12	38708487	CCDS8736.1	c.751G>T	p.G251X
SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter); member 5	ENSG00000142583	PAP55	44	29.5%	chr1	9020242	CCDS99.1	c.1496C>T	p.S499L
SLC22A6	solute carrier family 22 (organic anion transporter); member 6	ENSG00000197901	PAP55	79	35.4%	chr11	62503788	CCDS31591.1	c.1246C>T	p.P416S
SLC22A15	solute carrier family 22; member 15	ENSG00000163393	PAP55	100	27.0%	chr1	116410797	NM_018420	c.1499C>T	p.S500L
SLC25A12	solute carrier family 25 (mitochondrial carrier; Aralar); member 12	ENSG00000115840	PAP55	210	29.0%	chr2	172350119	CCDS33327.1	c.1948G>A	p.E650K
SLC25A19	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier); member 19	ENSG00000125454	PAP55	36	30.6%	chr17	70791143	CCDS11720.1	c.415G>A	p.V139M
SLC25A46	solute carrier family 25; member 46	ENSG00000164209	PAP55	111	31.5%	chr5	110125110	CCDS4100.1	c.986T>C	p.V329A
SLC27A5	solute carrier family 27 (fatty acid transporter); member 5	ENSG00000083807	PAP55	56	30.4%	chr19	63714010	CCDS12983.1	c.788C>T	p.A263V
SLC35C2	solute carrier family 35; member C2	ENSG00000080189	PAP55	60	25.0%	chr20	44419722	CCDS13396.1	c.218G>A	p.R73K
SLC35E4	solute carrier family 35; member E4	ENSG00000100036	PAP55	222	23.9%	chr22	29362756	CCDS13882.1	c.319C>T	p.R107C
SLC37A3	solute carrier family 37 (glycerol-3-phosphate transporter); member 3	ENSG00000157800	PAP55	107	26.2%	chr7	139697697	CCDS5859.1	c.727G>T	p.E243X
SLC38A10	solute carrier family 38; member 10	ENSG00000157637	PAP55	190	31.1%	chr17	76840826	CCDS42397.1	c.1709C>T	p.A570V
SLC43A1	solute carrier family 43; member 1	ENSG00000149150	PAP55	53	35.8%	chr11	57009198	CCDS7958.1	c.1627G>A	p.A543T
SLC43A3	solute carrier family 43; member 3	ENSG00000134802	PAP55	134	34.3%	chr11	56939096	CCDS7956.1	c.829C>T	p.R277W
SLC6A15	solute carrier family 6 (neutral amino acid transporter); member 15	ENSG00000072041	PAP55	37	29.7%	chr12	83803970	CCDS9026.1	c.298C>A	p.L100I
SLC7A7	solute carrier family 7 (cationic amino acid transporter; y+ system); member 7	ENSG00000155465	PAP55	62	27.4%	chr14	22315245	CCDS9574.1	c.893T>C	p.V298A
SLC9A6	solute carrier family 9 (sodium/hydrogen exchanger); member 6	ENSG00000198689	PAP55	110	19.1%	chrX	134954394	CCDS44003.1	c.1951A>T	p.R651X
SLC9A7	solute carrier family 9 (sodium/hydrogen exchanger); member 7	ENSG00000065923	PAP55	55	23.6%	chrX	46395764	CCDS14269.1	c.1164C>A	p.F388L
SLCO1A2	solute carrier organic anion transporter family; member 1A2	ENSG00000084453	PAP55	42	31.0%	chr12	21339933	CCDS8686.1	c.1136A>C	p.K379T
SLCO1B1	solute carrier organic anion transporter family; member 1B1	ENSG00000134538	PAP55	117	30.8%	chr12	21222836	CCDS8685.1	c.541C>T	p.R181C
SLCO1C1	solute carrier organic anion transporter family; member 1C1	ENSG00000139155	PAP55	66	25.8%	chr12	20777267	CCDS8683.1	c.1344A>C	p.E448D
SON	SON DNA binding protein	ENSG00000159140	PAP55	64	26.6%	chr21	33847889	CCDS13629.1	c.4482A>C	p.Q1494H
SORL1	sortilin-related receptor; L(DLR class) A repeats-containing	ENSG00000137642	PAP55	222	26.6%	chr11	120946091	CCDS8436.1	c.3239G>A	p.R1080H
SORCS1	sortilin-related VPS10 domain containing receptor 1	ENSG00000108018	PAP55	147	28.6%	chr10	108370256	CCDS31283.1	c.2716G>T	p.E906X
SNX32	sorting nexin 32	ENSG00000172803	PAP55	34	38.2%	chr11	65377347	CCDS8113.2	c.1177C>T	p.R393W
SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	ENSG00000151835	PAP55	83	32.5%	chr13	22805634	CCDS9300.1	c.9940G>T	p.E3314X
SACS	spastic ataxia of Charlevoix-Saguenay (sacsin)	ENSG00000151835	PAP55	141	33.3%	chr13	22837373	NM_014363	c.389A>C	p.K130T
SPG20	spastic paraplegia 20 (Troyer syndrome)	ENSG00000133104	PAP55	49	26.5%	chr13	35807222	CCDS9356.1	c.746G>A	p.R249Q
SYNE2	spectrin repeat containing; nuclear envelope 2	ENSG00000054654	PAP55	74	23.0%	chr14	63643969	CCDS9761.2	c.12500A>C	p.Y4167S
SPTBN1	spectrin; beta; non-erythrocytic 1	ENSG00000115306	PAP55	72	27.8%	chr2	54607178	CCDS33198.1	c.119T>G	p.F40C
SPACA4	sperm acrosome associated 4	ENSG00000177202	PAP55	107	33.6%	chr19	53802135	CCDS12725.1	c.88G>A	p.D30N
SPHKAP	SPHK1 interactor; AKAP domain containing	ENSG00000153820	PAP55	65	26.2%	chr2	228592027	CCDS33389.1	c.1787C>T	p.S596F
SFRS13A	splicing factor; arginine/serine-rich 13A	ENSG00000188529	PAP55	106	29.2%	chr1	24171044	CCDS30630.1	c.320C>T	p.S107F
SFRS15	splicing factor; arginine/serine-rich 15	ENSG00000156304	PAP55	56	33.9%	chr21	31996551	CCDS33537.1	c.334C>T	p.R112C
SFRS5	splicing factor; arginine/serine-rich 5	ENSG00000100650	PAP55	91	24.2%	chr14	69305300	CCDS32109.1	c.230G>A	p.R77Q
SHD	Src homology 2 domain containing transforming protein D	ENSG00000105251	PAP55	189	23.3%	chr19	4233937	CCDS12125.1	c.368A>G	p.Y123C

SOX3	SRY (sex determining region Y)-box 3	ENSG00000134595	PAP55	121	27.3%	chrX	139414403	CCDS14669.1	c.489G>T	p.K163N
SOX30	SRY (sex determining region Y)-box 30	ENSG00000039600	PAP55	122	29.5%	chr5	156986176	CCDS4339.1	c.2012C>A	p.S671Y
SOX30	SRY (sex determining region Y)-box 30	ENSG00000039600	PAP55	59	32.2%	chr5	156998042	CCDS4339.1	c.1654A>G	p.T552A
STAB1	stabilin 1	ENSG00000010327	PAP55	116	20.7%	chr3	52528579	CCDS33768.1	c.5194G>A	p.A1732T
STAB2	stabilin 2	ENSG00000136011	PAP55	104	27.9%	chr12	102622518	CCDS31888.1	c.3896C>A	p.S1299Y
SAMD7	sterile alpha motif domain containing 7	ENSG00000187033	PAP55	72	27.8%	chr3	171138839	CCDS3209.1	c.1192C>T	p.L398F
SOAT1	sterol O-acyltransferase 1	ENSG00000057252	PAP55	48	25.0%	chr1	177580732	CCDS1330.1	c.1015T>G	p.Y339D
SMC1A	structural maintenance of chromosomes 1A	ENSG00000072501	PAP55	299	28.8%	chrX	53440223	CCDS14352.1	c.2602G>T	p.A868S
SI	sucrase-isomaltase (alpha-glucosidase)	ENSG00000090402	PAP55	144	29.9%	chr3	166182756	CCDS3196.1	c.5384C>T	p.S1795L
SKIV2L2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	ENSG00000039123	PAP55	83	32.5%	chr5	54674918	CCDS3967.1	c.784C>T	p.R262C
SUPT4H1	suppressor of Ty 4 homolog 1 (S. cerevisiae)	ENSG00000213246	PAP55	75	21.3%	chr17	53778665	CCDS11606.1	c.295C>T	p.R99W
SYN3	synapsin III	ENSG00000185666	PAP55	64	25.0%	chr22	31322715	CCDS13908.1	c.719C>T	p.A240V
SYT13	synaptotagmin XIII	ENSG00000019505	PAP55	100	25.0%	chr11	45264181	CCDS31470.1	c.154A>G	p.K52E
SYTL2	synaptotagmin-like 2	ENSG00000137501	PAP55	186	25.8%	chr11	85112801	CCDS31651.1	c.2347G>A	p.E783K
SYTL4	synaptotagmin-like 4	ENSG00000102362	PAP55	155	31.6%	chrX	99822888	CCDS14472.1	c.1550G>A	p.R517Q
STXBP1	syntaxin binding protein 1	ENSG00000136854	PAP55	166	27.1%	chr9	129465332	CCDS6874.1	c.457T>G	p.F153V
TAF1L	TAF1 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 210kDa-like	ENSG00000122728	PAP55	201	24.4%	chr9	32622340	NM_153809	c.3238C>T	p.R1080C
TAF1	TAF1 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 250kDa	ENSG00000147133	PAP55	114	28.1%	chrX	70519336	CCDS14412.1	c.1726A>G	p.N576D
TAF7	TAF7 RNA polymerase II; TATA box binding protein (TBP)-associated factor; 55kDa	ENSG00000178913	PAP55	87	27.6%	chr5	140679392	CCDS4259.1	c.404G>A	p.G135E
TAS2R8	taste receptor; type 2; member 8	ENSG00000121314	PAP55	72	23.6%	chr12	10849960	CCDS8632.1	c.887T>G	p.F296C
TBPL2	TATA box binding protein like 2	ENSG00000182521	PAP55	123	24.4%	chr14	54965306	CCDS9724.1	c.928T>G	p.L310V
TBC1D8B	TBC1 domain family; member 8B (with GRAM domain)	ENSG00000133138	PAP55	42	23.8%	chrX	105984130	CCDS14522.1	c.2300G>A	p.R767Q
TBX21	T-box 21	ENSG00000073861	PAP55	124	28.2%	chr17	43177193	CCDS11514.1	c.1070C>A	p.P357H
TCP11L2	t-complex 11 (mouse)-like 2	ENSG00000166046	PAP55	38	26.3%	chr12	105264377	CCDS9104.1	c.1499G>A	p.R500Q
TNN	tenascin N	ENSG00000120332	PAP55	122	23.8%	chr1	173315343	CCDS30943.1	c.661G>A	p.E221K
TNN	tenascin N	ENSG00000120332	PAP55	162	26.5%	chr1	173315391	CCDS30943.1	c.709T>G	p.C237G
TNS1	tensin 1	ENSG00000079308	PAP55	69	30.4%	chr2	218463979	CCDS2407.1	c.442C>T	p.R148W
TEX9	testis expressed 9	ENSG00000151575	PAP55	132	31.1%	chr15	54445160	CCDS10157.1	c.119A>C	p.K40T
TSGA10	testis specific; 10	ENSG00000135951	PAP55	65	29.2%	chr2	99001131	CCDS2037.1	c.2036G>A	p.R679Q
TSGA10	testis specific; 10	ENSG00000135951	PAP55	65	29.2%	chr2	99001221	CCDS2037.1	c.1946G>A	p.R649H
TESK2	testis-specific kinase 2	ENSG00000070759	PAP55	247	33.6%	chr1	45695860	CCDS41323.1	c.185A>C	p.E62A
TET1	tet oncogene 1	ENSG00000138336	PAP55	96	27.1%	chr10	70074699	CCDS7281.1	c.2207C>T	p.S736L
TTC30A	tetratricopeptide repeat domain 30A	ENSG00000197557	PAP55	148	35.8%	chr2	178189707	CCDS2276.1	c.1969A>G	p.I657V
TH1L	TH1-like (Drosophila)	ENSG00000101158	PAP55	80	37.5%	chr20	57002156	CCDS13473.1	c.1550G>A	p.R517Q
THEMIS	thymocyte selection associated	ENSG00000172673	PAP55	65	26.2%	chr6	128176767	CCDS34534.1	c.712C>T	p.R238X
TOX	thymocyte selection-associated high mobility group box	ENSG00000198846	PAP55	80	28.8%	chr8	59926651	CCDS34897.1	c.679G>A	p.D227N
TG	thyroglobulin	ENSG00000042832	PAP55	216	25.9%	chr8	133969725	CCDS34944.1	c.2491G>A	p.D831N
THADA	thyroid adenoma associated	ENSG00000115970	PAP55	68	33.8%	chr2	43373793	NM_022065	c.4502C>T	p.T1501M
TRIP12	thyroid hormone receptor interactor 12	ENSG00000153827	PAP55	127	29.9%	chr2	230341608	CCDS33391.1	c.5750T>C	p.F1917S
TIGD6	tigger transposable element derived 6	ENSG00000164296	PAP55	188	29.3%	chr5	149354651	CCDS4301.1	c.1454A>G	p.D485G
TNIP3	TNFAIP3 interacting protein 3	ENSG00000050730	PAP55	134	20.9%	chr4	122287742	CCDS3718.1	c.647C>T	p.S216L
TNIP3	TNFAIP3 interacting protein 3	ENSG00000050730	PAP55	101	25.7%	chr4	122304711	CCDS3718.1	c.20G>A	p.G7D
TTPAL	tocopherol (alpha) transfer protein-like	ENSG00000124120	PAP55	92	26.1%	chr20	42548699	CCDS13332.2	c.689G>A	p.R230Q
TLL1	tolloid-like 1	ENSG00000038295	PAP55	91	26.4%	chr4	167239891	CCDS3811.1	c.2669G>A	p.R890Q
TOP1	topoisomerase (DNA) I	ENSG00000198900	PAP55	48	41.7%	chr20	39142222	CCDS13312.1	c.419G>A	p.R140Q
TCEAL7	transcription elongation factor A (SII)-like 7	ENSG00000182916	PAP55	122	24.6%	chrX	102473123	CCDS14506.1	c.136G>A	p.E46K
TCERG1	transcription elongation regulator 1	ENSG00000113649	PAP55	29	41.4%	chr5	145868904	CCDS4282.1	c.2998A>C	p.K1000Q
TFDP3	transcription factor Dp family; member 3	ENSG00000183434	PAP55	146	30.1%	chrX	132179806	NM_016521	c.148A>G	p.S50G
TRERF1	transcriptional regulating factor 1	ENSG00000124496	PAP55	62	32.3%	chr6	42345126	CCDS4867.1	c.181A>G	p.T61A
TBL3	transducin (beta)-like 3	ENSG00000183751	PAP55	134	33.6%	chr16	1965043	CCDS10453.1	c.578C>T	p.A193V

TLE1	transducin-like enhancer of split 1 (E(sp1) homolog; Drosophila)	ENSG00000196781	PAP55	51	31.4%	chr9	83420728	CCDS6661.1	c.907G>T	p.E303X
TGM4	transglutaminase 4 (prostate)	ENSG00000163810	PAP55	52	40.4%	chr3	44918074	CCDS2723.1	c.712G>A	p.E238K
TGM6	transglutaminase 6	ENSG00000166948	PAP55	279	26.2%	chr20	2332322	CCDS13025.1	c.1189G>A	p.A397T
TRPA1	transient receptor potential cation channel; subfamily A; member 1	ENSG00000104321	PAP55	80	30.0%	chr8	73136480	CCDS34908.1	c.878C>T	p.S293L
TRPC1	transient receptor potential cation channel; subfamily C; member 1	ENSG00000144935	PAP55	56	41.1%	chr3	144007700	CCDS3126.1	c.2213G>A	p.R738Q
TRPM3	transient receptor potential cation channel; subfamily M; member 3	ENSG00000083067	PAP55	58	20.7%	chr9	72354349	CCDS43835.1	c.3600A>C	p.E1200D
TKTL1	transketolase-like 1	ENSG00000007350	PAP55	85	29.4%	chrX	153196855	CCDS35448.1	c.1003G>A	p.E335K
TOMM7	translocase of outer mitochondrial membrane 7 homolog (yeast)	ENSG00000196683	PAP55	45	33.3%	chr7	22819255	ENST00000372879	c.364C>T	p.L122F
TM4SF5	transmembrane 4 L six family member 5	ENSG00000142484	PAP55	66	24.2%	chr17	4632624	CCDS11054.1	c.338G>A	p.R113Q
TM6SF1	transmembrane 6 superfamily member 1	ENSG00000136404	PAP55	47	29.8%	chr15	81582528	CCDS10323.1	c.497G>A	p.R166Q
TM7SF2	transmembrane 7 superfamily member 2	ENSG00000149809	PAP55	31	45.2%	chr11	64639444	CCDS41669.1	c.-1T>C	p.IVS8+2-1SpliceDonor
TM7SF4	transmembrane 7 superfamily member 4	ENSG00000164935	PAP55	132	25.0%	chr8	105430459	CCDS6301.1	c.503A>G	p.N168S
TMTC1	transmembrane and tetratricopeptide repeat containing 1	ENSG00000133687	PAP55	95	22.1%	chr12	29560565	CCDS8718.1	c.1967A>C	p.Q656P
TMPRSS11E	transmembrane protease; serine 11B	ENSG00000185873	PAP55	177	32.2%	chr4	68776293	CCDS3521.1	c.1182G>T	p.K394N
TMPRSS11D	transmembrane protease; serine 11D	ENSG00000153802	PAP55	117	28.2%	chr4	68375583	CCDS3518.1	c.943G>T	p.E315X
TMPRSS9	transmembrane protease; serine 9	ENSG00000178297	PAP55	170	29.4%	chr19	2359481	CCDS12088.1	c.868G>A	p.D290N
TMEM161A	transmembrane protein 161A	ENSG00000064545	PAP55	77	42.9%	chr19	19092844	CCDS12393.1	c.1046G>A	p.R349Q
TMEM168	transmembrane protein 168	ENSG00000146802	PAP55	74	31.1%	chr7	112194989	CCDS5757.1	c.1593A>C	p.E531D
TMEM195	transmembrane protein 195	ENSG00000187546	PAP55	94	24.5%	chr7	15391700	CCDS34604.1	c.970G>T	p.E324X
TMEM31	transmembrane protein 31	ENSG00000179363	PAP55	365	26.3%	chrX	102855394	CCDS35359.1	c.319G>T	p.D107Y
TMEM47	transmembrane protein 47	ENSG00000147027	PAP55	80	26.3%	chrX	34567329	CCDS14235.1	c.323G>A	p.R108Q
TMEM68	transmembrane protein 68	ENSG00000167904	PAP55	68	29.4%	chr8	56837842	CCDS6161.1	c.231G>T	p.K77N
TMEM74	transmembrane protein 74	ENSG00000164841	PAP55	82	31.7%	chr8	109865850	CCDS6310.1	c.654G>T	p.E218D
TNRC6A	trinucleotide repeat containing 6A	ENSG00000090905	PAP55	30	33.3%	chr16	24669603	CCDS10624.2	c.109G>A	p.D37N
TNRC6A	trinucleotide repeat containing 6A	ENSG00000090905	PAP55	107	31.8%	chr16	24710129	CCDS10624.2	c.2665G>A	p.E889K
TRIM13	tripartite motif-containing 13	ENSG00000204977	PAP55	277	29.2%	chr13	49484540	CCDS41888.1	c.472G>A	p.G158R
TRIM3	tripartite motif-containing 3	ENSG00000110171	PAP55	62	32.3%	chr11	6434754	CCDS7764.1	c.778C>T	p.R260C
TRIM37	tripartite motif-containing 37	ENSG00000108395	PAP55	64	23.4%	chr17	54489136	CCDS32694.1	c.1081C>T	p.R361X
TPP2	tripeptidyl peptidase II	ENSG00000134900	PAP55	90	42.2%	chr13	102099361	CCDS9502.1	c.2732C>A	p.S911Y
TRIO	triple functional domain (PTPRF interacting)	ENSG00000038382	PAP55	45	28.9%	chr5	14440901	CCDS3883.1	c.3826C>T	p.R1276X
TRMT6	tRNA methyltransferase 6 homolog (S. cerevisiae)	ENSG00000089195	PAP55	42	28.6%	chr20	5873534	CCDS13093.1	c.283C>T	p.R95X
TNNT2	troponin T type 2 (cardiac)	ENSG00000118194	PAP55	185	34.6%	chr1	199601419	CCDS30970.1	c.236C>T	p.S79L
TPH2	tryptophan hydroxylase 2	ENSG00000139287	PAP55	102	29.4%	chr12	70659047	CCDS31859.1	c.854G>A	p.R285Q
TTLL13	tubulin tyrosine ligase-like family; member 13	ENSG00000213471	PAP55	120	40.0%	chr15	88594957	CCDS32328.1	c.91A>G	p.N31D
TDRD5	tudor domain containing 5	ENSG00000162782	PAP55	45	28.9%	chr1	177828453	CCDS1332.1	c.80G>A	p.S27N
TNFSF14	tumor necrosis factor (ligand) superfamily; member 14	ENSG00000125735	PAP55	92	23.9%	chr19	6616272	CCDS12171.1	c.388G>A	p.D130N
UBQLNL	ubiquilin-like	ENSG00000175518	PAP55	110	36.4%	chr11	5493620	CCDS31385.1	c.628G>T	p.E210X
UBR1	ubiquitin protein ligase E3 component n-recognin 1	ENSG00000159459	PAP55	85	23.5%	chr15	41095260	CCDS10091.1	c.3127A>C	p.N1043H
UBR2	ubiquitin protein ligase E3 component n-recognin 2	ENSG00000024048	PAP55	66	25.8%	chr6	42681502	CCDS4870.1	c.728T>G	p.I243S
UBR5	ubiquitin protein ligase E3 component n-recognin 5	ENSG00000104517	PAP55	88	26.1%	chr8	103367141	CCDS34933.1	c.5260C>T	p.R1754W
USP33	ubiquitin specific peptidase 33	ENSG00000077254	PAP55	179	25.7%	chr1	77966855	CCDS678.1	c.941C>T	p.S314L
USP33	ubiquitin specific peptidase 33	ENSG00000077254	PAP55	101	26.7%	chr1	77979669	CCDS678.1	c.208A>C	p.N70H
USP34	ubiquitin specific peptidase 34	ENSG00000115464	PAP55	168	33.3%	chr2	61420069	CCDS42686.1	c.2665T>C	p.S889P
USP34	ubiquitin specific peptidase 34	ENSG00000115464	PAP55	65	33.8%	chr2	61431314	CCDS42686.1	c.1270T>C	p.Y424H
USP47	ubiquitin specific peptidase 47	ENSG00000170242	PAP55	160	33.1%	chr11	11898338	CCDS41619.1	c.825T>G	p.F275L
USP51	ubiquitin specific peptidase 51	ENSG00000185295	PAP55	125	22.4%	chrX	55530933	NM_201286	c.1165G>T	p.D389Y
B3GALT2	UDP-Gal:betaGlcNAc beta 1;3-galactosyltransferase; polypeptide 2	ENSG00000162630	PAP55	67	31.3%	chr1	191417251	CCDS1383.1	c.65T>G	p.L22R

GALNT1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	ENSG00000141429	PAP55	99	32.3%	chr18	31526265	CCDS11915.1	c.1282T>G	p.Y428D
GALNTL2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2	ENSG00000131386	PAP55	51	27.5%	chr3	16243901	CCDS33711.1	c.1810A>G	p.M604V
UHRF1BP1L	UHRF1 binding protein 1-like	ENSG00000111647	PAP55	46	21.7%	chr12	99013695	CCDS31882.1	c.721T>G	p.L241V
UPF3B	UPF3 regulator of nonsense transcripts homolog B (yeast)	ENSG00000125351	PAP55	228	31.1%	chrX	118852970	CCDS14588.1	c.1351C>T	p.R451X
UMODL1	uromodulin-like 1	ENSG00000177398	PAP55	125	34.4%	chr21	42416178	CCDS42935.1	c.3380T>C	p.V1127A
USH2A	Usher syndrome 2A (autosomal recessive; mild)	ENSG00000042781	PAP55	206	28.2%	chr1	213915317	CCDS31025.1	c.12559C>T	p.R4187C
UTRN	utrophin	ENSG00000152818	PAP55	40	27.5%	chr6	144801693	CCDS34547.1	c.1361A>C	p.K454T
VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	ENSG00000197969	PAP55	109	33.9%	chr9	79144403	CCDS6655.1	c.6530A>G	p.D2177G
VPS24	vacuolar protein sorting 24 homolog (S. cerevisiae)	ENSG00000115561	PAP55	116	35.3%	chr2	86685565	CCDS33237.1	c.970A>C	p.N324H
AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B; gamma)	ENSG00000117020	PAP55	61	26.2%	chr1	241867553	CCDS31077.1	c.544G>T	p.E182X
CRKL	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	ENSG00000099942	PAP55	116	31.9%	chr22	19602274	CCDS13785.1	c.52C>G	p.P18A
VEPH1	ventricular zone expressed PH domain homolog 1 (zebrafish)	ENSG00000197415	PAP55	57	24.6%	chr3	158466110	CCDS3179.1	c.2164A>C	p.K722Q
VWF	von Willebrand factor	ENSG00000110799	PAP55	92	30.4%	chr12	5931304	CCDS8539.1	c.8122A>T	p.I2708F
VWA5A	von Willebrand factor A domain containing 5A	ENSG00000110002	PAP55	58	31.0%	chr11	123499320	CCDS8444.1	c.968G>A	p.G323D
VWA5A	von Willebrand factor A domain containing 5A	ENSG00000110002	PAP55	42	35.7%	chr11	123513173	CCDS8444.1	c.1867A>C	p.K623Q
WDR11	WD repeat domain 11	ENSG00000120008	PAP55	152	25.0%	chr10	122616250	CCDS7619.1	c.1174C>T	p.R392X
WDR11	WD repeat domain 11	ENSG00000120008	PAP55	42	28.6%	chr10	122630345	CCDS7619.1	c.1681C>T	p.R561C
WDR47	WD repeat domain 47	ENSG00000085433	PAP55	81	24.7%	chr1	109358047	CCDS30787.1	c.266A>G	p.Q89R
WDR64	WD repeat domain 64	ENSG00000162843	PAP55	74	29.7%	chr1	239968384	CCDS1619.1	c.421T>G	p.Y141D
WDR67	WD repeat domain 67	ENSG00000156787	PAP55	38	31.6%	chr8	124164224	CCDS6338.1	c.326A>C	p.K109T
WBSCR22	Williams Beuren syndrome chromosome region 22	ENSG00000071462	PAP55	44	34.1%	chr7	72745678	CCDS5557.1	c.594G>T	p.K198N
WBSCR28	Williams-Beuren syndrome chromosome region 28	ENSG00000175877	PAP55	212	32.5%	chr7	72917935	CCDS43597.1	c.594G>A	p.W198X
WNK3	WNK lysine deficient protein kinase 3	ENSG00000196632	PAP55	97	15.5%	chrX	54281513	CCDS14357.1	c.4001G>A	p.R1334Q
WNK3	WNK lysine deficient protein kinase 3	ENSG00000196632	PAP55	66	19.7%	chrX	54282147	CCDS14357.1	c.3762C>A	p.S1254R
WNK3	WNK lysine deficient protein kinase 3	ENSG00000196632	PAP55	58	27.6%	chrX	54291869	CCDS14357.1	c.3637G>A	p.E1213K
WBP4	WW domain binding protein 4 (formin binding protein 21)	ENSG00000120688	PAP55	39	25.6%	chr13	40552879	CCDS9375.1	c.854C>T	p.S285L
WWC3	WWC family member 3	ENSG00000047644	PAP55	189	36.0%	chrX	10045339	CCDS14136.1	c.1240G>A	p.D414N
XKRX	XK; Kell blood group complex subunit-related; X-linked	ENSG00000182489	PAP55	283	23.7%	chrX	100056361	CCDS14476.1	c.1011C>A	p.F337L
YEATS2	YEATS domain containing 2	ENSG00000163872	PAP55	67	29.9%	chr3	184922420	CCDS43175.1	c.339G>T	p.K113N
YTHDC1	YTH domain containing 1	ENSG00000083896	PAP55	103	32.0%	chr4	68885738	CCDS33992.1	c.485G>A	p.R162H
ZBTB2	zinc finger and BTB domain containing 2	ENSG00000181472	PAP55	321	28.0%	chr6	151728674	CCDS5231.1	c.1220G>A	p.R407H
ZBTB2	zinc finger and BTB domain containing 2	ENSG00000181472	PAP55	195	25.1%	chr6	151729113	CCDS5231.1	c.781C>T	p.R261W
ZBTB33	zinc finger and BTB domain containing 33	ENSG00000177485	PAP55	100	17.0%	chrX	119271844	CCDS14596.1	c.546G>T	p.K182N
ZSCAN29	zinc finger and SCAN domain containing 29	ENSG00000140265	PAP55	248	32.3%	chr15	41441331	CCDS10095.2	c.1791T>G	p.I597M
ZFP106	zinc finger protein 106 homolog (mouse)	ENSG00000103994	PAP55	108	36.1%	chr15	40518816	CCDS32208.1	c.4962NULL>(	p.NULL-1FsIns1bp
ZNF14	zinc finger protein 14	ENSG00000105708	PAP55	72	33.3%	chr19	19684123	CCDS12409.1	c.967C>T	p.R323X
ZNF200	zinc finger protein 200	ENSG00000010539	PAP55	223	33.6%	chr16	3223660	CCDS10497.1	c.97C>T	p.R33X
ZNF211	zinc finger protein 211	ENSG00000121417	PAP55	82	29.3%	chr19	62844322	CCDS12956.1	c.695C>T	p.A232V
ZNF215	zinc finger protein 215	ENSG00000149054	PAP55	50	24.0%	chr11	6921424	CCDS7775.1	c.688G>T	p.E230X
ZNF229	zinc finger protein 229	ENSG00000167383	PAP55	63	22.2%	chr19	49626057	CCDS42574.1	c.739A>C	p.K247Q
ZNF235	zinc finger protein 235	ENSG00000159917	PAP55	247	27.9%	chr19	49483882	CCDS33048.1	c.1546C>T	p.R516X
ZNF256	zinc finger protein 256	ENSG00000152454	PAP55	108	30.6%	chr19	63145131	CCDS12966.1	c.857G>A	p.R286Q
ZNF317	zinc finger protein 317	ENSG00000130803	PAP55	100	11.0%	chr19	9132298	CCDS12210.1	c.977G>T	p.R326I
ZNF333	zinc finger protein 333	ENSG00000160961	PAP55	144	33.3%	chr19	14690800	CCDS12316.1	c.1661G>A	p.R554Q
ZNF334	zinc finger protein 334	ENSG00000198185	PAP55	93	30.1%	chr20	44564913	CCDS33480.1	c.472A>C	p.N158H
ZNF343	zinc finger protein 343	ENSG00000088876	PAP55	141	31.2%	chr20	2422452	CCDS13028.1	c.90G>T	p.K30N
ZNF347	zinc finger protein 347	ENSG00000197937	PAP55	122	31.1%	chr19	58337168	CCDS33097.1	c.725T>G	p.F242C
ZNF354A	zinc finger protein 354A	ENSG00000169131	PAP55	98	33.7%	chr5	178073030	CCDS4438.1	c.455T>C	p.I152T
ZNF354C	zinc finger protein 354C	ENSG00000177932	PAP55	66	25.8%	chr5	178438485	CCDS4443.1	c.446C>T	p.S149L
ZNF382	zinc finger protein 382	ENSG00000161298	PAP55	70	15.7%	chr19	41809668	CCDS33004.1	c.1029G>T	p.E343D

ZNF41	zinc finger protein 41	ENSG00000147124	PAP55	55	25.5%	chrX	47193390	CCDS14279.1	c.723T>G	p.N241K
ZNF418	zinc finger protein 418	ENSG00000196724	PAP55	145	29.0%	chr19	63130192	CCDS42642.1	c.1169G>A	p.R390Q
ZNF462	zinc finger protein 462	ENSG00000148143	PAP55	67	37.3%	chr9	108727401	CCDS35096.1	c.1387T>G	p.L463V
ZNF462	zinc finger protein 462	ENSG00000148143	PAP55	361	26.9%	chr9	108730107	CCDS35096.1	c.4093G>A	p.E1365K
ZNF470	zinc finger protein 470	ENSG00000197016	PAP55	44	34.1%	chr19	61781064	CCDS33122.1	c.1455A>C	p.E485D
ZNF483	zinc finger protein 483	ENSG00000173258	PAP55	94	25.5%	chr9	113344748	CCDS35106.1	c.1712G>T	p.R571I
ZNF516	zinc finger protein 516	ENSG00000101493	PAP55	162	38.3%	chr18	72220842	ENST00000217537	c.2216C>T	p.S739L
ZNF540	zinc finger protein 540	ENSG00000171817	PAP55	127	26.8%	chr19	42795145	CCDS12506.1	c.1124G>T	p.R375I
ZNF549	zinc finger protein 549	ENSG00000121406	PAP55	71	21.1%	chr19	62741829	CCDS12952.1	c.1606A>C	p.K536Q
ZNF555	zinc finger protein 555	ENSG00000186300	PAP55	211	22.7%	chr19	2804213	CCDS12096.1	c.1150C>T	p.R384X
ZNF560	zinc finger protein 560	ENSG00000198028	PAP55	88	26.1%	chr19	9439028	CCDS12214.1	c.1595G>A	p.R532H
ZNF585B	zinc finger protein 585B	ENSG00000197800	PAP55	100	33.0%	chr19	42372862	CCDS12500.1	c.103G>A	p.D35N
ZNF594	zinc finger protein 594	ENSG00000180626	PAP55	117	32.5%	chr17	5024978	ENST00000381752	c.933A>C	p.Q311H
ZNF596	zinc finger protein 596	ENSG00000172748	PAP55	72	16.7%	chr8	185715	CCDS5951.2	c.868C>T	p.H290Y
ZNF608	zinc finger protein 608	ENSG00000168916	PAP55	173	31.8%	chr5	124011203	CCDS34219.1	c.2773A>G	p.N925D
ZNF630	zinc finger protein 630	ENSG00000221994	PAP55	66	31.8%	chrX	47804866	NM_001037735	c.145T>C	p.C49R
ZNF655	zinc finger protein 655	ENSG00000197343	PAP55	100	27.0%	chr7	99008466	CCDS5669.1	c.799C>A	p.P267T
ZNF699	zinc finger protein 699	ENSG00000196110	PAP55	125	32.8%	chr19	9267896	CCDS42495.1	c.1184A>C	p.E395A
ZNF699	zinc finger protein 699	ENSG00000196110	PAP55	106	26.4%	chr19	9268002	CCDS42495.1	c.1078G>T	p.E360X
ZNF711	zinc finger protein 711	ENSG00000147180	PAP55	42	35.7%	chrX	84406890	CCDS35344.1	c.889G>T	p.D297Y
ZNF749	zinc finger protein 749	ENSG00000186230	PAP55	89	32.6%	chr19	62647326	NM_001023561	c.998A>C	p.K333T
ZNF749	zinc finger protein 749	ENSG00000186230	PAP55	79	22.8%	chr19	62648076	NM_001023561	c.1748G>A	p.R583H
ZNF781	zinc finger protein 781	ENSG00000196381	PAP55	98	42.9%	chr19	42852286	CCDS12507.1	c.604A>C	p.N202H
ZNF781	zinc finger protein 781	ENSG00000196381	PAP55	198	30.8%	chr19	42852732	CCDS12507.1	c.158G>A	p.R53Q
ZNF804B	zinc finger protein 804B	ENSG00000182348	PAP55	100	30.0%	chr7	88802759	CCDS5613.1	c.2527C>A	p.P843T
ZFP90	zinc finger protein 90 homolog (mouse)	ENSG00000184939	PAP55	45	28.9%	chr16	67156007	CCDS42183.1	c.1816G>T	p.E606X
ZFPM2	zinc finger protein; multitype 2	ENSG00000169946	PAP55	160	23.1%	chr8	106883353	NM_012082	c.1867A>G	p.T623A
ZIM2	zinc finger; imprinted 2	ENSG00000198300	PAP55	217	23.0%	chr19	62018856	CCDS12948.1	c.2766C>A	p.F922L
ZMYND8	zinc finger; MYND-type containing 8	ENSG00000101040	PAP55	147	29.3%	chr20	45338729	CCDS13405.1	c.1216G>A	p.A406T
ZSWIM1	zinc finger; SWIM-type containing 1	ENSG00000168612	PAP55	241	29.9%	chr20	43945442	CCDS13382.2	c.804C>A	p.F268L
ZP4	zona pellucida glycoprotein 4	ENSG00000116996	PAP55	80	33.8%	chr1	236120520	CCDS1615.1	c.39A>C	p.L13F
ACVR1	activin A receptor; type I	ENSG00000115170	PAP57	111	10.8%	chr2	158325778	CCDS2206.1	c.1124G>A	p.R375H
ADAM21	ADAM metallopeptidase domain 21	ENSG00000139985	PAP57	318	24.5%	chr14	69996014	CCDS9804.1	c.2045T>NULL	p.NULL-1FsDel1bp
ADAM21P1	ADAM metallopeptidase domain 21 pseudogene 1	ENSG00000139985	PAP57	318	24.5%	chr14	69996014	CCDS9804.1	c.2045T>NULL	p.NULL-1FsDel1bp
ADCYAP1R1	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	ENSG00000078549	PAP57	89	20.2%	chr7	31112674	CCDS5433.1	c.1258G>A	p.V420M
AGXT	alanine-glyoxylate aminotransferase	ENSG00000172482	PAP57	98	14.3%	chr2	241456981	CCDS2543.1	c.26NULL>C	p.NULL-1FsIns1bp
AGXT	alanine-glyoxylate aminotransferase	ENSG00000172482	PAP57	121	17.4%	chr2	241461116	CCDS2543.1	c.572C>NULL	p.NULL-1FsDel1bp
ALOX12B	arachidonate 12-lipoxygenase; 12R type	ENSG00000179477	PAP57	70	20.0%	chr17	7920712	CCDS11129.1	c.1436G>NUL	p.NULL-1FsDel1bp
AADACL3	arylacetamide deacetylase-like 3	ENSG00000188984	PAP57	184	22.3%	chr1	12708081	CCDS41253.1	c.584G>NULL	p.NULL-1FsDel1bp
ASTN2	astrotactin 2	ENSG00000148219	PAP57	300	20.3%	chr9	119016497	CCDS6815.1	c.976G>A	p.G326R
ARID1A	AT rich interactive domain 1A (SWI-like)	ENSG00000117713	PAP57	107	17.8%	chr1	26972763	CCDS285.1	c.3972C>NUL	p.NULL-1FsDel1bp
ATXN2L	ataxin 2-like	ENSG00000168488	PAP57	164	17.1%	chr16	28745763	CCDS10640.1	c.696G>NULL	p.NULL-1FsDel1bp
ATXN7	ataxin 7	ENSG00000163635	PAP57	73	24.7%	chr3	63948920	CCDS43102.1	c.1241C>T	p.P414L
AGBL5	ATP/GTP binding protein-like 5	ENSG00000084693	PAP57	120	25.8%	chr2	27143893	CCDS1732.3	c.2117A>G	p.Q706R

ATAD2	ATPase family; AAA domain containing 2	ENSG00000156802	PAP57	61	37.7%	chr8	124454074	CCDS6343.1	c.403A>NULL	p.NULL-1FsDel1bp
BRSK1	BR serine/threonine kinase 1	ENSG00000160469	PAP57	114	21.9%	chr19	60506848	CCDS12921.1	c.1128C>NULL	p.NULL-1FsDel1bp
BPTF	bromodomain PHD finger transcription factor	ENSG00000171634	PAP57	337	20.2%	chr17	63367196	CCDS11673.1	c.6439C>T	p.L2147F
CPAMD8	C3 and PZP-like; alpha-2-macroglobulin domain containing 8	ENSG00000160111	PAP57	73	27.4%	chr19	16893723	CCDS42519.1	c.3843G>NUL	p.NULL-1FsDel1bp
CACHD1	cache domain containing 1	ENSG00000158966	PAP57	64	15.6%	chr1	64916571	CCDS628.2	c.3081G>A	p.M1027I
CAMKK1	calcium/calmodulin-dependent protein kinase kinase 1; alpha	ENSG00000004660	PAP57	79	24.1%	chr17	3735417	CCDS11039.1	c.314G>A	p.R105Q
CIC	capicua homolog (Drosophila)	ENSG00000079432	PAP57	134	22.4%	chr19	47487584	CCDS12601.1	c.2733G>NUL	p.NULL-1FsDel1bp
CTNNB1	catenin (cadherin-associated protein); beta 1; 88kDa	ENSG00000168036	PAP57	183	19.7%	chr3	41241108	CCDS2694.1	c.101G>T	p.G34V
CDS1	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	ENSG00000163624	PAP57	112	25.9%	chr4	85775499	CCDS3608.1	c.781T>NULL	p.NULL-1FsDel1bp
CNTLN	centlein; centrosomal protein	ENSG00000044459	PAP57	73	35.6%	chr9	17447585	CCDS43789.1	c.3178T>C	p.S1060P
CLCN3	chloride channel 3	ENSG00000109572	PAP57	94	20.2%	chr4	170850035	CCDS34100.1	c.925A>NULL	p.NULL-1FsDel1bp
CHD5	chromodomain helicase DNA binding protein 5	ENSG00000116254	PAP57	262	23.3%	chr1	6094804	CCDS57.1	c.5123C>T	p.A1708V
C1orf116	chromosome 1 open reading frame 116	ENSG00000182795	PAP57	62	19.4%	chr1	205262369	CCDS1475.1	c.1363C>A	p.L455M
C12orf52	chromosome 12 open reading frame 52	ENSG00000139405	PAP57	58	19.0%	chr12	112109024	CCDS9166.1	c.90G>C	p.R30S
C14orf49	chromosome 14 open reading frame 49	ENSG00000176438	PAP57	54	22.2%	chr14	94988463	CCDS9935.1	c.1148C>T	p.A383V
C17orf98	chromosome 17 open reading frame 98	ENSG00000214556	PAP57	116	24.1%	chr17	34251164	CCDS42310.1	c.5C>T	p.A2V
C9orf114	chromosome 9 open reading frame 114	ENSG00000198917	PAP57	170	23.5%	chr9	130630941	CCDS6913.1	c.227A>NULL	p.NULL-1FsDel1bp
CIITA	class II; major histocompatibility complex; transactivator	ENSG00000179583	PAP57	97	25.8%	chr16	10908588	CCDS10544.1	c.1738C>T	p.R580C
CLDN20	claudin 20	ENSG00000171217	PAP57	255	19.6%	chr6	155638696	CCDS5249.1	c.151T>C	p.W51R
F8	coagulation factor VIII; procoagulant component	ENSG00000185010	PAP57	368	11.7%	chrX	153810880	CCDS35457.1	c.7484A>NULL	p.NULL-1FsDel1bp
COBLL1	COBL-like 1	ENSG00000082438	PAP57	89	23.6%	chr2	165259542	CCDS2223.2	c.4284T>NULL	p.NULL-1FsDel1bp
CCDC102A	coiled-coil domain containing 102A	ENSG00000135736	PAP57	117	22.2%	chr16	56107756	CCDS10784.1	c.1369C>T	p.R457W
CCDC52	coiled-coil domain containing 52	ENSG00000163611	PAP57	55	21.8%	chr3	114701090	CCDS2973.1	c.177G>C	p.K59N
CCDC73	coiled-coil domain containing 73	ENSG00000186714	PAP57	163	11.0%	chr11	32591757	CCDS41630.1	c.4203A>NULL	p.NULL-1FsDel1bp
COL5A1	collagen; type V; alpha 1	ENSG00000130635	PAP57	238	24.8%	chr9	136740506	ENST00000371814	c.416G>A	p.G139D
CIR1	corepressor interacting with RBPJ; 1	ENSG00000138433	PAP57	156	19.9%	chr2	174921959	CCDS2256.1	c.1540A>NULL	p.NULL-1FsDel1bp
CORIN	corin; serine peptidase	ENSG00000145244	PAP57	241	25.3%	chr4	47389860	CCDS3477.1	c.-1T>NULL	p.IVS5-3-1SpliceAcceptor
CRYGB	crystallin; gamma B	ENSG00000182187	PAP57	101	26.7%	chr2	208715657	CCDS2380.1	c.753G>NULL	p.NULL-1FsDel1bp
CYP2B6	cytochrome P450; family 2; subfamily B; polypeptide 6	ENSG00000197408	PAP57	241	25.3%	chr19	46189183	CCDS12570.1	c.133C>T	p.Q45X
cnot1	DAVID_CCR4-NOT transcription complex: subunit 1	NM_206999	PAP57	86	24.4%	chr16	57134817	NM_206999	c.5146TT>NUI	p.NULL-1FsDel2bp
Chmp1a	DAVID_chromatin modifying protein 1A	NM_001083314	PAP57	103	23.3%	chr16	88243359	NM_001083314	c.133C>T	p.R45C
c12orf51	DAVID_chromosome 12 open reading frame 51	NM_001109662	PAP57	74	24.3%	chr12	111132285	NM_001109662	c.6518A>G	p.N2173S
C2orf81	DAVID_chromosome 2 open reading frame 81	NM_001145054	PAP57	86	15.1%	chr2	74495629	NM_001145054	c.1102C>A	p.P368T
CCDC57	DAVID_coiled-coil domain containing 57	NM_198082	PAP57	63	25.4%	chr17	77709025	NM_198082	c.2129G>A	p.R710Q
DST	DAVID_dystonin	NM_020388	PAP57	120	32.5%	chr6	56576835	NM_020388	c.8939C>T	p.S2980F
FAM18A	DAVID_family with sequence similarity 18: member A	NM_001079512	PAP57	179	18.4%	chr16	10774704	NM_001079512	c.548T>NULL	p.NULL-1FsDel1bp
fbf1	DAVID_Fas (TNFRSF6) binding factor 1	NM_001080542	PAP57	231	33.8%	chr17	71433829	NM_001080542	c.703C>T	p.R235C
fgf13	DAVID_fibroblast growth factor 13	NM_001139500	PAP57	54	18.5%	chrX	137767489	NM_001139500	c.235C>NULL	p.NULL-1FsDel1bp

LOC643677	DAVID_hypothetical protein LOC643677	NM_001146197	PAP57	99	19.2%	chr13	102179997	NM_001146197	c.41987TT>NU	p.NULL-1FsDel2bp
LOXHD1	DAVID_lipoxygenase homology domains 1	NM_144612	PAP57	103	12.6%	chr18	42352171	NM_144612	c.5259NULL>(	p.NULL-1FsIns1bp
TRANK1	DAVID_lupus brain antigen 1	NM_014831	PAP57	119	16.0%	chr3	36847386	NM_014831	c.8560C>T	p.R2854W
Muc5ac	DAVID_mucin 5AC: oligomeric mucus/gel-forming; similar to hCG1778310	ENSG00000196292	PAP57	108	22.2%	chr11	1146571	ENST00000406844	c.-1G>A	p.IVS5-1-1SpliceAcceptor
NEB	DAVID_nebulin	NM_001164508	PAP57	97	12.4%	chr2	152133180	NM_001164508	c.-1T>NULL	p.IVS109-3-1SpliceAcceptor
NPHP4	DAVID_nephronophthisis 4	NM_015102	PAP57	123	20.3%	chr1	5930762	NM_015102	c.947G>A	p.R316H
PITRM1	DAVID_pitrilysin metallopeptidase 1	NM_014889	PAP57	238	18.5%	chr10	3180178	NM_014889	c.-1G>T	p.IVS18+1-1SpliceDonor
PPP1R12B	DAVID_protein phosphatase 1: regulatory (inhibitor) subunit 12B	NM_001167857	PAP57	63	20.6%	chr1	200673813	NM_001167857	c.1496T>NULL	p.NULL-1FsDel1bp
SLFN12L	DAVID_schlafen family member 12-like	NM_001145027	PAP57	153	18.3%	chr17	30826295	NM_001145027	c.2176A>NULL	p.NULL-1FsDel1bp
SEC16B	DAVID_SEC16 homolog B (S. cerevisiae)	NM_033127	PAP57	65	15.4%	chr1	176168556	NM_033127	c.2940C>NULL	p.NULL-1FsDel1bp
SENP1	DAVID_SUMO1/sentrin specific peptidase 1	NM_014554	PAP57	93	19.4%	chr12	46745163	NM_014554	c.1382A>NULL	p.NULL-1FsDel1bp
ZNF251	DAVID_zinc finger protein 251	NM_138367	PAP57	162	22.8%	chr8	145919342	NM_138367	c.512G>A	p.G171D
ZNF836	DAVID_zinc finger protein 836	NM_001102657	PAP57	74	31.1%	chr19	57350041	NM_001102657	c.2707T>C	p.S903P
DSEL	dermatan sulfate epimerase-like	ENSG00000171451	PAP57	225	23.6%	chr18	63330746	CCDS11995.1	c.2110T>A	p.F704I
DIAPH2	diaphanous homolog 2 (Drosophila)	ENSG00000147202	PAP57	164	11.6%	chrX	96023369	CCDS14467.1	c.583G>A	p.V195I
DPYD	dihydropyrimidine dehydrogenase	ENSG00000188641	PAP57	60	23.3%	chr1	97544371	CCDS30777.1	c.2129T>C	p.L710P
DPYD	dihydropyrimidine dehydrogenase	ENSG00000188641	PAP57	50	22.0%	chr1	97544379	CCDS30777.1	c.2241T>NULL	p.NULL-1FsDel1bp
DCLRE1A	DNA cross-link repair 1A (PSO2 homolog; S. cerevisiae)	ENSG00000198924	PAP57	141	21.3%	chr10	115591271	CCDS7584.1	c.2704C>T	p.Q902X
DOPEY2	dopey family member 2	ENSG00000142197	PAP57	94	22.3%	chr21	36508691	CCDS13643.1	c.1096G>A	p.V366I
DUSP9	dual specificity phosphatase 9	ENSG00000130829	PAP57	222	18.0%	chrX	152568217	CCDS14724.1	c.710C>NULL	p.NULL-1FsDel1bp
DNAH11	dynein; axonemal; heavy chain 11	ENSG00000105877	PAP57	109	15.6%	chr7	21710635	ENST00000409508	c.6353C>A	p.P2118Q
EVI2B	ecotropic viral integration site 2B	ENSG00000185862	PAP57	145	15.2%	chr17	26656161	CCDS11266.1	c.1939A>NULL	p.NULL-1FsDel1bp
ERMP1	endoplasmic reticulum metallopeptidase 1	ENSG00000099219	PAP57	112	14.3%	chr9	5820943	CCDS34983.1	c.725NULL>T	p.NULL-1FsIns4bp
EPHB2	EPH receptor B2	ENSG00000133216	PAP57	58	29.3%	chr1	23112833	ENST00000374630	c.3051A>NULL	p.NULL-1FsDel1bp
EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	ENSG00000128829	PAP57	187	14.4%	chr15	38052476	CCDS42016.1	c.1629A>NULL	p.NULL-1FsDel1bp
ERCC5	excision repair cross-complementing rodent repair deficiency; complementation group 5	ENSG00000134899	PAP57	220	23.2%	chr13	102322613	CCDS32004.1	c.2743A>NULL	p.NULL-1FsDel1bp
FAM135B	family with sequence similarity 135; member B	ENSG00000147724	PAP57	309	20.1%	chr8	139233247	CCDS6375.2	c.2653G>A	p.V885I
FAM59B	family with sequence similarity 59; member B	ENSG00000157833	PAP57	71	18.3%	chr2	26259375	NM_001168241	c.289C>T	p.R97W
FCGBP	Fc fragment of IgG binding protein	ENSG00000090920	PAP57	77	22.1%	chr19	45054953	CCDS12546.1	c.14957G>A	p.C4986Y
FCRLA	Fc receptor-like A	ENSG00000132185	PAP57	45	22.2%	chr1	159948411	CCDS30926.1	c.614T>C	p.M205T
FGFR2	fibroblast growth factor receptor 2	ENSG00000066468	PAP57	117	37.6%	chr10	123237505	CCDS7620.2	c.1979A>T	p.K660M
FSIP1	fibrous sheath interacting protein 1	ENSG00000150667	PAP57	133	21.8%	chr15	37697485	CCDS10050.1	c.1442G>A	p.G481D
FSIP2	fibrous sheath interacting protein 2	ENSG00000188738	PAP57	72	26.4%	chr2	186373284	ENST00000344648	c.2858A>NULL	p.NULL-1FsDel1bp
FOXK1	forkhead box K1	ENSG00000164916	PAP57	89	19.1%	chr7	4763160	CCDS34591.1	c.1060C>T	p.R354W
HERC4	hect domain and RLD 4	ENSG00000148634	PAP57	56	26.8%	chr10	69418433	CCDS41533.1	c.1799T>C	p.L600P
HK1	hexokinase 1	ENSG00000156515	PAP57	79	25.3%	chr10	70799328	CCDS7289.1	c.829A>G	p.I277V

HIST1H2BG	histone cluster 1; H2bg	ENSG00000187990	PAP57	78	19.2%	chr6	26324619	CCDS4594.1	c.232G>A	p.A78T
HCFC2	host cell factor C2	ENSG00000111727	PAP57	168	19.0%	chr12	103000665	CCDS9097.1	c.919A>NULL	p.NULL-1FsDel1bp
HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	ENSG00000095951	PAP57	310	27.1%	chr6	12128612	ENST00000379382	c.80C>T	p.T27M
HIVEP3	human immunodeficiency virus type I enhancer binding protein 3	ENSG00000127124	PAP57	59	20.3%	chr1	41818558	CCDS463.1	c.4498T>C	p.S1500P
ICOSLG	inducible T-cell co-stimulator ligand	ENSG00000160223	PAP57	179	21.2%	chr21	44481268	CCDS42952.1	c.666C>NULL	p.NULL-1FsDel1bp
IL1RAPL1	interleukin 1 receptor accessory protein-like 1	ENSG00000169306	PAP57	230	10.4%	chrX	29883547	CCDS14218.1	c.1780G>A	p.A594T
IQGAP1	IQ motif containing GTPase activating protein 1	ENSG00000140575	PAP57	39	25.6%	chr15	88820929	CCDS10362.1	c.2815A>NULI	p.NULL-1FsDel1bp
ISOC1	isochorismatase domain containing 1	ENSG00000066583	PAP57	186	23.1%	chr5	128468638	CCDS43357.1	c.400NULL>G	p.NULL-1FsIns1bp
KLK9	kallikrein-related peptidase 9	ENSG00000213022	PAP57	90	22.2%	chr19	56201751	CCDS12816.1	c.241T>C	p.W81R
KLHDC5	kelch domain containing 5	ENSG00000087448	PAP57	64	15.6%	chr12	27842036	CCDS31763.1	c.1188G>NUL	p.NULL-1FsDel1bp
KLHL10	kelch-like 10 (Drosophila)	ENSG00000161594	PAP57	79	20.3%	chr17	37257984	CCDS42340.1	c.1726G>A	p.A576T
KRT27	keratin 27	ENSG00000171446	PAP57	71	26.8%	chr17	36190203	CCDS11375.1	c.559G>A	p.V187M
KIAA0430	KIAA0430	ENSG00000166783	PAP57	96	20.8%	chr16	15640505	CCDS10562.2	c.87G>A	p.W29X
KIAA1267	KIAA1267	ENSG00000120071	PAP57	313	15.3%	chr17	41604508	CCDS11503.1	c.2067G>NUL	p.NULL-1FsDel1bp
KIFAP3	kinesin-associated protein 3	ENSG00000075945	PAP57	110	21.8%	chr1	168227994	CCDS1288.1	c.1210A>T	p.M404L
LRRC24	leucine rich repeat containing 24	ENSG00000177021	PAP57	131	35.1%	chr8	145720397	CCDS34969.1	c.512C>T	p.S171F
LHX1	LIM homeobox 1	ENSG00000132130	PAP57	104	26.9%	chr17	32374508	CCDS11316.1	c.1188C>NULI	p.NULL-1FsDel1bp
MST1R	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	ENSG00000164078	PAP57	153	24.8%	chr3	49914912	CCDS2807.1	c.1135G>A	p.D379N
MAMDC4	MAM domain containing 4	ENSG00000177943	PAP57	134	17.9%	chr9	138870640	ENST00000392881	c.1507C>T	p.R503C
MAN2A2	mannosidase; alpha; class 2A; member 2	ENSG00000196547	PAP57	125	24.8%	chr15	89254734	CCDS32332.1	c.-1G>NULL	p.IVS9-1-1SpliceAcceptor
MDM4	Mdm4 p53 binding protein homolog (mouse)	ENSG00000198625	PAP57	120	19.2%	chr1	202773744	ENST00000391947	c.-1T>NULL	p.IVS1+2-1SpliceDonor
MED1	mediator complex subunit 1	ENSG00000125686	PAP57	79	29.1%	chr17	34824833	CCDS11336.1	c.1471G>T	p.D491Y
MED12	mediator complex subunit 12	ENSG00000184634	PAP57	69	21.7%	chrX	70255396	CCDS43970.1	c.67G>T	p.D23Y
MED8	mediator complex subunit 8	ENSG00000159479	PAP57	133	16.5%	chr1	43622730	NM_052877	c.986NULL>A	p.NULL-1FsIns1bp
MEFV	Mediterranean fever	ENSG00000103313	PAP57	62	16.1%	chr16	3244354	CCDS10498.1	c.715C>T	p.R239X
MPPED2	metallophosphoesterase domain containing 2	ENSG00000066382	PAP57	156	22.4%	chr11	30389607	CCDS7870.1	c.869A>G	p.N290S
MECP2	methyl CpG binding protein 2 (Rett syndrome)	ENSG00000169057	PAP57	331	13.6%	chrX	152949172	CCDS14741.1	c.1301C>T	p.A434V
MBD6	methyl-CpG binding domain protein 6	ENSG00000166987	PAP57	121	10.7%	chr12	56207999	CCDS8944.1	c.2338NULL>(	p.NULL-1FsIns1bp
MON2	MON2 homolog (S. cerevisiae)	ENSG00000061987	PAP57	136	24.3%	chr12	61240588	CCDS31849.1	c.3460G>A	p.A1154T
MORC4	MORC family CW-type zinc finger 4	ENSG00000133131	PAP57	93	16.1%	chrX	106115014	CCDS14525.2	c.789A>NULL	p.NULL-1FsDel1bp
MORN1	MORN repeat containing 1	ENSG00000116151	PAP57	180	27.8%	chr1	2309570	CCDS40.1	c.215C>T	p.T72M
MSH3	mutS homolog 3 (E. coli)	ENSG00000113318	PAP57	145	15.2%	chr5	80006671	CCDS34195.1	c.1141A>NULI	p.NULL-1FsDel1bp
MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	ENSG00000055609	PAP57	120	27.5%	chr7	151505081	CCDS5931.1	c.10209A>NUI	p.NULL-1FsDel1bp
MYO1A	myosin IA	ENSG00000166866	PAP57	259	18.1%	chr12	55708840	CCDS8929.1	c.3224A>NULI	p.NULL-1FsDel1bp
NAPEPLD	N-acyl phosphatidylethanolamine phospholipase D	ENSG00000161048	PAP57	306	19.6%	chr7	102547359	CCDS5729.1	c.1488T>NULI	p.NULL-1FsDel1bp

NSFL1C	NSFL1 (p97) cofactor (p47)	ENSG00000088833	PAP57	167	21.6%	chr20	1381208	CCDS13015.1	c.715C>T	p.R239W
NRIP1	nuclear receptor interacting protein 1	ENSG00000180530	PAP57	141	15.6%	chr21	15262290	CCDS13568.1	c.3571G>NUL	p.NULL-1FsDel1bp
NR2E1	nuclear receptor subfamily 2; group E; member 1	ENSG00000112333	PAP57	171	19.3%	chr6	108615292	CCDS5063.1	c.1090NULL>A	p.NULL-1FsIns1bp
NOD2	nucleotide-binding oligomerization domain containing 2	ENSG00000167207	PAP57	98	24.5%	chr16	49302389	CCDS10746.1	c.1066C>T	p.P356S
OBSCN	obscurin; cytoskeletal calmodulin and titin-interacting RhoGEF	ENSG00000154358	PAP57	93	21.5%	chr1	226514085	ENST00000359599	c.4846C>T	p.R1616C
OCA2	oculocutaneous albinism II	ENSG00000104044	PAP57	195	12.3%	chr15	25902225	CCDS10020.1	c.-1G>T	p.IVS12-1-1SpliceAcceptor
ODZ3	odz; odd Oz/ten-m homolog 3 (Drosophila)	ENSG00000218336	PAP57	202	21.8%	chr4	183950448	NM_001080477	c.5629C>T	p.R1877W
OR2AT4	olfactory receptor; family 2; subfamily AT; member 4	ENSG00000171561	PAP57	171	25.1%	chr11	74477638	CCDS31639.1	c.769T>A	p.Y257N
PDZD7	PDZ domain containing 7	ENSG00000186862	PAP57	163	22.7%	chr10	102772049	CCDS31269.1	c.626G>A	p.R209H
PEPD	peptidase D	ENSG00000124299	PAP57	101	17.8%	chr19	38646806	CCDS42544.1	c.551G>A	p.R184Q
PHF12	PHD finger protein 12	ENSG00000109118	PAP57	68	25.0%	chr17	24258739	CCDS32598.1	c.2536G>A	p.D846N
PTEN	phosphatase and tensin homolog	ENSG00000171862	PAP57	207	44.0%	chr10	89682884	CCDS31238.1	c.388C>G	p.R130G
PIK3CA	phosphoinositide-3-kinase; catalytic; alpha polypeptide	ENSG00000121879	PAP57	105	25.7%	chr3	180434779	CCDS43171.1	c.3140A>G	p.H1047R
PIK3CB	phosphoinositide-3-kinase; catalytic; beta polypeptide	ENSG00000051382	PAP57	147	19.0%	chr3	139883541	CCDS3104.1	c.2462G>A	p.R821H
PLCH1	phospholipase C; eta 1	ENSG00000114805	PAP57	96	25.0%	chr3	156794472	CCDS33881.1	c.332G>A	p.G111D
PHIP	pleckstrin homology domain interacting protein	ENSG00000146247	PAP57	127	12.6%	chr6	79768389	CCDS4987.1	c.1825C>T	p.R609C
PLXNB2	plexin B2	ENSG00000196576	PAP57	105	26.7%	chr22	49062174	CCDS43035.1	c.3646C>NULL	p.NULL-1FsDel1bp
POLR2H	polymerase (RNA) II (DNA directed) polypeptide H	ENSG00000163882	PAP57	232	17.7%	chr3	185563976	CCDS3264.1	c.2T>C	p.M1T
KCND2	potassium voltage-gated channel; Shal-related subfamily; member 2	ENSG00000184408	PAP57	424	20.3%	chr7	119702199	CCDS5776.1	c.277C>T	p.R93C
PRRG3	proline rich Gla (G-carboxyglutamic acid) 3 (transmembrane)	ENSG00000130032	PAP57	132	15.9%	chrX	150619751	CCDS14699.1	c.286G>A	p.A96T
PCDH17	protocadherin 17	ENSG00000118946	PAP57	105	10.5%	chr13	57106128	CCDS31986.1	c.1447G>A	p.E483K
RAB3GAP2	RAB3 GTPase activating protein subunit 2 (non-catalytic)	ENSG00000118873	PAP57	53	24.5%	chr1	218391310	CCDS31028.1	c.4088A>G	p.K1363R
RAB40C	RAB40C; member RAS oncogene family	ENSG00000197562	PAP57	69	23.2%	chr16	617581	CCDS10413.1	c.804NULL>C	p.NULL-1FsIns1bp
RASAL1	RAS protein activator like 1 (GAP1 like)	ENSG00000111344	PAP57	43	34.9%	chr12	112038193	CCDS9165.1	c.778C>T	p.R260C
RPS27L	ribosomal protein S27-like	ENSG00000185088	PAP57	58	24.1%	chr15	61234986	CCDS42048.1	c.-1TT>NULL	p.IVS2-3-1SpliceAcceptor
RNF160	ring finger protein 160	ENSG00000198862	PAP57	66	25.8%	chr21	29261077	CCDS33527.1	c.2415AA>NU	p.NULL-1FsDel2bp
RG9MTD1	RNA (guanine-9-) methyltransferase domain containing 1	ENSG00000174173	PAP57	46	23.9%	chr3	102766699	CCDS43122.1	c.384A>NULL	p.NULL-1FsDel1bp
RBM6	RNA binding motif protein 6	ENSG00000004534	PAP57	236	16.5%	chr3	49980036	CCDS2809.1	c.174NULL>G	p.NULL-1FsIns1bp
RBMXL2	RNA binding motif protein; X-linked-like 2	ENSG00000170748	PAP57	77	22.1%	chr11	7067952	CCDS7777.1	c.1025G>A	p.R342Q
RUFY3	RUN and FYVE domain containing 3	ENSG00000018189	PAP57	71	29.6%	chr4	71849088	CCDS34001.1	c.503G>A	p.R168H
SLTM	SAFB-like; transcription modulator	ENSG00000137776	PAP57	360	18.1%	chr15	56969817	CCDS10168.2	c.2214NULL>C	p.NULL-1FsIns2bp
STIL	SCL/TAL1 interrupting locus	ENSG00000123473	PAP57	103	15.5%	chr1	47498678	CCDS41329.1	c.3200A>NULL	p.NULL-1FsDel1bp
SERTAD4	SERTA domain containing 4	ENSG00000082497	PAP57	200	18.0%	chr1	208479469	CCDS1494.1	c.184T>C	p.Y62H
SIRT3	sirtuin (silent mating type information regulation 2 homolog) 3 (S. cerevisiae)	ENSG00000142082	PAP57	45	26.7%	chr11	226090	CCDS7691.1	c.239G>A	p.R80Q
SIX4	SIX homeobox 4	ENSG00000100625	PAP57	134	15.7%	chr14	60256688	CCDS9749.2	c.1774CCTT>N	p.NULL-1FsDel4bp
SIX6	SIX homeobox 6	ENSG00000184302	PAP57	94	16.0%	chr14	60046338	CCDS9747.1	c.469NULL>A	p.NULL-1FsIns1bp

SKIL	SKI-like oncogene	ENSG00000136603	PAP57	122	18.0%	chr3	171560891	CCDS33890.1	c.78NULL>C	p.NULL-1FsIns1bp
SMAD7	SMAD family member 7	ENSG00000101665	PAP57	137	17.5%	chr18	44728793	CCDS11936.1	c.679C>NULL	p.NULL-1FsDel1bp
SLC16A4	solute carrier family 16; member 4 (monocarboxylic acid transporter 5)	ENSG00000168679	PAP57	79	27.8%	chr1	110707950	CCDS823.1	c.1552T>NULL	p.NULL-1FsDel1bp
SLC25A39	solute carrier family 25; member 39	ENSG00000013306	PAP57	91	14.3%	chr17	39754430	CCDS11482.1	c.391G>A	p.A131T
SLC26A10	solute carrier family 26; member 10	ENSG00000135502	PAP57	482	24.5%	chr12	56304176	ENST00000300189	c.871NULL>C	p.NULL-1FsIns1bp
SLC9A9	solute carrier family 9 (sodium/hydrogen exchanger); member 9	ENSG00000181804	PAP57	71	25.4%	chr3	145033756	CCDS33872.1	c.-1T>NULL	p.IVS1-3-1SpliceAcceptor
SPATS2L	spermatogenesis associated; serine-rich 2-like	ENSG00000196141	PAP57	85	27.1%	chr2	201042930	NM_015535	c.1006C>T	p.R336W
SMPD1	sphingomyelin phosphodiesterase 1; acid lysosomal	ENSG00000166311	PAP57	62	17.7%	chr11	6368484	CCDS31409.1	c.80C>NULL	p.NULL-1FsDel1bp
SAMD9	sterile alpha motif domain containing 9	ENSG00000205413	PAP57	102	20.6%	chr7	92572051	CCDS34680.1	c.1296G>T	p.K432N
STAG3	stromal antigen 3	ENSG00000066923	PAP57	274	22.3%	chr7	99647029	CCDS34703.1	c.3446T>A	p.F1149Y
SYNJ2	synaptojanin 2	ENSG00000078269	PAP57	120	28.3%	chr6	158427997	CCDS5254.1	c.3331C>NULL	p.NULL-1FsDel1bp
TRBV6-5	T cell receptor beta variable 6-5	ENSG00000211721	PAP57	140	19.3%	chr7	141819681	ENST00000390368	c.112A>G	p.M38V
TRPM4	transient receptor potential cation channel; subfamily M; member 4	ENSG00000130529	PAP57	180	22.8%	chr19	54377780	CCDS33073.1	c.1397C>T	p.A466V
TNPO3	transportin 3	ENSG00000064419	PAP57	73	23.3%	chr7	128397495	CCDS5809.1	c.2708NULL>(	p.NULL-1FsIns1bp
TRIM2	tripartite motif-containing 2	ENSG00000109654	PAP57	127	21.3%	chr4	154463302	CCDS3781.1	c.1754G>A	p.R585H
VPS33A	vacuolar protein sorting 33 homolog A (S. cerevisiae)	ENSG00000139719	PAP57	171	18.7%	chr12	121286350	CCDS9231.1	c.1513G>NUL	p.NULL-1FsDel1bp
ZFP90	zinc finger protein 90 homolog (mouse)	ENSG00000184939	PAP57	194	19.6%	chr16	67154809	CCDS42183.1	c.618NULL>A	p.NULL-1FsIns1bp
ZMPSTE24	zinc metallopeptidase (STE24 homolog; S. cerevisiae)	ENSG00000084073	PAP57	50	26.0%	chr1	40529130	CCDS449.1	c.1077T>NULL	p.NULL-1FsDel1bp

*Coordinates refer to the human reference genome hg18 release (NCBI 36.1, March 2006).

table S3. Clinical Characteristics and Mutations Assessed in Pap Specimens

Case #	Age	Tissue	Cancer subtype	Clinical stage (FIGO)	Race/Ethnicity	Total DNA recovered (µg)	Gene name	Gene ID	Genomic coordinate*	Transcript	Nucleotide	Amino acid change	Mutation type	Detected fraction
PAP 001	45	Endometrial	Endometrioid	IB	White	31	*PIK3CA*	ENSG00000121879	g.chr3:180434779A>G	CCDS43171.1	c.3140A>G	p.H1047R	Missense	10%
PAP 002	39	Ovarian	Papillary serous	IIIC	White	3.7	*TP53*	ENSG00000141510	g.chr17:7519215A>T	CCDS11118.1	c.440T>A	p.V147D	Missense	0.40%
PAP 003	53	Endometrial	Endometrioid	IB	White	5.2	*APC*	ENSG00000134982	g.chr5:112203538C>T	CCDS4107.1	c.4348C>T	p.R1450X	Nonsense	3.2%
PAP 004	38	Ovarian	Papillary serous	IB	White	0.36	*TP53*	ENSG00000141510	g.chr17:7519154delC	CCDS11118.1	c.501delG	Frameshift	Indel	<0.005%
PAP 005	59	Ovarian	Borderline papillary serous cystadenocarcinoma	IIIC	White	7.6	*NF1*	ENSG00000196712	g.chr17:26552610insC	CCDS42292.1	c.1241insC	Frameshift	Indel	<0.005%
PAP 006	57	Ovarian	Papillary serous	IIIC	White	8.2	*TP53*	ENSG00000141510	g.chr17:7517824C>T	CCDS11118.1	c.839G>A	p.R280K	Missense	<0.005%
PAP 007	63	Ovarian	Papillary serous	IIIC	White	6.8	*TP53*	ENSG00000141510	g.chr17:7517783C>A	CCDS11118.1	c.880G>T	p.E294X	Nonsense	<0.005%
PAP 010	73	Endometrial	Endometrioid	IB	White	8.6	*FBXW7*	ENSG00000109670	g.chr4:153466817G>A	CCDS3777.1	c.1435C>T	p.R479X	Nonsense	15%
PAP 011	58	Endometrial	Endometrioid	IB	White	11	*KRAS*	ENSG00000133703	g.chr12:25289551C>G	CCDS8703.1	c.35G>C	p.G12A	Missense	3.5%
PAP 024	56	Endometrial	Endometrioid with squamous differentiation	IA	White	5.6	*CTNNB1*	ENSG00000168036	g.chr3:41241108G>T	CCDS2694.1	c.101G>T	p.G34V	Missense	0.22%
PAP 025	75	Endometrial	Serous carcinoma	IA	Black	0.74	*TP53*	ENSG00000141510	g.chr17:7520119_7520120delGG	CCDS11118.1	c.292_293delCC	Frameshift	Indel	8.7%
PAP 026	86	Endometrial	Endometrioid carcinoma	IA	White	18	*PTEN*	ENSG00000171862	g.chr10:89710752G>A	CCDS31238.1	c.923G>A	p.R308H	Missense	0.01%
PAP 027	65	Ovarian	Papillary serous	IIIC	White	19	*SETD2*	ENSG00000181555	g.chr3:47138125G>A	NM_014159	c.805C>T	p.Q269X	Nonsense	<0.005%
PAP 030	73	Endometrial	Endometrioid	IA	White	18	*MSH6*	ENSG00000116062	g.chr2:47880779G>A	CCDS1836.1	c.2153G>A	p.S718N	Missense	0.24%
PAP 031	61	Endometrial	Endometrioid	IA	Asian	101	*CTNNB1*	ENSG00000168036	g.chr3:41241117C>A	CCDS2694.1	c.110C>A	p.S37Y	Missense	1.3%
PAP 032	82	Endometrial	Endometrioid	IA	White	2.2	*PTEN*	ENSG00000171862	g.chr10:89682884C>G	CCDS31238.1	c.388C>G	p.R130G	Missense	0.02%
PAP 033	68	Endometrial	Endometrioid with squamous differentiation	IA	White	11	*KRAS*	ENSG00000133703	g.chr12:25289551C>A	CCDS8703.1	c.35G>T	p.G12V	Missense	1.5%
PAP 034	55	Endometrial	Endometrioid	IA	White	11	*CTNNB1*	ENSG00000168036	g.chr3:41241107G>A	CCDS2694.1	c.100G>A	p. G34R	Missense	20%
PAP 035	50	Endometrial	Endometrioid	IVB	White	0.48	*KRAS*	ENSG00000133703	g.chr12:25289551C>T	CCDS8703.1	c.35G>A	p.G12D	Missense	6.1%
PAP 036	57	Ovarian	Endometrioid with squamous differentiation	IA	White	2.5	*PIK3CA*	ENSG00000121879	g.chr3:180418789A>T	CCDS43171.1	c.1637A>T	p.Q546L	Missense	<0.005%
PAP 037	64	Endometrial	Endometrioid	IA	Asian	10	*PIK3CA*	ENSG00000121879	g.chr3:180434712A>G	CCDS43171.1	c.3073A>G	p.T1025A	Missense	0.17%
PAP 038	47	Ovarian	Papillary serous	IA	Asian	5.2	*TP53*	ENSG00000141510	g.chr17:7518915T>C	CCDS11118.1	c.659A>G	p.Y220C	Missense	0.48%
PAP 039	73	Ovarian	Papillary serous	IA	Asian	9.0	*TP53*	ENSG00000141510	g.chr17:7518244delG	CCDS11118.1	c.871delC	Frameshift	Indel	5.9%
PAP 040	57	Endometrial	Endometrioid	IB	Asian	7.7	*CTNNB1*	ENSG00000168036	g.chr3:41241141C>A	CCDS2694.1	c.134C>A	p.S45Y	Missense	0.084%
PAP 041	66	Endometrial	Papillary serous	IA	Asian	5.7	*FGFR2*	ENSG00000066468	g.chr10:123269667G>C	CCDS7620.2	c.755C>G	p.S252W	Missense	0.13%
PAP 041	66	Endometrial	Papillary serous	IA	Asian	5.7	*PTEN*	ENSG00000171862	g.chr10:89682902T>C	CCDS31238.1	c.406T>C	p.C136R	Missense	0.087%
PAP 042	45	Ovarian	Adenosquamous carcinoma	IIIC	White	14	*TP53*	ENSG00000141510	g.chr17:7520074insA	CCDS11118.1	c.339insT	Frameshift	Indel	1.5%
PAP 058	62	Ovarian	Papillary serous	IIIC	White	14	*PIK3CA*	ENSG00000121879	g.chr3:180399630G>A	CCDS43171.1	c.323G>A	p.R108H	Missense	0.49%
PAP 060	69	Ovarian	Papillary serous	IIIC	White	9.3	*TP53*	ENSG00000141510	g.chr17:7519131C>T	CCDS11118.1	c.524G>A	p.R175H	Missense	<0.05%
PAP 061	70	Ovarian	Papillary serous	IIIC	White	5.9	*TP53*	ENSG00000141510	g.chr17:7517846G>A	CCDS11118.1	c.817C>T	p.R273C	Missense	0.021%
PAP 062	55	Ovarian	Papillary serous	IIIC	White	1.4	*TP53*	ENSG00000141510	g.chr17:7520213_7520216delGCAT	CCDS11118.1	c.196_199delATGC	Frameshift	Indel	<0.005%
PAP 063	66	Ovarian	Papillary serous	IIIB	White	7.4	*TP53*	ENSG00000141510	g.chr17:7519131C>T	CCDS11118.1	c.524G>A	p.R175H	Missense	<0.005%
PAP 064	50	Ovarian	Dysgerminoma	IIIA	Asian	5.6	*TP53*	ENSG00000141510	g.chr17:7518233T>G	CCDS11118.1	c.773A>C	p.E258A	Missense	4.2%
PAP 066	70	Endometrial	Endometrioid adenocarcinoma, villoglandular type	IIIC	Asian	7.2	*TP53*	ENSG00000141510	g.chr17:7518960T>C	CCDS11118.1	c.614A>G	p.Y205C	Missense	5.5%
PAP 067	61	Endometrial	Endometrioid	IB	Asian	9.3	*TP53*	ENSG00000141510	g.chr17:7518937G>A	CCDS11118.1	c.637C>T	p.R213X	Nonsense	2.7%
PAP 068	63	Endometrial	Endometrioid adenocarcinoma with mucinous differe	IB	Asian	8.6	*PIK3CA*	ENSG00000121879	g.chr3:180410674T>C	CCDS43171.1	c.1258T>C	p.C420R	Missense	0.029%
PAP 069	51	Endometrial	Endometrioid	IB	Asian	7.4	*TP53*	ENSG00000141510	g.chr17:7520084G>A	CCDS11118.1	c.328C>T	p.R110C	Missense	15%
PAP 070	49	Endometrial	Endometrioid	IIA	Asian	1.6	*PIK3CA*	ENSG00000121879	g.chr3:180399570G>A	CCDS43171.1	c.263G>A	p.R88Q	Missense	30%
PAP 071	57	Endometrial	Endometrioid	IA	White	4.4	*PIK3CA*	ENSG00000121879	g.chr3:180434779A>G	CCDS43171.1	C.3140A>G	p.H1047R	Missense	0.37%
PAP 072	64	Ovarian	Papillary serous	IV	White	4.2	*TP53*	ENSG00000141510	g.chr17:7518272C>T	CCDS11118.1	c.734G>A	p.G245D	Missense	0.81%

PAP 073	64	Ovarian	Papillary serous	IIIC	White	4.6	*TP53*	ENSG00000141510	g.chr17:7519167T>C	CCDS11118.1	c.488A>G	p.Y163C	Missense	<0.005%
PAP 074	73	Ovarian	Papillary serous	IV	White	8.3	*TP53*	ENSG00000141510	g.chr17:7519131C>T	CCDS11118.1	c.524G>A	p.R175H	Missense	<0.05%
PAP 075	54	Ovarian	Papillary serous	IIIC	White	7.4	*PIK3CA*	ENSG00000121879	g.chr3:180434768G>A	CCDS43171.1	c.3129G>A	p.M1043I	Missense	0.13%
PAP 076	53	Ovarian	Papillary serous	IIIC	White	9.4	*TP53*	ENSG00000141510	g.chr17:7519275G>A	CCDS11118.1	c.380C>T	p.S127F	Missense	<0.005%
PAP 078	53	Ovarian	Papillary serous	IIIC	White	1.4	*TP53*	ENSG00000141510	g.chr17:7519131C>T	CCDS11118.1	c.524G>A	p.R175H	Missense	<0.005%
PAP 080	94	Endometrial	Papillary serous	IIIA	Black	7.8	*TP53*	ENSG00000141510	g.chr17:7519008delG	CCDS11118.1	c.566delC	Frameshift	Indel	80%
PAP 083	51	Endometrial	Endometrioid	IA	Black	4.5	*PIK3CA*	ENSG00000121879	g.chr3:180434779A>G	CCDS43171.1	C.3140A>G	p.H1047R	Missense	0.14%
PAP 083	51	Endometrial	Endometrioid	IA	Black	4.5	*CTNNB1*	ENSG00000168036	g.chr3:41241105C>A	CCDS2694.1	c.98C>A	p.S33Y	Missense	0.07%

*Coordinates refer to the human reference genome hg18 release (NCBI 36.1, March 2006).

table S4. Primers Used to Assess Individual Mutations in Pap Specimens

Case #	Gene	Mutation	Amplicon length (bp)	Forward primer sequence	Reverse primer sequence
PAP 001	*PIK3CA*	p.H1047R	82	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNGATCCAATCCATTTTTGTTGTCCAG	CACACAGGAAACAGCTATGACCATGTGAGCAAGAGGCTTTGGAGT
PAP 002	*TP53*	p.V147D	93	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNGGCCAAGACCTGCCCTG	CACACAGGAAACAGCTATGACCATGTGCTGTGACTGCTTGTAGATGG
PAP 003	*APC*	p.R1450X	93	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCCACCTCCTCAAACAGCTCAA	CACACAGGAAACAGCTATGACCATGTGCAGCTTGCTTAGGTCCACT
PAP 004	*TP53*	p.Q167fs*(1 base deletion of C)	85	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNTGGCCATCTACAAGCAGTCA	CACACAGGAAACAGCTATGACCATGNNNNTCACCATCGCTATCTGAGCA
PAP 005	*NF1*	p.L414fs*(1 base insertion of C)	74	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCATTGGTGATGATTCGATGG	CACACAGGAAACAGCTATGACCATGCTGCCTGGCTCAGAATTCAC
PAP 006	*TP53*	p.R280K	90	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCCCTTTCTTGCGGAGATTC	CACACAGGAAACAGCTATGACCATGCTACTGGGACGGAACAGCTT
PAP 007	*TP53*	p.E294X	87	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNGGAAGAGAATCTCCGCAAGA	CACACAGGAAACAGCTATGACCATGGCTTCTTGTCCTGCTTGCTT
PAP 010	*FBXW7*	p.R479X	82	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNGGCCTGTCTCAATATCCCAAA	CACACAGGAAACAGCTATGACCATGTTGTTTTTCTGTTTCTCCCTCTG
PAP 011	*KRAS*	p.G12A	92	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCAAGGCACTCTTGCCTACG	CACACAGGAAACAGCTATGACCATGCATTTTCATTATTTTTATTATAAGGCCTG
PAP 024	*CTNNB1*	p.G34V	72	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCTGTGGTAGTGGCACCAGAA	CACACAGGAAACAGCTATGACCATGNNNNAAGCGGCTGTTAGTCACTGG
PAP 025	*TP53*	p.P98fs*(2 base deletion of CC)	91	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNGGCCCCTGTCATCTTCTGT	CACACAGGAAACAGCTATGACCATGGACTTGGCTGTCCCAGAATG
PAP 026	*PTEN*	p.R308H	99	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCAAGAAATCGATAGCATTTGCAG	CACACAGGAAACAGCTATGACCATGTTTATTTGCTTTGTCAAGATCATTTTT
PAP 027	*SETD2*	p.Q269X	85	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNAGGAAATATCTGCTTGCTCATTCAA	CACACAGGAAACAGCTATGACCATGGAAGCAGATACTAAGCAGGACACTATATC
PAP 030	*MSH6*	p.S718N	76	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNTTCCCTTGGATTCTGACACA	CACACAGGAAACAGCTATGACCATGAGCACCATTCGTTGATAGGC
PAP 031	*CTNNB1*	p.S37Y	85	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCACTGGCAGCAACAGTCTTACC	CACACAGGAAACAGCTATGACCATGGATTGCCTTTACCACTCAGAGAAG
PAP 032	*PTEN*	p.R130G	71	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNTTGCAGCAATTCACTGTAAAGC	CACACAGGAAACAGCTATGACCATGCCGATGTAATAAATATGCACATATCATTAC
PAP 033	*KRAS*	p.G12V	92	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCAAGGCACTCTTGCCTACG	CACACAGGAAACAGCTATGACCATGCATTTTCATTATTTTTATTATAAGGCCTG
PAP 034	*CTNNB1*	p.G34R	85	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCACTGGCAGCAACAGTCTTACC	CACACAGGAAACAGCTATGACCATGGATTGCCTTTACCACTCAGAGAAG
PAP 035	*KRAS*	p.G12D	92	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCAAGGCACTCTTGCCTACG	CACACAGGAAACAGCTATGACCATGCATTTTCATTATTTTTATTATAAGGCCTG
PAP 036	*PIK3CA*	p.Q546L	84	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNAGCTCAAAGCAATTTCTACACGA	CACACAGGAAACAGCTATGACCATGNNNNGCACTTACCTGTGACTCCATAGAA
PAP 037	*PIK3CA*	p.T1025A	70	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNTCTTTTGATGACATTGCATACATTC	CACACAGGAAACAGCTATGACCATGNNNNACTCCAAAGCCTCTTGCTCA
PAP 038	*TP53*	p.Y220C	83	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCAGTTGCAAACCAGACCTCA	CACACAGGAAACAGCTATGACCATGTGTGGAGTATTTGGATGACAGAAA
PAP 039	*TP53*	p.I254fs*(1 base deletion of C)	76	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNGTGGCAAGTGGCTCCTGA	CACACAGGAAACAGCTATGACCATGNNNNCATGGGCGGCATGAAC
PAP 040	*CTNNB1*	p.S45Y	90	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNACTGGCAGCAACAGTCTTACCT	CACACAGGAAACAGCTATGACCATGNNNNCCTCAGGATTGCCTTTACCA
PAP 041	*FGFR2*	p.S252W	71	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNAGTCCGGCTTGGAGGATG	CACACAGGAAACAGCTATGACCATGTCCCCACTCCTCCTTTCTTC
	PTEN	p.C136R	78	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNGGAAAGGGACGAACTGGTG	CACACAGGAAACAGCTATGACCATGNNNNTAGGGCCTCTTGTGCCTTTA
PAP 042	*TP53*	p.F113fs*(1 base insertion of T)	80	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNTCTTCTGTCCCTTCCCAGAA	CACACAGGAAACAGCTATGACCATGNNNNGACTTGGCTGTCCCAGAATG
PAP 058	*PIK3CA*	p.R108H	82	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNTCATACCAATTTCTCGATTGAGG	CACACAGGAAACAGCTATGACCATGNNNNCGGCTTTTTCAACCCTTTTT
PAP 060	*TP53*	p.R175H	85	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNTGGCCATCTACAAGCAGTCA	CACACAGGAAACAGCTATGACCATGNNNNTCACCATCGCTATCTGAGCA
PAP 061	*TP53*	p.R273C	76	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNGGGACGGAACAGCTTTGAG	CACACAGGAAACAGCTATGACCATGNNNNGCGGAGATTCTCTTCCTCTGT
PAP 062	*TP53*	p.M66fs*(4 base deletion of GCAT)	77	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCGGTGTAGGAGCTGCTGGT	CACACAGGAAACAGCTATGACCATGNNNNACCCAGGTCCAGATGAAGC
PAP 063	*TP53*	p.R175H	85	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNTGGCCATCTACAAGCAGTCA	CACACAGGAAACAGCTATGACCATGNNNNTCACCATCGCTATCTGAGCA
PAP 064	*TP53*	p.E258A	76	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNGTGGCAAGTGGCTCCTGA	CACACAGGAAACAGCTATGACCATGNNNNCATGGGCGGCATGAAC
PAP 066	*TP53*	p.Y205C	74	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCGAAAAGTGTTTCTGTCATCCA	CACACAGGAAACAGCTATGACCATGNNNNGCCCCTCCTCAGCATCTTAT
PAP 067	*TP53*	p.R213X	83	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCAGTTGCAAACCAGACCTCA	CACACAGGAAACAGCTATGACCATGNNNNTGTGGAGTATTTGGATGACAGAAA
PAP 068	*PIK3CA*	p.C420R	90	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNTTATATTTCCCCATGCCAATG	CACACAGGAAACAGCTATGACCATGNNNNGGTGTTTTGAAATGTGTTTTATAATTTAGA
PAP 069	*TP53*	p.R110C	80	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNTCTTCTGTCCCTTCCCAGAA	CACACAGGAAACAGCTATGACCATGNNNNGACTTGGCTGTCCCAGAATG
PAP 070	*PIK3CA*	p.R88Q	66	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNGAAAAAGCCGAAGGTCACAA	CACACAGGAAACAGCTATGACCATGNNNNCTCAAGAAGCAGAAAGGGAAGA
PAP 071	*PIK3CA*	p.H1047R	82	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNGATCCAATCCATTTTTGTTGTCCAG	CACACAGGAAACAGCTATGACCATGNNNNTGAGCAAGAGGCTTTGGAGT
PAP 072	*TP53*	p.G245D	74	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNTGTGATGATGGTGAGGATGG	CACACAGGAAACAGCTATGACCATGNNNNTCCACTACAACTACATGTGTAACAGTTC
PAP 073	*TP53*	p.Y163C	84	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCTCCGTCATGTGCTGTGACT	CACACAGGAAACAGCTATGACCATGNNNNCAGCTGTGGGTTGATTCCA
PAP 074	*TP53*	p.R175H	85	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNTGGCCATCTACAAGCAGTCA	CACACAGGAAACAGCTATGACCATGNNNNTCACCATCGCTATCTGAGCA
PAP 075	*PIK3CA*	p.M1043I	79	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCCAATCCATTTTTGTTGTCCA	CACACAGGAAACAGCTATGACCATGNNNNTGAGCAAGAGGCTTTGGAGT
PAP 076	*TP53*	p.S127F	82	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCTGCACAGGGCAGGTCTT	CACACAGGAAACAGCTATGACCATGNNNNCTCTGTCTCCTTCCTCTTCCTACA
PAP 078	*TP53*	p.R175H	85	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNTGGCCATCTACAAGCAGTCA	CACACAGGAAACAGCTATGACCATGNNNNTCACCATCGCTATCTGAGCA
PAP 080	*PIK3CA*	p.A189fs*(1 base deletion of C)	78	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNCACGCAAATTTCCTTCCACT	CACACAGGAAACAGCTATGACCATGNNNNGGCCTCTGATTCCTCACTGAT
PAP 083	*PIK3CA*	p.H1047R	82	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNGATCCAATCCATTTTTGTTGTCCAG	CACACAGGAAACAGCTATGACCATGNNNNTGAGCAAGAGGCTTTGGAGT
	CTNNB1	p.S33Y	90	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNACTGGCAGCAACAGTCTTACCT	CACACAGGAAACAGCTATGACCATGNNNNCCTCAGGATTGCCTTTACCA

table S5: Primers Used to Simultaneously Assess 12 Genes in Pap Specimens with the Multiplexed Safe-SeqS Strategy

Set #	Gene (codons)	Amplicon length (bp)	Forward primer sequence	Reverse primer sequence
1	*CTNNB1* 5-64	251	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNAAAGTAACATTTCCAATCTACTAATGCT	CACACAGGAAACAGCTATGACCATGNNNNTGAGAAAATCCCTGTTCCCAC
	EGFR 697-728	264	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNTGGAGCCTCTTACACCCAGT	CACACAGGAAACAGCTATGACCATGNNNNAAAAACACTGGAGTTTCCCAAA
	PIK3CA 23-88	241	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNGAAAAAGCCGAAGGTCACAA	CACACAGGAAACAGCTATGACCATGNNNNATGCCCCCAAGAATCCTAGT
	PTEN 1-26	257	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNCATCCGTCTACTCCCACGTT	CACACAGGAAACAGCTATGACCATGNNNNATCAGCTACCGCCAAGTCC
	PTEN 85-123	261	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNTTCGTCCCTTTCCAGCTTTA	CACACAGGAAACAGCTATGACCATGNNNNGGAATCCAGTGTTTCTTTTAAATACCT
	TP53 126-186	259	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNACCAGCCCTGTCGTCTCTC	CACACAGGAAACAGCTATGACCATGNNNNGCCCTGACTTTCAACTCTGTCT
	TP53 308-331	259	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNGCCTCAGATTCACTTTTATCACCT	CACACAGGAAACAGCTATGACCATGNNNNACCAGGAGCCATTGTCTTTG
2	*BRAF* 439-475	251	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNTCACCACATTACATACTTACCATGC	CACACAGGAAACAGCTATGACCATGNNNNAAGGGGATCTCTTCCTGTATCC
	EGFR 738-761	279	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNTCTGGATCCCAGAAGGTGAG	CACACAGGAAACAGCTATGACCATGNNNNGGCCAGTGCTGTCTCTAAGG
	KRAS 1-21	281	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNGTCCACAAAATGATTCTGAATTAGC	CACACAGGAAACAGCTATGACCATGNNNNACGATACACGTCTGCAGTCAAC
	PIK3CA 62-117	269	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNACAGAAATATTTTAGAAAGGGACAACA	CACACAGGAAACAGCTATGACCATGNNNNAGAAAATACCCCCTCCATCAAC
	PIK3CA 980-1049	272	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNGATCCAATCCATTTTTGTTGTCCAG	CACACAGGAAACAGCTATGACCATGNNNNTCCAAACTGACCAAACTGTTCTTA
	PTEN 100-164	294	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNGAAACCCAAAATCTGTTTTCCA	CACACAGGAAACAGCTATGACCATGNNNNGACCATAACCCACCACAGCTA
	TP53 186-224	251	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNCTCCTCCCAGAGACCCCAGT	CACACAGGAAACAGCTATGACCATGNNNNCATGAGCGCTGCTCAGATAG
	TP53 332-366	263	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNCCTAGGAAGGCAGGGGAGT	CACACAGGAAACAGCTATGACCATGNNNNTGCATGTTGCTTTTGTACCG
3	*AKT1* 17-58	279	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNACCACCCGCACGTCTGTAG	CACACAGGAAACAGCTATGACCATGNNNNAGCCAGTGCTTGTTGCTTG
	EGFR 762-823	251	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNCACACTGACGTGCCTCTCC	CACACAGGAAACAGCTATGACCATGNNNNTTATCTCCCCTCCCCGTATC
	NRAS 1-14	275	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNGATTGTCAGTGCGCTTTTCC	CACACAGGAAACAGCTATGACCATGNNNNGCTAAGGATGGGGGTTGCTA
	PIK3CA 272-347	279	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNTGACTTTACCTTATCAATGTCTCGAA	CACACAGGAAACAGCTATGACCATGNNNNGCTCGCCCCCTTAATCTCT
	PPP2R1A 176-217	277	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNGGTACTTCCGGAACCTGTGC	CACACAGGAAACAGCTATGACCATGNNNNCCGAGTCCTAGGGAGAGGAG
	PTEN 56-70	250	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNTTGTTAATGGTGGCTTTTTGTTT	CACACAGGAAACAGCTATGACCATGNNNNAAATGATCTAACAATGCTCTTGGAC
	PTEN 165-211	265	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNCATGGAAGGATGAGAATTTCAAG	CACACAGGAAACAGCTATGACCATGNNNNTGGCTACGACCCAGTTACCA
	TP53 33-102	256	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNAAACCGTAGCTGCCCTGGTA	CACACAGGAAACAGCTATGACCATGNNNNTGACTGCTCTTTTCACCCATC
	TP53 225-260	257	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNTCATCTTGGGCCTGTGTTATC	CACACAGGAAACAGCTATGACCATGNNNNGATGAGAGGTGGATGGGTAGTAGT
4	*EGFR* 830-875	258	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNTTCAGGGCATGAACTACTTGG	CACACAGGAAACAGCTATGACCATGNNNNATCCTCCCCTGCATGTGTTA
	KRAS 38-61	260	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNTCCCTCATTGCACTGTACTCC	CACACAGGAAACAGCTATGACCATGNNNNGGTGCTTAGTGGCCATTTGT
	NRAS 38-62	250	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNTGGTCTCTCATGGCACTGTACT	CACACAGGAAACAGCTATGACCATGNNNNATTAGCAATTTGAGGGACAAACC
	PTEN 71-84	250	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNTGTATCTCACTCGATAATCTGGATGAC	CACACAGGAAACAGCTATGACCATGNNNNTGTCACATTATAAAGATTCAGGCAAT
	PTEN 213-267	271	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNAGTTTGACAGTTAAAGGCATTTCC	CACACAGGAAACAGCTATGACCATGNNNNTGTCCTTATTTTGGATATTTCTCCC
	TP53 63-125	276	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNGAAGACCCAGGTCCAGATGA	CACACAGGAAACAGCTATGACCATGNNNNAGAAATGCAGGGGGATACG
	TP53 262-306	280	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNGAGGCATAACTGCACCCTTG	CACACAGGAAACAGCTATGACCATGNNNNGGGAGTAGATGGAGCCTGGT
5	*APC* 1254-1328	269	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNTGCTGGATTTGGTTCTAGGG	CACACAGGAAACAGCTATGACCATGNNNNTGCCACTTGCAAAGTTTCTTC
	APC 1403-1476	264	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNGGAAGAACCTGGACCCTCTG	CACACAGGAAACAGCTATGACCATGNNNNTTTTGAGAGTCGTTCGATTGC
	APC 1537-1617	289	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNTGCAACCTGTTTTGTGATGG	CACACAGGAAACAGCTATGACCATGNNNNAGGAAAATGACAATGGGAATGA
	FBXW7 474-548	296	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNTGATTCATCAGGAGAGCATTTAAG	CACACAGGAAACAGCTATGACCATGNNNNTTGTTTTTCTGTTTCTCCCTCTG
	FBXW7 558-618	289	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNGATGGTATCCATGTGGTGAGTG	CACACAGGAAACAGCTATGACCATGNNNNTTTGTGATGCTAAGGCTCCAT
	TP53 1-24	254	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNACTGCCTTCCGGGTCACT	CACACAGGAAACAGCTATGACCATGNNNNAGCCCAACCCTTGTCCTTAC
6	*TP53* 368-393	265	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNGAGGCTGTCAGTGGGGAAC	CACACAGGAAACAGCTATGACCATGNNNNAACATATTTGCATGGGGTGTG
	APC 1326-1405	283	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNCCACTGCATGGTTCACTCTG	CACACAGGAAACAGCTATGACCATGNNNNATCCTGTGAGCGAAGTTCCA
	APC 1475-1545	264	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNTGCCTCTTTCTCTTGGTTTTCA	CACACAGGAAACAGCTATGACCATGNNNNGGACCTAAGCAAGCTGCAGTAA
	FBXW7 243-287	257	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNACACCCAATGAAGAATGTAATTGAT	CACACAGGAAACAGCTATGACCATGNNNNGGTTGTGTGTAGATGTGAGTTTTCC
	FBXW7 329-374	276	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNTTCTGTTACATTGTGCAGAGTTCA	CACACAGGAAACAGCTATGACCATGNNNNTGGTTTTGAGCAGAGAGATGG
	FBXW7 413-472	266	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNGGAAGAAGTCCCAACCATGA	CACACAGGAAACAGCTATGACCATGNNNNTCACTTTTCCTTTCTACCCAAAAG
	FBXW7 549-593	259	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNGAATCTGCATTCCCAGAGACA	CACACAGGAAACAGCTATGACCATGNNNNCCTGTTTCCCATCCTCTTCC
	KRAS 134-150	267	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNGACACAAAACAGGCTCAGGAC	CACACAGGAAACAGCTATGACCATGNNNNAGAAACCAAAGCCAAAAGCA
	TP53 26-32	253	CGACGTAAAACGACGGCCAGTNNNNNNNNNNNNNNNNCCATGGGACTGACTTTCTGC	CACACAGGAAACAGCTATGACCATGNNNNTCATCTGGACCTGGGTCTTC

table S6. Mutations Identified in Pap Specimens through Simultaneous Assessment of 12 Genes

Case #	Tumor type	Gene name	Gene ID	Genomic coordinate*	Transcript	Nucleotide	Amino acid change	Mutation type	Detected fraction
PAP 001	Endometrial	*KRAS*	ENSG00000133703	g.chr12:25289551C>G	CCDS8703.1	c.35G>C	p.G12A	Missense	13%
		PIK3CA	ENSG00000121879	g.chr3:180434779A>G	CCDS43171.1	c.3140A>G	p.H1047R	Missense	5.7%
PAP 003	Endometrial	*PIK3CA*	ENSG00000121879	g.chr3:180399570G>A	CCDS43171.1	c.263G>A	p.R88Q	Missense	12%
		APC	ENSG00000134982	g.chr5:112203538C>T	CCDS4107.1	c.4348C>T	p.R1450X	Nonsense	13%
		PTEN	ENSG00000171862	g.chr10:89614243A>C	CCDS31238.1	c.38A>C	p.K13T	Missense	12%
PAP 010	Endometrial	*FBXW7*	ENSG00000109670	g.chr4:153466817G>A	CCDS3777.1	c.1435C>T	p.R479X	Nonsense	20%
PAP 011	Endometrial	*KRAS*	ENSG00000133703	g.chr12:25289551C>G	CCDS8703.1	c.35G>C	p.G12A	Missense	3.2%
PAP 025	Endometrial	*TP53*	ENSG00000141510	g.chr17:7520119_7520120delGG	CCDS11118.1	c.292_293delCC	Frameshift	Indel	10%
PAP 033	Endometrial	*PIK3CA*	ENSG00000121879	g.chr3:180404243T>G	CCDS43171.1	c.1031T>G	p.V344G	Missense	1.2%
		KRAS	ENSG00000133703	g.chr12:25289551C>A	CCDS8703.1	c.35G>T	p.G12V	Missense	1.1%
		PTEN	ENSG00000171862	g.chr10:89707637insC	CCDS31238.1	c.682insC	Frameshift	Indel	0.87%
PAP 034	Endometrial	*PIK3CA*	ENSG00000121879	g.chr3:180399630G>A	CCDS43171.1	c.323G>A	p.R108H	Missense	23%
		CTNNB1	ENSG00000168036	g.chr3:41241107G>A	CCDS2694.1	c.100G>A	p. G34R	Missense	18%
		PTEN	ENSG00000171862	g.chr10:89707750delA	CCDS31238.1	c.795delA	Frameshift	Indel	13%
		PIK3CA	ENSG00000121879	g.chr3:180399554T>G	CCDS43171.1	c.247T>G	p.F83V	Missense	4.5%
		KRAS	ENSG00000133703	g.chr12:25289551C>G	CCDS8703.1	c.35G>C	p.G12A	Missense	0.92%
PAP 035	Endometrial	*KRAS*	ENSG00000133703	g.chr12:25289551C>T	CCDS8703.1	c.35G>A	p.G12D	Missense	5.8%
		PIK3CA	ENSG00000121879	g.chr3:180399548G>A	CCDS43171.1	c.241G>A	p.E81K	Missense	5.3%
		PTEN	ENSG00000171862	g.chr10:89675287T>C	CCDS31238.1	c.202T>C	p.Y68H	Missense	4.7%
PAP 039	Ovarian	*TP53*	ENSG00000141510	g.chr17:7518244delG	CCDS11118.1	c.871delC	Frameshift	Indel	0.73%
PAP 067	Endometrial	*TP53*	ENSG00000141510	g.chr17:7518937G>A	CCDS11118.1	c.637C>T	p.R213X	Nonsense	2.3%
PAP 069	Endometrial	*TP53*	ENSG00000141510	g.chr17:7520084G>A	CCDS11118.1	c.328C>T	p.R110C	Missense	19%
		TP53	ENSG00000141510	g.chr17:7517747G>A	CCDS11118.1	c.916C>T	p.R306X	Nonsense	14%
PAP 070	Endometrial	*PIK3CA*	ENSG00000121879	g.chr3:180399570G>A	CCDS43171.1	c.263G>A	p.R88Q	Missense	28%

PAP 071	Endometrial	*KRAS*	ENSG00000133703	g.chr12:25289551C>T	CCDS8703.1	c.35G>A	p.G12D	Missense	0.39%
		PIK3CA	ENSG00000121879	g.chr3:180434779A>G	CCDS43171.1	c.3140A>G	p.H1047R	Missense	0.31%
PAP 072	Ovarian	*TP53*	ENSG00000141510	g.chr17:7518272C>T	CCDS11118.1	c.734G>A	p.G245D	Missense	0.54%

*Coordinates refer to the human reference genome hg18 release (NCBI 36.1, March 2006).