

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.pos	Ref.count	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase
2	SA018_12	SA018	12	1.16E+08	12,116175	missense	low	1.725	D871E	NOS1	12q24.2-q24.31				DOMAIN //	G:575490	665494	0.135244	0	TRUE	G:612236	A:47	612283	7.68E-05	1	FALSE	0	0	
3	SA018_17	SA018	17	70120448P	17,701204	missense	low	1.665	L186P	CD300E	17q25.1				TRANSMEN	A:533437	G:109501	642938	0.170313	0	TRUE	A:659863	G:75	659938	0.000114	1	FALSE	1	3
4	SA018_6	SA018	6	7176347	6,7176347	missense	low	1.7	Q1006K	REB1	6p25				COMPBIA	C:374691	A:93216	467907	0.199219	0	TRUE	C:452419	A:410	452829	0.000905	1	FALSE	1	11
5	SA030_12	SA030	12	70702459	12,707024	missense	high	4.285	T361K	TPH2	12q21.1					C:62138	A:5545	67683	0.081926	0	TRUE	C:40501	A:4	40505	9.88E-05	1	FALSE	0	0
6	SA030_19	SA030	19	18239109	19,182391	missense	low	0.805	R81S	KIAA1683	19p13.1					G:42605	T:9359	51964	0.180105	0	TRUE	G:67837	A:32	67869	0.000471	1	FALSE	1	2
7	SA030_22	SA030	22	15453170	22,154531	missense	low	1.61	R91W	CCT8L2	22q11.1					G:28429	A:9532	37961	0.2511	0	TRUE	G:94541	T:23	94564	0.000243	1	FALSE	0	0
8	SA031_10	SA031	10	60753841	10,607538	missense	medium	2.175	E119V	FAM13C1	10q21.1					T:415509	A:84911	500420	0.166979	0	TRUE	T:465549	G:408	465957	0.000876	1	FALSE	1	6
9	SA031_11	SA031	11	74824231	11,748242	missense	low	1.39	T596N	GMPD5	11q13.4-q13.5			TOPO_DON	G:151484	T:92900	244384	0.380139	0	TRUE	G:254936	T:147	255083	0.000576	1	FALSE	3	4	
10	SA031_12	SA031	12	1.3E+08	12,130188	missense	low	1.04	W824L	GPR133	12q24.33			TOPO_DON	G:75076	T:9383	84459	0.111095	0	TRUE	G:390978	A:40	391018	0.000102	1	FALSE	1	2	
11	SA051_19	SA051	19	11331516	19,113315	missense	low	1.06	A92V	LPPR2	19p13.2					C:251532	T:79025	330557	0.239066	0	TRUE	C:561762	T:208	561970	0.00037	1	FALSE	1	47
12	SA051_22	SA051	22	41944327	22,419443	missense	low	1.79	G590D	SCUBE1	22q13					C:259486	T:188841	448327	0.421213	0	TRUE	C:457145	A:92	457237	0.000201	1	FALSE	0	0
13	SA051_5	SA051	5	1.4E+08	5,1401821	missense	low	1.115	I212V	PCDHA5	5q31				DOMAIN //	A:130032	G:87777	217809	0.403	0	TRUE	A:135096	G:72	135168	0.000533	1	FALSE	3	0
14	SA051_9	SA051	9	701024	9,701024	missense	medium	2.295	W86C	ANKRD15	9p24.3					G:87627	C:6680	94307	0.070832	0	TRUE	G:69887	T:52	69939	0.000744	1	FALSE	1	37
15	SA052_1	SA052	1	39679297	1,3967929	missense	low	1.645	E4604D	MACF1	1p23-p31				COILED //	G:40360	T:3492	6552	0.532967	0	TRUE	G:404	N:0	404	0	1	FALSE	2	39
16	SA052_16	SA052	16	53919208	16,539192	missense	medium	2.36	N208S	JRX6	16q11.2-q13				COILD_BIND	A:59997	G:17839	77836	0.229187	0	TRUE	A:22395	G:2	22397	8.93E-05	1	FALSE	2	6
17	SA052_17	SA052	17	32556826	17,325568	missense	low	0.955	Q1946E	ACACA	17q21			Entrez Que	DOMAIN //	G:122017	C:50266	172283	0.291764	0	TRUE	G:178254	T:110	178364	0.000617	1	FALSE	1	8
18	SA052_19	SA052	19	17515343	19,175153	missense	medium	1.95	S517L	FAM129C	19p13.11					C:145831	T:18587	164418	0.113047	0	TRUE	C:149275	T:14	149289	9.38E-05	1	FALSE	0	0
19	SA052_20	SA052	20	50202897	20,502028	missense	low	0.975	R414Q	ZFP64	20q13.2					C:84522	T:70935	155457	0.4563	0	TRUE	C:159807	A:20	159827	0.000125	1	FALSE	2	5
20	SA052_6	SA052	6	31633931	6,3163393	missense	low	1.725	R237P	NFKB1L1	6p21.3				CONFLICT	G:22948	C:16518	39466	0.418537	0	TRUE	G:116388	A:14	116402	0.00012	1	FALSE	1	2
21	SA053_1	SA053	1	2.47E+08	1,2469119	missense	low	1.52	R86C	OR5BU1	1q44				TOPO_DON	G:281096	A:189581	470677	0.402784	0	TRUE	G:358280	A:36	358316	0.0001	1	FALSE	0	0
22	SA054_10	SA054	10	1.18E+08	10,117694	missense	neutral	0.345	R1374G	ACTR1L1	10q26				TOPO_DON	C:88919	G:14058	102977	0.136516	0	TRUE	C:127020	A:21	127041	0.000165	1	FALSE	0	0
23	SA054_10	SA054	10	1.25E+08	10,124581	missense	low	0.805	H557Q	CUZN1	10q26.13				TOPO_DON	A:15124	C:3128	18252	0.171378	0	TRUE	A:5025	N:0	5025	0	1	FALSE	1	1
24	SA054_1	SA054	1	1.55E+08	1,1550809	missense	medium	2.68	S887C	INSRR	1q21-q23			Entrez Que	DOMAIN //	G:82910	C:7995	90905	0.087949	0	TRUE	G:72402	A:34	72436	0.000469	1	FALSE	1	1
25	SA054_11	SA054	11	56225134	11,562251	missense	high	3.72	G232A	OR9G1					TOPO_DON	G:81158	C:6582	87740	0.075017	0	TRUE	G:61714	T:39	61753	0.000632	1	FALSE	0	0
26	SA054_1	SA054	1	1.58E+08	1,1583715	missense	medium	2.595	V662L	ATP1A2	1q21-q23				TOPO_DON	G:30012	C:10375	40387	0.25689	0	TRUE	G:55608	T:7	55615	0.000126	1	FALSE	1	1
27	SA054_1	SA054	1	1.74E+08	1,1736018	missense	medium	2.915	D687H	TNR	1q24				DOMAIN //	C:173080	G:34407	207487	0.165827	0	TRUE	C:192978	T:26	193004	0.000135	1	FALSE	1	1
28	SA054_12	SA054	12	12224157	12,122241	missense	low	0.86	E467Q	LRP6	12p11-p13			Cancer Cell	REGION //	C:66857	G:6723	73580	0.09137	0	TRUE	C:42607	T:15	42622	0.000352	1	FALSE	1	7
29	SA054_12	SA054	12	1.3E+08	12,129846	missense	neutral	0	W265C	STX2	12q24.33				TOPO_DON	C:72015	G:7918	79933	0.099058	0	TRUE	C:74343	T:11	74354	0.000148	1	FALSE	0	0
30	SA054_1	SA054	1	31428021	1,3142802	missense	neutral	0.795	F159L	INKA1N1	1p35.2				TRANSMEN	A:126686	G:26117	152803	0.170919	0	TRUE	A:106682	G:6	106688	5.62E-05	1	FALSE	2	7
31	SA054_1	SA054	1	32890201	1,3289020	missense	high	3.75	A39G	RBBP4	1p35.1				STRAND //	C:36592	G:3550	40142	0.088436	0	TRUE	C:19249	A:4	19253	0.000208	1	FALSE	1	148
32	SA054_17	SA054	17	10240483	17,102404	missense	medium	3.01	D1514E	MYH8	17p13.1				COILED //	G:122794	T:10747	133541	0.080477	0	TRUE	G:80603	T:59	80662	0.000731	1	FALSE	0	0
33	SA054_17	SA054	17	30616027	17,306160	missense	neutral	0.295	K617N	SLFN5	17q12					G:134459	C:8074	142533	0.056647	0	TRUE	G:88135	A:5	88140	5.67E-05	1	FALSE	1	31
34	SA054_19	SA054	19	13862103	19,138621	missense	neutral	0	S189Y	OR5orf57	19p13.12					G:74233	T:18153	92386	0.196491	0	TRUE	G:147617	A:18	147635	0.000122	1	FALSE	1	2
35	SA054_19	SA054	19	34793305	19,347933	missense	medium	2.305	K70N	POPA	19q12				COMPBIA	G:56130	C:27493	83623	0.282773	0	TRUE	G:206120	A:11	206131	5.34E-05	1	FALSE	2	70
36	SA054_19	SA054	19	35732111	19,357321	missense	low	0.895	P1249A	INZF536	19q12					C:66464	G:10753	77217	0.139257	0	TRUE	C:75480	T:38	75518	0.000503	1	FALSE	0	0
37	SA054_3	SA054	3	1.95E+08	3,1991252	missense	low	1.735	Q276K	IQCG	3q29					G:145639	T:13913	159552	0.08027	0	TRUE	G:211534	T:109	211643	0.000515	1	FALSE	1	10
38	SA054_3	SA054	3	48583689	3,4858368	missense	medium	2.155	K2365N	COL7A1	3p21.1				REGION //	T:191368	G:26771	218139	0.122725	0	TRUE	T:185896	G:36	185932	0.000194	1	FALSE	1	5
39	SA054_5	SA054	5	70884826	5,7088482	missense	low	0.895	D2375H	BDP1	5q13					G:22481	C:2676	25157	0.106372	0	TRUE	G:1642	N:0	1642	0	1	FALSE	2	3
40	SA054_6	SA054	6	1.3E+08	6,1297460	missense	low	1.28	R1687W	LAMA2	6q22-q23				COILED //	C:197972	T:17640	215612	0.081814	0	TRUE	C:154493	G:45	154538	0.000291	1	FALSE	1	2
41	SA054_6	SA054	6	26342949	6,2634294	missense	medium	3.385	K64N	HIST1H1D	6p21.3				DOMAIN //	C:124409	G:15750	140159	0.112372	0	TRUE	C:141935	G:10	141945	7.04E-05	1	FALSE	1	1
42	SA054_7	SA054	7	1.24E+08	7,1242525	missense	medium	2.215	M587T	POT1	7q31.33			Cancer Review :: Hahn	A:3353	G:651	4004	0.162587	0	TRUE	A:110	N:0	110	0	1	FALSE	1	27	
43	SA054_7	SA054	7	7591920	7,7591920	missense	medium	3.155	A593P	FLJ20323	7p22-p21					G:119751	C:22265	142016	0.156778	0	TRUE	G:103415	A:22	103437	0.000213	1	FALSE	1	32
44	SA054_9	SA054	9	1.15E+08	9,1148448	missense	NA		H629D	ZFP37	9q32					G:67596	C:10110	77706	0.130106	0	TRUE	G:16418	A:3	16421	0.000183	1	FALSE	1	3
45	SA054_X	SA054	X	1.49E+08	X,1493895	missense	neutral	0.345	P352T	MAMLD1	Xq28				COMPBIA	C:31150	A:7933	39083	0.202978	0	TRUE	C:205181	G:168	205349	0.000818	1	FALSE	1	15
46	SA056_18	SA056	18	72778139	18,727781	missense	low	1.04	P1543L	ZNF236	18q22-q23				CONFLICT	C:413779	T:31467	445246	0.070673	0	TRUE	C:614897	A:206	615103	0.000335	1	FALSE	1	15
47	SA056_2	SA056	2	1.8E+08	2,1796905	nonsense	NA		R489	SESTD1	2q31.2				REPEAT //	G:8154	A:1297	9451	0.137234	0	TRUE	G:2137	A:2	2139	0.000935	1			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func.Lmpa	Fi.score	A.A.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.pof	Ref.count	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase
71	SA065_8_1	SA065	8	1.11E+08	8,1105020	missense	low	1.79	Q876R	PKHD1L1	8q23.1-q23.2				TOPO_DON	A:51	G:10	61	0.163934	1.27E-16	TRUE	A:86	N:0	86	0	1	FALSE	0	0
72	SA067_10	SA067	10	49079392	10,4907939	missense	medium	2.085	K613N	FRMPD2	10q11.22				DOMAIN	//C:193114	A:21627	214741	0.100712	0	TRUE	C:188363	T:35	188398	0.000186	1	FALSE	0	0
73	SA067_1_1	SA067	1	1.2E+08	1,1200996	missense	low	1.265	K364L	HMGC52	1p13-p12				HELI	//35G:108108	C:13100	121208	0.08079	0	TRUE	G:109337	T:41	109378	0.000375	1	FALSE	1	4
74	SA067_1_1	SA067	1	50713763	1,5071376	nonsense	NA		W610	FAF1	1p33			Cancer Cell	DOMAIN	//C:15085	T:2160	17245	0.125254	0	TRUE	C:20356	A:24	20380	0.001178	0.581241	FALSE	2	107
75	SA067_15	SA067	15	32427606	15,324276	missense	neutral	0.66	V54G	C15orf55	15q14			Cancer Rev	COMPBIAS	T:79236	G:7524	86760	0.086722	0	TRUE	T:120877	C:31	120908	0.000256	1	FALSE	0	0
76	SA067_16	SA067	16	66202384	16,6620238	missense	medium	1.935	V50L	CTCF	16q21.1-q22.3			Cancer Cell	Map Pathw	G:107567	C:21337	128904	0.165526	0	TRUE	G:124465	A:11	124476	8.84E-05	1	FALSE	2	25
77	SA067_17	SA067	17	23926414	17,239264	missense	high	4.175	R60S	ALDOC	17cen-q12				HELI	//53G:100007	T:19245	119252	0.161381	0	TRUE	G:122537	A:78	122615	0.000636	1	FALSE	2	21
78	SA067_17	SA067	17	36109804	17,361098	missense	medium	3.5	E372V	KRT24	17q11.2				REGION	//T:102768	A:31775	134543	0.23617	0	TRUE	T:125067	C:12	125079	9.59E-05	1	FALSE	0	0
79	SA067_18	SA067	18	13045906	18,130459	missense	neutral	-0.345	S510C	CEP192	18p11.21				C:24885	G:3165	28050	0.112834	0	TRUE	C:22350	G:15	22365	0.000671	1	FALSE	2	19	
80	SA067_19	SA067	19	4992173	19,499217	missense	medium	2.22	F115V	KDM48	19p13.3				T:5791	G:2119	7910	0.267889	0	TRUE	T:8122	G:12	8134	0.001475	0.418338	FALSE	2	44	
81	SA067_19	SA067	19	60795781	19,607957	missense	NA		E446D	FIZ1	19q13.42			ZN_FING	//C:25565	G:4826	30391	0.158797	0	TRUE	C:30824	A:6	30830	0.000195	1	FALSE	2	14	
82	SA067_2_1	SA067	2	1.6E+08	2,1597340	missense	medium	2.25	W344G	TANC1	2q24.1-q24.2				T:152842	G:19357	172199	0.112411	0	TRUE	T:180657	C:25	180682	0.000138	1	FALSE	1	15	
83	SA067_2_1	SA067	2	1.97E+08	2,1974201	nonsense	NA		L672	PGAP1	2q33.1			TRANSMEN	A:54	C:12	66	0.181818	3.19E-21	TRUE	A:100	N:0	100	0	1	FALSE	1	3	
84	SA067_2_1	SA067	2	2.34E+08	2,2344153	missense	low	1.795	T259I	HJURP	2q37.1				G:58324	A:11392	69716	0.163406	0	TRUE	G:60945	C:8	60953	0.000131	1	FALSE	2	88	
85	SA067_4_1	SA067	4	1.57E+08	4,1565008	missense	low	1.61	S336C	MAP9	4q32.1				G:1101	C:156	1257	0.124105	2.24E-247	TRUE	G:789	A:2	791	0.002528	1	FALSE	1	1	
86	SA067_4_1	SA067	4	83568537	4,8356853	missense	medium	2.6	C177Y	HNRPDL	4q13-q21				DOMAIN	//C:32347	T:6625	38972	0.169994	0	TRUE	C:39599	T:14	39613	0.000353	1	FALSE	2	500
87	SA067_5_1	SA067	5	1.4E+08	5,1398190	missense	medium	2.565	S543C	ANKRD1	5q31.3				REPEAT	//C:126862	G:26545	153407	0.173036	0	TRUE	C:138850	A:10	138860	7.20E-05	1	FALSE	2	106
88	SA067_5_1	SA067	5	940546	5,940546	missense	high	4.81	N216S	BRD9	5p15.33				DOMAIN	//T:124322	C:17403	141725	0.122794	0	TRUE	T:123109	G:61	123170	0.000495	1	FALSE	2	41
89	SA067_6_1	SA067	6	64447895	6,6444789	missense	low	1.845	V94F	PHF3	6q12				G:78571	T:6796	85367	0.079609	0	TRUE	G:68830	A:3	68833	4.36E-05	1	FALSE	1	20	
90	SA067_8_1	SA067	8	1.23E+08	8,1226956	missense	medium	2.545	L512V	HAS2	8q24.12			Cancer Rev	TRANSMEN	G:74698	C:14312	89010	0.160791	0	TRUE	G:72304	T:32	72336	0.000442	1	FALSE	1	7
91	SA068_19	SA068	19	22063969	19,220639	missense	low	1.76	R526H	ZNF257	19q13			ZN_FING	//G:1889089	A:384904	2273993	0.169263	0	TRUE	G:1162004	T:602	1162606	0.000518	1	FALSE	1	5	
92	SA069_10	SA069	10	13304182	10,133041	missense	low	1.7	A115V	C10orf49	10p13			COILED	//G:164607	A:16859	163266	0.103261	0	TRUE	G:93304	T:17	93321	0.000182	1	FALSE	0	0	
93	SA069_10	SA069	10	32675759	10,326757	missense	medium	2.405	V31H	EPC1	10p11				A:79430	G:18330	97760	0.1875	0	TRUE	A:70709	C:86	70795	0.001215	1	FALSE	1	21	
94	SA069_1_1	SA069	1	1.7E+08	1,1698882	missense	medium	2.43	S55R	MYOC	1q23-q24				A:75731	T:13257	89898	0.148975	0	TRUE	A:265601	G:299	265900	0.001124	1	FALSE	1	2	
95	SA069_12	SA069	12	51127832	12,511278	missense	medium	2.45	C474V	KRT6B	12q12-q13			REGION	//C:267179	T:48439	315618	0.153474	0	TRUE	C:321935	G:279	322214	0.000866	1	FALSE	0	0	
96	SA069_1_1	SA069	1	34102507	1,3410250	missense	medium	2.415	R43T	HMGB4	1p35.1			DNA_BIND	G:30332	C:9369	39701	0.235989	0	TRUE	G:14949	N:0	14949	0	1	FALSE	0	0	
97	SA069_19	SA069	19	35732182	19,357321	missense	low	1.04	S1272R	ZNF536	19q12				T:285338	G:18719	304057	0.061564	0	TRUE	T:368149	G:77	368226	0.000209	1	FALSE	0	0	
98	SA069_19	SA069	19	51803970	19,518039	missense	medium	3.12	E105Q	CALM3	19q13.2-q13.3			CA_BIND	//G:109226	C:17364	126590	0.137167	0	TRUE	G:248306	T:54	248360	0.000217	1	FALSE	2	241	
99	SA069_20	SA069	20	62118620	20,621186	missense	medium	2.84	T542S	PRPF6	20q13.33			Cancer Cell	Map Pathw	C:2858	G:913	3771	0.242111	0	TRUE	C:9715	T:2	9717	0.000206	1	FALSE	2	101
100	SA069_2_1	SA069	2	54730332	2,5473033	missense	low	1.04	H1760P	SPTRB1	2p21			REGION	//J:121072	C:12651	133723	0.094606	0	TRUE	A:266525	C:31	266556	0.000116	1	FALSE	1	204	
101	SA071_11	SA071	11	1.01E+08	11,100848	missense	low	1.16	N694T	TRPC6	11q21-q22				TOPO_DON	T:1059	G:750	1809	0.414594	0	TRUE	T:1139	A:1	1140	0.000877	1	FALSE	1	1
102	SA071_11	SA071	11	1.17E+08	11,117156	missense	medium	2.215	N99I	OSCCML1	-			DISULFID	//T:72562	A:40154	112716	0.35624	0	TRUE	T:259972	G:238	260210	0.000915	1	FALSE	0	0	
103	SA071_11	SA071	11	20915930	11,209159	missense	low	1.5	K340N	NELL1	11p15.2-p15.1				DOMAIN	//A:10199	C:1831	12030	0.152203	0	TRUE	A:6634	G:5	6639	0.000753	1	FALSE	0	0
104	SA071_1_1	SA071	1	2.14E+08	2,1242389	missense	medium	2.19	Q2201H	USH2A	1q41				DOMAIN	//C:188113	A:94698	282811	0.334846	0	TRUE	C:247340	T:10	247350	4.04E-05	1	FALSE	0	0
105	SA071_1_1	SA071	1	40987896	1,4098789	missense	medium	3.49	T81I	NFYC	1p32 1p32			Cancer Cell	HELI	//64C:124169	T:55695	179864	0.309651	0	TRUE	C:177828	G:145	177973	0.000815	1	FALSE	2	61
106	SA071_14	SA071	14	68991362	14,689913	missense	high	4.235	H185D	SLC39A9	14q24.1			TRANSMEN	C:128248	G:12314	140562	0.0867605	0	TRUE	C:51326	A:21	51347	0.000409	1	FALSE	1	22	
107	SA071_20	SA071	20	44075304	20,440753	missense	low	1.245	P445R	MMP9	20q11.2-q13.1				C:29492	G:17780	47272	0.376121	0	TRUE	C:69652	A:9	69661	0.000129	1	FALSE	1	299	
108	SA071_2_1	SA071	2	1.32E+08	2,1319582	missense	low	0.975	L161R	FAM128A					C:54195	T:14291	68486	0.20867	0	TRUE	C:267350	A:30	267380	0.000112	1	FALSE	2	23	
109	SA071_7_1	SA071	7	1.29E+08	7,1289126	missense	medium	2.965	E763K	FAM40B	7q32.1				G:136209	A:144047	280256	0.513984	0	TRUE	G:132243	C:9	132252	6.81E-05	1	FALSE	1	3	
110	SA072_1_1	SA072	1	1.59E+08	1,1589213	missense	neutral	0.695	S97C	CD48	1q21.3-q22				DOMAIN	//G:155638	C:8513	164151	0.051861	0	TRUE	G:157490	T:43	157533	0.000273	1	FALSE	1	183
111	SA072_1_1	SA072	1	1.68E+08	1,1677776	missense	neutral	0	G1109A	F5	1q23			Entrez Que	PROPEP	//C:87488	G:10893	98381	0.110723	0	TRUE	C:201095	G:174	201269	0.000865	1	FALSE	1	11
112	SA072_1_1	SA072	1	1.74E+08	1,1735920	missense	medium	2.28	T1035S	TNR	1q24				CARBOHYD	T:53242	A:11959	65201	0.183417	0	TRUE	T:16829	G:9	16838	0.000535	1	FALSE	0	0
113	SA072_1_1	SA072	1	1.77E+08	1,1773439	missense	low	1.5	S1033I	ABL2	1q24-q25			Cancer Rev	COMPBIAS	A:104705	A:24072	128777	0.186928	0	TRUE	C:110497	G:52	110549	0.00047	1	FALSE	1	28
114	SA072_1_1	SA072	1	1.81E+08	1,1813463	missense	high	3.9	H309L	LAMC1	1q31				DISULFID	//A:77760	T:6417	84177	0.176232	0	TRUE	A:52373	T:3	52376	5.73E-05	1	FALSE	1	28
115	SA072_13	SA072	13	31843109	13,318431	nonsense	NA		S283S	BRCA2	13q12.1			Cancer Rev	VARIANT	//C:11232	A:2237	13469	0.166085	0	TRUE	C:7010	N:0	7010	0	1	FALSE	2	3
116	SA072_13	SA072	13	32526094	13,325260	missense	high	4.39	V373S	KL	13q12				REGION	//A:30311	C:2367	32678	0.072434	0	TRUE	A:23379	G:1	2338					

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.pos	Ref.count	Alt.count.T	Total.count	Alt.frequer	Binomial.te	Binomial.te	Ref.count	Alt.count.N	Total.count	Alt.frequer	Binomial.te	Binomial.te	SVNMix2.C	REF.RNASE	
140	SA076_1_1	SA076	1	1.84E+08	1,1843289	missense	medium	2.05	S3302R	HMCN1	1q25.3-q31.1				DISULFID //	C:313841	A:21138	334979	0.063102	0	TRUE	C:256819	A:45	256864	0.000175	1	FALSE	1	5	
141	SA076_1_1	SA076	6	141225648	1,4122564	missense	low	1.055	D119N	CTPS	1p34.1				HEUX // 11	G:48086	A:3364	51450	0.065384	0	TRUE	G:58680	T:25	58705	0.000426	1	FALSE	1	83	
142	SA076_15	SA076	15	69931572	15,699315	missense	medium	2.97	P2144S	MYO9A	15q22-q23				DOMAIN //	G:123531	A:8693	132224	0.065744	0	TRUE	G:167795	T:107	167902	0.000637	0.567019	FALSE	1	25	
143	SA076_19	SA076	19	36461366	19,364613	nonsense	NA		C391	TSZH3	19q12				ZN_FING //	A:517036	T:86277	603313	0.143005	0	TRUE	A:766635	C:281	766916	0.000366	1	FALSE	1	10	
144	SA076_2_2	SA076	2	2.34E+08	2,2341915	missense	low	1.115	A169V	UGT1A8	2q37					C:89195	T:15015	104210	0.144084	0	TRUE	C:150427	T:102	150529	0.000678	0.214954	FALSE	0	0	
145	SA076_2_2	SA076	2	2.7761549	2,2776154	missense	low	1.39	S673C	SLCA41AP	2p23.2			Entrez Query	COMPBIAS	A:20332	T:3095	23427	0.132113	0	TRUE	A:35847	G:9	35856	0.000251	1	FALSE	2	38	
146	SA077_11	SA077	11	60658132	11,606581	missense	medium	2.36	E73K	VP53C	11q12.2					C:95390	T:69338	164728	0.420924	0	TRUE	C:175104	G:33	175137	0.000188	1	FALSE	1	16	
147	SA077_16	SA077	16	57313665	16,573136	missense	medium	2.53	A89T	GOT2	16q21				MOD_RES	C:22211	T:19232	41443	0.464059	0	TRUE	C:46393	T:43	46436	0.000926	1	FALSE	2	15	
148	SA077_16	SA077	16	67413522	16,674135	missense	low	1.625	O610L	CDH1	16q22.1			Cancer Cell	DOMAIN //	A:136615	T:8104	144719	0.055998	0	TRUE	A:142381	C:152	142533	0.001066	1	FALSE	1	314	
149	SA077_19	SA077	19	21269047	19,212690	missense	NA		E187D	ZNF708	-				ZN_FING //	C:131716	G:12788	144504	0.088496	0	TRUE	C:89790	T:9	89799	0.0001	1	FALSE	1	3	
150	SA077_19	SA077	19	22732725	19,227327	missense	neutral	-1.58	R518T	ZNF99	19p12				ZN_FING //	C:42299	G:8603	50902	0.169011	0	TRUE	C:28611	T:4	28615	0.00014	1	FALSE	0	0	
151	SA077_19	SA077	19	41632645	19,416326	missense	neutral	0	R111C	ZNF566	19q13.12					G:211	A:14	225	0.062222	2.51E-14	0	TRUE	G:81	N:0	81	0	1	FALSE	1	9
152	SA077_2_2	SA077	2	2.2E+08	2,2200784	missense	medium	2.495	R272Q	GMPPA	2q35					G:249799	A:44721	294520	0.151844	0	TRUE	G:226080	A:26	226106	0.000115	1	FALSE	1	139	
153	SA077_3_1	SA077	3	1.34E+08	3,1336588	missense	low	1.245	R454H	DNAC13	3q22.1					G:2804	A:382	3186	0.1199	0	TRUE	G:2374	A:2	2376	0.000842	1	FALSE	2	6	
154	SA080_1_1	SA080	1	1.69E+08	1,1693197	missense	NA		A323P	LOC646804					G:689948	T:112400	802348	0.140089	0	TRUE	G:748896	T:94	748990	0.000126	1	FALSE	0	0		
155	SA080_1_8	SA080	1	84717716	1,847177	missense	medium	2.895	S55L	BDC05	1p22.3					C:897107	T:282089	1179196	0.239221	0	TRUE	C:1261052	T:374	1261426	0.000296	1	FALSE	2	108	
156	SA083_11	SA083	11	387564	11,387564	missense	medium	2.045	A324P	PKP3	11p15				REPEAT //	G:282123	C:3563	31786	0.112093	0	TRUE	G:48631	A:234	48654	0.000473	1	FALSE	2	62	
157	SA083_1_1	SA083	1	1.5E+08	1,1500179	missense	neutral	0.345	O224N	TDRKH						C:248915	T:29334	278249	0.105424	0	TRUE	C:317596	A:44	317640	0.000139	1	FALSE	1	48	
158	SA083_1_1	SA083	1	1.59E+08	1,1594465	missense	high	3.515	O256H	NDUF52	1q23					G:276470	C:14604	291074	0.050173	0	TRUE	G:242711	T:192	242903	0.00079	0.000539	FALSE	1	666	
159	SA083_1_1	SA083	1	2.14E+08	1,2144366	missense	medium	2.08	F1364L	USH2A	1q41				TOPO_DON	A:135478	G:41512	176990	0.234544	0	TRUE	A:181785	G:12	181797	6.40E-05	1	FALSE	0	0	
160	SA083_14	SA083	14	20556809	14,205568	missense	medium	3.2	P256A	NDRG2	14q11.2			Entrez Query	Query : Tumor	G:201718	C:30353	232071	0.130792	0	TRUE	G:242335	T:19	242354	7.84E-05	1	FALSE	1	747	
161	SA083_15	SA083	15	41715607	15,417156	missense	low	1.645	I315M	CATSPER2	15q14				TOPO_DON	G:145085	C:19417	164502	0.118035	0	TRUE	G:130538	T:30	130568	0.00023	1	FALSE	3	0	
162	SA083_17	SA083	17	71238113	17,712381	missense	low	1.05	R312H	ITGB4	17q25			Cancer Cell	DISULFID //	G:1273	A:151	1424	0.106039	1.13E-225	0	TRUE	G:4331	T:2	4333	0.000462	1	FALSE	1	265
163	SA083_18	SA083	18	46054162	18,460541	nonsense	NA		R406	MBD1	18q21					G:192932	A:22097	215029	0.102763	0	TRUE	G:338806	A:57	338863	0.000168	1	FALSE	1	24	
164	SA083_2_1	SA083	2	1.65E+08	2,1651845	missense	neutral	0.695	K66N	GRB14	2q22-q24			Cancer Cell	Map Pathw	T:50271	A:7668	57939	0.132346	0	TRUE	T:8658	G:7	8665	0.000808	1	FALSE	1	28	
165	SA083_2_1	SA083	2	2.7445072	2,2744507	missense	medium	2.395	D151H	E1F2B4	2p23.3					C:279180	G:47185	326365	0.144577	0	TRUE	C:251253	A:83	251336	0.00033	1	FALSE	2	39	
166	SA084_10	SA084	10	1.16E+08	10,115976	missense	low	0.975	K1102T	TDRD1	10q25.3					A:148846	C:62860	211706	0.296921	0	TRUE	A:115240	G:17	115257	0.000147	1	FALSE	0	0	
167	SA084_1_1	SA084	1	1.55E+08	1,1550337	missense	medium	1.95	Q456H	PRCC	1q21.1			Cancer Review	Future	G:238603	C:49019	287622	0.170429	0	TRUE	G:277047	T:133	277180	0.00048	1	FALSE	1	328	
168	SA084_11	SA084	11	69996762	11,699967	missense	neutral	0.45	I425E	SHANK2	11q13.3				DOMAIN //	T:151906	C:89437	241343	0.37058	0	TRUE	T:212837	G:19	212856	8.93E-05	1	FALSE	2	16	
169	SA084_12	SA084	12	55909857	12,559098	missense	neutral	0	A10G	SHMT2	12q12-q14				TRANSIT //	G:96457	G:42542	138999	0.30606	0	TRUE	C:137743	T:37	137780	0.000269	1	FALSE	2	116	
170	SA084_13	SA084	13	38323843	13,383238	nonsense	NA		E225S	FREM2	13q13.3				DOMAIN //	G:202751	T:74769	277520	0.266948	0	TRUE	G:266487	T:18	266505	6.75E-05	1	FALSE	0	0	
171	SA084_13	SA084	13	51565292	13,515652	missense	neutral	0.695	R369S	NEK5	13q14.3					C:25376	G:5273	30649	0.172045	0	TRUE	C:33098	A:3	33101	9.06E-05	1	FALSE	1	3	
172	SA084_14	SA084	14	51590759	14,515907	missense	medium	3.145	W266C	NR2	14q21-q22				DOMAIN //	C:217582	G:101620	319202	0.318356	0	TRUE	C:299246	A:36	299282	0.00012	1	FALSE	1	9	
173	SA084_16	SA084	16	2703678	16,270367	missense	low	1.66	I177M	PRSS27	16p13.3				DISULFID //	G:24508	C:27614	52122	0.529795	0	TRUE	G:172386	T:52	172438	0.000302	1	FALSE	3	0	
174	SA084_16	SA084	16	30919805	16,309198	missense	medium	2.195	E75D	STX1B	16p12-p11				TOPO_DON	C:46697	A:12260	58957	0.207948	0	TRUE	C:129105	T:63	129168	0.000488	1	FALSE	3	0	
175	SA084_17	SA084	17	32610438	17,326104	missense	medium	3.33	S1615C	ACACA	17q21			Entrez Query	Stability	A:44104	C:17132	61236	0.27977	0	TRUE	G:11822	T:7	11829	0.000592	1	FALSE	2	43	
176	SA084_19	SA084	19	10642785	19,106427	missense	medium	3.12	D47N	ILF3	19p13.2					G:134962	A:77804	212766	0.365679	0	TRUE	G:204160	T:106	204266	0.000519	1	FALSE	2	373	
177	SA084_20	SA084	20	5486603	20,548660	missense	medium	3.48	L606P	IFP5-1022P	20p12.3				DOMAIN //	A:86829	G:32163	118992	0.270295	0	TRUE	A:31440	C:2	31446	6.36E-05	1	FALSE	2	40	
178	SA084_2_1	SA084	2	1E+08	2,1003764	missense	high	3.77	H262L	CHST10	2q11.2				TOPO_DON	T:189686	A:48893	238579	0.204934	0	TRUE	T:139966	C:22	139988	0.000157	1	FALSE	1	32	
179	SA084_2_1	SA084	2	11638404	2,116384	missense	medium	2.14	A299G	GREB1	2p25.1					C:31299	G:15563	46862	0.332103	0	TRUE	C:121302	A:9	121311	7.42E-05	1	FALSE	2	32	
180	SA084_2_1	SA084	2	1.87E+08	2,1872368	missense	neutral	-0.035	D641E	ITGAV	2q31-q32				STRAND //	T:138523	A:43292	181815	0.23811	0	TRUE	T:155677	G:17	155694	0.000109	1	FALSE	2	224	
181	SA084_22	SA084	22	41286213	22,412862	missense	neutral	-0.16	T204K	SERHL2	22q13					C:68079	A:25326	93405	0.271142	0	TRUE	C:370709	A:202	370911	0.000545	1	FALSE	0	0	
182	SA089_16	SA089	16	30575021	16,305750	missense	neutral	0	N549S	PRR14	16p11.2					A:208378	G:54646	263024	0.207761	0	TRUE	A:32649	G:23	32672	0.000704	1	FALSE	2	14	
183	SA089_19	SA089	19	9582860	19,958286	missense	NA		H159Q	ZNF561	19p13.2					G:1734698	C:331672	2066370	0.160509	0	TRUE	G:1055023	T:608	1055631	0.000576	1	FALSE	1	31	
184	SA089_2_1	SA089	2	2.02E+08	2,2020608	missense	neutral	0	V458L	ALS2CR11	2q33.1					C:7364	G:481	7845	0.061313	0	TRUE	C:473	T:1	474	0.00211	1	FALSE	1	1	
185	SA090_1_1	SA090	1	12649124	1,126491																									

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.pof	Ref.count.	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNASE
209	SA092_12	SA092	12	39212301	12,392123	missense				LOC730512						C:24689	A:10251	34940	0.293389	0	TRUE	C:24474	A:17	24474	0.000695	1	FALSE	1	1
210	SA092_13	SA092	1	33006060	1,3300606	missense	low	1.895	N48K	KIAA1522	1p35.1					C:2145	A:201	2346	0.085678	1.21E-232	TRUE	C:7341	A:3	7344	0.000408	1	FALSE	1	112
211	SA092_13	SA092	13	41774275	13,417742	missense	medium	2.125	E1131D	AKAP11	13q14.11			Entrez Query :: Protein	G:33195	C:6876	40071	0.171595	0	TRUE	G:37467	T:6	37473	0.00016	1	FALSE	2	33	
212	SA092_15	SA092	15	29081438	15,290814	missense	neutral	0.255	Q1564P	TRPM1	15q13-q14			TOPO_DOM	T:38550	G:8462	47012	0.179997	0	TRUE	T:52893	C:19	52912	0.000359	1	FALSE	0	0	
213	SA092_15	SA092	15	40159239	15,401592	missense	neutral	0.445	H369N	PLA2G4D	15q15.1			DOMAIN //	G:13438	T:2704	16142	0.167513	0	TRUE	G:93919	T:19	39338	0.000483	1	FALSE	0	0	
214	SA092_15	SA092	15	40624635	15,406246	missense	medium	2.52	C204R	LRRCS7	15q15.1			REPEAT //	A:2434	G:681	3115	0.21862	0	TRUE	A:3292	C:1	3293	0.000304	1	FALSE	2	10	
215	SA092_16	SA092	16	18992853	16,189928	missense	low	1.57	A121V	COQ7	16p13.11-p12.3			REPEAT //	C:3144	T:643	3787	0.169791	0	TRUE	C:4097	T:2	4099	0.000488	1	FALSE	2	4	
216	SA092_17	SA092	17	16534689	17,165346	missense	low	1.525	L84V	CCDC144A						C:3250	G:493	3743	0.131713	0	TRUE	C:5144	G:1	5145	0.000194	1	FALSE	0	0
217	SA092_17	SA092	17	39816839	17,398168	missense	medium	2.93	M316T	ITGA2B	17q21.32			Entrez Query	REPEAT //	A:5736	G:1917	7653	0.25049	0	TRUE	A:31010	C:41	31051	0.00132	1	FALSE	3	0
218	SA092_17	SA092	17	58919790	17,589197	missense	medium	3.265	W785C	ACE	17q23.3			HELI // 78	G:10370	T:1432	11802	0.121335	0	TRUE	G:18744	T:9	18753	0.00048	1	FALSE	1	22	
219	SA092_17	SA092	17	7517810	17,751781	missense	medium	3.325	E285K	TP53	17p13.1	p.E285*,p.	carcinoma	Cancer Cell	DNA_BIND	C:18288	T:7082	25370	0.279149	0	TRUE	C:33670	A:4	33674	0.000119	1	FALSE	2	15
220	SA092_18	SA092	1	86727395	1,8672739	missense	low	1.53	L437F	CLCA1	1p31-p22			Cancer Cell	DOMAIN //	G:29669	C:7801	37470	0.208193	0	TRUE	G:33492	A:2	33494	5.97E-05	1	FALSE	0	0
221	SA092_18	SA092	1	89199758	1,8919975	missense	neutral	-0.68	R187K	CCBL2	1p22.2					C:16775	T:5926	22701	0.261046	0	TRUE	C:19672	G:21	19693	0.001066	1	FALSE	1	30
222	SA092_19	SA092	19	2060091	19,206009	missense	medium	2.7	F1094V	AP3D1	19p13.3					A:22855	C:4545	27400	0.165876	0	TRUE	A:33770	G:13	33783	0.000385	1	FALSE	2	96
223	SA092_19	SA092	19	21031439	19,210314	missense	medium	2.135	Y162C	ZNF430	19p12					A:815	N:0	1134	0.281305	0	TRUE	A:901	N:0	901	0	1	FALSE	2	14
224	SA092_19	SA092	19	4261561	19,426156	missense	medium	2.295	R153Q	FSF1	19p13.3			DOMAIN //	G:495	A:49	544	0.090074	5.35E-58	TRUE	G:1062	C:1	1063	0.000941	1	FALSE	0	0	
225	SA092_20	SA092	20	187835	20,187835	missense		NA		DEFB132	20p13					A:35735	G:2078	37813	0.055495	0	TRUE	A:39821	G:30	39851	0.000753	1	FALSE	1	1
226	SA092_20	SA092	20	31118342	20,311183	missense	low	1.345	E326K	C20orf185	20q11.21					G:47515	A:7555	55070	0.137189	0	TRUE	G:50163	A:2	50165	3.99E-05	1	FALSE	0	0
227	SA092_20	SA092	20	36790296	20,367902	missense	medium	3.315	S393C	SLC32A1	20q11.23			TRANSMEN	C:31864	G:2874	34738	0.082734	0	TRUE	C:46991	A:3	46994	6.38E-05	1	FALSE	0	0	
228	SA092_21	SA092	21	31520080	21,315200	missense		NA	T548P	TIAM1	21q22.11	21q22.11			DOMAIN //	T:20670	G:2719	23389	0.116251	0	TRUE	T:29601	C:9	29610	0.000304	1	FALSE	1	3
229	SA092_21	SA092	2	1.38E+08	2,1375304	missense	low	1.1	G54A	THSD7B	2q21-q22			DOMAIN //	G:27017	C:12792	39809	0.321334	0	TRUE	G:41412	T:34	41446	0.00082	1	FALSE	0	0	
230	SA092_21	SA092	2	1.66E+08	2,1659299	nonsense		NA	S1140	SCN2A	2q23-q24					C:7657	A:1769	9426	0.187672	0	TRUE	C:13526	T:2	13528	0.000148	1	FALSE	1	2
231	SA092_22	SA092	2	1.73E+08	2,1730422	nonsense		NA	R180	ITGA6	2q31.1			Cancer Cell	DISULFID	A:4756	T:1789	6545	0.273338	0	TRUE	A:5977	G:2	5979	0.000335	1	FALSE	1	35
232	SA092_22	SA092	22	16396840	22,163968	missense	medium	2.045	A406D	CECR2						C:16457	A:2945	19402	0.151788	0	TRUE	C:19128	G:5	19133	0.000261	1	FALSE	0	0
233	SA092_22	SA092	22	26756233	22,267562	missense	low	1.04	R1352C	TTC28						G:32153	A:15985	48138	0.332066	0	TRUE	G:45302	A:7	45309	0.000154	1	FALSE	2	14
234	SA092_24	SA092	2	42341907	2,4234190	missense	low	0.895	P161S	EMIL4	2p22-p21					C:2117	T:1033	3150	0.327937	0	TRUE	C:1497	N:0	1497	0	1	FALSE	2	46
235	SA092_24	SA092	2	73330983	2,7333098	missense	high	3.765	T371N	CCT7	2p13.2					C:5442	A:500	5942	0.084147	0	TRUE	C:17674	A:5	17679	0.000283	1	FALSE	1	367
236	SA092_24	SA092	2	73534150	2,7353415	missense	neutral	0	R2329W	ALMS1	2p13					A:29421	A:2840	32261	0.088032	0	TRUE	A:35353	G:13	35366	0.000368	1	FALSE	2	12
237	SA092_28	SA092	2	88177357	2,8817735	missense	medium	3.43	C276Y	SMYD1	2p11.2					G:16879	A:1456	18335	0.079411	0	TRUE	G:22797	A:8	22805	0.000351	1	FALSE	1	5
238	SA092_31	SA092	3	1.11E+08	3,1105060	missense	low	1.525	G272S	DPFA2	3q13.13					C:507	T:337	844	0.399289	0	TRUE	C:2343	A:1	2344	0.000427	1	FALSE	0	0
239	SA092_31	SA092	3	1.97E+08	3,1970018	missense	neutral	0.345	P351T	MUCA	3q29			Entrez Query :: Oncog	G:32060	T:1978	34038	0.058112	0	TRUE	G:25396	T:6	25402	0.000236	1	FALSE	1	1	
240	SA092_31	SA092	3	30817450	3,3081745	missense	low	1.885	M395I	GADL1	3p24.1-p23					C:8419	T:1226	9645	0.127112	0	TRUE	C:13184	G:3	13187	0.000227	1	FALSE	0	0
241	SA092_31	SA092	3	51248829	3,5124882	missense	medium	2.685	I644N	DOCK3	3p21.31			DOMAIN //	T:252	A:26	278	0.093525	2.86E-31	TRUE	T:344	N:0	344	0	1	FALSE	1	1	
242	SA092_31	SA092	3	9965571	3,9965571	missense	low	1.845	P348A	PRRT3	3p25.3			COMPBias	G:38479	C:3762	42241	0.08096	0	TRUE	G:40578	A:3	40581	7.39E-05	1	FALSE	1	13	
243	SA092_41	SA092	4	1.23E+08	4,1230731	missense	medium	2.42	R144C	TRPC3	4q27			TOPO_DOM	G:16259	A:2059	18318	0.112403	0	TRUE	G:40767	A:15	40782	0.000368	1	FALSE	0	0	
244	SA092_41	SA092	4	1.6E+08	4,1604822	missense		NA	E700K	RAPGEF2					G:220	A:20	240	0.083333	4.72E-23	TRUE	G:720	N:0	720	0	1	FALSE	1	17	
245	SA092_41	SA092	4	79527739	4,7952773	missense	medium	2.845	F1278L	FRAS1	4q21.21			REPEAT //	T:15210	C:2697	17907	0.150611	0	TRUE	T:19336	G:24	19360	0.00124	1	FALSE	1	1	
246	SA092_51	SA092	5	1.47E+08	5,1467604	missense	medium	2.905	V364A	DPYSL3	5q32					A:53680	G:7864	61544	0.127779	0	TRUE	A:56605	G:13	56618	0.00023	1	FALSE	1	50
247	SA092_61	SA092	6	11113619	6,1111361	missense	low	0.95	T76I	ELOV12	6p24.2			TRANSMEN	G:10335	A:2358	12693	0.185772	0	TRUE	G:14879	T:5	14884	0.000336	1	FALSE	2	3	
248	SA092_61	SA092	6	13429235	6,1342923	missense	medium	2.215	L89F	TBC1D7	6p24.1			DOMAIN //	G:60388	A:7050	67438	0.10454	0	TRUE	G:69847	T:79	69896	0.000113	1	FALSE	1	62	
249	SA092_61	SA092	6	1.52E+08	6,1519361	missense	neutral	-1.935	V316A	C6orf97	6q25.1					T:19740	C:3122	22862	0.136558	0	TRUE	T:24893	G:3	24896	0.000121	1	FALSE	1	2
250	SA092_71	SA092	7	1.49E+08	7,1491886	missense	low	1.87	P474A	LOC643641			ZN_FING //	C:41261	G:4663	45924	0.101537	0	TRUE	C:40674	A:1	40675	2.46E-05	1	FALSE	1	33		
251	SA092_71	SA092	7	22273110	7,2227311	missense	medium	2.2	S112C	RAPGEF5	7p15.3					G:7426	C:1125	8551	0.131564	0	TRUE	G:8753	A:1	8754	0.000114	1	FALSE	1	3
252	SA092_71	SA092	7	43444134	7,4344413	missense	low	0.96	S270T	HECW1	7p14.1-p13			DOMAIN //	G:13921	C:2108	16029	0.131512	0	TRUE	G:19469	A:1	19470	5.14E-05	1	FALSE	0	0	
253	SA092_71	SA092	7	6440949	7,6440949	missense	medium	2.6	S216I	DAGLB	7p22.1			TOPO_DOM	C:37884	A:7894	45778	0.172441	0	TRUE	C:44929	A:34	44963	0.000756	1	FALSE	2	31	
254	SA092_81	SA092	8	1.06E+08	8,1055057	missense	medium	3.42	M369R	DPY5	8q22			STRAND //	A:8466	C:1188	9654	0.123058	0	TRUE	A:11255	C:3	11258	0.000266	1	FALSE	1	1	
255	SA092_81	SA092	8	1.24E+08	8,1243367	missense	medium	2.045	E223G	ZHX1	8q24.13					T:14269	C:1231	15500	0.079419	0	TRUE	T:16408	C:1	16409	6.09E-0				

	T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC						
	1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.pof	Ref.count	Alt.count.T	Total.count	Alt.frequer	Binomial.te	Binomial.te	Ref.count	Alt.count	Total.count	Alt.frequer	Binomial.te	Binomial.te	Ref.count	Alt.count	Total.count	Alt.frequer	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase
278	SA097_10	SA097		10	61222751	10,6122277	missense	neutral	0.69	T452M	CDC6	10q21			Cancer Rev	MOTIF // 4	G:101803	A:36243	138046	0.262543	0	TRUE	G:221153	A:115	221268	0.00052	1	FALSE	2	5						
279	SA097_10	SA097		10	6593160	10,659316	missense	low	1.845	N41Y	PRKCQ	10p15				DOMAIN //	T:282518	A:19180	301698	0.063574	0	TRUE	T:267281	C:16	267297	5.99E-05	1	FALSE	1	4						
280	SA097_10	SA097		10	74726871	10,747268	missense	medium	1.91	L597V	PTC1C	10q22.2					G:39688	C:3215	42903	0.074936	0	TRUE	G:14760	A:1	14761	6.77E-05	1	FALSE	1	4						
281	SA097_11	SA097		11	1.24E+08	11,124048	missense	low	1.12	G9V	SIAE	11q24				SIGNAL // 3	C:45171	A:26035	71206	0.365629	0	TRUE	C:68332	T:48	68380	0.000702	1	FALSE	2	11						
282	SA097_1_1	SA097		1	1.55E+08	1,1549731	nonsense	NA		E47I	C1orf66	1q23.1					G:133699	T:28691	162390	0.17668	0	TRUE	G:111849	C:4	111853	3.58E-05	1	FALSE	1	17						
283	SA097_1_1	SA097		1	1.95E+08	1,1949132	missense	medium	2.68	P152T	CFH	1q32				DISULFID //	G:529407	A:81460	610867	0.133351	0	TRUE	C:458272	A:45	458317	9.82E-05	1	FALSE	1	65						
284	SA097_1_1	SA097		1	2.33E+08	1,2334125	missense	medium	2.015	R738W	ARID4B	1q42.1-q43					T:51213	A:43839	95052	0.461211	0	TRUE	T:49477	C:4	49481	0.08E-05	1	FALSE	2	19						
285	SA097_1_1	SA097		1	2.42E+08	1,2415710	nonsense	NA		Q42I	SDCCAG8	1q43-q44				REGION //	C:81353	T:4488	85841	0.052283	0	TRUE	C:56505	G:6	56511	0.000106	1	FALSE	1	23						
286	SA097_1_1	SA097		1	3340153	1,3340153	missense	medium	2.135	S1250C	PRDM16	1p36.23-p33			Cancer Rev	REGION //	C:40813	G:17868	58681	0.304494	0	TRUE	C:232344	A:28	232372	0.00012	1	FALSE	0	0						
287	SA097_19	SA097		19	15236428	19,152364	missense	medium	2.595	K333N	BRD4	19p13.1			Cancer Review :: Futre		G:132533	G:38335	170868	0.224354	0	TRUE	C:233174	G:168	233342	0.00072	1	FALSE	2	40						
288	SA097_21	SA097		21	39954498	21,399544	missense	low	1.895	P48A	B3GALT5	21q22.3				TOPO_DON	C:49710	G:55296	105006	0.526598	0	TRUE	C:140106	A:21	140127	0.00015	1	FALSE	3	0						
289	SA099_10	SA099		10	89682960	10,896829	missense	medium	3.055	Y155C	PTEN	10q23.3	p.F56fs*2,gastr	Cancer Cell	DOMAIN //	A:1113362	G:205478	1318840	0.155802	0	TRUE	A:1104084	G:179	1104263	0.000162	1	FALSE	2	13							
290	SA099_1_1	SA099		1	50805470	1,5080547	missense	medium	2.52	L379V	FAF1	1p33			Cancer Cell	STRAND //	G:1439821	C:355972	1795793	0.198226	0	TRUE	G:1146827	T:103	1146930	8.98E-05	1	FALSE	2	40						
291	SA102_11	SA102		11	22228924	11,222289	missense	neutral	0.255	V359L	TMM16E	11p14.3				TOPO_DON	G:187693	T:28146	215839	0.130403	0	TRUE	G:98769	T:17	98786	0.000172	1	FALSE	1	7						
292	SA102_13	SA102		13	50752858	13,507528	missense	low	1.5	G369A	FAM124A	13q14.3					G:123153	C:26673	149826	0.178027	0	TRUE	G:424	N:0	424	0	1	FALSE	0	0						
293	SA102_1_1	SA102		1	37063819	1,3706381	missense	high	4.05	V576F	GRM3	1p34-p33				TRANSMEN	C:217180	A:42641	259821	0.164117	0	TRUE	C:269424	A:238	269662	0.000883	1	FALSE	0	0						
294	SA102_16	SA102		16	88104445	16,881044	missense	low	0.975	G77A	SPG7	16q24.3			Entrez Que	TOPO_DON	G:8936	C:3776	12712	0.297042	0	TRUE	G:69714	T:8	69722	0.000115	1	FALSE	2	68						
295	SA102_17	SA102		17	7518257	17,751825	missense	high	3.54	P250L	TP53	17p13.1	p.P250P,p.	Cancer Cell	DNA_BIND	G:28050	A:12540	40590	0.308943	0	TRUE	G:130928	T:100	131028	0.000763	1	FALSE	2	43							
296	SA102_1_1	SA102		1	77870651	1,7787065	missense	low	1.04	A326G	ZZZ3	1p31.1					G:189716	C:38902	228618	0.170162	0	TRUE	G:201700	T:161	201861	0.000798	1	FALSE	1	53						
297	SA102_18	SA102		18	58187037	18,581870	missense	low	0.895	D030Y	TNFRSF11A	18q22.1			Cancer Cell	TOPO_DON	G:129955	T:9538	139493	0.068376	0	TRUE	G:145403	A:6	145409	4.13E-05	1	FALSE	1	14						
298	SA102_19	SA102		19	43726103	19,437261	missense	medium	2.925	A3957D	RYR1	19q13.1					C:38204	A:6798	45002	0.15106	0	TRUE	C:214073	A:31	214104	0.000145	1	FALSE	1	5						
299	SA102_20	SA102		20	33804795	20,338047	missense	NA			LOC729608						G:266175	A:18773	284948	0.056582	0	TRUE	G:249154	T:17	249171	6.82E-05	1	FALSE	0	0						
300	SA102_2_1	SA102		2	1.29E+08	2,1286550	missense	low	1.72	D1352E	UGCG1L	2q14.3				REGION //	C:2899	A:267	3166	0.084334	0	TRUE	C:658	N:0	658	0	1	FALSE	2	81						
301	SA102_2_1	SA102		2	1.58E+08	2,1578242	missense	medium	1.935	A484T	GALNT5	2q24.1				TOPO_DON	G:217338	A:51132	268470	0.190457	0	TRUE	G:256825	T:37	256862	0.000144	1	FALSE	1	5						
302	SA102_2_1	SA102		2	1.96E+08	2,1963011	missense	high	3.54	L736P	SLC39A10	2q32.3				TRANSMEN	T:35087	C:7026	42113	0.166837	0	TRUE	T:21094	C:8	21102	0.000379	1	FALSE	1	47						
303	SA102_2_1	SA102		2	2.19E+08	2,2190286	missense	medium	2.77	D924Y	USP37	2q35					C:101071	A:13474	114545	0.117631	0	TRUE	C:104605	T:10	104615	9.56E-05	1	FALSE	1	19						
304	SA103_14	SA103		14	52592175	14,525921	missense	low	1.79	R733Q	DDHD1	14q21				DOMAIN //	C:42473	T:3692	46165	0.079974	0	TRUE	C:32231	T:3	32234	9.31E-05	1	FALSE	1	10						
305	SA103_18	SA103		18	59412578	18,594125	missense	medium	3.285	K161M	SERPINB13	18q21.3-q22					A:335	T:193	528	0.36573	0	TRUE	A:284	T:4	288	0.013889	0.000849	FALSE	0	0						
306	SA103_19	SA103		19	61061413	19,610614	missense	medium	2.58	P281L	NLRP4	19q13.42			Cancer Cell	DOMAIN //	C:130917	T:11652	142569	0.0881729	0	TRUE	C:167359	A:17	167376	0.000102	1	FALSE	0	0						
307	SA106_10	SA106		10	21138777	10,211387	missense	medium	2.31	D859H	NEBL	10p12			Entrez Que	REGION //	C:88794	G:10372	99166	0.104592	0	TRUE	C:25326	G:3	25329	0.000118	1	FALSE	1	5						
308	SA106_10	SA106		10	26476372	10,264763	missense	high	4.675	R838F	MYO3A	10p11.1				DOMAIN //	A:24333	T:1834	26167	0.070088	0	TRUE	A:21507	C:36	21515	0.000372	1	FALSE	0	0						
309	SA106_10	SA106		10	38409386	10,384093	silent	NA			LOC340947						G:64072	T:3857	67929	0.05678	0	TRUE	G:59554	A:23	59577	0.000386	1	FALSE	1	1						
310	SA106_10	SA106		10	79286579	10,792865	missense	low	1.39	I151V	DLG5	10q23					T:18169	C:2501	20670	0.120997	0	TRUE	T:50716	A:7	50723	0.000138	1	FALSE	2	56						
311	SA106_1_1	SA106		1	1.08E+08	1,1080995	missense	low	0.805	F384L	VAV3	1p13.3			Cancer Cell	Map Pathw	A:98359	G:19268	117627	0.163806	0	TRUE	A:84169	G:13	84182	0.000154	1	FALSE	1	4						
312	SA106_1_1	SA106		1	1.12E+08	1,1117589	missense	low	1.845	P564T	OVGP1	1p13					G:77219	T:22114	99333	0.222625	0	TRUE	G:121744	T:30	121774	0.000246	1	FALSE	1	4						
313	SA106_1_1	SA106		1	1.17E+08	1,1173697	missense	neutral	-1.355	R833S	IGSF2	1p13				DISULFID //	C:64217	A:25409	89626	0.2835	0	TRUE	C:231339	G:63	231402	0.000272	1	FALSE	2	4						
314	SA106_1_1	SA106		1	1.44E+08	1,1435904	missense	low	1.735	L461V	PDG40IP	1q12			Cancer Review :: Futre	G:86599	C:9497	96096	0.098828	0	TRUE	G:266141	A:36	266177	0.000135	1	FALSE	1	22							
315	SA106_1_1	SA106		1	1.49E+08	1,1493296	missense	high	4.54	L75W	MGC29891	1q21.2				REPEAT //	T:148925	G:13467	162392	0.082929	0	TRUE	T:187385	A:23	187408	0.000123	1	FALSE	1	30						
316	SA106_1_1	SA106		1	1.53E+08	1,1533059	missense	medium	2.56	D79H	EFNA4	1q21-q22				DISULFID //	G:10166	C:585	10751	0.054414	0	TRUE	G:31472	T:24	31496	0.000762	1	FALSE	1	37						
317	SA106_1_1	SA106		1	1.54E+08	1,1537173	missense	low	0.975	L656F	ASH1L	1q22					C:19910	G:5469	25379	0.215493	0	TRUE	C:2098	T:1	2099	0.000476	1	FALSE	1	98						
318	SA106_1_1	SA106		1	1.56E+08	1,1558227	missense	medium	1.995	R338H	CFHL4	1q21			Cancer Rev	DISULFID //	C:63782	T:11486	75268	0.152601	0	TRUE	C:149967	A:29	149996	0.000193	1	FALSE	0	0						
319	SA106_1_1	SA106		1	1.57E+08	1,1565918	missense	medium	3.035	L727R	CD1E	1q22-q23					T:37568	G:8601	46169	0.186294	0	TRUE	T:10862	G:10	10872	0.00092	1	FALSE	1	5						
320	SA106_1_1	SA106		1	1.59E+08	1,1588605	missense	low	1.44	L260F	SLAMF1	1q22-q23				TOPO_DON	C:34783	G:5067	39850	0.127152	0	TRUE	C:60590	A:13	60603	0.000215	1	FALSE	1	1						
321	SA106_1_1	SA106		1	1.61E+08	1,1608239	missense	medium	3.045	R294G	UAP1	1q23.3				STRAND //	C:33039	G:3267	36306	0.089985	0	TRUE	C:4747	T:2	4749	0.000421	1	FALSE	1	129						
322	SA106_1_1	SA106		1	1.77E+08	1,1766788	missense	medium	2.945	K287E	RASAL2	1q24																								

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC						
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.pos	Ref.count.	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNAseq
347	SA212_12	SA212	12	94892152	12,948921	nonsense		NA	E65S	HAL	12q22-q24.1					C:224798	A:33396	258194	0.129345	0	TRUE	C:174840	T:27	174867	0.000154	1	FALSE	0	0						
348	SA212_1_6	SA212	1	35353064	1,3535306	missense	low	0.895	F1016V	ZMYM1	1p34.3					T:115615	G:46266	161881	0.285803	0	TRUE	T:78043	G:75	78118	0.00096	1	FALSE	2	55						
349	SA212_17	SA212	17	43984468	17,439844	missense	medium	2.175	S123F	H0XB3	17q21.3					G:67939	A:29742	97681	0.304481	0	TRUE	G:224384	T:27	224411	0.00012	1	FALSE	1	10						
350	SA212_18	SA212	18	9547358	18,954735	missense	medium	2.11	A684G	PPP4R1	18p11.22					G:270541	C:27198	297739	0.091348	0	TRUE	G:165842	T:77	165919	0.000464	1	FALSE	1	75						
351	SA212_2_2	SA212	2	2.39E+08	2,2389262	nonsense		NA	S48S	TRAF3IP1	2q37.3				REGION //	C:716699	A:48918	765617	0.063894	0	TRUE	C:880164	A:161	880325	0.000183	1	FALSE	1	14						
352	SA212_2_3	SA212	2	38830681	2,3883068	missense	high	3.87	A63V	SFR57	2p22.1				DOMAIN //	G:70693	A:8711	79404	0.109705	0	TRUE	G:84722	T:94	84816	0.001108	1	FALSE	1	832						
353	SA212_2_6	SA212	2	65285852	2,6528585	missense		NA		LKC279317						G:161988	T:12126	174114	0.069644	0	TRUE	G:287244	T:200	287444	0.000696	1	FALSE	1	87						
354	SA212_2_6	SA212	2	69027880	2,6902788	missense	low	1.4	S73Y	GN2	2p14				DOMAIN //	G:1390	T:93	1483	0.062711	4.88E-100	TRUE	G:4811	T:3	4814	0.000623	1	FALSE	0	0						
355	SA212_3_1	SA212	3	1.5E+08	3,1504098	missense	low	1.555	D206H	CP	3q23-q25			Entrez Query	DOMAIN //	C:664	G:103	767	0.134289	1.03E-145	TRUE	C:1269	N:0	1269	0	1	FALSE	1	26						
356	SA212_3_1	SA212	3	1.88E+08	3,1877727	missense	low	0.845	L70V	DNAJB11	3q27.3				DOMAIN //	C:269086	G:19854	288940	0.068713	0	TRUE	C:394754	G:35	394789	8.87E-05	1	FALSE	1	168						
357	SA213_1_1	SA213	1	1.44E+08	1,1436428	silent		NA	R70R	PDE4DIP	1q12					C:526388	A:95479	621867	0.153536	0	TRUE	C:1123591	T:110	1123701	9.79E-05	1	FALSE	1	90						
358	SA213_13	SA213	13	45620520	13,456205	missense	low	1.865	P316S	LCP1	13q14.3			Cancer Rev	DOMAIN //	G:138609	A:26686	165295	0.161445	0	TRUE	G:17591	T:13	17604	0.000738	1	FALSE	1	121						
359	SA213_17	SA213	17	36896299	17,368962	missense	low	0.895	P420R	KRT36	17q12-q21				REGION //	G:43731	C:321341	365072	0.880213	0	TRUE	G:502886	C:40	502926	7.95E-05	1	FALSE	0	0						
360	SA213_22	SA213	22	17504889	22,175048	missense	low	1.1	V328F	DGCR14	22q11.21	22q11.2				C:355042	A:74931	429973	0.174269	0	TRUE	C:343818	A:85	343903	0.000247	1	FALSE	1	106						
361	SA214_10	SA214	10	1.17E+08	10,116692	missense	neutral	-0.09	R125Q	TRUB1	10q25.3					G:24064	A:3237	27301	0.118567	0	TRUE	G:29111	T:12	29123	0.000412	1	FALSE	1	7						
362	SA214_10	SA214	10	14936159	10,149361	missense	medium	2.815	A255V	HSPA14	10p13					C:902	T:562	1464	0.38388	0	TRUE	C:593	T:2	595	0.003361	1	FALSE	2	44						
363	SA214_10	SA214	10	5878758	10,587875	missense	high	4.62	L76S	GD12	10p15					A:10504	G:989	11493	0.086052	0	TRUE	A:10452	G:6	10458	0.000574	1	FALSE	1	612						
364	SA214_10	SA214	10	76458349	10,764583	missense	medium	2.175	R1254H	MYST4	10q22.2			Cancer Review :: Futre	G:25038	A:2339	27377	0.085437	0	TRUE	G:42221	A:6	42227	0.000142	1	FALSE	1	34							
365	SA214_10	SA214	10	99190964	10,991909	missense	low	1.24	Y89H	EXOSC1	10q24				DOMAIN //	A:18224	G:1874	20098	0.093243	0	TRUE	A:24439	G:5	24444	0.000205	1	FALSE	2	131						
366	SA214_11	SA214	11	1.01E+08	11,101298	missense	low	1.845	R57C	KIAA1377	11q22.1				COILED //	C:794	T:54	848	0.063679	8.05E-64	TRUE	C:1370	N:0	1370	0	1	FALSE	1	3						
367	SA214_1_1	SA214	1	1.12E+08	1,1116942	missense	low	1.39	P141L	C1orf88	1p13.2					C:9689	T:1065	10754	0.099033	0	TRUE	C:20416	A:7	20423	0.000343	1	FALSE	1	21						
368	SA214_11	SA214	11	12272375	11,122723	missense	low	1.04	A274V	MICALCL	11p15.3					C:26797	T:2388	29185	0.081823	0	TRUE	C:33237	A:2	33239	6.02E-05	1	FALSE	0	0						
369	SA214_1_1	SA214	1	1.15E+08	1,1150647	missense	medium	2.045	V652I	CSD51	1p22				DOMAIN //	C:470	T:43	513	0.083821	5.19E-56	TRUE	C:910	A:1	911	0.001098	1	FALSE	2	1329						
370	SA214_1_1	SA214	1	1.18E+08	1,1184109	missense	low	1.735	R830C	SPAG17	1p12					G:28205	A:4328	32533	0.133034	0	TRUE	G:33818	A:12	33830	0.000355	1	FALSE	1	1						
371	SA214_1_1	SA214	1	1.54E+08	1,1538486	missense	neutral	0.05	A245V	MSTO1	1q22					C:9087	T:798	9885	0.080728	0	TRUE	C:18688	A:15	18703	0.000802	1	FALSE	1	30						
372	SA214_1_1	SA214	1	1.55E+08	1,1545098	missense	medium	2.32	E198K	SMG5	1q12.2			Entrez Query :: Stability	C:25754	T:7125	32879	0.216704	0	TRUE	C:29420	G:20	29440	0.000679	1	FALSE	2	52							
373	SA214_11	SA214	11	60397288	11,603972	missense	low	0.815	A397V	ZP1	11q12.2				DOMAIN //	C:11862	T:2297	14159	0.162229	0	TRUE	C:17101	A:4	17105	0.000234	1	FALSE	0	0						
374	SA214_11	SA214	11	60862100	11,608621	missense	high	3.71	R39C	DAK	11q12.2				DOMAIN //	C:8385	T:1214	9599	0.126472	0	TRUE	C:26406	T:4	26410	0.000151	1	FALSE	1	33						
375	SA214_11	SA214	11	6369893	11,636989	missense	low	0.985	R339H	SMPD1	11p15.4-p15.1					G:17894	A:2419	20313	0.119086	0	TRUE	G:41803	A:17	41820	0.000407	1	FALSE	1	116						
376	SA214_11	SA214	11	66039976	11,660399	missense	medium	1.965	R196Q	BBS1	11q13.1					G:28821	A:1948	30769	0.06631	0	TRUE	G:36176	A:14	36190	0.000387	1	FALSE	2	42						
377	SA214_1_1	SA214	1	1.69E+08	1,1692279	missense	neutral	0.55	A356V	C1orf129	1q24.3					C:18423	T:3685	22108	0.166682	0	TRUE	C:25197	A:5	25202	0.000198	1	FALSE	3	0						
378	SA214_11	SA214	11	76504975	11,765049	missense	neutral	0.435	V317M	CAPN5	11q14				DOMAIN //	G:15647	A:2129	17776	0.119768	0	TRUE	G:34208	A:41	34249	0.001197	1	FALSE	1	14						
379	SA214_1_1	SA214	1	1.85E+08	1,1845956	missense	medium	2.445	A434V	TPR	1q25			Cancer Rev	COILED //	G:3154	A:268	3422	0.078317	0	TRUE	G:4321	C:1	4322	0.000231	1	FALSE	1	70						
380	SA214_1_1	SA214	1	1.97E+08	1,1969884	missense	neutral	0.395	V1142I	PTPRC	1q31-q32				DOMAIN //	G:8990	A:589	9579	0.061489	0	TRUE	G:8066	A:2	8068	0.000248	1	FALSE	1	414						
381	SA214_1_1	SA214	1	1.99E+08	1,1993277	missense	high	3.86	R174Q	CACNA15	1q32				REPEAT //	C:15525	A:1754	20279	0.23443	0	TRUE	C:21827	T:3	21830	0.000137	1	FALSE	0	0						
382	SA214_1_2	SA214	1	2.02E+08	1,2024845	missense	low	1.59	R600C	PLEKHA6	1q32.1					G:15439	A:6360	16799	0.080957	0	TRUE	G:20420	T:12	20432	0.000587	1	FALSE	1	71						
383	SA214_1_2	SA214	1	2.04E+08	1,2035474	missense	medium	2.94	S105P	NUAK2	1q32.1				DOMAIN //	A:6958	G:836	7794	0.107262	0	TRUE	A:26854	C:46	26900	0.00171	0.024482	FALSE	1	24						
384	SA214_1_2	SA214	1	2.1E+08	1,2102569	missense	medium	2.555	R144H	INT57	1p36.13-q42.3					C:7297	T:816	8113	0.100579	0	TRUE	G:7946	T:1	7947	0.000126	1	FALSE	1	70						
385	SA214_12	SA214	12	1.08E+08	12,108061	missense	low	1.525	N131D	ACACB	12q24.11					A:5831	G:549	6380	0.08605	0	TRUE	A:30177	G:6	30183	0.000199	1	FALSE	1	1						
386	SA214_12	SA214	12	1.2E+08	12,119642	missense	medium	3.045	R226H	UNC119B	12q24.31					G:15575	A:1365	16940	0.080579	0	TRUE	G:22921	T:16	22937	0.000698	1	FALSE	1	12						
387	SA214_12	SA214	12	1.21E+08	12,121289	missense	neutral	0.71	H401R	VP533A	12q24.31					T:8367	C:570	8937	0.06378	0	TRUE	T:14539	C:4	14543	0.000275	1	FALSE	2	70						
388	SA214_12	SA214	12	1.24E+08	12,124016	missense	low	1.125	E547K	DHX37	12q24.31				DOMAIN //	C:16761	T:1312	18073	0.072594	0	TRUE	C:19520	G:16	19536	0.000819	1	FALSE	1	5						
389	SA214_1_2	SA214	1	2.21E+08	1,2212426	missense	low	1.845	R416H	DISP1	1q41					G:25409	A:1519	26928	0.05641	0	TRUE	G:28498	A:22	28520	0.000771	1	FALSE	1	6						
390	SA214_1_2	SA214	1	2.29E+08	1,2290461	missense	medium	2.075	A178T	C1orf198	1q42.13-q43					C:30143	T:2387	32530	0.073378	0	TRUE	C:35407	G:27	35434	0.000762	1	FALSE	1	68						
391	SA214_1_2	SA214	1	2.35E+08	1,2347889	missense	medium	2.455	D1621G	HEATR1	1q43					T:6954	C:533	7487	0.071119	0	TRUE	T:14395	G:7	14402	0.000486	1	FALSE	1	78						
392	SA214_1_2	SA214	1	2.36E+08	1,2361183	missense	low	1.7	A155V	ZP4	1q43				DOMAIN //	G:11048	A:1238	12286	0.100765	0	TRUE	G:10598	A:4	10602	0.000377	1	FALSE	0	0						
393	SA214_12																																		

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.pos	Ref.count.	Alt.count.T	Total.count	Alt.frequer	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.frequer	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase
416	SA214_16	SA214	16	23009557	16,2300955	missense	low	1.245	T4351	USP31	16p12.1					G:2566	A:224	2790	0.080287	1.11E-287	TRUE	G:2265	N:0	2265	0	1	FALSE	2	13
417	SA214_16	SA214	16	2446774	16,244677	missense	neutral	0.035	V7051	CCNF	16p13.3				REGION //	G:8850	A:651	9501	0.068519	0	TRUE	G:22428	T:8	22436	0.000357	1	FALSE	1	16
418	SA214_16	SA214	16	2751878	16,275187	missense	neutral	0	H450V	SRM2	16p13.3				COMPBIAS	C:30347	T:2848	33195	0.085796	0	TRUE	C:39441	G:37	39478	0.000937	1	FALSE	2	70
419	SA214_16	SA214	16	27670579	16,276705	missense	low	1.555	D1129N	KIAA0556	16p12.1-p11.2					G:12829	A:1199	14028	0.085472	0	TRUE	G:33297	A:7	33304	0.00021	1	FALSE	2	7
420	SA214_16	SA214	16	30958608	16,309586	missense	neutral	-0.205	V2931	STX4	16p11.2				TRANSMEN	G:3303	A:434	3737	0.116136	0	TRUE	G:18031	A:4	18035	0.000222	1	FALSE	2	251
421	SA214_16	SA214	16	3748891	16,374889	missense	high	4.09	R1112W	CREBBP	16p13.3			Cancer Cell	DOMAIN //	G:21845	A:2581	24426	0.105666	0	TRUE	G:29088	T:22	29110	0.000756	1	FALSE	2	29
422	SA214_16	SA214	1	64841079	1,6484107	missense	neutral	-0.345	F138Y	CACHD1	1p31.3				TOPO_DON	T:8190	A:605	8795	0.068789	0	TRUE	T:18066	G:3	18069	0.000166	1	FALSE	1	9
423	SA214_16	SA214	16	60408995	16,604089	missense	high	4.24	P389L	CDH8	16q22.1	p.P389P	serous_carcinoma	DOMAIN //	G:25413	A:2333	27746	0.084084	0	TRUE	G:30821	A:4	30825	0.00013	1	FALSE	1	2	
424	SA214_16	SA214	16	65170268	16,651702	missense	low	1.1	I125V	CMTM1	16q21				DOMAIN //	A:8266	G:804	9070	0.088644	0	TRUE	A:20685	G:5	20690	0.000242	1	FALSE	1	3
425	SA214_17	SA214	17	10383329	17,103833	missense	high	3.795	R445H	MYH2		p.R445H	serous_carcinoma	DOMAIN //	C:14712	T:1026	15738	0.065193	0	TRUE	C:17766	T:13	17779	0.000731	1	FALSE	0	0	
426	SA214_17	SA214	17	35894708	17,358947	nonsense	NA		R456	TNS4	17q21.2				DOMAIN //	G:9064	A:601	9665	0.062183	0	TRUE	G:13054	A:3	13057	0.00023	1	FALSE	1	23
427	SA214_17	SA214	1	74442677	1,7444267	nonsense	NA		R120	PPGT	1p31.1					C:3839	T:208	4047	0.051396	1.60E-226	TRUE	C:2171	A:2	2173	0.00092	1	FALSE	1	22
428	SA214_17	SA214	17	59349494	17,593494	missense	medium	3.42	A39T	GH1	17q24.2			Entrez Que	CONFLICT	C:14213	T:2674	16887	0.158347	0	TRUE	C:22229	T:5	22234	0.000225	1	FALSE	1	2
429	SA214_17	SA214	17	59645054	17,596450	missense	neutral	0.145	A86T	TEX2	17q23.3					C:19876	T:2588	22464	0.115207	0	TRUE	C:28549	G:20	28569	0.0007	1	FALSE	2	12
430	SA214_17	SA214	17	62168247	17,621682	missense	medium	3.225	A444V	PRKCA	17q22-q23.2			Cancer Cell	DOMAIN //	C:14498	T:1232	15730	0.092822	0	TRUE	C:30560	G:15	30575	0.000491	1	FALSE	2	9
431	SA214_17	SA214	17	65683698	17,656836	missense	medium	2.895	T308M	KCNJ2	17q23.1-q24.2				TOPO_DON	C:7781	T:410	8191	0.050055	0	TRUE	C:12231	T:5	12236	0.000409	1	FALSE	0	0
432	SA214_17	SA214	17	7518257	17,751825	missense	high	3.89	P250H	TP53	17p13.1	p.P250P.p	Bowen_dis	Cancer Cell	DNA_BIND	G:7502	T:530	8032	0.056986	0	TRUE	G:18987	T:9	18996	0.000474	1	FALSE	2	156
433	SA214_18	SA214	18	12496507	18,124965	missense	medium	2.75	R314H	SPIRE1	18p11.21				DOMAIN //	C:1727	T:118	1845	0.063957	9.82E-140	TRUE	C:2800	T:3	2803	0.00107	1	FALSE	2	44
434	SA214_18	SA214	18	14747912	18,147479	missense	NA			ANKRD30B						T:5499	C:1140	6639	0.171713	0	TRUE	T:6158	C:1	6159	0.000162	1	FALSE	0	0
435	SA214_18	SA214	1	82145364	1,8214536	nonsense	NA		R50	LPNH2	1p31.1				DOMAIN //	C:7948	T:680	8628	0.077813	0	TRUE	C:15384	G:14	15398	0.000909	1	FALSE	2	16
436	SA214_18	SA214	18	2903121	18,290312	missense	low	1.59	E961K	EMILIN2	18p11.3				DOMAIN //	G:5555	A:601	6156	0.097628	0	TRUE	G:20547	A:2	20549	9.73E-05	1	FALSE	1	34
437	SA214_18	SA214	18	8133737	18,813373	missense	medium	2.24	V754M	PTPRM	18p11.3			Entrez Que	TRANSMEN	G:11123	A:1129	12252	0.092148	0	TRUE	G:13613	A:2	13615	0.000147	1	FALSE	1	17
438	SA214_19	SA214	19	12637184	19,126371	nonsense	NA		R140	MAN2B1	19cen-q13.1				DISULFID //	G:13806	A:816	14622	0.055806	0	TRUE	G:26678	A:5	26683	0.000187	1	FALSE	1	265
439	SA214_19	SA214	19	15886613	19,158866	missense	medium	3.21	T403M	CYP4F11	19p13.1					G:19388	A:1965	21353	0.092025	0	TRUE	G:28716	T:5	28721	0.000174	1	FALSE	1	5
440	SA214_19	SA214	19	18997028	19,189970	missense	low	0.975	H377Y	SFRS14	19p12					G:10496	A:849	11345	0.074835	0	TRUE	G:15340	A:2	15342	0.00013	1	FALSE	1	55
441	SA214_19	SA214	19	47723105	19,477231	nonsense	NA		G118	CEACAM1	19q13.2			Entrez Que	DOMAIN //	C:29178	A:2704	31882	0.084813	0	TRUE	C:28591	T:2	28593	6.99E-05	1	FALSE	1	104
442	SA214_19	SA214	19	56320311	19,563203	nonsense	NA		R90	SIGLEC9	19q13.41				DISULFID //	C:15454	T:1213	16667	0.072779	0	TRUE	C:24426	G:25	24451	0.001022	1	FALSE	1	49
443	SA214_19	SA214	19	57901480	19,579014	missense	neutral	0.795	N214D	ZNF611	19q13.41					T:10630	C:605	11235	0.05385	0	TRUE	T:12505	A:1	12506	8.00E-05	1	FALSE	2	12
444	SA214_20	SA214	20	18091151	20,180911	missense	medium	2.24	K411N	CSR2BP	20p11.23					G:17981	T:1848	19829	0.093197	0	TRUE	G:24459	T:10	24469	0.000409	1	FALSE	2	18
445	SA214_20	SA214	20	35269150	20,352691	missense	medium	2.36	E251K	RPN2	20q12-q13.1				TOPO_DON	G:7291	A:880	8171	0.107698	0	TRUE	G:32208	T:17	32225	0.000528	1	FALSE	2	1143
446	SA214_20	SA214	20	35921775	20,359217	missense	high	3.63	R485C	CTNBNB1	20q11.23-q12					C:11030	T:795	11825	0.06723	0	TRUE	C:28792	G:13	28805	0.000451	1	FALSE	2	88
447	SA214_20	SA214	20	42983716	20,429837	missense	medium	2.425	R269H	PABPC1L					DOMAIN //	G:20873	A:2158	23031	0.0937	0	TRUE	G:26344	T:3	26347	0.000114	1	FALSE	1	22
448	SA214_20	SA214	2	1E+08	2,1002732	missense	medium	2.2	R623C	LONRF2	2q11.2				DOMAIN //	G:17050	A:1208	18258	0.066163	0	TRUE	G:11880	A:2	11882	0.000168	1	FALSE	0	0
449	SA214_20	SA214	2	1.09E+08	2,1086425	missense	low	1.585	A18V	LIMS1	2q12.3-q13				DOMAIN //	G:8713	T:579	9292	0.062312	0	TRUE	C:10658	T:19	10677	0.00178	0.328955	FALSE	1	21
450	SA214_20	SA214	2	1.21E+08	2,1205161	missense	medium	3.45	D82N	EPBA1L5	2q14.2				DOMAIN //	G:34409	A:4640	39049	0.118825	0	TRUE	G:30903	A:8	30911	0.000259	1	FALSE	2	20
451	SA214_20	SA214	2	1.35E+08	2,1354613	missense	neutral	0.55	N532D	YSK4	2q21.3					T:17278	C:1202	18480	0.065043	0	TRUE	T:18418	A:3	18421	0.000163	1	FALSE	0	0
452	SA214_20	SA214	2	1.45E+08	2,1448724	missense	low	0.805	P937H	ZE82	2q22					A:17107	G:975	18082	0.053921	0	TRUE	A:15205	G:6	15211	0.000394	1	FALSE	1	59
453	SA214_20	SA214	2	1.77E+08	2,1766675	missense	medium	2.43	B09V	HOKD13	2q31.1			Cancer Rev	DNA_BIND	A:4155	G:824	4979	0.165495	0	TRUE	A:5521	C:3	5524	0.000343	1	FALSE	1	51
454	SA214_20	SA214	2	1.98E+08	2,1983589	missense	NA			BOLL	2q33					C:10772	T:850	11622	0.073137	0	TRUE	C:21220	G:35	21255	0.001647	0.127708	FALSE	0	0
455	SA214_20	SA214	2	2.01E+08	2,2012321	missense	medium	1.955	P1066S	AOX1	2q33					C:24043	T:2467	26510	0.093059	0	TRUE	C:29716	T:10	29726	0.000336	1	FALSE	1	8
456	SA214_20	SA214	2	2.02E+08	2,2018396	missense	medium	2.62	L54S	CASP8	2q33-q34			Cancer Cell	DOMAIN //	T:30447	C:2865	33312	0.086005	0	TRUE	T:28045	A:3	28048	0.000107	1	FALSE	1	46
457	SA214_20	SA214	2	2.07E+08	2,2067355	missense	low	1.72	A156V	EEF1B2	2q33-q34				HELIX //	15C:13603	T:946	14549	0.065022	0	TRUE	C:11425	A:12	11437	0.001049	1	FALSE	1	1336
458	SA214_20	SA214	2	2.18E+08	2,2184659	nonsense	NA		R117	TNS1	2q35-q36			Entrez Que	DOMAIN //	G:5257	A:519	5776	0.089855	0	TRUE	G:14026	A:4	14030	0.000285	1	FALSE	1	24
459	SA214_22	SA214	22	20649678	22,206496	missense	high	3.775	R308C	TOP3B	22q11.22			Entrez Query ::	Stability	G:7708	A:703	8411	0.083581	0	TRUE	G:16017	T:2	16019	0.000125	1	FALSE	2	17
460	SA214_22	SA214	22	23048687	22,230486	missense	low	1.525	K580T	SPECC1L	22q11.23				COILED //	A:21446	C:2088	23534	0.088723	0	TRUE	A:31316	G:2	31318	6.39E-05	1	FALSE	1	20
461	SA214_22	SA214	2	26852015	2,2685201	missense	low	1.18	D168N	C2orf18	2p23.3					G:8515	A:1744	10259	0.169997	0	TRUE	G:24812	A:7	24819	0.000282	1	FALSE	2	121
462	SA214_22	SA214	2																										

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC						
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func...Impa	FI.score	AI.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.pof	Ref.count	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase
485	SA216_2_1	SA216	2	1.77E+08	2,1768963	missense	medium	2.085	MS01	MTX2	2q31.1					G:24694	A:2089	26783	0.077997	0	TRUE	G:24335	T:31	24366	0.001272	0.02635	FALSE	1	1	50					
486	SA217_12	SA217	12	4525792	12,452579	nonsense	NA		S106	RAD51AP1	12p13.2-p13.1			Entrez Query :: Stabilit	C:1736	A:173	1909	0.090623	7.65E-221	TRUE	C:605	N:0	605	0	1	FALSE	1	1	13						
487	SA217_14	SA217	14	91979510	14,919795	missense	medium	3.26	I182M	SLC24A4	14q32.12				TOPO_DON	C:83492	T:18432	101924	0.180841	0	TRUE	C:534470	T:68	534538	0.000127	0.000127	FALSE	0	0	0					
488	SA217_17	SA217	17	7517849	17,751784	missense	medium	2.825	V272L	TP53	17p13.1	p.V272M,p.carcinoma	Cancer Cell	DNA_BIND	C:100718	A:84632	185350	0.456606	0	TRUE	C:268000	A:26	268026	9.70E-05	1	FALSE	3	16							
489	SA217_18	SA217	18	32552422	18,325524	missense	neutral	0	V863L	FHD03	18q12			COMPBIAS	G:529124	C:67688	596812	0.113416	0	TRUE	G:518163	T:86	518249	0.000166	1	FALSE	1	2							
490	SA217_2_6	SA217	2	68947132	2,6894713	missense	medium	2.39	H137R	BMP10	2p14			PROPEP //	T:264137	C:29329	293466	0.09994	0	TRUE	T:258379	G:138	258517	0.000534	1	FALSE	0	0							
491	SA218_10	SA218	10	1.14E+08	10,114214	missense	medium	2.62	S76R	VT1A	10q25.2			COILED //	A:13264	C:2099	15363	0.136627	0	TRUE	A:11687	C:21	11708	0.001794	0.237447	FALSE	2	14							
492	SA218_10	SA218	10	14856409	10,148564	missense	NA			FAM107B	10p13			C:4669	T:614	5283	0.116222	0	TRUE	C:9063	N:0	9063	0	1	FALSE	0	0								
493	SA218_10	SA218	10	847334920	10,8473349	missense	low	1.245	S581N	NRG3	10q22-q23			Entrez Que	TOPO_DON	C:14583	A:5332	19915	0.267738	0	TRUE	G:11444	N:0	11444	0	1	FALSE	0	0						
494	SA218_10	SA218	10	97806610	10,978066	missense	low	1.87	A148V	CNNJ	10pter-q26.12			C:50042	T:3139	53181	0.059025	0	TRUE	C:32108	G:2	32110	6.23E-05	1	FALSE	1	44								
495	SA218_11	SA218	11	1.24E+08	11,123521	missense	medium	2.375	A752V	LOH11CR2	11q23			C:13112	T:964	14076	0.068485	0	TRUE	C:14959	A:2	14961	0.000134	1	FALSE	1	26								
496	SA218_11	SA218	11	1.25E+08	11,125275	missense	medium	2.175	A274V	HYLS1	11q24.2			C:282	T:18	300	0.06	4.48E-20	TRUE	C:464	N:0	464	0	1	FALSE	2	7								
497	SA218_11	SA218	11	19858138	11,198581	missense	low	1.735	C220Y	NAV2	11p15.1			COMPBIAS	G:23704	A:2927	26631	0.10991	0	TRUE	G:20879	A:10	20889	0.000479	1	FALSE	0	0							
498	SA218_1_1	SA218	1	1.53E+08	1,1534489	missense	medium	2.69	R299P	MTX1	1q21			C:26190	C:4007	30197	0.132695	0	TRUE	C:22698	C:4	22702	0.000176	1	FALSE	0	0								
499	SA218_1_1	SA218	1	1.54E+08	1,1542943	missense	medium	2.57	R80C	MAPBPBP	1q22			C:12174	T:1594	13768	0.115776	0	TRUE	C:15808	T:5	15813	0.000316	1	FALSE	1	70								
500	SA218_1_1	SA218	1	1.54E+08	1,1544969	missense	low	0.845	R741Q	SMG5	1q21.2			Entrez Query :: Stabilit	C:11203	T:841	12044	0.069827	0	TRUE	C:12546	G:7	12553	0.000558	1	FALSE	1	102							
501	SA218_1_1	SA218	1	1.81E+08	1,1813631	missense	medium	1.965	P1026S	LAMC1	1q31			DISULFID //	C:12959	T:1327	14286	0.092888	0	TRUE	C:10190	T:5	10195	0.00049	1	FALSE	1	170							
502	SA218_1_1	SA218	1	2.23E+08	1,2225624	missense	medium	2.005	G172E	NVL	1q41-q42.2			C:6957	T:756	7713	0.098016	0	TRUE	C:3676	N:0	3676	0	1	FALSE	2	61								
503	SA218_1_1	SA218	1	2.3062153	1,2306215	missense	low	1.89	D283G	EPH82	1p36.1-p35			Cancer Rev	COMPBIAS	A:14067	A:1299	18346	0.233239	0	TRUE	A:13633	G:9	13642	0.00066	1	FALSE	1	10						
504	SA218_12	SA218	12	53054074	12,530540	missense	neutral	0	A10AD	ZNF385A	12q13.13			C:14046	T:2191	16237	0.134939	0	TRUE	G:15779	T:4	15783	0.000253	1	FALSE	1	104								
505	SA218_12	SA218	12	54767879	12,547678	missense	medium	2.36	G216A	ERBB3	12q13			Entrez Query	DISULFID //	G:15879	C:3360	19239	0.174645	0	TRUE	G:25192	A:3	25195	0.000119	1	FALSE	2	42						
506	SA218_12	SA218	12	75273860	12,752738	missense	low	1.61	D870E	OSBPL8	12q14			G:9471	T:1256	10727	0.117088	0	TRUE	G:4943	N:0	4943	0	1	FALSE	1	110								
507	SA218_12	SA218	12	89969298	12,899692	missense	neutral	0.235	A339T	KERA	12q22			DISULFID //	C:38062	T:6177	44239	0.139628	0	TRUE	C:32100	A:1	32101	3.12E-05	1	FALSE	0	0							
508	SA218_12	SA218	12	93251435	12,932514	nonsense	NA		R503	CDC41C	12q22			COILED //	G:12523	A:1606	14129	0.113667	0	TRUE	G:9541	A:4	9545	0.000419	1	FALSE	1	18							
509	SA218_13	SA218	13	1.08E+08	13,107679	nonsense	NA		L31	ABHD13	13q33.3			T:870	A:108	978	0.110429	3.35E-150	TRUE	T:542	N:0	542	0	1	FALSE	2	42								
510	SA218_1_3	SA218	1	32565189	1,3256518	missense	high	4.84	H140Y	HDAC1	1p34			Cancer Cell	REGION //	C:27154	T:2371	29525	0.080305	0	TRUE	C:30924	G:6	30930	0.000194	1	FALSE	1	119						
511	SA218_13	SA218	13	34948136	13,349481	missense	low	1.715	V47A	MA2B21L1	13q13			A:15661	G:3594	19255	0.186653	0	TRUE	A:18920	C:9	18929	0.000475	1	FALSE	0	0								
512	SA218_13	SA218	13	44666129	13,446661	missense	low	0.805	N192H	KCTD4	13q14.12			T:19640	G:3660	23300	0.157082	0	TRUE	T:15419	G:3	15422	0.000195	1	FALSE	0	0								
513	SA218_14	SA218	14	24113319	14,241133	missense	low	1.51	D189G	CTSG	14q11.2			DISULFID //	T:7516	C:439	7955	0.055185	0	TRUE	T:31805	G:22	31827	0.000691	1	FALSE	0	0							
514	SA218_14	SA218	14	35203711	14,352037	missense	medium	2.845	I1233G	GARNL1	14q13.2			T:18097	C:4216	22313	0.188948	0	TRUE	T:12765	A:1	12766	7.83E-05	1	FALSE	3	0								
515	SA218_14	SA218	14	60259862	14,602598	nonsense	NA		Y228	SIX4	14q23			DNA_BIND	A:3325	C:706	4031	0.175143	0	TRUE	A:9594	G:5	9599	0.000521	1	FALSE	1	2							
516	SA218_14	SA218	14	64577317	14,645773	missense	high	3.695	G250D	FNTB	14q23-q24			REPEAT //	G:22694	A:2316	25010	0.092603	0	TRUE	G:26465	A:9	26474	0.00034	1	FALSE	1	26							
517	SA218_14	SA218	14	67319292	14,673192	missense	medium	1.95	S1444C	ZFYVE26	14q24.1			T:23828	A:2602	26430	0.098449	0	TRUE	T:23036	G:19	23055	0.000824	1	FALSE	2	20								
518	SA218_15	SA218	15	29451622	15,294516	missense	NA		C232Y	KLF13	15q12			ZN_FING //	G:3632	A:1102	4734	0.232784	0	TRUE	G:15768	T:7	15775	0.000444	1	FALSE	2	57							
519	SA218_15	SA218	15	37855996	15,378559	missense	medium	2.175	L81	FSIP1	15q14			G:11986	T:931	12917	0.070206	0	TRUE	G:8145	T:6	8151	0.000736	1	FALSE	1	1								
520	SA218_15	SA218	15	40401467	15,404014	missense	medium	2.075	N417S	GANC	15q15.2			A:1937	G:294	2231	0.131779	0	TRUE	A:1386	C:1	1387	0.000721	1	FALSE	2	21								
521	SA218_15	SA218	15	64573871	15,645738	missense	NA			SNAPC5	15q22.31			G:22481	C:1732	24213	0.071532	0	TRUE	G:12961	T:5	12966	0.000386	1	FALSE	1	54								
522	SA218_15	SA218	15	70809049	15,708090	missense	low	1.355	A228T	BS54	15q22.3-q23			REPEAT //	G:12352	A:3132	15484	0.202273	0	TRUE	G:10267	A:4	10271	0.000229	1	FALSE	2	29							
523	SA218_1_6	SA218	1	62683514	1,6268351	missense	medium	1.95	G359R	USP1	1p31.3			Entrez Query :: Stabilit	G:16446	A:3024	19470	0.155316	0	TRUE	G:12738	A:8	12746	0.000628	1	FALSE	2	53							
524	SA218_16	SA218	16	2808783	16,280878	missense	medium	2.62	V121A	PRSS21	16p13.3			DISULFID //	T:11021	A:1276	12497	0.118108	0	TRUE	T:14063	A:3	14066	0.000213	1	FALSE	1	3							
525	SA218_16	SA218	16	71389946	16,713899	missense	low	1.33	T1379M	ZFH3	16q22.3-q23.1			ZN_FING //	G:21031	A:1411	22242	0.054447	0	TRUE	G:20929	T:5	20934	0.000239	1	FALSE	1	24							
526	SA218_1_7	SA218	1	70419480	1,7041948	missense	medium	2.79	D180H	LRRCA4	1p31.1			REPEAT //	C:3470	G:530	4000	0.1325	0	TRUE	C:7818	T:2	7820	0.000256	1	FALSE	1	34							
527	SA218_17	SA218	17	24055036	17,240550	missense	neutral	0.55	K254N	PROCA1	17q11.2			COMPBIAS	C:21289	G:4145	25434	0.162971	0	TRUE	C:21787	A:5	21792	0.000229	1	FALSE	1	5							
528	SA218_17	SA218	17	39830472	17,398304	missense	low	1.1	H1500R	GPATC8	17q21.31			T:12515	C:1961	14476	0.135466	0	TRUE	T:256	N:0	256	0	1	FALSE	1	33								
529	SA218_17	SA218	17	49255551	17,492555	missense	low	1.775	N535	KIF2B	17q22			A:17097	G:3811	20908	0.182275	0	TRUE	A:14342	C:13	14355	0.000906	1	FALSE	0	0								
530	SA218_17	SA218	17	59349000	17,593490	missense	low	1.04	R103H	GH1	17q24.2			Entrez Que	DISULFID //	C:43290	T:3003	46293	0.064869	0	TRUE	C:36191	T:8	36199	0.000221	1	FALSE	0	0						
531	SA218_17	SA218	17	64623162	17,646231	missense	high	4.645	G519D	ABCA6	17q24.3			DOMAIN //	C:21134	T:2298	23432	0.098071	0	TRUE	C:14815	T:15	14830												

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC		
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	Fi.score	AA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.pos	Ref.count.	Alt.count.T	Total.count	Alt.frequer	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.frequer	Binomial.te	Binomial.te	SVNMix2.C	REF.RNAse		
554	SA218_2_	SA218		2 60541329	2,6054132	missense	neutral	0.695	5741N	BCL11A	2p16.1			Cancer Rev	ZN_FING	//C:28851	T:1995	30846	0.064676	0	TRUE	C:23060	G:17	23077	0.000737	1	FALSE	1	18		
555	SA218_2_	SA218		2 86158581	2,8615858	missense	medium	3.165	H431R	POLR1A	2p11.2			Cancer Cell	Map Pathw	T:44844	C:3779	48623	0.07772	0	TRUE	T:30174	G:27	30201	0.000894	1	FALSE	1	64		
556	SA218_3_	SA218		3 10239385	3,1023938	missense	medium	3.35	P360H	IRAK2	3p25.3					DOMAIN //	C:11700	A:1624	13324	0.121885	0	TRUE	C:16805	A:42	16847	0.002493	1.66E-05	FALSE	1	20	
557	SA218_3_	SA218		3 1.23E+08	3,1228997	missense	low	1.04	K754R	GOLGB1	3q13					TOPO_DON	T:5527	C:1285	6812	0.188638	0	TRUE	T:3652	G:1	3653	0.000274	1	FALSE	2	58	
558	SA218_3_	SA218		3 1.42E+08	3,1416052	missense	medium	2.43	V120D	CLSTN2	3q23-q24					DOMAIN //	T:8027	G:4141	12168	0.340319	0	TRUE	T:15303	G:17	15320	0.00111	1	FALSE	1	3	
559	SA218_3_	SA218		3 1.44E+08	3,1435780	nonsense		NA	G933	XRN1	3q23						C:414	A:26	400	0.050901	6.84E-29	TRUE	C:202	N:0	202	0	1	FALSE	1	72	
560	SA218_3_	SA218		3 1.44E+08	3,1437493	missense	neutral	0.755	S1095L	ATR	3q22-q24					Entrez Query ::	Stabilit	G:25954	A:4581	30535	0.150025	0	TRUE	G:17884	A:4	17888	0.000224	1	FALSE	2	23
561	SA218_3_	SA218		3 1.5E+08	3,1500283	missense	medium	1.955	T9I	CPB1	3q24					SIGNAL //	C:16940	T:1369	18309	0.074772	0	TRUE	C:22659	A:1	22660	0.000104	1	FALSE	0	0	
562	SA218_3_	SA218		3 1.8E+08	3,1804347	missense	low	0.935	H1047R	PIK3CA	3q26.3	p.H1047R	carcinoma	Cancer Cell	DOMAIN //	A:4451	G:2054	6505	0.315757	0	TRUE	A:3316	C:2	3318	0.000603	1	FALSE	2	35		
563	SA218_3_	SA218		3 51942780	3,5194278	missense	low	1.71	V440I	RRP9	3p21.1					REPEAT //	C:11261	T:2277	13538	0.168193	0	TRUE	C:14200	A:5	14205	0.000352	1	FALSE	2	19	
564	SA218_4_	SA218		4 1.07E+08	4,1068672	missense	medium	2.425	G336V	GSTCD	4q24					G:18477	T:2141	20618	0.103841	0	TRUE	G:12481	A:1	12482	8.01E-05	1	FALSE	1	24		
565	SA218_4_	SA218		4 1.39E+08	4,1386704	missense	medium	2.33	P750S	PCDH18	4q31					TOPO_DON	G:30199	A:5212	35411	0.147186	0	TRUE	G:22207	A:4	22211	0.00018	1	FALSE	2	53	
566	SA218_4_	SA218		4 1.57E+08	4,1570495	missense	high	3.67	V126M	TD02	4q31-q32						G:18670	A:7092	25762	0.275289	0	TRUE	G:13045	A:1	13046	7.67E-05	1	FALSE	1	7	
567	SA218_4_	SA218		4 1.66E+08	4,1661818	missense	medium	2.245	L406F	TRIM60	4q32.3					DOMAIN //	C:22383	T:3733	26116	0.142939	0	TRUE	C:16274	A:4	16278	0.000246	1	FALSE	0	0	
568	SA218_4_	SA218		4 57044154	5,704415	missense	medium	2.265	I306M	SRP72	4q11					Entrez Query ::	Protein	A:985	Q	1074	0.082868	2.59E-112	TRUE	G:684	N:0	684	0	1	FALSE	1	217
569	SA218_4_	SA218		4 70395876	4,7039587	missense	neutral	-0.345	A98V	UTG284	4q13					G:16864	A:2667	19531	0.136552	0	TRUE	G:10072	A:4	10076	0.000397	1	FALSE	0	0		
570	SA218_5_	SA218		5 1.68E+08	5,1677695	missense	medium	2.25	R305H	WWC1	5q35.1					COILED //	G:23174	A:5377	28551	0.18833	0	TRUE	G:17590	A:8	17598	0.000455	1	FALSE	2	28	
571	SA218_5_	SA218		5 1.75E+08	5,1750432	missense	medium	2.76	V130A	HRH2	5q35.2					DISULFID	T:36551	C:6927	43478	0.159322	0	TRUE	T:36814	G:10	36824	0.000272	1	FALSE	1	9	
572	SA218_5_	SA218		5 1.79E+08	5,1791973	missense	neutral	0.345	P236H	LOC51149	5q35.3					G:18926	T:3735	22661	0.164821	0	TRUE	G:19094	A:8	19102	0.000419	1	FALSE	1	25		
573	SA218_5_	SA218		5 37057947	5,3705794	missense	medium	2.93	R1789L	NIPBL	5p13.2					REPEAT //	G:27148	T:4359	31507	0.13835	0	TRUE	G:19767	A:5	19772	0.000253	1	FALSE	1	66	
574	SA218_5_	SA218		5 64303310	5,6430331	missense	neutral	0.65	A356V	SDCCA10	5q12.3					COILED //	C:1463	T:365	1828	0.199672	0	TRUE	C:989	G:1	990	0.00101	1	FALSE	1	32	
575	SA218_5_	SA218		5 78362566	5,7836256	missense	high	3.63	R510P	DMGDH	5q14.1					C:13560	G:2036	15596	0.130546	0	TRUE	C:9578	A:1	9579	0.000104	1	FALSE	1	1		
576	SA218_5_	SA218		5 81644227	5,8164422	missense	medium	2.74	W58L	LOC92270	5q14.2					G:22659	T:3883	26542	0.146296	0	TRUE	G:25918	A:3	25921	0.000116	1	FALSE	1	10		
577	SA218_6_	SA218		6 1.14E+08	6,1140094	missense		NA		LOC728590						A:14872	G:1591	16463	0.096641	0	TRUE	A:10102	G:1	10103	9.90E-05	1	FALSE	0	0		
578	SA218_6_	SA218		6 1.18E+08	6,1177940	missense	low	0.885	V915I	ROS1	6q22			Cancer Rev	TOPO_DON	C:27439	T:3435	30874	0.111259	0	TRUE	C:21776	A:4	21780	0.000184	1	FALSE	3	0		
579	SA218_6_	SA218		6 1.68E+08	6,1680949	missense	neutral	-0.755	P1350L	MLLT4	6q27			Cancer Rev	COMPBIAS	C:5877	T:477	6354	0.075071	0	TRUE	C:4604	A:3	4607	0.000651	1	FALSE	2	35		
580	SA218_6_	SA218		6 41358164	6,4135816	missense	medium	1.995	P118H	TREM1	6p22.1					DOMAIN //	G:13135	T:2640	15775	0.167353	0	TRUE	G:27883	T:7	27890	0.000251	1	FALSE	1	37	
581	SA218_6_	SA218		6 69703225	6,6970322	missense	low	1.455	P321L	BAI3	6q12					DISULFID	//C:15241	T:2160	17401	0.124131	0	TRUE	C:10651	A:1	10652	9.39E-05	1	FALSE	0	0	
582	SA218_6_	SA218		6 74533233	6,7453323	missense	neutral	0.46	A455T	CD109	6q13					G:38826	A:5795	44585	0.129169	0	TRUE	G:25082	C:1	25083	3.99E-05	1	FALSE	2	124		
583	SA218_6_	SA218		6 84291047	6,8429104	missense	medium	2.705	R390C	PRSS53	6q14.2					DOMAIN //	C:18787	T:5849	24636	0.237417	0	TRUE	C:14307	T:8	14315	0.000559	1	FALSE	3	0	
584	SA218_6_	SA218		6 90662079	6,9066207	missense	neutral	0.55	D391N	GJA10	6q15-q16					TOPO_DON	G:41717	A:8341	50058	0.166627	0	TRUE	G:32204	A:2	32206	6.21E-05	1	FALSE	0	0	
585	SA218_7_	SA218		7 1098968	7,1098968	missense	low	1.735	I360V	GPFR	7p22.3					TOPO_DON	A:17146	G:1970	19116	0.103055	0	TRUE	A:20868	G:3	20871	0.000144	1	FALSE	1	1	
586	SA218_7_	SA218		7 1.21E+08	7,1214792	missense	medium	3.485	V2082H	PTPRZ1	7q31.3					Entrez Que	DOMAIN //	T:33745	C:5980	39725	0.150535	0	TRUE	T:28596	A:4	28600	0.00014	1	FALSE	2	4
587	SA218_7_	SA218		7 1.32E+08	7,1315101	missense	high	3.79	R1323W	PLXNA4						TOPO_DON	G:26354	A:4875	31229	0.156105	0	TRUE	G:20991	A:21	21012	0.000999	1	FALSE	0	0	
588	SA218_7_	SA218		7 1.4E+08	7,1399019	missense	low	1.1	R679M	DEDN2D4	7q34					DOMAIN //	C:13365	A:3677	17042	0.215761	0	TRUE	C:8770	T:1	8771	0.000114	1	FALSE	1	3	
589	SA218_7_	SA218		7 43625813	7,4362581	missense	medium	2.345	E219D	STK17A	7p12-p14					Entrez Que	DOMAIN //	G:10662	C:2815	13487	0.050457	0	TRUE	G:6564	A:3	6567	0.000457	1	FALSE	1	154
590	SA218_7_	SA218		7 44519633	7,4451963	missense	neutral	0.345	G1340C	NPC1L1	7p13					TOPO_DON	C:16467	A:3411	19878	0.171597	0	TRUE	C:26021	A:4	26025	0.000154	1	FALSE	0	0	
591	SA218_7_	SA218		7 44585676	7,4458567	missense	medium	3.065	V204D	TMED4	7p13					TRANSMEN	A:5751	T:796	6547	0.121582	0	TRUE	G:21165	G:6	21171	0.000283	1	FALSE	1	133	
592	SA218_7_	SA218		7 5727257	7,5727257	missense	low	1.1	R469H	RNF216	7p22.1	p.R526H	serous_carc	Cancer Cell	Map Pathw	C:50312	T:7561	57873	0.130648	0	TRUE	C:37916	A:6	37922	0.000158	1	FALSE	2	56		
593	SA218_8_	SA218		8 1.13E+08	8,1134230	missense	low	1.365	V2177I	CSMD3	8q23.3					DOMAIN //	C:22510	T:1243	23753	0.05233	0	TRUE	C:13485	A:2	13487	0.000148	1	FALSE	0	0	
594	SA218_8_	SA218		8 1.34E+08	8,1336538	missense	neutral	0.205	R442Q	LRRC6	8q24.22						C:14259	T:792	15051	0.052621	0	TRUE	C:7798	A:5	7803	0.000641	1	FALSE	2	8	
595	SA218_8_	SA218		8 22920757	8,2292075	missense	low	1.65	D352N	RHOBTB2	8p21.3					DOMAIN //	G:2363	A:1040	3403	0.030513	0	TRUE	G:15974	A:3	15977	0.000188	1	FALSE	1	9	
596	SA218_8_	SA218		8 39032400	8,3903240	missense	high	4.405	G515S	ADAM9	8p11.23					Entrez Que	COMPBIAS	G:20143	A:1123	21266	0.052807	0	TRUE	G:13257	T:3	13260	0.000226	1	FALSE	1	1977
597	SA218_8_	SA218		8 87295786	8,8729578	missense	neutral	0.55	I462N	SLC7A13	8q21.3					TOPO_DON	A:44296	T:7243	51539	0.140534	0	TRUE	A:33207	G:3	33210	9.03E-05	1	FALSE	0	0	
598	SA218_9_	SA218		9 1.06E+08	9,1059413	missense	high	3.685	D1136Y	SMC2	9q31.1					G:7779	T:781	8560	0.091238	0	TRUE	G:6511	C:1	6512	0.000154	1	FALSE	1	31		
599	SA218_9_	SA218		9 1.16E+08	9,1161437	missense	neutral	0.55	A1315V	AKNA	9q32					G:25726															

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	A4.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.pos	Ref.count.	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase	
623	SA219_16	SA219	16	23131953	16,231319	missense	neutral	0.36	D487E	SCNN1G	16p12				Entrez Query :: Stability	C:8925	A:6173	15098	0.408862	0	TRUE	C:10772	G:10	10782	0.000927	1	FALSE	0	0	
624	SA219_16	SA219	16	65789020	16,657890	missense	medium	2.045	E351O	E2F4	16q21-q22				Cancer Cell	REGION //	G:16574	C:6032	22606	0.266832	0	TRUE	G:23085	T:2	23087	8.66E-05	1	FALSE	2	98
625	SA219_16	SA219	16	79276470	16,792764	nonsense	NA		R28	CDV12	16q23.2					DOMAIN //	G:62756	A:13772	76528	0.17996	0	TRUE	G:72992	T:30	73022	0.000411	1	FALSE	1	7
626	SA219_16	SA219	16	9765918	16,976591	missense	medium	2.34	T995M	GRIN2A	16p13.2					TOPO_DON	G:36060	A:19276	55336	0.348345	0	TRUE	G:39647	A:17	39664	0.000429	1	FALSE	1	1
627	SA219_17	SA219	17	34817996	17,348179	missense	low	1.79	S1335C	MED1	17q12-q21.1					REGION //	G:10993	C:15356	26349	0.582793	0	TRUE	G:28767	T:14	28781	0.000486	1	FALSE	2	9
628	SA219_17	SA219	17	54142222	17,541422	nonsense	NA		R237	RAD51C	17q22-q23				Entrez Query :: Stability	C:854	T:1234	2088	0.590996	0	TRUE	C:1690	A:2	1692	0.001182	1	FALSE	2	13	
629	SA219_1_7	SA219	1	76552141	1,7655214	missense	neutral	0.55	V28I	ST6GALNA4	1p31.1					TOPO_DON	G:59606	A:7856	67462	0.116451	0	TRUE	G:66807	A:24	66831	0.000359	1	FALSE	1	2
630	SA219_17	SA219	17	6951346	17,695134	missense	low	1.28	L147I	ASGR2	17p					TOPO_DON	G:15877	T:3354	19231	0.174406	0	TRUE	G:39950	A:6	39956	0.000515	1	FALSE	1	1
631	SA219_17	SA219	17	70438573	17,704385	missense	neutral	0.76	F416L	OTOP2	17q25.1					C:15301	G:14809	30110	0.49183	0	TRUE	C:34662	G:29	34691	0.000836	1	FALSE	0	0	
632	SA219_17	SA219	17	7517824	17,751782	missense	high	3.965	R280K	TP53	17p13.1	p.R280G,p.	carcinoma	Cancer Cell	DNA_BIND	C:4911	T:5184	10095	0.513522	0	TRUE	C:8176	G:2	8178	0.000245	1	FALSE	2	35	
633	SA219_17	SA219	17	8135407	17,813540	missense	medium	3.23	S188L	SLC25A35	17p13.1					TRANSMEN	G:22954	A:26236	49190	0.53336	0	TRUE	G:55753	A:35	55788	0.000627	1	FALSE	1	3
634	SA219_1_8	SA219	1	82208723	1,8220872	nonsense	NA		Y953	LPNH2	1p31.1					TOPO_DON	C:21465	G:7698	29163	0.263965	0	TRUE	C:22069	T:2	22071	9.06E-05	1	FALSE	1	34
635	SA219_2_2	SA219	2	16606834	2,1660683	nonsense	NA		Q119	FAM49A	2p24.3					G:36823	A:6846	43669	0.15677	0	TRUE	G:30622	C:35	30657	0.001142	1	FALSE	1	66	
636	SA219_4_4	SA219	4	1.56E+08	4,1563549	missense	high	4.25	V136E	NPY2R	4q31					DISULFID //	T:27046	A:18667	45713	0.408352	0	TRUE	T:43878	G:29	43907	0.00066	1	FALSE	0	0
637	SA219_4_4	SA219	4	3487718	4,3487718	missense	medium	1.995	E253Q	LRPAP1	4p16.3					COILED //	C:12087	G:5083	17170	0.296204	0	TRUE	C:52590	G:67	52657	0.001272	0.833673	FALSE	2	48
638	SA219_4_4	SA219	4	5069526	4,5069526	missense	medium	2.125	V89L	CYT1L	4p16-p15					C:45220	G:7737	52957	0.1461	0	TRUE	C:73159	G:6	73165	8.20E-05	1	FALSE	1	13	
639	SA219_4_4	SA219	4	52623171	4,5262317	missense	low	1.39	D113V	ATP1A8	4q12					A:24182	T:4657	28839	0.161483	0	TRUE	A:38364	G:2	38366	5.21E-05	1	FALSE	1	6	
640	SA219_5_3	SA219	5	33917243	5,3391724	missense	low	1.3	T76R	ADAMTS12	5q35				PROPEP //	G:65987	C:9247	75234	0.12291	0	TRUE	G:62202	T:42	62244	0.000675	1	FALSE	1	48	
641	SA219_6_3	SA219	6	1.43E+08	6,1431161	missense	medium	1.95	L2362Q	HIVEP2	6q23-q24					A:32906	T:5246	38152	0.137503	0	TRUE	A:55602	G:13	55615	0.000234	1	FALSE	1	33	
642	SA219_6_3	SA219	6	24958910	6,2495891	missense	medium	2.815	R231Q	C6orf32	6p22.3-p21.32					C:23507	T:6087	29594	0.205684	0	TRUE	C:44020	T:3	44023	6.81E-05	1	FALSE	1	13	
643	SA219_7_7	SA219	7	1.08E+08	7,1075437	nonsense	NA		Q55	LAMB4	7q22-q31.2					DOMAIN //	G:63473	A:6043	69516	0.08693	0	TRUE	G:82928	T:124	83052	0.001493	0.001964	FALSE	0	0
644	SA219_7_7	SA219	7	1.26E+08	7,1259603	missense	medium	2.39	G772S	GRM8	7q31.3-q32.1					TOPO_DON	C:17241	T:3155	20396	0.154687	0	TRUE	C:22343	G:3	22346	0.000134	1	FALSE	0	0
645	SA219_7_8	SA219	7	86407292	7,8640729	missense	medium	2.9	P273S	KIAA1324L	7q21.12					TOPO_DON	G:16262	A:2902	19164	0.15143	0	TRUE	G:12450	C:2	12452	0.000161	1	FALSE	1	8
646	SA219_8_8	SA219	8	1.33E+08	8,1330847	missense	medium	2.445	T86V	EFRA3	8q24.22					A:66733	G:5678	72411	0.078414	0	TRUE	A:46240	C:84	46324	0.0001813	5.39E-05	FALSE	1	106	
647	SA219_8_8	SA219	8	1.39E+08	8,1392328	missense	low	1.445	L1033V	FAM135B	8q24.23					A:54065	C:11940	66005	0.180895	0	TRUE	A:73668	G:41	73709	0.000556	1	FALSE	0	0	
648	SA219_9_3	SA219	X	1.35E+08	X,1353077	missense	low	1.73	T2749N	PPR112	Xq26.3					TRANSMEN	C:18169	A:1880	20049	0.09377	0	TRUE	C:21663	A:2	21665	9.23E-05	1	FALSE	0	0
649	SA219_9_3	SA219	X	18734557	X,1873455	missense	low	1.155	A456E	PPEF1	Xp22.3-p22.1					REGION //	C:13787	A:2288	16075	0.142333	0	TRUE	C:23404	G:17	23421	0.000726	1	FALSE	1	11
650	SA219_9_3	SA219	X	34058110	X,3405811	missense	low	1.39	P736L	FAM47A	Xp21.1					G:71121	A:11410	82531	0.138251	0	TRUE	G:59585	C:5	59590	8.39E-05	1	FALSE	0	0	
651	SA219_9_4	SA219	X	49848296	X,4984829	missense	neutral	0.69	K88E	AKAP4	Xp11.2				Entrez Query :: Stability	T:42425	C:8103	50528	0.136267	0	TRUE	T:35936	G:29	35965	0.000806	1	FALSE	0	0	
652	SA220_10_1	SA220	10	17211676	10,172116	missense	low	0.805	R32K	CUBN	10p12.31					PROPEP //	C:14382	T:5136	19518	0.263142	0	TRUE	C:53988	A:6	53994	0.000111	1	FALSE	0	0
653	SA220_10_1	SA220	10	17622184	10,176221	nonsense	NA		R149S	MYO3A	10p11.1					C:82326	T:35073	117399	0.29875	0	TRUE	C:142094	G:28	142122	0.000197	1	FALSE	0	0	
654	SA220_1_1	SA220	1	1.55E+08	1,1551880	nonsense	NA		R587	ARHGEF11	1q21					G:70503	A:11872	82375	0.144121	0	TRUE	G:111268	A:9	111277	8.09E-05	1	FALSE	1	36	
655	SA220_18_1	SA220	18	18860204	18,188602	missense	NA		R867H	RBBP8	18q11.2				Entrez Query :: Stability	G:27998	A:8090	36088	0.224174	0	TRUE	G:38143	T:28	38171	0.000734	1	FALSE	2	50	
656	SA220_18_1	SA220	18	27683594	18,276835	missense	low	0.895	T1223K	KIAA1012	18q12.1					G:905	T:7797	1682	0.46195	0	TRUE	G:3907	T:1	3908	0.000256	1	FALSE	2	11	
657	SA220_19_1	SA220	19	10999550	19,109995	missense	high	4.485	F1102L	SMARCA4	19p13.2				Cancer Cell	DOMAIN //	C:20503	G:27046	47949	0.564058	0	TRUE	C:66540	T:11	66551	0.000165	1	FALSE	2	57
658	SA220_19_1	SA220	19	57319001	19,573190	missense	high	4.13	N42K	PNF616	19q13.33					DOMAIN //	G:46278	T:29123	75401	0.386242	0	TRUE	G:77121	A:4	77125	5.19E-05	1	FALSE	1	2
659	SA220_20_1	SA220	20	49523947	20,495239	missense	low	1.04	T562N	NFKATC2	20q13.2-q13.3					DOMAIN //	G:81718	T:21053	102771	0.204854	0	TRUE	G:92807	T:20	92827	0.000215	1	FALSE	1	1
660	SA220_21_1	SA220	21	30907935	21,309079	missense	NA		KRTAP6-1	KRTAP6-1	21q22.1					G:9755	A:17643	27398	0.643952	0	TRUE	G:48441	A:11	48452	0.000227	1	FALSE	0	0	
661	SA220_3_3	SA220	3	1.44E+08	3,1437067	missense	neutral	0.735	R1716S	ATR	3q22-q24					Entrez Query :: Stability	C:4640	G:619	5259	0.117703	0	TRUE	C:5030	A:3	5033	0.000596	1	FALSE	1	8
662	SA220_3_3	SA220	3	51644663	3,5164466	missense	high	3.78	R386H	RAD54L2	3p21.2				Cancer Cell	DOMAIN //	G:33343	A:17550	50893	0.344841	0	TRUE	G:47154	A:8	47162	0.00017	1	FALSE	2	2
663	SA220_3_4	SA220	3	64501813	3,6450181	missense	low	1.895	L1840S	ADAMTS9	3p14.3-p14.2					DOMAIN //	A:5560	C:3128	8688	0.360037	0	TRUE	A:11961	G:1	11962	8.36E-05	1	FALSE	1	3
664	SA220_3_7	SA220	3	71109798	3,7110979	missense	medium	2.05	P407A	FOXP1	3p14.1					Entrez Query :: Tumor	G:9987	C:7337	17324	0.423517	0	TRUE	G:52186	A:4	52190	7.66E-05	1	FALSE	2	5
665	SA220_3_7	SA220	3	77754076	3,7775407	missense	medium	2.075	Q1188R	ROBO2	3p12.3					TOPO_DON	A:80289	G:48587	128876	0.377006	0	TRUE	A:118571	G:11	118582	9.28E-05	1	FALSE	0	0
666	SA220_5_5	SA220	5	1.78E+08	5,1782424	missense	low	0.805	E129Q	ZNF354B	5q35.3					G:148	C:70	218	0.321101	2.04E-130	0	TRUE	G:414	N:0	414	0	1	FALSE	2	9
667	SA220_6_8	SA220	6	89873683	6,8987368	missense	high	4.07	R27C	SRP35	6q15					DOMAIN //	G:46979	A:23904	70883	0.337232	0	TRUE	G:75684	A:41	75725	0.000541	1	FALSE	2	6
668	SA222_1_1	SA222	1	1.55E+08	1,1545223	missense																								

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC		
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	A4.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.ref	Ref.count	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNAse		
692	SA224_11	SA224	11	20761831	11,207618	missense	medium	2.005	H72Y	NELL1	11p15.2-p15.1					C:7753	T:2299	10052	0.228711	0	TRUE	C:7843	A:2	7845	0.000255	1	FALSE	1	37		
693	SA224_1_1	SA224	1	12708540	1,1270854	missense	medium	1.995	K348M	AADACL3						A:19329	T:17928	37257	0.481198	0	TRUE	A:37721	G:9	37730	0.000239	1	FALSE	0	0		
694	SA224_1_1	SA224	1	1.52E+08	1,1524931	missense	low	0.975	Q616E	UBAP2L	1q21.3					C:27719	G:10218	37937	0.269341	0	TRUE	C:30332	T:4	30336	0.000132	1	FALSE	1	2253		
695	SA224_1_1	SA224	1	16232307	1,1623230	missense	medium	2.94	G662V	CLNKA	1p36					DOMAIN //	G:13711	T:6092	19803	0.30763	0	TRUE	G:18668	A:2	18670	0.000107	1	FALSE	1	2	
696	SA224_1_1	SA224	1	1.75E+08	1,1748312	missense	medium	1.995	R623H	PAPPA2	1q23-q25					DISULFID //	G:347	A:365	712	0.51264	0	TRUE	G:709	N:0	709	0	1	FALSE	1	2	
697	SA224_11	SA224	11	9976412	11,997641	nonsense	NA		Q318	SBF2	11p15.4					G:2663	A:1131	3794	0.298102	0	TRUE	G:4541	T:3	4544	0.00066	1	FALSE	1	34		
698	SA224_1_1	SA224	1	20374158	1,2037415	missense	neutral	0.04	F36L	PLA2G2C						G:20919	T:14601	35520	0.411064	0	TRUE	G:43346	A:5	43351	0.000115	1	FALSE	1	1		
699	SA224_12	SA224	12	1.23E+08	12,122864	missense	medium	2.28	L1072R	DNAH10	12q24.31					COILED //	T:28124	G:7272	35396	0.205447	0	TRUE	T:27114	G:3	27117	0.000111	1	FALSE	0	0	
700	SA224_12	SA224	12	63110124	12,631101	missense	low	1.05	S589N	XPOT	12q14.2					REGION //	G:46840	A:5293	52133	0.101529	0	TRUE	G:82254	A:9	82263	0.000109	1	FALSE	1	689	
701	SA224_1_1	SA224	1	33809721	1,3380972	missense	NA		R2654P	CSMD2	1p35.1-p34.3					DISULFID //	C:460	G:134	594	0.225589	4.30E-219	TRUE	C:364	N:0	364	0	1	FALSE	1	14	
702	SA224_13	SA224	13	51940435	13,519404	missense	neutral	-0.55	T501A	CKAP2						A:43668	G:11480	55148	0.208167	0	TRUE	A:50965	G:16	50981	0.000314	1	FALSE	1	94		
703	SA224_1_4	SA224	1	43420017	1,4342001	missense	low	1.865	P128R	WDR65	1p34.2					REPEAT //	C:21311	G:7562	28873	0.261906	0	TRUE	C:21478	G:17	21495	0.000791	1	FALSE	0	0	
704	SA224_14	SA224	14	99445518	14,994455	nonsense	NA		Y396	EML1	14q32					REPEAT //	C:22796	A:18759	41555	0.451426	0	TRUE	C:45222	A:17	45239	0.000376	1	FALSE	1	29	
705	SA224_16	SA224	16	3234278	16,323427	missense	low	1.61	R579H	MEFV	16p13.3					DOMAIN //	C:19806	T:8358	28164	0.296762	0	TRUE	C:41826	A:3	41829	7.17E-05	1	FALSE	1	10	
706	SA224_16	SA224	16	70167750	16,701677	missense	neutral	0.205	V241	TAT	16q22.1					C:12124	T:21766	33890	0.642254	0	TRUE	C:33971	T:3	33974	8.83E-05	1	FALSE	0	0		
707	SA224_17	SA224	17	16344499	17,1634449	missense	medium	2.32	D631N	SMYD4	17p13.3					C:24235	T:14140	38355	0.368661	0	TRUE	C:36422	G:23	36445	0.000631	1	FALSE	1	54		
708	SA224_17	SA224	17	24983814	17,249838	missense	medium	2.015	E815K	SSH2	17q11.2					Entrez Query :: Phosph	C:1731	1884	0.080149	6.02E-175	TRUE	C:5615	G:4	5619	0.000712	1	FALSE	1	20		
709	SA224_17	SA224	17	71166043	17,711660	missense	low	0.84	R360L	RECQL5	17q25.2-q25.3					Entrez Que	DOMAIN //	C:8178	A:13621	21799	0.624845	0	TRUE	C:35395	T:6	35401	0.000169	1	FALSE	1	91
710	SA224_17	SA224	17	75972261	17,759722	missense	medium	2.32	H827D	RNF213	17q25.3					C:8098	G:4732	12830	0.368823	0	TRUE	C:8072	G:8	8080	0.00099	1	FALSE	1	187		
711	SA224_18	SA224	18	27945812	18,279458	missense	low	1.67	E70Q	RNF138	18q12.1					G:5670	C:1550	7220	0.214681	0	TRUE	G:7205	T:4	7209	0.000555	1	FALSE	1	65		
712	SA224_1_9	SA224	1	95065707	1,9506570	missense	neutral	0	R112L	SLC44A3	1p21.3					G:27205	T:20448	47653	0.421902	0	TRUE	G:45745	A:44	45789	0.000961	1	FALSE	1	49		
713	SA224_2_1	SA224	2	1.84E+08	2,1836685	missense	high	4.4	P189T	DUSP19	2q32.1					Entrez Que	DOMAIN //	C:35	A:41	76	0.539474	4.71E-86	TRUE	C:67	N:0	67	0	1	FALSE	1	13
714	SA224_22	SA224	22	29305777	22,293057	nonsense	NA		K439	PE51	22q12.1					Entrez Query :: Stabilit	T:13470	A:11943	25413	0.469956	0	TRUE	T:37346	G:37	37383	0.00099	1	FALSE	1	320	
715	SA224_3_1	SA224	3	1.26E+08	3,1258759	missense	medium	2.34	V2341L	ICALRN	3q21.1-q21.2					DOMAIN //	G:20760	T:3372	24132	0.139731	0	TRUE	G:57817	T:23	57840	0.000398	1	FALSE	1	84	
716	SA224_3_1	SA224	3	1.5E+08	3,1499421	missense	high	3.79	L197R	AGTR1	3q21-q25					TRANSMEN	T:22606	G:7626	30232	0.252249	0	TRUE	T:21399	G:8	21407	0.000374	1	FALSE	1	3	
717	SA224_3_4	SA224	3	4684132	3,4684132	missense	medium	2.375	I595M	ITPR1	3p26-p25					TOPO_DON	C:55541	G:13744	69285	0.198369	0	TRUE	C:70210	G:20	70230	0.000285	1	FALSE	1	13	
718	SA224_4_1	SA224	4	1.26E+08	4,1264611	missense	medium	2.14	V1386H	FAT4	4q28.1					Entrez Que	DOMAIN //	T:14958	C:5446	20404	0.266908	0	TRUE	T:18106	G:11	18117	0.000607	1	FALSE	1	4
719	SA224_4_1	SA224	4	1.3E+08	4,1300027	missense	low	0.975	Q482E	PHF17	4q26-q27					Entrez Query :: Tumor	C:43122	G:17556	60678	0.289331	0	TRUE	C:74177	T:8	74185	0.000108	1	FALSE	1	39	
720	SA224_4_1	SA224	4	1613089	4,1613089	missense	low	1.59	T315I	FAM53A	4p16.3					G:5455	A:9805	15260	0.642529	0	TRUE	G:15154	N:0	15154	0	1	FALSE	1	13		
721	SA224_5_1	SA224	5	1.58E+08	5,1580718	missense	low	0.97	A495T	EBF1	5q34					COMPBias	C:23207	T:8204	31411	0.261182	0	TRUE	C:35458	T:23	35481	0.000648	1	FALSE	1	25	
722	SA224_5_4	SA224	5	40889632	5,4088963	missense	neutral	0.55	R184K	CARD6	5p13.1					G:36918	A:15932	52850	0.301457	0	TRUE	C:66863	A:35	66898	0.000523	1	FALSE	1	13		
723	SA224_5_4	SA224	5	61035468	5,6103546	missense	neutral	0	P82S	FLJ37543	5q12.1					C:450	T:155	605	0.256198	3.58E-263	TRUE	C:433	T:1	434	0.002304	1	FALSE	0	0		
724	SA224_6_1	SA224	6	1875399	6,1875399	missense	neutral	0.055	E236D	GMD5	6p25					T:54306	A:18282	72588	0.25186	0	TRUE	T:60643	G:9	60652	0.000148	1	FALSE	1	107		
725	SA224_7_1	SA224	7	1E+08	7,1004717	missense	neutral	0	S3439P	MUC17	7q22.1					COMPBias	T:18489	C:4475	22964	0.19487	0	TRUE	T:13902	C:8	13910	0.000575	1	FALSE	0	0	
726	SA224_7_1	SA224	7	1.51E+08	7,1508127	missense	high	4.13	D60H	RHEB	7q36					MUTAGEN	C:17580	G:9918	27498	0.360681	0	TRUE	C:17691	A:2	17693	0.000113	1	FALSE	1	402	
727	SA224_7_9	SA224	7	93885039	7,9388503	missense	medium	3.45	E644G	COL1A2	7q22.1					Cancer Review :: Mitel	A:60282	G:15508	75790	0.206418	0	TRUE	A:63628	G:11	63639	0.000173	1	FALSE	1	2875	
728	SA224_9_1	SA224	9	1.07E+08	9,1066220	missense	medium	3.27	L1021F	ABCA1	9q31.1					DOMAIN //	C:7711	G:2635	10346	0.254688	0	TRUE	C:7140	A:7	7147	0.000979	1	FALSE	1	28	
729	SA224_9_1	SA224	9	1.38E+08	9,1375182	nonsense	NA		L701	ICALO649	9q34.3					T:6856	G:1515	8371	0.180982	0	TRUE	T:20186	G:20	20206	0.00099	1	FALSE	1	33		
730	SA224_X_1	SA224	X	1.05E+08	X,1050398	missense	low	1.1	Q506H	NRK	Xq22.3					COMPBias	G:41062	C:21467	62529	0.343313	0	TRUE	G:48033	T:20	48053	0.000416	1	FALSE	1	1	
731	SA224_X_1	SA224	X	56608306	X,5660830	missense	medium	3.105	Q425H	UBQLN2	Xp11.23-p11.1					G:28164	C:26497	54661	0.484751	0	TRUE	G:53269	T:5	53274	9.39E-05	1	FALSE	1	566		
732	SA224_X_9	SA224	X	9824322	X,9824322	missense	low	0.9	G792S	SHROOM2	Xp22.3					G:13625	A:2586	16211	0.159521	0	TRUE	G:28654	A:4	28658	0.00014	1	FALSE	1	21		
733	SA225_10	SA225	10	1.02E+08	10,102239	missense	low	0.975	A956G	SEC31B	10q24.31					COMPBias	G:5887	C:4587	10474	0.437942	0	TRUE	G:37567	A:1	37568	2.66E-05	1	FALSE	1	12	
734	SA225_10	SA225	10	1.03E+08	10,102722	missense	low	0.805	R25T	SEMA4G	10q24.31					TOPO_DON	G:8276	C:6352	14628	0.434236	0	TRUE	G:22764	A:5	22769	0.00022	1	FALSE	2	2	
735	SA225_1_1	SA225	1	1.5E+08	1,1504582	missense	neutral	0	G818R	HRNR	1q21.3					REPEAT //	C:4408	G:3532	7940	0.444836	0	TRUE	C:14729	G:3	14732	0.000204	1	FALSE	0	0	
736	SA225_1_1	SA225	1	1.52E+08	1,1523805	missense	low	1.385	N177K	NUP210L	1q21.3					G:5616	T:4316	9932	0.434555	0	TRUE	G:6029	T:2	6031	0.000332	1	FALSE	0	0		
737	SA225_1_1	SA225	1	1.53E+08	1,1532735	missense	low	1.87	W28C	DCST1	1q21.3					TOPO_DON	G:7965	C:4927	12892	0.382175	0	TRUE	G:10262	A:6							

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	Fi.score	AA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.ref	Pos.count	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count.T	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.RNase	SVNMix2.C	REF.RNase
761	SA225_20	SA225	20	31093466	20,31093466	nonsense		NA	S391	BPLI3	20q11.21					C:14281	A:41587	55868	0.74438	0	TRUE	C:54264	G:21	54285	0.000387	1	FALSE	0	0	
762	SA225_2_1	SA225	2	1.2E+08	2,1201549	missense	medium	1.95	R14T	TMEM177						G:9868	C:6996	16864	0.414848	0	TRUE	G:20027	A:7	20034	0.000349	1	FALSE	2	4	
763	SA225_2_1	SA225	2	1.63E+08	2,1627103	missense	low	1.12	G128R	GCG	2q36-q37				PEPTIDE //	C:12590	G:9127	21717	0.42027	0	TRUE	C:17317	A:5	17322	0.000289	1	FALSE	0	0	
764	SA225_2_1	SA225	2	1.79E+08	2,1792251	missense		NA		TTN	2q31					T:5874	C:5369	11243	0.477542	0	TRUE	T:9422	C:6	9428	0.000636	1	FALSE	0	0	
765	SA225_2_2	SA225	2	21084898	2,21084898	missense	medium	2.075	S2783T	APOB	2p24-p23					A:8198	T:5301	13499	0.392696	0	TRUE	A:14959	G:4	14963	0.000267	1	FALSE	0	0	
766	SA225_2_2	SA225	22	15453358	22,15453358	missense	neutral	0	E28G	CCT8L2	22q11.1					T:3017	C:15639	18656	0.838283	0	TRUE	T:15388	C:14	15402	0.000909	1	FALSE	0	0	
767	SA225_2_2	SA225	22	16443895	22,16443895	missense	medium	2.91	N38I	SLC25A18	22q11.2				REPEAT //	A:1840	T:13198	15038	0.877643	0	TRUE	A:10429	G:1	10430	9.59E-05	1	FALSE	3	0	
768	SA225_2_2	SA225	2	70018875	2,70018875	missense	medium	2.36	K207N	MXD1	2p13-p12			Entrez Query //	G:6487	T:7805	14292	0.54611	0	TRUE	G:18231	T:2	18233	0.00011	1	FALSE	2	17		
769	SA225_2_2	SA225	2	74502955	2,74502955	missense	medium	2.075	O56L	WDR54	2p13.1					A:3194	T:2642	5836	0.452707	0	TRUE	A:39597	G:7	39604	0.000177	1	FALSE	2	21	
770	SA225_2_2	SA225	2	96648938	2,96648938	missense	low	1.69	A183G	KIAA1310	2p12-p11.2					G:22645	C:34972	57617	0.606974	0	TRUE	G:58314	A:11	58325	0.000189	1	FALSE	2	47	
771	SA225_3_1	SA225	3	1.01E+08	3,1014966	missense	medium	3.49	L204V	TBC1D23	3q12.1-q12.2				DOMAIN //	C:1703	G:1411	3114	0.453115	0	TRUE	C:2776	A:1	2777	0.00036	1	FALSE	2	79	
772	SA225_3_1	SA225	3	1.24E+08	3,1239202	missense	low	0.895	I1511N	PARP14	3q21.1					T:37760	A:17840	55600	0.320863	0	TRUE	T:44473	G:7	44480	0.000157	1	FALSE	1	38	
773	SA225_3_1	SA225	3	1.75E+08	3,1754814	missense	low	1.79	L739V	NLGN1	3q26.31				TOPO_DON	C:16969	G:13347	30316	0.440263	0	TRUE	C:37126	T:7	37133	0.000189	1	FALSE	1	2	
774	SA225_3_1	SA225	3	1.93E+08	3,1926618	silent		NA		PCP2						G:17987	C:11765	29752	0.395436	0	TRUE	G:29153	T:7	29160	0.00024	1	FALSE	0	0	
775	SA225_3_1	SA225	3	1.98E+08	3,1981506	missense	high	3.645	V44F	NCBP2	3q29				BINDING //	C:8208	A:2923	11131	0.2626	0	TRUE	C:17584	G:2	17586	0.000114	1	FALSE	2	123	
776	SA225_3_1	SA225	3	9451095	3,9451095	missense	low	1.355	E85D	SETD5	3p25.3					A:6225	T:13856	20081	0.690005	0	TRUE	A:22591	G:3	22594	0.000133	1	FALSE	2	10	
777	SA225_4_1	SA225	4	13225330	4,13225330	missense	low	1.04	E254D	FAM44A	4p16.1					C:19860	G:12400	32260	0.384377	0	TRUE	C:49145	A:10	49155	0.000203	1	FALSE	2	48	
778	SA225_4_1	SA225	4	1.39E+08	4,1386709	missense		NA	R582H	PCDH18	4q31				CARBOHYD	C:8641	T:18463	27104	0.681191	0	TRUE	C:27028	T:8	27036	0.000296	1	FALSE	1	7	
779	SA225_4_1	SA225	4	37528239	4,37528239	nonsense		NA	C484	PGM2	4p14					C:478	A:389	867	0.448674	0	TRUE	C:995	G:2	997	0.002006	1	FALSE	1	127	
780	SA225_5_1	SA225	5	6676385	5,6676385	missense	medium	3.085	R160P	NSUN2	5p15.31					C:4453	G:12439	16892	0.736384	0	TRUE	C:21072	T:6	21078	0.000285	1	FALSE	3	17	
781	SA225_6_1	SA225	6	1.17E+08	6,1172208	missense	medium	3.185	G629V	GPRC6A	6q22.2				TOPO_DON	C:15098	A:20262	35360	0.57302	0	TRUE	C:25457	G:25	25482	0.000981	1	FALSE	0	0	
782	SA225_6_1	SA225	6	44500287	6,44500287	missense	medium	3.3	A520P	CDC5L	6p21				REGION //	G:21	C:61	82	0.743902	2.50E-133	0	TRUE	G:173	N:0	173	0	1	FALSE	3	12
783	SA225_6_1	SA225	6	7526785	6,7526785	missense	medium	1.955	Q1788R	DSP	6p24			Cancer Cell	REGION //	A:4279	G:14891	19170	0.776787	0	TRUE	A:14163	G:12	14175	0.000847	1	FALSE	3	1	
784	SA225_7_1	SA225	7	1E+08	7,1004733	missense	neutral	0	K3989N	MUC17	7q22.1				TOPO_DON	G:3293	C:14478	17771	0.814698	0	TRUE	G:26269	T:21	26290	0.000799	1	FALSE	0	0	
785	SA225_7_1	SA225	7	5293987	7,5293987	missense	medium	1.95	G5E	SLC29A4	7p22.1				TOPO_DON	G:300	A:279	579	0.481865	0	TRUE	G:600	N:0	600	0	1	FALSE	2	1	
786	SA225_7_1	SA225	7	7196685	7,7196685	missense		NA	P13S	PSCD3	7p22.1					G:306	A:347	653	0.531394	0	TRUE	G:642	N:0	642	0	1	FALSE	2	9	
787	SA225_8_1	SA225	8	1.46E+08	8,1461277	missense	low	1.545	D409Y	ZNFX16	8q24				ZN_FING	C:35878	A:26069	61947	0.420827	0	TRUE	C:55595	G:55	55650	0.000988	1	FALSE	2	27	
788	SA225_8_1	SA225	8	1.46E+08	8,1461423	missense	low	0.975	E10K	CZNF16	8q24					C:4336	T:19886	24222	0.820989	0	TRUE	C:32257	A:10	32267	0.00031	1	FALSE	2	3	
789	SA225_8_1	SA225	8	41698857	8,41698857	missense	medium	2.88	H284Q	ANK1	8p11.1				REGION //	G:25873	C:10893	36766	0.296279	0	TRUE	G:32492	T:3	32495	9.23E-05	1	FALSE	2	3	
790	SA225_9_1	SA225	9	1.15E+08	9,1148519	missense	low	1.5	K47N	ZFP37	9q32				DOMAIN //	C:8199	A:46552	54751	0.850249	0	TRUE	C:56033	A:5	56038	8.92E-05	1	FALSE	3	0	
791	SA225_9_1	SA225	9	1.34E+08	9,1342115	missense	medium	1.935	F106S	SETX	9q34.13					A:3146	G:7747	10893	0.711191	0	TRUE	A:10907	T:1	10908	9.17E-05	1	FALSE	2	3	
792	SA225_9_1	SA225	9	99173776	9,99173776	nonsense		NA	E1512	KIAA1529	9q22.33					G:1883	T:9634	11517	0.836503	0	TRUE	G:10566	A:2	10568	0.000189	1	FALSE	3	0	
793	SA225_X_1	SA225	X	1.02E+08	X,1015112	silent		NA		NXF2B						C:13731	T:8655	22386	0.386626	0	TRUE	C:20651	A:3	20654	0.000145	1	FALSE	0	0	
794	SA225_X_1	SA225	X	1.18E+08	X,1181416	missense	neutral	0	S149F	KIAA1210						G:17	A:33	50	0.66	5.57E-69	0	TRUE	G:68	N:0	68	0	1	FALSE	0	0
795	SA225_X_1	SA225	X	21665610	X,21665610	missense		NA		SMXP	Xp22.1					C:33146	G:11890	45036	0.264011	0	TRUE	C:29447	A:20	29467	0.000679	1	FALSE	2	1	
796	SA225_X_1	SA225	X	46919433	X,46919433	missense	medium	2.085	Q192E	RFM10	Xp11.23				DOMAIN //	C:3435	G:3495	7523	0.464575	0	TRUE	C:12778	A:5	12783	0.000391	1	FALSE	1	119	
797	SA225_X_1	SA225	X	53294130	X,53294130	missense	low	1.185	E815Q	IQSEC2					DOMAIN //	C:27547	G:18459	46006	0.40123	0	TRUE	C:42278	A:6	42284	0.000142	1	FALSE	2	10	
798	SA226_10_1	SA226	10	27375442	10,27375442	missense	neutral	0	O610E	ANKRD26	10pter-q22.1					G:8705	C:1315	10020	0.131238	0	TRUE	G:8017	T:4	8021	0.000499	1	FALSE	1	68	
799	SA226_1_1	SA226	1	1.52E+08	1,1524737	missense	neutral	0.345	S116A	UBAP2L	1q21.3					T:435955	G:187929	623884	0.301224	0	TRUE	T:585038	G:62	585100	0.000106	1	FALSE	1	484	
800	SA226_15_1	SA226	15	71641330	15,71641330	missense	low	1.62	N391D	NPTN	15q22				TOPO_DON	T:945062	C:83993	1029055	0.081621	0	TRUE	T:922527	G:60	922587	6.50E-05	1	FALSE	1	307	
801	SA227_10_1	SA227	10	1.28E+08	10,128182	missense	low	1.01	E276Q	C10orf90	10q26.2					C:40367	G:7505	47872	0.156772	0	TRUE	C:51626	G:41	51667	0.000794	1	FALSE	0	0	
802	SA227_10_1	SA227	10	89682759	10,89682759	missense	medium	1.94	Y88C	PTEN	10q23.3	p.Y88fs*3	gastricytoma	Cancer Cell	DOMAIN //	A:9491	G:17764	27255	0.65177	0	TRUE	A:28529	C:2	28531	7.01E-05	1	FALSE	2	2	
803	SA227_10_1	SA227	10	89707599	10,89707599	missense	medium	2.51	F215S	PTEN	10q23.3	p.F215fs*6	endometriosis	Cancer Cell	DOMAIN //	T:63	C:94	157	0.598726	6.80E-203	0	TRUE	T:166	G:1	167	0.005988	1	FALSE	2	13
804	SA227_12_1	SA227	12	29488415	12,29488415	missense	neutral	0.55	E983Q	OVCH1	12p11.22					C:13503	G:1499	15002	0.09992	0	TRUE	C:13798	A:8	13806	0.000579	1	FALSE	0	0	
805	SA227_14_1	SA227	14	43659419	14,43659419	missense		NA		LOC645086						T:35558	G:15263	50821	0.300329	0	TRUE	T:44963	G:37	45000	0.000822	1	FALSE	0	0	
806	SA227_16_1	SA227	16	75081152	16,75081152	missense		NA		CNTNAP4	16q23.1					A:27856	T:37336	65192	0.572708	0	TRUE	A:74333	G:9	74342	0.000121	1	FALSE	0	0	
807	SA227_17_1	SA227	17	36202242	17,36202242	missense	low	1.39	M453T	KRT28	17q21.2				REGION //	A:7540	G:272													

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.pos	Ref.count	Alt.count	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count	Alt.count	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNAseq	
830	SA229_12	SA229		12	14727385	12,1472733	missense	medium	2.585	L157I	GUCY2C	12q12		Entrez Query	TOPO_DON	A:893	T:83	976	0.085041	6.68E-100	TRUE	A:1134	N:0	1134	0	1	FALSE	0	0	
831	SA229_12	SA229		12	44607160	12,446071	missense	low	0.975	S86CA	SFRS2IP	12q13.11		Entrez Query	COMPBIAS	G:45992	C:13349	59341	0.224954	0	TRUE	G:27592	A:1	27593	3.62E-05	1	FALSE	2	17	
832	SA229_12	SA229		12	4790863	12,479086	nonsense		NA	Y46S	KCNAB6	12p13				G:9056	A:1810	10866	0.166575	0	TRUE	C:19837	A:3	19840	0.000151	1	FALSE	0	0	
833	SA229_12	SA229		12	54954863	12,549548	missense	medium	2.64	R329G	CS	12q13.2-q13.3				G:15556	C:4359	19915	0.21888	0	TRUE	G:18110	A:5	18115	0.000276	1	FALSE	2	2	
834	SA229_12	SA229		12	63371582	12,633715	missense	low	1.83	T175A	RASSF3	12q14.2		Entrez Query	DOMAIN	A:61731	G:17560	79291	0.221463	0	TRUE	A:55412	G:18	55430	0.000325	1	FALSE	1	3	
835	SA229_12	SA229		12	8867143	12,886714	missense	low	1.245	V54G	A2ZML1	12p13.31				T:95599	G:21081	116680	0.180674	0	TRUE	T:102708	C:16	102724	0.000156	1	FALSE	1	8	
836	SA229_13	SA229		13	47937162	13,479371	nonsense		NA	E747	RB1	13q14.2		Cancer Cell	REGION	G:55964	T:25177	81141	0.310287	0	TRUE	G:68125	T:34	68159	0.000499	1	FALSE	0	0	
837	SA229_14	SA229		14	93489508	14,934895	nonsense		NA	Q145	ASB2	14q31-q32				REPEAT	G:38109	A:40310	78419	0.514034	0	TRUE	G:70976	T:8	70984	0.000113	1	FALSE	1	1
838	SA229_16	SA229		16	24866364	16,248663	missense	high	3.775	M394T	ARHGAP17	16p12.1				DOMAIN	A:129881	G:26450	156331	0.169192	0	TRUE	A:120306	C:154	120460	0.001278	0.144416	FALSE	1	17
839	SA229_16	SA229		16	46956839	16,469568	missense		NA	SIH1	16q12					C:137	G:32	169	0.189349	3.29E-50	TRUE	C:159	N:0	159	0	1	FALSE	3	0	
840	SA229_16	SA229		16	54074460	16,540744	missense	medium	2.545	R98W	MMP2	16q13-q21		Entrez Query	PROPEP	C:50930	T:20273	71203	0.284721	0	TRUE	C:143352	T:82	143434	0.000572	1	FALSE	1	44	
841	SA229_16	SA229		16	55971065	16,559710	missense	low	1.7	T30M	CX3CL1	16q13				REGION	C:157701	T:54245	211946	0.255938	0	TRUE	C:173122	G:115	173237	0.000664	1	FALSE	1	4
842	SA229_16	SA229		16	66665518	16,666655	missense	low	1.83	Q297H	DUS2L	16q22.1				G:119790	T:35068	154858	0.226453	0	TRUE	G:149805	T:79	149884	0.000527	1	FALSE	2	16	
843	SA229_17	SA229		17	17016749	17,170167	missense	medium	2.775	M775R	M-RIP	17p11.2				REGION	T:71693	G:10399	82092	0.126675	0	TRUE	T:57986	C:9	57995	0.000155	1	FALSE	2	1
844	SA229_17	SA229		17	3511754	17,351175	missense		NA	N553I	CDC6	17q21.31		Entrez Query :: Protein	A:41333	T:20893	62226	0.33576	0	TRUE	A:37944	C:16	37960	0.000421	1	FALSE	1	15		
845	SA229_17	SA229		17	64411209	17,644112	missense	neutral	-0.21	A769S	ABCBA8	17q24				C:101933	A:24663	126596	0.194817	0	TRUE	C:80117	A:10	80127	0.000125	1	FALSE	0	0	
846	SA229_18	SA229		18	28603783	18,286037	missense	low	1.525	A257V	KLHL14	18q12.1				G:9866	A:2282	12148	0.18785	0	TRUE	G:86417	A:96	86513	0.00111	1	FALSE	0	0	
847	SA229_2	SA229		2	1.02E+08	2,1023309	missense	low	1.04	I355M	IL1RL1	2q12				TOPO_DON	T:340	G:123	463	0.265659	2.48E-213	TRUE	T:578	N:0	578	0	1	FALSE	0	0
848	SA229_2	SA229		2	1.79E+08	2,1793434	missense		NA	TTN	2q31	p.12725M	ductal_carcinoma			C:95467	G:20051	115518	0.173575	0	TRUE	C:97946	A:62	98008	0.000633	1	FALSE	0	0	
849	SA229_2	SA229		2	2.19E+08	2,2190831	missense	neutral	0	V291I	USP37	2q35				C:5428	T:1938	7366	0.263101	0	TRUE	C:9383	A:5	9388	0.000533	1	FALSE	0	0	
850	SA229_22	SA229		22	33811504	22,338115	missense	neutral	0.205	P186A	ISX	22q12.3				C:69742	G:45348	115090	0.394022	0	TRUE	C:113529	G:131	113660	0.001153	1	FALSE	0	0	
851	SA229_22	SA229		22	45159217	22,451592	missense	medium	2.095	N2257I	CCLSR1	22q13.31				REPEAT	T:55327	A:38928	94255	0.413007	0	TRUE	T:69589	G:99	69688	0.001421	0.038472	FALSE	2	4
852	SA229_2	SA229		2	44024471	2,4402447	missense	low	1.845	S788F	LRPPRC	2p21		Cancer Cell	REPEAT	G:3825	A:2264	6089	0.371818	0	TRUE	G:5301	A:1	5302	0.000189	1	FALSE	2	9	
853	SA229_3	SA229		3	17230831	3,1723083	missense	neutral	0.69	V542I	TBC1D5	3p24.3				MOD_RES	C:46312	G:34147	80459	0.424402	0	TRUE	C:58166	A:8	58174	0.000138	1	FALSE	0	0
854	SA230_1	SA230		1	1.57E+08	1,1569107	missense	medium	2.845	R448W	SPTA1	1q21				REPEAT	G:93168	A:23869	117037	0.203944	0	TRUE	G:65991	A:7	65998	0.000106	1	FALSE	0	0
855	SA230_1	SA230		1	25657517	1,2565751	missense	low	1.67	N233A	TMEM57	1p36.11	1p36.11			A:15921	G:6158	22079	0.278908	0	TRUE	A:1105	N:0	1105	0	1	FALSE	2	11	
856	SA230_1	SA230		1	26266481	1,2626648	missense	low	1.87	T131N	TMEM67	1p34-p33				ZN_FING	G:66817	T:19860	86677	0.229127	0	TRUE	G:155122	T:100	155222	0.000644	1	FALSE	1	1
857	SA230_1	SA230		1	26674204	1,2667420	missense		NA		HMGN2	1p36.1				A:19340	G:2143	21483	0.099753	0	TRUE	A:647	C:1	648	0.001543	1	FALSE	1	93	
858	SA230_14	SA230		14	31631014	14,316310	missense	neutral	0.39	Y463F	ARHGAP5	14q12		Entrez Query	DOMAIN	A:48441	T:3115	51556	0.06042	0	TRUE	A:49629	T:131	49760	0.002633	1	FALSE	1	26	
859	SA230_16	SA230		16	67734735	16,677347	missense	medium	2.96	T227M	CRH1A	16q22.1				REPEAT	G:71251	T:45268	116519	0.388503	0	TRUE	C:85926	A:62	85988	0.000721	1	FALSE	2	14
860	SA230_22	SA230		22	18507288	22,185072	nonsense		NA	R144	CDH8	22q11.21				TOPO_DON	C:51425	T:35498	86923	0.408384	0	TRUE	C:198168	T:26	198194	0.000131	1	FALSE	1	11
861	SA230_6	SA230		6	46934915	6,4693491	missense	medium	2.255	S895L	GPR116	6p12.3				TOPO_DON	G:204934	A:30336	235270	0.128941	0	TRUE	G:210647	C:151	210798	0.000716	1	FALSE	1	7
862	SA230_7	SA230		7	28810465	7,2881046	missense	medium	1.905	S276L	CREB5	7p15.1				C:147692	T:65805	213497	0.308224	0	TRUE	C:245444	A:52	245496	0.000212	1	FALSE	1	2	
863	SA230_8	SA230		8	1.39E+08	8,1392340	missense	low	1.79	N603I	FAM1358	8q24.23				T:210181	A:88039	298220	0.295215	0	TRUE	T:277125	A:23	277148	8.30E-05	1	FALSE	0	0	
864	SA230_X	SA230	X		17653762	X,1765376	missense	medium	2.3	E518K	NBS	Xp22.13				G:114825	A:11924	126749	0.094076	0	TRUE	G:275393	T:110	275503	0.000399	1	FALSE	1	9	
865	SA230_X	SA230	X		79169004	X,7916900	missense	high	4.1	T260M	THX2	Xq21.1				DNA_BIND	C:51930	T:21875	73805	0.296389	0	TRUE	C:29083	A:9	29092	0.000309	1	FALSE	0	0
866	SA231_1	SA231		1	1.15E+08	1,1153775	missense	neutral	0.775	M19L	TSBH	1p13				SIGNAL	A:12694	T:8223	20917	0.393125	0	TRUE	A:12820	T:3	12823	0.000234	1	FALSE	0	0
867	SA231_1	SA231		1	11692089	1,1169208	missense	medium	1.95	V208I	C1orf187	1p36.22				G:3238	A:15525	18763	0.872426	0	TRUE	G:28231	A:11	28242	0.000389	1	FALSE	1	1	
868	SA231_1	SA231		1	1.53E+08	1,1528410	nonsense		NA	S223	ADAR	1q21.1-q21.2				G:51609	C:8759	60368	0.145093	0	TRUE	G:34496	T:2	34498	5.80E-05	1	FALSE	1	104	
869	SA231_1	SA231		1	1.58E+08	1,1575132	missense		NA	W57R	LOC649458					T:10803	C:27742	38545	0.71973	0	TRUE	T:25680	C:6	25686	0.000234	1	FALSE	0	0	
870	SA231_11	SA231		11	65076107	11,650761	missense	low	1.79	F481L	LTBP3	11q12				G:14012	T:6017	20029	0.300414	0	TRUE	G:25876	T:9	25885	0.000348	1	FALSE	2	29	
871	SA231_11	SA231		11	75885098	11,7588509	missense	low	0.975	Q434E	C11orf30	11q13.5		Entrez Query	COMPBIAS	C:17024	G:5716	22740	0.251363	0	TRUE	C:20979	T:25	21004	0.00119	1	FALSE	2	14	
872	SA231_1	SA231		1	22095342	1,2209534	missense	neutral	0.345	I38L	HSPG2	1p36.1-p34				T:8373	A:23901	32274	0.740565	0	TRUE	T:23593	G:20	23613	0.000847	1	FALSE	1	3	
873	SA231_1	SA231		1	2.29E+08	1,2294114	missense	medium	1.935	V650A	TRIM67	1q42.2				DOMAIN	T:7419	C:4333	11752	0.368703	0	TRUE	T:44470	G:21	44491	0.000472	1	FALSE	0	0
874	SA231_12	SA231		12	30763326	12,307633	missense	medium	2.14	S750I	CAPRIN2	12p11				C:19891	A:10465	30356	0.344742	0	TRUE	C:21688	A:4	21692	0.000184	1	FALSE	2	1	
875	SA231_1	SA231		1	2.34E+08	1,2339327	missense	low	1.845	CA447D	LYST	1q42.1-q42.2				C:5307	G:22732	28039	0.810728	0	TRUE	C:18363	T:14	18367	0.000218</					

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.ref	Ref.count.	Alt.count.T	Total.count	Alt.frequer	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.frequer	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase
899	SA233_3_3	SA233	3	1.37E+08	3,1373533	missense	neutral	0.255	A368T	MLL2L1	3q22.2					C:14445	T:2492	16937	0.147133	0	TRUE	C:11446	G:10	11156	0.000896	1	FALSE	2	6
900	SA233_5_5	SA233	5	1.43E+08	5,1427594	missense	medium	3.085	G369V	NR3C1	5q31.3			Cancer Cell	REGION //	C:429	A:102	531	0.19209	1.06E-192	TRUE	C:228	A:1	229	0.004367	1	FALSE	2	7
901	SA233_9_8	SA233	9	8365963	9,8365963	missense	medium	3.39	P1545V	PTPRD	9p23-p24.3			Entrez Que	DOMAIN //	T:23917	A:17111	41028	0.417057	0	TRUE	T:47881	G:1	47885	8.35E-05	1	FALSE	0	0
902	SA234_10_10	SA234	10	1.15E+08	10,1153994	missense	medium	2.14	V262G	NRAP	10q24-q26				REPEAT //	A:538	C:314	852	0.368545	0	TRUE	A:55	G:1	56	0.017857	1	FALSE	0	0
903	SA234_1_1	SA234	1	10636835	1,10636835	missense	medium	2.465	K622N	CAS21	1p36.22				ZN_FING //	C:57165	G:24795	81960	0.302526	0	TRUE	C:71994	T:8	72002	0.000111	1	FALSE	2	5
904	SA234_11_11	SA234	11	62047346	11,62047346	missense	neutral	-0.27	I3707L	AHNAK	11q12.2				T:96444	G:8402	104846	0.080137	0	TRUE	T:57828	G:62	57890	0.001071	1	FALSE	1	106	
905	SA234_12_12	SA234	12	1.32E+08	12,131834	missense	neutral	0.755	R381K	KIA04692					C:19556	T:5523	25079	0.202024	0	TRUE	C:45247	A:4	45251	8.84E-05	1	FALSE	2	18	
906	SA234_1_1	SA234	1	2.14E+08	1,2142404	missense	medium	2.485	P2149R	USH2A	1q41				DOMAIN //	G:76360	C:19272	95632	0.201523	0	TRUE	G:46727	A:10	46737	0.000214	1	FALSE	0	0
907	SA234_12_12	SA234	12	4790780	12,4790780	missense	high	3.715	V438M	KCNA6	12p13				TRANSMEN	G:15067	A:4256	19323	0.220256	0	TRUE	G:81525	A:9	81534	0.00011	1	FALSE	1	1
908	SA234_1_1	SA234	1	63877042	1,63877042	missense	high	4.19	E376A	PGM1	1p31					A:49750	C:17700	67450	0.262417	0	TRUE	A:82590	G:92	82682	0.001113	1	FALSE	2	92
909	SA234_17_17	SA234	17	10486471	17,10486471	missense	low	1.71	A626T	MYH3	17p13.1				DOMAIN //	C:101669	T:16911	118580	0.142613	0	TRUE	C:116219	T:22	116241	0.000189	1	FALSE	1	2
910	SA234_17_17	SA234	17	70451328	17,70451328	missense	medium	2.215	L240R	OTOP3	17q25.1				TRANSMEN	T:57289	G:8146	65435	0.12449	0	TRUE	T:69853	C:3	69856	4.29E-05	1	FALSE	0	0
911	SA234_17_17	SA234	17	7518990	17,7518990	missense	high	3.77	I195S	TP53	17p13.1	p.1195fs*	adenocarci	Cancer Cell	DNA_BIND	C:28947	T:9278	106634	0.271461	0	TRUE	A:114346	G:101	114447	0.000883	1	FALSE	2	23
912	SA234_19_19	SA234	19	40742645	19,40742645	missense	neutral	0.055	V320L	ATP4A	19q13.1				TOPO_DON	C:34504	A:8894	43398	0.20494	0	TRUE	C:108700	A:25	108725	0.00023	1	FALSE	0	0
913	SA234_19_19	SA234	19	45046148	19,45046148	missense	low	1.7	Q5387H	FCGBP	19q13.1				DOMAIN //	C:24872	A:2617	27489	0.092452	0	TRUE	C:115513	A:8	115521	6.93E-05	1	FALSE	1	1312
914	SA234_20_20	SA234	20	33599751	20,33599751	missense	medium	2.82	I179M	ERGIC3	20pter-q12				TOPO_DON	T:34943	G:9862	44805	0.220109	0	TRUE	T:91437	C:1	91438	1.09E-05	1	FALSE	2	445
915	SA234_2_1	SA234	2	1.58E+08	2,1581059	missense	high	3.695	S385Y	ACRVC1	2q24.1				DOMAIN //	G:61325	T:19667	80992	0.242826	0	TRUE	G:41757	T:5	41762	0.00012	1	FALSE	0	0
916	SA234_2_1	SA234	2	1.79E+08	2,1793188	missense	low	1.04	G800A	TTN	2q31					C:68779	G:20722	89501	0.231528	0	TRUE	C:55371	A:6	55377	0.000108	1	FALSE	2	4
917	SA234_2_1	SA234	2	2.19E+08	2,2192218	missense	low	1.505	A335S	ZNF142	2q34-q35				ZN_FING //	G:26045	C:9341	35386	0.263974	0	TRUE	G:103301	A:34	103335	0.000329	1	FALSE	1	13
918	SA234_3_3	SA234	3	75797676	3,75797676	missense	neutral	0.205	R125W	GRG2C		p.R215W	serous_carcinoma		C:113818	T:9278	123096	0.075372	0	TRUE	C:127447	G:37	127484	0.00029	1	FALSE	0	0	
919	SA234_5_5	SA234	5	54492636	5,54492636	missense	medium	3.015	G88R	LOC493865	5q11.2					C:40048	A:11007	51055	0.215591	0	TRUE	G:79776	T:11	79787	0.000138	1	FALSE	2	9
920	SA234_6_2	SA234	6	26216009	6,26216009	missense	medium	1.915	V98L	HIST1H1T	6p21.3				DOMAIN //	C:112257	G:11438	123695	0.092469	0	TRUE	C:153783	G:112	153895	0.000728	1	FALSE	3	0
921	SA234_9_9	SA234	9	35065492	9,35065492	missense	medium	2.08	A468V	FANCG	9p13			Cancer Rev	REPEAT //	G:58651	A:23818	82469	0.288812	0	TRUE	G:65079	T:11	65090	0.000169	1	FALSE	2	6
922	SA234_9_9	SA234	9	85114313	9,85114313	missense	high	3.68	K295T	FRMD3	9q21.32				DOMAIN //	T:57769	G:3840	61609	0.062329	0	TRUE	T:42634	G:6	42640	0.000141	1	FALSE	1	10
923	SA234_X_7	SA234	X	1.03E+08	X,1028179	missense	medium	3.495	G236V	MORF4L2	Xq22			Entrez Query :: Stability	C:72490	A:23467	95957	0.244557	0	TRUE	C:59484	G:39	59523	0.000655	1	FALSE	2	96	
924	SA234_X_7	SA234	X	70695953	X,70695953	missense	high	3.925	H572D	OGT	Xq13					C:95258	G:28828	124086	0.232323	0	TRUE	C:77267	G:67	77334	0.000866	1	FALSE	2	95
925	SA235_10_10	SA235	10	5831311	10,5831311	missense	low	1.67	T1974S	C10orf18					C:23807	G:3971	27778	0.142955	0	TRUE	C:48598	A:7	48669	0.001459	0.568891	FALSE	2	73	
926	SA235_11_11	SA235	11	36554554	11,36554554	nonsense	NA		E104Z	RAG1	11p13				G:56040	T:8731	64771	0.134798	0	TRUE	G:39538	A:3	39541	7.59E-05	1	FALSE	0	0	
927	SA235_12_12	SA235	12	2838158	12,2838158	missense	medium	2.135	K733N	FXM1	12p13				C:19549	D:2662	22211	0.119851	0	TRUE	C:30379	T:2	30381	6.58E-05	1	FALSE	2	100	
928	SA235_17_17	SA235	17	59231647	17,59231647	missense	medium	2.87	G187R	DXD42	17q23.3					G:14744	A:5733	20477	0.279973	0	TRUE	G:11513	A:1	11514	8.69E-05	1	FALSE	2	58
929	SA235_17_17	SA235	17	162575251	17,162575251	missense	neutral	0.595	N839K	HELZ	17q24.2					G:19576	C:5562	25138	0.221259	0	TRUE	G:30839	T:3	30842	9.73E-05	1	FALSE	2	33
930	SA235_19_19	SA235	19	11546998	19,11546998	missense	low	1.59	R269W	ACP5	19p13.3-p13.2					G:17847	A:3338	21185	0.157564	0	TRUE	G:28093	T:26	28119	0.000925	1	FALSE	1	336
931	SA235_19_19	SA235	19	42852856	19,42852856	missense	neutral	0	A12S	ZNF781	19q13.12					C:1106	A:30	146	0.205479	2.59E-52	TRUE	C:71	N:0	71	0	1	FALSE	3	0
932	SA235_22_22	SA235	22	18282749	22,18282749	missense	low	1.14	R193S	TXNRD2					T:10844	A:3332	14136	0.23571	0	TRUE	T:15998	G:2	16000	0.000125	1	FALSE	2	33	
933	SA235_22_22	SA235	22	25190325	22,25190325	missense	low	1.78	S424N	HP5A	22cen-q12.3				C:27107	T:4539	31646	0.14343	0	TRUE	C:44894	A:8	44902	0.000178	1	FALSE	2	33	
934	SA235_2_8	SA235	2	85662226	2,85662226	missense	medium	2.36	T60M	VAMP8	2p12-p11.2				TOPO_DON	C:35929	T:6553	42482	0.154254	0	TRUE	C:32470	T:2	32472	6.16E-05	1	FALSE	1	570
935	SA235_3_2	SA235	3	23927353	3,23927353	missense	high	4.06	G16V	NKIRAS1	3p24.2			Cancer Cell	NP_BIND	C:13815	A:2243	16058	0.139681	0	TRUE	C:16444	G:2	16446	0.000122	1	FALSE	1	19
936	SA235_3_2	SA235	3	52412627	3,52412627	missense	medium	2.175	S52CS	BAP1	3p21.31-p21.2			Entrez Query :: Tumor	G:7016	A:8765	199544	0.000125	0	TRUE	G:29990	A:3	29993	0.0001	1	FALSE	2	27	
937	SA235_5_5	SA235	5	33917090	5,33917090	missense	medium	2.365	S127F	ADAMTS12	5q35				PROPEP //	G:42514	A:11793	54307	0.217154	0	TRUE	G:45961	T:34	45995	0.000739	1	FALSE	1	16
938	SA235_6_8	SA235	6	83902223	6,83902223	missense	low	1.105	R1013C	DOPEY1	6q15				C:13169	T:2596	15765	0.164669	0	TRUE	C:5296	G:3	5299	0.000566	1	FALSE	1	15	
939	SA235_7_2	SA235	7	21665004	7,21665004	missense	NA			DNAH11	7p21				G:17468	C:4487	21955	0.204373	0	TRUE	G:19483	N:0	19483	0	1	FALSE	1	1	
940	SA235_7_2	SA235	7	24876881	7,24876881	missense	high	3.575	L126V	OSBP1L	7p15				DOMAIN //	G:32787	C:8852	41639	0.212589	0	TRUE	G:57500	T:25	57525	0.000435	1	FALSE	1	19
941	SA235_8_8	SA235	8	1.36E+08	8,1356818	silent	NA			ZFA1	8q24.22				A:20784	T:5832	26616	0.219116	0	TRUE	A:27133	G:1	27134	3.69E-05	1	FALSE	0	0	
942	SA235_X_1	SA235	X	1.08E+08	X,1077165	missense	medium	2.505	G350W	COL4A5	Xq22				REGION //	G:313	T:41	354	0.115819	1.31E-60	TRUE	G:356	T:1	357	0.002801	1	FALSE	3	0
943	SA235_X_1	SA235	X	1.35E+08	X,1352547	missense	neutral	-0.205	T398M	GPR112	Xq26.3				TOPO_DON	C:37875	T:11818	49693	0.23782	0	TRUE	C:60855	G:18	60873	0.000296	1	FALSE	0	0
944	SA235_X_3	SA235	X	53579100	X,53579100	missense	neutral	0.735	V4207I	HUWE1	Xp11.22			Entrez Que	DOMAIN //	C:14838	T:2884	17722	0.162736	0	TRUE	C:27818	G:4	27822	0.000144	1	FALSE	2	

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	OA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.pos	Ref.count.	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase	
968	SA236_19	SA236	19	8931290	19,893129	missense	neutral		A5721V	MUC16	19p13.2				COMPBIAS	G:25620	A:17449	43069	0.405141	0	TRUE	G:39097	T:14	39111	0.000358	1	FALSE	2	8	
969	SA236_21	SA236	21	46490727	21,464907	missense	medium	2.175	L1523F	MTM3AP	21q22.3					C:7838	G:4627	12465	0.371199	0	TRUE	C:5979	A:6	5985	0.001003	1	FALSE	2	51	
970	SA236_2_2	SA236	2	1.79E+08	2,1793141	missense		NA		TTN	2q31					A:42502	C:26826	69328	0.386943	0	TRUE	A:66946	G:8	66954	0.000119	1	FALSE	0	0	
971	SA236_2_2	SA236	2	2.03E+08	2,2033699	missense	low	1.79	E310Q	ICA1L	2q33.1					C:2902	G:892	3794	0.235108	0	TRUE	C:4178	G:5	4183	0.001195	1	FALSE	1	6	
972	SA236_22	SA236	22	27521358	22,275213	silent		NA		XBP1	22q12.1	22q12				C:10226	T:7547	17773	0.424633	0	TRUE	C:13683	A:1	13684	7.31E-05	1	FALSE	2	393	
973	SA236_2_2	SA236	2	2.28E+08	2,2279132	missense	medium	2.095	R149T	C2orf33	2q36.3				TOPO_DON	G:643	C:213	856	0.248832	0	TRUE	G:1012	T:1	1013	0.000987	1	FALSE	1	106	
974	SA236_3_1	SA236	3	1.43E+08	3,1427312	missense	medium	2.63	I123M	RASA2	3q22-q23				DOMAIN //	C:1100	G:307	1407	0.218195	0	TRUE	C:608	N:0	608	0	1	FALSE	2	27	
975	SA236_3_1	SA236	3	1.74E+08	3,1743179	missense	medium	2.215	K95N	SPATA12	3q26.31					C:38196	G:19869	58065	0.342185	0	TRUE	C:41352	G:7	41359	0.000169	1	FALSE	0	0	
976	SA236_3_1	SA236	3	1.87E+08	3,1868899	missense		NA	D193N	IGF2BP2	3q27.2				DOMAIN //	C:22233	T:15098	37331	0.404436	0	TRUE	C:35982	A:4	35986	0.000111	1	FALSE	2	44	
977	SA236_3_2	SA236	3	21581122	3,2158112	missense	low	0.895	R75Q	ZNF385D	3p24.3					C:3674	T:7229	10903	0.663029	0	TRUE	C:7849	T:3	7852	0.000382	1	FALSE	3	0	
978	SA236_4_2	SA236	4	2804569	4,2804569	missense	low	0.975	E515Q	SH3BP2	4p16.3				DOMAIN //	G:651	C:890	1541	0.577547	0	TRUE	G:2048	N:0	2048	0	1	FALSE	2	36	
979	SA236_4_2	SA236	4	81340281	4,8134028	missense	low	1.245	R8P	PRDM8					DOMAIN //	G:34364	C:20695	55059	0.37587	0	TRUE	G:45915	T:8	45923	0.000174	1	FALSE	0	0	
980	SA236_4_2	SA236	4	85861668	4,8586166	missense	low	1.295	Q2508P	WDFY3	4q21.23					T:19193	G:9265	28458	0.325568	0	TRUE	T:26657	C:11	26668	0.000412	1	FALSE	2	7	
981	SA236_5_7	SA236	5	73204754	5,7320475	missense	medium	2.075	R914L	RGNEF	5q13.2				DOMAIN //	G:16420	T:6032	22452	0.268662	0	TRUE	G:19069	C:2	19071	0.000105	1	FALSE	1	9	
982	SA236_6_4	SA236	6	46931720	6,4693172	missense	low	0.895	S1304C	GPR116	6p12.3				TOPO_DON	G:1320	N:0	1470	0.102041	1.94E-194	0	TRUE	G:584	N:0	584	0	1	FALSE	1	10
983	SA236_6_4	SA236	6	48143933	6,4814393	missense	low	1.15	E140Q	CCOR1F38	6p12.3					C:29840	G:17707	47547	0.37241	0	TRUE	C:51809	T:3	51812	5.79E-05	1	FALSE	0	0	
984	SA236_7_1	SA236	7	1.02E+08	7,1023671	missense	low	1.04	L259F	LRRCT1	7q22.1				DOMAIN //	G:13288	C:7736	21024	0.36796	0	TRUE	G:22251	C:8	22259	0.000359	1	FALSE	1	1	
985	SA236_7_1	SA236	7	1.57E+08	7,1571068	missense	neutral	0.785	A754T	PTPRN2	7q36			Entrez Que	DOMAIN //	C:19751	T:9563	29314	0.326226	0	TRUE	C:64466	T:10	64476	0.000155	1	FALSE	3	0	
986	SA236_7_2	SA236	7	27107109	7,2710710	missense	medium	2.025	L298M	H0XA2	7p15-p14					A:12403	T:4921	17324	0.284057	0	TRUE	A:21592	G:7	21599	0.000324	1	FALSE	0	0	
987	SA236_7_2	SA236	7	82369929	7,8236992	missense	low	1.61	R4432K	PCLO					DOMAIN //	C:10770	T:4348	15118	0.287604	0	TRUE	C:11453	N:0	11453	0	1	FALSE	2	4	
988	SA236_9_1	SA236	9	1.13E+08	9,1132353	missense	medium	2.295	R273C	KIA0368	9q31.3					G:22705	A:14538	37243	0.390355	0	TRUE	G:44222	A:11	44233	0.000249	1	FALSE	2	42	
989	SA236_9_1	SA236	9	1.33E+08	9,1325674	missense	medium	3.245	P2075	OSGSC2	9q34				STRAND //	C:34950	T:17589	52539	0.33478	0	TRUE	C:62041	G:43	62048	0.000693	1	FALSE	2	74	
990	SA236_9_1	SA236	9	1.35E+08	9,1345137	nonsense		NA	S362	DDX31	9q34.13				DOMAIN //	G:15367	T:7433	22800	0.326009	0	TRUE	G:18729	A:5	18734	0.000267	1	FALSE	1	21	
991	SA237_10	SA237	10	1.06E+08	10,105752	missense	low	1.845	D438Y	SLK	10q25.1				COMPBIAS	G:13740	T:4301	18041	0.238401	0	TRUE	G:13625	T:5	13630	0.000367	1	FALSE	2	83	
992	SA237_10	SA237	10	18868462	10,188684	missense	low	1.8	G596R	CACNB2	10p12					G:23506	A:6929	30435	0.227666	0	TRUE	G:43520	T:13	43533	0.000299	1	FALSE	1	2	
993	SA237_10	SA237	10	34845919	10,348459	nonsense		NA	R133	PARD3	10p11.22-p11.21			Cancer Cell Map Pathw	G:23954	A:8800	32754	0.268669	0	TRUE	G:26737	C:22	26759	0.000822	1	FALSE	1	52		
994	SA237_10	SA237	10	53128112	10,531281	missense	medium	2.34	Q402E	CSTF2T	10q11				COMPBIAS	G:29832	C:12095	41927	0.288478	0	TRUE	G:39926	T:20	39946	0.000501	1	FALSE	1	20	
995	SA237_11	SA237	11	1.13E+08	11,1121701	missense	medium	2.19	K137N	TTC12	11q23.1				REPEAT //	G:31063	T:13642	44705	0.305156	0	TRUE	G:42058	T:40	42098	0.000195	1	FALSE	2	14	
996	SA237_1_1	SA237	1	11150117	1,1115011	missense	low	1.545	L1433S	FAM11	1p36.12				DOMAIN //	A:23546	G:7194	30740	0.234027	0	TRUE	A:26530	G:3	26533	0.000113	1	FALSE	2	12	
997	SA237_11	SA237	11	1.18E+08	11,117849	missense	low	0.895	S783Y	MLL	11q23					C:24712	A:8263	32975	0.250584	0	TRUE	C:28883	G:5	28888	0.000173	1	FALSE	2	7	
998	SA237_11	SA237	11	1.19E+08	11,118650	missense	medium	2.905	L281H	CBL	11q23.3			Cancer Cell	DOMAIN //	T:23426	A:5230	28656	0.18251	0	TRUE	T:24850	C:6	24856	0.000241	1	FALSE	1	4	
999	SA237_11	SA237	11	14858653	11,148586	missense	high	3.72	V202S	CYP2R1	11p15.2					T:20484	G:10574	31058	0.34046	0	TRUE	T:23450	G:18	23468	0.000767	1	FALSE	3	6	
1000	SA237_1_1	SA237	1	1.44E+08	1,1442504	missense	medium	2.42	Q1006H	ITGA10	1q21				TOPO_DON	A:570	C:385	955	0.403141	0	TRUE	A:1948	N:0	1948	0	1	FALSE	1	1	
1001	SA237_1_1	SA237	1	1.53E+08	1,1525669	silent		NA		ATP8B2	1q21.3					C:492	T:341	833	0.409364	0	TRUE	C:3835	N:0	3835	0	1	FALSE	0	0	
1002	SA237_1_1	SA237	1	1.57E+08	1,1571786	missense	low	1.285	K266E	PYHIN1	1q23.1			Entrez Que	DOMAIN //	A:224	G:171	395	0.432911	0	TRUE	A:645	N:0	645	0	1	FALSE	1	3	
1003	SA237_1_1	SA237	1	1.59E+08	1,1589215	missense	neutral	0.345	V31L	CD48	1q21.3-q22				DOMAIN //	C:19900	A:12064	31964	0.377425	0	TRUE	C:34297	G:15	34312	0.000437	1	FALSE	1	7	
1004	SA237_11	SA237	11	7021149	11,702114	missense	low	1.85	T439S	NLRP14	11p15.4				DOMAIN //	C:16612	G:9663	26275	0.367764	0	TRUE	C:34452	A:6	34458	0.000174	1	FALSE	0	0	
1005	SA237_1_1	SA237	1	1.81E+08	1,1814633	missense	medium	3.015	C470R	LAMC2	1q25-q31				DISULFID //	T:20399	C:13594	33993	0.399906	0	TRUE	T:35354	C:10	35364	0.000283	1	FALSE	2	2	
1006	SA237_11	SA237	11	93766399	11,937663	missense	low	0.9	I183V	GPR83	11q21				DISULFID //	T:36417	C:11193	47610	0.235098	0	TRUE	T:42537	G:44	42581	0.001033	1	FALSE	0	0	
1007	SA237_1_2	SA237	1	2.06E+08	1,2057108	missense	medium	2.135	L445M	CR2	1q32				DISULFID //	C:4568	A:3378	7946	0.42512	0	TRUE	C:10331	A:3	10334	0.00029	1	FALSE	2	5	
1008	SA237_12	SA237	12	1.2E+08	12,120139	missense	low	1.845	T65M	PRRX4	12q24.32				TOPO_DON	C:37237	T:9555	46792	0.204202	0	TRUE	C:43432	G:25	43457	0.000575	1	FALSE	1	29	
1009	SA237_12	SA237	12	29499500	12,294995	missense	medium	3.425	V796L	OVCH1	12p11.22				DOMAIN //	C:18889	G:5409	24298	0.222611	0	TRUE	C:25688	G:9	25697	0.00035	1	FALSE	0	0	
1010	SA237_15	SA237	15	15116332	15,351163	missense	medium	2.81	R292T	MEIS2	15q14				DNA_BIND	G:5238	C:15709	20947	0.25006	0	TRUE	C:29339	G:6	29345	0.000204	1	FALSE	1	9	
1011	SA237_15	SA237	15	36639374	15,366393	nonsense		NA	G54	RASGRP1	15q15				DOMAIN //	C:23208	A:5401	28609	0.188787	0	TRUE	C:28086	A:3	28089	0.000107	1	FALSE	0	0	
1012	SA237_15	SA237	15	81143191	15,811431	missense	medium	2.71	E460Q	AP3B2	15q					C:12801	G:8035	20836	0.385631	0	TRUE	C:29339	A:2	29341	6.82E-05	1	FALSE	0	0	
1013	SA237_16	SA237	16	3956705	16,395670	missense	medium	2.455	K1045M	ADCY9	16p13.3				TOPO_DON	T:18692	A:6365	25057	0.254021	0	TRUE	T:38130	C:4	38134	0.000105	1	FALSE	1	10	
1014	SA237_16	SA237	16	54289925	16,542899	missense	medium	3.32	G478D	SLC6A2	16q12.2</																			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func.Lmpa	Fi.score	AA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.pos	Ref.count.	Alt.count.T	Total.count	Alt.frequer	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.frequer	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase	
1037	SA237_7_1SA237			7 1.52E+08	7,1515220	missense	neutral		0.115451	MML3	7q36.1					G:30306	A:10269	40575	0.253087	0	TRUE	G:35838	T:4	35842	0.000112	1	FALSE	2	8	
1038	SA237_7_1SA237			7 36414010	7,3641401	missense	medium	1.905	S339C	ANLN	7p15-p14				REGION //	C:400292	G:10459	50751	0.206085	0	TRUE	C:39243	A:6	39249	0.000153	1	FALSE	1	73	
1039	SA237_7_4SA237			7 43317974	7,4331797	missense	medium	1.95	J9I	HECW1	7p14.1-p13					C:25168	A:5677	30845	0.184049	0	TRUE	C:34903	G:19	34922	0.000544	1	FALSE	1	1	
1040	SA237_7_1SA237			7 76708957	7,7670895	nonsense	NA		E85	CCDC146	7q11.23					G:13246	T:2706	15952	0.169634	0	TRUE	G:23764	A:4	23768	0.000168	1	FALSE	1	4	
1041	SA237_8_1SA237			8 1.03E+08	8,1033764	missense	low	0.995	V1369L	UBR5	8q22				Entrez Query :: Stability	C:38137	G:7720	45857	0.168349	0	TRUE	C:34419	G:6	34425	0.000174	1	FALSE	2	12	
1042	SA237_8_1SA237			8 1.08E+08	8,1077878	missense	medium	2.125	S323N	OXR1	8q23					G:26194	A:5333	31527	0.169157	0	TRUE	G:43798	A:6	43804	0.000137	1	FALSE	1	23	
1043	SA237_8_1SA237			8 1.34E+08	8,1340532	missense	medium	1.905	F1994S	TG	8q24				REPEAT //	T:34994	C:6903	41897	0.164761	0	TRUE	T:40142	C:3	40145	1.47E-05	1	FALSE	2	1	
1044	SA237_8_1SA237			8 67647319	8,6764731	missense	medium	3.035	K560N	MYBL1	8q22				Entrez Query :: Oncog	C:12667	G:3110	15777	0.197122	0	TRUE	G:10706	A:1	10707	9.34E-05	1	FALSE	1	7	
1045	SA237_9_2SA237			9 27552469	9,2755246	missense	low	1.61	Q170H	C9orf72	9p21.2					C:387	G:196	583	0.336192	0	TRUE	C:715	N:0	715	0	1	FALSE	1	7	
1046	SA237_X_1SA237	X		1.02E+08	X,1017973	missense	low	1.355	W618C	GPRASP1					COMPMIAS	G:31723	T:7822	39545	0.1978	0	TRUE	G:26282	C:11	26293	0.000418	1	FALSE	1	4	
1047	SA237_X_1SA237	X		19473991	X,1947399	missense	medium	2.015	K531N	SH3KBP1	Xp22.1-p21.3				Cancer Cell Map Pathw	C:34358	G:10367	44725	0.231794	0	TRUE	C:30458	A:7	30465	0.00023	1	FALSE	1	26	
1048	SA237_X_7SA237	X		76664477	X,7666447	missense	low	1.65	P2299S	ATRX	Xq13.1-q21.1				Entrez Query :: Stability	G:2279	A:269	2548	0.105573	0	TRUE	G:3400	T:1	3401	0.000294	1	FALSE	1	66	
1049	SA237_X_7SA237	X		77897900	X,7789790	missense	high	4.12	Y293C	GPR23	Xq13-q21.1				TOPO_DON	A:38092	G:17409	55501	0.31367	0	TRUE	A:46444	C:39	46483	0.000839	1	FALSE	1	1	
1050	SA065_16_1SA065		16	88140584	16,8814058	missense	low	1.885	F489L	SPG7	16q24.3				Entrez Query :: HELIX //	T:25	G:92	117	0.786325	5.43E-194	TRUE	T:57	N:0	57	0	1	FALSE	2	18	
1051	SA018_10_1SA018			10 1.26E+08	10,125518	missense	medium	2.94	S421A	CPXM2	10q26.13					A:15071	C:4513	19584	0.203443	0	TRUE	A:10483	G:8	10491	0.000763	1	FALSE	1	16	
1052	SA018_10_1SA018			10 26425588	10,2642558	missense	medium	2.82	C583R	MYO3A	10p11.1				DOMAIN //	T:1088	C:295	1383	0.213304	0	TRUE	T:1479	N:0	1479	0	1	FALSE	0	0	
1053	SA018_12_1SA018			12 1.03E+08	12,102572	missense	medium	2.605	487M	STAB2	12q23.3				DOMAIN //	A:1654	G:1270	2924	0.434337	0	TRUE	A:4391	C:1	4392	0.000228	1	FALSE	0	0	
1054	SA018_12_1SA018			12 21970262	12,2197026	missense	neutral	0	R96Q	ABCC9	12p12.1				TOPO_DON	C:1220	T:922	2142	0.430439	0	TRUE	C:1977	N:0	1977	0	1	FALSE	0	0	
1055	SA018_13_1SA018			13 85268197	13,8526819	missense	low	1.725	V150L	SLITRK6	13q31.1				TOPO_DON	C:845	G:522	1367	0.381858	0	TRUE	C:3348	N:0	3348	0	1	FALSE	0	0	
1056	SA018_14_1SA018			14 35299945	14,3529994	missense	medium	2.74	R130C	GARNL1	14q13.2					G:1702	A:704	2406	0.292602	0	TRUE	G:5754	A:2	5756	0.000347	1	FALSE	1	2	
1057	SA018_16_1SA018			16 27697402	16,276974	missense	medium	2.3	R1603H	KIAA0556	16p12.1-p11.2					G:1213	A:2446	3659	0.668489	0	TRUE	G:3906	A:1	3907	0.000256	1	FALSE	3	0	
1058	SA018_17_1SA018			17 36788783	17,3678877	missense	high	4.74	C192Q	KRT34	17q12-q21				REGION //	C:13191	G:2789	15980	0.174531	0	TRUE	C:8741	T:2	8743	0.000229	1	FALSE	0	0	
1059	SA018_17_1SA018			17 39207639	17,3920763	missense	low	1.9	D107N	DUSP3	17q21				Entrez Query :: DOMAIN //	C:932	T:2114	3046	0.694025	0	TRUE	C:2434	T:1	2435	0.000411	1	FALSE	2	11	
1060	SA018_17_1SA018			17 54642505	17,5464255	missense	low	0.975	G104V	C17orf71	17q22					G:2449	T:719	3168	0.226957	0	TRUE	G:3133	N:0	3133	0	1	FALSE	2	5	
1061	SA018_17_1SA018			17 71801610	17,7180161	missense	neutral	0.345	K99E	QRICH2	17q25.1					T:10830	C:3019	13849	0.217994	0	TRUE	T:10836	C:4	10840	0.000369	1	FALSE	1	2	
1062	SA018_18_1SA018			18 42813998	18,4281399	missense	low	1.32	D546N	TCEB3B	18q21.1				REGION //	C:10359	T:1822	12181	0.149577	0	TRUE	C:10381	A:2	10383	0.000193	1	FALSE	0	0	
1063	SA018_1_1SA018			1 1.5E+08	1,1504580	missense	neutral	0.345	S878L	HRNR	1q21.3				REPEAT //	G:10597	A:1996	12593	0.158501	0	TRUE	G:7573	C:1	7574	0.000132	1	FALSE	0	0	
1064	SA018_1_1SA018			1 2.25E+08	1,2252491	missense	medium	1.95	G1674S	CDC42BP4	1q42.11					C:22379	T:4333	26712	0.162212	0	TRUE	C:33468	A:3	33471	8.96E-05	1	FALSE	1	47	
1065	SA018_1_1SA018			1 57170133	1,5717013	missense	medium	2.175	R520L	C8B	1p32				DOMAIN //	C:36106	A:6833	42939	0.159133	0	TRUE	C:25918	T:6	25924	0.000231	1	FALSE	0	0	
1066	SA018_22_1SA018		22	40258099	22,4025809	missense	medium	3.245	G102R	POLR3H	22q13.2					C:4805	G:2099	6904	0.304027	0	TRUE	C:1698	N:0	1698	0	1	FALSE	2	88	
1067	SA018_2_1SA018			2 1.79E+08	2,1785873	missense	neutral	0.345	345T	PDE11A	2q31.2				DOMAIN //	A:1385	G:331	1716	0.19289	0	TRUE	A:365	N:0	365	0	1	FALSE	0	0	
1068	SA018_2_1SA018		2	2.04E+08	2,2037220	missense	medium	1.935	Q1768R	NBEA11						A:1101	G:388	1489	0.260578	0	TRUE	A:2687	G:1	2688	0.000372	1	FALSE	3	0	
1069	SA018_2_1SA018		2	2.32E+08	2,2320346	missense	low	1.245	D151N	NCL	2q12-qter				Entrez Query :: COMPMIAS	C:5054	T:1312	6366	0.206095	0	TRUE	C:6564	N:0	6564	0	1	FALSE	2	2767	
1070	SA018_2_1SA018		2	2.32E+08	2,2320346	missense	low	1.59	E143K	NCL	2q12-qter				Entrez Query :: COMPMIAS	C:31605	T:3081	34686	0.088825	0	TRUE	C:17495	A:1	17496	5.72E-05	1	FALSE	2	2608	
1071	SA018_2_1SA018		2	37121940	2,3712194	missense	NA		K899	HEATH5B	2p22.2					C:245270	A:63845	309115	0.206541	0	TRUE	C:318340	G:68	318408	0.000214	1	FALSE	3	0	
1072	SA018_4_1SA018		4	1.34E+08	4,1342931	missense	low	1.79	S793C	PCDH10	4q28.3				TOPO_DON	C:2958	G:1610	4568	0.352452	0	TRUE	C:4849	T:1	4850	0.000206	1	FALSE	1	2	
1073	SA018_5_1SA018		5	1.79E+08	5,1789805	missense	NA		D106G	HNRPH1	5q35.3				MOD_RES	T:8327	C:4096	12423	0.329711	0	TRUE	T:7376	C:3	7379	0.000407	1	FALSE	2	198	
1074	SA018_6_1SA018		6	1.02E+08	6,1024442	missense	high	3.86	D528N	GRIK2	6q16.3-q21				TOPO_DON	G:775	A:1117	1892	0.590381	0	TRUE	G:1561	A:1	1562	0.00064	1	FALSE	0	0	
1075	SA018_6_1SA018		6	26216141	6,2621614	missense	low	1.59	V54M	HIST1H1T	6p21.3				DOMAIN //	C:1513	T:200	1713	0.116754	8.39E-249	TRUE	C:463	N:0	463	0	1	FALSE	1	2	
1076	SA018_6_4SA018		6	45029071	6,4502907	missense	medium	2.61	S334I	SUPT3H	6p21.1-p21.3					C:7042	A:1407	8449	0.166529	0	TRUE	C:5765	A:1	5766	0.000173	1	FALSE	1	14	
1077	SA018_6_1SA018		6	56589207	6,5658920	missense	NA		DST		6p12.1					A:10315	C:2540	12855	0.197588	0	TRUE	A:17834	C:4	17838	0.000224	1	FALSE	0	0	
1078	SA018_7_1SA018		7	1.51E+08	7,1508190	missense	high	3.95	T23K	RHEB	7q36				HELI // 19	G:659	T:130	789	0.164766	2.77E-182	TRUE	G:1176	A:1	1177	0.00085	1	FALSE	1	12	
1079	SA018_9_1SA018		9	35795626	9,3579562	missense	low	1.325	R669Q	NPR2	9p21-p12				Entrez Query :: DOMAIN //	G:14073	A:1702	15775	0.107892	0	TRUE	G:9552	C:9	9561	0.000941	1	FALSE	1	4	
1080	SA018_X_1SA018	X		1.17E+08	X,1169173	missense	medium	2.77	A519V	KLHL13	Xq23-q24				REPEAT //	G:761	A:1909	2670	0.714981	0	TRUE	G:4696	A:2	4698	0.000426	1	FALSE	3	1	
1081	SA029_11_1SA029		11	85044324	11,8504433	missense	medium	1.995	G107R	TMEM126	11q14.1					G:20517	A:4712	25229	0.186769	0	TRUE	G:78048	A:9	78057	0.000115	1	FALSE	2	66	
1082	SA029_13_1SA029		13	47931834	13,4793183	missense	high	3.555	L657P	RB1	13q14.2				Cancer Cell	REGION //	T:283	C:239	522	0.457854	0	TRUE	T:270	N:0	270	0	1	FALSE	2	22
1083	SA029_16_1SA029		16	20284279	16,2028427	missense	medium	2.33	V401I	PDILT	16p12.3																			

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.pos	Ref.count	Alt.count.T	Total.count	Alt.frequen	Binomial.te	Binomial.te	Ref.count.T	Alt.count.N	Total.count	Alt.frequen	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase	
1106	SA031_10	SA031	10	1.28E+08	10,127727	missense	neutral	0.65	R612Q	ADAM12	10q26.3				COMPBIAS	C:6509	T:3044	9553	0.318643	0	TRUE	C:29876	A:8	29884	0.000268	1	FALSE	1	74	
1107	SA031_10	SA031	10	25918019	10,259180	missense	medium	2.91	R611C	GPR158	10p12.1				TOPO_DON	C:4476	T:1185	5661	0.209327	0	TRUE	C:5670	T:2	5672	0.000353	1	FALSE	0	0	
1108	SA031_11	SA031	11	1.02E+08	11,102331	missense	low	0.805	L12M	MMP13	11q22.3				SIGNAL //	A:14764	T:4842	19606	0.246965	0	TRUE	A:31628	G:5	31633	0.000158	1	FALSE	1	211	
1109	SA031_12	SA031	12	1.08E+08	12,108406	missense	medium	2.835	L84Q	UBE38	12q24.11					T:261	A:63	324	0.194444	3.81E-96	TRUE	T:940	N:0	940	0	1	FALSE	2	9	
1110	SA031_13	SA031	13	1.1E+08	13,109626	missense	high	3.87	G1011E	COL4A1	13q34				Entrez Que	CONFLICT	C:779	T:642	1421	0.451795	0	TRUE	C:1432	T:1	1433	0.000698	1	FALSE	1	408
1111	SA031_15	SA031	15	41273908	15,412739	missense	medium	1.935	A309P	CCND8P1	15q14-q15				Entrez Que	REGION //	G:10247	C:2481	12728	0.194925	0	TRUE	G:27703	A:4	27707	0.000144	1	FALSE	2	51
1112	SA031_15	SA031	15	41511751	15,415117	missense	medium	2.05	T1198I	TP53BP1	15q15-q21				Entrez Query :	Stabilit	G:72226	A:14819	87045	0.170245	0	TRUE	G:109777	C:44	109821	0.000401	1	FALSE	2	25
1113	SA031_15	SA031	15	45846112	15,458461	nonsense	NA		G552	SEMA6D	15q21.1				DOMAIN //	G:24535	T:7228	31763	0.22756	0	TRUE	G:73427	C:6	73433	8.17E-05	1	FALSE	1	2	
1114	SA031_17	SA031	17	24076521	17,240765	missense	medium	2.155	I96M	TLCD1	17q11.2				TRANSMEN	G:4299	C:1490	5789	0.257385	0	TRUE	G:3384	N:0	3384	0	1	FALSE	3	2	
1115	SA031_17	SA031	17	57967362	17,579673	missense	low	1.245	A155T	TLK2	17q23					G:336	A:53	389	0.136247	4.93E-72	TRUE	G:1541	A:1	1542	0.000649	1	FALSE	1	7	
1116	SA031_18	SA031	18	32552613	18,325526	missense	medium	2.15	K926N	FHOD3	18q12				DOMAIN //	G:4069	T:649	4718	0.137558	0	TRUE	G:12040	C:1	12041	8.30E-05	1	FALSE	1	12	
1117	SA031_18	SA031	18	53175626	18,531756	missense	medium	2.215	F263I	ST8SIA3	18q21.31				DISULFID //	T:4841	A:1497	6338	0.236194	0	TRUE	T:13790	N:0	13790	0	1	FALSE	0	0	
1118	SA031_19	SA031	19	51526303	19,515263	missense	neutral	0.255	G588E	HIF3A	19q13.32					G:17460	A:3843	21303	0.180397	0	TRUE	G:27356	C:4	27360	0.000146	1	FALSE	0	0	
1119	SA031_1_4	SA031	1	1.15E+08	1,1150602	missense	high	4.21	I24L	NRAS	1p13.2				Cancer Cell	HELIX //	T:18703	G:3135	21838	0.143557	0	TRUE	T:63410	C:9	63419	0.000142	1	FALSE	2	135
1120	SA031_1_1	SA031	1	1.44E+08	1,1436426	missense	medium	1.935	Y135S	PDE4DIP	1q12					T:13150	G:962	14112	0.068169	0	TRUE	T:15253	C:3	15256	0.000197	1	FALSE	1	147	
1121	SA031_1_1	SA031	1	1.81E+08	1,1808222	missense	medium	1.935	V105M	RNA5EL	1q25				Entrez Que	REPEAT //	C:7830	T:1311	9141	0.14342	0	TRUE	C:13923	T:5	13928	0.000359	1	FALSE	1	13
1122	SA031_1_2	SA031	1	26645437	1,2664543	missense	low	1.23	D123N	CHD5	1p36.11					G:2383	A:53	2922	0.184463	0	TRUE	G:4179	C:1	4180	0.000239	1	FALSE	2	30	
1123	SA031_1_4	SA031	1	62886498	1,6288649	missense	neutral	0.595	N200S	DOCK7	1p31.3					T:121	C:17	138	0.123188	5.27E-22	TRUE	T:446	N:0	446	0	1	FALSE	1	84	
1124	SA031_1_4	SA031	1	62886502	1,6288650	missense	low	0.895	K199Q	DOCK7	1p31.3					T:121	G:17	138	0.123188	5.27E-22	TRUE	T:446	N:0	446	0	1	FALSE	1	82	
1125	SA031_1_7	SA031	1	72513069	1,7251306	missense	NA			LOC100132353						G:4236	A:724	4960	0.145968	0	TRUE	G:7890	C:1	7891	0.000127	1	FALSE	1	1	
1126	SA031_20	SA031	20	2256892	20,225689	missense	neutral	0.715	T405N	TGM3	20q11.2				TURN //	C:1290	A:606	1896	0.31962	0	TRUE	C:5475	A:1	5476	0.000183	1	FALSE	0	0	
1127	SA031_2_2	SA031	2	1.16E+08	2,1159999	missense	high	3.62	P134L	PPP10	2q14.1				MOD_RES	C:5394	A:1004	6398	0.156924	0	TRUE	C:22859	A:8	22867	0.000135	1	FALSE	0	0	
1128	SA031_2_3	SA031	2	36594308	2,3659430	missense	medium	3.035	G29F	CRM1	2p21				DOMAIN //	G:17581	T:4186	21767	0.192309	0	TRUE	G:21988	C:6	21994	0.000273	1	FALSE	2	223	
1129	SA031_2_4	SA031	2	48811936	2,4881193	missense	low	1.04	L56P	ILCHGR	2p21				DOMAIN //	A:12519	G:2885	15404	0.187289	0	TRUE	A:24092	G:5	24097	0.000207	1	FALSE	0	0	
1130	SA031_6_4	SA031	6	1.51E+08	6,1512027	missense	low	0.895	I045S	PLEKHG1	6q25.1					T:15710	G:4555	20265	0.224772	0	TRUE	T:14813	C:4	14817	0.00027	1	FALSE	2	35	
1131	SA031_6_4	SA031	6	41225597	6,4122559	missense	low	0.975	G220A	TREML1	6p21.1				TOPO_DON	C:1680	G:477	2157	0.22114	0	TRUE	C:2437	G:1	2438	0.00041	1	FALSE	1	2	
1132	SA031_6_9	SA031	6	97668430	6,9766843	missense	neutral	0.76	E226D	KLHL32	6q16.1					G:2339	T:1128	3467	0.325353	0	TRUE	G:4318	C:3	4321	0.000694	1	FALSE	0	0	
1133	SA031_7_2	SA031	7	1.16E+08	7,116196934	G,A	NA								G:209569	A:87634	297203	0.294862	0	TRUE	G:270980	A:24	271004	8.86E-05	1	FALSE	1	1		
1134	SA031_7_7	SA031	7	1.4E+08	7,1401232	missense	medium	2.36	H539P	BRAF	7q34				DOMAIN //	T:32198	G:4637	36835	0.125886	0	TRUE	T:50034	C:50	50084	0.000998	1	FALSE	1	25	
1135	SA031_7_7	SA031	7	30668931	7,3066893	missense	high	4.45	W201R	CRHR2	7p15.1				TRANSMEN	A:1824	G:1509	3333	0.452745	0	TRUE	A:3820	G:2	3822	0.000523	1	FALSE	0	0	
1136	SA031_7_4	SA031	7	41696591	7,4169659	missense	low	1.615	V155F	INHBA	7p15-p13				Entrez Que	PROPEP //	C:25296	A:3044	10741	0.10741	0	TRUE	C:25709	A:6	25715	0.000233	1	FALSE	1	158
1137	SA031_7_7	SA031	7	55427079	7,5542707	missense	medium	2.47	A102P	LANCL2	7q31.1-q31.33					G:28475	C:5526	34001	0.162525	0	TRUE	G:35210	A:8	35218	0.000227	1	FALSE	2	38	
1138	SA031_7_7	SA031	7	6430947	7,6430947	missense	low	1.66	E367D	DAGLB	7p22.1				TOPO_DON	C:24259	G:4382	28641	0.152997	0	TRUE	C:12715	G:2	12717	0.000157	1	FALSE	1	19	
1139	SA031_8_8	SA031	8	1.4E+08	8,1398623	nonsense	NA		R550	COL22A1	8q24.23				COMPBIAS	T:2601	A:989	3590	0.275487	0	TRUE	T:4197	A:2	4199	0.000476	1	FALSE	0	0	
1140	SA031_8_8	SA031	8	69596604	8,6959660	missense	low	1.43	N175S	C8orf34	8q13					A:787	G:190	977	0.194473	8.36E-291	TRUE	A:1301	C:1	1302	0.000768	1	FALSE	0	0	
1141	SA031_8_7	SA031	8	74395778	8,7439577	missense	low	1.76	L228I	RDH10	8q21.11					C:176	A:56	232	0.241379	2.77E-91	TRUE	C:1248	N:0	1248	0	1	FALSE	2	44	
1142	SA031_8_9	SA031	8	92376944	8,9237694	missense	high	4.01	A105D	SLC26A7	8q23				TOPO_DON	C:21448	A:3058	24506	0.124786	0	TRUE	C:41909	T:6	41915	0.000143	1	FALSE	0	0	
1143	SA031_9_3	SA031	9	32620508	9,3262050	missense	low	1.5	L1690F	TAF1L	9p21.1					C:18742	A:4013	22755	0.176357	0	TRUE	C:80211	A:27	80238	0.000336	1	FALSE	0	0	
1144	SA031_9_9	SA031	9	5154175	9,5154175	missense	neutral	0.425	K127R	INS16	9p24				PROPEP //	T:3815	C:1081	4896	0.220792	0	TRUE	T:14095	C:5	14100	0.000355	1	FALSE	0	0	
1145	SA031_9_8	SA031	9	89409891	9,8940989	missense	low	1.235	V89I	DAPK1	9q34.1				Entrez Que	DOMAIN //	G:4261	A:2803	7064	0.396801	0	TRUE	G:13728	A:5	13733	0.000364	1	FALSE	2	11
1146	SA031_X_1	SA031	X	1E+08	X,1002867	missense	medium	2.36	L550V	CENPI	Xq22.1					T:362	G:44	406	0.108374	3.65E-55	TRUE	T:615	N:0	615	0	1	FALSE	1	15	
1147	SA031_X_1	SA031	X	1.07E+08	X,1069711	missense	low	1.175	M205L	MID2	Xq22				ZN_FING //	A:17726	T:2207	19933	0.110721	0	TRUE	A:13870	G:4	13874	0.000288	1	FALSE	1	15	
1148	SA031_X_1	SA031	X	1.29E+08	X,1289761	missense	low	1.1	T587N	BCORL1	Xq25-q26.1				COMPBIAS	C:1679	A:293	2172	0.22698	0	TRUE	C:4012	A:1	4013	0.000249	1	FALSE	1	8	
1149	SA031_X_1	SA031	X	1.35E+08	X,1352579	missense	neutral	0	L481F	GPR112	Xq26.3				TOPO_DON	C:247	T:45	292	0.15411	1.21E-63	TRUE	C:2768	N:0	2768	0	1	FALSE	0	0	
1150	SA031_X_1	SA031	X	1.49E+08	X,1491509	missense	NA			LOC389901						A:26097	T:1810	27907	0.064858	0	TRUE	A:39092	G:10	39102	0.000256	1	FALSE	0	0	
1151	SA031_X_7	SA031	X	34558472	X,3455847	missense	neutral	0.04	S142T	TME4F7	Xp11.4					C:535	G:155	690	0.224638	6.05E-248	TRUE	C:2040	N:0	2040	0	1	FALSE	2	35	
1152	SA031_X_4	SA031	X	41088518	X,4108851	missense	high	4.39	G316V	DDX3X	Xp11.3-p11.23																			

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC				
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AI.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.pos	Ref.count	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase
1175	SA051_5	SA051		5	9682783	5,9682783	missense	medium	2.935	R121T	TAS2R1	5p15			TOPO_DON	C:3806	G:1481	5287	0.280121	0	TRUE	C:3435	A:1	3436	0.000291	1	FALSE	0	0				
1176	SA051_6	SA051		6	46908941	6,4690894	missense	low	1.25	R439Q	MEP1A	6p12-p11			CARBOHYD	C:2572	A:1299	4301	0.402	0	TRUE	G:6159	C:3	6162	0.000487	1	FALSE	0	0				
1177	SA051_6	SA051		6	51884699	6,5188469	missense	low	1.39	F2116C	PKHD1	6p12.2			CARBOHYD	A:3252	C:2511	5763	0.435711	0	TRUE	A:10654	G:2	10656	0.000188	1	FALSE	0	0				
1178	SA051_6	SA051		6	90451368	6,9045136	missense	low	1.875	R3926Q	MDN1	6q15				C:814	T:572	1386	0.412698	0	TRUE	C:1058	N:0	1058	0	1	FALSE	2	10				
1179	SA051_9	SA051		9	1.3E+08	9,1300221	missense	medium	3.145	R217H	DNM1	9q34		Cancer Cell	Map Pathw	G:534	A:293	827	0.354293	0	TRUE	G:805	A:1	806	0.001241	1	FALSE	1	3				
1180	SA051_X	SA051	X	1	1.29E+08	X,1287540	missense	low	1.32	P166S	Cxor9	Xq26.13				C:18113	T:8387	26500	0.316491	0	TRUE	G:62170	A:15	62185	0.000241	1	FALSE	1	25				
1181	SA052_14	SA052		14	93664670	14,936646	missense	low	1.115	A45T	FAM14A	14q32.13				G:509	T:213	722	0.295014	0	TRUE	C:542	T:1	543	0.001842	1	FALSE	1	58				
1182	SA052_15	SA052		15	62749669	15,627496	missense	medium	2.375	D349Y	ZNF609	15q22.31				C:815	T:424	1239	0.342211	0	TRUE	G:1543	T:1	1544	0.000648	1	FALSE	2	10				
1183	SA052_16	SA052		16	22051894	16,220518	missense	medium	2.42	R682H	VWA3A			DOMAIN	//	G:31955	A:19602	51557	0.380201	0	TRUE	G:63188	A:26	63214	0.000411	1	FALSE	0	0				
1184	SA052_16	SA052		16	28514701	16,285147	missense	low	1.87	V18F	SULT1A2	16p12.1			STRAND	//	C:1331	A:280	1611	0.173805	0	TRUE	C:1072	N:0	1072	0	1	FALSE	0	0			
1185	SA052_17	SA052		17	37348458	17,373484	missense	medium	2.52	R250W	TTC25	17q21.2				C:11718	T:12904	24622	0.524084	0	TRUE	C:37878	T:18	37896	0.000475	1	FALSE	1	3				
1186	SA052_1	SA052		1	1.1E+08	1,1098354	missense	low	0.975	S569F	ATXN7L2	1p13.3				C:543	T:610	1153	0.529055	0	TRUE	C:772	T:3	775	0.003871	1	FALSE	2	9				
1187	SA052_1	SA052		1	2.11E+08	1,2108652	missense	neutral	-0.625	H134R	FAM71A	1q32.3				A:1462	G:2219	3681	0.602825	0	TRUE	A:2741	G:6	2747	0.002184	1	FALSE	0	0				
1188	SA052_2	SA052		2	31343024	2,3134302	missense	low	1.32	E520K	EH03	2p21		DOMAIN	//	G:11794	A:1776	3570	0.497479	0	TRUE	G:2355	A:6	2361	0.002541	1	FALSE	1	9				
1189	SA052_5	SA052		5	1.79E+08	5,1794002	missense	medium	2.865	G88R	RNF130	5q35.3		TOPO_DON	//	C:1126	G:1072	2143	0.474568	0	TRUE	C:4019	G:7	4026	0.001739	1	FALSE	2	117				
1190	SA052_6	SA052		6	25708867	6,2570886	missense	medium	2.14	R1156W	LRRC16	6p22.2				C:1962	T:477	2439	0.195572	0	TRUE	C:1370	N:0	1370	0	1	FALSE	1	11				
1191	SA053_17	SA053		17	7518264	17,751826	missense	high	4.015	R248B	TP53	17p13.1	p.R248Q	adenocarc	Cancer Cell	DNA_BIND	G:23936	A:4143	28079	0.147548	0	TRUE	G:28894	A:3	28897	0.000104	1	FALSE	2	39			
1192	SA053_2	SA053		2	24804706	2,2480470	nonsense	NA		E915	NCOA1	2p23		Cancer Cell	REGION	//	G:13276	T:2669	15945	0.167388	0	TRUE	G:23726	A:4	23730	0.000169	1	FALSE	1	27			
1193	SA053_2	SA053		2	27018373	2,2701837	missense	medium	1.99	A381T	DYP5L1	2p23.3		CONFLICT	//	G:12156	A:1395	13551	0.102944	0	TRUE	G:13606	C:4	13610	0.000294	1	FALSE	0	0				
1194	SA053_5	SA053		5	63532452	5,6353245	missense	medium	2.105	R21H	RNF180	5q12.2		TOPO_DON	G:7595	A:1446	9741	0.220306	0	TRUE	G:3175	T:1	3176	0.000315	1	FALSE	3	0					
1195	SA054_10	SA054		10	37548106	10,375481	missense	low	1.37	E1154K	ANKRD30A	10p11.21		COILED	//	G:622	A:183	805	0.227329	1.04E-300	TRUE	G:185	N:0	185	0	1	FALSE	1	1				
1196	SA054_10	SA054		10	856746	10,856746	missense	medium	2.19	K508N	LARP5	10p15.3				C:5289	G:382	5671	0.06736	0	TRUE	C:4081	A:1	4082	0.000245	1	FALSE	1	137				
1197	SA054_11	SA054		11	1.22E+08	11,122335	missense	neutral	-1.5	E747G	C11orf63	11q24.1				A:21545	G:7145	28690	0.249041	0	TRUE	A:19100	C:5	19105	0.000262	1	FALSE	1	8				
1198	SA054_11	SA054		11	18711700	11,187117	nonsense	NA		Y353	PTPN5	11p15.1		Entrez Que	DOMAIN	//	G:7761	T:966	8727	0.110691	0	TRUE	G:6832	A:2	6834	0.000293	1	FALSE	0	0			
1199	SA054_11	SA054		11	67927594	11,679275	missense	medium	2.695	F551C	LRP5	11q13.4		Cancer Cell	REGION	//	T:122	G:43	165	0.260606	3.44E-73	TRUE	T:125	N:0	125	0	1	FALSE	2	21			
1200	SA054_12	SA054		12	1.08E+08	12,107727	missense	medium	1.97	S162C	SSH1	12q24.11		Entrez Query :: Phosph	T:1847	A:378	2225	0.169888	0	TRUE	T:2827	C:1	2828	0.000354	1	FALSE	1	7					
1201	SA054_12	SA054		12	14867507	12,148675	missense	neutral	0	I124T	C12orf60	12p12.3				T:27953	C:4299	32252	0.133294	0	TRUE	T:24824	C:5	24829	0.000201	1	FALSE	1	3				
1202	SA054_12	SA054		12	53706700	12,537067	missense	low	1.04	R705S	NEUROD4	12q13.2				G:22350	T:3877	26227	0.147825	0	TRUE	G:19588	C:2	19590	0.000102	1	FALSE	0	0				
1203	SA054_12	SA054		12	54812323	12,548123	missense	low	1.54	L308F	FAM62A	12q13.2				A:14836	T:1867	16703	0.111776	0	TRUE	A:6241	G:1	6242	0.000106	1	FALSE	1	44				
1204	SA054_12	SA054		12	873988	12,873988	G,C	NA								G:10913	C:1108	12021	0.092172	0	TRUE	G:1780	N:0	1780	0	1	FALSE	1	4				
1205	SA054_13	SA054		13	27899347	13,278993	missense	medium	2.06	P462L	FLT1	13q12		Entrez Que	DISULFID	//	G:30432	A:5838	36270	0.160599	0	TRUE	G:39875	A:4	39879	0.0001	1	FALSE	1	13			
1206	SA054_14	SA054		14	31972716	14,319727	missense	low	1.61	V89F	AKAP6	14q13.1		Entrez Query :: Protein	A:35546	T:14311	49857	0.287041	0	TRUE	A:36740	C:9	36749	0.000245	1	FALSE	3	0					
1207	SA054_14	SA054		14	35166561	14,351665	missense	medium	2.86	D1609H	GARL1	14q13.2		REGION	//	C:208	G:29	237	0.122363	8.08E-39	TRUE	C:240	N:0	240	0	1	FALSE	1	7				
1208	SA054_14	SA054		14	60256864	14,602568	missense	medium	2.255	D306N	SIX4	14q13.2				C:15100	T:3372	18472	0.182547	0	TRUE	C:10177	T:2	10179	0.000196	1	FALSE	2	4				
1209	SA054_14	SA054		14	70513790	14,705137	missense	low	1.04	S328C	PCNX	14q24.2				C:910	G:391	1301	0.300538	0	TRUE	C:1756	N:0	1756	0	1	FALSE	2	6				
1210	SA054_15	SA054		15	49536935	15,495369	missense	low	1.4	R2718H	DMXL2	15q21.2				C:14935	T:4454	19389	0.229718	0	TRUE	C:21551	T:8	21559	0.000371	1	FALSE	1	9				
1211	SA054_15	SA054		15	64393430	15,643934	G,C	NA								G:514	C:75	589	0.127334	1.24E-84	TRUE	G:917	N:0	917	0	1	FALSE	3	0				
1212	SA054_17	SA054		17	10299092	17,102990	missense	medium	3.375	T776P	MYH4	17p13.1		DOMAIN	//	T:11906	G:1915	13821	0.138557	0	TRUE	T:18095	C:4	18099	0.000221	1	FALSE	1	1				
1213	SA054_17	SA054		17	20157950	17,201579	missense	high	4.12	V1063N	SPECC1	17p11.2		DOMAIN	//	T:1464	A:466	1930	0.241451	0	TRUE	T:1211	C:1	1212	0.000825	1	FALSE	1	10				
1214	SA054_17	SA054		17	3575620	17,357562	missense	neutral	0.61	E548K	GS2	17p13		Entrez Que	DOMAIN	//	G:5960	A:662	6622	0.09997	0	TRUE	G:4053	C:1	4054	0.000247	1	FALSE	1	4			
1215	SA054_18	SA054		18	50747050	18,507470	missense	medium	2.16	S221F	CDC68	18q21		COILED	//	G:12960	A:3219	25179	0.127845	0	TRUE	G:25488	T:4	25492	0.000157	1	FALSE	1	2				
1216	SA054_19	SA054		19	55911530	19,559115	missense	low	1.87	N91K	SHANK1	19q13.3				G:5949	T:2199	8148	0.269882	0	TRUE	G:1973	N:0	1973	0	1	FALSE	1	1				
1217	SA054_1	SA054		1	1E+08	1,1003596	missense	neutral	0.755	V110A	SA556	1p21.2				A:12579	G:1738	14317	0.121394	0	TRUE	A:21198	C:2	21200	9.43E-05	1	FALSE	1	2				
1218	SA054_1	SA054		1	9000908	1,9000908	missense	medium	2.805	Q184E	SLC2A7	1p36.2		TRANSMEN	G:578	C:857	1435	0.597213	0	TRUE	G:1341	T:2	1343	0.001489	1	FALSE	0	0					
1219	SA054_2	SA054		2	1.09E+08	2,1087554	missense	low	1.61	R2697T	RANBP2	2q12.3		Cancer Rev	REGION	//	G:6998	C:1063															

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.pos	Ref.count	Alt.count	Total.count	Alt.frequer	Binomial.te	Binomial.te	Ref.count	Alt.count	Total.count	Alt.frequer	Binomial.te	Binomial.te	SVNMix2.C	REF.RNASE
1244	SA056_6_1	SA056	6	1.3E+08	G.1296544	missense	neutral	0.02	H931D	LAMA2	6q22-q23				DISULFID //	C:19170	G:4577	23747	0.19274	0	TRUE	C:68615	A:26	68641	0.000379	1	FALSE	1	3
1245	SA056_6_2	SA056	6	1.37E+08	G.1366387	missense	low	0.805	A5397	BCLA1F	6q22-q23				C:20076	T:4169	24245	0.171953	0	TRUE	C:71520	A:8	71528	0.0000112	1	FALSE	1	235	
1246	SA056_6_3	SA056	6	1.53E+08	G.1527161	missense	low	1.61	M3742I	SYNE1	6q25				TOPO_DOM	C:836	A:187	1023	0.182796	1.21E-293	TRUE	C:590	N:0	590	0	1	FALSE	2	1
1247	SA056_6_3	SA056	6	35362119	G.6356211	missense	medium	2.34	D66G	ZNF76	6p21.3-p21.2				REPEAT //	A:16994	G:10369	27363	0.378942	0	TRUE	A:24145	G:5	24150	0.000207	1	FALSE	2	8
1248	SA063_17	SA063	17	7518269	G.1751826	missense	high	3.785	M246T	TP53	17p13.1	p.M246K,p	blast_phas	Cancer Cell	DNA_BIND	A:6886	G:11207	18093	0.619411	0	TRUE	A:19119	C:12	19131	0.000627	1	FALSE	3	16
1249	SA065_10	SA065	10	1.21E+08	G.10120857	missense	NA		T50R	FAM45A					C:58283	G:25236	83519	0.302159	0	TRUE	C:84918	A:33	84951	0.000388	1	FALSE	2	17	
1250	SA065_10	SA065	10	18282251	G.1018282	missense	low	1.52	L14V	SLC39A12	10p12.33				TOPO_DOM	T:19231	G:5494	24725	0.222204	0	TRUE	T:11911	C:2	11913	0.000168	1	FALSE	0	0
1251	SA065_10	SA065	10	25901779	G.10259017	missense	low	1.775	F570L	GPR158	10p12.1				TOPO_DOM	C:493	G:409	902	0.453437	0	TRUE	C:740	N:0	740	0	1	FALSE	1	3
1252	SA065_10	SA065	10	27392983	G.10273929	missense	neutral	0	D435V	ANKRD26	10pter-q22.1				C:195	A:43	238	0.180672	6.62E-57	TRUE	C:551	T:1	552	0.001812	1	FALSE	1	23	
1253	SA065_10	SA065	10	47991151	G.10479911	missense	neutral	0.695	G205C	ZNF488	10q11.22				G:108458	T:31449	139907	0.224785	0	TRUE	G:44102	C:4	44106	9.07E-05	1	FALSE	0	0	
1254	SA065_10	SA065	10	70935967	G.10709359	missense	neutral	0.505	M234V	TSPAN15	10q21.3				TOPO_DOM	A:1839	G:2027	3866	0.524315	0	TRUE	A:3045	N:0	3045	0	1	FALSE	2	45
1255	SA065_10	SA065	10	74928946	G.10749289	nonsense	NA		S150I	USP54	10q22.2				G:87054	C:26761	113815	0.235127	0	TRUE	G:117609	C:18	117627	0.000153	1	FALSE	1	23	
1256	SA065_11	SA065	11	1.11E+08	G.11111080	missense	NA		V334M	SNF1LK2	11q23.1				DOMAIN //	G:8881	A:1834	10715	0.171162	0	TRUE	G:15422	A:1	15423	6.48E-05	1	FALSE	1	61
1257	SA065_11	SA065	11	1.19E+08	G.11118796	missense	medium	2.3	K59N	THY1	11q22.3-q23				Entrez Quer	C:87473	G:15567	103040	0.151077	0	TRUE	C:41073	A:10	41083	0.000243	1	FALSE	1	460
1258	SA065_11	SA065	11	478590	G.11478590	missense	medium	1.905	E266V	PTDS22	11p15				TOPO_DOM	A:250	T:119	369	0.322493	7.68E-185	TRUE	A:460	N:0	460	0	1	FALSE	2	15
1259	SA065_11	SA065	11	56825978	G.11568259	missense	low	0.92	R1617Q	TNK51BP1	11q12.1				COMPIAS	C:1746	T:739	2485	0.297384	0	TRUE	C:1983	N:0	1983	0	1	FALSE	2	114
1260	SA065_12	SA065	12	1.19E+08	G.12119382	missense	NA		H135Q	GATC	12q24.31				C:61470	A:20532	82002	0.250384	0	TRUE	C:58573	T:9	58582	0.000154	1	FALSE	2	27	
1261	SA065_13	SA065	13	74821345	G.13748213	missense	medium	2.85	P457R	TBC1D4	13q22.2				DOMAIN //	G:474	C:230	704	0.326705	0	TRUE	G:649	N:0	649	0	1	FALSE	2	73
1262	SA065_14	SA065	14	30645895	G.14306458	missense	low	1.5	D2312N	HECTD1	14q12				DOMAIN //	C:1865	T:304	2169	0.140157	0	TRUE	C:492	N:0	492	0	1	FALSE	1	78
1263	SA065_14	SA065	14	35839781	G.14358397	missense	NA		V334M	SNF1LK2	11q23.1				C:18244	G:7066	25310	0.179178	0	TRUE	C:14051	N:0	14051	0	1	FALSE	2	5	
1264	SA065_14	SA065	14	37794204	G.14377942	missense	low	0.975	L259I	CLEC14A	14q21.1				DOMAIN //	G:20341	T:7390	27731	0.266489	0	TRUE	G:20113	A:4	20117	0.000199	1	FALSE	1	22
1265	SA065_15	SA065	15	69322466	G.15693224	nonsense	NA		Q297	THSD4	15q23				DOMAIN //	C:141	T:615	756	0.813492	0	TRUE	C:812	N:0	812	0	1	FALSE	3	0
1266	SA065_15	SA065	15	70430572	G.15704305	missense	medium	2.565	S210A	HEXA	15q23-q24				VARIANT //	A:178124	C:62268	240392	0.259027	0	TRUE	A:76266	G:17	76283	0.000223	1	FALSE	1	297
1267	SA065_15	SA065	15	98087153	G.15980871	missense	neutral	-0.145	H197D	LYSMOD4	15q26.3				TOPO_DOM	G:1154	C:945	2099	0.450214	0	TRUE	G:2502	T:1	2503	0.0004	1	FALSE	2	16
1268	SA065_16	SA065	16	30983133	G.16309831	missense	neutral	0.69	S50C	ZNF668	16p11.2				G:369	C:745	1114	0.668761	0	TRUE	G:1423	N:0	1423	0	1	FALSE	3	1	
1269	SA065_16	SA065	16	67930893	G.16679308	nonsense	NA		E22	COG8	16q22.1				C:323	A:179	502	0.356574	3.25E-287	TRUE	G:646	T:1	647	0.001546	1	FALSE	1	2	
1270	SA065_17	SA065	17	30703795	G.17307037	missense	medium	1.935	F800S	SLFN11					A:105	G:205	310	0.66129	0	TRUE	A:271	N:0	271	0	1	FALSE	2	52	
1271	SA065_17	SA065	17	30773380	G.17307733	missense	medium	2.265	E261Q	SLFN12	17q12				C:15013	G:2409	17422	0.138273	0	TRUE	C:21036	A:4	21040	0.00019	1	FALSE	1	11	
1272	SA065_17	SA065	17	34921344	G.17349213	nonsense	NA		Y90I	CRKRS					DOMAIN //	C:2283	A:3519	5802	0.606515	0	TRUE	C:24082	A:3	24085	0.000125	1	FALSE	2	17
1273	SA065_17	SA065	17	35134838	G.17351348	missense	high	3.61	R35F5	ERBB2	17q11.2-q12.1	17q21.1		Cancer Cell	DOMAIN //	A:30134	T:52347	82481	0.634655	0	TRUE	A:101443	C:66	101459	0.00065	1	FALSE	3	3
1274	SA065_17	SA065	17	36040603	G.17360406	nonsense	NA		E306	SMARCE1	17q21.2			Cancer Cell	COILED //	C:9717	A:5080	14797	0.343313	0	TRUE	C:11455	A:7	11462	0.000611	1	FALSE	1	258
1275	SA065_17	SA065	17	37590889	G.17375908	missense	medium	2.015	K7N	HCR1	17q21				SIGNAL //	C:10076	A:3127	13203	0.23684	0	TRUE	C:3947	A:1	3948	0.000253	1	FALSE	0	0
1276	SA065_17	SA065	17	59231599	G.17592315	missense	medium	2.74	G171R	DXD42	17q23.3				G:404	C:350	754	0.464191	0	TRUE	G:1029	N:0	1029	0	1	FALSE	2	139	
1277	SA065_17	SA065	17	70751148	G.17707511	missense	neutral	-0.125	D133E	GGA3	17q25.1				DOMAIN //	G:19419	T:9481	28900	0.328062	0	TRUE	G:29895	C:5	29900	0.000167	1	FALSE	2	51
1278	SA065_17	SA065	17	7517622	G.17751762	nonsense	NA		Q317	TP53	17p13.1				MOTIF //	3:G1208	A:3227	4435	0.727621	0	TRUE	G:14594	A:23	14617	0.001574	1	FALSE	2	35
1279	SA065_18	SA065	18	75760472	G.18757604	missense	high	4.335	P357S	KCNKG2	18q22-q23				INTRAMEM	C:179	T:289	468	0.617521	0	TRUE	C:372	N:0	372	0	1	FALSE	1	1
1280	SA065_19	SA065	19	10433667	G.19104336	missense	high	3.915	R579C	PDE4A	19p13.2				HELI //	57:C494	T:244	738	0.330623	0	TRUE	C:865	N:0	865	0	1	FALSE	1	17
1281	SA065_19	SA065	19	15330871	G.19153308	missense	low	1.59	L510F	AKAP8	19p13.1			Cancer Cell	Map Pathw	C:265	G:119	384	0.309896	2.14E-182	TRUE	C:381	T:1	382	0.002618	1	FALSE	2	41
1282	SA065_19	SA065	19	17705172	G.19177051	missense	medium	1.905	E987K	MAP15	19p13.11				REGION //	G:46365	A:23406	69771	0.335469	0	TRUE	G:76365	C:23	76388	0.000301	1	FALSE	2	33
1283	SA065_19	SA065	19	5102454	G.19510245	missense	low	1.1	S1075G	KDM4B	19p13.3				A:3088	G:15792	18880	0.836441	0	TRUE	A:22892	G:13	22905	0.000568	1	FALSE	2	8	
1284	SA065_19	SA065	19	57749713	G.19577497	missense	low	1.89	Q578E	ZNF808	19q13.41				ZN_FING //	C:27901	G:13614	41515	0.32793	0	TRUE	C:41010	G:4	41014	9.75E-05	1	FALSE	2	13
1285	SA065_19	SA065	19	62415911	G.19624159	missense	medium	3.395	G545E	ZNF264	19q13.4				ZN_FING //	G:1104	A:390	1494	0.261004	0	TRUE	G:1840	N:0	1840	0	1	FALSE	2	28
1286	SA065_1_1	SA065	1	1.5E+08	G.1504605	missense	medium	2.35	D50E	HRNR	1q21.3				DOMAIN //	A:1421	T:549	1970	0.27868	0	TRUE	A:180	G:1	181	0.005525	1	FALSE	0	0
1287	SA065_1_1	SA065	1	1.58E+08	G.151580519	missense	neutral	-0.895	S395T	FCRL6	1q23.2				TOPO_DOM	G:49981	C:13964	63945	0.218375	0	TRUE	G:31373	T:4	31377	0.000127	1	FALSE	2	17
1288	SA065_1_1	SA065	1	2.14E+08	G.12139150	missense	low	1.245	E4264K	USH2A	1q41				DOMAIN //	C:98452	T:77672	176124	0.441007	0	TRUE	C:104821	T:16	104837	0.000153	1	FALSE	0	0
1289	SA065_1_1	SA065	1	31969120	G.13196912	missense	low	1.7	Q1416H	BAI2	1p35				TOPO_DOM	C:135	A:607	742	0.818059	0	TRUE	C:606	A:1	607	0.001647	1	FALSE	2	1
1290	SA065_20	SA065	20	1386870	G.20138687	silent	NA		NSFL1C		20p13				C:3906	T:1281	5187	0.246964	0	TRUE	C:5044	N							

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func.Lmpa	FI.score	AA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.pos	Ref.count.	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase	
1313	SA067_17	SA067	17	7519259	17,7519259	missense	high	3.88	K132N	TP53	17p13.1	p.K132E,p	anaplastic	Cancer Cell	DNA_BIND	C:7452	A:1838	9290	0.197847	0	TRUE	C:18510	G:2	18512	0.000108	1	FALSE	2	41	
1314	SA067_21	SA067	21	46903243	21,46903243	missense	low	1.535	F271L	PRMT2	21q22.3				REGION //	C:12078	G:1142	13220	0.086384	0	TRUE	C:18878	A:14	18892	0.000741	1	FALSE	2	164	
1315	SA068_12	SA068	12	10657367	12,10657367	missense	high	4.11	Y11C	FLJ10292	12p13.2					T:41520	C:9444	50964	0.185307	0	TRUE	T:124421	C:230	124651	0.001845	1	FALSE	2	7	
1316	SA068_1_7	SA068	1	71316727	1,71316727	C,T		NA								C:4231	T:1288	5519	0.233376	0	TRUE	C:12489	G:2	12491	0.00016	1	FALSE	2	3	
1317	SA068_20	SA068	20	37065819	20,37065819	missense	medium	2.1	T289N	DHX35	20q11.22-q12				DOMAIN //	C:3246	A:1388	4634	0.299525	0	TRUE	C:4829	N:0	4829	0	1	FALSE	2	23	
1318	SA068_4	SA068	4	69845710	4,69845710	missense	medium	2.515	T26T	UGT2A3	4q13.2				TOPO_DON	A:161	G:81	242	0.334711	1.68E-128	TRUE	A:312	N:0	312	0	1	FALSE	0	0	
1319	SA068_5	SA068	5	1.32E+08	5,131572728	A,T		NA								A:189696	T:77112	266808	0.289017	0	TRUE	A:415691	G:79	415770	0.00019	1	FALSE	3	0	
1320	SA069_10	SA069	10	5812578	10,5812578	missense	neutral	0.55	T204P	C10orf18						A:4067	C:1067	5134	0.20783	0	TRUE	A:1669	N:0	1669	0	1	FALSE	2	103	
1321	SA069_11	SA069	11	32076582	11,32076582	missense	medium	2.16	T187S	RCN1	11p13				CA_BIND //	A:40655	T:12793	53448	0.239354	0	TRUE	A:28217	G:6	28223	0.000213	1	FALSE	2	510	
1322	SA069_12	SA069	12	1.16E+08	12,116080	missense	low	0.805	V468L	FBXO21	12q24.22					C:9960	G:1670	11630	0.143594	0	TRUE	C:16316	A:1	16317	6.13E-05	1	FALSE	2	37	
1323	SA069_12	SA069	12	25152940	12,25152940	missense	medium	2.615	K654Q	CASC1	12p12.1					T:179	G:22	201	0.109453	2.41E-25	TRUE	T:249	N:0	249	0	1	FALSE	1	6	
1324	SA069_14	SA069	14	64323220	14,64323220	missense	low	1.575	D1072E	SPTB	14q23-q24.2				REPEAT //	G:1283	T:539	1822	0.295829	0	TRUE	G:1966	N:0	1966	0	1	FALSE	1	1	
1325	SA069_14	SA069	14	74584520	14,74584520	missense	low	1.845	S531T	MLH3	14q24.3					C:8368	G:1866	10234	0.182333	0	TRUE	C:19283	T:3	19286	0.000156	1	FALSE	2	29	
1326	SA069_16	SA069	16	23609657	16,23609657	missense	neutral	0.345	R926K	ERN2	16p12.2				TOPO_DON	C:1898	T:314	2212	0.141953	0	TRUE	C:3529	N:0	3529	0	1	FALSE	1	5	
1327	SA069_16	SA069	16	27281598	16,27281598	missense	low	1.735	P475R	IL4R	16p12.1-p11.2				REGION //	C:455	G:81	536	0.151119	8.64E-106	TRUE	C:250	N:0	250	0	1	FALSE	1	69	
1328	SA069_16	SA069	16	83039796	16,83039796	missense	medium	2.73	V554M	ATP2C2	16q24.1				TOPO_DON	G:31074	A:4720	35794	0.131866	0	TRUE	G:29732	A:3	29735	0.000101	1	FALSE	2	10	
1329	SA069_17	SA069	17	24075902	17,24075902	missense	low	1.165	L166P	TLCD1	17q11.2				DOMAIN //	A:11097	G:3851	14948	0.257626	0	TRUE	A:10842	T:2	10844	0.000184	1	FALSE	2	50	
1330	SA069_17	SA069	17	69989053	17,69989053	missense	neutral	0.55	P220H	CD300A	17q25.1				TOPO_DON	C:6233	A:1377	7610	0.180946	0	TRUE	C:12552	A:4	12556	0.000319	1	FALSE	1	37	
1331	SA069_18	SA069	18	66143848	18,66143848	missense	low	1.54	I322L	SOC56	18q22.2				Cancer Cell	Map Pathw	A:4479	C:583	5062	0.115172	0	TRUE	A:1385	N:0	1385	0	1	FALSE	1	42
1332	SA069_19	SA069	19	14378953	19,14378953	missense	low	1.865	R763P	CD97	19p13				TOPO_DON	G:2113	C:408	2521	0.161841	0	TRUE	G:4939	T:1	4940	0.000202	1	FALSE	1	56	
1333	SA069_19	SA069	19	42561955	19,42561955	missense	medium	3.305	M43V	ZNF527					DOMAIN //	A:20703	G:2272	22975	0.09889	0	TRUE	A:29142	G:8	29150	0.000274	1	FALSE	1	33	
1334	SA069_1_1	SA069	1	1.58E+08	1,1582784	missense	medium	3.165	L153P	CNN10	1q22-q23				TRANSMEN	A:1815	G:701	2516	0.278617	0	TRUE	A:1607	G:1	1608	0.000622	1	FALSE	1	1	
1335	SA069_1_2	SA069	1	2.08E+08	1,2078498	missense	low	1.875	D252E	CAMK1G	1q32-q41				Entrez Que	DOMAIN //	C:21471	A:4943	25514	0.158462	0	TRUE	C:15876	T:5	15881	0.000315	1	FALSE	0	0
1336	SA069_1_4	SA069	1	44892966	1,44892966	missense	medium	2.945	T229V	TMEM53	1p34.1					T:61864	A:9563	71427	0.133885	0	TRUE	T:31374	G:4	31378	0.000127	1	FALSE	2	18	
1337	SA069_20	SA069	20	33704594	20,33704594	missense	low	1.83	G689R	RBM12	20q11.21				COMPMIAS	C:1080	G:224	1304	0.171779	0	TRUE	C:1643	N:0	1643	0	1	FALSE	2	37	
1338	SA069_20	SA069	20	60993799	20,60993799	missense	medium	2.885	K1110N	DIDO1	20q13.33				Entrez Query :: Tumor	C:5190	G:963	6153	0.156509	0	TRUE	C:3641	A:1	3642	0.000275	1	FALSE	2	34	
1339	SA069_22	SA069	22	30828132	22,30828132	missense	high	3.965	H525Y	SLC5A1	22q13.11	22q13.1			TOPO_DON	C:1969	T:394	2363	0.166737	0	TRUE	C:1155	N:0	1155	0	1	FALSE	2	7	
1340	SA069_2_2	SA069	2	1.49E+08	2,1498642	missense	low	1.04	E1281D	MBD5	2q23.1					G:692	C:168	860	0.195349	1.16E-239	TRUE	G:267	N:0	267	0	1	FALSE	1	86	
1341	SA069_2_2	SA069	2	2.38E+08	2,2379615	nonsense		NA	S250	COL6A3	2q37				CARBOHYD	G:5965	T:1152	7117	0.161866	0	TRUE	G:12813	A:5	12818	0.00039	1	FALSE	1	86	
1342	SA069_2_4	SA069	2	41900619	2,41900619	silent		NA		LDHAL3						T:6159	C:1294	7453	0.173621	0	TRUE	T:9310	C:3	9313	0.000322	1	FALSE	0	0	
1343	SA069_3_1	SA069	3	1.84E+08	3,1843544	missense	low	1.87	T144R	LAMP3	3q26.3-q27				COMPMIAS	G:33907	C:2566	36473	0.703053	0	TRUE	G:29301	C:9	29310	0.000307	1	FALSE	1	93	
1344	SA069_3_4	SA069	3	49666383	3,49666383	missense	low	1.7	P1464T	BSN	3p21.31					C:2283	A:567	2850	0.198947	0	TRUE	C:3809	N:0	3809	0	1	FALSE	0	0	
1345	SA069_4_1	SA069	4	1.39E+08	4,1393213	missense	low	1.52	H373Q	SLC7A11	4q28-q32				TRANSMEN	G:4352	T:942	5294	0.177937	0	TRUE	G:8231	C:1	8232	0.000121	1	FALSE	3	0	
1346	SA069_4_7	SA069	4	72535805	4,72535805	missense	medium	2.095	M415I	SLC4A4					TOPO_DON	G:523	A:215	738	0.291328	0	TRUE	G:529	C:1	530	0.001887	1	FALSE	0	0	
1347	SA069_5_1	SA069	5	1.69E+08	5,1689507	missense	low	1.85	V106M	CCDC99	5q35.1				COILED //	G:1442	A:647	2089	0.309718	0	TRUE	G:2256	N:0	2256	0	1	FALSE	2	16	
1348	SA069_6_1	SA069	6	1.53E+08	6,1525110	nonsense		NA	S8270	SYNE1	6q25				MOD_RES	G:16217	C:3388	19605	0.172813	0	TRUE	G:18954	C:4	18958	0.000211	1	FALSE	1	22	
1349	SA069_6_1	SA069	6	15605293	6,15605293	missense	medium	2.465	R620C	JARID2	6p24-p23				DOMAIN //	C:5000	T:786	5786	0.135845	0	TRUE	C:5435	G:2	5437	0.000368	1	FALSE	1	8	
1350	SA069_6_1	SA069	6	1.6E+08	6,1604129	missense	medium	2.215	N1482K	IGF2R	6q26				Entrez Que	REPEAT //	C:17904	G:3592	21496	0.167101	0	TRUE	C:17915	T:4	17919	0.000223	1	FALSE	2	41
1351	SA069_6_2	SA069	6	28651644	6,28651644	missense	low	1.735	L273M	ZNF452	6p22.1				COILED //	T:34974	T:18092	53066	0.340934	0	TRUE	A:34407	G:1	34408	2.91E-05	1	FALSE	0	0	
1352	SA069_7_1	SA069	7	1.06E+08	7,1062963	missense	low	0.975	K364M	PIK3CG	7q22.3				Cancer Cell	STRAND //	A:1857	T:724	2581	0.280511	0	TRUE	A:2589	G:2	2591	0.000772	1	FALSE	1	7
1353	SA069_7_1	SA069	7	1.43E+08	7,1427589	missense	medium	1.95	G898V	CLCN1	7q32-qter	7q35			TOPO_DON	G:1582	T:707	2289	0.308869	0	TRUE	G:2423	N:0	2423	0	1	FALSE	1	3	
1354	SA069_7_1	SA069	7	1.48E+08	7,1484327	missense	neutral	-0.135	I399T	ZNF425	7q36.1				ZN_FING //	A:853	G:245	1098	0.223133	0	TRUE	A:1028	N:0	1028	0	1	FALSE	0	0	
1355	SA069_7_4	SA069	7	43560770	7,43560770	missense	medium	2.635	F1522Y	HECW1	7p14.1-p13				DOMAIN //	T:564	A:161	725	0.222069	1.35E-239	TRUE	T:194	N:0	194	0	1	FALSE	3	0	
1356	SA069_7_4	SA069	7	43560771	7,43560771	missense	medium	2.485	F1522L	HECW1	7p14.1-p13				DOMAIN //	C:563	A:161	724	0.222376	1.08E-239	TRUE	C:194	N:0	194	0	1	FALSE	3	0	
1357	SA069_9_2	SA069	9	1.35E+08	9,1347625	missense	low	1.145	A944V	TSC1	9q34				Cancer Rev	COILED //	G:10110	A:2112	12222	0.172803	0	TRUE	G:11563	C:4	11567	0.000346	1	FALSE	1	38
1358	SA069_9_2	SA069	9	27940482	9,27940482	missense	medium	3.435	D63G	LINGO2	9p21.2-p21.1				REPEAT //	T:20883	C:3613	24496	0.147493	0	TRUE	T:20359	C:22	20381	0.001079	1	FALSE	0	0	
1359	SA069_9_1	SA069	X	17655314	X,17655314	missense	medium																							

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func.Lmpa	FI.score	AA.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.pos	Ref.count	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count.T	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase	
1382	SA071_17	SA071	17	11495115	17,11495115	missense	low	1.07	T701T	DNAH9	17p12				REGION //	T:45745	C:10890	56635	0.192284	0	TRUE	T:74264	C:20	74284	0.000269	1	FALSE	0	0	
1383	SA071_17	SA071	17	23628466	17,23628466	missense	neutral	0	P46T	FLJ40504	17q11.2				G:7909	T:4682	12591	0.371853	0	TRUE	G:35182	C:6	35188	0.000171	1	FALSE	0	0		
1384	SA071_17	SA071	17	36978333	17,36978333	missense	medium	2.58	H375Y	KRT9	17q21.1-q21.2				REGION //	T:4919	A:4914	6511	0.754723	0	TRUE	G:7721	A:5	7726	0.000647	1	FALSE	3	0	
1385	SA071_18	SA071	18	68568397	18,68568397	missense	medium	2.28	N474I	NETO1	18q22-q23				TOPO_DOM	T:17808	A:3627	21435	0.169209	0	TRUE	T:15342	C:4	15346	0.000261	1	FALSE	0	0	
1386	SA071_18	SA071	18	8623287	18,8623287	missense	high	3.725	F130I	RAB12	18p11.22				HELIX // 12	T:3796	A:566	4362	0.129757	0	TRUE	T:3234	N:0	3234	0	1	FALSE	1	167	
1387	SA071_19	SA071	19	22289454	19,22289454	nonsense	NA		C46S	LOC100130518					ZN_FING //	T:6889	A:3986	10875	0.366529	0	TRUE	T:28379	C:22	28401	0.000775	1	FALSE	0	0	
1388	SA071_19	SA071	19	39379479	19,39379479	missense	medium	2.085	V129G	LSM14A	19q13.11				T:453	G:119	572	0.208042	6.97E-168	0	TRUE	T:2824	N:0	2824	0	1	FALSE	2	69	
1389	SA071_19	SA071	19	58454336	19,58454336	missense	neutral	-0.09	C299F	VN1R2	19q13.41				TOPO_DOM	G:17110	T:9301	26411	0.352164	0	TRUE	G:13593	A:3	13596	0.000221	1	FALSE	0	0	
1390	SA071_1_1	SA071	1	1.03E+08	1,1032639	missense	medium	1.95	G309V	COL11A1	1p21				C:94	A:42	136	0.308824	3.28E-67	0	TRUE	C:144	N:0	144	0	1	FALSE	1	1	
1391	SA071_1_1	SA071	1	1.52E+08	1,1522077	missense	low	1.78	V37D	CREB3L4	1q21.3				TOPO_DOM	T:174	A:143	317	0.451104	2.68E-261	0	TRUE	T:360	G:1	361	0.00277	1	FALSE	1	8
1392	SA071_1_1	SA071	1	1.77E+08	1,1771008	missense	medium	2.075	L233V	ANGPTL1	1q25.2				G:18847	C:6445	25292	0.254824	0	TRUE	G:15668	A:1	15669	6.38E-05	1	FALSE	1	3		
1393	SA071_1_2	SA071	1	20096709	1,20096709	missense	medium	2.095	D191E	OTUD3					C:4843	G:2570	7413	0.346688	0	TRUE	C:27434	A:5	27439	0.000182	1	FALSE	2	5		
1394	SA071_1_2	SA071	1	2.04E+08	1,2041593	missense	medium	1.935	Q507K	SLC26A9	1q31-q32				G:8432	T:2916	11348	0.256962	0	TRUE	G:18657	A:7	18664	0.000375	1	FALSE	0	0		
1395	SA071_1_2	SA071	1	2.08E+08	1,2078725	missense	neutral	0.71	P269S	LAMB3	1q32				CONFLICT	G:1592	A:813	2405	0.338046	0	TRUE	G:3050	N:0	3050	0	1	FALSE	1	2	
1396	SA071_1_6	SA071	1	60293643	1,60293643	missense	low	0.805	T75A	C1orf87	1p32.1				T:512	C:223	735	0.330401	0	TRUE	T:772	C:1	773	0.001294	1	FALSE	0	0		
1397	SA071_22	SA071	22	30884998	22,30884998	missense	neutral	0	T69S	LOC15029	22q12.3				T:21798	A:5473	27271	0.200689	0	TRUE	T:23323	C:14	23337	0.0006	1	FALSE	0	0		
1398	SA071_2_2	SA071	2	1E+08	2,1004651	missense	NA		D147E	NMS	2q11.2				PROPEP //	T:561	G:165	726	0.227273	6.90E-240	0	TRUE	T:405	N:0	405	0	1	FALSE	0	0
1399	SA071_2_2	SA071	2	2.38E+08	2,2379684	missense	medium	3.47	F61I	COL6A3	2q37				DOMAIN //	A:3634	T:835	4469	0.186843	0	TRUE	A:10044	C:2	10046	0.000199	1	FALSE	1	3	
1400	SA071_2_2	SA071	2	26652377	2,26652377	missense	medium	2.125	S60G	LOC339778					A:17299	G:4774	22073	0.216282	0	TRUE	A:15260	C:4	15264	0.000262	1	FALSE	0	0		
1401	SA071_2_2	SA071	2	27654869	2,27654869	missense	neutral	0.345	E642D	C2orf16	2p23.3				A:15342	T:4427	19769	0.223936	0	TRUE	A:22425	C:6	22431	0.000267	1	FALSE	1	2		
1402	SA071_2_2	SA071	2	27656944	2,27656944	missense	neutral	0.55	T1334I	C2orf16	2p23.3				C:10751	T:3665	14416	0.254231	0	TRUE	C:9482	T:5	9487	0.000527	1	FALSE	3	0		
1403	SA071_2_2	SA071	2	9976649	2,9976649	missense	medium	2.015	V434H	TAF1B	2p25				T:3103	T:3660	4763	0.34852	0	TRUE	T:8300	C:1	8301	0.00012	1	FALSE	2	11		
1404	SA071_3_3	SA071	3	10322369	3,10322369	missense	medium	3.275	C153S	SEC13	3p25-p24				REPEAT //	C:1081	G:509	1590	0.320126	0	TRUE	C:1832	N:0	1832	0	1	FALSE	2	97	
1405	SA071_3_3	SA071	3	1.13E+08	3,1130857	missense	low	1.87	P40S	PHLDB2	3q13.2				C:302	T:123	425	0.289412	1.66E-193	0	TRUE	C:781	N:0	781	0	1	FALSE	1	6	
1406	SA071_3_3	SA071	3	1.15E+08	3,1148586	missense	medium	2.14	V1519G	KIAA2018	3q13.2				COMPBias	A:1112	C:551	1663	0.331329	0	TRUE	A:2052	G:1	2053	0.000487	1	FALSE	2	15	
1407	SA071_3_3	SA071	3	1.28E+08	3,1276201	missense	medium	2.06	R174Q	CDC37	3q21.2				COILED //	G:1069	A:533	1602	0.332709	0	TRUE	G:2030	N:0	2030	0	1	FALSE	0	0	
1408	SA071_3_3	SA071	3	32890383	3,32890383	missense	medium	2.28	G308C	TRIM71	3p22.3				ZN_FING //	G:862	T:1116	1978	0.546206	0	TRUE	G:2817	N:0	2817	0	1	FALSE	0	0	
1409	SA071_3_3	SA071	3	77654662	3,77654662	missense	medium	2.63	S285S	ROBO2	3p12.3				DISULFID //	A:83	T:96	179	0.536313	2.31E-185	0	TRUE	A:333	N:0	333	0	1	FALSE	0	0
1410	SA071_4_4	SA071	4	71102600	4,71102600	missense	neutral	0.425	P205S	ODAM	4q13.3				COMPBias	C:214	T:191	405	0.471605	0	TRUE	C:721	N:0	721	0	1	FALSE	0	0	
1411	SA071_5_5	SA071	5	1272669	5,1272669	missense	low	1.6	N476K	SLC6A19	5p15.33				TRANSMEN	C:853	A:396	1249	0.317054	0	TRUE	C:1173	N:0	1173	0	1	FALSE	0	0	
1412	SA071_5_5	SA071	5	1.5E+08	5,1498877	missense	medium	3.325	A241V	NDST1	5q33.1				REGION //	C:1863	T:1820	3683	0.494162	0	TRUE	C:4385	T:1	4386	0.000228	1	FALSE	2	5	
1413	SA071_5_5	SA071	5	1.5E+08	5,150390503	T,G	NA									T:55115	G:58354	113469	0.514273	0	TRUE	T:119084	C:19	119103	0.00016	1	FALSE	2	3	
1414	SA071_5_5	SA071	5	1.77E+08	5,1766548	missense	neutral	0.55	A2634S	NSD1	5q35.2-q35.3				Cancer Cell Map Pathw	G:729	T:875	1604	0.545511	0	TRUE	G:2599	C:1	2600	0.000385	1	FALSE	2	9	
1415	SA071_5_5	SA071	5	24523851	5,24523851	missense	medium	2.77	E682G	CDH10	5p14-p13				TOPO_DOM	T:327	C:1867	5074	0.367954	0	TRUE	T:15024	C:5	15029	0.000333	1	FALSE	0	0	
1416	SA071_5_5	SA071	5	7855337	5,7855337	missense	high	4.165	V879Y	ADCY2	5p15.3				TOPO_DOM	T:27313	C:12122	39435	0.307392	0	TRUE	T:21129	C:6	21135	0.000284	1	FALSE	2	22	
1417	SA071_6_6	SA071	6	1.14E+08	6,1144906	missense	low	1.845	L27I	H3S2T5	6q22.31				TRANSMEN	G:2141	T:1042	3183	0.327364	0	TRUE	G:1243	N:0	1243	0	1	FALSE	0	0	
1418	SA071_6_6	SA071	6	26312865	6,26312865	missense	NA			H1ST1H4E	6p21.3				G:17342	A:9044	26386	0.342758	0	TRUE	G:39921	A:46	39967	0.001151	1	FALSE	2	38		
1419	SA071_6_6	SA071	6	33277507	6,33277507	missense	low	1.605	G140V	SLC39A7	6p21.3				TRANSMEN	G:2656	T:1386	4042	0.3429	0	TRUE	G:7463	N:0	7463	0	1	FALSE	2	100	
1420	SA071_6_6	SA071	6	39155413	6,39155413	missense	medium	2.34	R380H	GLP1R	6p21				TOPO_DOM	G:973	A:425	1398	0.304006	0	TRUE	G:2058	A:1	2059	0.000486	1	FALSE	0	0	
1421	SA071_6_6	SA071	6	6211963	6,6211963	missense	medium	3.35	A133D	F13A1	6p25.3-p24.3				Entrez Que	STRAND //	G:4816	T:1859	6675	0.278502	0	TRUE	G:9690	A:5	9695	0.000516	1	FALSE	1	14
1422	SA071_6_6	SA071	6	75932096	6,75932096	missense	medium	2.19	D944H	COL12A1	6q12-q13				DOMAIN //	G:5030	G:2756	7786	0.353969	0	TRUE	C:25025	A:5	25030	0.0002	1	FALSE	1	14	
1423	SA071_6_6	SA071	6	83948193	6,83948193	missense	medium	1.98	S256R	PGM3	6q14.1-q15				A:434	C:310	744	0.416667	0	TRUE	A:838	G:1	839	0.001192	1	FALSE	2	34		
1424	SA071_7_7	SA071	7	1E+08	7,1004715	missense	low	0.805	V3365G	MUC17	7q22.1				COMPBias	T:25211	G:2378	27589	0.086194	0	TRUE	T:39506	C:7	39513	0.000177	1	FALSE	0	0	
1425	SA071_7_7	SA071	7	4180516	7,4180516	missense	NA		A1646	SDK1	7p22.2				DOMAIN //	G:20415	A:35444	55859	0.634526	0	TRUE	G:94334	A:12	94346	0.000127	1	FALSE	0	0	
1426	SA071_7_7	SA071	7	45692702	7,45692702	missense	medium	2.175	P787T	ADCY1	7p13-p12				TRANSMEN	C:205	A:468	673	0.695394	0	TRUE	G:766	N:0	766	0	1	FALSE	0	0	
1427	SA071_7_7	SA071	7	66047533	7,66047533	missense	medium	2.3	O99E	C7orf42	7q11.21				C:21316	G:10530	31846	0.330654	0	TRUE	C:16040	A:5	16045	0.000312	1	FALSE	2	104		
1428	SA071_7_7	SA071	7	92773211	7,92773211	missense	low	1.78	H530V	CCDC132	7q21.3				C:7239	T:2187	9436	0.232832	0	TRUE	C:26503	T:3	26506	0.000113	1	FALSE	1	34		

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.pos	Ref.count	Alt.count.T	Total.count	Alt.frequer	Binomial.te	Binomial.te	Ref.count.T	Alt.count.N	Total.count	Alt.frequer	Binomial.te	Binomial.te	SVNMix2.C	REF.RNASE
1451	SA074_19	SA074	19	59475500	19,594755	missense	neutral	-1.05	R105W	LILRB2	19q13.4				DOMAIN //	G:6224	A:1876	8100	0.231605	0	TRUE	G:4357	A:1	4358	0.000229	1	FALSE	1	19
1452	SA074_1	SA074	1	93452965	1,9345296	missense	low	1.175	E24V	CDCDC18	1p22.1				COILED //	A:1815	G:269	2084	0.129079	0	TRUE	A:459	N:0	459	0	1	FALSE	1	11
1453	SA074_20	SA074	20	2584036	20,258403	missense	medium	2.68	R121H	NOP56	20p13				G:20929	A:2357	23286	0.10122	0	TRUE	G:15054	A:4	15058	0.000266	1	FALSE	2	429	
1454	SA074_20	SA074	20	41521915	20,415219	missense	high	3.725	N116S	SFR56	20q12-q13.1				DOMAIN //	A:4088	G:506	4594	0.110144	0	TRUE	A:1644	G:1	1645	0.000608	1	FALSE	2	294
1455	SA074_20	SA074	20	51627127	20,516271	missense	low	1.2	D528G	ZNF217	20q13.2				T:11590	C:1262	12852	0.098195	0	TRUE	T:13724	C:4	13728	0.000291	1	FALSE	1	72	
1456	SA074_2	SA074	2	1.18E+08	2.1184324	missense	medium	2.825	R317G	CDCDC93	2q14.1				COILED //	G:14404	T:16975	16975	0.151458	0	TRUE	G:19826	T:3	19829	0.000151	1	FALSE	1	23
1457	SA074_2	SA074	2	2.19E+08	2.2192171	missense	medium	1.95	L794F	ZNF142	2q34-q35				C:18796	A:6839	25635	0.266784	0	TRUE	C:15372	T:7	15379	0.000455	1	FALSE	2	17	
1458	SA074_3	SA074	3	1.5E+08	3.1504079	missense	neutral	-1.235	A303T	CP	3q23-q25			Entrez Query	DISULFID //	C:8180	T:1675	9855	0.169964	0	TRUE	C:13029	A:2	13031	0.000153	1	FALSE	1	23
1459	SA074_6	SA074	6	43260253	6,4326025	missense	medium	2.445	C76F	PARC	6p21.1				G:7865	T:1325	9190	0.144178	0	TRUE	G:8653	A:6	8659	0.000693	1	FALSE	2	7	
1460	SA074_7	SA074	7	87237891	7,8723789	missense	medium	2.39	E247K	RUNCDC38	7q21.12				G:9598	A:1179	10777	0.1094	0	TRUE	G:14969	A:3	14972	0.0002	1	FALSE	1	3	
1461	SA074_9	SA074	9	85685087	9,8568508	missense	neutral	0.27	N863T	KIF27	9q21.32				COILED //	T:1565	G:212	1777	0.119302	3.51E-280	TRUE	T:2319	N:0	2319	0	1	FALSE	1	7
1462	SA074_X	SA074	X	70544230	X,7054423	missense	NA		M1396V	TAF1	Xq13.1				DOMAIN //	A:14607	G:4252	18859	0.225463	0	TRUE	A:25100	G:6	25106	0.000239	1	FALSE	2	10
1463	SA075_11	SA075	11	1.18E+08	11,118425	missense	medium	1.985	E561D	HYOU1	11q23.1-q23.3				C:14141	G:7073	21214	0.333412	0	TRUE	C:8993	T:2	8995	0.000222	1	FALSE	2	26	
1464	SA075_11	SA075	11	1.28E+08	11,128214	nonsense	NA		G143	KCNJ1	11q24				INTRAMEM	C:33555	A:14748	48303	0.305323	0	TRUE	C:17397	A:4	17401	0.00023	1	FALSE	0	0
1465	SA075_11	SA075	11	1.29E+08	11,129317	nonsense	low	1.075	N1314T	PRDM10	11q25				DOMAIN //	T:1022	G:295	1317	0.223994	0	TRUE	T:3639	A:1	3640	0.000275	1	FALSE	2	1
1466	SA075_12	SA075	12	47374052	12,473740	missense	medium	2.6	K404N	CCNT1	12pter-qter			Entrez Query	COILED //	C:67363	A:25447	92810	0.274184	0	TRUE	C:20908	T:4	20912	0.000191	1	FALSE	1	5
1467	SA075_17	SA075	17	7517743	17,7517743	C,T	NA								C:214431	T:63957	278388	0.229741	0	TRUE	C:278024	A:98	278122	0.000352	1	FALSE	3	0	
1468	SA075_18	SA075	18	59803341	18,598033	missense	low	1.105	A201G	SERPINB8	18q21.3				C:4066	G:1141	5207	0.219128	0	TRUE	C:1700	A:2	1702	0.001175	1	FALSE	1	33	
1469	SA075_1	SA075	1	1.51E+08	1.1505515	missense	neutral	0.345	G811R	FLG	1q21.3				COMPMAS	C:9777	T:4012	13789	0.290957	0	TRUE	C:4708	N:0	4708	0	1	FALSE	0	0
1470	SA075_1	SA075	1	1.54E+08	1.1543951	missense	neutral	0.185	L162F	SEMA4A	1q22				DOMAIN //	G:45490	T:12546	58036	0.216176	0	TRUE	G:21984	T:4	21988	0.000182	1	FALSE	1	61
1471	SA075_1	SA075	1	2.24E+08	1.2244878	missense	medium	2.08	Q426V	LIN9	1q42.12				T:845	A:118	963	0.122534	5.97E-162	TRUE	T:326	N:0	326	0	1	FALSE	1	21	
1472	SA075_1	SA075	1	65041317	1,6504131	missense	low	1.665	L392F	RAVER2	1p31.3				G:4919	C:688	5607	0.122704	0	TRUE	G:3472	A:1	3473	0.000288	1	FALSE	2	13	
1473	SA075_20	SA075	20	31469277	20,314692	missense	medium	1.97	P204A	SNTA1	20q11.12				DOMAIN //	G:27072	C:15475	42547	0.363715	0	TRUE	G:12195	A:1	12196	8.20E-05	1	FALSE	2	24
1474	SA075_20	SA075	20	9446845	20,944684	missense	low	1.735	D121H	C20orf103	20p12				TOPO_DOM	G:11840	C:1523	13363	0.113971	0	TRUE	G:7659	C:2	7661	0.000261	1	FALSE	1	20
1475	SA075_2	SA075	2	39103430	2,3910343	missense	medium	2.915	S548N	SOS1	2p22-q21			Cancer Cell	DOMAIN //	C:1297	T:371	1668	0.222422	0	TRUE	C:634	N:0	634	0	1	FALSE	1	11
1476	SA075_3	SA075	3	1.71E+08	3,1711274	missense	low	0.895	T245M	SAMD7	3q26.2				C:98307	T:18272	116579	0.156735	0	TRUE	C:47614	T:8	47622	0.000168	1	FALSE	0	0	
1477	SA075_3	SA075	3	38567894	3,3856789	missense	high	3.775	F1658Y	SCN5A	3p21				CONFLICT	A:32332	T:21557	53889	0.400026	0	TRUE	A:11607	G:5	11612	0.000431	1	FALSE	0	0
1478	SA075_3	SA075	3	99143915	3,9914391	missense	low	1.275	R973T	KDFZP667C	3q11.2				DOMAIN //	G:13686	C:2397	16083	0.149039	0	TRUE	G:10166	A:1	10167	9.84E-05	1	FALSE	1	22
1479	SA075_5	SA075	5	13939163	5,1393916	missense	medium	2.25	N885Y	DNAH5	5p15.2				REGION //	T:39188	A:10148	49336	0.205692	0	TRUE	T:27326	C:9	27335	0.000329	1	FALSE	0	0
1480	SA075_6	SA075	6	1.5E+08	6,1503093	missense	medium	2.705	W172L	ULBP2	6q25				DISULFID //	G:27687	T:2614	30301	0.086268	0	TRUE	G:20101	A:3	20104	0.000149	1	FALSE	1	4
1481	SA075_6	SA075	6	1.5E+08	6,1503093	missense	medium	2.825	E173Q	ULBP2	6q25				DISULFID //	G:27665	C:2614	30279	0.08633	0	TRUE	G:20083	A:3	20086	0.000149	1	FALSE	1	4
1482	SA075_7	SA075	7	1.08E+08	7,1076372	missense	low	1.68	T324S	NRCAM	7q31.1-q31.2				DISULFID //	G:376	C:90	466	0.193133	1.53E-142	TRUE	G:135	N:0	135	0	1	FALSE	0	0
1483	SA075_7	SA075	7	1.49E+08	7,1485074	nonsense	NA		C513	ZNF398	7q36.1				ZN_FING	C:7397	A:1491	8888	0.167754	0	TRUE	C:3401	A:1	3402	0.000294	1	FALSE	1	12
1484	SA075_7	SA075	7	29506007	7,2950600	G,T	NA								G:52412	T:10781	63193	0.170604	0	TRUE	G:53051	A:5	53056	9.42E-05	1	FALSE	0	0	
1485	SA075_8	SA075	8	1.24E+08	8,1241585	missense	medium	2.125	N30D	WDR67	8q24.13				A:13146	G:2125	15271	0.139153	0	TRUE	A:9153	G:2	9155	0.000218	1	FALSE	1	4	
1486	SA075_8	SA075	8	70650880	8,7065088	missense	medium	3.355	K98N	SULF1	8q13.2-q13.3				G:39316	T:8745	48061	0.181956	0	TRUE	G:15726	A:1	15727	6.36E-05	1	FALSE	1	68	
1487	SA075_9	SA075	9	1.37E+08	9,1367603	nonsense	NA		Y280	COL5A1	9q34.2-q34.3				REGION //	C:2032	A:1018	3050	0.33377	0	TRUE	C:3810	N:0	3810	0	1	FALSE	1	70
1488	SA075_9	SA075	9	1.39E+08	9,1392134	missense	medium	1.995	V04A	C9orf75					A:349	G:31	380	0.081579	1.05E-36	TRUE	A:160	N:0	160	0	1	FALSE	2	23	
1489	SA075_X	SA075	X	1.52E+08	X,1516207	missense	low	1.8	R259Q	MAGEA6	Xq28				DOMAIN //	G:8359	A:819	9178	0.089235	0	TRUE	G:4461	C:1	4462	0.000224	1	FALSE	0	0
1490	SA076_16	SA076	16	76327307	16,763273	missense	high	4.055	R91W	NUDT7					DOMAIN //	C:12804	T:2148	14952	0.143366	0	TRUE	G:12205	T:4	12209	0.000328	1	FALSE	1	1
1491	SA076_16	SA076	16	88481601	16,884816	missense	medium	2.125	A197T	TCF7	16q24.3				G:49764	A:11947	61711	0.193596	0	TRUE	G:84917	A:1	84934	0.0002	1	FALSE	2	93	
1492	SA076_17	SA076	17	1579263	17,157926	missense	high	3.61	N131I	TP53	17p13.1	p.Y126fs*1	adenocarci	Cancer Cell	DATA_BIND	T:15747	A:3009	18756	0.160429	0	TRUE	T:35219	G:72	35291	0.00204	1	FALSE	2	31
1493	SA076_1	SA076	1	1.57E+08	1.1565664	missense	medium	2.425	L139M	CD18	1q22-q23				DISULFID //	A:14312	T:2213	16525	0.133918	0	TRUE	A:20759	C:2	20761	9.63E-05	1	FALSE	0	0
1494	SA076_1	SA076	1	36064142	1,3606414	missense	NA		Q218H	EIF2C4	1p34.3				G:100419	T:17193	117612	0.146184	0	TRUE	G:67682	C:15	67697	0.000222	1	FALSE	1	10	
1495	SA076_7	SA076	7	37746968	7,3774696	missense	neutral	0.43	L150V	GPR141	7p14.1				TRANSMEN	C:30526	G:5042	35568	0.141757	0	TRUE	C:18904	T:15	18919	0.000793	1	FALSE	1	19
1496	SA076_X	SA076	X	79886266	X,7988626	missense	low	1.5	V245A	BRWD3	Xq21.1				REPEAT //	A:16911	G:2358	19269	0.122373	0	TRUE	A:15366	G:4	15370	0.00026	1	FALSE	2	3
1497	SA077_10	SA077	10	1.04E+08	10,104222	missense	medium	2.905	E292K	TMEM180	10q24.32				G:6273	A:1252	7525	0.166379	0	TRUE	G:2063	A:1	2064	0.000484	1	FALSE	1	7	
1498	SA077_10																												

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.pos	Ref.count.	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase	
1520	SA077_2_1	SA077		1	23290940	1,2329094	missense	medium	2.095	S801C	LUZP1	1p36				G:1975	C:423	2398	0.176397	0	TRUE	G:1316	N:0	1316	0	1	FALSE	1	20	
1521	SA077_1_1	SA077		1	28040143	1,2804014	missense	medium	3.23	L101F	PPP1R8	1p35			DOMAIN //	G:14756	T:2948	17704	0.166516	0	TRUE	G:4719	A:4	4723	0.000847	1	FALSE	1	73	
1522	SA077_20	SA077		20	44442316	20,444423	missense	medium	2.84	R264W	ELMO2	20q13				G:8290	A:949	9239	0.102717	0	TRUE	G:7114	A:1	7115	0.000141	1	FALSE	1	33	
1523	SA077_22	SA077		22	19715623	22,197156	missense	low	1	W160S	SLC7A4	22q11.21			CONFLICT //	C:4834	G:846	5680	0.148944	0	TRUE	C:2241	A:1	2242	0.000446	1	FALSE	0	0	
1524	SA077_2_1	SA077		2	1.75E+08	2,1745289	missense	medium	2.11	V168L	SP3	2q31			REGION //	C:2934	G:1910	4844	0.394302	0	TRUE	C:3418	A:1	3419	0.000292	1	FALSE	2	38	
1525	SA077_2_1	SA077		2	1.99E+08	2,1986572	missense	medium	2.195	L268T	PLCL1	2q33				T:1304	C:272	1576	0.172589	0	TRUE	T:395	C:1	396	0.002525	1	FALSE	1	2	
1526	SA077_2_1	SA077		2	27598855	2,2759885	nonsense	NA		R533	GCKR	2p23				C:10715	T:1965	12680	0.154968	0	TRUE	C:2635	N:0	2635	0	1	FALSE	0	0	
1527	SA077_2_1	SA077		2	55376666	2,5537666	missense	medium	2.08	T1708H	CDC88A	2p16.1			Entrez Query :: Stabilit	C:2650	G:534	3184	0.167714	0	TRUE	C:4466	T:1	4467	0.000224	1	FALSE	1	85	
1528	SA077_3_1	SA077		3	12752093	3,1275209	missense	NA		Q215E	TMEM40	3p25.1				G:11520	C:2308	13828	0.166908	0	TRUE	G:16746	C:3	16749	0.000179	1	FALSE	0	0	
1529	SA077_3_4	SA077		3	48562604	3,4856260	missense	medium	2.255	I55M	PKF84	3p22-p21			REGION //	G:18331	C:4589	22920	0.200218	0	TRUE	G:7876	N:0	7876	0	1	FALSE	1	12	
1530	SA077_3_8	SA077		3	89563141	3,8956314	missense	high	4.055	S763F	EPHA3	3p11.2			Entrez Que	DOMAIN //	C:304	T:83	387	0.21447	4.89E-137	TRUE	C:472	N:0	472	0	1	FALSE	1	10
1531	SA077_4_1	SA077		4	77879561	4,7787956	missense	low	1.555	W404L	SHROOM3	4q21.1				G:27790	T:5625	33415	0.168338	0	TRUE	G:7124	C:2	7126	0.000281	1	FALSE	2	9	
1532	SA077_5_1	SA077		5	13822176	5,1382217	missense	medium	3.015	D3264H	DNAH5	5p15.2			REGION //	C:1847	G:255	2102	0.121313	0	TRUE	C:2837	N:0	2837	0	1	FALSE	1	1	
1533	SA077_5_1	SA077		5	1.4E+08	5,1401568	missense	medium	3.1	A706V	PCDHA2	5q31			TRANSMEN	C:12032	T:4974	17006	0.292485	0	TRUE	C:5681	T:3	5684	0.000528	1	FALSE	0	0	
1534	SA077_5_1	SA077		5	1.76E+08	5,1759372	missense	low	0.99	D455E	CLCK	5q35.2			DOMAIN //	C:1393	A:845	2238	0.377569	0	TRUE	C:1841	N:0	1841	0	1	FALSE	0	0	
1535	SA077_5_4	SA077		5	40884850	5,4088485	missense	medium	2.095	M420T	CARD6	5p13.1				T:1787	C:828	2615	0.316635	0	TRUE	T:1391	N:0	1391	0	1	FALSE	1	13	
1536	SA077_5_9	SA077		5	9207621	5,9207621	missense	medium	2.705	C487F	SEMASA	5p15.2			DISULFID //	C:4130	G:712	5042	0.141214	0	TRUE	C:3966	T:1	3967	0.000252	1	FALSE	1	1	
1537	SA077_6_1	SA077		6	1.5E+08	6,1497605	nonsense	NA		S580	MAP3K7IP	6q25.1-q25.3			Cancer Cell	COILED //	C:6307	G:1253	7560	0.165741	0	TRUE	C:7707	A:3	7710	0.000389	1	FALSE	1	99
1538	SA077_6_1	SA077		6	1.68E+08	6,1676413	missense	low	0.81	V352I	UNC93A	6q27			TRANSMEN	G:2318	A:2275	4593	0.495319	0	TRUE	G:4025	A:1	4026	0.000248	1	FALSE	0	0	
1539	SA077_6_3	SA077		6	31851750	6,3185175	missense	low	1.87	Q161H	C6orf27	6p21.33				C:2398	A:816	3214	0.253889	0	TRUE	C:2581	A:1	2582	0.000387	1	FALSE	0	0	
1540	SA077_6_1	SA077		6	74130017	6,7413001	missense	neutral	0.345	A123T	C6orf221	6q13				G:847	A:193	1040	0.185577	1.48E-305	TRUE	G:997	N:0	997	0	1	FALSE	0	0	
1541	SA077_7_1	SA077		7	1.14E+08	7,1138538	missense	medium	2.48	A29T	FOX2	7q31			Entrez Que	CONFLICT //	G:23684	A:11349	35033	0.323952	0	TRUE	G:27057	C:5	27062	0.000185	1	FALSE	1	2
1542	SA077_7_1	SA077		7	1.4E+08	7,1397541	missense	NA		RAB19	RAB19	7q34				A:259	C:301	560	0.5375	0	TRUE	A:260	N:0	260	0	1	FALSE	0	0	
1543	SA077_7_3	SA077		7	30622045	7,3062204	missense	high	3.83	T347R	GARS	7p15			NP_BIND //	C:4744	G:373	5117	0.072894	0	TRUE	C:2898	A:1	2899	0.000345	1	FALSE	1	801	
1544	SA077_7_4	SA077		7	47872604	7,4787260	missense	low	1.39	Q1344E	PKD11	7p12.3			DOMAIN //	G:26556	C:6247	32803	0.190044	0	TRUE	G:21715	T:2	21717	9.21E-05	1	FALSE	0	0	
1545	SA077_7_7	SA077		7	76663626	7,7666362	missense	high	3.625	T409I	FGL2	7q11.23			DOMAIN //	G:10273	A:1455	11728	0.124062	0	TRUE	G:5698	A:2	5700	0.000351	1	FALSE	1	71	
1546	SA077_8_1	SA077		8	57241976	8,5724197	missense	neutral	0.51	F295L	PLAG1	8q12			Cancer Rev	REGION //	A:13760	G:3008	16768	0.179389	0	TRUE	A:12949	C:3	12952	0.000232	1	FALSE	1	1
1547	SA077_9_1	SA077		9	1.17E+08	9,1166079	missense	low	0.895	C40Y	TNFSF15	9q32			TRANSMEN	C:250	T:126	376	0.335106	1.98E-236	TRUE	C:135	N:0	135	0	1	FALSE	0	0	
1548	SA077_9_1	SA077		9	1.24E+08	9,1235620	missense	medium	1.905	V211M	DAB2IP	9q33.1-q33.3			Entrez Que	DOMAIN //	G:1168	A:546	1714	0.318553	0	TRUE	G:1504	N:0	1504	0	1	FALSE	1	17
1549	SA077_9_9	SA077		9	99807238	9,9980723	missense	neutral	0.345	E167K	ANP328	9q22.32			Entrez Que	COMPMIAS	G:322	A:144	466	0.309013	2.87E-231	TRUE	G:288	N:0	288	0	1	FALSE	2	967
1550	SA077_X_1	SA077	X		1.52E+08	X,1519104	missense	medium	2.515	L06Q	PNMA5	Xq28			VARIANT //	A:20182	T:12360	32542	0.379817	0	TRUE	A:37122	G:14	37136	0.000377	1	FALSE	1	2	
1551	SA080_13	SA080		13	93929421	13,939294	missense	medium	2.395	M30I	DCT				TOPO_DON	C:2153	A:347	2500	0.1388	0	TRUE	C:3221	N:0	3221	0	1	FALSE	0	0	
1552	SA080_15	SA080		15	46532138	15,465321	missense	medium	2.11	R1820C	FBN1	15q21.1			Entrez Que	DISULFID //	G:5113	A:603	5716	0.105493	0	TRUE	G:11324	A:2	11326	0.000177	1	FALSE	1	147
1553	SA080_17	SA080		17	7518915	17,751891	missense	medium	3.4	V220C	TP53	17p13.1	p.Y220C.p.	pleomorph	Cancer Cell	DNA_BIND	T:119872	C:13282	133154	0.099749	0	TRUE	T:161226	G:208	161434	0.001288	1	FALSE	2	31
1554	SA080_21	SA080		21	16168690	21,161686	missense	medium	2.08	S92SF	USP25	21q11.2				T:33069	C:7205	40274	0.1789	0	TRUE	T:43826	C:12	43838	0.000274	1	FALSE	1	39	
1555	SA083_10	SA083		10	24709856	10,247098	missense	low	0.97	P136L	KIAA1217					C:21198	T:3834	25032	0.153164	0	TRUE	C:33122	T:3	33125	9.06E-05	1	FALSE	1	19	
1556	SA083_10	SA083		10	26395929	10,263959	missense	low	1.845	K325E	MYO3A	10p11.1				A:2653	G:1447	4100	0.352927	0	TRUE	A:3295	C:2	3297	0.000607	1	FALSE	1	1	
1557	SA083_11	SA083		11	65380133	11,653801	missense	low	1.15	E54Q	CFL1	11q13			DOMAIN //	C:14428	G:2018	16446	0.122705	0	TRUE	C:8356	T:1	8357	0.00012	1	FALSE	2	1695	
1558	SA083_11	SA083		11	88026136	11,880261	missense	low	1	P332H	GRM5	11q14.2-q14.3			TOPO_DON	G:2986	T:734	3720	0.197312	0	TRUE	G:3771	N:0	3771	0	1	FALSE	0	0	
1559	SA083_14	SA083		14	72492017	14,724920	missense	medium	2.135	E347K	WDR21A	14q24.3				G:2926	A:1008	3934	0.256228	0	TRUE	G:5231	N:0	5231	0	1	FALSE	2	10	
1560	SA083_15	SA083		15	65468237	15,654682	missense	low	1.365	V491I	IQCH	15q23				G:653	A:92	745	0.12349	1.34E-128	TRUE	G:181	N:0	181	0	1	FALSE	1	3	
1561	SA083_16	SA083		16	71379858	16,713798	nonsense	NA		S3273	ZFXH3	16q22.3-q23.1				G:742	C:606	1348	0.449555	0	TRUE	G:1146	N:0	1146	0	1	FALSE	1	4	
1562	SA083_17	SA083		17	10375739	17,103757	missense	high	4.585	E878G	MYH2	17p13.1			COILED //	T:619	C:339	958	0.353862	0	TRUE	T:1103	N:0	1103	0	1	FALSE	0	0	
1563	SA083_19	SA083		19	50786269	19,507862	missense	low	1.61	I232M	GNP4	19q13.3			TRANSMEN	G:436	C:185	621	0.297907	5.40E-304	TRUE	G:605	N:0	605	0	1	FALSE	1	10	
1564	SA083_19	SA083		19	58037198	19,580371	missense	low	1.295	M54T	ZNF468	19q13.41			DOMAIN //	A:2965	G:1103	4068	0.271141	0	TRUE	A:13076	C:2	13078	0.000153	1	FALSE	2	23	
1565	SA083_1_1	SA083		1	1.44E+08	1,1441518	missense	medium	2.215	S254R	TXNIP	1q21.1				C:16302	A:1424	17726	0.080334	0	TRUE	C:5379	T:1	5380	0.000186	1	FALSE	1	4391	
1566	SA083_1_1	SA083		1	1.55E+08	1,1548317	missense	neutral	0.695	E322D	GPATCH4	1q22				C:24253	G:3274	27527	0.118938	0	TRUE	C:16299	A:2	163						

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC			
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.pos	Ref.count.	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count.T	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase			
1589	SA083_X_1	SA083	X	70511817	X,7051181	missense	medium	2.05	P163L	TAF1	Xq13.1					C:1801	T:1761	3562	0.494385	0	TRUE	C:10173	T:3	10176	0.000295	1	FALSE	3	3			
1590	SA083_X_8	SA083	X	84249588	X,8424958	missense	low	1.545	Q161P	SATL1	Xq21.1					COMPBIAS	T:27625	G:4132	31757	0.130113	0	TRUE	T:76812	C:9	76821	0.000117	1	FALSE	0	0		
1591	SA084_10	SA084		70587867	10,705878	missense	medium	1.245	L149V	VP526A	10q21.1					STRAND	C:264	G:248	512	0.484375	0	TRUE	C:299	N:0	299	0	1	FALSE	2	148		
1592	SA084_11	SA084		4099977	11,409997	missense	high	4	P357A	RRM1	11p15.5					DISULFID	C:225	G:251	476	0.527311	0	TRUE	C:462	N:0	462	0	1	FALSE	3	15		
1593	SA084_11	SA084		6380492	11,638049	missense	medium	2.89	E382K	APBB1	11p15					DOMAIN	C:1051	T:1334	2385	0.559329	0	TRUE	C:1463	N:0	1463	0	1	FALSE	2	5		
1594	SA084_11	SA084		85123065	11,851230	missense	neutral	0.695	E318Q	TYTL2	11q14					C:1631	G:1014	2645	0.383365	0	TRUE	C:3859	T:2	3861	0.000518	1	FALSE	1	4			
1595	SA084_13	SA084		51446171	13,514461	missense	low	1.655	E396K	ATP7B	13q14.3					Entrez Query	DOMAIN	C:758	T:589	1347	0.437268	0	TRUE	C:979	N:0	979	0	1	FALSE	3	0	
1596	SA084_14	SA084		34942654	14,349426	missense	medium	2.215	L110R	NFKBIA	14q13					Cancer Cell	REPEAT	A:254	C:121	375	0.322667	4.97E-210	0	TRUE	A:539	N:0	539	0	1	FALSE	3	35
1597	SA084_15	SA084		65283501	15,652835	missense	medium	2.215	L252P	FLJ11506	15q22.33-q23						A:1758	G:2125	3883	0.547257	0	TRUE	A:3545	N:0	3545	0	1	FALSE	2	11		
1598	SA084_16	SA084		56290333	16,562903	missense	low	1.18	E92K	CCDC135	16q13						G:651	A:327	978	0.334356	0	TRUE	G:948	N:0	948	0	1	FALSE	0	0		
1599	SA084_16	SA084		70668056	16,706680	missense	high	4.785	C208G	HPR	16q22.1					Cancer Rev	DOMAIN	T:1709	G:797	2506	0.318037	0	TRUE	T:3124	N:0	3124	0	1	FALSE	0	0	
1600	SA084_17	SA084		37295912	17,372959	missense	medium	3.325	G684D	ACLY	17q12-q21						C:2627	T:1380	4007	0.344397	0	TRUE	C:3862	N:0	3862	0	1	FALSE	2	171		
1601	SA084_18	SA084		17370102	18,173701	nonsense	NA		Q696	ESCO1	18q11.2					Entrez Query :: Stability	G:3369	A:3871	7240	0.534669	0	TRUE	G:26438	A:3	26441	0.000113	1	FALSE	2	11		
1602	SA084_18	SA084		46057290	18,460572	missense	low	1.04	G101A	MBD1	18q21						C:4113	G:2446	6559	0.372923	0	TRUE	C:4469	N:0	4469	0	1	FALSE	2	97		
1603	SA084_19	SA084		2029493	19,202949	nonsense	NA		E23	MOBK12A	19p13.3						C:13571	A:13591	27162	0.500368	0	TRUE	C:30553	A:9	30562	0.000294	1	FALSE	2	7		
1604	SA084_19	SA084		4506098	19,450609	missense	high	4.06	L191R	SEMA6B						DOMAIN	A:1030	C:1195	2225	0.537079	0	TRUE	A:1575	G:2	1577	0.001268	1	FALSE	1	4		
1605	SA084_19	SA084		9538032	19,953803	missense	NA		E253Q	ZNF121	19p						C:322	G:192	514	0.373541	0	TRUE	C:601	N:0	601	0	1	FALSE	2	100		
1606	SA084_1_1	SA084		1.51E+08	1,1505963	missense	neutral	0.55	G163E	FLG2	1q21.3					COMPBIAS	C:1357	T:892	2249	0.396621	0	TRUE	C:1287	N:0	1287	0	1	FALSE	0	0		
1607	SA084_1_2	SA084		22077659	1,2207765	missense	low	1.655	E852D	HSPG2	1p36.1-p34					DISULFID	C:1924	G:4006	5930	0.675548	0	TRUE	C:3928	N:0	3928	0	1	FALSE	2	5		
1608	SA084_1_3	SA084		36069625	1,3606962	nonsense	NA		Q287	E1F2C4	1p34.3					DOMAIN	A:391	T:460	851	0.540541	0	TRUE	C:819	N:0	819	0	1	FALSE	2	8		
1609	SA084_1_4	SA084		39870939	1,3987093	missense	neutral	0.695	S39L	HEYL	1p34.3						G:573	C:659	1232	0.534903	0	TRUE	G:1253	N:0	1253	0	1	FALSE	0	0		
1610	SA084_1_5	SA084		6452065	1,645206	missense	low	1.61	H712D	PLEKHG5	1p36.31					DOMAIN	G:2026	A:659	4295	0.226289	0	TRUE	G:3567	C:1	3568	0.00028	1	FALSE	3	3		
1611	SA084_1_8	SA084		86727310	1,8672731	missense	high	3.62	L409R	CLCA1	1p31-p22					Cancer Cell	DOMAIN	T:908	G:1013	1921	0.52733	0	TRUE	T:1498	A:1	1499	0.000667	1	FALSE	0	0	
1612	SA084_20	SA084		31083207	20,310832	missense	low	1.04	M31I	BP1L3	20q11.21						G:1818	A:846	2664	0.317568	0	TRUE	G:2175	N:0	2175	0	1	FALSE	0	0		
1613	SA084_20	SA084		5979574	20,597957	missense	neutral	0.55	K237N	LRRN4	20p12.3					REPEAT	C:1746	G:1350	3096	0.436047	0	TRUE	C:2778	A:1	2779	0.00036	1	FALSE	3	0		
1614	SA084_21	SA084		33321249	21,333212	missense	low	0.895	L70P	OLIG2	21q22.11					Cancer Review :: Future	T:446	C:519	965	0.537824	0	TRUE	T:788	C:2	790	0.002532	1	FALSE	0	0		
1615	SA084_21	SA084		44540721	21,445407	missense	low	1.77	L511V	AIRE	21q22.3						C:183	G:138	321	0.429907	7.65E-261	0	TRUE	C:170	N:0	170	0	1	FALSE	0	0	
1616	SA084_22	SA084		35011291	22,350112	missense	high	4.265	E176K	MYH9	22q13.1					Cancer Rev	COILED	C:730	T:310	1040	0.298077	0	TRUE	C:1153	N:0	1153	0	1	FALSE	2	430	
1617	SA084_2_1	SA084		2.1E+08	2,1097306	nonsense	NA		S429	ANKRD57	2q13						C:30350	G:13023	43373	0.300256	0	TRUE	C:51417	T:12	51429	0.000233	1	FALSE	2	77		
1618	SA084_2_2	SA084		2.18E+08	2,1833483	missense	medium	2.605	E761Q	DNAJC10	2q32.1					DOMAIN	G:111	C:78	189	0.412698	7.11E-146	0	TRUE	G:280	N:0	280	0	1	FALSE	2	121	
1619	SA084_2_3	SA084		2.37E+08	2,2371547	missense	medium	3.185	V299G	LOC100128709					Cancer Rev	TRANSMEN	T:3523	C:2307	5830	0.395712	0	TRUE	T:3553	C:2	3555	0.000563	1	FALSE	1	13		
1620	SA084_2_4	SA084		2.39E+08	2,2388464	missense	medium	2.67	E179K	PER2	2q37.3						C:741	T:409	1150	0.355652	0	TRUE	C:913	T:4	917	0.004362	0.254916	FALSE	2	4		
1621	SA084_2_5	SA084		74608461	2,7460846	missense	low	1.04	E317K	AUP1	2p13					TOPO_DON	C:687	T:807	1494	0.540161	0	TRUE	C:1226	N:0	1226	0	1	FALSE	2	45		
1622	SA084_3_1	SA084		3.141E+08	3,1406637	missense	neutral	0.55	D44N	RBP2	3q23					STRAND	C:446	T:176	622	0.282958	2.31E-293	0	TRUE	C:1414	N:0	1414	0	1	FALSE	3	0	
1623	SA084_3_4	SA084		34364892	3,4336489	missense	low	1.5	D713H	SNRK	3p22.1						G:2172	C:1115	3287	0.339215	0	TRUE	G:1801	N:0	1801	0	1	FALSE	2	44		
1624	SA084_3_4	SA084		49313520	3,4913523	missense	medium	3.005	L1495R	LAMB2	3p21					COILED	A:780	C:344	1214	0.283361	0	TRUE	A:692	N:0	692	0	1	FALSE	2	36		
1625	SA084_3_5	SA084		52703093	3,5270309	nonsense	NA		E501	GNL3	3p21.1					REGION	G:705	T:950	1700	0.558824	0	TRUE	G:2461	T:3	2464	0.001218	1	FALSE	3	16		
1626	SA084_4_1	SA084		4.123E+08	4,1234466	missense	low	1.845	K3280T	KIAA1109							G:260	C:192	398	0.482412	0	TRUE	G:547	N:0	547	0	1	FALSE	2	15		
1627	SA084_5_1	SA084		5.115E+08	5,1145011	missense	medium	1.975	S316C	TRIM36	5q22.3					COILED	G:116	C:158	274	0.576642	0	TRUE	G:516	N:0	516	0	1	FALSE	2	2		
1628	SA084_7_1	SA084		7.29885254	7,2988525	nonsense	NA		R110	WIFP3	7p15.1					C:83205	T:96197	179402	0.536209	0	TRUE	C:232594	T:105	232699	0.000451	1	FALSE	2	3			
1629	SA084_7_2	SA084		7.76754730	7,7675473	missense	medium	2.685	L772Q	CCDC146	7q11.23					COILED	T:403	A:363	766	0.47389	0	TRUE	T:801	N:0	801	0	1	FALSE	2	11		
1630	SA084_8_1	SA084		8.101E+08	8,1011452	missense	low	0.805	S318R	RG522	8q22.13						G:107	C:91	198	0.455956	1.19E-175	0	TRUE	G:256	N:0	256	0	1	FALSE	0	0	
1631	SA084_9_1	SA084		9.34638415	9,3463841	missense	medium	2.885	L217V	GALT	9p13					VARIANT	G:183	G:116	299	0.38796	9.52E-213	0	TRUE	C:183	N:0	183	0	1	FALSE	2	59	
1632	SA084_X_6	SA084	X	64875743	X,6487574	nonsense	NA		E511	MSN	Xq11.2-q12					Cancer Rev	HELIX	G:518	T:19341	44645	0.433218	0	TRUE	G:85430	A:18	85448	0.000211	1	FALSE	2	289	
1633	SA085_10	SA085		64644417	10,646444	missense	medium	2.19	P506A	JMJD1C	10q21.2						G:13852	C:46368	60220	0.769977	0	TRUE	G:103582	T:11	103593	0.000106	1	FALSE	2	16		
1634	SA089_10	SA089		46418936	10,464189	missense	low	0.805	R17H	GPRIN2	10q11.22						G:17605	A:2628	20233	0.129887	0	TRUE	G:16829	T:4	16833	0.000238	1	FALSE	1	4		
1635	SA089_11	SA089		15168881	11,151688	missense	low	1.61	G260V	INSC	11p15.2						G:5826	T:3242	9068	0.357521	0	TRUE	G:6116	N:0	6116	0	1	FALSE	0	0		
1636	SA089_12																															

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.ref	Ref.count	Alt.count	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count	Alt.count	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNASE
1658	SA089_4_5	SA089	4	8268869	4,8268869	missense		2.365	L2051	SH3TC1	4p16.1					C:5339	A:4397	9736	0.451623	0	TRUE	C:10542	N:0	10542	0	1	FALSE	1	4
1659	SA089_4_5	SA089	4	95420893	4,95420893	missense		3.395	L849W	SMARCAD1	4q22-q23					T:13359	G:5614	18973	0.295894	0	TRUE	T:50044	C:7	50051	0.00014	1	FALSE	2	19
1660	SA089_5_1	SA089	5	1.32E+08	5,1317835	missense	neutral	0	P15S	LOC441108	5q31.1					C:495	T:1323	1818	0.727723	0	TRUE	C:1686	N:0	1686	0	1	FALSE	2	9
1661	SA089_5_1	SA089	5	1.4E+08	5,1401690	missense	high	3.53	A706V	PCDH4	5q31				TRANSMEN	C:2003	T:4237	6240	0.679006	0	TRUE	C:6257	A:1	6258	0.00016	1	FALSE	0	0
1662	SA089_5_5	SA089	5	56578016	5,56578016	missense	low	1.845	G204V	GPBP1	5q11.2					G:52237	T:13156	65393	0.201184	0	TRUE	C:178520	A:32	178552	0.000179	1	FALSE	1	268
1663	SA089_5_5	SA089	5	94890538	5,94890538	missense	neutral	0	T3061	KIAA0372	5q15			REPEAT //	G:37513	A:39973	77486	0.515874	0	TRUE	C:160670	A:37	160707	0.00023	1	FALSE	3	0	
1664	SA089_6_1	SA089	6	1.45E+08	6,1449176	missense	low	1.1	H2344Q	UTRN	6q24					T:12126	G:6808	18934	0.359565	0	TRUE	T:46989	C:12	47001	0.000255	1	FALSE	1	30
1665	SA089_7_1	SA089	7	1.21E+08	7,1207591	missense	medium	3.07	H164P	WNT16	7q31					A:32558	C:12950	45508	0.284565	0	TRUE	A:51073	C:13	51086	0.000254	1	FALSE	0	0
1666	SA089_7_3	SA089	7	37265351	7,37265351	missense	medium	2.89	G125R	ELMO1	7p14.2			Entrez Query :: Stability	C:48567	G:21687	70254	0.308694	0	TRUE	C:42594	A:7	42601	0.000164	1	FALSE	1	22	
1667	SA089_9_3	SA089	9	35551257	9,35551257	missense	low	1.41	L1477V	RUSC2	9p13.3			DOMAIN //	C:2367	G:1107	3474	0.318653	0	TRUE	C:3874	T:2	3876	0.000516	1	FALSE	2	14	
1668	SA089_X_1	SA089	X	1.29E+08	X,1287764	missense	medium	2.995	F165L	ZDHHC9	Xq26.1			TOPO_DOM	C:478	T:202	680	0.297059	0	TRUE	G:482	N:0	482	0	1	FALSE	1	46	
1669	SA090_10_1	SA090	10	15929924	10,15929924	missense	medium	2.125	G40V	C10orf97	10p13					C:2205	A:329	2534	0.129834	0	TRUE	C:3638	N:0	3638	0	1	FALSE	1	71
1670	SA090_10_1	SA090	10	30642669	10,30642669	missense	neutral	0.69	T542P	PAPD1	10p11.23					T:289	G:70	359	0.194986	7.66E-123	TRUE	T:526	C:2	528	0.003788	1	FALSE	2	24
1671	SA090_10_1	SA090	10	96015435	10,96015435	missense	low	1.59	M1365I	PLCE1	10q23			Cancer Cell Map Pathw	C:2194	A:134	2328	0.05756	3.62E-161	TRUE	G:6815	C:1	6816	0.000147	1	FALSE	0	0	
1672	SA090_11_1	SA090	11	66769254	11,66769254	missense	neutral	0	P528S	FBXL11	11q13.1					C:45810	T:4553	50363	0.090404	0	TRUE	C:52723	A:35	52758	0.000663	1	FALSE	2	68
1673	SA090_11_1	SA090	11	67683155	11,67683155	missense	low	1.845	R412W	SUV420H1	11q13.2					T:9939	A:1808	11747	0.153912	0	TRUE	T:31358	C:11	31369	0.000351	1	FALSE	1	8
1674	SA090_12_1	SA090	12	41144715	12,41144715	missense	medium	2.725	A463G	PRICKLE1	12q12					G:10120	C:1094	11214	0.097557	0	TRUE	G:12950	A:5	12955	0.000386	1	FALSE	2	29
1675	SA090_16_1	SA090	16	87875737	16,87875737	missense	low	1.67	L1572F	ANKRD11	16q24.3			COMPMIAS	C:2333	A:724	3057	0.236833	0	TRUE	G:5473	A:1	5474	0.000183	1	FALSE	2	11	
1676	SA090_17_1	SA090	17	4007068	17,4007068	missense	medium	2.085	N246K	CYBSD2	17p13.2					C:14208	A:4496	18704	0.240376	0	TRUE	C:22053	A:5	22058	0.000227	1	FALSE	2	9
1677	SA090_19_1	SA090	19	49314268	19,49314268	missense	medium	1.915	E35K	ZNF225	19q13.2			DOMAIN //	G:8121	A:3035	11156	0.272051	0	TRUE	G:6361	N:0	6361	0	1	FALSE	1	10	
1678	SA090_1_1	SA090	1	1.72E+08	1,1718124	missense	low	0.855	L279I	SLCA11	1q25.1					A:11315	T:1637	12952	0.12639	0	TRUE	A:11925	G:2	11927	0.000168	1	FALSE	0	0
1679	SA090_1_2	SA090	1	2.4E+08	1,2398219	missense	neutral	0.55	H443L	KMO	1q42-q43			TRANSMEN	A:1086	1267	0.142857	1.06E-291	TRUE	A:1097	N:0	1097	0	1	FALSE	1	24		
1680	SA090_21_1	SA090	21	21629782	21,21629782	missense	high	3.83	D275V	NCAM2	21q21.1			DISULFID //	A:3152	T:397	3549	0.111862	0	TRUE	A:2912	N:0	2912	0	1	FALSE	1	12	
1681	SA090_2_2	SA090	2	55376402	2,55376402	missense	neutral	0.69	L1796C	CCDC88A	2p16.1					T:5994	A:854	6848	0.127408	0	TRUE	T:6743	A:1	6744	0.000148	1	FALSE	1	59
1682	SA090_3_1	SA090	3	1.15E+08	3,1151555	missense	low	0.94	L149V	ZDHHC23	3q13.31			TRANSMEN	C:15137	G:1956	17093	0.114433	0	TRUE	C:12583	A:4	12587	0.000318	1	FALSE	1	2	
1683	SA090_3_1	SA090	3	1.73E+08	3,1728625	missense	low	1.685	E771Q	PLD1	3q26			Cancer Cell REGION //	C:18986	G:2366	21352	0.110809	0	TRUE	C:12637	A:2	12639	0.000158	1	FALSE	2	16	
1684	SA090_4_4	SA090	4	89928045	4,89928045	missense	low	1.59	G385R	FAM13A1	4q22.1					C:26569	G:5163	31732	0.162706	0	TRUE	C:36943	A:4	36947	0.000108	1	FALSE	0	0
1685	SA090_5_1	SA090	5	1.57E+08	5,1565738	missense	medium	2.33	P122A	ITK	5q31-q32			Entrez Query	METAL // 1	C:1576	G:663	2239	0.296114	0	TRUE	C:1446	N:0	1446	0	1	FALSE	1	8
1686	SA090_5_3	SA090	5	34859764	5,34859764	nonsense	NA		L687	RAI14	5p13.3-p13.2			COILED //	T:20253	A:1262	21515	0.058657	0	TRUE	T:14605	C:11	14616	0.000753	1	FALSE	1	54	
1687	SA090_5_6	SA090	5	68698134	5,68698134	missense	neutral	-1.625	K26R	TA9F	5q11.2-q13.1			HELI // 1	T:7948	C:2697	10645	0.253358	0	TRUE	T:18355	C:1	18356	5.45E-05	1	FALSE	1	14	
1688	SA090_8_1	SA090	8	1.25E+08	8,1251728	missense	medium	2.42	L1478K	PRF16	-			TOPO_DOM	G:32678	A:3762	36440	0.103238	0	TRUE	G:82771	A:22	82793	0.000266	1	FALSE	0	0	
1689	SA090_8_6	SA090	8	61919979	8,61919979	missense	high	3.505	W1618L	CHD7	8q12.2					G:99988	T:10696	110684	0.096635	0	TRUE	G:106471	C:21	106492	0.000197	1	FALSE	2	3
1690	SA090_8_7	SA090	8	74748031	8,74748031	missense	low	0.88	G92D	STAU2	8q13-q21.1					C:490	T:35	525	0.066667	4.54E-44	TRUE	C:1056	N:0	1056	0	1	FALSE	1	53
1691	SA093_14_1	SA093	14	50417037	14,50417037	missense	medium	1.99	H151Q	ABHD128	14q22.1					C:4207	G:1718	5925	0.289958	0	TRUE	C:2987	N:0	2987	0	1	FALSE	0	0
1692	SA093_16_1	SA093	16	27425712	16,27425712	missense	low	1.265	N503K	GTF3C1	16p12					G:2210	C:1455	3665	0.396999	0	TRUE	G:2280	C:1	2281	0.000438	1	FALSE	2	7
1693	SA093_16_1	SA093	16	75784888	16,75784888	missense	neutral	-0.145	P63L	MON1B	16q23.1					C:2737	T:1941	4678	0.414921	0	TRUE	C:3201	T:2	3203	0.000624	1	FALSE	2	78
1694	SA093_16_1	SA093	16	83693385	16,83693385	missense	medium	2.795	A196V	FAM92B	16q24.1					G:821	A:587	1408	0.416903	0	TRUE	G:688	N:0	688	0	1	FALSE	0	0
1695	SA093_17_1	SA093	17	7520091	17,7520091	nonsense	NA		Y107	TP53	17p13.1	p.Y103_G1	adenocarcin	Cancer Cell	DNA_BIND	G:8886	T:28231	37117	0.760595	0	TRUE	G:44533	A:14	44547	0.000314	1	FALSE	3	1
1696	SA093_19_1	SA093	19	19122516	19,19122516	missense	high	4.035	R10H	MEF2B	19p12			DOMAIN //	C:94	T:137	231	0.593074	6.15E-303	TRUE	C:170	N:0	170	0	1	FALSE	2	11	
1697	SA093_19_1	SA093	19	42795447	19,42795447	missense	medium	3.29	F476V	ZNF540	19q13.12			ZN_FING //	T:6254	G:1666	7920	0.210354	0	TRUE	T:2122	C:1	2123	0.000471	1	FALSE	2	2	
1698	SA093_1_1	SA093	1	1.51E+08	1,1505492	missense	neutral	-0.145	R1567Q	FLG	1q21.3	p.R1567W	serous_carcinoma	COMPMIAS	C:16954	T:6399	23353	0.274012	0	TRUE	C:30117	T:5	30122	0.000166	1	FALSE	0	0	
1699	SA093_2_1	SA093	2	20267312	2,20267312	nonsense	NA		R124	SDC1	2p24.1			TOPO_DOM	G:2629	A:871	3500	0.248857	0	TRUE	G:1607	N:0	1607	0	1	FALSE	1	199	
1700	SA093_2_1	SA093	2	96769459	2,96769459	nonsense	NA		R16	LMAN2L	2q11.2			SIGNAL //	G:1576	A:1119	2695	0.415213	0	TRUE	G:1732	A:3	1735	0.001729	1	FALSE	3	0	
1701	SA093_5_1	SA093	5	1.4E+08	5,1401900	missense	high	3.635	T714M	PCDH6A	5q31			TRANSMEN	C:858	T:1339	2197	0.609467	0	TRUE	C:2800	T:2	2802	0.000714	1	FALSE	0	0	
1702	SA093_6_1	SA093	6	18279621	6,18279621	missense	low	0.895	E156K	AOF1	6p22.3			ZN_FING //	G:879	A:375	1254	0.299043	0	TRUE	G:1158	A:1	1159	0.000863	1	FALSE	1	44	
1703	SA093_6_1	SA093	6	52727791	6,52727791	missense	high	4.32	D61H	GSTA2	6p12.1			DOMAIN //	C:7734	G:701	8435	0.083106	0	TRUE	C:26374	A:2	26376	7.58E-05	1	FALSE	0	0	
1704	SA093_7_1	SA093	7	1.48E+08	7,1475003	nonsense	NA		E951	CNTNAP2	7q35-q36			DISULFID //	G:2030														

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.pos	Ref.count	Alt.count	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count	Alt.count	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase	
1727	SA096_14	SA096	14	87721907	14,877219	missense		2.34	G448R	KCNK10	14q31				TOPO_DON	C:2663	T:1194	3857	0.309567	0	TRUE	C:4251	A:1	4252	0.000235	1	FALSE	1	1	
1728	SA096_17	SA096	17	35121734	17,351217	missense		2.495	S310F	ERBB2	17q11.2-q21	p.S310F	serous_carc	Cancer Cell	DISULFID	C:60222	T:19189	79411	0.241642	0	TRUE	C:93407	A:50	93457	0.000535	1	FALSE	2	74	
1729	SA096_17	SA096	17	35133746	17,351337	missense		3.935	J755S	ERBB2	17q11.2-q21	p.L755P.p	bronchiolo	Cancer Cell	DOMAIN	T:23313	C:1555	24868	0.06253	0	TRUE	T:31827	C:33	31860	0.001036	1	FALSE	2	243	
1730	SA097_10	SA097	10	7658685	10,765868	missense		1.65	H572P	ITIH5	10p14				Entrez Query :: Stabilit	T:1040	G:470	1510	0.311258	0	TRUE	T:850	G:2	852	0.002347	1	FALSE	1	1	
1731	SA097_12	SA097	12	56178616	12,561786	missense		1.845	R345H	MARS	12q13.2					G:3690	A:2762	6452	0.428084	0	TRUE	G:4081	A:1	4082	0.000245	1	FALSE	2	21	
1732	SA097_12	SA097	12	6844663	12,684466	missense		3.06	K825E	USP5						A:5514	G:1184	6698	0.176769	0	TRUE	A:5178	N:0	5178	0	1	FALSE	2	47	
1733	SA097_15	SA097	15	70428633	15,704286	missense		1.635	P276L	HEXA	15q23-q24				DISULFID	G:8815	A:4825	13640	0.353739	0	TRUE	G:11639	A:1	11640	8.59E-05	1	FALSE	2	149	
1734	SA097_15	SA097	15	79369903	15,793699	missense		1.95	F463I	IL16	15q26.3					T:35343	A:13103	48446	0.270466	0	TRUE	T:104246	C:34	104280	0.000326	1	FALSE	0	0	
1735	SA097_16	SA097	16	15743029	16,157430	missense		NA								T:86981	G:30307	117288	0.258398	0	TRUE	T:90409	C:20	90429	0.000221	1	FALSE	2	1	
1736	SA097_16	SA097	16	20472698	16,204726	missense		0.185	E214D	ACSM2B						T:43681	A:12809	56490	0.226748	0	TRUE	T:106683	C:27	106710	0.000253	1	FALSE	0	0	
1737	SA097_16	SA097	16	4397605	16,439760	missense		0	V129L	CORO7	16p13.3				REPEAT	C:13985	G:1987	15972	0.124405	0	TRUE	C:18518	A:2	18520	0.000108	1	FALSE	2	12	
1738	SA097_17	SA097	17	5270295	17,527029	missense		1.43	I147M	RPAIN	17p13.2				Entrez Query	ZN_FING	C:499	G:528	1027	0.514119	0	TRUE	C:622	N:0	622	0	1	FALSE	2	11
1739	SA097_17	SA097	17	59349114	17,593491	missense		4.105	K96E	GH1	17q24.2				Entrez Query	DISULFID	T:8297	C:2347	10644	0.2205	0	TRUE	T:15561	C:3	15564	0.000193	1	FALSE	1	1
1740	SA097_18	SA097	18	44702017	18,447020	missense		2.645	R335H	SMAD7	18q21.1				Cancer Cell	DOMAIN	C:5685	T:3260	8945	0.364449	0	TRUE	C:6915	N:0	6915	0	1	FALSE	2	15
1741	SA097_19	SA097	19	42335702	19,423357	silent		NA	L258L	ZNF585A	19q13.12					A:23388	T:7995	31383	0.254756	0	TRUE	A:25920	G:5	25925	0.000193	1	FALSE	3	0	
1742	SA097_19	SA097	19	55965932	19,559659	missense		4.205	D88G	GNR32	19q13.3				TRANSMEN	A:8753	G:2276	11029	0.206365	0	TRUE	A:12932	C:13	12945	0.001004	1	FALSE	0	0	
1743	SA097_1_1	SA097	1	1.16E+08	1.16E+08	missense		1.3	V28M	C1orf161	1p13.1					G:13086	A:6462	19548	0.303571	0	TRUE	G:31791	A:4	31795	0.000126	1	FALSE	0	0	
1744	SA097_21	SA097	21	26063333	21,260633	missense		0.805	K428N	GABPA	21q21-q22.1	21q21.3				G:1022	C:307	1329	0.231001	0	TRUE	G:3568	N:0	3568	0	1	FALSE	2	3	
1745	SA097_2_1	SA097	2	1.09E+08	2,1088909	missense		2.135	N270K	EDAR	2q11-q13				TOPO_DON	G:2398	C:1976	4374	0.45176	0	TRUE	G:4171	T:2	4173	0.000479	1	FALSE	3	0	
1746	SA097_2_1	SA097	2	73306431	2,73306431	G,C		NA								G:82920	C:22831	105751	0.215894	0	TRUE	G:68227	T:5	68232	7.33E-05	1	FALSE	2	7	
1747	SA097_3_1	SA097	3	50620287	3,5062028	missense		0.805	P178S	CISH	3p21.3					G:4161	A:2740	6901	0.397004	0	TRUE	G:7234	N:0	7234	0	1	FALSE	2	11	
1748	SA097_5_1	SA097	5	1.76E+08	5,1759441	missense		1.845	E75SD	PLCKC					DOMAIN	G:3814	C:3151	6965	0.452405	0	TRUE	G:9197	A:1	9198	0.000109	1	FALSE	1	1	
1749	SA097_6_1	SA097	6	1.3E+08	6,129517341	A,T		NA								A:51684	T:17846	69530	0.256666	0	TRUE	A:89314	G:24	89338	0.000269	1	FALSE	0	0	
1750	SA097_6_2	SA097	6	24555132	6,2455513	missense		1.845	S578F	GPLD1	6p22.3-p22.2				REPEAT	G:19743	A:3893	23636	0.164706	0	TRUE	G:23414	A:4	23418	0.000171	1	FALSE	2	5	
1751	SA097_7_1	SA097	7	1.51E+08	7,1505661	missense		2.36	L592V	CSGICA-T	7q36.1				TOPO_DON	C:135	G:21	156	0.134615	1.04E-22	TRUE	C:111	N:0	111	0	1	FALSE	1	87	
1752	SA097_7_3	SA097	7	30982582	7,3098258	missense		3.02	S330P	GNRHR	7p14				TOPO_DON	T:6761	C:2234	8995	0.24836	0	TRUE	T:9750	C:15	9765	0.001536	1	FALSE	0	0	
1753	SA097_8_1	SA097	8	1.01E+08	8,1013412	missense		2.455	P606A	PRF19A	8q22					G:755	C:56	811	0.069051	8.71E-45	TRUE	G:374	N:0	374	0	1	FALSE	1	103	
1754	SA097_8_1	SA097	8	1.31E+08	8,131218467	C,T		NA								C:120876	T:26203	147079	0.178156	0	TRUE	C:308427	A:49	308476	0.000159	1	FALSE	2	3	
1755	SA097_X_1	SA097	X	2961418	X,2961418	missense		1.1	A561T	ARSH	Xp22.3					G:25216	A:7083	32299	0.219295	0	TRUE	G:83644	C:23	83667	0.000275	1	FALSE	1	2	
1756	SA097_X_1	SA097	X	84249861	X,8424986	missense		0	N70S	SAT1L	Xq21.1				COMPMIAS	T:7456	C:2821	10277	0.274496	0	TRUE	T:10191	C:5	10196	0.00049	1	FALSE	0	0	
1757	SA098_10	SA098	10	26326170	10,263261	missense		1.6	G162A	MYO3A	10p11.1				DOMAIN	G:578	C:381	959	0.397289	0	TRUE	G:840	N:0	840	0	1	FALSE	0	0	
1758	SA098_12	SA098	12	1.06E+08	12,106461	missense		1.79	H475Y	BTBD11	12q23.3					C:406	T:237	643	0.368585	0	TRUE	C:1105	N:0	1105	0	1	FALSE	3	0	
1759	SA098_17	SA098	17	57871710	17,578717	missense		NA								A:43883	G:43241	87124	0.496316	0	TRUE	A:129226	C:31	129257	0.00024	1	FALSE	2	16	
1760	SA098_19	SA098	19	23334272	19,233342	missense		-1.49	E1117Q	MTNF1	19p13.1-p12				ZN_FING	C:27852	G:30071	57923	0.519155	0	TRUE	C:89595	A:5	89600	5.58E-05	1	FALSE	2	18	
1761	SA098_19	SA098	19	23334293	19,233342	missense		2.63	E1110Q	ZNF91	19p13.1-p12				ZN_FING	C:28247	G:29610	57857	0.511779	0	TRUE	C:89479	T:10	89489	0.000112	1	FALSE	2	22	
1762	SA098_19	SA098	19	46041644	19,460416	missense		0.525	R461H	CYP2A6	19q13.2				Entrez Query	STRAND	T:1091	2560	0.261712	0	TRUE	C:2195	N:0	2195	0	1	FALSE	0	0	
1763	SA098_1_1	SA098	1	2.01E+08	1,2011304	missense		NA	R398C	KHLH12	1q32.1				REPEAT	G:13867	A:13001	26868	0.483884	0	TRUE	G:44101	A:9	44110	0.000204	1	FALSE	2	40	
1764	SA098_1_1	SA098	1	2.33E+08	1,2325225	missense		1.07	V336I	SLC35F3	1q42.2				TRANSMEN	G:1799	A:2066	3865	0.534541	0	TRUE	G:4094	A:1	4095	0.000244	1	FALSE	0	0	
1765	SA098_1_1	SA098	1	2.38E+08	1,2384384	missense		0.345	P1244L	FMN2	1q43				DOMAIN	C:2809	T:2055	4864	0.422492	0	TRUE	C:2084	N:0	2084	0	1	FALSE	2	8	
1766	SA098_1_1	SA098	1	1.768155	1,768155	missense		1.61	F66V	PER3	1p36.23					T:492	G:524	1016	0.515748	0	TRUE	T:936	N:0	936	0	1	FALSE	2	26	
1767	SA098_20	SA098	20	34673841	20,346738	missense		0	D121M	C2orf24	20q11.23				CONFLICT	C:7044	G:2933	9977	0.293976	0	TRUE	C:6999	N:0	6999	0	1	FALSE	2	206	
1768	SA098_3_1	SA098	3	1.15E+08	3,1146707	missense		1.61	A229P	CCDC52	3q13.2					C:1635	G:1151	2786	0.413137	0	TRUE	C:2311	N:0	2311	0	1	FALSE	2	29	
1769	SA098_3_1	SA098	3	58083878	3,5808387	missense		3.95	G1049S	FLNB	3p14.3				HELIX	T:10	G:1353	2090	0.352632	0	TRUE	G:1962	A:1	1963	0.000509	1	FALSE	2	43	
1770	SA098_6_1	SA098	6	1.07E+08	6,1066602	missense		1.935	S514N	PRDM1	6q21-q22.1				Entrez Query :: Tumor	G:45473	A:38659	84132	0.459504	0	TRUE	G:203269	C:30	203299	0.000148	1	FALSE	2	15	
1771	SA098_6_1	SA098	6	25907109	6,2590710	missense		2.345	W429C	SLC17A1	6p23-p21.3					C:1116	A:943	2059	0.457989	0	TRUE	C:1822	T:1	1823	0.000549	1	FALSE	0	0	
1772	SA098_6_1	SA098	6	71619003	6,7161900	missense		0.895	T235M	SMAP1	6q13					C:329	T:253	582	0.434708	0	TRUE	C:339	N:0	339	0	1	FALSE	2	18	
1773	SA098_8_1	SA098	8	2080062	8,2080062	missense		0.18	Q1383R	MYOM2	8p23.3				DOMAIN	A:3007	G:1756	4763	0.368675	0	TRUE	A:4488	C:1	4489	0.000223	1	FALSE	1	16	
1774	SA098_8_1	SA098	8	41516																										

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.pos	Ref.count	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count.T	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNASe	
1796	SA101_6_2	SA101	6	27907087	6,27907087	silent		NA		HIST1H4K	6p22-p21.3					C:45969	T:10453	56422	0.185265	0	TRUE	C:67564	T:13	67577	0.000192	1	FALSE	2	3	
1797	SA101_7_1	SA101	7	1.37E+08	7,1370251	missense	low	0.895	A165T	DGKI	7q32.3-q33				Entrez Query :: Protein	C:212	T:122	334	0.365269	2.45E-247	TRUE	C:229	N:0	229	0	1	FALSE	0	0	
1798	SA101_7_8	SA101	7	86920287	7,86920287	missense	high	3.555	I49F	ABCB4	7q21.1				DOMAIN //	T:537	A:112	849	0.367491	0	TRUE	T:529	N:0	529	0	1	FALSE	0	0	
1799	SA101_8_9	SA101	8	95003494	8,95003494	missense	medium	2.19	L11V	PPM2C	8q22.1				TRANSIT //	C:10348	G:6937	17285	0.401331	0	TRUE	C:14604	A:3	14607	0.000205	0	1	FALSE	2	48
1800	SA102_12_1	SA102	12	74710636	12,74710636	silent	neutral	0	H385V	LOC100131830					REGION //	G:966	T:755	1721	0.438698	0	TRUE	G:1984	N:0	1984	0	1	FALSE	1	60	
1801	SA102_15_1	SA102	15	56627980	15,56627980	missense	medium	2.78	T323M	LPC	15q21-q23					C:3735	T:555	4290	0.129371	0	TRUE	C:4650	A:2	4652	0.00043	1	FALSE	0	0	
1802	SA102_15_2	SA102	15	57170611	15,57170611	missense	low	1.79	I902T	HLF11	15q21					T:2010	C:327	2337	0.139923	0	TRUE	T:11879	C:6	11885	0.000505	1	FALSE	1	30	
1803	SA102_16_1	SA102	16	65531881	16,65531881	missense	high	4.73	D200N	CES2	16q22.1					G:35774	A:8570	44344	0.193262	0	TRUE	G:44515	A:10	44525	0.000225	1	FALSE	1	26	
1804	SA102_17_1	SA102	17	23944129	17,23944129	nonsense		NA	S87	SPAG5	17q11.2					C:372	C:167	539	0.309833	9.49E-257	TRUE	G:376	N:0	376	0	1	FALSE	2	9	
1805	SA102_17_1	SA102	17	35442520	17,35442520	missense	low	1.25	V282I	MED24	17q21.1					C:2874	T:2032	4906	0.414187	0	TRUE	C:4284	A:1	4285	0.000233	1	FALSE	2	15	
1806	SA102_20_1	SA102	20	23369006	20,23369006	missense	low	1.78	K34N	CSTL1	20p11.21					G:104403	C:36928	141331	0.261287	0	TRUE	G:451975	C:63	452038	0.000139	1	FALSE	0	0	
1807	SA102_22_1	SA102	22	16460985	22,16460985	missense	neutral	0.75	Q169K	ATP6V1E1	22pter-q11.2[22q11.1					G:60773	T:13058	73831	0.176863	0	TRUE	G:209526	A:30	209556	0.000143	1	FALSE	1	199	
1808	SA102_4_2	SA102	4	20200433	4,20200433	missense	medium	2.465	C1053S	SLIT2	4p15.2				Entrez Que	DISULFID //	T:145	A:26	171	0.152047	3.45E-40	TRUE	T:419	A:1	420	0.002381	1	FALSE	1	12
1809	SA103_12_1	SA103	12	7235494	12,7235494	missense	medium	2.14	D127N	PEX5	12p13.3					G:6901	A:385	7286	0.052841	0	TRUE	G:6933	C:1	6934	0.000144	1	FALSE	1	29	
1810	SA103_14_1	SA103	14	94363012	14,94363012	missense	medium	1.975	S1747L	DICER1	14q32.13				DOMAIN //	G:24560	A:6022	30582	0.196913	0	TRUE	G:30038	A:10	30048	0.000333	1	FALSE	1	40	
1811	SA103_2_1	SA103	2	1.63E+08	2,1629366	missense	medium	2.24	S1174L	KCNH7	2q24.2				TOPO_DON	G:6770	A:1222	7992	0.152903	0	TRUE	G:21854	A:3	21857	0.000137	1	FALSE	0	0	
1812	SA103_4_9	SA103	4	90388355	4,90388355	missense	low	0.805	E644Q	GRIN3C	4q22.1					C:312	G:174	486	0.358025	9.38E-294	TRUE	C:445	G:7	452	0.015487	0.008106	FALSE	1	9	
1813	SA103_7_6	SA103	7	65340349	7,65340349	missense	low	1.475	D68N	TPST1	7q11.21				TOPO_DON	G:56161	A:15869	72030	0.220311	0	TRUE	G:30026	C:4	30030	0.000133	1	FALSE	1	40	
1814	SA103_7_8	SA103	7	87011490	7,87011490	missense	low	1.545	M701R	ABCB1	7q21.1				Entrez Que	TOPO_DON	A:2176	C:256	2432	0.105263	0	TRUE	A:2642	G:2	2644	0.000756	1	FALSE	1	3
1815	SA106_10_1	SA106	10	1.27E+08	10,126673	missense	high	3.695	N249K	CTBP2	10q26.13				Cancer Cell	NP_BIND //	G:206	C:13	219	0.059361	5.26E-10	TRUE	G:253	C:4	257	0.015564	0.22741	FALSE	1	49
1816	SA106_10_1	SA106	10	37545309	10,37545309	missense	low	1.24	Q1022E	ANKRD30A	10p11.21				COILED //	C:3055	G:431	3486	0.123637	0	TRUE	C:428	N:0	428	0	1	FALSE	0	0	
1817	SA106_10_1	SA106	10	55261147	10,55261147	missense	low	1.65	A1379V	PCDH15	10q21.1				TRANSMEN	G:1787	A:835	2622	0.1318459	0	TRUE	G:874	N:0	874	0	1	FALSE	0	0	
1818	SA106_10_1	SA106	10	64085226	10,64085226	missense	neutral	0	Q74E	ZNF365	10q21.2					C:539	G:450	989	0.455005	0	TRUE	C:881	N:0	881	0	1	FALSE	1	1	
1819	SA106_11_1	SA106	11	1.18E+08	11,118284	missense	low	0.975	M38V	BCI9L	11q23.3					T:527	C:241	768	0.313802	0	TRUE	T:186	N:0	186	0	1	FALSE	2	72	
1820	SA106_11_1	SA106	11	1.2E+08	11,120489	missense	medium	1.945	V239I	TECTA	11q22-q24				DOMAIN //	G:4895	A:3778	8673	0.435605	0	TRUE	G:1303	N:0	1303	0	1	FALSE	0	0	
1821	SA106_11_1	SA106	11	66129597	11,66129597	missense	high	4.505	G210E	CCS	11q13				REGION //	G:8830	A:3244	12074	0.268676	0	TRUE	G:4078	N:0	4078	0	1	FALSE	2	34	
1822	SA106_11_1	SA106	11	67681762	11,67681762	missense	low	0.895	R876T	SUV420H1	11q13.2					C:754	G:199	953	0.208814	0	TRUE	C:127	N:0	127	0	1	FALSE	2	13	
1823	SA106_12_1	SA106	12	10042960	12,10042960	missense	low	0.975	D3H	CLEC1B					TOPO_DON	C:37743	G:12158	49901	0.243642	0	TRUE	C:13988	T:5	13993	0.000357	1	FALSE	0	0	
1824	SA106_12_1	SA106	12	1.07E+08	12,107124	missense	low	1.765	R166L	WSCD2	12q23.3				DOMAIN //	G:3632	T:2704	6336	0.426768	0	TRUE	G:6996	A:1	6997	0.000143	1	FALSE	0	0	
1825	SA106_12_1	SA106	12	12209468	12,12209468	missense	low	1.66	R525Q	LRP6	12p11-p13				Cancer Cell	REGION //	C:5001	T:1557	6558	0.23742	0	TRUE	C:2828	N:0	2828	0	1	FALSE	2	33
1826	SA106_12_1	SA106	12	91682047	12,91682047	missense	medium	2.19	P294S	PLEKHG7	12q22				DOMAIN //	G:24636	T:5393	30029	0.175953	0	TRUE	C:11604	G:4	11608	0.000345	1	FALSE	0	0	
1827	SA106_13_1	SA106	13	1.13E+08	13,112778	missense	medium	2.35	E520A	MCF2L					COILED //	A:5577	C:977	6554	0.149069	0	TRUE	A:3640	C:1	3641	0.000275	1	FALSE	2	18	
1828	SA106_13_1	SA106	13	1.13E+08	13,113336	missense	high	3.935	I189M	TFDP1	13q34				Cancer Cell	DNA_BIND	C:3396	G:704	4100	0.171707	0	TRUE	C:1656	N:0	1656	0	1	FALSE	1	138
1829	SA106_13_1	SA106	13	26743848	13,26743848	missense	low	1.61	G85A	RASL11A	-				Entrez Que	NP_BIND //	G:1323	C:283	1606	0.176214	0	TRUE	G:1244	N:0	1244	0	1	FALSE	1	36
1830	SA106_14_1	SA106	14	1.03E+08	14,103263	missense	medium	2.365	L101F	ZFYVE21	14q32.33				ZN_FING //	C:332	T:854	1186	0.720067	0	TRUE	C:1793	N:0	1793	0	1	FALSE	3	1	
1831	SA106_14_1	SA106	14	61277634	14,61277634	missense	medium	1.955	V690M	HIF1A	14q21-q24				Entrez Que	REGION //	G:1269	A:495	1764	0.280612	0	TRUE	G:1094	C:1	1095	0.000913	1	FALSE	1	120
1832	SA106_15_1	SA106	15	39138160	15,39138160	missense	high	4.295	D652H	JNOC1	15q15.1				DOMAIN //	C:757	G:1745	2502	0.697442	0	TRUE	C:2443	N:0	2443	0	1	FALSE	2	6	
1833	SA106_15_1	SA106	15	63277239	15,63277239	missense	medium	2.51	D813A	CILP	15q22					T:2029	G:775	2804	0.276391	0	TRUE	T:622	N:0	622	0	1	FALSE	1	4	
1834	SA106_16_1	SA106	16	20906138	16,20906138	missense	neutral	0.37	T2339N	DNAH3	16p12.2					G:2012	T:1631	3643	0.447708	0	TRUE	G:2060	N:0	2060	0	1	FALSE	0	0	
1835	SA106_16_1	SA106	16	55001	16,55001	missense	medium	2.56	R5G	RHBDP1	16p13.3				CONFLICT	G:1063	C:221	1284	0.172118	2.08E-279	TRUE	G:1633	A:1	1634	0.000612	1	FALSE	1	20	
1836	SA106_16_1	SA106	16	65849822	16,65849822	missense	medium	2.485	I533F	SLC9A5	16q22.1					A:1750	T:554	2304	0.240451	0	TRUE	A:7129	C:1	7130	0.00014	1	FALSE	1	1	
1837	SA106_16_1	SA106	16	66882690	16,66882690	missense	medium	2.61	T291R	SLC7A6	16q22.1				TOPO_DON	C:47413	G:28182	75595	0.372802	0	TRUE	C:18172	A:8	18180	0.00044	1	FALSE	1	19	
1838	SA106_16_1	SA106	16	67149973	16,67149973	missense		NA	D86	ZFP90	16q22.1				DOMAIN //	G:198502	G:78454	276956	0.283272	0	TRUE	G:148462	A:17	148479	0.000114	1	FALSE	2	3	
1839	SA106_16_1	SA106	16	82650430	16,82650430	missense	medium	2.425	P937A	MBTPS1	16p16q24				TOPO_DON	G:66048	C:18684	84732	0.220507	0	TRUE	G:15148	C:2	15150	0.000132	1	FALSE	2	76	
1840	SA106_17_1	SA106	17	17072002	17,17072002	missense	medium	2.075	R59G	FLCN	17p11.2				Cancer Review :: Futre	G:24550	C:13704	38254	0.358237	0	TRUE	G:11080	T:4	11084	0.000361	1	FALSE	2	5	
1841	SA106_17_1	SA106	17	46296242	17,46296242	missense	medium	3.06	P46A	TOB1	17q21				Entrez Query :: Oncog	G:625	C:213	838	0.254177	0	TRUE	G:564	N:0	564	0	1	FALSE	1	98	
1842</																														

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func.Impa	FI.score	AA.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.pof	Ref.count	Alt.count	Total.count	Alt.frequer	Binomial.te	Binomial.te	Ref.count	Alt.count	Total.count	Alt.frequer	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase
1865	SA106_1_1	SA106	1	7769484	1,7769484,G,C			NA								G:145553	C:56180	201733	0.278487	0	TRUE	G:325063	C:29	325092	8.92E-05	1	FALSE	1	6
1866	SA106_20	SA106	20	32513571	20,32513571	missense		NA	E477D	ITCH	20q11.22-q11.23				DOMAIN //	A:25782	C:7975	33757	0.236247	0	TRUE	A:25217	G:5	22522	0.000222	1	FALSE	1	44
1867	SA106_20	SA106	20	52208926	20,52208926	missense	medium	2.385	K378N	CYP2A41	20p13			Entrez Query :: Oncog	T:313	A:181	494	0.366397	1.32E-296	0	TRUE	T:353	N:0	353	0	1	FALSE	1	2
1868	SA106_20	SA106	20	5852138	20,5852138	nonsense		NA	E450	CHGB	20pter-p12			PEPTIDE //	G:4487	T:2494	6981	0.357255	0	TRUE	G:6818	N:0	6818	0	1	FALSE	0	0	
1869	SA106_21	SA106	21	43063936	21,43063936	missense	low	0.805	R549C	PDE9A	21q22.3			HELIX // 53	C:88238	T:31731	119969	0.264493	0	TRUE	C:25101	T:8	25109	0.000319	1	FALSE	1	26	
1870	SA106_22	SA106	22	17882541	22,17882541	missense	medium	2.28	S470R	CDC45L	22q11.21			C:13232	G:2819	16051	0.175628	0	TRUE	C:3260	G:1	3261	0.000307	1	FALSE	1	29		
1871	SA106_22	SA106	22	29666821	22,29666821	missense	low	1.18	M276I	MORC2	22q12.2			C:231413	G:75133	306546	0.245095	0	TRUE	C:37326	A:13	37339	0.000348	1	FALSE	2	44		
1872	SA106_2_1	SA106	2	1.36E+08	2,1362648	missense	low	1.73	E1738K	LCT	2q21			REGION //	C:517	T:110	627	0.175439	5.31E-140	0	TRUE	C:449	N:0	449	0	1	FALSE	2	2
1873	SA106_2_1	SA106	2	1.7E+08	2,1698059	missense	neutral	0.475	L1289I	LRP2	2q24-q31			DISULFID //	G:2668	T:2768	5436	0.509198	0	TRUE	G:4423	N:0	4423	0	1	FALSE	2	15	
1874	SA106_2_4	SA106	2	43305982	2,43305982	missense	high	4.08	K155N	ZFP36L2	2p22.3-p21			ZN_FING //	C:139	G:176	315	0.55873	0	TRUE	C:528	N:0	528	0	1	FALSE	2	94	
1875	SA106_2_8	SA106	2	84630693	2,84630693,G,A			NA						G:206583	A:39376	245959	0.160092	0	TRUE	G:172617	A:17	172634	9.85E-05	1	FALSE	3	0		
1876	SA106_3_1	SA106	3	1.31E+08	3,13078609	missense	low	1.53	G618D	PLXND1	3q21.3			TOPO_DON	C:2540	T:2742	5282	0.519122	0	TRUE	C:6245	T:4	6249	0.00064	1	FALSE	1	49	
1877	SA106_3_1	SA106	3	13402856	3,13402856	missense	medium	2.175	N246Y	NUP210	3p25.1			TOPO_DON	T:1324	A:384	1708	0.224824	0	TRUE	T:591	N:0	591	0	1	FALSE	1	76	
1878	SA106_3_1	SA106	3	1.67E+08	3,1670305	missense	low	1.445	S315S	BCHE	3q26.1-q26.2			G:32151	A:14799	46950	0.315208	0	TRUE	G:11683	C:5	11688	0.000428	1	FALSE	0	0		
1879	SA106_3_1	SA106	3	21442159	3,21442159	missense	medium	1.935	K227N	ZNF385D	3p24.3			ZN_FING //	C:20709	G:12131	32840	0.369397	0	TRUE	C:4877	N:0	4877	0	1	FALSE	2	6	
1880	SA106_4_1	SA106	4	1.09E+08	4,1090880	missense	high	3.755	M400I	CYP2U1	4q25			G:6314	T:2626	8940	0.293736	0	TRUE	G:3759	A:2	3761	0.000532	1	FALSE	1	7		
1881	SA106_4_1	SA106	4	1.7E+08	4,1698391	nonsense		NA	G381	PALLD	4q32.3			G:2294	T:1328	3622	0.366648	0	TRUE	G:3779	A:2	3781	0.000529	1	FALSE	2	6		
1882	SA106_5_1	SA106	5	1.8E+08	5,1802683	missense	high	3.895	Y81H	BTNL8	5q35.3			DISULFID //	T:46197	C:12748	58945	0.216269	0	TRUE	T:8407	C:8	8415	0.000951	1	FALSE	0	0	
1883	SA106_5_1	SA106	5	34064704	5,34064704	missense	low	0.83	Q131H	CIQTNF3	-			DOMAIN //	C:166	A:54	220	0.245455	1.57E-93	0	TRUE	C:152	N:0	152	0	1	FALSE	1	3
1884	SA106_5_1	SA106	5	9683045	5,9683045	missense	medium	2.715	D34N	TAS2R1	5p15			TOPO_DON	C:5371	T:1741	7112	0.244798	0	TRUE	C:14298	A:3	14301	0.00021	1	FALSE	0	0	
1885	SA106_6_1	SA106	6	1.16E+08	6,1163954	missense	medium	2.25	K265R	FRK	6q21-q22.3			Entrez Query	DOMAIN //	T:18508	C:3436	21944	0.15658	0	TRUE	T:2653	N:0	2653	0	1	FALSE	1	15
1886	SA106_6_1	SA106	6	1.5E+08	6,1500469	missense	low	0.895	S321T	LATS1	6q24-q25.1			Entrez Query :: Protein	C:6308	G:6792	13100	0.158473	0	TRUE	C:10960	N:0	10960	0	1	FALSE	2	10	
1887	SA106_6_2	SA106	6	26360203	6,26360203	missense	high	3.655	T116A	HIST1H2BH	6p21.3			A:14200	G:1361	15561	0.087462	0	TRUE	A:9783	C:2	9785	0.000204	1	FALSE	1	84		
1888	SA106_6_4	SA106	6	43433108	6,43433108	missense	medium	2.015	P308T	ZNF318	6pter-p12.1			MOD_RES	G:57176	T:18239	75415	0.218488	0	TRUE	G:19736	T:2	19738	0.000101	1	FALSE	1	21	
1889	SA106_6_4	SA106	6	43716201	6,43716201	missense	medium	2.28	V260N	MAD2L1BP	6p21.1			TURN // 25	T:18062	A:3809	21871	0.174158	0	TRUE	T:7135	C:7	7142	0.00098	1	FALSE	2	35	
1890	SA106_6_7	SA106	6	75870224	6,75870224	missense	low	1.83	P2763H	COL12A1	6q12-q13			REGION //	G:703	T:1320	2023	0.652496	0	TRUE	G:701	N:0	701	0	1	FALSE	1	56	
1891	SA106_7_1	SA106	7	1.39E+08	7,1393017	missense	neutral	-1.725	W202L	TBXAS1	7q34-q35			TOPO_DON	G:185	T:409	594	0.688552	0	TRUE	G:634	N:0	634	0	1	FALSE	1	18	
1892	SA106_7_2	SA106	7	23266755	7,23266755	missense	medium	2.495	G286R	GNMNB	7p15			DOMAIN //	G:387	C:158	545	0.289908	1.16E-239	0	TRUE	G:706	N:0	706	0	1	FALSE	1	220
1893	SA106_7_2	SA106	7	94879590	7,94879590	missense	medium	3.21	P113A	PON2	7q21.3			ACT_SITE //	G:76241	C:29323	105564	0.277775	0	TRUE	G:47927	A:6	47933	0.000125	1	FALSE	2	113	
1894	SA106_8_1	SA106	8	1.11E+08	8,1110541	missense	medium	2.515	E172G	KCNV1	8q22.3-q24.1			TOPO_DON	T:10956	C:2194	13150	0.166844	0	TRUE	T:2886	N:0	2886	0	1	FALSE	0	0	
1895	SA106_8_1	SA106	8	1.13E+08	8,1133102	missense	low	1.61	Q3622L	C5MD3	8q23.3			TOPO_DON	T:115	A:73	188	0.388298	8.77E-122	0	TRUE	T:101	N:0	101	0	1	FALSE	0	0
1896	SA106_8_2	SA106	8	25359658	8,25359658	missense	medium	2.19	S25C	KCTD9	8p21.1			DOMAIN //	G:21753	C:6953	28706	0.242214	0	TRUE	G:10148	A:2	10150	0.000197	1	FALSE	2	5	
1897	SA106_9_1	SA106	9	1.03E+08	9,1033375	missense	medium	2.25	G14V	RNF20	9q22			G:3294	T:831	4125	0.201455	0	TRUE	G:1117	N:0	1117	0	1	FALSE	1	7		
1898	SA106_9_1	SA106	9	1.31E+08	9,1309311	missense	high	4.21	R134W	PPP2R4	9q34			Entrez Query	STRAND //	C:1102	T:939	2041	0.460069	0	TRUE	C:2217	T:1	2218	0.000451	1	FALSE	2	61
1899	SA208_10	SA208	10	13521272	10,13521272	missense	neutral	0	S489L	C10orf30	10p13			G:54396	A:14411	68807	0.209441	0	TRUE	G:63647	A:7	63654	0.00011	1	FALSE	0	0		
1900	SA208_11	SA208	11	62043991	11,62043991	missense	medium	1.975	L4825S	AHNAK	11q12.2			A:39663	C:33034	72697	0.554407	0	TRUE	A:79333	C:17	79350	0.000214	1	FALSE	2	693		
1901	SA208_12	SA208	12	68051017	12,68051017	missense	medium	2.755	T170R	YEATS4	12q13-q15			Entrez Query	REGION //	C:594	G:961	1555	0.618006	0	TRUE	C:2050	N:0	2050	0	1	FALSE	2	15
1902	SA208_15	SA208	15	71328474	15,71328474	missense	low	1.245	P543A	NEO1	15q22.3-q23			DOMAIN //	G:269	C:671	400894	0.210592	0	TRUE	C:812	N:0	812	0	1	FALSE	1	65	
1903	SA208_16	SA208	16	72896716	16,72896716	missense	high	4.095	L187M	PSMD7	16q23-q24			Cancer Cell	MOD_RES	C:992	A:1965	2957	0.664525	0	TRUE	C:3617	N:0	3617	0	1	FALSE	2	83
1904	SA208_17	SA208	17	58903142	17,58903142	missense		NA			LOC342541			A:5817	G:8222	14039	0.585654	0	TRUE	A:33496	G:5	33501	0.000149	1	FALSE	0	0		
1905	SA208_19	SA208	19	19684432	19,19684432	nonsense		NA	K220		19p13.3-p13.2			T:705	ZNF14	1081	0.347826	0	TRUE	T:418	N:0	418	0	1	FALSE	2	13		
1906	SA208_19	SA208	19	54533860	19,54533860	missense	medium	3.395	S180C	CD37	19q13.3			TOPO_DON	C:4399	G:2924	7323	0.39929	0	TRUE	C:8625	T:1	8626	0.000116	1	FALSE	1	39	
1907	SA208_1_1	SA208	1	1.49E+08	1,1487931	missense	low	1.79	P362A	ADAMTSL4	1q21.2			C:3474	G:1043	4517	0.230905	0	TRUE	C:11590	A:2	11592	0.000173	1	FALSE	2	22		
1908	SA208_1_1	SA208	1	1.55E+08	1,1553356	missense	high	3.825	G81S	ETV3L	1q23.1			DNA_BIND	C:665	T:927	1592	0.582286	0	TRUE	C:1283	N:0	1283	0	1	FALSE	0	0	
1909	SA208_1_2	SA208	1	2.38E+08	1,2384879	missense	low	1.86	L375V	FMN2	1q43			DOMAIN //	C:7558	G:1212	12679	0.403896	0	TRUE	C:27139	A:8	27147	0.000295	1	FALSE	0	0	
1910	SA208_1_2	SA208	1	26454317	1,26454317	missense	medium	2.39	H93Y	CCDC21	1p36.11			G:514	T:1084	1598	0.678348	0	TRUE	C:1847	A:1	1848	0.000541	1	FALSE	3	1		
1911	SA208_20	SA208	20	25217120	20,25217120,G,T			NA						G:5837	T:4163	10000	0.4163	0	TRUE	G:5803	A:2	5805	0.000345	1	FALSE	1	9		
1912	SA208_20	SA208	20	30253480	20,30253480	missense	neutral	0	L55V	PLAGL2	20q11.21			Entrez Query :: Stability															

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	KA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.pos	Ref.count.	Alt.count.T	Total.count	Alt.frequer	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.frequer	Binomial.te	Binomial.te	SVNMix2.C	REF.RNAse
1934	SA210_18	SA210	18	5281019	18,5281019	missense	medium	3.27	K396N	ZFP161								42558	0.21305	0	TRUE	C:32747	A:4	32751	0.000122	1	FALSE	2	41
1935	SA210_19	SA210	19	11268037	19,11268037	missense	neutral	-0.92	V22L	TSPAN16	19p13.2							7921	0.236334	0	TRUE	G:5452	T:2	5454	0.000367	1	FALSE	0	0
1936	SA210_19	SA210	19	6701327	19,6701327	missense	medium	2.125	R418G	TRIP10	19p13.3							712	0.217697	1.16E-242	TRUE	C:1603	N:0	1603	0	1	FALSE	2	90
1937	SA210_1_1	SA210	1	1.1E+08	1,10966714	missense	low	1.64	Q652H	SORT1	1p21.3-p13.1	1p21.3-p13.1						55780	0.181176	0	TRUE	C:30991	T:5	30996	0.000161	1	FALSE	2	449
1938	SA210_1_1	SA210	1	1.66E+08	1,16600811	missense	neutral	0.655	P102R	MP2L1	1q24.2							21926	0.163687	0	TRUE	C:19172	A:1	19173	5.22E-05	1	FALSE	1	207
1939	SA210_1_1	SA210	1	1.72E+08	1,17246707	missense	medium	2.945	P173L	RABGAP1L	1q24							94414	0.170907	0	TRUE	C:57016	A:15	57031	0.000263	1	FALSE	1	19
1940	SA210_1_2	SA210	1	2.1E+08	1,21059711	missense	low	1.075	K390Q	PPP2R5A	1q32.2-q32.3							3717	0.189131	0	TRUE	A:3327	N:0	3327	0	1	FALSE	2	269
1941	SA210_1_2	SA210	1	2.14E+08	1,21431011	missense	low	1.575	L1989V	USH2A	1q41							21228	0.207132	0	TRUE	G:25651	C:3	25654	0.000117	1	FALSE	0	0
1942	SA210_1_2	SA210	1	2.15E+08	1,2146049	missense	medium	2.075	Q258H	USH2A	1q41							8941	0.186221	0	TRUE	C:12193	T:4	12197	0.000328	1	FALSE	0	0
1943	SA210_1_2	SA210	1	27627945	1,27627945	missense	medium	2.715	R15G	WASF2	1p36.11-p34.3							1645	0.164742	0	TRUE	G:320	N:0	320	0	1	FALSE	1	162
1944	SA210_1_3	SA210	1	35798690	1,35798690	missense	neutral	0.49	D117E	NCDN	1p34.3							2941	0.365522	0	TRUE	C:1867	N:0	1867	0	1	FALSE	2	37
1945	SA210_1_3	SA210	1	59021034	1,59021034	nonsense	NA		C99	JUN	1p32-p31							4748	0.267692	0	TRUE	G:3773	A:3	3776	0.000794	1	FALSE	2	249
1946	SA210_22	SA210	22	30682433	22,30682433	missense	high	4.385	R132H	YWHAH	22q12.3							24583	0.196843	0	TRUE	G:19849	A:8	19857	0.000403	1	FALSE	2	934
1947	SA210_2_1	SA210	2	1.13E+08	2,1130215	missense	low	1.34	K144N	POLR1B	2q13							52185	0.225295	0	TRUE	G:74543	C:7	74550	9.39E-05	1	FALSE	2	22
1948	SA210_2_2	SA210	2	1.13E+08	2,1134527	missense	neutral	0	V15L	ILF19	2q12-q21							10703	0.18079	0	TRUE	G:10219	C:2	10221	0.000196	1	FALSE	0	0
1949	SA210_2_2	SA210	2	1.31E+08	2,1305490	missense	medium	2.975	E807K	ACE1B								5939	0.170062	0	TRUE	C:4989	N:0	4989	0	1	FALSE	1	2
1950	SA210_2_2	SA210	2	1.41E+08	2,1407998	missense	medium	2.32	S4093P	LRP1B	2q21.2							38528	0.188979	0	TRUE	A:62337	C:13	62350	0.000209	1	FALSE	0	0
1951	SA210_2_2	SA210	2	1.73E+08	2,1725305	missense	medium	2.14	C168R	HAT1	2q31.2-q33.1							28545	0.237835	0	TRUE	T:25344	C:6	25350	0.000237	1	FALSE	2	134
1952	SA210_2_2	SA210	2	2.38E+08	2,2379181	missense	low	0.83	Q2415E	COL6A3	2q37							2572	0.241835	0	TRUE	G:1416	N:0	1416	0	1	FALSE	1	1330
1953	SA210_3_1	SA210	3	1.51E+08	3,1507283	missense	low	1.575	M288I	WWTR1	3q23-q24							6050	0.216216	0	TRUE	C:2162	N:0	2162	0	1	FALSE	1	409
1954	SA210_3_1	SA210	3	18368683	3,18368683	missense	medium	2.215	L528F	SATB1	3p23							23458	0.169537	0	TRUE	C:30928	T:9	30937	0.000291	1	FALSE	2	189
1955	SA210_3_1	SA210	3	49854319	3,49854319	missense	medium	2.075	M187I	TRAIP	3p21.31							1169	0.202737	0	TRUE	C:164	N:0	164	0	1	FALSE	1	19
1956	SA210_3_1	SA210	3	53827110	3,53827110	missense	medium	2.32	D507N	CHDH	3p21.1							3646	0.233132	0	TRUE	C:4351	T:1	4352	0.00023	1	FALSE	2	42
1957	SA210_4_1	SA210	4	1.26E+08	4,1258121	missense	neutral	0.345	H579Y	ANKRD50	4q28.1							30717	0.231924	0	TRUE	G:35356	A:3	35359	8.48E-05	1	FALSE	1	35
1958	SA210_4_1	SA210	4	74666422	4,74666422	missense	medium	3.12	L265F	RASF56	4q13.3							197	0.203046	5.07E-61	TRUE	G:118	N:0	118	0	1	FALSE	2	7
1959	SA210_5_1	SA210	5	64502234	5,64502234	missense	medium	2.79	S1070R	ADAMTS6	5q12							545	0.185321	3.11E-150	TRUE	G:275	N:0	275	0	1	FALSE	1	6
1960	SA210_6_1	SA210	6	1.22E+08	6,1216444	missense	medium	1.995	E513K	C6orf170	6q22.31							3022	0.130377	0	TRUE	C:1459	N:0	1459	0	1	FALSE	1	8
1961	SA210_6_1	SA210	6	1.47E+08	6,1467617	missense	medium	2.815	D619A	GRM1	6q24							10387	0.12506	0	TRUE	A:8058	C:2	8060	0.000248	1	FALSE	0	0
1962	SA210_6_1	SA210	6	32519014	6,32519014	missense	medium	2.925	D135N	HLA-DRA	6p21.3							733227	0.149118	0	TRUE	G:1399336	A:210	1399546	0.00015	1	FALSE	1	803
1963	SA210_7_1	SA210	7	1.07E+08	7,1073568	missense	medium	2.08	S1582T	LAMB1	7q22							141604	0.165221	0	TRUE	C:276521	T:54	276575	0.000195	1	FALSE	1	29
1964	SA210_7_1	SA210	7	91546627	7,91546627	missense	low	1.59	V2427G	AKAP9	7q21-q22							7176	0.143116	0	TRUE	T:3057	C:1	3058	0.000327	1	FALSE	1	118
1965	SA210_8_1	SA210	8	1.04E+08	8,1039161	missense	medium	2.545	E204Q	AZIN1	8q22.3							62705	0.201866	0	TRUE	C:37576	G:5	37581	0.000133	1	FALSE	1	192
1966	SA210_8_1	SA210	8	57243247	8,57243247	missense	NA		V46F	PLAG1	8q12							26704	0.122118	0	TRUE	C:20922	T:5	20927	0.000239	1	FALSE	1	1
1967	SA210_9_1	SA210	9	39075765	9,39075765	missense	medium	2.415	A1137G	CNTNAP3	9p13.1							49226	0.224001	0	TRUE	G:10008	T:2	10010	0.0002	1	FALSE	1	2
1968	SA210_10_1	SA210	X	1.01E+08	X,1009792	missense	medium	2.08	Q332E	NXF5	Xq22							99070	0.292551	0	TRUE	G:42428	A:9	42437	0.000212	1	FALSE	0	0
1969	SA210_10_1	SA210	X	1.32E+08	X,1322859	missense	medium	3.105	V203G	GPC4	Xq26.1							33077	0.211053	0	TRUE	A:15344	C:7	15351	0.000456	1	FALSE	1	39
1970	SA210_10_1	SA210	X	34871072	X,34871072	missense	neutral	-0.09	T68M	FAM47B	Xp21.1							7815	0.144082	0	TRUE	C:14093	A:7	14100	0.000496	1	FALSE	0	0
1971	SA212_10	SA212	10	1.16E+08	10,115647	missense	neutral	0.695	G353R	NHLRC2	10q25.3							4463	0.156136	0	TRUE	G:4623	N:0	4623	0	1	FALSE	1	19
1972	SA212_11	SA212	11	47776109	11,47776109	missense	low	0.845	N1060K	NUP160	11p11.2							500	0.272	9.61E-201	TRUE	A:419	N:0	419	0	1	FALSE	2	62
1973	SA212_11	SA212	11	64259232	11,64259232	nonsense	NA		S447	RASGRP2								732	0.219945	7.67E-262	TRUE	G:1194	N:0	1194	0	1	FALSE	1	22
1974	SA212_11	SA212	11	75885114	11,75885114	missense	neutral	0.695	P439R	C11orf30	11q13.5							6736	0.103771	0	TRUE	C:9375	A:3	9378	0.00032	1	FALSE	1	19
1975	SA212_11	SA212	11	77060791	11,77060791	missense	low	1.87	R1232H	RSF1	11q14.1							3358	0.124777	0	TRUE	C:4664	A:2	4666	0.000429	1	FALSE	2	49
1976	SA212_12	SA212	12	11041221	12,11041221	missense	medium	2.155	L174R	TAS2R49	12p13.2							23290	0.226621	0	TRUE	A:37142	C:3	37145	8.08E-05	1	FALSE	1	2
1977	SA212_12	SA212	12	1.23E+08	12,122724	missense	medium	2.125	R100S	TCTN2	12q24.31							43003	0.109667	0	TRUE	A:34532	G:7	34539	0.000203	1	FALSE	1	9
1978	SA212_13	SA212	13	27495543	13,27495543	missense	medium	2.875	L788I	FLT3	13q12							3865	0.098577	0	TRUE	G:7382	A:1	7383	0.000135	1	FALSE	1	11
1979	SA212_14	SA212	14	70060228	14,70060228	missense	neutral	0.6	V334F	ADAM20	14q24.1							37721	0.268153	0	TRUE	C:33613	A:10	33623	0.000297	1	FALSE	0	0
1980	SA212_16	SA212	16	27658956	16,27658956	missense	low	1.04	A613P	KIAA0556	16p12.1-p11.2							15846	0.280954	0	TRUE	G:21466	A:4	21470	0.000186	1	FALSE	1	5
1981	SA212_16	SA212	16	60416453	16,60416453	missense	high	3.61	T267P	CDH8	16q22.1							14082	0.300383	0	TRUE	T:27046	C:17	27063	0.000628	1	FALSE	3	0
1982	SA212_17	SA212	17	7517845	17,7517845	missense	medium	3.105	R273H	TP53	17p13.1	p.R273C,p. carcinoma	Cancer Cell					2177	0.381259	0	TRUE	C:3795	T:1	3796	0.000263	1	FALSE	2	14
1983	SA212_18	SA212																											

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.pof	Ref.count.	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase	
2003	SA212_X_2	SA212	X	27908511	X,27908511	missense	neutral	-0.99	P288A	WDR42B	Xp21.3				REPEAT //	G:512	C:125	637	0.196232	1.15E-164	TRUE	G:1489	T:1	1490	0.000671	1	FALSE	0	0	
2004	SA212_X_3	SA212	X	53605899	X,53605899	missense	neutral	0.55	E2412D	HWEU1	Xp11.22				Entrez Query	COMPBIAS	C:65431	A:13348	78779	0.169436	0	TRUE	C:39112	A:8	39120	0.000204	1	FALSE	2	108
2005	SA213_10	SA213		97433289	10,97433289	missense	low	1.245	T3955	TCTN3	10q23.33				TOPO_DON	T:85	A:34	119	0.285714	2.95E-58	TRUE	T:160	N:0	160	0	1	FALSE	2	113	
2006	SA213_11	SA213		1.02E+08	11,1020988	missense	low	0.92	E61K	MMP8	11q22.3				PROPEP //	C:420	T:122	542	0.225092	7.06E-193	TRUE	C:760	N:0	760	0	1	FALSE	0	0	
2007	SA213_11	SA213		62753604	11,62753604	missense	neutral	-1.2	H33N	SLC22A25	11q12.3				TOPO_DON	G:41472	T:3485	44957	0.077519	0	TRUE	G:45926	A:7	45933	0.000152	1	FALSE	0	0	
2008	SA213_11	SA213		63786836	11,63786836	nonsense	NA		E779	PLCB3	11q13				DOMAIN //	G:5372	T:3409	8781	0.388225	0	TRUE	G:7157	C:3	7160	0.000419	1	FALSE	2	29	
2009	SA213_13	SA213		1.02E+08	13,102124	missense	low	1.79	E1157G	TPP2	13q32-q33					C:6302	G:6125	42127	0.145394	0	TRUE	A:10551	G:2	10553	0.00019	1	FALSE	1	480	
2010	SA213_13	SA213		23942079	13,23942079	missense	medium	2.63	V667L	PARP4	13q11				Entrez Query	DOMAIN //	C:6317	T:1230	8447	0.252161	0	TRUE	C:5023	T:1	5024	0.000199	1	FALSE	2	111
2011	SA213_16	SA213		14218647	16,14218647	silent	NA		G161G	MKL2	16p13.12					C:10247	T:9197	19444	0.472799	0	TRUE	C:18261	T:39	18300	0.002131	1	FALSE	1	5	
2012	SA213_16	SA213		88183840	16,88183840	missense	medium	3.285	R441G	CPNE7	16q24.3				DOMAIN //	C:2474	G:1441	3915	0.368072	0	TRUE	C:5047	A:2	5049	0.000396	1	FALSE	2	28	
2013	SA213_16	SA213		88291425	16,88291425	missense	low	0.805	A365T	SPATA2L	16q24.3					C:722	T:255	977	0.261003	0	TRUE	C:1893	G:1	1894	0.000528	1	FALSE	1	17	
2014	SA213_17	SA213		36806740	17,36806740	missense	low	1.715	V128L	KRT31	17q12-q21				REGION //	C:203	A:121	324	0.373457	1.52E-222	TRUE	C:396	N:0	396	0	1	FALSE	0	0	
2015	SA213_18	SA213		21058381	18,21058381	missense	low	1.265	D1167N	ZNF521	18q11.2					C:1080	T:913	1993	0.458103	0	TRUE	C:2942	N:0	2942	0	1	FALSE	2	409	
2016	SA213_18	SA213		45619654	18,45619654	missense	medium	2.47	M1570I	MYO5B	18q21				DOMAIN //	C:2896	T:835	3731	0.223801	0	TRUE	C:1653	N:0	1653	0	1	FALSE	1	109	
2017	SA213_19	SA213		38358287	19,38358287	missense	neutral	0	S463L	WDR88	19q13.11					C:405	T:211	616	0.342532	0	TRUE	C:1100	N:0	1100	0	1	FALSE	1	4	
2018	SA213_1_2	SA213		2.21E+08	1,2213506	missense	low	1.5	S773N	TLR5	1q41-q42				DOMAIN //	C:100232	T:8306	108538	0.076526	0	TRUE	C:37547	T:6	37553	0.00016	1	FALSE	1	94	
2019	SA213_22	SA213		22438319	22,22438319	missense	low	1.865	V104G	PWIL3	22q11.23					A:33407	C:5741	39148	0.146649	0	TRUE	A:16036	G:2	16038	0.000125	1	FALSE	0	0	
2020	SA213_3_1	SA213		1.23E+08	3,1225829	missense	low	1.845	A834P	STXBPL5					REPEAT //	G:499	C:240	739	0.324763	0	TRUE	G:386	N:0	386	0	1	FALSE	2	34	
2021	SA213_3_1	SA213		1.4E+08	3,1396758	silent	NA		T823	FAM62C	3q22.3				DOMAIN //	G:53706	C:35410	89116	0.397347	0	TRUE	G:46148	A:11	46159	0.000238	1	FALSE	3	1	
2022	SA213_3_1	SA213		1.53E+08	3,1525663	missense	medium	2.82	I1039R	MED12L	3q25.1					G:521	T:799	7820	0.066624	0	TRUE	C:2091	N:0	2091	0	1	FALSE	1	10	
2023	SA213_3_1	SA213		1.59E+08	3,1586145	missense	neutral	0.035	N251S	VEPH1	3q24-q25					T:233	C:345	578	0.596886	0	TRUE	T:323	N:0	323	0	1	FALSE	2	16	
2024	SA213_3_1	SA213		1.86E+08	3,1859115	missense	low	1.085	H268Q	MAGEF1	3q13				DOMAIN //	G:8641	C:1762	10403	0.169374	0	TRUE	G:5287	A:1	5288	0.000189	1	FALSE	1	271	
2025	SA213_4_1	SA213		4.12E+08	4,1207477	missense	medium	2.47	A103T	PDE5A	4q25-q27				MOD_RES	C:9166	T:3718	12884	0.288575	0	TRUE	C:6031	A:1	6032	0.000166	1	FALSE	1	38	
2026	SA213_4_1	SA213		4.1679671	4,4167967	missense	neutral	0.695	A369T	WDR21B	4p13					G:218	A:271	489	0.554192	0	TRUE	G:698	N:0	698	0	1	FALSE	1	1	
2027	SA213_5_1	SA213		1.77E+08	5,1774812	missense	low	1.79	R435W	N4BP3	5q35.3				COILED //	C:1050	T:5017	6067	0.826933	0	TRUE	C:4394	N:0	4394	0	1	FALSE	3	4	
2028	SA213_6_1	SA213		1E+08	6,1000982	missense	low	1.175	S266T	CCNC	6q21				Entrez Query :: Tumor	C:9862	G:2736	12598	0.217177	0	TRUE	C:8397	A:2	8399	0.000238	1	FALSE	1	77	
2029	SA213_6_1	SA213		6.11E+08	6,1106741	missense	medium	2.74	I263N	Gcorf186					A:12178	T:856	13034	0.065674	0	TRUE	A:5424	C:2	5426	0.000369	1	FALSE	1	25		
2030	SA213_6_1	SA213		6.4126513	6,4142651	missense	neutral	0.695	R255K	NCR2	6p21.1				TOPO_DON	G:333	A:222	555	0.4	0	TRUE	G:752	N:0	752	0	1	FALSE	0	0	
2031	SA213_6_1	SA213		6.56593450	6,5659345	missense	NA			DST					G:433	A:317	750	0.422667	0	TRUE	G:1197	N:0	1197	0	1	FALSE	2	25		
2032	SA213_7_1	SA213		7.38400182	7,3840018	missense	neutral	0	G519D	AMPH	7p14-p13					C:990	T:941	1931	0.487312	0	TRUE	C:2951	A:1	2952	0.000339	1	FALSE	1	1	
2033	SA213_8_1	SA213		8.105E+08	8,1054307	missense	medium	2.24	R263G	TM7SF4	8q23					A:27553	G:11385	38938	0.292388	0	TRUE	A:20316	C:4	20320	0.000197	1	FALSE	0	0	
2034	SA213_8_1	SA213		8.59646063	8,5964606	missense	low	1.06	I39L	SDCBP	8q12				Entrez Query :: Tumor	A:1203	C:158	1361	0.116091	5.22E-238	TRUE	A:872	N:0	872	0	1	FALSE	1	190	
2035	SA213_9_1	SA213		9.135E+08	9,1351982	missense	low	1.04	S167L	MED22	9q34.2					G:71	A:285	356	0.800562	0	TRUE	G:1420	N:0	1420	0	1	FALSE	3	6	
2036	SA213_9_1	SA213		9.138E+08	9,1378157	missense	medium	2.065	S954T	KCNT1	9q34.3				TOPO_DON	G:2511	C:1304	3815	0.341809	0	TRUE	G:3462	T:1	3463	0.000289	1	FALSE	1	1	
2037	SA213_X_1	SA213	X	13700971	X,1370097	missense	low	1.895	L287W	GPMB6	Xp22.2					G:580	T:685	1545	0.443366	0	TRUE	G:1438	N:0	1438	0	1	FALSE	2	104	
2038	SA214_10	SA214		14603894	10,146038	missense	medium	3.045	R87W	FAM107B	10p13				COILED //	G:5369	A:967	6356	0.152124	0	TRUE	G:6730	A:1	6731	0.000149	1	FALSE	1	96	
2039	SA214_10	SA214		10.27440995	10,2744099	missense	medium	2.31	A747T	YME1L1						C:318	T:42	360	0.116667	2.96E-65	TRUE	C:341	N:0	341	0	1	FALSE	2	366	
2040	SA214_10	SA214		10.27498964	10,2749899	missense	low	1.245	T357M	MASTL	10p12.1				DOMAIN //	C:3877	T:850	4727	0.179818	0	TRUE	C:2542	N:0	2542	0	1	FALSE	2	25	
2041	SA214_11	SA214		11.64435213	11,644352	missense	medium	2.4	G447R	ATG2A	11q13.1					C:14465	T:2283	16748	0.136315	0	TRUE	C:7704	A:1	7705	0.00013	1	FALSE	1	9	
2042	SA214_11	SA214		11.77073845	11,770738	missense	medium	2.215	R970C	RSF1	11q14.1				Entrez Query	COILED //	G:821	A:82	903	0.090808	1.58E-118	TRUE	G:874	N:0	874	0	1	FALSE	2	58
2043	SA214_12	SA214		12.11E+08	12,110474	missense	medium	2.36	R321C	ATXN2	12q24.1					G:5323	A:1194	6517	0.183213	0	TRUE	G:8021	A:3	8024	0.000374	1	FALSE	2	30	
2044	SA214_12	SA214		12.116E+08	12,116068	nonsense	NA		Q616	FBXO21	12q24.22				G:20334	A:2410	22744	0.105962	0	TRUE	G:10409	T:2	10411	0.000192	1	FALSE	2	45		
2045	SA214_12	SA214		12.30724780	12,307247	missense	low	1.63	R181H	IPO8	12p11.21					C:458	T:27	485	0.05567	6.78E-33	TRUE	G:736	N:0	736	0	1	FALSE	2	18	
2046	SA214_12	SA214		12.44530949	12,445309	missense	medium	1.905	V926I	ARID2	12q12				COMPBIAS	G:16320	A:1411	17731	0.079578	0	TRUE	G:8587	C:2	8589	0.000233	1	FALSE	1	25	
2047	SA214_12	SA214		12.44608667	12,446086	missense	low	0.805	A362T	SFRS2IP	12q13.11					C:50759	T:4560	55319	0.082431	0	TRUE	C:49764	G:5	49769	0.0001	1	FALSE	1	55	
2048	SA214_12	SA214		12.48238967	12,482389	missense	medium	2.865	A410W	MCRS1	12q13.12				DOMAIN //	G:22618	A:1418	24036	0.058995	0	TRUE	G:8510	A:3	8513	0.000352	1	FALSE	2	177	
2049	SA214_12	SA214		12.51933712	12,519337	missense	medium	3.375	P276T	MFS05	12q13.13					C:2101	A:245	2346	0.104433	0	TRUE	C:2354	N:0	2354	0	1	FALSE	2	96	
2050	SA214_13	SA214		13.113E+08	13,112898	silent	NA		A97A	PCID2	</																			

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	
1	id	PatientID	Chr	Coord	Mutation	RG.var.type	Func.Lmpa	FI.score	AA.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.pos	Ref.count	Alt.count	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count	Alt.count	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase	
2072	SA214_1_1	SA214	1	2.34E+08	1,2340217	nonsense		NA	W1466	LYST	1q42.1-q42.2					C:37068	T:3445	40513	0.085034	0	TRUE	C:29034	A:2	29036	6.89E-05	1	FALSE	1	5	
2073	SA214_1_2	SA214	1	2.43E+08	1,2428025	missense	neutral		A604V	C1orf101	1q44				TOPO_DON	C:15542	T:1295	16837	0.076914	0	TRUE	C:21731	T:4	21735	0.000184	1	FALSE	2	7	
2074	SA214_1_3	SA214	1	38225859	1,3822585	missense	medium	3.24	K92N	SF3A3	1p34.3				HELI // 80	C:2587	A:1295	2732	0.053075	2.04E-175	TRUE	C:4577	T:1	4578	0.000218	1	FALSE	2	133	
2075	SA214_1_4	SA214	1	39114062	1,3911406	missense	medium	1.95	R99Q	GIA9	1p34				TRANSMEN	C:5344	T:613	5957	0.102904	0	TRUE	C:2774	A:2	2776	0.00072	1	FALSE	1	10	
2076	SA214_1_8	SA214	1	89251600	1,8925160	missense	medium	3.245	R242C	GBP3	1p22.2				G:9754	A:976	10730	0.09096	0	TRUE	G:13811	A:3	13814	0.000217	1	FALSE	1	28		
2077	SA214_20	SA214	20	25604765	20,256047	missense	low	1.7	V387M	ZNF337	20p11.21				ZN_FING // C:32018	T:3425	35443	0.096634	0	TRUE	C:16769	T:5	16774	0.000298	1	FALSE	2	54		
2078	SA214_20	SA214	20	33775923	20,337759	missense	NA		I224V	RBM39	20q11.22				DOMAIN // T:554	C:104	658	0.158055	8.20E-177	TRUE	T:688	N:0	688	0	1	FALSE	1	410		
2079	SA214_20	SA214	20	44108464	20,441084	missense	medium	3.31	R613H	SLC12A5	20q13.12				TOPO_DON	C:24752	A:2425	27177	0.08923	0	TRUE	G:21726	A:3	21729	0.000138	1	FALSE	0	0	
2080	SA214_21	SA214	21	37460102	21,374601	missense	low	0.805	P1239H	TTC3	21q22.2				C:3949	A:482	4431	0.108779	0	TRUE	C:3523	T:1	3524	0.000284	1	FALSE	2	131		
2081	SA214_22	SA214	22	39088981	22,390889	missense	medium	2.42	T354M	ADSL	22q13.11	22q13.2			HELI // 33	C:161	T:17	178	0.095506	1.30E-24	TRUE	C:166	N:0	166	0	1	FALSE	2	146	
2082	SA214_2_1	SA214	2	1.36E+08	2,1363254	missense	low	1.715	M624V	MCM6	2q21				T:3221	C:274	3495	0.078398	0	TRUE	T:3955	C:2	3957	0.000505	1	FALSE	2	152		
2083	SA214_2_2	SA214	2	1.67E+08	2,1674684	missense	NA			XIRP2	2q24.3				A:38423	G:5063	43486	0.116428	0	TRUE	A:58038	G:18	58056	0.00031	1	FALSE	0	0		
2084	SA214_2_3	SA214	2	1.7E+08	2,1697353	missense	medium	2.14	R3791W	LRP2	2q24-q31				DISULFID // G:23841	A:2174	26015	0.083567	0	TRUE	G:16319	A:4	16323	0.000245	1	FALSE	1	19		
2085	SA214_2_4	SA214	2	2.34E+08	2,2343029	missense	medium	2.305	A159T	UGT1A3	2q37				VARIANT // G:8953	A:497	9450	0.052593	0	TRUE	G:8656	A:5	8661	0.000577	1	FALSE	0	0		
2086	SA214_2_4	SA214	2	4366718	2,4436671	missense	high	3.66	R270Q	SLC3A1	2p16.3				TOPO_DON	C:535	A:504	5939	0.084863	0	TRUE	G:6216	A:2	6218	0.000322	1	FALSE	1	1	
2087	SA214_2_4	SA214	2	47880481	2,4788048	nonsense	NA		E619	MSPH6	2p16				Cancer Rev	VARIANT // G:16261	T:1418	17679	0.080208	0	TRUE	G:8416	N:0	8416	0	1	FALSE	1	32	
2088	SA214_2_6	SA214	2	64632408	2,6463240	missense	low	1.79	P99H	AFTHP	2p14				C:3815	A:427	4242	0.10066	0	TRUE	C:3538	N:0	3538	0	1	FALSE	1	71		
2089	SA214_2_8	SA214	2	88256037	2,8825603	silent	NA		V191	THNSL2	2p11.2				T:191181	G:34876	226057	0.15428	0	TRUE	T:171196	G:111	171307	0.000648	1	FALSE	1	1		
2090	SA214_3_1	SA214	3	1.15E+08	3,1148615	missense	medium	1.95	M567T	KIAA2018	3q13.2				A:31116	G:2765	33881	0.081609	0	TRUE	A:15235	C:5	15240	0.000328	1	FALSE	1	11		
2091	SA214_3_1	SA214	3	1.22E+08	3,1219522	nonsense	NA		R60	GTF2F1	3q21-q24				Entrez Que	DOMAIN // C:45775	T:10019	55794	0.179571	0	TRUE	C:44837	T:7	44844	0.000156	1	FALSE	2	25	
2092	SA214_3_1	SA214	3	1.8E+08	3,1380564	missense	medium	2.9	R140H	TMEM22	3q22.3				TRANSMEN	G:16444	A:2937	19381	0.15154	0	TRUE	G:19197	A:6	19203	0.000312	1	FALSE	2	5	
2093	SA214_3_1	SA214	3	1.8E+08	3,1804347	missense	low	0.935	H1047R	PIK3CA	3q26.3	p.H1047R, carcinoma	Cancer Cell	DOMAIN // A:136669	G:31806	168475	0.188788	0	TRUE	A:120642	G:23	120665	0.000191	1	FALSE	2	62			
2094	SA214_3_1	SA214	3	1.85E+08	3,1853059	missense	neutral	0.375	V238M	HTR3E	3q27.1				TOPO_DON	G:20619	A:1654	22273	0.07426	0	TRUE	G:11213	A:3	11216	0.000267	1	FALSE	0	0	
2095	SA214_3_1	SA214	3	1.87E+08	3,1868757	missense	medium	2.05	A355V	IGF2BP2	3q27.2				G:1181	A:242	1423	0.170063	0	TRUE	G:699	N:0	699	0	1	FALSE	2	6		
2096	SA214_4_1	SA214	4	3086884	4,3086884	missense	medium	3.12	R268Q	HTT	4p16.3				REPEAT // G:16233	A:2308	18541	0.124481	0	TRUE	G:11060	A:2	11062	0.000181	1	FALSE	2	2		
2097	SA214_5_1	SA214	5	1.38E+08	5,1375344	missense	low	1.39	R121W	BRD8	5q31				COILED // G:10410	A:1680	12090	0.138958	0	TRUE	G:15791	A:3	15794	0.00019	1	FALSE	2	32		
2098	SA214_5_1	SA214	5	71515338	5,7151533	missense	medium	2.565	L100R	MAP1B	5q13				Cancer Cell Map Pathw	T:5822	G:508	6330	0.080253	0	TRUE	T:3526	C:2	3528	0.000567	1	FALSE	2	2	
2099	SA214_6_1	SA214	6	1.39E+08	6,1392654	missense	neutral	0.145	N8965	C6orf91	6q24.1				A:4182	G:479	4661	0.102768	0	TRUE	A:4027	N:0	4027	0	1	FALSE	1	4		
2100	SA214_6_1	SA214	6	1.49E+08	6,1489089	missense	medium	2.08	R1158C	SASH1	6q24.3				Entrez Que	CONFLICT // C:1770	T:164	1934	0.084798	2.36E-232	TRUE	C:2519	T:1	2520	0.000397	1	FALSE	2	22	
2101	SA214_6_1	SA214	6	28649330	6,2864933	missense	neutral	0.755	K772R	ZNF452	6p22.1				T:7326	C:1393	8719	0.159766	0	TRUE	T:10887	C:2	10889	0.000184	1	FALSE	1	1		
2102	SA214_7_1	SA214	7	1.07E+08	7,1068402	missense	medium	2.045	L246I	COG5	7q22-q31				G:3117	T:495	3612	0.137043	0	TRUE	G:4626	T:2	4628	0.000432	1	FALSE	2	30		
2103	SA214_7_1	SA214	7	1.43E+08	7,1428513	missense	high	3.6	A241T	TAS2R60	7q35				TRANSMEN	G:22426	A:2746	25172	0.109089	0	TRUE	G:26400	C:9	26409	0.000341	1	FALSE	0	0	
2104	SA214_7_1	SA214	7	1.51E+08	7,1514413	nonsense	NA		R384	GALNT11	7q34-q36				TOPO_DON	C:7465	T:630	8095	0.077826	0	TRUE	C:3120	N:0	3120	0	1	FALSE	1	103	
2105	SA214_8_1	SA214	8	1.23E+08	8,1226957	missense	medium	3.005	S466P	HAS2	8q24.12				Cancer Rev	TOPO_DON	A:212	G:12	224	0.053571	3.42E-14	TRUE	A:263	N:0	263	0	1	FALSE	1	1
2106	SA214_8_1	SA214	8	1.25E+08	8,1247330	missense	low	1.04	R447C	C8ORF36	8q24.13				REPEAT // G:23299	A:3787	27086	0.139814	0	TRUE	G:15003	A:8	15011	0.000533	1	FALSE	3	0		
2107	SA214_8_1	SA214	8	94890344	8,9489034	missense	low	1.05	H847R	TMEM67	8q22.13				A:5281	G:624	5905	0.105673	0	TRUE	A:8154	G:2	8156	0.000245	1	FALSE	1	10		
2108	SA214_9_1	SA214	9	1.01E+08	9,1006510	missense	high	3.605	C547Y	GALNT12	9q22.33				TOPO_DON	G:27046	A:1555	28601	0.054369	0	TRUE	G:8783	A:1	8784	0.000114	1	FALSE	1	5	
2109	SA214_9_1	SA214	9	1.03E+08	9,1033968	missense	neutral	-1.115	V61I	PPP3R2	9q31.1				DOMAIN // C:48292	T:3652	51944	0.073036	0	TRUE	C:21389	T:6	21395	0.00028	1	FALSE	0	0		
2110	SA214_9_1	SA214	9	1.23E+08	9,1225666	missense	low	1.1	G454S	FBXW2	9q34				C:26307	T:2963	29270	0.10123	0	TRUE	C:19804	T:7	19811	0.000353	1	FALSE	2	114		
2111	SA214_9_8	SA214	9	88157632	9,8815763	nonsense	NA		W101	ZCCHC6	9q21				C:23694	T:2624	26318	0.099704	0	TRUE	C:27281	A:4	27285	0.000147	1	FALSE	1	36		
2112	SA214_X_1	SA214	X	1.49E+08	X,1491503	silent	NA			LOC389901					C:4444	T:285	4729	0.060266	0	TRUE	C:6178	A:1	6179	0.000162	1	FALSE	0	0		
2113	SA214_X_1	SA214	X	54487601	X,5448760	missense	low	1.04	T157A	TSR2	Xp11.22				A:32504	G:2782	35286	0.078841	0	TRUE	A:45606	T:5	45611	0.00011	1	FALSE	2	42		
2114	SA214_X_1	SA214	X	70273906	X,7027390	missense	low	1.61	R1899Q	MED12	Xq13				REGION // G:9960	A:1040	11000	0.094545	0	TRUE	G:5246	A:1	5247	0.000191	1	FALSE	1	132		
2115	SA215_14	SA215	14	78504386	14,785043	missense	low	1.61	P781I	NRXN3	14q31				C:12913	T:1880	14793	0.127087	0	TRUE	C:12240	A:6	12246	0.00049	1	FALSE	0	0		
2116	SA215_1_1	SA215	1	27747012	1,2774701	missense	neutral	0.205	T1401N	AHDC1	1p36.13				G:616	T:104	720	0.144444	7.02E-160	TRUE	G:550	N:0	550	0	1	FALSE	2	42		
2117	SA215_20	SA215	20	3789993	20,378999	missense	neutral	0.55	P103S	MAVS	20p13				TOPO_DON	C:980	T:666	1646	0.040617	0	TRUE	C:1206	G:1	1207	0.000829	1	FALSE	2	95	
2118	SA215_2_1	SA215	2	1.72E+08	2,1718906	missense	low	0.895	D91S	MTTL8	2q31.1				A:5422	C:1247	6669	0.186985	0	TRUE	A:7659	C:1	7660	0.000131	1	FALSE	1	35		
2119	SA215_2_1	SA215	2</																											

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC		
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.pos	Ref.count.	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase		
2141	SA222_6_1	SA222		6	1.49E+08	6,1488031	missense	low	1.24	E113K	SASH1	6q24.3				G:50123	A:4411	54534	0.080885	0	TRUE	G:55053	C:13	55066	0.000236	1	FALSE	1	9		
2142	SA222_9_1	SA222		9	1.36E+08	9,1364534	missense	high	3.76	R285W	RXRA	9q34.3				C:15527	T:7467	22994	0.324737	0	TRUE	C:17226	A:4	17229	0.000174	1	FALSE	2	33		
2143	SA226_10_1	SA226		10	1.21E+08	10,121388	missense		NA		LOC646119					G:2619	C:3498	6117	0.571849	0	TRUE	G:11230	A:3	11234	0.000356	1	FALSE	0	0		
2144	SA226_10_1	SA226		10	98147041	10,9814704	missense	high	4.78	C426R	TLL2	10q23-q24				DISULFID //	A:7657	G:8527	16184	0.526878	0	TRUE	A:39824	C:6	39830	0.000151	1	FALSE	0	0	
2145	SA226_11_1	SA226		11	1.24E+08	11,124029	missense	medium	2.575	A147V	SIAE	11q24				G:62761	A:7450	70211	0.106109	0	TRUE	G:60265	A:16	60281	0.000265	1	FALSE	1	16		
2146	SA226_11_1	SA226		11	59816420	11,598164	missense	low	0.895	P63R	MSA44A	11q12				TOPO_DON	C:25509	G:5416	30925	0.175133	0	TRUE	C:65170	A:15	65185	0.00023	1	FALSE	1	41	
2147	SA226_18_1	SA226		18	31077206	18,310772	silent		NA	P169P	ZNF397	18q12.2				C:25315	T:21043	46358	0.453924	0	TRUE	C:78390	A:13	78403	0.000166	1	FALSE	1	58		
2148	SA226_19_1	SA226		19	18756041	19,187560	missense	high	3.585	R683C	COMP	19p13.1				DISULFID //	G:4301	A:1556	5857	0.265665	0	TRUE	G:10012	A:8	10020	0.000798	1	FALSE	1	45	
2149	SA226_1_8	SA226		1	89253612	1,8925361	missense	medium	2.22	K88N	GBP3	1p22.2				C:87208	G:28484	115692	0.246205	0	TRUE	C:112347	A:23	112370	0.000205	1	FALSE	1	46		
2150	SA226_2_1	SA226		2	1.36E+08	2,1361130	missense	medium	2.125	S380G	R3HDM1	2q21.3				MOD_RES	A:80	G:31	111	0.279279	2.18E-50	TRUE	A:327	N:0	327	0	1	FALSE	1	83	
2151	SA226_2_2	SA226		2	2.29E+08	2,2285547	missense	medium	1.97	A1674V	SPHKAP	2q36				G:2182	A:810	2992	0.270722	0	TRUE	G:2948	C:2	2950	0.000678	1	FALSE	0	0		
2152	SA226_3_1	SA226		3	73179151	3,7317915	missense	medium	2.485	D81H	PPP4R2	3p13				G:858	C:268	1126	0.238011	0	TRUE	G:2577	N:0	2577	0	1	FALSE	1	54		
2153	SA226_5_1	SA226		5	1.72E+08	5,1723281	missense	low	1.425	H96N	RPL26L1	5q35.2				C:20736	A:4461	25197	0.177045	0	TRUE	C:18576	T:5	18581	0.000269	1	FALSE	1	92		
2154	SA226_6_1	SA226		6	46768647	6,4676864	missense	neutral	0.185	I1608N	TDRD6	6p12.3				DOMAIN //	T:974	A:2603	3577	0.727705	0	TRUE	T:4244	C:2	4246	0.000471	1	FALSE	0	0	
2155	SA228_2_1	SA228		6	76717353	6,7671735	missense	neutral	-0.585	S490R	IMPJ1	6q14.2-q15				G:4567	C:850	5417	0.156913	0	TRUE	G:6533	T:1	6534	0.000153	1	FALSE	0	0		
2156	SA228_12_1	SA228		12	55003610	12,550036	missense	low	1.65	V742L	PAN2	12q13.2-q13.3				C:37507	G:5555	43062	0.129	0	TRUE	C:25883	A:7	25890	0.00027	1	FALSE	2	18		
2157	SA228_14_1	SA228		14	92746746	14,9274674	G,C		NA							G:51308	C:18165	69473	0.261468	0	TRUE	G:41958	T:9	41967	0.000214	1	FALSE	0	0		
2158	SA228_17_1	SA228		17	7518937	17,751893	nonsense		NA	R213	TP53	17p13.1	p.R213>p.	carcinoma	Cancer Cell	DNA_BIND	G:82068	A:57659	139727	0.412655	0	TRUE	G:140451	A:29	140480	0.000206	1	FALSE	2	9	
2159	SA228_1_1	SA228		1	2E+08	1,1995991	missense	medium	2.115	R168L	TNNT2	1q32				C:24306	A:8268	32574	0.253822	0	TRUE	C:21096	T:3	21099	0.000142	1	FALSE	3	0		
2160	SA228_2_1	SA228		2	1.16E+08	2,1157833	missense	low	1.535	V44I	DPP10	2q14.1				REGION //	G:12361	A:2556	14917	0.171348	0	TRUE	G:14307	C:3	14310	0.00021	1	FALSE	0	0	
2161	SA228_2_2	SA228		2	2.03E+08	2,2033323	missense	low	1.525	S484W	ALS2CR13	2q33.1				C:75091	G:22553	97644	0.230972	0	TRUE	C:63695	T:15	63710	0.000235	1	FALSE	2	4		
2162	SA228_2_2	SA228		2	2.19E+08	2,2192372	missense	neutral	0	R367H	RNF25	2q35				C:1082	T:294	1376	0.213663	0	TRUE	C:564	T:1	565	0.00177	1	FALSE	2	11		
2163	SA228_2_2	SA228		2	2.2E+08	2,2198752	missense	low	1.2	P297T	PTPRN	2q35-q36.1				Entrez Query: Topo_DON	G:17254	T:5274	22528	0.234109	0	TRUE	G:23099	A:32	23131	0.001383	1	FALSE	1	1	
2164	SA228_2_2	SA228		2	61284984	2,6128498	missense	low	1.1	3099V	USP34	2p15				T:30640	C:7824	38464	0.203411	0	TRUE	T:28370	A:1	28371	3.52E-05	1	FALSE	2	53		
2165	SA228_4_1	SA228		4	1.85E+08	4,1846685	missense	low	0.825	S93T	ING2	4q35.1				COILED //	G:20987	C:3472	24459	0.141952	0	TRUE	G:19155	A:2	19157	0.000104	1	FALSE	2	25	
2166	SA228_5_1	SA228		5	45297865	5,4529786	missense	medium	1.95	P863L	HCN1	5p12				COMPBIAS	G:18907	A:3041	21948	0.138555	0	TRUE	G:9694	A:1	9695	0.000103	1	FALSE	0	0	
2167	SA228_7_1	SA228		7	5993603	7,5993603	missense	low	0.805	P54L	PM52	7p22.2				Cancer Review :: Futre	G:1275	A:139	1414	0.098303	7.92E-165	TRUE	G:3170	A:1	3171	0.000315	1	FALSE	1	12	
2168	SA228_8_1	SA228		8	91005958	8,9100595	missense	medium	2.38	H181Y	OSGIN2	8q21				C:13532	T:1590	15122	0.105145	0	TRUE	C:26600	A:9	26609	0.000338	1	FALSE	1	26		
2169	SA228_9_1	SA228		9	15961688	9,1596168	missense	low	1.61	L1279I	C9orf93	9p22.3				T:9149	A:1768	10917	0.161949	0	TRUE	T:16883	C:3	16886	0.000178	1	FALSE	3	0		
2170	SA228_X_6	SA228	X		68299281	X,6829928	nonsense		NA	R176	PIA1	Xq13.1				T:67081	A:19216	86297	0.222673	0	TRUE	T:125890	A:24	125914	0.000191	1	FALSE	2	3		
2171	SA083_14_1	SA083		14	63617012	14,636170	missense	low	1.06	G3750E	SYNE2	14q23.2				TOPO_DON	G:6097	A:1072	7169	0.145933	0	TRUE	G:4560	C:1	4561	0.000219	1	FALSE	2	21	
2172	SA031_17_1	SA031		17	76841585	17,768415	missense	low	1.385	L447V	MGC15523	17q25.3				G:64	C:20	84	0.238095	3.87E-32	TRUE	G:172	N:0	172	0	1	FALSE	2	87		
2173	SA031_4_1	SA031		4	75396781	4,7539678	missense	neutral	0.11	G50E	EPGN	4q13.3				TOPO_DON	G:51	A:21	72	0.291667	2.76E-37	TRUE	G:1626	N:0	1626	0	1	FALSE	1	1	
2174	SA056_X_1	SA056	X		1.18E+08	X,1175840	missense	medium	2.345	R237G	DOCK11	Xq24				DOMAIN //	C:44	G:20	64	0.3125	2.35E-37	TRUE	G:127	N:0	127	0	1	FALSE	1	15	
2175	SA069_4_1	SA069		4	26231347	4,2623134	missense	low	1.04	S78N	TBC1D19	4p15.2				G:96	A:21	117	0.179487	8.39E-31	TRUE	G:92	N:0	92	0	1	FALSE	1	8		
2176	SA074_16_1	SA074		16	82828357	16,828283	missense	neutral	0.435	R79Q	KCNGA4	16q24.1				TOPO_DON	C:485	T:61	546	0.111722	1.31E-78	TRUE	C:83	N:0	83	0	1	FALSE	0	0	
2177	SA089_5_1	SA089		5	79845248	5,7984524	missense	medium	3.205	M74T	FAM151B	5q14.1				T:232	C:230	462	0.497835	0	TRUE	T:69	G:1	70	0.014286	1	FALSE	2	2		
2178	SA094_7_1	SA094		7	75023289	7,7502328	nonsense		NA	Q602	HIP1	7q11.23				Cancer Cell	COILED //	G:365	T:33	98	0.336735	1.33E-53	TRUE	G:24948	A:6	24954	0.00024	1	FALSE	1	32
2179	SA098_5_1	SA098		5	13819269	5,1381926	missense	high	4.255	I3306N	DNAH5	5p15.2				REGION //	A:50	T:47	97	0.484536	4.65E-97	TRUE	A:308	N:0	308	0	1	FALSE	0	0	
2180	SA210_15_1	SA210		15	33043727	15,330437	missense	low	1.175	K44N	AQR	15q14				C:507	A:43	550	0.078182	6.02E-47	TRUE	C:96	N:0	96	0	1	FALSE	2	17		
2181	SA210_9_1	SA210		9	2634736	9,2634736	missense	low	1.115	I357L	VLDLR	9p24				DOMAIN //	A:657	C:262	919	0.285092	0	TRUE	A:96	N:0	96	0	1	FALSE	1	50	
2182	SA213_5_1	SA213		5	43523776	5,4352377	missense	low	1.79	K571M	C5orf34	5p12				T:33	A:39	72	0.541667	1.79E-80	TRUE	T:52	N:0	52	0	1	FALSE	2	4		
2183	SA214_8_1	SA214		8	1.1E+08	8,1095679	missense	low	1.3	A284V	TTC35	8q23.1				C:61	T:6	67	0.089552	3.40E-08	TRUE	C:109	N:0	109	0	1	FALSE	2	187		
2184	SA103_8_1	SA103		8	1.03E+08	8,1032896	missense	medium	3.415	F323L	RRM2B	8q23.1				Entrez Query :: Stability	G:11562	C:1269	12831	0.098901	0	TRUE	G:12863	A:6	12869	0.000466	1	FALSE	1	40	
2185	SA210_7_1	SA210		7	29001915	7,2900191	stop loss		NA		CPVL	7p15-p14				A:645	T:167	812	0.205665	5.75E-196	TRUE	A:765	N:0	765	0	1	FALSE	1	134		
2186	SA018_17_1	SA018		17	7519131	17,751913	missense	high	3.63	R175H	TP53	17p13.1	p.R175H.p.	adenocarci	Cancer Cell	DNA_BIND	C:20568	T:119074	139642	0.852709	0	TRUE	C:136015	A:87	136102	0.000639	1	FALSE	3	2	
2187	SA029_19_1	SA029		19	60995612	19,609956	missense	low	1.435	A794T	NLRP11																				

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC							
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.pos	Ref.count.	Alt.count.T	Total.count	Alt.freq	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.freq	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.freq	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase	
2210	SA051_19	SA051		19	5987021	19,5987021	missense	medium	2.285	V331M	KIR2DL1	1p36.13				TOPO_DON	G:428425	A:415989	844414	0.492636	0	TRUE	G:692876	A:87	692963	0.000126	1	FALSE	0	0						
2211	SA051_3	SA051		3	1.92E+08	3,1916105	missense	low	0.975	D302H	CLDN16	3q28				TOPO_DON	G:6953	C:1870	8823	0.211946	0	TRUE	G:5804	T:1	5805	0.000172	1	FALSE	1	1						
2212	SA051_8	SA051		8	1.45E+08	8,1446922	missense	low	0.895	G134S	ZC3H3	8q24.3					C:106395	T:48100	154495	0.311337	0	TRUE	C:106994	A:4	106998	3.74E-05	1	FALSE	2	4						
2213	SA051_X_1	SA051	X		1.52E+08	X,1523397	nonsense		NA	Q227	ZFP92					ZN_FING	//C:133998	T:56316	190314	0.295911	0	TRUE	C:147292	T:12	147304	8.15E-05	1	FALSE	0	0						
2214	SA052_11	SA052		11	1.08E+08	11,1076268	nonsense		NA	Q513	ATM	11q22-q23				Cancer Rev	VARIANT	//G:80038	T:57259	137297	0.417045	0	TRUE	C:125464	A:8	125472	6.38E-05	1	FALSE	2	2					
2215	SA052_1	SA052		1	1.362251	1,1362251	missense	low	1.31	R52L	VWA1	1p36.33				DOMAIN	//G:69287	T:8470	77757	0.108929	0	TRUE	G:61613	A:2	61615	3.25E-05	1	FALSE	0	0						
2216	SA052_13	SA052		13	25686305	13,25686305	nonsense		NA	R572	RNF6	13q12.12				Entrez Que	VARIANT	//G:425876	A:111794	537670	0.207923	0	TRUE	G:384028	A:57	384085	0.000148	1	FALSE	1	21					
2217	SA052_17	SA052		17	74480687	17,74480687	missense	low	0.975	V197M	LGALS3BP	17q25				DOMAIN	//T:33422	T:258089	291511	0.114651	0	TRUE	C:186230	G:68	186298	0.000365	1	FALSE	1	672						
2218	SA052_22	SA052		22	18146919	22,18146919	missense	neutral	0	R396C	TBX1	22q11.21					C:205725	T:32984	238709	0.138177	0	TRUE	C:164538	T:83	164621	0.000504	1	FALSE	3	0						
2219	SA052_5	SA052		5	1.46E+08	5,1456233	missense	low	1.24	D761G	RBM27						A:435968	G:148315	584283	0.253841	0	TRUE	A:499398	G:39	499437	7.81E-05	1	FALSE	1	6						
2220	SA052_6	SA052		6	1.37E+08	6,1365367	missense	low	1.32	T268I	PDE7B	6q23-q24				HELIX	//26	C:94414	T:43536	137950	0.315593	0	TRUE	C:136467	T:23	136490	0.000169	1	FALSE	1	1					
2221	SA052_6	SA052		6	72068156	6,72068156	missense	low	0.975	K347Q	OGFR1	6q13					A:105278	C:22584	127862	0.176628	0	TRUE	A:109146	G:8	109154	7.73E-05	1	FALSE	1	102						
2222	SA052_8	SA052		8	1.26E+08	8,1256443	missense	medium	2.36	R300C	MTSS1	8p22				Entrez Que	COMPBIAS	G:36057	A:24691	60748	0.40645	0	TRUE	G:53428	A:10	53438	0.000187	1	FALSE	2	4					
2223	SA052_X_1	SA052	X		1.33E+08	X,1334351	missense	high	3.59	L41P	HPRT1	Xq26.1				Entrez Que	HELIX	//39	T:11871	C:77956	89827	0.867846	0	TRUE	T:64912	C:4	64916	6.16E-05	1	FALSE	2	8				
2224	SA052_X_1	SA052	X		1.43E+08	X,1425444	missense	low	1.11	W721I	SLITRK4	Xq27.3				TOPO_DON	C:81481	G:53700	135181	0.397245	0	TRUE	C:135285	T:11	135296	8.13E-05	1	FALSE	1	3						
2225	SA052_X_4	SA052	X		48254779	X,48254779	missense	low	1.255	V97I	PORCN	Xp11.23				TRANSMEN	G:13082	A:44999	58081	0.774763	0	TRUE	G:71085	C:60	71145	0.000843	0.018935	FALSE	3	2						
2226	SA053_17	SA053		17	26339089	17,26339089	missense	neutral	0.345	A173G	RNF135	17q11.2					C:92763	G:96718	189481	0.510436	0	TRUE	C:109240	A:23	109263	0.000211	1	FALSE	3	9						
2227	SA054_10	SA054		10	70638380	10,70638380	missense	medium	2.645	M648I	SUPV3L1	10q22.1					G:53157	A:5597	58754	0.095262	0	TRUE	G:66958	A:4	66962	5.97E-05	1	FALSE	2	79						
2228	SA054_11	SA054		11	47397030	11,47397030	missense	high	3.64	E418K	PSMC3	11p12-p13				Cancer Cell Map Pathw	C:173911	T:46686	220597	0.211635	0	TRUE	C:140930	A:53	140983	0.000376	1	FALSE	2	51						
2229	SA054_12	SA054		12	1.07E+08	12,1066933	missense	neutral	0.205	P6A	ASCL4	12q23.3					C:50957	G:5297	55308	0.095773	0	TRUE	C:64020	T:4	64024	6.25E-05	1	FALSE	0	0						
2230	SA054_1	SA054		1	44214631	1,44214631	missense	high	3.605	L91M	ATP6V0B	1p32.3				TOPO_DON	C:107726	A:21244	128970	0.164672	0	TRUE	C:98196	A:7	98203	7.13E-05	1	FALSE	1	439						
2231	SA054_17	SA054		17	17988000	17,17988000	missense	medium	2.295	N2046K	MYO15A	17p11.2				REGION	//	C:270812	A:63783	334595	0.196272	0	TRUE	C:390701	A:25	390726	6.40E-05	1	FALSE	1	1					
2232	SA054_2	SA054		2	36889501	2,36889501	missense	medium	2.91	A576V	VIT	2p22-p21				DOMAIN	//C:403672	T:224726	628398	0.357617	0	TRUE	C:543604	G:37	543641	6.81E-05	1	FALSE	2	5						
2233	SA054_5	SA054		5	1.43E+08	5,1427602	missense	low	1.5	L119V	RN3C1	5q05.5				Cancer Cell	REGION	//A:334421	C:75135	409556	0.183455	0	TRUE	A:251517	G:12	251529	4.77E-05	1	FALSE	2	19					
2234	SA054_5	SA054		5	52401750	5,52401750	missense	medium	3.275	S713C	ITGA2	5q23-q31				DISULFID	C:23963	G:4775	34138	0.139873	0	TRUE	C:54195	A:4	54199	7.38E-05	1	FALSE	1	21						
2235	SA054_6	SA054		6	26077557	6,26077557	missense	low	1.24	K146I	TRIM38	6p21.3					A:80410	T:24144	104554	0.230924	0	TRUE	A:128831	G:7	128838	5.43E-05	1	FALSE	2	62						
2236	SA054_7	SA054		7	1.03E+08	7,1034168	missense	medium	1.995	N64K	RELN	7q22				DISULFID	//G:25572	T:6542	32114	0.203712	0	TRUE	G:22843	T:18	22861	0.000787	1	FALSE	0	0						
2237	SA065_11	SA065		11	1.01E+08	11,1011442	missense	medium	2.545	M108I	C11orf70	11q22.1					G:155436	T:25723	181159	0.141991	0	TRUE	G:117324	A:20	117344	0.00017	1	FALSE	1	1						
2238	SA065_13	SA065		13	31827243	13,31827243	missense	low	1.23	R2418T	BRCA2	13q12.3				Cancer Rev	REGION	//	C:1405	C:291	1696	0.171158	0	TRUE	G:569	T:1	570	0.001754	1	FALSE	1	15				
2239	SA065_13	SA065		13	47821138	13,47821138	nonsense		NA	W195	RB1	13q14.2				Cancer Cell	HELIX	//18	G:8639	A:9323	17962	0.51904	0	TRUE	G:31267	T:3	31270	9.59E-05	1	FALSE	1	13				
2240	SA065_13	SA065		13	69354524	13,69354524	missense	medium	2.805	E373D	KLHL1	13q21					T:19330	G:39608	58938	0.672028	0	TRUE	T:36700	G:10	36710	0.000272	1	FALSE	0	0						
2241	SA065_16	SA065		16	69075354	16,69075354	missense	medium	2.91	F573S	COG4	16q22.1				HELIX	//53	A:9063	G:2232	11295	0.19761	0	TRUE	A:10094	T:1	10095	9.91E-05	1	FALSE	2	142					
2242	SA065_17	SA065		17	33708934	17,33708934	missense	low	1.24	T115I	MRPL45	17q21.2					C:2259	T:1197	3456	0.346354	0	TRUE	C:6337	G:2	6339	0.000316	1	FALSE	3	8						
2243	SA065_17	SA065		17	78152540	17,78152540	missense	medium	1.905	N620I	FOXK2	17q25.1					A:11394	T:8087	19481	0.415122	0	TRUE	A:15813	G:1	15814	6.32E-05	1	FALSE	2	23						
2244	SA065_18	SA065		18	13046603	18,13046603	missense	low	1.59	Q742H	CEP192	18p11.21					G:21237	C:23560	44797	0.525928	0	TRUE	G:31768	C:4	31772	0.000126	1	FALSE	2	46						
2245	SA065_18	SA065		18	13665574	18,13665574	missense	low	0.975	L242F	C18orf19					COILED	//	G:140036	A:42334	182370	0.232132	0	TRUE	G:106491	T:24	106515	0.000225	1	FALSE	1	29					
2246	SA065_19	SA065		19	20049893	19,20049893	silent		NA		ZNF90						C:34853	T:14604	49457	0.295287	0	TRUE	C:40537	A:22	40559	0.000542	1	FALSE	0	0						
2247	SA065_19	SA065		19	54177874	19,54177874	nonsense		NA	K286	GYS1	19q13.3					T:183508	A:96813	280321	0.345365	0	TRUE	T:290888	C:64	290952	0.00022	1	FALSE	1	39						
2248	SA065_2	SA065		2	2.29E+08	2,2285947	missense	neutral	0.345	I196L	SPHKAP	2q36					T:342760	G:125368	468128	0.267807	0	TRUE	T:353340	C:19	353359	5.38E-05	1	FALSE	0	0						
2249	SA065_2	SA065		2	26005850	2,26005850	missense	low	1.355	A706P	KIF3C	2p23				REGION	//	C:67247	G:32193	99440	0.323743	0	TRUE	C:81521	T:9	81530	0.00011	1	FALSE	2	18					
2250	SA065_4	SA065		4	71726717	4,71726717	missense	medium	3.105	S237I	ENAM	4q13.3					G:77594	T:31905	109499	0.291373	0	TRUE	G:110819	A:20	110839	0.00018	1	FALSE	0	0						
2251	SA065_6	SA065		6	31941117	6,31941117	missense	medium	2.105	V572F	SLC44A4	6p21.3				TRANSMEN	C:20342	A:18143	38485	0.47143	0	TRUE	C:27564	A:13	27577											

T	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func.Lmpa	Fi.score	EA.variant	Gene	Location	mutations	cancer.type	gene.s.kno	regions.pos	Ref.count	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase	
2279	SA074_3_3	SA074	3	1.8E+08	3,1804187	missense	medium	2.105	E545K	PIK3CA	3q26.3	p.E545K,p	carcinoma	Cancer Cell	VARIENT //	G:6262	A:802	7064	0.113533	0	TRUE	G:24175	A:2	24177	8.27E-05	1	FALSE	2	35	
2280	SA075_10	SA075	10	44750145	10,447501	missense	low	1.445	L129I	KSP37					TRANSMEN	C:43249	A:2894	46143	0.062718	0	TRUE	C:33697	A:18	33715	0.000534	1	FALSE	0	0	
2281	SA075_18	SA075	18	75760218	18,757602	missense	neutral	-0.445	A227E	CKNG2	18q22-q23				TRANSMEN	C:43792	A:25844	69636	0.37113	0	TRUE	C:59604	G:7	59611	0.000117	1	FALSE	0	0	
2282	SA075_20	SA075	20	32559168	20,325591	missense	high	4.255	R874C	ITCH	20q11.22-q11.23				DOMAIN //	C:3074	T:612	3686	0.166034	0	TRUE	C:5188	A:1	5189	0.000193	1	FALSE	2	34	
2283	SA075_2_2	SA075	2	2.19E+08	2,2192137	missense	medium	3.145	R1500Q	ZNF142	2q34-q35				ZN_FING //	C:173787	T:36240	210027	0.172549	0	TRUE	C:154248	T:38	154286	0.000246	1	FALSE	2	7	
2284	SA075_22	SA075	22	37775460	22,377754	missense	medium	2.25	W217C	APOBEC3F	22q13.1				G:1056116	T:202170	1258286	0.160671	0	TRUE	G:1160774	A:263	1161037	0.000227	1	FALSE	2	15		
2285	SA077_1_1	SA077	1	1.1E+08	1,1098236	missense	neutral	0	K271N	SPYL2	1p13.3				TOPO_DON	G:10061	T:8637	18698	0.461921	0	TRUE	G:15164	A:1	15165	6.59E-05	1	FALSE	0	0	
2286	SA077_11	SA077	11	1.18E+08	11,118007	missense	low	1.23	A642T	PHLDB1	11q23.3				G:5956	A:2222	8178	0.271705	0	TRUE	G:8148	A:2	8150	0.000245	1	FALSE	1	7		
2287	SA077_1_1	SA077	1	12844033	1,1284403	missense	medium	2.995	P413T	PRAMEF2	1p36.21				C:355632	A:29396	385028	0.076348	0	TRUE	C:366849	T:36	366885	9.81E-05	1	FALSE	0	0		
2288	SA077_12	SA077	12	1.01E+08	12,101096	missense	low	1.04	1383M	C12orf48	12q23.2				C:7971	G:8970	16941	0.529485	0	TRUE	C:16721	G:16	16737	0.000956	1	FALSE	2	20		
2289	SA077_14	SA077	14	22619468	14,226194	missense	neutral	-0.69	T364A	ACIN1	14q11.2				COMPMIAS	T:1877	C:447	2324	0.192341	0	TRUE	T:1551	N:0	1551	0	1	FALSE	1	122	
2290	SA077_15	SA077	15	29008776	15,290087	missense	low	1.065	H891N	MTMR15	15q13.2-q13.3				C:258954	A:39308	298262	0.13179	0	TRUE	C:262439	T:19	262458	7.24E-05	1	FALSE	1	20		
2291	SA077_15	SA077	15	72212827	15,722128	missense	low	1.845	A227T	ISLR2	15q24.1				DOMAIN //	G:72395	A:21960	94355	0.232738	0	TRUE	G:65359	A:11	65370	0.000168	1	FALSE	0	0	
2292	SA077_17	SA077	17	7519277	17,751927	nonsense	NA		Y126	TP53	17p13.1	p.Y126fs*1	adenocarci	Cancer Cell	DNA_BIND	G:68022	C:110211	178233	0.618354	0	TRUE	G:102452	A:5	102457	4.88E-05	1	FALSE	2	13	
2293	SA077_18	SA077	18	54738027	18,547380	missense	low	1.7	S510T	ZNF532	18q21.32				T:85741	A:15930	101671	0.156682	0	TRUE	T:98654	C:55	98670	0.000557	1	FALSE	1	11		
2294	SA077_2_2	SA077	2	1.21E+08	2,1208238	missense	high	3.635	S381F	INHBB	2cen-q13				DISULFID //	C:12174	T:15034	27208	0.552558	0	TRUE	C:28222	A:6	28228	0.000213	1	FALSE	2	8	
2295	SA077_4_5	SA077	4	53989050	4,539890	missense	neutral	0.695	P373T	FIP1L1	4q12				Cancer Rev	COMPMIAS	C:9954	A:18715	28669	0.652796	0	TRUE	C:21544	T:3	21547	0.000139	1	FALSE	2	69
2296	SA077_5_5	SA077	5	68751581	5,687515	missense	medium	2.295	A205P	MARVELD2	5q13.2				TRANSMEN	G:21113	C:9366	30479	0.307294	0	TRUE	G:11978	T:2	11980	0.000167	1	FALSE	0	0	
2297	SA077_6_6	SA077	6	1.55E+08	6,1551710	missense	medium	2.08	1368T	RBM16	6q25.1-q25.3				COMPMIAS	T:162216	C:58333	220549	0.26449	0	TRUE	T:177085	C:10	177095	5.65E-05	1	FALSE	2	36	
2298	SA077_6_6	SA077	6	1.59E+08	6,1591830	missense	neutral	-0.245	V14I	LOC202455	6q25.3				C:8339	T:2264	10603	0.213524	0	TRUE	C:11788	G:4	11792	0.000339	1	FALSE	0	0		
2299	SA077_7_2	SA077	7	23206737	7,2320673	missense	low	1.1	S374A	NUPL2	7p15				REGION //	T:3949	G:377	4326	0.087147	0	TRUE	T:2675	C:1	2676	0.000374	1	FALSE	1	140	
2300	SA077_8_2	SA077	8	27207642	8,2720764	missense	medium	2.33	E121Q	TRIM35	8p21.2				Entrez Que	C:321821	G:49992	371813	0.134455	0	TRUE	C:272740	G:155	27285	0.000568	1	FALSE	1	9	
2301	SA083_11	SA083	11	31438785	11,314387	missense	low	1.7	A53G	JMMP1L	11p13				G:81303	C:13928	95231	0.140451	0	TRUE	G:76836	T:34	76870	0.000442	0.017677	FALSE	1	25		
2302	SA083_1_1	SA083	1	2.13E+08	2,1218846	missense	medium	1.95	Q178H	CENPF	1q32-q41				G:362765	T:95550	458315	0.268288	0	TRUE	G:351174	A:6	351180	1.71E-05	1	FALSE	2	122		
2303	SA083_13	SA083	13	47984155	13,479841	nonsense	NA		E225	RCBT82	13q14.3				REPEAT //	C:178015	A:54026	232041	0.23283	0	TRUE	C:210140	A:5	210145	2.38E-05	1	FALSE	2	7	
2304	SA083_16	SA083	16	66567534	16,665675	missense	low	1.225	R398H	DPEP3	16q22.1				C:261478	T:124703	386181	0.322913	0	TRUE	C:387801	T:57	387858	0.000147	1	FALSE	0	0		
2305	SA083_5_5	SA083	5	56581153	5,565811	missense	low	1.39	S322L	GGBP1	5q11.2				C:2584	T:658	3242	0.202961	0	TRUE	C:3360	N:0	3360	0	1	FALSE	2	254		
2306	SA083_6_6	SA083	6	33277240	6,3327724	missense	neutral	0.425	D80E	SLC39A7	6p21.3				COMPMIAS	C:632504	G:1077166	1709670	0.630043	0	TRUE	C:1043934	A:94	1044028	9.00E-05	1	FALSE	2	96	
2307	SA084_1_1	SA084	1	1.18E+08	1,1183408	missense	medium	1.995	D1596H	SPAG17	1p12				C:46964	G:44012	90976	0.483776	0	TRUE	C:102164	T:7	102171	6.85E-05	1	FALSE	2	7		
2308	SA084_17	SA084	17	7519119	17,751911	missense	high	3.97	H179R	TP53	17p13.1	p.H179N,p	carcinoma	Cancer Cell	DNA_BIND	T:21155	C:30398	51553	0.589646	0	TRUE	T:64032	G:10	64042	0.000156	1	FALSE	3	8	
2309	SA084_3_3	SA084	3	1.26E+08	3,1256943	nonsense	NA		Q1580	KALRN	3q21.1-q21.2				DOMAIN //	C:175272	T:260193	435465	0.597506	0	TRUE	C:425733	T:39	425772	9.16E-05	1	FALSE	2	1	
2310	SA084_6_6	SA084	6	30788388	6,3078838	missense	low	0.895	Q437L	MDC1	6p21.3				Entrez Que	REGION //	T:63395	A:81764	145159	0.563272	0	TRUE	T:141921	C:11	141932	7.75E-05	1	FALSE	0	0
2311	SA084_6_6	SA084	6	54914603	6,5491460	missense	neutral	-1.15	N959H	FAM83B	6p12.1				A:67347	C:64977	132324	0.491045	0	TRUE	A:185971	T:11	185982	5.91E-05	1	FALSE	3	2		
2312	SA089_10	SA089	10	79249128	10,792491	missense	low	1.7	P1210A	DLG5	10q23				MOD_RES	G:2290	C:24001	46971	0.510975	0	TRUE	G:53570	C:8	53578	0.000149	1	FALSE	3	0	
2313	SA089_12	SA089	12	1.3E+08	12,130159	missense	low	1.115	T630N	GPR133	12q24.33				TOPO_DON	C:329265	A:159838	489103	0.326798	0	TRUE	C:212772	A:20	212792	9.40E-05	1	FALSE	0	0	
2314	SA089_7_7	SA089	7	57383065	7,573830	missense	medium	2.695	L2065R	MED13	7q12-q23				A:94023	C:247929	341952	0.72504	0	TRUE	A:259677	G:15	259692	7.58E-05	1	FALSE	3	6		
2315	SA089_17	SA089	17	64621097	17,646210	C,G	NA								C:170318	G:51591	221909	0.232487	0	TRUE	C:206372	A:93	206465	0.00045	1	FALSE	0	0		
2316	SA089_19	SA089	19	4769358	19,476935	missense	NA								G:99705	T:48996	148701	0.329493	0	TRUE	G:141738	T:36	141774	0.000254	1	FALSE	2	48		
2317	SA089_19	SA089	19	49867836	19,498678	missense	medium	1.95	D62H	CEACAM19	19q13.31				TOPO_DON	G:206481	C:116092	322573	0.359894	0	TRUE	G:275941	T:16	275957	5.80E-05	1	FALSE	1	5	
2318	SA089_19	SA089	19	8574717	19,857471	missense	low	1.065	G163R	ADAMTS10	19p13.3-p13.2				PROPEP //	C:188723	G:115351	304074	0.379352	0	TRUE	C:271322	T:26	271348	9.58E-05	1	FALSE	2	8	
2319	SA089_22	SA089	22	41552928	22,415529	missense	medium	2.97	S196I	ARFGAP3	22q13.2-q13.3				C:631708	A:148708	780416	0.19055	0	TRUE	C:271171	T:11	271182	4.06E-05	1	FALSE	2	101		
2320	SA089_6_6	SA089	6	1.13E+08	6,1125470	missense	neutral	0.395	Q1607K	LAMA4					DOMAIN //	G:44263	T:24740	69003	0.358535	0	TRUE	G:38428	C:12	38440	0.000312	1	FALSE	1	60	
2321	SA089_7_7	SA089	7	73573536	7,7357353	missense	low	1.1	L327F	GTF2IRD1	7q11.23				C:4665	T:4243	8908	0.476313	0	TRUE	C:11897	G:19	11916	0.001594	1	FALSE	2	28		
2322	SA089_8_8	SA089	8	1.45E+08	8,1447334	missense	neutral	0.66	R241Q	EEF1D	8q24.3				C:284025	T:22017	306042	0.071941	0	TRUE	C:255404	A:26	255430	0.000102	1	FALSE	2	140		
2323	SA090_1_1	SA090	1	52845092	1,528450	missense	neutral	0.67	S96T	GPK7	1p32				HELEX // 97	G:193000	C:49327	242327	0.203556	0	TRUE	G:139007	A:22	139029	0.000158	1	FALSE	2	107	
2324	SA094_1_1	SA094	1	26388564	1,263885	missense	low	1.61	E701Q	CNKSR1	1p36.11																			

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC		
1	id	Patient.ID	Chr	Coord	Mutation	RG.var.type	Func..Impa	FI.score	AA.variant	Gene	Location	mutations.	cancer.type	gene.s.kno	regions.pos	Ref.count.	Alt.count.T	Total.count	Alt.frequency	Binomial.te	Binomial.te	Ref.count.	Alt.count.N	Total.count	Alt.frequency	Binomial.te	Binomial.te	SVNMix2.C	REF.RNase		
2347	SA106_14	SA106		14	81022422	14,8102242	missense	medium	2.725	V588M	SELI1	14q24.3-q31			REGION //	C:252568	T:186320	438888	0.424527	0	TRUE	C:347462	T:14	347476	4.03E-05	1	FALSE	2	20		
2348	SA106_19	SA106		19	50069540	19,5006954	missense	medium	3.425	G336V	PVRL2	19q13.2			DOMAIN //	G:93557	T:25664	119221	0.215264	0	TRUE	G:120709	A:31	120740	0.000257	1	FALSE	2	134		
2349	SA106_22	SA106		22	45238397	22,4523839	missense	medium	2.93	P1352S	CELSR1	22q13.3			DISULFID //	G:4403	A:4476	8879	0.504111	0	TRUE	G:22146	A:2	22148	9.03E-05	1	FALSE	2	10		
2350	SA106_3_1	SA106		3	1.2E+08	3,1203959	missense	low	1.585	V209E	UPK1B	3q13.3-q21			TOPO_DON	T:192625	A:34076	226701	0.150313	0	TRUE	T:176308	C:26	176334	0.000147	1	FALSE	0	0		
2351	SA106_3_1	SA106		3	1.81E+08	3,1805345	missense	medium	1.905	F367S	ZNF639	3q26.32				T:78445	C:24797	103242	0.240183	0	TRUE	T:75502	C:24	75526	0.000318	1	FALSE	1	85		
2352	SA106_4_1	SA106		4	1.29E+08	4,1287843	missense	low	1.795	P109H	INTU	4q28.1				T:162	A:83	245	0.338776	8.01E-146	0	TRUE	C:96	N:0	96	0	1	FALSE	2	3	
2353	SA106_6_1	SA106		6	1.52E+08	6,1517290	missense	medium	2.075	P280L	ZBTB2	6q25.1				G:27836	A:6320	34156	0.185033	0	TRUE	G:32017	G:14	32018	3.12E-05	1	FALSE	1	22		
2354	SA106_6_1	SA106		6	71000988	6,7100098	missense	medium	2.34	K763N	COL9A1	6q12-q14			REGION //	C:12803	A:26344	39147	0.672951	0	TRUE	C:21092	G:14	21106	0.000663	1	FALSE	0	0		
2355	SA106_7_1	SA106		7	5934506	7,5934506	missense	neutral	0	T760M	RSPH10B	7p22.1				G:32965	A:7920	40885	0.193714	0	TRUE	G:24876	A:8	24884	0.000321	1	FALSE	0	0		
2356	SA106_8_1	SA106		8	1.45E+08	8,1450652	missense	low	1.78	G3713C	PLEC1	8q24			REGION //	T:7497	A:2409	9906	0.243186	0	TRUE	C:4632	T:1	4633	0.000216	1	FALSE	1	114		
2357	SA208_15	SA208		15	81013033	15,8101303	missense	high	3.685	R475P	CPFB1	15q25.2			DOMAIN //	C:540059	G:357646	897705	0.3984	0	TRUE	C:584488	A:79	584567	0.000135	1	FALSE	3	0		
2358	SA210_11	SA210		11	68603909	11,6860390	missense	low	1.445	R524Q	TPCN2	11q13.2			TOPO_DON	G:59872	A:12273	72145	0.170116	0	TRUE	G:64765	T:8	64773	0.000124	1	FALSE	1	22		
2359	SA210_15	SA210		15	42566067	15,4256606	missense	medium	2.08	Q118E	CTDSP2	15q15.3				G:98890	G:32515	131405	0.247441	0	TRUE	C:150734	A:5	150739	3.32E-05	1	FALSE	2	26		
2360	SA210_16	SA210		16	66477394	16,6647739	missense	medium	2.275	H77D	NRN1L	16q22.1				C:383780	G:97692	481472	0.202903	0	TRUE	C:526245	G:185	526430	0.000351	0.395262	FALSE	2	4		
2361	SA210_3_1	SA210		3	1.44E+08	3,1437001	missense	low	1.63	E1849K	ATR	3q22-q24			Entrez Que	C:291893	T:85311	377204	0.226167	0	TRUE	C:366521	T:154	366675	0.00042	0.002009	FALSE	2	37		
2362	SA210_7_1	SA210		7	99547385	7,9954738	missense	medium	2.195	R268C	TAFF6	7q22.1				G:671467	A:128375	799842	0.1605	0	TRUE	G:653914	A:81	653995	0.000124	1	FALSE	1	230		
2363	SA210_8_1	SA210		8	55703391	8,5570339	nonsense	NA		E1466	RP1	8q11-q13				G:57939	T:16700	74639	0.223744	0	TRUE	G:47427	T:11	47438	0.000232	1	FALSE	0	0		
2364	SA210_9_1	SA210		9	17779460	9,1777946	missense	low	1.455	P179L	SH3GL2	9p22			DOMAIN //	T:78219	T:12812	91031	0.140743	0	TRUE	C:56977	T:11	56988	0.000193	1	FALSE	0	0		
2365	SA212_17	SA212		17	26206285	17,2620628	NA	NA								A:408	T:208	616	0.337662	0	TRUE	A:1036	N:0	1036	0	1	FALSE	1	1		
2366	SA212_18	SA212		18	84734154	18,8473415	missense	medium	2.35	R234T	BXDC5	1p22.3			DOMAIN //	G:101479	C:12257	113736	0.107767	0	TRUE	G:79565	C:8	79573	0.000101	1	FALSE	1	191		
2367	SA212_7_1	SA212		7	1.01E+08	7,1006308	missense	neutral	0	Q17L	MOGAT3	7q22.1				T:237574	A:53925	291499	0.184992	0	TRUE	T:349204	C:103	349307	0.000295	1	FALSE	3	0		
2368	SA212_X_1	SA212	X		1.54E+08	X,1543899	missense	medium	3.455	F275I	TMLHE	Xq28.1				A:471901	T:64252	536153	0.119839	0	TRUE	A:340056	G:170	340226	0.0005	0.0023	FALSE	1	45		
2369	SA213_1_1	SA213		1	41751501	1,4175150	missense	low	1.525	S1993F	HIVEP3	1p34			Cancer Cell	G:43243	A:23814	67057	0.355131	0	TRUE	G:64490	A:26	64492	3.10E-05	1	FALSE	2	12		
2370	SA213_7_1	SA213		7	7514737	7,7514737	nonsense	NA		E339	TP53	17p13.1	p.E339*,p.	medullary	Cancer Cell	HELI	X://33	C:37369	A:177417	214786	0.206018	0	TRUE	C:206450	T:46	206496	0.000223	1	FALSE	2	19
2371	SA213_3_1	SA213		3	1.15E+08	3,1148658	missense	medium	1.995	E75K	KIAA2018	3q13.2				C:212	T:63	275	0.229091	2.17E-96	0	TRUE	C:423	N:0	423	0	1	FALSE	2	60	
2372	SA213_3_1	SA213		3	1.27E+08	3,1272525	missense	neutral	-0.11	T104I	SLC41A3	3q21.2				G:176970	A:85197	262167	0.324972	0	TRUE	G:235450	A:77	235527	0.000327	1	FALSE	2	156		
2373	SA213_5_1	SA213		5	1347307	5,1347307	missense	neutral	0.14	L232V	TERC	5p15.33			Cancer Rev	REGION //	G:4476	T:5077	10253	0.563445	0	TRUE	G:11725	N:0	11725	0	1	FALSE	2	1	
2374	SA213_6_1	SA213		6	29071581	6,2907158	missense	medium	2.28	G393R	ZNF311	6p22.1				ZN_FING //	G:74955	T:54562	129517	0.421273	0	TRUE	C:91146	T:21	91167	0.00023	1	FALSE	0	0	
2375	SA213_7_1	SA213		7	55191971	7,5519197	missense	medium	2.865	L387V	ENFR	7p12			Cancer Cell	TOPO_DON	C:5214	G:5033	10247	0.491168	0	TRUE	C:4660	G:2	4662	0.000429	1	FALSE	2	9	
2376	SA214_10	SA214		10	26486324	10,2648632	missense	medium	2.49	R958H	MYO3A	10p11.1			DOMAIN //	G:16610	A:1652	18262	0.090461	0	TRUE	G:10073	N:0	10073	0	1	FALSE	0	0		
2377	SA214_12	SA214		12	1.23E+08	12,1233933	missense	medium	1.935	R1647C	NCOR2	12q24			Cancer Cell	Map Pathw	G:3528	A:800	4328	0.184843	0	TRUE	G:2005	A:1	2006	0.000499	1	FALSE	1	98	
2378	SA214_15	SA214		15	41894165	15,4189416	missense	low	1.7	R148Q	MFAF1	15q15-q21				C:196877	T:37252	234129	0.159109	0	TRUE	C:191239	T:10	191249	5.23E-05	1	FALSE	2	28		
2379	SA214_16	SA214		16	56007195	16,5600719	missense	NA	NA		CC17	16q13				G:50619	A:6117	56736	0.107815	0	TRUE	G:26405	A:3	26408	0.000114	1	FALSE	1	4		
2380	SA214_3_1	SA214		3	1.22E+08	3,1218914	missense	neutral	0	R222W	RABL3	3q13.33			REGION //	G:151832	A:22980	174812	0.131456	0	TRUE	G:140673	A:24	140697	0.000171	1	FALSE	2	19		
2381	SA214_4_1	SA214		4	48580057	4,4858005	missense	medium	2.59	P2667L	COL7A1	3p21.1			MOD_RES	G:7950	A:1029	8979	0.114601	0	TRUE	G:7061	C:13	7074	0.001838	1	FALSE	1	5		
2382	SA214_4_1	SA214		4	1.52E+08	4,1516283	missense	medium	2.52	V2177A	LRBA	4q31.3			HELI	X://21	A:73385	G:4511	77896	0.957911	0	TRUE	A:53560	T:6	53566	0.000112	1	FALSE	1	45	
2383	SA214_5_1	SA214		5	1.48E+08	5,1477621	missense	low	0.975	R169H	FBXO38	5q33.1				G:125537	A:11646	137183	0.084894	0	TRUE	G:122479	T:102	122581	0.000832	1	FALSE	2	13		
2384	SA214_8_1	SA214		8	95574152	8,9557415	missense	medium	2.175	R1571H	KIAA1429	8q22.1				C:8087	T:1312	9399	0.193589	0	TRUE	T:7128	A:5	7133	0.000701	1	FALSE	2	86		
2385	SA214_X_1	SA214	X		1.22E+08	X,1223895	missense	high	4.62	T649A	GRIA3	Xq25-q26			TRANSMEN	A:112718	G:12079	124797	0.096789	0	TRUE	A:86471	G:56	86527	0.000647	1	FALSE	0	0		
2386	SA215_12	SA215		12	93500256	12,9350025	missense	medium	3.095	D90Y	TMCC3	12q22			C:3000963	A:304659	3305622	0.092164	0	TRUE	C:2565391	T:234	2565625	9.12E-05	1	FALSE	1	105			
2387	SA217_13	SA217		13	23769756	13,2376975	missense	low	0.855	V531I	SPATA13	13q12.12			DOMAIN //	G:293858	A:35247	329105	0.1071	0	TRUE	G:264432	A:36	264468	0.000136	1	FALSE	1	34		
2388	SA217_8_1	SA217		8	1.46E+08	8,1460035	missense	neutral	0	G144R	ZNF517	8q24.3				G:121090	A:55733	176823	0.315191	0	TRUE	G:174880	A:15	174895	8.58E-05	1	FALSE	2	5		
2389	SA222_8_1	SA222		8	1E+08	8,1002170	missense	medium	2.075	S503R	VP5138	8q22.1				C:50013	A:8410	58423	0.14395	0	TRUE	C:44694	A:38	44732	0.00085	1	FALSE	1	4		
2390	SA226_15	SA226		15	89257524	15,8925752	silent	neutral	0	G865L	MAN2A2	15q26.1				C:36004	T:35965	66569	0.540266	0	TRUE	C:44325	A:7	44332	0.000158	1	FALSE	1	94		
2391	SA226_17	SA226		17	7519127	17,7519127	nonsense	NA		C176	TP53	17p13.1	p.C176Y,p.	adenocarci	Cancer Cell	DNA_BIND	G:30600	T:33757	39757	0.849083	0	TRUE	G:109645	T:21	109666	0.000191	1	FALSE	1	103	
2392	SA226_5_1	SA226		5	1.77E+08	5,1767574	missense	medium	2.495	M500V	SLC34A1	5q35			DISULFID //	A															

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
2	0	NOS1	-1	12:116175	Basal	FALSE	HETD	-0.3234	2n Somatic	2	0.8	NLOH	NA	NA	NA	NA	-0.75447	NA	0.009709	0.189235	MISSENSE		
3	0	CD300E	-1	17:701204	Basal	FALSE	NEUT	0.1133	4n Somatic	4	0.875	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.194018	MISSENSE		
4	0	RREB1	1	6:7176152	Basal	FALSE	GAIN	0.3081	5n non-mo	5	0.58	HET	NA	NA	NA	NA	NA	NA	0.016181	0.350578	MISSENSE		
5	0	TPH2	1	12:707024	Other	FALSE	NEUT	0.0407	4n balance	4	0.6047	HET	HET	0.6047	GAIN	0.084	-0.50281	NA	0.006472	0.514095	MISSENSE		
6	0	KIAA1683	-1	19:182390	Other	FALSE	NEUT	-0.094	3n duplicat	3	0.6129	HET	HET	0.6129	NEUT	-0.1566	NA	NA	0.006472	0.509712	MISSENSE		
7	0	CESK1	-1	22:154531	Other	FALSE	HETD	-0.284	2n Somatic	2	0.75	DLOH	DLOH	0.75	HETD	-0.361	NA	NA	NA	0.511478	MISSENSE		
8	0	FAM13C	-1	10:607538	Basal	FALSE	NEUT	-0.0194	3n Somatic	3	0.6891	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.995589	MISSENSE		
9	69	GDPD5	-1	11:748241	Basal	FALSE	NEUT	-0.0064	3n Somatic	3	0.697	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.496946	MISSENSE		
10	0	GPR133	1	12:130188	Basal	FALSE	NEUT	-0.087	2n Somatic	2	0.6667	NLOH	NA	NA	NA	NA	NA	NA	0.012945	0.355659	MISSENSE		
11	16	AC024575	1	19:113314	Basal	FALSE	GAIN	0.1528	4n Germilin	4	0.5769	HET	NA	NA	NA	NA	NA	NA	NA	0.788352	MISSENSE		
12	0	SCUBE1	-1	22:419442	Basal	FALSE	NEUT	-0.1317	2n Somatic	2	0.6954	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.193991	MISSENSE		
13	2	PCDHA2,PC1,1,1	5:1401821	Basal	FALSE	NEUT	-0.0904	2n Germilin	2	0.7	NLOH	NA	NA	NA	NA	NA	NA	NA	NA	0.789916	MISSENSE		
14	5	KANK1	1	9:700983	Basal	FALSE	NEUT	-0.0596	3n duplicat	3	0.6585	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.513051	MISSENSE		
15	68	MACF1	1	1:3967926	Basal	FALSE	HETD	-0.1994	Hemizygou	1	0.6471	DLOH	DLOH	0.6471	HETD	-0.2282	-0.22547	NA	0.02589	0.244373	MISSENSE		
16	5	IRX6	1	16:539189	Basal	FALSE	NEUT	-0.0014	2n Germilin	2	0.6087	HET	HET	0.6087	NEUT	-0.009	NA	NA	0.003236	0.192135	MISSENSE		
17	1	ACACA	-1	17:325567	Basal	FALSE	HETD	-0.1844	Hemizygou	1	0.6522	DLOH	DLOH	0.6522	HETD	-0.227	-0.55327	NA	0.003236	0.512449	MISSENSE		
18	0	FAM129C	1	19:175153	Basal	FALSE	GAIN	0.5713	6n Somatic	6	0.7778	LOH	LOH	0.7778	HLAMP	1.1717	NA	NA	NA	0.517401	MISSENSE		
19	13	ZFP64	-1	20:502028	Basal	FALSE	NEUT	0.0289	Normal (A	2	0.6015	HET	HET	0.6015	NEUT	0.0571	NA	NA	0.003236	0.190145	MISSENSE		
20	0	NFKBIL1	1	6:3163390	Basal	FALSE	NEUT	-0.012	Normal (A	2	0.625	HET	HET	0.625	NEUT	0.009	-0.03493	NA	NA	0.779542	MISSENSE		
21	0	OR14I1	-1	1:2469119	Basal	FALSE	NEUT	0.1141	6n Somatic	6	0.7083	NLOH	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE		
22	0	ATRN1	1	10:117694	Basal	FALSE	NEUT	-0.1184	Normal (A	2	0.58	HET	NA	NA	NA	NA	NA	NA	0.016181	0.509052	MISSENSE		
23	1	CUZD1,ACC-1,1	10:124581	Basal	FALSE	NEUT	-0.1184	Normal (A	2	0.58	HET	NA	NA	NA	NA	NA	NA	NA	NA	0.517516	MISSENSE		
24	0	NTRK1,INS1,1,1	1:1550809	Basal	FALSE	NEUT	0.0978	4n balance	4	0.5758	HET	NA	NA	NA	NA	NA	NA	NA	NA	0.509318	MISSENSE		
25	0	OR9G9	1	11:562251	Basal	FALSE	NEUT	0.0875	5n non-mo	5	0.7879	NLOH	NA	NA	NA	NA	NA	NA	NA	0.193844	MISSENSE		
26	0	ATP1A2	1	1:1583715	Basal	FALSE	NEUT	0.0978	4n balance	4	0.5758	HET	NA	NA	NA	NA	NA	-0.1552	0.006803	0.006472	0.225016	MISSENSE	
27	0	TNR	-1	1:1736018	Basal	FALSE	NEUT	-0.0642	2n Somatic	2	0.6901	NLOH	NA	NA	NA	NA	NA	-0.08506	NA	0.009709	0.370004	MISSENSE	
28	1	LRP6,BCL2L1,1	12:122241	Basal	FALSE	NEUT	-0.1688	Hemizygou	1	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	NA	0.364646	MISSENSE		
29	0	STX2	-1	12:129846	Basal	FALSE	NEUT	-0.0678	Normal (A	2	0.5795	HET	NA	NA	NA	NA	NA	-0.03477	NA	NA	1	MISSENSE	
30	4	NKAIN1	-1	1:3142798	Basal	FALSE	NEUT	0.003	3n duplicat	3	0.5932	HET	NA	NA	NA	NA	NA	NA	0.003236	0.195635	MISSENSE		
31	32	RBBP4	1	1:3289016	Basal	FALSE	GAIN	0.2001	5n Germilin	5	0.5932	HET	NA	NA	NA	NA	NA	-0.32749	NA	0.003236	0.51943	MISSENSE	
32	0	MYH8	-1	17:102404	Basal	FALSE	NEUT	-0.0018	3n Somatic	3	0.72	NLOH	NA	NA	NA	NA	NA	-0.22775	NA	0.009709	0.355221	MISSENSE	
33	9	SUFN5	1	17:306159	Basal	FALSE	GAIN	0.1503	3n Germilin	3	0.5854	HET	NA	NA	NA	NA	NA	NA	0.003236	0.516385	MISSENSE		
34	0	C19orf57	-1	19:138620	Basal	FALSE	NEUT	-0.0258	3n Somatic	3	0.7	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.510704	MISSENSE		
35	38	POP4	1	19:347932	Basal	FALSE	NEUT	0.0943	5n non-mo	5	0.6	HET	NA	NA	NA	NA	NA	NA	NA	0.999135	MISSENSE		
36	0	ZNF536	1	19:357320	Basal	FALSE	NEUT	0.0943	5n non-mo	5	0.6	HET	NA	NA	NA	NA	NA	NA	0.022654	0.787524	MISSENSE		
37	1	IQCG	-1	3:1991251	Basal	FALSE	NEUT	0.02	3n duplicat	3	0.6667	NLOH	NA	NA	NA	NA	NA	NA	NA	0.995269	MISSENSE		
38	0	COL7A1	3:4858365	Basal	FALSE	NEUT	-0.0737	3n Somatic	3	0.6818	NLOH	NA	NA	NA	NA	NA	-0.0811	NA	0.009709	0.99144	MISSENSE		
39	2	BDP1	1:57088479	Basal	FALSE	NEUT	-0.1268	2n Germilin	2	0.6667	NLOH	NA	NA	NA	NA	NA	-0.07935	NA	0.995364	MISSENSE			
40	0	LAMA2	1:61297460	Basal	FALSE	GAIN	0.3537	6n non-mo	6	0.652	NLOH	NA	NA	NA	NA	NA	-0.31832	NA	0.022654	0.999695	MISSENSE		
41	0	HIST1H1D	-1:62634291	Basal	FALSE	GAIN	0.1798	5n Germilin	5	0.5806	HET	NA	NA	NA	NA	NA	-0.05895	NA	NA	0.452352	MISSENSE		
42	6	POT1	-1:71242525	Basal	FALSE	NEUT	-0.069	3n Germilin	3	0.6923	NLOH	NA	NA	NA	NA	NA	-0.06986	NA	NA	0.994874	MISSENSE		
43	8	MIOS	1:7591886	Basal	FALSE	NEUT	0.029	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.757942	MISSENSE			
44	0	ZFP37	-1:91148448	Basal	FALSE	NEUT	-0.0993	2n Somatic	2	0.6667	NLOH	NA	NA	NA	NA	NA	NA	NA	0.003236	0.99482	MISSENSE		
45	0	MAMLD1	1:1493895	Basal	FALSE	NEUT	0.0823	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE		
46	0	ZNF236	1:18727780	Basal	FALSE	NEUT	-0.01	4n balance	4	0.5897	HET	NA	NA	NA	NA	NA	NA	NA	0.012945	0.992332	MISSENSE		
47	8	SESTD1	-1:21796905	Basal	FALSE	NEUT	0.1331	5n non-mo	5	0.5833	HET	NA	NA	NA	NA	NA	NA	NA	0.003236	1	TRUNCATING		
48	0	ERBB4	-1:2119565	Basal	FALSE	NEUT	0.1074	5n non-mo	5	0.5833	HET	NA	NA	NA	NA	NA	-0.76042	NA	NA	0.268347	MISSENSE		
49	0	SPHKAP,AC-1,1	2:2285903	Basal	FALSE	NEUT	0.1001	4n Germilin	4	0.5833	HET	NA	NA	NA	NA	NA	NA	NA	NA	0.590896	MISSENSE		
50	28	TACC2	1:10123960	Basal	FALSE	HETD	-0.2059	2n Somatic	2	0.8696	DLOH	DLOH	0.8696	HETD	-0.3381	NA	NA	NA	0.012945	NA	MISSENSE		
51	0	GUCY1A2	-1:1106063	Basal	FALSE	GAIN	0.3261	4n monoal	4	0.72	ASCN	ASCN	0.72	AMP	0.4734	-0.3576	NA	NA	0.003236	NA	MISSENSE		
52	0	MS4A15	1:11602878	Basal	FALSE	NEUT	0.0747	3n duplicat	3	0.6364	HET	HET	0.6364	NEUT	0.0437	NA	NA	NA	0.003236	NA	MISSENSE		
53	0	RASGRP2	-1:11642634	Basal	FALSE	NEUT	0.0747	3n duplicat	3	0.6364	HET	HET	0.6364	NEUT	-0.0068	-0.48831	NA	NA	NA	NA	MISSENSE		
54	10	SRGAP2	1:12046949	Basal	FALSE	NEUT	-0.0252	3n duplicat	3	0.6667	HET	HET	0.6667	NEUT	0.0248	-0.15151	NA	NA	0.006472	NA	MISSENSE		
55	0	ISL2	1:15744177	Basal	FALSE	NEUT	0.0681	3n Somatic	3	0.9	NLOH	NLOH	0.9	NEUT	0.0268	NA	NA	NA	NA	NA	MISSENSE		
56	4	BAIAP3	1:16133144	Basal	FALSE	HETD	-0.2194	2n Somatic	2	NA	NA	NA	NA	NA	HETD	-0.2593	NA	NA	NA	NA	MISSENSE		
57	94	CENPT	-1:16664208	Basal	FALSE	NEUT	0.0048	2n Somatic	2	NA	NA	NA	NA	NA	NEUT	-0.0177	-0.0671	NA	NA	NA	MISSENSE		
58	11	TNRC6C	1:17735941	Basal	FALSE	HETD	-0.2301	2n Somatic	2	0.88	DLOH	DLOH	0.88	HETD	-0.386	NA	NA	NA	0.003236	NA	MISSENSE		
59	5	MRI1	1:19137401	Basal	FALSE	HETD	-0.2478	2n Somatic	2	0.875	DLOH	DLOH	0.875	HETD	-0.4928	NA	NA	NA	NA	NA	MISSENSE		
60	0	FCER2	-1:19766008	Basal	FALSE	HETD	-0.275	2n Somatic	2	0.8515	DLOH	DLOH	0.8515	HETD	-0.4412	-0.30021	NA	NA	NA	NA	MISSENSE		
61	0	TTN	-1:21791071	Basal	FALSE	HETD	-0.1757	2n Somatic	2	0.8048	NLOH	NLOH	0.8048	NEUT	-0.0729	-0.11939	NA	NA	0.20712	NA	MISSENSE		
62	83	MYF	1:2279297	Basal	FALSE	NEUT	0.059	3n Somatic	3	0.8977	NLOH	NLOH	0.8977	NEUT	-0.0216	NA	NA	NA	NA	NA	MISSENSE		
63	0	TRIOBP	1:22364613	Basal	FALSE	NEUT	0.0155	3n duplicat	3	0.678	HET	HET	0.678	NEUT	0.0165	NA	NA	NA	0.003236	NA	MISSENSE		
64	0	AC019172	1:23778233	Basal	FALSE	HETD	-0.2003	Normal (A	2	0.6061	HET	HET	0.6061	HETD	-0.3313	NA	NA	NA	NA	NA	MISSENSE		
65	26	SPTBN1	1:5470977	Basal	FALSE	NEUT	-0.093	2n Somatic	2	0.825	NLOH	NLOH	0.825	HETD	-0.292								

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
71	0	PKHD11	Basal	1:8:1105019	Basal	FALSE	GAIN	0.3797	4n monoal	4	0.7418	ASCNA	ASCNA	0.7418	AMP	0.5155	NA	NA	0.029126	NA	MISSENSE		
72	0	FRMPD2	-1	10:490793	Basal	FALSE	NEUT	-0.0255	4n balance	4	0.6	HET	NA	NA	NA	NA	NA	NA	NA	0.421448	MISSENSE		
73	0	HMGCS2	-1	1:1200996	Basal	FALSE	NEUT	0.0296	5n non-mo	5	0.5778	HET	NA	NA	NA	NA	-1.32758	NA	0.006472	0.427801	MISSENSE		
74	83	FAF1	-1	1:5071358	Basal	FALSE	NEUT	-0.0276	Normal (A	2	0.6	HET	NA	NA	NA	NA	-0.20194	NA	0.003236	0.42193	TRUNCATING		
75	0	C15orf55	1	15:324275	Basal	FALSE	NEUT	0.04	4n balance	4	0.6	HET	NA	NA	NA	NA	NA	NA	0.003236	0.422049	MISSENSE		
76	16	CTCF	1	16:662023	Basal	FALSE	NEUT	-0.0743	2n Germli	2	0.6087	HET	NA	NA	NA	NA	-0.17154	NA	0.003236	0.985389	MISSENSE		
77	20	ALDOC	-1	17:329263	Basal	FALSE	NEUT	-0.0987	Hemizygou	1	0.6	HET	NA	NA	NA	NA	-1.34054	NA	0.003236	0.587697	MISSENSE		
78	0	KRT24	-1	17:361097	Basal	FALSE	NEUT	-0.0143	3n Somatic	3	0.6667	NLOH	NA	NA	NA	NA	NA	NA	0.184502	MISSENSE			
79	18	CEP192	1	18:130458	Basal	FALSE	NEUT	-0.028	4n balance	4	0.5882	HET	NA	NA	NA	NA	-0.08983	NA	0.012945	0.179848	MISSENSE		
80	16	JMJD28	1	19:499198	Basal	FALSE	NEUT	-0.0241	3n duplicat	3	0.6	HET	NA	NA	NA	NA	NA	NA	0.271486	MISSENSE			
81	8	FIZ1	-1	19:607957	Basal	FALSE	NEUT	-0.0809	5n monoal	5	0.6021	HET	NA	NA	NA	NA	NA	NA	NA	0.425794	MISSENSE		
82	3	TANC1	1	2:1597340	Basal	FALSE	NEUT	0.0175	3n duplicat	3	0.5862	HET	NA	NA	NA	NA	NA	NA	0.006472	0.501152	MISSENSE		
83	0	PGAP1	-1	2:1974200	Basal	FALSE	NEUT	0.1053	4n Germli	4	0.5862	HET	NA	NA	NA	NA	-1.48166	NA	0.009709	0.587845	TRUNCATING		
84	39	HJURP	-1	2:2344153	Basal	FALSE	NEUT	0.1002	4n balance	4	0.6	HET	NA	NA	NA	NA	NA	NA	0.003236	0.429703	MISSENSE		
85	0	MAP9	-1	4:1565007	Basal	FALSE	NEUT	-0.007	4n Germli	4	0.6	HET	NA	NA	NA	NA	NA	NA	0.003236	0.422865	MISSENSE		
86	536	HNRPD	-1	4:8356834	Basal	FALSE	NEUT	-0.0097	Hemizygou	1	0.6	HET	NA	NA	NA	NA	NA	NA	NA	0.426237	MISSENSE		
87	71	ANKHD1	1	5:1398190	Basal	FALSE	NEUT	-0.0325	4n balance	4	0.6	HET	NA	NA	NA	NA	NA	NA	0.003236	0.27067	MISSENSE		
88	17	BRD9	-1	5:940517	Basal	FALSE	NEUT	-0.0989	Normal (A	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	1	MISSENSE		
89	7	PHF3	1	6:6444786	Basal	FALSE	NEUT	0.096	3n Germli	3	0.5789	HET	NA	NA	NA	NA	NA	NA	0.006472	0.736026	MISSENSE		
90	0	HAS2	-1	8:1226956	Basal	FALSE	GAIN	0.2474	6n balance	6	0.5858	HET	NA	NA	NA	NA	NA	NA	0.016181	0.584475	MISSENSE		
91	0	ZNF257	1	19:220637	Basal	FALSE	NEUT	-0.0756	2n Germli	2	NA	NA	NA	NA	NA	NA	NA	NA	0.006472	NA	MISSENSE		
92	0	C10orf49	-1	10:133040	Basal	FALSE	NEUT	-0.0419	4n monoal	4	0.6842	NLOH	NA	NA	NA	NA	NA	NA	NA	0.614781	MISSENSE		
93	2	EPC1	-1	10:326757	Basal	FALSE	NEUT	-0.0224	Normal (A	2	0.5909	HET	NA	NA	NA	NA	NA	NA	0.009709	0.38191	MISSENSE		
94	0	MYOC	-1	1:1698881	Basal	FALSE	NEUT	0.1143	3n duplicat	3	0.5833	HET	NA	NA	NA	NA	NA	NA	NA	0.832183	MISSENSE		
95	0	KRT6B	-1	12:511277	Basal	FALSE	NEUT	-0.0152	2n Somatic	2	0.7273	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.470634	MISSENSE		
96	0	HMG84,CS 1,-1	1	1:3410247	Basal	FALSE	NEUT	-0.0602	2n Somatic	2	0.7353	NLOH	NA	NA	NA	NA	NA	NA	NA	0.687384	MISSENSE		
97	0	ZNF536	1	19:357321	Basal	FALSE	GAIN	0.5304	6n Somatic	6	0.8242	NLOH	NA	NA	NA	NA	NA	NA	0.022654	0.456799	MISSENSE		
98	101	CALM3	1	19:518039	Basal	FALSE	NEUT	-0.0793	Normal (A	2	0.5926	HET	NA	NA	NA	NA	-0.52918	NA	0.003236	0.556016	MISSENSE		
99	79	ZNF512B,P -1,1	20:621185	Basal	FALSE	NEUT	0.0379	3n Germli	3	0.6	HET	NA	NA	NA	NA	NA	NA	NA	NA	0.437858	MISSENSE		
100	51	SPTBN1	1	2:5473029	Basal	FALSE	GAIN	0.3833	4n balance	4	0.6	HET	NA	NA	NA	NA	-0.29399	NA	0.006472	1	MISSENSE		
101	0	TRPC6	-1	11:100848	Basal	FALSE	NEUT	0.0448	Normal (A	2	0.566	HET	NA	NA	NA	NA	-0.13785	NA	0.003236	0.453976	MISSENSE		
102	0	DSCAML1	-1	11:117156	Basal	FALSE	NEUT	0.0448	Normal (A	2	0.566	HET	NA	NA	NA	NA	NA	NA	0.009709	0.383823	MISSENSE		
103	0	NELL1	1	11:209158	Basal	FALSE	HETD	-0.3334	Hemizygou	1	0.7547	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.471871	MISSENSE		
104	0	USH2A	-1	1:2142387	Basal	FALSE	NEUT	0.1152	Normal (A	2	0.5688	HET	NA	NA	NA	NA	NA	NA	0.064725	0.558826	MISSENSE		
105	42	NYFC	1	1:4098786	Basal	FALSE	NEUT	0.0054	2n Germli	2	0.5714	HET	NA	NA	NA	NA	-0.08712	NA	NA	0.371141	MISSENSE		
106	4	SLC39A9	1	14:689913	Basal	FALSE	HETD	-0.3594	Hemizygou	1	0.76	NLOH	NA	NA	NA	NA	NA	NA	NA	0.560756	MISSENSE		
107	1	MMIP9	1	20:440752	Basal	FALSE	NEUT	0.0091	Normal (A	2	0.5789	HET	NA	NA	NA	NA	-0.5585	NA	0.003236	0.997391	MISSENSE		
108	11	FAM128A	-1	2:1319582	Basal	FALSE	NEUT	0.0651	Normal (A	2	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.704	MISSENSE		
109	1	FAM40B	1	7:1289126	Basal	FALSE	GAIN	0.2767	3n duplicat	3	0.6364	HET	NA	NA	NA	NA	NA	NA	NA	0.687054	MISSENSE		
110	0	CD48	-1	1:1589213	Basal	FALSE	GAIN	0.2074	6n monoal	6	0.7	NLOH	NA	NA	NA	NA	-0.31279	NA	NA	0.46464	MISSENSE		
111	0	F5	-1	1:1677775	Basal	FALSE	GAIN	0.3551	6n non-mo	6	0.6154	HET	NA	NA	NA	NA	-0.18683	NA	0.009709	0.361717	MISSENSE		
112	0	TNR	-1	1:1735920	Basal	FALSE	GAIN	0.3551	6n non-mo	6	0.6154	HET	NA	NA	NA	NA	-0.2344	NA	0.009709	0.696598	MISSENSE		
113	9	ABL2	-1	1:1773438	Basal	FALSE	GAIN	0.3551	6n non-mo	6	0.6154	HET	NA	NA	NA	NA	-0.33166	NA	0.003236	0.46035	MISSENSE		
114	2	LAMC1	1	1:1813462	Basal	FALSE	NEUT	0.1192	5n non-mo	5	0.6154	HET	NA	NA	NA	NA	-1.18022	NA	0.009709	0.460815	MISSENSE		
115	6	BRCA2	1	13:318430	Basal	FALSE	NEUT	-0.0782	2n Somatic	2	0.625	HET	NA	NA	NA	NA	-0.51411	0.020408	0.032362	0.69702	TRUNCATING		
116	1	KL	1	13:325260	Basal	FALSE	NEUT	-0.0782	2n Somatic	2	0.625	HET	NA	NA	NA	NA	-0.04377	NA	0.003236	0.687308	MISSENSE		
117	1	KCNJ12	1	17:212602	Basal	FALSE	NEUT	-0.1346	2n Somatic	2	0.7143	NLOH	NA	NA	NA	NA	NA	NA	0.009709	0.38336	MISSENSE		
118	1	ACE	1	17:589198	Basal	FALSE	NEUT	-0.0089	3n Somatic	3	0.6191	HET	NA	NA	NA	NA	-0.25787	NA	0.006472	0.448589	MISSENSE		
119	5	GBP5	-1	1:8950473	Basal	FALSE	GAIN	0.2039	6n Germli	6	0.7273	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.411139	MISSENSE		
120	0	THEG	-1	19:313273	Basal	FALSE	NEUT	-0.1249	2n Somatic	2	0.625	HET	NA	NA	NA	NA	NA	NA	0.003236	0.474332	MISSENSE		
121	5	KIAA0406	-1	20:360747	Basal	FALSE	NEUT	-0.0351	2n Somatic	2	0.6548	HET	NA	NA	NA	NA	NA	NA	0.009709	0.470108	MISSENSE		
122	0	C21orf34	1	21:164886	Basal	FALSE	NEUT	0.096	5n monoal	5	0.6667	HET	NA	NA	NA	NA	NA	NA	NA	0.688996	MISSENSE		
123	0	SYN1	-1	21:329519	Basal	FALSE	NEUT	0.09	4n monoal	4	0.6667	HET	NA	NA	NA	NA	-1.15456	NA	0.012945	0.993122	MISSENSE		
124	1	UBR3	1	2:1706057	Basal	FALSE	GAIN	0.2059	5n non-mo	5	0.6	HET	NA	NA	NA	NA	NA	NA	NA	0.420628	MISSENSE		
125	0	C2orf16	1	2:2765579	Basal	FALSE	NEUT	-0.0087	Normal (A	2	0.6	HET	NA	NA	NA	NA	NA	NA	0.009709	0.997325	MISSENSE		
126	10	TMC1	-1	3:1308724	Basal	FALSE	NEUT	0.0264	3n Germli	3	0.6	HET	NA	NA	NA	NA	NA	NA	NA	0.696288	MISSENSE		
127	0	FAT4	1	4:1265474	Basal	FALSE	NEUT	-0.0518	Normal (A	2	0.6	HET	NA	NA	NA	NA	NA	NA	0.019417	0.686893	MISSENSE		
128	16	KIAA0196	-1	8:1261562	Basal	FALSE	NEUT	0.1088	6n monoal	6	0.7333	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.383582	MISSENSE		
129	0	TRPM3	-1	9:7261593	Basal	FALSE	GAIN	0.3746	6n non-mo	6	0.6229	HET	NA	NA	NA	NA	NA	0.006803	0.012945	0.563032	MISSENSE		
130	0	MSL3	1	X:1169377	Basal	FALSE	NEUT	-0.0909	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.003236	NA	MISSENSE		
131	0	FUNDC2	1	X:1539360	Basal	FALSE	NEUT	-0.022	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE		
132	0	BMP15	1	X:5067574	Basal	FALSE	NEUT	-0.0588	NA	NA	NA	NA	NA	NA	NA	NA	-0.12156	NA	0.006472	NA	MISSENSE		
133	9	ZNF408	1	11:466824	Basal	FALSE	NEUT	0.0484	3n Somatic	3	0.6	HET	HET	0.6	NEUT	0.0492	NA	NA	NA	0.438433	MISSENSE		
134	0	NT5C1A	-1	1:3990384	Basal	FALSE	NEUT	0.0039	3n duplicat	3	0.6667	NLOH	NLOH	0.6667	NEUT	0.0735	-0.59612	NA	0.003236	0.472176	MISSENSE		
135	32	NCOR1	-1	17:159015	Basal	FALSE	NEUT	-0.0671	3n Somatic</														

NEOGENOMICS EX.1102.038

1	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDos	HMMDos	OncoSNP	OncoSNP	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh	
209	0	AC024935	1	12:392121	Other	FALSE	NEUT	0.078	4n balance	4	0.5652	HET	NA	NA	NA	NA	NA	NA	NA	0.12198	MISSENSE		
210	32	KIAA1522	1	1:3300603	Other	FALSE	NEUT	0.0675	3n duplicat	3	0.6451	NLOH	NA	NA	NA	NA	NA	NA	NA	0.449335	MISSENSE		
211	16	AKAP11	1	13:417742	Other	FALSE	HETD	-0.1581	2n Somatic	2	0.7213	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.346605	MISSENSE		
212	0	TRPM1	-1	15:290814	Other	FALSE	HETD	-0.1841	2n Somatic	2	0.6923	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.454212	MISSENSE		
213	0	PLA2G4D	-1	15:401592	Other	FALSE	HETD	-0.1841	2n Somatic	2	0.6923	NLOH	NA	NA	NA	NA	-0.05303	NA	NA	0.329099	MISSENSE		
214	7	LRRCS7	-1	15:406246	Other	FALSE	HETD	-0.1841	2n Somatic	2	0.6923	NLOH	NA	NA	NA	NA	NA	NA	NA	0.339648	MISSENSE		
215	5	COQ7	1	16:189928	Other	FALSE	HETD	-0.1652	Normal (A	2	0.5692	HET	NA	NA	NA	NA	-0.67317	NA	NA	0.406467	MISSENSE		
216	0	CCDC144A	1	17:165346	Other	FALSE	HETD	-0.1679	2n Somatic	2	0.7181	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.986385	MISSENSE		
217	1	ITGA2B	-1	17:398168	Other	FALSE	HETD	-0.1719	2n Somatic	2	0.7222	NLOH	NA	NA	NA	NA	-0.58146	NA	0.006472	0.498716	MISSENSE		
218	1	ACE	1	17:589197	Other	FALSE	GAIN	0.2817	6n Germlin	6	0.56	HET	NA	NA	NA	NA	-0.12047	NA	0.006472	0.589477	MISSENSE		
219	122	TP53	-1	17:751760	Other	FALSE	HETD	-0.1679	2n Somatic	2	0.7181	NLOH	NA	NA	NA	NA	-1.03436	0.306122	0.812298	0.290377	MISSENSE		
220	0	CLCA1	1	1:8672735	Other	FALSE	NEUT	0.0895	4n balance	4	0.5672	HET	NA	NA	NA	NA	-0.28421	NA	0.003236	0.287806	MISSENSE		
221	10	CCBL2	-1	1:8919971	Other	FALSE	NEUT	0.0883	5n Germlin	5	0.5672	HET	NA	NA	NA	NA	NA	NA	NA	0.840289	MISSENSE		
222	48	AP3D1	-1	19:206006	Other	FALSE	HETD	-0.2067	Normal (A	2	0.6	HET	NA	NA	NA	NA	-0.07456	NA	NA	0.288508	MISSENSE		
223	8	ZNF430	1	19:210314	Other	FALSE	HETD	-0.1489	3n Germlin	3	0.5896	HET	NA	NA	NA	NA	NA	NA	NA	0.290373	MISSENSE		
224	0	FSD1	1	19:426153	Other	FALSE	HETD	-0.2067	Normal (A	2	0.6	HET	NA	NA	NA	NA	NA	NA	NA	0.292159	MISSENSE		
225	0	DEFB132	1	20:187794	Other	FALSE	NEUT	0.0901	4n monoal	4	0.6562	NLOH	NA	NA	NA	NA	NA	NA	NA	0.591797	MISSENSE		
226	0	C20orf185	1	20:311183	Other	FALSE	NEUT	0.0439	4n balance	4	0.56	HET	NA	NA	NA	NA	NA	NA	0.009709	0.223293	MISSENSE		
227	0	SLC32A1	1	20:367902	Other	FALSE	NEUT	0.0439	4n balance	4	0.56	HET	NA	NA	NA	NA	NA	NA	NA	0.292214	MISSENSE		
228	0	TIAM1	-1	21:315200	Other	FALSE	NEUT	-0.0193	3n duplicat	3	0.7011	NLOH	NA	NA	NA	NA	-0.66199	NA	0.006472	0.289181	MISSENSE		
229	0	THSD7B	1	2:1375304	Other	FALSE	GAIN	0.2068	6n balance	6	0.5714	HET	NA	NA	NA	NA	NA	NA	0.012945	0.295243	MISSENSE		
230	0	SCN2A2	1	2:1659297	Other	FALSE	GAIN	0.1891	6n balance	6	0.5741	HET	NA	NA	NA	NA	NA	NA	NA	0.565353	TRUNCATING		
231	0	ITGA6	2	2:1730422	Other	FALSE	GAIN	0.1917	5n Germlin	5	0.5741	HET	NA	NA	NA	NA	-0.51722	NA	0.003236	0.387791	TRUNCATING		
232	0	CECR2	1	22:163968	Other	FALSE	NEUT	-0.0362	3n duplicat	3	0.5862	HET	NA	NA	NA	NA	NA	NA	0.003236	0.290193	MISSENSE		
233	14	TTC28	-1	22:267561	Other	FALSE	NEUT	-0.0109	3n duplicat	3	0.6	HET	NA	NA	NA	NA	NA	NA	NA	0.216306	MISSENSE		
234	39	EMIL4	1	2:4234187	Other	FALSE	GAIN	0.3128	6n non-mo	6	0.612	HET	NA	NA	NA	NA	NA	NA	0.006472	0.214034	MISSENSE		
235	102	CCT7	1	2:7333095	Other	FALSE	NEUT	0.0434	4n monoal	4	0.65	NLOH	NA	NA	NA	NA	-0.11708	NA	NA	0.300707	MISSENSE		
236	6	ALMS1	1	2:7353411	Other	FALSE	NEUT	0.0434	4n monoal	4	0.65	NLOH	NA	NA	NA	NA	-0.06111	NA	0.006472	0.286465	MISSENSE		
237	0	SMYD1	1	2:8817731	Other	FALSE	NEUT	0.0434	4n balance	4	0.5532	HET	NA	NA	NA	NA	NA	NA	0.006472	0.289102	MISSENSE		
238	0	DPPE2	-1	3:1105060	Other	FALSE	NEUT	-0.0098	3n Somatic	3	0.775	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.50295	MISSENSE		
239	0	MUC4	-1	3:1970017	Other	FALSE	NEUT	-0.0325	3n Somatic	3	0.775	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.216173	MISSENSE		
240	0	GADL1	-1	3:3081741	Other	FALSE	NEUT	0.0071	4n Somatic	4	0.7273	NLOH	NA	NA	NA	NA	NA	NA	NA	0.384425	MISSENSE		
241	0	DOCK3	1	3:5124878	Other	FALSE	HETD	-0.168	2n Germlin	2	0.7273	NLOH	NA	NA	NA	NA	NA	NA	0.019417	0.291744	MISSENSE		
242	2	PRRT3,CRE	-1,1	3:996538	Other	FALSE	NEUT	0.0071	4n Somatic	4	0.7273	NLOH	NA	NA	NA	NA	NA	NA	NA	0.835357	MISSENSE		
243	0	TRPC3	-1	4:1230731	Other	FALSE	NEUT	-0.0302	3n duplicat	3	0.5918	HET	NA	NA	NA	NA	-0.12368	NA	0.006472	0.289999	MISSENSE		
244	6	RAPGEF2	1	4:1604821	Other	FALSE	NEUT	-0.0364	2n Germlin	2	0.5918	HET	NA	NA	NA	NA	-0.13813	NA	NA	0.503517	MISSENSE		
245	0	FRAS1	4	4:7952769	Other	FALSE	NEUT	0.0622	4n balance	4	0.5714	HET	NA	NA	NA	NA	NA	NA	0.012945	0.215825	MISSENSE		
246	1	DPYSL3	-1	5:1467604	Other	FALSE	HETD	-0.1518	2n Germlin	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.499963	MISSENSE		
247	3	ELOVL2	-1	6:1111358	Other	FALSE	NEUT	0.1187	4n balance	4	0.5643	HET	NA	NA	NA	NA	-0.01512	NA	NA	0.284421	MISSENSE		
248	15	TBC1D7	-1	6:1342920	Other	FALSE	NEUT	0.1187	5n Germlin	5	0.5643	HET	NA	NA	NA	NA	NA	NA	0.003236	0.289649	MISSENSE		
249	0	C6orf97	1	6:1519361	Other	FALSE	NEUT	-0.0348	3n duplicat	3	0.5922	HET	NA	NA	NA	NA	NA	NA	NA	0.38582	MISSENSE		
250	10	ZNF862	1	7:1491885	Other	FALSE	GAIN	0.275	6n non-mo	6	0.6316	NLOH	NA	NA	NA	NA	NA	NA	NA	1	MISSENSE		
251	0	RAPGEF5	-1	7:2227307	Other	FALSE	GAIN	0.2109	6n balance	6	0.5714	HET	NA	NA	NA	NA	NA	NA	0.006472	0.384842	MISSENSE		
252	0	HECW1	1	7:4344410	Other	FALSE	NEUT	0.0269	4n balance	4	0.5714	HET	NA	NA	NA	NA	NA	NA	0.022654	0.291894	MISSENSE		
253	14	DAGLB	-1	7:6440923	Other	FALSE	GAIN	0.4091	6n non-mo	6	0.6616	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.496773	MISSENSE		
254	0	DPYS	-1	8:1055057	Other	FALSE	GAIN	0.2441	6n monoal	6	0.6957	NLOH	NA	NA	NA	NA	-0.6844	NA	0.003236	0.386721	MISSENSE		
255	2	ZHX1	-1	8:1243366	Other	FALSE	GAIN	0.2441	6n monoal	6	0.6957	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.388262	MISSENSE		
256	0	TG	1	8:1339681	Other	FALSE	GAIN	0.2441	6n monoal	6	0.6957	NLOH	NA	NA	NA	NA	-0.01794	NA	0.02589	0.221192	MISSENSE		
257	0	EYA1	-1	8:7240887	Other	FALSE	GAIN	0.2441	6n non-mo	6	0.591	HET	NA	NA	NA	NA	NA	0.013605	0.006472	0.832091	MISSENSE		
258	31	GTF3C4	1	9:1345438	Other	FALSE	NEUT	0.0243	4n balance	4	0.5625	HET	NA	NA	NA	NA	-0.07585	NA	0.003236	0.217932	MISSENSE		
259	7	RANBP6	1	9:6003756	Other	FALSE	HETD	-0.1504	2n Somatic	2	0.7078	NLOH	NA	NA	NA	NA	NA	NA	0.009709	0.216781	MISSENSE		
260	0	ALDH1A1	-1	9:7472178	Other	FALSE	NEUT	-0.046	3n Germlin	3	0.5882	HET	NA	NA	NA	NA	-0.69076	NA	0.009709	0.975255	MISSENSE		
261	6	ZNF449	1	X:1343107	Other	FALSE	HETD	-0.1483	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.006472	NA	MISSENSE		
262	0	CNGB1	-1	16:565559	Basal	FALSE	GAIN	0.2646	NA	NA	0.564	HET	NA	NA	NA	NA	-0.39506	NA	NA	NA	TRUNCATING		
263	0	AC005829	1	17:416778	Basal	FALSE	NEUT	-0.0654	4n Germlin	4	0.8684	NLOH	NA	NA	NA	NA	NA	NA	NA	0.384563	MISSENSE		
264	0	ZNF560	-1	19:943979	Basal	FALSE	HETD	-0.2018	2n Somatic	2	0.8636	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.999613	MISSENSE		
265	17	DFFA	-1	1:1044422	Other	FALSE	NEUT	0.0794	4n balance	4	0.5588	HET	NA	NA	NA	NA	-0.27496	NA	NA	0.216395	MISSENSE		
266	0	MMP27	-1	11:102080	Other	FALSE	HETD	-0.1738	2n Somatic	2	0.7059	NLOH	NA	NA	NA	NA	-0.08593	NA	0.006472	0.386237	MISSENSE		
267	0	PRH1	1	12:109745	Other	FALSE	NEUT	-0.0246	3n duplicat	3	0.5862	HET	NA	NA	NA	NA	-0.06089	NA	NA	0.288659	TRUNCATING		
268	9	ARHGDI8	-1	12:149867	Other	FALSE	NEUT	-0.0385	3n duplicat	3	0.5785	HET	NA	NA	NA	NA	-0.3586	NA	NA	0.496656	MISSENSE		
269	2	TAOX2	1	16:299101	Other	FALSE	NEUT	0.0602	4n balance	4	0.5385	HET	NA	NA	NA	NA	-0.44423	NA	NA	0.496837	MISSENSE		
270	4	MKI67	-1	10:129797	Other	FALSE	NEUT	-0.026	Normal (A	2	NA	NA	NA	NA	NA	NA	NA	NA	0.012945	0.218555	MISSENSE		
271	1	PRKG1	1	10:537011	Other	FALSE	NEUT	-0.026	Normal (A	2	NA	NA	NA	NA	NA	NA	-1.06065	NA	0.003236	0.498504	MISSENSE		
272	8	C11orf30	1	11:758849	Other	FALSE	NEUT	-0.0115	Normal (A	2	NA	NA	NA	NA	NA	NA	NA	NA	0.016181	0.500869	MISSENSE		
273	8	PTPRU	1	1:2950446	Other	FALSE																	

1	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDos	HMMDos	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type			
278	27	CDC6	-1	10:612227	Basal	FALSE	HETD	-0.5041	Hemizygou	1	0.6856	NLOH	NA	NA	NA	NA	-0.26489	NA	0.009709	0.288438	MISSENSE		
279	0	PRKQ	-1	10:659312	Basal	FALSE	NEUT	0.1125	Normal (A)	2	0.6087	HET	NA	NA	NA	NA	-0.91935	NA	0.009709	0.589294	MISSENSE		
280	0	TTC18	-1	10:747268	Basal	FALSE	NEUT	0.0718	Normal (A)	2	0.5575	HET	NA	NA	NA	NA	NA	0.006472	0.290156	MISSENSE			
281	68	SIAE	-1	11:124048	Basal	FALSE	NEUT	-0.1175	2n Somatic	2	0.8235	NLOH	NA	NA	NA	NA	NA	NA	0.605628	MISSENSE			
282	2	C1orf66	1	1:1549731	Basal	FALSE	AMP	0.6664	5n monoal	5	0.7	NLOH	NA	NA	NA	NA	NA	NA	0.292769	TRUNCATING			
283	4	CFH	1	1:1949132	Basal	FALSE	GAIN	0.4283	4n balance	4	0.5833	HET	NA	NA	NA	NA	-0.06441	NA	0.003236	0.389131	MISSENSE		
284	42	ARID4B	-1	1:2334123	Basal	FALSE	GAIN	0.3378	4n monoal	4	0.7241	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.294761	MISSENSE		
285	3	SDCCAG8	1	1:2415709	Basal	FALSE	GAIN	0.3378	4n monoal	4	0.7241	NLOH	NA	NA	NA	NA	-0.08202	NA	0.596375	TRUNCATING			
286	0	PRDM16	1	1:3340118	Basal	FALSE	GAIN	0.2088	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.293463	MISSENSE		
287	30	BRD4	-1	19:152363	Basal	FALSE	NEUT	0.1334	Normal (A)	2	0.6	HET	NA	NA	NA	NA	NA	NA	0.006472	0.391016	MISSENSE		
288	3	B3GALT5	1	21:399544	Basal	FALSE	HETD	-0.386	Hemizygou	1	0.8182	NLOH	NA	NA	NA	NA	-0.94636	NA	NA	0.593529	MISSENSE		
289	19	PTEN	1	10:896829	Other	FALSE	NEUT	-0.0119	5n non-mo	5	0.5556	HET	NA	NA	NA	NA	-0.80322	0.251701	0.006472	NA	MISSENSE		
290	28	FAF1	-1	1:5080543	Other	FALSE	NEUT	-0.0155	4n Germlin	4	0.5579	HET	NA	NA	NA	NA	-0.12492	NA	0.003236	NA	MISSENSE		
291	0	ANO5	1	11:222288	Other	FALSE	NEUT	0.1615	6n non-mo	6	0.5952	HET	NA	NA	NA	NA	NA	NA	0.003236	0.598046	MISSENSE		
292	0	FAM124A	1	13:507528	Other	FALSE	HETD	-0.2354	2n Germlin	2	0.6667	NLOH	NA	NA	NA	NA	NA	NA	0.30984	MISSENSE			
293	0	GRIK3	-1	1:3706378	Other	FALSE	NEUT	-0.0738	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	-0.35222	NA	0.009709	0.671444	MISSENSE		
294	31	SPG7	1	16:881044	Other	FALSE	NEUT	0.1187	4n monoal	4	0.6	HET	NA	NA	NA	NA	NA	NA	0.003236	0.674441	MISSENSE		
295	92	TP53	-1	17:751822	Other	FALSE	NEUT	-0.1244	2n Somatic	2	0.7	NLOH	NA	NA	NA	NA	-1.34495	0.306122	0.812298	0.684253	MISSENSE		
296	15	ZZZ3	-1	1:7787062	Other	FALSE	NEUT	-0.0273	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	NA	NA	0.012945	0.677364	MISSENSE		
297	0	TNFRSF11A	1	18:581869	Other	FALSE	NEUT	-0.0695	Hemizygou	1	0.5652	HET	NA	NA	NA	NA	-0.25101	NA	0.310117	MISSENSE			
298	0	RYR1	1	19:437260	Other	FALSE	NEUT	0.023	3n duplicat	3	0.6	HET	NA	NA	NA	NA	-0.18424	NA	0.022654	0.893368	MISSENSE		
299	0	AL357374	1	20:338047	Other	FALSE	GAIN	0.1834	4n Germlin	4	0.5897	HET	NA	NA	NA	NA	NA	NA	1	MISSENSE			
300	37	UGCG1	1	12:86550	Other	FALSE	NEUT	-0.0425	2n Germlin	2	NA	NA	NA	NA	NA	NA	-0.01316	NA	NA	0.882028	MISSENSE		
301	0	GALNT5	1	2:1578242	Other	FALSE	NEUT	0.0097	3n duplicat	3	0.5652	HET	NA	NA	NA	NA	-0.75933	NA	NA	0.87417	MISSENSE		
302	11	SLC39A10	1	2:1963009	Other	FALSE	NEUT	-0.0283	3n duplicat	3	0.5633	HET	NA	NA	NA	NA	NA	NA	NA	0.894442	MISSENSE		
303	0	USP37	-1	2:2190285	Other	FALSE	NEUT	-0.0182	Normal (A)	2	0.5633	HET	NA	NA	NA	NA	NA	NA	0.003236	0.883598	MISSENSE		
304	0	DDHD1	-1	14:525921	Other	FALSE	GAIN	0.2371	4n balance	4	0.5789	HET	NA	NA	NA	NA	NA	NA	0.003236	0.637292	MISSENSE		
305	0	SERPINF13	1	18:594125	Other	FALSE	NEUT	0.0101	Normal (A)	2	0.6	HET	NA	NA	NA	NA	-0.0963	NA	0.003236	0.638612	MISSENSE		
306	0	NLRP4	1	19:610613	Other	FALSE	GAIN	0.2319	4n Somatic	4	0.7778	NLOH	NA	NA	NA	NA	-0.0997	NA	0.009709	0.723264	MISSENSE		
307	0	NEBL	-1	10:211387	Basal	FALSE	GAIN	0.5229	6n Germlin	6	0.7	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.635257	MISSENSE		
308	0	MYO3A	1	10:264761	Basal	FALSE	GAIN	0.5203	6n non-mo	6	0.7	NLOH	NA	NA	NA	NA	NA	0.006803	0.009709	0.956375	MISSENSE		
309	0	RP11-508N	-1	10:384093	Basal	FALSE	NEUT	0.0824	4n balance	4	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.954885	MISSENSE		
310	21	DLG5	-1	10:792865	Basal	FALSE	NEUT	0.1359	4n balance	4	0.6	HET	NA	NA	NA	NA	NA	NA	0.016181	0.720883	MISSENSE		
311	0	VAV3	-1	1:1080994	Basal	FALSE	GAIN	0.3521	6n non-mo	6	0.6207	HET	NA	NA	NA	NA	-0.41324	NA	0.012945	0.724141	MISSENSE		
312	1	OVGP1	-1	1:1117589	Basal	FALSE	GAIN	0.3118	5n non-mo	5	NA	NA	NA	NA	NA	NA	NA	NA	0.012945	0.734842	MISSENSE		
313	3	IGSF2	1	1:1173696	Basal	FALSE	GAIN	0.3118	5n non-mo	5	0.5938	HET	NA	NA	NA	NA	NA	NA	NA	0.947542	MISSENSE		
314	1	PDE4DIP	-1	1:1435904	Basal	FALSE	GAIN	0.3118	4n monoal	4	0.5571	HET	NA	NA	NA	NA	NA	NA	0.009709	0.717459	MISSENSE		
315	4	GABPB2	1	1:1493295	Basal	FALSE	GAIN	0.2821	4n monoal	4	0.7407	NLOH	NA	NA	NA	NA	NA	NA	NA	0.956666	MISSENSE		
316	10	EFNA4	1	1:1533059	Basal	FALSE	GAIN	0.3088	5n monoal	5	0.7407	NLOH	NA	NA	NA	NA	-0.05906	NA	NA	0.954247	MISSENSE		
317	14	ASH1L	-1	1:1537172	Basal	FALSE	GAIN	0.3088	5n monoal	5	0.7407	NLOH	NA	NA	NA	NA	-0.08992	NA	0.009709	0.724457	MISSENSE		
318	0	FCRL4	-1	1:1558226	Basal	FALSE	GAIN	0.3088	5n monoal	5	0.7407	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.954326	MISSENSE		
319	0	CD1E	1	1:1565918	Basal	FALSE	GAIN	0.3088	5n Germlin	5	0.7407	NLOH	NA	NA	NA	NA	-0.0372	NA	NA	0.963141	MISSENSE		
320	0	SLAMF1	-1	1:1588604	Basal	FALSE	GAIN	0.3088	5n monoal	5	0.7407	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.722679	MISSENSE		
321	23	UAP1	1	1:1608239	Basal	FALSE	GAIN	0.3088	5n monoal	5	0.7218	NLOH	NA	NA	NA	NA	-0.49726	NA	0.006472	0.634574	MISSENSE		
322	9	RASAL2	1	1:1766787	Basal	FALSE	NEUT	0.1298	4n monoal	4	0.7143	NLOH	NA	NA	NA	NA	-0.09316	NA	0.006472	0.719642	MISSENSE		
323	1	MYBPC1	1	12:100547	Basal	FALSE	NEUT	-0.0491	3n duplicat	3	0.6207	HET	NA	NA	NA	NA	-0.01278	NA	0.006472	1	MISSENSE		
324	1	RHOA	1	1:2269458	Basal	FALSE	GAIN	0.3935	6n monoal	6	0.7945	NLOH	NA	NA	NA	NA	-0.05379	NA	NA	0.72218	MISSENSE		
325	1	CLEC4C	-1	12:779116	Basal	FALSE	NEUT	-0.04	3n duplicat	3	0.6154	HET	NA	NA	NA	NA	NA	NA	0.003236	0.251528	MISSENSE		
326	83	SLC2A1	-1	1:4316534	Basal	FALSE	NEUT	0.1346	4n balance	4	0.5714	HET	NA	NA	NA	NA	-0.23774	NA	0.003236	0.625585	MISSENSE		
327	21	MAST2	1	1:4625781	Basal	FALSE	NEUT	0.1346	4n balance	4	0.5714	HET	NA	NA	NA	NA	NA	NA	0.016181	0.598624	MISSENSE		
328	0	SLC1A7	-1	1:5333176	Basal	FALSE	GAIN	0.4473	6n Germlin	6	0.5714	HET	NA	NA	NA	NA	NA	NA	0.006472	0.301149	MISSENSE		
329	0	PPP1R14D	-1	1:15389079	Basal	FALSE	HETD	-0.28	2n Somatic	2	0.8	NLOH	NA	NA	NA	NA	NA	NA	NA	0.437463	MISSENSE		
330	0	PCSK9	1	1:5529569	Basal	FALSE	GAIN	0.4473	6n Germlin	6	0.7021	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.308143	MISSENSE		
331	7	ZNF668	-1	16:309830	Basal	FALSE	NEUT	-0.0908	3n duplicat	3	0.619	HET	NA	NA	NA	NA	NA	NA	NA	0.588467	MISSENSE		
332	0	KCNJ12	1	17:212602	Basal	FALSE	HETD	-0.289	2n Somatic	2	0.7034	NLOH	NA	NA	NA	NA	NA	NA	0.009709	0.993096	MISSENSE		
333	0	SLFN12L	-1	17:308261	Basal	FALSE	NEUT	-0.0555	3n duplicat	3	0.6301	HET	NA	NA	NA	NA	NA	NA	0.003236	0.579055	MISSENSE		
334	0	WDR63	1	1:8534832	Basal	FALSE	GAIN	0.4622	6n non-mo	6	0.636	HET	NA	NA	NA	NA	NA	NA	0.006472	0.380028	MISSENSE		
335	0	WDR63	1	1:8536484	Basal	FALSE	GAIN	0.4622	6n non-mo	6	0.636	HET	NA	NA	NA	NA	NA	NA	0.006472	0.630442	MISSENSE		
336	0	PDCD2L	1	19:395876	Basal	FALSE	NEUT	0.0039	4n balance	4	0.6	HET	NA	NA	NA	NA	NA	NA	0.003236	0.288714	MISSENSE		
337	0	FCAR	1	19:600784	Basal	FALSE	NEUT	-0.118	3n duplicat	3	0.6515	HET	NA	NA	NA	NA	-0.05421	NA	0.003236	0.302229	MISSENSE		
338	9	ZNF133	1	20:182436	Basal	FALSE	NEUT	0.0753	4n balance	4	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.592543	MISSENSE		
339	0	FOXA2	-1	20:225107	Basal	FALSE	NEUT	0.0753	4n Germlin	4	0.5714	HET	NA	NA	NA	NA	-0.0752	NA	0.006472	0.371742	MISSENSE		
340	72	CSE1L	1	20:471407	Basal	FALSE	NEUT	0.1323	4n Germlin	4	0.5625	HET	NA	NA	NA	NA	NA	NA	NA	0.301756	MISSENSE		
341	150	E1F2AK2	-1	2:3720326	Basal	FALSE	NEUT	-0.0461	3n Somatic	3	0.8365	NLOH	NA	NA	NA	NA	-0.12343	NA	0.006472	0.594321	MISSENSE		
342	0	MORC1	-1	3:1102645	Basal	TRUE	NEUT	0.1578	Normal (A)	2	0.5455	HET	NA	NA	NA	NA	NA	NA	0.009709	0.279455	SPICE		
343	160	SF3B3	1	16:691553	Other	FALSE	HETD	-0.1711	2n Germlin	2	0.7015	NLOH	NA	NA	NA	NA	-						

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ	
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type			
347	0	HAL	-1	12:948919	Basal	FALSE	HETD	-0.1406	Normal (A)	2	0.5866	HET	NA	NA	NA	NA	-0.6412	NA	0.006472	0.380523	TRUNCATING			
348	58	ZMYM1	-1	1:3535302	Basal	FALSE	NEUT	-0.0538	3n Germli	3	0.5897	HET	NA	NA	NA	NA	NA	NA	NA	0.555947	MISSENSE			
349	1	HOBX3	-1	17:439844	Basal	FALSE	GAIN	0.2598	6n Somatic	6	0.7941	NLOH	NA	NA	NA	NA	NA	NA	NA	0.601302	MISSENSE			
350	14	PPP4R1	-1	18:954732	Basal	FALSE	NEUT	-0.0038	3n duplicat	3	0.5882	HET	NA	NA	NA	NA	NA	NA	NA	0.534601	MISSENSE			
351	2	TRAF3IP1	-1	2:2389260	Basal	FALSE	NEUT	-0.0867	2n Somatic	2	0.6557	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.597589	TRUNCATING			
352	138	SFRS7	-1	2:3883065	Basal	FALSE	NEUT	-0.0307	3n Germli	3	0.6	HET	NA	NA	NA	NA	-0.21713	NA	0.595661	MISSENSE				
353	0	AC007318	-1	2:6528581	Basal	FALSE	NEUT	0.0728	4n balance	4	0.5652	HET	NA	NA	NA	NA	NA	NA	0.306779	MISSENSE				
354	0	GKN2	-1	2:6902783	Basal	FALSE	NEUT	0.0728	4n balance	4	0.5652	HET	NA	NA	NA	NA	NA	NA	0.377389	MISSENSE				
355	2	CP	-1	3:1504098	Basal	FALSE	NEUT	0.0051	4n monoal	4	0.6042	HET	NA	NA	NA	NA	-0.05706	NA	0.003236	0.444695	MISSENSE			
356	15	DNAJB11	-1	3:1877726	Basal	FALSE	NEUT	0.0348	4n Somatic	4	0.75	NLOH	NA	NA	NA	NA	-0.08016	NA	0.003236	0.598575	MISSENSE			
357	20	PDE4DIP	-1	1:1436426	Basal	FALSE	GAIN	0.1722	5n monoal	5	0.5806	HET	NA	NA	NA	NA	NA	NA	0.009709	0.377624	MISSENSE			
358	32	LCP1	-1	13:456204	Basal	FALSE	NEUT	0.1093	4n Germli	4	0.963	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.378332	MISSENSE			
359	0	KRT36	-1	17:368962	Basal	FALSE	HETD	-0.2424	2n Somatic	2	0.9375	NLOH	NA	NA	NA	NA	NA	NA	NA	0.307001	MISSENSE			
360	17	DGCR14	-1	22:175048	Basal	FALSE	NEUT	0.0439	4n balance	4	0.5778	HET	NA	NA	NA	NA	NA	NA	0.003236	0.592204	MISSENSE			
361	3	TRUB1	-1	10:116692	Other	FALSE	NEUT	-0.1415	Hemizygou	1	0.5789	HET	NA	NA	NA	NA	NA	NA	0.593724	MISSENSE				
362	48	HSPA14	-1	10:149359	Other	FALSE	NEUT	0.0089	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.615568	MISSENSE			
363	138	GDI2	-1	10:587873	Other	FALSE	NEUT	0.0089	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	-0.19551	NA	0.392	MISSENSE				
364	7	MYST4	-1	10:764583	Other	FALSE	NEUT	-0.0882	Hemizygou	1	0.5789	HET	NA	NA	NA	NA	-0.76453	0.020408	0.009709	0.304848	MISSENSE			
365	48	EXOSC1	-1	10:991909	Other	FALSE	NEUT	-0.1339	2n Germli	2	0.5789	HET	NA	NA	NA	NA	-0.07918	NA	1	MISSENSE				
366	0	KIAA1377	-1	11:101298	Other	FALSE	NEUT	-0.0496	Normal (A)	2	0.5667	HET	NA	NA	NA	NA	NA	NA	0.003236	0.541959	MISSENSE			
367	7	C1orf88	-1	1:1116942	Other	FALSE	NEUT	-0.0428	Normal (A)	2	0.563	HET	NA	NA	NA	NA	NA	NA	0.003236	0.594851	MISSENSE			
368	0	MICALCL	-1	1:122723	Other	FALSE	NEUT	-0.0562	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	NA	NA	0.840274	MISSENSE				
369	533	CSDE1	-1	1:1150647	Other	FALSE	NEUT	-0.0428	Normal (A)	2	0.563	HET	NA	NA	NA	NA	NA	NA	0.003236	0.431064	MISSENSE			
370	0	SPAG17	-1	1:1184109	Other	FALSE	NEUT	-0.0428	Normal (A)	2	0.5741	HET	NA	NA	NA	NA	NA	NA	0.006472	0.430288	MISSENSE			
371	5	MSTO1	-1	1:1538486	Other	FALSE	NEUT	0.074	3n Germli	3	0.5882	HET	NA	NA	NA	NA	NA	NA	NA	0.37423	MISSENSE			
372	82	SMG5	-1	1:1545097	Other	FALSE	NEUT	0.074	4n monoal	4	0.5882	HET	NA	NA	NA	NA	-0.20828	NA	0.006472	0.302483	MISSENSE			
373	0	ZP1	-1	11:603972	Other	FALSE	NEUT	-0.0562	3n Germli	3	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.37741	MISSENSE			
374	9	DAK	-1	11:608619	Other	FALSE	NEUT	-0.0562	2n Germli	2	0.5714	HET	NA	NA	NA	NA	-1.44429	NA	NA	0.59083	MISSENSE			
375	31	APBB1,SM	-1,1	11:636987	Other	FALSE	NEUT	-0.0562	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	NA	NA	NA	0.594809	MISSENSE			
376	21	BB51	-1	11:660399	Other	FALSE	NEUT	-0.0562	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.855565	MISSENSE			
377	1	C1orf129	-1	1:1692279	Other	FALSE	NEUT	0.0683	4n monoal	4	0.5882	HET	NA	NA	NA	NA	NA	NA	NA	0.818797	MISSENSE			
378	3	CAPN5	-1	11:765049	Other	FALSE	NEUT	-0.0562	2n Somatic	2	0.5667	HET	NA	NA	NA	NA	-0.22598	NA	NA	0.302834	MISSENSE			
379	13	TPR	-1	1:1845956	Other	FALSE	NEUT	0.0908	4n monoal	4	0.5882	HET	NA	NA	NA	NA	-0.93579	NA	0.006472	0.982504	MISSENSE			
380	0	PTPRC	-1	1:1969884	Other	FALSE	NEUT	0.0732	3n duplicat	3	0.5882	HET	NA	NA	NA	NA	-1.30286	NA	0.006472	0.901537	MISSENSE			
381	0	CACNA1S	-1	1:1993277	Other	FALSE	NEUT	0.0732	4n monoal	4	0.5882	HET	NA	NA	NA	NA	-0.9663	NA	0.009709	0.17317	MISSENSE			
382	23	PLEKHA6,A	-1,-1	1:2024845	Other	FALSE	NEUT	0.0732	4n monoal	4	0.5882	HET	NA	NA	NA	NA	NA	NA	NA	0.880784	MISSENSE			
383	0	NUAK2	-1	1:2035474	Other	FALSE	NEUT	0.0732	4n monoal	4	0.5882	HET	NA	NA	NA	NA	NA	NA	0.006472	0.811967	MISSENSE			
384	11	INTS7	-1	1:2102567	Other	FALSE	NEUT	0.0637	4n Germli	4	0.5882	HET	NA	NA	NA	NA	NA	NA	NA	0.109468	MISSENSE			
385	0	ACACB	-1	12:108061	Other	FALSE	NEUT	-0.0487	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	-1.61752	NA	0.016181	0.979586	MISSENSE			
386	1	UNC119B	-1	12:119642	Other	FALSE	NEUT	-0.0487	2n Germli	2	0.5625	HET	NA	NA	NA	NA	NA	NA	NA	0.600599	MISSENSE			
387	29	VPS33A	-1	12:121288	Other	FALSE	NEUT	-0.0487	Hemizygou	1	0.5625	HET	NA	NA	NA	NA	NA	NA	NA	0.981069	MISSENSE			
388	2	DHX37	-1	12:124016	Other	FALSE	NEUT	-0.0487	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	NA	NA	NA	0.639312	MISSENSE			
389	0	DHSP1	-1	1:2212425	Other	FALSE	NEUT	0.0637	4n Germli	4	0.5854	HET	NA	NA	NA	NA	-0.11135	NA	NA	0.879744	MISSENSE			
390	17	C1orf198	-1	1:2290460	Other	FALSE	NEUT	0.0637	3n Somatic	3	0.5854	HET	NA	NA	NA	NA	NA	NA	NA	0.898274	MISSENSE			
391	15	HEATR1	-1	1:2347889	Other	FALSE	NEUT	0.0637	4n monoal	4	0.5854	HET	NA	NA	NA	NA	NA	NA	0.006472	0.991306	MISSENSE			
392	0	ZP4	-1	1:2361183	Other	FALSE	NEUT	0.0637	4n monoal	4	0.5854	HET	NA	NA	NA	NA	NA	NA	0.003236	0.647655	MISSENSE			
393	728	ATP5B	-1	12:553248	Other	FALSE	NEUT	-0.0487	Hemizygou	1	0.5588	HET	NA	NA	NA	NA	-1.67682	NA	0.003236	0.684806	MISSENSE			
394	20	R3HDM2	-1	12:559483	Other	FALSE	NEUT	-0.0487	Hemizygou	1	0.5588	HET	NA	NA	NA	NA	NA	NA	NA	0.003236	0.811164	MISSENSE		
395	15	STMN1	-1	1:2610068	Other	FALSE	NEUT	-0.0713	Hemizygou	1	0.5714	HET	NA	NA	NA	NA	-1.09346	NA	NA	0.882383	TRUNCATING			
396	4	PTPRU	-1	1:2952428	Other	FALSE	NEUT	-0.0713	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-0.10015	NA	0.003236	0.98103	MISSENSE			
397	3	NEDD1	-1	12:958306	Other	FALSE	NEUT	-0.0487	Normal (A)	2	0.5519	HET	NA	NA	NA	NA	-0.13077	NA	NA	0.683442	MISSENSE			
398	17	TMPO	-1	12:974654	Other	FALSE	NEUT	-0.0487	Normal (A)	2	0.5519	HET	NA	NA	NA	NA	NA	NA	0.009709	0.982843	MISSENSE			
399	3	LATS2	-1	13:204470	Other	FALSE	NEUT	-0.1156	Hemizygou	1	0.5865	HET	NA	NA	NA	NA	-0.17832	0.013605	0.003236	0.899135	MISSENSE			
400	0	FGF9	-1	13:211734	Other	FALSE	NEUT	-0.1156	Hemizygou	1	0.5865	HET	NA	NA	NA	NA	-0.95013	NA	NA	0.812488	MISSENSE			
401	46	HSPH1	-1	13:306094	Other	FALSE	NEUT	-0.1432	Hemizygou	1	0.5714	HET	NA	NA	NA	NA	-0.29308	NA	NA	0.81297	MISSENSE			
402	0	THSD1	-1	13:518501	Other	FALSE	NEUT	-0.1306	Hemizygou	1	0.5714	HET	NA	NA	NA	NA	NA	NA	0.006472	0.650068	MISSENSE			
403	19	MACF1	-1	1:3967607	Other	FALSE	NEUT	-0.0573	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-0.68383	NA	0.02589	0.893539	MISSENSE			
404	37	MACF1	-1	1:3972288	Other	FALSE	NEUT	-0.0573	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-0.68383	NA	0.02589	0.899808	MISSENSE			
405	0	MYH6	-1	14:229331	Other	FALSE	NEUT	-0.1306	Hemizygou	1	0.5747	HET	NA	NA	NA	NA	-0.85429	NA	0.003236	0.814424	MISSENSE			
406	131	PTPRF	-1	1:4384234	Other	FALSE	NEUT	-0.0573	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-0.54171	NA	0.012945	0.647816	MISSENSE			
407	0	FANCM	-1	14:447033	Other	FALSE	NEUT	-0.1306	Hemizygou	1	0.5747	HET	NA	NA	NA	NA	NA	NA	0.006472	0.880499	MISSENSE			
408	0	C14orf37	-1	14:575415	Other	FALSE	NEUT	-0.1306	Hemizygou	1	0.5747	HET	NA	NA	NA	NA	NA	NA	NA	0.68474	MISSENSE			
409	15	C14orf133	-1	14:769873	Other	FALSE	NEUT	-0.1433	Hemizygou	1	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.254003	MISSENSE			
410	2	OSBPL9	-1	1:5195224	Other	FALSE	NEUT	-0.0573	Hemizygou	1	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.252139	TRUNCATING			
411	1632	B2M	-1	15:427949	Other	FALSE	NEUT	-0.1358																

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	Ens54Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloh.joh	apolloh.cal	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
416	21	USP31	-1	16:230095	Other	FALSE	NEUT	-0.0535	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.006472	0.603702	MISSENSE		
417	3	CNCF	1	16:244674	Other	FALSE	NEUT	-0.0743	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.878431	MISSENSE		
418	28	SRRM2	1	16:275183	Other	FALSE	NEUT	-0.0743	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.883627	MISSENSE		
419	5	KIAA0556	1	16:276705	Other	FALSE	NEUT	-0.0535	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.012945	1	MISSENSE		
420	99	STX4	1	16:309585	Other	FALSE	NEUT	-0.0535	Hemizygous	1	0.5714	HET	NA	NA	NA	NA	-0.86828	NA	NA	0.987695	MISSENSE		
421	17	CREBBP	-1	16:374885	Other	FALSE	NEUT	-0.0743	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-3.04078	NA	0.019417	0.902869	MISSENSE		
422	0	CACHD1	1	16:484088	Other	FALSE	NEUT	-0.0573	2n Germlin	2	0.56	HET	NA	NA	NA	NA	NA	NA	0.006472	0.983545	MISSENSE		
423	0	CDH8	-1	16:604089	Other	FALSE	NEUT	-0.0535	2n Germlin	2	0.5714	HET	NA	NA	NA	NA	-0.3762	NA	0.019417	0.884461	MISSENSE		
424	0	CMTM1	1	16:651702	Other	FALSE	NEUT	-0.0535	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.810897	MISSENSE		
425	0	MYH2	-1	17:103832	Other	FALSE	NEUT	-0.0697	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-0.67979	NA	0.016181	0.610181	MISSENSE		
426	0	TNS4	-1	17:358946	Other	FALSE	NEUT	-0.0517	Normal (A)	2	0.56	HET	NA	NA	NA	NA	NA	NA	0.003236	0.951929	TRUNCATING		
427	3	TNNI3K	1	17:444263	Other	FALSE	NEUT	-0.0311	Normal (A)	2	0.5503	HET	NA	NA	NA	NA	NA	NA	0.006472	0.856056	TRUNCATING		
428	0	GH1	-1	17:593494	Other	FALSE	NEUT	-0.0582	Hemizygous	1	0.5714	HET	NA	NA	NA	NA	-1.08416	NA	NA	0.891846	MISSENSE		
429	7	TEX2	-1	17:596450	Other	FALSE	NEUT	-0.0582	Hemizygous	1	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.982597	MISSENSE		
430	7	PRKCA	1	17:621682	Other	FALSE	NEUT	-0.0582	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-3.48497	0.013605	0.003236	0.893272	MISSENSE		
431	0	KCNJ2	1	17:656836	Other	FALSE	NEUT	-0.0582	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-0.12728	NA	NA	0.810189	MISSENSE		
432	109	TP53	-1	17:751822	Other	FALSE	NEUT	-0.0697	Normal (A)	2	0.5706	HET	NA	NA	NA	NA	-2.55666	0.306122	0.812298	0.809295	MISSENSE		
433	20	SPIRE1	-1	18:124964	Other	FALSE	NEUT	-0.108	Normal (A)	2	0.5897	HET	NA	NA	NA	NA	-0.06007	NA	NA	0.881525	MISSENSE		
434	0	ANKRD30B	1	18:147478	Other	FALSE	NEUT	-0.108	3n duplicat	3	0.5608	HET	NA	NA	NA	NA	NA	NA	0.003236	0.88032	MISSENSE		
435	15	LPHN2	1	18:214532	Other	FALSE	NEUT	-0.0311	Normal (A)	2	0.5503	HET	NA	NA	NA	NA	NA	NA	0.006472	0.688075	TRUNCATING		
436	7	EMILIN2	1	18:290309	Other	FALSE	NEUT	-0.108	Normal (A)	2	0.5652	HET	NA	NA	NA	NA	NA	NA	0.003236	0.684134	MISSENSE		
437	0	PTPRM	1	18:813370	Other	FALSE	NEUT	-0.108	Normal (A)	2	0.5652	HET	NA	NA	NA	NA	-0.4611	NA	0.003236	0.647196	MISSENSE		
438	7	MAN2B1	-1	19:126371	Other	FALSE	NEUT	-0.0615	Normal (A)	2	0.5758	HET	NA	NA	NA	NA	-0.23783	NA	0.012945	0.813895	TRUNCATING		
439	0	CYP4F11	-1	19:158865	Other	FALSE	NEUT	-0.0615	Normal (A)	2	0.5758	HET	NA	NA	NA	NA	NA	NA	0.003236	0.648241	MISSENSE		
440	14	SFRS14	-1	19:189968	Other	FALSE	NEUT	-0.0615	Normal (A)	2	0.5758	HET	NA	NA	NA	NA	NA	NA	NA	0.683422	MISSENSE		
441	13	CEACAM1	-1	19:477230	Other	FALSE	NEUT	-0.0615	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-0.23292	NA	0.003236	0.687578	TRUNCATING		
442	0	SIGLEC9	1	19:563202	Other	FALSE	NEUT	-0.0615	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.982001	TRUNCATING		
443	6	AC022150	-1,-1	19:579014	Other	FALSE	NEUT	-0.0615	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.812233	MISSENSE		
444	9	CSRP2BP	1	20:180911	Other	FALSE	NEUT	-0.0676	Normal (A)	2	0.5664	HET	NA	NA	NA	NA	NA	NA	0.006472	0.898137	MISSENSE		
445	401	RPN2	1	20:352691	Other	FALSE	NEUT	-0.0676	Normal (A)	2	0.566	HET	NA	NA	NA	NA	-1.65821	NA	0.006472	0.899943	MISSENSE		
446	40	CTNBNB1	1	20:359217	Other	FALSE	NEUT	-0.0676	Normal (A)	2	0.566	HET	NA	NA	NA	NA	-0.14144	NA	0.006472	0.902847	MISSENSE		
447	7	PABPC1L	1	20:429835	Other	FALSE	NEUT	-0.0676	Normal (A)	2	0.566	HET	NA	NA	NA	NA	NA	NA	0.003236	0.810067	MISSENSE		
448	0	LONRF2	-1	2:1002731	Other	FALSE	NEUT	-0.0679	Normal (A)	2	0.566	HET	NA	NA	NA	NA	NA	NA	NA	0.997187	MISSENSE		
449	8	LIMS1	1	2:1086423	Other	FALSE	NEUT	-0.0679	2n Germlin	2	0.5667	HET	NA	NA	NA	NA	-0.27595	NA	0.003236	0.901398	MISSENSE		
450	10	EPB41L5	1	2:1205160	Other	FALSE	NEUT	-0.0543	Normal (A)	2	0.57	HET	NA	NA	NA	NA	NA	NA	0.003236	0.983201	MISSENSE		
451	0	YSK4	-1	2:1354612	Other	FALSE	NEUT	-0.0543	2n Germlin	2	0.5556	HET	NA	NA	NA	NA	NA	NA	0.019417	0.109358	MISSENSE		
452	0	ZEB2	-1	2:1448723	Other	FALSE	NEUT	-0.0543	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	NA	NA	0.016181	0.811034	MISSENSE		
453	0	RPLP1P4,H	-1,1	2:1766675	Other	FALSE	NEUT	-0.0419	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	NA	NA	NA	0.901458	MISSENSE		
454	0	BOLL	-1	2:1983589	Other	FALSE	NEUT	-0.0346	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	NA	NA	0.006472	0.89889	MISSENSE		
455	0	AOX1	1	2:2012321	Other	FALSE	NEUT	-0.0346	2n Germlin	2	0.5556	HET	NA	NA	NA	NA	-1.44925	NA	0.012945	0.902061	MISSENSE		
456	12	CASP8	1	2:2018395	Other	FALSE	NEUT	-0.0346	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	-2.0339	NA	NA	0.64943	MISSENSE		
457	236	EEF1B2	1	2:2067353	Other	FALSE	NEUT	-0.0346	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	-0.20601	NA	NA	0.685636	MISSENSE		
458	1	TNS1	-1	2:2184659	Other	FALSE	NEUT	-0.0552	Hemizygous	1	0.5556	HET	NA	NA	NA	NA	-0.07818	NA	0.009709	0.900506	TRUNCATING		
459	17	TOP3B	-1	2:206496	Other	FALSE	NEUT	-0.1364	Hemizygous	1	0.6154	HET	NA	NA	NA	NA	-0.04386	NA	NA	0.890829	MISSENSE		
460	4	ADORA2A,(1,1		22:230486	Other	FALSE	NEUT	-0.1364	Hemizygous	1	0.5833	HET	NA	NA	NA	NA	NA	NA	NA	0.881406	MISSENSE		
461	74	C2orf18		2:2685199	Other	FALSE	NEUT	0.0243	3n Germlin	3	0.5625	HET	NA	NA	NA	NA	NA	NA	NA	0.647341	MISSENSE		
462	47	DCTN1	-1	2:7445084	Other	FALSE	NEUT	0.0237	3n Germlin	3	0.5625	HET	NA	NA	NA	NA	-0.52934	NA	0.009709	0.812212	MISSENSE		
463	1	TSGA10	-1	2:9908843	Other	FALSE	NEUT	-0.0679	2n Germlin	2	0.566	HET	NA	NA	NA	NA	NA	NA	0.003236	0.879596	TRUNCATING		
464	103	NIT2	1	3:1015471	Other	FALSE	NEUT	0.0176	3n duplicat	3	0.5625	HET	NA	NA	NA	NA	-0.05041	NA	0.003236	0.98168	MISSENSE		
465	2	SENp7	-1	3:1025299	Other	FALSE	NEUT	0.0176	3n Germlin	3	0.5625	HET	NA	NA	NA	NA	NA	NA	0.006472	0.649622	TRUNCATING		
466	0	KCNH8	1	3:1954995	Other	FALSE	NEUT	-0.0453	2n Somatic	2	0.5942	HET	NA	NA	NA	NA	NA	NA	0.003236	0.977395	MISSENSE		
467	0	SCN10A	-1	3:3877349	Other	FALSE	NEUT	-0.0477	2n Somatic	2	0.5942	HET	NA	NA	NA	NA	NA	NA	0.016181	0.649751	MISSENSE		
468	1	PDE5A	-1	4:1206661	Other	FALSE	NEUT	-0.0188	2n Germlin	2	0.5571	HET	NA	NA	NA	NA	-0.26482	NA	NA	0.684342	MISSENSE		
469	1	KLHL3	-1	5:1370559	Other	FALSE	NEUT	-0.1228	Hemizygous	1	0.5652	HET	NA	NA	NA	NA	NA	NA	NA	0.173766	MISSENSE		
470	0	ATP10B	-1	5:1600457	Other	FALSE	NEUT	-0.1321	Hemizygous	1	0.575	HET	NA	NA	NA	NA	NA	NA	0.009709	0.811478	MISSENSE		
471	0	C10orf79	-1	10:105937	Other	FALSE	NEUT	-0.09	4n Germlin	4	0.5804	HET	NA	NA	NA	NA	NA	NA	0.012945	0.98114	MISSENSE		
472	125	HIF1A	1	14:612812	Other	FALSE	NEUT	-0.0727	3n duplicat	3	0.5641	HET	NA	NA	NA	NA	-0.41807	NA	NA	0.902257	TRUNCATING		
473	5	ZNF780A	-1	19:452728	Other	FALSE	NEUT	-0.0324	4n balance	4	0.5691	HET	NA	NA	NA	NA	NA	NA	NA	0.898182	MISSENSE		
474	1	PLCE1	1	10:960085	Other	FALSE	NEUT	-0.0702	4n Germlin	3	0.5625	HET	NA	NA	NA	NA	-1.55449	NA	0.006472	0.24476	MISSENSE		
475	16	QSER1	1	11:329101	Other	FALSE	NEUT	-0.0406	Hemizygous	1	0.5625	HET	NA	NA	NA	NA	NA	NA	0.009709	0.272368	MISSENSE		
476	0	RAG2	-1	11:365717	Other	FALSE	NEUT	-0.0406	6n non-mo	6	0.5625	HET	NA	NA	NA	NA	-0.03741	NA	0.003236	0.269882	MISSENSE		
477	14	EPHA2	-1	11:633121	Other	FALSE	NEUT	-0.1151	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-0.19613	0.006803	0.006472	0.996979	MISSENSE		
478	1	DLG2	-1	11:833539	Other	FALSE	NEUT	-0.044	5n Germlin	5	0.5528	HET	NA	NA	NA	NA	-0.11831	NA	0.012945	1	MISSENSE		
479	4	ATP55	1	14:498579	Other	FALSE	NEUT	-0.0451	Hemizygous	2	0.5573	HET	NA	NA	NA	NA	NA	NA	0.003236	0.269041	MISSENSE		
480	144	KTN1	1																				

table_S3

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ	
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDos	HMMDos	OncoSNP	OncoSNP	apolloh.jo	apolloh.cal	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type			
554	4	BCL11A	-1	2:6054130	Other	FALSE	NEUT	-0.0123	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	0.040816	0.003236	0.30209	MISSENSE			
555	10	POLR1A	-1	2:8615855	Other	FALSE	NEUT	-0.0123	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	-1.25508	0.006472	0.306969	MISSENSE			
556	2	IRAK2	-1	3:1023935	Other	FALSE	NEUT	-0.0737	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	-0.19239	NA	0.673955	MISSENSE			
557	22	GOLGB1	-1	3:1228997	Other	FALSE	NEUT	-0.0734	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	0.019417	0.588023	MISSENSE			
558	0	CLSTN2	-1	3:1416052	Other	FALSE	NEUT	-0.0533	2n Somatic	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.298956	MISSENSE			
559	5	XRN1	-1	3:1435780	Other	FALSE	NEUT	-0.0533	2n Somatic	2	NA	NA	NA	NA	NA	NA	NA	-0.05947	0.009709	0.275923	TRUNCATING			
560	11	ATR	-1	3:1437492	Other	FALSE	NEUT	-0.0533	2n Somatic	2	NA	NA	NA	NA	NA	NA	NA	-0.25996	0.006803	0.670091	MISSENSE			
561	0	CPB1	-1	3:1500282	Other	FALSE	NEUT	-0.0533	2n Germlin	2	NA	NA	NA	NA	NA	NA	NA	-0.07747	0.003236	0.585159	MISSENSE			
562	21	PIK3CA	-1	3:1804345	Other	FALSE	NEUT	-0.0781	2n Somatic	2	NA	NA	NA	NA	NA	NA	NA	-2.04007	0.047619	0.016181	0.30048	MISSENSE		
563	9	RRP9	-1	3:5194274	Other	FALSE	NEUT	-0.0737	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	0.003236	0.28617	MISSENSE			
564	7	GSTCD	-1	4:1068672	Other	FALSE	NEUT	-0.0419	2n Germlin	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.677682	MISSENSE			
565	22	PCDH18	-1	4:1386704	Other	FALSE	NEUT	-0.0419	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	-0.20214	NA	0.589272	MISSENSE			
566	0	TD02	-1	4:1570495	Other	FALSE	NEUT	-0.0419	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	-1.02725	NA	0.304832	MISSENSE			
567	0	TRIM60	-1	4:1661818	Other	FALSE	NEUT	-0.0419	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.584188	MISSENSE			
568	43	SRP72	-1	4:5704411	Other	FALSE	NEUT	-0.0509	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	-0.07519	0.003236	0.416316	MISSENSE			
569	0	UGT2B4	-1	4:7039584	Other	FALSE	NEUT	-0.0419	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	-1.05948	NA	0.332593	MISSENSE			
570	30	WWC1	-1	5:1677695	Other	FALSE	NEUT	-0.0623	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	0.006472	0.543889	MISSENSE			
571	0	HRH2	-1	5:1750431	Other	FALSE	NEUT	-0.1359	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	-0.50547	0.003236	0.544217	MISSENSE			
572	6	C5orf45, SC-1,1	-1	5:1791972	Other	FALSE	NEUT	-0.1359	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.545111	MISSENSE			
573	20	NIPBL	-1	5:3705791	Other	FALSE	NEUT	-0.0568	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	0.009709	0.988856	MISSENSE			
574	10	SOCCAG10	-1	5:6430327	Other	FALSE	NEUT	-0.0623	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	1	MISSENSE			
575	1	DMGDH	-1	5:7836252	Other	FALSE	NEUT	-0.0623	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	-1.0166	0.006472	0.985164	MISSENSE			
576	2	ATP6AP1L	-1	5:8164419	Other	FALSE	NEUT	-0.0623	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.984995	MISSENSE			
577	0	RP11-367G	-1	6:1140094	Other	FALSE	NEUT	0.014	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.719258	MISSENSE			
578	1	ROS1	-1	6:1177939	Other	FALSE	NEUT	0.014	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	0.013605	0.016181	0.550416	MISSENSE			
579	17	MLLT4	-1	6:1680949	Other	FALSE	NEUT	0.014	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	-0.32151	0.006472	0.989337	MISSENSE			
580	0	TREM1	-1	6:4135814	Other	FALSE	NEUT	0.0071	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	-0.09042	NA	0.548525	MISSENSE			
581	0	BAI3	-1	6:6970304	Other	FALSE	NEUT	0.0071	3n Germlin	3	NA	NA	NA	NA	NA	NA	NA	0.020408	0.022654	0.991848	MISSENSE			
582	66	CD109	-1	6:7453320	Other	FALSE	NEUT	0.0071	3n Germlin	3	NA	NA	NA	NA	NA	NA	NA	0.006472	0.981832	MISSENSE				
583	1	PRSS35	-1	6:8429101	Other	FALSE	NEUT	0.014	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	0.003236	0.562444	MISSENSE			
584	0	GJA10	-1	6:9066203	Other	FALSE	NEUT	0.014	2n Germlin	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.577581	MISSENSE			
585	0	GPR30, C7orf1,1	-1	7:1098931	Other	FALSE	HETD	-0.2903	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.172095	MISSENSE			
586	3	PTPRZ1	-1	7:1214791	Other	FALSE	NEUT	-0.0083	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	-0.07374	0.006803	0.016181	0.174696	MISSENSE		
587	0	PLXNA4	-1	7:1315100	Other	FALSE	NEUT	-0.0618	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.016181	0.685618	MISSENSE		
588	0	DENND2A	-1	7:1399018	Other	FALSE	NEUT	-0.0618	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.009709	0.172534	MISSENSE		
589	33	STK17A	-1	7:4362562	Other	FALSE	NEUT	-0.0523	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.40907	MISSENSE			
590	0	NPCL1L	-1	7:4451960	Other	FALSE	NEUT	-0.0523	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.009709	0.17212	MISSENSE		
591	29	TMED4	-1	7:4458565	Other	FALSE	NEUT	-0.0523	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.238505	MISSENSE			
592	31	RNF216	-1	7:5727219	Other	FALSE	NEUT	-0.0454	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.009709	0.360683	MISSENSE		
593	0	CSMD3	-1	8:1134229	Other	FALSE	GAIN	0.3602	6n monoal	6	NA	NA	NA	NA	NA	NA	NA	0.013605	0.061489	0.172605	MISSENSE			
594	4	LRRC6	-1	8:1336537	Other	FALSE	GAIN	0.3602	6n monoal	6	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.003236	0.705096	MISSENSE		
595	1	RHOBTB2	-1	8:2292073	Other	FALSE	HETD	-0.2549	Hemizygous	1	NA	NA	NA	NA	NA	NA	NA	-0.19374	0.003236	0.384678	MISSENSE			
596	171	ADAM9	-1	8:3903237	Other	FALSE	AMP	0.6943	6n monoal	6	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.003236	0.23885	MISSENSE		
597	0	SLC7A13	-1	8:8729575	Other	FALSE	GAIN	0.3885	6n monoal	6	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.172704	MISSENSE			
598	9	SMC2	-1	9:1059412	Other	FALSE	NEUT	-0.0966	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	-0.0831	0.012945	0.471596	MISSENSE			
599	0	AKNA	-1	9:1161437	Other	FALSE	NEUT	-0.0966	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.016181	0.173372	MISSENSE		
600	0	FAM73B	-1	9:1308520	Other	FALSE	NEUT	-0.0966	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.473834	MISSENSE			
601	0	PNPLA7	-1	9:1395579	Other	FALSE	NEUT	-0.0966	2n Germlin	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.171515	MISSENSE			
602	1	S1PR3	-1	9:9080597	Other	FALSE	NEUT	-0.0966	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	-0.35595	NA	0.006472	0.46808	MISSENSE		
603	5	ACSL4	-1	X:1088112	Other	FALSE	NEUT	-0.0823	NA	NA	NA	NA	NA	NA	NA	NA	NA	-1.12353	NA	0.003236	NA	MISSENSE		
604	0	RP13-102H	-1	X:1300481	Other	FALSE	NEUT	-0.0823	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE		
605	2	SCML2	-1	X:1825204	Other	FALSE	NEUT	-0.1001	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE		
606	0	CNKSR2	-1	X:2135461	Other	FALSE	NEUT	-0.1001	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE		
607	0	BCOR	-1	X:3981671	Other	FALSE	NEUT	-0.1001	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0.08842	NA	0.006472	NA	MISSENSE		
608	13	UTX	-1	X:4483470	Other	FALSE	NEUT	-0.1001	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE		
609	0	KIF4A	-1	X:6948052	Other	FALSE	NEUT	-0.0823	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.012945	NA	MISSENSE		
610	36	ABC87	-1	X:7420586	Other	FALSE	NEUT	-0.0823	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0.05067	0.003236	NA	MISSENSE			
611	0	P2RY10	-1	X:7810308	Other	FALSE	NEUT	-0.0823	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0.24735	0.006472	NA	MISSENSE			
612	23	MPP7	-1	10:283830	Basal	FALSE	GAIN	0.2501	6n balance	6	0.6071	HET	HET	0.6071	AMP	0.4231	NA	NA	0.003236	0.474943	MISSENSE			
613	4	KIAA1324	-1	11:1095421	Basal	FALSE	NEUT	0.0446	4n balance	4	0.6087	HET	HET	0.6087	GAIN	0.1693	NA	NA	0.006472	0.848391	MISSENSE			
614	81	S100A16	-1	11:1518471	Basal	FALSE	GAIN	0.2889	6n non-mo	6	0.7273	LOH	LOH	0.7273	AMP	0.6198	NA	NA	NA	0.839294	MISSENSE			
615	9	KIF21A	-1	12:380202	Basal	FALSE	GAIN	0.4227	6n monoal	6	0.7556	LOH	LOH	0.7556	AMP	0.7025	NA	NA	0.012945	0.573806	TRUNCATING			
616	0	ADAMTS20	-1	12:420566	Basal	FALSE	NEUT	-0.0177	3n duplicat	3	0.6136	HET	HET	0.6136	NEUT	-0.0386	NA	0.020408	0.022654	0.171821	MISSENSE			
617	18	SFN	-1	12:706239	Basal	FALSE	HETD	-0.2153	Normal (A)	2	0.6111	HET	HET	0.6111	HETD	-0.1762	-0.98709	NA	NA	0.834395	MISSENSE			
618	63	TMPO	-1	12:974456	Basal	FALSE	HETD	-0.2202	Normal (A)	2	0.6061	HET	HET	0.6061	HETD	-0.2431	NA	NA	0.009709	0.853631	MISSENSE			
619	32</																							

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ	
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type			
623	0	SCNN1G		1:16:231319	Basal	FALSE	HETD	-0.3681	2n Somatic	2	0.7143	DLOH	DLOH	0.7143	HETD	-0.1875	-0.07191	NA	0.006472	0.237448	MISSENSE			
624	48	E2F4		1:16:657889	Basal	FALSE	NEUT	0.0199	3n Germinal	3	0.7297	LOH	LOH	0.7297	GAIN	0.1861	-0.27996	NA	NA	0.238141	MISSENSE			
625	0	CDYL2		-1:16:792764	Basal	FALSE	NEUT	-0.0116	3n Somatic	3	0.75	NLOH	NLOH	0.75	NEUT	0.067	NA	NA	NA	0.241367	TRUNCATING			
626	0	GRIN2A		-1:16:976587	Basal	FALSE	GAIN	0.1994	5n non-mo	5	0.6129	HET	HET	0.6129	AMP	0.4024	-0.87274	NA	0.009709	0.178665	MISSENSE			
627	33	PPARBP		-1:17:348179	Basal	FALSE	NEUT	-0.0014	3n Somatic	3	0.7413	NLOH	NLOH	0.7413	NEUT	0.0846	NA	NA	NA	1	MISSENSE			
628	23	RAD51C		1:17:541420	Basal	FALSE	NEUT	0.1168	5n Somatic	5	0.78	LOH	LOH	0.78	GAIN	0.2789	-0.02938	NA	NA	0.471879	TRUNCATING			
629	1	ST6GALNA		1:17:655210	Basal	FALSE	NEUT	0.0176	4n Germinal	4	0.6087	HET	HET	0.6087	GAIN	0.1419	-1.11069	NA	0.009709	0.405898	MISSENSE			
630	0	ASGR2		-1:17:695131	Basal	FALSE	NEUT	-0.0666	3n Somatic	3	0.75	LOH	LOH	0.75	GAIN	0.2393	NA	NA	0.003236	0.468567	MISSENSE			
631	0	OTOP2		1:17:704385	Basal	FALSE	NEUT	0.0692	4n Somatic	4	0.7778	LOH	LOH	0.7778	GAIN	0.2408	NA	NA	0.009709	0.234484	MISSENSE			
632	204	TP53		-1:17:751778	Basal	FALSE	NEUT	-0.0666	3n Somatic	3	0.7143	NLOH	NLOH	0.7143	NEUT	0.0605	-1.75605	0.306122	0.812298	0.238849	MISSENSE			
633	1	SLC25A35		-1:17:813538	Basal	FALSE	NEUT	-0.0666	3n Somatic	3	0.7353	NLOH	NLOH	0.7353	NEUT	-0.0236	NA	NA	NA	0.24259	MISSENSE			
634	1	LPIN2		1:18:220852	Basal	FALSE	NEUT	0.0176	5n non-mo	5	0.6111	HET	HET	0.6111	GAIN	0.1377	NA	NA	0.006472	0.471536	TRUNCATING			
635	4	FAM49A		-1:2:1660681	Basal	FALSE	NEUT	-0.0691	3n duplicat	3	0.625	HET	HET	0.625	NEUT	0.0026	NA	NA	NA	0.171831	TRUNCATING			
636	0	NPY2R		1:4:1563549	Basal	FALSE	NEUT	-0.0675	2n Somatic	2	0.7143	NLOH	NLOH	0.7143	NEUT	-0.0524	-0.36251	NA	NA	0.383037	MISSENSE			
637	49	LRPA1		-1:4:3487696	Basal	FALSE	HETD	-0.343	Hemizygou	1	0.6875	DLOH	DLOH	0.6875	HETD	-0.3089	-0.14714	NA	0.003236	0.474654	MISSENSE			
638	0	CYT1L		-1:4:5069489	Basal	FALSE	HETD	-0.343	Hemizygou	1	0.6522	DLOH	DLOH	0.6522	HOMD	-0.3788	NA	NA	NA	0.839665	MISSENSE			
639	0	SPATA18		1:4:5262313	Basal	FALSE	HETD	-0.331	2n Germinal	2	0.6875	DLOH	DLOH	0.6875	HETD	-0.2295	NA	NA	0.006472	0.172553	MISSENSE			
640	0	ADAMTS12		-1:5:3391706	Basal	FALSE	NEUT	-0.1208	3n duplicat	3	0.6324	HET	HET	0.6324	NEUT	-0.0964	NA	NA	0.012945	0.365138	MISSENSE			
641	3	HIVEP2		-1:6:1431161	Basal	FALSE	NEUT	-0.0326	3n duplicat	3	0.6111	HET	HET	0.6111	NEUT	-9.00E-04	NA	NA	0.009709	0.639711	MISSENSE			
642	0	FAM65B		-1:6:2495888	Basal	FALSE	NEUT	-0.047	3n duplicat	3	0.6111	HET	HET	0.6111	NEUT	0.0031	NA	NA	0.003236	0.702632	MISSENSE			
643	0	LAMB4		-1:7:1075436	Basal	FALSE	NEUT	0.0693	4n balance	4	0.6111	HET	HET	0.6111	GAIN	0.1862	-0.55342	NA	0.012945	0.238938	TRUNCATING			
644	0	GRM8		-1:7:1259603	Basal	FALSE	GAIN	0.3916	6n non-mo	6	0.6341	ASCNA	ASCNA	0.6341	AMP	0.5585	-0.35913	NA	0.012945	0.845375	MISSENSE			
645	0	KIAA1324L		-1:7:8640709	Basal	FALSE	NEUT	0.0744	4n Germinal	4	NA	NA	NA	NA	NEUT	0.0857	NA	NA	0.019417	0.70801	MISSENSE			
646	2	EFRA3A		1:8:1330846	Basal	FALSE	NEUT	-0.0043	3n Somatic	3	0.6858	LOH	LOH	0.6858	GAIN	0.1929	NA	NA	0.009709	0.169688	MISSENSE			
647	0	FAM135B		-1:8:1392372	Basal	FALSE	NEUT	-0.0579	3n Somatic	3	0.7419	NLOH	NLOH	0.7419	NEUT	0.0304	NA	NA	0.022654	0.477529	MISSENSE			
648	0	GPR112		1:X:1353075	Basal	FALSE	HETD	-0.2453	NA	NA	NA	NA	NA	NA	0.622	HETD	-0.1825	NA	NA	0.016181	NA	MISSENSE		
649	0	PPEF1		1:X:1873451	Basal	FALSE	NEUT	0.0297	NA	NA	NA	NA	NA	NA	0.6316	NEUT	0.0366	NA	NA	NA	NA	MISSENSE		
650	0	FAM47A		-1:X:3405807	Basal	FALSE	NEUT	0.0297	NA	NA	NA	NA	NA	NA	0.625	GAIN	0.1324	NA	NA	0.012945	NA	MISSENSE		
651	0	AKAP4		-1:X:4984825	Basal	FALSE	NEUT	0.0297	NA	NA	NA	NA	LOH	0.8286	GAIN	0.1767	NA	NA	0.003236	NA	MISSENSE			
652	0	CUBN		-1:10:172116	Basal	FALSE	HETD	-0.2664	3n Somatic	3	0.6471	HET	HET	0.6471	HETD	-0.3186	-0.0355	NA	0.029126	NA	MISSENSE			
653	0	MYO3A		1:10:265221	Basal	FALSE	HETD	-0.247	3n duplicat	3	0.6667	HET	HET	0.6667	HETD	-0.3186	NA	0.006803	0.009709	NA	TRUNCATING			
654	9	ARHGGEF11		-1:1:1551879	Basal	FALSE	GAIN	0.2713	6n non-mo	6	0.6667	ASCNA	ASCNA	0.6667	AMP	0.4518	-0.0762	NA	0.009709	NA	TRUNCATING			
655	29	RBBP8		1:18:188601	Basal	FALSE	HETD	-0.2502	3n duplicat	3	0.6667	HET	HET	0.6667	HETD	-0.2896	-0.01675	NA	0.003236	NA	MISSENSE			
656	18	KIAA1012		-1:18:276835	Basal	FALSE	HETD	-0.2512	3n duplicat	3	0.6667	HET	HET	0.6667	HETD	-0.3061	NA	NA	0.016181	NA	MISSENSE			
657	124	SMARCA4		1:19:109995	Basal	FALSE	GAIN	0.2366	6n non-mo	6	0.697	HET	HET	0.697	AMP	0.4626	-0.17766	NA	0.019417	NA	MISSENSE			
658	1	ZNF616		-1:19:573189	Basal	FALSE	NEUT	-0.0805	4n balance	4	0.6429	HET	HET	0.6429	NEUT	-0.0789	NA	NA	NA	NA	MISSENSE			
659	0	NFATC2		-1:20:495239	Basal	FALSE	GAIN	0.3295	6n non-mo	6	0.7143	ASCNA	ASCNA	0.7143	AMP	0.5728	-0.51793	NA	0.006472	NA	MISSENSE			
660	0	KRTAP6-1		-1:21:309079	Basal	FALSE	GAIN	0.2063	5n monoal	5	0.7143	HET	HET	0.7143	GAIN	0.1949	NA	NA	NA	NA	MISSENSE			
661	0	ATR		-1:3:1437066	Basal	FALSE	NEUT	-0.0103	4n balance	4	0.8	NLOH	NLOH	0.8	NEUT	0.0141	-0.12269	0.006803	0.006472	NA	MISSENSE			
662	8	RAD54L2		1:3:5164462	Basal	FALSE	NEUT	-0.0651	4n balance	4	0.625	HET	HET	0.625	NEUT	-0.0292	NA	NA	0.009709	NA	MISSENSE			
663	0	ADAMTS9		-1:3:6450178	Basal	FALSE	NEUT	-0.0386	4n balance	4	0.6333	HET	HET	0.6333	NEUT	-0.0292	NA	NA	0.006472	NA	MISSENSE			
664	5	FOXPI		-1:3:7110976	Basal	FALSE	NEUT	-0.0386	4n balance	4	0.6333	HET	HET	0.6333	NEUT	-0.0292	NA	NA	NA	NA	MISSENSE			
665	0	ROBO2		1:3:7775389	Basal	FALSE	NEUT	-0.0386	4n balance	4	0.6364	HET	HET	0.6364	NEUT	-0.0738	-0.04312	NA	0.003236	NA	MISSENSE			
666	7	ZNF354B		1:5:1782422	Basal	FALSE	HOMD	-0.537	2n Somatic	2	0.85	DLOH	DLOH	0.85	HOMD	-0.6499	NA	NA	0.006472	NA	MISSENSE			
667	3	RP11-63L7		-1:6:8987365	Basal	FALSE	NEUT	0.124	5n non-mo	5	0.6364	HET	HET	0.6364	GAIN	0.1788	NA	NA	NA	NA	MISSENSE			
668	11	C1orf85,TN-1,1		1:15:45223	Other	FALSE	NEUT	0.1267	4n monoal	4	0.619	HET	NA	NA	NA	NA	NA	NA	NA	0.358376	MISSENSE			
669	7	RNF2		1:1:1833287	Other	FALSE	NEUT	0.1233	5n non-mo	5	0.619	HET	NA	NA	NA	NA	NA	NA	NA	NA	0.473233	MISSENSE		
670	186	USP5		1:12:684192	Other	FALSE	AMP	0.642	6n monoal	6	0.7414	NLOH	NA	NA	NA	NA	NA	NA	NA	NA	0.703097	MISSENSE		
671	0	NPAS3		1:14:333391	Other	FALSE	HETD	-0.2384	Normal (A)	2	0.5816	HET	NA	NA	NA	NA	NA	NA	0.003236	0.837813	MISSENSE			
672	1	LPO		1:17:536985	Other	FALSE	HETD	-0.1923	2n Somatic	2	0.7809	NLOH	NA	NA	NA	NA	-0.0589	NA	0.003236	0.838945	MISSENSE			
673	0	ZNF311		-1:6:2907228	Other	FALSE	NEUT	0.08	4n Germinal	4	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.57913	MISSENSE			
674	417	HSPA8		-1:11:122436	Other	FALSE	NEUT	-0.0291	3n duplicat	3	0.6667	HET	HET	0.6667	NEUT	-0.0159	-0.44389	0.020408	NA	0.708137	MISSENSE			
675	5	TRAF6		-1:11:364683	Other	FALSE	NEUT	-0.023	3n Germinal	3	0.7303	NLOH	NLOH	0.7303	NEUT	-0.0045	-0.64886	NA	0.003236	0.236834	MISSENSE			
676	4	UACA		-1:15:687482	Other	FALSE	HETD	-0.3822	2n Somatic	2	0.9333	DLOH	DLOH	0.9333	HETD	-0.4081	NA	NA	0.006472	0.703069	MISSENSE			
677	0	PSG5		-1:19:483712	Other	FALSE	GAIN	0.1828	4n balance	4	0.6154	HET	HET	0.6154	GAIN	0.2461	NA	NA	NA	0.239075	MISSENSE			
678	0	NLRP9		-1:19:609358	Other	FALSE	NEUT	0.1103	4n balance	4	0.625	HET	HET	0.625	GAIN	0.2242	NA	NA	0.006472	0.252989	MISSENSE			
679	7	ZSWIM1		1:20:439455	Other	FALSE	NEUT	0.1176	4n balance	4	0.619	HET	HET	0.619	GAIN	0.268	NA	NA	NA	0.29109	MISSENSE			
680	28	YPEL1		-1:22:203876	Other	FALSE	HETD	-0.3238	2n Somatic	2	0.7143	DLOH	DLOH	0.7143	HETD	-0.4061	NA	NA	NA	0.834615	MISSENSE			
681	36	PIK3CA		1:3:1804345	Other	FALSE	NEUT	0.0537	3n duplicat	3	0.6667	HET	HET	0.6667	NEUT	0.054	-0.89988	0.047619	0.016181	0.173438	MISSENSE			
682	0	FGA		-1:4:1557248	Other	FALSE	HETD	-0.2284	2n Somatic	2	0.8	DLOH	DLOH	0.8	HETD	-0.2973	-0.08207	NA	0.006472	0.708979	MISSENSE			
683	19	GRIA2		1:4:1585034	Other	FALSE	HETD	-0.2213	2n Somatic	2	0.8	DLOH	DLOH	0.8	HETD	-0.2973	-0.19506	0.013605	0.003236	0.849445	MISSENSE			
684	34	DIAPH1		-1:5:1409439																				

1	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
Non.ref.RN	Ens54Gene	Strand	primer	PAM50	Splice.site	HMMDos	HMMDos	OncoSNP	OncoSNP	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh	apolloh
692	0	NELL1	1:11:207617	Basal	FALSE	NEUT	-0.0613	3n duplicat	3	0.6471	HET	HET	0.6471	NEUT	-0.061	NA	NA	0.006472	NA	MISSENSE			
693	0	AADACL3	1:12:1270850	Basal	FALSE	HETD	-0.303	2n Somatic	2	0.7826	DLOH	DLOH	0.7826	HETD	-0.401	NA	NA	NA	NA	MISSENSE			
694	1	UBAP2L	1:1:1524931	Basal	FALSE	GAIN	0.3742	6n Germilin	6	0.9	LOH	LOH	0.9	AMP	0.6266	NA	NA	0.003236	NA	MISSENSE			
695	0	CLCNKA	1:1:1623226	Basal	FALSE	HETD	-0.303	2n Somatic	2	0.7917	DLOH	DLOH	0.7917	HETD	-0.3967	NA	NA	0.003236	NA	MISSENSE			
696	0	PAPPA2	1:1:1748312	Basal	FALSE	GAIN	0.4141	NA	NA	0.9	LOH	LOH	0.9	AMP	0.6363	-0.01033	0.020408	0.022654	NA	MISSENSE			
697	0	SBF2	-1:11:997638	Basal	FALSE	HETD	-0.2867	3n Somatic	2	0.7857	DLOH	DLOH	0.7857	HETD	-0.3614	NA	NA	0.003236	NA	TRUNCATING			
698	0	PLA2G2C	-1:1:2037412	Basal	FALSE	HETD	-0.303	2n Somatic	2	0.7857	DLOH	DLOH	0.7857	HETD	-0.3846	-0.82195	NA	NA	NA	MISSENSE			
699	0	DNAH10	1:12:122864	Basal	FALSE	NEUT	-0.1042	3n Somatic	3	0.8333	NLOH	NLOH	0.8333	NEUT	-0.105	-0.09193	NA	0.012945	NA	MISSENSE			
700	1	XPOT	1:12:631100	Basal	FALSE	NEUT	-0.079	3n duplicat	3	0.6316	HET	HET	0.6316	NEUT	-0.0888	NA	NA	0.006472	NA	MISSENSE			
701	1	CSMD2	-1:1:3380968	Basal	FALSE	NEUT	-0.0769	3n Somatic	3	0.8	NLOH	NLOH	0.8	NEUT	-0.0639	NA	NA	0.019417	NA	MISSENSE			
702	0	CKAP2	1:13:519404	Basal	FALSE	HETD	-0.2269	2n Somatic	2	0.75	DLOH	DLOH	0.75	HETD	-0.2854	NA	NA	0.003236	NA	MISSENSE			
703	0	WDR65	1:1:4341998	Basal	FALSE	GAIN	0.2766	5n Germilin	5	0.6364	HET	HET	0.6364	AMP	0.427	NA	NA	NA	NA	MISSENSE			
704	0	EML1	1:14:994454	Basal	FALSE	NEUT	-0.0662	3n Somatic	3	0.8276	NLOH	NLOH	0.8276	NEUT	-0.0743	NA	NA	0.003236	NA	TRUNCATING			
705	0	MEFV	-1:16:323424	Basal	FALSE	HETD	-0.3201	Normal (A	2	0.625	HET	HET	0.625	HETD	-0.4102	-0.04743	NA	0.003236	NA	MISSENSE			
706	0	TAT	-1:16:701677	Basal	FALSE	GAIN	0.2884	NA	NA	0.7241	ASCNA	ASCNA	0.7241	AMP	0.5503	-0.56634	NA	0.006472	NA	MISSENSE			
707	0	SMYD4	-1:17:163446	Basal	FALSE	NEUT	-0.1358	3n Somatic	3	NA	NA	NA	NA	NEUT	-0.1725	NA	NA	NA	NA	MISSENSE			
708	0	SSH2	-1:17:249837	Basal	FALSE	HETD	-0.288	2n Somatic	2	0.7895	DLOH	DLOH	0.7895	HETD	-0.386	-0.12252	NA	NA	NA	MISSENSE			
709	0	RECQL5	-1:17:711660	Basal	FALSE	GAIN	0.314	4n Germilin	4	0.875	LOH	LOH	0.875	AMP	0.4398	NA	NA	NA	NA	MISSENSE			
710	0	RNF213	1:17:759722	Basal	FALSE	NEUT	0.1413	4n Somatic	4	0.875	LOH	LOH	0.875	GAIN	0.2649	NA	NA	0.02589	NA	MISSENSE			
711	0	RNF138	1:18:279457	Basal	FALSE	NEUT	-0.0113	3n duplicat	3	0.6111	HET	HET	0.6111	NEUT	-0.0641	NA	NA	NA	NA	MISSENSE			
712	0	SLC44A3	1:1:9506568	Basal	FALSE	NEUT	-0.0259	3n duplicat	3	0.6471	HET	HET	0.6471	NEUT	-0.0192	NA	NA	NA	NA	MISSENSE			
713	0	DUSP19	2:1836685	Basal	FALSE	HETD	-0.2638	2n Somatic	2	0.7857	DLOH	DLOH	0.7857	HETD	-0.3422	-0.04019	NA	0.012945	NA	MISSENSE			
714	0	PES1	-1:22:293057	Basal	FALSE	NEUT	-0.0645	3n duplicat	3	0.6429	HET	HET	0.6429	NEUT	-0.0615	NA	NA	NA	NA	TRUNCATING			
715	0	KALRN	1:13:258759	Basal	FALSE	NEUT	0.107	4n balance	4	0.6071	HET	HET	0.6071	GAIN	0.1914	-0.43438	0.013605	0.012945	NA	MISSENSE			
716	0	AGTR1	1:13:1499420	Basal	FALSE	NEUT	0.1526	4n balance	4	0.6129	HET	HET	0.6129	GAIN	0.1972	-0.55884	NA	NA	NA	MISSENSE			
717	0	ITPR1	1:3:4684103	Basal	FALSE	NEUT	-0.0658	3n Somatic	3	0.8333	NLOH	NLOH	0.8333	NEUT	-0.0516	-0.67535	NA	0.012945	NA	MISSENSE			
718	0	FAT4	1:4:1264609	Basal	FALSE	HETD	-0.2659	2n Somatic	2	0.7778	DLOH	DLOH	0.7778	HETD	-0.3604	NA	NA	0.019417	NA	MISSENSE			
719	0	PHF17	1:4:1300027	Basal	FALSE	HETD	-0.2659	2n Somatic	2	0.7778	DLOH	DLOH	0.7778	HETD	-0.3604	NA	NA	NA	NA	MISSENSE			
720	0	FAM53A	-1:4:1613053	Basal	FALSE	HETD	-0.3028	2n Somatic	2	0.8	DLOH	DLOH	0.8	HETD	-0.4117	NA	NA	NA	NA	MISSENSE			
721	0	EBF1	-1:5:1580717	Basal	FALSE	HETD	-0.2841	Normal (A	2	0.6154	HET	HET	0.6154	HETD	-0.3578	NA	NA	0.003236	NA	MISSENSE			
722	0	CARD6	1:5:4088960	Basal	FALSE	NEUT	0.1212	4n balance	4	0.6136	HET	HET	0.6136	GAIN	0.1863	-0.04743	NA	0.006472	NA	MISSENSE			
723	0	AC094086	1:5:6103543	Basal	FALSE	HOMD	-0.5948	Hemizygou	1	0.6957	HOMD	HOMD	0.6957	HOMD	-0.7509	NA	NA	NA	NA	MISSENSE			
724	0	GMD5	-1:6:1875362	Basal	FALSE	HETD	-0.2899	2n Somatic	2	NA	NA	NA	NA	HETD	-0.3392	-0.57093	NA	NA	NA	MISSENSE			
725	0	MUC17	1:7:1004716	Basal	FALSE	NEUT	-0.0357	3n Germilin	3	NA	NA	NA	NA	HETD	-0.2594	NA	NA	0.045307	NA	MISSENSE			
726	0	RHEB	-1:7:1508127	Basal	FALSE	NEUT	0.1024	4n balance	4	0.619	HET	HET	0.619	GAIN	0.1783	-0.49763	NA	NA	NA	MISSENSE			
727	1	COL1A2	1:7:9388500	Basal	FALSE	NEUT	-0.0357	4n Germilin	4	0.6129	HET	HET	0.6129	GAIN	0.1939	-0.57512	0.020408	0.006472	NA	MISSENSE			
728	0	ABCA1	-1:9:1066220	Basal	FALSE	NEUT	-0.0483	3n duplicat	3	0.6296	HET	HET	0.6296	NEUT	-0.0374	-0.09761	0.006803	0.009709	NA	MISSENSE			
729	0	KIAA0649	9:1375182	Basal	FALSE	GAIN	0.3207	6n non-mo	6	0.6506	HET	HET	0.6506	AMP	0.4843	NA	NA	0.003236	NA	TRUNCATING			
730	0	NRK	1:X:1050397	Basal	FALSE	CNVG1	0.5721	NA	NA	NA	NA	ASCNA	0.6923	AMP	0.7024	-0.20994	NA	0.006472	NA	MISSENSE			
731	0	UBQLN2	1:X:5660826	Basal	FALSE	GAIN	0.2749	NA	NA	NA	NA	HET	0.6087	GAIN	0.2781	-0.10023	NA	0.003236	NA	MISSENSE			
732	1	SHROOM2	1:X:9824295	Basal	FALSE	NEUT	-0.0584	NA	NA	NA	NA	HET	0.6364	NEUT	-0.0651	NA	NA	0.009709	NA	MISSENSE			
733	0	SEC31B	-1:10:102239	Basal	FALSE	NEUT	-0.0115	Normal (A	2	0.6233	HET	HET	0.6233	NEUT	0.0202	-0.08609	NA	0.003236	0.110219	MISSENSE			
734	2	SEMA4G	1:10:102722	Basal	FALSE	NEUT	-0.0115	Normal (A	2	0.6233	HET	HET	0.6233	GAIN	0.1509	-0.04781	NA	NA	0.113896	MISSENSE			
735	0	HRNR	-1:1:1504582	Basal	FALSE	NEUT	-0.0068	2n Somatic	2	0.6229	HET	HET	0.6229	GAIN	0.203	NA	NA	0.003236	0.266545	MISSENSE			
736	0	NUP210L	-1:1:1523805	Basal	FALSE	NEUT	-0.0089	2n Somatic	2	0.625	HET	HET	0.625	GAIN	0.1973	NA	NA	0.009709	0.27219	MISSENSE			
737	0	DCST1	1:1:1532735	Basal	FALSE	NEUT	-0.0089	2n Somatic	2	0.9509	LOH	LOH	0.9509	GAIN	0.1973	NA	NA	0.003236	0.117425	MISSENSE			
738	0	PADI6	1:1:1759303	Basal	FALSE	NEUT	-0.0155	Normal (A	2	0.625	HET	HET	0.625	GAIN	0.2057	NA	NA	NA	0.115263	MISSENSE			
739	1	NCF2	-1:1:1818046	Basal	FALSE	GAIN	0.4174	3n duplicat	3	0.6667	ASCNA	ASCNA	0.6667	AMP	0.6077	-0.13909	NA	0.012945	0.221166	MISSENSE			
740	0	CRB1	1:1:1957133	Basal	FALSE	GAIN	0.4174	3n duplicat	3	0.6429	ASCNA	ASCNA	0.6429	AMP	0.6169	NA	NA	0.016181	0.21474	MISSENSE			
741	12	ZNF281	-1:1:1986437	Basal	FALSE	GAIN	0.4174	3n duplicat	3	0.6429	ASCNA	ASCNA	0.6429	AMP	0.6169	NA	NA	0.003236	0.132973	TRUNCATING			
742	1	PPPIA4	1:1:2012961	Basal	FALSE	GAIN	0.2653	3n duplicat	3	0.6538	ASCNA	ASCNA	0.6538	AMP	0.6169	NA	NA	0.012945	0.287198	MISSENSE			
743	36	DHX37	-1:12:124036	Basal	FALSE	NEUT	-0.0372	Normal (A	2	0.6207	HET	HET	0.6207	GAIN	0.2374	NA	NA	NA	0.749908	MISSENSE			
744	0	RIMBP2	-1:12:129501	Basal	FALSE	NEUT	-0.0372	Normal (A	2	0.63	HET	HET	0.63	GAIN	0.1337	NA	NA	0.009709	0.285579	MISSENSE			
745	0	C1orf65	1:1:2216350	Basal	FALSE	GAIN	0.2741	3n Somatic	3	0.9333	LOH	LOH	0.9333	AMP	0.6442	NA	NA	NA	0.462186	MISSENSE			
746	5	IL22RA1	-1:1:2432729	Basal	FALSE	NEUT	-0.0155	Normal (A	2	0.6316	HET	HET	0.6316	GAIN	0.2057	-0.11197	NA	NA	0.283187	MISSENSE			
747	5	MAP3K12	-1:12:521671	Basal	FALSE	NEUT	0.0076	2n Somatic	2	0.9333	LOH	LOH	0.9333	GAIN	0.1949	-0.36952	NA	0.003236	0.117331	TRUNCATING			
748	0	AL391382	-1:13:182914	Basal	FALSE	GAIN	0.435	4n balance	4	0.6957	ASCNA	ASCNA	0.6957	AMP	0.5777	NA	NA	NA	0.464581	MISSENSE			
749	58	ZMYM6	-1:1:3524693	Basal	FALSE	NEUT	-0.0155	2n Somatic	2	0.6296	HET	HET	0.6296	GAIN	0.1953	NA	NA	0.009709	0.369837	MISSENSE			
750	5	POMGNT1	-1:1:4643187	Basal	FALSE	NEUT	-0.0155	Normal (A	2	0.625	HET	HET	0.625	GAIN	0.1858	-0.00311	NA	0.003236	0.599747	MISSENSE			
751	5	CASC5	1:15:387020	Basal	FALSE	HETD	-0.4239	Hemizygou	1	0.8824	DLOH	DLOH	0.8824	HETD	-0.4621	-0.04843	NA	NA	0.585758	MISSENSE			
752	41	TUN2	1:15:608412	Basal	FALSE	NEUT	-0.0095	Normal (A	2	0.619	HET	HET	0.619	GAIN	0.1922	-0.0872	NA	0.012945	0.117914	MISSENSE			
753	57	ZNF609	1:15:627552	Basal	FALSE	NEUT	-0.0095	Normal (A	2	0.619	HET	HET	0.619	GAIN	0.1922	NA	NA	0.003236	0.118475	MISSENSE			
754</																							

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
761	0	BPL13	-1	20:310934	Basal	FALSE	HETD	-0.4318	Hemizygous	1	0.8571	DLOH	DLOH	0.8571	HETD	-0.4631	NA	NA	0.003236	0.464344	TRUNCATING		
762	6	TMEM177	-1	2:1201548	Basal	FALSE	NEUT	-0.0166	Normal (A)	2	0.9338	LOH	LOH	0.9338	GAIN	0.2017	NA	NA	0.003236	0.597858	MISSENSE		
763	0	GCG	-1	2:1627100	Basal	FALSE	NEUT	0.0394	Normal (A)	2	0.6316	HET	HET	0.6316	GAIN	0.1601	-0.04473	NA	NA	0.112407	MISSENSE		
764	0	TTN	-1	2:1792251	Basal	FALSE	NEUT	0.0394	Normal (A)	2	0.6154	HET	HET	0.6154	GAIN	0.1351	-0.04924	NA	0.20712	0.116555	MISSENSE		
765	0	APOB	-1	2:2108486	Basal	FALSE	HETD	-0.4012	Hemizygous	1	0.8824	DLOH	DLOH	0.8824	HETD	-0.4491	-0.11816	NA	0.035599	0.280331	MISSENSE		
766	0	CEK1	-1	22:154533	Basal	FALSE	NEUT	-0.0153	2n Somatic	2	0.9	LOH	LOH	0.9	GAIN	0.1931	NA	NA	NA	0.757693	MISSENSE		
767	1	SLC25A18	-1	22:164438	Basal	FALSE	NEUT	-0.0153	2n Somatic	2	0.9259	LOH	LOH	0.9259	GAIN	0.1931	-0.0048	NA	NA	0.354246	MISSENSE		
768	17	MXD1	-1	2:7001884	Basal	FALSE	NEUT	0.0092	Normal (A)	2	0.6207	HET	HET	0.6207	GAIN	0.1761	-0.08651	NA	NA	0.212999	MISSENSE		
769	13	WDR54	-1	2:7450292	Basal	FALSE	NEUT	0.0092	2n Somatic	2	0.6154	HET	HET	0.6154	GAIN	0.1555	NA	NA	NA	0.206691	MISSENSE		
770	66	KIAA1310	-1	2:9664890	Basal	FALSE	GAIN	0.2701	3n duplicat	3	0.6364	ASCNA	ASCNA	0.6364	AMP	0.6685	NA	NA	NA	0.226997	MISSENSE		
771	83	TBC1D23	-1	3:1014966	Basal	FALSE	NEUT	0.0157	Normal (A)	2	0.6154	HET	HET	0.6154	GAIN	0.1418	NA	NA	0.003236	0.45737	MISSENSE		
772	4	PARP14	-1	3:1239201	Basal	FALSE	NEUT	-0.0036	Normal (A)	2	0.625	HET	HET	0.625	GAIN	0.1553	-0.17594	NA	0.006472	0.107334	MISSENSE		
773	0	NLGN1	-1	3:1754814	Basal	FALSE	NEUT	0.0193	Normal (A)	2	0.625	HET	HET	0.625	GAIN	0.1577	-0.04601	NA	0.003236	0.107963	MISSENSE		
774	0	PYDC2	-1	3:1926617	Basal	FALSE	NEUT	0.023	Normal (A)	2	0.6154	HET	HET	0.6154	GAIN	0.1493	NA	NA	NA	0.465789	MISSENSE		
775	92	NCBP2	-1	3:1981504	Basal	FALSE	NEUT	-0.011	Normal (A)	2	0.6316	HET	HET	0.6316	GAIN	0.2384	-0.21987	NA	NA	0.144789	MISSENSE		
776	57	SETD5	-1	3:9451057	Basal	FALSE	HETD	-0.4329	Hemizygous	1	0.875	DLOH	DLOH	0.875	HETD	-0.4955	NA	NA	0.012945	0.290848	MISSENSE		
777	44	FAM44A	-1	4:1322529	Basal	FALSE	NEUT	-0.0041	Normal (A)	2	0.6364	HET	HET	0.6364	GAIN	0.1362	NA	NA	NA	0.220394	MISSENSE		
778	2	PCDH18	-1	4:1386709	Basal	FALSE	HETD	-0.4218	Hemizygous	1	0.875	DLOH	DLOH	0.875	HETD	-0.5151	-0.1256	NA	NA	0.227357	MISSENSE		
779	9	PGM2	-1	4:3752819	Basal	FALSE	NEUT	-0.0041	Normal (A)	2	0.619	HET	HET	0.619	GAIN	0.1805	-0.51721	NA	NA	0.341162	TRUNCATING		
780	333	NSUN2	-1	5:6676360	Basal	FALSE	HETD	-0.4791	Hemizygous	1	0.8629	DLOH	DLOH	0.8629	HETD	-0.5579	-0.03833	NA	0.003236	0.216364	MISSENSE		
781	0	GPRC6A	-1	6:1172208	Basal	FALSE	GAIN	0.3071	3n duplicat	3	0.6522	ASCNA	ASCNA	0.6522	AMP	0.5835	NA	NA	0.012945	1	MISSENSE		
782	147	CDC5L	-1	6:4450025	Basal	FALSE	HETD	-0.4466	Hemizygous	1	0.875	DLOH	DLOH	0.875	HETD	-0.4913	-0.06116	NA	0.003236	0.32109	MISSENSE		
783	387	DSP	-1	6:7526744	Basal	FALSE	HETD	-0.433	Hemizygous	1	0.875	DLOH	DLOH	0.875	HETD	-0.4733	-0.1131	0.034014	0.003236	0.557963	MISSENSE		
784	0	MUC17	-1	7:1004733	Basal	FALSE	HETD	-0.4429	Hemizygous	1	0.8983	DLOH	DLOH	0.8983	HETD	-0.3679	NA	NA	0.045307	0.390147	MISSENSE		
785	2	SLC29A4	-1	7:5293949	Basal	FALSE	NEUT	0.0339	Normal (A)	2	0.6364	HET	HET	0.6364	GAIN	0.2011	NA	NA	NA	0.326	MISSENSE		
786	7	CYTH3	-1	7:6196651	Basal	FALSE	NEUT	0.0339	Normal (A)	2	0.6364	HET	HET	0.6364	GAIN	0.2011	-0.32761	NA	NA	0.56385	MISSENSE		
787	33	ZNF16	-1	8:1461277	Basal	FALSE	NEUT	-0.0225	Normal (A)	2	0.6364	HET	HET	0.6364	GAIN	0.2508	NA	NA	0.012945	0.336709	MISSENSE		
788	9	ZNF16	-1	8:1461423	Basal	FALSE	NEUT	-0.0225	Normal (A)	2	0.6364	HET	HET	0.6364	GAIN	0.2508	NA	NA	0.012945	0.333634	MISSENSE		
789	3	ANK1	-1	8:4169966	Basal	FALSE	NEUT	0.0882	3n duplicat	3	0.6571	ASCNA	ASCNA	0.6571	AMP	0.5931	NA	0.013605	0.009709	0.561867	MISSENSE		
790	11	ZFP37	-1	9:1148517	Basal	FALSE	NEUT	0.0057	2n Somatic	2	0.9286	LOH	LOH	0.9286	GAIN	0.118	NA	NA	0.003236	0.428053	MISSENSE		
791	19	SETX	-1	9:1342115	Basal	FALSE	HETD	-0.3971	Hemizygous	1	NA	NA	NA	NA	GAIN	0.0601	NA	NA	0.006472	0.56653	MISSENSE		
792	22	KIAA1529	-1	9:9917374	Basal	FALSE	NEUT	0.0057	2n Somatic	2	0.913	LOH	LOH	0.913	GAIN	0.1904	NA	NA	0.006472	0.563122	TRUNCATING		
793	0	NXF2B	-1	X:1015111	Basal	FALSE	HETD	-0.4423	NA	NA	NA	NA	DLOH	0.8824	HOMD	-0.6411	NA	NA	NA	NA	MISSENSE		
794	0	KIAA1210	-1	X:1181415	Basal	FALSE	HETD	-0.4423	NA	NA	NA	NA	DLOH	0.8485	HETD	-0.4762	NA	NA	0.016181	NA	MISSENSE		
795	2	SMPX	-1	X:2166542	Basal	FALSE	GAIN	0.3088	NA	NA	NA	NA	ASCNA	0.6	AMP	0.5828	NA	NA	NA	NA	MISSENSE		
796	0	RBM10	-1	X:4691940	Basal	FALSE	NEUT	-0.0215	NA	NA	NA	NA	HET	0.6364	GAIN	0.1569	NA	NA	0.003236	NA	MISSENSE		
797	7	IQSEC2	-1	X:5329410	Basal	FALSE	NEUT	-0.0215	NA	NA	NA	NA	HET	0.6667	NEUT	0.043	-0.28584	NA	0.009709	NA	MISSENSE		
798	0	ANKRD26	-1	X:10273754	Basal	FALSE	NEUT	0.0511	Normal (A)	2	0.5789	HET	NA	NA	NA	NA	NA	NA	0.003236	0.563346	MISSENSE		
799	0	UBAP2L	-1	1:1524737	Basal	FALSE	GAIN	0.5453	6n non-mo	6	0.6944	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.43002	MISSENSE		
800	0	NPTN	-1	15:716412	Basal	FALSE	HETD	-0.2348	Normal (A)	2	0.5882	HET	NA	NA	NA	NA	NA	NA	NA	0.343408	MISSENSE		
801	0	C10orf90	-1	10:128182	Basal	FALSE	NEUT	-0.0828	4n Somatic	4	0.8235	NLOH	NLOH	0.8235	NEUT	-0.0131	NA	NA	NA	0.360315	MISSENSE		
802	2	PTEN	-1	10:896827	Basal	FALSE	NEUT	-0.0828	4n Somatic	4	0.8261	NLOH	NLOH	0.8261	NEUT	-0.0128	-0.84748	0.251701	0.006472	0.562793	MISSENSE		
803	35	PTEN	-1	10:897075	Basal	FALSE	NEUT	-0.0828	4n Somatic	4	0.8261	NLOH	NLOH	0.8261	NEUT	-0.0128	-0.84748	0.251701	0.006472	0.710876	MISSENSE		
804	0	OVC1	-1	12:294883	Basal	FALSE	NEUT	0.0817	5n non-mo	5	0.6452	HET	HET	0.6452	GAIN	0.1537	NA	NA	0.009709	0.561996	MISSENSE		
805	0	AL109766	-1	14:436593	Basal	FALSE	NEUT	0.0255	5n non-mo	5	0.6	HET	HET	0.6	NEUT	0.0629	NA	NA	NA	0.564	MISSENSE		
806	0	CNTNAP4	-1	16:750811	Basal	FALSE	HETD	-0.2131	3n Somatic	3	0.8	DLOH	DLOH	0.8	HETD	-0.232	NA	NA	0.006472	0.391394	MISSENSE		
807	0	KRT28	-1	17:362022	Basal	FALSE	NEUT	0.0562	5n Germli	5	0.8571	LOH	LOH	0.8571	GAIN	0.2253	NA	NA	0.003236	0.431004	MISSENSE		
808	86	TP53	-1	17:751888	Basal	FALSE	NEUT	-0.1254	3n Somatic	3	0.84	NLOH	NLOH	0.84	NEUT	-0.1158	-1.13499	0.306122	0.812298	0.334484	MISSENSE		
809	50	OSBPL1A	-1	18:199990	Basal	FALSE	NEUT	-0.0478	4n monoal	4	0.7059	NLOH	NLOH	0.7059	NEUT	-0.0151	NA	NA	0.012945	0.562524	MISSENSE		
810	1	TSHZ3	-1	19:364607	Basal	FALSE	AMP	0.672	6n monoal	6	0.6667	ASCNA	ASCNA	0.6667	HLAMP	1.1078	NA	NA	0.012945	0.33833	MISSENSE		
811	1	KLHL29	-1	2:2376815	Basal	FALSE	NEUT	-0.0375	4n monoal	4	0.6207	HET	HET	0.6207	NEUT	0.029	NA	NA	0.003236	0.326016	MISSENSE		
812	16	IFT122	-1	3:1306936	Basal	FALSE	GAIN	0.2795	6n non-mo	6	0.6296	ASCNA	ASCNA	0.6296	AMP	0.4946	NA	NA	0.003236	0.338204	MISSENSE		
813	22	ATR	-1	3:1436608	Basal	FALSE	GAIN	0.2938	6n non-mo	6	0.6	ASCNA	ASCNA	0.6	AMP	0.4457	-0.17946	0.006803	0.006472	0.563613	MISSENSE		
814	69	TCERG1	-1	5:1458667	Basal	FALSE	HETD	-0.4369	2n Somatic	2	0.75	DLOH	DLOH	0.75	HOMD	-0.507	-0.08187	NA	NA	0.56249	MISSENSE		
815	0	CNR1	-1	6:8891138	Basal	FALSE	GAIN	0.3269	6n balance	6	0.6291	ASCNA	ASCNA	0.6291	AMP	0.4732	-0.15972	NA	NA	0.551954	MISSENSE		
816	0	FCN2	-1	9:1369188	Basal	FALSE	HETD	-0.2231	3n Somatic	3	0.8194	NLOH	NLOH	0.8194	HETD	-0.1934	NA	NA	NA	0.562066	MISSENSE		
817	5	SETBP1	-1	18:407858	Basal	FALSE	NEUT	0.0227	4n Germli	4	0.5625	HET	NA	NA	NA	NA	NA	NA	NA	0.563112	MISSENSE		
818	0	COL6A3	-1	2:2379422	Basal	FALSE	HETD	-0.1872	NA	NA	0.6471	NLOH	NA	NA	NA	NA	-0.16807	0.027211	0.02589	NA	MISSENSE		
819	30	MTDH	-1	8:9880438	Basal	FALSE	NEUT	0.0503	4n balance	4	0.5581	HET	NA	NA	NA	NA	NA	NA	NA	0.595778	MISSENSE		
820	0	CUGBP2	-1	10:114076	Basal	FALSE	GAIN	0.4719	6n monoal	6	0.7405	NLOH	NA	NA	NA	NA	NA	NA	NA	0.70277	MISSENSE		
821	1	ANK3	-1	10:616028	Basal	FALSE	HETD	-0.2633	Hemizygous	1	0.6667	NLOH	NA	NA	NA	NA	NA	NA	0.019417	0.561659	MISSENSE		
822	0	SORL1	-1	11:120931	Basal	FALSE																	

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDos	HMMDos	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
830	0	GUCY2C	-1	12:147273	Basal	FALSE	NEUT	0.0237	2n Germlin	2	0.575	HET	NA	NA	NA	NA	-0.07463	NA	0.012945	0.566035	MISSENSE		
831	10	SFRS2IP	-1	12:446071	Basal	FALSE	NEUT	-0.0563	Normal (A)	2	0.5679	HET	NA	NA	NA	NA	NA	NA	0.003236	0.564678	MISSENSE		
832	0	KCNA6	1	12:479083	Basal	FALSE	NEUT	0.0812	3n duplicat	3	0.6084	HET	NA	NA	NA	NA	NA	NA	0.003236	0.428437	TRUNCATING		
833	5	CS	-1	12:549548	Basal	FALSE	NEUT	-0.0563	2n Germlin	2	0.5625	HET	NA	NA	NA	NA	-0.36211	NA	NA	0.3447	MISSENSE		
834	0	RASSF3	1	12:633715	Basal	FALSE	NEUT	-0.0563	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	NA	NA	NA	0.563007	MISSENSE		
835	0	A2ML1	1	12:886710	Basal	FALSE	NEUT	0.0812	3n duplicat	3	0.5952	HET	NA	NA	NA	NA	NA	NA	0.012945	0.430397	MISSENSE		
836	0	RB1	1	13:479371	Basal	FALSE	HETD	-0.2516	Hemizygou	1	0.6598	NLOH	NA	NA	NA	NA	-0.34796	0.07483	0.019417	0.34076	TRUNCATING		
837	0	ASB2	-1	14:934894	Basal	FALSE	NEUT	-0.0695	2n Somatic	2	0.6943	NLOH	NA	NA	NA	NA	NA	NA	NA	0.571134	TRUNCATING		
838	4	ARHGAP17	-1	16:248663	Basal	FALSE	NEUT	0.056	3n duplicat	3	0.5788	HET	NA	NA	NA	NA	-0.0288	NA	NA	0.561737	MISSENSE		
839	3	SLAH1	-1	16:469567	Basal	FALSE	HETD	-0.2377	Hemizygou	1	0.701	NLOH	NA	NA	NA	NA	-0.18736	NA	0.003236	0.711619	MISSENSE		
840	0	MMP2	1	16:540744	Basal	FALSE	HETD	-0.2402	Hemizygou	1	0.701	NLOH	NA	NA	NA	NA	-0.26946	NA	0.009709	0.564135	MISSENSE		
841	0	CX3CL1	1	16:559710	Basal	FALSE	NEUT	-0.0744	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-0.13513	NA	NA	0.562277	MISSENSE		
842	11	DUS2L	1	16:666654	Basal	FALSE	NEUT	-0.0672	Normal (A)	2	0.5588	HET	NA	NA	NA	NA	NA	NA	NA	0.996751	MISSENSE		
843	2	C17orf84	N,1,1	17:170167	Basal	FALSE	NEUT	-0.0956	2n Somatic	2	0.7138	NLOH	NA	NA	NA	NA	NA	NA	NA	0.705021	MISSENSE		
844	1	CDC6	1	17:357115	Basal	FALSE	GAIN	0.2546	4n Germlin	4	0.7273	NLOH	NA	NA	NA	NA	-0.07218	NA	0.003236	0.564223	MISSENSE		
845	0	ABCA8	-1	17:644111	Basal	FALSE	NEUT	-0.0711	2n Somatic	2	0.7273	NLOH	NA	NA	NA	NA	-0.00923	NA	0.006472	0.709384	MISSENSE		
846	0	KLHL14	-1	18:286037	Basal	FALSE	NEUT	-0.0621	Normal (A)	2	0.5664	HET	NA	NA	NA	NA	NA	NA	0.003236	0.596253	MISSENSE		
847	0	IL18R1	IL1F1,1	2:1023308	Basal	FALSE	HETD	-0.2922	Hemizygou	1	0.6863	NLOH	NA	NA	NA	NA	NA	NA	NA	0.597397	MISSENSE		
848	0	TTN	-1	2:1793434	Basal	FALSE	NEUT	-0.0418	2n Somatic	2	0.6923	NLOH	NA	NA	NA	NA	-0.03953	NA	0.20712	0.564098	MISSENSE		
849	0	USP37	-1	2:190830	Basal	FALSE	HETD	-0.2742	Hemizygou	1	0.6923	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.555809	MISSENSE		
850	0	ISX	1	22:338114	Basal	FALSE	HETD	-0.2905	Hemizygou	1	0.6889	NLOH	NA	NA	NA	NA	NA	NA	0.009709	0.564557	MISSENSE		
851	4	CELSR1	-1	22:451591	Basal	FALSE	NEUT	-0.0276	NA	NA	0.5882	HET	NA	NA	NA	NA	-0.08213	NA	NA	MISSENSE			
852	16	LRPPRC	-1	22:4402443	Basal	FALSE	NEUT	0.1003	3n duplicat	3	0.6	HET	NA	NA	NA	NA	-0.06968	NA	0.006472	0.704835	MISSENSE		
853	0	TBC1D5	-1	3:1723079	Basal	FALSE	NEUT	-0.0621	2n Somatic	2	0.6842	NLOH	NA	NA	NA	NA	NA	NA	0.003236	1	MISSENSE		
854	0	SPTA1	-1	1:1569107	Other	FALSE	GAIN	0.3455	4n monoal	4	NA	NA	NA	NA	NA	NA	NA	NA	0.012945	0.5682	MISSENSE		
855	17	TMEM57	-1	1:2565749	Other	FALSE	NEUT	0.0474	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.505397	MISSENSE		
856	0	TRIM63	-1	1:2626444	Other	FALSE	NEUT	0.0474	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.172432	MISSENSE		
857	7	HMG2	1	1:2667416	Other	FALSE	NEUT	0.0474	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.336276	MISSENSE		
858	0	ARHGAP5	1	14:316309	Other	FALSE	NEUT	-0.0588	Normal (A)	2	NA	NA	NA	NA	NA	NA	-0.34846	NA	0.009709	0.998579	MISSENSE		
859	8	CIRH1A	1	16:677347	Other	FALSE	NEUT	-0.136	Hemizygou	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.870828	MISSENSE		
860	2	ZDHHC8	1	22:185072	Other	FALSE	HETD	-0.3077	Hemizygou	1	NA	NA	NA	NA	NA	NA	NA	NA	0.003236	0.879788	TRUNCATING		
861	0	GPR116	-1	6:4693487	Other	FALSE	NEUT	0.0376	2n Germlin	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.517102	MISSENSE		
862	1	CREB5	1	7:2881043	Other	FALSE	NEUT	-0.0071	Normal (A)	2	NA	NA	NA	NA	NA	NA	-0.27597	NA	NA	0.998081	MISSENSE		
863	0	FAM135B	-1	8:1392340	Other	FALSE	NEUT	0.0366	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	NA	0.022654	0.683266	MISSENSE		
864	0	NHS	1	X:1765373	Other	FALSE	NEUT	0.0281	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.006472	NA	MISSENSE		
865	0	TBX22	1	X:7916897	Other	FALSE	NEUT	0.0281	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.003236	NA	MISSENSE		
866	0	TSB8	1	1:1153775	Basal	FALSE	NEUT	0.108	4n Germlin	4	0.9437	LOH	LOH	0.9437	GAIN	0.1841	-0.24066	NA	NA	0.992506	MISSENSE		
867	0	C1orf187	1	1:1169206	Basal	FALSE	HETD	-0.3854	2n Somatic	2	0.8947	DLOH	DLOH	0.8947	HOMD	-0.6152	NA	NA	NA	0.888632	MISSENSE		
868	11	ADAR	-1	1:1528410	Basal	FALSE	GAIN	0.4471	6n non-mo	6	0.6471	ASCNA	ASCNA	0.6471	AMP	0.6501	-0.04591	NA	0.009709	0.888939	TRUNCATING		
869	0	AL513323	1	1:1575132	Basal	FALSE	HETD	-0.4442	2n Somatic	2	0.8835	DLOH	DLOH	0.8835	HETD	-0.5326	NA	NA	NA	0.644525	MISSENSE		
870	15	LTBP3	-1	1:1650760	Basal	FALSE	NEUT	0.1102	4n balance	4	0.6316	HET	HET	0.6316	GAIN	0.1873	NA	NA	NA	0.893972	MISSENSE		
871	11	C11orf30	1	11:758849	Basal	FALSE	NEUT	-0.1104	3n Somatic	3	0.9167	NLOH	NLOH	0.9167	NEUT	-0.0873	NA	NA	0.016181	0.868223	MISSENSE		
872	0	HSPG2	-1	1:2209530	Basal	FALSE	HETD	-0.3849	2n Somatic	2	0.8938	DLOH	DLOH	0.8938	HOMD	-0.6469	-0.0997	NA	0.016181	0.998673	MISSENSE		
873	0	TRIM67	1	1:2294114	Basal	FALSE	NEUT	0.0079	4n Somatic	4	0.9091	NLOH	NLOH	0.9091	NEUT	0.0319	NA	NA	0.009709	0.998484	MISSENSE		
874	2	CAPRIN2	-1	12:307632	Basal	FALSE	HETD	-0.3857	2n Somatic	2	0.8462	DLOH	DLOH	0.8462	HETD	-0.47	NA	NA	0.003236	0.992359	MISSENSE		
875	1	LYST	-1	1:2339326	Basal	FALSE	NEUT	0.0079	3n Somatic	3	0.9333	NLOH	NLOH	0.9333	NEUT	9.00E-04	NA	NA	0.019417	0.998964	MISSENSE		
876	0	PDZRN4	1	12:402528	Basal	FALSE	HETD	-0.3918	2n Somatic	2	0.875	DLOH	DLOH	0.875	HETD	-0.4656	NA	NA	0.006472	0.879232	MISSENSE		
877	0	SLTRK1	-1	13:833524	Basal	FALSE	HETD	-0.3516	2n Somatic	2	0.875	DLOH	DLOH	0.875	HETD	-0.4429	NA	NA	0.006472	0.998937	MISSENSE		
878	14	KIAA0430	-1	16:156172	Basal	FALSE	NEUT	0.0755	4n balance	4	0.6316	HET	HET	0.6316	GAIN	0.1632	NA	NA	NA	0.997826	MISSENSE		
879	1	CD19	1	16:288511	Basal	FALSE	NEUT	0.0843	4n balance	4	0.6154	HET	HET	0.6154	NEUT	0.0618	-0.39693	NA	0.006472	0.997554	MISSENSE		
880	8	ESP8	1	1:6439810	Basal	FALSE	NEUT	0.0877	4n Somatic	4	0.9667	NLOH	NLOH	0.9667	NEUT	0.0377	NA	NA	NA	0.657654	MISSENSE		
881	134	MBD2	-1	18:499854	Basal	FALSE	NEUT	0.1231	4n balance	4	0.6087	HET	HET	0.6087	GAIN	0.1976	-0.05379	NA	NA	0.336889	MISSENSE		
882	18	DSCR1	-1	21:348123	Basal	FALSE	NEUT	0.1259	4n balance	4	0.6207	HET	HET	0.6207	GAIN	0.2235	NA	NA	NA	0.336918	MISSENSE		
883	15	XRN1	-1	3:1436242	Basal	FALSE	GAIN	0.4812	6n non-mo	6	0.7021	ASCNA	ASCNA	0.7021	AMP	0.695	-0.03982	NA	0.009709	0.649642	MISSENSE		
884	0	PDZD2	1	5:3183524	Basal	FALSE	NEUT	0.143	4n balance	4	0.619	HET	HET	0.619	GAIN	0.2083	NA	0.013605	0.006472	0.863145	MISSENSE		
885	39	MTMR12	-1	5:3228383	Basal	FALSE	NEUT	0.143	4n balance	4	0.619	HET	HET	0.619	GAIN	0.2083	NA	NA	0.003236	0.998395	MISSENSE		
886	0	GRM1	1	6:1467620	Basal	FALSE	GAIN	0.4163	6n non-mo	6	0.6786	ASCNA	ASCNA	0.6786	AMP	0.613	-0.39621	0.013605	0.012945	0.893293	MISSENSE		
887	4	ALDH5A1	1	6:2462323	Basal	FALSE	NEUT	0.0704	4n Germlin	4	0.9545	NLOH	NLOH	0.9545	NEUT	0.0347	-0.61296	NA	NA	0.305398	MISSENSE		
888	0	HTR1B	-1	6:7822925	Basal	FALSE	NEUT	0.1119	4n balance	4	0.619	HET	HET	0.619	GAIN	0.1509	-0.25823	NA	NA	0.68547	MISSENSE		
889	14	DUS4L	1	7:1070041	Basal	FALSE	NEUT	0.146	4n balance	4	0.6154	HET	HET	0.6154	GAIN	0.21	NA	NA	NA	0.998855	MISSENSE		
890	0	PKD11	-1	7:4783925	Basal	FALSE	NEUT	0.1408	4n balance	4	0.625	HET	HET	0.625	GAIN	0.2077	NA	NA	0.019417	0.863446	MISSENSE		
891	0	RP1	1	8:5570006	Basal	FALSE	HETD	-0.4008	2n Somatic	2	0.8929	DLOH	DLOH	0.8929	HETD	-0.5133	NA	NA	0.012945	0.869749	MISSENSE		
892	0	NHSL2	1	X:172523	Basal	FALSE	NEUT	-0.1156	NA	NA	NA	DLOH	0.8333	HETD	-0.2977	NA	NA	NA	NA	MISSENSE			

1	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDos	HMMDos	OncoSNP	OncoSNP	apollo.ho	apollo.ho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type			
899	4	MSL2	-1	3:173532	Basal	FALSE	NEUT	-0.0159	Normal (A)	2	0.625	HET	0.625	NEUT	0.0593	NA	NA	NA	NA	MISSENSE			
900	5	NR3C1	-1	5:1427594	Basal	FALSE	HETD	-0.1672	Hemizygou	1	0.6364	HET	0.6364	NEUT	-0.0763	-0.52751	NA	0.006472	NA	MISSENSE			
901	0	PTPRD	-1	9:8365931	Basal	FALSE	GAIN	0.3387	6n Germli	6	0.7143	LOH	LOH	0.7143	AMP	0.6066	NA	0.006472	NA	MISSENSE			
902	0	NRAP	-1	10:115399	Basal	FALSE	NEUT	-0.076	3n Somatic	3	NA	NA	NA	NA	NA	NA	0.013605	0.019417	0.880506	MISSENSE			
903	23	CAS21	-1	1:1063679	Basal	FALSE	HETD	-0.2338	2n Somatic	2	NA	NA	NA	NA	NA	NA	NA	NA	0.683834	MISSENSE			
904	17	AHNAK	-1	11:620471	Basal	FALSE	HETD	-0.1982	2n Germli	2	NA	NA	NA	NA	NA	NA	NA	0.032362	0.684162	MISSENSE			
905	30	ANKLE2	-1	12:131834	Basal	FALSE	HETD	-0.2601	2n Somatic	2	NA	NA	NA	NA	NA	NA	NA	NA	0.885492	MISSENSE			
906	0	USH2A	-1	1:2142403	Basal	FALSE	NEUT	0.0092	5n non-mo	5	NA	NA	NA	NA	NA	NA	NA	0.064725	0.998398	MISSENSE			
907	0	KCNA6	1	12:479074	Basal	FALSE	NEUT	0.0051	4n Germli	4	NA	NA	NA	NA	NA	NA	NA	0.003236	0.333679	MISSENSE			
908	45	PGM1	1	1:6387702	Basal	FALSE	NEUT	0.1091	5n non-mo	5	NA	NA	NA	NA	NA	NA	-0.9837	0.003236	0.998162	MISSENSE			
909	0	MYH3	-1	17:104864	Basal	FALSE	HETD	-0.2452	2n Somatic	2	NA	NA	NA	NA	NA	NA	-0.4602	0.012945	0.998249	MISSENSE			
910	0	OTOP3	1	17:704512	Basal	FALSE	NEUT	-0.0072	4n Somatic	4	NA	NA	NA	NA	NA	NA	NA	0.003236	1	MISSENSE			
911	85	TP53	-1	17:751894	Basal	FALSE	HETD	-0.2452	2n Somatic	2	NA	NA	NA	NA	NA	NA	-1.58285	0.306122	0.812298	0.880989	MISSENSE		
912	0	ATP4A	-1	19:407426	Basal	FALSE	NEUT	-0.0315	3n duplicat	3	NA	NA	NA	NA	NA	NA	-0.15633	NA	0.998632	MISSENSE			
913	3	FCGBP	-1	19:450461	Basal	FALSE	NEUT	-0.0315	3n duplicat	3	NA	NA	NA	NA	NA	NA	NA	0.012945	0.68231	MISSENSE			
914	271	ERGIC3	1	20:335997	Basal	FALSE	NEUT	-0.0065	3n Germli	3	NA	NA	NA	NA	NA	NA	NA	NA	0.172425	MISSENSE			
915	0	ACVR1C	-1	2:1581058	Basal	FALSE	NEUT	-0.0307	3n duplicat	3	NA	NA	NA	NA	NA	NA	-0.34913	NA	0.003236	0.202243	MISSENSE		
916	6	TTN	-1	2:1793187	Basal	FALSE	NEUT	-0.0516	3n duplicat	3	NA	NA	NA	NA	NA	NA	-0.16082	NA	0.20712	0.215315	MISSENSE		
917	5	ZNF142	-1	2:2192218	Basal	FALSE	HETD	-0.1446	Normal (A)	2	NA	NA	NA	NA	NA	NA	NA	0.003236	0.349598	MISSENSE			
918	0	FRG2C	1	3:7579763	Basal	FALSE	HETD	-0.1993	2n Somatic	2	NA	NA	NA	NA	NA	NA	NA	0.003236	0.210237	MISSENSE			
919	24	CDC20B,GF-1,1	1	5:5449260	Basal	FALSE	NEUT	0.0374	4n balance	4	NA	NA	NA	NA	NA	NA	NA	NA	0.979333	MISSENSE			
920	1	HIST1H4A,1,-1	1	6:2621596	Basal	FALSE	NEUT	0.0226	4n balance	4	NA	NA	NA	NA	NA	NA	NA	NA	0.29662	MISSENSE			
921	16	FANCG	-1	9:3506545	Basal	FALSE	HETD	-0.2227	2n Somatic	2	NA	NA	NA	NA	NA	NA	-0.03042	NA	0.006472	0.444445	MISSENSE		
922	1	FRMD3	-1	9:8511428	Basal	FALSE	NEUT	-0.0192	4n monoal	4	NA	NA	NA	NA	NA	NA	NA	0.003236	0.546093	MISSENSE			
923	465	MORF4L2	-1	X:1028178	Basal	FALSE	HETD	-0.1614	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE			
924	88	OGT	1	X:7069592	Basal	FALSE	HETD	-0.179	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.009709	NA	MISSENSE			
925	34	C10orf18	1	10:583128	Basal	FALSE	GAIN	0.2774	5n non-mo	5	0.6296	ASCNA	ASCNA	0.6296	GAIN	0.3274	NA	0.003236	0.209796	MISSENSE			
926	0	RAG1	1	11:365545	Basal	FALSE	NEUT	-0.0087	4n balance	4	0.6154	HET	HET	0.6154	NEUT	0.0736	-0.10086	NA	0.003236	0.209208	TRUNCATING		
927	97	FOXN1	-1	12:283812	Basal	FALSE	NEUT	-0.0018	4n balance	4	0.625	HET	HET	0.625	NEUT	0.1059	-0.05242	NA	0.439633	MISSENSE			
928	121	DDX42	1	17:592316	Basal	FALSE	NEUT	-0.0104	4n monoal	4	0.6923	NLOH	NLOH	0.6923	NEUT	-0.0113	-0.18491	NA	0.006472	0.350437	MISSENSE		
929	21	HELZ	-1	17:625752	Basal	FALSE	NEUT	-0.0104	4n monoal	4	0.7143	LOH	LOH	0.7143	NEUT	0.083	NA	0.003236	0.209375	MISSENSE			
930	6	ACP5	-1	19:115469	Basal	FALSE	NEUT	2.00E-04	4n balance	4	0.6296	HET	HET	0.6296	NEUT	0.0686	-0.17245	NA	NA	0.350195	MISSENSE		
931	1	ZNF781	-1	19:428528	Basal	FALSE	NEUT	-0.0244	4n balance	4	0.6216	HET	HET	0.6216	NEUT	0.0784	NA	NA	0.543198	MISSENSE			
932	15	TXNRD2	-1	22:182827	Basal	FALSE	NEUT	-0.0454	4n balance	4	0.6341	HET	HET	0.6341	NEUT	0.0187	-0.16713	NA	0.006472	0.355445	MISSENSE		
933	13	HP54	-1	22:251902	Basal	FALSE	NEUT	-0.0648	4n Germli	4	0.6216	HET	HET	0.6216	NEUT	0.0051	NA	NA	0.437345	MISSENSE			
934	172	VAMP8	1	2:8566219	Basal	FALSE	NEUT	-0.0561	4n balance	4	0.625	HET	HET	0.625	NEUT	0.0092	-0.14822	NA	NA	0.44662	MISSENSE		
935	5	NKIRAS1	-1	3:2392717	Basal	FALSE	NEUT	0.0919	5n monoal	5	0.7419	LOH	LOH	0.7419	GAIN	0.2322	NA	NA	NA	1	MISSENSE		
936	33	BAP1	-1	3:5241259	Basal	FALSE	HETD	-0.1862	3n duplicat	3	0.6842	NLOH	NLOH	0.6842	HETD	-0.1641	NA	NA	0.003236	0.439672	MISSENSE		
937	5	ADAMTS12	-1	5:3391706	Basal	FALSE	HETD	-0.1957	3n duplicat	3	0.6471	NLOH	NLOH	0.6471	HETD	-0.1926	NA	NA	0.012945	0.553724	MISSENSE		
938	5	DOPEY1	1	6:8390218	Basal	FALSE	NEUT	-0.0011	4n balance	4	0.6154	HET	HET	0.6154	NEUT	0.0609	NA	NA	0.006472	0.437675	MISSENSE		
939	0	DNAH11	1	7:2166496	Basal	FALSE	HETD	-0.1873	3n duplicat	3	0.65	NLOH	NLOH	0.65	HETD	-0.1664	-0.23241	NA	0.02589	0.445204	MISSENSE		
940	1	OSBPL3	-1	7:2487684	Basal	FALSE	HETD	-0.1873	3n duplicat	3	0.65	NLOH	NLOH	0.65	HETD	-0.1655	NA	NA	NA	0.436571	MISSENSE		
941	0	ZFAT	-1	8:1356817	Basal	FALSE	NEUT	0.143	5n non-mo	5	0.6136	HET	HET	0.6136	GAIN	0.3618	NA	NA	NA	0.30877	MISSENSE		
942	1	COL4A5	1	X:1077164	Basal	FALSE	NEUT	0.0988	NA	NA	NA	NA	LOH	0.7647	GAIN	0.2094	-0.40567	NA	0.009709	NA	MISSENSE		
943	0	GPR112	1	X:1352546	Basal	FALSE	NEUT	0.079	NA	NA	NA	NA	LOH	0.6818	GAIN	0.2193	NA	NA	0.016181	NA	MISSENSE		
944	361	HUWE1	-1	X:5357906	Basal	FALSE	GAIN	0.2175	NA	NA	NA	NA	HET	0.6429	GAIN	0.2214	-0.22363	NA	0.02589	NA	MISSENSE		
945	5	ITIH5L	-1	X:5479816	Basal	FALSE	NEUT	-0.0174	NA	NA	NA	NA	HET	0.6429	GAIN	0.2561	NA	NA	0.003236	NA	MISSENSE		
946	95	RBM17	1	10:618327	Basal	FALSE	HETD	-0.3279	2n Somatic	2	0.7931	DLOH	DLOH	0.7931	HETD	-0.3485	-0.05299	NA	NA	0.548813	MISSENSE		
947	0	DENND2C	-1	1:1149450	Basal	FALSE	NEUT	0.0675	4n balance	4	0.6129	HET	HET	0.6129	GAIN	0.2051	NA	NA	NA	0.5538	MISSENSE		
948	10	TUT1,EEF1,-1,-1	1	11:620998	Basal	FALSE	NEUT	0.0473	4n balance	4	0.6154	HET	HET	0.6154	GAIN	0.1285	NA	NA	NA	0.2085	MISSENSE		
949	3	MAP4K2	-1	11:643215	Basal	FALSE	NEUT	0.0473	4n balance	4	0.6154	HET	HET	0.6154	NEUT	0.0731	-0.24336	NA	0.003236	0.457282	MISSENSE		
950	2	ALG10	1	12:340702	Basal	FALSE	HETD	-0.3247	2n Somatic	2	0.7974	DLOH	DLOH	0.7974	HETD	-0.3934	-0.55006	NA	NA	0.368513	MISSENSE		
951	24	ARID2	1	12:445306	Basal	FALSE	HETD	-0.3247	2n Somatic	2	0.7857	DLOH	DLOH	0.7857	HETD	-0.3764	NA	NA	0.019417	0.355581	TRUNCATING		
952	0	KIF5A	1	12:562490	Basal	FALSE	HETD	-0.3247	2n Somatic	2	0.7778	DLOH	DLOH	0.7778	HETD	-0.3857	NA	NA	0.006472	0.211728	MISSENSE		
953	0	ACRBP	-1	12:662382	Basal	FALSE	NEUT	-0.0691	3n Somatic	3	0.8261	NLOH	NLOH	0.8261	NEUT	-0.0047	NA	NA	NA	0.351278	MISSENSE		
954	0	FLT3	-1	13:275295	Basal	FALSE	NEUT	-0.0984	3n duplicat	3	0.6552	HET	HET	0.6552	NEUT	-0.0535	-0.36568	0.006803	0.006472	0.543011	MISSENSE		
955	0	FLT3	-1	13:275295	Basal	FALSE	NEUT	-0.0984	3n duplicat	3	0.6552	HET	HET	0.6552	NEUT	-0.0535	-0.36568	0.006803	0.006472	0.547186	TRUNCATING		
956	21	YLPN1	1	14:743390	Basal	FALSE	HETD	-0.3447	2n Somatic	2	0.7778	DLOH	DLOH	0.7778	HETD	-0.396	NA	NA	0.006472	0.21243	MISSENSE		
957	30	CATSPERB	-1	14:911577	Basal	FALSE	HETD	-0.3447	2n Somatic	2	0.7838	DLOH	DLOH	0.7838	HETD	-0.4006	NA	NA	0.003236	0.372856	MISSENSE		
958	6	MORF4L1	1	15:769643	Basal	FALSE	HETD	-0.3344	2n Somatic	2	0.7778	DLOH	DLOH	0.7778	HETD	-0.3689	NA	NA	NA	0.367493	MISSENSE		
959	0	TPSD1,PRS1,-1	1	16:124833	Basal	FALSE	NEUT	-0.1047	3n duplicat	3	0.6667	HET	HET	0.6667	NEUT	-0.0941	NA	NA	NA	0.446352	MISSENSE		
960	21	BRD7	-1	16:489150	Basal	FALSE	NEUT	-0.1107	3n duplicat	3	0.7889	NLOH	NLOH	0.7889	NEUT	-0.0907	NA	NA	NA	0.236307	MISSENSE		
961	0	HYDIN	-1	16:694419	Basal	FALSE	GAIN	0.404	6n Germli	6	0.6923	ASCNA	ASCNA	0.6923	AMP	0.7369	NA	NA	0.02589	0.207876	MISSENSE		
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	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDos	HMMDos	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
968	15	MUC16	-1	19:893124	Basal	FALSE	NEUT	0.0048	4n balance	4	0.6207	HET	HET	0.6207	GAIN	0.1428	NA	NA	0.064725	0.233773	MISSENSE		
969	71	MCM3AP	-1,1	21:464905	Basal	FALSE	NEUT	0.0899	5n non-mo	5	0.623	HET	HET	0.623	GAIN	0.206	NA	NA	NA	0.556048	MISSENSE		
970	0	TTN	-1	2:1793140	Basal	FALSE	NEUT	0.0244	4n Germli	4	0.8519	LOH	LOH	0.8519	GAIN	0.1382	-0.08197	NA	0.20712	0.443726	MISSENSE		
971	0	ICA1L	-1	2:2033698	Basal	FALSE	NEUT	0.0244	3n Somatic	3	0.8571	NLOH	NLOH	0.8571	NEUT	0.022	NA	NA	NA	0.400475	MISSENSE		
972	337	XBP1	-1	22:275213	Basal	FALSE	NEUT	0.054	4n balance	4	0.619	HET	HET	0.619	GAIN	0.1669	-0.11519	NA	NA	0.124239	MISSENSE		
973	22	MFF	-1	2:2279132	Basal	FALSE	HETD	-0.2039	2n Somatic	2	0.8333	NLOH	NLOH	0.8333	NEUT	-0.1733	NA	NA	NA	0.237577	MISSENSE		
974	15	RASA2	-1	3:1427312	Basal	FALSE	GAIN	0.3827	6n Somatic	6	0.8679	LOH	LOH	0.8679	AMP	0.6202	-0.1462	NA	0.006472	0.233593	MISSENSE		
975	0	SPATA16	-1	3:1743178	Basal	FALSE	GAIN	0.2306	5n Somatic	5	0.8679	LOH	LOH	0.8679	AMP	0.3798	NA	NA	0.006472	0.200382	MISSENSE		
976	37	IGF2BP2	-1	3:1868899	Basal	FALSE	NEUT	0.1394	4n Germli	4	0.8679	LOH	LOH	0.8679	GAIN	0.309	NA	NA	NA	0.330932	MISSENSE		
977	1	ZNF385D	-1	3:2158109	Basal	FALSE	NEUT	0.0474	4n Somatic	4	0.8636	NLOH	NLOH	0.8636	NEUT	0.0895	NA	NA	0.003236	0.224498	MISSENSE		
978	57	SH3BP2	1	4:2804529	Basal	FALSE	HETD	-0.3002	2n Somatic	2	0.8248	DLOH	DLOH	0.8248	HETD	-0.3565	-0.13336	NA	NA	0.177041	MISSENSE		
979	0	PRDM8	1	4:8134025	Basal	FALSE	NEUT	0.0346	4n balance	4	0.6087	HET	HET	0.6087	GAIN	0.1075	NA	NA	NA	0.365551	MISSENSE		
980	4	WDFY3	-1	4:8586163	Basal	FALSE	NEUT	0.0346	3n duplicat	3	0.619	HET	HET	0.619	GAIN	0.1042	NA	NA	0.006472	0.232128	MISSENSE		
981	3	AC093283	1	5:7320471	Basal	FALSE	HETD	-0.3372	2n Somatic	2	0.7841	DLOH	DLOH	0.7841	HETD	-0.3693	NA	NA	NA	0.367155	MISSENSE		
982	0	GPR116	-1	6:4693168	Basal	FALSE	NEUT	0.073	4n balance	4	0.6119	HET	HET	0.6119	GAIN	0.1965	NA	NA	NA	0.555968	MISSENSE		
983	0	C6orf138	-1	6:4814390	Basal	FALSE	NEUT	0.073	4n balance	4	0.6071	HET	HET	0.6071	GAIN	0.1965	NA	NA	NA	0.366469	MISSENSE		
984	1	LRRIC17,FB1	-1,1	7:1023669	Basal	FALSE	NEUT	-0.0691	3n Germli	3	0.7704	NLOH	NLOH	0.7704	NEUT	-0.1015	NA	NA	NA	0.233884	MISSENSE		
985	1	PTPRN2	-1	7:1571068	Basal	FALSE	NEUT	0.0269	4n balance	4	0.6348	HET	HET	0.6348	GAIN	0.1388	-0.01088	NA	0.012945	0.367403	MISSENSE		
986	0	HOXA2	-1	7:2710707	Basal	FALSE	NEUT	0.0662	4n balance	4	0.6129	HET	HET	0.6129	GAIN	0.1863	NA	NA	0.003236	0.124304	MISSENSE		
987	4	PCL0	-1	7:8236989	Basal	FALSE	NEUT	-0.0691	3n duplicat	3	0.619	HET	HET	0.619	NEUT	-0.066	NA	NA	0.019417	0.126193	MISSENSE		
988	47	KIAA0368	-1	9:1132353	Basal	FALSE	NEUT	0.0571	4n balance	4	0.6087	HET	HET	0.6087	GAIN	0.133	NA	NA	NA	0.367984	MISSENSE		
989	73	EXOSC2	1	9:1325674	Basal	FALSE	NEUT	0.0257	4n balance	4	0.6154	HET	HET	0.6154	NEUT	0.0633	-0.03889	NA	0.003236	0.226408	MISSENSE		
990	6	DDX31	-1	9:1345136	Basal	FALSE	NEUT	0.0257	4n balance	4	0.6154	HET	HET	0.6154	GAIN	0.1361	NA	NA	NA	0.171714	TRUNCATING		
991	55	SLK	1	10:105752	Other	FALSE	NEUT	-0.0603	2n Germli	2	0.7742	NLOH	NLOH	0.7742	NEUT	-0.0096	-0.26289	NA	0.003236	0.449546	MISSENSE		
992	1	CACNB2	1	10:188684	Other	FALSE	NEUT	-0.0542	Normal (A	2	0.6061	HET	HET	0.6061	NEUT	-0.0135	-0.24071	NA	0.003236	0.368797	MISSENSE		
993	10	PARD3	-1	10:348457	Other	FALSE	NEUT	-0.0542	2n Germli	2	0.6061	HET	HET	0.6061	NEUT	-0.0172	-0.51899	NA	0.003236	0.553493	TRUNCATING		
994	4	PRKG1,CST1	-1,1	10:531280	Other	FALSE	NEUT	-0.0542	2n Somatic	2	0.7692	NLOH	NLOH	0.7692	NEUT	-0.004	NA	NA	NA	0.439018	MISSENSE		
995	22	TTC12	1	11:1127011	Other	FALSE	NEUT	-0.0934	Normal (A	2	0.6042	HET	HET	0.6042	NEUT	-0.0499	NA	NA	NA	0.43993	MISSENSE		
996	12	FRAP1	-1	11:115008	Other	FALSE	NEUT	-0.071	Normal (A	2	0.6071	HET	HET	0.6071	NEUT	-0.0115	-0.50953	0.027211	NA	0.66754	MISSENSE		
997	4	MLL	1	11:117849	Other	FALSE	NEUT	-0.0934	Normal (A	2	0.6154	HET	HET	0.6154	NEUT	-0.0499	NA	NA	0.016181	0.1232	MISSENSE		
998	2	CBL	1	11:118650	Other	FALSE	NEUT	-0.0934	Normal (A	2	0.6154	HET	HET	0.6154	NEUT	-0.0499	-0.88616	0.006803	0.003236	0.124655	MISSENSE		
999	109	CYP2R1	-1	11:148586	Other	FALSE	HETD	-0.3205	Hemizygou	1	0.7	DLOH	DLOH	0.7	HETD	-0.3736	NA	NA	0.003236	0.234129	MISSENSE		
1000	0	ITGA10	1	11:1442504	Other	FALSE	NEUT	0.0467	3n duplicat	3	0.64	HET	HET	0.64	GAIN	0.2797	-0.32015	NA	0.006472	0.554733	MISSENSE		
1001	0	ATP8B2	1	11:1525668	Other	FALSE	NEUT	0.0908	2n Germli	2	0.625	HET	HET	0.625	GAIN	0.3112	NA	NA	0.003236	0.128367	MISSENSE		
1002	0	PYHIN1	1	11:1571785	Other	FALSE	GAIN	0.1702	3n duplicat	3	0.5814	HET	HET	0.5814	GAIN	0.2953	NA	NA	0.009709	0.17517	MISSENSE		
1003	0	C048	-1	11:1589215	Other	FALSE	GAIN	0.2179	3n duplicat	3	0.6316	HET	HET	0.6316	GAIN	0.2953	-0.08532	NA	NA	0.124375	MISSENSE		
1004	0	NLRP14	1	11:702112	Other	FALSE	HETD	-0.3205	Hemizygou	1	0.695	DLOH	DLOH	0.695	HETD	-0.3751	NA	NA	0.009709	0.124155	MISSENSE		
1005	4	LAMC2	1	11:1814633	Other	FALSE	NEUT	0.1211	3n Germli	3	0.6216	HET	HET	0.6216	GAIN	0.2943	-0.42386	NA	0.003236	0.334584	MISSENSE		
1006	0	GPR83	-1	11:937663	Other	FALSE	NEUT	-0.0811	Normal (A	2	0.6111	HET	HET	0.6111	NEUT	-0.0523	-0.16504	NA	0.003236	0.230038	MISSENSE		
1007	4	CR2	1	11:2057106	Other	FALSE	GAIN	0.1709	3n duplicat	3	0.6316	HET	HET	0.6316	GAIN	0.321	-0.10491	NA	0.003236	0.375321	MISSENSE		
1008	9	P2RX4	1	12:120139	Other	FALSE	HETD	-0.2303	Normal (A	2	0.6162	HET	HET	0.6162	HETD	-0.2105	-0.23658	NA	NA	0.172913	MISSENSE		
1009	0	OVCCH1	-1	12:294994	Other	FALSE	NEUT	-0.1095	Normal (A	2	0.6154	HET	HET	0.6154	NEUT	-0.094	NA	NA	0.009709	0.552423	MISSENSE		
1010	2	MEIS2	-1	15:351163	Other	FALSE	NEUT	-0.0524	3n Germli	3	0.6111	HET	HET	0.6111	NEUT	-0.0325	NA	NA	0.006472	0.235637	MISSENSE		
1011	0	RASGRP1	-1	15:366393	Other	FALSE	NEUT	-0.0524	Normal (A	2	0.6053	HET	HET	0.6053	NEUT	-0.0325	-0.28239	NA	0.003236	0.366793	TRUNCATING		
1012	0	AP3B2	-1	15:811431	Other	TRUE	HETD	-0.3347	Hemizygou	1	0.7037	DLOH	DLOH	0.7037	HETD	-0.3934	-0.10391	NA	0.009709	0.126862	SPICE		
1013	1	ADCY9	-1	16:395667	Other	FALSE	NEUT	-0.0443	Normal (A	2	0.6087	HET	HET	0.6087	NEUT	0.0027	-0.72745	NA	0.012945	0.551773	MISSENSE		
1014	0	SLCGA2	1	16:542898	Other	FALSE	NEUT	-0.0443	Normal (A	2	0.6	HET	HET	0.6	NEUT	0.065	NA	NA	0.006472	0.368742	MISSENSE		
1015	0	MPP2	-1	17:393159	Other	FALSE	HETD	-0.348	Hemizygou	1	0.7083	DLOH	DLOH	0.7083	HETD	-0.3952	NA	NA	NA	0.226067	MISSENSE		
1016	24	GNA13	-1	17:604800	Other	FALSE	NEUT	-0.064	Normal (A	2	NA	NA	NA	NA	NEUT	-0.0034	-0.448	NA	NA	0.175498	MISSENSE		
1017	86	SAFB	1	19:559263	Other	FALSE	NEUT	0.0826	3n duplicat	3	0.9045	LOH	LOH	0.9045	GAIN	0.2388	NA	NA	0.003236	0.123701	MISSENSE		
1018	0	AC018755	-1	19:567892	Other	FALSE	HETD	-0.3607	Hemizygou	1	0.7027	DLOH	DLOH	0.7027	HETD	-0.3951	NA	NA	NA	0.125318	MISSENSE		
1019	14	MZF1	-1	19:637736	Other	FALSE	HETD	-0.3607	Hemizygou	1	0.973	NLOH	NLOH	0.973	NEUT	-0.1582	-0.01795	NA	0.003236	0.205905	MISSENSE		
1020	0	SLC24A3	1	20:196254	Other	FALSE	NEUT	-0.058	Normal (A	2	0.6	HET	HET	0.6	NEUT	0.0364	NA	NA	0.003236	0.556413	MISSENSE		
1021	89	RRM2	1	21:1018139	Other	FALSE	NEUT	-0.0215	Normal (A	2	0.6	HET	HET	0.6	NEUT	0.0757	-1.09513	NA	NA	0.235194	MISSENSE		
1022	88	FAR5LB	-1	22:231728	Other	FALSE	HETD	-0.3334	Hemizygou	1	0.6923	DLOH	DLOH	0.6923	HETD	-0.3845	NA	NA	NA	0.36646	MISSENSE		
1023	60	SREBF2	1	22:405929	Other	FALSE	NEUT	-0.1307	Normal (A	2	0.6111	HET	HET	0.6111	NEUT	-0.0432	NA	NA	0.003236	0.349891	MISSENSE		
1024	100	ADI1	-1	23:3496670	Other	FALSE	NEUT	-0.0283	Normal (A	2	0.6154	HET	HET	0.6154	NEUT	0.0681	-0.93411	NA	0.003236	1	MISSENSE		
1025	84	HAAO	-1	24:285078	Other	FALSE	NEUT	-0.0226	Normal (A	2	0.6	HET	HET	0.6	NEUT	0.0277	-0.93701	NA	0.003236	0.355755	MISSENSE		
1026	7	EHBP1	1	2:6307399	Other	FALSE	NEUT	-0.0147	Normal (A	2	0.634	NLOH	NLOH	0.634	NEUT	0.0201	NA	NA	0.003236	0.789517	MISSENSE		
1027	33	ASAP2	1	2:9392320	Other	FALSE	NEUT	-0.0215	Normal (A	2	0.6	HET	HET	0.6	NEUT	0.0582	-0.38917	NA	NA	0.796085	MISSENSE		
1028	0	GRM2	1	3:5172160	Other	FALSE	NEUT	-0.1059	Normal (A	2	0.6031												

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	Ens54Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloho	apolloho	apolloho	apolloho	apolloho	apolloho	apolloho	mut_freq	mut_freq	clonality	mut_type		
1037	4	MLL3	-1	7:151218	Other	FALSE	NEUT	-0.0751	2n Somatic	2	0.77	NLOH	NLOH	0.77	NEUT	0.0375	NA	0.013605	0.022654	0.352753	MISSENSE		
1038	19	ANLN	1	7:3641397	Other	FALSE	GAIN	0.1882	3n duplicat	3	0.6364	HET	HET	0.6364	GAIN	0.3299	NA	NA	0.006472	0.79425	MISSENSE		
1039	0	HECW1	1	7:4331793	Other	FALSE	GAIN	0.1927	3n duplicat	3	0.6364	HET	HET	0.6364	GAIN	0.3299	NA	NA	0.022654	0.798229	MISSENSE		
1040	1	CCDC146	1	7:7670893	Other	FALSE	GAIN	0.231	3n duplicat	3	0.6429	HET	HET	0.6429	GAIN	0.3151	NA	NA	0.003236	0.833849	TRUNCATING		
1041	10	UBR5	-1	8:1033764	Other	FALSE	GAIN	0.3383	4n monoal	4	0.7308	ASCNA	ASCNA	0.7308	AMP	0.5261	-0.10526	NA	0.009709	0.650484	MISSENSE		
1042	0	OKR1	1	8:1077878	Other	FALSE	GAIN	0.3383	5n Germlin	5	0.6667	ASCNA	ASCNA	0.6667	AMP	0.506	NA	NA	0.048112	MISSENSE			
1043	2	TG	1	8:1340531	Other	FALSE	GAIN	0.2421	4n monoal	4	0.6615	ASCNA	ASCNA	0.6615	AMP	0.4845	-0.01626	NA	0.02589	0.372493	MISSENSE		
1044	1	MYBL1	-1	8:6764729	Other	FALSE	GAIN	0.3414	4n monoal	4	NA	NA	NA	NA	GAIN	0.3944	-0.22655	NA	0.006472	0.646557	MISSENSE		
1045	0	C9orf72	1	9:2755243	Other	FALSE	NEUT	-0.0445	Normal (A/	2	0.6047	HET	HET	0.6047	NEUT	0.0058	NA	0.006803	0.009709	0.649909	MISSENSE		
1046	0	GPRASP1	1	X:1017973	Other	FALSE	NEUT	0.0564	NA	NA	NA	NA	NLOH	0.7241	NEUT	0.0883	NA	NA	0.003236	NA	MISSENSE		
1047	1	SH3KBP1	-1	X:1947395	Other	FALSE	GAIN	0.2132	NA	NA	NA	NA	HET	0.6203	GAIN	0.3154	-0.33189	NA	NA	NA	MISSENSE		
1048	0	ATRX	-1	X:7666443	Other	FALSE	NEUT	0.0564	NA	NA	NA	NA	HET	0.6	NEUT	0.0705	NA	NA	NA	MISSENSE			
1049	0	LPAR4	1	X:7789770	Other	FALSE	NEUT	0.0564	NA	NA	NA	NA	NLOH	0.683	NEUT	0.0705	-0.22887	NA	0.009709	NA	MISSENSE		
1050	49	SPG7	1	16:881405	Basal	FALSE	NEUT	-0.0283	2n Somatic	2	0.8855	DLOH	DLOH	0.8855	HETD	-0.2085	NA	NA	0.003236	NA	MISSENSE		
1051	6	CPXM2	-1	10:125518	Basal	FALSE	NEUT	-0.0936	3n duplicat	3	0.625	HET	NA	NA	NA	NA	NA	NA	0.006472	0.651571	MISSENSE		
1052	0	MYO3A	1	10:264253	Basal	FALSE	NEUT	0.1262	4n Somatic	4	0.5614	HET	NA	NA	NA	NA	NA	0.006803	0.009709	0.986407	MISSENSE		
1053	0	STAB2	1	12:102572	Basal	FALSE	HETD	-0.3234	2n Somatic	2	0.8	NLOH	NA	NA	NA	NA	NA	NA	0.029126	0.983223	MISSENSE		
1054	0	ABCC9	-1	12:219702	Basal	FALSE	NEUT	0.1234	4n balance	4	0.5538	HET	NA	NA	NA	NA	-0.03346	NA	0.012945	0.370569	MISSENSE		
1055	0	SUTRK6	-1	13:852681	Basal	FALSE	GAIN	0.4942	6n monoal	6	0.7838	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.833585	MISSENSE		
1056	0	GARNL1	-1	14:352999	Basal	FALSE	HETD	-0.3386	2n Somatic	2	0.8125	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.649351	MISSENSE		
1057	11	KIAA0556	1	16:276973	Basal	FALSE	HETD	-0.3573	2n Somatic	2	0.8205	NLOH	NA	NA	NA	NA	NA	NA	0.012945	0.419314	MISSENSE		
1058	0	KRT34	-1	17:367887	Basal	FALSE	GAIN	0.2776	4n Somatic	4	0.8611	NLOH	NA	NA	NA	NA	NA	NA	NA	0.42192	MISSENSE		
1059	29	DUSP3	-1	17:392076	Basal	FALSE	GAIN	0.2776	5n Somatic	5	0.8611	NLOH	NA	NA	NA	NA	-0.20544	NA	NA	0.420181	MISSENSE		
1060	6	C17orf71	1	17:546424	Basal	FALSE	NEUT	0.1133	4n Somatic	4	0.875	NLOH	NA	NA	NA	NA	NA	NA	0.009709	0.89316	MISSENSE		
1061	1	QRICH2	-1	17:718015	Basal	FALSE	NEUT	0.1133	4n Somatic	4	0.875	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.996685	MISSENSE		
1062	0	KATNAL2	1	18:428139	Basal	FALSE	GAIN	0.4326	6n Germlin	6	0.7672	NLOH	NA	NA	NA	NA	NA	NA	NA	0.646343	MISSENSE		
1063	0	HRNR	-1	1:1504580	Basal	FALSE	GAIN	0.3581	5n Germlin	5	NA	NA	NA	NA	NA	NA	NA	NA	0.003236	0.643232	MISSENSE		
1064	5	CDC42BPA	-1	1:2252491	Basal	FALSE	GAIN	0.3581	5n non-mo	5	0.6117	HET	NA	NA	NA	NA	NA	NA	0.003236	1	MISSENSE		
1065	0	CBB	-1	1:5717010	Basal	FALSE	NEUT	0.1117	4n monoal	4	0.6929	NLOH	NA	NA	NA	NA	-0.13898	NA	0.003236	0.989861	MISSENSE		
1066	48	POLR3H	-1	22:402579	Basal	FALSE	NEUT	-0.0654	3n Somatic	3	0.625	HET	NA	NA	NA	NA	-0.62316	NA	NA	0.982989	MISSENSE		
1067	0	PDE11A	-1	2:1785872	Basal	FALSE	NEUT	-0.0755	3n duplicat	3	0.6219	HET	NA	NA	NA	NA	-0.09163	NA	0.009709	0.994525	MISSENSE		
1068	1	NBEAL1	1	2:2037218	Basal	FALSE	NEUT	-0.0755	3n Somatic	3	0.6219	HET	NA	NA	NA	NA	NA	NA	0.003236	0.421977	MISSENSE		
1069	1005	NCL	-1	2:2320346	Basal	FALSE	NEUT	-0.0755	3n duplicat	3	0.6219	HET	NA	NA	NA	NA	-0.10632	NA	0.006472	0.886993	MISSENSE		
1070	1018	NCL	-1	2:2320346	Basal	FALSE	NEUT	-0.0755	3n duplicat	3	0.6219	HET	NA	NA	NA	NA	-0.10632	NA	0.006472	0.651565	MISSENSE		
1071	5	HEATR5B	-1	2:3712191	Basal	TRUE	NEUT	0.1317	4n monoal	4	0.6842	NLOH	NA	NA	NA	NA	NA	NA	0.016181	0.705629	SPICE		
1072	0	PCDH10	1	4:1342930	Basal	FALSE	HETD	-0.3574	Normal (A/	2	0.5684	HET	NA	NA	NA	NA	-0.12578	NA	0.003236	0.660058	MISSENSE		
1073	188	HNRNP1	-1	5:1789805	Basal	FALSE	HETD	-0.3636	Normal (A/	2	0.5769	HET	NA	NA	NA	NA	-0.16489	NA	NA	0.709231	MISSENSE		
1074	0	GRIK2	1	6:1024442	Basal	FALSE	GAIN	0.2172	4n monoal	4	0.5912	HET	NA	NA	NA	NA	-0.16483	NA	0.009709	0.665554	MISSENSE		
1075	0	HIST1H4A	1	6:2621610	Basal	FALSE	GAIN	0.3081	5n non-mo	5	0.58	HET	NA	NA	NA	NA	NA	NA	NA	0.697172	MISSENSE		
1076	1	SUPT3H	-1	6:4502904	Basal	FALSE	GAIN	0.3235	5n non-mo	5	0.5641	HET	NA	NA	NA	NA	NA	NA	0.006472	0.632567	MISSENSE		
1077	0	DST	-1	6:5658916	Basal	FALSE	GAIN	0.3235	5n non-mo	5	0.5641	HET	NA	NA	NA	NA	-0.01971	0.068027	0.038835	0.838862	MISSENSE		
1078	0	RHEB	-1	7:1508189	Basal	FALSE	GAIN	0.244	5n non-mo	5	0.5879	HET	NA	NA	NA	NA	-0.37316	NA	NA	0.656348	MISSENSE		
1079	2	NPR2	1	9:3579558	Basal	FALSE	AMP	0.7282	6n non-mo	6	0.6623	NLOH	NA	NA	NA	NA	-0.13719	NA	0.006472	1	MISSENSE		
1080	24	KLHL13	-1	X:1169172	Basal	FALSE	HETD	-0.3483	NA	NA	NA	NA	NA	NA	NA	NA	-0.1295	NA	NA	NA	MISSENSE		
1081	24	TMEM126A	1	11:850442	Other	FALSE	NEUT	0.0553	3n duplicat	3	0.5755	HET	HET	0.6129	NEUT	0.0915	NA	NA	0.006472	0.267938	MISSENSE		
1082	44	RB1	1	13:479318	Other	FALSE	HETD	-0.134	2n Somatic	2	0.6429	NLOH	DLOH	0.6667	HETD	-0.204	-1.22447	0.07483	0.019417	0.410454	MISSENSE		
1083	0	PDILT	-1	16:202842	Other	FALSE	NEUT	0.029	4n balance	4	0.5882	HET	HET	0.6154	NEUT	0.1175	NA	NA	NA	0.210065	MISSENSE		
1084	6	B4GALT5	-1	20:476904	Other	FALSE	NEUT	0.06	4n balance	4	0.6111	HET	HET	0.6111	NEUT	0.1619	-0.04918	NA	0.003236	0.21178	MISSENSE		
1085	17	HP54	-1	22:251792	Other	FALSE	NEUT	0.0367	4n balance	4	0.6154	HET	HET	0.6154	NEUT	0.1211	NA	NA	NA	0.536278	MISSENSE		
1086	28	XPO1	-1	2:6157759	Other	FALSE	HETD	-0.1463	2n Somatic	2	0.6667	DLOH	DLOH	0.6667	HETD	-0.1931	-1.49217	NA	0.003236	0.288139	MISSENSE		
1087	0	A4GNT	-1	3:1393262	Other	FALSE	NEUT	0.0743	4n balance	4	0.6111	HET	HET	0.6111	NEUT	0.0647	NA	NA	NA	0.685973	MISSENSE		
1088	0	MASP1	-1	3:1884236	Other	FALSE	NEUT	0.0754	4n balance	4	0.6111	HET	HET	0.6111	NEUT	0.0795	-0.12237	NA	0.012945	0.693807	MISSENSE		
1089	2	ULK4	-1	3:4192764	Other	FALSE	NEUT	0.0567	4n balance	4	0.6154	HET	HET	0.6154	NEUT	0.0064	NA	NA	0.006472	0.212978	MISSENSE		
1090	7	HIVEP2	-1	6:1431160	Other	FALSE	NEUT	0.1136	4n balance	4	0.6111	HET	HET	0.6111	NEUT	0.1556	NA	NA	0.009709	0.695627	MISSENSE		
1091	0	SAGE1	1	X:1348172	Other	FALSE	HETD	-0.1254	NA	NA	NA	NA	DLOH	0.7	HETD	-0.1694	NA	NA	0.003236	NA	MISSENSE		
1092	2	TAF5	1	10:105129	Other	FALSE	NEUT	-0.0775	3n duplicat	3	0.625	HET	HET	0.625	NEUT	-0.0803	-0.12115	NA	0.006472	0.694831	MISSENSE		
1093	0	BTBD16	1	10:124033	Other	FALSE	NEUT	-0.0775	3n duplicat	3	0.6364	HET	HET	0.6364	NEUT	-0.0803	NA	NA	NA	0.811461	MISSENSE		
1094	2	C10orf18	1	10:580902	Other	FALSE	NEUT	0.0692	4n balance	4	0.6071	HET	HET	0.6071	GAIN	0.1149	NA	NA	0.003236	0.979717	MISSENSE		
1095	95	ERBB3	1	12:547651	Other	FALSE	NEUT	0.0407	3n Somatic	3	0.6061	HET	HET	0.6061	NEUT	0.0384	-0.38038	0.006803	0.006472	0.692366	MISSENSE		
1096	0	KCNH5	-1	14:622440	Other	FALSE	NEUT	0.004	4n monoal	4	0.6429	NLOH	NLOH	0.6429	NEUT	0.0104	NA	NA	0.012945	0.286659	MISSENSE		
1097	3	SYNE2	-1	14:636615	Other	FALSE	NEUT	0.004	3n duplicat	3	0.6429	NLOH	NLOH	0.6429	NEUT	0.0104	NA	NA	0.02589	0.532677	MISSENSE		
1098	19	TCF12	1	15:553328	Other	FALSE	HETD	-0.1636	3n duplicat	3	0.6154	HET	HET	0.6154	HETD	-0.264	-0.01392	0.020408	0.006472	0.413518	MISSENSE		

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDos	HMMDos	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
1106	1	ADAM12	-1	10:127727	Basal	FALSE	NEUT	0.0254	4n Somatic	4	0.7018	NLOH	NA	NA	NA	NA	-0.22408	0.006803	0.006472	0.67817	MISSENSE		
1107	0	GPR158	-1	10:259179	Basal	FALSE	NEUT	-0.0155	2n Somatic	2	0.6891	NLOH	NA	NA	NA	NA	NA	NA	0.012945	1	MISSENSE		
1108	0	MMP13	-1	11:102331	Basal	FALSE	NEUT	-0.0064	2n Somatic	2	0.697	NLOH	NA	NA	NA	NA	-0.09675	NA	0.006472	0.694166	MISSENSE		
1109	19	UBE3B	-1	12:108406	Basal	FALSE	HETD	-0.1842	Hemizygous	1	0.6212	HET	NA	NA	NA	NA	-0.13405	NA	0.006472	0.693046	MISSENSE		
1110	0	COL4A1	-1	13:109626	Basal	FALSE	NEUT	0.0833	4n Somatic	4	0.7071	NLOH	NA	NA	NA	NA	-0.42461	0.006803	0.009709	0.52707	MISSENSE		
1111	24	CNDDBP1	-1	15:412738	Basal	FALSE	NEUT	-0.0213	2n Somatic	2	0.6923	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.688078	MISSENSE		
1112	14	TP53BP1	-1	15:415117	Basal	FALSE	NEUT	-0.0213	2n Somatic	2	0.6923	NLOH	NA	NA	NA	NA	-0.09287	NA	0.006472	0.692309	MISSENSE		
1113	0	SEMA6D	-1	15:458460	Basal	FALSE	NEUT	-0.0213	3n Somatic	3	0.6923	NLOH	NA	NA	NA	NA	-0.07446	NA	NA	0.815105	TRUNCATING		
1114	39	TLCID1	-1	17:240764	Basal	FALSE	HETD	-0.1947	Hemizygous	1	0.6154	HET	NA	NA	NA	NA	NA	NA	NA	0.280701	MISSENSE		
1115	3	TLK2	-1	17:579673	Basal	FALSE	NEUT	0.0075	4n Somatic	4	0.7188	NLOH	NA	NA	NA	NA	NA	NA	NA	0.68517	MISSENSE		
1116	1	FHOD3	-1	18:325525	Basal	FALSE	NEUT	0.1139	5n non-mo	5	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.406924	MISSENSE		
1117	0	ST8SIA3	-1	18:531755	Basal	FALSE	NEUT	0.0214	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.210144	MISSENSE		
1118	0	HIF3A	-1	19:515262	Basal	FALSE	NEUT	0.0202	4n monoal	4	0.5855	HET	NA	NA	NA	NA	-0.05083	NA	NA	0.283054	MISSENSE		
1119	62	NRAS	-1	1:1150601	Basal	FALSE	NEUT	-0.0105	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-1.14222	NA	0.006472	0.411804	MISSENSE		
1120	1	PDE4DIP	-1	1:1436426	Basal	FALSE	GAIN	0.2837	6n monoal	6	0.594	HET	NA	NA	NA	NA	NA	NA	0.009709	0.209806	MISSENSE		
1121	0	RNASEL	-1	1:1808222	Basal	FALSE	NEUT	-0.0111	3n Somatic	3	0.7258	NLOH	NA	NA	NA	NA	NA	NA	0.009709	0.24344	MISSENSE		
1122	23	DHDDS	-1	1:2664540	Basal	FALSE	NEUT	0.0358	Normal (A)	2	0.5882	HET	NA	NA	NA	NA	-0.013	NA	NA	0.527255	MISSENSE		
1123	0	DOCK7	-1	1:6288646	Basal	FALSE	NEUT	-0.0034	Normal (A)	2	0.5682	HET	NA	NA	NA	NA	NA	NA	0.006472	0.9946	MISSENSE		
1124	0	DOCK7	-1	1:6288646	Basal	FALSE	NEUT	-0.0034	Normal (A)	2	0.5682	HET	NA	NA	NA	NA	NA	NA	0.006472	0.29113	MISSENSE		
1125	0	RP5-10170	1,-1	1:7251304	Basal	FALSE	NEUT	-0.0034	5n non-mo	5	0.5682	HET	NA	NA	NA	NA	NA	NA	NA	0.533488	MISSENSE		
1126	0	TGM3	-1	2:2025686	Basal	FALSE	NEUT	-0.0374	3n Somatic	3	0.6923	NLOH	NA	NA	NA	NA	NA	NA	0.009709	0.662725	MISSENSE		
1127	0	DPP10	-1	2:1159999	Basal	FALSE	NEUT	-0.0082	2n Germli	2	0.7091	NLOH	NA	NA	NA	NA	NA	NA	0.016181	0.694114	MISSENSE		
1128	112	CRIM1	-1	2:3659426	Basal	FALSE	NEUT	0.1179	4n Somatic	4	0.7091	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.693008	MISSENSE		
1129	0	LHCGR-TC	1,-1	2:4881191	Basal	FALSE	NEUT	0.117	4n Somatic	4	0.7091	NLOH	NA	NA	NA	NA	NA	NA	NA	0.852166	MISSENSE		
1130	26	PLEKHG1	-1	1:61512026	Basal	FALSE	NEUT	2.00E-04	2n Somatic	2	0.6786	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.745725	MISSENSE		
1131	0	TREML1	-1	6:4122556	Basal	FALSE	HETD	-0.2171	Hemizygous	1	0.6061	HET	NA	NA	NA	NA	NA	NA	NA	0.999904	MISSENSE		
1132	0	KLHL32	-1	6:9766839	Basal	FALSE	NEUT	0.1256	4n Germli	4	0.7	NLOH	NA	NA	NA	NA	NA	NA	0.009709	0.999876	MISSENSE		
1133	0	MET	-1	7:1161967	Basal	TRUE	GAIN	0.2587	6n balance	6	0.569	HET	NA	NA	NA	NA	-0.84817	0.020408	0.012945	0.999718	SPICE		
1134	6	BRAF	-1	7:1401232	Basal	FALSE	GAIN	0.2328	6n balance	6	0.569	HET	NA	NA	NA	NA	-0.85365	NA	0.006472	0.870645	MISSENSE		
1135	0	CRHR2	-1	7:3066890	Basal	FALSE	NEUT	0.0936	4n Somatic	4	0.7097	NLOH	NA	NA	NA	NA	-0.16638	NA	0.003236	0.997917	MISSENSE		
1136	7	INHBA	-1	7:4169656	Basal	FALSE	GAIN	0.2293	6n Germli	6	0.7097	NLOH	NA	NA	NA	NA	-0.19785	NA	0.003236	0.999812	MISSENSE		
1137	22	LANCL2	-1	7:5542705	Basal	FALSE	NEUT	0.0961	3n duplicat	3	0.6	HET	NA	NA	NA	NA	NA	NA	0.003236	0.866148	MISSENSE		
1138	4	DAGLB	-1	7:6430912	Basal	FALSE	NEUT	0.1028	4n Somatic	4	0.7097	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.999685	MISSENSE		
1139	0	COL22A1	-1	8:1398623	Basal	FALSE	GAIN	0.2795	6n Somatic	6	0.7365	NLOH	NA	NA	NA	NA	-0.1452	NA	0.032362	0.870515	TRUNCATING		
1140	0	C8orf34	-1	8:6959657	Basal	FALSE	NEUT	-0.018	3n Somatic	3	0.7365	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.869616	MISSENSE		
1141	40	RDH10	-1	8:7439575	Basal	FALSE	NEUT	-0.018	3n Somatic	3	0.7365	NLOH	NA	NA	NA	NA	-0.73035	NA	NA	0.739968	MISSENSE		
1142	0	SILC26A7	-1	8:9237690	Basal	FALSE	NEUT	-0.018	2n Germli	2	0.7365	NLOH	NA	NA	NA	NA	-0.07082	NA	0.006472	0.994811	MISSENSE		
1143	0	TAF1L	-1	9:3262046	Basal	FALSE	NEUT	-0.0085	2n Somatic	2	0.6875	NLOH	NA	NA	NA	NA	-0.04738	NA	NA	0.992326	MISSENSE		
1144	0	INSLB	-1	9:5153978	Basal	FALSE	NEUT	-0.0028	2n Germli	2	0.6875	NLOH	NA	NA	NA	NA	NA	NA	NA	0.871085	MISSENSE		
1145	19	DAPK1	-1	9:8940986	Basal	FALSE	NEUT	-0.0216	3n Somatic	3	0.6875	NLOH	NA	NA	NA	NA	-0.39927	NA	0.003236	0.747047	MISSENSE		
1146	0	CENPI	-1	X:1002867	Basal	FALSE	NEUT	0.0452	NA	NA	NA	NA	NA	NA	NA	NA	-0.10234	NA	NA	NA	MISSENSE		
1147	0	MID2	-1	X:1069711	Basal	FALSE	NEUT	0.0452	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.003236	NA	MISSENSE		
1148	0	BCORL1	-1	X:1289759	Basal	FALSE	NEUT	0.0452	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.012945	NA	MISSENSE		
1149	0	GPR112	-1	X:1352579	Basal	FALSE	NEUT	0.0452	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.016181	NA	MISSENSE		
1150	0	RP13-50712	-1	X:1491509	Basal	FALSE	NEUT	0.1309	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE		
1151	19	TMEM47	-1	X:3455843	Basal	FALSE	NEUT	-0.0843	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE		
1152	84	DDX3X	-1	X:4108848	Basal	FALSE	NEUT	0.0632	NA	NA	NA	NA	NA	NA	NA	NA	-0.12374	NA	0.003236	NA	MISSENSE		
1153	0	LPAR4	-1	X:7789765	Basal	FALSE	NEUT	0.0632	NA	NA	NA	NA	NA	NA	NA	NA	-0.2281	NA	0.009709	NA	MISSENSE		
1154	73	USMG5	-1	10:105141	Basal	FALSE	NEUT	-0.1273	2n Somatic	2	0.7083	NLOH	NA	NA	NA	NA	NA	NA	NA	1	MISSENSE		
1155	12	ZEB1	-1	10:318504	Basal	FALSE	NEUT	-0.116	2n Somatic	2	0.7091	NLOH	NA	NA	NA	NA	-0.13225	NA	0.009709	0.995347	MISSENSE		
1156	23	NRP1	-1	10:335853	Basal	FALSE	NEUT	-0.116	2n Somatic	2	0.7091	NLOH	NA	NA	NA	NA	-0.16693	NA	0.003236	0.870342	MISSENSE		
1157	366	PHLDA1	-1	12:747109	Basal	FALSE	NEUT	-0.1208	2n Somatic	2	0.7037	NLOH	NA	NA	NA	NA	NA	NA	NA	0.870945	MISSENSE		
1158	42	PCCA	-1	13:995531	Basal	FALSE	NEUT	-0.055	2n Somatic	2	0.7143	NLOH	NA	NA	NA	NA	-1.16069	NA	NA	0.999048	MISSENSE		
1159	56	BAZ1A	-1	14:343151	Basal	FALSE	NEUT	-0.1139	2n Somatic	2	0.7	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.716181	MISSENSE		
1160	2	NTRK3	-1	15:865284	Basal	TRUE	NEUT	-0.1307	2n Somatic	2	0.7037	NLOH	NA	NA	NA	NA	-0.25041	0.013605	0.019417	0.761593	SPICE		
1161	0	MSLN1	-1	16:759455	Basal	FALSE	NEUT	-0.0236	3n duplicat	3	0.6203	HET	NA	NA	NA	NA	NA	NA	0.003236	0.751822	MISSENSE		
1162	0	CLT7orf47	-1	17:539754	Basal	FALSE	GAIN	0.1874	4n Somatic	4	0.7368	NLOH	NA	NA	NA	NA	NA	NA	NA	0.996831	MISSENSE		
1163	24	TP53	-1	17:751759	Basal	FALSE	NEUT	-0.1379	2n Somatic	2	0.7021	NLOH	NA	NA	NA	NA	-2.01044	0.306122	0.812298	0.991072	TRUNCATING		
1164	31	LDLR	-1	19:110877	Basal	FALSE	GAIN	0.1528	5n non-mo	5	0.5769	HET	NA	NA	NA	NA	-0.30296	NA	0.006472	0.885923	MISSENSE		
1165	70	PGM1	-1	1:6386766	Basal	FALSE	GAIN	0.2197	6n balance	6	0.5676	HET	NA	NA	NA	NA	-1.3769	NA	0.003236	0.876751	MISSENSE		
1166	15	ARFGEF2	-1	20:470223	Basal	FALSE	GAIN	0.178	4n balance	4	0.5789	HET	NA	NA	NA	NA	-0.23175	NA	NA	0.995139	MISSENSE		
1167	123	PPIG	-1	2:1701956	Basal	FALSE	NEUT	-0.1028	2n Somatic	2	0.7045	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.989842	MISSENSE		
1168	46	CASP8	-1	2:2018582	Basal	FALSE	NEUT	-0.1028	2n Germli	2	0.7045	NLOH	NA	NA	NA	NA	-1.61767	NA	NA	0.883039	MISSENSE		
1169	0	EMILIN1	-1	2:2715993	Basal	FALSE	NEUT	-0.1196	2n Germli	2	0.7105												

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	Ens54Gene	Strand	primer	PAM50	Splice.site	HMMDos	HMMDos	OncoSNP	OncoSNP	apolloh.jo	apolloh.cal	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
1175	0	TAS2R1	-1	5:9682752	Basal	FALSE	GAIN	0.1976	4n balance	4	0.5714	NA	NA	NA	NA	NA	-0.04069	NA	0.009709	1	MISSENSE		
1176	0	MEP1A	-1	6:4690890	Basal	FALSE	NEUT	-0.0951	2n Somatic	2	0.7059	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.905232	MISSENSE		
1177	0	PKHD1	-1	6:5188466	Basal	FALSE	NEUT	-0.0951	2n Somatic	2	0.7059	NLOH	NA	NA	NA	NA	NA	NA	0.032362	0.612127	MISSENSE		
1178	11	MDN1	-1	6:9045134	Basal	FALSE	NEUT	-0.09	2n Somatic	2	0.7059	NLOH	NA	NA	NA	NA	NA	NA	0.02589	0.426439	MISSENSE		
1179	0	DNM1	-1	9:1300221	Basal	FALSE	NEUT	-0.064	2n Somatic	2	0.625	HET	NA	NA	NA	NA	-0.7214	NA	0.006472	0.750061	MISSENSE		
1180	0	SASH3	-1	X:1287540	Basal	FALSE	NEUT	-0.1034	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.006472	NA	MISSENSE		
1181	20	IFI27L2	-1	14:936646	Basal	FALSE	HETD	-0.2016	Hemizygous	1	0.65	DLOH	DLOH	0.65	HETD	-0.2504	NA	NA	NA	0.748982	MISSENSE		
1182	12	ZNF609	-1	15:627496	Basal	FALSE	NEUT	-0.0395	Hemizygous	1	0.6087	HET	HET	0.6087	NEUT	-0.0473	NA	NA	0.003236	0.752144	MISSENSE		
1183	0	VWA3A	-1	16:220518	Basal	FALSE	NEUT	-0.0189	Normal (A)	2	0.6071	HET	HET	0.6071	NEUT	0.0019	NA	NA	0.003236	0.756755	MISSENSE		
1184	0	SULT1A2	-1	16:285146	Basal	FALSE	NEUT	-0.0189	Normal (A)	2	0.6071	HET	HET	0.6071	NEUT	0.0019	-0.03601	NA	NA	0.424283	MISSENSE		
1185	0	TTC25	-1	17:373484	Basal	FALSE	HETD	-0.1686	Hemizygous	1	0.6522	DLOH	DLOH	0.6522	HETD	-0.227	NA	NA	0.003236	0.743245	MISSENSE		
1186	19	ATXN7L2	-1	1:1098353	Basal	FALSE	HETD	-0.1845	Hemizygous	1	0.6538	DLOH	DLOH	0.6538	HETD	-0.2424	NA	NA	0.006472	0.425817	MISSENSE		
1187	0	FAM71A	-1	1:2108652	Basal	FALSE	GAIN	0.4577	6n monoal	6	0.6842	ASCNA	ASCNA	0.6842	AMP	0.6505	NA	NA	0.003236	0.425155	MISSENSE		
1188	1	EHD3	-1	2:3134298	Basal	FALSE	NEUT	0.0348	Normal (A)	2	0.6061	HET	HET	0.6061	NEUT	0.0572	-0.10418	NA	NA	0.991708	MISSENSE		
1189	101	RNF130	-1	5:1794002	Basal	FALSE	HETD	-0.1558	Hemizygous	1	0.6207	HET	HET	0.6207	HETD	-0.1347	NA	NA	0.003236	0.766599	MISSENSE		
1190	2	LRRC16A	-1	6:2570883	Basal	FALSE	NEUT	-0.012	Normal (A)	2	0.6098	HET	HET	0.6098	NEUT	0.006	NA	NA	0.003236	0.611039	MISSENSE		
1191	232	TP53	-1	17:751822	Basal	FALSE	NEUT	-0.1048	2n Somatic	2	0.6057	HET	NA	NA	NA	NA	-0.93756	0.306122	0.812298	NA	MISSENSE		
1192	3	NCOA1	-1	2:2480467	Basal	FALSE	NEUT	0.0274	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	-0.39208	NA	0.003236	NA	TRUNCATING		
1193	0	AC011740	-1,1	2:2701833	Basal	FALSE	NEUT	0.0274	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE		
1194	4	RNF180	-1	5:6353223	Basal	FALSE	NEUT	-0.065	2n Germlin	2	0.6069	HET	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE		
1195	0	ANKRD30A	-1	10:375479	Basal	FALSE	GAIN	0.2857	6n monoal	6	0.72	NLOH	NA	NA	NA	NA	NA	NA	0.022654	1	MISSENSE		
1196	9	LARP5	-1	10:856710	Basal	FALSE	GAIN	0.3911	6n non-mo	6	0.5957	HET	NA	NA	NA	NA	NA	NA	NA	0.611005	MISSENSE		
1197	2	CL1orf63	-1	11:122335	Basal	FALSE	NEUT	-0.0274	Normal (A)	2	0.5872	HET	NA	NA	NA	NA	NA	NA	0.009709	0.734572	MISSENSE		
1198	0	PTPN5	-1	11:187116	Basal	FALSE	GAIN	0.2292	6n balance	6	0.5789	HET	NA	NA	NA	NA	-0.16902	NA	0.009709	0.98913	TRUNCATING		
1199	47	LRP5	-1	11:679275	Basal	FALSE	NEUT	-0.0522	NA	NA	0.6	HET	NA	NA	NA	NA	-0.17863	NA	NA	NA	MISSENSE		
1200	1	SSH1	-1	12:107727	Basal	FALSE	NEUT	-0.0618	3n duplicat	3	0.5795	HET	NA	NA	NA	NA	-0.21047	NA	0.012945	0.750102	MISSENSE		
1201	0	CL2orf60	-1	12:148674	Basal	FALSE	HETD	-0.2374	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.993137	MISSENSE		
1202	0	NEUROD4	-1	12:537066	Basal	FALSE	NEUT	-0.041	2n Germlin	2	0.5849	HET	NA	NA	NA	NA	NA	NA	0.009709	0.980607	MISSENSE		
1203	13	FAM62A	-1	12:548122	Basal	FALSE	GAIN	0.1629	5n non-mo	5	0.5849	HET	NA	NA	NA	NA	NA	NA	0.003236	0.425244	MISSENSE		
1204	1	WNK1	-1	12:873960	Basal	TRUE	NEUT	-0.0661	3n duplicat	3	0.5847	HET	NA	NA	NA	NA	NA	NA	0.012945	0.425399	SPICE		
1205	1	FLT1	-1	13:278993	Basal	FALSE	GAIN	0.2114	5n non-mo	5	0.5833	HET	NA	NA	NA	NA	-0.46552	0.013605	0.006472	0.745009	MISSENSE		
1206	1	AKAP6	-1	14:319726	Basal	FALSE	NEUT	0.103	5n non-mo	5	0.5714	HET	NA	NA	NA	NA	NA	NA	0.016181	0.631039	MISSENSE		
1207	1	GARNL1	-1	14:351662	Basal	FALSE	NEUT	-0.0953	4n balance	4	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.227628	MISSENSE		
1208	3	SIX4	-1	14:602568	Basal	FALSE	NEUT	-0.0953	2n Somatic	2	0.6709	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.783007	MISSENSE		
1209	3	PCNX	-1	14:705137	Basal	FALSE	NEUT	-0.1211	2n Somatic	2	0.6709	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.219094	MISSENSE		
1210	2	DMXL2	-1	15:495368	Basal	FALSE	HETD	-0.2832	Hemizygous	1	0.6111	HET	NA	NA	NA	NA	NA	NA	0.019417	0.218532	MISSENSE		
1211	1	DIS3L	-1	15:643931	Basal	TRUE	NEUT	0.0813	3n Germlin	3	0.6111	HET	NA	NA	NA	NA	NA	NA	0.006472	0.464941	SPICE		
1212	0	MYH4	-1	17:102990	Basal	FALSE	NEUT	-0.0018	3n Somatic	3	0.72	NLOH	NA	NA	NA	NA	-0.21608	NA	0.032362	0.984313	MISSENSE		
1213	0	CYTSB	-1	17:201579	Basal	FALSE	NEUT	0.0875	4n balance	4	0.5833	HET	NA	NA	NA	NA	NA	NA	0.003236	0.774092	MISSENSE		
1214	1	ITGAE, GSG	-1,1	17:357558	Basal	FALSE	GAIN	0.2029	5n Somatic	5	0.72	NLOH	NA	NA	NA	NA	NA	NA	NA	0.476457	MISSENSE		
1215	0	CCDC68	-1	18:507470	Basal	FALSE	NEUT	-0.0848	2n Somatic	2	0.6869	NLOH	NA	NA	NA	NA	NA	NA	NA	0.218947	MISSENSE		
1216	0	SHANK1	-1	19:559114	Basal	FALSE	NEUT	0.0944	4n monoal	4	0.6111	HET	NA	NA	NA	NA	NA	NA	NA	0.219117	MISSENSE		
1217	0	SASS6	-1	1:1003596	Basal	FALSE	NEUT	0.0355	3n duplicat	3	0.5833	HET	NA	NA	NA	NA	NA	NA	0.003236	0.53362	MISSENSE		
1218	0	SLC2A7	-1	1:9000884	Basal	FALSE	GAIN	0.3343	6n Somatic	6	0.75	NLOH	NA	NA	NA	NA	NA	NA	NA	0.758407	MISSENSE		
1219	18	RANBP2	-1	2:1087554	Basal	FALSE	NEUT	0.0807	4n Somatic	4	0.7356	NLOH	NA	NA	NA	NA	-0.28855	NA	NA	1	MISSENSE		
1220	0	CSRP3	-1	2:1662438	Basal	FALSE	NEUT	-0.1065	2n Somatic	2	0.6769	NLOH	NA	NA	NA	NA	NA	NA	0.009709	0.996948	MISSENSE		
1221	0	CN1A	-1	2:1666060	Basal	FALSE	NEUT	-0.1065	2n Somatic	2	0.6769	NLOH	NA	NA	NA	NA	NA	NA	0.019417	0.218307	MISSENSE		
1222	0	CASP10	-1	2:2018020	Basal	FALSE	NEUT	-0.1065	2n Somatic	2	0.6769	NLOH	NA	NA	NA	NA	-0.27245	NA	0.003236	0.329151	MISSENSE		
1223	0	APOB	-1	2:2108538	Basal	FALSE	NEUT	0.0431	3n Somatic	3	0.6667	NLOH	NA	NA	NA	NA	-0.11675	NA	0.035599	0.087938	MISSENSE		
1224	5	REV1	-1	2:9940706	Basal	FALSE	NEUT	0.097	4n Somatic	4	0.7356	NLOH	NA	NA	NA	NA	-0.05452	NA	0.006472	0.092798	MISSENSE		
1225	0	SPATA16	-1	3:1741259	Basal	FALSE	GAIN	0.3319	6n non-mo	6	0.5739	HET	NA	NA	NA	NA	NA	NA	0.006472	0.257628	MISSENSE		
1226	1	PHF7	-1	3:5242993	Basal	FALSE	NEUT	-0.0737	2n Germlin	2	0.6818	NLOH	NA	NA	NA	NA	NA	NA	NA	0.253022	TRUNCATING		
1227	0	EPHA5	-1	4:6591334	Basal	FALSE	NEUT	0.0971	4n Germlin	4	0.7059	NLOH	NA	NA	NA	NA	-0.0694	NA	0.006472	0.757896	MISSENSE		
1228	0	F13A1	-1	6:6119838	Basal	FALSE	NEUT	0.0275	3n duplicat	3	0.5806	HET	NA	NA	NA	NA	-0.08533	0.006803	0.006472	0.442541	MISSENSE		
1229	0	FILIP1	-1	6:7612006	Basal	FALSE	NEUT	0.1103	5n Germlin	5	0.5949	HET	NA	NA	NA	NA	NA	NA	NA	0.326012	MISSENSE		
1230	2	MDN1	-1	6:9058595	Basal	FALSE	GAIN	0.2407	6n non-mo	6	0.5949	HET	NA	NA	NA	NA	NA	NA	0.02589	0.091558	TRUNCATING		
1231	0	TMEM176A	-1	7:1501323	Basal	FALSE	NEUT	0.1005	4n Somatic	4	0.75	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.087184	MISSENSE		
1232	24	UBR5	-1	8:1033771	Basal	FALSE	NEUT	0.0233	3n Somatic	3	0.7179	NLOH	NA	NA	NA	NA	-0.08224	NA	0.009709	0.253876	MISSENSE		
1233	0	BTX	-1	X:1005000	Basal	TRUE	GAIN	0.2172	NA	NA	NA	NA	NA	NA	NA	NA	-0.28305	0.006803	0.003236	NA	SPICE		
1234	0	ATP1B4	-1	X:1199332	Basal	FALSE	NEUT	0.0888	NA	NA	NA	NA	NA	NA	NA	NA	-0.1552	NA	0.003236	NA	MISSENSE		
1235	0	TUR7	-1	X:1281616	Basal	FALSE	NEUT	0.0063	NA	NA	NA	NA	NA	NA	NA	NA	-0.06148	NA	0.003236	NA	MISSENSE		
1236	0	GK	-1	X:3062244	Basal	FALSE	NEUT	0.0971	NA	NA	NA	NA	NA	NA	NA	NA	-0.5876	NA	NA	NA	MISSENSE		
1237	10	PTPN23	-1	3:4742755	Basal	FALSE	HETD	-0.2146	Hemizygous	1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE		
1238	239	TGFB1	-1	5:1354227	Bas																		

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
1244	0	LAMA2	1	6:1296544	Basal	FALSE	NEUT	0.0137	3n Germlin	3	0.5645	HET	NA	NA	NA	NA	-0.9752	NA	0.022654	0.255059	MISSENSE		
1245	1	BCLAF1	-1	6:1366387	Basal	FALSE	NEUT	-0.0232	3n Germlin	3	0.5248	HET	NA	NA	NA	NA	NA	NA	0.003236	0.555939	MISSENSE		
1246	3	SYNE1	-1	6:1527160	Basal	FALSE	NEUT	-0.0232	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	NA	0.047619	0.022654	0.445013	MISSENSE		
1247	17	ZNF76	1	6:3536208	Basal	FALSE	NEUT	-0.0855	2n Somatic	2	0.6818	NLOH	NA	NA	NA	NA	NA	NA	NA	0.63963	MISSENSE		
1248	238	TP53	-1	17:751822	Basal	FALSE	HETD	-0.3275	2n Somatic	2	0.5526	HET	NA	NA	NA	NA	-1.14852	0.306122	0.812298	NA	MISSENSE		
1249	13	FAM45A	1	10:120857	Basal	FALSE	HETD	-0.2059	2n Somatic	2	0.8426	HOMD	HOMD	0.8426	HOMD	-0.681	NA	NA	0.003236	NA	MISSENSE		
1250	0	SLC39A12	1	10:182822	Basal	FALSE	NEUT	0.0919	3n duplicat	3	0.6667	HET	HET	0.6667	NEUT	-0.0343	NA	NA	0.003236	NA	MISSENSE		
1251	0	GPR158	1	10:259017	Basal	FALSE	NEUT	0.0777	3n duplicat	3	0.6429	HET	HET	0.6429	NEUT	-0.0361	NA	NA	0.012945	NA	MISSENSE		
1252	2	ANKRD26	-1	10:273929	Basal	FALSE	NEUT	0.0777	3n duplicat	3	0.6429	HET	HET	0.6429	HETD	-0.3651	NA	NA	0.003236	NA	MISSENSE		
1253	0	ZNF488	1	10:479911	Basal	FALSE	NEUT	0.0823	NA	NA	0.6282	HET	HET	0.6282	NEUT	0.1072	NA	NA	0.003236	NA	MISSENSE		
1254	29	TSPAN15	1	10:709359	Basal	FALSE	NEUT	0.0624	3n duplicat	3	0.6571	HET	HET	0.6571	NEUT	0.0408	NA	NA	NA	NA	MISSENSE		
1255	8	USP54	-1	10:749289	Basal	FALSE	NEUT	0.0624	2n Germlin	2	0.651	HET	HET	0.651	HETD	-0.2699	NA	NA	0.003236	NA	TRUNCATING		
1256	15	SIK2	1	11:111080	Basal	FALSE	GAIN	0.3261	4n monoal	4	0.7048	HET	HET	0.7048	GAIN	0.2606	NA	NA	NA	NA	MISSENSE		
1257	4	THY1	-1	11:118796	Basal	FALSE	GAIN	0.2772	4n monoal	4	0.6923	HET	HET	0.6923	GAIN	0.3653	-0.32269	NA	NA	NA	MISSENSE		
1258	26	TPD52	1	11:478564	Basal	FALSE	HETD	-0.198	2n Somatic	2	0.8837	DLOH	DLOH	0.8837	HETD	-0.4005	-0.78415	NA	NA	NA	MISSENSE		
1259	46	TNKS1BP1	-1	11:568259	Basal	FALSE	NEUT	0.1156	3n duplicat	3	0.6364	HET	HET	0.6364	NEUT	0.0511	NA	NA	NA	NA	MISSENSE		
1260	23	GATC	1	12:119382	Basal	FALSE	HETD	-0.2449	2n Somatic	2	NA	NA	NA	NA	HOMD	-0.6403	NA	NA	NA	NA	MISSENSE		
1261	26	TBC1D4	-1	13:748213	Basal	FALSE	NEUT	0.1597	3n Somatic	3	0.8889	NLOH	NLOH	0.8889	NEUT	0.078	-0.48212	NA	0.012945	NA	MISSENSE		
1262	13	HECTD1	-1	14:306458	Basal	FALSE	NEUT	0.1183	3n Somatic	3	0.8636	DLOH	DLOH	0.8636	HETD	-0.3352	NA	NA	0.006472	NA	MISSENSE		
1263	3	MBIP	-1	14:358397	Basal	TRUE	NEUT	0.1042	3n Somatic	3	0.9	LOH	LOH	0.9	GAIN	0.1755	NA	NA	NA	NA	SPICE		
1264	0	CLEC14A	-1	14:377941	Basal	FALSE	NEUT	0.1042	3n Somatic	3	0.9091	NLOH	NLOH	0.9091	NEUT	0.0572	NA	NA	0.009709	NA	MISSENSE		
1265	4	THSD4	1	15:693224	Basal	FALSE	NEUT	0.0681	3n Somatic	3	0.8889	NLOH	NLOH	0.8889	NEUT	0.0685	NA	NA	0.006472	NA	TRUNCATING		
1266	97	HEXA	-1	15:704305	Basal	FALSE	NEUT	0.0681	3n Germlin	3	0.9091	NLOH	NLOH	0.9091	NEUT	-0.0231	-0.83267	NA	0.009709	NA	MISSENSE		
1267	15	LYSMD4	AC-1,-1	15:980871	Basal	FALSE	NEUT	0.0503	3n Somatic	3	0.8966	NLOH	NLOH	0.8966	NEUT	0.0568	NA	NA	NA	NA	MISSENSE		
1268	19	ZNF668	-1	16:309830	Basal	FALSE	HETD	-0.2319	2n Somatic	2	0.8571	DLOH	DLOH	0.8571	HETD	-0.4637	NA	NA	NA	NA	MISSENSE		
1269	0	COG8	-1	16:679308	Basal	FALSE	NEUT	0.0048	2n Somatic	2	NA	NA	NA	NA	NEUT	-0.0569	NA	NA	0.003236	NA	TRUNCATING		
1270	93	SLFN11	-1	17:307037	Basal	FALSE	HETD	-0.2227	2n Somatic	2	0.8571	DLOH	DLOH	0.8571	HETD	-0.3973	NA	NA	0.003236	NA	MISSENSE		
1271	3	SLFN12	-1	17:307733	Basal	FALSE	HETD	-0.2227	2n Somatic	2	0.8571	DLOH	DLOH	0.8571	HETD	-0.3973	NA	NA	NA	NA	MISSENSE		
1272	27	CRKRS	-1	17:349213	Basal	FALSE	HETD	-0.2066	2n Somatic	2	0.8	HOMD	HOMD	0.8	HOMD	-0.7416	NA	NA	0.019417	NA	TRUNCATING		
1273	242	ERBB2	1	17:351348	Basal	FALSE	HETD	-0.2066	2n Somatic	2	0.8611	DLOH	DLOH	0.8611	HETD	-0.3733	-0.55758	0.061224	0.003236	NA	MISSENSE		
1274	26	KRT22ZP	5,-1,-1	17:360405	Basal	FALSE	HETD	-0.2066	2n Somatic	2	0.8667	DLOH	DLOH	0.8667	HETD	-0.3564	NA	NA	NA	NA	TRUNCATING		
1275	0	HCRT	-1	17:375908	Basal	FALSE	HETD	-0.1919	2n Somatic	2	0.8667	DLOH	DLOH	0.8667	HETD	-0.3564	-0.12147	NA	NA	NA	MISSENSE		
1276	69	DDX42	1	17:592315	Basal	FALSE	HETD	-0.1871	2n Somatic	2	0.85	DLOH	DLOH	0.85	HETD	-0.3651	-0.09985	NA	0.006472	NA	MISSENSE		
1277	22	GGA3	-1	17:707511	Basal	FALSE	HETD	-0.2301	2n Somatic	2	0.8776	DLOH	DLOH	0.8776	HETD	-0.4255	-0.5463	NA	0.003236	NA	MISSENSE		
1278	67	TP53	-1	17:751759	Basal	FALSE	NEUT	-0.0162	3n Somatic	3	0.8983	DLOH	DLOH	0.8983	HETD	-0.2421	-1.33579	0.306122	0.812298	NA	TRUNCATING		
1279	0	KCNQ2	1	18:757602	Basal	FALSE	NEUT	-0.001	3n duplicat	3	0.6212	HET	HET	0.6212	NEUT	0.0253	NA	NA	NA	NA	MISSENSE		
1280	3	PDE4A	1	19:104336	Basal	FALSE	HETD	-0.2478	2n Somatic	2	0.85	DLOH	DLOH	0.85	HOMD	-0.6048	-0.20645	NA	0.003236	NA	MISSENSE		
1281	26	AKAP8	-1	19:153308	Basal	FALSE	HETD	-0.2478	2n Somatic	2	0.875	DLOH	DLOH	0.875	HETD	-0.4272	-0.13162	NA	0.003236	NA	MISSENSE		
1282	23	MAP15	1	19:177051	Basal	FALSE	HETD	-0.2478	Hemizygou	1	0.8722	DLOH	DLOH	0.8722	HETD	-0.4973	NA	NA	NA	NA	MISSENSE		
1283	7	JMJD2B	1	19:510226	Basal	FALSE	HETD	-0.275	2n Somatic	2	0.8462	DLOH	DLOH	0.8462	HETD	-0.4628	NA	NA	NA	NA	MISSENSE		
1284	8	ZNF808	1	19:577496	Basal	FALSE	HETD	-0.2631	2n Somatic	2	0.8889	DLOH	DLOH	0.8889	HOMD	-0.6008	NA	NA	NA	NA	MISSENSE		
1285	22	ZNF264	1	19:624158	Basal	FALSE	HETD	-0.2631	2n Somatic	2	0.8684	DLOH	DLOH	0.8684	HETD	-0.4012	NA	NA	0.006472	NA	MISSENSE		
1286	0	HRNR	-1	1:1504605	Basal	FALSE	GAIN	0.2871	4n balance	4	0.6129	HET	HET	0.6129	GAIN	0.3245	NA	NA	0.003236	NA	MISSENSE		
1287	10	FCRL6	1	1:1580519	Basal	TRUE	NEUT	0.0675	4n balance	4	0.5957	HET	HET	0.5957	AMP	0.4701	NA	NA	0.006472	NA	SPICE		
1288	0	USH2A	-1	1:2139150	Basal	FALSE	NEUT	0.013	3n duplicat	3	0.6761	HET	HET	0.6761	NEUT	0.0447	NA	NA	0.064725	NA	MISSENSE		
1289	2	BAI2	-1	1:3196908	Basal	FALSE	NEUT	0.0387	3n Somatic	3	0.8919	LOH	LOH	0.8919	GAIN	0.2237	NA	NA	0.006472	NA	MISSENSE		
1290	71	NSFL1C	-1	20:138683	Basal	FALSE	HETD	-0.2892	2n Somatic	2	0.8696	DLOH	DLOH	0.8696	HETD	-0.3779	-0.13127	NA	NA	NA	MISSENSE		
1291	5	HEMK2	-1	21:291706	Basal	FALSE	NEUT	0.1582	4n balance	4	0.6	HET	HET	0.6	NEUT	0.0483	NA	NA	NA	NA	MISSENSE		
1292	0	C22orf33	-1	22:357279	Basal	FALSE	NEUT	0.0155	3n duplicat	3	0.6238	HET	HET	0.6238	NEUT	0.0165	NA	NA	NA	NA	MISSENSE		
1293	1	EPB41L5	1	2:1206171	Basal	FALSE	HETD	-0.1701	2n Somatic	2	0.871	DLOH	DLOH	0.871	HETD	-0.2972	NA	NA	0.003236	NA	MISSENSE		
1294	0	SCN3A	-1	2:1656550	Basal	FALSE	GAIN	0.2038	3n Somatic	3	NA	NA	NA	NA	GAIN	0.1874	NA	NA	0.012945	NA	MISSENSE		
1295	0	UGT1A8	1	2:2342453	Basal	FALSE	NEUT	0.059	3n Somatic	3	0.9062	NLOH	NLOH	0.9062	NEUT	-0.0129	-0.83795	NA	0.006472	NA	MISSENSE		
1296	11	MFSO1	1	3:1600056	Basal	FALSE	GAIN	0.3884	4n monoal	4	0.6765	ASCNA	ASCNA	0.6765	AMP	0.5295	NA	NA	NA	NA	MISSENSE		
1297	11	KDR	-1	4:5565578	Basal	FALSE	HETD	-0.1715	Normal (A)	2	0.6111	HET	HET	0.6111	HETD	-0.2441	-0.54809	0.013605	0.006472	NA	MISSENSE		
1298	0	PCDHA9	PC1,1,1,1,1,1,1,5	5:1402429	Basal	FALSE	HETD	-0.1781	2n Somatic	2	0.8667	DLOH	DLOH	0.8667	HETD	-0.3227	NA	NA	NA	NA	MISSENSE		
1299	5	AC026713	-1	5:3903821	Basal	FALSE	GAIN	0.219	3n duplicat	3	0.6412	HET	HET	0.6412	NEUT	-0.106	NA	NA	NA	NA	MISSENSE		
1300	0	RFPL4B	1	6:1127780	Basal	FALSE	GAIN	0.2197	3n duplicat	3	0.6667	HET	HET	0.6667	GAIN	0.1962	NA	NA	NA	NA	MISSENSE		
1301	40	MRPL14	-1	6:4419226	Basal	FALSE	GAIN	0.4172	5n non-mo	5	0.6216	HET	HET	0.6216	AMP	0.7559	NA	NA	0.003236	NA	MISSENSE		
1302	10	ORAI2	1	7:1018664	Basal	FALSE	NEUT	0.1056	3n Somatic	3	0.9226	NLOH	NLOH	0.9226	NEUT	0.074	NA	NA	0.003236	NA	TRUNCATING		
1303	0	SLC13A1	1	7:1225504	Basal	FALSE	NEUT	0.1277	3n Somatic	3	NA	NA	NA	NA	GAIN	0.1854	NA	NA	0.009709	NA	MISSENSE		
1304	41	MLL3	-1	7:1514915	Basal	FALSE	GAIN	0.2694	4n monoal	4	0.7826	HET	HET	0.7826	GAIN	0.2651	NA	0.013605	0.022654	NA	MISSENSE		
1305	132	UBR5	-1	8:1033695	Basal	FALSE	NA	NA	3n duplicat	3	0.6383	HET	HET	0.6383	GAIN	0.2163	-0.14583	NA	0.009709	NA	MISSENSE		
1306	33																						

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
1313	60	TP53	-1	17:751907	Basal	FALSE	NEUT	-0.1238	Hemizygous	1	0.6111	HET	NA	NA	NA	NA	-1.97634	0.306122	0.812298	0.456216	MISSENSE		
1314	69	PRMT2	-1	21:469032	Basal	FALSE	GAIN	0.2877	6n balance	6	0.6	HET	NA	NA	NA	NA	NA	NA	0.003236	0.191009	MISSENSE		
1315	34	MAGOH	-1	12:106573	Basal	FALSE	NEUT	-0.0972	2n Somatic	2	0.6792	NLOH	NA	NA	NA	NA	-0.25254	NA	NA	NA	MISSENSE		
1316	2	ZRANB2	-1	1:7131649	Basal	TRUE	NEUT	0.1112	4n balance	4	0.5492	HET	NA	NA	NA	NA	NA	NA	0.006472	NA	SPICE		
1317	16	DHX35	-1	20:370657	Basal	FALSE	NEUT	0.0697	3n duplicat	3	0.5909	HET	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE		
1318	0	UGT2A3	-1	4:6984567	Basal	FALSE	NEUT	-0.0158	2n Somatic	2	0.7083	NLOH	NA	NA	NA	NA	-1.63621	NA	0.003236	NA	MISSENSE		
1319	49	P4HA2	-1	5:1315727	Basal	TRUE	NEUT	-0.032	2n Germlin	2	0.7087	NLOH	NA	NA	NA	NA	-1.54737	NA	NA	NA	SPICE		
1320	66	C10orf18	-1	10:581254	Basal	FALSE	GAIN	0.3301	5n monoal	5	0.6842	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.441615	MISSENSE		
1321	330	RCN1	-1	11:320765	Basal	FALSE	GAIN	0.2509	4n balance	4	0.6	HET	NA	NA	NA	NA	NA	NA	NA	0.3992	MISSENSE		
1322	17	FBXO21	-1	12:116080	Basal	FALSE	NEUT	0.0114	3n Somatic	3	0.7273	NLOH	NA	NA	NA	NA	NA	NA	NA	0.09696	MISSENSE		
1323	0	CASC1	-1	12:251529	Basal	FALSE	HETD	-0.1863	Hemizygous	1	0.709	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.438306	MISSENSE		
1324	0	SPTB	-1	14:643231	Basal	FALSE	NEUT	-0.0242	2n Somatic	2	0.7	NLOH	NA	NA	NA	NA	NA	NA	0.022654	0.256057	MISSENSE		
1325	14	MLH3	-1	14:745844	Basal	FALSE	NEUT	-0.0321	2n Somatic	2	0.7	NLOH	NA	NA	NA	NA	-0.02063	NA	0.003236	0.319725	MISSENSE		
1326	1	ERN2	-1	16:236096	Basal	FALSE	HETD	-0.1763	Hemizygous	1	0.7066	NLOH	NA	NA	NA	NA	-0.05584	NA	0.016181	0.44435	MISSENSE		
1327	14	IL4R	-1	16:272815	Basal	FALSE	NEUT	0.0113	3n duplicat	3	0.6129	HET	NA	NA	NA	NA	-0.30666	NA	0.003236	0.441752	MISSENSE		
1328	9	ATP2C2	-1	16:830397	Basal	FALSE	NEUT	-0.0677	2n Somatic	2	0.7273	NLOH	NA	NA	NA	NA	NA	NA	NA	0.440529	MISSENSE		
1329	65	TLCOD1	-1	17:240757	Basal	FALSE	NEUT	0.03	2n Somatic	2	0.75	NLOH	NA	NA	NA	NA	NA	NA	NA	0.254722	MISSENSE		
1330	0	CD300A	-1	17:699890	Basal	FALSE	NEUT	0.0699	3n Somatic	3	0.75	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.548098	MISSENSE		
1331	10	SOC56	-1	18:661438	Basal	FALSE	NEUT	-0.0351	Normal (A)	2	0.5797	HET	NA	NA	NA	NA	-0.06146	NA	NA	0.759582	MISSENSE		
1332	2	CD97	-1	19:143789	Basal	FALSE	NEUT	-0.0653	Normal (A)	2	0.6	HET	NA	NA	NA	NA	NA	NA	0.006472	0.516439	MISSENSE		
1333	9	ZNF527	-1	19:425617	Basal	FALSE	AMP	0.8856	6n Somatic	6	0.8242	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.441291	MISSENSE		
1334	0	KCNJ10	-1	1:1582784	Basal	FALSE	NEUT	0.1358	3n duplicat	3	0.6	HET	NA	NA	NA	NA	-0.03884	NA	0.003236	0.093889	MISSENSE		
1335	0	CAMK1G	-1	1:2078497	Basal	FALSE	NEUT	0.071	5n non-mo	5	0.5833	HET	NA	NA	NA	NA	NA	NA	NA	0.247224	MISSENSE		
1336	10	TMEM53	-1	1:4489277	Basal	FALSE	NEUT	0.0309	3n duplicat	3	0.6	HET	NA	NA	NA	NA	NA	NA	0.006472	0.755367	MISSENSE		
1337	23	CPNE1	-1	20:337045	Basal	FALSE	NEUT	-0.0558	2n Germlin	2	0.6	HET	NA	NA	NA	NA	NA	NA	NA	0.998236	MISSENSE		
1338	15	DIDO1	-1	20:609936	Basal	FALSE	NEUT	0.0379	3n duplicat	3	0.6	HET	NA	NA	NA	NA	NA	NA	0.009709	0.753909	MISSENSE		
1339	7	SLCSA1	-1	22:308280	Basal	FALSE	NEUT	-0.0769	2n Somatic	2	0.7242	NLOH	NA	NA	NA	NA	-0.08992	NA	NA	0.987696	MISSENSE		
1340	0	MBD5	-1	2:1489641	Basal	FALSE	NEUT	0.0057	2n Germlin	2	0.7059	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.624097	MISSENSE		
1341	0	COL6A3	-1	2:2379614	Basal	FALSE	GAIN	0.2532	3n duplicat	3	0.6087	HET	NA	NA	NA	NA	-0.17692	0.027211	0.02589	0.443037	TRUNCATING		
1342	0	LDHAL3	-1	2:4190058	Basal	FALSE	NEUT	0.1039	3n duplicat	3	0.6	HET	NA	NA	NA	NA	NA	NA	NA	0.549474	MISSENSE		
1343	10	LAMP3	-1	3:1843544	Basal	FALSE	GAIN	0.3787	6n Somatic	6	0.7778	NLOH	NA	NA	NA	NA	-0.07545	NA	0.006472	0.980871	MISSENSE		
1344	0	BSN	-1	3:4966634	Basal	FALSE	HETD	-0.2407	Hemizygous	1	0.6364	HET	NA	NA	NA	NA	NA	NA	0.016181	0.555636	MISSENSE		
1345	2	SLC7A11	-1	4:1393213	Basal	FALSE	NEUT	0.0023	2n Somatic	2	0.6857	NLOH	NA	NA	NA	NA	-0.12954	NA	NA	0.440089	MISSENSE		
1346	0	SLCA4A	-1	4:7253576	Basal	FALSE	NEUT	-0.0113	2n Germlin	2	0.7241	NLOH	NA	NA	NA	NA	-0.05979	NA	0.009709	0.183288	MISSENSE		
1347	56	CDC99	-1	5:1689507	Basal	FALSE	NEUT	-0.0479	2n Somatic	2	0.7059	NLOH	NA	NA	NA	NA	-0.07638	NA	0.003236	0.193462	MISSENSE		
1348	0	SYNE1	-1	6:1525110	Basal	FALSE	NEUT	0.0353	Normal (A)	2	0.5926	HET	NA	NA	NA	NA	NA	0.047619	0.022654	0.192984	TRUNCATING		
1349	1	JARID2	-1	6:1560526	Basal	FALSE	GAIN	0.2314	4n balance	4	0.5645	HET	NA	NA	NA	NA	NA	NA	0.006472	0.766139	MISSENSE		
1350	18	IGF2R	-1	6:1604129	Basal	FALSE	HETD	-0.2541	Hemizygous	1	0.5926	HET	NA	NA	NA	NA	-0.12729	NA	0.009709	0.31707	MISSENSE		
1351	0	SCAND3	-1	6:2865145	Basal	FALSE	GAIN	0.3347	5n Germlin	5	0.5645	HET	NA	NA	NA	NA	NA	NA	0.003236	0.760052	MISSENSE		
1352	0	PIK3CG	-1	7:1062963	Basal	FALSE	NEUT	0.1059	3n duplicat	3	0.6	HET	NA	NA	NA	NA	-0.70245	0.040816	0.006472	0.62111	MISSENSE		
1353	1	CLCN1	-1	7:1427588	Basal	FALSE	NEUT	0.0981	3n duplicat	3	0.6	HET	NA	NA	NA	NA	NA	NA	0.003236	0.991147	MISSENSE		
1354	0	ZNF425	-1	7:1484326	Basal	FALSE	NEUT	0.0332	2n Germlin	2	0.6	HET	NA	NA	NA	NA	NA	NA	0.003236	0.194424	MISSENSE		
1355	2	HECW1	-1	7:4356073	Basal	FALSE	HETD	-0.2078	Hemizygous	1	0.6195	HET	NA	NA	NA	NA	NA	NA	0.022654	0.255938	MISSENSE		
1356	2	HECW1	-1	7:4356073	Basal	FALSE	HETD	-0.2078	Hemizygous	1	0.6195	HET	NA	NA	NA	NA	NA	NA	0.022654	0.439001	MISSENSE		
1357	11	TSC1	-1	9:1347624	Basal	FALSE	NEUT	-0.059	2n Somatic	2	0.7097	NLOH	NA	NA	NA	NA	-0.39927	0.013605	0.003236	0.320493	MISSENSE		
1358	0	LINGO2	-1	9:2794044	Basal	FALSE	NEUT	0.1108	3n Somatic	3	0.725	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.244457	MISSENSE		
1359	9	NHS	-1	X:1765528	Basal	FALSE	NEUT	-0.0238	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.006472	NA	MISSENSE		
1360	24	PEO1	-1	10:102738	Basal	FALSE	GAIN	0.3127	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.438938	MISSENSE		
1361	6	ARHGAP21	-1	10:249298	Basal	TRUE	NEUT	0.0357	2n Germlin	2	0.5882	HET	NA	NA	NA	NA	NA	NA	0.022654	0.55747	SPICE		
1362	0	ZNF365	-1	10:638064	Basal	FALSE	NEUT	0.0629	2n Germlin	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	1	MISSENSE		
1363	1	PRKCQ	-1	10:659298	Basal	FALSE	GAIN	0.2798	3n duplicat	3	0.612	HET	NA	NA	NA	NA	-0.64375	NA	0.009709	0.447375	MISSENSE		
1364	1	ALKBH8	-1	11:106932	Basal	FALSE	NEUT	0.0448	Normal (A)	2	0.566	HET	NA	NA	NA	NA	NA	NA	0.003236	0.618721	MISSENSE		
1365	0	SLC22A10	-1	11:628264	Basal	FALSE	HETD	-0.3557	Hemizygous	1	0.75	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.757061	MISSENSE		
1366	35	ANAPC5	-1	12:120230	Basal	FALSE	NEUT	0.0127	Normal (A)	2	0.5652	HET	NA	NA	NA	NA	-0.25918	NA	0.003236	0.256874	MISSENSE		
1367	0	STX2	-1	12:129863	Basal	FALSE	NEUT	0.0127	Normal (A)	2	0.5652	HET	NA	NA	NA	NA	-0.03451	NA	NA	0.545296	MISSENSE		
1368	17	CHFR	-1	12:131944	Basal	FALSE	NEUT	-0.0412	Normal (A)	2	0.5652	HET	NA	NA	NA	NA	NA	NA	NA	0.320775	MISSENSE		
1369	21	EP58	-1	12:156685	Basal	FALSE	HETD	-0.3185	Hemizygous	1	0.75	NLOH	NA	NA	NA	NA	-0.10636	NA	0.006472	0.317796	MISSENSE		
1370	10	MLL2	-1	12:477267	Basal	FALSE	NEUT	0.0313	Normal (A)	2	0.5769	HET	NA	NA	NA	NA	NA	NA	0.009709	0.329272	MISSENSE		
1371	0	MYO1A	-1	12:557179	Basal	FALSE	NEUT	0.0467	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	-0.03459	NA	0.006472	0.454328	MISSENSE		
1372	33	NUP107	-1	12:673706	Basal	FALSE	NEUT	0.0467	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	-0.2831	NA	NA	0.094579	MISSENSE		
1373	10	C13orf3	-1	13:206339	Basal	FALSE	NEUT	0.0256	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	NA	NA	NA	0.188984	MISSENSE		
1374	0	B3GALT1	-1	13:306869	Basal	TRUE	NEUT	0.0256	Normal (A)	2	0.5667	HET	NA	NA	NA	NA	NA	NA	0.003236	0.55354	SPICE		
1375	0	RP11-396A	-1	13:408570	Basal	FALSE	NEUT	0.0552	Normal (A)	2	0.5667	HET	NA	NA	NA	NA	NA	NA	NA	0.441196	MISSENSE		
1376	0	ABCC4	-1	13:945245	Basal	FALSE	NEUT	0.0936	Normal (A)	2	0.5667												

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
1382	0	DNAH9		1:17:114950	Basal	FALSE	HETD	-0.4038	Hemizygou	1	0.7442	NLOH	NA	NA	NA	NA	-0.1225	NA	0.012945	0.49432	MISSENSE		
1383	0	AC061975		-1:17:236284	Basal	FALSE	NEUT	-0.0098	2n Somatic	2	0.8182	NLOH	NA	NA	NA	NA	NA	NA	NA	0.243324	MISSENSE		
1384	1	KRT9		-1:17:369782	Basal	FALSE	NEUT	0.0412	2n Somatic	2	0.8182	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.440382	MISSENSE		
1385	0	NETO1		-1:18:685683	Basal	FALSE	AMP	0.7782	6n Germlin	6	0.75	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.624156	MISSENSE		
1386	21	RAB12		1:18:862310	Basal	FALSE	AMP	0.7893	6n monoal	6	0.7525	NLOH	NA	NA	NA	NA	NA	NA	NA	0.560694	MISSENSE		
1387	0	ZNF729		1:19:222894	Basal	FALSE	NEUT	-0.0422	2n Germlin	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.621217	TRUNCATING		
1388	59	LSM14A		1:19:393794	Basal	FALSE	NEUT	-0.0411	Normal (A)	2	0.5833	HET	NA	NA	NA	NA	NA	NA	NA	0.762351	MISSENSE		
1389	0	VN1R2		1:19:584542	Basal	FALSE	NEUT	-0.0533	Normal (A)	2	0.5721	HET	NA	NA	NA	NA	NA	NA	NA	0.317078	MISSENSE		
1390	0	COL11A1		-1:1:1032639	Basal	FALSE	NEUT	0.0844	2n Germlin	2	0.5622	HET	NA	NA	NA	NA	-0.20188	0.006803	0.019417	0.191624	MISSENSE		
1391	0	CREB3L4		1:1:1522077	Basal	FALSE	NEUT	-0.0408	Normal (A)	2	0.6154	HET	NA	NA	NA	NA	-0.25008	NA	0.003236	0.268464	MISSENSE		
1392	0	ANGPTL1, R-1,1		1:1771008	Basal	FALSE	GAIN	0.3426	3n duplicat	3	0.6308	HET	NA	NA	NA	NA	NA	NA	NA	0.436201	MISSENSE		
1393	6	OTUD3		1:1:2009667	Basal	FALSE	NEUT	0.0054	Normal (A)	2	0.5811	HET	NA	NA	NA	NA	NA	NA	NA	0.557514	MISSENSE		
1394	0	SLC26A9		-1:1:2041591	Basal	FALSE	GAIN	0.4556	4n monoal	4	0.6818	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.623984	MISSENSE		
1395	0	LAMB3		-1:1:2078725	Basal	FALSE	NEUT	0.0148	Normal (A)	2	0.5738	HET	NA	NA	NA	NA	-0.40027	NA	0.003236	0.264849	MISSENSE		
1396	0	C1orf87		-1:1:6029361	Basal	FALSE	NEUT	0.0054	Normal (A)	2	0.56	HET	NA	NA	NA	NA	NA	NA	0.003236	0.560803	MISSENSE		
1397	0	C22orf42		-1:22:308849	Basal	FALSE	GAIN	0.2395	NA	NA	0.581	HET	NA	NA	NA	NA	NA	NA	0.003236	NA	MISSENSE		
1398	0	NMS		1:1:1004651	Basal	FALSE	NEUT	0.0393	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.546196	MISSENSE		
1399	0	COL6A3		-1:2:2379684	Basal	FALSE	AMP	0.6793	5n monoal	5	0.7413	NLOH	NA	NA	NA	NA	-0.17711	0.027211	0.02589	0.322598	MISSENSE		
1400	0	C2orf70		1:2:2665233	Basal	FALSE	GAIN	0.3659	4n monoal	4	0.6964	NLOH	NA	NA	NA	NA	NA	NA	NA	0.779509	MISSENSE		
1401	1	C2orf16		1:2:2765483	Basal	FALSE	GAIN	0.3659	3n duplicat	3	NA	NA	NA	NA	NA	NA	NA	NA	0.009709	0.321829	MISSENSE		
1402	1	C2orf16		1:2:2765691	Basal	FALSE	GAIN	0.3659	3n duplicat	3	0.6154	HET	NA	NA	NA	NA	NA	NA	0.009709	0.438535	MISSENSE		
1403	16	TAF1B		1:2:9976623	Basal	FALSE	NEUT	0.0366	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	-0.08986	NA	0.003236	0.24388	MISSENSE		
1404	54	SEC13L1		-1:3:1032233	Basal	FALSE	NEUT	0.0249	2n Somatic	2	0.7812	NLOH	NA	NA	NA	NA	NA	NA	NA	0.256062	MISSENSE		
1405	0	PLCX2		1:3:1130857	Basal	FALSE	NEUT	0.0699	Normal (A)	2	0.5586	HET	NA	NA	NA	NA	NA	NA	NA	0.256274	MISSENSE		
1406	8	KIAA2018		-1:3:1148586	Basal	FALSE	NEUT	0.0339	Normal (A)	2	0.5586	HET	NA	NA	NA	NA	NA	NA	0.003236	0.185525	MISSENSE		
1407	0	CCDC37		3:1:1276201	Basal	FALSE	NEUT	0.0339	Normal (A)	2	0.5732	HET	NA	NA	NA	NA	NA	NA	0.003236	0.619741	MISSENSE		
1408	0	TRIM71		3:3:289034	Basal	FALSE	HETD	-0.3636	Hemizygou	1	0.7812	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.094188	MISSENSE		
1409	0	ROBO2		3:7:765462	Basal	FALSE	HETD	-0.3374	Hemizygou	1	0.7087	NLOH	NA	NA	NA	NA	-0.10532	NA	0.003236	0.256964	MISSENSE		
1410	0	ODAM		4:7:110256	Basal	FALSE	HETD	-0.3294	Hemizygou	1	0.7671	NLOH	NA	NA	NA	NA	NA	NA	0.009709	0.194861	MISSENSE		
1411	0	SLC6A19		5:1:1272635	Basal	FALSE	NEUT	0.0397	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	NA	NA	NA	0.757936	MISSENSE		
1412	39	NDST1		5:1:1498877	Basal	FALSE	HETD	-0.38	Hemizygou	1	0.7568	NLOH	NA	NA	NA	NA	-0.66204	NA	NA	0.760402	MISSENSE		
1413	9	TNIP1		-1:5:1503904	Basal	TRUE	HETD	-0.38	Hemizygou	1	0.7568	NLOH	NA	NA	NA	NA	-0.08428	NA	0.003236	0.321339	SPICE		
1414	27	NSD1		5:1:1766548	Basal	FALSE	HETD	-0.38	Hemizygou	1	0.7568	NLOH	NA	NA	NA	NA	-0.08283	NA	0.006472	0.318836	MISSENSE		
1415	0	CDH10		-1:5:2452381	Basal	FALSE	NEUT	0.0397	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	-0.21152	NA	0.019417	0.277579	MISSENSE		
1416	21	ADCY2		5:7:7855304	Basal	FALSE	NEUT	0.0397	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	-0.73601	NA	0.016181	0.624281	MISSENSE		
1417	0	HS3ST5		-1:6:1144905	Basal	FALSE	NEUT	0.0716	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	-0.01621	NA	0.003236	0.258363	MISSENSE		
1418	17	HIST1H4A, 1,1		6:2631282	Basal	FALSE	NEUT	0.0031	2n Germlin	2	0.5818	HET	NA	NA	NA	NA	NA	NA	NA	0.246571	MISSENSE		
1419	50	SLC39A7		6:3327747	Basal	FALSE	NEUT	0.0031	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	NA	NA	NA	0.553227	MISSENSE		
1420	0	GLP1R		6:3915537	Basal	FALSE	NEUT	0.0443	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	-0.16477	NA	NA	0.516668	MISSENSE		
1421	0	F13A1		-1:6:6211934	Basal	FALSE	GAIN	0.2712	3n duplicat	3	0.5818	HET	NA	NA	NA	NA	-0.08113	0.006803	0.006472	0.320291	MISSENSE		
1422	0	COL12A1		-1:6:7593205	Basal	FALSE	NEUT	0.0737	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	-0.0941	NA	0.016181	0.4414	MISSENSE		
1423	22	PGM3		-1:6:8394816	Basal	FALSE	NEUT	0.0513	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	-0.03435	NA	NA	0.444554	MISSENSE		
1424	0	MUC17		7:1004712	Basal	FALSE	NEUT	0.1347	3n duplicat	3	0.7022	NLOH	NA	NA	NA	NA	NA	NA	0.045307	0.55604	MISSENSE		
1425	0	SDK1		7:4180478	Basal	TRUE	HETD	-0.3718	2n Somatic	2	0.8273	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.317911	SPICE		
1426	0	ADCY1		7:4569250	Basal	FALSE	NEUT	0.0189	2n Somatic	2	0.8273	NLOH	NA	NA	NA	NA	-0.77874	NA	0.009709	0.25895	MISSENSE		
1427	39	C7orf42		7:6604749	Basal	FALSE	NEUT	-0.0231	Normal (A)	2	0.6	HET	NA	NA	NA	NA	NA	NA	0.003236	0.329855	MISSENSE		
1428	11	CCDC132		7:9277317	Basal	FALSE	GAIN	0.3649	3n duplicat	3	0.6273	HET	NA	NA	NA	NA	NA	NA	0.009709	0.196382	MISSENSE		
1429	0	UNC5D		8:3572557	Basal	FALSE	HETD	-0.3752	Hemizygou	1	0.7674	NLOH	NA	NA	NA	NA	-0.10532	NA	0.006472	0.76047	MISSENSE		
1430	22	MYST3		-8:4191799	Basal	FALSE	HETD	-0.3664	Hemizygou	1	0.7674	NLOH	NA	NA	NA	NA	NA	NA	0.009709	0.242374	MISSENSE		
1431	15	SETX		-9:1341923	Basal	FALSE	NEUT	0.0263	2n Somatic	2	0.8	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.424177	MISSENSE		
1432	0	GPR50		X:1501005	Basal	FALSE	NEUT	0.0273	NA	NA	NA	NA	NA	NA	NA	NA	-0.2157	NA	0.003236	NA	TRUNCATING		
1433	64	TP53		-1:17:751913	Basal	FALSE	NEUT	-0.13	2n Somatic	2	0.6667	HET	NA	NA	NA	NA	-2.09299	0.306122	0.812298	0.441798	MISSENSE		
1434	0	USHBP1		-1:19:172301	Basal	FALSE	NEUT	0.1299	4n Somatic	4	0.7059	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.762764	MISSENSE		
1435	0	TRPV4		-1:12:108736	Basal	FALSE	NEUT	-0.0653	3n duplicat	3	0.6111	HET	HET	0.6111	NEUT	-0.0414	-0.02445	NA	0.006472	0.93855	MISSENSE		
1436	0	HAO2		1:1:1197308	Basal	FALSE	AMP	0.9644	6n Somatic	6	0.8615	LOH	LOH	0.8615	HLAMP	1.7485	-0.58934	NA	0.003236	0.940853	MISSENSE		
1437	1915	PHGDH		1:1:200654	Basal	FALSE	HLAMP	1.4465	6n Somatic	6	0.8615	LOH	LOH	0.8615	HLAMP	1.7485	-0.56561	NA	0.003236	0.673438	MISSENSE		
1438	0	OR6K3		-1:1:1569539	Basal	FALSE	GAIN	0.3164	6n non-mo	6	0.6429	ASCNA	ASCNA	0.6429	AMP	0.4852	-0.09818	NA	0.003236	0.936746	TRUNCATING		
1439	4	DGCR2		-1:22:174159	Basal	FALSE	NEUT	-0.1264	2n Somatic	2	0.6667	DLOH	DLOH	0.6667	HETD	-0.2925	NA	NA	NA	0.758206	TRUNCATING		
1440	0	REG3A		-1:2:7923828	Basal	FALSE	NEUT	-0.0226	5n Germlin	5	0.6154	HET	HET	0.6154	NEUT	-0.0117	NA	NA	NA	0.671695	MISSENSE		
1441	0	LAMA4		-1:6:1125677	Basal	FALSE	NEUT	-0.0593	3n duplicat	3	0.6111	HET	HET	0.6111	NEUT	-0.0267	-0.33248	NA	0.012945	0.759616	MISSENSE		
1442	0	MRAP2		6:8485559	Basal	FALSE	NEUT	-0.0567	3n duplicat	3	0.6111	HET	HET	0.6111	NEUT	-0.0267	NA	NA	NA	0.936906	MISSENSE		
1443	46	PHF14		7:1:111756	Basal	FALSE	NEUT	-0.0253	3n duplicat	3	0.6154	HET	HET	0.6154	NEUT	0.0176	NA	NA	NA	0.761383	MISSENSE		
1444	0	DNAH11		7:2:157613	Basal	FALSE	NEUT	-0.0253	3n duplicat	3	0.6154	HET	HET	0.6154	NEUT	0.0255	-0.06019	NA	0.02589	0.940901	MISSENSE		
1445																							

NEOGENOMICS EX.1102.057

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
1520	2	LUZP1	-1	1:2329092	Other	FALSE	NEUT	-0.0532	2n Somatic	2	0.7368	NLOH	NA	NA	NA	NA	NA	NA	NA	0.253127	MISSENSE		
1521	19	PPP1R8	-1	1:2804011	Other	FALSE	NEUT	-0.0769	2n Germlin	2	0.7368	NLOH	NA	NA	NA	NA	NA	NA	NA	0.748571	MISSENSE		
1522	4	ELMO2	-1	20:444422	Other	FALSE	NEUT	0.0409	3n Germlin	3	0.5777	HET	NA	NA	NA	NA	-0.06297	NA	0.003236	0.249919	MISSENSE		
1523	0	SLC7A4	-1	22:197155	Other	FALSE	NEUT	0.0323	4n monoal	4	0.6575	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.981125	MISSENSE		
1524	32	SP3	-1	2:1745289	Other	FALSE	NEUT	0.0108	3n duplicat	3	0.6043	HET	NA	NA	NA	NA	-0.17259	NA	0.003236	0.556521	MISSENSE		
1525	0	PLCL1	-1	2:1986572	Other	FALSE	NEUT	0.0134	3n duplicat	3	0.6	HET	NA	NA	NA	NA	-0.0334	NA	0.003236	0.377839	MISSENSE		
1526	0	GCKR	-1	2:2759882	Other	FALSE	NEUT	-0.0437	3n duplicat	3	0.5974	HET	NA	NA	NA	NA	-0.07206	NA	0.006472	0.251749	TRUNCATING		
1527	28	CCDC88A	-1	2:5537662	Other	FALSE	NEUT	-0.017	3n duplicat	3	0.5974	HET	NA	NA	NA	NA	NA	NA	0.006472	0.380866	MISSENSE		
1528	0	TMEM40	-1	3:1275205	Other	FALSE	NEUT	0.0722	4n Somatic	4	0.7778	NLOH	NA	NA	NA	NA	NA	NA	0.250018	MISSENSE			
1529	0	PFKFB4	-1	3:4856256	Other	FALSE	HETD	-0.2435	2n Somatic	2	0.7778	NLOH	NA	NA	NA	NA	-0.25954	NA	NA	0.248777	MISSENSE		
1530	0	EPHA3	-1	3:8956310	Other	FALSE	NEUT	-0.0068	3n Germlin	3	0.7778	NLOH	NA	NA	NA	NA	-0.06091	0.013605	0.016181	0.550936	MISSENSE		
1531	4	SHROOM3	-1	4:7787952	Other	FALSE	NEUT	0.0082	3n duplicat	3	0.5914	HET	NA	NA	NA	NA	NA	NA	0.003236	0.251594	MISSENSE		
1532	0	DNAH5	-1	5:1382213	Other	FALSE	NEUT	0.1517	5n monoal	5	0.6914	NLOH	NA	NA	NA	NA	-0.06471	NA	0.035599	0.252572	MISSENSE		
1533	0	PCDHA2	-1	5:1401568	Other	FALSE	HETD	-0.2398	2n Somatic	2	0.7143	NLOH	NA	NA	NA	NA	-0.12337	NA	0.012945	0.979101	MISSENSE		
1534	0	PCDH24	-1	5:1759372	Other	FALSE	HETD	-0.2398	2n Somatic	2	0.7143	NLOH	NA	NA	NA	NA	-0.12337	NA	0.006472	0.746613	MISSENSE		
1535	3	CARD6	-1	5:4088841	Other	FALSE	NEUT	0.0848	3n Germlin	3	0.5714	HET	NA	NA	NA	NA	-0.02056	NA	0.006472	0.379909	MISSENSE		
1536	0	SEMA5A	-1	5:9207596	Other	FALSE	GAIN	0.2219	5n monoal	5	0.6914	NLOH	NA	NA	NA	NA	-0.05404	NA	0.003236	0.387455	MISSENSE		
1537	6	MAP3K7IP1	-1	6:1497605	Other	FALSE	NEUT	0.1012	4n balance	4	0.5667	HET	NA	NA	NA	NA	-0.26212	NA	NA	0.384475	TRUNCATING		
1538	0	UNC93A	-1	6:1676413	Other	FALSE	HETD	-0.2967	2n Somatic	2	0.7083	NLOH	NA	NA	NA	NA	NA	NA	0.379854	MISSENSE			
1539	0	C6orf27	-1	6:3185172	Other	FALSE	NEUT	0.0613	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.009709	0.374116	MISSENSE		
1540	0	C6orf221	-1	6:7412997	Other	FALSE	HETD	-0.1632	2n Germlin	2	0.7143	NLOH	NA	NA	NA	NA	NA	NA	NA	0.551983	MISSENSE		
1541	0	FOXP2	-1	7:1138538	Other	FALSE	NEUT	0.0839	3n Germlin	3	0.5714	HET	NA	NA	NA	NA	NA	NA	0.012945	0.981826	MISSENSE		
1542	0	RAB19	-1	7:1397540	Other	FALSE	HETD	-0.2354	2n Somatic	2	0.7097	NLOH	NA	NA	NA	NA	NA	NA	NA	0.557111	MISSENSE		
1543	82	GARS	-1	7:3062201	Other	FALSE	GAIN	0.3646	6n Germlin	6	0.6364	HET	NA	NA	NA	NA	-0.02823	NA	0.003236	0.72127	MISSENSE		
1544	0	PKD1L1	-1	7:4787257	Other	FALSE	NEUT	-0.0588	3n duplicat	3	0.5926	HET	NA	NA	NA	NA	NA	NA	0.019417	0.980561	MISSENSE		
1545	0	FGL2,CCDC -1,1	-1	7:7666359	Other	FALSE	NEUT	0.026	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.557817	MISSENSE		
1546	0	PLAG1	-1	8:5724193	Other	FALSE	NEUT	0.0702	2n Germlin	2	0.5779	HET	NA	NA	NA	NA	NA	0.006803	NA	0.379337	MISSENSE		
1547	0	TNFSF15	-1	9:1166079	Other	FALSE	GAIN	0.236	5n non-mo	5	0.583	HET	NA	NA	NA	NA	-0.0764	NA	NA	0.743052	MISSENSE		
1548	6	DAB2IP	-1	9:1235619	Other	FALSE	NEUT	0.1406	5n non-mo	5	0.583	HET	NA	NA	NA	NA	NA	NA	0.003236	1	MISSENSE		
1549	967	ANP32B	-1	9:9980720	Other	FALSE	NEUT	0.1121	4n balance	4	0.5806	HET	NA	NA	NA	NA	NA	NA	NA	0.558713	MISSENSE		
1550	0	PNMA5	-1	X:1519104	Other	FALSE	GAIN	0.3771	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.003236	NA	MISSENSE		
1551	0	DCT	-1	13:939293	Other	FALSE	NEUT	0.0202	5n non-mo	5	0.5577	HET	NA	NA	NA	NA	-0.88886	NA	0.006472	NA	MISSENSE		
1552	1	FBN1	-1	15:465321	Other	FALSE	NEUT	-0.0429	4n Germlin	4	0.5654	HET	NA	NA	NA	NA	-0.05693	NA	0.006472	NA	MISSENSE		
1553	23	TP53	-1	17:751888	Other	FALSE	HETD	-0.2342	Hemizygou	1	0.6	HET	NA	NA	NA	NA	-1.38019	0.306122	0.812298	NA	MISSENSE		
1554	9	USP25	-1	21:161686	Other	FALSE	NEUT	0.0171	5n Germlin	6	0.569	HET	NA	NA	NA	NA	NA	NA	0.009709	NA	MISSENSE		
1555	5	KIAA1217	-1	10:247098	Basal	FALSE	NEUT	0.0045	3n duplicat	3	0.5952	HET	NA	NA	NA	NA	NA	NA	0.016181	0.248005	MISSENSE		
1556	1	MYO3A	-1	10:263959	Basal	FALSE	NEUT	0.0045	3n duplicat	3	0.5952	HET	NA	NA	NA	NA	NA	0.006803	0.009709	0.995725	MISSENSE		
1557	638	CFL1	-1	11:653800	Basal	FALSE	NEUT	-0.0812	Normal (A)	2	0.5872	HET	NA	NA	NA	NA	-0.30652	NA	NA	0.556055	MISSENSE		
1558	0	GRM5	-1	11:880261	Basal	FALSE	NEUT	-0.0698	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	-0.49359	0.013605	0.003236	0.985697	MISSENSE		
1559	69	WDR21A	-1	14:724919	Basal	FALSE	HETD	-0.1893	2n Somatic	2	0.6835	NLOH	NA	NA	NA	NA	NA	NA	NA	0.560093	MISSENSE		
1560	0	IQCH	-1	15:654682	Basal	FALSE	HETD	-0.207	Hemizygou	1	0.6923	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.746575	MISSENSE		
1561	2	ATBF1	-1	16:713798	Basal	FALSE	NEUT	-0.0525	2n Somatic	2	0.6923	NLOH	NA	NA	NA	NA	NA	NA	NA	0.380399	TRUNCATING		
1562	0	MYH2	-1	17:103757	Basal	FALSE	HETD	-0.2474	2n Somatic	2	0.6895	NLOH	NA	NA	NA	NA	-0.29933	NA	0.016181	0.979245	MISSENSE		
1563	0	GPR4	-1	19:507862	Basal	FALSE	NEUT	-0.0121	Normal (A)	2	0.5614	HET	NA	NA	NA	NA	NA	NA	0.006472	0.97799	MISSENSE		
1564	18	ZNF468	-1	19:580371	Basal	FALSE	NEUT	-0.0121	4n balance	4	0.5614	HET	NA	NA	NA	NA	NA	NA	0.003236	0.727214	MISSENSE		
1565	434	TXNIP	-1	1:1441517	Basal	FALSE	GAIN	0.311	6n non-mo	6	0.6021	HET	NA	NA	NA	NA	NA	NA	0.006472	0.559364	MISSENSE		
1566	41	GPATCH4	-1	1:1548317	Basal	FALSE	GAIN	0.3524	6n non-mo	6	0.6442	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.559692	MISSENSE		
1567	0	LY9	-1	1:1590508	Basal	FALSE	GAIN	0.3524	6n Germlin	6	0.6442	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.379379	MISSENSE		
1568	0	TNFSF4	-1	1:1714225	Basal	FALSE	GAIN	0.388	6n non-mo	6	0.6335	NLOH	NA	NA	NA	NA	-0.16729	NA	NA	0.412628	TRUNCATING		
1569	137	KCTD3	-1	1:2138601	Basal	FALSE	GAIN	0.3746	6n non-mo	6	0.6288	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.560938	TRUNCATING		
1570	37	ZNF669	-1	1:2453305	Basal	FALSE	GAIN	0.3746	6n non-mo	6	0.6356	NLOH	NA	NA	NA	NA	NA	NA	NA	0.380373	MISSENSE		
1571	15	IPO13	-1	1:4419487	Basal	FALSE	NEUT	0.0719	4n balance	4	0.5562	HET	NA	NA	NA	NA	NA	NA	NA	0.373683	MISSENSE		
1572	25	BCAS4	-1	20:489264	Basal	FALSE	NEUT	0.0134	4n balance	4	0.5652	HET	NA	NA	NA	NA	NA	NA	0.003236	0.385668	MISSENSE		
1573	33	GCC2	-1	2:1084651	Basal	FALSE	GAIN	0.1952	4n balance	4	0.5652	HET	NA	NA	NA	NA	NA	NA	0.003236	0.269653	MISSENSE		
1574	54	MTIF2	-1	2:5532069	Basal	FALSE	NEUT	0.07	3n Somatic	3	0.7273	NLOH	NA	NA	NA	NA	-0.11835	NA	0.003236	0.378666	MISSENSE		
1575	24	TF	-1	3:1349583	Basal	FALSE	NEUT	0.1088	4n Somatic	4	0.75	NLOH	NA	NA	NA	NA	-0.12377	NA	0.003236	1	MISSENSE		
1576	8	IFT80	-1	3:1615081	Basal	FALSE	GAIN	0.2262	4n Somatic	4	0.75	NLOH	NA	NA	NA	NA	NA	NA	NA	0.379515	TRUNCATING		
1577	7	C4orf14	-1	4:5753791	Basal	FALSE	NEUT	0.0129	2n Somatic	2	0.6849	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.376052	MISSENSE		
1578	4	PDSS2	-1	6:1076382	Basal	FALSE	NEUT	0.0722	3n duplicat	3	0.5916	HET	NA	NA	NA	NA	-0.02062	NA	0.006472	0.263557	MISSENSE		
1579	8	SYNE1	-1	6:1527393	Basal	FALSE	NEUT	0.0365	3n duplicat	3	0.5855	HET	NA	NA	NA	NA	NA	0.047619	0.022654	0.092208	MISSENSE		
1580	11	KIAA0240,1,-1	-1	6:4290439	Basal	FALSE	GAIN	0.1558	4n balance	4	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.426395	MISSENSE		
1581	0	CTTNBP2	-1	7:1172189	Basal	FALSE	GAIN	0.2381	4n Germlin	4	0.5556	HET	NA	NA	NA	NA	NA	NA	0.012945	0.661717	MISSENSE		
1582	0	PKD1L1	-1	7:4794297	Basal	FALSE	NEUT	0.014	3n Germlin	3	0.5857	HET	NA	NA	NA	NA	NA	NA	0.019417	0.278292	TRUNCATING		
1583	8	TRIB1	-1	8:1265149	Basal	FALSE	NEUT	0.0036															

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	Ens54Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
1589	70	TAF1		1:X:7051178	Basal	FALSE	GAIN	0.3104	NA	NA	NA	NA	NA	NA	NA	NA	-0.31112	0.013605	0.012945	NA	MISSENSE		
1590	0	SATL1		-1:X:8424956	Basal	FALSE	NEUT	0.0386	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE		
1591	140	VPS26A		1:10:705878	Basal	FALSE	GAIN	0.269	4n balance	4	0.581	HET	NA	NA	NA	NA	NA	NA	NA	NA	0.398699	MISSENSE	
1592	217	RRM1		1:11:409995	Basal	FALSE	NEUT	-0.0951	2n Somatic	2	0.8	NLOH	NA	NA	NA	NA	-0.68097	NA	NA	NA	0.773791	MISSENSE	
1593	9	APB81		-1:11:638045	Basal	FALSE	NEUT	-0.1041	2n Somatic	2	0.8	NLOH	NA	NA	NA	NA	-0.15943	NA	NA	NA	0.266756	MISSENSE	
1594	1	SYTL2		-1:11:851230	Basal	FALSE	HETD	-0.4433	Hemizygous	1	0.7692	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.429605	MISSENSE		
1595	15	ATP7B		-1:13:514461	Basal	FALSE	NEUT	-0.103	2n Somatic	2	0.8204	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.578487	MISSENSE		
1596	321	NFKB1A		-1:14:349424	Basal	FALSE	NEUT	-0.0899	2n Germlin	2	0.8	NLOH	NA	NA	NA	NA	-0.96104	NA	NA	NA	0.654809	MISSENSE	
1597	76	AC012568		-1:15:652834	Basal	FALSE	NEUT	-0.1284	2n Somatic	2	0.8077	NLOH	NA	NA	NA	NA	NA	NA	NA	NA	0.262721	MISSENSE	
1598	0	C16orf50		1:16:562903	Basal	FALSE	HETD	-0.4277	Hemizygous	1	0.7174	NLOH	NA	NA	NA	NA	NA	NA	NA	NA	0.999434	MISSENSE	
1599	0	HP		1:16:706680	Basal	FALSE	HETD	-0.4327	Hemizygous	1	0.7174	NLOH	NA	NA	NA	NA	-0.02757	NA	NA	NA	0.378872	MISSENSE	
1600	116	ACLY		-1:17:372958	Basal	FALSE	NEUT	-0.0899	2n Somatic	2	0.8046	NLOH	NA	NA	NA	NA	-0.64818	NA	0.006472	0.30081	MISSENSE		
1601	18	ESCO1		-1:18:173700	Basal	FALSE	NEUT	-0.0163	2n Somatic	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.650314	TRUNCATING		
1602	63	MBD1		-1:18:460572	Basal	FALSE	GAIN	0.3122	4n balance	4	0.5625	HET	NA	NA	NA	NA	NA	NA	0.003236	0.920668	MISSENSE		
1603	41	MOBK12A		-1:19:202946	Basal	FALSE	NEUT	-0.0794	2n Somatic	2	0.8	NLOH	NA	NA	NA	NA	NA	NA	NA	0.948351	TRUNCATING		
1604	0	SEMA6B		-1:19:450606	Basal	FALSE	NEUT	-0.0794	2n Somatic	2	0.8	NLOH	NA	NA	NA	NA	-0.06531	NA	NA	NA	0.270847	MISSENSE	
1605	73	ZNF121		-1:19:953800	Basal	FALSE	GAIN	0.3178	4n Germlin	4	0.5647	HET	NA	NA	NA	NA	NA	NA	0.003236	0.65601	MISSENSE		
1606	0	FLG2		-1:1:1505963	Basal	FALSE	GAIN	0.4059	5n non-mo	5	0.5806	HET	NA	NA	NA	NA	NA	NA	0.029126	0.665665	MISSENSE		
1607	31	HSPG2		-1:1:2207763	Basal	FALSE	GAIN	0.1721	3n Somatic	3	0.8095	NLOH	NA	NA	NA	NA	-0.10647	NA	0.016181	0.791471	MISSENSE		
1608	7	EIF2C4		1:1:3606944	Basal	FALSE	NEUT	-0.0928	2n Germlin	2	0.8095	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.932686	TRUNCATING		
1609	0	HEYL		-1:1:3987090	Basal	FALSE	NEUT	-0.0928	2n Somatic	2	0.8095	NLOH	NA	NA	NA	NA	-0.01129	NA	0.003236	0.37952	MISSENSE		
1610	79	PLEKHG5		-1:1:6452035	Basal	FALSE	NEUT	-0.0822	2n Somatic	2	0.7933	NLOH	NA	NA	NA	NA	-0.06849	NA	NA	0.921145	MISSENSE		
1611	0	CLCA1		1:1:8672728	Basal	FALSE	NEUT	-0.1077	2n Somatic	2	0.8095	NLOH	NA	NA	NA	NA	-0.3489	NA	0.003236	0.377758	MISSENSE		
1612	0	BPII3		1:20:310830	Basal	FALSE	GAIN	0.3056	4n balance	4	0.5521	HET	NA	NA	NA	NA	NA	NA	0.003236	0.651575	MISSENSE		
1613	2	LRRN4		-1:20:597953	Basal	FALSE	NEUT	0.1149	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.377809	MISSENSE		
1614	0	OLIG2		1:21:333210	Basal	FALSE	NEUT	-0.0975	2n Somatic	2	0.8049	NLOH	NA	NA	NA	NA	NA	NA	NA	0.920248	MISSENSE		
1615	0	AIRE		1:21:445406	Basal	FALSE	NEUT	-0.0712	2n Somatic	2	0.8049	NLOH	NA	NA	NA	NA	-0.11103	NA	NA	0.391165	MISSENSE		
1616	330	MYH9		-1:22:350112	Basal	FALSE	NEUT	-0.0779	2n Somatic	2	0.8	NLOH	NA	NA	NA	NA	-0.21396	NA	0.006472	0.760157	MISSENSE		
1617	43	ANKRD57		1:2:1097306	Basal	FALSE	NEUT	0.1267	3n duplicat	3	0.6173	HET	NA	NA	NA	NA	NA	NA	NA	0.651499	TRUNCATING		
1618	184	DNAJC10		2:1:1833481	Basal	FALSE	GAIN	0.173	3n duplicat	3	0.6182	HET	NA	NA	NA	NA	-0.11502	NA	0.003236	0.776548	MISSENSE		
1619	0	CKCR7		1:2:2371547	Basal	FALSE	HETD	-0.4307	Hemizygous	1	0.7143	NLOH	NA	NA	NA	NA	-0.22671	NA	NA	0.582407	MISSENSE		
1620	10	PER2		-1:2:2388464	Basal	FALSE	HETD	-0.4307	Hemizygous	1	0.7143	NLOH	NA	NA	NA	NA	-0.0347	NA	NA	0.279943	MISSENSE		
1621	246	AUP1		-1:2:7460843	Basal	FALSE	NEUT	-0.1071	2n Germlin	2	0.8	NLOH	NA	NA	NA	NA	NA	NA	NA	1	MISSENSE		
1622	1	RBP2		-1:3:1406637	Basal	FALSE	GAIN	0.3447	4n balance	4	0.55	HET	NA	NA	NA	NA	-0.04466	NA	NA	0.207108	MISSENSE		
1623	29	SNRK		1:3:4336485	Basal	FALSE	GAIN	0.3191	4n Somatic	4	0.8462	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.208646	MISSENSE		
1624	34	LAMB2	CC-1	3:4913520	Basal	FALSE	NEUT	-0.1005	2n Somatic	2	0.8462	NLOH	NA	NA	NA	NA	NA	NA	NA	0.213924	MISSENSE		
1625	199	GNL3		3:5270306	Basal	FALSE	NEUT	-0.1005	2n Germlin	2	0.8462	NLOH	NA	NA	NA	NA	NA	NA	NA	0.153494	TRUNCATING		
1626	13	KIAA1109		1:4:1234466	Basal	FALSE	GAIN	0.1842	3n duplicat	3	0.5873	HET	NA	NA	NA	NA	NA	NA	0.022654	0.273584	MISSENSE		
1627	7	TRIM36		-1:5:1145009	Basal	FALSE	NEUT	-0.1136	2n Somatic	2	0.8065	NLOH	NA	NA	NA	NA	NA	NA	0.012945	0.208513	MISSENSE		
1628	11	WIPF3		1:7:2988521	Basal	FALSE	NEUT	-0.103	2n Somatic	2	0.7895	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.208447	TRUNCATING		
1629	8	CDC146		1:7:7675469	Basal	FALSE	NEUT	0.1167	3n Germlin	3	0.6316	HET	NA	NA	NA	NA	NA	NA	0.003236	0.30411	MISSENSE		
1630	0	RGS22		-1:8:1011451	Basal	FALSE	GAIN	0.4757	5n Germlin	5	0.6	HET	NA	NA	NA	NA	NA	NA	0.009709	0.208167	MISSENSE		
1631	36	GALT		9:3463838	Basal	FALSE	GAIN	0.507	5n non-mo	5	0.5705	HET	NA	NA	NA	NA	-0.62447	NA	NA	0.277299	MISSENSE		
1632	323	MSN		1:X:6487571	Basal	FALSE	HETD	-0.4664	NA	NA	NA	NA	NA	NA	NA	NA	-0.28468	NA	0.006472	NA	TRUNCATING		
1633	72	JMID1C		-1:10:646442	Basal	FALSE	NEUT	0.0136	Hemizygous	1	NA	NA	NLOH		1	NEUT	0.006026	NA	NA	0.012945	NA	MISSENSE	
1634	1	GPRIN2		1:10:464187	Basal	FALSE	NEUT	0.0083	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	NA	NA	NA	0.209404	MISSENSE		
1635	0	INSC		1:11:151688	Basal	FALSE	NEUT	0.0056	Normal (A)	2	0.561	HET	NA	NA	NA	NA	NA	NA	0.006472	0.298802	MISSENSE		
1636	23	CRY1		-1:12:105919	Basal	FALSE	NEUT	0.0162	Normal (A)	2	0.5652	HET	NA	NA	NA	NA	-0.01984	NA	0.009709	0.290913	MISSENSE		
1637	0	LRK2		1:12:390204	Basal	FALSE	NEUT	0.0162	Normal (A)	2	0.55	HET	NA	NA	NA	NA	-0.11484	NA	0.029126	0.153996	MISSENSE		
1638	0	KIAA1409		1:14:931732	Basal	FALSE	HETD	-0.2491	Hemizygous	1	0.6667	NLOH	NA	NA	NA	NA	NA	NA	0.029126	0.210101	MISSENSE		
1639	4	PAK6		1:15:383519	Basal	FALSE	NEUT	0.0019	2n Germlin	2	0.56	HET	NA	NA	NA	NA	-0.39375	NA	0.003236	0.28314	MISSENSE		
1640	20	C16orf91		-1:16:141010	Basal	FALSE	NEUT	-0.015	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.207114	MISSENSE		
1641	0	DNAH3		-1:16:209941	Basal	FALSE	NEUT	-0.015	2n Germlin	2	0.5462	HET	NA	NA	NA	NA	-0.24545	NA	0.032362	0.152126	MISSENSE		
1642	60	PHKB		1:16:462804	Basal	FALSE	NEUT	0.0049	Normal (A)	2	0.5663	HET	NA	NA	NA	NA	-0.26154	NA	0.003236	0.284725	MISSENSE		
1643	17	LRRK37A3		-1:17:602870	Basal	FALSE	NEUT	0.1	2n Germlin	2	0.7273	NLOH	NA	NA	NA	NA	NA	NA	NA	0.206648	MISSENSE		
1644	40	TP53		-1:17:751762	Basal	TRUE	HETD	-0.2464	Hemizygous	1	0.6667	NLOH	NA	NA	NA	NA	-1.33494	0.306122	0.812298	0.270939	SPLICE		
1645	165	GPI		1:19:395602	Basal	FALSE	NEUT	0.0079	Normal (A)	2	0.5721	HET	NA	NA	NA	NA	-0.75374	NA	0.003236	0.259873	MISSENSE		
1646	0	ATP1A3		-1:19:471839	Basal	FALSE	NEUT	0.0079	Normal (A)	2	0.5721	HET	NA	NA	NA	NA	-0.18459	NA	0.003236	0.207987	MISSENSE		
1647	91	UBAP2L		1:1:1524737	Basal	FALSE	GAIN	0.1961	3n duplicat	3	0.5926	HET	NA	NA	NA	NA	NA	NA	0.003236	0.207342	MISSENSE		
1648	8	GON4L		-1:1:1540413	Basal	FALSE	GAIN	0.1961	3n duplicat	3	0.5926	HET	NA	NA	NA	NA	NA	NA	0.016181	0.153182	TRUNCATING		
1649	106	KCTD3		1:1:2138591	Basal	FALSE	GAIN	0.2029	3n duplicat	3	0.5926	HET	NA	NA	NA	NA	NA	NA	0.006472	0.153919	MISSENSE		
1650	0	USH2A		-1:1:2143180	Basal	FALSE	GAIN	0.2029	3n duplicat	3	0.5926	HET	NA	NA	NA	NA	NA	NA	0.064725	0.152656	MISSENSE		
1651	0	FMN2		1:1:2383225	Basal	FALSE	NEUT	0.0858	4n monoal	4	0.6116	HET	NA	NA	NA	NA	-0.01336	NA	0.012945	0.153288	TRUNCATING		
1652	45	SEC23B		1:20:184542	Basal	FALSE	NEUT	-0.0031	Normal (A)	2	0.5603												

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	Ens54Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
1658	1	SH3TC1	-1	4:8268846	Basal	FALSE	HETD	-0.2607	Hemizygou	1	0.6407	NLOH	NA	NA	NA	NA	NA	NA	NA	0.205201	NA		
1659	28	SMARCAD1	-1	4:9542085	Basal	FALSE	NEUT	0.0311	2n Germli	2	0.5643	HET	NA	NA	NA	NA	NA	NA	0.003236	0.154382	MISSENSE		
1660	19	AC116366	-1	5:1317834	Basal	FALSE	NEUT	-0.0482	2n Somatic	2	0.6875	NLOH	NA	NA	NA	NA	NA	NA	NA	0.257945	MISSENSE		
1661	0	PCDHA2,PC1	1,1	5:1401690	Basal	FALSE	NEUT	-0.0482	2n Somatic	2	0.6875	NLOH	NA	NA	NA	NA	NA	NA	NA	0.209001	MISSENSE		
1662	0	GPBP1	-1	5:5657797	Basal	FALSE	NEUT	-0.0531	2n Germli	2	0.6747	NLOH	NA	NA	NA	NA	NA	NA	NA	0.207662	MISSENSE		
1663	35	TTC37	-1	5:9489051	Basal	FALSE	HETD	-0.2221	Hemizygou	1	0.6747	NLOH	NA	NA	NA	NA	-0.03428	NA	0.003236	0.207896	MISSENSE		
1664	8	UTRN	-1	6:1449175	Basal	FALSE	NEUT	0.0331	2n Germli	2	0.5488	HET	NA	NA	NA	NA	-0.04118	NA	0.009709	0.213546	MISSENSE		
1665	0	WNT16	-1	7:1207590	Basal	FALSE	NEUT	0.0243	2n Germli	2	0.5581	HET	NA	NA	NA	NA	-0.49227	NA	0.006472	0.207218	MISSENSE		
1666	7	ELMO1	-1	7:3726532	Basal	FALSE	NEUT	0.0067	Normal (A	2	0.5667	HET	NA	NA	NA	NA	-0.41685	NA	0.009709	0.344551	MISSENSE		
1667	13	RUSC2	-1	9:3555123	Basal	FALSE	NEUT	0.0163	Normal (A	2	0.5779	HET	NA	NA	NA	NA	NA	NA	0.003236	0.208373	MISSENSE		
1668	0	ZDHHCH9	-1	X:1287764	Basal	FALSE	NEUT	0.0107	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.003236	NA	MISSENSE		
1669	7	C10orf97	-1	10:159298	Other	FALSE	NEUT	0.1128	5n non-mo	5	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.212849	MISSENSE		
1670	30	MTAPAP	-1	10:306426	Other	FALSE	NEUT	0.0293	2n Germli	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.209124	MISSENSE		
1671	0	PLCE1	-1	10:960153	Other	FALSE	NEUT	-0.0334	Normal (A	2	0.5738	HET	NA	NA	NA	NA	-0.62467	NA	0.006472	0.205481	MISSENSE		
1672	32	FBXL11	-1	11:667692	Other	FALSE	NEUT	-0.0211	4n balance	4	0.573	HET	NA	NA	NA	NA	NA	NA	NA	0.208677	MISSENSE		
1673	3	SUV420H1	-1	11:676831	Other	FALSE	NEUT	-0.0211	4n balance	4	0.573	HET	NA	NA	NA	NA	-0.02791	NA	0.006472	0.153225	MISSENSE		
1674	18	PRICKLE1	-1	12:411446	Other	FALSE	NEUT	-0.0045	4n balance	4	0.5833	HET	NA	NA	NA	NA	-0.06757	NA	0.009709	0.208312	MISSENSE		
1675	16	ANKRD11	-1	16:878757	Other	FALSE	NEUT	-0.0759	2n Somatic	2	0.6667	NLOH	NA	NA	NA	NA	NA	NA	0.012945	0.2088	MISSENSE		
1676	5	CYB5D2	-1	17:400703	Other	FALSE	NEUT	-0.0505	2n Somatic	2	0.5904	HET	NA	NA	NA	NA	NA	NA	0.003236	0.152714	MISSENSE		
1677	1	ZNF225	-1	19:493142	Other	FALSE	NEUT	0.0337	6n Germli	6	0.5788	HET	NA	NA	NA	NA	NA	NA	NA	0.153441	MISSENSE		
1678	0	SLC9A11	-1	1:1718124	Other	FALSE	NEUT	0.0425	2n Germli	2	0.5769	HET	NA	NA	NA	NA	NA	NA	0.006472	0.206974	MISSENSE		
1679	2	KMO	-1	1:2398217	Other	FALSE	NEUT	0.1144	6n non-mo	6	0.5721	HET	NA	NA	NA	NA	-0.51413	NA	0.006472	0.154063	MISSENSE		
1680	0	NCAM2	-1	21:216297	Other	FALSE	NEUT	-0.004	4n monoal	4	0.6	HET	NA	NA	NA	NA	-0.07141	NA	0.012945	0.209527	MISSENSE		
1681	7	CCDC88A	-1	2:5537637	Other	FALSE	NEUT	-0.0359	2n Somatic	2	0.5849	HET	NA	NA	NA	NA	NA	NA	0.006472	0.208798	MISSENSE		
1682	0	ZDHHCH23	-1	3:1151554	Other	FALSE	NEUT	0.0725	4n balance	4	0.566	HET	NA	NA	NA	NA	NA	NA	0.006472	0.28061	MISSENSE		
1683	17	PLD1	-1	3:1728625	Other	FALSE	GAIN	0.2162	6n balance	6	0.566	HET	NA	NA	NA	NA	-0.89609	NA	0.006472	0.279233	MISSENSE		
1684	0	FAM13A	-1	4:8992801	Other	FALSE	NEUT	-0.0208	2n Somatic	2	0.5882	HET	NA	NA	NA	NA	NA	NA	0.003236	0.205358	MISSENSE		
1685	0	ITK	-1	5:1565737	Other	FALSE	NEUT	-0.032	5n monoal	5	0.5833	HET	NA	NA	NA	NA	-0.37404	NA	0.022654	0.208913	MISSENSE		
1686	0	RAI14	-1	5:3485973	Other	FALSE	NEUT	0.0629	5n non-mo	5	0.5789	HET	NA	NA	NA	NA	NA	NA	0.003236	0.208249	TRUNCATING		
1687	5	TAF9,AC14	-1,-1	5:6869793	Other	FALSE	NEUT	-0.032	2n Germli	2	0.5789	HET	NA	NA	NA	NA	NA	NA	NA	0.154295	MISSENSE		
1688	0	FER1L6	-1	8:1251728	Other	FALSE	NEUT	0.1005	5n Germli	6	0.5803	HET	NA	NA	NA	NA	NA	NA	0.016181	0.152443	MISSENSE		
1689	3	CHD7	-1	8:6191994	Other	FALSE	NEUT	-0.0044	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	NA	NA	0.012945	0.15194	MISSENSE		
1690	17	STAU2	-1	8:7474799	Other	FALSE	NEUT	-0.0044	2n Germli	2	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.200975	MISSENSE		
1691	0	C14orf29	-1	14:504170	Basal	FALSE	HETD	-0.2791	2n Somatic	2	0.8611	NLOH	NA	NA	NA	NA	NA	NA	NA	0.278916	MISSENSE		
1692	37	GTF3C1	-1	16:274256	Basal	FALSE	GAIN	0.2571	4n balance	4	0.5714	HET	NA	NA	NA	NA	-0.07514	NA	0.009709	0.207365	MISSENSE		
1693	48	MON18	-1	16:757848	Basal	FALSE	GAIN	0.2922	4n Germli	4	0.5625	HET	NA	NA	NA	NA	NA	NA	NA	0.151682	MISSENSE		
1694	0	FAM92B	-1	16:836933	Basal	FALSE	GAIN	0.2922	5n non-mo	5	0.5625	HET	NA	NA	NA	NA	NA	NA	NA	0.205451	MISSENSE		
1695	28	TP53	-1	17:752006	Basal	FALSE	NEUT	-0.0957	2n Somatic	2	0.8605	NLOH	NA	NA	NA	NA	-0.80089	0.306122	0.812298	0.204085	TRUNCATING		
1696	27	MEF2B	-1	19:191224	Basal	FALSE	AMP	0.6769	6n non-mo	6	0.6522	HET	NA	NA	NA	NA	-0.05328	NA	NA	0.209041	MISSENSE		
1697	2	ZNF540	-1	19:427954	Basal	FALSE	GAIN	0.2911	4n balance	4	0.5763	HET	NA	NA	NA	NA	NA	NA	NA	0.208042	MISSENSE		
1698	0	FLG	-1	1:1505492	Basal	FALSE	AMP	0.6908	6n Germli	6	0.5429	HET	NA	NA	NA	NA	NA	NA	0.02589	0.277961	MISSENSE		
1699	16	SOC1	-1	2:2026727	Basal	FALSE	GAIN	0.2322	4n Germli	4	0.5593	HET	NA	NA	NA	NA	-0.30924	NA	0.012945	0.209825	TRUNCATING		
1700	3	LMAN2L	-1	2:9676941	Basal	FALSE	GAIN	0.249	4n balance	4	0.5638	HET	NA	NA	NA	NA	NA	NA	NA	0.151788	TRUNCATING		
1701	0	PCDHA2,PC1	1,1,1	5:1401899	Basal	FALSE	HETD	-0.2971	2n Somatic	2	0.8571	NLOH	NA	NA	NA	NA	NA	NA	NA	0.278294	MISSENSE		
1702	10	AOF1	-1	6:1827958	Basal	FALSE	NEUT	0.0962	4n balance	4	0.5818	HET	NA	NA	NA	NA	NA	NA	NA	0.207168	MISSENSE		
1703	0	GSTA2	-1	6:5272775	Basal	FALSE	GAIN	0.2314	4n balance	4	0.5698	HET	NA	NA	NA	NA	-0.05071	NA	0.003236	0.208251	MISSENSE		
1704	0	CNTNAP2	-1	7:1475003	Basal	FALSE	GAIN	0.264	4n balance	4	0.5607	HET	NA	NA	NA	NA	-0.04193	NA	0.02589	0.205953	TRUNCATING		
1705	14	PFTK1	-1	7:9042303	Basal	TRUE	GAIN	0.2094	4n balance	4	0.5607	HET	NA	NA	NA	NA	NA	NA	NA	0.151934	TRUNCATING		
1706	0	NKRF	-1	X:1186079	Basal	FALSE	GAIN	0.2341	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.003236	NA	MISSENSE		
1707	0	BRWD3	-1	X:7981924	Basal	FALSE	NEUT	0.1125	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.012945	NA	MISSENSE		
1708	0	PRKCQ	-1	10:659306	Other	FALSE	HETD	-0.2184	2n Somatic	2	0.6923	NLOH	NA	NA	NA	NA	-0.6459	NA	0.009709	0.209208	MISSENSE		
1709	1	ZMYND17	-1	10:748543	Other	FALSE	HETD	-0.1948	2n Somatic	2	0.7	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.274898	MISSENSE		
1710	27	TRIP11	-1	14:915412	Other	FALSE	NEUT	0.0581	4n balance	4	0.5556	HET	NA	NA	NA	NA	NA	0.006803	0.012945	0.152619	MISSENSE		
1711	6	ADCY9	-1	16:398346	Other	FALSE	NEUT	0.0602	4n balance	4	0.5714	HET	NA	NA	NA	NA	-0.7769	NA	0.012945	0.212019	MISSENSE		
1712	1	SPAG9	-1	17:464289	Other	FALSE	NEUT	0.0577	4n Somatic	4	0.7619	NLOH	NA	NA	NA	NA	NA	NA	NA	0.15498	MISSENSE		
1713	15	QRICH2	-1	17:718007	Other	FALSE	NEUT	0.0577	4n Somatic	4	0.7619	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.152749	MISSENSE		
1714	24	TCF4	-1	18:510505	Other	FALSE	HETD	-0.1971	2n Somatic	2	0.7006	NLOH	NA	NA	NA	NA	-0.33909	NA	0.003236	0.27809	MISSENSE		
1715	89	RAB13	-1	1:1522218	Other	FALSE	NEUT	0.0591	4n balance	4	0.5667	HET	NA	NA	NA	NA	-0.08546	NA	NA	0.153736	MISSENSE		
1716	0	C1orf26	-1	1:1834577	Other	FALSE	NEUT	0.064	4n balance	4	0.5556	HET	NA	NA	NA	NA	NA	NA	0.003236	0.152495	MISSENSE		
1717	0	CST9L	-1	20:234946	Other	FALSE	NEUT	-0.0131	4n balance	4	0.56	HET	NA	NA	NA	NA	NA	NA	NA	0.210663	MISSENSE		
1718	0	SEMG2	-1	20:432844	Other	FALSE	NEUT	-0.0131	3n duplicat	3	0.5664	HET	NA	NA	NA	NA	NA	NA	NA	0.205579	MISSENSE		
1719	5	C2orf34	-1	2:4484706	Other	FALSE	NEUT	0.0628	4n balance	4	0.5673	HET	NA	NA	NA	NA	NA	NA	NA	0.210682	MISSENSE		
1720	1	TSPYL6,AC	-1,1	2:5433644	Other	FALSE	NEUT	0.0628	3n Germli	3	0.56	HET	NA	NA	NA	NA	NA	NA	NA	0.21135	MISSENSE		
1721	15	YTHDC1	-1	4:6888110	Other	FALSE	NEUT	0.0601	4n balance	4	0.5556	HET	NA	NA	NA	NA	NA	NA	0.003236	0.15356	TRUNCATING		
1722	8	RBM28	-1	7:1277518	Other	FALSE	NEUT	-0.0057	3n duplicat	3	0.5735	HET	NA	NA	NA	NA	NA	NA	0.006472	0.208952	MISSENSE		
1723	5	DGKI	-1</																				

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
1727	0	KCNK10	-1	14:877218	Other	FALSE	NEUT	0.1059	3n duplicat	3	NA	NA	NA	NA	NA	NA	-0.08984	NA	0.006472	0.436473	MISSENSE		
1728	203	ERBB2	1	17:351217	Other	FALSE	NEUT	-0.09	Hemizygou	1	NA	NA	NA	NA	NA	NA	-0.66367	0.061224	0.003236	0.263847	MISSENSE		
1729	140	ERBB2	1	17:351337	Other	FALSE	NEUT	-0.09	Hemizygou	1	NA	NA	NA	NA	NA	NA	-0.66367	0.061224	0.003236	0.205223	MISSENSE		
1730	0	ITIH5	-1	10:765865	Basal	FALSE	NEUT	0.1125	Normal (A	2	0.6087	HET	NA	NA	NA	NA	NA	NA	0.006472	0.372619	MISSENSE		
1731	167	MARS	1	12:561785	Basal	FALSE	NEUT	0.0141	2n Somatic	2	0.8182	NLOH	NA	NA	NA	NA	-0.08408	NA	0.006472	0.153102	MISSENSE		
1732	43	USP5	1	12:684463	Basal	FALSE	GAIN	0.2667	2n Somatic	2	0.6881	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.238792	MISSENSE		
1733	160	HEXA	-1	15:704286	Basal	FALSE	GAIN	0.4075	4n Germlin	4	0.7899	NLOH	NA	NA	NA	NA	-1.03212	NA	0.009709	0.211184	MISSENSE		
1734	0	IL16	1	15:793698	Basal	FALSE	NEUT	0.0517	2n Somatic	2	0.7899	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.207456	MISSENSE		
1735	3	MYH11	-1	16:157429	Basal	TRUE	NEUT	0.0817	Normal (A	2	0.5789	HET	NA	NA	NA	NA	-0.26304	NA	0.012945	0.282099	SPICE		
1736	0	ACSM2	-1	16:204726	Basal	FALSE	NEUT	0.0817	2n Germlin	2	0.5789	HET	NA	NA	NA	NA	NA	NA	0.006472	0.208594	MISSENSE		
1737	5	CORO7	-1	16:439756	Basal	FALSE	HETD	-0.4178	Hemizygou	1	0.618	HET	NA	NA	NA	NA	NA	NA	0.006472	0.352936	MISSENSE		
1738	57	RPAIN,ACD	1,1	17:527025	Basal	FALSE	HETD	-0.281	Hemizygou	1	0.8103	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.278785	MISSENSE		
1739	0	GH1	-1	17:593490	Basal	FALSE	NEUT	0.1112	3n Somatic	3	0.8284	NLOH	NA	NA	NA	NA	-0.53694	NA	0.006472	0.211106	MISSENSE		
1740	26	SMAD7	-1	18:447019	Basal	FALSE	GAIN	0.235	Normal (A	2	0.6	HET	NA	NA	NA	NA	-0.78336	NA	0.006472	0.349635	MISSENSE		
1741	5	ZNF585A	-1	19:423356	Basal	FALSE	GAIN	0.3042	3n duplicat	3	0.5978	HET	NA	NA	NA	NA	NA	NA	0.003236	0.208936	MISSENSE		
1742	0	GPR32	1	19:559658	Basal	FALSE	NEUT	0.0982	Normal (A	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.006472	0.218202	MISSENSE		
1743	0	Clorf161	1	11:1164650	Basal	FALSE	NEUT	0.0556	2n Germlin	2	0.5556	HET	NA	NA	NA	NA	NA	NA	0.006472	0.272586	MISSENSE		
1744	10	GABPA	1	21:260633	Basal	FALSE	NEUT	0.0431	Normal (A	2	0.5823	HET	NA	NA	NA	NA	NA	NA	0.003236	0.152482	MISSENSE		
1745	1	EDAR	-1	2:1088907	Basal	FALSE	NEUT	-0.0736	2n Somatic	2	0.7857	NLOH	NA	NA	NA	NA	-0.20245	NA	0.006472	0.208255	MISSENSE		
1746	14	SMYD5	1	2:7330639	Basal	TRUE	GAIN	0.4054	3n duplicat	3	0.5612	HET	NA	NA	NA	NA	NA	NA	0.006472	0.206544	SPICE		
1747	54	CISH	-1	3:5062025	Basal	FALSE	NEUT	-0.096	2n Germlin	2	0.8041	NLOH	NA	NA	NA	NA	-0.27793	NA	0.006472	0.15244	MISSENSE		
1748	0	PCDH24	1	5:1759441	Basal	FALSE	NEUT	-0.0947	2n Somatic	2	0.8	NLOH	NA	NA	NA	NA	-0.36941	NA	0.006472	0.2089	MISSENSE		
1749	0	LAMA2	1	6:1295171	Basal	TRUE	NEUT	0.0427	Normal (A	2	NA	NA	NA	NA	NA	NA	-0.56446	NA	0.022654	0.271434	SPICE		
1750	3	GPLD1	-1	6:2455510	Basal	FALSE	AMP	0.7221	5n monoal	5	0.6875	NLOH	NA	NA	NA	NA	-0.07326	NA	0.006472	0.371371	MISSENSE		
1751	29	AC021097	1	7:1505661	Basal	FALSE	GAIN	0.3597	4n monoal	4	0.625	HET	NA	NA	NA	NA	NA	NA	0.006472	0.208551	MISSENSE		
1752	0	GHRHR	1	7:3098254	Basal	FALSE	HETD	-0.4419	Hemizygou	1	0.6545	NLOH	NA	NA	NA	NA	-0.25075	NA	0.003236	0.153139	MISSENSE		
1753	4	RNF19A	-1	8:1013410	Basal	FALSE	NEUT	0.0984	Normal (A	2	0.601	HET	NA	NA	NA	NA	NA	NA	0.006472	0.153028	MISSENSE		
1754	2	ASAP1	-1	8:1312184	Basal	TRUE	NEUT	0.0782	2n Somatic	2	0.8571	NLOH	NA	NA	NA	NA	-0.83171	NA	0.012945	0.26248	SPICE		
1755	1	ARSH	1	X:2961381	Basal	FALSE	NEUT	-0.0159	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.006472	0.208551	MISSENSE		
1756	0	SATL1	-1	X:8424983	Basal	FALSE	NEUT	-0.0086	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.006472	0.208551	MISSENSE		
1757	0	MYO3A	1	10:263261	Other	FALSE	NEUT	-0.1066	Normal (A	2	0.563	HET	NA	NA	NA	NA	NA	0.006803	0.009709	0.205534	MISSENSE		
1758	2	BTBD11	1	12:106461	Other	FALSE	NEUT	-0.1201	2n Germlin	2	0.5556	HET	NA	NA	NA	NA	NA	NA	0.003236	0.274324	MISSENSE		
1759	9	METTL2A	1	17:578716	Other	FALSE	NEUT	-0.1077	Normal (A	2	0.5652	HET	NA	NA	NA	NA	NA	NA	0.006472	0.379157	MISSENSE		
1760	24	ZNF91	-1	19:233342	Other	FALSE	NEUT	-0.1323	Normal (A	2	0.5423	HET	NA	NA	NA	NA	NA	NA	0.009709	0.206667	MISSENSE		
1761	16	ZNF91	-1	19:233342	Other	FALSE	NEUT	-0.1323	Normal (A	2	0.5423	HET	NA	NA	NA	NA	NA	NA	0.009709	0.296708	MISSENSE		
1762	0	CYP2A6	1	19:460416	Other	FALSE	NEUT	-0.1334	Normal (A	2	0.5625	HET	NA	NA	NA	NA	-0.34789	NA	0.006472	0.208076	MISSENSE		
1763	26	KLHL12	-1	1:2011304	Other	FALSE	NEUT	-0.1064	Normal (A	2	0.553	HET	NA	NA	NA	NA	NA	NA	0.006472	0.208646	MISSENSE		
1764	0	SLC35F3	1	1:2325224	Other	FALSE	NEUT	-0.1321	Normal (A	2	0.553	HET	NA	NA	NA	NA	NA	NA	0.006472	0.201813	MISSENSE		
1765	7	FMN2	1	1:2384384	Other	FALSE	NEUT	-0.1321	Normal (A	2	0.553	HET	NA	NA	NA	NA	-0.0097	NA	0.012945	0.208633	MISSENSE		
1766	30	PER3,VAM1	1,1	1:7768114	Other	FALSE	NEUT	-0.1063	Normal (A	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.006472	0.210264	MISSENSE		
1767	81	SLA2,C20orf	-1,1	20:346738	Other	FALSE	GAIN	0.2059	3n duplicat	3	0.6591	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.20756	MISSENSE		
1768	27	CCDC52	-1	3:1146705	Other	FALSE	NEUT	-0.0723	Normal (A	2	0.55	HET	NA	NA	NA	NA	NA	NA	0.003236	0.211755	MISSENSE		
1769	19	FLNB	1	3:5808384	Other	FALSE	NEUT	-0.088	Normal (A	2	0.5556	HET	NA	NA	NA	NA	-0.19626	NA	0.009709	0.288308	MISSENSE		
1770	9	PRDM1	1	6:1066602	Other	FALSE	NEUT	-0.0781	Normal (A	2	0.55	HET	NA	NA	NA	NA	NA	NA	0.003236	0.152887	MISSENSE		
1771	0	SLC17A1	-1	6:2590692	Other	FALSE	NEUT	-0.0908	Normal (A	2	0.5577	HET	NA	NA	NA	NA	NA	NA	0.006472	0.235328	MISSENSE		
1772	24	SMAP1	1	6:7161898	Other	FALSE	NEUT	-0.079	Normal (A	2	0.55	HET	NA	NA	NA	NA	-0.09438	NA	0.006472	0.285385	MISSENSE		
1773	0	MYOM2	1	8:2080033	Other	FALSE	NEUT	-0.1009	Normal (A	2	0.5455	HET	NA	NA	NA	NA	NA	NA	0.012945	0.208233	MISSENSE		
1774	8	GINS4	1	8:4151661	Other	FALSE	NEUT	-0.0997	Normal (A	2	0.5581	HET	NA	NA	NA	NA	-0.0318	NA	0.006472	0.208101	MISSENSE		
1775	30	MED12	1	X:7025595	Other	FALSE	HOMD	-0.635	NA	NA	NA	NA	NA	NA	NA	NA	-0.00819	NA	0.003236	NA	MISSENSE		
1776	5	LRP1	1	12:558594	Other	FALSE	NEUT	0.0196	3n duplicat	3	0.5556	HET	NA	NA	NA	NA	-0.32011	NA	0.019417	0.208551	MISSENSE		
1777	3	ZNF773	1	19:627099	Other	FALSE	NEUT	-0.0543	3n duplicat	3	0.5541	HET	NA	NA	NA	NA	NA	NA	0.003236	0.208551	MISSENSE		
1778	2	KBTBD10	1	2:1700749	Other	FALSE	NEUT	0.0196	4n Germlin	4	0.5487	HET	NA	NA	NA	NA	NA	NA	0.006472	0.208551	MISSENSE		
1779	24	TDO2	1	4:1570587	Other	FALSE	NEUT	0.012	5n non-mo	5	0.5512	HET	NA	NA	NA	NA	-0.80678	NA	0.006472	0.208551	MISSENSE		
1780	0	ENAM	1	4:7172889	Other	FALSE	NEUT	0.012	6n Germlin	6	0.5556	HET	NA	NA	NA	NA	NA	NA	0.009709	0.208551	MISSENSE		
1781	3	BRAF	-1	7:1400995	Other	FALSE	NEUT	-0.0387	4n balance	4	0.5592	HET	NA	NA	NA	NA	-0.76705	NA	0.006472	0.208551	MISSENSE		
1782	0	UTP14A	1	X:1288878	Other	FALSE	NEUT	-0.015	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.006472	0.208551	MISSENSE		
1783	20	E2F8	-1	11:192078	Other	FALSE	HETD	-0.2244	2n Somatic	2	0.7778	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.152302	MISSENSE		
1784	23	GAB2	-1	11:776153	Other	FALSE	HETD	-0.2078	2n Somatic	2	0.7778	NLOH	NA	NA	NA	NA	-0.2116	NA	0.016181	0.277277	MISSENSE		
1785	88	TJP1	-1	15:277979	Other	FALSE	HETD	-0.2241	2n Somatic	2	0.8	NLOH	NA	NA	NA	NA	-0.23102	NA	0.012945	0.209087	MISSENSE		
1786	0	C16orf54	1	16:296631	Other	FALSE	NEUT	0.1162	4n balance	4	0.5714	HET	NA	NA	NA	NA	NA	NA	0.006472	0.204409	TRUNCATING		
1787	0	MYH2	-1	17:103698	Other	FALSE	NEUT	0.1139	3n Somatic	3	0.8592	NLOH	NA	NA	NA	NA	-0.19733	NA	0.016181	0.209912	MISSENSE		
1788	200	TP53	-1	17:751915	Other	FALSE	NEUT	0.1139	4n Somatic	4	0.8592	NLOH	NA	NA	NA	NA	-0.80679	0.306122	0.812298	0.213014	MISSENSE		
1789	0	CDH2	-1	18:237861	Other	FALSE	NEUT	0.1554	4n balance	4	0.5556	HET	NA	NA	NA	NA	-0.29318	NA	0.006472	0			

1	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
	Non.ref.RN	Ens54Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
1796	2	HIST1H4K1	-1,1	6:2790706	Other	FALSE	NEUT	0.1482	3n	Germ	3	NA	NA	NA	NA	NA	NA	NA	NA	0.273852	MISSENSE		
1797	0	DGKI		7:13702511	Other	FALSE	NEUT	0.1524	4n	Germ	4	0.5676	HET	NA	NA	NA	NA	-0.5432	NA	0.003236	0.382482	MISSENSE	
1798	0	ABC84		7:8692003	Other	FALSE	NEUT	0.1675	4n	balance	4	0.5652	HET	NA	NA	NA	NA	-0.02288	NA	0.012945	0.207752	MISSENSE	
1799	26	PPM2C		1:89500346	Other	FALSE	NEUT	0.1785	4n	balance	4	0.5429	HET	NA	NA	NA	NA	NA	NA	NA	0.212362	MISSENSE	
1800	9	PHLDA1		12:747104	Other	FALSE	NEUT	-0.0337	3n	Somatic	3	0.6667	NLOH	NA	NA	NA	NA	NA	NA	NA	0.374531	MISSENSE	
1801	0	LIPC		1:15566279	Other	FALSE	NEUT	-0.0469	3n	duplicat	3	0.5541	HET	NA	NA	NA	NA	-0.833	NA	0.003236	0.249172	MISSENSE	
1802	8	RNF111		1:15571705	Other	FALSE	NEUT	-0.0469	Hemizygo		1	0.5541	HET	NA	NA	NA	NA	-0.3773	NA	0.006472	0.204355	MISSENSE	
1803	9	CES2		1:16655318	Other	FALSE	NEUT	-0.0451	2n	Germ	2	0.5652	HET	NA	NA	NA	NA	-0.03167	NA	NA	0.206554	MISSENSE	
1804	25	AC005726	-1,-1	17:239440	Other	FALSE	NEUT	-0.0472	2n	Germ	2	0.7	NLOH	NA	NA	NA	NA	NA	NA	NA	0.283061	TRUNCATING	
1805	29	THRAP4		17:354424	Other	FALSE	NEUT	-0.0179	3n	Somatic	3	0.7	NLOH	NA	NA	NA	NA	NA	NA	NA	0.287502	MISSENSE	
1806	0	CSTL1		1:20233689	Other	FALSE	GAIN	0.2464	6n	balance	6	0.5606	HET	NA	NA	NA	NA	NA	NA	NA	0.208331	MISSENSE	
1807	51	ATP6V1E1		22:164609	Other	FALSE	HETD	-0.2322	Hemizygo		1	0.6667	NLOH	NA	NA	NA	NA	-0.85917	0.006803	NA	0.264964	MISSENSE	
1808	0	SUT2		1:42020039	Other	FALSE	HETD	-0.1972	2n	Somatic	2	0.6	HET	NA	NA	NA	NA	-0.4072	0.020408	0.009709	0.207976	MISSENSE	
1809	6	PEX5		12:723546	Other	FALSE	NEUT	-0.0828	Normal (A		2	0.5754	HET	NA	NA	NA	NA	-0.05668	NA	0.003236	0.207677	MISSENSE	
1810	12	DICER1		1:14946300	Other	FALSE	NEUT	-0.1358	2n	Somatic	2	0.7179	NLOH	NA	NA	NA	NA	-0.01958	NA	0.003236	0.351825	MISSENSE	
1811	0	KCNH7		2:1629366	Other	FALSE	GAIN	0.1975	4n	balance	4	0.5556	HET	NA	NA	NA	NA	NA	NA	0.009709	0.279449	MISSENSE	
1812	0	GPRIN3		1:49038813	Other	FALSE	NEUT	-0.16	2n	Somatic	2	0.7234	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.205827	MISSENSE	
1813	0	TPST1		7:6534302	Other	FALSE	NEUT	-0.1405	2n	Somatic	2	0.7143	NLOH	NA	NA	NA	NA	NA	NA	NA	0.153018	MISSENSE	
1814	0	ABC81		7:8701144	Other	FALSE	NEUT	-0.1636	2n	Somatic	2	0.7273	NLOH	NA	NA	NA	NA	-0.10657	NA	0.012945	0.285919	MISSENSE	
1815	0	CTBP2		10:126673	Basal	FALSE	HETD	-0.2864	2n	Somatic	2	0.8	NLOH	NA	NA	NA	NA	-0.36723	NA	NA	0.272989	MISSENSE	
1816	0	ANKRD30A		1:3075452	Basal	FALSE	NEUT	0.0824	4n	balance	4	0.5714	HET	NA	NA	NA	NA	NA	NA	0.022654	0.15262	MISSENSE	
1817	0	PCDH15		1:10552611	Basal	FALSE	NEUT	0.1074	4n	balance	4	0.5979	HET	NA	NA	NA	NA	-0.21143	NA	0.022654	0.153888	MISSENSE	
1818	0	ZNF365		1:10640851	Basal	FALSE	NEUT	-0.0395	3n	duplicat	3	0.6	HET	NA	NA	NA	NA	NA	NA	0.003236	0.264407	MISSENSE	
1819	27	BCL9L		11:118284	Basal	FALSE	NEUT	-0.0436	3n	duplicat	3	0.619	HET	NA	NA	NA	NA	NA	NA	0.003236	0.212046	MISSENSE	
1820	0	TCTA		11:120489	Basal	FALSE	NEUT	-0.0436	3n	duplicat	3	0.619	HET	NA	NA	NA	NA	NA	NA	0.006472	0.20735	MISSENSE	
1821	20	CCS		11:661295	Basal	FALSE	NEUT	-0.0491	3n	duplicat	3	0.6316	HET	NA	NA	NA	NA	-0.02105	NA	NA	0.210508	MISSENSE	
1822	7	SUV420H1		11:676815	Basal	FALSE	NEUT	-0.0491	3n	duplicat	3	0.6316	HET	NA	NA	NA	NA	-0.02696	NA	0.006472	0.219845	MISSENSE	
1823	0	CLEC1B,CLC	-1,1	12:100429	Basal	FALSE	NEUT	-0.04	3n	duplicat	3	0.625	HET	NA	NA	NA	NA	NA	NA	NA	0.203573	MISSENSE	
1824	0	WSCD2		12:107124	Basal	FALSE	NEUT	-0.0491	3n	duplicat	3	0.6207	HET	NA	NA	NA	NA	NA	NA	0.003236	0.277218	MISSENSE	
1825	15	LRP6,BCL2L	-1,1	12:122094	Basal	FALSE	NEUT	-0.0385	3n	Germ	3	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.315759	MISSENSE	
1826	0	PLEKHG7		1:12916818	Basal	FALSE	NEUT	-0.0491	3n	Germ	3	0.6207	HET	NA	NA	NA	NA	NA	NA	0.003236	0.27955	MISSENSE	
1827	11	MCF2L		13:112778	Basal	FALSE	NEUT	0.1234	4n	Somatic	4	0.8722	NLOH	NA	NA	NA	NA	-0.11837	NA	0.003236	0.152733	MISSENSE	
1828	35	TFFD1		13:113336	Basal	FALSE	GAIN	0.2298	4n	Somatic	4	0.8722	NLOH	NA	NA	NA	NA	-0.22372	NA	0.006472	0.208736	MISSENSE	
1829	9	RASL11A		13:267438	Basal	FALSE	NEUT	0.1142	4n	Germ	4	0.8722	NLOH	NA	NA	NA	NA	NA	NA	NA	0.288318	MISSENSE	
1830	32	ZFYVE21		14:103263	Basal	FALSE	NEUT	-0.07	3n	Somatic	3	0.8421	NLOH	NA	NA	NA	NA	NA	NA	NA	0.279493	MISSENSE	
1831	35	HIF1A		14:612776	Basal	FALSE	NEUT	-0.0529	3n	Somatic	3	0.8421	NLOH	NA	NA	NA	NA	-0.28197	NA	NA	0.208843	MISSENSE	
1832	26	INO80		1:15391381	Basal	FALSE	HETD	-0.28	2n	Somatic	2	0.8	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.478679	MISSENSE	
1833	0	CILP		1:15632771	Basal	FALSE	NEUT	-0.0314	3n	Germ	3	0.625	HET	NA	NA	NA	NA	NA	NA	0.012945	0.487402	MISSENSE	
1834	0	DNAH3		1:16209061	Basal	FALSE	NEUT	-0.0781	3n	duplicat	3	0.6356	HET	NA	NA	NA	NA	-0.15596	NA	0.032362	0.278425	MISSENSE	
1835	5	RHBDF1		1:1654804	Basal	FALSE	HETD	-0.2279	2n	Germ	2	0.625	HET	NA	NA	NA	NA	NA	NA	0.003236	0.69513	MISSENSE	
1836	1	SLC9A5		1:16658496	Basal	FALSE	HETD	-0.2951	2n	Germ	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.72558	MISSENSE	
1837	7	SLC7A6		1:1668826	Basal	FALSE	HETD	-0.2951	2n	Germ	2	0.5714	HET	NA	NA	NA	NA	-0.09128	NA	NA	1	MISSENSE	
1838	6	ZFP90		1:16671499	Basal	TRUE	HETD	-0.2951	Normal (A		2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.984003	SPICE	
1839	28	MBTPS1		1:16826504	Basal	FALSE	NEUT	0.1562	4n	monoal	4	0.7338	NLOH	NA	NA	NA	NA	-0.07842	NA	0.006472	0.984142	MISSENSE	
1840	8	FLCN		17:170718	Basal	FALSE	HETD	-0.3206	2n	Somatic	2	0.7958	NLOH	NA	NA	NA	NA	-0.03037	NA	NA	0.729044	MISSENSE	
1841	29	T0B1		17:462962	Basal	FALSE	NEUT	-0.0449	3n	duplicat	3	0.619	HET	NA	NA	NA	NA	NA	NA	NA	0.715683	MISSENSE	
1842	0	MPO		17:537057	Basal	FALSE	NEUT	-0.0449	3n	duplicat	3	0.619	HET	NA	NA	NA	NA	-0.09445	NA	0.003236	0.983954	MISSENSE	
1843	36	TMEM49		17:552438	Basal	FALSE	NEUT	-0.0449	2n	Germ	2	0.619	HET	NA	NA	NA	NA	NA	NA	NA	0.486638	MISSENSE	
1844	74	SOX9		17:676292	Basal	FALSE	NEUT	-0.0449	3n	duplicat	3	0.619	HET	NA	NA	NA	NA	NA	NA	NA	0.668187	MISSENSE	
1845	3	MGAT5B		17:724138	Basal	FALSE	NEUT	-0.0449	3n	duplicat	3	0.619	HET	NA	NA	NA	NA	-0.49336	NA	0.006472	1	MISSENSE	
1846	24	ZNF532		18:547370	Basal	FALSE	HETD	-0.2944	2n	Somatic	2	0.8117	NLOH	NA	NA	NA	NA	NA	NA	NA	0.979061	MISSENSE	
1847	0	CCDC123		19:381223	Basal	TRUE	NEUT	0.0039	4n	balance	4	0.6	HET	NA	NA	NA	NA	NA	NA	0.009709	0.681754	SPICE	
1848	2	ZNF180		19:496733	Basal	FALSE	NEUT	-0.1161	3n	Germ	3	0.6471	HET	NA	NA	NA	NA	NA	NA	0.006472	0.728823	MISSENSE	
1849	145	SNRPD2		19:508836	Basal	FALSE	NEUT	-0.1161	3n	duplicat	3	0.6471	HET	NA	NA	NA	NA	-0.23562	NA	NA	0.999039	MISSENSE	
1850	20	ALKBH7		19:632549	Basal	FALSE	NEUT	0.0039	3n	duplicat	3	0.625	HET	NA	NA	NA	NA	NA	NA	NA	0.668019	MISSENSE	
1851	0	STXBP3		1:1091235	Basal	FALSE	GAIN	0.3521	5n	non-mo	5	0.6207	HET	NA	NA	NA	NA	-0.0549	NA	0.009709	0.689121	MISSENSE	
1852	0	FLG2		1:1505929	Basal	FALSE	GAIN	0.2821	5n	monoal	5	0.7407	NLOH	NA	NA	NA	NA	NA	NA	0.029126	0.671691	MISSENSE	
1853	51	SMG5		1:1545046	Basal	FALSE	GAIN	0.3088	5n	monoal	5	0.7407	NLOH	NA	NA	NA	NA	-0.08984	NA	0.006472	0.984661	MISSENSE	
1854	20	SPEN		1:1613780	Basal	FALSE	NEUT	-0.0503	3n	Germ	3	NA	NA	NA	NA	NA	NA	-0.03641	NA	0.022654	0.686995	MISSENSE	
1855	2	RP5-1056L	1,1	1:1980749	Basal	FALSE	NEUT	-0.0503	3n	duplicat	3	0.6	HET	NA	NA	NA	NA	NA	NA	NA	0.682547	MISSENSE	
1856	15	PPP1R15B		1:2026453	Basal	FALSE	NEUT	0.1545	4n	monoal	4	0.6961	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.997258	MISSENSE	
1857	68	PCTK3		1:2037670	Basal	FALSE	NEUT	0.1529	4n	monoal	4	0.6961	NLOH	NA	NA	NA	NA	NA	NA	NA	0.993579	MISSENSE	
1858	45	AOF2		1:2325658	Basal	FALSE	NEUT	-0.0503	3n	duplicat	3	0.5936	HET	NA	NA	NA	NA	-0.05461	NA	NA	0.724292	MISSENSE	
1859	16	RCC1		1:2873571	Basal	FALSE	NEUT	-0.0353	2n	Somatic	2	0.5936	HET	NA	NA	NA	NA	-0.00854	NA				

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
1865	0	PER3,VAM1	1,1	1:7769450	Basal	TRUE	NEUT	-0.0564	3n Germlin	3	0.6195	HET	NA	NA	NA	NA	NA	NA	NA	0.263221	SPLICE		
1866	10	ITCH		1:20:325133	Basal	FALSE	NEUT	0.0753	4n balance	4	0.5625	HET	NA	NA	NA	NA	-0.49237	NA	NA	0.420143	MISSENSE		
1867	0	CYP24A1		-1:20:522088	Basal	FALSE	GAIN	0.2431	4n balance	4	0.5625	HET	NA	NA	NA	NA	-0.05095	NA	0.003236	1	MISSENSE		
1868	0	CHGB		1:20:585210	Basal	FALSE	NEUT	0.0753	4n balance	4	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.432997	TRUNCATING		
1869	9	PDE9A		1:21:430639	Basal	FALSE	GAIN	0.2809	5n Somatic	5	0.8916	NLOH	NA	NA	NA	NA	-0.07801	NA	NA	0.663546	MISSENSE		
1870	8	CDC45L		1:22:178825	Basal	FALSE	NEUT	-0.0618	3n Somatic	3	0.8387	NLOH	NA	NA	NA	NA	-0.08917	NA	NA	0.663962	MISSENSE		
1871	18	MORC2		-1:22:296667	Basal	FALSE	NEUT	-0.0838	3n Somatic	3	0.8387	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.28052	MISSENSE		
1872	2	LCT		-1:2:1362647	Basal	FALSE	NEUT	-0.0498	3n duplicat	3	0.6062	HET	NA	NA	NA	NA	-0.52023	NA	0.019417	0.255923	MISSENSE		
1873	29	LRP2		-1:2:1698058	Basal	FALSE	NEUT	-0.053	3n duplicat	3	0.6162	HET	NA	NA	NA	NA	-0.09157	NA	0.038835	0.66515	MISSENSE		
1874	95	ZFP36L2		-1:2:4330579	Basal	FALSE	NEUT	-0.0468	3n Somatic	3	0.8365	NLOH	NA	NA	NA	NA	NA	NA	0.620323	MISSENSE			
1875	1	DNHL1		1:2:8463066	Basal	TRUE	GAIN	0.2267	4n Germlin	4	NA	NA	NA	NA	NA	NA	NA	NA	0.533372	SPLICE			
1876	16	PLXND1		-1:3:1307858	Basal	FALSE	NEUT	-0.0273	3n Germlin	3	0.625	HET	NA	NA	NA	NA	NA	NA	0.621372	MISSENSE			
1877	16	NUP210		-1:3:1340282	Basal	FALSE	NEUT	0.1567	4n balance	4	0.5616	HET	NA	NA	NA	NA	-0.32131	NA	0.009709	0.243102	MISSENSE		
1878	0	BCHC		-1:3:1670305	Basal	FALSE	GAIN	0.4532	6n Germlin	6	0.7719	NLOH	NA	NA	NA	NA	-0.02247	NA	0.009709	0.347103	MISSENSE		
1879	5	ZNF385D		-1:3:2144213	Basal	FALSE	NEUT	0.1604	4n balance	4	NA	NA	NA	NA	NA	NA	NA	NA	0.003236	0.300263	MISSENSE		
1880	1	CYP2U1		4:1090880	Basal	FALSE	HETD	-0.2785	Normal (A)	2	0.5797	HET	NA	NA	NA	NA	-0.49529	NA	NA	0.477356	MISSENSE		
1881	7	PALLD		14:1698389	Basal	FALSE	HETD	-0.4203	2n Somatic	2	0.75	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.535027	TRUNCATING		
1882	0	BTNL8		1:5:1802683	Basal	FALSE	HETD	-0.2892	2n Somatic	2	0.8	NLOH	NA	NA	NA	NA	NA	NA	NA	0.531786	MISSENSE		
1883	0	AMACR		-1:5:3406467	Basal	FALSE	HETD	-0.2799	Normal (A)	2	0.5806	HET	NA	NA	NA	NA	-0.51475	NA	NA	0.347727	MISSENSE		
1884	0	TAS2R1		-1:5:9683010	Basal	FALSE	HETD	-0.3124	Normal (A)	2	0.5806	HET	NA	NA	NA	NA	-0.01888	NA	0.009709	0.473056	MISSENSE		
1885	1	FRK		-1:6:1163953	Basal	FALSE	GAIN	0.3256	5n Germlin	5	0.8718	NLOH	NA	NA	NA	NA	-0.0278	NA	0.009709	0.476343	MISSENSE		
1886	18	LATS1		-1:6:1500469	Basal	FALSE	NEUT	0.1423	4n Somatic	4	0.875	NLOH	NA	NA	NA	NA	NA	NA	0.019417	0.520648	MISSENSE		
1887	22	HIST1H2BH		3:2636017	Basal	FALSE	NEUT	0.1385	4n Somatic	4	0.8718	NLOH	NA	NA	NA	NA	-0.10316	NA	0.009709	0.628137	MISSENSE		
1888	4	ZNF318		-1:6:4343307	Basal	FALSE	NEUT	-0.0351	3n Somatic	3	0.8718	NLOH	NA	NA	NA	NA	-0.05461	NA	0.006472	0.731429	MISSENSE		
1889	19	MAD2L1BP		1:6:4371616	Basal	FALSE	NEUT	-0.0351	3n Somatic	3	0.8718	NLOH	NA	NA	NA	NA	NA	NA	NA	0.522274	MISSENSE		
1890	0	COL12A1		-1:6:7587019	Basal	FALSE	NEUT	-0.0506	3n Somatic	3	0.8718	NLOH	NA	NA	NA	NA	-0.05792	NA	0.016181	0.577624	MISSENSE		
1891	3	TBXAS1		1:7:1393015	Basal	FALSE	NEUT	-0.0569	3n Somatic	3	0.8421	NLOH	NA	NA	NA	NA	-0.51734	NA	0.006472	0.493669	MISSENSE		
1892	5	GPNMB		1:7:2326672	Basal	FALSE	HETD	-0.2833	2n Somatic	2	0.8	NLOH	NA	NA	NA	NA	NA	NA	0.009709	0.478619	MISSENSE		
1893	48	PON2		-1:7:9487956	Basal	FALSE	NEUT	-0.0567	3n Somatic	3	0.8421	NLOH	NA	NA	NA	NA	-0.49244	NA	NA	0.349464	MISSENSE		
1894	0	KCNV1		-1:8:1110541	Basal	FALSE	GAIN	0.5577	6n balance	6	0.5368	HET	NA	NA	NA	NA	NA	NA	NA	0.737117	MISSENSE		
1895	0	CSMD3		-1:8:1133102	Basal	FALSE	GAIN	0.5396	6n balance	6	0.5368	HET	NA	NA	NA	NA	NA	0.013605	0.061489	0.725926	MISSENSE		
1896	8	KCTD9		-1:8:2535961	Basal	FALSE	HETD	-0.3157	2n Somatic	2	0.7961	NLOH	NA	NA	NA	NA	NA	NA	NA	0.238714	MISSENSE		
1897	1	RNF20		1:9:1033375	Basal	FALSE	NEUT	-0.0653	3n Somatic	3	0.8333	NLOH	NA	NA	NA	NA	NA	NA	0.012945	0.893026	MISSENSE		
1898	89	PPP2R4		1:9:1309311	Basal	FALSE	NEUT	-0.0499	3n Somatic	3	0.8333	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.72917	MISSENSE		
1899	0	BEND7		-1:10:135212	Basal	FALSE	AMP	0.6607	4n balance	4	0.6042	HET	NA	NA	NA	NA	NA	NA	0.003236	0.476329	MISSENSE		
1900	442	AHNAK		-1:11:620439	Basal	FALSE	NEUT	0.1045	2n Germlin	2	0.5676	HET	NA	NA	NA	NA	NA	NA	0.032362	0.476418	MISSENSE		
1901	69	YEATS4		1:12:680509	Basal	FALSE	HETD	-0.3007	Hemizygou	1	0.82	NLOH	NA	NA	NA	NA	NA	NA	NA	0.509491	MISSENSE		
1902	0	NEO1		1:15:713284	Basal	FALSE	NEUT	0.1202	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	-0.15771	NA	NA	0.300056	MISSENSE		
1903	281	PSMD7		1:16:728966	Basal	FALSE	HETD	-0.2815	Hemizygou	1	0.746	NLOH	NA	NA	NA	NA	-0.52401	NA	NA	0.573577	MISSENSE		
1904	0	AC113554		1:17:589031	Basal	FALSE	HETD	-0.2392	Hemizygou	1	0.8367	NLOH	NA	NA	NA	NA	NA	NA	NA	0.300685	MISSENSE		
1905	14	ZNF14		-1:19:196842	Basal	FALSE	NEUT	0.0821	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	NA	NA	0.009709	0.982887	TRUNCATING		
1906	1	CD37,AC011	1,-1	19:545338	Basal	FALSE	NEUT	0.0821	Normal (A)	2	0.564	HET	NA	NA	NA	NA	NA	NA	NA	0.725176	MISSENSE		
1907	14	ADAMTSL4		1:1487931	Basal	FALSE	GAIN	0.4034	3n duplicat	3	0.6389	HET	NA	NA	NA	NA	NA	NA	0.003236	0.524688	MISSENSE		
1908	0	ETV3L		-1:15:53355	Basal	FALSE	GAIN	0.4051	3n duplicat	3	0.6445	HET	NA	NA	NA	NA	NA	NA	0.003236	0.240284	MISSENSE		
1909	0	FMN2		1:12384878	Basal	FALSE	NEUT	0.1107	Normal (A)	2	0.6122	HET	NA	NA	NA	NA	-0.03291	NA	0.012945	0.708524	MISSENSE		
1910	36	CDC21		1:12645429	Basal	FALSE	HETD	-0.3277	Hemizygou	1	0.8235	NLOH	NA	NA	NA	NA	NA	NA	NA	0.729363	MISSENSE		
1911	0	PYGB		1:20:252170	Basal	TRUE	NEUT	0.1047	2n Germlin	2	NA	NA	NA	NA	NA	NA	-0.27227	NA	NA	0.72742	SPLICE		
1912	23	PLAGL2		-1:20:302534	Basal	FALSE	NEUT	0.0535	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	NA	NA	0.003236	0.737709	MISSENSE		
1913	25	RNF149		-1:2:1012647	Basal	FALSE	NEUT	0.1272	2n Germlin	2	0.5625	HET	NA	NA	NA	NA	NA	NA	0.003236	0.30084	TRUNCATING		
1914	0	IL1B		-1:2:1133068	Basal	FALSE	NEUT	0.1272	2n Germlin	2	0.5814	HET	NA	NA	NA	NA	-1.37728	NA	NA	0.475781	MISSENSE		
1915	13	XRN1		-1:3:1435848	Basal	FALSE	GAIN	0.4765	3n duplicat	3	0.6301	HET	NA	NA	NA	NA	-0.07187	NA	0.009709	0.735416	MISSENSE		
1916	19	C3orf58		1:3:1451742	Basal	FALSE	GAIN	0.4765	3n duplicat	3	0.6301	HET	NA	NA	NA	NA	NA	NA	0.003236	0.72725	MISSENSE		
1917	2	VEPH1		-1:3:1584660	Basal	FALSE	GAIN	0.4765	3n duplicat	3	0.6301	HET	NA	NA	NA	NA	NA	NA	0.003236	0.730181	MISSENSE		
1918	0	SERPINI2		-1:3:1686660	Basal	FALSE	AMP	0.7372	4n monoal	4	0.7092	NLOH	NA	NA	NA	NA	NA	NA	NA	0.72972	MISSENSE		
1919	1	C3orf70		-1:3:1862836	Basal	FALSE	NEUT	0.1412	2n Germlin	2	0.5676	HET	NA	NA	NA	NA	NA	NA	NA	0.240613	MISSENSE		
1920	98	DPYSL3		-1:5:1467604	Basal	FALSE	HETD	-0.2953	Hemizygou	1	0.8222	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.473076	MISSENSE		
1921	71	PIK3R1		1:5:672680	Basal	TRUE	HETD	-0.2953	Hemizygou	1	0.8151	NLOH	NA	NA	NA	NA	-2.45496	0.081633	0.003236	0.350609	SPLICE		
1922	234	NCUBE1		-1:6:9009636	Basal	FALSE	HETD	-0.3015	Hemizygou	1	0.8132	NLOH	NA	NA	NA	NA	NA	NA	NA	0.950821	MISSENSE		
1923	32	TAf2		-1:8:1209139	Basal	FALSE	NEUT	0.1218	2n Somatic	2	0.8831	NLOH	NA	NA	NA	NA	-0.046	NA	0.006472	0.724706	MISSENSE		
1924	0	SHROOM4		-1:X:5039365	Basal	FALSE	NEUT	0.1212	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE		
1925	106	EIF4G2		-1:11:107777	Other	FALSE	HETD	-0.1689	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	-0.09665	NA	0.003236	0.300018	TRUNCATING		
1926	0	NELL1		1:11:208257	Other	FALSE	GAIN	0.5255	6n Germlin	6	0.6866	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.482869	MISSENSE		
1927	570	EIF3M		1:11:325730	Other	FALSE	GAIN	0.2596	4n monoal	4	0.6866	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.480033	MISSENSE		
1928	184	MANSC1		-1:12:123750	Other	FALSE	HETD	-0.1579	2n Germlin	2	0.5652</												

NEOGENOMICS EX.1102.064

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDos	HMMDos	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
2003	0	WDR42B	-1	X:2790827	Basal	FALSE	HETD	-0.2733	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
2004	90	HUWE1	-1	X:5360586	Basal	FALSE	HETD	-0.2733	NA	NA	NA	NA	NA	NA	NA	NA	-0.06902	NA	0.02589	NA	NA	NA	NA
2005	57	TCTN3	-1	10:974330	Basal	FALSE	HETD	-0.3649	2n Somatic	2	0.9444	NLOH	NA	NA	NA	NA	NA	NA	NA	0.460985	NA	NA	NA
2006	0	MMMP8	-1	11:102098	Basal	FALSE	HETD	-0.2567	3n Somatic	3	0.5792	HET	NA	NA	NA	NA	-0.04876	NA	0.009709	0.30866	NA	NA	NA
2007	0	SLC22A25	-1	11:627535	Basal	FALSE	HETD	-0.265	Normal (A)	2	0.5792	HET	NA	NA	NA	NA	NA	NA	0.009709	0.873859	NA	NA	NA
2008	15	PLCB3	-1	11:637868	Basal	FALSE	HETD	-0.265	Normal (A)	2	0.5792	HET	NA	NA	NA	NA	-0.94991	NA	0.003236	0.995394	NA	NA	NA
2009	56	TPP2	-1	13:102124	Basal	FALSE	AMP	0.9076	6n Germli	6	0.9867	NLOH	NA	NA	NA	NA	NA	NA	0.003236	1	NA	NA	NA
2010	72	PARP4	-1	13:239420	Basal	FALSE	NEUT	0.0921	4n Somatic	4	0.958	NLOH	NA	NA	NA	NA	-0.03187	NA	0.009709	0.451613	NA	NA	NA
2011	1	MKL2	-1	16:142186	Basal	TRUE	GAIN	0.207	4n balance	4	0.5769	HET	NA	NA	NA	NA	NA	NA	0.009709	0.306751	NA	NA	NA
2012	13	CPNE7	-1	16:881838	Basal	FALSE	NEUT	0.077	4n balance	4	0.5758	HET	NA	NA	NA	NA	NA	NA	0.860593	NA	NA	NA	NA
2013	3	C16orf76	-1	16:882913	Basal	FALSE	NEUT	0.077	4n balance	4	0.5758	HET	NA	NA	NA	NA	NA	NA	0.861372	NA	NA	NA	NA
2014	0	KRT31	-1	17:368067	Basal	FALSE	HETD	-0.2424	2n Somatic	2	0.9375	NLOH	NA	NA	NA	NA	NA	NA	0.880476	NA	NA	NA	NA
2015	388	ZNF521	-1	18:210583	Basal	FALSE	GAIN	0.1798	4n balance	4	0.6387	HET	NA	NA	NA	NA	NA	NA	0.012945	0.862323	NA	NA	NA
2016	36	MYO5B	-1	18:456196	Basal	FALSE	GAIN	0.4468	6n non-mo	6	0.6387	HET	NA	NA	NA	NA	-0.02152	NA	0.003236	0.506993	NA	NA	NA
2017	2	WDR88	-1	19:383582	Basal	FALSE	NEUT	0.0076	4n balance	4	0.6078	HET	NA	NA	NA	NA	NA	NA	0.003236	0.703169	NA	NA	NA
2018	11	TLR5	-1	1:2213506	Basal	FALSE	GAIN	0.2909	5n non-mo	5	0.641	HET	NA	NA	NA	NA	-0.11762	NA	0.006472	0.502536	NA	NA	NA
2019	0	PIWIL3	-1	22:234838	Basal	FALSE	GAIN	0.2055	4n balance	4	0.5778	HET	NA	NA	NA	NA	-0.01099	NA	0.009709	0.283466	NA	NA	NA
2020	23	STXBPSL	-1	3:1225827	Basal	FALSE	GAIN	0.1797	4n monoal	4	0.6543	HET	NA	NA	NA	NA	NA	NA	0.022654	0.306851	NA	NA	NA
2021	9	FAM62C	-1	3:1396758	Basal	TRUE	GAIN	0.3098	5n Germli	5	0.5943	HET	NA	NA	NA	NA	NA	NA	NA	0.453091	NA	NA	NA
2022	0	P2RY12,ME-1,1	-1	3:1525663	Basal	FALSE	GAIN	0.3098	5n non-mo	5	0.625	HET	NA	NA	NA	NA	NA	NA	NA	0.49898	NA	NA	NA
2023	19	VEPH1	-1	3:1586144	Basal	FALSE	GAIN	0.3098	5n non-mo	5	0.625	HET	NA	NA	NA	NA	NA	NA	0.003236	0.702343	NA	NA	NA
2024	30	MAGEF1	-1	3:1859114	Basal	FALSE	NEUT	0.1346	5n non-mo	5	0.625	HET	NA	NA	NA	NA	NA	NA	0.003236	0.3064	NA	NA	NA
2025	5	PDESA	-1	4:1207477	Basal	FALSE	HETD	-0.3629	2n Somatic	2	0.9333	NLOH	NA	NA	NA	NA	-0.05932	NA	NA	0.862785	NA	NA	NA
2026	0	WDR21B	-1	4:4167964	Basal	FALSE	HETD	-0.3748	2n Somatic	2	0.9333	NLOH	NA	NA	NA	NA	NA	NA	0.504923	NA	NA	NA	NA
2027	36	AC136632	-1	5:1774810	Basal	FALSE	HETD	-0.3882	2n Somatic	2	0.9333	NLOH	NA	NA	NA	NA	NA	NA	NA	0.307217	NA	NA	NA
2028	12	CCNC	-1	6:1000981	Basal	TRUE	AMP	0.676	6n non-mo	6	0.5738	HET	NA	NA	NA	NA	-0.01368	NA	NA	0.308273	NA	NA	NA
2029	3	C6orf186,C-1,1	-1	6:1106741	Basal	FALSE	AMP	0.7215	6n non-mo	6	0.5738	HET	NA	NA	NA	NA	NA	NA	NA	0.782501	NA	NA	NA
2030	0	NCR2	-1	6:4142648	Basal	FALSE	GAIN	0.1823	4n balance	4	0.5738	HET	NA	NA	NA	NA	-0.08695	NA	0.003236	0.45054	NA	NA	NA
2031	29	DST	-1	6:5659342	Basal	FALSE	GAIN	0.2264	4n balance	4	0.5738	HET	NA	NA	NA	NA	-0.01862	0.068027	0.038835	0.778511	NA	NA	NA
2032	0	AMPH	-1	7:3840014	Basal	FALSE	GAIN	0.1876	4n balance	4	0.5625	HET	NA	NA	NA	NA	-0.05261	NA	0.009709	0.429151	NA	NA	NA
2033	0	TM7SF4	-1	8:1054307	Basal	FALSE	GAIN	0.4148	6n non-mo	6	0.6678	HET	NA	NA	NA	NA	NA	NA	0.003236	0.119542	NA	NA	NA
2034	25	SDCBP	-1	8:5964602	Basal	FALSE	GAIN	0.1745	4n balance	4	0.6	HET	NA	NA	NA	NA	-0.12646	NA	NA	0.463151	NA	NA	NA
2035	65	MED22	-1	9:1351980	Basal	FALSE	HETD	-0.3522	2n Somatic	2	0.9314	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.539263	NA	NA	NA
2036	0	KCNT1	-1	9:1378155	Basal	FALSE	HETD	-0.3522	2n Somatic	2	0.9314	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.539147	NA	NA	NA
2037	762	GPM6B	-1	X:1370094	Basal	FALSE	HOMD	-0.7031	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
2038	22	FAM107B	-1	10:146038	Other	FALSE	NEUT	0.0089	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.119505	NA	NA	NA
2039	238	YME1L1	-1	10:274409	Other	FALSE	NEUT	-0.0882	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.469427	NA	NA	NA
2040	17	MASTL	-1	10:274987	Other	FALSE	NEUT	-0.0882	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.540463	NA	NA	NA
2041	3	ATG2A	-1	11:644351	Other	FALSE	NEUT	-0.0562	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	1	NA	NA	NA
2042	38	RSF1	-1	11:770738	Other	FALSE	NEUT	-0.0562	Hemizygou	1	0.5667	HET	NA	NA	NA	NA	NA	NA	0.006472	0.120178	NA	NA	NA
2043	12	ATXN2	-1	12:110474	Other	FALSE	NEUT	-0.0487	Hemizygou	1	0.5625	HET	NA	NA	NA	NA	NA	NA	0.003236	0.461344	NA	NA	NA
2044	18	FBXO21	-1	12:116068	Other	FALSE	NEUT	-0.0487	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	NA	NA	NA	0.543275	NA	NA	NA
2045	18	IPO8	-1	12:307247	Other	FALSE	NEUT	-0.0487	Normal (A)	2	0.5661	HET	NA	NA	NA	NA	NA	NA	NA	0.690122	NA	NA	NA
2046	7	ARID2	-1	12:445309	Other	FALSE	NEUT	-0.0487	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	NA	NA	0.019417	0.241107	NA	NA	NA
2047	7	SFRS2IP	-1	12:446086	Other	FALSE	NEUT	-0.0487	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	NA	NA	0.003236	0.399126	NA	NA	NA
2048	85	MCRS1	-1	12:482387	Other	FALSE	NEUT	-0.0487	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	NA	NA	NA	0.988535	NA	NA	NA
2049	42	MFSO5	-1	12:519336	Other	FALSE	NEUT	-0.0487	Normal (A)	2	0.5588	HET	NA	NA	NA	NA	NA	NA	NA	0.411885	NA	NA	NA
2050	21	PCID2	-1	13:112898	Other	FALSE	NEUT	-0.0409	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.999388	NA	NA	NA
2051	3	MDGA2	-1	14:463939	Other	FALSE	NEUT	-0.1306	Hemizygou	1	0.5747	HET	NA	NA	NA	NA	NA	NA	0.009709	0.690632	NA	NA	NA
2052	73	SYNE2	-1	14:637597	Other	FALSE	NEUT	-0.1306	Hemizygou	1	0.5747	HET	NA	NA	NA	NA	NA	NA	0.02589	0.788245	NA	NA	NA
2053	0	TRPM1	-1	15:291121	Other	FALSE	NEUT	-0.1358	Hemizygou	1	0.5769	HET	NA	NA	NA	NA	NA	NA	0.006472	0.150504	NA	NA	NA
2054	2	MYO5A	-1	15:504517	Other	FALSE	NEUT	-0.1358	Hemizygou	1	0.581	HET	NA	NA	NA	NA	-0.15045	NA	0.009709	0.252572	NA	NA	NA
2055	5	CREBBP	-1	16:375769	Other	FALSE	NEUT	-0.0743	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-3.04078	NA	0.019417	0.998626	NA	NA	NA
2056	3	ZFP90	-1	16:671549	Other	FALSE	NEUT	-0.0535	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.690223	NA	NA	NA
2057	0	MYH4	-1	17:102960	Other	FALSE	NEUT	-0.0697	Normal (A)	2	NA	NA	NA	NA	NA	NA	-0.67979	NA	0.032362	0.696819	NA	NA	NA
2058	0	MYO15A	-1	17:179637	Other	FALSE	NEUT	-0.0697	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-0.07158	NA	0.006472	0.262598	NA	NA	NA
2059	0	DNAH2	-1	17:763707	Other	FALSE	NEUT	-0.0697	Normal (A)	2	0.5706	HET	NA	NA	NA	NA	-0.26133	NA	0.019417	1	NA	NA	NA
2060	253	MYO5B	-1	18:456157	Other	FALSE	NEUT	-0.108	Hemizygou	1	0.5714	HET	NA	NA	NA	NA	-0.07158	NA	0.003236	0.240697	NA	NA	NA
2061	208	PRKCSH	-1	19:114142	Other	FALSE	NEUT	-0.0615	Normal (A)	2	0.5758	HET	NA	NA	NA	NA	-0.29308	NA	NA	0.882511	NA	NA	NA
2062	7	ZNF616	-1	19:573104	Other	FALSE	NEUT	-0.0615	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.839082	NA	NA	NA
2063	0	LILRA5	-1	19:595151	Other	FALSE	NEUT	-0.0582	Normal (A)	2	0.5686	HET	NA	NA	NA	NA	NA	NA	NA	0.88145	NA	NA	NA
2064	0	NTNG1	-1	1:1074927	Other	FALSE	NEUT	-0.0428	Normal (A)	2	0.563	HET	NA	NA	NA	NA	-0.22262	NA	0.009709	0.883493	NA	NA	NA
2065	38	GON4L	-1	1:1540015	Other	FALSE	NEUT	0.074	3n Germli	3	0.5882	HET	NA	NA	NA	NA	NA	NA	0.016181	0.403171	NA	NA	NA

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	Ens54Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloh.joh	apolloh.cal	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
2072	0	LYST	-1	1:2340217	Other	FALSE	NEUT	0.0637	4n monoal	4	0.5854	HET	NA	NA	NA	NA	NA	0.019417	0.886294	TRUNCATING			
2073	8	C1orf101	-1	1:2428023	Other	FALSE	NEUT	0.0637	3n duplicat	3	0.5854	HET	NA	NA	NA	NA	NA	0.003236	0.892828	MISSENSE			
2074	49	SF3A3	-1	1:3822582	Other	FALSE	NEUT	-0.0573	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-0.27298	NA	0.831712	MISSENSE			
2075	3	GIA9	-1	1:3911403	Other	FALSE	NEUT	-0.0573	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.865887	MISSENSE			
2076	5	GBP3	-1	1:8925156	Other	FALSE	NA	NA	Normal (A)	2	0.563	HET	NA	NA	NA	NA	NA	0.003236	NA	MISSENSE			
2077	24	ZNF337	-1	20:256047	Other	FALSE	NEUT	-0.0676	3n duplicat	3	0.7343	NLOH	NA	NA	NA	NA	NA	NA	0.770425	MISSENSE			
2078	113	RBM39	-1	20:337757	Other	FALSE	NEUT	-0.0676	Normal (A)	2	0.566	HET	NA	NA	NA	NA	NA	0.003236	0.884131	MISSENSE			
2079	0	SLC12A5	1	20:441084	Other	FALSE	NEUT	-0.0765	Normal (A)	2	0.566	HET	NA	NA	NA	NA	NA	0.006472	0.833209	MISSENSE			
2080	57	TTC3	1	21:374600	Other	FALSE	NEUT	-0.0527	Normal (A)	2	0.57	HET	NA	NA	NA	NA	NA	0.006472	0.827115	MISSENSE			
2081	74	ADSL	1	22:390889	Other	FALSE	NEUT	-0.1364	Hemizygou	1	0.5833	HET	NA	NA	NA	NA	-1.44053	0.003236	0.836708	MISSENSE			
2082	78	MCM6	-1	2:1363254	Other	FALSE	NEUT	-0.0543	2n Germlin	2	0.5556	HET	NA	NA	NA	NA	-0.31306	NA	0.840204	MISSENSE			
2083	0	XIRP2	1	2:1674684	Other	FALSE	NEUT	-0.0419	2n Germlin	2	0.5556	HET	NA	NA	NA	NA	NA	0.02589	0.55005	MISSENSE			
2084	3	LRP2	-1	2:1697352	Other	FALSE	NEUT	-0.0419	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	-0.27034	0.038835	0.825967	MISSENSE			
2085	0	UGT1A8	1	2:2343029	Other	FALSE	NEUT	-0.0552	Normal (A)	2	0.565	HET	NA	NA	NA	NA	-1.44494	0.006472	0.767593	MISSENSE			
2086	0	SLC3A1	1	2:4436668	Other	FALSE	NEUT	0.0243	3n Germlin	3	0.5625	HET	NA	NA	NA	NA	-0.16561	NA	0.547277	MISSENSE			
2087	5	MSH6,FBX1	-1	2:4788044	Other	FALSE	NEUT	0.0243	3n duplicat	3	0.5625	HET	NA	NA	NA	NA	NA	NA	1	TRUNCATING			
2088	23	AFTPH	1	2:6463237	Other	FALSE	NEUT	0.0237	3n duplicat	3	0.5625	HET	NA	NA	NA	NA	NA	0.006472	0.549743	MISSENSE			
2089	0	THNSL2	1	2:8825601	Other	TRUE	NEUT	0.0237	3n duplicat	3	0.6	HET	NA	NA	NA	NA	NA	0.003236	0.884412	SPICE			
2090	0	KIAA2018	-1	3:1148614	Other	FALSE	NEUT	0.0176	3n duplicat	3	0.5625	HET	NA	NA	NA	NA	NA	0.003236	0.766099	MISSENSE			
2091	30	GTF2E1	1	3:1219522	Other	FALSE	NEUT	0.0176	3n duplicat	3	0.5625	HET	NA	NA	NA	NA	-0.44478	0.003236	0.407578	TRUNCATING			
2092	5	TMEM22	1	3:1380562	Other	FALSE	NEUT	0.0393	3n duplicat	3	0.5588	HET	NA	NA	NA	NA	NA	0.003236	0.837021	MISSENSE			
2093	40	PIK3CA	1	3:1804345	Other	FALSE	NEUT	0.0519	3n duplicat	3	0.5588	HET	NA	NA	NA	NA	-3.60877	0.047619	0.016181	0.898915	MISSENSE		
2094	0	HTR3E	1	3:1853058	Other	FALSE	NEUT	0.0519	3n duplicat	3	0.5588	HET	NA	NA	NA	NA	NA	0.003236	0.401211	MISSENSE			
2095	6	IGF2BP2	-1	3:1868757	Other	FALSE	NEUT	0.0519	3n duplicat	3	0.5588	HET	NA	NA	NA	NA	NA	NA	0.833031	MISSENSE			
2096	10	HTT	1	4:3086844	Other	FALSE	NEUT	-0.137	Hemizygou	1	0.5833	HET	NA	NA	NA	NA	-0.57331	0.003236	0.882401	MISSENSE			
2097	20	BRD8	-1	5:1375344	Other	FALSE	NEUT	-0.1228	Hemizygou	1	0.5652	HET	NA	NA	NA	NA	NA	0.003236	0.548898	MISSENSE			
2098	8	MAP1B	1	5:151530	Other	FALSE	NEUT	-0.1166	Hemizygou	1	0.5688	HET	NA	NA	NA	NA	-0.17602	0.003236	0.884936	MISSENSE			
2099	0	C6orf91	1	6:1392654	Other	FALSE	NEUT	-0.0606	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	NA	NA	0.888133	MISSENSE			
2100	15	SASH1	1	6:1489089	Other	FALSE	NEUT	-0.0606	Normal (A)	2	0.5556	HET	NA	NA	NA	NA	NA	NA	0.89588	MISSENSE			
2101	0	SCAND3	-1	6:2864929	Other	FALSE	NEUT	-0.053	3n duplicat	2	0.56	HET	NA	NA	NA	NA	NA	0.003236	0.682426	MISSENSE			
2102	19	COG5	-1	7:1068401	Other	FALSE	NEUT	-0.0345	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	NA	NA	0.887645	MISSENSE			
2103	0	TAS2R60	1	7:1428513	Other	FALSE	NEUT	-0.0556	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	-0.07452	NA	0.830649	MISSENSE			
2104	9	GALNT11	1	7:1514413	Other	FALSE	NEUT	-0.0556	Normal (A)	2	NA	NA	NA	NA	NA	NA	-1.34572	NA	0.549247	TRUNCATING			
2105	0	HAS2	-1	8:1226957	Other	FALSE	NEUT	0.009	4n Germlin	4	0.5714	HET	NA	NA	NA	NA	NA	0.016181	0.685573	MISSENSE			
2106	1	KLHL38	-1	8:1247329	Other	FALSE	NEUT	0.009	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	NA	NA	0.828059	MISSENSE			
2107	4	TMEM67	1	8:9489030	Other	FALSE	NEUT	0.0042	3n duplicat	3	0.5676	HET	NA	NA	NA	NA	NA	0.006472	0.684579	MISSENSE			
2108	0	GALNT12	1	9:1006510	Other	FALSE	NEUT	-0.0521	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-1.34572	0.003236	0.884782	MISSENSE			
2109	0	PPP3R2,GR	-1	9:1033968	Other	FALSE	NEUT	-0.0521	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.743504	MISSENSE			
2110	49	FBXW2	-1	9:1225666	Other	FALSE	NEUT	-0.0623	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-0.20601	0.003236	0.88272	MISSENSE			
2111	2	ZCCHC6	-1	9:8815759	Other	FALSE	NEUT	-0.0521	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	NA	0.006472	0.772903	TRUNCATING			
2112	0	RP13-507i2	-1	X:1491502	Other	FALSE	NEUT	-0.0578	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE			
2113	49	TSR2	1	X:5448757	Other	FALSE	NEUT	-0.0578	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE			
2114	0	MED12	1	X:7027371	Other	FALSE	NEUT	-0.0578	NA	NA	NA	NA	NA	NA	NA	NA	-0.05151	0.003236	NA	MISSENSE			
2115	0	NRXN3	1	14:785043	Other	FALSE	NEUT	-0.0727	3n duplicat	3	0.5641	HET	NA	NA	NA	NA	-0.07785	0.006803	0.009709	0.769805	MISSENSE		
2116	18	AHDC1	-1	1:2774698	Other	FALSE	NEUT	-0.1064	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.829508	MISSENSE			
2117	48	RP11-119B	1	20:378996	Other	FALSE	NEUT	-0.0245	5n non-mo	5	0.564	HET	NA	NA	NA	NA	NA	NA	0.996802	MISSENSE			
2118	11	METTL8	-1	2:1718906	Other	FALSE	NEUT	-0.0358	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	NA	0.003236	0.547774	MISSENSE			
2119	56	ZNF638	1	2:7142981	Other	FALSE	NEUT	0.0178	5n Germlin	5	0.5667	HET	NA	NA	NA	NA	NA	0.003236	0.833487	MISSENSE			
2120	26	POLR1A	-1	2:8616155	Other	FALSE	NEUT	0.0096	4n Germlin	4	0.5667	HET	NA	NA	NA	NA	-1.30337	0.006472	0.829384	MISSENSE			
2121	32	PIK3CA	1	3:1804345	Other	FALSE	NEUT	-0.1033	2n Somatic	2	0.5841	HET	NA	NA	NA	NA	-1.45855	0.047619	0.016181	0.551485	MISSENSE		
2122	0	MASP1	-1	3:1884862	Other	FALSE	NEUT	-0.0997	2n Somatic	2	0.5841	HET	NA	NA	NA	NA	-0.08342	0.012945	0.84497	MISSENSE			
2123	102	PTEN	1	10:896828	Other	FALSE	NEUT	-0.0702	Hemizygou	1	0.5625	HET	NA	NA	NA	NA	-1.61977	0.251701	0.006472	0.74184	MISSENSE		
2124	0	GPR52,RAE1	1	1:1726840	Other	FALSE	NEUT	-0.058	3n duplicat	3	0.5568	HET	NA	NA	NA	NA	NA	NA	0.842462	MISSENSE			
2125	0	OSR1	-1	2:1941555	Other	FALSE	NEUT	0.0151	6n non-mo	6	0.5667	HET	NA	NA	NA	NA	NA	0.003236	0.262418	MISSENSE			
2126	4	PLEKHM3	-1	2:2085499	Other	FALSE	NEUT	0.0397	6n non-mo	6	0.5658	HET	NA	NA	NA	NA	NA	0.003236	0.321487	MISSENSE			
2127	16	TRPM7	-1	15:486716	Other	FALSE	HETD	-0.2423	2n Somatic	2	0.6923	NLOH	NA	NA	NA	NA	NA	0.006472	0.086575	MISSENSE			
2128	9	LPIN2	-1	18:291150	Other	FALSE	NEUT	-0.0308	4n monoal	4	0.6667	NLOH	NA	NA	NA	NA	NA	0.003236	0.566232	MISSENSE			
2129	11	ZNF211	1	19:628440	Other	FALSE	NEUT	-0.0953	3n Somatic	3	0.7333	NLOH	NA	NA	NA	NA	NA	0.006472	0.562408	MISSENSE			
2130	0	NEXN,FUB1	-1	1:7817409	Other	FALSE	NEUT	-0.0305	4n balance	4	0.5692	HET	NA	NA	NA	NA	NA	NA	0.184517	MISSENSE			
2131	26	FYCO1	-1	3:4597871	Other	FALSE	NEUT	-0.1391	3n duplicat	3	0.6296	NLOH	NA	NA	NA	NA	NA	NA	0.335493	MISSENSE			
2132	27	FYCO1	-1	3:4597871	Other	FALSE	NEUT	-0.1391	3n duplicat	3	0.6296	NLOH	NA	NA	NA	NA	NA	NA	0.451058	TRUNCATING			
2133	0	SPOCK3	-1	4:1678926	Other	FALSE	GAIN	0.1776	4n Somatic	4	0.75	NLOH	NA	NA	NA	NA	NA	0.003236	0.262254	MISSENSE			
2134	0	SATL1	-1	X:8423655	Other	FALSE	NEUT	-0.1062	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE			
2135	0	SPRR1A	1	1:1512245	Other	FALSE	NEUT	0.1273	3n duplicat	3	0.619	HET	NA	NA	NA	NA	NA	NA	0.781398	MISSENSE			
2136	5	SLC25A44	1	1:1544362	Other	FALSE	NEUT	0.1267	4n monoal	4	0.619	HET	NA	NA	NA	NA	NA	0.003236	0.56246	MISSENSE			
2137	0	ADCY10	-1	1:1660588	Other	FALSE	GAIN	0.2312	3n duplicat	3	0.619	HET	NA	NA	NA	NA	-0.25339	0.003236	0.564483	MISSENSE			
2138	109																						

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDos	HMMDos	OncoSNP	OncoSNP	apollohoJ	apollohoJ	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
2141	1	SASH1		1:6:1488031	Other	FALSE	HETD	-0.1479	Normal (A)	2	0.6	HET	NA	NA	NA	NA	NA	NA	NA	0.328563	MISSENSE		
2142	30	RXRA.AL66	1,1	9:1364533	Other	FALSE	HETD	-0.274	2n Somatic	2	0.7609	NLOH	NA	NA	NA	NA	NA	NA	NA	0.565015	MISSENSE		
2143	0	RPS8P4		1:10:121388	Basal	FALSE	NEUT	-0.1585	Normal (A)	2	0.6364	HET	NA	NA	NA	NA	NA	NA	NA	0.886679	MISSENSE		
2144	0	TLL2		-1:10:981470	Basal	FALSE	HETD	-0.2306	Normal (A)	2	0.6364	HET	NA	NA	NA	NA	-0.07361	NA	0.003236	0.793736	MISSENSE		
2145	0	SIAE		-1:11:124029	Basal	FALSE	NEUT	-0.1413	Normal (A)	2	0.6667	HET	NA	NA	NA	NA	NA	NA	NA	1	MISSENSE		
2146	0	MS4A4A		1:11:598163	Basal	FALSE	NEUT	-0.1386	Normal (A)	2	0.6506	HET	NA	NA	NA	NA	NA	NA	NA	0.185925	MISSENSE		
2147	1	ZNF397		1:18:310771	Basal	FALSE	HETD	-0.265	Normal (A)	2	0.5889	HET	NA	NA	NA	NA	NA	NA	NA	0.726779	MISSENSE		
2148	0	COMP		-1:19:187558	Basal	FALSE	HETD	-0.2214	Normal (A)	2	0.5842	HET	NA	NA	NA	NA	-0.26733	NA	0.639709	MISSENSE			
2149	0	GBP3		-1:18:925357	Basal	FALSE	GAIN	0.4059	4n monoal	4	0.6582	HET	NA	NA	NA	NA	NA	NA	0.003236	0.189781	MISSENSE		
2150	1	R3HDM1		2:1361130	Basal	FALSE	NEUT	-0.1138	2n Germlin	2	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.643595	MISSENSE		
2151	0	SPHKAP.AC-1,1		2:285547	Basal	FALSE	NEUT	-0.0152	Normal (A)	2	0.6	HET	NA	NA	NA	NA	NA	NA	NA	0.640363	MISSENSE		
2152	0	PPP4R2		1:3:7317911	Basal	FALSE	NEUT	0.0532	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.633041	MISSENSE		
2153	0	RPL26L1		1:5:1723281	Basal	FALSE	HETD	-0.5017	Hemizygou	1	0.9062	NLOH	NA	NA	NA	NA	-0.20959	NA	NA	0.63998	MISSENSE		
2154	0	TDRD6		1:6:4676861	Basal	FALSE	AMP	0.6844	6n monoal	6	0.7567	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.546103	MISSENSE		
2155	0	IMPG1		-1:6:7671732	Basal	FALSE	NEUT	-0.1489	Normal (A)	2	0.5833	HET	NA	NA	NA	NA	NA	NA	0.006472	0.639915	MISSENSE		
2156	9	PAN2		-1:12:550035	Basal	FALSE	NEUT	0.0223	4n balance	4	0.5714	HET	NA	NA	NA	NA	NA	NA	0.006472	1	MISSENSE		
2157	0	UBR7		1:14:927465	Basal	TRUE	HETD	-0.1882	3n duplicat	3	0.6418	NLOH	NA	NA	NA	NA	NA	NA	NA	0.527557	SPICE		
2158	10	TP53		-1:17:751891	Basal	FALSE	NEUT	-0.0211	4n monoal	4	0.7054	NLOH	NA	NA	NA	NA	-1.22507	0.306122	0.812298	0.995288	TRUNCATING		
2159	1	TNNT2		-1:1:1995991	Basal	FALSE	NEUT	0.0158	4n Germlin	4	0.5679	HET	NA	NA	NA	NA	-0.08407	NA	NA	0.541515	MISSENSE		
2160	0	DPP10		1:2:1157833	Basal	FALSE	NEUT	-0.0046	4n balance	4	0.5645	HET	NA	NA	NA	NA	NA	NA	0.016181	0.982584	MISSENSE		
2161	6	FAM117B		1:2:2033322	Basal	FALSE	HETD	-0.1458	3n duplicat	3	0.6471	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.639753	MISSENSE		
2162	13	RNF25		-1:2:192371	Basal	FALSE	HETD	-0.1872	3n duplicat	3	0.6471	NLOH	NA	NA	NA	NA	-0.10016	NA	0.003236	0.983659	MISSENSE		
2163	0	PTPRN		-1:2:198750	Basal	FALSE	HETD	-0.1872	3n duplicat	3	0.6471	NLOH	NA	NA	NA	NA	-0.01908	NA	0.006472	0.990686	MISSENSE		
2164	26	USP34		-1:2:128495	Basal	FALSE	NEUT	0.0212	4n balance	4	0.5581	HET	NA	NA	NA	NA	NA	NA	0.022654	0.603585	MISSENSE		
2165	13	ING2		1:4:1846685	Basal	FALSE	NEUT	0.0018	4n monoal	4	0.6842	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.604004	MISSENSE		
2166	0	HCN1		-1:5:4529782	Basal	FALSE	GAIN	0.3169	6n Germlin	6	0.6364	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.999973	MISSENSE		
2167	2	PMS2		-1:7:5993569	Basal	FALSE	NEUT	0.035	4n balance	4	0.5714	HET	NA	NA	NA	NA	-0.01823	0.006803	NA	0.609967	MISSENSE		
2168	8	OSGIN2		1:8:9100592	Basal	FALSE	NEUT	0.0503	4n Germlin	4	0.5581	HET	NA	NA	NA	NA	NA	NA	NA	0.971502	MISSENSE		
2169	1	C9orf93		9:1596165	Basal	FALSE	GAIN	0.2665	5n non-mo	5	0.5913	HET	NA	NA	NA	NA	NA	NA	NA	0.600834	MISSENSE		
2170	5	PIA1		-1:5:6829924	Basal	FALSE	HETD	-0.1782	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	TRUNCATING		
2171	11	SYNE2		1:14:636169	Basal	FALSE	HETD	-0.2094	2n Somatic	2	0.6835	NLOH	NA	NA	NA	NA	NA	NA	0.02589	0.599097	MISSENSE		
2172	30	SLC38A10		-1:17:768415	Basal	FALSE	NEUT	0.0672	4n Somatic	4	0.7188	NLOH	NA	NA	NA	NA	NA	NA	NA	0.601154	MISSENSE		
2173	0	EPGN		1:4:7539674	Basal	FALSE	NEUT	0.0303	4n Germlin	4	0.566	HET	NA	NA	NA	NA	NA	NA	NA	1	MISSENSE		
2174	0	DOCK11		1:11:75839	Basal	FALSE	HETD	-0.2189	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.009709	NA	MISSENSE		
2175	3	TBC1D19		1:4:2623131	Basal	FALSE	HETD	-0.2253	Hemizygou	1	0.6	HET	NA	NA	NA	NA	NA	NA	NA	0.618105	MISSENSE		
2176	0	KCNG4		-1:16:828283	Other	FALSE	NEUT	-0.0438	2n Somatic	2	0.6327	NLOH	NA	NA	NA	NA	NA	NA	NA	0.98672	MISSENSE		
2177	6	FAM151B		1:5:7984521	Basal	FALSE	NEUT	-0.0495	2n Somatic	2	0.6747	NLOH	NA	NA	NA	NA	NA	NA	NA	0.598646	MISSENSE		
2178	6	HIP1		-1:7:7502325	Other	FALSE	NEUT	0.1045	4n balance	4	0.5554	HET	NA	NA	NA	NA	-0.26709	NA	0.003236	0.600329	TRUNCATING		
2179	0	DNAH5		-1:5:1381908	Other	FALSE	NEUT	-0.0871	Normal (A)	2	0.5577	HET	NA	NA	NA	NA	-0.05307	NA	0.035599	0.603714	MISSENSE		
2180	10	AQR		-1:15:330436	Other	FALSE	HETD	-0.1745	2n Somatic	2	0.7143	NLOH	NA	NA	NA	NA	-0.16326	NA	NA	0.394984	MISSENSE		
2181	16	VLDLR		1:9:2634542	Other	FALSE	NEUT	0.0205	3n duplicat	3	0.6	HET	NA	NA	NA	NA	-0.05641	0.006803	0.003236	0.644738	MISSENSE		
2182	16	CSorf34		-1:5:4352373	Basal	FALSE	HETD	-0.3817	2n Somatic	2	0.9524	NLOH	NA	NA	NA	NA	NA	NA	NA	0.577499	MISSENSE		
2183	177	TTC35		1:8:1095679	Other	FALSE	NEUT	0.0042	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.576958	MISSENSE		
2184	3	RRM2B		-1:8:1032895	Other	FALSE	NEUT	-0.057	2n Somatic	2	0.73	NLOH	NA	NA	NA	NA	-0.8627	NA	0.006472	0.99891	MISSENSE		
2185	3	CPVL		-1:7:2900172	Other	FALSE	NEUT	0.0094	3n duplicat	3	0.6	HET	NA	NA	NA	NA	NA	NA	0.006472	0.575663	MISSENSE		
2186	149	TP53		-1:17:751907	Basal	FALSE	GAIN	0.2747	5n Somatic	5	0.9048	NLOH	NA	NA	NA	NA	-0.91968	0.306122	0.812298	0.792666	MISSENSE		
2187	0	NLRP11		-1:19:609951	Other	FALSE	NEUT	0.0175	4n balance	4	0.5779	HET	HET	0.6111	NEUT	0.0653	NA	NA	0.009709	0.647421	MISSENSE		
2188	1	PIBF1		1:13:722994	Other	FALSE	HETD	-0.2356	2n Somatic	2	0.7273	DLOH	DLOH	0.7273	HETD	-0.3398	NA	NA	0.003236	0.576122	MISSENSE		
2189	40	NOB1		-1:16:683393	Other	FALSE	NEUT	0.0743	4n balance	4	0.6053	HET	HET	0.6053	NEUT	0.023	NA	NA	NA	0.801462	MISSENSE		
2190	107	TP53		-1:17:751877	Other	FALSE	HETD	-0.2637	2n Somatic	2	0.7297	DLOH	DLOH	0.7297	HETD	-0.366	-0.87544	0.306122	0.812298	0.377582	MISSENSE		
2191	0	FAP		-1:2:1627806	Other	FALSE	NEUT	-0.0668	3n duplicat	3	0.6882	NLOH	NLOH	0.6882	NEUT	-0.0898	NA	NA	0.009709	0.990341	MISSENSE		
2192	161	GSR		-1:8:3067710	Other	FALSE	NEUT	0.095	4n Germlin	4	0.75	LOH	LOH	0.75	GAIN	0.166	-0.0514	NA	0.006472	0.644812	MISSENSE		
2193	0	HABP2		1:10:115333	Basal	FALSE	NEUT	0.0526	4n Somatic	4	0.7018	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.803877	MISSENSE		
2194	4	CAMK1D		1:10:129108	Basal	FALSE	NEUT	-0.0151	3n Somatic	3	0.6891	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.813053	MISSENSE		
2195	0	FRMPD2		-1:10:490707	Basal	FALSE	NEUT	-0.0194	3n Somatic	3	0.6891	NLOH	NA	NA	NA	NA	NA	NA	NA	0.797885	MISSENSE		
2196	0	CDC38		-1:12:948539	Basal	FALSE	HETD	-0.1842	2n Germlin	2	0.6284	NLOH	NA	NA	NA	NA	NA	NA	NA	0.580419	MISSENSE		
2197	19	TUBGCP5		1:15:204154	Basal	FALSE	NEUT	-0.0088	3n Somatic	3	0.6923	NLOH	NA	NA	NA	NA	-0.09387	NA	NA	0.996403	MISSENSE		
2198	0	C16orf65		-1:16:219032	Basal	FALSE	NEUT	-0.025	3n Somatic	3	0.7	NLOH	NA	NA	NA	NA	NA	NA	NA	0.64742	MISSENSE		
2199	6	ZNF267		1:16:318333	Basal	FALSE	NEUT	-0.025	2n Somatic	2	0.5985	HET	NA	NA	NA	NA	NA	NA	0.006472	0.377903	MISSENSE		
2200	0	C16orf78		1:16:479653	Basal	FALSE	NEUT	-0.0286	3n Somatic	3	0.6812	NLOH	NA	NA	NA	NA	NA	NA	NA	0.580095	MISSENSE		
2201	2	ZNF284		1:19:492825	Basal	FALSE	NEUT	0.0202	4n monoal	4	0.5806	HET	NA	NA	NA	NA	NA	NA	NA	1	MISSENSE		
2202	20	CELSR1		-1:22:451861	Basal	FALSE	NEUT	-0.0707	3n Somatic	3	0.695	NLOH	NA	NA	NA	NA	-0.18394	NA	NA	0.989388	MISSENSE		
2203	9	DDIT4L		-1:4:1013281	Basal	FALSE	NEUT	0.0303	Normal (A)	2	0.566	HET	NA	NA	NA	NA	NA	NA	0.003236	0.568866	MISSENSE		
2204	0	EPHA5		-1:4:6614984	Basal	FALSE	NEUT	0.0301	Normal (A)	2	0.566	HET	NA	NA	NA	NA	-0.08299	NA	0.006472				

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apollohoJ	apollohoJ	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
2210	0	KIR2DL1		1:19:599867	Basal	FALSE	GAIN	0.1572	4n Somatic	4	0.75	NLOH	NA	NA	NA	NA	-0.2689	NA	0.003236	0.574747	MISSENSE		
2211	0	CLDN16		1:3:1916103	Basal	FALSE	GAIN	0.2312	5n Somatic	4	0.7143	NLOH	NA	NA	NA	NA	-0.27849	NA	0.003236	0.802483	MISSENSE		
2212	5	ZC3H3		-1:8:1446922	Basal	FALSE	NEUT	-0.1463	2n Somatic	2	0.6875	NLOH	NA	NA	NA	NA	NA	NA	NA	0.795079	MISSENSE		
2213	0	ZFP92		1:X:1523393	Basal	FALSE	NEUT	-0.1034	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	TRUNCATING		
2214	3	ATM		1:11:107626	Basal	FALSE	NEUT	-0.0068	Normal (A)	2	0.6042	HET	HET	0.6042	NEUT	-0.002	-0.53343	0.013605	0.012945	0.803864	TRUNCATING		
2215	0	VWA1		1:1:1362068	Basal	FALSE	HETD	-0.2067	Hemizygous	1	0.6522	DLOH	DLOH	0.6522	HETD	-0.2379	NA	NA	NA	0.780562	MISSENSE		
2216	5	RNF6		-1:13:256862	Basal	FALSE	NEUT	0.0871	Normal (A)	2	0.6071	HET	HET	0.6071	NEUT	0.1318	NA	NA	0.003236	0.776517	TRUNCATING		
2217	100	LGALS3BP		-1:17:744806	Basal	FALSE	GAIN	0.5242	6n monoal	6	0.6974	ASCNA	ASCNA	0.6974	AMP	0.7387	NA	0.020408	0.003236	0.677064	MISSENSE		
2218	2	TBX1		1:22:181466	Basal	FALSE	GAIN	0.3754	5n monoal	5	0.7059	ASCNA	ASCNA	0.7059	AMP	0.5839	NA	NA	0.003236	0.301762	MISSENSE		
2219	0	RBM27		1:5:1456232	Basal	FALSE	HETD	-0.1499	Hemizygous	1	NA	NA	NA	NA	NEUT	-0.046	NA	NA	NA	0.154118	MISSENSE		
2220	0	PDE7B		1:6:1365362	Basal	FALSE	HETD	-0.2721	Hemizygous	1	0.6875	DLOH	DLOH	0.6875	HETD	-0.3122	-0.07516	NA	0.003236	1	MISSENSE		
2221	28	OGFR1		1:6:7206811	Basal	FALSE	NEUT	-0.0198	2n Somatic	2	0.7714	NLOH	NLOH	0.7714	NEUT	-0.0814	NA	NA	NA	0.525444	MISSENSE		
2222	3	MTSS1		-1:8:1256442	Basal	FALSE	NEUT	0.0354	2n Germli	2	0.6	HET	HET	0.6	NEUT	0.0753	-0.03045	NA	0.003236	0.308146	MISSENSE		
2223	39	HPRT1		1:X:1334351	Basal	FALSE	HOMD	-0.5218	NA	NA	NA	NA	NA	NA	NEUT	0.0112	-0.49317	NA	NA	MISSENSE			
2224	0	SLITRK4		-1:X:1425444	Basal	FALSE	HOMD	-0.5218	NA	NA	NA	NA	DLOH	0.875	HOMD	-0.6572	NA	NA	NA	MISSENSE			
2225	17	PORCN		1:X:4825473	Basal	FALSE	HOMD	-0.5218	NA	NA	NA	NA	DLOH	0.8889	HOMD	-0.7024	-0.07395	NA	0.006472	NA	MISSENSE		
2226	84	RNF135		1:17:263390	Basal	FALSE	GAIN	0.2477	6n Somatic	6	0.7329	NLOH	NA	NA	NA	NA	NA	NA	NA	NA	MISSENSE		
2227	29	SUPV3L1		1:10:706383	Basal	FALSE	NEUT	-0.0376	4n monoal	4	0.58	HET	NA	NA	NA	NA	NA	NA	0.003236	0.781698	MISSENSE		
2228	35	PSMC3		-1:11:473970	Basal	FALSE	NEUT	0.051	4n Germli	4	0.5714	HET	NA	NA	NA	NA	-0.26072	NA	0.012945	0.779021	MISSENSE		
2229	0	ASCL4		1:12:106692	Basal	FALSE	NEUT	-0.0618	4n Germli	4	0.5795	HET	NA	NA	NA	NA	NA	NA	NA	0.422997	MISSENSE		
2230	141	ATP6V0B		1:1:4421458	Basal	FALSE	GAIN	0.2431	6n non-mo	6	0.5932	HET	NA	NA	NA	NA	-0.70003	NA	NA	0.898805	MISSENSE		
2231	1	MYO15A		1:17:179879	Basal	FALSE	NEUT	-0.0018	4n Somatic	4	0.72	NLOH	NA	NA	NA	NA	-0.02424	NA	0.006472	0.458659	MISSENSE		
2232	6	VIT		1:2:3688945	Basal	FALSE	NEUT	0.0654	3n Somatic	3	0.6667	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.780004	MISSENSE		
2233	8	NR3C1		-1:5:1427602	Basal	FALSE	NEUT	-0.1303	2n Somatic	2	0.6667	NLOH	NA	NA	NA	NA	-0.47195	NA	0.006472	0.6673	MISSENSE		
2234	4	ITGA2		1:5:5240172	Basal	FALSE	GAIN	0.1645	6n balance	6	0.5789	HET	NA	NA	NA	NA	-0.50996	NA	NA	0.282023	MISSENSE		
2235	35	TRIM38		1:6:2607753	Basal	FALSE	GAIN	0.1798	5n Germli	5	0.5806	HET	NA	NA	NA	NA	NA	NA	NA	0.800544	MISSENSE		
2236	0	RELN		-1:7:1034163	Basal	FALSE	NEUT	-0.0999	4n balance	4	NA	NA	NA	NA	NA	NA	-0.10392	0.013605	0.02589	0.418059	MISSENSE		
2237	0	C11orf70		1:11:101442	Basal	FALSE	GAIN	0.3261	4n monoal	4	0.7179	HET	HET	0.7179	NEUT	0.018	NA	NA	NA	MISSENSE			
2238	5	BRCA2		1:13:18272	Basal	FALSE	GAIN	0.4822	6n monoal	6	0.7521	ASCNA	ASCNA	0.7521	AMP	0.6402	-0.36009	0.020408	0.032362	NA	MISSENSE		
2239	2	RL1		1:13:478211	Basal	FALSE	HOMD	-0.4927	Hemizygous	1	0.7895	HOMD	HOMD	0.7895	HOMD	-0.8295	-0.74715	0.07483	0.019417	NA	TRUNCATING		
2240	0	KHLH1		-1:13:693544	Basal	FALSE	GAIN	0.2689	3n Germli	3	0.9545	LOH	LOH	0.9545	GAIN	0.1618	NA	NA	NA	MISSENSE			
2241	55	COG4		-1:16:690748	Basal	FALSE	NEUT	0.0048	3n Somatic	3	0.9212	NLOH	NLOH	0.9212	HETD	-0.2646	NA	NA	NA	MISSENSE			
2242	68	MRPL45		1:17:337088	Basal	FALSE	HETD	-0.2066	2n Somatic	2	0.9054	HOMD	HOMD	0.9054	HOMD	-0.6719	NA	NA	NA	MISSENSE			
2243	32	FOXK2		1:17:781524	Basal	FALSE	HETD	-0.2301	2n Somatic	2	0.881	DLOH	DLOH	0.881	HETD	-0.4351	NA	NA	NA	MISSENSE			
2244	61	CEP192		1:18:130465	Basal	FALSE	NEUT	0.0503	3n duplicat	3	0.6667	HET	HET	0.6667	NEUT	0.0046	-0.0815	NA	0.012945	NA	MISSENSE		
2245	6	C18orf19		-1:18:136562	Basal	FALSE	NEUT	0.0503	3n duplicat	3	0.6286	HET	HET	0.6286	NEUT	0.0046	NA	NA	NA	MISSENSE			
2246	0	ZNF90		1:19:200498	Basal	FALSE	HETD	-0.2478	2n Somatic	2	0.9289	DLOH	DLOH	0.9289	HETD	-0.3973	NA	NA	0.003236	NA	MISSENSE		
2247	2	GYS1		-1:19:541777	Basal	FALSE	HETD	-0.2685	2n Somatic	2	0.8636	DLOH	DLOH	0.8636	HETD	-0.4972	-0.53623	NA	0.006472	NA	TRUNCATING		
2248	0	SPHKAP	AC-1,1	2:2285947	Basal	FALSE	NEUT	0.059	3n Somatic	3	0.8817	NLOH	NLOH	0.8817	NEUT	0.0154	NA	NA	NA	MISSENSE			
2249	9	KIF3C		-1:2:2600546	Basal	FALSE	HETD	-0.1611	2n Somatic	2	0.86	DLOH	DLOH	0.86	HETD	-0.3674	NA	NA	0.009709	NA	MISSENSE		
2250	0	ENAM		4:7:172667	Basal	FALSE	HETD	-0.1488	2n Somatic	2	0.5926	HET	HET	0.5926	HETD	-0.3399	NA	NA	0.009709	NA	MISSENSE		
2251	0	SLC44A4		-1:6:3194107	Basal	FALSE	GAIN	0.3373	4n Germli	4	0.6714	ASCNA	ASCNA	0.6714	AMP	0.624	NA	NA	0.003236	NA	MISSENSE		
2252	206	AODP		-1:9:1910591	Basal	FALSE	GAIN	0.3955	5n monoal	5	0.7436	HET	HET	0.7436	GAIN	0.2195	-0.05201	NA	NA	NA	MISSENSE		
2253	1	SRPK3		1:X:1527001	Basal	FALSE	GAIN	0.3101	NA	NA	NA	NA	HET	0.6074	GAIN	0.3469	NA	NA	NA	MISSENSE			
2254	0	MECP2		-1:X:1529495	Basal	FALSE	NEUT	0.046	NA	NA	NA	NA	HET	0.6074	NEUT	0.0733	NA	NA	NA	TRUNCATING			
2255	0	PNLIPRP3		1:10:118220	Basal	FALSE	NEUT	-0.055	2n Germli	2	0.7038	NLOH	NA	NA	NA	NA	-0.62642	NA	0.003236	0.396434	MISSENSE		
2256	54	NCOR2		-1:12:123398	Basal	FALSE	NEUT	-0.0096	3n Somatic	3	0.7273	NLOH	NA	NA	NA	NA	-0.25688	NA	0.003236	0.897711	MISSENSE		
2257	269	TP53		-1:17:751823	Basal	FALSE	NEUT	0.0446	3n Somatic	3	0.7547	NLOH	NA	NA	NA	NA	-1.03827	0.306122	0.812298	0.778945	MISSENSE		
2258	10	AC026713		-1:5:3900291	Basal	FALSE	NEUT	-0.0325	Normal (A)	2	0.6087	HET	NA	NA	NA	NA	NA	NA	NA	0.395077	MISSENSE		
2259	105	MXRA5		-1:X:3258362	Basal	FALSE	NEUT	-0.0582	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.016181	NA	MISSENSE		
2260	1	ZMYND17		-1:10:748558	Basal	FALSE	NEUT	0.0351	2n Germli	2	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.898244	MISSENSE		
2261	7	TRIM45		-1:1:1174626	Basal	FALSE	NEUT	0.0184	Normal (A)	2	0.5736	HET	NA	NA	NA	NA	NA	NA	0.666927	MISSENSE			
2262	19	PRKCZ		1:1:1980827	Basal	FALSE	HETD	-0.4091	Hemizygous	1	0.75	NLOH	NA	NA	NA	NA	-1.05341	0.020408	NA	0.990603	MISSENSE		
2263	0	STAB2		1:12:102653	Basal	FALSE	NEUT	0.0127	Normal (A)	2	0.5652	HET	NA	NA	NA	NA	NA	NA	0.029126	1	MISSENSE		
2264	47	ISGF3G	RN 1,1	14:236969	Basal	FALSE	NEUT	0.0234	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.667985	MISSENSE		
2265	12	ZFYVE1		-1:14:725121	Basal	FALSE	NEUT	-0.0465	2n Somatic	2	0.76	NLOH	NA	NA	NA	NA	NA	NA	NA	0.779874	MISSENSE		
2266	1	DNAH2		1:17:762011	Basal	FALSE	HETD	-0.4038	Hemizygous	1	0.7442	NLOH	NA	NA	NA	NA	-0.13138	NA	0.019417	0.891332	MISSENSE		
2267	21	XRCC1		-1:19:487425	Basal	FALSE	NEUT	-0.0533	Normal (A)	2	0.5819	HET	NA	NA	NA	NA	-0.08176	NA	0.006472	0.893705	MISSENSE		
2268	0	LILRA1		1:19:597991	Basal	FALSE	NEUT	-0.0668	Normal (A)	2	0.5721	HET	NA	NA	NA	NA	-0.02139	NA	0.003236	0.994183	MISSENSE		
2269	13	MOV10L1		1:22:488939	Basal	FALSE	NEUT	-0.0486	Normal (A)	2	0.581	HET	NA	NA	NA	NA	NA	NA	0.006472	0.445573	MISSENSE		
2270	0	ADAM19		-1:5:1568540	Basal	FALSE	HETD	-0.38	Hemizygous	1	0.7568	NLOH	NA	NA	NA	NA	NA	NA	0.009709	0.895852	MISSENSE		
2271	5	RPP40		-1:6:4943947	Basal	FALSE	GAIN	0.2712	3n duplicat	3	0.5818	HET	NA	NA	NA	NA	NA	NA	NA	0.996074	MISSENSE		
2272	5	ZNF588		7:6380533	Basal	FALSE	NEUT	-0.0231	Normal (A)	2	0.6	HET	NA	NA	NA	NA	NA	NA	NA	0.99088	MISSENSE		
2273	22	ACO1		9:3239853	Basal																		

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ
1	Non.ref.RN	Ens54Gene	Strand	primer	PAM50	Splice.site	HMMDosage	HMMDosage	OncoSNP	OncoSNP	apolloh.joh	apolloh.cal	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type		
2279	14	PIK3CA	1	3:1804186	Other	FALSE	NEUT	0.0266	Normal (A)	2	0.5641	HET	NA	NA	NA	NA	-1.3086	0.047619	0.016181	0.592132	MISSENSE		
2280	0	TMEM72	1	10:447500	Other	FALSE	NEUT	-0.0518	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.375418	MISSENSE		
2281	0	KCNQ2	1	18:757601	Other	FALSE	HETD	-0.1727	2n Somatic	2	0.6341	NLOH	NA	NA	NA	NA	NA	NA	NA	0.191577	MISSENSE		
2282	27	ITCH	1	20:325591	Other	FALSE	NEUT	0.0031	4n balance	4	0.5714	HET	NA	NA	NA	NA	-1.29903	NA	NA	0.376755	MISSENSE		
2283	34	ZNF142	-1	2:2192133	Other	FALSE	NEUT	-0.0548	2n Somatic	2	0.6591	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.378665	MISSENSE		
2284	8	APOBEC3F	1	22:377754	Other	FALSE	NEUT	0.0248	4n balance	4	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.589544	MISSENSE		
2285	0	SVPL2	1	1:1098236	Other	FALSE	HETD	-0.2072	2n Somatic	2	0.7368	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.283811	MISSENSE		
2286	1	PHLDB1	1	11:118007	Other	FALSE	NEUT	0.0593	4n balance	4	0.5641	HET	NA	NA	NA	NA	NA	NA	NA	0.592309	MISSENSE		
2287	0	PRAMEF1	1,1	1:1284380	Other	FALSE	NEUT	-0.0797	2n Somatic	2	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.607469	MISSENSE		
2288	25	C12orf48	1	12:101096	Other	FALSE	GAIN	0.2976	6n non-mo	6	0.5972	HET	NA	NA	NA	NA	NA	NA	NA	0.600887	MISSENSE		
2289	34	ACIN1	-1	14:226194	Other	FALSE	NEUT	0.1035	4n monoal	4	0.6587	NLOH	NA	NA	NA	NA	-0.12257	NA	0.006472	0.378759	MISSENSE		
2290	3	MTMR15	1	15:290087	Other	FALSE	GAIN	0.2011	5n non-mo	5	0.5828	HET	NA	NA	NA	NA	NA	NA	NA	0.113293	MISSENSE		
2291	0	ISLR2	1	15:722124	Other	FALSE	GAIN	0.3423	6n monoal	6	0.8	NLOH	NA	NA	NA	NA	NA	NA	NA	0.589896	MISSENSE		
2292	7	TP53	-1	17:751924	Other	FALSE	NEUT	0.0298	3n Somatic	3	0.7619	NLOH	NA	NA	NA	NA	-0.93225	0.306122	0.812298	0.282972	TRUNCATING		
2293	3	ZNF532	1	18:547377	Other	FALSE	NEUT	-0.0427	2n Somatic	2	0.7586	NLOH	NA	NA	NA	NA	NA	NA	NA	0.379642	MISSENSE		
2294	5	INHBB	2	12:208238	Other	FALSE	HETD	-0.2215	2n Somatic	2	0.7037	NLOH	NA	NA	NA	NA	-0.12554	NA	NA	0.183744	MISSENSE		
2295	54	FIP1L1	1	4:5398902	Other	FALSE	NEUT	0.1287	4n balance	4	0.5638	HET	NA	NA	NA	NA	NA	NA	0.003236	0.710005	MISSENSE		
2296	0	MARVELD2	1	5:6875154	Other	FALSE	HETD	-0.2088	2n Somatic	2	0.7105	NLOH	NA	NA	NA	NA	NA	NA	NA	0.966287	MISSENSE		
2297	25	RBM16	1	6:1551709	Other	FALSE	NEUT	0.1012	4n balance	4	0.5667	HET	NA	NA	NA	NA	NA	NA	0.003236	0.711302	MISSENSE		
2298	0	OSTCL	-1	6:1591830	Other	FALSE	NEUT	0.1012	4n balance	4	0.5667	HET	NA	NA	NA	NA	NA	NA	NA	0.962757	MISSENSE		
2299	12	NUPL2	1	7:2320625	Other	FALSE	GAIN	0.5046	6n non-mo	6	0.6	HET	NA	NA	NA	NA	-0.21483	NA	0.003236	0.708847	MISSENSE		
2300	1	TRIM35	-1	8:2720759	Other	FALSE	NEUT	0.0702	4n balance	4	0.5556	HET	NA	NA	NA	NA	NA	NA	NA	0.967855	MISSENSE		
2301	6	IMMP1L	-1	11:314382	Basal	FALSE	NEUT	0.0437	3n Germilin	3	0.5796	HET	NA	NA	NA	NA	-0.01881	NA	NA	1	MISSENSE		
2302	49	CENPF	1	21:28845	Basal	FALSE	GAIN	0.4037	6n non-mo	6	0.6288	NLOH	NA	NA	NA	NA	-0.10313	0.006803	0.019417	0.721371	MISSENSE		
2303	4	RCBTB2	-1	13:479837	Basal	FALSE	NEUT	-0.0486	2n Somatic	2	0.6857	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.986871	TRUNCATING		
2304	0	DPEP3	-1	16:665674	Basal	FALSE	HETD	-0.2344	2n Somatic	2	0.6923	NLOH	NA	NA	NA	NA	NA	NA	NA	0.990455	MISSENSE		
2305	125	GPBP1	1	5:5658077	Basal	FALSE	NEUT	-0.1062	2n Somatic	2	0.6824	NLOH	NA	NA	NA	NA	NA	NA	NA	0.966924	MISSENSE		
2306	78	SLC39A7	1	6:3327721	Basal	FALSE	GAIN	0.2517	5n non-mo	5	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.708933	MISSENSE		
2307	16	SPAG17	-1	1:1183405	Basal	FALSE	GAIN	0.4059	5n non-mo	5	0.5775	HET	NA	NA	NA	NA	NA	NA	0.006472	0.710836	MISSENSE		
2308	269	TP53	-1	17:751907	Basal	FALSE	NEUT	-0.1024	2n Somatic	2	0.8049	NLOH	NA	NA	NA	NA	-1.12814	0.306122	0.812298	0.997299	MISSENSE		
2309	6	KALRN	1	3:1256942	Basal	FALSE	NEUT	-0.0995	2n Somatic	2	0.806	NLOH	NA	NA	NA	NA	-0.33277	0.013605	0.012945	0.710572	TRUNCATING		
2310	0	MDC1	-1	6:3078795	Basal	FALSE	NEUT	-0.1075	2n Germilin	2	0.8159	NLOH	NA	NA	NA	NA	-0.06019	NA	0.006472	0.710355	MISSENSE		
2311	54	FAM83B	1	6:5491457	Basal	FALSE	NEUT	-0.1166	2n Germilin	2	0.7907	NLOH	NA	NA	NA	NA	NA	NA	0.016181	0.711077	MISSENSE		
2312	30	DLG5	-1	10:792486	Basal	FALSE	HETD	-0.2453	Hemizygou	1	0.6471	NLOH	NA	NA	NA	NA	NA	NA	0.016181	0.669415	MISSENSE		
2313	0	GPR133	1	12:130159	Basal	FALSE	NEUT	-0.0195	Normal (A)	2	0.5652	HET	NA	NA	NA	NA	NA	NA	0.012945	0.851312	MISSENSE		
2314	134	MED13	-1	17:573828	Basal	FALSE	NEUT	0.1	2n Somatic	2	0.7273	NLOH	NA	NA	NA	NA	-0.01231	NA	0.003236	0.778891	MISSENSE		
2315	0	ABCA6	-1	17:646210	Basal	TRUE	NEUT	0.1125	2n Germilin	2	0.7273	NLOH	NA	NA	NA	NA	-0.04264	NA	0.006472	0.663457	SPUCE		
2316	36	TICAM1	-1	19:476897	Basal	FALSE	NEUT	0.0079	Normal (A)	2	0.5769	HET	NA	NA	NA	NA	-0.22553	NA	NA	0.480647	MISSENSE		
2317	1	CEACAM19	1	19:498677	Basal	FALSE	NEUT	0.0079	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	NA	NA	NA	0.662088	MISSENSE		
2318	8	ADAMTS10	-1	19:857448	Basal	FALSE	NEUT	0.0079	Normal (A)	2	0.5769	HET	NA	NA	NA	NA	NA	NA	NA	0.664076	MISSENSE		
2319	52	ARFGAP3	-1	22:415528	Basal	FALSE	GAIN	0.2076	3n duplicat	3	0.6	HET	NA	NA	NA	NA	-0.20788	NA	NA	0.853297	MISSENSE		
2320	6	LAMA4	-1	6:1125470	Basal	FALSE	NEUT	0.0331	Normal (A)	2	0.5526	HET	NA	NA	NA	NA	-0.40351	NA	0.012945	0.664686	MISSENSE		
2321	17	GTF2IRD1	1	7:7357348	Basal	FALSE	NEUT	0.0243	Normal (A)	2	0.5601	HET	NA	NA	NA	NA	-0.02778	NA	0.012945	0.666135	MISSENSE		
2322	111	EEF1D	-1	8:1447330	Basal	FALSE	NEUT	0.0141	Normal (A)	2	0.561	HET	NA	NA	NA	NA	-0.12818	NA	0.003236	0.662663	MISSENSE		
2323	55	GPX7	1	1:5284505	Other	FALSE	NEUT	0.109	4n Germilin	4	0.6571	NLOH	NA	NA	NA	NA	-0.05981	NA	NA	0.662193	MISSENSE		
2324	11	CNKSR1	1	1:2638851	Other	FALSE	NEUT	0.1001	4n Germilin	4	1	NLOH	NA	NA	NA	NA	NA	NA	NA	0.663545	MISSENSE		
2325	41	ARL6IP1	-1	16:187175	Other	FALSE	NEUT	0.0602	4n Germilin	4	0.5556	HET	NA	NA	NA	NA	NA	NA	NA	0.482504	TRUNCATING		
2326	13	TP53	-1	17:751778	Other	FALSE	HETD	-0.1814	2n Somatic	2	0.703	NLOH	NA	NA	NA	NA	-1.16039	0.306122	0.812298	0.481496	TRUNCATING		
2327	42	EXOSC8	1	13:364790	Basal	FALSE	HETD	-0.4558	Hemizygou	1	0.7	NLOH	NA	NA	NA	NA	-0.06114	NA	NA	0.774819	MISSENSE		
2328	25	EIF2AK4	1	15:380575	Basal	FALSE	HETD	-0.4658	Hemizygou	1	0.6053	HET	NA	NA	NA	NA	-0.22311	NA	NA	0.664321	MISSENSE		
2329	1	CCDC8	-1	19:516067	Basal	FALSE	GAIN	0.285	3n Somatic	3	0.6875	NLOH	NA	NA	NA	NA	NA	NA	0.009709	0.661854	MISSENSE		
2330	0	KIR3DL2	1	19:600551	Basal	FALSE	NEUT	0.0982	Normal (A)	2	0.7565	NLOH	NA	NA	NA	NA	-0.17497	NA	0.003236	0.777029	MISSENSE		
2331	0	ZNF667	-1	19:616442	Basal	FALSE	NEUT	0.0982	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	NA	NA	NA	0.99493	MISSENSE		
2332	39	MF12	-1	3:1982209	Basal	FALSE	GAIN	0.4197	3n duplicat	3	0.6643	NLOH	NA	NA	NA	NA	NA	NA	NA	0.653398	MISSENSE		
2333	39	WHSC1	1	4:1927522	Basal	FALSE	NEUT	0.0899	2n Somatic	2	0.7872	NLOH	NA	NA	NA	NA	-0.05031	NA	0.009709	0.307849	MISSENSE		
2334	0	CFTR	1	7:1170378	Basal	FALSE	GAIN	0.2692	3n Germilin	3	0.5909	HET	NA	NA	NA	NA	-0.2242	NA	0.003236	0.995003	MISSENSE		
2335	19	PTPN3	-1	9:1111816	Basal	FALSE	GAIN	0.3267	3n duplicat	3	0.6162	HET	NA	NA	NA	NA	NA	NA	0.009709	0.849866	MISSENSE		
2336	42	NRAS	-1	1:1150580	Other	FALSE	NEUT	-0.0964	2n Somatic	2	0.5495	HET	NA	NA	NA	NA	-0.7738	NA	0.006472	0.48161	MISSENSE		
2337	23	SETD2	-1	3:4713745	Other	FALSE	NEUT	-0.088	2n Somatic	2	0.5556	HET	NA	NA	NA	NA	-0.0107	NA	0.016181	0.301635	TRUNCATING		
2338	0	PCDHA2	1,1,1,1	5:1402018	Other	FALSE	NEUT	-0.0886	Normal (A)	2	0.5532	HET	NA	NA	NA	NA	NA	NA	NA	1	MISSENSE		
2339	0	FAM123C	1	12:1312380	Other	FALSE	NEUT	0.0196	5n non-mo	5	0.7139	NLOH	NA	NA	NA	NA	NA	NA	0.003236	NA	MISSENSE		
2340	0	ITGA8	-1	10:156792	Other	FALSE	NEUT	0.1053	4n balance	4	0.5625	HET	NA	NA	NA	NA	-0.2371	NA	0.009709	0.306113	MISSENSE		
2341	0	C10orf93	-1	10:134604	Other	FALSE	NEUT	-0.0461	3n Somatic	3	0.6842	NLOH	NA	NA	NA	NA	NA	NA	NA	0.28566	MISSENSE		
2342	0	FAM71F1	1	7:1281572	Other	FALSE	NEUT	-0.0089	Normal (A)	2	0												

	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY	AZ	
1	Non.ref.RN	EnS4Gene	Strand	primer	PAM50	Splice.site	HMMDos	HMMDos	OncoSNP	OncoSNP	apolloho	apolloho	APOLLOH	APOLLOH	HMMcopy	HMMcopy	driver	mut_freq	mut_freq	clonality	mut_type			
2347	24	SEL1L	-1	14:810222	Basal	FALSE	NEUT	-0.07	3n Somatic	3	0.8421	NLOH	NA	NA	NA	NA	-0.07842	NA	0.003236	0.860975	MISSENSE			
2348	56	PVR12	-1	19:500694	Basal	FALSE	NEUT	-0.1161	3n Germlin	3	0.6471	HET	NA	NA	NA	NA	-0.12125	NA	NA	0.779811	MISSENSE			
2349	20	CELSR1	-1	22:452383	Basal	FALSE	NEUT	-0.078	3n Somatic	3	0.8387	NLOH	NA	NA	NA	NA	-0.21143	NA	NA	0.306985	MISSENSE			
2350	0	UPK1B	1	3:1203956	Basal	FALSE	NEUT	-0.0273	3n duplicat	3	0.6176	HET	NA	NA	NA	NA	NA	NA	NA	0.301118	MISSENSE			
2351	25	ZNF639	1	3:1805343	Basal	FALSE	GAIN	0.4484	5n monoal	5	0.7719	NLOH	NA	NA	NA	NA	NA	NA	NA	0.989349	MISSENSE			
2352	3	INTU	1	4:1287841	Basal	FALSE	HETD	-0.266	Normal (A)	2	0.5989	HET	NA	NA	NA	NA	NA	NA	0.003236	0.469068	MISSENSE			
2353	2	ZBTB2	-1	6:1517290	Basal	FALSE	NEUT	0.1423	4n Somatic	4	0.875	NLOH	NA	NA	NA	NA	NA	NA	NA	0.776626	MISSENSE			
2354	0	COL9A1	-1	6:7100093	Basal	FALSE	NEUT	-0.0605	3n Somatic	3	0.8718	NLOH	NA	NA	NA	NA	-0.06921	NA	0.012945	0.66606	MISSENSE			
2355	0	RSPH10B	-1	7:5934455	Basal	FALSE	HETD	-0.2833	2n Somatic	2	0.8	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.673661	MISSENSE			
2356	20	PLEC1	-1	8:1450652	Basal	FALSE	GAIN	0.2977	5n non-mo	5	0.5909	HET	NA	NA	NA	NA	-0.14253	NA	0.003236	0.992878	MISSENSE			
2357	1	CPEB1	-1	15:810129	Basal	FALSE	NEUT	0.1356	Normal (A)	2	0.5663	HET	NA	NA	NA	NA	-0.23582	NA	0.003236	0.842833	MISSENSE			
2358	5	TPCN2	1	11:686038	Other	FALSE	NEUT	-0.0068	3n duplicat	3	0.5882	HET	NA	NA	NA	NA	-0.11177	NA	NA	0.845221	MISSENSE			
2359	14	CTDSP12	1	15:425658	Other	FALSE	HETD	-0.1745	2n Germlin	2	0.7143	NLOH	NA	NA	NA	NA	NA	NA	NA	0.358409	MISSENSE			
2360	3	NRN1L	1	16:664773	Other	FALSE	HETD	-0.1711	2n Germlin	2	0.7015	NLOH	NA	NA	NA	NA	NA	NA	NA	0.786429	MISSENSE			
2361	18	ATR	-1	3:1436998	Other	FALSE	GAIN	0.3489	6n monoal	6	0.6765	NLOH	NA	NA	NA	NA	-0.28931	0.006803	0.006472	0.79808	MISSENSE			
2362	49	TAF6	-1	7:9954734	Other	FALSE	NEUT	0.1416	4n balance	4	0.5641	HET	NA	NA	NA	NA	-0.31651	NA	0.003236	0.513381	MISSENSE			
2363	0	RP1	1	8:5570334	Other	FALSE	NEUT	0.0135	3n duplicat	3	0.6	HET	NA	NA	NA	NA	NA	NA	0.012945	0.987882	TRUNCATING			
2364	0	SH3GL2	1	9:1777907	Other	FALSE	NEUT	0.0135	3n Germlin	3	0.6	HET	NA	NA	NA	NA	-0.45756	NA	NA	0.791565	MISSENSE			
2365	1	ATAD5	1	17:262062	Basal	TRUE	HETD	-0.1796	2n Somatic	2	0.7931	NLOH	NA	NA	NA	NA	NA	NA	0.009709	0.792863	SPICE			
2366	35	BXDC5	1	1:8473410	Basal	FALSE	NEUT	-0.0042	5n Germlin	5	0.5833	HET	NA	NA	NA	NA	NA	NA	NA	0.534683	MISSENSE			
2367	1	MOGAT3	-1	7:1006307	Basal	FALSE	NEUT	0.1216	4n monoal	4	0.6512	NLOH	NA	NA	NA	NA	NA	NA	0.006472	0.534326	MISSENSE			
2368	0	TMLHE	-1	X:1543898	Basal	FALSE	HETD	-0.1676	NA	NA	NA	NA	NA	NA	NA	NA	-0.03535	NA	0.003236	NA	MISSENSE			
2369	10	HIVEP3	-1	1:4175145	Basal	FALSE	HETD	-0.348	2n Somatic	2	0.9333	NLOH	NA	NA	NA	NA	NA	NA	0.012945	0.645022	MISSENSE			
2370	136	TP53	-1	17:751441	Basal	FALSE	HETD	-0.3777	2n Somatic	2	0.9294	NLOH	NA	NA	NA	NA	-0.83906	0.306122	0.812298	0.646254	TRUNCATING			
2371	32	KIAA2018	-1	3:1148658	Basal	FALSE	GAIN	0.2035	4n monoal	4	0.6543	HET	NA	NA	NA	NA	NA	NA	0.003236	0.990041	MISSENSE			
2372	60	SLC41A3	-1	3:1272525	Basal	FALSE	NEUT	0.0848	5n non-mo	5	0.5943	HET	NA	NA	NA	NA	NA	NA	NA	0.808806	MISSENSE			
2373	4	TERT	-1	5:1347285	Basal	FALSE	NEUT	0.0828	4n Somatic	4	0.9524	NLOH	NA	NA	NA	NA	-0.14918	0.013605	0.003236	0.536915	MISSENSE			
2374	0	ZNF311	-1	6:2907155	Basal	FALSE	GAIN	0.2001	4n balance	4	0.5534	HET	NA	NA	NA	NA	NA	NA	NA	0.641097	MISSENSE			
2375	12	EGFR	1	7:5519192	Basal	FALSE	NEUT	0.114	4n balance	4	0.5625	HET	NA	NA	NA	NA	-0.80051	0.163265	0.006472	0.790641	MISSENSE			
2376	0	MYO3A	1	10:264862	Other	FALSE	NEUT	-0.0882	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	NA	0.006803	0.009709	0.991079	MISSENSE			
2377	27	NCOR2	-1	12:123393	Other	FALSE	NEUT	-0.0487	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	-0.63681	NA	0.003236	0.337805	MISSENSE			
2378	46	MFA1	-1	15:418941	Other	FALSE	NEUT	-0.1358	Hemizygou	1	0.5769	HET	NA	NA	NA	NA	NA	NA	NA	0.791729	MISSENSE			
2379	0	CCL17	1	16:560071	Other	FALSE	NEUT	-0.0535	Normal (A)	2	0.5714	HET	NA	NA	NA	NA	-1.12854	NA	0.003236	0.795826	MISSENSE			
2380	12	RAB13	-1	3:1218910	Other	FALSE	NEUT	0.0176	3n duplicat	3	0.5625	HET	NA	NA	NA	NA	NA	NA	NA	0.635365	MISSENSE			
2381	0	COL7A1	-1	3:4858001	Other	FALSE	NEUT	-0.0477	Hemizygou	1	0.5942	HET	NA	NA	NA	NA	-0.27595	NA	0.009709	0.639393	MISSENSE			
2382	15	LRBA	-1	4:1516283	Other	FALSE	NEUT	-0.0188	Hemizygou	1	0.5571	HET	NA	NA	NA	NA	NA	NA	0.009709	0.788404	MISSENSE			
2383	8	FBXO38	1	5:1477618	Other	FALSE	NEUT	-0.1228	Hemizygou	1	0.575	HET	NA	NA	NA	NA	NA	NA	0.012945	0.9874	MISSENSE			
2384	88	KIAA1429	-1	8:9557411	Other	FALSE	NEUT	0.0042	3n duplicat	3	0.5676	HET	NA	NA	NA	NA	NA	NA	0.003236	0.641754	MISSENSE			
2385	0	GRIA3	1	X:1223894	Other	FALSE	NEUT	-0.0578	NA	NA	NA	NA	NA	NA	NA	NA	-0.48639	NA	0.009709	NA	MISSENSE			
2386	25	TMC3	-1	12:935002	Other	FALSE	NEUT	-0.0743	3n duplicat	3	0.5714	HET	NA	NA	NA	NA	NA	NA	0.003236	0.793456	MISSENSE			
2387	10	SPATA13	1	13:237697	Other	FALSE	NEUT	-0.1161	3n Somatic	3	0.7253	NLOH	NA	NA	NA	NA	NA	NA	NA	0.003236	0.512568	MISSENSE		
2388	17	AF235103.-1,1	-1	8:1460031	Other	FALSE	GAIN	0.2779	6n monoal	6	0.6667	NLOH	NA	NA	NA	NA	NA	NA	NA	0.532631	MISSENSE			
2389	2	VPS13B	1	8:1002170	Other	FALSE	GAIN	0.2075	4n Germlin	4	0.5714	HET	NA	NA	NA	NA	NA	NA	0.022654	0.534584	MISSENSE			
2390	0	MAN2A2	1	15:892574	Basal	FALSE	HETD	-0.2192	Normal (A)	2	0.5882	HET	NA	NA	NA	NA	-0.62456	NA	0.003236	0.535319	MISSENSE			
2391	0	TP53	-1	17:751877	Basal	FALSE	NEUT	-0.0153	2n Somatic	2	0.9362	NLOH	NA	NA	NA	NA	-1.1693	0.306122	0.812298	0.79128	TRUNCATING			
2392	0	SLC34A1	1	5:1767574	Basal	FALSE	HETD	-0.4855	Hemizygou	1	0.9062	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.533507	MISSENSE			
2393	0	PPAPDC3	1	9:1331732	Basal	FALSE	NEUT	0.0288	Normal (A)	2	0.5745	HET	NA	NA	NA	NA	NA	NA	NA	0.642657	MISSENSE			
2394	0	NBP16	1	1:1470060	Basal	FALSE	NEUT	-0.0198	2n Somatic	2	0.7538	NLOH	NA	NA	NA	NA	NA	NA	NA	0.791085	MISSENSE			
2395	0	PLA2G2E	-1	1:2012134	Basal	FALSE	NEUT	0.0054	Normal (A)	2	0.5811	HET	NA	NA	NA	NA	-0.9744	NA	NA	0.989437	MISSENSE			
2396	10	LTBP1	1	2:3347655	Basal	FALSE	GAIN	0.4001	3n duplicat	3	0.6154	HET	NA	NA	NA	NA	-0.06013	NA	0.009709	0.793768	MISSENSE			
2397	7	PRDM4	-1	12:106669	Other	FALSE	NEUT	-0.0762	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	-0.26824	NA	NA	0.798952	MISSENSE			
2398	26	SLC25A13	-1	7:9567585	Other	FALSE	NEUT	0.0808	4n balance	4	0.5714	HET	NA	NA	NA	NA	-0.15909	0.013605	NA	0.991905	MISSENSE			
2399	0	KRT28	-1	17:362021	Basal	FALSE	NEUT	-0.0899	2n Somatic	2	0.8046	NLOH	NA	NA	NA	NA	NA	NA	0.003236	0.785608	MISSENSE			
2400	33	UBA2	1	19:396156	Basal	FALSE	GAIN	0.3178	4n Germlin	4	0.5646	HET	NA	NA	NA	NA	-0.0977	NA	0.003236	0.974482	TRUNCATING			
2401	131	TP53	-1	17:751877	Basal	FALSE	NEUT	-0.1354	Hemizygou	1	0.8103	NLOH	NA	NA	NA	NA	-1.71496	0.306122	0.812298	0.799038	MISSENSE			
2402	1	VDAC2	1	10:766501	Other	FALSE	NEUT	0.0409	3n duplicat	3	0.6	HET	NA	NA	NA	NA	-0.25952	NA	0.003236	0.990581	MISSENSE			
2403	0	KCNJ5	1	11:128286	Other	FALSE	NEUT	-0.1118	2n Somatic	2	0.7487	NLOH	NA	NA	NA	NA	-0.10984	NA	NA	0.642715	MISSENSE			
2404	11	DCAMK1L	-1	13:352830	Other	FALSE	NEUT	-0.0056	3n Somatic	3	0.75	NLOH	NA	NA	NA	NA	NA	NA	NA	0.795184	MISSENSE			
2405	8	IDH3B	-1	20:259214	Other	FALSE	AMP	0.721	6n non-mo	6	0.6562	NLOH	NA	NA	NA	NA	-0.79962	NA	NA	0.533317	TRUNCATING			
2406	54	LONP1	-1	19:565903	Other	FALSE	HETD	-0.1758	2n Somatic	2	0.7143	NLOH	NA	NA	NA	NA	NA	NA	NA	0.99794	MISSENSE			
2407	0	RLBP1L2	1	6:1234113	Other	FALSE	HETD	0.1539	4n balance	4	0.5556	HET	NA	NA	NA	NA	NA	NA	0.003236	0.797747	MISSENSE			
2408	5	ZNF324	1	19:636740	Basal	FALSE	NEUT	0.0368	4n balance	4	0.5714	HET	NA	NA	NA	NA	NA	NA	NA	0.99323	MISSENSE			
2409	0	WSCD2	1	12:107142	Other	FALSE	NEUT	-0.0487	Normal (A)	2	0.5625	HET	NA	NA	NA	NA	NA	NA	0.003236	0.799925	MISSENSE			
2410	1	CIT	-1	12:118664	Other	FALSE	NEUT	-0.0487	Normal (A)	2	0.5625													