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Mutational and selective effects on copy-number variants in the human genome

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Comprehensive descriptions of large insertion/deletion or segmental duplication polymorphisms (SDs) in the human genome have recently been generated. These annotations, known collectively as structural or copy-number variants (CNVs), include thousands of discrete genomic regions and span hundreds of millions of nucleotides. Here we review the genomic distribution of CNVs, which is strongly correlated with gene, repeat and segmental duplication content. We explore the evolutionary mechanisms giving rise to this nonrandom distribution, considering the available data on both human polymorphisms and the fixed changes that differentiate humans from other species. It is likely that mutational biases, selective effects and interactions between these forces all contribute substantially to the spectrum of human copy-number variation. Although defining these variants with nucleotide-level precision remains a largely unmet but critical challenge, our understanding of their potential medical impact and evolutionary importance is rapidly emerging.

The HapMap project[1] provides a powerful resource for studying the relationship between genetic and phenotypic variation in humans as well as the evolutionary and genealogical history of modern human populations. Technical and practical concerns have led to a variation map composed almost exclusively of single nucleotide polymorphisms (SNPs), despite the fact that other types of variation in the human genome are likely to be of considerable importance. Recent advances, however, have facilitated insights into a number of other variants in the human genome (**Table 1**, see http://genome.ucsc.edu and http://projects.tcag.ca/variation/). These include small insertion and deletion (indel) polymorphisms identified in sequence traces[2–4], common deletion polymorphisms mined from HapMap genotype data[5,6] and variants identified by comparing clone paired-end sequence data to the reference human assembly[7]. There have also been studies using comparative genomic hybridization with microarrays (array-CGH) to identify large (>50 kb) CNVs among dozens of individuals[8–10]. Finally, two recent studies using genome-wide BAC and oligonucleotide arrays have identified large CNVs in hundreds of individuals[11,12], including the reference HapMap samples.

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Based on these studies, there are now over 400,000 annotated indel polymorphisms smaller than 1,000 nucleotides in length[2–4] (**Table 1**). These polymorphisms, particularly for the smallest events affecting from one to a handful of nucleotides, are the second most commonly occurring form of variation in the human genome. They behave similarly to SNPs in terms of their broad genomic distribution, allelic associations with other variants, frequency distributions in human populations and contributions to evolutionary divergence among mammals[2–4,13]. The sequence properties of the larger (>1 kb) variants are less clear. Thus far, more than 4,000 distinct regions of the reference genome assembly have been annotated to harbor CNVs (along with a small number of inversions, which are more difficult to detect and presently less explored), and many are frequently polymorphic in human populations. Although they affect dramatically fewer regions compared with SNPs or small indels, these variants span an estimated 600 Mb of the human genome (see **Table 1** and references therein). We note that this number should be interpreted cautiously, as it is likely to be too large; most known CNVs were identified through BAC array-CGH, a method that lacks precision in identifying breakpoints and is likely to substantially overestimate variant size. Also, there are different degrees of quality control among the different studies and only a minority have been validated across platforms. However, even assuming an order of magnitude difference between currently estimated and true variant sizes, an estimated 60 Mb would still be within CNVs, representing a sizable fraction of the genome (~2%).

Comparisons between chimpanzee and human genomic sequences confirm a similar relative influence of copy-number changes when compared with single-nucleotide substitutions[14–17] (**Table 2**). Whereas ~35 million fixed nucleotide substitutions contribute to a human-chimp sequence divergence of ~1.2%, ~5 million mutations involving gain or loss of DNA raise the total amount of human-chimp genomic divergence to ~5%. Even after excluding small indels, mobile-element insertions and microsatellite expansions, several thousand indel differences (>5 kb) spanning ~115 Mb remain between the two species[15]. Although it is possible that assembly errors may contribute to this estimate, it should be emphasized that many of the larger events were annotated using approaches independent from chimpanzee assembly (namely mapping of whole-genome shotgun sequence and paired-end sequence data from the chimpanzee genome against the high-quality human genome assembly to identify duplications and structurally variant regions[15–17]). Furthermore, the limited number and the size of these events facilitated identification and validation for many of them, and efforts are underway to provide high quality BAC-based sequence data from these regions.

EX1091

Table 1 Summary of recent analyses of structural variation in the human genome

Reference	Coverage	Analysis	No. of individuals	No. events or regions	Size range (bp)	Average size (bp) Median size (bp)	Total bp
Mills *et al.*, *Genome Res.* 2006	16 million whole-genome shotgun traces	Alignment of sequence traces from SNP Consortium resequencing	36	415,434	1–9,989	20 2	8,360,235
Conrad *et al.*, *Nat. Genet.* 2006	1.3 million SNPs	HapMap SNP-genotyping data mining based on Mendelian inconsistencies	180 (60 parent-offspring trios from CEU and YRI populations)	609	25–993,000	34,996 17,217	21,313,127
McCarroll *et al.*, *Nat. Genet.* 2006	1.3 million SNPs	HapMap SNP-genotyping data mining based on null genotypes, Mendelian inconsistencies and deviations from Hardy-Weinberg equilibrium	269 (CEU, YRI and CHB+JPT populations, including 60 trios)	538	96–745,418	16,874 6,887	9,078,084
Hinds *et al.*, *Nat. Genet.* 2006	100 million to 200 million bp	Oligonucleotide array hybridization	24	1,000	72–8,001	1,379 947	137,912
Tuzun *et al.*, *Nat. Genet.* 2005	×8 coverage fosmid library	Paired end-sequencing	1	297	700–1,944,156	55,706 25,230	14,984,826
Iafrate *et al.*, *Nat. Genet.* 2004	5,264 BACs	BAC array-CGH	55[a]	246	19,597–337,967	146,189 150,395	35,962,540
Sharp *et al.*, *Am. J. Hum. Genet.* 2005	1,986 BACs	BAC array-CGH	47	124	29,514–410,301	170,019 164,704	21,082,320
Sebat *et al.*, *Science* 2004	85,000 oligonucleotides	ROMA-CGH	20	72	754–1,698,859	350,670 199,800	25,248,203
Wong *et al.*, *Am. J. Hum. Genet.* 2007	26,363 BACs	BAC array-CGH	105	1,365[b]	50,459–1,037,332	185,504 175,314	253,212,685
Redon *et al.*, *Nature* 2006	26,574 BACs	BAC array-CGH	269 (CEU, YRI and CHB+JPT populations, including 60 trios)	913	2,639–7,378,760	349,880 227,889	319,440,476
Redon *et al.*, *Nature* 2006	500,000 SNPs	Affyx 500K SNP array analysis	269 (CEU, YRI and CHB+JPT populations, including 60 trios)	980	1,033–3,605,436	165,996 63,140	162,675,683
All variations	NA	NA	NA	323,573	1–7,442,054	1,901 2	615,095,095
All variations >1 kb	NA	NA	NA	4,131	1,004–7,442,053	148,578 93,356	613,774,371

NA, not applicable; ROMA, representational oligonucleotide microarray analysis; CEU (Utah residents with ancestry from northern and western Europe); YRI, Yoruba in Ibadan, Nigeria; CHB+JPT, Han Chinese in Beijing, China and Japanese in Tokyo.
[a]39 healthy controls, 16 with karyotype abnormalities. [b]Accounting for only those sites that showed in two or more individuals.

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Thus, CNVs contribute substantially, if not predominantly, to per-nucleotide heterozygosity in human populations and divergence between humans and other species. CNVs are likely to inform all aspects of human genetic analysis, including associations with both rare and common traits, clinical diagnostics and treatments, population demographics, and the molecular and phenotypic evolution of the human species. In this perspective, we focus our analysis on the large (>1 kb) variants identified in recent genome-wide surveys. Although still incomplete, the available data allow us to assess the genomic landscape of CNVs and provide insight into the likely influences of biased mutational mechanisms and natural selection.

Distribution of CNVs in the human genome

We combined published human CNVs (along with a small number of inversions) into a single nonredundant set (**Table 1** and **Supplementary Table 1** online) and evaluated the density of these variants across the reference human genome assembly in 1-Mb nonoverlapping windows (see **Supplementary Note** and **Supplementary Table 2** online). The average genome-wide per-nucleotide density is ~21%, and the median 1-Mb window has a density of ~16.6%. Consistent with previous analyses[9–12], the distribution of CNVs in the genome is nonrandom and highly correlated with other genomic features, including exons ($P = 2 \times 10^{-12}$), segmental duplications (SDs; $P < 2 \times 10^{-16}$) and mobile elements such as *Alu* repeats ($P = 3 \times 10^{-7}$). These correlations are at least partially transitive, but remain very significant even when considered simultaneously (see **Supplementary Note**). Additionally, there are both 'cold' and 'hot' regions of copy-number variation: there are 250 1-Mb regions in which more than half of all bases are within an annotated CNV and 60 regions where more than 90% of all bases are annotated. Not surprisingly, these hotspots cluster in pericentromeric and subtelomeric regions of chromosomes, regions previously recognized as evolutionarily unstable and highly polymorphic[18–20]. This accounts for only ~1/3 of all hotspots, however, with the remainder occurring elsewhere in the genome (**Fig. 1**; **Supplementary Table 2**).

CNVs and segmental duplications. There is a strong relationship between duplicated sequences in the reference genome assembly and copy-number variation in the human genome. More than half of all nucleotides annotated to be within SDs (http://humanparalogy.gs.washington.edu)[21] overlap with CNVs. The average SD density in the most CNV-rich fraction of the genome is ~25%, in contrast to a genome-wide average density of 4–5% and a density of 2–3% in CNV-poor regions (see **Supplementary Note** online). These findings confirm

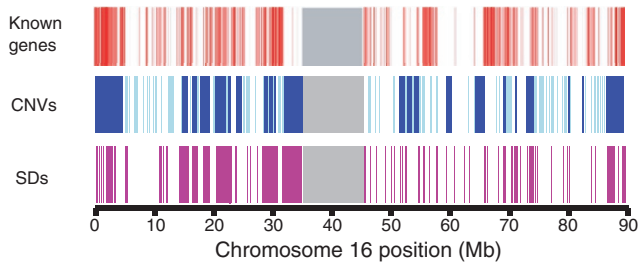


Figure 1 Copy-number variation along human chromosome 16. Regional densities of segmental duplications (SDs), CNVs and exons vary and co-vary across the genome, as seen here for human chromosome 16 (*x* axis corresponds to coordinates in the hg17 assembly). On the bottom row, the positions of all SDs are marked in purple. In the middle row, positions of all CNVs (nonredundant set of all CNVs > 1 kb described in **Table 1** and **Supplementary Table 1**) are marked in light blue and common (>3% frequency as estimated in refs. 11,12) CNVs are marked in darker blue. On the top row, exons of known genes are colored red. Heterochromatic sequence is gray. Note that CNVs are enriched in telomeric (for example, near 0 Mb) and pericentromeric (for example, near 35 Mb) regions and that there is a strong correlation between SDs and CNVs, particularly for common variants. Also note that CNVs and SDs often overlap gene-rich regions (for example, near 30 Mb), but that CNVs may also reside in regions that are poor in both gene and segmental duplication content (for example, 60–66 Mb).

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previous estimates that duplicated regions of the genome are enriched 4–10-fold for copy-number variation[9–12] (**Fig. 1**). This strong correlation in part reflects the fundamentally similar nature of CNVs and SDs. Indeed, many SDs represent the reference assembly alleles of CNVs rather than duplication events that are fixed in the human population. To ameliorate this circularity, we stratified SDs using sequence identity as a surrogate for evolutionary age (**Fig. 2**). We reasoned that older duplications (as measured by divergence) are less likely to be presently polymorphic. Consistent with previous analyses[11], the correlation between SDs and CNVs is most striking when only young, high-identity duplications are considered (**Fig. 2a**, red bars). However, the relationship remains pronounced even when only relatively old, divergent SDs are considered (**Fig. 2a**, blue and purple bars). This indicates that the relationship between these two features is not strictly dependent upon sequence identity—that is, longer blocks of nearly perfect sequence identity predisposing to nonallelic homologous recombination—and that the presence of ancient (and probably fixed) copy-number mutations is associated with the presence of currently polymorphic CNVs. Indeed, it is known that more divergent repeat sequences such as *Alu* elements and LINEs may contribute to nonallelic homologous recombination, although in these cases it is the proximity of the homologous repeats that predisposes to the arrangement. Such events are less likely to be recurrent.

However, not all CNVs map to duplicated regions of the reference genome assembly, as approximately half of all CNV nucleotides are within annotations that do not overlap SDs. Interestingly, CNVs that do not overlap SDs are characterized by significantly fewer individuals that show copy number deviation[11,12]. For example, from the BAC array-CGH data presented in Redon *et al.*[12], the average frequency for CNVs associated with SDs is 10.9%, in contrast to only 3.2% for variants that are not associated with SDs ($P = 1.9 \times 10^{-12}$). This difference is even larger when comparing CNVs overlapping young SDs (98–100% identical) versus the remaining sites (20% versus 3.7%, $P = 7.4 \times 10^{-15}$). Thus, both the density and population frequency of copy-number variation are correlated with the presence of duplicated sequences in the reference genome assembly. We note, however, that for many variants it is not allele frequency *per se* that is measured, but rather a measure of how many individuals show some deviation in copy number from the reference sample or assembly, which effectively prohibits distinguishing common alleles from recurrent mutational events and allelic heterogeneity.

CNVs and gene content. There is also a significant relationship between the genomic regions affected by CNVs and gene content. The exon density (including both coding and untranslated regions) in the most CNV-rich regions of the genome is over 2.7%, in contrast to the genome-wide average of 2.1% ($P = 0.0013$; see **Supplementary Note**). Conversely, the density of CNVs in the most gene-rich regions of the genome is over 30%, compared with a genome-wide average of 21% ($P = 3.3 \times 10^{-9}$). Thus, gene-rich regions tend to be rich in copy-number variation and vice versa. However, given that there is a strong correlation between SDs and gene content[21–23], we asked whether the association between copy-number variation and gene content could be separated from its association with SDs (**Fig. 2b**). We partitioned variants that do not overlap SDs from those that do; we still find a significant ($P = 0.019$), albeit weaker, enrichment for copy-number variation in gene-rich regions. However, unlike CNVs that overlap SDs (**Fig. 2b**, red bars), CNVs that are not associated with SDs are also enriched in the most gene-poor regions of the genome ($P = 2.6 \times 10^{-6}$; **Fig. 2b**, blue bars). Thus, the spectrum of copy-number variation in the genome can be separated based on overlap with SDs, and these two groups have distinct gene density profiles.

We also sought to characterize the types of genes seen in CNVs, considering the two groups independently. GO-term[24] and PANTHER[25] analyses reveal that CNVs associated with segmental duplication are highly enriched for genes involved in sensory perception (for example, olfactory receptors) and the immune response, consistent with previous studies[19,20,26–28] (**Fig. 3** and **Supplementary Note**). Other functional categories such as 'cell adhesion' and 'structural proteins' are also enriched, although these observations are driven largely by a few gene clusters, namely the *LCE* and keratin (structural proteins) and protocadherin (cell adhesion) loci (that is, these enrichment values result from a 'jackpot' effect in which one or a few CNVs overlap with dozens of distinct but functionally related genes because these genes reside in a genomic cluster). Interestingly, the protocadherin cluster on human chromosome 5, thought to be important for generating combinatorial complexity in synaptic connections in the brain[29], is particularly rich in copy-number variation, harboring gain and loss annotations from many of the CNV annotation efforts. In fact, detailed analyses of this cluster show that it has been prone to frequent copy-number mutations and gene-conversion events throughout mammalian and vertebrate evolution[30].

CNVs that do not overlap SDs show no enrichment for olfactory receptors and only weak enrichment for defense and immunity proteins (probably as a consequence of the tight association of olfactory receptors and immunoglobulin genes with SDs). These regions are enriched, however, for genes involved in signaling ($P = 2 \times 10^{-7}$; **Fig. 3**). This functional category includes members of the *FGF*, *EGF*, *WNT* and *BMP* families that collectively play a wide variety of roles in regulating organismal

Table 2 Human versus chimpanzee genetic variation

Type	Size	No. events	Mb
Substitution	1 bp	35,000,000	35
Structural	<80 bp	4,930,000	18.1
	80 bp–15 kb	70,000	48.9
	>15 kb	~1,000	21
	SD (LS)	~940	46
	SD (QD)	~590	26
Total structural	>1 bp	5,000,000	160

Between-species differences based principally on a comparison of two representative individuals. QD, quantitative differences between shared SDs; LS, lineage-specific duplications (see refs. 14–17).

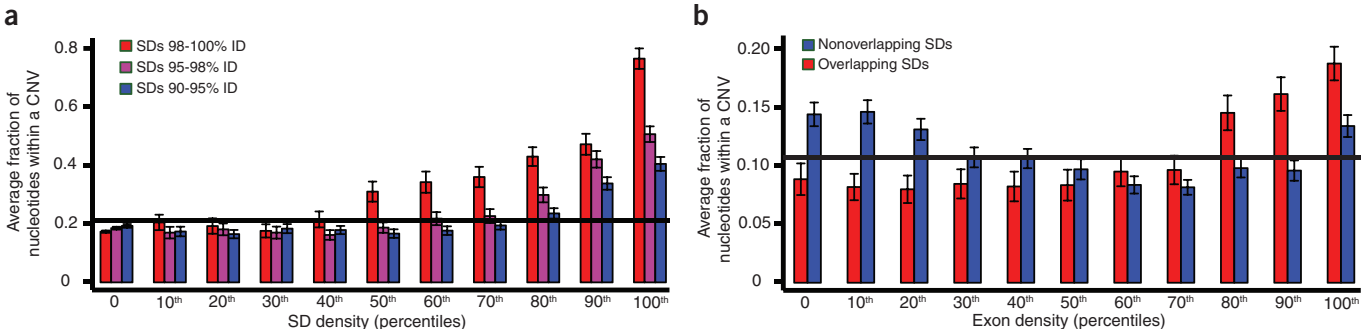


Figure 2 Relationships among copy-number variants, segmental duplications, and genes. (**a**) Copy-number variation and segmental duplication similarity. Nonoverlapping 1-Mb windows were binned according to their segmental duplication content, treating SDs of each of the three indicated levels of percent identity separately (see **Supplementary Note**). Those windows with no SDs of the given similarity level (excluding heterochromatic sequences) were binned into one group ('0'), and the remainder were ranked and binned into deciles (0–10th percentile, 10th–20th, etc.). For the windows within each bin, the average number of nucleotides that are within a CNV is plotted as a vertical bar. For example, nearly 80% of nucleotides within the windows containing the highest density of young (98–100% identity) SDs are within a CNV (red column, 100th-percentile bin). The genome-wide average density of CNVs (~21%) is plotted as a horizontal line; error bars, s.e.m. (**b**) Copy-number variation gene content in duplicated and unique regions of the reference genome assembly. Nonoverlapping 1-Mb windows were binned as described above according to their exon density; those with no annotations (excluding heterochromatic sequences) were binned into one group ('0'), and the remainder were ranked and placed into deciles. For the windows within each bin, the average number of nucleotides that are within a CNV is plotted as a vertical bar, with those CNVs that overlap SDs separated from those that do. For example, nearly 20% of nucleotides within the windows containing the highest density of exons are within a CNV that overlaps an SD (red column, 100th-percentile bin). A horizontal line is drawn at ~10.5%, close to the average density of each class of CNV (that is, those that overlap SDs and those that do not); error bars, s.e.m.

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development and cellular growth, proliferation and differentiation. Interestingly, this observation is in direct contrast with previous results[12]; this difference is likely to be due to the rapidly expanding set of CNVs identified in the human genome (~70% increase in total genomic coverage) and the focus on CNVs that do not overlap SDs. We further note that this enrichment is unlikely to be driven by a single study, as there is still a weak enrichment for signaling molecules even after eliminating genes that overlap a CNV from only one study (not shown). We also find a significant ($P = 0.0023$) enrichment for ion channel genes specifically for CNVs that do not overlap duplicated sequence. Although it is unclear at present whether the copy-number variation occurs at these genes *per se* or in their sequence vicinity, this bias suggests two things: (i) forces other than nonallelic homologous recombination of duplicated sequence are likely to be responsible for this variation and (ii) individual humans may differ considerably in the expression or actual complement of such genes. As these genes are involved in a variety of physiological and developmental processes, including medically relevant ones such as cancer (for example, receptor tyrosine kinases) and are frequently targets of therapeutic drugs (for example, voltage-gated ion channels[31]), understanding such differences in the human population is likely to be important in our understanding and treatment of diseases.

Evolutionary mechanisms influencing CNVs

The nonrandom genomic distribution of large CNVs led us to explore the evolutionary processes impacting these variants. Although there is considerable work on the evolutionary fates of gene duplicates[32–34] that is relevant to characterizing many individual loci, these analyses do not explain the spectrum of CNVs in the genome *per se*. Furthermore, these models generally assume that a fundamentally random process underlies the initial generation of duplicated sequence. If particular regions are systematically more or less prone to copy-number mutations for mechanistic reasons, then evolutionary inferences must account for such bias when defining the neutral expectation. Therefore, we undertake a more general exploration and consider to what extent this genomic distribution is likely to be driven by neutral evolutionary processes versus natural selection. Although enforcing a dichotomy between these two is artificial, it provides a context in which to discuss the evolution and population dynamics of CNVs and relate evidence from other analyses. We consider each in turn.

Neutrality of CNVs. A key tenet of a neutralist view of CNVs is that such mutations can exist with weak or no phenotypic consequences. Although it is difficult to establish with certainty that any given mutation does not contribute to a phenotype, several observations support the validity of this prediction. The existence of many CNVs in a large sample of 'normal' individuals indicates that many such mutations confer minimal to no phenotypic consequence within humans. At the very least such variants do not have substantial deleterious effects. More specific albeit anecdotal studies also provide support. An analysis of autistic children and their unaffected parents, for example, found no phenotypic link with a common deletion that effectively eliminates three of the protocadherin genes (discussed above) on chromosome 5 (ref. 35). Also, studies in mice in which large (~1-Mb) deletions are shown to have no major phenotype confirm that even very large variants may be of minimal, or at the very least not seriously deleterious, influence[36]. Finally, very high levels of indel and genomic structural polymorphism are seen in wild-type individuals of the tunicate *Ciona savignyi*, in which 15–20% of all nucleotides are either allele specific or in an inverted orientation when comparing any two homologous chromosomes[37]. This demonstrates that even extreme levels of genomic structural variation are tolerable, if not phenotypically inconsequential, in a healthy, wild population.

Another prediction of the neutralist hypothesis is that the mechanisms that give rise to copy-number mutations are strongly correlated with local genomic features, making particular regions systematically more prone to such mutations. Evidence confirming this prediction is abundant. For example, recent studies show directly that regions flanked by SDs of high sequence similarity are much more likely to harbor copy-number variation than other genomic sites, probably as a result of nonallelic homologous recombination[9,12]. Further evidence for this effect comes from comparisons between the human and chimpanzee genomes: lineage-specific duplications are substantially (~10-fold) more likely to occur in regions near ancestrally duplicated sequence, a phenomenon termed 'duplication shadowing'[17]. The strong correlation between the presence of SDs and the complete collection of known CNVs genome-wide provides further corroboration for a tight mechanistic link.

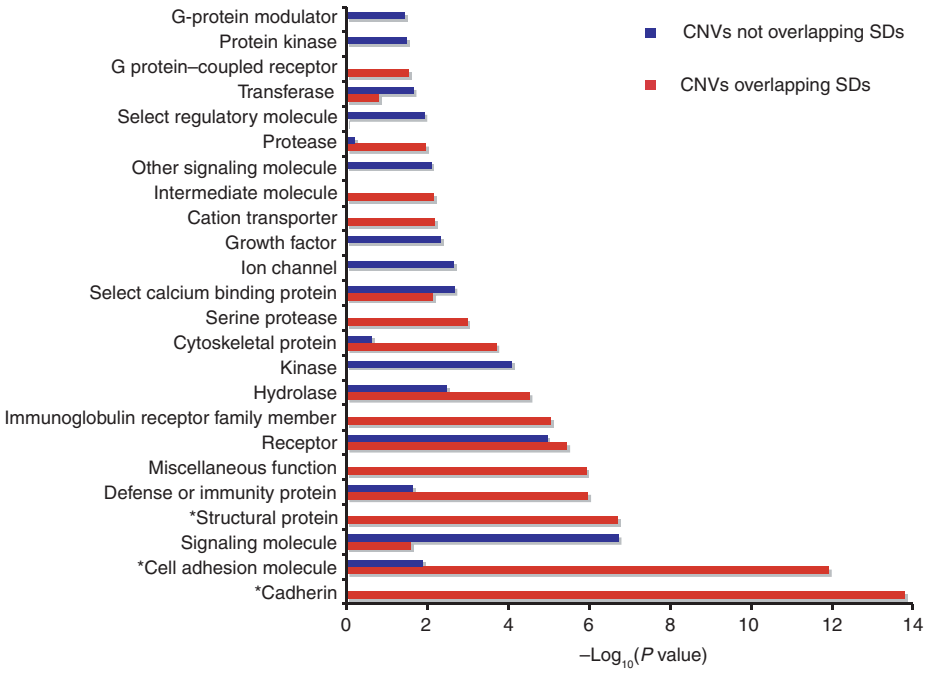


Figure 3 Functional annotation of copy-number variation gene content. Molecular function annotations for the genes affected by either CNVs that overlap SDs (red) or CNVs that do not overlap SDs (blue) were obtained using the PANTHER[25] classification system (see **Supplementary Note**). Negative log transformed *P* values, after Bonferroni adjustment, for the most significantly enriched functional groups are plotted as horizontal bars for each of the molecular functions indicated along the *y* axis. Some molecular functions are commonly enriched (for example, 'receptor'), but others are unique to either category of CNVs, such as 'signaling molecule' or 'serine protease'. Functional annotations with an asterisk show enrichment largely as a result of a few gene clusters (for example, clusters of keratin or protocadherin genes) that harbor CNVs. Note also that these categories are not independent as they share substantial overlap in some cases (for example, cytoskeletal protein, intermediate filament and miscellaneous function).

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Insights from studies of chromosome evolution. Also important to the 'neutralist' perspective are results from analyses of chromosome evolution within mammals. Genome sequence assemblies[38–41] and high-resolution genetic maps of mammalian species have led to the reconstruction of ancestral mammalian karyotypes. Concomitant with such reconstructions are inferences regarding the numbers, types and locations of mutational events that must have occurred to generate the extant karyotypes[42–44]. The most relevant conclusion from these analyses is that the distribution of rearrangement breakpoints throughout evolution is nonrandom, highlighted by the existence of long stretches of genomic sequence being stable and short stretches, known as 'fragile sites', being prone to breakage[45,46]. Some regions are sufficiently unstable as to yield recurrent changes even among the closely related great apes, where a pericentromeric region of human chromosome 16 has been independently inverted in both chimpanzees and gorillas[47]. Furthermore, sites subject to rearrangement 'reuse' throughout mammalian chromosomal evolution are strongly correlated with segmental duplication content[48]. Interestingly, however, it appears that the relationship between SDs and evolutionarily 'fragile sites' is not necessarily causative[49] and may in fact be correlated through another mechanism. In any case, the strong correlations that exist among SDs, CNVs and chromosomal rearrangement hotspots provide substantial evidence that mutational mechanisms can explain much of the distribution of copy-number variation in the genome.

Selective pressure on CNVs: a boost in prior probability. An alternative to the neutralist perspective suggests that natural selection actively influences the distribution of CNVs in the genome. Intuitively, CNVs are highly likely to be subjected to selective pressure. Consider that large variants, in contrast with SNPs and small indels, often affect entire protein-coding genes and substantial amounts of flanking DNA. They may alter gene expression levels through a copy-number effect, duplicate or delete transcriptional regulatory elements for genes both within and near the variant, and also result in hybrid or truncated transcripts[27,28,50–52]. It is also clear that some CNVs contribute to human phenotypes, including many genetic disorders[28,53], color vision[54] (**Fig. 4**), glomerulonephritis[55], Parkinson's disease[56], Alzheimer's disease[57], Crohn's disease[58], hereditary pancreatitis[59], autism[60,61] and HIV-AIDS susceptibility[62]. The fact that large copy-number mutations have a higher likelihood, relative to SNPs and microindels, of altering genomic functionality and contributing to a phenotype increases the prior probability that selection has affected any particular mutation. Although difficult to quantify precisely, this increase in prior probability is likely to be at least several orders of magnitude. For example, of the 297 variant sites identified by Tuzun *et al.*, 6 or 7 (~2%) are thought to influence disease or disease susceptibility, a rate far greater than would be seen for any similar evaluation of SNPs[7].

Evidence for negative and positive selection on CNVs. The effects of negative selection are particularly visible for deletions, as might be expected for loss-of-function alleles: they tend to be at lower frequencies in human populations than other types of variants[6,63] and also tend to be biased away from genes[12]. Negative selection is also likely to contribute to the enrichment in gene-poor regions for CNVs not overlapping SDs (**Fig. 2b**), because such variants would have a lower likelihood of disrupting protein-coding sequence than mutations that arise in gene-rich regions. In fact, although it is possible that mutational mechanisms can explain the bias toward both gene-poor and gene-rich regions of the genome seen for CNVs that are not associated with segmental duplication (**Fig. 2b**, blue bars), such a pattern may instead reflect both negative and positive selective pressures (see below). Furthermore, regions of the genome known to be under intense purifying selection ('ultraconserved' elements[64]) are significantly depleted within CNVs[65]; deletion or amplification of these functionally critical regions probably results in deleterious consequences. Finally, the 'fragile-site' model of chromosome evolution[46] may be at least partially a consequence of purifying selection against breakpoints that disrupt blocks of coregulated genes (for example, *HOX* clusters[66]) or regulatory domains of genes encoding key developmental proteins (for example, *DACH*[67]); this is more of a 'stable-site' model than a 'fragile-site' model, but either mechanism would result in a nonrandom distribution of chromosomal breakpoints.

Adaptive selection is also likely to be a prominent influence on copy-number polymorphisms. One study found evidence for positive selection acting on a large (900-kb) inversion polymorphism, potentially as a consequence of increased fertility[68]. Functional biases in the genes that are associated with CNVs provide an indication of adaptive selection. Many genes affected by CNVs, particularly those variants that overlap

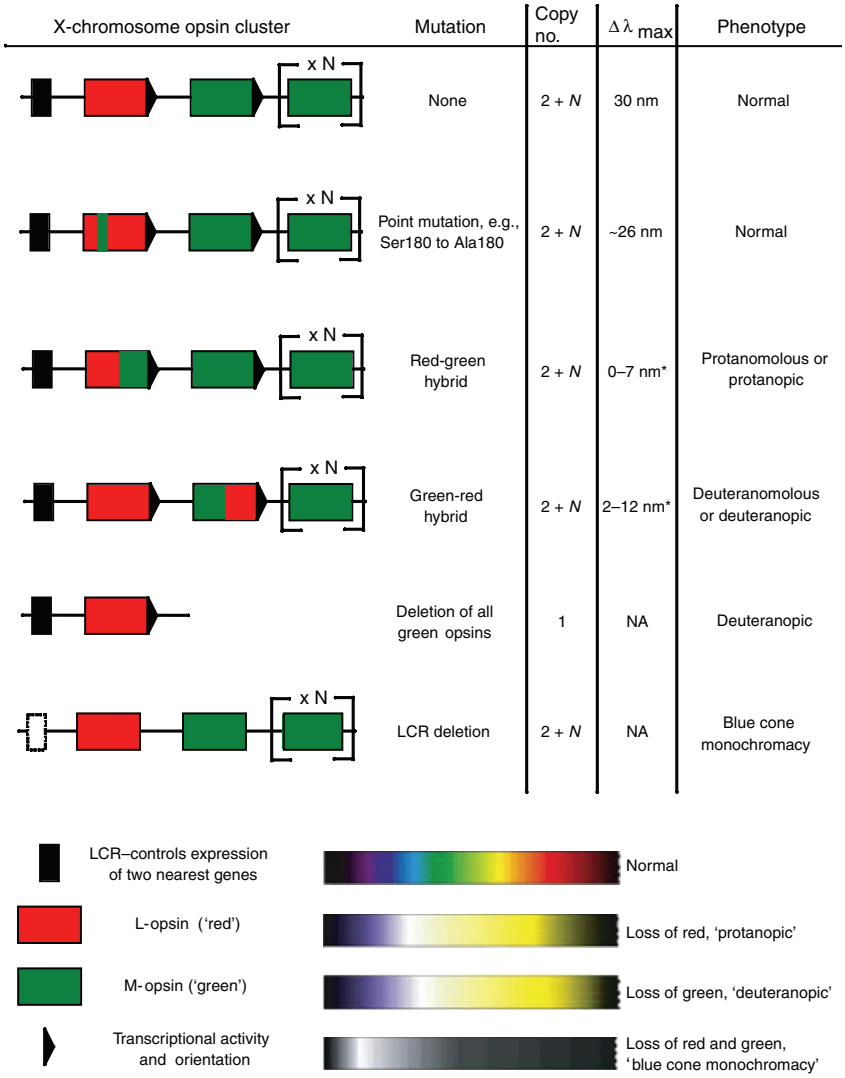


Figure 4 Variation in the X-chromosome opsin locus sequence, structure and resulting phenotype. A locus control region (LCR; black rectangle) activates transcription of the two nearest, and only the two nearest, genes, as indicated by black arrowheads. Normal individuals (first row) have both red and green photopigment genes immediately downstream of the LCR, and a variable number of downstream green opsins. Total copy number (2 + *N*) is polymorphic among humans and typically ranges from 2 to 6; however, variation in copy number by itself does not dictate phenotype. The difference in maximal wavelength absorption ($\Delta\lambda_{max}$; third column) between the two expressed proteins is generally indicative of a person's ability to discriminate colors (fourth column): defects arise when $\Delta\lambda_{max}$ values are small, ranging from moderate (protanomolous and deuteranomolous) to severe (protanopic and deuteranopic) when $\Delta\lambda_{max}$ is near 0. The legend includes simulated images of how these individuals view the color spectrum (from ref. 54). A common SNP alters the red photopigment such that it responds to a wavelength closer to that of the green photopigment (second row). Hybrid opsin genes generated by unequal crossing-over commonly cause defects in color vision (rows three and four); note that a range of $\Delta\lambda_{max}$ values (asterisks in the third column) are observed depending on the crossover breakpoints. Some mutation events result in loss of all green opsins (fifth row). Deletion of the LCR, which is outside of the copy-number variable region, eliminates expression altogether (last row). Figure adapted with permission from figures in ref. 54 and with advice from Samir Deeb.

SDs, belong to categories of environmentally responsive functions such as sensory perception and immunity. These genes have long been considered, and in many cases shown, to be subject to rapid adaptive changes throughout mammalian evolution[39,40]. A variety of studies have also found signatures of positive selection at the level of amino acid replacements within recently duplicated gene families, including the morpheus[69], RanBP2 (ref. 70) and DUF1220 (ref. 71) families, as well as more global elevations of amino acid replacement rates among CNV-affected genes[26].

The associations between CNVs, SDs and genes may reflect a combination of positive and negative selective pressures. Consider the distinctions in gene density observed when CNVs are partitioned according to whether or not they overlap SDs (**Fig. 2b**). CNVs that overlap SDs are enriched for high-frequency events, and SDs are themselves a mixture of both high-frequency CNVs and fixed duplication events. Their lack of enrichment in gene-poor regions, in contrast to that seen for CNVs not overlapping SDs, may be due to a fixation bias between CNVs that arise in gene-poor versus gene-rich regions. Although, on the one hand, copy-number mutations are less likely to be deleterious (and removed by negative selection) in gene-poor regions, resulting in an enrichment in these areas, such events are also less likely to be given a boost in fixation probability by adaptive selection. Those CNVs that affect gene-rich regions without resulting in deleterious effects, on the other hand, would more likely be subjected to adaptive selection and therefore pushed to higher frequency and fixed more often. Although this argument must be tempered by the ability of SDs to induce recurrent mutation events, making them appear to be 'high frequency', such a scenario would explain why SDs and high-frequency CNVs would be enriched in gene-rich regions but not gene-poor regions. At the same time, other copy-number mutations would be enriched in both gene-rich regions (owing to the presence of very young but beneficial variants) and gene-poor regions (owing to variants that are not deleterious but subject to genetic drift).

Unifying the hypotheses. Of course, the reality is that the distribution of CNVs is likely to be a complex product of both mutational and selective effects. Several recent studies highlight this concept. First, one expects that the interplay between neutral and selective effects would be at least partially mediated by variant size. This dynamic has in fact been observed directly in a recent study of children affected by idiopathic mental retardation, where CNVs found in the unaffected parents are several times smaller than the putatively causative variants identified in the affected children[72]. Second, in another study of idiopathic mental retardation, several duplication-mediated regions of genomic instability were discovered in which large, recurrent deletions consistently result in a well defined and dramatic disorder[73]. One of these regions, located on chromosome 17q21.31, corresponded to the same region that is frequently inverted in European populations (see above) and is associated with positive selection and apparently increased fecundity in Icelandic populations[68]. Interestingly, in every case studied thus far, the germline rearrangement associated with disease (under negative selection) occurred in a parent who carried the inverted haplotype (under positive selection)[73–75]. These data indicate that the inversion structure or some other property of the inversion haplotype may act

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as premutation state for disease. Collectively, these studies imply that interactions between biased mutational effects and selective pressures are key influences on the evolution and population dynamics of human genomic structural variation (including both CNV and inversion polymorphisms).

Future directions

Although an impressive knowledge of the copy-number variation landscape has emerged, many unresolved questions and technological challenges remain. First, our current view of this variation is, for the most part, top-down and largely impressionistic. Our reliance on BAC-based arrays or commercial SNP platforms for detecting many of the known variants limits our ability to define the true extent of variation. This has several ramifications. First, many of the common smaller variants (<50 kb) have simply not yet been discovered. Second, lack of resolution in inferring variant breakpoints means that the annotations for many known variants include more DNA than is in reality affected. It will be important to determine which genomic functional elements are internal and external to a given variant, rather than knowing only that they are in the vicinity. The lack of breakpoint resolution also precludes many analyses, particularly evolutionary and population genetic, which need to distinguish between recurrent mutation events and legitimate allele-frequency differences. It is very difficult, if not impossible, to accurately delineate neutral and selective effects on particular loci without such information. Third, although current approaches have had some success in classifying CNVs in the range of 0, 1 or 2 copies, multicopy expansions remain more opaque. Distinguishing between 3, 4 or more copies will ultimately be necessary to characterize variants as to both their potential phenotypic effects and their population genetic and evolutionary histories. Fourth, most of the current technology has not been able to discover balanced rearrangement events, such as inversions, or sequences that are not represented within the human reference genome assembly. Thus, our understanding of genomic structural variation has largely been limited to regions of copy-number difference with respect to the reference genome assembly.

Ultimately, a more careful, sequence-based description of allelic states will be necessary. Consider the examples of gene amplifications that have been subject to adaptive selection pressure[69–71], in which a variety of smaller-scale nucleotide changes (for example, amino acid replacements) accompany copy-number mutations. The red-green opsin gene family also highlights this issue[54] (**Fig. 4**). Although mutation breakpoints and copy number differences are important to predicting the color-vision phenotype, allelic states that differ by single-nucleotide changes, gene order and status of nearby sequence elements are also critical (**Fig. 4**). Mutations at all scales contribute to the genotype, which is the unit that contributes (or fails to contribute) to a change in phenotype. Ultimately, it is the sequence that matters. Future technology development that cost-effectively and comprehensively captures both single-nucleotide and structural variation remains one of the most important goals of human genetics.

Note: Supplementary information is available on the Nature Genetics website.

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COMPETING INTERESTS STATEMENT

The authors declare no competing financial interests.

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Mutational and selective effects on copy-number variants in the human genome

Supplementary Note

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Sequence and annotation data

Analyses were carried out using the human genome assembly hg17 (NCBI build35, May 2004). All sequence and annotations were obtained from the UCSC genome browser (http://genome.ucsc.edu) except where otherwise indicated. Gene annotations used correspond to the 'Known Gene' track, and include coding and UTR exons. Repeats were obtained via UCSC but generated by RepeatMasker (www.repeatmasker.org). *Alus* were identified by by using the "grep" Unix command to identify lines containing 'Alu' from the RepeatMasker annotation output.

We obtained structural variants (mostly copy-number variants; CNVs) annotated by a variety of analyses spanning multiple experimental techniques, populations, and sample sizes; details are listed in Table 1 of the main manuscript. Annotations from the Mills et al study were obtained through that paper's supplemental material (www.genome.org); the Wong et al. annotations were obtained directly from the authors (courtesy of Ze Cheng), and we used only those variants that were seen in more than 1 individual for the subsequent analysis; the Redon et al. annotations were obtained through the Database of Genomic Variants (http://projects.tcag.ca/variation). We then merged all variants > 1 kbp in size that have any amount of overlap, generating a single, non-redundant feature set with 4,131 distinct genomic regions spanning ~613 Mbp; these regions are listed in Supplementary Table 1. This merged set of 'CNVs' is used in all subsequent analyses.

Sliding window analyses

Sliding window density calculations were performed in consecutive non-overlapping 1-Mbp windows with custom perl scripts; we treated the 'overhang' at the end of each chromosome as a whole window. We merged all annotations within a given feature set with any overlap so that each base is counted at most once. We excluded Y, M, unk, and random chromosomes. GC% and N% were determined for these same windows by counting nucleotides. Features that span breakpoints between windows were split accordingly. Supplementary Table 2 lists the density values for each feature within each window across the genome, totaling 3,030 windows.

Density correlations

For these and all following analyses, we eliminated from consideration any window that contains greater than 50% missing sequence, annotated as 'N's in hg17, reducing the total number of windows to 2,852; retaining these windows inflates correlations among features due to co-occurrence of '0' densities. Relationships between feature sets were then grossly evaluated with simple linear regression models using the R programming environment (http://cran.r-project.org/), regressing the per-window CNV density against the per-window density of each listed feature (exons, segmental duplications (SDs), and *Alus*). The *p*-values reported in the first paragraph under "Distribution of copy-number variants in the human genome" correspond to the probability that the per-window densities of these feature pairs are uncorrelated genome-wide. We also regressed CNV density against exon, SD, and *Alu* density simultaneously; each of these variables remain significant at $p < 0.01$. We note that in truth these relationships are complex and non-linear, and thus these models should only be interpreted to mean that there exist strong relationships rather than that the relationships are truly linear. Also see Figures 2 and 3 for more analyses of the relationships between CNVs, genes, and SDs.

Stratification of windows into density deciles

We ranked the per-window density values for each feature set and divided the windows into 10 evenly spaced bins ('deciles'); ties in ranking were broken randomly. Note that we placed all windows with zero density into a separate bin, generating 11 total bins: 10 equal-sized bins of windows containing at least 1 nucleotide of the feature and a zero-density bin consisting of all those windows that are devoid of the feature. This was necessary since some features have a zero-density tail that comprises more than 10% of all windows. 'Rich' and 'poor' fractions of the genome (as in "the most CNV-rich fraction of the genome") correspond to the highest-density bin and the zero-density bin of the genome, respectively. The genome-wide average refers to the average density across all bins. Statistical tests differentiating 'rich' vs 'poor' or 'rich' vs 'average', were conducted using a t-test comparing the designated sets of bins to each other.

Stratification of segmental duplication annotations

For some of the analyses, we subdivided the annotations of SDs according to the percent identities of the paralogous sequence blocks (available in the 'Genomic SuperDup' track at http://genome.ucsc.edu or http://humanparalogy.gs.washington.edu). Since SDs of varying percent identities often overlap with one another, we nested this subdivision such that any base within a segmental duplication was considered to belong to the highest percent identity of all the segmental duplications to which it belongs. In this way, all bases within a duplication of 98-100% identity are parsed out first, bases within 95%-98% are parsed from the remaining nucleotides, and 90%-95% from the regions remaining after these two steps.

Allele frequency comparisons

To compare the 'allele frequencies' for variants that do or do not overlap SDs, we considered only those variants identified in the Redon et al. study via BAC-CGH; we use the 'frequency' count as supplied in the annotations in the Database of Genomic Variants (http://projects.tcag.ca/variation). We then performed a t-test comparing the frequencies for those variants that do overlap SDs versus those that do not, and also compared those variants that overlap 98%-100% identical SDs versus those that do not.

Functional biases in gene content

We used Panther analyses to test for enrichment of functional categories of genes that overlap CNVs; we considered CNVs that do not overlap SDs independently from CNVs that do overlap SDs. We identified genes that overlap these two groups using the Table Browser at UCSC (http://genome.ucsc.edu), with the 'Known Gene' track, mapping them to 'Gene Symbols' to eliminate some of the redundancy of multiple transcripts mapping to the same gene. These lists were uploaded to a published Panther web-tool (http://www.pantherdb.org/; Thomas et al. 2003). We focused on "Molecular Function" annotations, using the set of all annotated human genes as the background set, and used Bonferroni correction for multiple-testing. Both CNVs that overlap SDs and CNVs that do not overlap SDs were depleted for genes with "Molecular function unclassified" and "Ribosomal proteins". All other significant associations are enrichments and are shown in Figure 3 using the arbitrary threshold of 0.05 (after Bonferroni correction).

To check for consistency with an independent classification system, we also performed GO-term analyses using a published web tool (http://gostat.wehi.edu.au/; Beissbarth and Speed 2004). The highest-scoring enrichment categories seen for Panther were largely consistent with the GO results, although differences in the number of genes annotated to specific categories and the organizational hierarchies (GO-terms are richer and more complex), exclude direct correspondence of functional categories in some cases.

For CNVs that overlap SDs, the top-scoring GO-terms (all significant at $p < 0.001$ after correction for multiple testing) indicated enrichment for olfactory receptor activities ('sensory perception of chemical stimulus', 'neurophysiological process', 'sensory perception of smell', etc), cell adhesion activity ('cell-cell adhesion'), and the immune response ('response to pest, pathogen, or parasite', 'response to wounding'), among others. These are similar to the enrichments seen using Panther in Figure 4 (olfactory receptor enrichment can be seen indirectly with Panther in 'receptor' and 'G-protein coupled receptor').

For CNVs that do not overlap SDs, GO-terms strongly confirmed the enrichments seen using Panther. Again using a multiple testing correction and threshold of $p < 0.001$, GO-term enrichments include signaling molecules ('development-morphogenesis', 'cell-cell signaling', 'signal transduction', 'embryonic development', etc), calcium binding proteins ('calcium ion binding'), and kinase activity ('protein serine/threonine kinase activity'), among others.

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Chr*	Start	Stop	Count**
chr1	377	1058627	8
chr1	1193016	1197883	1
chr1	1239243	1359795	1
chr1	1409796	2056500	3
chr1	2081232	2356539	2
chr1	2408416	2412411	1
chr1	2488752	2521167	1
chr1	2615721	2623251	3
chr1	2636643	2641218	1
chr1	2642730	2648431	1
chr1	2650139	2665166	5
chr1	2946306	3034294	1
chr1	3149962	3572010	5
chr1	3600497	3743996	2
chr1	3783062	3784419	1
chr1	4357954	4579734	1
chr1	5200140	5470944	1
chr1	5824356	6057323	2
chr1	6123617	6258744	1
chr1	6423652	6599669	2
chr1	6636417	6738013	1
chr1	7425623	7622325	2
chr1	7790663	7799206	1
chr1	8137673	8288423	1
chr1	8511882	8515501	1
chr1	8680537	8850906	2
chr1	9696862	9700374	1
chr1	10172336	10516820	5
chr1	10638954	11057241	5
chr1	12149530	12365909	1
chr1	12533434	13709230	9
chr1	14050388	14117706	1
chr1	15232750	15235630	1
chr1	15246185	15255968	1
chr1	15395307	15600631	1
chr1	15678279	15683728	1
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chrY	57491257	57649991	1

UCSC BED format (http://genome.ucsc.edu)
o the number of distinct annotations (from any source within Table 1) that overlapped thi

s interval

Chr	Window	N %	GC %	Repeat %	Alu %	Exon %
chr1	0	0.2	0.367152	0.347985	0.087134	0.027638
chr1	1	0.1	0.515449	0.328107	0.200611	0.103625
chr1	2	0.05	0.551608	0.243594	0.069092	0.052106
chr1	3	0.06	0.531766	0.212762	0.063085	0.043763
chr1	4	0	0.476987	0.420283	0.050301	0.002634
chr1	5	0.06	0.445509	0.39874	0.050328	0.009666
chr1	6	0	0.515581	0.400816	0.2155	0.071696
chr1	7	0	0.477829	0.411675	0.12151	0.02708
chr1	8	0	0.445757	0.468273	0.266713	0.015491
chr1	9	0	0.501281	0.495338	0.31109	0.044334
chr1	10	0	0.480678	0.432622	0.266564	0.037517
chr1	11	0	0.500756	0.457263	0.237197	0.062461
chr1	12	0	0.465776	0.471416	0.194847	0.047894
chr1	13	0.1	0.410045	0.467938	0.195583	0.028831
chr1	14	0	0.443172	0.441401	0.092417	0.000963
chr1	15	0	0.484472	0.455226	0.255284	0.056268
chr1	16	0.05	0.472145	0.406977	0.199267	0.051212
chr1	17	0	0.508876	0.470914	0.190724	0.041185
chr1	18	0	0.49617	0.417371	0.078885	0.012318
chr1	19	0	0.474893	0.443278	0.206393	0.067596
chr1	20	0	0.466346	0.508237	0.166039	0.047378
chr1	21	0	0.473582	0.474566	0.240198	0.042634
chr1	22	0	0.498163	0.451867	0.1507	0.026653
chr1	23	0	0.462029	0.518456	0.288197	0.054449
chr1	24	0	0.462591	0.502717	0.230554	0.056453
chr1	25	0.05	0.45837	0.449382	0.175855	0.03513
chr1	26	0	0.485438	0.507009	0.308321	0.065555
chr1	27	0	0.487605	0.522085	0.296746	0.066818
chr1	28	0.2	0.364567	0.488954	0.337099	0.02413
chr1	29	0.005	0.466963	0.491548	0.155751	0.018823
chr1	30	0	0.483389	0.518294	0.046521	0.008378
chr1	31	0	0.475568	0.492988	0.22836	0.047518
chr1	32	0	0.466141	0.56408	0.360084	0.060479
chr1	33	0	0.463206	0.451712	0.111585	0.049321
chr1	34	0	0.449387	0.472908	0.054347	0.012272
chr1	35	0	0.429187	0.541139	0.261738	0.053603
chr1	36	0	0.47436	0.455668	0.204855	0.046233
chr1	37	0	0.47562	0.42583	0.126274	0.037229
chr1	38	0	0.45738	0.477633	0.122587	0.016843
chr1	39	0	0.454208	0.473048	0.264509	0.04824
chr1	40	0	0.446468	0.507254	0.239275	0.053322
chr1	41	0	0.46767	0.468966	0.105457	0.021622
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chr1	43	0	0.46859	0.496378	0.163314	0.05753
chr1	44	0	0.477492	0.433235	0.184579	0.044016
chr1	45	0.05	0.409834	0.588205	0.280244	0.039134
chr1	46	0	0.454212	0.498678	0.187859	0.062111
chr1	47	0	0.449034	0.510662	0.103579	0.03258

chr1	48	0	0.429249	0.494638	0.043341	0.016301
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chr1	59	0	0.411193	0.476685	0.047421	0.004177
chr1	60	0	0.380908	0.507958	0.03759	0.008195
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chr1	68	0	0.389599	0.494464	0.067409	0.013247
chr1	69	0	0.366059	0.512023	0.041335	0.000627
chr1	70	0	0.372672	0.460419	0.104247	0.020784
chr1	71	0	0.366771	0.417732	0.045289	0.01307
chr1	72	0	0.347043	0.396304	0.045694	0.000603
chr1	73	0	0.351348	0.520727	0.03734	0
chr1	74	0	0.361925	0.402328	0.036337	0.025389
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chr1	77	0	0.38768	0.480298	0.108569	0.022151
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chr1	83	0	0.374383	0.391385	0.033882	0
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chr1	113	0	0.410869	0.555832	0.185466	0.017308
chr1	114	0	0.415163	0.458203	0.153157	0.058801
chr1	115	0	0.408976	0.489172	0.060609	0.022568
chr1	116	0	0.422354	0.413713	0.080954	0.024543
chr1	117	0	0.417812	0.450435	0.087903	0.036666
chr1	118	0	0.376814	0.509678	0.042749	0.01452
chr1	119	0	0.41366	0.426963	0.058167	0.019532
chr1	120	0.1	0.36325	0.39022	0.071502	0.029382
chr1	121	0.902524	0.041663	0.097018	0	0
chr1	122	1	0	0	0	0
chr1	123	1	0	0	0	0
chr1	124	1	0	0	0	0
chr1	125	1	0	0	0	0
chr1	126	1	0	0	0	0
chr1	127	1	0	0	0	0
chr1	128	1	0	0	0	0
chr1	129	1	0	0	0	0
chr1	130	1	0	0	0	0
chr1	131	1	0	0	0	0
chr1	132	1	0	0	0	0
chr1	133	1	0	0	0	0
chr1	134	1	0	0	0	0
chr1	135	1	0	0	0	0
chr1	136	1	0	0	0	0
chr1	137	1	0	0	0	0
chr1	138	1	0	0	0	0
chr1	139	1	0	0	0	0
chr1	140	1	0	0	0	0
chr1	141	0.708377	0.118441	0.117587	0.036148	0.00066
chr1	142	0.129099	0.364282	0.339874	0.110295	0.034712
chr1	143	0.1	0.380386	0.418011	0.118696	0.051373
chr1	144	0.05	0.398021	0.481983	0.093112	0.016655
chr1	145	0.25	0.305787	0.316911	0.070039	0.014352

chr1	146	0.1	0.382422	0.400055	0.154611	0.044645
chr1	147	0	0.448997	0.515446	0.361823	0.09387
chr1	148	0	0.446927	0.453221	0.202228	0.076899
chr1	149	0	0.408109	0.482774	0.03245	0.054307
chr1	150	0	0.463629	0.48866	0.257917	0.069817
chr1	151	0	0.488406	0.426257	0.211632	0.090005
chr1	152	0	0.465667	0.529286	0.346114	0.095644
chr1	153	0	0.494356	0.364303	0.174856	0.081599
chr1	154	0	0.42152	0.518409	0.059891	0.035315
chr1	155	0	0.382584	0.490215	0.043684	0.041839
chr1	156	0	0.42441	0.431869	0.057735	0.056134
chr1	157	0	0.441341	0.498783	0.158213	0.087903
chr1	158	0	0.431217	0.424784	0.120539	0.039174
chr1	159	0	0.399567	0.447082	0.091752	0.033084
chr1	160	0	0.372464	0.503921	0.035573	0.001981
chr1	161	0	0.409132	0.364304	0.068814	0.005334
chr1	162	0	0.423893	0.44005	0.096789	0.01416
chr1	163	0	0.399755	0.487246	0.068431	0.016518
chr1	164	0	0.417678	0.451236	0.14575	0.036862
chr1	165	0	0.397119	0.431912	0.055752	0.008533
chr1	166	0	0.378042	0.454595	0.061214	0.036082
chr1	167	0	0.38065	0.488252	0.054874	0.024781
chr1	168	0	0.393442	0.47952	0.120051	0.023589
chr1	169	0	0.385278	0.465319	0.042432	0.022
chr1	170	0	0.397008	0.560665	0.160253	0.032709
chr1	171	0	0.393866	0.50678	0.10956	0.025523
chr1	172	0	0.412653	0.420621	0.075538	0.009411
chr1	173	0	0.402971	0.366332	0.037597	0.01887
chr1	174	0	0.400258	0.456269	0.055366	0.008763
chr1	175	0	0.410253	0.451805	0.171164	0.038009
chr1	176	0	0.413003	0.483579	0.143171	0.044
chr1	177	0	0.41374	0.479105	0.120139	0.02101
chr1	178	0	0.425763	0.437247	0.059991	0.013497
chr1	179	0	0.418063	0.4316	0.142177	0.05339
chr1	180	0	0.406784	0.411953	0.094025	0.026907
chr1	181	0	0.391921	0.42023	0.110953	0.038585
chr1	182	0	0.375407	0.4073	0.059742	0.020942
chr1	183	0	0.362871	0.442651	0.069477	0.025886
chr1	184	0	0.354277	0.468275	0.046801	0.002387
chr1	185	0	0.340713	0.49179	0.041796	0
chr1	186	0	0.338437	0.463092	0.04573	0.002416
chr1	187	0	0.338484	0.493621	0.042497	0.000468
chr1	188	0	0.345035	0.476281	0.048833	0.002143
chr1	189	0	0.367133	0.421011	0.071775	0.018675
chr1	190	0	0.360592	0.471923	0.045722	0
chr1	191	0	0.341339	0.472229	0.054019	0
chr1	192	0	0.345261	0.502933	0.043177	0.00338
chr1	193	0	0.35019	0.457059	0.046853	0.041857
chr1	194	0	0.366182	0.41096	0.056495	0.018608

chr1	195	0	0.35691	0.367981	0.044044	0.007897
chr1	196	0	0.386547	0.471088	0.129773	0.005082
chr1	197	0	0.445418	0.399064	0.175891	0.041693
chr1	198	0	0.490218	0.381384	0.181699	0.056876
chr1	199	0	0.450152	0.382403	0.148265	0.062366
chr1	200	0	0.466433	0.44501	0.209114	0.055908
chr1	201	0	0.470233	0.373953	0.149727	0.068308
chr1	202	0.1	0.415068	0.365847	0.134831	0.046279
chr1	203	0	0.43219	0.398472	0.086977	0.060573
chr1	204	0	0.430581	0.328935	0.066281	0.032017
chr1	205	0	0.405901	0.416525	0.06442	0
chr1	206	0	0.416913	0.429712	0.087237	0.034652
chr1	207	0	0.412706	0.481973	0.103917	0.023487
chr1	208	0	0.427238	0.489666	0.172929	0.027895
chr1	209	0	0.423244	0.460222	0.145281	0.027474
chr1	210	0	0.412591	0.328302	0.059935	0.011275
chr1	211	0	0.382605	0.432496	0.071485	0.014423
chr1	212	0	0.363957	0.38081	0.049754	0.024118
chr1	213	0	0.381052	0.306999	0.059669	0.006597
chr1	214	0	0.375071	0.392095	0.098264	0.007671
chr1	215	0	0.376598	0.432631	0.052125	0.001745
chr1	216	0	0.394247	0.428959	0.115168	0.023932
chr1	217	0	0.396678	0.44653	0.063213	0.019307
chr1	218	0	0.397975	0.444944	0.053145	0.005584
chr1	219	0.05	0.395781	0.405919	0.102732	0.026584
chr1	220	0.05	0.40985	0.458222	0.219843	0.030515
chr1	221	0	0.407304	0.540461	0.07976	0.021193
chr1	222	0	0.449802	0.485126	0.252849	0.034285
chr1	223	0	0.433294	0.443967	0.131436	0.023843
chr1	224	0	0.493406	0.45959	0.096244	0.081977
chr1	225	0	0.452294	0.471563	0.132269	0.030046
chr1	226	0	0.441785	0.438165	0.102497	0.020019
chr1	227	0	0.43052	0.435143	0.12722	0.049075
chr1	228	0	0.419366	0.395023	0.07673	0.022423
chr1	229	0	0.410496	0.410475	0.098653	0.02155
chr1	230	0	0.413752	0.463337	0.096104	0.011211
chr1	231	0.05	0.416899	0.402562	0.209329	0.027927
chr1	232	0	0.430033	0.484594	0.20727	0.036956
chr1	233	0	0.405652	0.396992	0.132044	0.024633
chr1	234	0	0.381902	0.426849	0.081273	0.014527
chr1	235	0	0.365868	0.454713	0.070891	0
chr1	236	0	0.394231	0.37432	0.106789	0.012354
chr1	237	0	0.397727	0.431684	0.135413	0.003929
chr1	238	0	0.40505	0.462714	0.146485	0.023458
chr1	239	0	0.402822	0.426347	0.128585	0.01264
chr1	240	0	0.404393	0.426864	0.11655	0.015252
chr1	241	0	0.433564	0.499729	0.209896	0.023064
chr1	242	0	0.415942	0.394812	0.105939	0.00441
chr1	243	0	0.433209	0.536889	0.185583	0.037792

chr1	244	0	0.37934	0.544838	0.047455	0.035265
chr1	245	0.24863823	0.31123195	0.39309704	0.04971808	0.04058732
chr10	0	0.05	0.43311	0.342155	0.093295	0.023522
chr10	1	0	0.458585	0.302167	0.065174	0.032521
chr10	2	0	0.403558	0.355421	0.06549	0
chr10	3	0	0.443603	0.321021	0.096281	0.008129
chr10	4	0	0.389531	0.386661	0.06285	0.003021
chr10	5	0.05	0.410845	0.442885	0.105035	0.03944
chr10	6	0	0.438636	0.430272	0.136866	0.022584
chr10	7	0	0.425878	0.37099	0.131459	0.020361
chr10	8	0	0.401886	0.341874	0.118293	0.005284
chr10	9	0	0.361096	0.427228	0.061269	0
chr10	10	0	0.387677	0.420324	0.076555	0
chr10	11	0	0.438816	0.342797	0.129097	0.016145
chr10	12	0	0.448087	0.471014	0.279203	0.020487
chr10	13	0	0.442496	0.443201	0.212346	0.025622
chr10	14	0	0.42627	0.39581	0.134563	0.016165
chr10	15	0	0.420943	0.449164	0.19405	0.019664
chr10	16	0	0.39878	0.473193	0.134896	0.014347
chr10	17	0	0.399696	0.449317	0.15324	0.034893
chr10	18	0.05	0.382184	0.425389	0.157903	0.01981
chr10	19	0	0.365364	0.466367	0.083327	0.00308
chr10	20	0	0.378619	0.421971	0.081788	0.002761
chr10	21	0	0.41006	0.450628	0.201229	0.013275
chr10	22	0	0.396565	0.457144	0.122136	0.014661
chr10	23	0	0.405878	0.511485	0.142227	0.01001
chr10	24	0	0.404065	0.414788	0.123267	0.0167
chr10	25	0	0.391598	0.488431	0.130212	0.015734
chr10	26	0	0.400217	0.463133	0.12995	0.01958
chr10	27	0	0.398892	0.492217	0.188781	0.027955
chr10	28	0	0.39732	0.44266	0.163239	0.013646
chr10	29	0	0.426596	0.409149	0.161642	0.015589
chr10	30	0	0.434209	0.479924	0.19766	0.01741
chr10	31	0	0.404623	0.455745	0.089397	0.017523
chr10	32	0	0.402294	0.578927	0.172875	0.024278
chr10	33	0	0.403686	0.45232	0.095256	0.016031
chr10	34	0	0.404955	0.338026	0.129453	0.005623
chr10	35	0	0.431688	0.458551	0.234703	0.014829
chr10	36	0	0.390584	0.440406	0.106139	0
chr10	37	1.00E-06	0.387509	0.481197	0.124623	0.004447
chr10	38	0.05	0.385936	0.556	0.128708	0.028986
chr10	39	0.805059	0.076184	0.144335	0.01542	0.00132
chr10	40	1	0	0	0	0
chr10	41	0.724941	0.10418	0.231957	0.002148	0
chr10	42	0	0.433168	0.54771	0.105711	0.024431
chr10	43	0	0.451795	0.491419	0.132768	0.021865
chr10	44	0	0.42989	0.460883	0.04871	0.017206
chr10	45	0.15	0.355857	0.44278	0.099062	0.023805
chr10	46	0.15	0.357479	0.375569	0.121133	0.015672

chr10	47	0.3	0.310034	0.287267	0.065627	0.011342
chr10	48	0.15	0.364643	0.353355	0.075189	0.017204
chr10	49	0	0.445064	0.387723	0.042393	0.022484
chr10	50	0.05	0.41291	0.412228	0.087528	0.026014
chr10	51	0.05	0.385076	0.400683	0.12926	0.034567
chr10	52	0	0.378031	0.335611	0.057593	0.006383
chr10	53	0	0.365947	0.377379	0.062732	0.009222
chr10	54	2.00E-06	0.366699	0.495676	0.054617	0.003568
chr10	55	0	0.351962	0.435941	0.056202	0.007995
chr10	56	0	0.342909	0.412492	0.047028	0.000486
chr10	57	0	0.347075	0.493386	0.042279	0.001851
chr10	58	0	0.35091	0.501206	0.038235	0
chr10	59	1.00E-06	0.373273	0.488882	0.06333	0.007277
chr10	60	0	0.382687	0.398196	0.048544	0.007164
chr10	61	1.00E-06	0.390674	0.363197	0.097637	0.031595
chr10	62	0	0.37834	0.412386	0.056567	0.013313
chr10	63	2.00E-06	0.38507	0.380224	0.076746	0.015676
chr10	64	1.00E-06	0.401624	0.437149	0.161114	0.020176
chr10	65	0	0.387491	0.457826	0.077331	0.002029
chr10	66	0	0.35237	0.510441	0.051324	0
chr10	67	0	0.355173	0.476078	0.069013	0.001657
chr10	68	0	0.363106	0.433092	0.057935	0.00628
chr10	69	0	0.408027	0.539391	0.268063	0.039866
chr10	70	0	0.446233	0.511502	0.312642	0.042138
chr10	71	0	0.478932	0.418455	0.137239	0.034548
chr10	72	0	0.493091	0.401115	0.072236	0.024844
chr10	73	0	0.476578	0.446637	0.209303	0.044135
chr10	74	0	0.401852	0.545307	0.255434	0.041442
chr10	75	0	0.420133	0.455001	0.232069	0.042565
chr10	76	0	0.433396	0.480311	0.206735	0.021242
chr10	77	0	0.408615	0.330378	0.049537	0.00089
chr10	78	0	0.420042	0.356678	0.051925	0.014147
chr10	79	0	0.468614	0.41952	0.110383	0.017184
chr10	80	0	0.499988	0.35481	0.056245	0.016978
chr10	81	0.01	0.418039	0.497096	0.108342	0.015925
chr10	82	0	0.413659	0.513965	0.090599	0.021278
chr10	83	0	0.366568	0.508604	0.050619	0
chr10	84	0	0.374435	0.409823	0.058717	0
chr10	85	0	0.394488	0.531285	0.061923	0.011219
chr10	86	0	0.399883	0.514168	0.073683	0.009418
chr10	87	0	0.42028	0.468042	0.031664	0.005513
chr10	88	0	0.448935	0.484211	0.204952	0.032549
chr10	89	0	0.392525	0.428895	0.093201	0.020464
chr10	90	0	0.37551	0.383069	0.046271	0.027354
chr10	91	0	0.391091	0.492407	0.070193	0.028714
chr10	92	0	0.389179	0.496284	0.050275	0.012106
chr10	93	0	0.395879	0.464635	0.128598	0.033486
chr10	94	0	0.415937	0.532518	0.246909	0.028115
chr10	95	0	0.420613	0.421393	0.129909	0.029001

chr10	96	0	0.391387	0.66107	0.113805	0.026966
chr10	97	0	0.414621	0.43299	0.127794	0.03495
chr10	98	0	0.441765	0.394162	0.154366	0.046544
chr10	99	0	0.467689	0.456014	0.187446	0.05689
chr10	100	0	0.404579	0.511728	0.078522	0.014799
chr10	101	0	0.426981	0.487112	0.190239	0.043974
chr10	102	0	0.479204	0.384677	0.175481	0.062107
chr10	103	0	0.450856	0.417532	0.23769	0.042464
chr10	104	0	0.457935	0.470367	0.280772	0.055103
chr10	105	0	0.460556	0.408727	0.170731	0.060818
chr10	106	0	0.417702	0.360832	0.058162	0.013306
chr10	107	0	0.376914	0.4496	0.044057	0.002425
chr10	108	0	0.390842	0.397528	0.096558	0.007573
chr10	109	0	0.370472	0.511929	0.04114	0
chr10	110	0	0.375824	0.481742	0.043685	0
chr10	111	0	0.403961	0.473522	0.081535	0.009035
chr10	112	0	0.42202	0.400929	0.098761	0.027298
chr10	113	0	0.404324	0.439829	0.0443	0.006368
chr10	114	0	0.422651	0.324543	0.120993	0.010949
chr10	115	0	0.422609	0.361669	0.095925	0.045457
chr10	116	1.00E-06	0.414008	0.411135	0.123108	0.027198
chr10	117	0	0.378865	0.443467	0.04882	0.003544
chr10	118	0	0.423836	0.405297	0.106714	0.028543
chr10	119	0	0.422391	0.352357	0.070721	0.019566
chr10	120	0	0.434735	0.450289	0.148892	0.025016
chr10	121	0	0.448415	0.442186	0.153865	0.026824
chr10	122	0	0.418675	0.409266	0.05877	0.008941
chr10	123	0	0.444958	0.388071	0.159923	0.019951
chr10	124	0	0.438725	0.354813	0.072514	0.044673
chr10	125	0.05	0.442838	0.335856	0.049646	0.015916
chr10	126	0	0.481738	0.369881	0.176767	0.030653
chr10	127	0	0.426751	0.386812	0.082091	0.024932
chr10	128	0.05	0.412806	0.354476	0.072761	0.014207
chr10	129	0	0.44498	0.346471	0.067678	0.022732
chr10	130	0	0.437778	0.267644	0.036998	0
chr10	131	0	0.462552	0.308264	0.062583	0.008953
chr10	132	0	0.472456	0.35607	0.046277	0.002616
chr10	133	0.06	0.473317	0.333669	0.060128	0.018588
chr10	134	0.05	0.536606	0.249536	0.044289	0.05079
chr10	135	0	0.49647389	0.48895508	0.07454748	0.0620411
chr11	0	0.05	0.52066	0.371627	0.182593	0.107198
chr11	1	0.016576	0.55884	0.318356	0.08694	0.050826
chr11	2	0	0.531708	0.362482	0.05848	0.042975
chr11	3	0	0.469509	0.493587	0.183273	0.032513
chr11	4	0	0.399128	0.475736	0.061434	0.034134
chr11	5	0	0.38372	0.435554	0.053646	0.046152
chr11	6	0	0.419804	0.486844	0.076073	0.070461
chr11	7	0	0.404302	0.480772	0.052615	0.026439
chr11	8	0	0.445287	0.421592	0.108242	0.035334

chr11	9	0	0.422123	0.531904	0.271786	0.033244
chr11	10	0	0.416917	0.481911	0.104022	0.02702
chr11	11	0	0.431486	0.394149	0.042548	0.019047
chr11	12	0	0.434513	0.384699	0.0851	0.026506
chr11	13	0	0.408	0.487981	0.060068	0.015515
chr11	14	0	0.398662	0.507205	0.100312	0.015065
chr11	15	0	0.415154	0.397547	0.033771	0.002926
chr11	16	0	0.387443	0.409612	0.079859	0.008339
chr11	17	0	0.450577	0.450334	0.132856	0.036749
chr11	18	0	0.423092	0.520769	0.171271	0.044522
chr11	19	0	0.435164	0.383373	0.051785	0.015332
chr11	20	0	0.407643	0.440099	0.082562	0.017333
chr11	21	0	0.37058	0.480281	0.039358	0.002695
chr11	22	0	0.364825	0.472512	0.048847	0.015743
chr11	23	0	0.358574	0.515168	0.047071	0
chr11	24	0	0.352781	0.472656	0.045344	0.005786
chr11	25	0	0.352095	0.506705	0.038669	0.004254
chr11	26	0	0.365228	0.429168	0.047542	0.013996
chr11	27	0	0.394889	0.430744	0.067444	0.021414
chr11	28	0	0.365731	0.438206	0.040057	0.006675
chr11	29	0	0.367246	0.47183	0.033196	0.003613
chr11	30	0	0.383446	0.405363	0.047105	0.009018
chr11	31	0	0.377608	0.388146	0.072357	0.009899
chr11	32	0	0.411866	0.49598	0.161523	0.015422
chr11	33	0	0.419598	0.439219	0.16802	0.032016
chr11	34	0	0.423409	0.42184	0.114379	0.028923
chr11	35	0	0.419333	0.394394	0.069265	0.027029
chr11	36	0	0.412276	0.413527	0.064343	0.026149
chr11	37	0	0.355025	0.484419	0.034195	0
chr11	38	0	0.352022	0.51227	0.047037	0
chr11	39	0	0.365109	0.517286	0.080014	0
chr11	40	0	0.367285	0.408672	0.056199	0.006762
chr11	41	0	0.368164	0.464356	0.05406	0
chr11	42	0	0.376804	0.526078	0.049811	0
chr11	43	0	0.407597	0.457904	0.101359	0.012754
chr11	44	0	0.476554	0.41119	0.084213	0.015668
chr11	45	0	0.473347	0.40861	0.086808	0.037969
chr11	46	0	0.447633	0.443497	0.240216	0.047593
chr11	47	0	0.466251	0.521944	0.338738	0.055044
chr11	48	0	0.391743	0.671647	0.053639	0.010403
chr11	49	0	0.365425	0.444412	0.055413	0.004494
chr11	50	0.207	0.303769	0.654583	0.049312	0.001004
chr11	51	0.549219	0.16907	0.382958	0.005936	0.000948
chr11	52	1	0	0	0	0
chr11	53	1	0	0	0	0
chr11	54	0.450781	0.202635	0.440219	0.007747	0.003466
chr11	55	0	0.359334	0.475604	0.044557	0.035531
chr11	56	0	0.410954	0.498096	0.061436	0.029629
chr11	57	0	0.416998	0.542384	0.149242	0.044422

chr11	58	0	0.3972	0.547838	0.045442	0.027038
chr11	59	0	0.400185	0.501054	0.115456	0.04004
chr11	60	0	0.466167	0.481293	0.1472	0.055964
chr11	61	0	0.499265	0.467421	0.193705	0.051126
chr11	62	0	0.452265	0.588051	0.185674	0.08863
chr11	63	0	0.512868	0.450649	0.244865	0.068743
chr11	64	0	0.520541	0.424484	0.228233	0.097438
chr11	65	0	0.511378	0.486016	0.240275	0.113111
chr11	66	0	0.503604	0.469022	0.298325	0.093028
chr11	67	0	0.496315	0.525101	0.210743	0.040984
chr11	68	0.002605	0.49421	0.439093	0.138967	0.028102
chr11	69	0.017888	0.496642	0.404531	0.154799	0.034903
chr11	70	0	0.507239	0.403081	0.103898	0.023944
chr11	71	0	0.455972	0.530886	0.169042	0.039819
chr11	72	0	0.463941	0.452124	0.151188	0.04248
chr11	73	0	0.424145	0.5483	0.219946	0.047935
chr11	74	0	0.466262	0.471009	0.129665	0.040321
chr11	75	0	0.437836	0.481604	0.124388	0.024557
chr11	76	0	0.450175	0.518504	0.123652	0.033922
chr11	77	0	0.418551	0.547694	0.220578	0.02843
chr11	78	0	0.438885	0.402112	0.046793	0.008974
chr11	79	0	0.385322	0.461529	0.044339	0
chr11	80	0	0.361035	0.397897	0.042894	0
chr11	81	0	0.361679	0.543211	0.039616	0
chr11	82	0	0.398417	0.501492	0.10214	0.029439
chr11	83	0	0.370532	0.39268	0.063274	0.002712
chr11	84	0	0.367748	0.530232	0.040831	0.000767
chr11	85	0	0.402722	0.447917	0.123522	0.03252
chr11	86	0	0.396542	0.496591	0.090217	0.018509
chr11	87	0.012	0.370517	0.502313	0.038146	0.007029
chr11	88	0	0.355539	0.452377	0.042912	0.005868
chr11	89	0	0.369087	0.421464	0.070043	0.011324
chr11	90	0	0.352131	0.51365	0.035836	0
chr11	91	0	0.381992	0.401613	0.04151	0.003607
chr11	92	0	0.400753	0.446885	0.059261	0.02234
chr11	93	0	0.407152	0.512295	0.09805	0.044303
chr11	94	0	0.405421	0.413797	0.046803	0.016257
chr11	95	0.015562	0.378235	0.39694	0.067093	0.025814
chr11	96	0	0.361317	0.540798	0.032607	0
chr11	97	0	0.353914	0.539919	0.067769	0
chr11	98	0	0.349679	0.443275	0.055899	0.000394
chr11	99	0	0.36289	0.453281	0.040254	0.00377
chr11	100	0	0.379548	0.455612	0.068588	0.013237
chr11	101	0	0.39201	0.503187	0.126869	0.031779
chr11	102	0	0.374367	0.457166	0.073791	0.019178
chr11	103	0	0.369114	0.416001	0.042365	0.00644
chr11	104	0	0.357183	0.472171	0.046819	0.007336
chr11	105	0	0.367557	0.429616	0.049245	0.014394
chr11	106	0	0.370617	0.480769	0.05863	0.010318

chr11	107	0	0.406851	0.543888	0.237157	0.048137
chr11	108	0	0.384007	0.498449	0.061255	0.005526
chr11	109	0	0.393984	0.484094	0.106517	0.013356
chr11	110	0	0.402411	0.414724	0.063956	0.020712
chr11	111	0	0.420683	0.443896	0.146164	0.034213
chr11	112	0	0.432892	0.348065	0.045331	0.012634
chr11	113	0	0.432339	0.417965	0.117829	0.030698
chr11	114	0	0.408904	0.361148	0.050397	0.011185
chr11	115	0	0.449897	0.407017	0.057776	0
chr11	116	0	0.462182	0.421348	0.18193	0.047614
chr11	117	0	0.464379	0.386247	0.138273	0.073054
chr11	118	0	0.483836	0.486259	0.24371	0.08312
chr11	119	0	0.478847	0.348459	0.080838	0.030481
chr11	120	0	0.438113	0.420988	0.078942	0.019475
chr11	121	0	0.397803	0.456171	0.072984	0.001464
chr11	122	0	0.445132	0.430948	0.206202	0.020228
chr11	123	0	0.383988	0.487074	0.058466	0.035303
chr11	124	0	0.449087	0.410746	0.10433	0.055098
chr11	125	0	0.455297	0.420567	0.12091	0.038921
chr11	126	0	0.41747	0.349682	0.042162	0.000356
chr11	127	0	0.391879	0.414044	0.04251	0.005491
chr11	128	0	0.419869	0.4228	0.066653	0.027009
chr11	129	0	0.44313	0.47937	0.152701	0.038475
chr11	130	0	0.427941	0.379656	0.042268	0.010002
chr11	131	0	0.423344	0.336854	0.034194	0.013588
chr11	132	0	0.420274	0.318093	0.038073	0.000695
chr11	133	0	0.470623	0.376656	0.059993	0.044531
chr11	134	0	0.45329752	0.39894338	0.03430264	0.00320081
chr12	0	0.016	0.443617	0.444387	0.197002	0.033493
chr12	1	0	0.424951	0.403228	0.146682	0.028454
chr12	2	0	0.477224	0.342892	0.110392	0.030761
chr12	3	0	0.469281	0.390536	0.086125	0.023992
chr12	4	0	0.428447	0.424332	0.089861	0.029098
chr12	5	0	0.438777	0.367869	0.043319	0.01431
chr12	6	2.00E-06	0.498258	0.422795	0.24119	0.093897
chr12	7	0.073	0.392709	0.555742	0.193326	0.046874
chr12	8	0	0.432612	0.54862	0.194787	0.048208
chr12	9	0	0.399351	0.506463	0.07133	0.031225
chr12	10	0	0.376258	0.502262	0.088938	0.052726
chr12	11	0	0.400196	0.44534	0.082013	0.01655
chr12	12	0	0.426409	0.477044	0.230983	0.033371
chr12	13	0	0.415864	0.354633	0.057627	0.022337
chr12	14	0	0.397183	0.511099	0.141348	0.022394
chr12	15	0	0.374528	0.418468	0.07082	0.015545
chr12	16	0	0.368244	0.397342	0.050479	0.006449
chr12	17	0	0.355326	0.551042	0.037058	0
chr12	18	0	0.362032	0.478003	0.044944	0.00482
chr12	19	0	0.391968	0.471327	0.163391	0.013263
chr12	20	0	0.366144	0.452917	0.05748	0.01059

chr12	21	0	0.365004	0.506524	0.049275	0.03321
chr12	22	0	0.377837	0.481756	0.083073	0.013615
chr12	23	0	0.361538	0.37263	0.045845	0.004343
chr12	24	0	0.376769	0.356578	0.084309	0.014021
chr12	25	0	0.390537	0.508237	0.126582	0.014877
chr12	26	0	0.39092	0.357251	0.079586	0.016634
chr12	27	0	0.397444	0.42331	0.128643	0.031266
chr12	28	0	0.367601	0.455125	0.039921	0.00392
chr12	29	0	0.385994	0.438753	0.07042	0.019063
chr12	30	0	0.399289	0.48528	0.066173	0.009953
chr12	31	0	0.433446	0.524155	0.242004	0.026293
chr12	32	0	0.412309	0.479956	0.254794	0.022319
chr12	33	0	0.368683	0.555561	0.043243	0.003286
chr12	34	0.252039	0.318091	0.586514	0.027234	0.003125
chr12	35	1	0	0	0	0
chr12	36	0.142961	0.330877	0.691279	0.052275	0.000369
chr12	37	0	0.367013	0.491298	0.055093	0.007495
chr12	38	0	0.366058	0.430046	0.071822	0.023058
chr12	39	0	0.363544	0.352484	0.042816	0.009721
chr12	40	0	0.384028	0.452529	0.0916	0.011313
chr12	41	0	0.386742	0.422039	0.09829	0.009656
chr12	42	0	0.370288	0.460154	0.067088	0.016118
chr12	43	0	0.376656	0.458777	0.05432	0.011551
chr12	44	0	0.385616	0.498749	0.096028	0.028137
chr12	45	0	0.39072	0.52504	0.074338	0.017406
chr12	46	0	0.43529	0.421086	0.092808	0.054377
chr12	47	0	0.458003	0.543339	0.25531	0.078003
chr12	48	0	0.467037	0.460115	0.252531	0.075691
chr12	49	0	0.429908	0.579892	0.331188	0.045268
chr12	50	0	0.471775	0.407347	0.13881	0.048458
chr12	51	0	0.486639	0.36112	0.160998	0.090211
chr12	52	0	0.469642	0.352647	0.219607	0.058055
chr12	53	0	0.408882	0.476247	0.080163	0.027941
chr12	54	0	0.446324	0.477824	0.220887	0.08605
chr12	55	0	0.470482	0.481528	0.238189	0.102308
chr12	56	0	0.441324	0.496814	0.161308	0.07947
chr12	57	0	0.375481	0.431027	0.042381	0.004611
chr12	58	0	0.356683	0.476856	0.04044	0.005723
chr12	59	0	0.348845	0.587137	0.036387	0
chr12	60	0	0.367359	0.469737	0.047182	0.005312
chr12	61	0	0.391954	0.426569	0.098397	0.021058
chr12	62	0	0.38724	0.495241	0.125885	0.013745
chr12	63	0	0.404827	0.454577	0.177946	0.020621
chr12	64	0	0.394211	0.389741	0.089197	0.022061
chr12	65	0	0.384445	0.394255	0.082759	0.007615
chr12	66	0	0.397649	0.452837	0.057483	0.008848
chr12	67	0	0.406012	0.478198	0.185245	0.024728
chr12	68	0	0.390856	0.489349	0.109222	0.021641
chr12	69	0	0.378592	0.433017	0.067973	0.022181

chr12	70	0	0.379535	0.408339	0.085648	0.031634
chr12	71	0	0.357517	0.512261	0.031069	0.004468
chr12	72	0	0.348922	0.534506	0.045641	0
chr12	73	0	0.350119	0.423154	0.042767	0.007038
chr12	74	0.229723	0.29682	0.329831	0.068911	0.013823
chr12	75	0.020277	0.382798	0.480835	0.125017	0.02263
chr12	76	0	0.365577	0.378659	0.051277	0.002681
chr12	77	0	0.350074	0.375306	0.044015	0.006165
chr12	78	0	0.375949	0.438891	0.099936	0.009913
chr12	79	0	0.361096	0.400489	0.054086	0.006713
chr12	80	0	0.351045	0.427191	0.041417	0.006683
chr12	81	0	0.366192	0.436766	0.070176	0.00766
chr12	82	0	0.360498	0.527453	0.037905	0.002081
chr12	83	0	0.344817	0.446556	0.043989	0.012217
chr12	84	0	0.347972	0.421371	0.047173	0.007526
chr12	85	0	0.344019	0.496816	0.039282	0.000408
chr12	86	0	0.355328	0.485569	0.040924	0.011178
chr12	87	0	0.366087	0.478182	0.047896	0.017974
chr12	88	0	0.382634	0.37765	0.078088	0.019452
chr12	89	0	0.354923	0.4735	0.039113	0.007324
chr12	90	0	0.366251	0.430475	0.048392	0.004102
chr12	91	0	0.395564	0.433088	0.120664	0.016475
chr12	92	0	0.414093	0.498027	0.157028	0.017754
chr12	93	0	0.41787	0.484151	0.161667	0.014798
chr12	94	0	0.412617	0.476255	0.217031	0.027777
chr12	95	0	0.395258	0.459265	0.129768	0.012764
chr12	96	0	0.386793	0.434866	0.049746	0
chr12	97	0	0.406283	0.43465	0.147984	0.022448
chr12	98	0	0.371126	0.554998	0.068554	0.010065
chr12	99	0	0.400512	0.460806	0.120045	0.026689
chr12	100	0	0.399288	0.469989	0.187085	0.035787
chr12	101	0	0.392941	0.465435	0.045546	0.01734
chr12	102	0	0.404118	0.45006	0.085079	0.025168
chr12	103	0	0.425106	0.470529	0.142641	0.014896
chr12	104	0	0.415948	0.452952	0.059844	0.015549
chr12	105	0	0.412998	0.467092	0.112081	0.030561
chr12	106	0	0.435252	0.477711	0.097267	0.014584
chr12	107	0.057	0.43438	0.448016	0.146167	0.0339
chr12	108	0	0.476933	0.455565	0.217128	0.056676
chr12	109	0	0.452532	0.5361	0.301341	0.039287
chr12	110	0	0.459609	0.546464	0.304083	0.044431
chr12	111	0	0.445915	0.515064	0.210787	0.048211
chr12	112	0	0.488608	0.466996	0.165461	0.034846
chr12	113	0	0.440561	0.429847	0.138975	0.008676
chr12	114	0	0.42067	0.423503	0.078247	0.010307
chr12	115	0	0.447763	0.467884	0.215683	0.015594
chr12	116	0	0.456902	0.478017	0.191558	0.020968
chr12	117	0	0.424013	0.509249	0.156277	0.010453
chr12	118	0	0.44057	0.480173	0.182865	0.025907

chr12	119	0	0.475052	0.521142	0.315275	0.058499
chr12	120	0.035253	0.473807	0.540669	0.359176	0.043348
chr12	121	0.114947	0.411173	0.459486	0.319384	0.067489
chr12	122	3.00E-04	0.47081	0.494523	0.302411	0.062586
chr12	123	0	0.514041	0.44148	0.151922	0.028298
chr12	124	0	0.442399	0.478457	0.115202	0.010109
chr12	125	0	0.405003	0.435573	0.07154	0
chr12	126	0	0.413708	0.463086	0.077213	0.001113
chr12	127	0	0.448827	0.430316	0.119856	0.005826
chr12	128	0	0.430557	0.431267	0.073652	0.005776
chr12	129	0	0.469797	0.414693	0.100711	0.035044
chr12	130	0.144	0.434888	0.318508	0.055645	0.017828
chr12	131	0.045	0.527665	0.316539	0.125837	0.060694
chr12	132	0.13338906	0.38394929	0.50788996	0.22027202	0.05351124
chr13	0	1	0	0	0	0
chr13	1	1	0	0	0	0
chr13	2	1	0	0	0	0
chr13	3	1	0	0	0	0
chr13	4	1	0	0	0	0
chr13	5	1	0	0	0	0
chr13	6	1	0	0	0	0
chr13	7	1	0	0	0	0
chr13	8	1	0	0	0	0
chr13	9	1	0	0	0	0
chr13	10	1	0	0	0	0
chr13	11	1	0	0	0	0
chr13	12	1	0	0	0	0
chr13	13	1	0	0	0	0
chr13	14	1	0	0	0	0
chr13	15	1	0	0	0	0
chr13	16	1	0	0	0	0
chr13	17	0.918	0.030771	0.053406	0.007435	0
chr13	18	0	0.415112	0.480317	0.100187	0.003405
chr13	19	0	0.428879	0.506974	0.230738	0.021286
chr13	20	0	0.421659	0.510882	0.2194	0.028729
chr13	21	0	0.405072	0.398515	0.068736	0.0019
chr13	22	0	0.400833	0.497022	0.116909	0.016413
chr13	23	0	0.426044	0.407968	0.106581	0.027524
chr13	24	0	0.420334	0.446882	0.136831	0.033446
chr13	25	0	0.409913	0.419302	0.10843	0.012797
chr13	26	0	0.434289	0.432402	0.130815	0.011431
chr13	27	0	0.417447	0.4252	0.167501	0.025986
chr13	28	0	0.414727	0.486348	0.083151	0.013623
chr13	29	0	0.425178	0.434723	0.118355	0.017772
chr13	30	0	0.425236	0.422862	0.094988	0.015137
chr13	31	0	0.39244	0.406455	0.109316	0.02906
chr13	32	0	0.397074	0.418071	0.094895	0.026087
chr13	33	0	0.385968	0.431893	0.068125	0.002796
chr13	34	0	0.36531	0.425182	0.057493	0.002445

chr13	35	0	0.393953	0.376334	0.080249	0.020057
chr13	36	0	0.385801	0.448664	0.08431	0.017414
chr13	37	0	0.356516	0.485159	0.047454	0.009823
chr13	38	0	0.381422	0.396071	0.066525	0.021781
chr13	39	0	0.40453	0.385474	0.066567	0.012755
chr13	40	0	0.409172	0.528407	0.184382	0.034271
chr13	41	0	0.386414	0.413355	0.078969	0.023138
chr13	42	0	0.399347	0.390476	0.069033	0.008008
chr13	43	0	0.402145	0.387715	0.067008	0.010423
chr13	44	0	0.420998	0.463057	0.232524	0.021404
chr13	45	0	0.408502	0.433946	0.083699	0.023381
chr13	46	0	0.384024	0.426646	0.060111	0.009384
chr13	47	0	0.394394	0.518431	0.09882	0.023301
chr13	48	0	0.395006	0.486406	0.105187	0.022006
chr13	49	0	0.408073	0.467876	0.16676	0.029558
chr13	50	0	0.405151	0.392267	0.055618	0.015138
chr13	51	0	0.415819	0.449148	0.128826	0.049214
chr13	52	0	0.408937	0.372887	0.081641	0.012265
chr13	53	0	0.355531	0.43151	0.038775	0
chr13	54	0	0.350151	0.511317	0.052151	0
chr13	55	0	0.342732	0.506117	0.043624	0
chr13	56	0	0.343304	0.49753	0.043522	0.009235
chr13	57	0	0.346243	0.404768	0.045942	0.004951
chr13	58	0	0.3707	0.415841	0.057515	0
chr13	59	0	0.372117	0.410984	0.074148	0.004349
chr13	60	0	0.366582	0.486375	0.045304	0.007885
chr13	61	0	0.345584	0.485992	0.054252	0
chr13	62	0	0.338408	0.475568	0.048323	0
chr13	63	0	0.344541	0.441161	0.037533	0.003223
chr13	64	0	0.343205	0.499371	0.050727	0
chr13	65	0	0.349608	0.408583	0.041215	0.002194
chr13	66	0	0.348472	0.295203	0.052819	0.004027
chr13	67	0	0.34635	0.456157	0.043036	0
chr13	68	0	0.33609	0.468331	0.03789	0
chr13	69	0	0.34474	0.443614	0.053809	0.003983
chr13	70	0	0.343121	0.398671	0.046654	0.00324
chr13	71	0	0.35581	0.318885	0.048764	0.001999
chr13	72	0	0.386374	0.427181	0.149747	0.020933
chr13	73	0	0.379596	0.35298	0.066356	0.015576
chr13	74	0	0.379302	0.430529	0.068411	0.006618
chr13	75	0	0.371265	0.422499	0.058797	0.009492
chr13	76	0	0.382152	0.390296	0.078239	0.025336
chr13	77	0	0.371561	0.405696	0.044697	0.010416
chr13	78	0	0.376558	0.394573	0.062941	0.011571
chr13	79	0	0.384953	0.483922	0.086961	0.004205
chr13	80	0	0.353253	0.468209	0.051839	0
chr13	81	0	0.343997	0.514713	0.043992	0.001142
chr13	82	0	0.341363	0.483766	0.0405	0.001428
chr13	83	0	0.348708	0.452886	0.054289	0.005185

chr13	84	0	0.348776	0.436342	0.058183	0
chr13	85	0.05	0.325644	0.416516	0.048631	0.004181
chr13	86	0	0.34413	0.490034	0.046785	0
chr13	87	0	0.347401	0.437951	0.043246	0.004444
chr13	88	0	0.341441	0.489012	0.053465	0
chr13	89	0	0.350938	0.471567	0.062769	0
chr13	90	0	0.367444	0.385768	0.054377	0.005397
chr13	91	0	0.357036	0.39643	0.057702	0.001236
chr13	92	0	0.364721	0.392288	0.055279	0.001885
chr13	93	0	0.376653	0.294954	0.059141	0.006375
chr13	94	0	0.415242	0.444776	0.177214	0.014915
chr13	95	0	0.385665	0.451762	0.075829	0.019537
chr13	96	0	0.39119	0.395326	0.056209	0.018654
chr13	97	0	0.430686	0.454454	0.137904	0.021564
chr13	98	0	0.431927	0.419157	0.144875	0.021808
chr13	99	0	0.424118	0.425335	0.187756	0.012349
chr13	100	0	0.400248	0.40612	0.071873	0.014367
chr13	101	0	0.372218	0.335506	0.044033	0.004821
chr13	102	0	0.386561	0.366589	0.066652	0.021029
chr13	103	0	0.357344	0.378667	0.043919	0
chr13	104	0	0.360005	0.327702	0.043884	0.003682
chr13	105	0	0.38743	0.301752	0.055318	0.005151
chr13	106	0	0.387495	0.35241	0.06105	0.004161
chr13	107	0	0.374635	0.402133	0.048821	0.011709
chr13	108	0	0.392569	0.382759	0.056619	0.007963
chr13	109	0	0.441169	0.28737	0.055196	0.020881
chr13	110	0	0.458206	0.403296	0.079289	0.032814
chr13	111	0.4	0.288244	0.156191	0.020139	0.004108
chr13	112	0	0.488805	0.33122	0.085277	0.041598
chr13	113	0.2	0.417256	0.253893	0.067254	0.028747
chr13	114	0.10490904	0.38992593	0.35133339	0.15804897	0.07563243
chr14	0	1	0	0	0	0
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chr14	2	1	0	0	0	0
chr14	3	1	0	0	0	0
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chr14	13	1	0	0	0	0
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chr14	15	1	0	0	0	0
chr14	16	1	0	0	0	0
chr14	17	1	0	0	0	0

chr14	18	0.07	0.380888	0.527309	0.178463	0.007792
chr14	19	0	0.391629	0.489971	0.088178	0.03735
chr14	20	0	0.433639	0.480882	0.189186	0.056397
chr14	21	0	0.395072	0.449869	0.096289	0.020469
chr14	22	0	0.46417	0.426791	0.200976	0.09481
chr14	23	0	0.46651	0.42923	0.113142	0.110188
chr14	24	0	0.39351	0.480832	0.044953	0.008577
chr14	25	0	0.369867	0.403251	0.036086	0.003081
chr14	26	0	0.348319	0.406124	0.042368	0.00121
chr14	27	0	0.347458	0.522652	0.035408	0
chr14	28	0	0.357792	0.425904	0.049551	0.002584
chr14	29	0	0.374089	0.403292	0.061746	0.003677
chr14	30	0	0.391192	0.492184	0.220281	0.026201
chr14	31	0	0.392597	0.506343	0.102957	0.006462
chr14	32	0	0.376904	0.310463	0.058231	0.011979
chr14	33	0	0.407391	0.378109	0.085557	0.008489
chr14	34	0	0.42729	0.557824	0.351245	0.026555
chr14	35	0	0.38228	0.464901	0.117295	0.014953
chr14	36	0	0.385881	0.377539	0.082221	0.018453
chr14	37	0	0.376712	0.48551	0.047553	0.015869
chr14	38	0	0.387379	0.544905	0.130379	0.024638
chr14	39	0	0.364764	0.537263	0.034261	0
chr14	40	0	0.34415	0.506603	0.03624	0
chr14	41	0	0.348184	0.509481	0.042255	0.003148
chr14	42	0	0.341859	0.538135	0.041668	0
chr14	43	0	0.352308	0.517972	0.042158	0
chr14	44	0	0.381037	0.527367	0.106995	0.027784
chr14	45	0	0.358062	0.583059	0.032468	0
chr14	46	0	0.348084	0.389792	0.045379	0.004221
chr14	47	0	0.357038	0.49015	0.045305	0.000234
chr14	48	0	0.369965	0.496484	0.043007	0
chr14	49	0	0.416966	0.511982	0.253572	0.035651
chr14	50	0	0.401261	0.433638	0.114992	0.034971
chr14	51	0	0.403859	0.417888	0.07639	0.022578
chr14	52	0	0.39268	0.514539	0.144455	0.021163
chr14	53	0	0.395974	0.41094	0.061884	0.004269
chr14	54	0	0.417509	0.408469	0.185115	0.041691
chr14	55	0	0.402951	0.435496	0.069875	0.011843
chr14	56	0	0.395982	0.391839	0.103945	0.01812
chr14	57	0	0.396367	0.470028	0.115033	0.018676
chr14	58	0	0.397491	0.425982	0.087532	0.011638
chr14	59	0	0.382821	0.490418	0.0609	0.023064
chr14	60	0	0.400194	0.442187	0.110818	0.019968
chr14	61	0	0.39478	0.448776	0.074736	0.017054
chr14	62	0	0.378926	0.461119	0.066266	0.009422
chr14	63	0	0.416803	0.503994	0.2848	0.044358
chr14	64	0	0.447767	0.415023	0.192332	0.043835
chr14	65	0	0.402754	0.465107	0.055439	0.00289
chr14	66	0	0.378214	0.526533	0.113912	0.018748

chr14	67	0	0.409849	0.398776	0.126082	0.032419
chr14	68	0	0.454801	0.384361	0.137594	0.034144
chr14	69	0	0.438646	0.436131	0.107347	0.030481
chr14	70	0	0.412192	0.501241	0.123239	0.022317
chr14	71	0	0.407827	0.443903	0.09847	0.012229
chr14	72	0	0.447531	0.435918	0.214137	0.037966
chr14	73	0	0.454623	0.512991	0.319095	0.04816
chr14	74	0	0.456663	0.410523	0.197481	0.051993
chr14	75	0	0.436241	0.40905	0.117982	0.024039
chr14	76	0	0.474646	0.442889	0.180771	0.04619
chr14	77	0	0.439436	0.442389	0.174621	0.020111
chr14	78	0	0.388559	0.292736	0.053856	0.005499
chr14	79	0	0.379355	0.379631	0.046971	0.011588
chr14	80	0	0.385221	0.446746	0.082282	0.013586
chr14	81	0	0.381032	0.451771	0.062123	0.004092
chr14	82	0	0.353535	0.414986	0.047733	0
chr14	83	0	0.354202	0.406853	0.049735	0
chr14	84	0	0.365628	0.403477	0.05267	0
chr14	85	0	0.368542	0.411686	0.048009	0.007178
chr14	86	0	0.366117	0.438413	0.048737	0
chr14	87	0	0.401219	0.453239	0.0552	0.016226
chr14	88	0	0.418825	0.419505	0.132079	0.028634
chr14	89	0	0.431365	0.453294	0.172488	0.024993
chr14	90	0	0.459163	0.435331	0.174434	0.026572
chr14	91	0	0.426255	0.490998	0.169772	0.03318
chr14	92	0	0.464658	0.486641	0.172075	0.040523
chr14	93	0	0.444283	0.451882	0.076183	0.035965
chr14	94	0	0.463586	0.40993	0.099297	0.036648
chr14	95	0	0.451579	0.450171	0.093155	0.037327
chr14	96	0	0.430081	0.375102	0.077468	0.007476
chr14	97	0	0.415517	0.35111	0.04502	0.004677
chr14	98	0	0.448377	0.360513	0.064971	0.014785
chr14	99	0	0.488831	0.406369	0.153935	0.038167
chr14	100	0	0.480781	0.388452	0.059573	0.020137
chr14	101	0	0.471227	0.490727	0.209111	0.044353
chr14	102	0	0.486634	0.494588	0.256615	0.031839
chr14	103	0	0.509164	0.408446	0.187109	0.040553
chr14	104	0	0.561633	0.358337	0.133372	0.071912
chr14	105	0	0.483032	0.462232	0.041398	0.025942
chr14	106	0.02170457	0.40521344	0.49887679	0.04207702	0.00987829
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chr15	12	1	0	0	0	0
chr15	13	1	0	0	0	0
chr15	14	1	0	0	0	0
chr15	15	1	0	0	0	0
chr15	16	1	0	0	0	0
chr15	17	1	0	0	0	0
chr15	18	0.26	0.316527	0.423504	0.105174	0.001978
chr15	19	0.1	0.369836	0.428942	0.074601	0.004521
chr15	20	0.1	0.398203	0.411038	0.196684	0.028544
chr15	21	0.05	0.389042	0.594414	0.116365	0.009675
chr15	22	0	0.403311	0.567042	0.1038	0.014644
chr15	23	0	0.428616	0.458578	0.093894	0.016398
chr15	24	0.044	0.390851	0.468802	0.075347	0.003177
chr15	25	0.101	0.375896	0.42283	0.052131	0.002799
chr15	26	0.2	0.345934	0.334095	0.143588	0.034615
chr15	27	0	0.438545	0.46117	0.124895	0.015302
chr15	28	0	0.426758	0.470172	0.132606	0.009714
chr15	29	0	0.448004	0.482775	0.096692	0.027384
chr15	30	0	0.417689	0.437885	0.099394	0.019839
chr15	31	0	0.409496	0.366405	0.089525	0.023809
chr15	32	0	0.409912	0.400943	0.143489	0.038192
chr15	33	0	0.37631	0.394066	0.092145	0.014707
chr15	34	0	0.369978	0.331203	0.057807	0.004666
chr15	35	0	0.371438	0.391154	0.042125	0.002525
chr15	36	0	0.396002	0.438147	0.068788	0.014519
chr15	37	0	0.395345	0.374617	0.052624	0.018429
chr15	38	0	0.471707	0.413955	0.222424	0.078846
chr15	39	0	0.464509	0.481402	0.329599	0.069839
chr15	40	0	0.434605	0.464252	0.200553	0.067872
chr15	41	0	0.438182	0.429339	0.231841	0.074209
chr15	42	0	0.411991	0.51956	0.2448	0.025806
chr15	43	0	0.433297	0.481544	0.168948	0.044118
chr15	44	0	0.371002	0.533651	0.034257	0
chr15	45	0	0.382314	0.391836	0.040573	0.007189
chr15	46	0	0.38906	0.303679	0.063207	0.033746
chr15	47	0	0.378047	0.497779	0.055867	0.028729
chr15	48	0	0.402481	0.520124	0.235239	0.024915
chr15	49	0	0.409004	0.444823	0.100779	0.039374
chr15	50	0	0.419588	0.427896	0.165502	0.037694
chr15	51	0	0.384041	0.396774	0.041018	0.009798
chr15	52	0	0.365908	0.49369	0.041878	0.002048
chr15	53	0	0.401247	0.522353	0.175682	0.024632
chr15	54	0	0.379254	0.579644	0.096452	0.020061
chr15	55	0	0.408613	0.364177	0.108161	0.021715
chr15	56	0	0.407916	0.433067	0.121193	0.020335
chr15	57	0	0.417534	0.452455	0.213614	0.022195

chr15	58	0	0.409291	0.314485	0.090489	0.012205
chr15	59	0	0.404318	0.355671	0.05654	0.007206
chr15	60	0	0.421247	0.354751	0.100427	0.023562
chr15	61	0	0.427936	0.385289	0.159939	0.039619
chr15	62	0	0.449252	0.481425	0.294339	0.030033
chr15	63	0	0.442599	0.462611	0.257884	0.058193
chr15	64	0	0.474719	0.425466	0.173621	0.023035
chr15	65	0	0.424627	0.416392	0.12944	0.018192
chr15	66	0	0.446336	0.451248	0.13524	0.032342
chr15	67	0	0.44653	0.421309	0.091515	0.024657
chr15	68	0	0.45634	0.395523	0.076455	0.018185
chr15	69	0	0.412881	0.452653	0.095099	0.014597
chr15	70	0	0.425443	0.488806	0.195124	0.032454
chr15	71	0	0.436208	0.426118	0.104301	0.018351
chr15	72	0	0.502798	0.403875	0.184132	0.070644
chr15	73	0	0.4795	0.460188	0.252941	0.069357
chr15	74	0	0.402707	0.589021	0.122392	0.018897
chr15	75	0	0.463687	0.382986	0.092569	0.025797
chr15	76	0	0.470383	0.426914	0.185755	0.049314
chr15	77	0	0.43583	0.436257	0.069262	0.019334
chr15	78	0	0.4392	0.409675	0.122241	0.017422
chr15	79	0	0.413379	0.466472	0.078458	0.02578
chr15	80	0.06	0.419164	0.340418	0.104466	0.033417
chr15	81	0	0.431648	0.478746	0.173883	0.026296
chr15	82	0.06	0.394275	0.410685	0.102987	0.034719
chr15	83	0	0.437603	0.442839	0.175787	0.032558
chr15	84	0	0.416385	0.420082	0.088038	0.019319
chr15	85	0	0.384363	0.48109	0.045033	0
chr15	86	0	0.446329	0.375987	0.06518	0.017205
chr15	87	0	0.465479	0.445774	0.157334	0.032076
chr15	88	0	0.464806	0.481266	0.266938	0.054864
chr15	89	0	0.433969	0.480189	0.152599	0.035873
chr15	90	0	0.439203	0.377671	0.054341	0.012682
chr15	91	0	0.434668	0.442814	0.157485	0.014532
chr15	92	0	0.388822	0.413298	0.060287	0.007103
chr15	93	0	0.383408	0.392601	0.066311	0
chr15	94	0	0.397659	0.285062	0.07947	0.005735
chr15	95	0	0.378774	0.427092	0.045897	0.001022
chr15	96	0.022	0.409744	0.41248	0.092603	0.007342
chr15	97	0	0.432594	0.396855	0.115915	0.019873
chr15	98	0	0.429839	0.430313	0.077074	0.028459
chr15	99	0	0.468097	0.389454	0.088616	0.029229
chr15	100	0	0.41438291	0.44040116	0.06752411	0.03196367
chr16	0	2.00E-06	0.573848	0.31687	0.202902	0.112122
chr16	1	0	0.577928	0.304391	0.186486	0.091558
chr16	2	0	0.550235	0.362414	0.220817	0.133474
chr16	3	0	0.487769	0.452616	0.273016	0.086188
chr16	4	0	0.515621	0.465088	0.318221	0.063502
chr16	5	0	0.456039	0.468072	0.15291	0.007463

chr16	6	0	0.412883	0.40547	0.132875	0.004563
chr16	7	0	0.411351	0.34966	0.102148	0.003396
chr16	8	0.0175	0.436336	0.477179	0.178777	0.018727
chr16	9	0	0.432156	0.513503	0.156129	0.007225
chr16	10	0	0.454223	0.555799	0.215658	0.018284
chr16	11	0	0.483321	0.485672	0.282628	0.04312
chr16	12	0	0.458926	0.466672	0.189519	0.007532
chr16	13	0	0.419647	0.49498	0.124276	0.002886
chr16	14	0	0.446959	0.501266	0.250257	0.028729
chr16	15	0	0.462327	0.527386	0.295801	0.033064
chr16	16	0	0.458159	0.533365	0.221182	0.021832
chr16	17	0	0.434696	0.468312	0.127529	0.004178
chr16	18	0	0.448479	0.52265	0.23838	0.032648
chr16	19	0	0.447339	0.53347	0.225391	0.027845
chr16	20	0	0.426963	0.509473	0.132617	0.049318
chr16	21	0	0.437705	0.494373	0.259161	0.038227
chr16	22	0	0.442973	0.489115	0.208201	0.023683
chr16	23	0	0.452195	0.540542	0.257681	0.039416
chr16	24	0	0.438019	0.521233	0.251144	0.034753
chr16	25	0	0.423396	0.520981	0.163077	0.011492
chr16	26	0	0.420689	0.554242	0.10585	0.004537
chr16	27	0	0.479468	0.513424	0.196579	0.029862
chr16	28	0	0.4919	0.563748	0.368836	0.055113
chr16	29	0	0.495105	0.479626	0.28418	0.066911
chr16	30	0	0.504712	0.539681	0.359849	0.115161
chr16	31	0	0.45114	0.583971	0.175856	0.060542
chr16	32	0	0.412695	0.528523	0.088459	0.010011
chr16	33	0.069349	0.397601	0.498778	0.09589	0.015454
chr16	34	0.030651	0.399003	0.589407	0.056827	0.002226
chr16	35	0.856698	0.05299	0.140707	0.000305	0
chr16	36	1	0	0	0	0
chr16	37	1	0	0	0	0
chr16	38	1	0	0	0	0
chr16	39	1	0	0	0	0
chr16	40	1	0	0	0	0
chr16	41	1	0	0	0	0
chr16	42	1	0	0	0	0
chr16	43	1	0	0	0	0
chr16	44	0.943302	0.020532	0.054938	0	0
chr16	45	0	0.413225	0.540001	0.176877	0.033877
chr16	46	0	0.41473	0.48442	0.104018	0.026485
chr16	47	0	0.433865	0.509874	0.099667	0.018468
chr16	48	0	0.477698	0.409902	0.172425	0.019006
chr16	49	0	0.452797	0.394775	0.081126	0.025112
chr16	50	0	0.396904	0.387763	0.06055	0
chr16	51	0	0.40013	0.468943	0.12774	0.012163
chr16	52	0	0.419081	0.402065	0.129768	0.017362
chr16	53	0	0.432581	0.405765	0.076742	0.004814
chr16	54	0	0.437601	0.432797	0.05363	0.017854

chr16	55	0	0.4659	0.441469	0.198235	0.052113
chr16	56	0	0.485749	0.472735	0.191276	0.069505
chr16	57	0	0.414933	0.505432	0.164783	0.021268
chr16	58	0	0.370012	0.497175	0.068728	0
chr16	59	0	0.359433	0.43753	0.050366	0
chr16	60	0	0.366387	0.379638	0.059269	0.002929
chr16	61	0	0.365594	0.472935	0.060666	0
chr16	62	0	0.363357	0.444399	0.065356	0
chr16	63	0	0.38268	0.409696	0.05361	0.003825
chr16	64	0	0.438168	0.385679	0.068977	0.004089
chr16	65	0	0.482851	0.429171	0.242349	0.0916
chr16	66	0	0.496849	0.441142	0.304655	0.094737
chr16	67	0	0.45712	0.520826	0.330943	0.043369
chr16	68	0	0.450226	0.51218	0.336837	0.057992
chr16	69	0	0.452743	0.450509	0.152695	0.04189
chr16	70	0	0.429246	0.469555	0.203	0.057418
chr16	71	0	0.422163	0.391701	0.133323	0.013306
chr16	72	0	0.413609	0.396381	0.152378	0.003614
chr16	73	0	0.457045	0.514809	0.295085	0.046919
chr16	74	0	0.3981	0.505087	0.144626	0.021614
chr16	75	0	0.379319	0.421941	0.077074	0.012458
chr16	76	0	0.424093	0.386495	0.136653	0.007703
chr16	77	0	0.431376	0.328959	0.114765	0.004227
chr16	78	0	0.416593	0.340694	0.055204	0.006364
chr16	79	0	0.433212	0.486587	0.165596	0.028861
chr16	80	0	0.458787	0.453346	0.114955	0.020661
chr16	81	0	0.418062	0.354633	0.064469	0.000901
chr16	82	0	0.469103	0.419967	0.136918	0.035343
chr16	83	0	0.511621	0.419623	0.18515	0.042283
chr16	84	0	0.512311	0.35808	0.100585	0.020268
chr16	85	0	0.490002	0.353725	0.091297	0.01851
chr16	86	0.02	0.517799	0.357929	0.144386	0.034288
chr16	87	0	0.577683	0.275428	0.120131	0.071088
chr16	88	0.00604409	0.51490895	0.41305281	0.25289784	0.07855861
chr17	0	0.046522	0.486092	0.386533	0.208672	0.033683
chr17	1	0	0.513799	0.4712	0.342412	0.06315
chr17	2	0	0.477586	0.511281	0.285553	0.050932
chr17	3	0	0.471265	0.491918	0.199572	0.064909
chr17	4	0	0.497674	0.459087	0.299057	0.084778
chr17	5	0	0.453148	0.508334	0.190958	0.041692
chr17	6	0	0.465744	0.512032	0.152306	0.038058
chr17	7	0	0.514477	0.415261	0.25478	0.143095
chr17	8	0	0.466155	0.463297	0.20698	0.055702
chr17	9	0	0.458811	0.457284	0.206182	0.019466
chr17	10	0	0.429718	0.436254	0.146541	0.042359
chr17	11	0	0.422345	0.40847	0.117288	0.022452
chr17	12	0	0.41424	0.476265	0.127544	0.019199
chr17	13	0	0.396421	0.441303	0.099434	0.003355
chr17	14	0	0.409688	0.454696	0.098781	0.007767

chr17	15	0	0.432619	0.43065	0.153025	0.029
chr17	16	0	0.46215	0.489496	0.201645	0.027297
chr17	17	0	0.513157	0.413001	0.198488	0.066357
chr17	18	0	0.48094	0.458119	0.22125	0.058753
chr17	19	0	0.461274	0.530159	0.254534	0.043551
chr17	20	0	0.43791	0.48095	0.178432	0.019376
chr17	21	0.1	0.411311	0.427105	0.116927	0.01431
chr17	22	0.1	0.385714	0.472511	0.099336	0.009116
chr17	23	0	0.456612	0.444056	0.1678	0.055095
chr17	24	0	0.477183	0.43832	0.290989	0.086428
chr17	25	0	0.411329	0.486697	0.202363	0.038204
chr17	26	0	0.441736	0.501644	0.272685	0.044305
chr17	27	0	0.44408	0.51512	0.295275	0.030471
chr17	28	0	0.437612	0.434283	0.078874	0.009251
chr17	29	0	0.445974	0.397688	0.042408	0.01625
chr17	30	0	0.43788	0.506452	0.145689	0.054392
chr17	31	0.1	0.410355	0.387948	0.160224	0.054009
chr17	32	0	0.448914	0.404384	0.209889	0.037229
chr17	33	0.1	0.423608	0.401396	0.216675	0.046107
chr17	34	0	0.481218	0.500372	0.348782	0.061207
chr17	35	0	0.49236	0.412445	0.241432	0.083716
chr17	36	0	0.424575	0.383858	0.085522	0.067547
chr17	37	0	0.500847	0.437848	0.301904	0.102339
chr17	38	0.1	0.426476	0.456575	0.295478	0.079794
chr17	39	0	0.498155	0.4573	0.26703	0.079881
chr17	40	0	0.49555	0.44876	0.286952	0.068079
chr17	41	0	0.451467	0.424507	0.212971	0.045812
chr17	42	0	0.436572	0.468917	0.222245	0.040273
chr17	43	0	0.454128	0.354081	0.217843	0.052021
chr17	44	0	0.476689	0.467415	0.270698	0.059612
chr17	45	0	0.49765	0.384509	0.181835	0.066348
chr17	46	0	0.44975	0.457305	0.212813	0.042171
chr17	47	0	0.388714	0.450319	0.039246	0.0055
chr17	48	0	0.358217	0.496135	0.045888	0
chr17	49	0	0.366826	0.533601	0.052684	0.002312
chr17	50	0	0.393587	0.462633	0.091326	0.021353
chr17	51	0	0.398001	0.444007	0.052917	0.006026
chr17	52	0	0.453373	0.403127	0.150241	0.016772
chr17	53	0	0.462789	0.378177	0.151622	0.070402
chr17	54	0	0.423944	0.55774	0.33741	0.031481
chr17	55	0	0.420262	0.475139	0.275192	0.048405
chr17	56	0	0.413318	0.458423	0.197635	0.014316
chr17	57	0	0.402262	0.554454	0.265159	0.030093
chr17	58	0	0.428814	0.453319	0.162896	0.033847
chr17	59	0	0.460657	0.39596	0.238374	0.066548
chr17	60	0	0.449166	0.447707	0.215944	0.035895
chr17	61	0	0.405245	0.466366	0.152382	0.003967
chr17	62	0	0.44869	0.433253	0.19924	0.024276
chr17	63	0.09	0.40598	0.461416	0.28087	0.028477

chr17	64	0	0.390005	0.424407	0.106286	0.046315
chr17	65	0	0.381386	0.40163	0.074667	0.014499
chr17	66	0	0.372301	0.352845	0.06612	0
chr17	67	0	0.41725	0.346159	0.085779	0.003935
chr17	68	0	0.476738	0.419701	0.203245	0.028093
chr17	69	0	0.504182	0.394841	0.135428	0.018477
chr17	70	0	0.50194	0.45814	0.283959	0.077098
chr17	71	0	0.520669	0.395667	0.278413	0.123027
chr17	72	0	0.507053	0.459154	0.248346	0.050157
chr17	73	0	0.503333	0.39528	0.182686	0.050288
chr17	74	0	0.522133	0.346423	0.159548	0.04703
chr17	75	0.153	0.446537	0.329069	0.145878	0.05331
chr17	76	0	0.541295	0.318741	0.132023	0.064363
chr17	77	0.065	0.532013	0.314021	0.20291	0.114458
chr17	78	0.15489007	0.44397303	0.32396937	0.17066692	0.0411388
chr18	0	0	0.423024	0.465325	0.177653	0.024798
chr18	1	0	0.365162	0.566083	0.039758	0.002175
chr18	2	0	0.391154	0.447325	0.121184	0.021352
chr18	3	0	0.416212	0.430829	0.191986	0.016537
chr18	4	0	0.376253	0.520437	0.053744	0
chr18	5	0	0.398488	0.402538	0.056108	0.00973
chr18	6	0	0.399364	0.433755	0.085774	0.020005
chr18	7	0	0.417647	0.408949	0.129503	0.007466
chr18	8	0	0.42649	0.395879	0.098373	0.013342
chr18	9	0	0.411006	0.474123	0.16834	0.034765
chr18	10	0	0.426223	0.336759	0.070243	0.012769
chr18	11	0	0.424634	0.458283	0.140342	0.008212
chr18	12	0	0.43647	0.500268	0.216084	0.027979
chr18	13	0	0.438458	0.424978	0.094193	0.031544
chr18	14	0	0.409912	0.471293	0.074184	0.008784
chr18	15	0.599102	0.147292	0.234235	0.031115	0
chr18	16	0.764896	0.088976	0.133373	0.042885	0.004065
chr18	17	0	0.41537	0.500918	0.267203	0.022925
chr18	18	0	0.408595	0.483332	0.127695	0.011055
chr18	19	0	0.436157	0.396813	0.17302	0.03458
chr18	20	0	0.409365	0.389582	0.112566	0.01332
chr18	21	0	0.386719	0.416001	0.077346	0.00785
chr18	22	0	0.402076	0.408754	0.114661	0.012704
chr18	23	0	0.372974	0.381782	0.053483	0.004024
chr18	24	0	0.358413	0.446209	0.038089	0.000265
chr18	25	0	0.346732	0.506119	0.051388	0
chr18	26	0	0.356336	0.418093	0.051259	0.015578
chr18	27	0	0.396242	0.428811	0.156186	0.034735
chr18	28	0	0.379591	0.396604	0.06681	0.010923
chr18	29	0	0.355505	0.446754	0.042766	0.010275
chr18	30	0	0.377073	0.403327	0.053193	0.012194
chr18	31	0	0.405938	0.56403	0.109751	0.042358
chr18	32	0	0.40933	0.446847	0.082462	0.014096
chr18	33	0	0.444801	0.315221	0.035396	0.008965

chr18	34	0	0.367534	0.391839	0.039438	0
chr18	35	0	0.369414	0.36719	0.051172	0
chr18	36	0	0.355003	0.36999	0.041845	0
chr18	37	0	0.372496	0.347338	0.053786	0.003065
chr18	38	0	0.369229	0.404149	0.043353	0.001156
chr18	39	0	0.36016	0.496873	0.042776	0.004487
chr18	40	0	0.393828	0.375979	0.042123	0.007145
chr18	41	0	0.427985	0.373392	0.118991	0.02134
chr18	42	0	0.439575	0.40634	0.125697	0.037584
chr18	43	0	0.442338	0.373106	0.062873	0.007727
chr18	44	0	0.465456	0.386091	0.076626	0.013072
chr18	45	0	0.43003	0.413486	0.115894	0.020155
chr18	46	0	0.426696	0.47994	0.136433	0.023215
chr18	47	0	0.395851	0.472934	0.066638	0
chr18	48	0	0.371936	0.329849	0.051669	0.001911
chr18	49	0	0.374263	0.420657	0.061617	0.004937
chr18	50	0.047	0.364734	0.378765	0.072823	0.016725
chr18	51	0	0.38231	0.312159	0.061655	0.008908
chr18	52	0	0.392757	0.363434	0.074111	0.010385
chr18	53	0	0.430594	0.436308	0.157648	0.020601
chr18	54	0	0.434823	0.363746	0.152065	0.025362
chr18	55	0	0.415045	0.434057	0.127871	0.01429
chr18	56	0	0.359766	0.428114	0.05211	0.000999
chr18	57	0	0.394824	0.401135	0.064162	0.011521
chr18	58	0	0.413451	0.397821	0.143774	0.026102
chr18	59	0	0.395445	0.407948	0.085091	0.028369
chr18	60	0	0.360731	0.440032	0.047503	0
chr18	61	0	0.347498	0.385162	0.050655	0.00588
chr18	62	0	0.342589	0.444853	0.048583	0.003749
chr18	63	0	0.350527	0.410906	0.047697	0.009281
chr18	64	0	0.355101	0.401695	0.051349	0.007849
chr18	65	0	0.367011	0.391146	0.057539	0.01103
chr18	66	0	0.385698	0.477136	0.081188	0.004007
chr18	67	0	0.350857	0.445019	0.051382	0
chr18	68	0	0.368466	0.424349	0.057589	0.006654
chr18	69	0	0.386813	0.414306	0.049243	0.002999
chr18	70	0.028	0.405322	0.312953	0.062245	0.022709
chr18	71	0	0.418517	0.315333	0.034931	0.009631
chr18	72	0	0.44869	0.357608	0.10214	0.024733
chr18	73	0.022	0.404603	0.363825	0.048118	0.003057
chr18	74	0	0.45719	0.303294	0.046449	0.006538
chr18	75	0	0.493678	0.360052	0.079517	0.03808
chr18	76	0	0.46925414	0.34532325	0.09516534	0.00965396
chr19	0	0.011	0.543475	0.423775	0.217322	0.076562
chr19	1	0	0.588722	0.372891	0.26946	0.105485
chr19	2	0	0.544977	0.483034	0.329613	0.071217
chr19	3	0	0.556693	0.489699	0.328851	0.077654
chr19	4	0	0.540482	0.540279	0.39455	0.061933
chr19	5	0	0.528216	0.476445	0.287952	0.059515

chr19	6	0	0.486854	0.588832	0.327672	0.050767
chr19	7	0.005	0.509473	0.518108	0.33906	0.080893
chr19	8	0.005	0.495135	0.550301	0.352644	0.044919
chr19	9	0	0.45514	0.658827	0.315431	0.056803
chr19	10	0	0.524033	0.554826	0.435099	0.094198
chr19	11	0	0.487706	0.63165	0.373501	0.084669
chr19	12	0	0.480188	0.583081	0.360787	0.103219
chr19	13	0	0.504313	0.543351	0.344484	0.052504
chr19	14	0	0.489789	0.571153	0.350707	0.063805
chr19	15	0	0.480763	0.524824	0.227447	0.063706
chr19	16	0	0.505839	0.528252	0.349363	0.054696
chr19	17	0	0.528255	0.553272	0.401615	0.079236
chr19	18	0	0.543923	0.473196	0.33789	0.08207
chr19	19	0	0.490925	0.532306	0.299404	0.091961
chr19	20	0	0.407987	0.706314	0.199497	0.027194
chr19	21	0	0.4093	0.736668	0.209396	0.03008
chr19	22	0	0.410895	0.698723	0.159139	0.007117
chr19	23	0	0.4161	0.738068	0.193829	0.015388
chr19	24	0.576378	0.165292	0.377978	0.031179	0.00411
chr19	25	1	0	0	0	0
chr19	26	1	0	0	0	0
chr19	27	1	0	0	0	0
chr19	28	1	0	0	0	0
chr19	29	1	0	0	0	0
chr19	30	1	0	0	0	0
chr19	31	1	0	0	0	0
chr19	32	0.423622	0.221393	0.548863	0.006741	0.000471
chr19	33	0	0.421883	0.532293	0.066551	0.007566
chr19	34	0	0.475897	0.446462	0.116765	0.006953
chr19	35	0	0.458167	0.360352	0.107742	0.011885
chr19	36	0	0.435412	0.364684	0.073867	0.004865
chr19	37	0	0.436187	0.48171	0.18297	0.022363
chr19	38	0	0.499258	0.44727	0.235969	0.034908
chr19	39	0	0.443966	0.570118	0.226524	0.024113
chr19	40	0	0.500836	0.520443	0.237278	0.094758
chr19	41	0	0.469881	0.607877	0.318424	0.073826
chr19	42	0	0.421543	0.59229	0.2186	0.064542
chr19	43	0	0.509976	0.531472	0.321001	0.058688
chr19	44	0	0.484176	0.580056	0.269992	0.07018
chr19	45	0	0.494001	0.567394	0.298212	0.100304
chr19	46	0	0.473359	0.569174	0.207155	0.058589
chr19	47	0	0.499542	0.503125	0.193499	0.076404
chr19	48	0	0.461418	0.551103	0.168342	0.046785
chr19	49	0	0.429037	0.587177	0.176146	0.063835
chr19	50	0	0.52967	0.554904	0.388078	0.086823
chr19	51	0	0.491914	0.572596	0.272392	0.061347
chr19	52	0	0.507116	0.545166	0.369311	0.049481
chr19	53	0	0.500879	0.578549	0.342874	0.076808
chr19	54	0	0.524239	0.540786	0.349347	0.095426

chr19	55	0	0.522093	0.52305	0.275203	0.088584
chr19	56	0	0.479534	0.51096	0.161941	0.066951
chr19	57	0	0.436558	0.585456	0.256979	0.088882
chr19	58	0	0.452977	0.569264	0.324379	0.067045
chr19	59	0	0.494696	0.500811	0.234345	0.081199
chr19	60	0	0.521562	0.503928	0.25963	0.109333
chr19	61	0	0.447444	0.522138	0.176852	0.055737
chr19	62	0	0.444192	0.531026	0.202989	0.101877
chr19	63	0.00616028	0.48925525	0.50215117	0.27626495	0.12780354
chr2	0	0	0.440526	0.367538	0.031253	0.010008
chr2	1	0.026	0.45221	0.285168	0.043433	0.010314
chr2	2	0	0.442209	0.375335	0.040087	0.00067
chr2	3	0.05	0.402034	0.423175	0.051163	0.005591
chr2	4	0.1	0.381025	0.353524	0.04804	0.003473
chr2	5	0.05	0.387413	0.343488	0.058667	0.018071
chr2	6	0	0.40078	0.389709	0.045358	0.005749
chr2	7	0	0.41156	0.372715	0.046842	0.009633
chr2	8	0	0.438631	0.321355	0.061474	0.014938
chr2	9	0	0.445927	0.422118	0.167281	0.01677
chr2	10	0	0.485094	0.415987	0.178752	0.035293
chr2	11	0	0.450506	0.414578	0.117529	0.035124
chr2	12	0	0.407422	0.409633	0.05064	0.004194
chr2	13	0	0.357427	0.520513	0.034318	0.002568
chr2	14	0	0.376064	0.469718	0.048623	0.00408
chr2	15	0	0.415038	0.42963	0.079489	0.009988
chr2	16	0.075	0.397234	0.367051	0.070834	0.004864
chr2	17	0	0.385777	0.425438	0.056136	0.010123
chr2	18	0	0.39099	0.4421	0.035149	0.006587
chr2	19	0	0.411354	0.380689	0.038319	0.005218
chr2	20	0	0.442838	0.406837	0.104226	0.03502
chr2	21	0.025	0.385111	0.38911	0.037703	0.016209
chr2	22	0	0.370483	0.443543	0.044459	0
chr2	23	0	0.443334	0.358363	0.065244	0.008127
chr2	24	0	0.415551	0.5151	0.215391	0.034291
chr2	25	0	0.452832	0.460824	0.219345	0.025387
chr2	26	0	0.466012	0.477145	0.225754	0.040107
chr2	27	0	0.462963	0.423797	0.22229	0.098798
chr2	28	0	0.428202	0.401004	0.143035	0.020684
chr2	29	0	0.435775	0.36222	0.088032	0.01457
chr2	30	0	0.426919	0.431432	0.09158	0.014029
chr2	31	0.000855	0.425895	0.507089	0.051937	0.012895
chr2	32	0	0.397347	0.503651	0.271429	0.037345
chr2	33	0.002	0.404979	0.436123	0.129933	0.016496
chr2	34	0	0.37624	0.489618	0.070956	0
chr2	35	0	0.355312	0.539592	0.039521	0
chr2	36	0	0.392021	0.388603	0.061227	0.012914
chr2	37	0	0.399144	0.426826	0.138814	0.031201
chr2	38	0	0.421905	0.469474	0.182495	0.029569
chr2	39	0	0.394265	0.451361	0.147052	0.019089

chr2	40	0	0.371712	0.355424	0.041203	0.006214
chr2	41	0	0.368532	0.460025	0.04862	0.000772
chr2	42	0	0.436003	0.437459	0.21232	0.026581
chr2	43	0	0.440867	0.407565	0.155716	0.026869
chr2	44	0	0.398744	0.421712	0.165705	0.020159
chr2	45	0	0.430655	0.351795	0.075079	0.015311
chr2	46	0	0.433611	0.365524	0.086653	0.027748
chr2	47	0	0.458286	0.471767	0.223927	0.029976
chr2	48	0	0.402438	0.503184	0.140305	0.023635
chr2	49	0	0.380057	0.455143	0.041851	0.002382
chr2	50	0	0.359383	0.249308	0.047984	0.003914
chr2	51	0	0.351635	0.436952	0.042236	0
chr2	52	0	0.359186	0.516014	0.042415	0
chr2	53	0	0.379771	0.473294	0.07765	0.007992
chr2	54	0	0.40586	0.386509	0.142773	0.02072
chr2	55	0	0.398464	0.459525	0.18868	0.033786
chr2	56	0	0.376453	0.418612	0.040241	0.005084
chr2	57	0	0.355159	0.537102	0.035612	0
chr2	58	0	0.364264	0.35494	0.050803	0.003211
chr2	59	0	0.379489	0.346824	0.034444	0
chr2	60	0	0.426004	0.355054	0.099531	0.011751
chr2	61	0	0.409331	0.533869	0.303408	0.019927
chr2	62	0	0.414267	0.533657	0.175586	0.009108
chr2	63	0	0.37669	0.547383	0.092327	0.016314
chr2	64	0	0.411012	0.389122	0.110504	0.026964
chr2	65	0	0.434691	0.432524	0.180363	0.031432
chr2	66	0	0.395321	0.349504	0.0435	0.004334
chr2	67	0	0.383081	0.362347	0.041492	0.003417
chr2	68	0	0.398556	0.442697	0.089741	0.024734
chr2	69	0	0.415175	0.422472	0.144372	0.027093
chr2	70	0	0.440982	0.451637	0.193787	0.039193
chr2	71	0	0.454461	0.434719	0.094578	0.035257
chr2	72	0	0.400229	0.509247	0.081936	0.009008
chr2	73	0	0.444218	0.499796	0.13382	0.039514
chr2	74	0	0.456956	0.415202	0.170174	0.065257
chr2	75	0	0.402178	0.482276	0.052577	0.019811
chr2	76	0	0.362254	0.488774	0.041826	0.000352
chr2	77	0	0.350241	0.43485	0.045792	0.003616
chr2	78	0	0.350315	0.514881	0.049382	0
chr2	79	0	0.381946	0.407833	0.052327	0.004204
chr2	80	0	0.388317	0.324129	0.052691	0.007604
chr2	81	0	0.357935	0.505655	0.03845	0.001898
chr2	82	0	0.350994	0.475797	0.05072	0.000967
chr2	83	0	0.35591	0.476925	0.060241	0
chr2	84	0	0.389856	0.465608	0.048153	0.009979
chr2	85	0	0.467993	0.463346	0.235785	0.045276
chr2	86	0	0.429604	0.473578	0.156941	0.040663
chr2	87	0	0.42587	0.421926	0.122948	0.021159
chr2	88	0	0.419287	0.494274	0.152949	0.01838

chr2	89	0.15	0.344084	0.380593	0.035275	0.005389
chr2	90	0.983023	0.007818	0.009286	0.002374	0
chr2	91	0.268932	0.30443	0.413077	0.076639	0.007599
chr2	92	1	0	0	0	0
chr2	93	1	0	0	0	0
chr2	94	0.748045	0.101357	0.096658	0.017939	0.001455
chr2	95	0	0.444203	0.403989	0.085068	0.027823
chr2	96	0	0.477855	0.44295	0.180378	0.072395
chr2	97	0.05	0.399286	0.399265	0.084373	0.017942
chr2	98	0	0.431541	0.464456	0.09915	0.019436
chr2	99	0	0.4076	0.483824	0.141871	0.025277
chr2	100	0	0.433716	0.43558	0.112065	0.007972
chr2	101	0	0.433848	0.435781	0.173774	0.028418
chr2	102	0	0.407598	0.410812	0.054111	0.035489
chr2	103	0	0.364762	0.47907	0.048545	0
chr2	104	0	0.391097	0.358294	0.05807	0.001503
chr2	105	0	0.429412	0.40382	0.095182	0.013103
chr2	106	0	0.423679	0.455633	0.108283	0.009875
chr2	107	0	0.385035	0.475027	0.072363	0.00807
chr2	108	0	0.398352	0.493779	0.120026	0.039463
chr2	109	0.05	0.437565	0.3605	0.134261	0.017891
chr2	110	0.291512	0.310183	0.339763	0.083341	0.023408
chr2	111	0.008488	0.42849	0.395584	0.074811	0.020192
chr2	112	0	0.422122	0.472646	0.153108	0.02989
chr2	113	0	0.440769	0.421848	0.114152	0.0544
chr2	114	0	0.402701	0.45211	0.097644	0.014397
chr2	115	0	0.370233	0.38423	0.055295	0.00043
chr2	116	0	0.360856	0.540289	0.050179	0.003965
chr2	117	0	0.369009	0.550676	0.040348	0
chr2	118	0	0.40871	0.451809	0.049862	0.010449
chr2	119	0	0.448689	0.409178	0.070919	0.018373
chr2	120	0	0.434564	0.468355	0.10641	0.022901
chr2	121	0	0.481687	0.382318	0.102186	0.017005
chr2	122	0	0.423374	0.492452	0.115465	0.005938
chr2	123	0	0.361841	0.524482	0.044732	0
chr2	124	0	0.376439	0.479117	0.047525	0.001841
chr2	125	0	0.374683	0.489948	0.051681	0.003494
chr2	126	0	0.376559	0.513593	0.046615	0
chr2	127	0	0.449538	0.49414	0.10895	0.028752
chr2	128	0	0.47072	0.491581	0.205583	0.042005
chr2	129	0	0.426535	0.577497	0.061669	0
chr2	130	0	0.445659	0.449991	0.101607	0.032181
chr2	131	0.15	0.385929	0.390009	0.121145	0.019275
chr2	132	0	0.410156	0.510466	0.095342	0.017046
chr2	133	0	0.40237	0.350532	0.057808	0.009147
chr2	134	0	0.414143	0.385839	0.055643	0.006133
chr2	135	0	0.412139	0.509663	0.141831	0.027529
chr2	136	0	0.408437	0.443633	0.157305	0.027282
chr2	137	0	0.387724	0.420295	0.043307	0

chr2	138	0	0.373702	0.434878	0.04317	0.002479
chr2	139	0	0.371978	0.43894	0.060112	0.006544
chr2	140	0	0.355347	0.43065	0.047033	0.005145
chr2	141	0	0.34772	0.376882	0.063325	0.010071
chr2	142	0	0.351842	0.321619	0.05027	0.001315
chr2	143	0	0.36292	0.395562	0.055851	0.002452
chr2	144	0	0.375101	0.281999	0.05702	0.015812
chr2	145	0	0.367861	0.273594	0.036345	0.006896
chr2	146	0	0.352879	0.389004	0.042545	0
chr2	147	0	0.365276	0.445566	0.042367	0.003297
chr2	148	0	0.373876	0.43364	0.063751	0.007396
chr2	149	0.1	0.361504	0.340363	0.069315	0.010512
chr2	150	0	0.381106	0.450507	0.04753	0.006812
chr2	151	0	0.387604	0.396252	0.078062	0.006823
chr2	152	0	0.398532	0.390255	0.162	0.040416
chr2	153	0	0.38634	0.438105	0.081086	0.010479
chr2	154	0	0.361905	0.529822	0.042633	0.002627
chr2	155	0	0.349737	0.431434	0.044705	0.00683
chr2	156	0	0.351358	0.468235	0.04111	0
chr2	157	0	0.37448	0.409595	0.064128	0.012769
chr2	158	0	0.388985	0.460888	0.073002	0.01572
chr2	159	0	0.410053	0.392662	0.111695	0.016475
chr2	160	0	0.383047	0.411393	0.11307	0.041335
chr2	161	0	0.383437	0.431596	0.068745	0.003587
chr2	162	0	0.3662	0.406373	0.052735	0.022954
chr2	163	0	0.354512	0.385803	0.035986	0.006652
chr2	164	0	0.361897	0.366799	0.053194	0.004539
chr2	165	0	0.364695	0.356233	0.06827	0.020539
chr2	166	0	0.3625	0.361978	0.056837	0.031249
chr2	167	0	0.358613	0.471539	0.042966	0.017624
chr2	168	0	0.385607	0.363609	0.071962	0.005441
chr2	169	0	0.392349	0.390278	0.068857	0.033938
chr2	170	0	0.391331	0.503401	0.144499	0.026138
chr2	171	0	0.408831	0.449139	0.172783	0.02342
chr2	172	0	0.407598	0.486609	0.183955	0.027269
chr2	173	0	0.408955	0.393786	0.103989	0.027619
chr2	174	0	0.40389	0.407438	0.121752	0.020028
chr2	175	0	0.397826	0.397903	0.123589	0.028913
chr2	176	0	0.404058	0.385331	0.066301	0.022016
chr2	177	0	0.394131	0.31767	0.075883	0.008875
chr2	178	0	0.390034	0.406211	0.092294	0.017117
chr2	179	0	0.380941	0.333272	0.064652	0.03615
chr2	180	0	0.369137	0.415372	0.047174	0.006222
chr2	181	0	0.360545	0.422731	0.035505	0.00304
chr2	182	0	0.369268	0.362971	0.048465	0.022485
chr2	183	0	0.374321	0.43612	0.090188	0.0197
chr2	184	0	0.358672	0.519748	0.034904	0
chr2	185	0	0.340081	0.473595	0.039192	0.005998
chr2	186	0	0.348874	0.521167	0.043115	0.007019

chr2	187	0	0.368777	0.486971	0.070015	0.014608
chr2	188	0	0.355954	0.447607	0.05207	0.005393
chr2	189	0	0.351717	0.418414	0.042738	0.012915
chr2	190	0	0.376279	0.473252	0.093937	0.027164
chr2	191	0	0.393474	0.393116	0.092597	0.023829
chr2	192	0	0.37985	0.322117	0.056873	0.014953
chr2	193	0	0.343865	0.474776	0.038093	0
chr2	194	0	0.341177	0.49153	0.043174	0
chr2	195	0	0.34567	0.461319	0.032602	0
chr2	196	0	0.381732	0.438895	0.109618	0.024106
chr2	197	0	0.390181	0.402526	0.108315	0.028502
chr2	198	0	0.395473	0.451071	0.131802	0.026278
chr2	199	0	0.363081	0.421546	0.037152	0.00337
chr2	200	0	0.395283	0.410302	0.088633	0.014508
chr2	201	0	0.413069	0.449452	0.175944	0.052287
chr2	202	0	0.413209	0.45732	0.162707	0.037591
chr2	203	0	0.402462	0.569256	0.297932	0.034666
chr2	204	0	0.406439	0.40188	0.14092	0.023208
chr2	205	0	0.376777	0.356567	0.049882	0.003797
chr2	206	0	0.418574	0.371107	0.148066	0.020017
chr2	207	0	0.398124	0.394671	0.066469	0.013125
chr2	208	0	0.416738	0.450383	0.190826	0.024515
chr2	209	0	0.370732	0.543419	0.038577	0.010477
chr2	210	0	0.367452	0.363996	0.079668	0.027063
chr2	211	0	0.363235	0.433331	0.037199	0.01161
chr2	212	0	0.349736	0.322215	0.056834	0.00537
chr2	213	0	0.358954	0.327931	0.04677	0.007583
chr2	214	0	0.35835	0.505802	0.058432	0.006679
chr2	215	0	0.379055	0.416559	0.090107	0.012178
chr2	216	0	0.406623	0.39223	0.114591	0.024352
chr2	217	0	0.437198	0.3686	0.090021	0.016124
chr2	218	0	0.459801	0.401628	0.076601	0.025655
chr2	219	0	0.475891	0.430633	0.22184	0.105051
chr2	220	0	0.453853	0.383625	0.096845	0.035886
chr2	221	0	0.382352	0.372246	0.060683	0
chr2	222	0	0.392998	0.321721	0.07596	0.011975
chr2	223	0	0.403563	0.441145	0.106515	0.010939
chr2	224	0	0.40696	0.455253	0.124358	0.014755
chr2	225	0	0.393231	0.391766	0.115959	0.017663
chr2	226	0	0.36911	0.400696	0.049704	0.002279
chr2	227	0	0.397522	0.36965	0.078634	0.014234
chr2	228	0	0.399417	0.467189	0.141825	0.029708
chr2	229	0	0.380275	0.444991	0.05082	0.002925
chr2	230	0	0.411432	0.43731	0.141181	0.026715
chr2	231	0	0.434916	0.472407	0.154855	0.031731
chr2	232	0	0.459799	0.474662	0.217272	0.020016
chr2	233	0.02	0.471338	0.408697	0.190983	0.043927
chr2	234	0	0.432511	0.420092	0.087687	0.034552
chr2	235	0	0.448804	0.403776	0.106448	0.009129

chr2	236	0	0.469084	0.328183	0.13368	0.012622
chr2	237	0	0.444101	0.363632	0.052892	0.009313
chr2	238	0	0.481293	0.364844	0.126016	0.045195
chr2	239	0.03	0.467574	0.343503	0.064361	0.018788
chr2	240	0.025	0.478844	0.360507	0.046244	0.011615
chr2	241	0	0.534338	0.347583	0.08546	0.06302
chr2	242	0.292771	0.348682	0.303047	0.117438	0.051421
chr2	243	0.99994515	0	0	0	0
chr20	0	0.008	0.459245	0.560442	0.159128	0.049982
chr20	1	0	0.446314	0.514011	0.06484	0.051472
chr20	2	0	0.45349	0.519876	0.19001	0.04902
chr20	3	0	0.46689	0.4904	0.247902	0.072658
chr20	4	0	0.444655	0.505836	0.161942	0.026397
chr20	5	0	0.431588	0.504386	0.211704	0.033514
chr20	6	0	0.390106	0.406488	0.06509	0.007154
chr20	7	0	0.37009	0.447762	0.047941	0.004111
chr20	8	0	0.383914	0.376401	0.067762	0.014689
chr20	9	0	0.390149	0.370726	0.061527	0.016057
chr20	10	0	0.403429	0.351452	0.066552	0.010749
chr20	11	0	0.38718	0.424473	0.049465	0.004983
chr20	12	0	0.385517	0.501642	0.04019	0.00226
chr20	13	0	0.396927	0.467372	0.118795	0.012187
chr20	14	0	0.373679	0.39003	0.073235	0.003977
chr20	15	0	0.385518	0.347063	0.052824	0.003475
chr20	16	0	0.40697	0.437091	0.062644	0.010868
chr20	17	0	0.441912	0.414447	0.113663	0.021553
chr20	18	0	0.423607	0.527932	0.122722	0.024701
chr20	19	0	0.432133	0.384659	0.077112	0.016017
chr20	20	0	0.419244	0.382137	0.082394	0.016184
chr20	21	0	0.412973	0.438802	0.08441	0.009885
chr20	22	0	0.417224	0.409588	0.040647	0.009106
chr20	23	0	0.448834	0.443323	0.047213	0.027746
chr20	24	0	0.456374	0.410195	0.039017	0.017808
chr20	25	0	0.450139	0.545504	0.15803	0.02697
chr20	26	0.732431	0.102049	0.147243	0.019376	0.002067
chr20	27	1	0	0	0	0
chr20	28	0.765661	0.094242	0.118525	0.017712	0.004194
chr20	29	0.267569	0.334372	0.421397	0.169672	0.026777
chr20	30	0	0.48499	0.511338	0.261512	0.057785
chr20	31	0	0.479183	0.504958	0.239543	0.041209
chr20	32	0	0.445236	0.544565	0.273592	0.050441
chr20	33	0	0.45756	0.518236	0.293728	0.066252
chr20	34	0.02	0.476738	0.505775	0.277032	0.043826
chr20	35	0	0.466567	0.506723	0.206691	0.024831
chr20	36	0	0.462519	0.463126	0.152075	0.053678
chr20	37	0	0.415458	0.424295	0.062516	0.005112
chr20	38	0	0.421145	0.40609	0.050395	0.003362
chr20	39	0	0.43215	0.450988	0.113013	0.036545
chr20	40	0	0.422559	0.410852	0.050493	0.01243

chr20	41	0	0.451937	0.507651	0.176912	0.016554
chr20	42	0	0.468185	0.512183	0.180588	0.050418
chr20	43	0	0.437351	0.52998	0.146739	0.071365
chr20	44	0	0.46813	0.445185	0.103002	0.05872
chr20	45	0	0.463388	0.501383	0.239371	0.025461
chr20	46	0	0.47991	0.472911	0.096388	0.012033
chr20	47	0	0.457239	0.514843	0.261565	0.053042
chr20	48	0	0.489755	0.497544	0.245017	0.024107
chr20	49	0	0.466921	0.479626	0.204229	0.020093
chr20	50	0	0.411639	0.429485	0.13257	0.005335
chr20	51	0	0.429658	0.429679	0.196866	0.014494
chr20	52	0	0.395589	0.452021	0.082792	0.00854
chr20	53	0	0.38023	0.477218	0.053793	0
chr20	54	0	0.449131	0.484732	0.175176	0.02164
chr20	55	0	0.492071	0.370955	0.071408	0.029143
chr20	56	0	0.462473	0.36162	0.090394	0.042413
chr20	57	0	0.450552	0.358825	0.060115	0.035791
chr20	58	0	0.431823	0.398631	0.043179	0.009735
chr20	59	0	0.50571	0.280009	0.046733	0.007206
chr20	60	0.13705	0.488114	0.23648	0.088753	0.095791
chr20	61	0	0.570644	0.286075	0.128019	0.10514
chr20	62	0	0.53604532	0.28203411	0.13147615	0.10804078
chr21	0	1	0	0	0	0
chr21	1	1	0	0	0	0
chr21	2	1	0	0	0	0
chr21	3	1	0	0	0	0
chr21	4	1	0	0	0	0
chr21	5	1	0	0	0	0
chr21	6	1	0	0	0	0
chr21	7	1	0	0	0	0
chr21	8	1	0	0	0	0
chr21	9	0.719767	0.110272	0.215546	0.01083	0.0024
chr21	10	0.79	0.085022	0.108684	0.036985	0.002216
chr21	11	1	0	0	0	0
chr21	12	1	0	0	0	0
chr21	13	0.26	0.279925	0.401564	0.069891	0.004222
chr21	14	0	0.390953	0.455266	0.062393	0.019343
chr21	15	0	0.376371	0.389778	0.056832	0.009475
chr21	16	0	0.356381	0.361764	0.064407	0.005216
chr21	17	0	0.382215	0.54555	0.095161	0.004443
chr21	18	0	0.366296	0.444754	0.057428	0.013442
chr21	19	0	0.352242	0.469379	0.050226	0
chr21	20	0	0.349962	0.469082	0.058059	0
chr21	21	0	0.348055	0.376763	0.064228	0.0037
chr21	22	0	0.350544	0.499845	0.065599	0
chr21	23	0	0.344839	0.465895	0.066264	0
chr21	24	0	0.355641	0.450496	0.078261	0.002908
chr21	25	0	0.368687	0.453024	0.070137	0.003881
chr21	26	0	0.390266	0.417056	0.107519	0.016379

chr21	27	0	0.367679	0.406077	0.057482	0.010186
chr21	28	0	0.368024	0.484003	0.052361	0.001177
chr21	29	0	0.395777	0.400241	0.110142	0.030603
chr21	30	0	0.368828	0.380539	0.062186	0.007184
chr21	31	0	0.417337	0.410286	0.164738	0.011449
chr21	32	3.00E-05	0.440455	0.445586	0.148588	0.029106
chr21	33	0	0.434047	0.431135	0.193528	0.047841
chr21	34	0	0.436098	0.408779	0.124869	0.024397
chr21	35	0	0.416256	0.308824	0.057241	0.012204
chr21	36	0	0.449268	0.467784	0.208773	0.024087
chr21	37	0	0.42816	0.427613	0.153849	0.037173
chr21	38	0	0.421904	0.353661	0.052802	0.011115
chr21	39	1.00E-05	0.433592	0.44399	0.132579	0.042904
chr21	40	0	0.416355	0.3743	0.068041	0.00685
chr21	41	0.001199	0.44806	0.437739	0.083995	0.022948
chr21	42	0.001842	0.497198	0.31631	0.08422	0.064138
chr21	43	0.001369	0.506146	0.457706	0.169194	0.04194
chr21	44	0	0.526288	0.400473	0.131151	0.085044
chr21	45	0	0.517023	0.353477	0.068391	0.049373
chr21	46	0	0.49980515	0.42968515	0.11789174	0.06665721
chr22	0	1	0	0	0	0
chr22	1	1	0	0	0	0
chr22	2	1	0	0	0	0
chr22	3	1	0	0	0	0
chr22	4	1	0	0	0	0
chr22	5	1	0	0	0	0
chr22	6	1	0	0	0	0
chr22	7	1	0	0	0	0
chr22	8	1	0	0	0	0
chr22	9	1	0	0	0	0
chr22	10	1	0	0	0	0
chr22	11	1	0	0	0	0
chr22	12	1	0	0	0	0
chr22	13	1	0	0	0	0
chr22	14	0.4319	0.240055	0.313864	0.03805	0.005141
chr22	15	0.15	0.352683	0.465356	0.097007	0.01671
chr22	16	0	0.473899	0.447531	0.290728	0.042362
chr22	17	2.10E-05	0.478658	0.446682	0.190029	0.039335
chr22	18	0.05	0.514893	0.325239	0.148133	0.063155
chr22	19	0	0.49006	0.426001	0.241141	0.069123
chr22	20	0	0.484759	0.471134	0.250857	0.05358
chr22	21	0	0.478663	0.398802	0.105303	0.041555
chr22	22	0	0.504961	0.452077	0.196258	0.062557
chr22	23	0	0.473427	0.499553	0.21588	0.034251
chr22	24	0	0.447465	0.444894	0.120258	0.019025
chr22	25	0	0.460101	0.451534	0.116334	0.02622
chr22	26	0	0.454024	0.417252	0.092077	0.023172
chr22	27	0	0.431742	0.498456	0.231043	0.029545
chr22	28	0	0.467606	0.45658	0.239176	0.056404

chr22	29	0	0.491328	0.463532	0.245037	0.07207
chr22	30	0	0.458485	0.519098	0.306067	0.05546
chr22	31	0	0.444429	0.477618	0.128295	0.024476
chr22	32	0	0.433044	0.476638	0.13392	0.00245
chr22	33	0	0.425603	0.534787	0.075137	0.004841
chr22	34	0	0.458533	0.470812	0.176615	0.038129
chr22	35	0	0.505157	0.435567	0.159848	0.05453
chr22	36	0	0.537103	0.4526	0.243892	0.076011
chr22	37	0	0.497104	0.493421	0.242662	0.068193
chr22	38	0	0.477363	0.442959	0.183905	0.049673
chr22	39	0	0.451512	0.531634	0.337045	0.054762
chr22	40	0	0.49512	0.50137	0.302206	0.083863
chr22	41	0	0.522146	0.454157	0.266464	0.043356
chr22	42	0.011	0.481807	0.442989	0.129815	0.022752
chr22	43	0.02	0.501714	0.454589	0.171657	0.028711
chr22	44	0.02	0.482956	0.415037	0.155353	0.053732
chr22	45	0	0.516044	0.338922	0.122885	0.036131
chr22	46	0	0.458079	0.48425	0.071861	0.005274
chr22	47	0.012	0.508168	0.319556	0.052946	0.003566
chr22	48	0.05	0.499782	0.337282	0.115398	0.053693
chr22	49	0.08112332	0.49468823	0.3750836	0.18167298	0.10155018
chr3	0	0.035	0.356445	0.387866	0.045412	0.00765
chr3	1	0	0.365911	0.449352	0.045612	0.00353
chr3	2	0	0.377391	0.349635	0.078848	0.005075
chr3	3	0	0.394036	0.427324	0.061585	0.017262
chr3	4	0	0.409454	0.447588	0.09233	0.015791
chr3	5	0	0.406959	0.499182	0.1009	0.010915
chr3	6	0	0.372828	0.456723	0.049569	0.000668
chr3	7	0	0.381723	0.394924	0.05092	0.003783
chr3	8	0	0.41941	0.459943	0.045549	0.015059
chr3	9	0	0.460232	0.478636	0.19638	0.066672
chr3	10	0	0.478631	0.417615	0.130446	0.039934
chr3	11	0	0.44646	0.488919	0.165057	0.020593
chr3	12	0	0.444737	0.443359	0.16903	0.02162
chr3	13	0	0.506475	0.452512	0.088034	0.011363
chr3	14	0	0.470258	0.471648	0.085278	0.025578
chr3	15	0	0.419918	0.459391	0.154286	0.036188
chr3	16	0	0.414103	0.448993	0.052851	0.014647
chr3	17	0	0.382336	0.398583	0.075004	0.01807
chr3	18	0	0.373916	0.357874	0.03097	0.004586
chr3	19	0	0.374077	0.494983	0.058257	0.009547
chr3	20	0	0.37793	0.533085	0.083356	0.010167
chr3	21	0	0.36501	0.443503	0.04046	0.001652
chr3	22	0	0.36844	0.477355	0.037254	0
chr3	23	0	0.399411	0.438373	0.13104	0.011992
chr3	24	0	0.385002	0.383724	0.055636	0.001814
chr3	25	0	0.387583	0.37179	0.064768	0.015029
chr3	26	0	0.380622	0.513904	0.030629	0.001689
chr3	27	0	0.394113	0.454326	0.126246	0.018376

chr3	28	0	0.373672	0.448735	0.046618	0.004064
chr3	29	0	0.363915	0.34522	0.05251	0.002888
chr3	30	0	0.380986	0.413198	0.043948	0.006769
chr3	31	0	0.402523	0.423015	0.081774	0.007991
chr3	32	0	0.432639	0.531759	0.23723	0.01769
chr3	33	0	0.401182	0.530731	0.166182	0.033541
chr3	34	0	0.382554	0.518309	0.039577	0
chr3	35	0	0.360832	0.444708	0.033634	0.006198
chr3	36	0	0.395896	0.50386	0.062607	0.002963
chr3	37	0	0.423363	0.39984	0.128475	0.033481
chr3	38	0	0.446167	0.447558	0.084887	0.059286
chr3	39	0	0.415434	0.527482	0.087191	0.040323
chr3	40	0	0.415575	0.494733	0.081802	0.025321
chr3	41	0	0.401496	0.509649	0.101225	0.005524
chr3	42	0	0.446647	0.445152	0.136118	0.050576
chr3	43	0	0.424147	0.447037	0.077564	0.017701
chr3	44	0	0.4265	0.434382	0.134598	0.049882
chr3	45	0	0.444491	0.414931	0.121609	0.046756
chr3	46	0	0.453832	0.498815	0.092105	0.048528
chr3	47	0	0.451343	0.504652	0.326348	0.063253
chr3	48	0	0.478357	0.519429	0.317237	0.080448
chr3	49	0	0.496313	0.474499	0.345206	0.112948
chr3	50	0	0.490243	0.430875	0.146654	0.073634
chr3	51	0	0.440817	0.56642	0.168656	0.03972
chr3	52	0	0.494061	0.357883	0.170271	0.088308
chr3	53	0	0.449431	0.404137	0.148841	0.029796
chr3	54	0	0.425277	0.366443	0.066066	0.004228
chr3	55	0	0.414673	0.35624	0.057214	0.011246
chr3	56	0	0.405486	0.42972	0.125473	0.014435
chr3	57	0	0.418208	0.51766	0.252927	0.040021
chr3	58	0	0.436365	0.473584	0.129892	0.031081
chr3	59	0	0.400491	0.393942	0.048904	0.000926
chr3	60	2.00E-06	0.384805	0.38377	0.062362	0.000213
chr3	61	0	0.402164	0.40037	0.109001	0.00354
chr3	62	0	0.401306	0.314998	0.072997	0.018789
chr3	63	0	0.393048	0.422716	0.061983	0.014955
chr3	64	0	0.406858	0.35152	0.058085	0.018925
chr3	65	0	0.401769	0.378813	0.097594	0.007382
chr3	66	0.26	0.309174	0.311261	0.093222	0.007134
chr3	67	0	0.387826	0.458534	0.05973	0.006962
chr3	68	0	0.383827	0.446103	0.041033	0.00357
chr3	69	0	0.402993	0.40703	0.127581	0.01714
chr3	70	0	0.374921	0.379605	0.039077	0.009523
chr3	71	0	0.411924	0.287404	0.110708	0.012232
chr3	72	0	0.443705	0.45223	0.110567	0.002846
chr3	73	0	0.412822	0.397141	0.128767	0.010191
chr3	74	0	0.37127	0.38424	0.051208	0
chr3	75	0	0.410495	0.548177	0.09443	0.002635
chr3	76	0	0.355514	0.323884	0.044335	0

chr3	77	0	0.360436	0.280174	0.057732	0.006011
chr3	78	0	0.362665	0.41231	0.046194	0.00613
chr3	79	0	0.350723	0.340564	0.050645	0.001517
chr3	80	0	0.346508	0.457969	0.048912	0
chr3	81	0	0.359335	0.402132	0.052587	0.002886
chr3	82	0	0.357547	0.44985	0.043133	0
chr3	83	0	0.337732	0.477841	0.039948	0
chr3	84	0	0.344883	0.543221	0.041236	0
chr3	85	0	0.342633	0.298216	0.059486	0.000874
chr3	86	0	0.350834	0.45492	0.046386	0.003112
chr3	87	0	0.360641	0.441021	0.05061	0.003656
chr3	88	0	0.360491	0.482185	0.056947	0.009447
chr3	89	0	0.350931	0.392414	0.044296	0.006672
chr3	90	0.412456	0.216451	0.394161	0.022342	0
chr3	91	1	0	0	0	0
chr3	92	1	0	0	0	0
chr3	93	1	0	0	0	0
chr3	94	0.987544	0.004627	0.012456	0	0
chr3	95	0	0.369822	0.465635	0.064105	0.01341
chr3	96	0	0.345348	0.515471	0.045372	0
chr3	97	0	0.349783	0.532847	0.042807	0
chr3	98	0	0.353895	0.410991	0.038877	0.004203
chr3	99	0	0.376856	0.474259	0.062033	0.02153
chr3	100	0	0.376573	0.506369	0.038859	0.008966
chr3	101	0	0.390872	0.408406	0.09566	0.029562
chr3	102	0	0.388295	0.500742	0.117004	0.028875
chr3	103	0	0.375272	0.436524	0.056647	0.011029
chr3	104	0	0.348538	0.478021	0.039638	0
chr3	105	0	0.348463	0.536337	0.039847	0
chr3	106	0	0.357597	0.405221	0.052492	0.008978
chr3	107	0	0.365434	0.47087	0.05553	0.000741
chr3	108	0	0.377054	0.452979	0.066481	0.006608
chr3	109	0	0.387985	0.38502	0.051802	0.019398
chr3	110	0	0.388616	0.526566	0.132597	0.012644
chr3	111	0	0.358835	0.494906	0.039532	0
chr3	112	0	0.3775	0.482389	0.035849	0.011212
chr3	113	0	0.388899	0.43017	0.074596	0.041751
chr3	114	0	0.398144	0.473958	0.092797	0.04697
chr3	115	0	0.387457	0.35369	0.093167	0.033245
chr3	116	0	0.371083	0.417502	0.046064	0.002769
chr3	117	0	0.373277	0.335831	0.048793	0.001537
chr3	118	0	0.36988	0.313917	0.046359	0.004143
chr3	119	0	0.369624	0.479844	0.032473	0
chr3	120	0	0.407102	0.472621	0.086783	0.044911
chr3	121	0	0.401498	0.475365	0.103807	0.025301
chr3	122	0	0.378928	0.614274	0.09724	0.031191
chr3	123	0	0.399971	0.517364	0.114402	0.046255
chr3	124	0	0.455405	0.347418	0.103913	0.031618
chr3	125	0	0.426106	0.335167	0.083763	0.030477

chr3	126	0	0.42896	0.48053	0.188103	0.028484
chr3	127	0	0.465512	0.506479	0.075923	0.030758
chr3	128	0	0.493888	0.418371	0.063228	0.029358
chr3	129	0	0.468819	0.449865	0.143199	0.02719
chr3	130	0	0.478729	0.464735	0.196074	0.059338
chr3	131	0	0.412647	0.510461	0.109768	0.019247
chr3	132	0	0.389712	0.444005	0.057873	0.021279
chr3	133	0	0.385677	0.433021	0.066051	0.028589
chr3	134	0	0.410833	0.459632	0.083838	0.0223
chr3	135	0	0.440487	0.424215	0.073225	0.026204
chr3	136	0	0.426813	0.421389	0.031382	0.00424
chr3	137	0	0.401774	0.573776	0.207859	0.022749
chr3	138	0	0.399948	0.549089	0.072196	0.006901
chr3	139	0	0.416915	0.492369	0.140579	0.042755
chr3	140	0	0.431658	0.483827	0.115351	0.025372
chr3	141	0	0.418113	0.410305	0.030174	0.006951
chr3	142	0	0.420651	0.476445	0.090438	0.017382
chr3	143	0	0.392164	0.532371	0.205431	0.040267
chr3	144	0	0.400708	0.37291	0.064485	0.015871
chr3	145	0	0.365032	0.419272	0.044099	0.004576
chr3	146	0	0.349208	0.512332	0.03999	0
chr3	147	0	0.361595	0.471888	0.039584	0.01318
chr3	148	0	0.359441	0.381481	0.044491	0.010702
chr3	149	0	0.359311	0.438535	0.046432	0.002405
chr3	150	0	0.396481	0.399726	0.117741	0.025713
chr3	151	0	0.391738	0.451866	0.108128	0.021797
chr3	152	0	0.389558	0.421439	0.072044	0.031418
chr3	153	0	0.365642	0.398407	0.065122	0.01101
chr3	154	0	0.380866	0.472548	0.120718	0.009339
chr3	155	0	0.371282	0.481039	0.057476	0.005948
chr3	156	0	0.386985	0.515321	0.093039	0.015852
chr3	157	0	0.400959	0.398119	0.096628	0.0172
chr3	158	0	0.388387	0.436511	0.060682	0.014336
chr3	159	0	0.37532	0.438261	0.072111	0.015103
chr3	160	0	0.390895	0.414783	0.045726	0.003165
chr3	161	0	0.398639	0.429036	0.119328	0.023227
chr3	162	0	0.377987	0.458427	0.063889	0.011651
chr3	163	0	0.3547	0.495502	0.038886	0
chr3	164	0	0.343241	0.575972	0.04361	0
chr3	165	0	0.349114	0.541441	0.040536	0
chr3	166	0	0.345993	0.466599	0.055855	0.010998
chr3	167	0	0.345407	0.498704	0.042164	0.001674
chr3	168	0	0.363625	0.49247	0.037297	0.009681
chr3	169	0	0.365678	0.397564	0.048417	0.004108
chr3	170	0	0.372636	0.300623	0.055419	0.012392
chr3	171	0	0.410611	0.458985	0.187218	0.040299
chr3	172	0	0.394775	0.401545	0.076612	0.02361
chr3	173	0	0.399933	0.413765	0.134832	0.020511
chr3	174	0	0.363635	0.429573	0.051822	0.005037

chr3	175	0	0.355986	0.370963	0.063672	0.004002
chr3	176	0	0.351366	0.361822	0.053585	0.002939
chr3	177	0	0.362086	0.49223	0.042812	0.002634
chr3	178	0	0.404407	0.432926	0.147327	0.006541
chr3	179	0	0.372492	0.431515	0.043344	0.000276
chr3	180	0	0.39769	0.502276	0.148854	0.028218
chr3	181	0	0.374593	0.47185	0.053201	0.011583
chr3	182	0	0.37877	0.433361	0.104278	0.007013
chr3	183	0	0.389217	0.421723	0.108437	0.000284
chr3	184	0	0.417625	0.477937	0.200459	0.045399
chr3	185	0	0.483215	0.42959	0.213134	0.072258
chr3	186	0	0.41028	0.490689	0.178366	0.02696
chr3	187	0	0.432382	0.428305	0.165423	0.024808
chr3	188	0	0.423453	0.499071	0.09636	0.031318
chr3	189	0	0.401529	0.349991	0.079003	0.003924
chr3	190	0	0.383299	0.441333	0.059058	0.010174
chr3	191	0	0.37598	0.391627	0.067552	0.02353
chr3	192	0	0.369357	0.522301	0.063463	0.004132
chr3	193	0	0.372278	0.423603	0.057675	0.005737
chr3	194	0	0.398662	0.433515	0.090676	0.013101
chr3	195	0.02	0.449643	0.389404	0.138699	0.032858
chr3	196	0.1	0.410987	0.380573	0.12572	0.030492
chr3	197	0	0.467591	0.517488	0.287028	0.042379
chr3	198	0	0.439943	0.470814	0.177613	0.033096
chr3	199	0.10875132	0.37833595	0.41645032	0.18304824	0.02831291
chr4	0	0	0.482347	0.513325	0.139224	0.053492
chr4	1	0.051	0.514541	0.343779	0.133316	0.071039
chr4	2	0.15	0.422212	0.385738	0.164731	0.058363
chr4	3	0.049373	0.492347	0.369864	0.092944	0.0388
chr4	4	0.030627	0.447093	0.478292	0.11852	0.012913
chr4	5	0	0.443113	0.547412	0.064929	0.020048
chr4	6	0	0.49805	0.415286	0.106532	0.03853
chr4	7	0	0.518296	0.349254	0.081411	0.028797
chr4	8	0.149089	0.446279	0.335239	0.0919	0.039743
chr4	9	0.000911	0.456416	0.425592	0.081207	0.024132
chr4	10	0	0.404275	0.444371	0.065549	0.008715
chr4	11	0	0.379309	0.502938	0.042667	0.001965
chr4	12	0	0.383988	0.504954	0.0474	0
chr4	13	0	0.394089	0.445498	0.041719	0.009026
chr4	14	0	0.389499	0.481326	0.041397	0.008708
chr4	15	0	0.410905	0.425018	0.081416	0.029899
chr4	16	0	0.402087	0.438912	0.061228	0.002606
chr4	17	0	0.402625	0.499133	0.109025	0.018269
chr4	18	0	0.369143	0.482455	0.037446	0
chr4	19	0	0.364904	0.464238	0.048381	0.000599
chr4	20	0	0.37573	0.367659	0.061601	0.008199
chr4	21	0	0.376795	0.427666	0.052805	0.003843
chr4	22	0	0.380264	0.450244	0.057534	0.005877
chr4	23	0	0.386747	0.368509	0.046117	0.006317

chr4	24	0	0.421155	0.457855	0.105316	0.022957
chr4	25	0	0.436613	0.468252	0.202608	0.013912
chr4	26	0	0.39341	0.461334	0.087247	0.01681
chr4	27	0	0.359287	0.476768	0.047359	0
chr4	28	0	0.351093	0.417371	0.046204	0
chr4	29	0	0.345731	0.442773	0.056722	0
chr4	30	0	0.356762	0.353546	0.061204	0.006232
chr4	31	0.15	0.298464	0.385891	0.045548	0
chr4	32	0.059	0.325539	0.409558	0.044908	0
chr4	33	0	0.346507	0.470821	0.048202	0
chr4	34	0	0.344841	0.492593	0.044061	0
chr4	35	0	0.349956	0.461255	0.041279	0.005401
chr4	36	0	0.368624	0.491799	0.049414	0.003239
chr4	37	0	0.411952	0.421877	0.096543	0.014702
chr4	38	0	0.412296	0.47093	0.137533	0.024161
chr4	39	0	0.416034	0.569173	0.350746	0.041195
chr4	40	0.02	0.419644	0.444688	0.240296	0.016351
chr4	41	0	0.404776	0.382334	0.109958	0.022766
chr4	42	0	0.389834	0.446601	0.077069	0.003793
chr4	43	0	0.356175	0.518324	0.042303	0
chr4	44	0	0.360175	0.476306	0.037766	0.008067
chr4	45	0	0.350763	0.538386	0.038319	0.006766
chr4	46	0	0.360998	0.453494	0.048027	0.015421
chr4	47	0	0.379546	0.429542	0.08232	0.032871
chr4	48	0	0.392845	0.52304	0.110368	0.021352
chr4	49	0.648955	0.15466	0.235427	0.026279	0
chr4	50	1	0	0	0	0
chr4	51	1	0	0	0	0
chr4	52	0.501045	0.199761	0.259027	0.023774	0.016096
chr4	53	0	0.406122	0.533217	0.073696	0.012745
chr4	54	0	0.40856	0.465275	0.108086	0.016373
chr4	55	0	0.404409	0.453186	0.069937	0.014115
chr4	56	0	0.394028	0.506285	0.153554	0.022779
chr4	57	0	0.422488	0.487389	0.214629	0.033703
chr4	58	0	0.37272	0.476875	0.037708	0
chr4	59	0.05	0.332471	0.490466	0.03686	0
chr4	60	0	0.346265	0.513341	0.039195	0
chr4	61	0	0.353782	0.441247	0.052699	0
chr4	62	0	0.354121	0.366693	0.066853	0.008255
chr4	63	0	0.351429	0.559489	0.043267	0
chr4	64	0	0.341412	0.541617	0.038366	0.003034
chr4	65	0	0.349013	0.50094	0.042786	0.000766
chr4	66	0	0.343514	0.426641	0.038268	0.007768
chr4	67	0	0.358635	0.469194	0.043202	0
chr4	68	0	0.370808	0.512137	0.073208	0.029344
chr4	69	0.1	0.333157	0.530324	0.060823	0.018523
chr4	70	0	0.354699	0.527567	0.033238	0.01331
chr4	71	0.175	0.301694	0.349451	0.068745	0.026214
chr4	72	0	0.387353	0.469118	0.125152	0.02617

chr4	73	0	0.365305	0.498313	0.035102	0.008366
chr4	74	0	0.377104	0.487878	0.075103	0.024857
chr4	75	0.075	0.342946	0.412259	0.041909	0.022225
chr4	76	0	0.393482	0.518237	0.07729	0.028076
chr4	77	0	0.405853	0.466243	0.150503	0.03481
chr4	78	0	0.41558	0.449641	0.081157	0.020547
chr4	79	0	0.392793	0.442272	0.092081	0.011194
chr4	80	0	0.365024	0.43995	0.052166	0.01086
chr4	81	0	0.363512	0.440339	0.04288	0.009105
chr4	82	0	0.375652	0.427112	0.047972	0.016702
chr4	83	0	0.404539	0.469007	0.115743	0.010852
chr4	84	0	0.409544	0.505553	0.207913	0.038011
chr4	85	0	0.383714	0.407486	0.055582	0.009511
chr4	86	0	0.36971	0.452966	0.066816	0.01583
chr4	87	0	0.370365	0.418647	0.067272	0.010313
chr4	88	0	0.398216	0.470162	0.157244	0.034618
chr4	89	0	0.399823	0.512707	0.133778	0.035595
chr4	90	0	0.378982	0.436653	0.065299	0.012528
chr4	91	0	0.35586	0.395561	0.058699	0.008845
chr4	92	0	0.351106	0.490898	0.039702	0.001641
chr4	93	0	0.350897	0.506062	0.037796	0.000244
chr4	94	0	0.348771	0.368514	0.045704	0.002116
chr4	95	0	0.37493	0.442967	0.094717	0.015797
chr4	96	0	0.371362	0.343431	0.068369	0.006014
chr4	97	0	0.355304	0.449041	0.040714	0.001382
chr4	98	0	0.355351	0.494978	0.031194	0.000351
chr4	99	0	0.379163	0.517083	0.073434	0.005189
chr4	100	0	0.387347	0.523541	0.096131	0.028441
chr4	101	0	0.375415	0.474959	0.054406	0.017131
chr4	102	0	0.366721	0.443303	0.064406	0.007691
chr4	103	0	0.373666	0.451438	0.056188	0.013415
chr4	104	0	0.37346	0.548818	0.074292	0.022088
chr4	105	0	0.35405	0.544215	0.031406	0.000746
chr4	106	0	0.368943	0.452998	0.059932	0.014797
chr4	107	0	0.367791	0.482384	0.047307	0.012554
chr4	108	0	0.365471	0.474254	0.034218	0.006516
chr4	109	0	0.400127	0.417195	0.094242	0.014992
chr4	110	0	0.386711	0.396382	0.122298	0.018526
chr4	111	0	0.396657	0.438847	0.118554	0.023689
chr4	112	0	0.356467	0.423715	0.033891	0
chr4	113	0	0.38355	0.424519	0.112941	0.02472
chr4	114	0	0.374231	0.332317	0.107202	0.018628
chr4	115	0	0.363899	0.4908	0.046226	0.008601
chr4	116	0	0.344435	0.443806	0.041107	0.003339
chr4	117	0	0.344743	0.510872	0.043743	0
chr4	118	0	0.344017	0.500821	0.036446	0.002023
chr4	119	0	0.376728	0.450279	0.094942	0.010746
chr4	120	0	0.381978	0.384001	0.085361	0.038918
chr4	121	0	0.363691	0.466697	0.045972	0.001979

chr4	122	0	0.37944	0.433995	0.0557	0.009948
chr4	123	0	0.376508	0.428839	0.076137	0.03107
chr4	124	0	0.386211	0.446806	0.103565	0.016742
chr4	125	0	0.362319	0.440356	0.036821	0.007761
chr4	126	0	0.355356	0.379151	0.052701	0.009669
chr4	127	0	0.350085	0.452771	0.047174	0
chr4	128	0	0.368862	0.490628	0.043739	0.005737
chr4	129	0	0.397789	0.537288	0.171079	0.021838
chr4	130	0	0.374897	0.457341	0.07401	0.01129
chr4	131	0	0.351587	0.454077	0.044418	0
chr4	132	0	0.344638	0.535585	0.049437	0
chr4	133	0	0.355492	0.518977	0.043058	0
chr4	134	0	0.346204	0.476303	0.047675	0.005843
chr4	135	0	0.344609	0.493402	0.040559	0
chr4	136	0	0.344867	0.477509	0.039598	0
chr4	137	0	0.343164	0.439261	0.043579	0
chr4	138	0	0.353677	0.4477	0.05258	0.005143
chr4	139	0	0.369676	0.420704	0.048268	0.003667
chr4	140	0	0.415067	0.485692	0.208119	0.022934
chr4	141	0	0.405761	0.360433	0.091821	0.019221
chr4	142	0	0.382074	0.484086	0.06541	0.008346
chr4	143	0	0.36592	0.46033	0.045966	0.005195
chr4	144	0	0.380912	0.469651	0.070759	0.017924
chr4	145	0	0.373512	0.445022	0.045739	0.006438
chr4	146	0	0.385644	0.526776	0.085746	0.020627
chr4	147	0	0.393038	0.397962	0.063417	0.016894
chr4	148	0	0.381166	0.421648	0.076332	0.011678
chr4	149	0	0.391365	0.391165	0.08555	0.011109
chr4	150	0	0.367314	0.454829	0.037916	0
chr4	151	0	0.371432	0.409601	0.086688	0.011318
chr4	152	0	0.399461	0.46832	0.179655	0.015421
chr4	153	0	0.408048	0.367041	0.076825	0.011329
chr4	154	0	0.415729	0.4377	0.145898	0.030383
chr4	155	0	0.38955	0.400636	0.055986	0.026212
chr4	156	0	0.375266	0.438859	0.060567	0.018681
chr4	157	0	0.361682	0.426225	0.053024	0.009291
chr4	158	0	0.356464	0.385322	0.051598	0.009176
chr4	159	0	0.371437	0.468032	0.065403	0.015885
chr4	160	0	0.393177	0.455032	0.120513	0.011478
chr4	161	0	0.35953	0.52182	0.038478	0
chr4	162	0	0.343761	0.462161	0.061957	0.003667
chr4	163	0	0.344485	0.435541	0.05858	0.001163
chr4	164	0	0.371395	0.438399	0.060483	0.01288
chr4	165	0	0.360891	0.459583	0.044453	0.001793
chr4	166	0	0.397026	0.442384	0.164379	0.017428
chr4	167	0.03	0.343835	0.420882	0.045194	0.007162
chr4	168	0	0.352833	0.47183	0.045718	0.003307
chr4	169	0	0.372059	0.468542	0.064328	0.014661
chr4	170	0	0.393972	0.470834	0.134354	0.024513

chr4	171	0	0.389987	0.502443	0.078658	0.008678
chr4	172	0	0.348277	0.50182	0.049456	0
chr4	173	0	0.357057	0.423163	0.059463	0
chr4	174	0	0.392764	0.40844	0.076752	0.015118
chr4	175	0	0.366572	0.399151	0.062325	0.010887
chr4	176	0	0.359418	0.525437	0.0559	0.006709
chr4	177	0	0.367306	0.409165	0.081168	0.01507
chr4	178	0	0.371634	0.42611	0.089976	0.005448
chr4	179	0	0.352377	0.471886	0.052352	0
chr4	180	0	0.35566	0.47784	0.064045	0
chr4	181	0	0.358488	0.339431	0.063671	0
chr4	182	0	0.376355	0.317393	0.06367	0
chr4	183	0	0.386853	0.303698	0.090388	0.002257
chr4	184	0	0.426595	0.433107	0.157814	0.021349
chr4	185	0	0.433232	0.416705	0.125906	0.01919
chr4	186	0	0.421578	0.386168	0.14139	0.039451
chr4	187	0	0.417524	0.398111	0.10194	0.032354
chr4	188	0	0.395538	0.383557	0.070333	0.003453
chr4	189	0	0.40571	0.480032	0.15697	0.006029
chr4	190	0	0.39452	0.421677	0.051681	0
chr4	191	0.02431794	0.4260771	0.4337178	0.04714033	0.00760179
chr5	0	0.063	0.485729	0.319746	0.05469	0.049972
chr5	1	0	0.539626	0.305087	0.059671	0.04124
chr5	2	0	0.453897	0.314598	0.043246	0.003347
chr5	3	0	0.440914	0.317783	0.048851	0.001858
chr5	4	0	0.399571	0.385431	0.042412	0
chr5	5	0	0.418999	0.381956	0.050302	0.010422
chr5	6	0	0.441535	0.36296	0.054897	0.015165
chr5	7	0	0.406134	0.380168	0.050468	0.012248
chr5	8	0	0.38644	0.456746	0.042267	0
chr5	9	0	0.402101	0.358301	0.047493	0.008852
chr5	10	0	0.439763	0.451314	0.107721	0.016989
chr5	11	0	0.394566	0.316023	0.06141	0.005436
chr5	12	0	0.356749	0.521599	0.043316	0
chr5	13	0	0.376951	0.44872	0.044015	0.013971
chr5	14	0	0.431874	0.325289	0.116789	0.028889
chr5	15	0	0.394594	0.441173	0.057608	0.004562
chr5	16	0	0.415704	0.408541	0.1113	0.014059
chr5	17	0	0.415327	0.435307	0.157441	0.004736
chr5	18	0	0.3568	0.481491	0.052379	0
chr5	19	0	0.349734	0.452449	0.052333	0.002807
chr5	20	0	0.350828	0.447319	0.057189	0.000121
chr5	21	0	0.357313	0.459432	0.074936	0.004657
chr5	22	0	0.353267	0.378991	0.06313	0.00353
chr5	23	0	0.354767	0.527406	0.062699	0.000456
chr5	24	0	0.351398	0.482365	0.057165	0.004789
chr5	25	0	0.349292	0.514327	0.055058	0
chr5	26	0	0.349128	0.499437	0.052183	0.002682
chr5	27	0	0.344861	0.460111	0.050617	0.000382

chr5	28	0	0.348177	0.499742	0.047353	0
chr5	29	0	0.346984	0.524172	0.053325	0
chr5	30	0	0.355677	0.477452	0.040072	0
chr5	31	0	0.414033	0.380602	0.14435	0.015805
chr5	32	0	0.424364	0.494783	0.188714	0.033553
chr5	33	0	0.395099	0.468674	0.062973	0.012158
chr5	34	0	0.398738	0.473272	0.106842	0.033102
chr5	35	0	0.392791	0.439428	0.0599	0.020597
chr5	36	0	0.391128	0.448206	0.073439	0.019327
chr5	37	0	0.398304	0.512415	0.168603	0.027289
chr5	38	0	0.4101	0.391908	0.071043	0.021252
chr5	39	0	0.373698	0.402847	0.068387	0.01254
chr5	40	0	0.382555	0.51159	0.090439	0.025731
chr5	41	0	0.3768	0.445	0.047099	0.02569
chr5	42	0	0.381311	0.500676	0.049622	0.010024
chr5	43	0	0.404381	0.549719	0.129349	0.029611
chr5	44	0	0.364526	0.48673	0.038562	0.003808
chr5	45	0	0.357478	0.47943	0.044286	0.002748
chr5	46	0.558602	0.161638	0.428622	0.002085	0
chr5	47	1	0	0	0	0
chr5	48	1	0	0	0	0
chr5	49	0.441398	0.209714	0.380814	0.021394	0.005359
chr5	50	0	0.361226	0.343911	0.042515	0.0054
chr5	51	0	0.351469	0.437883	0.040292	0
chr5	52	0	0.38069	0.416835	0.064568	0.01801
chr5	53	0	0.397835	0.443596	0.100468	0.008863
chr5	54	0	0.400588	0.439503	0.121994	0.022213
chr5	55	0	0.414	0.44161	0.134565	0.012124
chr5	56	0	0.40337	0.447125	0.133297	0.010242
chr5	57	0	0.378969	0.41092	0.044761	0.005521
chr5	58	0	0.378389	0.342103	0.055411	0.008353
chr5	59	0	0.376593	0.405325	0.047338	0.006365
chr5	60	0	0.392957	0.443766	0.08656	0.012628
chr5	61	0	0.401194	0.432483	0.10806	0.014234
chr5	62	0	0.373181	0.504213	0.042209	0
chr5	63	0	0.373621	0.510603	0.04069	0.002996
chr5	64	0	0.37013	0.461739	0.100262	0.028626
chr5	65	0	0.395378	0.461251	0.112584	0.021585
chr5	66	0	0.389266	0.343629	0.052355	0.004997
chr5	67	0	0.395529	0.433602	0.059424	0.006931
chr5	68	0	0.417506	0.525045	0.246273	0.03098
chr5	69	0	0.379699	0.47048	0.12915	0.025631
chr5	70	0	0.389136	0.476982	0.184687	0.040365
chr5	71	0	0.410529	0.399916	0.070171	0.020553
chr5	72	0	0.406698	0.428954	0.11555	0.015792
chr5	73	0	0.407647	0.320418	0.065188	0.008152
chr5	74	0	0.391173	0.511397	0.133384	0.026685
chr5	75	0	0.403078	0.445063	0.086299	0.009135
chr5	76	0	0.412646	0.465843	0.130311	0.027601

chr5	77	0	0.395362	0.401379	0.107161	0.016393
chr5	78	0	0.404164	0.467855	0.186176	0.02211
chr5	79	0	0.417055	0.4794	0.176943	0.045901
chr5	80	0	0.389958	0.439826	0.113644	0.017637
chr5	81	0	0.390846	0.450434	0.074888	0.006649
chr5	82	0	0.370379	0.380169	0.055363	0.015907
chr5	83	0	0.357618	0.371044	0.052811	0.0049
chr5	84	0	0.343634	0.523354	0.039171	0
chr5	85	0	0.349242	0.473268	0.049419	0.003041
chr5	86	0	0.364569	0.468622	0.065039	0.016472
chr5	87	0	0.366691	0.442924	0.050768	0.007673
chr5	88	0	0.363992	0.324544	0.044103	0.004072
chr5	89	0	0.366141	0.42826	0.054235	0.015781
chr5	90	0	0.377201	0.413797	0.102347	0.020011
chr5	91	0.04	0.33509	0.414178	0.032934	0
chr5	92	0	0.3714	0.345411	0.036903	0.009496
chr5	93	0	0.365505	0.424247	0.073646	0.0095
chr5	94	0	0.372745	0.381756	0.061816	0.016606
chr5	95	0	0.390526	0.384113	0.064473	0.020793
chr5	96	0	0.382648	0.424181	0.067229	0.029353
chr5	97	0.023	0.358633	0.489749	0.034737	0
chr5	98	0	0.3729	0.514938	0.081196	0.012069
chr5	99	0	0.353098	0.466775	0.051162	0.00124
chr5	100	0	0.35093	0.520793	0.034747	0.007069
chr5	101	0	0.359081	0.534037	0.0458	0.007855
chr5	102	0	0.366914	0.359943	0.047785	0.019775
chr5	103	0	0.356	0.423497	0.056121	0.000902
chr5	104	0	0.342805	0.478259	0.036585	0
chr5	105	0	0.344762	0.458204	0.055353	0
chr5	106	0	0.366165	0.327016	0.044267	0.003033
chr5	107	0	0.374249	0.408029	0.057255	0.006873
chr5	108	0	0.377503	0.47338	0.071678	0.008599
chr5	109	0	0.372312	0.472894	0.033841	0.009345
chr5	110	0	0.372945	0.468693	0.043126	0.014978
chr5	111	0	0.392174	0.452136	0.052932	0.009965
chr5	112	0	0.401096	0.422808	0.120353	0.03677
chr5	113	0	0.379632	0.503181	0.043139	0.002915
chr5	114	0	0.388608	0.500154	0.048443	0.023023
chr5	115	0	0.388196	0.411479	0.052501	0.019971
chr5	116	0	0.372193	0.408197	0.070706	0
chr5	117	0	0.362633	0.42569	0.039498	0
chr5	118	0	0.38603	0.501399	0.104958	0.019535
chr5	119	0	0.362366	0.497436	0.041178	0.000493
chr5	120	0	0.350312	0.500569	0.039905	0.001356
chr5	121	0	0.376767	0.433916	0.040179	0.013361
chr5	122	0	0.385292	0.403347	0.089707	0.013026
chr5	123	0	0.382544	0.446896	0.048928	0
chr5	124	0	0.383565	0.388898	0.071727	0.005645
chr5	125	0	0.382167	0.494894	0.083842	0.006461

chr5	126	0	0.403096	0.44927	0.126476	0.019828
chr5	127	0	0.378063	0.403616	0.064725	0.017016
chr5	128	0	0.364241	0.513002	0.047731	0.006509
chr5	129	0	0.362178	0.495371	0.051622	0.005882
chr5	130	0	0.385037	0.567039	0.127363	0.01091
chr5	131	0	0.429741	0.515131	0.107864	0.043709
chr5	132	0	0.448922	0.42246	0.15615	0.047799
chr5	133	0	0.462926	0.446473	0.202091	0.028812
chr5	134	0	0.455564	0.410362	0.160995	0.033564
chr5	135	0	0.42093	0.437248	0.040485	0.010994
chr5	136	0	0.417825	0.426953	0.039597	0.009846
chr5	137	0	0.431384	0.470289	0.259808	0.059286
chr5	138	0.005	0.448234	0.486548	0.258053	0.027071
chr5	139	0	0.458389	0.42401	0.165819	0.03945
chr5	140	0	0.417008	0.41225	0.133734	0.190916
chr5	141	0	0.462466	0.445981	0.181481	0.038853
chr5	142	0	0.411705	0.384969	0.082735	0.013843
chr5	143	0	0.383379	0.437516	0.048623	0.007541
chr5	144	0	0.369923	0.541406	0.040383	0
chr5	145	0	0.404482	0.444443	0.132682	0.018459
chr5	146	0	0.392901	0.448495	0.06984	0.009125
chr5	147	0	0.375314	0.444779	0.044813	0.019201
chr5	148	0	0.433132	0.433693	0.100289	0.036904
chr5	149	0	0.486747	0.412731	0.141161	0.052455
chr5	150	0	0.438446	0.495454	0.110056	0.063815
chr5	151	0	0.403841	0.490907	0.072518	0.010338
chr5	152	0	0.384589	0.517508	0.036708	0.000363
chr5	153	0	0.430068	0.456035	0.090259	0.01833
chr5	154	0	0.417758	0.502827	0.137524	0.019141
chr5	155	0.0041	0.383272	0.440426	0.056869	0.001032
chr5	156	0	0.419843	0.510294	0.149986	0.039555
chr5	157	0	0.413026	0.437382	0.121444	0.013419
chr5	158	0	0.403766	0.363486	0.060385	0.014319
chr5	159	0	0.434568	0.465814	0.156383	0.031091
chr5	160	0	0.380028	0.472043	0.0473	0.004247
chr5	161	0	0.358836	0.47426	0.049148	0.009269
chr5	162	0	0.375033	0.504881	0.077549	0.010191
chr5	163	0	0.362232	0.389702	0.053167	0
chr5	164	0	0.358852	0.433624	0.077078	0
chr5	165	0	0.36751	0.397759	0.072151	0
chr5	166	0	0.383006	0.333232	0.089946	0
chr5	167	0	0.428924	0.358282	0.111814	0.011869
chr5	168	0	0.431255	0.381436	0.071594	0.00762
chr5	169	0	0.448741	0.365697	0.054319	0.023698
chr5	170	0	0.423528	0.473012	0.113006	0.014101
chr5	171	0	0.455293	0.506201	0.176029	0.019976
chr5	172	0	0.467826	0.457336	0.159767	0.028315
chr5	173	0	0.441482	0.450716	0.094833	0.009377
chr5	174	0	0.429769	0.526787	0.10714	0.008895

chr5	175	0	0.469763	0.51629	0.159344	0.041459
chr5	176	0	0.497791	0.461975	0.223141	0.076497
chr5	177	0	0.477572	0.480675	0.16958	0.036679
chr5	178	0	0.482538	0.481886	0.177674	0.030664
chr5	179	0	0.484927	0.485309	0.225862	0.051343
chr5	180	0.02331364	0.43621331	0.54469749	0.1242815	0.03272069
chr6	0	0.005	0.428765	0.3703	0.062576	0.016442
chr6	1	0	0.436574	0.326614	0.074609	0.010727
chr6	2	0	0.42614	0.434171	0.096227	0.031297
chr6	3	0	0.454078	0.403831	0.110771	0.03008
chr6	4	0	0.425541	0.492214	0.107007	0.021066
chr6	5	0	0.427227	0.364717	0.073629	0.00553
chr6	6	0	0.429343	0.435429	0.092916	0.007532
chr6	7	0	0.433837	0.379243	0.162725	0.049055
chr6	8	0	0.384674	0.410637	0.080851	0.008932
chr6	9	0.05	0.352537	0.3978	0.045806	0.000316
chr6	10	0	0.41854	0.427469	0.167853	0.026643
chr6	11	0	0.414421	0.418319	0.098191	0.01865
chr6	12	0	0.39472	0.379902	0.08527	0.011313
chr6	13	0	0.423832	0.411051	0.134431	0.022906
chr6	14	0	0.428897	0.37548	0.087997	0.010553
chr6	15	0	0.433914	0.435955	0.211729	0.012343
chr6	16	0	0.423146	0.379515	0.118207	0.015217
chr6	17	0	0.414196	0.497431	0.204303	0.023605
chr6	18	0	0.400808	0.454746	0.153632	0.018817
chr6	19	0	0.383659	0.462	0.067663	0.002343
chr6	20	0	0.403375	0.431968	0.137278	0.011524
chr6	21	0	0.412627	0.419136	0.184059	0.007423
chr6	22	0	0.381829	0.37969	0.078572	0.003391
chr6	23	0	0.369442	0.452322	0.046962	0
chr6	24	0	0.402794	0.445557	0.14471	0.03799
chr6	25	0	0.39734	0.390446	0.091487	0.021528
chr6	26	0	0.416866	0.436766	0.146467	0.060655
chr6	27	0	0.409663	0.516213	0.168183	0.034545
chr6	28	0	0.406154	0.463297	0.127582	0.046825
chr6	29	0	0.41424	0.520611	0.085921	0.043227
chr6	30	0	0.456368	0.497943	0.16998	0.096984
chr6	31	0	0.480525	0.486669	0.205303	0.109805
chr6	32	0	0.442982	0.455384	0.112112	0.095485
chr6	33	0	0.491885	0.413873	0.170048	0.095715
chr6	34	0	0.477353	0.508291	0.250034	0.027724
chr6	35	0	0.460092	0.464363	0.218494	0.044208
chr6	36	0	0.454642	0.446933	0.206993	0.050173
chr6	37	0	0.467384	0.454911	0.203084	0.044086
chr6	38	0	0.401364	0.419265	0.128358	0.02322
chr6	39	0	0.437897	0.370131	0.076889	0.042602
chr6	40	0	0.452149	0.412377	0.030642	0.007155
chr6	41	0	0.468902	0.402115	0.118139	0.044804
chr6	42	0	0.451645	0.50181	0.269441	0.041263

chr6	43	0	0.492028	0.400373	0.223003	0.106967
chr6	44	0	0.462602	0.40692	0.104766	0.033528
chr6	45	0	0.389421	0.380488	0.068849	0.011212
chr6	46	0	0.395335	0.382244	0.054298	0.034655
chr6	47	0	0.392308	0.400456	0.085604	0.022686
chr6	48	0	0.356823	0.482042	0.044012	0.000905
chr6	49	0	0.363448	0.500117	0.05574	0.016871
chr6	50	0	0.36364	0.39314	0.046872	0.004015
chr6	51	0	0.37816	0.371323	0.035793	0.013507
chr6	52	0	0.419379	0.409076	0.09737	0.039264
chr6	53	0	0.405262	0.405703	0.117531	0.026098
chr6	54	0	0.360826	0.432122	0.055752	0.008233
chr6	55	0	0.353319	0.427706	0.041978	0.008426
chr6	56	0	0.376874	0.386438	0.077231	0.03824
chr6	57	0	0.378147	0.486461	0.087173	0.015874
chr6	58	0.161875	0.317275	0.47291	0.039044	0.000886
chr6	59	1	0	0	0	0
chr6	60	1	0	0	0	0
chr6	61	0.938125	0.022405	0.061816	0	0
chr6	62	0.05	0.338801	0.496925	0.026388	0.001962
chr6	63	0	0.358798	0.555856	0.03869	0.001946
chr6	64	0	0.377201	0.460778	0.102326	0.014183
chr6	65	0	0.347171	0.446392	0.035892	0
chr6	66	0	0.345912	0.472366	0.039012	0.005576
chr6	67	0	0.342951	0.510969	0.043442	0
chr6	68	0	0.345791	0.54231	0.038838	0
chr6	69	0	0.351681	0.416207	0.037574	0.004553
chr6	70	0	0.364492	0.394331	0.04422	0.014195
chr6	71	0	0.384249	0.487914	0.0891	0.013905
chr6	72	0	0.369343	0.418454	0.043844	0.00667
chr6	73	0	0.370653	0.370375	0.072259	0.011319
chr6	74	0	0.407622	0.549737	0.212279	0.021556
chr6	75	0	0.36551	0.489123	0.034505	0.011525
chr6	76	0	0.381058	0.444596	0.124442	0.026282
chr6	77	0	0.361608	0.59207	0.034417	0
chr6	78	0	0.365074	0.554841	0.037068	0.001643
chr6	79	0	0.365681	0.491327	0.051215	0.008893
chr6	80	0	0.380716	0.443473	0.060817	0.020456
chr6	81	0	0.359399	0.531271	0.033553	0.002694
chr6	82	0	0.367171	0.459593	0.047615	0.010926
chr6	83	0	0.381638	0.486612	0.080499	0.017389
chr6	84	0	0.379099	0.50367	0.077147	0.023468
chr6	85	0	0.381394	0.455119	0.031714	0
chr6	86	0	0.392385	0.608833	0.08295	0.012808
chr6	87	0	0.38634	0.581523	0.050875	0.004015
chr6	88	0	0.39659	0.424137	0.144773	0.023982
chr6	89	0	0.394636	0.518775	0.11922	0.016954
chr6	90	0	0.420781	0.412217	0.172364	0.053525
chr6	91	0	0.385376	0.362825	0.046021	0.003427

chr6	92	0	0.356518	0.398226	0.0336	0
chr6	93	0	0.352186	0.458437	0.041506	0
chr6	94	0	0.343582	0.368963	0.03245	0.006077
chr6	95	0.2	0.277246	0.390183	0.027987	0
chr6	96	0	0.355966	0.486223	0.041613	0.008009
chr6	97	0	0.373773	0.416819	0.062478	0.017095
chr6	98	0	0.353772	0.416391	0.037417	0
chr6	99	0	0.388649	0.34963	0.062957	0.017443
chr6	100	0	0.378739	0.441524	0.0686	0.015134
chr6	101	0	0.363149	0.43706	0.047685	0.009511
chr6	102	0	0.340054	0.399855	0.038142	0.004038
chr6	103	0	0.342535	0.527619	0.038485	0
chr6	104	0	0.358056	0.495685	0.038833	0
chr6	105	0	0.389255	0.439202	0.11746	0.021883
chr6	106	0	0.399598	0.371974	0.097433	0.00853
chr6	107	0	0.41645	0.473551	0.214765	0.020383
chr6	108	0	0.422251	0.433945	0.177816	0.025115
chr6	109	0	0.413732	0.394517	0.120084	0.036504
chr6	110	0	0.405185	0.473815	0.076723	0.021749
chr6	111	0	0.405292	0.511123	0.239428	0.03123
chr6	112	0	0.402908	0.339794	0.060682	0.020043
chr6	113	0	0.363979	0.417119	0.046213	0
chr6	114	0	0.382789	0.364077	0.103312	0.00785
chr6	115	1.00E-06	0.35722	0.50735	0.033511	0
chr6	116	0	0.374061	0.38998	0.041466	0.030092
chr6	117	0	0.375816	0.461561	0.064363	0.031296
chr6	118	0	0.383196	0.48421	0.061236	0.009515
chr6	119	0	0.389874	0.440573	0.090506	0.016233
chr6	120	0	0.351727	0.508286	0.036986	0
chr6	121	0	0.367269	0.530691	0.086108	0.008409
chr6	122	0	0.365082	0.443702	0.063927	0.006148
chr6	123	0	0.363247	0.423773	0.04873	0.016648
chr6	124	0	0.360415	0.367489	0.048647	0.000501
chr6	125	0	0.383834	0.422792	0.048554	0.010107
chr6	126	0	0.374501	0.4486	0.054794	0.013259
chr6	127	0	0.368407	0.398764	0.059954	0.01725
chr6	128	0	0.357058	0.345543	0.054342	0.01107
chr6	129	0	0.362879	0.39021	0.051399	0.002857
chr6	130	0	0.384728	0.416256	0.077074	0.012816
chr6	131	0	0.389603	0.434504	0.083375	0.018631
chr6	132	0	0.377753	0.401104	0.075378	0.021161
chr6	133	0	0.377592	0.374761	0.076476	0.014085
chr6	134	0	0.400542	0.443344	0.146272	0.016144
chr6	135	0	0.390197	0.402883	0.119225	0.023558
chr6	136	0	0.388121	0.380184	0.092942	0.019755
chr6	137	0	0.39898	0.435172	0.105972	0.017128
chr6	138	0	0.408902	0.40353	0.11034	0.019827
chr6	139	0	0.406864	0.439843	0.168137	0.017931
chr6	140	0	0.364127	0.466107	0.057416	0

chr6	141	0	0.350008	0.551985	0.047081	0.001653
chr6	142	0	0.366958	0.494491	0.04844	0.012062
chr6	143	0	0.394143	0.366893	0.071703	0.024185
chr6	144	0	0.396273	0.456148	0.117059	0.014656
chr6	145	0	0.378382	0.448162	0.051888	0.002632
chr6	146	0	0.370337	0.466102	0.036744	0.025745
chr6	147	0	0.374022	0.414719	0.06548	0.01175
chr6	148	0	0.406846	0.371502	0.126175	0.007709
chr6	149	0	0.411533	0.428931	0.127442	0.014878
chr6	150	0	0.442552	0.465906	0.167519	0.035829
chr6	151	0	0.428882	0.414018	0.225703	0.024278
chr6	152	0	0.390822	0.373882	0.093301	0.044622
chr6	153	0	0.371354	0.477788	0.067596	0.011377
chr6	154	0	0.388541	0.468003	0.111764	0.009836
chr6	155	0	0.41031	0.398869	0.171187	0.016233
chr6	156	0	0.390534	0.432588	0.055952	0
chr6	157	0.05	0.401627	0.306227	0.110725	0.016992
chr6	158	0	0.445375	0.434388	0.15846	0.043851
chr6	159	0	0.436961	0.420722	0.126665	0.033091
chr6	160	0	0.430915	0.448906	0.086494	0.043283
chr6	161	0	0.417351	0.415181	0.079573	0.024774
chr6	162	0	0.401299	0.334825	0.107309	0.000925
chr6	163	0	0.395935	0.352098	0.06789	0.012804
chr6	164	0	0.406671	0.409366	0.059478	0
chr6	165	0	0.382406	0.507617	0.043704	0.006224
chr6	166	0	0.442192	0.341342	0.068865	0.021375
chr6	167	0.05	0.439248	0.346823	0.063681	0.028107
chr6	168	0	0.468327	0.279835	0.049284	0.028177
chr6	169	0	0.435125	0.435299	0.049166	0.017026
chr6	170	0.1568105	0.39798299	0.29988624	0.04382392	0.01779235
chr7	0	0.184	0.436639	0.289106	0.116979	0.037849
chr7	1	0	0.560367	0.359402	0.132199	0.048912
chr7	2	0	0.513423	0.474812	0.248515	0.0425
chr7	3	0	0.427264	0.410951	0.102544	0.005237
chr7	4	0	0.479972	0.559115	0.282804	0.026725
chr7	5	0	0.498401	0.518794	0.379322	0.045062
chr7	6	0	0.466037	0.573797	0.292393	0.028402
chr7	7	0	0.381102	0.409514	0.074312	0.008368
chr7	8	0	0.36868	0.410239	0.038084	0.004004
chr7	9	0	0.347363	0.49214	0.043085	0
chr7	10	0	0.365115	0.478277	0.060965	0.0054
chr7	11	0	0.358596	0.395406	0.033821	0
chr7	12	0	0.369784	0.424115	0.073516	0.023993
chr7	13	0	0.356771	0.42106	0.062848	0.006491
chr7	14	0	0.35229	0.388692	0.04447	0.002125
chr7	15	0	0.355219	0.389932	0.05522	0.004832
chr7	16	0	0.377535	0.426783	0.077688	0.01271
chr7	17	0	0.37345	0.421923	0.061514	0.013483
chr7	18	0	0.360736	0.31213	0.046814	0.009493

chr7	19	0	0.361815	0.493813	0.042402	0.007168
chr7	20	0	0.380612	0.370309	0.074311	0.010796
chr7	21	0	0.395779	0.434983	0.099489	0.013613
chr7	22	0	0.405229	0.439494	0.103826	0.019441
chr7	23	0	0.407228	0.544307	0.166273	0.028586
chr7	24	0	0.405305	0.443526	0.091514	0.024383
chr7	25	0	0.41364	0.339828	0.068175	0.004529
chr7	26	0	0.414662	0.360539	0.120478	0.040177
chr7	27	0	0.410182	0.344883	0.105876	0.011951
chr7	28	0	0.406572	0.337666	0.081817	0.010552
chr7	29	0	0.416286	0.413133	0.091823	0.021543
chr7	30	0	0.451691	0.420443	0.063955	0.030315
chr7	31	0	0.394042	0.391624	0.046163	0.012374
chr7	32	0	0.413045	0.523856	0.154046	0.02143
chr7	33	0	0.394441	0.348761	0.053186	0.009462
chr7	34	0	0.388976	0.494956	0.047554	0.008724
chr7	35	0	0.412008	0.39908	0.093677	0.009248
chr7	36	0	0.416866	0.388665	0.083348	0.016818
chr7	37	0	0.3933	0.457651	0.068349	0.010541
chr7	38	0	0.390043	0.346108	0.065479	0.02071
chr7	39	0	0.409827	0.451751	0.176387	0.016995
chr7	40	0	0.38832	0.393132	0.090736	0.001448
chr7	41	0	0.403229	0.331495	0.066989	0.008416
chr7	42	0	0.396115	0.470895	0.063632	0.009888
chr7	43	0	0.448392	0.455248	0.16328	0.039381
chr7	44	0	0.481734	0.473931	0.220719	0.054431
chr7	45	0	0.428812	0.51379	0.076906	0.016775
chr7	46	0	0.390389	0.50573	0.049805	0.002047
chr7	47	0.025336	0.443033	0.400984	0.115366	0.026829
chr7	48	0.014664	0.375394	0.443417	0.038147	0.02224
chr7	49	0	0.373796	0.544896	0.04685	0.003068
chr7	50	0.04	0.416894	0.357829	0.049567	0.024147
chr7	51	0	0.407693	0.470387	0.077237	0.000949
chr7	52	0	0.372065	0.474408	0.063154	0.001269
chr7	53	0	0.363027	0.496978	0.046958	0.003484
chr7	54	0	0.391898	0.4689	0.050792	0.005396
chr7	55	0	0.448297	0.536655	0.23033	0.038705
chr7	56	0.05	0.422004	0.515756	0.240253	0.005145
chr7	57	0.135012	0.358881	0.49016	0.104471	0.003072
chr7	58	1	0	0	0	0
chr7	59	1	0	0	0	0
chr7	60	0.864988	0.050163	0.122327	0.000848	0
chr7	61	0.1	0.340095	0.803277	0.024084	0
chr7	62	0	0.431294	0.532224	0.221171	0.011867
chr7	63	0	0.414057	0.671037	0.185287	0.028612
chr7	64	0	0.418549	0.576475	0.244474	0.016489
chr7	65	0	0.450711	0.596939	0.350346	0.019499
chr7	66	0	0.441878	0.576497	0.256334	0.00276
chr7	67	0	0.430288	0.55019	0.231999	0

chr7	68	0	0.420543	0.444405	0.198354	0.001256
chr7	69	0	0.424572	0.398178	0.14052	0.005383
chr7	70	0	0.44064	0.536213	0.233343	0.008493
chr7	71	0	0.441115	0.599698	0.291017	0.020951
chr7	72	0	0.501633	0.560368	0.372706	0.048011
chr7	73	0	0.49341	0.584009	0.459343	0.044979
chr7	74	0.25	0.363506	0.430336	0.304601	0.036169
chr7	75	0	0.47963	0.545018	0.343248	0.030646
chr7	76	0	0.403628	0.462693	0.171863	0.012862
chr7	77	0	0.382904	0.374317	0.099981	0.016334
chr7	78	0	0.356037	0.397813	0.053947	0.000672
chr7	79	0	0.361844	0.434688	0.063858	0.00565
chr7	80	0	0.360961	0.395467	0.077666	0.006772
chr7	81	0	0.358665	0.363223	0.071348	0.006505
chr7	82	0	0.346946	0.346491	0.051708	0.011398
chr7	83	0	0.344456	0.346812	0.05539	0.00252
chr7	84	0	0.345443	0.399206	0.036468	0.006259
chr7	85	0	0.351732	0.521015	0.038805	0.000959
chr7	86	0	0.378021	0.445935	0.058116	0.029273
chr7	87	0	0.369959	0.458672	0.06796	0.018459
chr7	88	0	0.352218	0.448837	0.034448	0.005607
chr7	89	0	0.375326	0.475953	0.071172	0.022907
chr7	90	0	0.384842	0.419335	0.045116	0.00909
chr7	91	0	0.384976	0.457436	0.132293	0.042629
chr7	92	0	0.371173	0.408248	0.03794	0.025141
chr7	93	0	0.367257	0.363139	0.045576	0.021599
chr7	94	0	0.37469	0.504354	0.073271	0.014704
chr7	95	0	0.386217	0.403648	0.067137	0.011497
chr7	96	0	0.392932	0.476865	0.085498	0.002886
chr7	97	0	0.458556	0.550193	0.259784	0.03235
chr7	98	0	0.465633	0.47485	0.271157	0.069998
chr7	99	0	0.490646	0.509293	0.303788	0.104912
chr7	100	0	0.510986	0.540104	0.360428	0.063176
chr7	101	0	0.493876	0.460731	0.311591	0.042759
chr7	102	0	0.389115	0.457262	0.117144	0.038014
chr7	103	0	0.384923	0.440317	0.072553	0.005433
chr7	104	0	0.42477	0.450789	0.245288	0.02561
chr7	105	0	0.415032	0.470789	0.078628	0.011359
chr7	106	0	0.388943	0.477696	0.11817	0.034607
chr7	107	0	0.396843	0.395851	0.093445	0.031132
chr7	108	0	0.356373	0.516471	0.037514	0
chr7	109	0	0.363315	0.492345	0.041223	0.00203
chr7	110	0	0.367491	0.380247	0.069211	0.009437
chr7	111	0	0.38948	0.390733	0.081012	0.010502
chr7	112	0	0.363249	0.49386	0.040206	0.008538
chr7	113	0	0.356345	0.36847	0.060295	0.019055
chr7	114	0	0.355746	0.357537	0.040612	0.004598
chr7	115	0	0.372153	0.381305	0.05025	0.021394
chr7	116	0	0.38451	0.386926	0.097341	0.023311

chr7	117	0	0.363779	0.420191	0.049606	0.009261
chr7	118	0	0.344183	0.523378	0.034031	0
chr7	119	0	0.351655	0.420631	0.043763	0.005333
chr7	120	0	0.370689	0.38863	0.052404	0.018232
chr7	121	0	0.36702	0.382054	0.061834	0.018082
chr7	122	0	0.369711	0.441766	0.056838	0.020761
chr7	123	0	0.367944	0.488607	0.05279	0.008077
chr7	124	0	0.353215	0.468566	0.048126	0.004996
chr7	125	0	0.35516	0.473805	0.040538	0.002012
chr7	126	0	0.394042	0.387764	0.059688	0.015058
chr7	127	0	0.451748	0.388901	0.178971	0.030808
chr7	128	0	0.446342	0.467312	0.212184	0.050349
chr7	129	0	0.430737	0.49596	0.215328	0.040463
chr7	130	0	0.42684	0.453666	0.175923	0.008356
chr7	131	0	0.453075	0.300506	0.052904	0.010949
chr7	132	0	0.387402	0.348976	0.101322	0.003121
chr7	133	0	0.409754	0.398429	0.085355	0.01753
chr7	134	0	0.413039	0.439685	0.138813	0.036571
chr7	135	0	0.377316	0.487209	0.059026	0.003738
chr7	136	0	0.379768	0.373009	0.047666	0.014768
chr7	137	0	0.420729	0.570338	0.227051	0.02212
chr7	138	0.025	0.42713	0.423373	0.191914	0.026101
chr7	139	0	0.444353	0.487683	0.241765	0.02482
chr7	140	0	0.417802	0.434582	0.106303	0.014174
chr7	141	0	0.411389	0.377474	0.056165	0.019074
chr7	142	0	0.424064	0.458103	0.079699	0.058878
chr7	143	0	0.38913	0.417617	0.079402	0.038127
chr7	144	0	0.364828	0.527381	0.057388	0
chr7	145	0	0.35821	0.390948	0.06247	0.000542
chr7	146	0	0.36831	0.410462	0.057118	0.001696
chr7	147	0	0.415258	0.43053	0.137081	0.013771
chr7	148	0	0.470791	0.506441	0.198766	0.044765
chr7	149	0	0.437131	0.473054	0.081619	0.040256
chr7	150	0	0.503703	0.352144	0.13034	0.063821
chr7	151	0	0.429696	0.519854	0.250696	0.027332
chr7	152	0	0.418172	0.514163	0.073033	0.004842
chr7	153	0.1	0.389444	0.287962	0.073454	0.000979
chr7	154	0.08	0.435938	0.312569	0.074207	0.021906
chr7	155	0	0.457922	0.326759	0.054501	0.016001
chr7	156	0	0.469092	0.424269	0.165829	0.030132
chr7	157	0	0.503183	0.27169	0.04476	0.01441
chr7	158	0	0.45461362	0.42007833	0.10171777	0.02902856
chr8	0	0	0.460344	0.375228	0.059648	0.01731
chr8	1	0	0.482314	0.281784	0.060655	0.037918
chr8	2	0	0.412586	0.339393	0.078298	0.004219
chr8	3	0	0.388675	0.318823	0.069212	0
chr8	4	0	0.377694	0.295254	0.060636	0
chr8	5	0	0.382883	0.456693	0.054265	0
chr8	6	0	0.436733	0.399163	0.128071	0.015096

chr8	7	0.1	0.410035	0.331503	0.060774	0.006268
chr8	8	0	0.430649	0.475167	0.175616	0.011365
chr8	9	0	0.41756	0.452716	0.133829	0.010717
chr8	10	0	0.461107	0.337194	0.070652	0.022788
chr8	11	0	0.451085	0.443387	0.118955	0.04644
chr8	12	0.1	0.387384	0.419981	0.11566	0.031166
chr8	13	0	0.372674	0.393297	0.08755	0.007013
chr8	14	0	0.352152	0.394166	0.063113	0.000705
chr8	15	0	0.372616	0.454705	0.075073	0.001585
chr8	16	0	0.363156	0.440401	0.064591	0.005894
chr8	17	0	0.395097	0.384643	0.123863	0.046945
chr8	18	0	0.397953	0.487799	0.091056	0.013959
chr8	19	0	0.412328	0.456312	0.117911	0.013095
chr8	20	0	0.437781	0.406442	0.084344	0.011355
chr8	21	0.0174	0.450208	0.405602	0.099442	0.010535
chr8	22	0	0.486712	0.39698	0.176607	0.0724
chr8	23	0	0.435316	0.459835	0.12203	0.031212
chr8	24	0	0.382044	0.431135	0.06462	0.012249
chr8	25	0	0.414523	0.415246	0.127347	0.018835
chr8	26	0	0.417819	0.469965	0.131093	0.024525
chr8	27	0	0.447297	0.43127	0.112949	0.033852
chr8	28	0	0.421056	0.433403	0.173306	0.029807
chr8	29	0.0661	0.397143	0.403127	0.124547	0.008962
chr8	30	0	0.419154	0.507272	0.247185	0.032921
chr8	31	0	0.37828	0.456711	0.077329	0.009143
chr8	32	0	0.381938	0.355148	0.091455	0.009815
chr8	33	0	0.409695	0.530103	0.162595	0.012941
chr8	34	0	0.375484	0.480503	0.061236	0
chr8	35	0	0.382575	0.415935	0.073458	0.007433
chr8	36	0	0.384661	0.496045	0.071974	0
chr8	37	0	0.451973	0.41227	0.145504	0.033069
chr8	38	0	0.44299	0.456994	0.248839	0.051824
chr8	39	0	0.368108	0.664553	0.086471	0.024031
chr8	40	0	0.405976	0.446907	0.091751	0.003922
chr8	41	0	0.452419	0.440828	0.159459	0.032315
chr8	42	0	0.439508	0.517271	0.268792	0.032031
chr8	43	0.041948	0.382006	0.757083	0.066647	0.008796
chr8	44	1	0	0	0	0
chr8	45	1	0	0	0	0
chr8	46	0.958052	0.015711	0.041917	0.000315	0
chr8	47	0	0.442448	0.849741	0.035788	0
chr8	48	0.06	0.385736	0.526566	0.135404	0.002729
chr8	49	0	0.432143	0.474297	0.113088	0.012745
chr8	50	0	0.371838	0.548193	0.043205	0.002181
chr8	51	0	0.357652	0.523102	0.045384	0.001694
chr8	52	0	0.376163	0.494409	0.069982	0.005851
chr8	53	0	0.396503	0.445159	0.102998	0.013878
chr8	54	0	0.403965	0.564953	0.075721	0.00561
chr8	55	0	0.404584	0.482734	0.155519	0.01691

chr8	56	0	0.403818	0.458579	0.110126	0.012099
chr8	57	0	0.399407	0.485133	0.09689	0.019443
chr8	58	0	0.394128	0.470935	0.05317	0.006402
chr8	59	0	0.388244	0.41825	0.06967	0.018868
chr8	60	0	0.365554	0.447879	0.04516	0.000632
chr8	61	0	0.398599	0.41331	0.090053	0.01613
chr8	62	0	0.397917	0.430038	0.061231	0.011555
chr8	63	0	0.371608	0.468848	0.038325	0.000664
chr8	64	0	0.382744	0.452578	0.065682	0.012523
chr8	65	0	0.369826	0.420745	0.039077	0.005604
chr8	66	0	0.38937	0.50071	0.1075	0.010323
chr8	67	0	0.409742	0.475079	0.161267	0.033571
chr8	68	0	0.39567	0.4881	0.146323	0.018619
chr8	69	0	0.370426	0.436123	0.056944	0.015248
chr8	70	0	0.390973	0.438213	0.090021	0.008743
chr8	71	0	0.397383	0.508259	0.166598	0.015832
chr8	72	0	0.38222	0.37369	0.043364	0.00647
chr8	73	0	0.383641	0.426844	0.042263	0.009235
chr8	74	0	0.403603	0.46158	0.149792	0.031457
chr8	75	0	0.389717	0.457651	0.087939	0.0153
chr8	76	0	0.356942	0.472825	0.061269	0.008159
chr8	77	0	0.352703	0.382001	0.037642	0.008087
chr8	78	0	0.347161	0.464031	0.036634	0.00163
chr8	79	0	0.353261	0.429462	0.034936	0.005499
chr8	80	0	0.379937	0.478375	0.056133	0.003205
chr8	81	0	0.40894	0.452378	0.178224	0.012909
chr8	82	0	0.386085	0.437727	0.06833	0.026228
chr8	83	0	0.346798	0.473627	0.050656	0
chr8	84	0	0.351648	0.510441	0.039133	0
chr8	85	0	0.353062	0.412014	0.042463	0.003037
chr8	86	0.2114	0.308329	0.348568	0.074775	0.046875
chr8	87	0	0.378438	0.438047	0.105404	0.021987
chr8	88	0	0.358302	0.530175	0.054926	0.004594
chr8	89	0	0.356633	0.47066	0.050865	0.00288
chr8	90	0	0.366809	0.544702	0.051947	0.003263
chr8	91	0	0.376568	0.448688	0.048923	0.015385
chr8	92	0	0.369334	0.443241	0.049374	0.014784
chr8	93	0	0.371578	0.378045	0.050272	0.005518
chr8	94	0	0.390035	0.416026	0.084141	0.010624
chr8	95	0	0.409084	0.489617	0.18416	0.034691
chr8	96	0	0.405694	0.438799	0.087149	0.012125
chr8	97	0	0.404312	0.418734	0.069397	0.015139
chr8	98	0	0.416411	0.49	0.15376	0.01166
chr8	99	0	0.406842	0.460027	0.129353	0.024146
chr8	100	0	0.372371	0.45138	0.099116	0.020126
chr8	101	0	0.414639	0.458829	0.163564	0.022464
chr8	102	0	0.421861	0.408916	0.113122	0.014523
chr8	103	0	0.424938	0.439639	0.165647	0.022889
chr8	104	0	0.387824	0.500485	0.09719	0.025907

chr8	105	0	0.378869	0.419518	0.070736	0.014273
chr8	106	0	0.363064	0.359185	0.050358	0.004478
chr8	107	0	0.370868	0.440022	0.071337	0.006398
chr8	108	0	0.373254	0.412068	0.047236	0.00689
chr8	109	0	0.372292	0.433643	0.067442	0.005825
chr8	110	0	0.370038	0.415761	0.052146	0.024974
chr8	111	0	0.347075	0.487729	0.046085	0.002927
chr8	112	0	0.34501	0.498839	0.047277	0
chr8	113	0	0.345252	0.421196	0.050008	0.01133
chr8	114	0	0.340738	0.437071	0.036512	0.002021
chr8	115	0	0.344466	0.513412	0.050174	0
chr8	116	0	0.360896	0.372278	0.046061	0.010017
chr8	117	0	0.385368	0.394301	0.069211	0.007766
chr8	118	0	0.389122	0.412529	0.061118	0.007931
chr8	119	0	0.39597	0.386771	0.080611	0.003835
chr8	120	0	0.390156	0.472237	0.099317	0.017039
chr8	121	0	0.392524	0.446009	0.114617	0.019239
chr8	122	0	0.378463	0.439155	0.083529	0.003006
chr8	123	0	0.400426	0.441986	0.064297	0.000348
chr8	124	0	0.426806	0.460348	0.163082	0.036681
chr8	125	0	0.425629	0.460265	0.127921	0.021895
chr8	126	0	0.421968	0.439992	0.122691	0.011994
chr8	127	0	0.395795	0.532681	0.08576	0.005232
chr8	128	0	0.414588	0.456369	0.101329	0.004072
chr8	129	0	0.406563	0.444365	0.055147	0.002889
chr8	130	0	0.388573	0.485347	0.058617	0.007388
chr8	131	0	0.425831	0.449553	0.120283	0.009867
chr8	132	0	0.388376	0.514889	0.038375	0.003574
chr8	133	0	0.412193	0.396178	0.052209	0.024165
chr8	134	0	0.459911	0.40164	0.075911	0.018026
chr8	135	0	0.419005	0.423692	0.055348	0.007773
chr8	136	0	0.41931	0.452307	0.046923	0.001954
chr8	137	0	0.379108	0.482709	0.046517	0
chr8	138	0	0.376218	0.465576	0.043672	0.003657
chr8	139	0	0.432748	0.40688	0.057061	0.008449
chr8	140	0	0.456255	0.412382	0.049548	0.002656
chr8	141	0	0.450102	0.435691	0.15838	0.01868
chr8	142	0	0.52764	0.342089	0.083199	0.023406
chr8	143	0	0.549001	0.342607	0.031628	0.03268
chr8	144	0.1	0.499646	0.367549	0.125117	0.066777
chr8	145	0.0071	0.559079	0.371293	0.193088	0.125012
chr8	146	0	0.46246548	0.6502527	0.16630462	0.08417295
chr9	0	0	0.424611	0.394117	0.1553	0.038984
chr9	1	0	0.396479	0.466532	0.046709	0.002939
chr9	2	0	0.402007	0.423963	0.063416	0.014396
chr9	3	0	0.377348	0.404119	0.057191	0.010686
chr9	4	0	0.407726	0.432529	0.117552	0.018017
chr9	5	0	0.388169	0.510827	0.083041	0.029303
chr9	6	0	0.411427	0.532546	0.201252	0.022651

chr9	7	0	0.394426	0.421346	0.047855	0.005829
chr9	8	0	0.373826	0.32615	0.063293	0.006213
chr9	9	0	0.350607	0.379967	0.039053	4.10E-05
chr9	10	0	0.351542	0.401824	0.044856	0
chr9	11	0	0.34891	0.535357	0.038911	0
chr9	12	0	0.355932	0.457492	0.045423	0.005494
chr9	13	0	0.376065	0.37584	0.05788	0.00674
chr9	14	0	0.387312	0.327344	0.064397	0.021029
chr9	15	0	0.387609	0.52654	0.131793	0.023093
chr9	16	0	0.412681	0.309455	0.096306	0.010375
chr9	17	0	0.38073	0.484093	0.070789	0.00914
chr9	18	0	0.390535	0.385129	0.054227	0.01049
chr9	19	0	0.406334	0.477791	0.16737	0.030538
chr9	20	0	0.379274	0.377886	0.068283	0.009816
chr9	21	0	0.38277	0.462422	0.046418	0.032472
chr9	22	0	0.366447	0.511195	0.043753	0.002775
chr9	23	0	0.371614	0.435056	0.045004	0.004297
chr9	24	0	0.357507	0.464081	0.036304	0
chr9	25	0	0.355065	0.500402	0.040296	0.00246
chr9	26	0	0.374982	0.448278	0.068975	0.012495
chr9	27	0	0.395313	0.410963	0.066812	0.021175
chr9	28	0	0.359571	0.379784	0.037092	0.000615
chr9	29	0	0.351163	0.494305	0.04018	0
chr9	30	0	0.346212	0.512795	0.034836	0
chr9	31	0	0.357735	0.479012	0.037817	0
chr9	32	0	0.398876	0.502595	0.086465	0.031266
chr9	33	0	0.438069	0.492713	0.211574	0.045134
chr9	34	0	0.460006	0.497938	0.212377	0.062696
chr9	35	0	0.447247	0.454318	0.156035	0.081765
chr9	36	0	0.448232	0.464015	0.220293	0.023033
chr9	37	0	0.431857	0.402095	0.17449	0.036819
chr9	38	0	0.438817	0.489115	0.118985	0.014661
chr9	39	0.145271	0.336411	0.422978	0.112167	0.010445
chr9	40	0.154729	0.333425	0.424295	0.113801	0.017713
chr9	41	0.1	0.359997	0.463317	0.117619	0.009303
chr9	42	0.105	0.359113	0.469049	0.11509	0.003374
chr9	43	0.162942	0.343581	0.41061	0.092959	0
chr9	44	0.137058	0.357328	0.452285	0.101139	0.009409
chr9	45	0.214072	0.306	0.327827	0.059258	0.028305
chr9	46	1	0	0	0	0
chr9	47	1	0	0	0	0
chr9	48	1	0	0	0	0
chr9	49	1	0	0	0	0
chr9	50	1	0	0	0	0
chr9	51	1	0	0	0	0
chr9	52	1	0	0	0	0
chr9	53	1	0	0	0	0
chr9	54	1	0	0	0	0
chr9	55	1	0	0	0	0

chr9	56	1	0	0	0	0
chr9	57	1	0	0	0	0
chr9	58	1	0	0	0	0
chr9	59	1	0	0	0	0
chr9	60	1	0	0	0	0
chr9	61	1	0	0	0	0
chr9	62	1	0	0	0	0
chr9	63	1	0	0	0	0
chr9	64	0.335928	0.249076	0.436961	0.04927	0.005066
chr9	65	0.35	0.264002	0.336816	0.061921	0.009261
chr9	66	0.112535	0.351236	0.425405	0.087549	0.011342
chr9	67	0.187465	0.321123	0.427409	0.054908	0.019382
chr9	68	0.05	0.390062	0.394716	0.110964	0.031306
chr9	69	0	0.407347	0.437861	0.090045	0.031802
chr9	70	0	0.392089	0.395034	0.093953	0.024327
chr9	71	0	0.389274	0.442422	0.132702	0.01665
chr9	72	0	0.389322	0.418907	0.123182	0.013226
chr9	73	0	0.352334	0.467618	0.048339	0.001339
chr9	74	0	0.382827	0.407856	0.106929	0.022341
chr9	75	0	0.389816	0.477101	0.060005	0.001789
chr9	76	0	0.416231	0.44959	0.166849	0.026998
chr9	77	0	0.394189	0.432884	0.107454	0.0178
chr9	78	0	0.393782	0.430734	0.072755	0.00393
chr9	79	0	0.388405	0.373006	0.053445	0.005598
chr9	80	0	0.367313	0.483093	0.045919	0
chr9	81	0	0.405562	0.443053	0.138025	0.019172
chr9	82	0	0.38504	0.426047	0.047514	0.003825
chr9	83	0	0.404424	0.465699	0.132563	0.023966
chr9	84	0	0.412467	0.383496	0.095061	0.017607
chr9	85	0	0.404133	0.489269	0.126347	0.015199
chr9	86	0	0.409022	0.440863	0.102993	0.018572
chr9	87	0	0.437517	0.443644	0.126881	0.023786
chr9	88	0	0.431027	0.528969	0.140449	0.020963
chr9	89	0.1	0.412932	0.336617	0.066596	0.022139
chr9	90	0	0.417047	0.495815	0.07594	0.012172
chr9	91	0	0.429979	0.491218	0.124017	0.015898
chr9	92	0	0.447366	0.499168	0.167149	0.053519
chr9	93	0	0.460318	0.489417	0.090162	0.030964
chr9	94	0	0.432733	0.478846	0.185803	0.01669
chr9	95	0	0.431002	0.414439	0.10741	0.015424
chr9	96	0	0.430591	0.552891	0.214128	0.030226
chr9	97	0	0.43323	0.476216	0.136397	0.042186
chr9	98	0	0.45867	0.434978	0.094065	0.033849
chr9	99	0	0.400669	0.456497	0.072945	0.020845
chr9	100	0	0.392027	0.508157	0.089018	0.012735
chr9	101	0	0.377446	0.425943	0.041173	0.028344
chr9	102	0	0.34804	0.54809	0.044102	0.002685
chr9	103	0	0.356241	0.480212	0.045839	0.004341
chr9	104	0	0.394816	0.454698	0.122435	0.022395

chr9	105	0	0.394068	0.483671	0.095217	0.020706
chr9	106	0	0.392058	0.452645	0.045118	0.010368
chr9	107	0	0.431535	0.439696	0.160988	0.007643
chr9	108	0	0.40662	0.424703	0.079939	0.015263
chr9	109	0	0.431061	0.39086	0.12495	0.027068
chr9	110	0	0.38713	0.451146	0.104381	0.027022
chr9	111	0	0.405699	0.49532	0.201056	0.025917
chr9	112	0	0.41961	0.498286	0.178858	0.029352
chr9	113	0	0.456943	0.440694	0.122086	0.051124
chr9	114	0	0.453503	0.430804	0.104912	0.042739
chr9	115	0	0.383689	0.495773	0.048491	0.002768
chr9	116	0	0.418202	0.42363	0.067141	0.02024
chr9	117	0	0.393626	0.412411	0.042048	0.00505
chr9	118	0	0.374132	0.466603	0.05057	0
chr9	119	0	0.410708	0.454241	0.051323	0.003459
chr9	120	0	0.424526	0.453672	0.125895	0.03416
chr9	121	0	0.466398	0.445734	0.130159	0.028744
chr9	122	0	0.414979	0.509487	0.120026	0.053091
chr9	123	0	0.442932	0.427726	0.138725	0.01654
chr9	124	0	0.45663	0.459148	0.219203	0.030543
chr9	125	0	0.435482	0.444153	0.200564	0.023341
chr9	126	0	0.469343	0.45282	0.129302	0.022139
chr9	127	0	0.505977	0.446845	0.228666	0.077272
chr9	128	0	0.51374	0.506862	0.357961	0.0938
chr9	129	0	0.506566	0.491026	0.268531	0.055282
chr9	130	0.1	0.461872	0.384351	0.196431	0.033166
chr9	131	0	0.480476	0.424374	0.197036	0.034835
chr9	132	0	0.478725	0.413015	0.172924	0.056078
chr9	133	0	0.546177	0.359095	0.119558	0.070603
chr9	134	0.263	0.408657	0.214166	0.051209	0.017274
chr9	135	0	0.530626	0.376408	0.080272	0.041749
chr9	136	0.13	0.503472	0.249818	0.11063	0.08069
chr9	137	0	0.566592	0.359262	0.188563	0.130957
chr9	138	0	0.48730749	0.50676149	0.13008859	0.04002152
chrX	0	0.13	0.423445	0.457106	0.236631	0.011823
chrX	1	0.3	0.342868	0.431118	0.228874	0.020226
chrX	2	0.15	0.385058	0.451881	0.219959	0.017619
chrX	3	0.1	0.373791	0.426433	0.130459	0.013057
chrX	4	0	0.373329	0.445882	0.100458	0
chrX	5	0	0.382531	0.404968	0.092389	0.0057
chrX	6	0	0.404876	0.41421	0.087638	0.007257
chrX	7	0	0.393735	0.363248	0.065167	0.008656
chrX	8	0	0.39233	0.363172	0.072516	0.011334
chrX	9	0	0.456696	0.362376	0.163669	0.024883
chrX	10	0	0.394576	0.366187	0.055172	0.011892
chrX	11	0	0.389484	0.369308	0.044286	0.005732
chrX	12	0	0.404753	0.376547	0.080501	0.022507
chrX	13	0	0.40563	0.400532	0.089708	0.02354
chrX	14	0	0.378339	0.445621	0.043634	0.009145

chrX	15	0	0.39984	0.393557	0.095764	0.027176
chrX	16	0	0.413698	0.500738	0.147344	0.014879
chrX	17	0	0.417831	0.400644	0.051939	0.018901
chrX	18	0	0.425137	0.478176	0.194637	0.022778
chrX	19	0	0.42649	0.422555	0.170821	0.033164
chrX	20	0	0.384074	0.54037	0.036247	0.000334
chrX	21	0	0.385346	0.416207	0.080166	0.019053
chrX	22	0	0.376712	0.458007	0.055522	0.00651
chrX	23	0	0.418062	0.546063	0.221757	0.020284
chrX	24	0	0.410577	0.411365	0.136343	0.014687
chrX	25	0	0.372761	0.513375	0.03869	0.003757
chrX	26	0	0.360627	0.515468	0.054633	0
chrX	27	0	0.364853	0.496382	0.060563	0.007029
chrX	28	0	0.361947	0.416688	0.070427	0.000712
chrX	29	0	0.36902	0.402956	0.071233	0.004514
chrX	30	0	0.396272	0.451945	0.097274	0.022604
chrX	31	0	0.370019	0.338878	0.061432	0.003362
chrX	32	0	0.357416	0.367597	0.064485	0.008543
chrX	33	0	0.356457	0.578339	0.040502	0.000351
chrX	34	0	0.365745	0.511407	0.047001	0.006157
chrX	35	0	0.363264	0.561237	0.05934	0.005535
chrX	36	0.05	0.356322	0.480409	0.036003	0.003294
chrX	37	0	0.39133	0.435998	0.05757	0.029423
chrX	38	0	0.40584	0.449354	0.043709	0.005105
chrX	39	0	0.480065	0.432828	0.133461	0.006668
chrX	40	0	0.429436	0.543463	0.219126	0.02815
chrX	41	0	0.399341	0.528514	0.124633	0.013402
chrX	42	0	0.379796	0.604829	0.04368	0.000794
chrX	43	0	0.397028	0.465329	0.072828	0.011586
chrX	44	0	0.407374	0.593833	0.217087	0.0146
chrX	45	0	0.392046	0.616373	0.078085	0
chrX	46	0	0.434004	0.570769	0.230403	0.037628
chrX	47	0	0.434943	0.604158	0.204275	0.042408
chrX	48	0.05	0.465135	0.488671	0.255688	0.087301
chrX	49	0.18	0.338433	0.418448	0.074439	0.019981
chrX	50	0	0.398375	0.603847	0.046536	0.014435
chrX	51	0	0.399733	0.67784	0.056333	0.019508
chrX	52	0.1	0.391452	0.440137	0.129068	0.021482
chrX	53	0	0.438751	0.604994	0.211085	0.047698
chrX	54	0	0.420312	0.661701	0.176655	0.036285
chrX	55	0	0.394336	0.685073	0.036344	0.010489
chrX	56	0	0.393902	0.779969	0.041443	0.01582
chrX	57	0	0.38508	0.856412	0.021952	0.014582
chrX	58	0.534967	0.191642	0.462162	0.003222	0
chrX	59	1	0	0	0	0
chrX	60	1	0	0	0	0
chrX	61	0.465033	0.199752	0.508987	0.004813	0
chrX	62	0	0.391523	0.778957	0.029855	0.01071
chrX	63	0	0.393513	0.752541	0.035895	0.008021

chrX	64	0	0.404706	0.700792	0.082178	0.013443
chrX	65	0	0.38262	0.705607	0.023798	0.010033
chrX	66	0	0.378488	0.711719	0.025103	0.004496
chrX	67	0	0.428661	0.566909	0.121603	0.01893
chrX	68	0	0.429726	0.569384	0.054345	0.011139
chrX	69	0	0.4148	0.611575	0.148769	0.036912
chrX	70	0	0.450326	0.562154	0.220806	0.049216
chrX	71	0	0.423226	0.557561	0.092815	0.032988
chrX	72	0	0.390639	0.787597	0.064443	0.014613
chrX	73	0	0.40448	0.642736	0.100605	0.023616
chrX	74	0	0.388504	0.778584	0.029666	0.009573
chrX	75	0	0.384177	0.863217	0.028217	0.004823
chrX	76	0.08	0.364475	0.664787	0.116875	0.015479
chrX	77	0	0.37819	0.690738	0.060413	0.019369
chrX	78	0	0.366101	0.745758	0.032147	0.004634
chrX	79	0	0.372986	0.698346	0.053115	0.011503
chrX	80	0	0.365241	0.728152	0.028706	0.003606
chrX	81	0	0.360444	0.789914	0.034842	0
chrX	82	0	0.360897	0.746666	0.030349	0.003745
chrX	83	0	0.361472	0.661452	0.034341	0.009177
chrX	84	0	0.369545	0.664054	0.033346	0.018639
chrX	85	0	0.363358	0.544069	0.04347	0.006143
chrX	86	0	0.359736	0.676401	0.034907	0.006832
chrX	87	0	0.358186	0.711201	0.045267	0.001593
chrX	88	0	0.354895	0.699399	0.046536	0.000845
chrX	89	0	0.358873	0.723366	0.041562	0
chrX	90	0	0.361355	0.643489	0.039398	0.009695
chrX	91	0	0.361748	0.583275	0.059224	0.007304
chrX	92	0	0.361912	0.646758	0.035205	0.005833
chrX	93	0	0.362608	0.714437	0.042706	0
chrX	94	0	0.358531	0.670102	0.032333	0
chrX	95	0	0.370658	0.520112	0.068363	0.003097
chrX	96	0	0.37674	0.401369	0.107812	0.00859
chrX	97	0	0.366635	0.600212	0.03269	0
chrX	98	0	0.358668	0.645688	0.021262	0
chrX	99	0	0.395362	0.505618	0.069207	0.024986
chrX	100	0	0.411222	0.551958	0.155035	0.048699
chrX	101	0	0.400389	0.625142	0.037098	0.031771
chrX	102	0	0.407899	0.554598	0.0851	0.022575
chrX	103	0	0.401595	0.514578	0.076848	0.014035
chrX	104	0	0.370259	0.449647	0.039424	0.008313
chrX	105	0	0.380122	0.591667	0.045571	0.028091
chrX	106	0	0.415944	0.504459	0.106253	0.016012
chrX	107	0	0.381318	0.540061	0.043169	0.031253
chrX	108	0	0.392127	0.605222	0.059217	0.013188
chrX	109	0	0.399214	0.486267	0.05419	0.020423
chrX	110	0	0.389269	0.44668	0.0572	0.023622
chrX	111	0	0.392872	0.517239	0.049807	0.012942
chrX	112	0	0.370275	0.654836	0.059317	0

chrX	113	0.07	0.335874	0.525066	0.063617	0.004751
chrX	114	0	0.39976	0.52297	0.118129	0.013594
chrX	115	0.02	0.358427	0.682361	0.025418	0.007486
chrX	116	0	0.374569	0.584917	0.033237	0.003125
chrX	117	0	0.41139	0.499955	0.181769	0.024404
chrX	118	0	0.44201	0.555604	0.236577	0.03177
chrX	119	0	0.410482	0.526418	0.111161	0.051276
chrX	120	0	0.367107	0.652415	0.035111	0
chrX	121	0	0.370821	0.673933	0.028918	0
chrX	122	0	0.400686	0.476387	0.171277	0.021001
chrX	123	0	0.375936	0.420042	0.063831	0.010728
chrX	124	0	0.364815	0.66531	0.029397	0
chrX	125	0	0.359358	0.635718	0.031095	0.0048
chrX	126	0	0.353893	0.703387	0.031643	0.001433
chrX	127	0	0.376557	0.55211	0.032342	0
chrX	128	0	0.436513	0.481559	0.134403	0.03277
chrX	129	0	0.400521	0.490878	0.085107	0.019945
chrX	130	0	0.39086	0.535852	0.06164	0.012822
chrX	131	0	0.396854	0.436542	0.072694	0.014245
chrX	132	0	0.409818	0.424152	0.128501	0.007701
chrX	133	0	0.413173	0.516385	0.163928	0.024859
chrX	134	0	0.41577	0.514131	0.096111	0.044882
chrX	135	0	0.409717	0.486509	0.128642	0.036782
chrX	136	0	0.39495	0.529899	0.08071	0.003937
chrX	137	0	0.38434	0.504821	0.028208	0.00538
chrX	138	0	0.392686	0.52383	0.078832	0.014175
chrX	139	0	0.394546	0.570958	0.092135	0.007068
chrX	140	0	0.381733	0.617414	0.060266	0.009602
chrX	141	0	0.374042	0.592188	0.033627	0.002292
chrX	142	0	0.370726	0.573766	0.039913	0.006505
chrX	143	0.03	0.354374	0.635213	0.035063	0
chrX	144	0	0.381759	0.586861	0.051733	0.011582
chrX	145	0	0.369419	0.649654	0.044324	0
chrX	146	0	0.378981	0.549971	0.045359	0.005702
chrX	147	0	0.390577	0.417433	0.02122	0.013813
chrX	148	0.07	0.395604	0.507369	0.0332	0.029639
chrX	149	0	0.437901	0.489523	0.093761	0.027152
chrX	150	0	0.414672	0.535639	0.046207	0.02358
chrX	151	0	0.425116	0.539312	0.040116	0.035622
chrX	152	0.05	0.505085	0.3539	0.124528	0.083527
chrX	153	0.05	0.436304	0.503649	0.123864	0.080357
chrX	154	0	0.39405288	0.69902034	0.04434132	0.05384919

Seg Dup %	CNV %
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0.145101	0.774253
0.067046	0.454752
0	0.601202
0.002024	0.221781
0.007191	0.446449
0.033545	0.470067
0	0.205247
0.022619	0.324741
0.001968	0.003513
0	0.705531
0.008256	0.057242
0.200437	0.682946
0.414808	0.709231
0	0.067319
0.048904	0.251068
0.45061	0.661853
0.029945	0.557201
0	0.207187
0.025073	0
0.006634	0.170068
0.074594	0.437066
0.055352	0.175163
0.003665	0.181899
0.012597	0.011089
0.142374	0.425735
0.020039	0.159183
0.017726	0.178478
0.008355	0.002259
0.011931	0.18802
0.015269	0.035322
0	0.650247
0.008941	0.140316
0.003852	0.006261
0	0.025052
0.003304	0
0.004929	0.362351
0.001101	0.274354
0.00589	0.009055
0.054883	0.239324
0.005803	0.408113
0	0.001209
0.002983	0
0.005822	0.018638
0.007672	0.341188
0.005737	0.015101
0.007311	0.22523
0.177538	0

0.002068	0.170763
0.003369	0.311245
0.004199	0.218639
0.005262	0.004181
0.00161	0.397829
0.001504	0.327811
0.004358	0.018328
0.001196	0.033354
0.005045	0
0.002658	0.150001
0.001532	0
0.001046	0.162756
0.00183	0
0.00255	0.003865
0.002435	0.055355
0.001264	0.171624
0.001076	0.104326
0.007149	0.066106
0.002131	0.003888
0.006719	0.12229
0.004971	0
0	0
0.004238	0
0.001251	0
0.002569	0.394725
0.001113	0.356943
0.003035	0
0.001531	0.200845
0.001231	0.049561
0.003378	0.030874
0.002997	0.192149
0.011897	0.009001
0.001217	0
0.008485	0.183546
0.001374	0.012671
0.352794	0.67975
0	0.163746
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0	0.212746
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0.004096	0.136348
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0.018813	1
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0.003773	0
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0	0
0	0
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0.289138	0.465269
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0.565686	0.888524
0.059708	0.286353
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0.005537	0.22689
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0	0.063723
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0	0.026291
0	0.224761

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0	0
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0	0.001658

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0.113987	0.218723
0.08943	0.134272
0.164739	1
0.416221	0.187727
0	0.022813
0.001844	0.019658
0.053461	0.497792
0.055774	0.500354
0.138459	0
0.011836	0.310459
0.017028	0.041748
0.01332	0.037753
0.032262	0
0.005651	0
0.003852	0

0.01159	0.065235
0.004564	0.036903
0.009623	0
0.006367	0
0.002529	0
0	0
0.003671	0.001977
0.005947	0.120865
0.019584	0
0.020404	0.192144
0.016658	0
0.005913	0
0.020981	0.248812
0.001004	1
0.001422	1
0.004667	1
0.001262	0.356625
0	0.037045
0.001588	0.102451
0.017684	0
0.001169	0
0.10438	0.001687
0.100029	0.003596
0.001334	0.031184
0.003581	0
0.015738	0
0.002739	0
0.0023	0
0.018551	0
0.011117	0
0.002779	0
0.02449	0.023452
0.312233	0.382237
0.100314	0.196818
0.08202	0
0.101722	0
0.249406	0
0.717809	0
0.02569	0
0.06125	0
0.106801	0
0.010056	0.173283
0.05751	0.318619
0	0.024738
0	0
0	0
0.00145	0.015241
0.117117	0.329083
0.018236	0.627137

0.030519	0
0.006653	0
0.001189	0.978634
0.009798	0.102116
0.003919	0
0.001317	0
0.149491	0.348107
0.260492	0.083438
0.028893	0.012979
0.039442	0.074252
0.024133	0
0.002124	0.082018
0.420026	0
0.008129	0.227593
0.002927	0.015559
0.005422	0.094863
0.014865	0
0.001129	0.01563
0.010479	0.114613
0.029831	0.14694
0	0.012762
0.003208	0.013077
0.001049	0
0.002338	0
0.726135	0.199266
0.683697	0.535842
0.64004	0.259255
0.888943	0
0.186073	0.182931
0.001088	0.002327
0.00219	0
0.001691	0.009437
0	0.120044
0	0
0.002715	0.005767
0.009075	0
0.081012	0.029865
0.336477	0
0.042889	0.111454
0.096173	0.261207
0.003377	0.165218
0.04931	0.171657
0.005954	0.082051
0.007863	0
0.003084	0.201892
0.004631	0.131666
0.007849	0
0.005363	0
0	0

0.003647	0
0.045626	0.026414
0.006919	0.469043
0.006444	0
0.014811	0.009507
0.051378	0.260679
0.123691	0.328265
0.002258	0.005564
0.002563	0.163765
0.00642	0.19775
0.001318	0
0	0
0.001345	0.152919
0.003107	0.131397
0.00279	0.027719
0.006516	0.266511
0.003818	0
0.018156	0.00193
0	0
0.048412	0
0.041216	0.138795
0.373979	0.776041
0.012991	0.008463
0.002447	0
0.002476	0
0.028328	0
0.147331	0.288217
0.205563	0.684031
0.006705	0.200706
0.152565	0
0.021214	0
0.01835	0
0.034718	0.170545
0.011952	0.634878
0.006937	0
0.186033	0.383192
0.00692	0
0.009657	0.001599
0.129755	0.234075
0.086934	0.045137
0.151271	0.051007
0.17053981	0.19748382