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Supplementary Information

Human DNA Methylation Signatures Differentiate Persistent from Resolving MRSA Bacteremia

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Materials and Methods

Reduced representation bisulfite sequencing (RRBS)

Library preparation

Genomic DNA was extracted from whole blood samples using QIAGEN's QIAamp DNA Blood Midi/Maxi Kit, performed at Duke. The purified genomic DNA was shipped on ice to University of California, Los Angeles (UCLA) for RRBS library preparation. Genomic DNA was first quantified by Qubit dsDNA BR Assay Kit (ThermoFisher cat. Q32850). The RRBS libraries were prepared as described(1) with the following conditions. For each sample, 100 ng of purified genomic DNA was digested with 20 U of MspI (NEB, cat # R0106L) at 37°C o/n in the presence of RNase Cocktail Mix (Ambion, cat # AM2286). End-repair and adenylation tailing were performed by the addition of Klenow Fragment 3′->5′ exo- (NEB, cat # M0212L) in the presence of dATP, dGTP, and d^{5me}CTP (Fermentas). Adapter Ligation was performed by the addition of 0.3 µl of Illumina TruSeq methylated Adapters (Illumina, TruSeq Nano cat# FC-121-4001) and 1 µl of Quick T4 DNA Ligase (NEB cat# M2200L). Samples were pooled and purified using an equal volume of SPRI beads (Beckman Coulter, cat # B23318). Size-selection was performed using SPRI beads to enrich for fragments from 200 to 400 bp. Bisulfite treatment was performed using EpiTect Bisulfite kit (QIAGEN, cat # 59104) according to manufacturer's protocol, except that two consecutive rounds of conversion were performed, for a total of 10 hr of incubation. Purified converted DNA was PCR amplified using MyTaq HS Mix (Bioline, cat# BIO-25045) and TruSeq PCR Primer Cocktail (Illumina, TruSeq Nano cat# FC-121-4001) according to the following protocol: initial denaturation at 98°C for 30 s; 12 cycles of 98°C for 15 s, 60°C for 30 s,

72°C for 30 s; final extension at 72°C for 5 min. Amplified libraries were purified twice with an equal amount of SPRI beads to remove primer and adapter dimers.

Sequence data generation

Libraries were sequenced in 100 bp single-end (SE) mode (Illumina; HiSeq 3000) at the UCLA BSCRC sequencing core following manufacturer's instructions. Each pool of eight indexed libraries was sequenced in one lane.

Sequence data processing

The sequencing data were pre-processed with the following steps. The sequencing data were first demultiplexed based on the barcodes of each sample pooled in the lanes. The data were subjected to a quality control step using FastQC (version 0.11.7), where the low quality reads were discarded from further analysis based on the per base sequence quality and per sequence quality score using the default criteria setting in FastQC(2). Sequencing data were trimmed to remove the adaptors and the terminal CG using the trimmomatic software (v0.38) (3). The reads were aligned to the human genome GRCh38/hg38 (release 93, downloaded from Ensembl) and DNA methylation levels were determined using the BS-Seeker2 pipeline(4) with the aligner bowtie (v1.2.2) and the default settings for the fragment length (20 for lower bound, 500 for upper bound). Samples with less than 5 M total raw reads (3 samples) were excluded from further analyses. On average each sample generated about 36 M total raw reads with 73.7% mappability. Within the study, sequencing data were generated from two sequencing runs, termed batch.

Targeted Bisulfite Sequencing (TBS-seq)

Probe design

The probes were designed by Integrated DNA Technologies based on the coordinates of the DMS we discovered using RRBS data. A total 871 sites, which included 72 regions, (the cut-off of q-value < 0.01 and methylation difference larger than 8% in methylkit analysis) were initially included for the probe design to capture both strands of the CpG. To improve specificity, probes categorized as high off-target risk were removed from the panel before the synthesis of the Discovery Pool probes. The final probe design file is included as **SI Appendix, Table S6**. A total of 1117 probes were designed, including the 160 DMS and 5 DMR reported from the RRBS analysis.

Library Preparation and Data Generation

500 ng of purified DNA was fragmented to an average of 250 bp using a Bioruptor Pico sonicator (Diagenode) for 15 cycles (30s ON; 90s OFF). End-repair and dA-tailing were performed using the NEBNext Ultra II DNA kit (New England Biolabs) according to manufacturer's instructions. Ligation was performed according the protocol with the addition of 2.5 µl of custom pre-methylated unique-dual indexed adapters (15 µM, IDT). After purification with 0.8 volumes of Purification Beads (New England Biolabs), samples were pooled in groups of 16. After the addition of human Cot DNA and Universal Blockers TS mix (IDT), the pools were dried in a Vacufuge (Eppendorf). Dried pellets were resuspended with a mixture of Hybridization Buffer, Hybridization Enhancer and custom Discovery Pool probes according to manufacturer's recommendations (IDT – xGen Hybridization Capture of DNA libraries). The hybridization was performed for 24 hrs at 65°C, followed by washes and elution of the captured DNA for 5 minutes at 95°C with TBS elution buffer (10 mM Tris-HCl pH = 8, 0.05% Tween-20). Library pools were then subject to bisulfite treatment (EZ DNA Methylation-Lightning, Zymo Research) and then amplified as follows: 2 min at 98°C; 16 cycles of (98°C for 20 sec;

60°C for 30 sec; 72°C for 30 sec); 72°C for 5 minutes; hold at 4°C. Library QC was performed using the High-Sensitivity D1000 Assay on a 2200 Agilent TapeStation. Libraries were sequenced on a NovaSeq6000 as paired-end 150 bases.

Data processing

1. ***DNA methylation data***

   The demultiplexed data were subject to FastQC (v0.11.8) before and after adapter sequences were removed with cutadapt (v2.10). Trimmed reads were aligned against the GRCh38 genome using BSBolt (5) according to the pipeline described in (6). Methylation was called on aligned reads after PCR duplicates removal and the DNA methylation matrix was assembled using the common CpG sites covered by at least 20 reads across all samples.

   A total of 3614 intersecting CpG detected from both RRBS and TBS-seq were collected, which included the 121 DMS and 5 DMR reported from RRBS. The correlation between data generated from the two methods was computed and the two-factor ANOVA was used to determine the statistical difference among factors including the disease outcomes and techniques.

2. ***Genotype data***

   As bisulfite conversion leads to the deamination of unmethylated cytosines, it is not possible to distinguish C to T SNPs from conversion events. Therefore, we were only able to detect AA, AG and GG alleles based on reads mapping to the forward strand, and CC, CT and TT alleles based on reads mapping to the reverse strand. As we designed probes to capture both forward and reverse strands at most target regions, we were able to

genotype the majority of alleles in our target regions, and we assign NN genotypes to loci that we could not genotype. To determine which of the possible genotypes was the most probable, we first converted bam files to pileup files using samtools, and then further converted these to ATCGmap files using a custom script. The ATCGmap files contain the counts of ATCG on the forward and atcg on the reverse strands at each position. From these counts vectors we were able to determine the genotypes by correlating the observed counts with the expected counts for each allele combination. We called only alleles for which the correlation was 0.98.

Fisher's exact test was used to determine the association between SNP genotypes and APMB/ARMB outcomes, and the association between genotypes and race group was also tested as a positive control. The adjusted p-values were calculated based on the FDR method.

Data Analysis

Classification of patients

The classification algorithm, logistic regression, was used to build a classifier using the Python package, scikit-learn version 0.21.2. To build a generalizable classifier and reduce model overfitting, we incorporated a regularization method, elastic net (7), in our classification model. We first optimized the parameter sets for logistic regression including, solvers, modes of penalty, and related C or λ1_ratio with corresponding solvers by cross-validated grid-search over a parameter grid. We included all 749,212 CpG in the optimization phase and used both precision and recall score for the model evaluation. We found that the optimal parameter set for our data was a logistic regression model using saga solver with elastic net penalty, setting the C equal to 1, λ1_ratio equal to 0.5, and max_iter equal 1000. Then, the classifiers were trained and tested using

a ten-fold cross-validation strategy. Receiver operating curves (ROC) were used to estimate the sensitivity and specificity of the APMB classification method. The AUC was calculated for each ROC to evaluate the accuracy of APMB classification. The average AUC for the true class label was shown (blue bold line in **Fig. 1A** and **Fig. 2B**; red boxplot in **Fig. 2A**). Within each cross-validation run, the class labels (APMB and ARMB) of samples were randomly shuffled and generated the AUC for random background distribution (black bold line in **Fig. 1A** and **Fig. 2B**; blue boxplot in **Fig. 2A**).

To rank the feature importance of DMS, the logistic regression classification models were developed and evaluated using a 10-fold leave-one-class-out cross-validation strategy. A recursive feature elimination algorithm(8) was used to prune the less important features. Using only the samples in the developing set, we first built the classifiers using all DMS to train the logistic regression model. Next, we selected the top 80% of the DMS with the largest feature importance scores and retrained the logistic regression model using only the selected DMS. This process was iterated until the number of selected DMS reach zero, resulting in the last iteration in a logistic regression classifier trained on only one DMS. Each of the classifiers was evaluated using the samples in the evaluating set; while the permuted class labels (APMB and ARMB) for the evaluating samples were used to calculate the performance for chance outcomes. This iterative backward elimination procedure was repeated using each of the 10 folds as the evaluating set. Note that the evaluating samples were never used for developing the classifiers. The feature importance was measured by regression coefficients generated during developing the classifiers. A 10-fold cross-validation was used among the only developing samples to estimate the feature importance for each DMS, calculating the absolute sum of 10 coefficients for a given DMS, generated during developing of the logistic regression. The absolute sum of coefficient for each DMS (from highest

to lowest) were used to rank the importance of DMS. The following iteration was then used the top 80% ranked DMS to build the new classifiers.

Based on the **Fig. 2A**, a minimum of 16 top ranked DMS was used to generate an optimal classification model using all 142 samples (**Fig. 2B** and **Fig. 2C**). The coefficients were used to calculate the odds ratio by taking an exponent of coefficient. The 95% confidence interval were generated based on the 10-fold cross validation. The mean and 95% confidence interval of odds ratio were plotted using Prism GraphPad.

GREAT Analysis

To map to the human genome assembly provided in Genomic regions enrichment of annotations tool (GREAT) analysis, we used the command line version of batch coordinate conversion (liftOver) created by the UCSC Genome Browser Group. The program converts genome coordinate and genome annotation files between GRCh37/hg19 and GRCh38/hg38 assemblies.

Functional annotation of the differentially methylated sites was determined using the GREAT tool (http://great.stanford.edu/public/html/). This website accepts genomic positions as input. For each run, we provided the list of genomic coordinates of differentially methylated sites (DMS) in the human genome assembly GRCh37/hg19 using the bed file format and used the RRBS-detected CpG sites (after filtering for a minimum of 15x coverage) as background. The analysis was carried out based on the basal plus extension association rules by applying the parameters, proximal 5.0 kb upstream and 1.0 kb downstream, plus distal up to 1Mb. The output is a list of GO classes that are deemed significant by the hypergeometric test. As threshold for significance we set as a False Discovery Rate (FDR) < 0.05 for the region-based hypergeometric test.

Region Set Enrichment Analysis

We used LOLA(9) to identify significant overlaps of DMS regions with transcription factor binding sites based on ChIP-seq datasets obtained from ENCODE(10) and CODEX(11) database. The Fisher's exact test was used with a significance threshold of 0.05 on FDR adjusted p-values. To facilitate the data interpretation, we manually annotated and grouped the results into broader categories based on cell types and origin of tissue. The figures included all the significant transcription factors that were enriched in at least one of the relevant comparisons. The cutoff was the p-values < 0.05 as previously described(12). The whole enrichment results together with their original and curated annotations are presented in **SI Appendix, Table S4**.

Cell Composition Estimation

A reference-based cell estimation approach was utilized to estimate proportions of six blood cell types: neutrophils, monocytes, CD4+ T cells, CD8+ T cells, B cells, and NK cells, as previously described (13-15). In summary, whole genome bisulfite sequencing (WGBS) methylomes were obtained from the Blueprint Epigenome Project (16). In total, 34 methylation profiles were analyzed from venous blood-derived cell types (**SI Appendix, Table S5**). First, to process the reference dataset, we used a sliding window to aggregate the methylation values into regions composed of at least two CpG loci that have similar methylation (≤ 25% methylation difference) and are within 500bp distance from each other. Second, cell-specific regions were selected that were uniquely hypomethylated in one cell type by at least 30% than all other cell types. An exception to this criteria were CD4+ and CD8+ T cells which because of their similarity led to a dearth of unique regions, therefore additional regions specific to T cells as a whole and regions at least 30% methylation difference between CD4+ and CD8+ T cells were also included. As a result, 145 cell-specific hypomethylated regions were selected and these regions represented 1075 reference CpG loci (**SI Appendix, Fig. S4**). Second, a non-negative least squares regression was

performed on the methylation values of the cell-specific regions of the references and samples to estimate the proportion of each cell type within the samples.

Figures

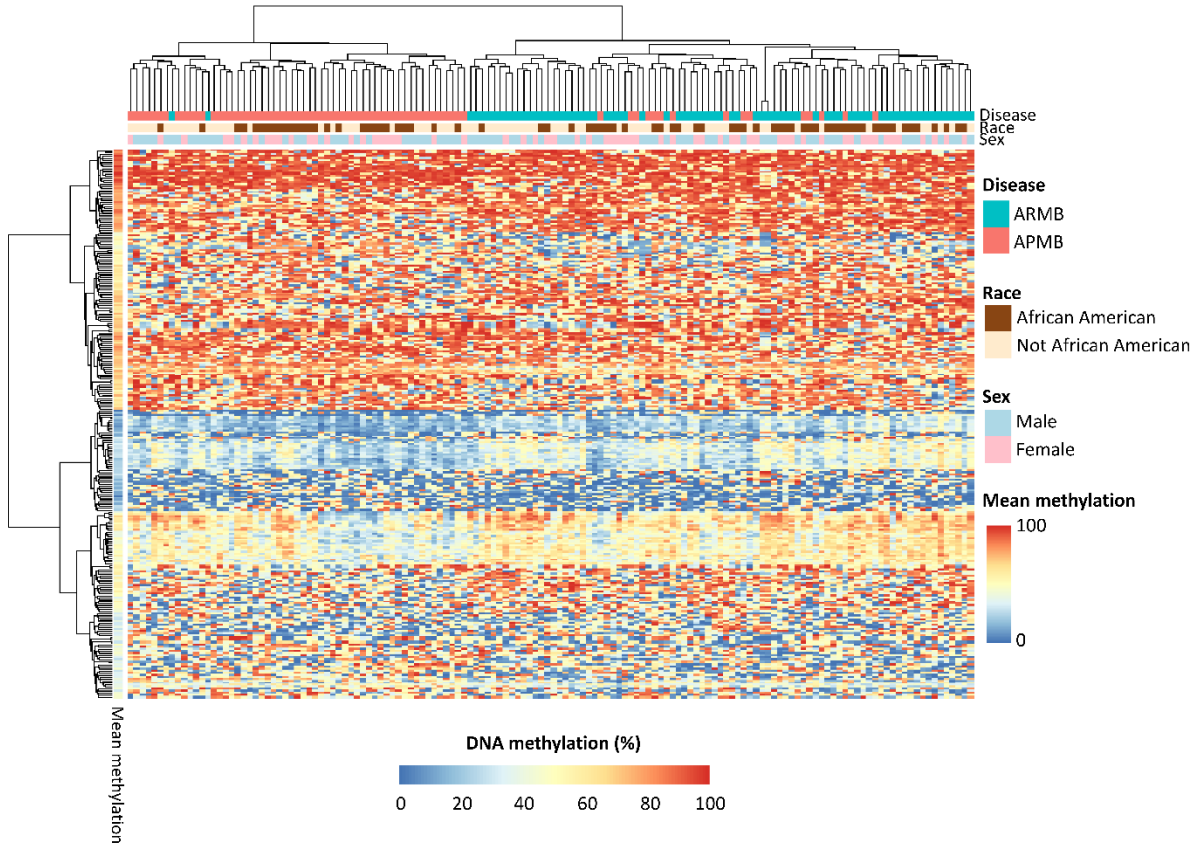

Figure S1. DNA methylation levels were analyzed after sex, race and batch correction. The clustered heatmap for the corrected DNA methylation levels of DMS (row) detected within each sample (column) were generated based on the Ward.D2 method. The standardized methylation levels were applied and present in Figure 1.

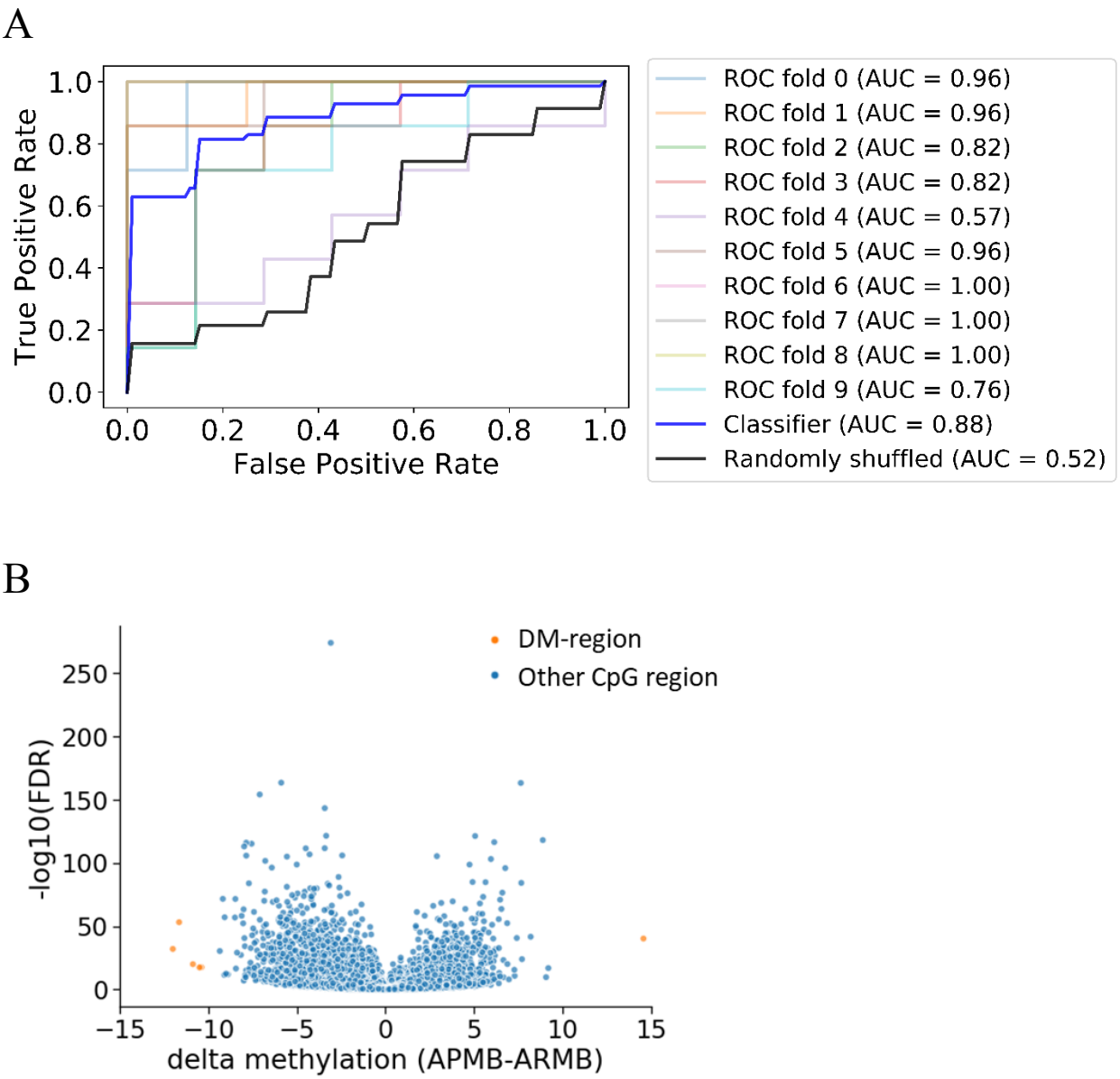

Figure S2. Study differential DNA methylation patterns using clustered CpG regions. **A** ROC curve summarizes the test set classification performance (estimated by 10-fold cross validation) of a logistic regression model that uses the DNA methylation levels of 126,144 CpG regions to distinguish APMB and ARMB samples. **B** Volcano plot represents the methylation difference for 126,144 CpG regions by delta methylation (%) and –log 10 adjusted p-value (FDR) generated from methylkit. The cut-off to define DMS (orange dot) was set as FDR < 0.01 and |delta methylation| > 10%.

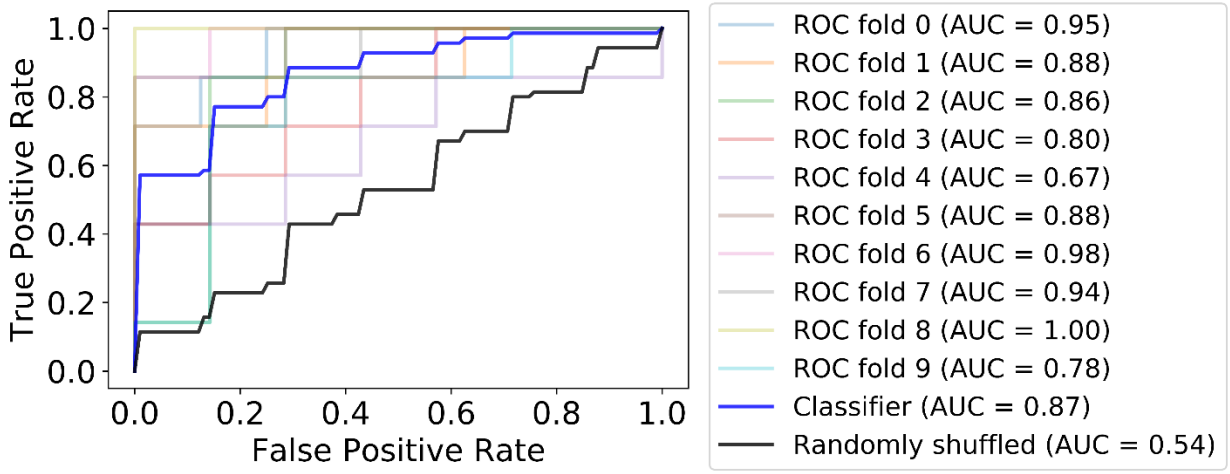

Figure S3. Cell-type composition played a moderate effect on the APMB classification. ROC curve of the logistic regression model that uses the DNA methylation levels of 749,212 CpG sites and 6 estimated cell-type proportions to distinguish APMB and ARMB samples.

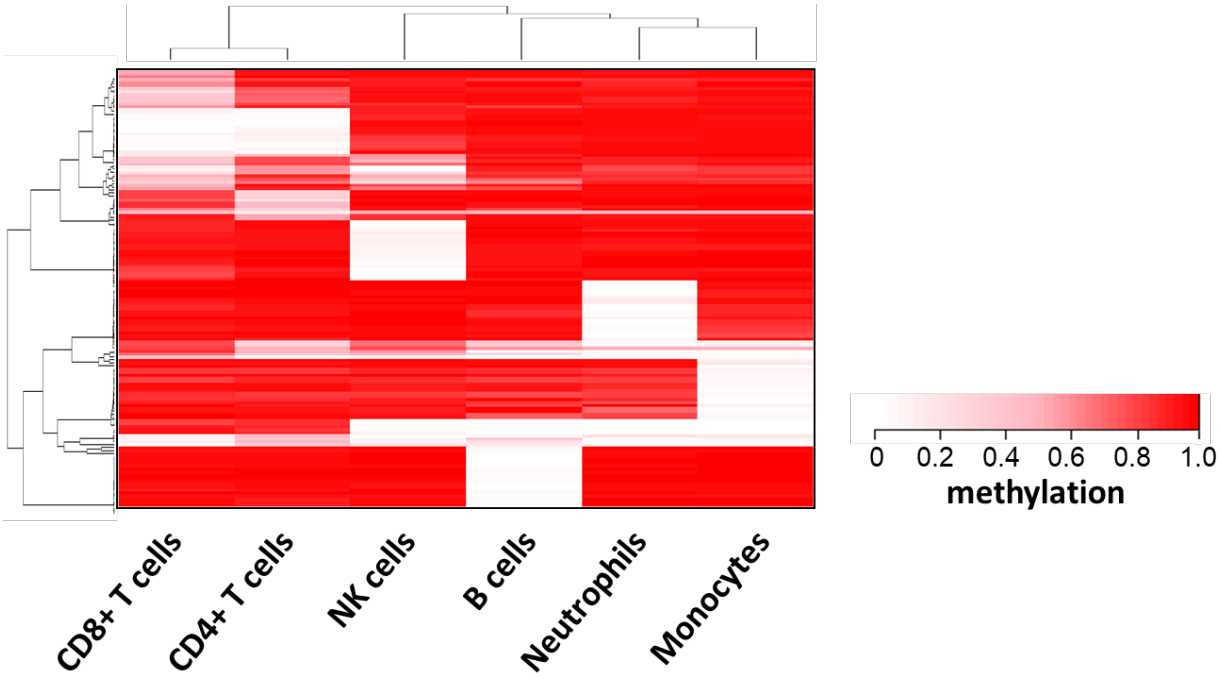

Figure S4. Hierarchical clustering of cell-specific methylation across the purified cell references used for estimation of cell quantity in all samples. The average methylation value for each region (rows) from the designated cell type (columns) is depicted.

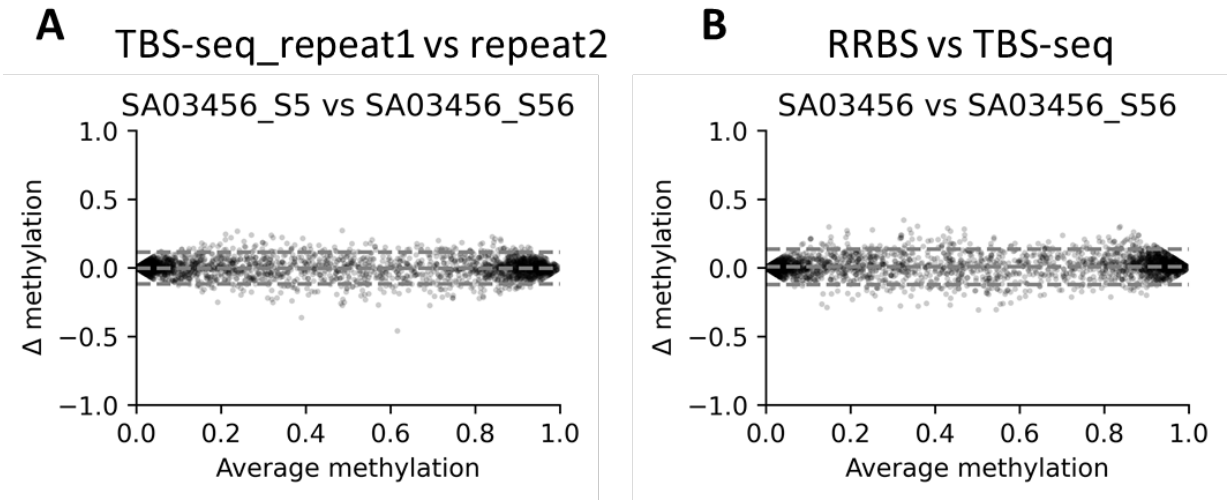

Figure S5. Bland-Altman plots demonstrated the good intra-sample correlations among **A** two technical replicates from TBS-seq; **B** two techniques, TBS-seq and RRBS; **A and B** A total of 3614 detected sites were presented. (Representative sample)

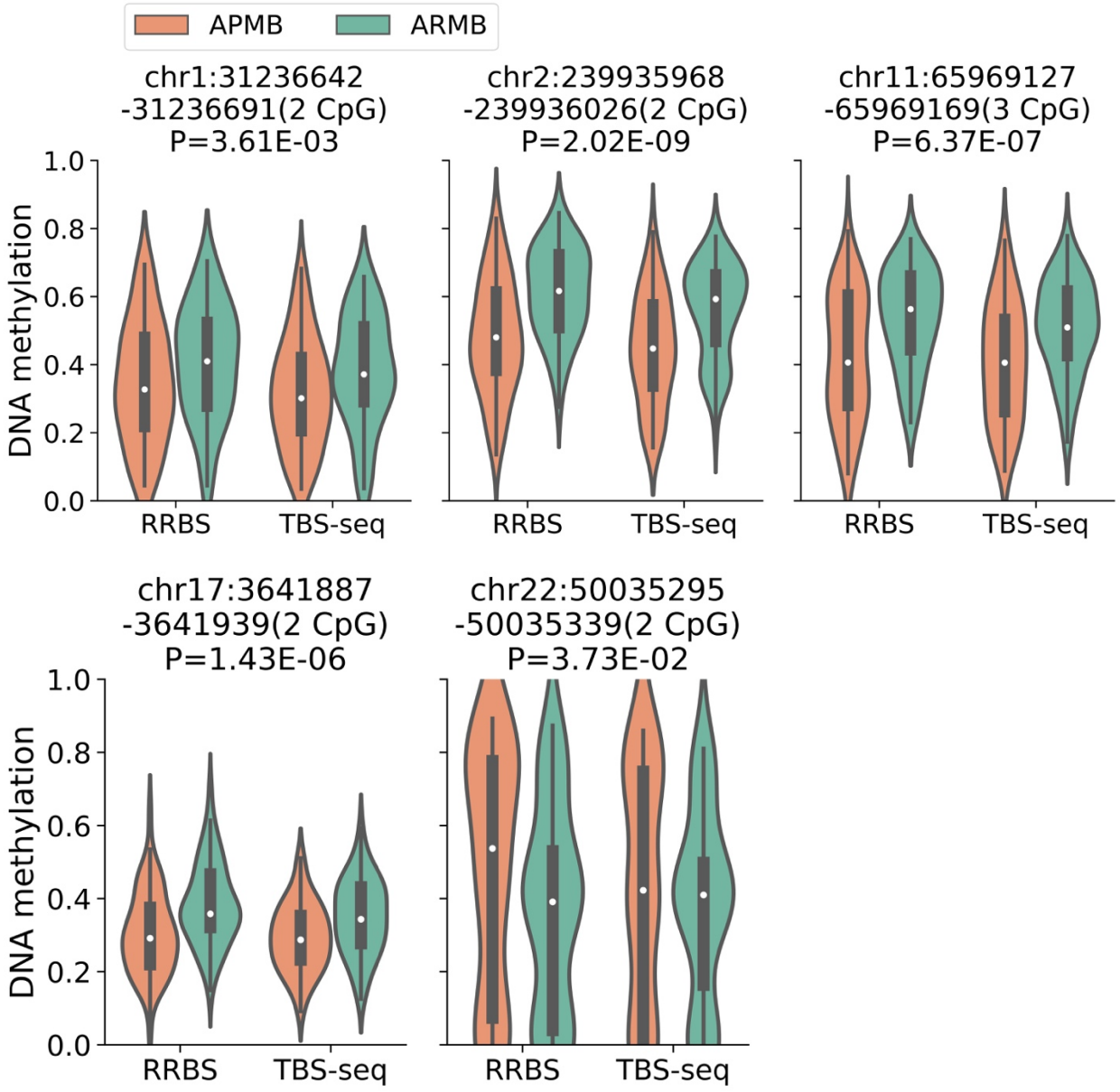

Figure S6. Violin plots of methylation levels in RRBS and TBS-seq for DMR reported in Table S3. Numbers of CpG included within the regions were indicated. Two-way ANOVA was used to determine the disease associated (p-value shown).

Table S1. DMS identified from Methylkit

Chromosome coordinate (GRCh38/Hg38)	p-value	FDR-adjusted p-value	Delta methylation (APMB-ARMB)
chr1:2036515	5.98E-28	1.36E-24	-10.59
chr1:3556781	1.53E-28	3.68E-25	12.15
chr1:13525959	3.34E-17	1.83E-14	-10.03
chr1:18407222	1.32E-20	1.20E-17	-10.26
chr1:20410039	1.32E-45	1.71E-41	10.49
chr1:21943065	5.37E-51	1.09E-46	13.21
chr1:22001786	6.51E-38	4.10E-34	-11.66
chr1:25046088	1.90E-17	1.09E-14	10.65
chr1:28097690	9.30E-21	8.60E-18	-10.53
chr1:31236690	5.76E-25	9.46E-22	-11.66
chr1:34031251	2.33E-21	2.33E-18	10.84
chr1:54748336	1.75E-64	9.36E-60	-18.85
chr1:58814495	7.52E-25	1.21E-21	-12.11
chr1:64215091	6.62E-29	1.69E-25	-13.46
chr1:89088798	4.37E-30	1.31E-26	-10.39
chr1:106412524	5.23E-34	2.14E-30	-10.12
chr1:116982836	1.09E-28	2.72E-25	-12.11
chr1:177964307	3.63E-24	5.39E-21	-11.95
chr1:201956727	4.95E-111	1.85E-105	-20.79
chr1:206797125	4.87E-29	1.28E-25	-10.82
chr1:232531806	6.40E-28	1.44E-24	-11.92
chr1:243267458	1.50E-29	4.25E-26	-13.03
chr1:246696421	3.86E-16	1.77E-13	-10.05
chr1:248804251	7.22E-20	6.02E-17	-11.59
chr10:3515012	8.28E-28	1.85E-24	10.38
chr10:56911268	8.98E-21	8.32E-18	10.05
chr10:75108239	3.55E-15	1.37E-12	-10.11
chr10:94360188	1.27E-48	2.02E-44	10.84
chr10:94368118	2.96E-55	7.39E-51	15.99
chr10:101037017	2.61E-30	7.99E-27	12.45
chr10:103361885	4.28E-22	4.82E-19	-11.25
chr10:110736940	6.44E-43	6.27E-39	-10.19
chr10:125835395	3.32E-29	8.99E-26	10.92
chr11:10901923	2.24E-40	1.88E-36	15.02
chr11:57663997	2.92E-35	1.37E-31	-11.43
chr11:65969127	1.21E-36	6.79E-33	-12.77
chr11:65969132	1.26E-31	4.33E-28	-12.10
chr11:65969168	1.41E-27	3.08E-24	-10.40
chr11:70457091	5.18E-27	1.07E-23	-14.59
chr11:71306949	7.89E-61	3.11E-56	13.21
chr11:71478444	7.24E-27	1.47E-23	-10.17
chr11:71478468	3.28E-27	6.90E-24	-10.12
chr11:72465345	1.74E-25	2.98E-22	11.31

chr11:72685944	3.11E-19	2.35E-16	10.23
chr11:97011585	1.69E-16	8.18E-14	10.30
chr11:104278040	4.40E-58	1.37E-53	11.78
chr11:117838312	1.46E-72	1.22E-67	12.38
chr11:126186929	4.06E-47	5.73E-43	-13.39
chr11:134843845	1.44E-25	2.50E-22	12.65
chr12:9222322	7.68E-27	1.55E-23	-10.25
chr12:11884467	1.37E-26	2.70E-23	-10.77
chr12:14441806	4.27E-18	2.68E-15	-10.82
chr12:19422599	1.09E-16	5.49E-14	-10.29
chr12:38202864	4.00E-22	4.53E-19	11.03
chr12:48520748	4.90E-27	1.02E-23	11.58
chr12:69649244	2.15E-70	1.61E-65	14.71
chr12:87429642	8.82E-28	1.96E-24	11.74
chr12:114730634	1.17E-26	2.35E-23	10.16
chr12:116497224	1.45E-45	1.84E-41	-10.72
chr12:124105868	8.97E-22	9.62E-19	11.59
chr12:124301507	3.42E-47	4.93E-43	10.30
chr12:132875488	9.85E-32	3.45E-28	-12.04
chr13:23974260	5.48E-19	3.99E-16	11.48
chr13:79097784	1.02E-31	3.55E-28	-10.07
chr13:99390832	8.03E-49	1.34E-44	16.50
chr13:109818476	2.56E-23	3.43E-20	-11.15
chr13:110452404	1.15E-26	2.30E-23	-11.80
chr13:110668271	1.25E-30	3.94E-27	10.29
chr14:39296965	5.72E-29	1.49E-25	-13.50
chr14:58447700	8.63E-15	3.11E-12	-10.45
chr14:63315206	2.15E-53	4.87E-49	-15.52
chr14:64655178	9.72E-22	1.04E-18	-11.42
chr14:76160039	4.56E-21	4.41E-18	-10.80
chr14:100603571	2.75E-26	5.15E-23	-10.48
chr14:100603659	1.18E-39	9.50E-36	-11.18
chr14:104285093	7.96E-38	4.93E-34	-10.35
chr14:104314729	7.38E-59	2.51E-54	11.14
chr14:104878424	4.04E-25	6.68E-22	10.17
chr15:49947207	4.65E-83	6.97E-78	-16.85
chr15:63105996	3.58E-20	3.09E-17	10.03
chr15:85338841	1.04E-19	8.53E-17	-10.12
chr15:94317448	2.19E-16	1.05E-13	-10.07
chr15:99148275	3.09E-17	1.71E-14	-10.80
chr16:3339677	5.43E-39	3.99E-35	12.99
chr16:3339702	3.54E-34	1.48E-30	12.20
chr16:3484891	2.64E-17	1.49E-14	10.14
chr16:9574393	7.68E-28	1.72E-24	10.10
chr16:11135755	1.95E-19	1.53E-16	-11.68
chr16:12584582	1.30E-28	3.18E-25	11.40
chr16:14283074	1.02E-20	9.36E-18	-10.71

chr16:17134510	2.22E-27	4.75E-24	13.38
chr16:51108332	3.62E-58	1.18E-53	10.58
chr16:55760866	1.29E-32	4.72E-29	-10.84
chr16:55760868	1.08E-32	4.02E-29	-11.03
chr16:57893654	1.48E-25	2.56E-22	-10.02
chr16:59532978	6.33E-40	5.21E-36	10.22
chr16:76048126	6.81E-34	2.77E-30	14.88
chr16:79167175	9.22E-45	1.06E-40	12.43
chr16:84434719	6.71E-47	9.31E-43	-12.30
chr16:87808561	4.08E-24	6.02E-21	-10.25
chr16:88909597	3.44E-18	2.19E-15	-11.10
chr17:493917	2.33E-18	1.50E-15	-11.10
chr17:1469598	2.34E-26	4.43E-23	-12.07
chr17:3641887	3.08E-21	3.05E-18	-10.96
chr17:3641938	9.57E-34	3.83E-30	-10.31
chr17:31512677	1.36E-30	4.26E-27	-13.57
chr17:32183905	1.21E-25	2.13E-22	-10.41
chr17:50612438	1.13E-33	4.50E-30	-12.30
chr17:55270937	1.42E-31	4.81E-28	-11.68
chr17:55434242	1.40E-56	3.76E-52	12.96
chr17:64832779	5.08E-50	9.06E-46	12.26
chr17:67273601	4.41E-60	1.57E-55	14.01
chr17:75988992	7.20E-36	3.62E-32	-10.30
chr17:76521054	5.49E-23	7.03E-20	-10.26
chr17:76532692	1.31E-16	6.45E-14	-10.11
chr17:79453012	1.01E-44	1.14E-40	13.54
chr17:81071756	7.54E-17	3.88E-14	10.55
chr17:81501247	1.39E-38	9.81E-35	10.97
chr18:514511	5.79E-38	3.81E-34	-10.77
chr18:8478171	5.58E-63	2.61E-58	-12.25
chr18:9689202	1.84E-47	2.70E-43	-11.62
chr18:10128034	1.37E-61	6.02E-57	-12.24
chr18:12747013	1.91E-21	1.94E-18	-11.09
chr18:14224865	4.13E-55	9.98E-51	-14.91
chr18:29179128	6.22E-39	4.53E-35	-10.47
chr18:44127233	4.19E-20	3.58E-17	-10.40
chr18:68625631	4.19E-27	8.72E-24	-11.37
chr18:79320288	3.78E-15	1.45E-12	10.03
chr19:502553	2.82E-35	1.33E-31	10.89
chr19:660423	8.27E-31	2.65E-27	10.42
chr19:1012120	2.02E-57	5.61E-53	10.10
chr19:1882286	5.73E-26	1.04E-22	10.08
chr19:4735650	6.02E-19	4.33E-16	10.02
chr19:8111756	3.00E-20	2.62E-17	11.63
chr19:9708272	8.15E-18	4.91E-15	-10.70
chr19:9708293	1.08E-16	5.44E-14	-10.44
chr19:14554121	1.65E-19	1.30E-16	10.72

chr19:17846094	6.34E-26	1.14E-22	-10.77
chr19:18453069	1.60E-69	1.09E-64	14.90
chr19:35785184	1.58E-26	3.07E-23	-11.97
chr19:40289873	2.16E-24	3.29E-21	-11.10
chr19:44110849	1.28E-68	7.97E-64	11.33
chr19:47385025	2.93E-39	2.24E-35	-10.77
chr19:48573344	2.20E-44	2.39E-40	10.92
chr19:48573429	1.04E-25	1.83E-22	11.04
chr19:48864414	1.15E-29	3.31E-26	-10.91
chr19:53984703	1.33E-22	1.61E-19	12.28
chr19:57736140	3.03E-50	5.67E-46	12.00
chr2:1267654	3.35E-23	4.38E-20	10.60
chr2:1269996	6.61E-17	3.44E-14	10.42
chr2:10274802	1.55E-34	6.67E-31	-11.33
chr2:24879194	6.87E-58	2.06E-53	-14.41
chr2:24879198	3.96E-30	1.20E-26	-14.23
chr2:24879200	7.52E-31	2.43E-27	-14.82
chr2:24879238	1.99E-25	3.39E-22	-13.51
chr2:24879268	2.33E-25	3.94E-22	-13.59
chr2:28545482	4.18E-44	4.35E-40	13.62
chr2:107392572	1.03E-52	2.27E-48	-10.81
chr2:111716295	2.03E-28	4.81E-25	11.73
chr2:112308828	1.93E-24	2.94E-21	-11.60
chr2:127631768	1.79E-25	3.08E-22	-12.40
chr2:187638001	1.31E-26	2.59E-23	12.58
chr2:205806274	5.98E-37	3.45E-33	12.06
chr2:227667841	4.80E-36	2.49E-32	12.76
chr2:233485840	1.44E-22	1.73E-19	10.76
chr2:239374107	1.26E-81	1.57E-76	-11.41
chr2:239935968	9.79E-35	4.26E-31	-11.95
chr2:239936025	4.06E-42	3.81E-38	-11.56
chr2:241768418	9.56E-39	6.82E-35	12.02
chr20:37033404	4.50E-39	3.37E-35	11.22
chr20:37033434	1.70E-40	1.45E-36	11.44
chr20:56487815	2.03E-27	4.35E-24	10.83
chr20:56958543	5.37E-51	1.09E-46	-14.91
chr20:62887880	2.29E-21	2.30E-18	12.73
chr21:13373641	9.03E-38	5.55E-34	-14.33
chr21:34595581	2.05E-21	2.08E-18	-12.65
chr21:41550703	1.83E-44	2.01E-40	11.91
chr21:43842363	9.01E-17	4.59E-14	-10.17
chr21:45386566	1.16E-39	9.43E-36	12.19
chr22:17230982	9.26E-44	9.25E-40	13.20
chr22:30858049	1.88E-21	1.91E-18	-10.04
chr22:30922757	9.78E-54	2.29E-49	-18.26
chr22:37697965	4.46E-83	6.97E-78	-17.62
chr22:44396248	1.90E-33	7.42E-30	10.63

chr22:45585413	1.16E-21	1.22E-18	11.52
chr22:45585505	4.47E-43	4.41E-39	16.64
chr22:45585567	7.92E-35	3.49E-31	12.37
chr22:46806142	1.17E-28	2.89E-25	-12.38
chr22:49017306	3.72E-15	1.43E-12	10.68
chr22:49164475	1.75E-35	8.37E-32	10.27
chr22:50035295	6.08E-38	3.93E-34	13.52
chr22:50035338	4.90E-34	2.03E-30	15.14
chr22:50692955	1.26E-48	2.02E-44	-11.62
chr3:54626248	4.03E-19	2.98E-16	-10.75
chr3:58123434	3.06E-27	6.46E-24	-14.13
chr3:70439711	5.39E-35	2.43E-31	-10.89
chr3:103234006	6.24E-46	8.50E-42	-12.98
chr3:138896490	8.64E-32	3.04E-28	-12.30
chr3:138920773	7.77E-41	7.01E-37	11.81
chr3:156221516	2.25E-19	1.75E-16	10.83
chr3:156221548	1.68E-36	9.11E-33	10.90
chr3:160954639	1.86E-37	1.12E-33	-16.10
chr3:170190991	9.16E-26	1.63E-22	10.69
chr3:170923555	1.58E-31	5.30E-28	-10.24
chr3:197547814	4.21E-25	6.95E-22	-11.41
chr4:1533561	3.24E-19	2.44E-16	11.55
chr4:8286793	1.27E-19	1.02E-16	-11.36
chr4:9761350	1.23E-45	1.62E-41	12.03
chr4:54650215	3.39E-33	1.30E-29	-10.66
chr4:55447223	5.51E-27	1.14E-23	-12.66
chr4:72534065	1.25E-22	1.52E-19	-11.63
chr4:108399799	1.97E-23	2.66E-20	-10.44
chr4:131141731	4.25E-31	1.39E-27	10.83
chr4:184933072	1.23E-63	6.16E-59	-13.68
chr4:187958977	1.22E-23	1.70E-20	-11.10
chr4:189266846	5.65E-35	2.54E-31	-13.94
chr5:18672185	3.88E-44	4.09E-40	11.78
chr5:33549454	2.69E-23	3.59E-20	10.56
chr5:36364346	5.15E-38	3.42E-34	10.51
chr5:119849603	4.65E-37	2.70E-33	10.49
chr5:173795168	3.64E-18	2.31E-15	-10.08
chr5:177082849	1.30E-26	2.57E-23	-10.62
chr5:177223143	8.20E-19	5.73E-16	-10.63
chr5:177386403	3.89E-27	8.12E-24	-11.58
chr5:180771485	8.89E-41	7.93E-37	-10.48
chr6:8449026	4.43E-36	2.32E-32	-13.21
chr6:15219516	3.57E-39	2.70E-35	-10.05
chr6:26309151	3.29E-33	1.27E-29	-10.17
chr6:36458313	1.26E-30	3.98E-27	11.50
chr6:37519993	8.03E-44	8.13E-40	12.13
chr6:38881770	1.40E-50	2.70E-46	-16.78

chr6:110595457	1.18E-21	1.24E-18	-11.25
chr6:118946385	3.18E-31	1.05E-27	12.15
chr6:139771822	3.09E-29	8.39E-26	-10.30
chr6:155256689	8.97E-21	8.32E-18	-10.75
chr6:159316215	6.35E-30	1.87E-26	-10.16
chr6:169240434	2.56E-55	6.62E-51	12.14
chr6:170242079	1.93E-20	1.72E-17	-10.88
chr6:170248145	2.28E-19	1.77E-16	-10.77
chr7:376995	1.07E-28	2.67E-25	11.75
chr7:4116423	2.38E-41	2.20E-37	-13.30
chr7:23904440	4.79E-33	1.81E-29	10.68
chr7:28531768	3.25E-21	3.20E-18	-11.99
chr7:29645809	1.22E-49	2.13E-45	-12.04
chr7:34992017	8.53E-39	6.15E-35	10.68
chr7:66706159	5.77E-61	2.40E-56	11.47
chr7:71174455	4.28E-30	1.29E-26	-10.94
chr7:105129213	1.33E-19	1.06E-16	-10.62
chr7:149822095	5.37E-36	2.76E-32	-12.68
chr7:158279847	1.12E-31	3.89E-28	-11.01
chr8:11849347	1.23E-21	1.28E-18	10.30
chr8:29711287	1.35E-39	1.08E-35	11.63
chr8:97813316	2.76E-25	4.63E-22	-11.47
chr8:133065543	1.73E-38	1.20E-34	-10.47
chr8:142017087	1.98E-15	7.98E-13	10.11
chr8:142765584	3.95E-26	7.25E-23	10.08
chr8:143310432	1.23E-52	2.63E-48	15.21
chr8:144398572	2.20E-38	1.49E-34	-16.19
chr9:446276	1.35E-30	4.24E-27	-11.54
chr9:27921848	1.92E-22	2.26E-19	-12.43
chr9:34539872	1.26E-23	1.75E-20	-11.10
chr9:100332543	5.47E-32	1.95E-28	-11.85
chr9:106530763	1.21E-18	8.23E-16	-10.08
chr9:108616106	3.54E-38	2.37E-34	-11.89
chr9:113294725	7.56E-37	4.32E-33	-13.67
chr9:119361013	8.56E-21	7.98E-18	11.68
chr9:124096410	4.43E-22	4.97E-19	-10.99
chr9:126420976	2.02E-18	1.32E-15	-10.17
chr9:132197921	1.50E-60	5.60E-56	13.43
chr9:133708289	3.70E-22	4.23E-19	11.89
chr9:134333485	1.00E-65	5.77E-61	-19.32
chr9:134416396	2.29E-20	2.02E-17	10.63
chr9:134690733	5.07E-45	6.03E-41	16.13
chr9:136600128	5.52E-18	3.40E-15	10.21
chr9:137041339	2.88E-27	6.13E-24	-10.62
chr9:137265634	3.00E-31	9.89E-28	-10.30

Table S2. Biological annotation for DMS in GREAT and RegulomeDB

Chromosome coordinate of DMS (GRCh38/Hg38)	RegulomeDB score	SNP	CpG island	The first closest gene to DMS	Distance to the TSS of the first closest gene	The second closest gene to DMS	Distance to the TSS of the second closest gene
chr1:2036515	4	n/a	Others	PRKCZ	-13954	GABRD	17175
chr1:3556781	5	n/a	Others	MEGF6	54713	ARHGEF16	102356
chr1:13525959	6	rs12031108	Others	PDPN	-57505	LRRC38	-11912
chr1:18407222	5	rs6695244	Others	KLHDC7A	-73707	IGSF21	299477
chr1:20410039	5	rs76402501	Others	CAMK2N1	76180	VWA5B1	119121
chr1:21943065	4	rs6656791	Others	CELA3B	-33955	HSPG2	-5769
chr1:22001786	5	n/a	Others	CELA3A	131		
chr1:25046088	2b	rs12731221	Others	RUNX3	-81079	SYF2	186404
chr1:28097690	5	rs61786971	Others	EYA3	-8995	PTAFR	79497
chr1:31236690	5	n/a	Shores	PUM1	-170996	NKAIN1	2863
chr1:34031251	7	n/a	Others	CSMD2	134590	HMGB4	170752
chr1:54748336	5	rs369910060	Others	PARS2	16177	ENSG00000271723	106537
chr1:58814495	2b	n/a	Shores	FGGY	-482485	JUN	-30383
chr1:64215091	7	rs12081070	Others	CACHD1	-255700	UBE2U	11285
chr1:89088798	4	n/a	Others	GBP1	-23439	GBP2	37315
chr1:106412524	7	n/a	Others	PRMT6	-644154		
chr1:116982836	2a	n/a	Others	CD101	-18923	PTGFRN	72780
chr1:177964307	7	rs3813651	Others	SEC16B	5607	FAM5B	792810
chr1:201956727	5	n/a	Shores	RNPEP	-25896	TIMM17A	1237
chr1:206797125	4	n/a	Others	IL19	-1744		
chr1:232531806	7	n/a	Others	SIPA1L2	29751	DISC1	904992
chr1:243267458	7	n/a	Others	SDCCAG8	11403	AKT3	582669
chr1:246696421	4	n/a	Others	SCCPDH	-27625	CNST	129976
chr1:248804251	5	n/a	Others	OR14I1	-252822	ZNF672	-34028
chr10:3515012	5	n/a	Others	PITRM1	-342202	KLF6	270262
chr10:56911268	5	n/a	Others	ZWINT	-549993		
chr10:75108239	5	n/a	Shores	SAMD8	-3395	DUSP13	951
chr10:94360188	7	rs12773803	Shores	NOC3L	2750	PLCE1	366200
chr10:94368118	6	rs34032820	Others	TBC1D12	-34385	NOC3L	-5180
chr10:101037017	5	n/a	Others	KAZALD1	-24823	SFXN3	5779
chr10:103361885	4	n/a	Others	PCGF6	-10752	TAF5	-6081
chr10:110736940	7	n/a	Others	PDCD4	-134866	RBM20	92544
chr10:125835395	7	n/a	Others	BCCIP	11850	DHX32	45919
chr11:10901923	5	rs10840511	Others	ZBED5	-43851	CSNK2A3	451433
chr11:57663997	7	rs1783985	Shores	ZDHHC5	-3898		
chr11:65969127	4	n/a	Others	BANF1	-32951	SART1	7439
chr11:65969132	4	n/a	Others	BANF1	-32946	SART1	7444
chr11:65969168	4	n/a	Others	BANF1	-32910	SART1	7480
chr11:70457091	5	rs3132897	Others	CTTN	58550	SHANK2	555175
chr11:71306949	2b	rs1792206	Others	SHANK2	-159624	DHCR7	141485
chr11:71478444	5	rs201214062	Others	KRTAP5-7	-48822	NADSYN1	25336
chr11:71478468	5	rs34989018	Others	KRTAP5-7	-48798	NADSYN1	25360
chr11:72465345	7	rs1984826	Others	CLPB	-30698	PDE2A	209107
chr11:72685944	5	rs12805218	Others	PDE2A	-11493	ARAP1	66458
chr11:97011585	6	rs35218107	Others	JRKL	759428		
chr11:104278040	6	n/a	Others	PDGFD	-113934	CASP12	620391
chr11:117838312	5	rs516655	Others	FXYD2	-13569	FXYD6	38869
chr11:126186929	1f	rs632918	Others	CDON	-123638	RPUSD4	24762
chr11:134843845	5	rs2846150	Others	B3GAT1	-451493		
chr12:9222322	6	rs7301059	Others	PZP	-13953	KLRB1	385563
chr12:11884467	5	n/a	Others	BCL2L14	-186471	ETV6	234614
chr12:14441806	5	n/a	Others	ATF7IP	76125	PLBD1	126542
chr12:19422599	7	n/a	Others	AEBP2	-17074	PLEKHA5	292832
chr12:38202864	6	rs7301806	Others	ALG10B	-113713		
chr12:48520748	6	rs11612973	Others	OR8S1	-4883		
chr12:69649244	7	n/a	Others	LRRC10	-38083	BEST3	50171
chr12:87429642	7	n/a	Others	CEP290	712573		
chr12:114730634	7	rs10774764	Others	TBX3	-47045		
chr12:116497224	4	n/a	Others	MED13L	-219887	MAP1LC3B2	-62156
chr12:124105868	5	rs10128763	Others	ZNF664	132745	NCOR2	389383
chr12:124301507	5	rs77263762	Shores	NCOR2	193744	ZNF664	328384
chr12:132875488	6	rs11147135	Others	GOLGA3	-46787	CHFR	12119
chr13:23974260	7	rs372370712	Others	C1QTNF9B	-77206	SPATA13	-5544
chr13:79097784	6	n/a	Others	RNF219	-438606	RBM26	308003

chr13:99390832	5	rs7983036	Others	TM9SF2	-110584	GPR183	-83428
chr13:109818476	5	rs336229	Others	IRS2	-31909	COL4A1	488672
chr13:110452404	7	rs35131825	Others	RAB20	109328	COL4A2	145138
chr13:110668271	7	n/a	Others	CARS2	37885	CARKD	52611
chr14:39296965	7	rs12588386	Others	CTAGE5	29842	FBXO33	135534
chr14:58447700	6	rs1743728	Others	DACT1	-190478	TIMM9	-20087
chr14:63315206	7	rs12232119	Others	RHOJ	110796	PPP2R5E	228170
chr14:64655178	4	n/a	Others	PLEKHG3	-49257	PPP1R36	105277
chr14:76160039	7	rs1900119	Others	ESRRB	-247498	GPATCH2L	8104
chr14:100603571	5	n/a	Others	DLK1	-123255	BEGAIN	-35502
chr14:100603659	5	n/a	Others	DLK1	-123167	BEGAIN	-35590
chr14:104285093	5	n/a	Others	C14orf180	-294590	C14orf144	40890
chr14:104314729	5	n/a	Others	C14orf180	-264954	C14orf144	70526
chr14:104878424	4	rs368570320	Others	PLD4	-46398	CEP170B	13112
chr15:49947207	7	n/a	Others	ATP8B4	172014	FGF7	524112
chr15:63105996	5	rs2134265	Others	LACTB	-15803	TPM1	63312
chr15:85338841	7	n/a	Others	AKAP13	-41887	PDE8A	358402
chr15:94317448	5	n/a	Others	MCTP2	19183		
chr15:99148275	7	rs8039020	Others	MEF2A	-417424	SYNM	43195
chr16:3339677	6	n/a	Others	TIGD7	-34033	OR2C1	-16211
chr16:3339702	6	rs11642109	Others	TIGD7	-34058	OR2C1	-16186
chr16:3484891	5	rs13740	CpG_island	CLUAP1	-16032	NAA60	41281
chr16:9574393	5	n/a	Others	USP7	-610910	GRIN2A	608360
chr16:11135755	4	n/a	Others	SOCS1	120423	CIITA	258558
chr16:12584582	3a	n/a	Others	CPPED1	219434	SNX29	607845
chr16:14283074	7	rs189369584	Shores	MKL2	203787	PARN	347192
chr16:17134510	4	rs12708815	Others	XYLT1	336370	NOMO3	902016
chr16:51108332	7	rs11644161	Others	SALL1	42942	CYLD	365573
chr16:55760866	5	n/a	Others	CES1	72291	SLC6A2	104223
chr16:55760868	5	n/a	Others	CES1	72289	SLC6A2	104225
chr16:57893654	3a	n/a	Others	KIFC3	-91059	CNGB1	77457
chr16:59532978	7	rs7184791	Others	GOT2	-798622		
chr16:76048126	7	rs160953	Others	ENSG00000214325	-347936	CNTNAP4	-261769
chr16:79167175	7	rs1946279	Others	MAF	433538		
chr16:84434719	7	n/a	Others	ATP2C2	66193	TLDC1	70038
chr16:87808561	4	n/a	Others	KLHDC4	-42613	SLC7A5	60926
chr16:88909597	5	rs2549208	CpG_island	PABPN1L	-42980	CBFA2T3	67606
chr17:493917	5	n/a	Shores	FAM101B	-101428	VPS53	220938
chr17:1469598	4	n/a	Shores	CRK	-13341	MYO1C	23213
chr17:3641887	2a	n/a	Others	CTNS	5409	TAX1BP3	26794
chr17:3641938	4	rs114273516	Others	CTNS	5460	TAX1BP3	26743
chr17:31512677	5	rs9910757	Others	RAB11FIP4	121054	COPRS	346660
chr17:32183905	6	n/a	Others	RHBDL3	-82270	RHOT1	41440
chr17:50612438	5	rs3785914	Others	ABCC3	-22418	CACNA1G	50979
chr17:55270937	4	n/a	Others	HLF	5926	MMD	151054
chr17:55434242	4	rs9907421	Others	MMD	-12251	TMEM100	297878
chr17:64832779	7	n/a	Shores	SMURF2	-170712	LRRC37A3	86005
chr17:67273601	6	rs11659146	Others	HELZ	-28419	PSMD12	93025
chr17:75988992	7	rs113617218	Others	CDK3	-12345	ACOX1	-9630
chr17:76521054	7	n/a	Others	RHBDF2	-19648	CYGB	16850
chr17:76532692	7	n/a	Others	RHBDF2	-31286	CYGB	5212
chr17:79453012	5	rs12450239	Others	RBFOX3	29468	ENGASE	378068
chr17:81071756	5	rs35663354	CpG_island	BAIAP2	36595	AATK	94260
chr17:81501247	7	rs8064656	Shores	ACTG1	11533	ENSG00000171282	94734
chr18:514511	5	rs111692475	CpG_island	CETN1	-65855	COLEC12	-13790
chr18:8478171	5	n/a	Others	RAB12	-131273	PTPRM	911390
chr18:9689202	6	n/a	Others	PPP4R1	-74644	RAB31	-18962
chr18:10128034	4	rs630147	Shores	APCDD1	-326593	VAPA	213973
chr18:12747013	5	n/a	Others	CEP76	-44240	PTPN2	137221
chr18:14224865	7	rs11873382	Others	ANKRD30B	-523374	ZNF519	-92436
chr18:29179128	6	rs28737314	Others	NONE			
chr18:44127233	7	rs1963128	Others	SYT4	-849584	SETBP1	-553664
chr18:68625631	6	rs62099966	Others	TMX3	89666		
chr18:79320288	5	n/a	Others	NFATC1	-80047	ATP9B	250895
chr19:502553	5	rs4919835	Shores	TPGS1	-4745		
chr19:660423	4	n/a	Shores	RNF126	2853	FGF22	20529
chr19:1012120	5	rs7145	Shores	TMEM259	8997	GRIN3B	11702
chr19:1882286	4	n/a	Shores	KLF16	-18719	ABHD17A	3146
chr19:4735650	7	rs10411311	Others	FEM1A	-56065	DPP9	-11788

chr19:8111756	5	n/a	Others	FBN3	38089	CCL25	58757
chr19:9708272	4	n/a	Others	ZNF812	-7497	ZNF846	60344
chr19:9708293	4	n/a	Others	ZNF812	-7518	ZNF846	60323
chr19:14554121	5	n/a	Others	NDUFB7	17940	TECR	24562
chr19:17846094	7	n/a	Shores	INSL3	-24521	JAK3	1937
chr19:18453069	6	rs10405479	Others	ISYNA1	-14769	ELL	69057
chr19:35785184	3a	rs199806241	Others	ARHGAP33	9610	PRODH2	28114
chr19:40289873	6	n/a	Others	AKT2	-4479		
chr19:44110849	4	rs78799625	Shores	ZNF225	-2508		
chr19:47385025	7	n/a	Others	MEIS3	34262	DHX34	35745
chr19:48573344	4	rs3760800	Others	SPACA4	-33398	SULT2B1	21270
chr19:48573429	4	rs3760802	Others	SPACA4	-33313	SULT2B1	21355
chr19:48864414	7	rs538372	Others	HSD17B14	-27737	PLEKHA4	4217
chr19:53984703	5	rs2362381	Shores	CACNG6	-7584	CACNG8	21664
chr19:57736140	7	rs76147066	Others	ZNF776	-10655	ZNF671	-8517
chr2:1267654	7	n/a	Others	TPO	-145806	SNTG2	324873
chr2:1269996	7	n/a	Others	TPO	-143464	SNTG2	327215
chr2:10274802	6	n/a	Others	HPCAL1	-28897	RRM2	152474
chr2:24879194	5	n/a	Others	PTRHD1	-85813	ADCY3	40644
chr2:24879198	5	n/a	Others	PTRHD1	-85817	ADCY3	40640
chr2:24879200	5	n/a	Others	PTRHD1	-85819	ADCY3	40638
chr2:24879238	4	n/a	Others	PTRHD1	-85857	ADCY3	40600
chr2:24879268	4	n/a	Others	PTRHD1	-85887	ADCY3	40570
chr2:28545482	4	rs12467291	Others	PPP1CB	-206369	PLB1	49412
chr2:107392572	6	rs11894951	Others	ST6GAL2	-505927	RGPD4	-434364
chr2:111716295	5	n/a	Others	ANAPC1	168394	BCL2L11	595367
chr2:112308828	6	rs7564052	Others	ZC3H6	33235	RGPD8	124816
chr2:127631768	5	rs200293641	Others	GPR17	-14095	MYO7B	95966
chr2:187638001	5	n/a	Others	GULP1	-654830	TFPI	-83510
chr2:205806274	4	rs10932128	Others	NRP2	123775	INO80D	279907
chr2:227667841	7	rs6436725	Others	C2orf83	-34670	SLC19A3	50170
chr2:233485840	5	rs1048603	Others	USP40	79749	DGKD	131334
chr2:239374107	7	rs114465705	Others	HDAC4	26840	TWIST2	539130
chr2:239935968	4	n/a	Shores	HDAC4	-552743	NDUFA10	89433
chr2:239936025	4	n/a	Shores	HDAC4	-552800	NDUFA10	89376
chr2:241768418	4	n/a	Shores	GAL3ST2	-8406	D2HGDH	33840
chr20:37033404	7	n/a	Others	SAMHD1	-81562	RBL1	62590
chr20:37033434	6	n/a	Others	SAMHD1	-81592	RBL1	62560
chr20:56487815	7	n/a	Others	FAM209A	-36670	RTFDC1	19225
chr20:56958543	6	n/a	Others	BMP7	308084	TFAP2C	329242
chr20:62887880	2b	n/a	Others	TCFL5	-26118	DIDO1	50041
chr21:13373641	5	rs55923962	Others	POTED	-236535		
chr21:34595581	2b	n/a	Others	KCNE1	-84267	RCAN1	19561
chr21:41550703	7	rs61614992	Others	TMPRSS2	-42639	RIPK4	264635
chr21:43842363	5	n/a	Others	AGPAT3	-82644	RRP1	52851
chr21:45386566	2b	n/a	Others	POFUT2	-98669	COL18A1	-68921
chr22:17230982	5	rs5748969	Others	CECR2	-244754	CECR1	-8994
chr22:30858049	5	n/a	Others	MORC2	110150	OSBP2	163244
chr22:30922757	5	n/a	Shores	MORC2	45442	OSBP2	227952
chr22:37697965	6	n/a	Others	TRIOBP	962		
chr22:44396248	5	n/a	Others	PRR5	-280836	KIAA1644	-83398
chr22:45585413	4	rs3788659	Others	ATXN10	-86385	FBLN1	82523
chr22:45585505	4	rs141579499	Others	ATXN10	-86293	FBLN1	82615
chr22:45585567	2b	n/a	Others	ATXN10	-86231	FBLN1	82677
chr22:46806142	4	n/a	Others	TBC1D22A	43522		
chr22:49017306	4	rs2318433	Others	FAM19A5	527847	BRD1	805333
chr22:49164475	5	n/a	Shores	BRD1	657964	FAM19A5	675216
chr22:50035295	5	rs181659854	Shores	TTLL8	21639	PIM3	119564
chr22:50035338	5	n/a	Shores	TTLL8	21596	PIM3	119607
chr22:50692955	7	rs4428117	Others	ACR	-45240	SHANK3	18314
chr3:54626248	5	rs595993	CpG_island	LRTM1	301825	CACNA2D3	503583
chr3:58123434	4	rs1131356	CpG_island	DNASE1L3	91236	FLNB	115035
chr3:70439711	7	n/a	Others	FOXP1	691125	MITF	700277
chr3:103234006	6	rs9683380	Others	ZPLD1	798992		
chr3:138896490	7	rs12485482	Others	PIK3CB	-61739	FOXL2	50649
chr3:138920773	7	rs11720941	Others	PIK3CB	-86022	FOXL2	26366
chr3:156221516	7	rs11915832	Others	KCNAB1	100969	SSR3	333667
chr3:156221548	7	n/a	Others	KCNAB1	101001	SSR3	333635
chr3:160954639	5	n/a	Others	B3GALNT1	150711	PPM1L	198432

chr3:170190991	7	n/a	Others	PRKCI	-31373	PHC3	-9245
chr3:170923555	7	n/a	Others	EIF5A2	-14863	SLC2A2	103194
chr3:197547814	2b	n/a	Others	DLG1	-249239	BDH1	8172
chr4:1533561	4	n/a	Shores	NKX1-1	-135170	FAM53A	150699
chr4:8286793	5	rs7692567	Others	HTRA3	17029	ACOX3	153917
chr4:9761350	5	rs13140817	Others	DRD5	-20283	DEFB131	316715
chr4:54650215	6	rs34269143	Others	KIT	-7702	PDGFRA	421119
chr4:55447223	5	n/a	Others	TMEM165	51267	CLOCK	62803
chr4:72534065	7	n/a	Others	ADAMTS3	34733	NPFFR2	502262
chr4:108399799	5	rs219455	Others	LEF1	-231378	RPL34	-220856
chr4:131141731	7	rs7693301	Others	NONE			
chr4:184933072	7	rs6841615	Others	ACSL1	-106255	HELT	-85856
chr4:187958977	6	rs113110760	Others	ZFP42	-36793		
chr4:189266846	7	rs11942078	Others	FRG1	-673942		
chr5:18672185	7	rs62348334	Others	NONE			
chr5:33549454	5	n/a	Others	TARS	108489	ADAMTS12	342737
chr5:36364346	6	n/a	Others	SLC1A3	-242008	RANBP3L	-62447
chr5:119849603	7	n/a	Others	FAM170A	220006		
chr5:173795168	4	n/a	Others	BOD1	-178509	CPEB4	-93111
chr5:177082849	7	rs384250	Shores	FGFR4	-4036		
chr5:177223143	5	n/a	Others	RAB24	80564	NSD1	89219
chr5:177386403	5	rs368438452	Others	SLC34A1	1960	PFN3	14232
chr5:180771485	7	rs112065232	Others	OR2Y1	-31387	MGAT1	38343
chr6:8449026	7	rs1855767	Others	SLC35B3	-13544		
chr6:15219516	5	n/a	Others	JARID2	-26779		
chr6:26309151	6	rs9393700	Others	BTN3A2	-56079	HIST1H4H	-23618
chr6:36458313	6	n/a	Others	PXT1	-15425	STK38	89156
chr6:37519993	6	rs4714072	Others	CCDC167	-20072	MDGA1	177996
chr6:38881770	7	rs862428	Others	GLP1R	-167027	DNAH8	158649
chr6:110595457	6	n/a	Others	SLC22A16	-118817	CDK19	219858
chr6:118946385	7	rs9374764	Others	MCM9	-11224	FAM184A	132357
chr6:139771822	4	n/a	Others	CITED2	-397203		
chr6:155256689	5	n/a	Others	CLDN20	-7323	TIAM2	423993
chr6:159316215	5	n/a	Shores	FNDC1	146819	SOD2	377112
chr6:169240434	5	n/a	Shores	THBS2	13609	SMOC2	798699
chr6:170242079	6	rs7772458	Others	DLL1	48393	C6orf70	399447
chr6:170248145	5	rs2983214	Others	DLL1	42327	C6orf70	405513
chr7:376995	5	rs146197992	Shores	PDGFA	142069	FAM20C	223993
chr7:4116423	5	n/a	Shores	FOXK1	-565884	SDK1	814976
chr7:23904440	7	rs61512807	Others	NPY	-379747	STK31	194274
chr7:28531768	7	n/a	Others	CHN2	-662641	CREB5	119243
chr7:29645809	7	rs117988574	Shores	WIPF3	-188915	PRR15	81999
chr7:34992017	1f	rs2023328	Others	DPY19L1	46023	NPSR1	333733
chr7:66706159	7	n/a	Others	KCTD7	-34496	TPST1	500961
chr7:71174455	6	n/a	Others	WBSCR17	42287		
chr7:105129213	7	rs113117338	Others	KMT2E	115035	SRPK2	259680
chr7:149822095	5	n/a	Others	ZNF467	-48617	ZNF862	-16271
chr7:158279847	5	rs13231012	Others	PTPRN2	307831	DNAJB6	942880
chr8:11849347	4	n/a	Others	CTSB	18881	FDFT1	46737
chr8:29711287	6	rs143977863	Others	DUSP4	-360619	TMEM66	371919
chr8:97813316	7	n/a	Others	MATN2	-74660	LAPTM4B	38260
chr8:133065543	6	rs55814750	Others	WISP1	-125493	SLA	-5186
chr8:142017087	5	n/a	Others	TSNARE1	386094	PTP4A3	696356
chr8:142765584	5	rs13272651	Others	LYPD2	-13051	LYNX1	12637
chr8:143310432	2b	n/a	Shores	ZNF696	19044	TOP1MT	24463
chr8:144398572	4	rs4317614	Shores	CPSF1	10790	ADCK5	26222
chr9:446276	3a	n/a	Others	KANK1	-24014	DOCK8	231412
chr9:27921848	7	rs1888916	Others	C9orf72	-348399	LINGO2	748436
chr9:34539872	7	rs142048455	Others	ENHO	-16832	CNTFR	49864
chr9:100332543	6	n/a	Others	TEX10	20395	INVS	233288
chr9:106530763	7	n/a	Others	ZNF462	-332333	TMEM38B	836220
chr9:108616106	7	n/a	Others	ACTL7B	240852		
chr9:113294725	7	rs7849326	Others	RNF183	5039	PRPF4	19084
chr9:119361013	5	rs183792476	Others	DBC1	8453		
chr9:124096410	5	n/a	Others	NEK6	-161552	LHX2	84801
chr9:126420976	2b	n/a	Others	LMX1B	-193466	MVB12B	94128
chr9:132197921	5	rs11243663	Shores	NTNG2	35975	SETX	157063
chr9:133708289	5	rs2073815	Others	SARDH	31630	DBH	71930
chr9:134333485	2b	rs3818732	Others	COL5A1	-308288	RXRA	6906

chr9:134416396	5	n/a	Others	COL5A1	-225377	RXRA	89817
chr9:134690733	5	rs16832	Others	FCN2	-190078	COL5A1	48960
chr9:136600128	5	n/a	Others	EGFL7	-58727	NOTCH1	-54267
chr9:137041339	4	n/a	Shores	FUT7	-8330	NPDC1	4863
chr9:137265634	6	n/a	Shores	TOR4A	-12114	NELFB	10462

Table S3. DM-region identified from Methylkit

Chromosome coordinate (GRCh38/Hg38)	p-value	FDR-adjusted p-value	Delta methylation (APMB-ARMB)	Size (bp)	nCpG in Region	In original DMS table	Found with TF binding	Found in GeneHancer
chr1:31236642-31236691	2.13E-20	2.62E-18	-10.39	49	2	Yes for one (31236690); t	No	No
chr2:239935968-239936026	2.41E-35	8.20E-33	-12.01	58	2	Yes for both 2 sites	CEBPbeta	No
chr10:103361871-103361886	2.51E-20	3.06E-18	-10.50	15	2	Yes for one (103361885);	CEBPbeta	No
chr11:65969127-65969169	5.69E-57	6.03E-54	-11.65	42	3	Yes for all 3 sites	No	No
chr17:3641887-3641939	6.06E-23	9.02E-21	-10.87	52	2	Yes for both 2 sites	CEBPbeta+STAT1	GH17J003639
chr22:50035295-50035339	9.50E-44	5.08E-41	14.58	44	2	Yes for both 2 sites	No	No

Table S4. Result of LOLA analysis on 276 DMS

userSet	DataSource	Target (curate)	Tissue (curate)	Cell Type (curate)	pValueLog	OddsRatio	support	rnkPV	rnkOR	rnkSup	maxRnk	meanRnk	b	c	d	Filename	Description	qValue	size
dms.bed	encode_tfbs	CEBPB	Liver	HepG2	3.65419973	5.19919822	8	15	36	71	71	40.7	4276	268	744656	wgEncodeAv	ChIP HepG2 CE	0.044521	18125
dms.bed	encode_tfbs	CEBPB	Liver	HepG2	2.65911874	3.31127767	9	20	51	62	62	44.3	7547	267	741385	wgEncodeAv	ChIP HepG2 CE	0.330146	56629
dms.bed	encode_tfbs	GR	Lung	A549	1.94022713	3.2924027	6	27	52	89	89	56	5021	270	743911	wgEncodeAv	ChIP A549 GR	1	23324
dms.bed	encode_tfbs	p300	Cervix	HeLa-S3	1.44996062	4.24887734	3	37	40	155	155	77.3	1932	273	747000	wgEncodeAv	ChIP HeLa-S3 p	1	25854
dms.bed	encode_tfbs	CEBPB	Liver	HepG2	1.36593115	2.22566361	7	39	73	80	80	64	8655	269	740277	wgEncodeAv	ChIP HepG2 CE	1	18443
dms.bed	encode_tfbs	STAT1	Blood	K562	1.32593637	3.78167461	3	42	44	155	155	80.3	2170	273	746762	wgEncodeAv	ChIP K562 STA	1	2203
dms.bed	codex	GATA1	Blood	Leukaemia cell	0.83026926	6.28578886	1	71	33	315	315	140	433	275	748499	GSM610335	Adult chronic n	1	7135
dms.bed	encode_tfbs	STAT1	Blood	K562	0.77643953	2.14860649	3	75	75	155	155	102	3811	273	745121	wgEncodeAv	ChIP K562 STA	1	2333
dms.bed	encode_tfbs	HNF4A	Liver	HepG2	0.74492513	1.6925279	5	78	94	102	102	91.3	8076	271	740856	wgEncodeAv	ChIP HepG2 HN	1	11130
dms.bed	encode_tfbs	p300	Liver	HepG2	0.69083306	1.47922779	7	81	105	80	105	88.7	12947	269	735985	wgEncodeAv	ChIP HepG2 p3	1	27913
dms.bed	encode_tfbs	c-Fos	Breast	MCF10A-Er-Src	0.60458967	1.58936299	4	84	99	127	127	103	6866	272	742066	wgEncodeAv	ChIP MCF10A-E	1	92358
dms.bed	encode_tfbs	FOXA1	Liver	HepG2	0.56001847	1.43343711	5	89	109	102	109	100	9517	271	739415	wgEncodeAv	ChIP HepG2 FO	1	51264
dms.bed	encode_tfbs	FOXA2	Liver	HepG2	0.54073216	1.48290247	4	95	104	127	127	109	7354	272	741578	wgEncodeAv	ChIP HepG2 FO	1	40989
dms.bed	encode_tfbs	HNF4G	Liver	HepG2	0.53615608	1.40049087	5	96	111	102	111	103	9738	271	739194	wgEncodeAv	ChIP HepG2 HN	1	20384
dms.bed	encode_tfbs	GR	Lung	A549	0.48446766	2.52738366	1	102	66	315	315	161	1076	275	747856	wgEncodeAv	ChIP A549 GR	1	10279
dms.bed	encode_tfbs	GR	Uterus	ECC-1	0.45857807	1.63284478	2	104	97	211	211	137	3333	274	745599	wgEncodeAv	ChIP ECC-1 GR	1	9255
dms.bed	encode_tfbs	FOXA1	Liver	HepG2	0.41347615	1.23124707	5	107	120	102	120	110	11057	271	737875	wgEncodeAv	ChIP HepG2 FO	1	43114
dms.bed	encode_tfbs	c-Jun	Blood	K562	0.36527039	1.77749413	1	115	89	315	315	173	1529	275	747403	wgEncodeAv	ChIP K562 c-Ju	1	6596
dms.bed	encode_tfbs	CEBPB	Lung	A549	0.33635817	1.19451921	3	118	123	155	155	132	6827	273	742105	wgEncodeAv	ChIP A549 CEB	1	38845
dms.bed	codex	CBX2	Blood	Erythrocytic leukaem	0.3142295	1.51099738	1	120	102	315	315	179	1798	275	747134	GSM830986	K562 erythrocy	1	8296
dms.bed	encode_tfbs	ERalpha_a	Breast	T47D	0.30068656	1.44493418	1	121	107	315	315	181	1880	275	747052	wgEncodeAv	ChIP T-47D ERa	1	10505
dms.bed	encode_tfbs	ERalpha_a	Breast	T47D	0.29782253	1.43119781	1	122	110	315	315	182	1898	275	747034	wgEncodeAv	ChIP T-47D ERa	1	10547
dms.bed	encode_tfbs	TFIIIC-110	Blood	K562	0.28169358	1.35533735	1	124	113	315	315	184	2004	275	746928	wgEncodeAv	ChIP K562 TFIII	1	1858
dms.bed	encode_tfbs	TR4	Blood	K562	0.24644687	1.19767943	1	127	122	315	315	188	2267	275	746665	wgEncodeAv	ChIP K562 TR4	1	587
dms.bed	encode_tfbs	c-Fos	Breast	MCF10A-Er-Src	0.23974456	1.03637045	2	128	129	211	211	156	5238	274	743694	wgEncodeAv	ChIP MCF10A-E	1	86323
dms.bed	encode_tfbs	c-Fos	Breast	MCF10A-Er-Src	0.22466549	0.97334567	3	130	134	155	155	140	8361	273	740571	wgEncodeAv	ChIP MCF10A-E	1	70462
dms.bed	encode_tfbs	GATA-2	Blood vessel	HUVEC	0.21590388	0.97573564	2	132	133	211	211	159	5561	274	743371	wgEncodeAv	ChIP HUVEC GA	1	27454
dms.bed	codex	LMO2	Blood	Leukaemia cell	0.19351856	0.97953662	1	134	132	315	315	194	2770	275	746162	GSM108231	Juvenile acute	1	7923
dms.bed	codex	TP53	ESC	Embryonic Stem Cell	0.18509572	0.94660414	1	136	135	315	315	195	2866	275	746066	GSM981236	codex Embryor	1	4067
dms.bed	encode_tfbs	p300	Lung	A549	0.17804438	0.88268734	4	137	137	127	137	134	12273	272	736659	wgEncodeAv	ChIP A549 p30	1	18216
dms.bed	codex	CEBPB	Blood	Macrophage	0.17716624	0.8769194	3	138	139	155	155	144	9269	273	739663	GSM785502	Macrophages v	1	35161
dms.bed	codex	KDM1A	Blood	Erythrocytic leukaem	0.17321136	0.86750595	2	139	143	211	211	164	6249	274	742683	GSM831002	K562 erythrocy	1	13355
dms.bed	encode_tfbs	SETDB1	Bone	U2OS	0.17075139	0.86125139	2	140	144	211	211	165	6294	274	742638	wgEncodeAv	ChIP U2OS SET	1	23538
dms.bed	encode_tfbs	CEBPB	Cervix	HeLa-S3	0.17004527	0.87978486	6	141	138	89	141	123	18451	270	730481	wgEncodeAv	ChIP HeLa-S3 C	1	61004
dms.bed	encode_tfbs	CEBPB	Lung	IMR90	0.16764991	0.8571569	3	142	145	155	155	147	9480	273	739452	wgEncodeAv	ChIP IMR90 CEI	1	70445
dms.bed	encode_tfbs	c-Fos	Breast	MCF10A-Er-Src	0.15704074	0.8262869	2	146	146	211	211	168	6558	274	742374	wgEncodeAv	ChIP MCF10A-E	1	67918
dms.bed	codex	RUNX1T1	Blood	Acute Myeloid Leuke	0.14802977	0.80317637	2	147	150	211	211	169	6745	274	742187	GSM722705	Kasumi-1 (AML	1	5124
dms.bed	encode_tfbs	HNF4A	Liver	HepG2	0.14728423	0.80125837	2	149	151	211	211	170	6761	274	742171	wgEncodeAv	ChIP HepG2 HN	1	20805
dms.bed	encode_tfbs	FOSL2	Liver	HepG2	0.14307777	0.81802562	4	150	147	127	150	141	13226	272	735706	wgEncodeAv	ChIP HepG2 FO	1	25211
dms.bed	encode_tfbs	ERalpha_a	Uterus	ECC-1	0.12953201	0.75524202	2	152	153	211	211	172	7169	274	741763	wgEncodeAv	ChIP ECC-1 ERa	1	16091
dms.bed	codex	FOS	Blood	Leukaemia cell	0.12776256	0.732415	1	153	156	315	315	208	3700	275	745232	GSM610336	Adult chronic n	1	11110
dms.bed	encode_tfbs	TAL1	Blood	K562	0.12655676	0.74745132	2	154	154	211	211	173	7243	274	741689	wgEncodeAv	ChIP K562 TAL1	1	26260
dms.bed	encode_tfbs	NFKB	Blood	GM19193	0.11713592	0.69413206	1	155	160	315	315	210	3903	275	745029	wgEncodeAv	ChIP GM19193	1	5280
dms.bed	codex	POU5F1	ESC	Embryonic Stem Cell	0.1124165	0.67721119	1	156	164	315	315	212	4000	275	744932	GSM112406	codex Embryor	1	10380
dms.bed	encode_tfbs	STAT3	Breast	MCF10A-Er-Src	0.1058634	0.69238827	2	158	161	211	211	177	7813	274	741119	wgEncodeAv	ChIP MCF10A-E	1	39908
dms.bed	codex	FOSB	Blood	Leukaemia cell	0.0986449	0.67271799	2	160	165	211	211	179	8039	274	740893	GSM610337	Adult chronic n	1	23883
dms.bed	encode_tfbs	STAT3	Breast	MCF10A-Er-Src	0.09321824	0.69183107	3	161	162	155	162	159	11710	273	737222	wgEncodeAv	ChIP MCF10A-E	1	44494
dms.bed	encode_tfbs	STAT3	Breast	MCF10A-Er-Src	0.09161815	0.6029094	1	163	182	315	315	220	4490	275	744442	wgEncodeAv	ChIP MCF10A-E	1	12334
dms.bed	encode_tfbs	STAT3	Breast	MCF10A-Er-Src	0.08468282	0.63372546	2	165	172	211	211	183	8528	274	740404	wgEncodeAv	ChIP MCF10A-E	1	45110
dms.bed	encode_tfbs	c-Jun	Blood vessel	HUVEC	0.08363336	0.57433277	1	167	186	315	315	223	4712	275	744220	wgEncodeAv	ChIP HUVEC c-J	1	29524
dms.bed	encode_tfbs	HDAC2	Liver	HepG2	0.0808241	0.726043	6	169	157	89	169	138	22242	270	726690	wgEncodeAv	ChIP HepG2 HD	1	18836
dms.bed	encode_tfbs	ARID3A	Liver	HepG2	0.07916625	0.61789044	2	171	177	211	211	186	8744	274	740188	wgEncodeAv	ChIP HepG2 AR	1	17622
dms.bed	encode_tfbs	BAF170	Cervix	HeLa-S3	0.06152097	0.49397574	1	172	200	315	315	229	5473	275	743459	wgEncodeAv	ChIP HeLa-S3 B	1	2632
dms.bed	encode_tfbs	CEBPB	ESC	H1-hESC	0.06095951	0.49189336	1	173	201	315	315	230	5496	275	743436	wgEncodeAv	ChIP H1-hESC C	1	15557
dms.bed	encode_tfbs	MBD4	Liver	HepG2	0.05482704	0.4689361	1	177	206	315	315	233	5763	275	743169	wgEncodeAv	ChIP HepG2 MI	1	5912

dms.bed	codex	TAL1	Blood	Erythroid Progenitor	0.05407313	0.46608347	1	178	207	315	315	233	5798	275	743134	GSM651545	CD36+ erythroi	1	17834
dms.bed	encode_tfbs	TEAD4	Liver	HepG2	0.0482517	0.44378267	1	179	212	315	315	235	6087	275	742845	wgEncodeAv	ChIP HepG2 TE	1	15160
dms.bed	codex	TAL1	Blood	T-Cell	0.04606831	0.4352744	1	180	214	315	315	236	6205	275	742727	GSM151964	codex T-Cell TA	1	18234
dms.bed	encode_tfbs	ERalpha_a	Uterus	ECC-1	0.04236907	0.42064223	1	184	220	315	315	240	6419	275	742513	wgEncodeAv	ChIP ECC-1 ERa	1	11452
dms.bed	encode_tfbs	GATA3	Breast	T47D	0.0421825	0.50075449	2	185	196	211	211	197	10760	274	738172	wgEncodeAv	ChIP T-47D GA	1	37199
dms.bed	encode_tfbs	NFKB	Blood	GM19099	0.0417617	0.41821072	1	186	222	315	315	241	6456	275	742476	wgEncodeAv	ChIP GM19099	1	7777
dms.bed	encode_tfbs	SP1	Liver	HepG2	0.04174954	0.63298366	6	187	173	89	187	150	25401	270	723531	wgEncodeAv	ChIP HepG2 SP	1	25477
dms.bed	encode_tfbs	USF2	Liver	HepG2	0.03929917	0.40825822	1	189	227	315	315	244	6612	275	742320	wgEncodeAv	ChIP HepG2 US	1	6291
dms.bed	encode_tfbs	CTCF	Skin	NHEK	0.03656113	0.61754394	6	193	178	89	193	153	26014	270	722918	wgEncodeAv	ChIP NHEK CTC	1	42465
dms.bed	encode_tfbs	TCF7L2	Kidney	HEK293	0.03622084	0.39557939	1	194	230	315	315	246	6822	275	742110	wgEncodeAv	ChIP HEK293 T	1	8961
dms.bed	encode_tfbs	c-Jun	Blood	K562	0.03497931	0.39038145	1	195	232	315	315	247	6912	275	742020	wgEncodeAv	ChIP K562 c-Ju	1	9848
dms.bed	encode_tfbs	TCF12	ESC	H1-hESC	0.03417623	0.38699071	1	196	234	315	315	248	6972	275	741960	wgEncodeAv	ChIP H1-hESC T	1	7833
dms.bed	codex	EP300	Blood	Leukaemia cell	0.0335216	0.38420935	1	198	235	315	315	249	7022	275	741910	GSM749524	Acute promyel	1	8952
dms.bed	encode_tfbs	JunB	Blood	K562	0.03085115	0.37268747	1	201	239	315	315	252	7237	275	741695	wgEncodeAv	ChIP K562 eGFI	1	12287
dms.bed	codex	SUZ12	Blood	Erythrocytic leukaem	0.02734985	0.3570868	1	205	244	315	315	255	7550	275	741382	GSM831021	K562 erythrocy	1	2804
dms.bed	encode_tfbs	KAP1	Bone	U2OS	0.02601379	0.49084193	3	207	202	155	207	188	16400	273	732532	wgEncodeAv	ChIP U2OS KAP	1	14647
dms.bed	encode_tfbs	c-Myc	Blood vessel	HUVEC	0.02309621	0.33718029	1	209	251	315	315	258	7991	275	740941	wgEncodeAv	ChIP HUVEC c-M	1	5145
dms.bed	codex	LMO2	Blood	Acute Myeloid Leuke	0.02063264	0.41228049	2	212	225	211	225	216	13028	274	735904	GSM150116	Kasumi-1 (AML	1	11106
dms.bed	encode_tfbs	STAT3	Breast	MCF10A-Er-Src	0.01754331	0.30897563	1	214	258	315	315	262	8712	275	740220	wgEncodeAv	ChIP MCF10A-E	1	41355
dms.bed	encode_tfbs	CEBPB	Blood	K562	0.01706941	0.30641335	1	215	259	315	315	263	8784	275	740148	wgEncodeAv	ChIP K562 CEBI	1	22240
dms.bed	codex	BACH2	Blood	Lymphoma cell	0.01468022	0.29300693	1	218	266	315	315	266	9181	275	739751	GSM108480	Adult B cell No	1	10250
dms.bed	encode_tfbs	SMC3	Liver	HepG2	0.0141929	0.29015902	1	219	268	315	315	267	9270	275	739662	wgEncodeAv	ChIP HepG2 SM	1	30797
dms.bed	codex	ZNF143	Cervix	Cervical cancer cells	0.0140839	0.37697326	2	220	236	211	236	222	14225	274	734707	GSM959045	ChIP-seq_ZNF1	1	4407
dms.bed	encode_tfbs	USF-1	Liver	HepG2	0.01350906	0.37349319	2	221	238	211	238	223	14355	274	734577	wgEncodeAv	ChIP HepG2 US	1	21890
dms.bed	encode_tfbs	CTCF	ESC	H1-hESC	0.01346866	0.49969372	5	222	197	102	222	174	26668	271	722264	wgEncodeAv	ChIP H1-hESC C	1	66551
dms.bed	encode_tfbs	JunD	Liver	HepG2	0.01334631	0.42792242	3	223	217	155	223	198	18751	273	730181	wgEncodeAv	ChIP HepG2 Ju	1	21614
dms.bed	codex	FOXA2	Endoderm	Endoderm	0.01285127	0.28208403	1	224	274	315	315	271	9532	275	739400	GSM112406	Day 5 of in vitr	1	34457
dms.bed	encode_tfbs	GR	Lung	A549	0.01274505	0.4954159	5	226	198	102	226	175	26890	271	722042	wgEncodeAv	ChIP A549 GR	1	16720
dms.bed	encode_tfbs	CTCF	ESC	H1-hESC	0.01215883	0.42048988	3	227	221	155	227	201	19074	273	729858	wgEncodeAv	ChIP H1-hESC C	1	43247
dms.bed	encode_tfbs	ZKSCAN1	Cervix	HeLa-S3	0.01195469	0.27647156	1	229	276	315	315	273	9723	275	739209	wgEncodeAv	ChIP HeLa-S3 Z	1	4131
dms.bed	encode_tfbs	RXRA	Liver	HepG2	0.01170843	0.27489607	1	230	277	315	315	274	9778	275	739154	wgEncodeAv	ChIP HepG2 RX	1	17063
dms.bed	encode_tfbs	TEAD4	Blood	K562	0.011629	0.4170341	3	231	223	155	231	203	19228	273	729704	wgEncodeAv	ChIP K562 TEAI	1	31030
dms.bed	encode_tfbs	CTCF	Lung	A549	0.01137165	0.45558379	4	232	210	127	232	190	23419	272	725513	wgEncodeAv	ChIP A549 CTCI	1	45732
dms.bed	encode_tfbs	CTCF	Esophagus	HEEpiC	0.01111572	0.45388303	4	233	211	127	233	190	23504	272	725428	wgEncodeAv	ChIP HEEpiC CT	1	46226
dms.bed	encode_tfbs	Rad21	ESC	H1-hESC	0.01058259	0.40991972	3	235	226	155	235	205	19553	273	729379	wgEncodeAv	ChIP H1-hESC F	1	55674
dms.bed	encode_tfbs	c-Fos	Blood	K562	0.01045256	0.26660517	1	236	280	315	315	277	10078	275	738854	wgEncodeAv	ChIP K562 c-Fo	1	7646
dms.bed	encode_tfbs	Rad21	Liver	HepG2	0.01017117	0.35145044	2	237	245	211	245	231	15237	274	733695	wgEncodeAv	ChIP HepG2 Ra	1	37233
dms.bed	encode_tfbs	CEBPB	Blood	K562	0.01015658	0.26458258	1	238	281	315	315	278	10154	275	738778	wgEncodeAv	ChIP K562 CEBI	1	38715
dms.bed	encode_tfbs	COREST	Liver	HepG2	0.00996956	0.34999656	2	239	248	211	248	233	15299	274	733633	wgEncodeAv	ChIP HepG2 CC	1	5336
dms.bed	encode_tfbs	CTCF	Liver	HepG2	0.00994015	0.2630854	1	240	282	315	315	279	10211	275	738721	wgEncodeAv	ChIP HepG2 CT	1	40800
dms.bed	encode_tfbs	CTCF	Liver	HepG2	0.00958205	0.40270499	3	241	228	155	241	208	19894	273	729038	wgEncodeAv	ChIP HepG2 CT	1	55778
dms.bed	encode_tfbs	USF2	Cervix	HeLa-S3	0.00914404	0.25743523	1	244	285	315	315	281	10432	275	738500	wgEncodeAv	ChIP HeLa-S3 U	1	12306
dms.bed	encode_tfbs	SETDB1	Blood	K562	0.0086569	0.25385639	1	246	291	315	315	284	10577	275	738355	wgEncodeAv	ChIP K562 SETI	1	3882
dms.bed	encode_tfbs	CTCF	Breast	MCF-7	0.0081164	0.39124102	3	247	231	155	247	211	20461	273	728471	wgEncodeAv	ChIP MCF-7 CT	1	58994
dms.bed	encode_tfbs	CTCF	Kidney	RPTEC	0.00741139	0.45752182	5	249	209	102	249	187	29031	271	719901	wgEncodeAv	ChIP RPTEC CT	1	58785
dms.bed	codex	ZNF143	Blood	Chronic myelogenous	0.00709337	0.24161424	1	250	295	315	315	287	11105	275	737827	GSM959047	ChIP-seq_ZNF1	1	3419
dms.bed	encode_tfbs	CTCF	Blood	K562	0.00696301	0.50116805	7	251	195	80	251	175	36967	269	711965	wgEncodeAv	ChIP K562 CTCI	1	51992
dms.bed	encode_tfbs	p300	Blood	K562	0.00610667	0.31791835	2	252	254	211	254	239	16808	274	732124	wgEncodeAv	ChIP K562 p30	1	25881
dms.bed	encode_tfbs	ZEB1	Blood	GM12878	0.00480988	0.22078039	1	253	308	315	315	292	12136	275	736796	wgEncodeAv	ChIP GM12878	1	4845
dms.bed	encode_tfbs	CTCF	Blood	K562	0.00469414	0.30308923	2	255	264	211	264	243	17611	274	731321	wgEncodeAv	ChIP K562 CTCI	1	56058
dms.bed	encode_tfbs	Rad21	Blood	GM12878	0.00456802	0.21827544	1	256	309	315	315	293	12273	275	736659	wgEncodeAv	ChIP GM12878	1	40019
dms.bed	encode_tfbs	NFKB	Blood	GM12878	0.00424622	0.21482246	1	258	311	315	315	295	12467	275	736465	wgEncodeAv	ChIP GM12878	1	17036
dms.bed	encode_tfbs	CTCF	Breast	MCF-7	0.00413298	0.42348361	5	259	218	102	259	193	31267	271	717665	wgEncodeAv	ChIP MCF-7 CT	1	82176
dms.bed	encode_tfbs	ELF1	Liver	HepG2	0.00394436	0.42100992	5	260	219	102	260	194	31443	271	717489	wgEncodeAv	ChIP HepG2 EL	1	18001
dms.bed	encode_tfbs	TCF7L2	Cervix	HeLa-S3	0.0038731	0.38813665	4	261	233	127	261	207	27340	272	721592	wgEncodeAv	ChIP HeLa-S3 T	1	19242
dms.bed	encode_tfbs	Max	Blood vessel	HUVEC	0.00363033	0.2899247	2	263	269	211	269	248	18391	274	730541	wgEncodeAv	ChIP HUVEC M	1	9122
dms.bed	encode_tfbs	EBF1	Blood	GM12878	0.00326371	0.20322491	1	265	317	315	317	299	13166	275	735766	wgEncodeAv	ChIP GM12878	1	33410

dms.bed	encode_tfbs	c-Myc	Breast	MCF10A-Er-Src	0.00313485	0.20155741	1	266	319	315	319	300	13273	275	735659	wgEncodeAv	ChIP MCF10A-E	1	25703
dms.bed	encode_tfbs	c-Fos	Blood vessel	HUVEC	0.00295605	0.1991739	1	267	322	315	322	301	13429	275	735503	wgEncodeAv	ChIP HUVEC c-F	1	46726
dms.bed	codex	MYB	Blood	T-Cell	0.00293167	0.19884221	1	268	323	315	323	302	13451	275	735481	GSM144200	codex T-Cell M	1	17978
dms.bed	encode_tfbs	BHLHE40	Liver	HepG2	0.00273383	0.33059102	3	269	253	155	269	226	24094	273	724838	wgEncodeAv	ChIP HepG2 BH	1	14628
dms.bed	encode_tfbs	NFKB	Blood	GM10847	0.00260874	0.19428119	1	271	327	315	327	304	13761	275	735171	wgEncodeAv	ChIP GM10847	1	9262
dms.bed	codex	GATA1	Blood	Erythroblast	0.00212678	0.35935047	4	273	243	127	273	214	29444	272	719488	GSM127824	Proerythroblas	1	53723
dms.bed	encode_tfbs	CTCF	Cervix	HeLa-S3	0.0019661	0.31600171	3	275	255	155	275	228	25169	273	723763	wgEncodeAv	ChIP HeLa-S3 C	1	52783
dms.bed	encode_tfbs	SMC3	Blood	K562	0.00194776	0.18371686	1	276	339	315	339	310	14537	275	734395	wgEncodeAv	ChIP K562 SMC	1	23598
dms.bed	codex	GATA1	Blood	Erythroblast	0.00193827	0.41333157	6	277	224	89	277	197	38211	270	710721	GSM970258	Proerythroblas	1	71670
dms.bed	encode_tfbs	CTCF	Blood	K562	0.00178671	0.31202325	3	278	257	155	278	230	25479	273	723453	wgEncodeAv	ChIP K562 CTCI	1	45603
dms.bed	encode_tfbs	Rad21	Blood	K562	0.00177808	0.18064925	1	279	341	315	341	312	14779	275	734153	wgEncodeAv	ChIP K562 Rad2	1	34725
dms.bed	encode_tfbs	CTCF	Choroid plexus	HCPEpiC	0.0017233	0.35033721	4	280	247	127	280	218	30171	272	718761	wgEncodeAv	ChIP HCPEpiC C	1	61062
dms.bed	encode_tfbs	CTCF	Liver	HepG2	0.00167491	0.25659125	2	281	286	211	286	259	20714	274	728218	wgEncodeAv	ChIP HepG2 CT	1	46448
dms.bed	encode_tfbs	CTCF	ESC	H1-hESC	0.00157193	0.25420515	2	283	290	211	290	261	20903	274	728029	wgEncodeAv	ChIP H1-hESC C	1	54111
dms.bed	encode_tfbs	CTCF	Blood	GM12865	0.0015442	0.30616049	3	284	260	155	284	233	25950	273	722982	wgEncodeAv	ChIP GM12865	1	44069
dms.bed	encode_tfbs	SIX5	Lung	A549	0.00146343	0.1744209	1	285	346	315	346	315	15296	275	733636	wgEncodeAv	ChIP A549 SIX5	1	4909
dms.bed	encode_tfbs	TCF12	Lung	A549	0.0014548	0.30383118	3	286	263	155	286	235	26142	273	722790	wgEncodeAv	ChIP A549 TCF1	1	20896
dms.bed	encode_tfbs	YY1	Blood	K562	0.00127441	0.17024915	1	287	348	315	348	317	15663	275	733269	wgEncodeAv	ChIP K562 YY1	1	4948
dms.bed	encode_tfbs	CTCF	Breast	MCF-7	0.00127284	0.24658935	2	288	292	211	292	264	21530	274	727402	wgEncodeAv	ChIP MCF-7 CT	1	66592
dms.bed	encode_tfbs	CTCF	Intestine	Caco-2	0.00115532	0.24324938	2	289	294	211	294	265	21817	274	727115	wgEncodeAv	ChIP Caco-2 CT	1	46852
dms.bed	encode_tfbs	USF-1	Blood	K562	0.00112408	0.16662953	1	290	350	315	350	318	15996	275	732936	wgEncodeAv	ChIP K562 USF-	1	18521
dms.bed	encode_tfbs	CTCF	Lung	SAEC	0.00111905	0.29401894	3	291	265	155	291	237	26983	273	721949	wgEncodeAv	ChIP SAEC CTCI	1	42446
dms.bed	encode_tfbs	NFKB	Blood	GM12892	0.00100918	0.16363897	1	292	351	315	351	319	16282	275	732650	wgEncodeAv	ChIP GM12892	1	8152
dms.bed	encode_tfbs	CTCF	Eye	WERI-Rb-1	0.00100231	0.23851701	2	293	297	211	297	267	22237	274	726695	wgEncodeAv	ChIP WERI-Rb-1	1	50308
dms.bed	codex	CBFB	Blood	Leukaemia cell	0.00091699	0.16106976	1	295	352	315	352	321	16536	275	732396	GSM112232	U937 (histiocyt	1	9623
dms.bed	encode_tfbs	CTCF	Blood	K562	0.00081965	0.23213183	2	296	299	211	299	269	22830	274	726102	wgEncodeAv	ChIP K562 CTCI	1	43247
dms.bed	encode_tfbs	CTCF	Breast	HMF	0.00081603	0.23199556	2	297	300	211	300	269	22843	274	726089	wgEncodeAv	ChIP HMF CTCF	1	54171
dms.bed	encode_tfbs	USF1	Brain	SK-N-SH_RA	0.00070543	0.22759431	2	299	304	211	304	271	23271	274	725661	wgEncodeAv	ChIP SK-N-SH_I	1	19622
dms.bed	encode_tfbs	USF-1	ESC	H1-hESC	0.00070149	0.15428952	1	300	358	315	358	324	17246	275	731686	wgEncodeAv	ChIP H1-hESC U	1	26042
dms.bed	encode_tfbs	NFKB	Blood	GM18951	0.00062923	0.15169577	1	302	360	315	360	326	17534	275	731398	wgEncodeAv	ChIP GM18951	1	13535
dms.bed	encode_tfbs	CTCF	Breast	HMEC	0.00050774	0.14682221	1	303	368	315	368	329	18102	275	730830	wgEncodeAv	ChIP HMEC CTC	1	40048
dms.bed	encode_tfbs	CTCF	Skin	NHEK	0.00047453	0.21644104	2	304	310	211	310	275	24431	274	724501	wgEncodeAv	ChIP NHEK CTC	1	47113
dms.bed	encode_tfbs	CTCF	Blood	K562	0.00044413	0.21468733	2	305	312	211	312	276	24624	274	724308	wgEncodeAv	ChIP K562 CTCI	1	54387
dms.bed	encode_tfbs	ATF3	Blood	K562	0.00043966	0.143721	1	306	369	315	369	330	18483	275	730449	wgEncodeAv	ChIP K562 ATF3	1	16011
dms.bed	encode_tfbs	c-Myc	Breast	MCF-7	0.00039835	0.14166932	1	307	370	315	370	331	18744	275	730188	wgEncodeAv	ChIP MCF-7 c-M	1	10072
dms.bed	encode_tfbs	CTCF	Breast	MCF-7	0.00038201	0.26000309	3	308	284	155	308	249	30370	273	718562	wgEncodeAv	ChIP MCF-7 CT	1	54343
dms.bed	encode_tfbs	CTCF	Blood	GM12878	0.00035724	0.13947069	1	309	372	315	372	332	19032	275	729900	wgEncodeAv	ChIP GM12878	1	48916
dms.bed	codex	LMO2	Blood	Acute Myeloid Leuke	0.00035691	0.20909792	2	310	316	211	316	279	25260	274	723672	GSM150116	Kasumi-1 (AML	1	13782
dms.bed	encode_tfbs	NFIC	Liver	HepG2	0.00032859	0.13782816	1	311	373	315	373	333	19253	275	729679	wgEncodeAv	ChIP HepG2 NF	1	16091
dms.bed	encode_tfbs	AP-2alpha	Cervix	HeLa-S3	0.00031235	0.29215125	4	312	267	127	312	235	35892	272	713040	wgEncodeAv	ChIP HeLa-S3 A	1	18970
dms.bed	encode_tfbs	CTCF	Heart	HCFaa	0.00030476	0.13638107	1	313	374	315	374	334	19452	275	729480	wgEncodeAv	ChIP HCFaa CT	1	41571
dms.bed	encode_tfbs	ETS1	Lung	A549	0.00029234	0.1355938	1	314	375	315	375	335	19562	275	729370	wgEncodeAv	ChIP A549 ETS1	1	5525
dms.bed	encode_tfbs	Rad21	Liver	HepG2	0.00025918	0.13336689	1	315	376	315	376	335	19880	275	729052	wgEncodeAv	ChIP HepG2 Ra	1	54315
dms.bed	encode_tfbs	CTCF	Breast	MCF-7	0.00022206	0.28294603	4	316	273	127	316	239	37002	272	711930	wgEncodeAv	ChIP MCF-7 CT	1	58608
dms.bed	encode_tfbs	CTCF	Liver	HepG2	0.00018983	0.12792753	1	317	379	315	379	337	20702	275	728230	wgEncodeAv	ChIP HepG2 CT	1	48708
dms.bed	encode_tfbs	CTCF	Skin	NHEK	0.00018039	0.19342699	2	319	328	211	328	286	27232	274	721700	wgEncodeAv	ChIP NHEK CTC	1	53797
dms.bed	encode_tfbs	CTCF	Blood	GM19240	0.00016571	0.19164438	2	321	331	211	331	288	27476	274	721456	wgEncodeAv	ChIP GM19240	1	46036
dms.bed	encode_tfbs	JunD	Blood	K562	0.00016455	0.12557473	1	322	380	315	380	339	21079	275	727853	wgEncodeAv	ChIP K562 eGFI	1	26674
dms.bed	encode_tfbs	JunD	Blood	K562	0.0001595	0.23793063	3	323	298	155	323	259	33063	273	715869	wgEncodeAv	ChIP K562 JunD	1	40052
dms.bed	codex	MYH11	Blood	Leukaemia cell	0.00015089	0.18971546	2	325	333	211	333	290	27745	274	721187	GSM112232	U937 (histiocyt	1	29434
dms.bed	encode_tfbs	Rad21	ESC	H1-hESC	0.00014127	0.18838241	2	326	334	211	334	290	27934	274	720998	wgEncodeAv	ChIP H1-hESC F	1	75680
dms.bed	encode_tfbs	CTCF	Kidney	HEK293	0.0001369	0.12266892	1	327	382	315	382	341	21564	275	727368	wgEncodeAv	ChIP HEK293 C	1	47331
dms.bed	encode_tfbs	CTCF	Breast	MCF-7	0.00011711	0.18469145	2	329	337	211	337	292	28471	274	720461	wgEncodeAv	ChIP MCF-7 CT	1	57936
dms.bed	encode_tfbs	MYBL2	Liver	HepG2	0.00011651	0.2309284	3	330	301	155	330	262	34020	273	714912	wgEncodeAv	ChIP HepG2 M	1	17898
dms.bed	encode_tfbs	CTCF	Blood	GM12873	0.00011549	0.18442208	2	331	338	211	338	293	28511	274	720421	wgEncodeAv	ChIP GM12873	1	51005
dms.bed	encode_tfbs	CTCF	Bone	Osteobl	0.00011472	0.23059464	3	332	303	155	332	263	34067	273	714865	wgEncodeAv	ChIP Osteobl C	1	56264
dms.bed	encode_tfbs	STAT1	Cervix	HeLa-S3	9.4795E-05	0.11724327	1	333	389	315	389	346	22532	275	726400	wgEncodeAv	ChIP HeLa-S3 S	1	16158

dms.bed	encode_tfbs	Egr-1	ESC	H1-hESC	9.44E-05	0.11718429	1	334	390	315	390	346	22543	275	726389	wgEncodeAv	ChIP H1-hESC E	1	8743
dms.bed	encode_tfbs	CBX3	Blood	K562	9.39E-05	0.18052847	2	335	342	211	342	296	29102	274	719830	wgEncodeAv	ChIP K562 CBX3	1	20723
dms.bed	encode_tfbs	CTCF	Blood	GM12878	8.8682E-05	0.17948226	2	336	343	211	343	297	29265	274	719667	wgEncodeAv	ChIP GM12878	1	44982
dms.bed	encode_tfbs	CTCF	Breast	HMEC	7.6927E-05	0.17693256	2	337	345	211	345	298	29670	274	719262	wgEncodeAv	ChIP HMEC CTC	1	55897
dms.bed	encode_tfbs	TCF12	Blood	GM12878	7.6244E-05	0.1142458	1	338	392	315	392	348	23105	275	725827	wgEncodeAv	ChIP GM12878	1	20437
dms.bed	encode_tfbs	CEBPD	Liver	HepG2	7.3623E-05	0.11377833	1	339	393	315	393	349	23197	275	725735	wgEncodeAv	ChIP HepG2 CE	1	11433
dms.bed	encode_tfbs	AP-2gamma	Cervix	HeLa-S3	7.2919E-05	0.28607085	5	340	271	102	340	238	45376	271	703556	wgEncodeAv	ChIP HeLa-S3 A	1	25452
dms.bed	encode_tfbs	CTCF	Blood	GM19239	5.9136E-05	0.11093379	1	341	395	315	395	350	23773	275	725159	wgEncodeAv	ChIP GM19239	1	41085
dms.bed	encode_tfbs	CTCF	Blood	GM12892	5.5231E-05	0.17126892	2	343	347	211	347	300	30611	274	718321	wgEncodeAv	ChIP GM12892	1	48306
dms.bed	encode_tfbs	CTCF	Skin	AG09309	4.6472E-05	0.10796262	1	344	399	315	399	353	24406	275	724526	wgEncodeAv	ChIP AG09309	1	43928
dms.bed	encode_tfbs	ELF1	Lung	A549	4.537E-05	0.10767532	1	345	400	315	400	353	24469	275	724463	wgEncodeAv	ChIP A549 ELF1	1	8611
dms.bed	encode_tfbs	CTCF	Kidney	HRPEpiC	4.004E-05	0.10620313	1	346	402	315	402	354	24797	275	724135	wgEncodeAv	ChIP HRPEpiC C	1	53134
dms.bed	encode_tfbs	CTCF	Blood	GM06990	3.9554E-05	0.10606158	1	347	403	315	403	355	24829	275	724103	wgEncodeAv	ChIP GM06990	1	45500
dms.bed	encode_tfbs	FOXP2	Brain	SK-N-MC	3.6165E-05	0.10503318	1	350	404	315	404	356	25064	275	723868	wgEncodeAv	ChIP SK-N-MC I	1	14695
dms.bed	encode_tfbs	CTCF	Skin	AG04449	3.555E-05	0.10483845	1	351	405	315	405	357	25109	275	723823	wgEncodeAv	ChIP AG04449	1	50260
dms.bed	encode_tfbs	CTCF	Lung	IMR90	3.2466E-05	0.10382003	1	352	406	315	406	358	25347	275	723585	wgEncodeAv	ChIP IMR90 CTC	1	45920
dms.bed	encode_tfbs	ELK4	Cervix	HeLa-S3	3.1635E-05	0.10353255	1	353	407	315	407	358	25415	275	723517	wgEncodeAv	ChIP HeLa-S3 E	1	5916
dms.bed	encode_tfbs	CTCF	Blood	GM12872	3.0393E-05	0.10309167	1	354	408	315	408	359	25520	275	723412	wgEncodeAv	ChIP GM12872	1	47151
dms.bed	encode_tfbs	CTCF	Blood	GM12864	2.7303E-05	0.10192943	1	355	410	315	410	360	25801	275	723131	wgEncodeAv	ChIP GM12864	1	46798
dms.bed	encode_tfbs	Mxi1	Cervix	HeLa-S3	2.636E-05	0.20289468	3	357	318	155	357	277	38479	273	710453	wgEncodeAv	ChIP HeLa-S3 M	1	12009
dms.bed	encode_tfbs	CTCF	Lung	NHLF	2.0124E-05	0.09875889	1	359	411	315	411	362	26600	275	722332	wgEncodeAv	ChIP NHLF CTC	1	39537
dms.bed	encode_tfbs	E2F6	Cervix	HeLa-S3	1.923E-05	0.0983029	1	360	412	315	412	362	26719	275	722213	wgEncodeAv	ChIP HeLa-S3 E	1	4775
dms.bed	encode_tfbs	TCF7L2	Pancreas	PANC-1	1.7571E-05	0.09741051	1	363	415	315	415	364	26955	275	721977	wgEncodeAv	ChIP PANC-1 TC	1	13366
dms.bed	encode_tfbs	c-Myc	Breast	MCF10A-Er-Src	1.3539E-05	0.15083646	2	365	361	211	365	312	34566	274	714366	wgEncodeAv	ChIP MCF10A-E	1	35153
dms.bed	encode_tfbs	BHLHE40	Blood	K562	1.3394E-05	0.15069932	2	366	362	211	366	313	34596	274	714336	wgEncodeAv	ChIP K562 BHLI	1	22497
dms.bed	encode_tfbs	COREST	Blood	K562	1.3009E-05	0.09454787	1	367	418	315	418	367	27741	275	721191	wgEncodeAv	ChIP K562 COR	1	35741
dms.bed	encode_tfbs	CTCF	Blood	GM12891	1.2167E-05	0.09393245	1	368	420	315	420	368	27916	275	721016	wgEncodeAv	ChIP GM12891	1	42632
dms.bed	codex	TCF3	Blood	Leukaemia cell	1.161E-05	0.14889779	2	369	365	211	369	315	34995	274	713937	GSM108230	Juvenile acute	1	43270
dms.bed	codex	MYB	Blood	T-Cell	1.001E-05	0.14707581	2	370	367	211	370	316	35408	274	713524	GSM144200	codex T-Cell M	1	30659
dms.bed	encode_tfbs	CTCF	Brain	Gliobla	6.3088E-06	0.08828918	1	372	423	315	423	370	29630	275	719302	wgEncodeAv	ChIP Gliobla CT	1	62772
dms.bed	encode_tfbs	CTCF	Blood vessel	HBMEC	6.0783E-06	0.08798926	1	373	424	315	424	371	29727	275	719205	wgEncodeAv	ChIP HBMEC CT	1	58376
dms.bed	codex	CTCF	Blood	Erythroid Progenitor	5.8765E-06	0.08771887	1	374	425	315	425	371	29815	275	719117	GSM651543	CD36+ erythroi	1	21602
dms.bed	encode_tfbs	YY1	ESC	H1-hESC	3.4388E-06	0.08363613	1	375	430	315	430	373	31210	275	717722	wgEncodeAv	ChIP H1-hESC Y	1	18328
dms.bed	encode_tfbs	CTCF	Blood	GM19238	2.7333E-06	0.08199832	1	376	433	315	433	375	31807	275	717125	wgEncodeAv	ChIP GM19238	1	49938
dms.bed	encode_tfbs	CTCF	Lung	A549	2.5631E-06	0.08155112	1	377	435	315	435	376	31974	275	716958	wgEncodeAv	ChIP A549 CTC	1	55351
dms.bed	encode_tfbs	NFKB	Blood	GM15510	2.2809E-06	0.08075155	1	378	437	315	437	377	32277	275	716655	wgEncodeAv	ChIP GM15510	1	12803
dms.bed	encode_tfbs	NFKB	Blood	GM12891	1.5727E-06	0.07830219	1	380	440	315	440	378	33242	275	715690	wgEncodeAv	ChIP GM12891	1	28683
dms.bed	encode_tfbs	GABP	Lung	A549	9.0247E-07	0.07490291	1	381	442	315	442	379	34681	275	714251	wgEncodeAv	ChIP A549 GAB	1	12348
dms.bed	encode_tfbs	YY1	Lung	A549	4.1467E-07	0.07060111	1	383	448	315	448	382	36691	275	712241	wgEncodeAv	ChIP A549 YY1_	1	10259
dms.bed	codex	SPI1	Blood	Monocyte	3.6532E-07	0.06994544	1	384	449	315	449	383	37018	275	711914	GSM785495	Peripheral bloc	1	33822
dms.bed	encode_tfbs	CHD2	Cervix	HeLa-S3	3.2541E-07	0.14992035	3	385	363	155	385	301	51147	273	697785	wgEncodeAv	ChIP HeLa-S3 C	1	20500
dms.bed	encode_tfbs	YY1	Brain	SK-N-SH_RA	3.0493E-07	0.06903084	1	386	450	315	450	384	37484	275	711448	wgEncodeAv	ChIP SK-N-SH_I	1	15684
dms.bed	encode_tfbs	ELF1	Blood	K562	1.3565E-07	0.10857986	2	390	397	211	397	333	47170	274	701762	wgEncodeAv	ChIP K562 ELF1	1	27780
dms.bed	encode_tfbs	CREB1	Lung	A549	1.336E-07	0.10847922	2	391	398	211	398	333	47211	274	701721	wgEncodeAv	ChIP A549 CREI	1	15913
dms.bed	encode_tfbs	GABP	Liver	HepG2	1.1616E-07	0.06451541	1	392	457	315	457	388	39968	275	708964	wgEncodeAv	ChIP HepG2 GA	1	10109
dms.bed	encode_tfbs	TCF7L2	Colon	HCT-116	8.9446E-08	0.06339036	1	393	458	315	458	389	40639	275	708293	wgEncodeAv	ChIP HCT-116 T	1	19463
dms.bed	encode_tfbs	Ini1	Cervix	HeLa-S3	8.5128E-08	0.06318159	1	394	459	315	459	389	40766	275	708166	wgEncodeAv	ChIP HeLa-S3 Ir	1	7780
dms.bed	codex	MYB	Blood	T-Cell	8.0671E-08	0.06295621	1	395	460	315	460	390	40904	275	708028	GSM151963	codex T-Cell M	1	20147
dms.bed	codex	RUNX1	Blood	Acute Myeloid Leuke	6.7981E-08	0.06224924	1	396	462	315	462	391	41343	275	707589	GSM722708	Peripheral bloc	1	44582
dms.bed	codex	SAP30	ESC	Embryonic Stem Cell	6.2635E-08	0.06191633	1	397	463	315	463	392	41553	275	707379	GSM831040	K562 erythrocy	1	16520
dms.bed	encode_tfbs	Pol2-4H8	Brain	SK-N-MC	3.4166E-08	0.05955658	1	400	466	315	466	394	43105	275	705827	wgEncodeAv	ChIP SK-N-MC I	1	24130
dms.bed	codex	RUNX1	Blood	Lymphoma cell	2.3731E-08	0.09815646	2	402	413	211	413	342	51832	274	697100	GSM125293	T cell Lymphob	1	26549
dms.bed	encode_tfbs	Max	Cervix	HeLa-S3	2.1639E-08	0.15565589	4	404	357	127	404	296	64649	272	684283	wgEncodeAv	ChIP HeLa-S3 M	1	29647
dms.bed	encode_tfbs	MAZ	Liver	HepG2	1.7813E-08	0.05720827	1	405	467	315	467	396	44769	275	704163	wgEncodeAv	ChIP HepG2 MA	1	12090
dms.bed	encode_tfbs	Max	Blood	NB4	1.6541E-08	0.05695254	1	406	468	315	468	396	44958	275	703974	wgEncodeAv	ChIP NB4 Max	1	34659
dms.bed	encode_tfbs	RUNX3	Blood	GM12878	1.1271E-08	0.05566286	1	407	469	315	469	397	45936	275	702996	wgEncodeAv	ChIP GM12878	1	67965
dms.bed	codex	EP300	Blood	Leukaemia cell	9.3196E-09	0.09334446	2	410	421	211	421	347	54310	274	694622	GSM112231	Acute myelom	1	33890

dms.bed	encode_tfbs	Pol2-4H8	Blood	K562	8.0305E-09	0.05456959	1	412	471	315	471	399	46799	275	702133	wgEncodeAv	ChIP K562 Pol2	1	23352
dms.bed	encode_tfbs	c-Myc	Blood	NB4	4.6042E-09	0.0528629	1	413	474	315	474	401	48213	275	700719	wgEncodeAv	ChIP NB4 c-My	1	26252
dms.bed	codex	P300	Blood	Lymphoma cell	4.4649E-09	0.05277166	1	414	475	315	475	401	48291	275	700641	GSM125294	T cell Lymphob	1	19253
dms.bed	encode_tfbs	FOXP2	Brain	PFSK-1	4.323E-09	0.05267607	1	415	476	315	476	402	48373	275	700559	wgEncodeAv	ChIP PFSK-1 FO	1	18182
dms.bed	encode_tfbs	TAF1	Cervix	HeLa-S3	3.4917E-09	0.05205225	1	416	477	315	477	403	48915	275	700017	wgEncodeAv	ChIP HeLa-S3 T	1	16100
dms.bed	encode_tfbs	Max	Blood	K562	3.0677E-09	0.11761528	3	417	388	155	417	320	63995	273	684937	wgEncodeAv	ChIP K562 Max	1	31436
dms.bed	encode_tfbs	YY1	Liver	HepG2	2.3409E-09	0.08702713	2	418	426	211	426	352	57947	274	690985	wgEncodeAv	ChIP HepG2 YY	1	17876
dms.bed	encode_tfbs	Egr-1	Blood	K562	1.7254E-09	0.05009102	1	419	480	315	480	405	50701	275	698231	wgEncodeAv	ChIP K562 Egr-1	1	36997
dms.bed	codex	POLR2A	Blood	Erythrocytic leukaem	5.4606E-10	0.04718015	1	421	481	315	481	406	53606	275	695326	GSM831016	K562 erythrocy	1	35672
dms.bed	encode_tfbs	Sin3Ak-20	Liver	HepG2	3.6533E-10	0.04623883	1	422	482	315	482	406	54618	275	694314	wgEncodeAv	ChIP HepG2 Sir	1	16459
dms.bed	encode_tfbs	Mxi1	Blood	GM12878	1.4734E-10	0.04423994	1	424	488	315	488	409	56899	275	692033	wgEncodeAv	ChIP GM12878	1	17735
dms.bed	codex	NOTCH1	Blood	T-cell acute lymphobl	1.1641E-10	0.10216501	3	425	409	155	425	330	72733	273	676199	GSM959056	ChIP-seq_ICN1	1	43398
dms.bed	encode_tfbs	E2F6	Blood	K562	9.2855E-11	0.04328607	1	426	489	315	489	410	58056	275	690876	wgEncodeAv	ChIP K562 E2F6	1	16312
dms.bed	encode_tfbs	c-Myc	Breast	MCF-7	7.8605E-11	0.04295154	1	427	490	315	490	411	58473	275	690459	wgEncodeAv	ChIP MCF-7 c-M	1	20956
dms.bed	codex	BRD4	Blood	Lymphoma cell	6.7824E-11	0.07411059	2	429	444	211	444	361	67140	274	681792	GSM125294	T cell Lymphob	1	23553
dms.bed	encode_tfbs	TBP	ESC	H1-hESC	5.6697E-11	0.04230975	1	430	491	315	491	412	59290	275	689642	wgEncodeAv	ChIP H1-hESC T	1	17194
dms.bed	encode_tfbs	E2F6	Blood	K562	4.7443E-11	0.07301238	2	432	446	211	446	363	68058	274	680874	wgEncodeAv	ChIP K562 E2F6	1	24570
dms.bed	encode_tfbs	Pol2	Liver	HepG2	2.6133E-11	0.04085951	1	433	493	315	493	414	61223	275	687709	wgEncodeAv	ChIP HepG2 Po	1	22928
dms.bed	encode_tfbs	ELF1	Blood	GM12878	2.0531E-11	0.04042708	1	435	494	315	494	415	61824	275	687108	wgEncodeAv	ChIP GM12878	1	23008
dms.bed	encode_tfbs	c-Myc	Breast	MCF-7	2.0416E-11	0.04041711	1	436	495	315	495	415	61838	275	687094	wgEncodeAv	ChIP MCF-7 c-M	1	27697
dms.bed	encode_tfbs	Pol2-4H8	Blood vessel	HUVEC	1.7981E-11	0.09501892	3	437	416	155	437	336	77636	273	671296	wgEncodeAv	ChIP HUVEC Po	1	32525
dms.bed	codex	CBFB	Blood	Leukaemia cell	1.198E-11	0.03949257	1	438	497	315	497	417	63164	275	685768	GSM112232	U937 (histiocyt	1	15852
dms.bed	encode_tfbs	c-Myc	Blood	K562	1.0626E-11	0.03929011	1	439	498	315	498	417	63462	275	685470	wgEncodeAv	ChIP K562 c-My	1	24153
dms.bed	encode_tfbs	Pol2	Liver	HepG2	9.597E-12	0.03911971	1	440	499	315	499	418	63715	275	685217	wgEncodeAv	ChIP HepG2 Po	1	15108
dms.bed	encode_tfbs	c-Myc	Blood	K562	3.5358E-12	0.03752146	1	441	500	315	500	419	66190	275	682742	wgEncodeAv	ChIP K562 c-My	1	31092
dms.bed	codex	POLR2A	Blood	Erythroblast	3.0954E-12	0.06556438	2	442	454	211	454	369	75014	274	673918	GSM970259	Proerythroblas	1	35015
dms.bed	codex	CBFB	Blood	Leukaemia cell	1.7714E-12	0.03648645	1	446	501	315	501	421	67898	275	681034	GSM112230	Acute myelom	1	12533
dms.bed	encode_tfbs	Pol2	Liver	HepG2	1.4459E-12	0.0867978	3	447	427	155	447	343	84163	273	664769	wgEncodeAv	ChIP HepG2 Po	1	25927
dms.bed	codex	RUNX3	Blood	B-cells	6.3438E-13	0.06187883	2	449	464	211	464	375	79010	274	669922	GSM101089	GM12878 cell f	1	104018
dms.bed	encode_tfbs	MAZ	Blood	K562	5.8853E-13	0.03494482	1	450	502	315	502	422	70612	275	678320	wgEncodeAv	ChIP K562 MAZ	1	33323
dms.bed	encode_tfbs	TAF1	Liver	HepG2	2.8236E-13	0.03398455	1	452	504	315	504	424	72415	275	676517	wgEncodeAv	ChIP HepG2 TA	1	16659
dms.bed	codex	ERG	Blood	Leukaemia cell	2.0762E-13	0.08135563	3	454	436	155	454	348	89123	273	659809	GSM112231	Acute myelom	1	25083
dms.bed	encode_tfbs	HMGN3	Blood	K562	1.582E-13	0.03326177	1	455	506	315	506	425	73834	275	675098	wgEncodeAv	ChIP K562 HMG	1	14587
dms.bed	encode_tfbs	Pol2	Cervix	HeLa-S3	6.731E-14	0.03224784	1	457	510	315	510	427	75921	275	673011	wgEncodeAv	ChIP HeLa-S3 P	1	15736
dms.bed	encode_tfbs	Pol2	Breast	MCF-7	5.487E-14	0.03201408	1	458	511	315	511	428	76419	275	672513	wgEncodeAv	ChIP MCF-7 Po	1	20449
dms.bed	encode_tfbs	Pol2	Uterus	ECC-1	1.5815E-14	0.03065496	1	460	513	315	513	429	79449	275	669483	wgEncodeAv	ChIP ECC-1 Pol2	1	20137
dms.bed	encode_tfbs	Pol2-4H8	Colon	HCT-116	1.244E-14	0.03041036	1	462	514	315	514	430	80020	275	668912	wgEncodeAv	ChIP HCT-116 F	1	29178
dms.bed	codex	CBFB	Blood	Leukaemia cell	6.2681E-15	0.02971338	1	466	515	315	515	432	81693	275	667239	GSM112230	Acute myelom	1	18365
dms.bed	codex	BCOR	Blood	B-Cells	1.7358E-15	0.02850598	1	467	517	315	517	433	84763	275	664169	GSM898061	Cell line: Germ	1	31772
dms.bed	encode_tfbs	Max	Blood	K562	1.2536E-15	0.0505651	2	468	478	211	478	386	94456	274	654476	wgEncodeAv	ChIP K562 Max	1	46171
dms.bed	encode_tfbs	HA-E2F1	Breast	MCF-7	7.2325E-16	0.02770938	1	471	520	315	520	435	86918	275	662014	wgEncodeAv	ChIP MCF-7 HA	1	21946
dms.bed	codex	KDM4A	ESC	Embryonic Stem Cell	0	0.04446761	2	478	487	211	487	392	105580	274	643352	GSM831035	K562 erythrocy	1	20642
dms.bed	encode_tfbs	Pol2	Lung	A549	0	0.03974337	2	478	496	211	496	395	116181	274	632751	wgEncodeAv	ChIP A549 Pol2	1	27603
dms.bed	encode_tfbs	Pol2	Lung	A549	0	0.01994613	1	478	526	315	526	440	115547	275	633385	wgEncodeAv	ChIP A549 Pol2	1	27685
dms.bed	encode_tfbs	Pol2	Blood	GM12878	0	0.01607451	1	478	530	315	530	441	138258	275	610674	wgEncodeAv	ChIP GM12878	1	27558
dms.bed	codex	STAT5	Blood	Erythroid Leukaemia	0	0	0	478	534	534	534	515	92	276	748840	BG22_STAT5	No drug (DMSC	1	127
dms.bed	codex	RUNX1T1	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	52486	276	696446	GSM108230	Juvenile acute	1	16941
dms.bed	codex	TCF12	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	38783	276	710149	GSM108230	Juvenile acute	1	18869
dms.bed	codex	BCL6	Blood	Lymphoma cell	0	0	0	478	534	534	534	515	29301	276	719631	GSM108480	Adult B cell No	1	8053
dms.bed	codex	ERG	Blood	Hematopoietic Stem	0	0	0	478	534	534	534	515	3240	276	745692	GSM109787	Mobilised CD34	1	2783
dms.bed	codex	FLI1	Blood	Hematopoietic Stem	0	0	0	478	534	534	534	515	15727	276	733205	GSM109788	Mobilised CD34	1	10750
dms.bed	codex	TAL1	Blood	Hematopoietic Stem	0	0	0	478	534	534	534	515	1267	276	747665	GSM109788	Mobilised CD34	1	528
dms.bed	codex	LYL1	Blood	Hematopoietic Stem	0	0	0	478	534	534	534	515	961	276	747971	GSM109788	Mobilised CD34	1	1972
dms.bed	codex	GATA2	Blood	Hematopoietic Stem	0	0	0	478	534	534	534	515	3137	276	745795	GSM109788	Mobilised CD34	1	7046
dms.bed	codex	RUNX1	Blood	Hematopoietic Stem	0	0	0	478	534	534	534	515	28103	276	720829	GSM109788	Mobilised CD34	1	14287
dms.bed	codex	LMO2	Blood	Hematopoietic Stem	0	0	0	478	534	534	534	515	2118	276	746814	GSM109788	Mobilised CD34	1	1790
dms.bed	codex	MYH11	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	53746	276	695186	GSM112230	Acute myelom	1	9071

dms.bed	codex	MYH11	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	21208	276	727724	GSM112230	Acute myelom	1	6452
dms.bed	codex	RUNX1	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	71939	276	676993	GSM112230	Acute myelom	1	17308
dms.bed	codex	MED21	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	61895	276	687037	GSM112230	Acute myelom	1	10213
dms.bed	codex	TBP	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	52425	276	696507	GSM112230	Acute myelom	1	8207
dms.bed	codex	TCF12	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	70117	276	678815	GSM112230	Acute myelom	1	17269
dms.bed	codex	GATA2	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	35647	276	713285	GSM112231	Acute myelom	1	6162
dms.bed	codex	TAL1	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	50332	276	698600	GSM112231	Acute myelom	1	9472
dms.bed	codex	FLI1	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	25340	276	723592	GSM112231	Acute myelom	1	4027
dms.bed	codex	ELF1	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	61611	276	687321	GSM112231	Acute myelom	1	9602
dms.bed	codex	SPI1	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	31489	276	717443	GSM112231	Acute myelom	1	5553
dms.bed	codex	HDAC1	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	49047	276	699885	GSM112231	Acute myelom	1	20782
dms.bed	codex	MYH11	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	47398	276	701534	GSM112231	CD34+ acute m	1	7941
dms.bed	codex	CBFB	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	38395	276	710537	GSM112232	CD34+ acute m	1	6608
dms.bed	codex	FOXA2	Endoderm	Endoderm	0	0	0	478	534	534	534	515	89070	276	659862	GSM112406	Day 5 of in vitr	1	31741
dms.bed	codex	SOX2	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	372	276	748560	GSM112406	codex Embryor	1	2311
dms.bed	codex	SOX2	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	847	276	748085	GSM112406	codex Embryor	1	5206
dms.bed	codex	NANOG	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	2133	276	746799	GSM112407	codex Embryor	1	13465
dms.bed	codex	NANOG	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	2369	276	746563	GSM112407	codex Embryor	1	18537
dms.bed	codex	MAFK	Blood	Lymphoma cell	0	0	0	478	534	534	534	515	3394	276	745538	GSM115967	Adult B cell No	1	6721
dms.bed	codex	POLR2A	Blood	Leukemia cell	0	0	0	478	534	534	534	515	57199	276	691733	GSM122478	Jurkat T-ALL ce	1	12283
dms.bed	codex	POLR2A	Blood	Leukemia cell	0	0	0	478	534	534	534	515	29142	276	719790	GSM122478	Jurkat T-ALL ce	1	4956
dms.bed	codex	POLR2A	Blood	Leukemia cell	0	0	0	478	534	534	534	515	62202	276	686730	GSM122478	Jurkat T-ALL ce	1	17457
dms.bed	codex	POLR2A	Blood	Leukemia cell	0	0	0	478	534	534	534	515	53258	276	695674	GSM122478	Jurkat T-ALL ce	1	11078
dms.bed	codex	ETS1	Blood	Lymphoma cell	0	0	0	478	534	534	534	515	75691	276	673241	GSM125292	T cell Lymphob	1	41378
dms.bed	codex	GABPA	Blood	Lymphoma cell	0	0	0	478	534	534	534	515	7350	276	741582	GSM125293	T cell Lymphob	1	14021
dms.bed	codex	NOTCH1	Blood	Lymphoma cell	0	0	0	478	534	534	534	515	15292	276	733640	GSM125293	T cell Lymphob	1	3633
dms.bed	codex	RBPJ	Blood	Lymphoma cell	0	0	0	478	534	534	534	515	17978	276	730954	GSM125293	T cell Lymphob	1	4115
dms.bed	codex	NOTCH1	Blood	Lymphoma cell	0	0	0	478	534	534	534	515	41923	276	707009	GSM125293	T cell Lymphob	1	10849
dms.bed	codex	RBPJ	Blood	Lymphoma cell	0	0	0	478	534	534	534	515	36313	276	712619	GSM125293	T cell Lymphob	1	9754
dms.bed	codex	MED1	Blood	Lymphoma cell	0	0	0	478	534	534	534	515	68208	276	680724	GSM125294	T cell Lymphob	1	27299
dms.bed	codex	NR2F2	Endometrium	Endometrial Stromal	0	0	0	478	534	534	534	515	4924	276	744008	GSM125739	codex Endome	1	19929
dms.bed	codex	TAL1	Blood	Erythroblast	0	0	0	478	534	534	534	515	4966	276	743966	GSM127824	Proerythroblas	1	18003
dms.bed	codex	GFI1B	Blood	Erythroblast	0	0	0	478	534	534	534	515	612	276	748320	GSM127824	Proerythroblas	1	3000
dms.bed	codex	CDK7	Blood	Leukemia cell	0	0	0	478	534	534	534	515	48628	276	700304	GSM129638	Untreated Jurk	1	14641
dms.bed	codex	CDK7	Blood	Multiple myeloma ce	0	0	0	478	534	534	534	515	11575	276	737357	GSM131392	MM1-S cell line	1	3839
dms.bed	codex	POLR2A	Blood	Multiple myeloma ce	0	0	0	478	534	534	534	515	58236	276	690696	GSM131392	MM1-S cell line	1	13717
dms.bed	codex	CDK9	Blood	Multiple myeloma ce	0	0	0	478	534	534	534	515	29010	276	719922	GSM131392	MM1-S cell line	1	7705
dms.bed	codex	EP300	Blood	Acute Myeloid Leuke	0	0	0	478	534	534	534	515	258	276	748674	GSM146600	Kasumi-1 (AML	1	581
dms.bed	codex	EP300	Blood	Acute Myeloid Leuke	0	0	0	478	534	534	534	515	336	276	748596	GSM146600	Kasumi-1 (AML	1	839
dms.bed	codex	CEBPA	Blood	Acute Myeloid Leuke	0	0	0	478	534	534	534	515	243	276	748689	GSM150116	Kasumi-1 (AML	1	612
dms.bed	codex	CEBPA	Blood	Acute Myeloid Leuke	0	0	0	478	534	534	534	515	2915	276	746017	GSM150116	Kasumi-1 (AML	1	7279
dms.bed	codex	SPI1	Blood	Acute Myeloid Leuke	0	0	0	478	534	534	534	515	9035	276	739897	GSM150116	Kasumi-1 (AML	1	25538
dms.bed	codex	SPI1	Blood	Acute Myeloid Leuke	0	0	0	478	534	534	534	515	12422	276	736510	GSM150116	Kasumi-1 (AML	1	21287
dms.bed	codex	MYB	Blood	T-Cell	0	0	0	478	534	534	534	515	47938	276	700994	GSM151963	codex T-Cell M	1	26035
dms.bed	codex	MYB	Blood	T-Cell	0	0	0	478	534	534	534	515	49047	276	699885	GSM151964	codex T-Cell M	1	24032
dms.bed	codex	MYB	Blood	T-Cell	0	0	0	478	534	534	534	515	45095	276	703837	GSM151964	codex T-Cell M	1	21401
dms.bed	codex	GATA1	Blood	Myeloid Leukemia	0	0	0	478	534	534	534	515	3042	276	745890	GSM467647	Human K562 e	1	4065
dms.bed	codex	GATA2	Blood	Myeloid Leukemia	0	0	0	478	534	534	534	515	3444	276	745488	GSM467648	Human K562 e	1	8820
dms.bed	codex	GATA1	Blood	Megakaryocyte	0	0	0	478	534	534	534	515	1570	276	747362	GSM607949	CD34+ Umbilic	1	1867
dms.bed	codex	GATA2	Blood	Megakaryocyte	0	0	0	478	534	534	534	515	680	276	748252	GSM607950	CD34+ Umbilic	1	409
dms.bed	codex	RUNX1	Blood	Megakaryocyte	0	0	0	478	534	534	534	515	25116	276	723816	GSM607951	CD34+ Umbilic	1	7868
dms.bed	codex	FLI1	Blood	Megakaryocyte	0	0	0	478	534	534	534	515	10598	276	738334	GSM607952	CD34+ Umbilic	1	3674
dms.bed	codex	TAL1	Blood	Megakaryocyte	0	0	0	478	534	534	534	515	830	276	748102	GSM607953	CD34+ Umbilic	1	1498
dms.bed	codex	RUNX1	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	4023	276	744909	GSM610330	Infantile acute	1	6857
dms.bed	codex	RUNX1	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	5309	276	743623	GSM610332	Adult chronic n	1	5430
dms.bed	codex	RUNX1	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	17214	276	731718	GSM610334	Adult chronic n	1	15982
dms.bed	codex	TAL1	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	201	276	748731	GSM614003	T-cell acute lyn	1	1077

dms.bed	codex	TAL1	Blood	Erythroblast	0	0	0	478	534	534	534	515	1296	276	747636	GSM614004	Proerythroblas	1	4799
dms.bed	codex	SPI1	Blood	Umbilical Cord Blood	0	0	0	478	534	534	534	515	3754	276	745178	GSM638310	CD133+ Umbili	1	11445
dms.bed	codex	IKAROS	Blood	Umbilical Cord Blood	0	0	0	478	534	534	534	515	4931	276	744001	GSM638312	CD133+ Umbili	1	1118
dms.bed	codex	MEIS1	Blood	Umbilical Cord Blood	0	0	0	478	534	534	534	515	159	276	748773	GSM638314	CD133+ Umbili	1	420
dms.bed	codex	CTCF	Blood	Hematopoietic Stem	0	0	0	478	534	534	534	515	19640	276	729292	GSM651541	Mobilised CD34	1	18624
dms.bed	codex	CTCF	Blood	Erythroid Progenitor	0	0	0	478	534	534	534	515	28903	276	720029	GSM651542	CD36+ erythroi	1	25290
dms.bed	codex	TAL1	Blood	Erythroid Progenitor	0	0	0	478	534	534	534	515	4543	276	744389	GSM651544	CD36+ erythroi	1	9130
dms.bed	codex	GATA1	Blood	Erythroid Progenitor	0	0	0	478	534	534	534	515	12930	276	736002	GSM651546	CD36+ erythroi	1	10328
dms.bed	codex	GATA1	Blood	Erythroid Progenitor	0	0	0	478	534	534	534	515	6335	276	742597	GSM651547	CD36+ erythroi	1	16428
dms.bed	codex	SMARCA4	Blood	Hematopoietic Stem	0	0	0	478	534	534	534	515	13710	276	735222	GSM651552	Mobilised CD34	1	6462
dms.bed	codex	SMARCA4	Blood	Erythroid Progenitor	0	0	0	478	534	534	534	515	1586	276	747346	GSM651553	CD36+ erythroi	1	7687
dms.bed	codex	SMAD1	Blood	Erythroblast	0	0	0	478	534	534	534	515	223	276	748709	GSM722397	Proerythroblas	1	1035
dms.bed	codex	SMAD1	Blood	Erythroblast	0	0	0	478	534	534	534	515	276	276	748656	GSM722398	Proerythroblas	1	1293
dms.bed	codex	TCF7L2	Blood	Hematopoietic Stem	0	0	0	478	534	534	534	515	770	276	748162	GSM722400	Mobilised CD34	1	9717
dms.bed	codex	TCF7L2	Blood	Hematopoietic Stem	0	0	0	478	534	534	534	515	2806	276	746126	GSM722401	Mobilised CD34	1	3739
dms.bed	codex	TCF7L2	Blood	Hematopoietic Stem	0	0	0	478	534	534	534	515	3088	276	745844	GSM722402	Mobilised CD34	1	6212
dms.bed	codex	RUNX1	Blood	Acute Myeloid Leuke	0	0	0	478	534	534	534	515	18122	276	730810	GSM722704	Kasumi-1 (AML	1	10203
dms.bed	codex	RUNX1T1	Blood	Acute Myeloid Leuke	0	0	0	478	534	534	534	515	3187	276	745745	GSM722706	Kasumi-1 (AML	1	3283
dms.bed	codex	POLR2A	Blood	Acute Myeloid Leuke	0	0	0	478	534	534	534	515	44757	276	704175	GSM722709	Kasumi-1 (AML	1	10124
dms.bed	codex	POLR2A	Blood	Acute Myeloid Leuke	0	0	0	478	534	534	534	515	42268	276	706664	GSM722710	Kasumi-1 (AML	1	10018
dms.bed	codex	SPI1	Blood	Macrophage	0	0	0	478	534	534	534	515	7080	276	741852	GSM785501	Macrophages v	1	26490
dms.bed	codex	EGR2	Blood	Macrophage	0	0	0	478	534	534	534	515	4335	276	744597	GSM785503	Macrophages v	1	1020
dms.bed	codex	CBX8	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	1640	276	747292	GSM830987	K562 erythrocy	1	7114
dms.bed	codex	CHD1	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	30680	276	718252	GSM830988	K562 erythrocy	1	6998
dms.bed	codex	HDAC1	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	55005	276	693927	GSM830993	K562 erythrocy	1	11727
dms.bed	codex	HDAC2	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	22983	276	725949	GSM830995	K562 erythrocy	1	5605
dms.bed	codex	KDM5C	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	17020	276	731912	GSM831000	K562 erythrocy	1	3472
dms.bed	codex	CREBBP	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	118	276	748814	GSM831001	K562 erythrocy	1	2277
dms.bed	codex	NCOR1	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	721	276	748211	GSM831004	K562 erythrocy	1	624
dms.bed	codex	WHSC1	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	1364	276	747568	GSM831005	K562 erythrocy	1	2085
dms.bed	codex	EP300	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	1723	276	747209	GSM831006	K562 erythrocy	1	2174
dms.bed	codex	PHF8	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	72957	276	675975	GSM831008	K562 erythrocy	1	16510
dms.bed	codex	PHF8	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	73051	276	675881	GSM831009	K562 erythrocy	1	17229
dms.bed	codex	KDM5B	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	67490	276	681442	GSM831010	K562 erythrocy	1	21221
dms.bed	codex	KDM5B	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	27359	276	721573	GSM831011	K562 erythrocy	1	5601
dms.bed	codex	RBBP5	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	70671	276	678261	GSM831012	K562 erythrocy	1	15698
dms.bed	codex	REST	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	5424	276	743508	GSM831015	K562 erythrocy	1	5610
dms.bed	codex	RNF2	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	2897	276	746035	GSM831017	K562 erythrocy	1	4105
dms.bed	codex	SAP30	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	52026	276	696906	GSM831018	K562 erythrocy	1	10433
dms.bed	codex	SIRT6	Blood	Erythrocytic leukaem	0	0	0	478	534	534	534	515	2900	276	746032	GSM831020	K562 erythrocy	1	1838
dms.bed	codex	CHD1	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	13009	276	735923	GSM831025	K562 erythrocy	1	4814
dms.bed	codex	EZH2	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	13316	276	735616	GSM831028	K562 erythrocy	1	3205
dms.bed	codex	HDAC2	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	45879	276	703053	GSM831029	K562 erythrocy	1	8835
dms.bed	codex	EP300	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	4099	276	744833	GSM831036	K562 erythrocy	1	2276
dms.bed	codex	PHF8	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	77297	276	671635	GSM831037	K562 erythrocy	1	13630
dms.bed	codex	RBBP5	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	65483	276	683449	GSM831038	K562 erythrocy	1	12525
dms.bed	codex	SUZ12	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	13467	276	735465	GSM831042	K562 erythrocy	1	2682
dms.bed	codex	EP300	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	3596	276	745336	GSM835863	Acute myeloid	1	5120
dms.bed	codex	RUNX1	Blood	Acute Myeloid Leuke	0	0	0	478	534	534	534	515	13089	276	735843	GSM850823	Kasumi-1 (AML	1	12817
dms.bed	codex	RUNX1	Blood	Acute Myeloid Leuke	0	0	0	478	534	534	534	515	13499	276	735433	GSM850824	Kasumi-1 (AML	1	17787
dms.bed	codex	RUNX1T1	Blood	Acute Myeloid Leuke	0	0	0	478	534	534	534	515	890	276	748042	GSM850826	Blast cells from	1	1125
dms.bed	codex	POLR2A	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	49089	276	699843	GSM897115	codex Embryor	1	12277
dms.bed	codex	SMAD3	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	1021	276	747911	GSM897117	codex Embryor	1	947
dms.bed	codex	SMC3	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	3770	276	745162	GSM897119	codex Embryor	1	4240
dms.bed	codex	SMC1A	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	5434	276	743498	GSM897120	codex Embryor	1	4560
dms.bed	codex	BCL6	Blood	B-Cells	0	0	0	478	534	534	534	515	52428	276	696504	GSM898060	Cell line: Germ	1	23912
dms.bed	codex	NCOR2	Blood	B-Cells	0	0	0	478	534	534	534	515	6236	276	742696	GSM898062	Cell line: Germ	1	5917

dms.bed	codex	TAL1	Blood	Erythroblast	0	0	0	478	534	534	534	515	101	276	748831	GSM908054	Proerythroblas	1	584
dms.bed	codex	TAL1	Blood	Erythroblast	0	0	0	478	534	534	534	515	369	276	748563	GSM908055	Proerythroblas	1	1137
dms.bed	codex	NFE2	Blood	Erythroblast	0	0	0	478	534	534	534	515	166	276	748766	GSM908059	Proerythroblas	1	404
dms.bed	codex	POLR2A	Blood	Erythroblast	0	0	0	478	534	534	534	515	726	276	748206	GSM908069	Proerythroblas	1	235
dms.bed	codex	POLR2A	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	71791	276	677141	GSM937544	codex Embryor	1	14514
dms.bed	codex	POLR2A	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	75452	276	673480	GSM937545	codex Embryor	1	15798
dms.bed	codex	KMT2A	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	12612	276	736320	GSM941543	Adult acute B c	1	3495
dms.bed	codex	AFF1	Blood	Leukaemia cell	0	0	0	478	534	534	534	515	2154	276	746778	GSM941544	Adult acute B c	1	5219
dms.bed	codex	ZNF143	Kidney	Embryonic kidney cel	0	0	0	478	534	534	534	515	7616	276	741316	GSM959048	ChIP-seq_ZNF1	1	2276
dms.bed	codex	ZNF143	Blood	T-cell acute lymphobl	0	0	0	478	534	534	534	515	7656	276	741276	GSM959049	ChIP-seq_ZNF1	1	1901
dms.bed	codex	ZNF143	Kidney	Embryonic kidney cel	0	0	0	478	534	534	534	515	5227	276	743705	GSM959050	ChIP-seq_ZNF1	1	4353
dms.bed	codex	ZNF143	Kidney	Embryonic kidney cel	0	0	0	478	534	534	534	515	11289	276	737643	GSM959051	ChIP-seq_ZNF1	1	6459
dms.bed	codex	ZNF143	Kidney	Embryonic kidney cel	0	0	0	478	534	534	534	515	9745	276	739187	GSM959052	ChIP-seq_ZNF7	1	7031
dms.bed	codex	GATA1	Blood	Erythroblast	0	0	0	478	534	534	534	515	7683	276	741249	GSM970257	Proerythroblas	1	10094
dms.bed	codex	POLR2A	Blood	Erythroblast	0	0	0	478	534	534	534	515	70563	276	678369	GSM970260	Proerythroblas	1	25986
dms.bed	codex	IRF2	Blood	Erythroblast	0	0	0	478	534	534	534	515	1571	276	747361	GSM970261	Proerythroblas	1	1789
dms.bed	codex	TP53	ESC	Embryonic Stem Cell	0	0	0	478	534	534	534	515	5964	276	742968	GSM981237	codex Embryor	1	3420
dms.bed	encode_tfbs	CTCF	Blood	Dnd41	0	0	0	478	534	534	534	515	28059	276	720873	wgEncodeAv	ChIP Dnd41 CT	1	50070
dms.bed	encode_tfbs	EZH2	Blood	Dnd41	0	0	0	478	534	534	534	515	7424	276	741508	wgEncodeAv	ChIP Dnd41 EZ	1	1732
dms.bed	encode_tfbs	EZH2	Blood	GM12878	0	0	0	478	534	534	534	515	3127	276	745805	wgEncodeAv	ChIP GM12878	1	2472
dms.bed	encode_tfbs	CHD1	ESC	H1-hESC	0	0	0	478	534	534	534	515	23090	276	725842	wgEncodeAv	ChIP H1-hESC C	1	7247
dms.bed	encode_tfbs	EZH2	ESC	H1-hESC	0	0	0	478	534	534	534	515	39533	276	709399	wgEncodeAv	ChIP H1-hESC E	1	6370
dms.bed	encode_tfbs	JARID1A	ESC	H1-hESC	0	0	0	478	534	534	534	515	6418	276	742514	wgEncodeAv	ChIP H1-hESC J	1	1625
dms.bed	encode_tfbs	RBBP5	ESC	H1-hESC	0	0	0	478	534	534	534	515	97540	276	651392	wgEncodeAv	ChIP H1-hESC F	1	16151
dms.bed	encode_tfbs	EZH2	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	714	276	748218	wgEncodeAv	ChIP HeLa-S3 E	1	1818
dms.bed	encode_tfbs	Pol2(b)	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	10050	276	738882	wgEncodeAv	ChIP HeLa-S3 P	1	3149
dms.bed	encode_tfbs	EZH2	Liver	HepG2	0	0	0	478	534	534	534	515	13093	276	735839	wgEncodeAv	ChIP HepG2 EZ	1	3286
dms.bed	encode_tfbs	EZH2	Breast	HMEC	0	0	0	478	534	534	534	515	15807	276	733125	wgEncodeAv	ChIP HMEC EZH	1	4626
dms.bed	encode_tfbs	CTCF	Muscle	HSMM	0	0	0	478	534	534	534	515	22764	276	726168	wgEncodeAv	ChIP HSMM CT	1	50924
dms.bed	encode_tfbs	EZH2	Muscle	HSMM	0	0	0	478	534	534	534	515	5858	276	743074	wgEncodeAv	ChIP HSMM EZ	1	1540
dms.bed	encode_tfbs	CTCF	Muscle	HSMMtube	0	0	0	478	534	534	534	515	25939	276	722993	wgEncodeAv	ChIP HSMMtub	1	47949
dms.bed	encode_tfbs	EZH2	Muscle	HSMMtube	0	0	0	478	534	534	534	515	14832	276	734100	wgEncodeAv	ChIP HSMMtub	1	2700
dms.bed	encode_tfbs	CTCF	Blood vessel	HUVEC	0	0	0	478	534	534	534	515	28288	276	720644	wgEncodeAv	ChIP HUVEC CT	1	37412
dms.bed	encode_tfbs	EZH2	Blood vessel	HUVEC	0	0	0	478	534	534	534	515	44338	276	704594	wgEncodeAv	ChIP HUVEC EZ	1	6234
dms.bed	encode_tfbs	Pol2(b)	Blood vessel	HUVEC	0	0	0	478	534	534	534	515	21432	276	727500	wgEncodeAv	ChIP HUVEC Po	1	5298
dms.bed	encode_tfbs	CHD1	Blood	K562	0	0	0	478	534	534	534	515	35872	276	713060	wgEncodeAv	ChIP K562 CHD	1	9350
dms.bed	encode_tfbs	EZH2	Blood	K562	0	0	0	478	534	534	534	515	1670	276	747262	wgEncodeAv	ChIP K562 EZH2	1	1685
dms.bed	encode_tfbs	HDAC1	Blood	K562	0	0	0	478	534	534	534	515	55352	276	693580	wgEncodeAv	ChIP K562 HDA	1	11833
dms.bed	encode_tfbs	HDAC2	Blood	K562	0	0	0	478	534	534	534	515	15020	276	733912	wgEncodeAv	ChIP K562 HDA	1	5247
dms.bed	encode_tfbs	HDAC6	Blood	K562	0	0	0	478	534	534	534	515	2691	276	746241	wgEncodeAv	ChIP K562 HDA	1	1114
dms.bed	encode_tfbs	p300	Blood	K562	0	0	0	478	534	534	534	515	1410	276	747522	wgEncodeAv	ChIP K562 p30(	1	2674
dms.bed	encode_tfbs	PHF8	Blood	K562	0	0	0	478	534	534	534	515	112486	276	636446	wgEncodeAv	ChIP K562 PHF8	1	22302
dms.bed	encode_tfbs	PLU1	Blood	K562	0	0	0	478	534	534	534	515	69985	276	678947	wgEncodeAv	ChIP K562 PLU1	1	15520
dms.bed	encode_tfbs	Pol2(b)	Blood	K562	0	0	0	478	534	534	534	515	42861	276	706071	wgEncodeAv	ChIP K562 Pol2	1	11424
dms.bed	encode_tfbs	RBBP5	Blood	K562	0	0	0	478	534	534	534	515	76962	276	671970	wgEncodeAv	ChIP K562 RBBI	1	14258
dms.bed	encode_tfbs	SAP30	Blood	K562	0	0	0	478	534	534	534	515	52151	276	696781	wgEncodeAv	ChIP K562 SAP3	1	9753
dms.bed	encode_tfbs	CTCF	Brain	NH-A	0	0	0	478	534	534	534	515	18813	276	730119	wgEncodeAv	ChIP NH-A CTC	1	38474
dms.bed	encode_tfbs	EZH2	Brain	NH-A	0	0	0	478	534	534	534	515	40938	276	707994	wgEncodeAv	ChIP NH-A EZH	1	6493
dms.bed	encode_tfbs	CTCF	Skin	NHDF-Ad	0	0	0	478	534	534	534	515	23565	276	725367	wgEncodeAv	ChIP NHDF-Ad	1	48995
dms.bed	encode_tfbs	EZH2	Skin	NHDF-Ad	0	0	0	478	534	534	534	515	35851	276	713081	wgEncodeAv	ChIP NHDF-Ad	1	5739
dms.bed	encode_tfbs	EZH2	Skin	NHEK	0	0	0	478	534	534	534	515	31931	276	717001	wgEncodeAv	ChIP NHEK EZH	1	7978
dms.bed	encode_tfbs	Pol2(b)	Skin	NHEK	0	0	0	478	534	534	534	515	13251	276	735681	wgEncodeAv	ChIP NHEK Pol2	1	5784
dms.bed	encode_tfbs	EZH2	Lung	NHLF	0	0	0	478	534	534	534	515	29188	276	719744	wgEncodeAv	ChIP NHLF EZH	1	7030
dms.bed	encode_tfbs	ATF3	Lung	A549	0	0	0	478	534	534	534	515	8387	276	740545	wgEncodeAv	ChIP A549 ATF3	1	6580
dms.bed	encode_tfbs	BCL3	Lung	A549	0	0	0	478	534	534	534	515	10733	276	738199	wgEncodeAv	ChIP A549 BCL3	1	7740
dms.bed	encode_tfbs	CTCF	Lung	A549	0	0	0	478	534	534	534	515	13795	276	735137	wgEncodeAv	ChIP A549 CTCI	1	40841
dms.bed	encode_tfbs	CTCF	Lung	A549	0	0	0	478	534	534	534	515	15487	276	733445	wgEncodeAv	ChIP A549 CTCI	1	38133

dms.bed	encode_tfbs	FOSL2	Lung	A549	0	0	0	478	534	534	534	515	9378	276	739554	wgEncodeAv	ChIP A549 FOS	1	28756
dms.bed	encode_tfbs	FOXA1	Lung	A549	0	0	0	478	534	534	534	515	355	276	748577	wgEncodeAv	ChIP A549 FOX	1	7695
dms.bed	encode_tfbs	GR	Lung	A549	0	0	0	478	534	534	534	515	365	276	748567	wgEncodeAv	ChIP A549 GR	1	1009
dms.bed	encode_tfbs	NRSF	Lung	A549	0	0	0	478	534	534	534	515	23615	276	725317	wgEncodeAv	ChIP A549 NRS	1	11970
dms.bed	encode_tfbs	Sin3Ak-20	Lung	A549	0	0	0	478	534	534	534	515	17380	276	731552	wgEncodeAv	ChIP A549 Sin3	1	6024
dms.bed	encode_tfbs	TAF1	Lung	A549	0	0	0	478	534	534	534	515	41046	276	707886	wgEncodeAv	ChIP A549 TAF	1	9984
dms.bed	encode_tfbs	USF-1	Lung	A549	0	0	0	478	534	534	534	515	11929	276	737003	wgEncodeAv	ChIP A549 USF	1	11980
dms.bed	encode_tfbs	USF-1	Lung	A549	0	0	0	478	534	534	534	515	14356	276	734576	wgEncodeAv	ChIP A549 USF	1	11932
dms.bed	encode_tfbs	USF-1	Lung	A549	0	0	0	478	534	534	534	515	11839	276	737093	wgEncodeAv	ChIP A549 USF	1	8004
dms.bed	encode_tfbs	ZBTB33	Lung	A549	0	0	0	478	534	534	534	515	15358	276	733574	wgEncodeAv	ChIP A549 ZBTI	1	7152
dms.bed	encode_tfbs	CTCF	Uterus	ECC-1	0	0	0	478	534	534	534	515	10655	276	738277	wgEncodeAv	ChIP ECC-1 CTC	1	23192
dms.bed	encode_tfbs	ERalpha_a	Uterus	ECC-1	0	0	0	478	534	534	534	515	1783	276	747149	wgEncodeAv	ChIP ECC-1 ERa	1	4260
dms.bed	encode_tfbs	FOXA1	Uterus	ECC-1	0	0	0	478	534	534	534	515	2136	276	746796	wgEncodeAv	ChIP ECC-1 FOX	1	5892
dms.bed	encode_tfbs	ATF2)	Blood	GM12878	0	0	0	478	534	534	534	515	22151	276	726781	wgEncodeAv	ChIP GM12878	1	23467
dms.bed	encode_tfbs	ATF3	Blood	GM12878	0	0	0	478	534	534	534	515	3644	276	745288	wgEncodeAv	ChIP GM12878	1	1677
dms.bed	encode_tfbs	BATF	Blood	GM12878	0	0	0	478	534	534	534	515	3797	276	745135	wgEncodeAv	ChIP GM12878	1	32427
dms.bed	encode_tfbs	BCL11A	Blood	GM12878	0	0	0	478	534	534	534	515	4385	276	744547	wgEncodeAv	ChIP GM12878	1	17876
dms.bed	encode_tfbs	BCL3	Blood	GM12878	0	0	0	478	534	534	534	515	11619	276	737313	wgEncodeAv	ChIP GM12878	1	15455
dms.bed	encode_tfbs	BCLAF1	Blood	GM12878	0	0	0	478	534	534	534	515	15042	276	733890	wgEncodeAv	ChIP GM12878	1	6114
dms.bed	encode_tfbs	CEBPB	Blood	GM12878	0	0	0	478	534	534	534	515	4896	276	744036	wgEncodeAv	ChIP GM12878	1	5786
dms.bed	encode_tfbs	EBF1	Blood	GM12878	0	0	0	478	534	534	534	515	21614	276	727318	wgEncodeAv	ChIP GM12878	1	36140
dms.bed	encode_tfbs	Egr-1	Blood	GM12878	0	0	0	478	534	534	534	515	35027	276	713905	wgEncodeAv	ChIP GM12878	1	16331
dms.bed	encode_tfbs	ETS1	Blood	GM12878	0	0	0	478	534	534	534	515	10912	276	738020	wgEncodeAv	ChIP GM12878	1	4120
dms.bed	encode_tfbs	FOXM1	Blood	GM12878	0	0	0	478	534	534	534	515	28891	276	720041	wgEncodeAv	ChIP GM12878	1	22926
dms.bed	encode_tfbs	GABP	Blood	GM12878	0	0	0	478	534	534	534	515	24267	276	724665	wgEncodeAv	ChIP GM12878	1	6566
dms.bed	encode_tfbs	IRF4	Blood	GM12878	0	0	0	478	534	534	534	515	9182	276	739750	wgEncodeAv	ChIP GM12878	1	17771
dms.bed	encode_tfbs	MEF2A	Blood	GM12878	0	0	0	478	534	534	534	515	10202	276	738730	wgEncodeAv	ChIP GM12878	1	17605
dms.bed	encode_tfbs	MEF2C	Blood	GM12878	0	0	0	478	534	534	534	515	7154	276	741778	wgEncodeAv	ChIP GM12878	1	9216
dms.bed	encode_tfbs	MTA3	Blood	GM12878	0	0	0	478	534	534	534	515	16432	276	732500	wgEncodeAv	ChIP GM12878	1	12032
dms.bed	encode_tfbs	NFATC1	Blood	GM12878	0	0	0	478	534	534	534	515	8928	276	740004	wgEncodeAv	ChIP GM12878	1	10812
dms.bed	encode_tfbs	NFIC	Blood	GM12878	0	0	0	478	534	534	534	515	19655	276	729277	wgEncodeAv	ChIP GM12878	1	29060
dms.bed	encode_tfbs	NRSF	Blood	GM12878	0	0	0	478	534	534	534	515	13470	276	735462	wgEncodeAv	ChIP GM12878	1	6906
dms.bed	encode_tfbs	p300	Blood	GM12878	0	0	0	478	534	534	534	515	3725	276	745207	wgEncodeAv	ChIP GM12878	1	5168
dms.bed	encode_tfbs	PAX5-C20	Blood	GM12878	0	0	0	478	534	534	534	515	28204	276	720728	wgEncodeAv	ChIP GM12878	1	25342
dms.bed	encode_tfbs	PAX5-N19	Blood	GM12878	0	0	0	478	534	534	534	515	21947	276	726985	wgEncodeAv	ChIP GM12878	1	19740
dms.bed	encode_tfbs	Pbx3	Blood	GM12878	0	0	0	478	534	534	534	515	9572	276	739360	wgEncodeAv	ChIP GM12878	1	9941
dms.bed	encode_tfbs	PML	Blood	GM12878	0	0	0	478	534	534	534	515	51547	276	697385	wgEncodeAv	ChIP GM12878	1	16678
dms.bed	encode_tfbs	Pol2-4H8	Blood	GM12878	0	0	0	478	534	534	534	515	73928	276	675004	wgEncodeAv	ChIP GM12878	1	19234
dms.bed	encode_tfbs	POU2F2	Blood	GM12878	0	0	0	478	534	534	534	515	30704	276	718228	wgEncodeAv	ChIP GM12878	1	22891
dms.bed	encode_tfbs	PU.1	Blood	GM12878	0	0	0	478	534	534	534	515	13935	276	734997	wgEncodeAv	ChIP GM12878	1	42938
dms.bed	encode_tfbs	RXRA	Blood	GM12878	0	0	0	478	534	534	534	515	2470	276	746462	wgEncodeAv	ChIP GM12878	1	1704
dms.bed	encode_tfbs	SIX5	Blood	GM12878	0	0	0	478	534	534	534	515	13195	276	735737	wgEncodeAv	ChIP GM12878	1	4839
dms.bed	encode_tfbs	SP1	Blood	GM12878	0	0	0	478	534	534	534	515	32997	276	715935	wgEncodeAv	ChIP GM12878	1	18248
dms.bed	encode_tfbs	SRF	Blood	GM12878	0	0	0	478	534	534	534	515	14857	276	734075	wgEncodeAv	ChIP GM12878	1	8544
dms.bed	encode_tfbs	STAT5A	Blood	GM12878	0	0	0	478	534	534	534	515	12479	276	736453	wgEncodeAv	ChIP GM12878	1	7423
dms.bed	encode_tfbs	TAF1	Blood	GM12878	0	0	0	478	534	534	534	515	42203	276	706729	wgEncodeAv	ChIP GM12878	1	14278
dms.bed	encode_tfbs	TCF3	Blood	GM12878	0	0	0	478	534	534	534	515	26500	276	722432	wgEncodeAv	ChIP GM12878	1	16021
dms.bed	encode_tfbs	USF-1	Blood	GM12878	0	0	0	478	534	534	534	515	17405	276	731527	wgEncodeAv	ChIP GM12878	1	9778
dms.bed	encode_tfbs	YY1	Blood	GM12878	0	0	0	478	534	534	534	515	51971	276	696961	wgEncodeAv	ChIP GM12878	1	30994
dms.bed	encode_tfbs	ZBTB33	Blood	GM12878	0	0	0	478	534	534	534	515	5832	276	743100	wgEncodeAv	ChIP GM12878	1	2144
dms.bed	encode_tfbs	PAX5-C20	Blood	GM12891	0	0	0	478	534	534	534	515	3378	276	745554	wgEncodeAv	ChIP GM12891	1	3156
dms.bed	encode_tfbs	Pol2-4H8	Blood	GM12891	0	0	0	478	534	534	534	515	46596	276	702336	wgEncodeAv	ChIP GM12891	1	16236
dms.bed	encode_tfbs	Pol2	Blood	GM12891	0	0	0	478	534	534	534	515	48533	276	700399	wgEncodeAv	ChIP GM12891	1	16585
dms.bed	encode_tfbs	POU2F2	Blood	GM12891	0	0	0	478	534	534	534	515	21378	276	727554	wgEncodeAv	ChIP GM12891	1	14630
dms.bed	encode_tfbs	PU.1	Blood	GM12891	0	0	0	478	534	534	534	515	13266	276	735666	wgEncodeAv	ChIP GM12891	1	48830
dms.bed	encode_tfbs	TAF1	Blood	GM12891	0	0	0	478	534	534	534	515	39826	276	709106	wgEncodeAv	ChIP GM12891	1	11883
dms.bed	encode_tfbs	YY1	Blood	GM12891	0	0	0	478	534	534	534	515	36175	276	712757	wgEncodeAv	ChIP GM12891	1	13593

dms.bed	encode_tfbs	PAX5-C20	Blood	GM12892	0	0	0	478	534	534	534	515	32046	276	716886	wgEncodeAv	ChIP	GM12892	1	10300
dms.bed	encode_tfbs	Pol2-4H8	Blood	GM12892	0	0	0	478	534	534	534	515	49812	276	699120	wgEncodeAv	ChIP	GM12892	1	17407
dms.bed	encode_tfbs	Pol2	Blood	GM12892	0	0	0	478	534	534	534	515	71314	276	677618	wgEncodeAv	ChIP	GM12892	1	20075
dms.bed	encode_tfbs	TAF1	Blood	GM12892	0	0	0	478	534	534	534	515	34654	276	714278	wgEncodeAv	ChIP	GM12892	1	9442
dms.bed	encode_tfbs	YY1	Blood	GM12892	0	0	0	478	534	534	534	515	36075	276	712857	wgEncodeAv	ChIP	GM12892	1	15951
dms.bed	encode_tfbs	ATF2	ESC	H1-hESC	0	0	0	478	534	534	534	515	15564	276	733368	wgEncodeAv	ChIP	H1-hESC A	1	5998
dms.bed	encode_tfbs	ATF3	ESC	H1-hESC	0	0	0	478	534	534	534	515	10001	276	738931	wgEncodeAv	ChIP	H1-hESC A	1	4808
dms.bed	encode_tfbs	BCL11A	ESC	H1-hESC	0	0	0	478	534	534	534	515	309	276	748623	wgEncodeAv	ChIP	H1-hESC B	1	2518
dms.bed	encode_tfbs	FOSL1	ESC	H1-hESC	0	0	0	478	534	534	534	515	2718	276	746214	wgEncodeAv	ChIP	H1-hESC F	1	1113
dms.bed	encode_tfbs	GABP	ESC	H1-hESC	0	0	0	478	534	534	534	515	17251	276	731681	wgEncodeAv	ChIP	H1-hESC G	1	5653
dms.bed	encode_tfbs	HDAC2	ESC	H1-hESC	0	0	0	478	534	534	534	515	8952	276	739980	wgEncodeAv	ChIP	H1-hESC H	1	5644
dms.bed	encode_tfbs	JunD	ESC	H1-hESC	0	0	0	478	534	534	534	515	15096	276	733836	wgEncodeAv	ChIP	H1-hESC J	1	8447
dms.bed	encode_tfbs	NANOG	ESC	H1-hESC	0	0	0	478	534	534	534	515	3203	276	745729	wgEncodeAv	ChIP	H1-hESC N	1	5473
dms.bed	encode_tfbs	NRSF	ESC	H1-hESC	0	0	0	478	534	534	534	515	7606	276	741326	wgEncodeAv	ChIP	H1-hESC N	1	13286
dms.bed	encode_tfbs	p300	ESC	H1-hESC	0	0	0	478	534	534	534	515	16327	276	732605	wgEncodeAv	ChIP	H1-hESC p	1	8934
dms.bed	encode_tfbs	Pol2-4H8	ESC	H1-hESC	0	0	0	478	534	534	534	515	53779	276	695153	wgEncodeAv	ChIP	H1-hESC P	1	21342
dms.bed	encode_tfbs	Pol2	ESC	H1-hESC	0	0	0	478	534	534	534	515	84073	276	664859	wgEncodeAv	ChIP	H1-hESC P	1	20317
dms.bed	encode_tfbs	POU5F1	ESC	H1-hESC	0	0	0	478	534	534	534	515	841	276	748091	wgEncodeAv	ChIP	H1-hESC P	1	3997
dms.bed	encode_tfbs	RXRA	ESC	H1-hESC	0	0	0	478	534	534	534	515	1259	276	747673	wgEncodeAv	ChIP	H1-hESC R	1	1306
dms.bed	encode_tfbs	Sin3Ak-20	ESC	H1-hESC	0	0	0	478	534	534	534	515	23827	276	725105	wgEncodeAv	ChIP	H1-hESC S	1	8977
dms.bed	encode_tfbs	SIX5	ESC	H1-hESC	0	0	0	478	534	534	534	515	5870	276	743062	wgEncodeAv	ChIP	H1-hESC S	1	3425
dms.bed	encode_tfbs	SP1	ESC	H1-hESC	0	0	0	478	534	534	534	515	24488	276	724444	wgEncodeAv	ChIP	H1-hESC S	1	15110
dms.bed	encode_tfbs	SP2	ESC	H1-hESC	0	0	0	478	534	534	534	515	8840	276	740092	wgEncodeAv	ChIP	H1-hESC S	1	2469
dms.bed	encode_tfbs	SP4	ESC	H1-hESC	0	0	0	478	534	534	534	515	31863	276	717069	wgEncodeAv	ChIP	H1-hESC S	1	5752
dms.bed	encode_tfbs	SRF	ESC	H1-hESC	0	0	0	478	534	534	534	515	6721	276	742211	wgEncodeAv	ChIP	H1-hESC S	1	5105
dms.bed	encode_tfbs	TAF1	ESC	H1-hESC	0	0	0	478	534	534	534	515	83950	276	664982	wgEncodeAv	ChIP	H1-hESC T	1	20547
dms.bed	encode_tfbs	TAF7	ESC	H1-hESC	0	0	0	478	534	534	534	515	39715	276	709217	wgEncodeAv	ChIP	H1-hESC T	1	10475
dms.bed	encode_tfbs	TEAD4	ESC	H1-hESC	0	0	0	478	534	534	534	515	11981	276	736951	wgEncodeAv	ChIP	H1-hESC T	1	19857
dms.bed	encode_tfbs	YY1	Colon	HCT-116	0	0	0	478	534	534	534	515	28070	276	720862	wgEncodeAv	ChIP	HCT-116 Y	1	12749
dms.bed	encode_tfbs	ZBTB33	Colon	HCT-116	0	0	0	478	534	534	534	515	12037	276	736895	wgEncodeAv	ChIP	HCT-116 Z	1	4325
dms.bed	encode_tfbs	GABP	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	17337	276	731595	wgEncodeAv	ChIP	HeLa-S3 G	1	6761
dms.bed	encode_tfbs	NRSF	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	5673	276	743259	wgEncodeAv	ChIP	HeLa-S3 N	1	10247
dms.bed	encode_tfbs	Pol2	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	89307	276	659625	wgEncodeAv	ChIP	HeLa-S3 P	1	25332
dms.bed	encode_tfbs	ATF3	Liver	HepG2	0	0	0	478	534	534	534	515	7149	276	741783	wgEncodeAv	ChIP	HepG2 AT	1	3291
dms.bed	encode_tfbs	BHLHE40	Liver	HepG2	0	0	0	478	534	534	534	515	2881	276	746051	wgEncodeAv	ChIP	HepG2 BH	1	2859
dms.bed	encode_tfbs	NRSF	Liver	HepG2	0	0	0	478	534	534	534	515	11112	276	737820	wgEncodeAv	ChIP	HepG2 NR	1	6024
dms.bed	encode_tfbs	NRSF	Liver	HepG2	0	0	0	478	534	534	534	515	33833	276	715099	wgEncodeAv	ChIP	HepG2 NR	1	12828
dms.bed	encode_tfbs	Pol2-4H8	Liver	HepG2	0	0	0	478	534	534	534	515	55219	276	693713	wgEncodeAv	ChIP	HepG2 Po	1	19586
dms.bed	encode_tfbs	SP2	Liver	HepG2	0	0	0	478	534	534	534	515	3655	276	745277	wgEncodeAv	ChIP	HepG2 SP	1	2626
dms.bed	encode_tfbs	SRF	Liver	HepG2	0	0	0	478	534	534	534	515	4527	276	744405	wgEncodeAv	ChIP	HepG2 SR	1	5314
dms.bed	encode_tfbs	TCF12	Liver	HepG2	0	0	0	478	534	534	534	515	716	276	748216	wgEncodeAv	ChIP	HepG2 TC	1	2061
dms.bed	encode_tfbs	ZBTB33	Liver	HepG2	0	0	0	478	534	534	534	515	5908	276	743024	wgEncodeAv	ChIP	HepG2 ZB	1	2879
dms.bed	encode_tfbs	ZBTB7A	Liver	HepG2	0	0	0	478	534	534	534	515	13679	276	735253	wgEncodeAv	ChIP	HepG2 ZB	1	9189
dms.bed	encode_tfbs	Pol2	Blood vessel	HUVEC	0	0	0	478	534	534	534	515	74490	276	674442	wgEncodeAv	ChIP	HUVEC Po	1	19254
dms.bed	encode_tfbs	BCL3	Blood	K562	0	0	0	478	534	534	534	515	1490	276	747442	wgEncodeAv	ChIP	K562 BCL3	1	1603
dms.bed	encode_tfbs	BCLAF1	Blood	K562	0	0	0	478	534	534	534	515	11843	276	737089	wgEncodeAv	ChIP	K562 BCLA	1	4444
dms.bed	encode_tfbs	CTCFL	Blood	K562	0	0	0	478	534	534	534	515	12294	276	736638	wgEncodeAv	ChIP	K562 CTCF	1	11533
dms.bed	encode_tfbs	ETS1	Blood	K562	0	0	0	478	534	534	534	515	37939	276	710993	wgEncodeAv	ChIP	K562 ETS1	1	10726
dms.bed	encode_tfbs	FOSL1	Blood	K562	0	0	0	478	534	534	534	515	4569	276	744363	wgEncodeAv	ChIP	K562 FOSL	1	11174
dms.bed	encode_tfbs	GABP	Blood	K562	0	0	0	478	534	534	534	515	33517	276	715415	wgEncodeAv	ChIP	K562 GAB	1	14393
dms.bed	encode_tfbs	GATA2	Blood	K562	0	0	0	478	534	534	534	515	3786	276	745146	wgEncodeAv	ChIP	K562 GAT.	1	19322
dms.bed	encode_tfbs	HDAC2	Blood	K562	0	0	0	478	534	534	534	515	6630	276	742302	wgEncodeAv	ChIP	K562 HDA	1	6672
dms.bed	encode_tfbs	MEF2A	Blood	K562	0	0	0	478	534	534	534	515	2911	276	746021	wgEncodeAv	ChIP	K562 MEF	1	5631
dms.bed	encode_tfbs	NR2F2	Blood	K562	0	0	0	478	534	534	534	515	13148	276	735784	wgEncodeAv	ChIP	K562 NR2	1	16678
dms.bed	encode_tfbs	NRSF	Blood	K562	0	0	0	478	534	534	534	515	13072	276	735860	wgEncodeAv	ChIP	K562 NRS	1	15849
dms.bed	encode_tfbs	PML	Blood	K562	0	0	0	478	534	534	534	515	44197	276	704735	wgEncodeAv	ChIP	K562 PML	1	15895
dms.bed	encode_tfbs	Pol2	Blood	K562	0	0	0	478	534	534	534	515	113609	276	635323	wgEncodeAv	ChIP	K562 Pol2	1	24989

dms.bed	encode_tfbs	PU.1	Blood	K562	0	0	0	478	534	534	534	515	10781	276	738151	wgEncodeAv	ChIP K562 PU.1	1	28677
dms.bed	encode_tfbs	Sin3Ak-20	Blood	K562	0	0	0	478	534	534	534	515	34562	276	714370	wgEncodeAv	ChIP K562 Sin3	1	12700
dms.bed	encode_tfbs	SIX5	Blood	K562	0	0	0	478	534	534	534	515	9976	276	738956	wgEncodeAv	ChIP K562 SIX5	1	4194
dms.bed	encode_tfbs	SP1	Blood	K562	0	0	0	478	534	534	534	515	18028	276	730904	wgEncodeAv	ChIP K562 SP1	1	7206
dms.bed	encode_tfbs	SP2	Blood	K562	0	0	0	478	534	534	534	515	8512	276	740420	wgEncodeAv	ChIP K562 SP2_	1	3124
dms.bed	encode_tfbs	SRF	Blood	K562	0	0	0	478	534	534	534	515	7406	276	741526	wgEncodeAv	ChIP K562 SRF	1	4717
dms.bed	encode_tfbs	STAT5A	Blood	K562	0	0	0	478	534	534	534	515	5881	276	743051	wgEncodeAv	ChIP K562 STA1	1	9811
dms.bed	encode_tfbs	TAF1	Blood	K562	0	0	0	478	534	534	534	515	52624	276	696308	wgEncodeAv	ChIP K562 TAF1	1	15246
dms.bed	encode_tfbs	TAF7	Blood	K562	0	0	0	478	534	534	534	515	9184	276	739748	wgEncodeAv	ChIP K562 TAF7	1	3422
dms.bed	encode_tfbs	THAP1	Blood	K562	0	0	0	478	534	534	534	515	13124	276	735808	wgEncodeAv	ChIP K562 THA	1	3506
dms.bed	encode_tfbs	TRIM28	Blood	K562	0	0	0	478	534	534	534	515	13171	276	735761	wgEncodeAv	ChIP K562 TRIM	1	12137
dms.bed	encode_tfbs	YY1	Blood	K562	0	0	0	478	534	534	534	515	40256	276	708676	wgEncodeAv	ChIP K562 YY1_	1	12677
dms.bed	encode_tfbs	YY1	Blood	K562	0	0	0	478	534	534	534	515	46331	276	702601	wgEncodeAv	ChIP K562 YY1	1	24059
dms.bed	encode_tfbs	ZBTB33	Blood	K562	0	0	0	478	534	534	534	515	6600	276	742332	wgEncodeAv	ChIP K562 ZBTE	1	3285
dms.bed	encode_tfbs	ZBTB7A	Blood	K562	0	0	0	478	534	534	534	515	58073	276	690859	wgEncodeAv	ChIP K562 ZBTE	1	21711
dms.bed	encode_tfbs	NRSF	Pancreas	PANC-1	0	0	0	478	534	534	534	515	8793	276	740139	wgEncodeAv	ChIP PANC-1 N	1	5507
dms.bed	encode_tfbs	Pol2-4H8	Pancreas	PANC-1	0	0	0	478	534	534	534	515	36827	276	712105	wgEncodeAv	ChIP PANC-1 Pc	1	10324
dms.bed	encode_tfbs	Sin3Ak-20	Pancreas	PANC-1	0	0	0	478	534	534	534	515	36499	276	712433	wgEncodeAv	ChIP PANC-1 Si	1	7182
dms.bed	encode_tfbs	NRSF	Brain	PFSK-1	0	0	0	478	534	534	534	515	11999	276	736933	wgEncodeAv	ChIP PFSK-1 NR	1	11390
dms.bed	encode_tfbs	Sin3Ak-20	Brain	PFSK-1	0	0	0	478	534	534	534	515	10064	276	738868	wgEncodeAv	ChIP PFSK-1 Sir	1	5950
dms.bed	encode_tfbs	TAF1	Brain	PFSK-1	0	0	0	478	534	534	534	515	25236	276	723696	wgEncodeAv	ChIP PFSK-1 TA	1	5844
dms.bed	encode_tfbs	NRSF	Brain	SK-N-SH	0	0	0	478	534	534	534	515	31988	276	716944	wgEncodeAv	ChIP SK-N-SH N	1	18845
dms.bed	encode_tfbs	NRSF	Brain	SK-N-SH	0	0	0	478	534	534	534	515	10883	276	738049	wgEncodeAv	ChIP SK-N-SH N	1	11029
dms.bed	encode_tfbs	Pol2-4H8	Brain	SK-N-SH	0	0	0	478	534	534	534	515	51956	276	696976	wgEncodeAv	ChIP SK-N-SH P	1	28168
dms.bed	encode_tfbs	Sin3Ak-20	Brain	SK-N-SH	0	0	0	478	534	534	534	515	39383	276	709549	wgEncodeAv	ChIP SK-N-SH S	1	15561
dms.bed	encode_tfbs	TAF1	Brain	SK-N-SH	0	0	0	478	534	534	534	515	43119	276	705813	wgEncodeAv	ChIP SK-N-SH T	1	13993
dms.bed	encode_tfbs	CTCF	Brain	SK-N-SH_RA	0	0	0	478	534	534	534	515	15595	276	733337	wgEncodeAv	ChIP SK-N-SH_I	1	40588
dms.bed	encode_tfbs	p300	Brain	SK-N-SH_RA	0	0	0	478	534	534	534	515	15645	276	733287	wgEncodeAv	ChIP SK-N-SH_I	1	46485
dms.bed	encode_tfbs	Rad21	Brain	SK-N-SH_RA	0	0	0	478	534	534	534	515	22305	276	726627	wgEncodeAv	ChIP SK-N-SH_I	1	62275
dms.bed	encode_tfbs	CTCF	Breast	T47D	0	0	0	478	534	534	534	515	16091	276	732841	wgEncodeAv	ChIP T-47D CTC	1	29285
dms.bed	encode_tfbs	ERalpha_a	Breast	T47D	0	0	0	478	534	534	534	515	516	276	748416	wgEncodeAv	ChIP T-47D ERa	1	3902
dms.bed	encode_tfbs	FOXA1	Breast	T47D	0	0	0	478	534	534	534	515	13123	276	735809	wgEncodeAv	ChIP T-47D FO)	1	41555
dms.bed	encode_tfbs	p300	Breast	T47D	0	0	0	478	534	534	534	515	11761	276	737171	wgEncodeAv	ChIP T-47D p3(	1	13973
dms.bed	encode_tfbs	NRSF	Brain	U87	0	0	0	478	534	534	534	515	33158	276	715774	wgEncodeAv	ChIP U87 NRSF	1	11746
dms.bed	encode_tfbs	Pol2-4H8	Brain	U87	0	0	0	478	534	534	534	515	55287	276	693645	wgEncodeAv	ChIP U87 Pol2-	1	22873
dms.bed	encode_tfbs	BHLHE40	Lung	A549	0	0	0	478	534	534	534	515	7053	276	741879	wgEncodeAv	ChIP A549 BHL	1	3123
dms.bed	encode_tfbs	Max	Lung	A549	0	0	0	478	534	534	534	515	31592	276	717340	wgEncodeAv	ChIP A549 Max	1	9881
dms.bed	encode_tfbs	Pol2(phosphoS2)	Lung	A549	0	0	0	478	534	534	534	515	3200	276	745732	wgEncodeAv	ChIP A549 Pol2	1	3454
dms.bed	encode_tfbs	Rad21	Lung	A549	0	0	0	478	534	534	534	515	11843	276	737089	wgEncodeAv	ChIP A549 Rad1	1	24465
dms.bed	encode_tfbs	ZNF274	Blood	GM08714	0	0	0	478	534	534	534	515	33	276	748899	wgEncodeAv	ChIP GM08714	1	667
dms.bed	encode_tfbs	Pol2	Blood	GM10847	0	0	0	478	534	534	534	515	52372	276	696560	wgEncodeAv	ChIP GM10847	1	9683
dms.bed	encode_tfbs	BHLHE40	Blood	GM12878	0	0	0	478	534	534	534	515	22777	276	726155	wgEncodeAv	ChIP GM12878	1	13986
dms.bed	encode_tfbs	BRCA1	Blood	GM12878	0	0	0	478	534	534	534	515	2324	276	746608	wgEncodeAv	ChIP GM12878	1	551
dms.bed	encode_tfbs	c-Fos	Blood	GM12878	0	0	0	478	534	534	534	515	6451	276	742481	wgEncodeAv	ChIP GM12878	1	2239
dms.bed	encode_tfbs	CHD1	Blood	GM12878	0	0	0	478	534	534	534	515	15940	276	732992	wgEncodeAv	ChIP GM12878	1	6668
dms.bed	encode_tfbs	CHD2	Blood	GM12878	0	0	0	478	534	534	534	515	40573	276	708359	wgEncodeAv	ChIP GM12878	1	15597
dms.bed	encode_tfbs	COREST	Blood	GM12878	0	0	0	478	534	534	534	515	4144	276	744788	wgEncodeAv	ChIP GM12878	1	1397
dms.bed	encode_tfbs	CTCF	Blood	GM12878	0	0	0	478	534	534	534	515	24866	276	724066	wgEncodeAv	ChIP GM12878	1	55551
dms.bed	encode_tfbs	E2F4	Blood	GM12878	0	0	0	478	534	534	534	515	13570	276	735362	wgEncodeAv	ChIP GM12878	1	3440
dms.bed	encode_tfbs	ELK1	Blood	GM12878	0	0	0	478	534	534	534	515	21924	276	727008	wgEncodeAv	ChIP GM12878	1	5584
dms.bed	encode_tfbs	IKZF1_(IkN)	Blood	GM12878	0	0	0	478	534	534	534	515	1777	276	747155	wgEncodeAv	ChIP GM12878	1	9047
dms.bed	encode_tfbs	JunD	Blood	GM12878	0	0	0	478	534	534	534	515	62	276	748870	wgEncodeAv	ChIP GM12878	1	2472
dms.bed	encode_tfbs	Max	Blood	GM12878	0	0	0	478	534	534	534	515	46986	276	701946	wgEncodeAv	ChIP GM12878	1	12542
dms.bed	encode_tfbs	MAZ	Blood	GM12878	0	0	0	478	534	534	534	515	65012	276	683920	wgEncodeAv	ChIP GM12878	1	18952
dms.bed	encode_tfbs	NF-E2	Blood	GM12878	0	0	0	478	534	534	534	515	1620	276	747312	wgEncodeAv	ChIP GM12878	1	772
dms.bed	encode_tfbs	NF-YA	Blood	GM12878	0	0	0	478	534	534	534	515	6090	276	742842	wgEncodeAv	ChIP GM12878	1	1841
dms.bed	encode_tfbs	NF-YB	Blood	GM12878	0	0	0	478	534	534	534	515	22477	276	726455	wgEncodeAv	ChIP GM12878	1	13295

dms.bed	encode_tfbs	Nrf1	Blood	GM12878	0	0	0	478	534	534	534	515	20932	276	728000	wgEncodeAv	ChIP	GM12878	1	5683
dms.bed	encode_tfbs	p300	Blood	GM12878	0	0	0	478	534	534	534	515	11238	276	737694	wgEncodeAv	ChIP	GM12878	1	17461
dms.bed	encode_tfbs	p300	Blood	GM12878	0	0	0	478	534	534	534	515	1105	276	747827	wgEncodeAv	ChIP	GM12878	1	6189
dms.bed	encode_tfbs	Pol2	Blood	GM12878	0	0	0	478	534	534	534	515	67488	276	681444	wgEncodeAv	ChIP	GM12878	1	21947
dms.bed	encode_tfbs	Pol2	Blood	GM12878	0	0	0	478	534	534	534	515	43318	276	705614	wgEncodeAv	ChIP	GM12878	1	11086
dms.bed	encode_tfbs	Pol2(phosphoS2)	Blood	GM12878	0	0	0	478	534	534	534	515	44571	276	704361	wgEncodeAv	ChIP	GM12878	1	9370
dms.bed	encode_tfbs	Pol3	Blood	GM12878	0	0	0	478	534	534	534	515	258	276	748674	wgEncodeAv	ChIP	GM12878	1	211
dms.bed	encode_tfbs	Rad21	Blood	GM12878	0	0	0	478	534	534	534	515	12304	276	736628	wgEncodeAv	ChIP	GM12878	1	33085
dms.bed	encode_tfbs	RFX5	Blood	GM12878	0	0	0	478	534	534	534	515	12178	276	736754	wgEncodeAv	ChIP	GM12878	1	4341
dms.bed	encode_tfbs	SIN3A	Blood	GM12878	0	0	0	478	534	534	534	515	49236	276	699696	wgEncodeAv	ChIP	GM12878	1	10392
dms.bed	encode_tfbs	SMC3	Blood	GM12878	0	0	0	478	534	534	534	515	14630	276	734302	wgEncodeAv	ChIP	GM12878	1	30517
dms.bed	encode_tfbs	STAT1	Blood	GM12878	0	0	0	478	534	534	534	515	5076	276	743856	wgEncodeAv	ChIP	GM12878	1	1769
dms.bed	encode_tfbs	STAT3	Blood	GM12878	0	0	0	478	534	534	534	515	3164	276	745768	wgEncodeAv	ChIP	GM12878	1	6487
dms.bed	encode_tfbs	TBLR1	Blood	GM12878	0	0	0	478	534	534	534	515	22942	276	725990	wgEncodeAv	ChIP	GM12878	1	13702
dms.bed	encode_tfbs	TBP	Blood	GM12878	0	0	0	478	534	534	534	515	29537	276	719395	wgEncodeAv	ChIP	GM12878	1	14893
dms.bed	encode_tfbs	TR4	Blood	GM12878	0	0	0	478	534	534	534	515	2338	276	746594	wgEncodeAv	ChIP	GM12878	1	1263
dms.bed	encode_tfbs	USF2	Blood	GM12878	0	0	0	478	534	534	534	515	12767	276	736165	wgEncodeAv	ChIP	GM12878	1	9022
dms.bed	encode_tfbs	WHIP	Blood	GM12878	0	0	0	478	534	534	534	515	14416	276	734516	wgEncodeAv	ChIP	GM12878	1	14102
dms.bed	encode_tfbs	YY1	Blood	GM12878	0	0	0	478	534	534	534	515	1274	276	747658	wgEncodeAv	ChIP	GM12878	1	2077
dms.bed	encode_tfbs	Znf143	Blood	GM12878	0	0	0	478	534	534	534	515	25617	276	723315	wgEncodeAv	ChIP	GM12878	1	20024
dms.bed	encode_tfbs	ZNF274	Blood	GM12878	0	0	0	478	534	534	534	515	3	276	748929	wgEncodeAv	ChIP	GM12878	1	233
dms.bed	encode_tfbs	ZZZ3	Blood	GM12878	0	0	0	478	534	534	534	515	463	276	748469	wgEncodeAv	ChIP	GM12878	1	713
dms.bed	encode_tfbs	Pol2	Blood	GM12891	0	0	0	478	534	534	534	515	61669	276	687263	wgEncodeAv	ChIP	GM12891	1	20390
dms.bed	encode_tfbs	Pol2	Blood	GM12892	0	0	0	478	534	534	534	515	78354	276	670578	wgEncodeAv	ChIP	GM12892	1	22544
dms.bed	encode_tfbs	Pol2	Blood	GM15510	0	0	0	478	534	534	534	515	77351	276	671581	wgEncodeAv	ChIP	GM15510	1	18661
dms.bed	encode_tfbs	NFKB	Blood	GM18505	0	0	0	478	534	534	534	515	9331	276	739601	wgEncodeAv	ChIP	GM18505	1	8805
dms.bed	encode_tfbs	Pol2	Blood	GM18505	0	0	0	478	534	534	534	515	77858	276	671074	wgEncodeAv	ChIP	GM18505	1	21784
dms.bed	encode_tfbs	NFKB	Blood	GM18526	0	0	0	478	534	534	534	515	3303	276	745629	wgEncodeAv	ChIP	GM18526	1	3070
dms.bed	encode_tfbs	Pol2	Blood	GM18526	0	0	0	478	534	534	534	515	65479	276	683453	wgEncodeAv	ChIP	GM18526	1	16856
dms.bed	encode_tfbs	Pol2	Blood	GM18951	0	0	0	478	534	534	534	515	88138	276	660794	wgEncodeAv	ChIP	GM18951	1	21218
dms.bed	encode_tfbs	Pol2	Blood	GM19099	0	0	0	478	534	534	534	515	76843	276	672089	wgEncodeAv	ChIP	GM19099	1	22219
dms.bed	encode_tfbs	Pol2	Blood	GM19193	0	0	0	478	534	534	534	515	82602	276	666330	wgEncodeAv	ChIP	GM19193	1	21404
dms.bed	encode_tfbs	Bach1	ESC	H1-hESC	0	0	0	478	534	534	534	515	25055	276	723877	wgEncodeAv	ChIP	H1-hESC E	1	11457
dms.bed	encode_tfbs	BRCA1	ESC	H1-hESC	0	0	0	478	534	534	534	515	6692	276	742240	wgEncodeAv	ChIP	H1-hESC E	1	2025
dms.bed	encode_tfbs	CHD1	ESC	H1-hESC	0	0	0	478	534	534	534	515	6756	276	742176	wgEncodeAv	ChIP	H1-hESC C	1	2191
dms.bed	encode_tfbs	CHD2	ESC	H1-hESC	0	0	0	478	534	534	534	515	21085	276	727847	wgEncodeAv	ChIP	H1-hESC C	1	6849
dms.bed	encode_tfbs	c-Jun	ESC	H1-hESC	0	0	0	478	534	534	534	515	2286	276	746646	wgEncodeAv	ChIP	H1-hESC c	1	2148
dms.bed	encode_tfbs	c-Myc	ESC	H1-hESC	0	0	0	478	534	534	534	515	13647	276	735285	wgEncodeAv	ChIP	H1-hESC c	1	4551
dms.bed	encode_tfbs	CtBP2	ESC	H1-hESC	0	0	0	478	534	534	534	515	29330	276	719602	wgEncodeAv	ChIP	H1-hESC C	1	7089
dms.bed	encode_tfbs	GTF2F1	ESC	H1-hESC	0	0	0	478	534	534	534	515	14994	276	733938	wgEncodeAv	ChIP	H1-hESC G	1	3548
dms.bed	encode_tfbs	JunD	ESC	H1-hESC	0	0	0	478	534	534	534	515	11090	276	737842	wgEncodeAv	ChIP	H1-hESC J	1	9550
dms.bed	encode_tfbs	MafK	ESC	H1-hESC	0	0	0	478	534	534	534	515	2319	276	746613	wgEncodeAv	ChIP	H1-hESC M	1	11425
dms.bed	encode_tfbs	Max	ESC	H1-hESC	0	0	0	478	534	534	534	515	17159	276	731773	wgEncodeAv	ChIP	H1-hESC M	1	11129
dms.bed	encode_tfbs	Mxi1	ESC	H1-hESC	0	0	0	478	534	534	534	515	20321	276	728611	wgEncodeAv	ChIP	H1-hESC M	1	6351
dms.bed	encode_tfbs	Nrf1	ESC	H1-hESC	0	0	0	478	534	534	534	515	15205	276	733727	wgEncodeAv	ChIP	H1-hESC M	1	4513
dms.bed	encode_tfbs	RFX5	ESC	H1-hESC	0	0	0	478	534	534	534	515	2917	276	746015	wgEncodeAv	ChIP	H1-hESC F	1	1695
dms.bed	encode_tfbs	SIN3A	ESC	H1-hESC	0	0	0	478	534	534	534	515	77976	276	670956	wgEncodeAv	ChIP	H1-hESC S	1	21309
dms.bed	encode_tfbs	SUZ12	ESC	H1-hESC	0	0	0	478	534	534	534	515	9211	276	739721	wgEncodeAv	ChIP	H1-hESC S	1	4789
dms.bed	encode_tfbs	USF2	ESC	H1-hESC	0	0	0	478	534	534	534	515	10919	276	738013	wgEncodeAv	ChIP	H1-hESC U	1	6952
dms.bed	encode_tfbs	Znf143	ESC	H1-hESC	0	0	0	478	534	534	534	515	30032	276	718900	wgEncodeAv	ChIP	H1-hESC Z	1	30687
dms.bed	encode_tfbs	Pol2	Colon	HCT-116	0	0	0	478	534	534	534	515	68846	276	680086	wgEncodeAv	ChIP	HCT-116 P	1	12864
dms.bed	encode_tfbs	ELK4	Kidney	HEK293	0	0	0	478	534	534	534	515	7129	276	741803	wgEncodeAv	ChIP	HEK293 El	1	1375
dms.bed	encode_tfbs	KAP1	Kidney	HEK293	0	0	0	478	534	534	534	515	20142	276	728790	wgEncodeAv	ChIP	HEK293 K/	1	19774
dms.bed	encode_tfbs	Pol2	Kidney	HEK293	0	0	0	478	534	534	534	515	55500	276	693432	wgEncodeAv	ChIP	HEK293 P(	1	11490
dms.bed	encode_tfbs	ZNF263	Kidney	HEK293-T-REx	0	0	0	478	534	534	534	515	55967	276	692965	wgEncodeAv	ChIP	HEK293-T-	1	31453
dms.bed	encode_tfbs	BAF155	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	17304	276	731628	wgEncodeAv	ChIP	HeLa-S3 B	1	8650
dms.bed	encode_tfbs	BDP1	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	236	276	748696	wgEncodeAv	ChIP	HeLa-S3 B	1	508

dms.bed	encode_tfbs	BRCA1	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	16379	276	732553	wgEncodeAv	ChIP	HeLa-S3	B	1	8114
dms.bed	encode_tfbs	BRF1	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	115	276	748817	wgEncodeAv	ChIP	HeLa-S3	B	1	193
dms.bed	encode_tfbs	BRF2	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	3	276	748929	wgEncodeAv	ChIP	HeLa-S3	B	1	303
dms.bed	encode_tfbs	Brg1	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	3540	276	745392	wgEncodeAv	ChIP	HeLa-S3	B	1	1357
dms.bed	encode_tfbs	c-Fos	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	3346	276	745586	wgEncodeAv	ChIP	HeLa-S3	c	1	9325
dms.bed	encode_tfbs	c-Jun	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	3414	276	745518	wgEncodeAv	ChIP	HeLa-S3	c	1	21903
dms.bed	encode_tfbs	c-Myc	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	24704	276	724228	wgEncodeAv	ChIP	HeLa-S3	c	1	10226
dms.bed	encode_tfbs	COREST	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	27227	276	721705	wgEncodeAv	ChIP	HeLa-S3	C	1	16322
dms.bed	encode_tfbs	E2F1	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	26276	276	722656	wgEncodeAv	ChIP	HeLa-S3	E	1	5116
dms.bed	encode_tfbs	E2F4	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	14240	276	734692	wgEncodeAv	ChIP	HeLa-S3	E	1	2831
dms.bed	encode_tfbs	ELK1	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	20302	276	728630	wgEncodeAv	ChIP	HeLa-S3	E	1	4809
dms.bed	encode_tfbs	GTF2F1	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	23728	276	725204	wgEncodeAv	ChIP	HeLa-S3	G	1	11730
dms.bed	encode_tfbs	HA-E2F1	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	50409	276	698523	wgEncodeAv	ChIP	HeLa-S3	H	1	10283
dms.bed	encode_tfbs	IRF3	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	5314	276	743618	wgEncodeAv	ChIP	HeLa-S3	IF	1	1587
dms.bed	encode_tfbs	JunD	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	6465	276	742467	wgEncodeAv	ChIP	HeLa-S3	Ju	1	31633
dms.bed	encode_tfbs	MafK	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	6348	276	742584	wgEncodeAv	ChIP	HeLa-S3	M	1	14185
dms.bed	encode_tfbs	MAZ	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	56066	276	692866	wgEncodeAv	ChIP	HeLa-S3	M	1	13409
dms.bed	encode_tfbs	NF-YA	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	18079	276	730853	wgEncodeAv	ChIP	HeLa-S3	N	1	5978
dms.bed	encode_tfbs	NF-YB	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	13674	276	735258	wgEncodeAv	ChIP	HeLa-S3	N	1	7156
dms.bed	encode_tfbs	Nrf1	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	11528	276	737404	wgEncodeAv	ChIP	HeLa-S3	N	1	2915
dms.bed	encode_tfbs	Pol2	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	107441	276	641491	wgEncodeAv	ChIP	HeLa-S3	P	1	21270
dms.bed	encode_tfbs	Pol2(phosphoS2)	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	50469	276	698463	wgEncodeAv	ChIP	HeLa-S3	P	1	12797
dms.bed	encode_tfbs	PRDM1	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	845	276	748087	wgEncodeAv	ChIP	HeLa-S3	P	1	4577
dms.bed	encode_tfbs	Rad21	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	10946	276	737986	wgEncodeAv	ChIP	HeLa-S3	R	1	43420
dms.bed	encode_tfbs	RFX5	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	18975	276	729957	wgEncodeAv	ChIP	HeLa-S3	R	1	19284
dms.bed	encode_tfbs	RPC155	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	1364	276	747568	wgEncodeAv	ChIP	HeLa-S3	R	1	2668
dms.bed	encode_tfbs	SMC3	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	21726	276	727206	wgEncodeAv	ChIP	HeLa-S3	S	1	39567
dms.bed	encode_tfbs	SPT20	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	146	276	748786	wgEncodeAv	ChIP	HeLa-S3	S	1	4088
dms.bed	encode_tfbs	STAT3	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	2231	276	746701	wgEncodeAv	ChIP	HeLa-S3	S	1	13834
dms.bed	encode_tfbs	TBP	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	32528	276	716404	wgEncodeAv	ChIP	HeLa-S3	T	1	18489
dms.bed	encode_tfbs	TCF7L2	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	4581	276	744351	wgEncodeAv	ChIP	HeLa-S3	T	1	3198
dms.bed	encode_tfbs	TFIIIC-110	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	1596	276	747336	wgEncodeAv	ChIP	HeLa-S3	T	1	2616
dms.bed	encode_tfbs	TR4	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	4416	276	744516	wgEncodeAv	ChIP	HeLa-S3	T	1	2115
dms.bed	encode_tfbs	Znf143	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	16222	276	732710	wgEncodeAv	ChIP	HeLa-S3	Z	1	7048
dms.bed	encode_tfbs	ZNF274	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	9	276	748923	wgEncodeAv	ChIP	HeLa-S3	Z	1	101
dms.bed	encode_tfbs	ZZZ3	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	79	276	748853	wgEncodeAv	ChIP	HeLa-S3	Z	1	251
dms.bed	encode_tfbs	BRCA1	Liver	HepG2	0	0	0	478	534	534	534	515	6200	276	742732	wgEncodeAv	ChIP	HepG2	BR	1	1497
dms.bed	encode_tfbs	CHD2	Liver	HepG2	0	0	0	478	534	534	534	515	18227	276	730705	wgEncodeAv	ChIP	HepG2	CH	1	5169
dms.bed	encode_tfbs	c-Jun	Liver	HepG2	0	0	0	478	534	534	534	515	2544	276	746388	wgEncodeAv	ChIP	HepG2	c-J	1	12672
dms.bed	encode_tfbs	ERRA	Liver	HepG2	0	0	0	478	534	534	534	515	1597	276	747335	wgEncodeAv	ChIP	HepG2	ER	1	1177
dms.bed	encode_tfbs	GRp20	Liver	HepG2	0	0	0	478	534	534	534	515	3317	276	745615	wgEncodeAv	ChIP	HepG2	GR	1	597
dms.bed	encode_tfbs	HSF1	Liver	HepG2	0	0	0	478	534	534	534	515	2243	276	746689	wgEncodeAv	ChIP	HepG2	HS	1	1435
dms.bed	encode_tfbs	IRF3	Liver	HepG2	0	0	0	478	534	534	534	515	1884	276	747048	wgEncodeAv	ChIP	HepG2	IRF	1	684
dms.bed	encode_tfbs	JunD	Liver	HepG2	0	0	0	478	534	534	534	515	7110	276	741822	wgEncodeAv	ChIP	HepG2	Ju	1	32275
dms.bed	encode_tfbs	MafF	Liver	HepG2	0	0	0	478	534	534	534	515	2960	276	745972	wgEncodeAv	ChIP	HepG2	Ma	1	37637
dms.bed	encode_tfbs	MafK	Liver	HepG2	0	0	0	478	534	534	534	515	2799	276	746133	wgEncodeAv	ChIP	HepG2	Ma	1	61944
dms.bed	encode_tfbs	MafK	Liver	HepG2	0	0	0	478	534	534	534	515	2964	276	745968	wgEncodeAv	ChIP	HepG2	Ma	1	37628
dms.bed	encode_tfbs	Max	Liver	HepG2	0	0	0	478	534	534	534	515	36440	276	712492	wgEncodeAv	ChIP	HepG2	Ma	1	11854
dms.bed	encode_tfbs	Mxi1	Liver	HepG2	0	0	0	478	534	534	534	515	61008	276	687924	wgEncodeAv	ChIP	HepG2	Mx	1	20371
dms.bed	encode_tfbs	Nrf1	Liver	HepG2	0	0	0	478	534	534	534	515	7798	276	741134	wgEncodeAv	ChIP	HepG2	Nr	1	1902
dms.bed	encode_tfbs	p300	Liver	HepG2	0	0	0	478	534	534	534	515	9618	276	739314	wgEncodeAv	ChIP	HepG2	p3	1	6613
dms.bed	encode_tfbs	PGC1A	Liver	HepG2	0	0	0	478	534	534	534	515	2231	276	746701	wgEncodeAv	ChIP	HepG2	PG	1	1308
dms.bed	encode_tfbs	Pol2	Liver	HepG2	0	0	0	478	534	534	534	515	60927	276	688005	wgEncodeAv	ChIP	HepG2	Po	1	19572
dms.bed	encode_tfbs	Pol2(phosphoS2)	Liver	HepG2	0	0	0	478	534	534	534	515	10442	276	738490	wgEncodeAv	ChIP	HepG2	Po	1	4091
dms.bed	encode_tfbs	RFX5	Liver	HepG2	0	0	0	478	534	534	534	515	15380	276	733552	wgEncodeAv	ChIP	HepG2	RF	1	6017
dms.bed	encode_tfbs	TBP	Liver	HepG2	0	0	0	478	534	534	534	515	39386	276	709546	wgEncodeAv	ChIP	HepG2	TB	1	13806
dms.bed	encode_tfbs	TCF7L2	Liver	HepG2	0	0	0	478	534	534	534	515	826	276	748106	wgEncodeAv	ChIP	HepG2	TC	1	2742

dms.bed	encode_tfbs	TR4	Liver	HepG2	0	0	0	478	534	534	534	515	9815	276	739117	wgEncodeAv	ChIP HepG2 TR	1	2953
dms.bed	encode_tfbs	ZNF274	Liver	HepG2	0	0	0	478	534	534	534	515	6	276	748926	wgEncodeAv	ChIP HepG2 ZN	1	245
dms.bed	encode_tfbs	Pol2	Blood vessel	HUVEC	0	0	0	478	534	534	534	515	40325	276	708607	wgEncodeAv	ChIP HUVEC Po	1	12305
dms.bed	encode_tfbs	MafK	Lung	IMR90	0	0	0	478	534	534	534	515	3329	276	745603	wgEncodeAv	ChIP IMR90 Ma	1	40788
dms.bed	encode_tfbs	Pol2	Lung	IMR90	0	0	0	478	534	534	534	515	66558	276	682374	wgEncodeAv	ChIP IMR90 Po	1	17647
dms.bed	encode_tfbs	Rad21	Lung	IMR90	0	0	0	478	534	534	534	515	17773	276	731159	wgEncodeAv	ChIP IMR90 Ra	1	37417
dms.bed	encode_tfbs	ARID3A	Blood	K562	0	0	0	478	534	534	534	515	4385	276	744547	wgEncodeAv	ChIP K562 ARI	1	9026
dms.bed	encode_tfbs	ATF1	Blood	K562	0	0	0	478	534	534	534	515	13434	276	735498	wgEncodeAv	ChIP K562 ATF	1	14864
dms.bed	encode_tfbs	ATF3	Blood	K562	0	0	0	478	534	534	534	515	4424	276	744508	wgEncodeAv	ChIP K562 ATF	1	1233
dms.bed	encode_tfbs	Bach1	Blood	K562	0	0	0	478	534	534	534	515	2490	276	746442	wgEncodeAv	ChIP K562 Bach	1	3806
dms.bed	encode_tfbs	BDP1	Blood	K562	0	0	0	478	534	534	534	515	370	276	748562	wgEncodeAv	ChIP K562 BDP	1	570
dms.bed	encode_tfbs	BRF1	Blood	K562	0	0	0	478	534	534	534	515	253	276	748679	wgEncodeAv	ChIP K562 BRF	1	221
dms.bed	encode_tfbs	BRF2	Blood	K562	0	0	0	478	534	534	534	515	46	276	748886	wgEncodeAv	ChIP K562 BRF	1	1087
dms.bed	encode_tfbs	Brg1	Blood	K562	0	0	0	478	534	534	534	515	2768	276	746164	wgEncodeAv	ChIP K562 Brg1	1	2463
dms.bed	encode_tfbs	CCNT2	Blood	K562	0	0	0	478	534	534	534	515	75327	276	673605	wgEncodeAv	ChIP K562 CCN	1	20057
dms.bed	encode_tfbs	CHD2	Blood	K562	0	0	0	478	534	534	534	515	23251	276	725681	wgEncodeAv	ChIP K562 CHD	1	7797
dms.bed	encode_tfbs	c-Jun	Blood	K562	0	0	0	478	534	534	534	515	7114	276	741818	wgEncodeAv	ChIP K562 c-Ju	1	8827
dms.bed	encode_tfbs	c-Jun	Blood	K562	0	0	0	478	534	534	534	515	2418	276	746514	wgEncodeAv	ChIP K562 c-Ju	1	5218
dms.bed	encode_tfbs	c-Jun	Blood	K562	0	0	0	478	534	534	534	515	3214	276	745718	wgEncodeAv	ChIP K562 c-Ju	1	8587
dms.bed	encode_tfbs	c-Myc	Blood	K562	0	0	0	478	534	534	534	515	23835	276	725097	wgEncodeAv	ChIP K562 c-My	1	7746
dms.bed	encode_tfbs	c-Myc	Blood	K562	0	0	0	478	534	534	534	515	29698	276	719234	wgEncodeAv	ChIP K562 c-My	1	10583
dms.bed	encode_tfbs	c-Myc	Blood	K562	0	0	0	478	534	534	534	515	46627	276	702305	wgEncodeAv	ChIP K562 c-My	1	19290
dms.bed	encode_tfbs	c-Myc	Blood	K562	0	0	0	478	534	534	534	515	15105	276	733827	wgEncodeAv	ChIP K562 c-My	1	5023
dms.bed	encode_tfbs	COREST	Blood	K562	0	0	0	478	534	534	534	515	6093	276	742839	wgEncodeAv	ChIP K562 COR	1	6371
dms.bed	encode_tfbs	E2F4	Blood	K562	0	0	0	478	534	534	534	515	34408	276	714524	wgEncodeAv	ChIP K562 E2F4	1	8181
dms.bed	encode_tfbs	ELK1	Blood	K562	0	0	0	478	534	534	534	515	12821	276	736111	wgEncodeAv	ChIP K562 ELK1	1	2961
dms.bed	encode_tfbs	GATA-1	Blood	K562	0	0	0	478	534	534	534	515	2224	276	746708	wgEncodeAv	ChIP K562 GAT	1	4074
dms.bed	encode_tfbs	GATA-2	Blood	K562	0	0	0	478	534	534	534	515	3139	276	745793	wgEncodeAv	ChIP K562 GAT	1	10648
dms.bed	encode_tfbs	GTF2B	Blood	K562	0	0	0	478	534	534	534	515	9553	276	739379	wgEncodeAv	ChIP K562 GTF	1	2928
dms.bed	encode_tfbs	GTF2F1	Blood	K562	0	0	0	478	534	534	534	515	15910	276	733022	wgEncodeAv	ChIP K562 GTF	1	3621
dms.bed	encode_tfbs	Ini1	Blood	K562	0	0	0	478	534	534	534	515	2089	276	746843	wgEncodeAv	ChIP K562 Ini1	1	1942
dms.bed	encode_tfbs	IRF1	Blood	K562	0	0	0	478	534	534	534	515	622	276	748310	wgEncodeAv	ChIP K562 IRF1	1	1299
dms.bed	encode_tfbs	IRF1	Blood	K562	0	0	0	478	534	534	534	515	15565	276	733367	wgEncodeAv	ChIP K562 IRF1	1	8352
dms.bed	encode_tfbs	IRF1	Blood	K562	0	0	0	478	534	534	534	515	26007	276	722925	wgEncodeAv	ChIP K562 IRF1	1	10323
dms.bed	encode_tfbs	IRF1	Blood	K562	0	0	0	478	534	534	534	515	42873	276	706059	wgEncodeAv	ChIP K562 IRF1	1	12576
dms.bed	encode_tfbs	KAP1	Blood	K562	0	0	0	478	534	534	534	515	610	276	748322	wgEncodeAv	ChIP K562 KAP	1	5489
dms.bed	encode_tfbs	MafF	Blood	K562	0	0	0	478	534	534	534	515	3404	276	745528	wgEncodeAv	ChIP K562 Maf	1	25074
dms.bed	encode_tfbs	MafK	Blood	K562	0	0	0	478	534	534	534	515	3161	276	745771	wgEncodeAv	ChIP K562 Maf	1	19317
dms.bed	encode_tfbs	Mxi1	Blood	K562	0	0	0	478	534	534	534	515	21392	276	727540	wgEncodeAv	ChIP K562 Mxi	1	6711
dms.bed	encode_tfbs	NELFe	Blood	K562	0	0	0	478	534	534	534	515	2423	276	746509	wgEncodeAv	ChIP K562 NEL	1	458
dms.bed	encode_tfbs	NF-E2	Blood	K562	0	0	0	478	534	534	534	515	1310	276	747622	wgEncodeAv	ChIP K562 NF-E	1	2637
dms.bed	encode_tfbs	NF-YA	Blood	K562	0	0	0	478	534	534	534	515	9989	276	738943	wgEncodeAv	ChIP K562 NF-Y	1	4286
dms.bed	encode_tfbs	NF-YB	Blood	K562	0	0	0	478	534	534	534	515	13744	276	735188	wgEncodeAv	ChIP K562 NF-Y	1	10096
dms.bed	encode_tfbs	Nrf1	Blood	K562	0	0	0	478	534	534	534	515	14724	276	734208	wgEncodeAv	ChIP K562 Nrf1	1	4211
dms.bed	encode_tfbs	Pol2	Blood	K562	0	0	0	478	534	534	534	515	56586	276	692346	wgEncodeAv	ChIP K562 Pol2	1	13845
dms.bed	encode_tfbs	Pol2	Blood	K562	0	0	0	478	534	534	534	515	53810	276	695122	wgEncodeAv	ChIP K562 Pol2	1	13582
dms.bed	encode_tfbs	Pol2	Blood	K562	0	0	0	478	534	534	534	515	55820	276	693112	wgEncodeAv	ChIP K562 Pol2	1	16558
dms.bed	encode_tfbs	Pol2	Blood	K562	0	0	0	478	534	534	534	515	62753	276	686179	wgEncodeAv	ChIP K562 Pol2	1	16522
dms.bed	encode_tfbs	Pol2	Blood	K562	0	0	0	478	534	534	534	515	22346	276	726586	wgEncodeAv	ChIP K562 Pol2	1	9974
dms.bed	encode_tfbs	Pol2	Blood	K562	0	0	0	478	534	534	534	515	65220	276	683712	wgEncodeAv	ChIP K562 Pol2	1	18081
dms.bed	encode_tfbs	Pol2(phosphoS2)	Blood	K562	0	0	0	478	534	534	534	515	15993	276	732939	wgEncodeAv	ChIP K562 Pol2	1	5397
dms.bed	encode_tfbs	Pol2(phosphoS2)	Blood	K562	0	0	0	478	534	534	534	515	1700	276	747232	wgEncodeAv	ChIP K562 Pol2	1	2220
dms.bed	encode_tfbs	Pol3	Blood	K562	0	0	0	478	534	534	534	515	473	276	748459	wgEncodeAv	ChIP K562 Pol3	1	207
dms.bed	encode_tfbs	Rad21	Blood	K562	0	0	0	478	534	534	534	515	5231	276	743701	wgEncodeAv	ChIP K562 Rad	1	17627
dms.bed	encode_tfbs	RFX5	Blood	K562	0	0	0	478	534	534	534	515	4863	276	744069	wgEncodeAv	ChIP K562 RFX	1	2201
dms.bed	encode_tfbs	RPC155	Blood	K562	0	0	0	478	534	534	534	515	1246	276	747686	wgEncodeAv	ChIP K562 RPC	1	1310
dms.bed	encode_tfbs	SETDB1	Blood	K562	0	0	0	478	534	534	534	515	497	276	748435	wgEncodeAv	ChIP K562 SET	1	2967

dms.bed	encode_tfbs	SIRT6	Blood	K562	0	0	0	478	534	534	534	515	1037	276	747895	wgEncodeAv	ChIP K562 SIRT	1	2305
dms.bed	encode_tfbs	STAT1	Blood	K562	0	0	0	478	534	534	534	515	1230	276	747702	wgEncodeAv	ChIP K562 STA1	1	1503
dms.bed	encode_tfbs	STAT1	Blood	K562	0	0	0	478	534	534	534	515	1506	276	747426	wgEncodeAv	ChIP K562 STA1	1	1476
dms.bed	encode_tfbs	STAT2	Blood	K562	0	0	0	478	534	534	534	515	3974	276	744958	wgEncodeAv	ChIP K562 STA1	1	3040
dms.bed	encode_tfbs	STAT2	Blood	K562	0	0	0	478	534	534	534	515	1099	276	747833	wgEncodeAv	ChIP K562 STA1	1	1923
dms.bed	encode_tfbs	TBLR1	Blood	K562	0	0	0	478	534	534	534	515	11507	276	737425	wgEncodeAv	ChIP K562 TBLF	1	5086
dms.bed	encode_tfbs	TBLR1	Blood	K562	0	0	0	478	534	534	534	515	10282	276	738650	wgEncodeAv	ChIP K562 TBLF	1	8505
dms.bed	encode_tfbs	TBP	Blood	K562	0	0	0	478	534	534	534	515	50960	276	697972	wgEncodeAv	ChIP K562 TBP	1	17558
dms.bed	encode_tfbs	UBF	Blood	K562	0	0	0	478	534	534	534	515	28927	276	720005	wgEncodeAv	ChIP K562 UBF_	1	6002
dms.bed	encode_tfbs	UBTF	Blood	K562	0	0	0	478	534	534	534	515	51472	276	697460	wgEncodeAv	ChIP K562 UBT	1	13692
dms.bed	encode_tfbs	USF2	Blood	K562	0	0	0	478	534	534	534	515	4714	276	744218	wgEncodeAv	ChIP K562 USF2	1	3083
dms.bed	encode_tfbs	Znf143	Blood	K562	0	0	0	478	534	534	534	515	27747	276	721185	wgEncodeAv	ChIP K562 Znf1	1	29069
dms.bed	encode_tfbs	ZNF263	Blood	K562	0	0	0	478	534	534	534	515	6069	276	742863	wgEncodeAv	ChIP K562 ZNF2	1	3081
dms.bed	encode_tfbs	ZNF274	Blood	K562	0	0	0	478	534	534	534	515	15	276	748917	wgEncodeAv	ChIP K562 ZNF2	1	305
dms.bed	encode_tfbs	ZNF274	Blood	K562	0	0	0	478	534	534	534	515	1647	276	747285	wgEncodeAv	ChIP K562 ZNF2	1	1997
dms.bed	encode_tfbs	E2F4	Breast	MCF10A-Er-Src	0	0	0	478	534	534	534	515	38685	276	710247	wgEncodeAv	ChIP MCF10A-E	1	15516
dms.bed	encode_tfbs	Pol2	Breast	MCF10A-Er-Src	0	0	0	478	534	534	534	515	80084	276	668848	wgEncodeAv	ChIP MCF10A-E	1	22298
dms.bed	encode_tfbs	Pol2	Breast	MCF10A-Er-Src	0	0	0	478	534	534	534	515	77361	276	671571	wgEncodeAv	ChIP MCF10A-E	1	19467
dms.bed	encode_tfbs	GATA3	Breast	MCF-7	0	0	0	478	534	534	534	515	194	276	748738	wgEncodeAv	ChIP MCF-7 GA	1	6081
dms.bed	encode_tfbs	GATA3	Breast	MCF-7	0	0	0	478	534	534	534	515	2637	276	746295	wgEncodeAv	ChIP MCF-7 GA	1	12077
dms.bed	encode_tfbs	TCF7L2	Breast	MCF-7	0	0	0	478	534	534	534	515	6114	276	742818	wgEncodeAv	ChIP MCF-7 TCI	1	10293
dms.bed	encode_tfbs	ZNF217	Breast	MCF-7	0	0	0	478	534	534	534	515	2178	276	746754	wgEncodeAv	ChIP MCF-7 ZN	1	9933
dms.bed	encode_tfbs	Pol2	Blood	NB4	0	0	0	478	534	534	534	515	63223	276	685709	wgEncodeAv	ChIP NB4 Pol2	1	16703
dms.bed	encode_tfbs	SUZ12	Testis	NT2-D1	0	0	0	478	534	534	534	515	18784	276	730148	wgEncodeAv	ChIP NT2-D1 SU	1	3308
dms.bed	encode_tfbs	YY1	Testis	NT2-D1	0	0	0	478	534	534	534	515	14605	276	734327	wgEncodeAv	ChIP NT2-D1 YY	1	4862
dms.bed	encode_tfbs	ZNF274	Testis	NT2-D1	0	0	0	478	534	534	534	515	55	276	748877	wgEncodeAv	ChIP NT2-D1 ZN	1	745
dms.bed	encode_tfbs	GATA-1	Blood	PBDE	0	0	0	478	534	534	534	515	24317	276	724615	wgEncodeAv	ChIP PBDE GAT	1	25001
dms.bed	encode_tfbs	Pol2	Blood	PBDE	0	0	0	478	534	534	534	515	76406	276	672526	wgEncodeAv	ChIP PBDE Pol2	1	18332
dms.bed	encode_tfbs	GATA-1	Blood	PBDEFetal	0	0	0	478	534	534	534	515	1221	276	747711	wgEncodeAv	ChIP PBDEFeta	1	2157
dms.bed	encode_tfbs	Pol2	Blood	Raji	0	0	0	478	534	534	534	515	77623	276	671309	wgEncodeAv	ChIP Raji Pol2	1	19732
dms.bed	encode_tfbs	GATA-2	Brain	SH-SY5Y	0	0	0	478	534	534	534	515	11153	276	737779	wgEncodeAv	ChIP SH-SY5Y G	1	35620
dms.bed	encode_tfbs	GATA3	Brain	SH-SY5Y	0	0	0	478	534	534	534	515	859	276	748073	wgEncodeAv	ChIP SH-SY5Y G	1	15879
dms.bed	encode_tfbs	eGFP-FOS	Blood	K562	0	0	0	478	534	534	534	515	3015	276	745917	wgEncodeAv	ChIP K562 eGFI	1	10256
dms.bed	encode_tfbs	GATA2	Blood	K562	0	0	0	478	534	534	534	515	3179	276	745753	wgEncodeAv	ChIP K562 eGFI	1	11478
dms.bed	encode_tfbs	HDAC8	Blood	K562	0	0	0	478	534	534	534	515	3249	276	745683	wgEncodeAv	ChIP K562 eGFI	1	1718
dms.bed	encode_tfbs	Pol2	Lung	A549	0	0	0	478	534	534	534	515	60743	276	688189	wgEncodeAv	ChIP A549 Pol2	1	17011
dms.bed	encode_tfbs	CTCF	Skin	Fibrobl	0	0	0	478	534	534	534	515	29001	276	719931	wgEncodeAv	ChIP Fibrobl CT	1	45978
dms.bed	encode_tfbs	Pol2	Brain	Gliobla	0	0	0	478	534	534	534	515	55542	276	693390	wgEncodeAv	ChIP Gliobla Po	1	17417
dms.bed	encode_tfbs	c-Myc	Blood	GM12878	0	0	0	478	534	534	534	515	25325	276	723607	wgEncodeAv	ChIP GM12878	1	3690
dms.bed	encode_tfbs	Pol2	Blood	GM12878	0	0	0	478	534	534	534	515	60801	276	688131	wgEncodeAv	ChIP GM12878	1	14237
dms.bed	encode_tfbs	c-Myc	ESC	H1-hESC	0	0	0	478	534	534	534	515	1066	276	747866	wgEncodeAv	ChIP H1-hESC c	1	1217
dms.bed	encode_tfbs	Pol2	ESC	H1-hESC	0	0	0	478	534	534	534	515	62203	276	686729	wgEncodeAv	ChIP H1-hESC P	1	12915
dms.bed	encode_tfbs	c-Myc	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	6741	276	742191	wgEncodeAv	ChIP HeLa-S3 c-	1	2835
dms.bed	encode_tfbs	CTCF	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	15725	276	733207	wgEncodeAv	ChIP HeLa-S3 C	1	58806
dms.bed	encode_tfbs	c-Myc	Liver	HepG2	0	0	0	478	534	534	534	515	10287	276	738645	wgEncodeAv	ChIP HepG2 c-M	1	4413
dms.bed	encode_tfbs	CTCF	Blood vessel	HUVEC	0	0	0	478	534	534	534	515	14036	276	734896	wgEncodeAv	ChIP HUVEC CT	1	44033
dms.bed	encode_tfbs	Pol2	Blood vessel	HUVEC	0	0	0	478	534	534	534	515	43411	276	705521	wgEncodeAv	ChIP HUVEC Po	1	17190
dms.bed	encode_tfbs	c-Myc	Blood	K562	0	0	0	478	534	534	534	515	19373	276	729559	wgEncodeAv	ChIP K562 c-My	1	11738
dms.bed	encode_tfbs	Pol2	Blood	K562	0	0	0	478	534	534	534	515	65667	276	683265	wgEncodeAv	ChIP K562 Pol2	1	19255
dms.bed	encode_tfbs	c-Myc	Breast	MCF-7	0	0	0	478	534	534	534	515	10257	276	738675	wgEncodeAv	ChIP MCF-7 c-M	1	6930
dms.bed	encode_tfbs	Pol2	Breast	MCF-7	0	0	0	478	534	534	534	515	62378	276	686554	wgEncodeAv	ChIP MCF-7 Po	1	19412
dms.bed	encode_tfbs	Pol2	Breast	MCF-7	0	0	0	478	534	534	534	515	56138	276	692794	wgEncodeAv	ChIP MCF-7 Po	1	16136
dms.bed	encode_tfbs	CTCF	Skin	ProgFib	0	0	0	478	534	534	534	515	21861	276	727071	wgEncodeAv	ChIP ProgFib CT	1	43918
dms.bed	encode_tfbs	Pol2	Skin	ProgFib	0	0	0	478	534	534	534	515	61199	276	687733	wgEncodeAv	ChIP ProgFib Po	1	16338
dms.bed	encode_tfbs	CTCF	Lung	AG04450	0	0	0	478	534	534	534	515	26245	276	722687	wgEncodeAv	ChIP AG04450	1	46500
dms.bed	encode_tfbs	CTCF	Gingival	AG09319	0	0	0	478	534	534	534	515	29897	276	719035	wgEncodeAv	ChIP AG09319	1	49675
dms.bed	encode_tfbs	CTCF	Skin	AG10803	0	0	0	478	534	534	534	515	22387	276	726545	wgEncodeAv	ChIP AG10803	1	47656

dms.bed	encode_tfbs	CTCF	Blood vessel	AoAF	0	0	0	478	534	534	534	515	21048	276	727884	wgEncodeAv	ChIP AoAF CTC	1	45960
dms.bed	encode_tfbs	CTCF	Brain	BE2_C	0	0	0	478	534	534	534	515	25341	276	723591	wgEncodeAv	ChIP BE2_C CT(	1	54655
dms.bed	encode_tfbs	CTCF	Skin	BJ	0	0	0	478	534	534	534	515	30329	276	718603	wgEncodeAv	ChIP BJ CTCF	1	44668
dms.bed	encode_tfbs	CTCF	Blood	GM12801	0	0	0	478	534	534	534	515	1384	276	747548	wgEncodeAv	ChIP GM12801	1	2883
dms.bed	encode_tfbs	CTCF	Blood	GM12874	0	0	0	478	534	534	534	515	22832	276	726100	wgEncodeAv	ChIP GM12874	1	37517
dms.bed	encode_tfbs	CTCF	Blood	GM12875	0	0	0	478	534	534	534	515	23356	276	725576	wgEncodeAv	ChIP GM12875	1	39184
dms.bed	encode_tfbs	CTCF	Blood	GM12878	0	0	0	478	534	534	534	515	21125	276	727807	wgEncodeAv	ChIP GM12878	1	40122
dms.bed	encode_tfbs	CTCF	Cerebellum	HAc	0	0	0	478	534	534	534	515	29823	276	719109	wgEncodeAv	ChIP HAc CTCF	1	45591
dms.bed	encode_tfbs	CTCF	Spinal cord	HA-sp	0	0	0	478	534	534	534	515	23898	276	725034	wgEncodeAv	ChIP HA-sp CTC	1	46546
dms.bed	encode_tfbs	CTCF	Heart	HCM	0	0	0	478	534	534	534	515	36843	276	712089	wgEncodeAv	ChIP HCM CTCF	1	50703
dms.bed	encode_tfbs	CTCF	Colon	HCT-116	0	0	0	478	534	534	534	515	21528	276	727404	wgEncodeAv	ChIP HCT-116 (	1	50294
dms.bed	encode_tfbs	CTCF	Cervix	HeLa-S3	0	0	0	478	534	534	534	515	16413	276	732519	wgEncodeAv	ChIP HeLa-S3 C	1	38400
dms.bed	encode_tfbs	CTCF	Skin	HFF	0	0	0	478	534	534	534	515	20068	276	728864	wgEncodeAv	ChIP HFF CTCF	1	34889
dms.bed	encode_tfbs	CTCF	Skin	HFF-Myc	0	0	0	478	534	534	534	515	27541	276	721391	wgEncodeAv	ChIP HFF-Myc (	1	43821
dms.bed	encode_tfbs	CTCF	Blood	HL-60	0	0	0	478	534	534	534	515	8526	276	740406	wgEncodeAv	ChIP HL-60 CTC	1	16683
dms.bed	encode_tfbs	CTCF	Blood vessel	HPAF	0	0	0	478	534	534	534	515	28327	276	720605	wgEncodeAv	ChIP HPAF CTC	1	56686
dms.bed	encode_tfbs	CTCF	Lung	HPF	0	0	0	478	534	534	534	515	22897	276	726035	wgEncodeAv	ChIP HPF CTCF	1	46150
dms.bed	encode_tfbs	CTCF	Kidney	HRE	0	0	0	478	534	534	534	515	22928	276	726004	wgEncodeAv	ChIP HRE CTCF	1	42295
dms.bed	encode_tfbs	CTCF	Blood vessel	HUVEC	0	0	0	478	534	534	534	515	25385	276	723547	wgEncodeAv	ChIP HUVEC CT	1	37920
dms.bed	encode_tfbs	CTCF	Placenta	HVMF	0	0	0	478	534	534	534	515	26355	276	722577	wgEncodeAv	ChIP HVMF CT(	1	46460
dms.bed	encode_tfbs	CTCF	Blood	NB4	0	0	0	478	534	534	534	515	16374	276	732558	wgEncodeAv	ChIP NB4 CTCF	1	38253
dms.bed	encode_tfbs	CTCF	Skin	NHDF-neo	0	0	0	478	534	534	534	515	27938	276	720994	wgEncodeAv	ChIP NHDF-nec	1	45920
dms.bed	encode_tfbs	CTCF	Lung	NHLF	0	0	0	478	534	534	534	515	21642	276	727290	wgEncodeAv	ChIP NHLF CTC	1	35446
dms.bed	encode_tfbs	CTCF	Brain	SK-N-SH_RA	0	0	0	478	534	534	534	515	28125	276	720807	wgEncodeAv	ChIP SK-N-SH_I	1	46232
dms.bed	encode_tfbs	CTCF	Lung	WI-38	0	0	0	478	534	534	534	515	21501	276	727431	wgEncodeAv	ChIP WI-38 CT(	1	31518

Table S5. Blueprint data included in the cell type specific DNA methylation

CELL_TYPE	MARKERS	DONOR_ID	DONOR_AGE	DONOR_SEX	BIOMATERIAL_PROVIDER	USED_FOR_CELLULAR_QUANTIFICATION
Band neutrophils	CD11b+/CD16dim	BM030613	65 - 70	Male	Sanquin Amsterdam	NO
Band neutrophils	CD11b+/CD16dim	BM060814	80 - 85	Female	Sanquin Amsterdam	NO
Band neutrophils	CD11b+/CD16dim	BM190913	70 - 75	Female	Sanquin Amsterdam	NO
CD4+ naïve T cells	CD3+CD4+CD45RA+	5.2	50 - 55	Male	Queen Mary University of London	YES
CD4+ naïve T cells	CD3+CD4+CD45RA+	145.2	40 - 45	Female	Queen Mary University of London	YES
CD4+ naïve T cells	CD3+CD4+CD45RA+	299.2	35 - 40	Male	Queen Mary University of London	YES
CD4+ naïve T cells	CD3+CD4+CD45RA+	329.2	70 - 75	Female	Queen Mary University of London	YES
CD4+ central memory T cells	CD3+ CD4+ CD45RA- CD62+	S006YC	65 - 70	Female	NIHR Cambridge BioResource	YES
CD4+ central memory T cells	CD3+ CD4+ CD45RA- CD62+	S014QS	55 - 60	Male	NIHR Cambridge BioResource	NO
CD4+ effector memory T cells	CD3+ CD4+ CD45RA- CD62-	S001U3	40 - 45	Female	NIHR Cambridge BioResource	YES
CD4+ effector memory T cells	CD3+ CD4+ CD45RA- CD62-	S014QS	55 - 60	Male	NIHR Cambridge BioResource	YES
CD4+ naïve T cells	CD3+CD4+CD45RA+	S007DD	50 - 55	Female	NIHR Cambridge BioResource	YES
CD4+ naïve T cells	CD3+CD4+CD45RA+	S008H1	50 - 55	Male	NIHR Cambridge BioResource	YES
CD4+ naïve T cells	CD3+CD4+CD45RA+	S009W4	45 - 50	Female	NIHR Cambridge BioResource	YES
CD8+ naïve T cells	CD3+CD8+CD45RA+	S002ND	60 - 65	Male	NIHR Cambridge BioResource	YES
CD8+ naïve T cells	CD3+CD8+CD45RA+	S0164R	65 - 70	Female	NIHR Cambridge BioResource	YES
CD8+ effector memory T cells	CD3+ CD8+ CD62L- CD45RA-	S014WG	65 - 70	Female	NIHR Cambridge BioResource	YES
CD8+ central memory T cells	CD3+ CD8+ CD62L+ CD45RA-	C003VO	65 - 70	Female	NIHR Cambridge BioResource	NO
CD8+ central memory T cells	CD3+ CD8+ CD62L+ CD45RA-	C005UI	55 - 60	Male	NIHR Cambridge BioResource	YES
CD8+ effector memory T cells	CD3+ CD8+ CD62L- CD45RA-	C00256	40 - 45	Male	NIHR Cambridge BioResource	YES
CD8+ effector memory T cells	CD3+ CD8+ CD62L- CD45RA-	S014WG	65 - 70	Female	NIHR Cambridge BioResource	YES
CD8+ naïve T cells	CD3+CD8+CD45RA+	C00256	40 - 45	Male	NIHR Cambridge BioResource	YES
CD8+ naïve T cells	CD3+CD8+CD45RA+	C003VO	65 - 70	Female	NIHR Cambridge BioResource	YES
class-switch memory B cells	CD19+ CD27- IgD-	C003JB	55 - 60	Male	NIHR Cambridge BioResource	NO
class-switch memory B cells	CD19+ CD27+ IgA+ IgG+	NC11_41	60 - 65	Female	Jose I. Martin-Subero	NO
Mature neutrophils	CD66b+CD16+	C000S5	65 - 70	Male	NIHR Cambridge BioResource	YES
Mature neutrophils	CD66b+CD16+	C0010K	60 - 65	Female	NIHR Cambridge BioResource	YES
Mature neutrophils	CD66b+CD16+	C0011I	50 - 55	Female	NIHR Cambridge BioResource	YES
Mature neutrophils	CD66b+CD16+	C001UY	60 - 65	Male	NIHR Cambridge BioResource	YES
Mature neutrophils	CD66b+CD16+	PB100713	55 - 60	Male	Sanquin Amsterdam	YES
Mature neutrophils	CD66b+CD16+	PB270313	70 - 75	Male	Sanquin Amsterdam	YES
Mature neutrophils	CD66b+CD16+	PB130513	30 - 35	Male	Sanquin Amsterdam	YES
memory B cells	CD19+ CD27+ IgD+	C003N3	50 - 55	Male	NIHR Cambridge BioResource	NO
memory B cells	CD19+ CD27+ IgD+	S017RE	50 - 55	Female	NIHR Cambridge BioResource	NO
Monocytes	CD14+CD16-	C000S5	65 - 70	Male	NIHR Cambridge BioResource	YES
Monocytes	CD14+CD16-	C0010K	60 - 65	Female	NIHR Cambridge BioResource	YES
Monocytes	CD14+CD16-	C001UY	60 - 65	Male	NIHR Cambridge BioResource	YES
Monocytes	CD14+CD16-	C004SQ	60 - 65	Female	NIHR Cambridge BioResource	YES
naïve B cells	CD19+ CD27- IgD+	NC11_41	60 - 65	Female	Jose I. Martin-Subero	YES
naïve B cells	CD19+ CD27- IgD+	NC11_83	45 - 50	Female	Jose I. Martin-Subero	YES
naïve B cells	CD19+ CD27- IgD+	NC15_72	60 - 65	Female	Jose I. Martin-Subero	YES

naïve B cells	CD19+ CD27- IgD+	S001JP	70 - 75	Female	NIHR Cambridge BioResource	NO
naïve B cells	CD19+ CD27- IgD+	S00DM8	50 - 55	Male	NIHR Cambridge BioResource	NO
NK cells	CD3- CD56+ CD16dim	C002CT	50 - 55	Male	NIHR Cambridge BioResource	YES
NK cells	CD3- CD56+ CD16dim	C006G5	70 - 75	Female	NIHR Cambridge BioResource	YES

Table S6 Probes used in TBS-seq

Chromosome	Start	Stop	Score	Strand	Seq
chr1	204070973	204071093	14	+	GTGCTGGGATTACAGGCGCGAGCCACCGCGCCCGGCAATTTGGGTAACCCTTTCATGATTTCTAGGATGGCTTCATCCATAGTTATCCAAACATCAAGCCTTTAATGTTGGCTTCTCCCA
chr1	89088699	89088819	5	+	CTCTCACCCAGAGGAGGAAGGAATGTTAATAAATGTGTCCATGGGTTATCAGTTCCCTCCTGTTTGCATAGTTCCCTTGGCTGCGGGTGGGAGGTCCCCGGCTTCTTGCACTTCCTGGGT
chr1	22001697	22001817	2	+	CCTCCTCCTTGTGGCCGTTGGTAAGACCCCAACCTGTCTGTGTGCTCCCTGGGCTGCCCTGGACTAGGAATCCTTGAAATCTACCACTCGCTCTGAGTCCCATGACATGCTATGCCTGGT
chr1	28097601	28097721	2	+	CCAGCCCAGAATTTCAGTTTCTAGTCTCTCTGAGTCTTGAAAGGTAGTAGCAGCAATAGGCCGGGTGCAGTGTCTCACAACTGGAATCCGAGCACTTTGGGTGGATCTCTTGAGGCCAGG
chr1	77351022	77351142	2	+	GTGAGGACATAATTCCATTAAAGCACTGTGCAATAATTGGTCTTCACCAAAAATAAAAGGTTTGTTTCATTACAATAAAAGAATAACTGGGCCGGGCGCGGTGGCTCATGTCTGTAATCC
chr1	22001757	22001877	2	-	ATAAGCTGAAAGCCCCTACAGTCATGCCCCCGGGTACAAGCTGAGACCCCCTCCTGTGGAACCAGGCATAGCATGTCATGGGACTCAGAGCGAGTGGTAGATTTCAAGGATTCCTAGTCC
chr1	154321036	154321156	2	+	CTGAGCTAATGGTTTTAAAGTCTGTTCCTTATCTTTGCTGGAGGCAGGCAGTAGCTGTGCAGTGACAGTGTGCCTATGCAGACAGAGGGAGCAGTGAATAGCAATAGGGTGTTTCCACCA
chr1	158289863	158289983	2	+	TAGTTCAGAGCAGGTGGGGAAATGAGAGATTGAGTAGGAGGACCAAGGTTGAGGGAAGCAGATCTTCTTAGTTGCTGTCAGCGGCTGATGGGGAAGATTGTTGGTAGAAGGAAGTCAGAA
chr1	1755623	1755743	1	+	GGGGGACGTCGCAGGCCAGGGTGGGCCGGGCCACCAGGGCCAAGGTTGGTGTGGGGAGCTGGTGAGGAACAAAGGTGGCAGGGCTGAGCGGCCCCCTGGGCACGGAGGGCTGGGGGAGCT
chr1	1947556	1947676	1	+	GGCCCCGGGTAGCAGAGCTGTTTCCTTGCAAGTCTGAGCAGGACTTTTTGTTGACTTTGCACCTGAACAGAGGCAATTCGAGAGGCCACGCGCAGGTTGGCATTCTCCTTTGGCCTCTGT
chr1	2036426	2036546	1	+	ACACCCACCTTGCCTCCAGCGGTTGGCGCAGCCACACGGCTCCCATGGCAGGACCCGGGGCAGCACTTCCTCCTGCTAACATCGTCCACGCAGCTCAGCTCTCCAGGAGCTTCTCAGCAG
chr1	2590863	2590983	1	+	CTGGCAGGCAGGCTTGGCATGGTTGGCCGGGGCGGGACGTACACTGGGTCGCCGCTAGCTGCACCTTCGCACAGATGCCTCCGAGCAGCGGGTGGGCGTGGGCCGCACAGCGCGGCAGGG
chr1	3167207	3167327	1	+	TGAAGGCCCCTGTCCCTCCCAGGCCTTCAGCCTGTACACAAAGCCCAGCAGTTGCCCTTTACGTGAGAGGAATTTCTGAAAACGACCCCGTTAAAAGCCATTCCGGAAATCCGTCATCCG
chr1	3556692	3556812	1	+	CAAGGGGTGGCACGTACGTTATCCTTCAAAACAGGACACTGGAGAGCAGAAGAGGCTCCAGTGAAAACACAAGGATGCAGGTACTTCACGTCCCTGTCCCAACCACACGCGCTCACAGAC
chr1	3947902	3948022	1	+	CTACCAGCCAAGGAAAAGCAAAAATCCATAGGCGCTGCGCAGGGTGTGATTTACCTCCCGAGAAGTGCACATTCCCTCCACCCGGCATCGTCATCATCGTGTTGATCTCCTTCTGGAGCG
chr1	4058726	4058846	1	+	GCGCCTTGGCTCATTGCTCCCCAACACTGACAGCCCCTCACCCCATTGTCGGATCTGTCCAGGGCTTCTAAGCCGGGGAGCACCCCTCACCTTCATGTCGGGACTCATGCCGCCCACCTG
chr1	4058846	4058966	1	+	TGGACCCCTTCTTGGCCTCCAGGCCCCTCCCACATGTGGTTGTGGGTGGTGAGAAGGGGCCTCTGGCTGCAGTTGTGGTTTGGGGCCTCTCTTCCCCGGATGGCTCTGTTCCGGGGCAGT
chr1	5503299	5503419	1	+	TCCTTCCTGACCTTCCTTGTCTACAAATTGAGACTCATCGCCTTCCTCGCCGAATTAGCATGCAGGTTCAAAGAGGGGCCCGGAGGCTCCTACACGACCAGCCAACAAACTCTAATTTCA
chr1	5651330	5651450	1	+	CCTGTGCCTGCAAGGGTGCGGAGGTGTGCACAGGCTGGCGTACACCCACTTGGTGGAGAAACCAGCCAGGATAACCCCAGGGGCTCCACCTGATGGGCTGGGCCACTGAGGAACCAGAGC
chr1	9233268	9233388	1	+	CATGGGAAGGGCTCTAGGCCAAGAGTCCCGGCATCATTCGAGTCTGCTCTGGCCCGCTCCTGCCCTAAGCCCTCCTGCTCACTTCCAGCTGTGGAGGTAGCCCAGAGAGTGCCTGGCTCC
chr1	10642717	10642837	1	+	AGACCAGCTGGCTCTGCTGCACGCCAGCCTGTCCTCCTCGGAGGCCGCGTGCCCCGGACCTTCTGTCCCAAGCTGCACCCAGCGGTGCTGGGCTTTGGGAGTGGGGCCTGGCCCTGCCAG
chr1	11964149	11964269	1	+	CTACTGAGGTGCTCCCTTCCCTCAGGAACGTCATTGCCCCGCTGATGACCCGGCATGGGAGGCTGTGGTCGAACTTCTGGGGGGCTCTCAGTGCAGATGGCTACTATGCCCGTTCCGAGG
chr1	12035048	12035168	1	+	ACAGGCATGAGCCACTGCCCCTGGCCTCCGGAGAACGGCAGGGAGGTGCTTGAGAAAGCCCTGGGCCTGGGGCTGCCTCTCCAGTCACTTCTTAGGACTGATTTCAGCATGGGATACAGG
chr1	14949973	14950093	1	+	GAAGAGCCTCTGCACGGAAGACGGTTTCAACACCACCTAACGGAAAAAACAGTTACTGTGCAATATGAGAAAAGGACAAAGGCTGTATTACCTGAGTCCCTGCACCCTCCACACCCACCC
chr1	14950093	14950213	1	+	GTAGTAAGAATTACCAAGCGGCTCTCCGGGCTGGGGAGCGCCGTGGAAGAAACCCTGTGGAGGAGTGGGTGGGTGTTATTTGAGAGTCTTCTCCTATTTGGGGATTGCTGTACTGCTTCC
chr1	15118535	15118655	1	+	GGACGCCCCAGCACAGTGCCCTTCAGACCGCCCCATGGCCTCGGATCACCTGGTGGGGAGGTATTTTGGGAGTGCAGGTGCAGATGCGGGAATTCTGGAGTCCCACCTGAGATCAGCATT
chr1	17394863	17394983	1	+	TCCCTGGAGGCAGCATGACACCAAGTGGCGGGTGACCAGCCCTGGGCCACACTGGCTCAAGAGCTGTTCTTTCCATCTTCCTTCTAGCGCAGAGGGCCGGGCCATGAGTAAGACCCTCCG
chr1	18407193	18407313	1	+	TCTGTGGCCGGGGGAGTTTGGGAAGCACCGCACAGCTGTGTCTTTTCTGGAAGCTGCATCAGGTTTCTGAGAAACCGTGTAGTAAAGAAACCTGCTTAGCTCTGCTGAGCCCAGCCTTTC
chr1	19920354	19920474	1	+	ATATTTGCGGTTGTAGGTGCCCAGGTTGCGGCGAAAGCAGAGGGCAGCCCTCTTGTCACACTCGCAGGTCAGCCGCTGGCAGGTGGTCCTGCCGGCTGGATGGGACAAAGTGAGTCAGGG
chr1	20410010	20410130	1	+	GGTTCCTGCCCTGCCACTAACCAACCATCGGAGGGACACTTCTGGGCCTCAGTTTCCTCATCTGTAAAGCCCTGGTGATTCTCGAGAGTTCTTCACACTTCTTTGTAGACAGACGCCGGG
chr1	21882879	21882999	1	+	CAACCACAGGGGAATCCAGCTCCTCACCCGCAGAATGACCGAGCACAGCCCCGGGTCTAGGTTACTCAATCCTCTTTCCTCCCTGCCTTCCGGGGATGTCTTCAGGCCTCCTCCCTCCTG
chr1	25045989	25046109	1	+	ATTGTGGCTTTGGGGTCTCAACCACCAGCCACAGGAGTCCAGCTGGTCCAGACCACAGGTCCACCCGGGGCTGGAGCTGGGAATTGAGGAGGTGACAGCGGGTGGGGTGGGTGTGAGCTG
chr1	26282679	26282799	1	+	CAATGGTGTTGTCAGGCTGCATCATCAGTAGGAAGGCCTGTTCCCCATTCTCAGACTTGATGCGCAGCATGGAGAGCGGGGGTGCCGGCGTGTTGGGTGACTCCTGGCTCCTGCACAGCC
chr1	31236553	31236673	1	+	CATGGAGGTTAGTGACAACTGGAGGGCCCACTCTGCAATGAGCCCAGATAGTGCAACAGAGCCAAGAGAGCAATTTTCAAGTTCCTCCCGCAAATGATCTTGTGCAACCTTCACAAGCTG
chr1	31236673	31236793	1	+	CCCAAAGCCACCCAGCCGGGATGTGGGAGAAACCAGAATGCCACCCAGGTCTCATCTAACTCAAGCCTCTAGTGCTGGTGAGCTCCTCTAAGTGGAAGAGTGGGGTTAGCTTAGCAAGGG
chr1	33338780	33338900	1	+	TGCCTGTATACAGTCAGGCACCTGAAACCGAAAGGTGGAGGCAGGATAAGGCCGATGGGAGAGGCTGGGGGAGGGGAGTAAAGCTAGGCTTCGGTGGGGGAAGGGGGAGGTAAAATCTTG
chr1	44801697	44801817	1	+	CTGGCCTCAAGTACTTGCACCAGCGCGGCATCTTGCACCGGGACCTCAAGTTGGGTGAGACTCCTGAGCCTGGAGGATGGGAGGTTGGGGAGGGAGGGAGGGAGGGAGGAAGGAAAGAAT
chr1	53071554	53071674	1	+	CTACCCTGAGGAGCTCTCCCGGCTGCACCGGCTGGAGACGCTGAACCTGCAAAACAACCGCCTGACTTCCCGAGGTGAGGGGCCACCCAGAGCCCAGGGTCAGGGACACCAAGTGGGGCC
chr1	54748237	54748357	1	+	GGTACAGCTGCACCTGGCATTCTGGTTCCTGCCCACAGAAAGTGCAGGGCTTCCCTCTGCCCTGAGCCCGCAGAGGGAAGGACTAGAACTGGGCCGGGCGGGAGCCCCAGCTGTGGCTGG
chr1	58814406	58814526	1	+	GCCGGGAAAAGAGGCGCCTAGACCAGTTAGTTTCCTTTGCTCCAGGACCGGATGCGGAGCCGGGACTCAGGTGGAGGCAGGAGAAATACGCACCCTGGGTGCACCTGTAAGTCCTCCAGG
chr1	110229687	110229807	1	+	TCACTGGGTGAGCAGGGGTACACCTTGCGCAGGGGCAGCTGAGGGGAAGTGTGGGGACAGAAGCCATCTTGCCCCCACCTGCTCCTGCCGCTCCCGGGAAGGGGGCCCTCCACAGCCTGA
chr1	116982747	116982867	1	+	GACTGGGCTTTTCTGTCCCTTCACTAGTCAGTCATTGTCCACAGGCTGAGTGGCAAAGAAGCGAGAGCAGTTCATAACCTCCAGGTGGCGGCTTCCATCAGCCTAAGCCCGGCCTCTGGA
chr1	154861677	154861797	1	+	CCTCCCAAGCACCAACACCATAAACCACCGTCCGCCTGGGATGGATGCCATCTGGGTGCTGTCTGACACCCCTAAGAACAGGACTCTCCGGACTGTGGCTGCTCATCCTCGTGATGAAAC
chr1	163885635	163885755	1	+	GTGCCTCACTCATAGGGCAGCATCTGATTGAAGTCCACCGCTGGACTCAGCTGAGCACGGCTCCGTGATGACCGCAGCCACTCCTGCTGCACCTCCAGTTCCCAGGTTTCCTAGATAGCC
chr1	177964278	177964398	1	+	TCTGCAGCAAAATGACAGGAGCAGTGAGCGGGGTCCTGGGCAAGCCAGCAAGGCTGAGGCACTCTCCGCCGGAAGCTGACCTGCTCCAAAGCGTGGGCAGGTACCATGTCAGCCTGGGTG
chr1	200916088	200916208	1	+	AGGCAGAGGGTAGAGATGGGTGGCTCAGCGCCTCCAAGCCATTCCTGGAGCTTTGACTGCCCGGAGCCCAGGCTCATGAGAAACAGCCCCTTCCCCATACCTGGAAGACTGGGACCCCTC
chr1	201889720	201889840	1	+	ATTCTTAGCTGAATAGAGTCACCAGGACTCAAGCCTGGCGGCAGAGCTAGGTGCTTAGGTGCTGGTGCCTGGGAGTTCCAGAAAAGGCATGTTAGTTACCTTCATAGGCTTTGACTGGGC
chr1	206797096	206797216	1	+	CACTCCCTGCAGTGTAGAGACTTTGCTGCGGGACAGGATGTGAACATCCTTGGCTTTTGCATGGTCAAGTTAAGTCACTTGTCCGGGGTCATAGTGACACAATCATTGCCAAACCTGTTC
chr1	228211046	228211166	1	+	GAGGAGGGAGTAAGGGCTTTGCCCAGGGCGGAGGGTGCATCTCACCTAGAAGAGGCTCAAAGGGGAGCCTGCCAGGGTGGAGAACCGGTGACCTCCTTGTGCGATAGGCAGAGGAGACGG
chr1	232531752	232531872	1	+	ATCAGAAAGGTTGGGGACATGTAGGTGCCGGTATGGGCGTTAACGGAAGGGTACGGTGGCTAAGGAAATACCTGAAGAAAAGGATGAGGAAATCAGCCACACAGATAGAAAGGAAGGGAG
chr1	1755683	1755803	1	-	CATTAGCACCTGTGGGGCGCGAGGCTCCGACCCCAAGGCTGCCTCCCACCCGCCCTCGCCAGCTCCCCCAGCCCTCCGTGCCCAGGGGGCCGCTCAGCCCTGCCACCTTTGTTCCTCACC
chr1	1947616	1947736	1	-	TCTCCACAGTGACCTGGCCTGGCTGGTGGCCCAGCTGCTCTGACCCGACCGGGCAGCACGACAGAGGCCAAAGGAGAATGCCAACCTGCGCGTGGCCTCTCGAATTGCCTCTGTTCAGGT
chr1	2036486	2036606	1	-	GAGGGCCCGGAGGACACAGCCATAGTGGAGCGGCCAGCATGGTGCTAGCACAAAGCAGAGCTGCTGAGAAGCTCCTGGAGAGCTGAGCTGCGTGGACGATGTTAGCAGGAGGAAGTGCTG
chr1	2590923	2591043	1	-	CACTGTGCCCGGGGCACCCCCATGCACCCCAAGGAGCGATGCCGCGTGTGGTAGCCAAGGCCCTGCCGCGCTGTGCGGCCCACGCCCACCCGCTGCTCGGAGGCATCTGTGCGAAGGTGC
chr1	3167267	3167387	1	-	CCTGAGGCTCTCCCACGCAGGCCTGAATTCCCAGAAAACTGGGAGCAGCTTTGAGTTCTGCGGATGACGGATTTCCGGAATGGCTTTTAACGGGGTCGTTTTCAGAAATTCCTCTCACGT
chr1	3556752	3556872	1	-	TACCATGAGGCAGCCTCACCATCCTCACCCGGCAGGCTCGGCAGTTTTTAACATTCTCCGGTCTGTGAGCGCGTGTGGTTGGGACAGGGACGTGAAGTACCTGCATCCTTGTGTTTTCAC
chr1	3947962	3948082	1	-	TCTCGCTTTATGAAAGAGATGCCATTTGGGGAAGACTCGCATTGTCGGGAGCGCTGTGGACGCTCCAGAAGGAGATCAACACGATGATGACGATGCCGGGTGGAGGGAATGTGCACTTCT
chr1	4058786	4058906	1	-	GCCCCTTCTCACCACCCACAACCACATGTGGGAGGGGCCTGGAGGCCAAGAAGGGGTCCACAGGTGGGCGGCATGAGTCCCGACATGAAGGTGAGGGGTGCTCCCCGGCTTAGAAGCCCT
chr1	5503239	5503359	1	-	TGCTAATTCGGCGAGGAAGGCGATGAGTCTCAATTTGTAGACAAGGAAGGTCAGGAAGGAACTGCCCAAGGCCCCCAGCTCAGAGCAACTCAGGAAGACCCTGAGACACCATCTTCCCAG
chr1	5651270	5651390	1	-	TTCTCCACCAAGTGGGTGTACGCCAGCCTGTGCACACCTCCGCACCCTTGCAGGCACAGGTGTCCGGCTGAGCACGCCCTCTCTAAGCCCCTCTGTCAACTCGAATTCTGCATTTTCCTG
chr1	9233208	9233328	1	-	GGAGCGGGCCAGAGCAGACTCGAATGATGCCGGGACTCTTGGCCTAGAGCCCTTCCCATGTTCTGTGGCCCTGAGTGTGTCAGGCACCCACATAGCTCTGAAAACCAGGGCCCAGGAAGG
chr1	10642657	10642777	1	-	GGTCCGGGGCACGCGGCCTCCGAGGAGGACAGGCTGGCGTGCAGCAGAGCCAGCTGGTCTGTGGGACTGGGTCATCGAGGCCCCTCCCGCCATCCTCCCGCCTCCCTGGCACTGCCCTTT
chr1	11964089	11964209	1	-	TCCCATGCCGGGTCATCAGCGGGGCAATGACGTTCCTGAGGGAAGGGAGCACCTCAGTAGGAGGTCGCTGCCCACTGGGAGTAGGAGACAGCACTAACCAGGGATGGGGGGAGGTAGGTG
chr1	14949913	14950033	1	-	CACAGTAACTGTTTTTTCCGTTAGGTGGTGTTGAAACCGTCTTCCGTGCAGAGGCTCTTCCGGTGAAGCCGCTGGCCTGTAAACACACCTTTAGCCAGACCCTCCTCGGTGCCCTGAGTG
chr1	14950033	14950153	1	-	CCACAGGGTTTCTTCCACGGCGCTCCCCAGCCCGGAGAGCCGCTTGGTAATTCTTACTACGGGTGGGTGTGGAGGGTGCAGGGACTCAGGTAATACAGCCTTTGTCCTTTTCTCATATTG
chr1	15118475	15118595	1	-	CTCCCCACCAGGTGATCCGAGGCCATGGGGCGGTCTGAAGGGCACTGTGCTGGGGCGTCCCACCACTAGAAATCCAGTCCGGTAATCTGAAGATGTAAGTGCCCCCAGGAGGAGTGACGG
chr1	17394803	17394923	1	-	TTGAGCCAGTGTGGCCCAGGGCTGGTCACCCGCCACTTGGTGTCATGCTGCCTCCAGGGAGCTGGCCTCTGACCGTTGTGTGAAAGAGGCCGGTCCATAGCGGATGTGTTGGTTACGAAT
chr1	18407133	18407253	1	-	GATGCAGCTTCCAGAAAAGACACAGCTGTGCGGTGCTTCCCAAACTCCCCCGGCCACAGAACCTCCTTGTTCCAGAAGCATCTTGTCAAACCAGATGCTGATTTGAGGAAGGCTGGTGCT
chr1	19920294	19920414	1	-	TGTGACAAGAGGGCTGCCCTCTGCTTTCGCCGCAACCTGGGCACCTACAACCGCAAATATGCCCATTATCCCAACAAGCTGTGCACCGGGCCCACCCCGCCCTGCTGAGGCTATGCTCGG
chr1	20409950	20410070	1	-	TGAGGAAACTGAGGCCCAGAAGTGTCCCTCCGATGGTTGGTTAGTGGCAGGGCAGGAACCTGAACTTCAGACTCCCGGTTCTCAGCACAGATCCCCTTTTGTAATACTCACTTTTCCCAC
chr1	21882819	21882939	1	-	CTAGACCCGGGGCTGTGCTCGGTCATTCTGCGGGTGAGGAGCTGGATTCCCCTGTGGTTGCAGGGGGTTAATTCAGGATGAGGGGGAGAAGCTATTGGCAGACAGATGTGGACTCTGTAT
chr1	21882939	21883059	1	-	CCAGGGGAGGGAGTGGTGGGAATTCCAGGGTGAGCAGGTGGCCTGTGTGTGGATGGTGACCAGGAGGGAGGAGGCCTGAAGACATCCCCGGAAGGCAGGGAGGAAAGAGGATTGAGTAAC
chr1	25046049	25046169	1	-	CCCGGGGCTGGCGTCAGCAGAGTGCAGGCCCCTGTGGACCCACAGAAGTAACGCAGGTGACAGCTCACACCCACCCCACCCGCTGTCACCTCCTCAATTCCCAGCTCCAGCCCCGGGTGG
chr1	26282739	26282859	1	-	GGGCGGGATGAGGAGGTGAGGGCCTGGGGGCGTTGGGTCACCGCGTGCTGATGGCCTCTGGGCTGTGCAGGAGCCAGGAGTCACCCAACACGCCGGCACCCCCGCTCTCCATGCTGCGCA
chr1	31236613	31236733	1	-	GTTAGATGAGACCTGGGTGGCATTCTGGTTTCTCCCACATCCCGGCTGGGTGGCTTTGGGCAGCTTGTGAAGGTTGCACAAGATCATTTGCGGGAGGAACTTGAAAATTGCTCTCTTGGC
chr1	33338720	33338840	1	-	TCCCATCGGCCTTATCCTGCCTCCACCTTTCGGTTTCAGGTGCCTGACTGTATACAGGCATTTGAGACCTGTGGGAATGCCCGGCAGCACTTATAGCCTCTGAACTGGTCAAGGGAATTG
chr1	38836168	38836288	1	-	GGATTACAGGCATGAGCCACCGTGCCAGGTGAGTGTTATTTGTTAATAGTAACTTCCCGGAACGGTACATTAGGATACTTTGGATACAAATAACATCCAAGAAGGACTTGAAGGGAAAGC
chr1	44801637	44801757	1	-	TCTCACCCAACTTGAGGTCCCGGTGCAAGATGCCGCGCTGGTGCAAGTACTTGAGGCCAGAAAGGATCTGCCGCAGGTAGTAGCGCACTTCTGGCTCCAACAGGGTGTGCCGGGCCTTCC
chr1	53071494	53071614	1	-	CGGTTGTTTTGCAGGTTCAGCGTCTCCAGCCGGTGCAGCCGGGAGAGCTCCTCAGGGTAGATCTTTTCCAGCTGGTTGTTCTAGGGGGGTAGGGGGCCGCAAGGAAGCAGCATCAGCCTA
chr1	54748297	54748417	1	-	AGCAGGGCCTAGGCTCTGTGCCTGCCGTAAGCAACAGGACCCTCCTGCACTGCGCTCAAGCCAGCCACAGCTGGGGCTCCCGCCCGGCCCAGTTCTAGTCCTTCCCTCTGCGGGCTCAGG
chr1	58814466	58814586	1	-	CACGCCCGGTGACCACCGACCCAGAGCCCCTGGTCATGTCATAGCCAAAACCAATGTAGTCCTGGAGGACTTACAGGTGCACCCAGGGTGCGTATTTCTCCTGCCTCCACCTGAGTCCCG
chr1	110229747	110229867	1	-	GTCAGGTCTAATTCCCATCAGGTGAAAGAGGAAACGTCTTGGCTGAGGCAACCTTGTTCCTCAGGCTGTGGAGGGCCCCCTTCCCGGGAGCGGCAGGAGCAGGTGGGGGCAAGATGGCTT
chr1	116982807	116982927	1	-	TGGGCCTCTGGCCACTGCAGGTACTGGCTGTTAAAATTCACACACCTGTACCCTCCCCCCTCCAGAGGCCGGGCTTAGGCTGATGGAAGCCGCCACCTGGAGGTTATGAACTGCTCTCGC
chr1	154861617	154861737	1	-	AGCACCCAGATGGCATCCATCCCAGGCGGACGGTGGTTTATGGTGTTGGTGCTTGGGAGGACTGAGGAAGGAGACAGTGACTCAGACTGGGGATGCTGGGTGGATTCCCTGTAGGAGGTT
chr1	163885575	163885695	1	-	CCGTGCTCAGCTGAGTCCAGCGGTGGACTTCAATCAGATGCTGCCCTATGAGTGAGGCACAGGGGCAGGCTGAACACATGAAGACAAAATCCGGGAGGTAGGGAACCAAATGTATCAGGC
chr1	177964218	177964338	1	-	GCCTCAGCCTTGCTGGCTTGCCCAGGACCCCGCTCACTGCTCCTGTCATTTTGCTGCAGATCTAACAGTAGGAACCCTTGTAAAGACAGCCCTGCTTCCAACTCTGGACAGGAGTGGCCG
chr1	200916028	200916148	1	-	GCAGTCAAAGCTCCAGGAATGGCTTGGAGGCGCTGAGCCACCCATCTCTACCCTCTGCCTGGCCAGTGCCCTGTCCTTGGGGAAGTGACTCCCACAGGCCAGCTCCTCAAGCTGAAGAGG
chr1	201889660	201889780	1	-	ACCTAAGCACCTAGCTCTGCCGCCAGGCTTGAGTCCTGGTGACTCTATTCAGCTAAGAATGTGGAGGTCGACAACGGAGGAGGCAGGAGTCCGGGAGGGAGGAAGAGGAGGCCTCTGGAG
chr1	206797036	206797156	1	-	GCAAAAGCCAAGGATGTTCACATCCTGTCCCGCAGCAAAGTCTCTACACTGCAGGGAGTGAGCCCTGACCCTTAGAGGCTGACCCCAGCGAAGGAGTCAGGGAAGGTTCTTCTTCCTCCA
chr1	228210986	228211106	1	-	TTGAGCCTCTTCTAGGTGAGATGCACCCTCCGCCCTGGGCAAAGCCCTTACTCCCTCCTCTTCCCCCCGACCCCTACGCAGCTCTCCTTCAGCAGCCCCTCCAGGTTGCACTGAGGGGCC
chr1	232531692	232531812	1	-	GCCACCGTACCCTTCCGTTAACGCCCATACCGGCACCTACATGTCCCCAACCTTTCTGATCCTGTCCCATGATAGCAGTCGCTTTGAACAAGTTATGTAGACCCTACCCAAATTCAGTTG
chr1	232531812	232531932	1	-	GCATGTGCCAGGCTTGCTTTCAATTCCAGTCCCTGATTGGAGCTCCTTCCCCTCCTCCCTCTCCCTTCCTTTCTATCTGTGTGGCTGATTTCCTCATCCTTTTCTTCAGGTATTTCCTTA
chr1	246696382	246696502	1	-	CATTGACTGAGTGCTACCAGGAGCCAAGAAATGGACAATGATCCATGTTCATTGCTATAGTACCTGAACACTTAAAAACACGCTCCCGGGCGGGTGACGCACGCCTGTAATCCCAGCTAC
chr1	2425920	2426040	1	+	GGTCCCCCGGCTAATTCAGCTGGAGTCCCCGTCGCTCGAGAGCCTCCTCCCAGGAAAACGCCCTTTGCTGCGGCAGCTTTCTGTTCTCCCTGGCTCCCTGCACGGAACTGAGCTTTGGTA
chr1	3471544	3471664	1	+	GGGGGAGGGGTCTGGGATAGCGGCTGCCCCTCCCCCAGCTCTGCCCCCAGCCAGGCAGGCTTTGTGTTCTCTGAGCTCTGTGTCCTCCGGTCCCCTCTGCCTCAGGCAGCTGCATGTTTG
chr1	19484343	19484463	1	+	CGATTGTGCGTTCATCCTTGTCCTGTGGGCCACCCATCCTCGCCCCTCGGCTCCCACTCAGGCCCGGGCGCCGTGGACCCCGGCCTGCCCTGCAGAATGCTTCGCACGCACAGCACCCAC
chr1	24502264	24502384	1	+	GGATGGGAGGGGAGGGGAAGGAGTGGGTAAGGGGAAGAGGGTTGTACCCGCCAGGGCGGGACCCAGCCTGTGCCGTCCCACACCTTGTGCTAGCTCCAGCTCAGCTACCTGCGGCCGCCT
chr1	26234120	26234240	1	+	TCGACTCCCGATTGGCCAGAGGCGGCAGAACGGGGTGGGGCCAAACGACGCGCGTTCTGTGGCGCGCGGCCTGGCGGGCGTGCAACGGCCGTTAGAGGAGCTGAGGGAGGGAACCACCGC
chr1	32251185	32251305	1	+	GTGGTTGGGCTGCTGGGGCCCGGTTGGCTGCGGAGCCCTCCGGAGGAGGCAGGAAGTCAGGGTGGGACGTGGGCGCGGGGAGACAGGTGGTGGCTACGACGGCGAAGGGAGCTGAGACTG
chr1	158931472	158931592	1	+	TAACAGGATGGAAAGCAAAAAATATGGGTGGGAGGAGTCTGCACGTTGTTTCACAACTTCTCTCTCCCCAGGGCAAAGCAGAGTATGAGGAAGCCAGCACTAGTCAAGTGACTCTAAGAA
chr1	161707149	161707269	1	+	GACCCCAGATGCAAGGAGATGAGACAGTTAAATTTACTTCCTCTTTTCTAATCTGAGAGGTTTCATGTTGAAGAAAATCAGTGTTGGGGTTGCAGGAGACCTAAACACAGTCACCATGAA
chr1	183023350	183023470	1	+	CTTTCTCCTCGCCCAGACCCCACCCCACCCTGCCGACCCCACCCCCTGCTCCTTCCTCCCCGGGGGCGCGCACTCGGGCACGCGCTCGGAAGTCGGGGGTCGGCGCGGAGTGCAGGCTGC
chr1	1206540	1206660	1	-	TCATGAACGGTCCCAGCCACCTCCGGGCAGGGCGGGTGAGGACGGGGACGGGGCGTGTCCAACTGGCTGTGGGCTCTTGAAACCCGAGCATGGCACAGCACGGGGCGATGGGCGCGTTTC
chr1	6466111	6466231	1	-	CCGCCCGCCAGGCGGGCCCTTCTCGACGGCGCGGGGCGGGCCCTGCGGGCGCGGGGCTGAAGGCGGAACCACGACGGGCAGAGAGCACGGAGCCGGGAAGCCCCTGGGCGCCCGTCGGAG
chr1	6497383	6497503	1	-	CGCTCCTGTCCCCCCGCCCCCCGCCCCCGAGGCGGGGCCGCCGCGGCTCCTCCCCGCCCACCTGCCCCGCCCGCCTCCCGTGCGAGGGTCCGGCGGCGGCGGCTCTGCGGCCTCCCAGTC
chr1	23424707	23424827	1	-	CACCCCTCCCCCGCACAGTTGGGAGGCGGGCGGTGGGGGGGTGGGGGTGGGGAGAGCCCCGCCCCCGCCGGGCGTGTGTGTCGTGTGTGTTTGGGGCCCGCGCGGGTTGCGCGCCCTCCG
chr1	23559458	23559578	1	-	CCGAGGCGGGCCATTTTGAATAAAGAGGCGTGCCTTCCAGGCAGGCTCTATAAGTGACCGCCGCGGCGAGCGTGCGCGCGTTGCAGGTCACTGTAGCGGGACTTCTTTTGGTTTTCTTTC
chr1	42035893	42036013	1	-	TGGGCGGAGGAGGCGGGGCAAGCCGCGCGGCCAGGAAGGGGGCGGGGCCCGGGGTCTGGAGGCGGGGCCTGGGGCTGTCAGTCCCGCGCCCGCCGCCGCGCCACGGCTCCTCGCATGCCG
chr1	54887154	54887274	1	-	CCCACCGAACCTCGGCGACCCGAGCCAATCGCGAGGCGGCGGGCGATCCCGGGCTCCCCGGGCTGTGGGCTACAGGCGCAGAGCGGGCCAGGCGCGGAGCTGGCGGCAGTGACAGGAGGC
chr1	85708374	85708494	1	-	AAGAGCTCTACAAGTCGTGAAGGGGCGAGGCGCAAAAGCGTAGCTTTACGGCGATTCGAGCAGTCGCGTCAAGCAGGCTATTCCGGGTTTGTGGCTGCTTGGCTCCACACGTGGGCCGCC
chr1	109509679	109509799	1	-	GCACGTGCGCCCCGCCCCCGCCGCGCGCACGCGCCCCGAGGCTCCGGCGGCGGCGACGGGCGCGCGCGCGGTGCTCGCTGCCCCCACGCCGCTCCCTCCGCTGGGATCGCTGCGCCTCCG

chr1	151831757	151831877	1 -	GGAGGGCCAGGTGCTCCCGCCTTCCACCCTCCGCCCTCCTCCCTCCCCTGGGCCCTGCTCCCTGCCCTCCTGGGCAGCCAGGGCAGCCAGGACGGCACCAAGGGAGCTGCCCCATGGACA
chr1	156601430	156601550	1 -	CTGGAAAAACCGTGATTTTGGTTCCCGCGGACGTCTCTATGGTTTCGACAGCCTAGAAGGAACAAAACGGCATTTCCGGGAAGATGGCGGCGCACAAGTCAGGTCCGGCACATGTTTCCG
chr1	157552436	157552556	1 -	AGCAGCTGAAGACGGGTACTCCCACTTCCTTTTTTCAATTCACTAATGCATTCTGCTCTTTTTGAGAGCACAGCTTCTCAGATGTGCTCCTTGGAGCTGGTGTGCAGTGTCCTGACTGTA
chr1	157700728	157700848	1 -	GTTTCCCATATGAAAAATACAGAAAGAATTATTTGAATACTAGCAAATACACAACTTGATATTTCTAGAGAACCCAGGCACAGTCTTGGAGACATTACTCCTGAGAGACTGCAGCTGATG
chr1	157777091	157777211	1 -	AACATAGTGGCACTATTCTACTTCCTTTTTTGCTAATTATACAAAACCTATTCTGAAAACCACATTTCATCGCCTGCTCAGAGTCTCCAGTTGGTGACCAAGAGTACATCTCTTTTCAAA
chr1	157820079	157820199	1 -	GAGACTGGTCACTAGAGGGTTCTTCTTCCTTCTACTTCTGCTGAAGGGTAACTTCCGATATCAACTTCCTCAAACCTCTGATGAGCTGCTGCTGCTCGACTCTGAGGTGCATTCTTTTTT
chr1	160646981	160647101	1 -	AGTCCCAGTGATACAGGAAGCGGGTTCAGGAACCTGCTGGTTCCTGATACATAAATCAGACAGCCTCTGCTGCATGACACGAAGCTTGCTTCTGCCTGGCATCTGTGAGCAGCTGCCAGG
chr1	206772453	206772573	1 -	CCTTGATTGTGGCTTTTTAATGAATGAAGAGGCCTCCCTGAGCTTACAATATAAAAGGGGGACAGAGAGGTGAAGGTCTACACATCAGGGGCTTGCTCTTGCAAAACCAAACCACAAGAC
chr1	228416661	228416781	1 -	ACCTCTCCTAAGAGGCGCCGCCCCAGTCCCGGCCGCCGAACACTCCCTCGCCCAGCATTCCCCTCCCCCGCCGCCCCCCAGCCCCCGCTGACGCCACAAAGTCCCTAGGCCTCCCGACCC
chr10	34815255	34815375	4 -	TCCTCCCCCTCCCCTCCCCTCCCCTCCCCTCCCCTCCCGCCGTCCCCTCCCCCAGCGGCCCCGAGCGAGCGCCAGCGCCACACAGCCCCGGGCAGCCGCCGGCGAGCGCGCCGCGACGCC
chr10	3514923	3515043	1 +	AGAACATCCCTGCAGGCCAAGGGAGCAGCAAGATAATTATGCAAAGTTAATGAACTTTACAGGTGGCTTTGCTTAGCCAGGAATGGGCCGAGACCCGGAGTTTTAATGGATTAAATGTTT
chr10	6143789	6143909	1 +	CTTAAGTCGCACTATTACTTCCCTTGAGTAAGGGACGTAATATTGAGTAATATTTATTGAGCTGTGTGTGAGAGACTGTTTCAGGCTCCGGGAAAACAGCGAACAAAATAAAAACAAATT
chr10	6215666	6215786	1 +	GCAAGTCCTGTTCATCGGGAGTGTCTGTTTATGTTTGGAAAGGATTTCTTGTTAAGTGCGAGTTGATTGTGAAACCCTAGTGCAAGGGTGTTCAGCCCCGGCTGTATGCTGGAGTCTCCT
chr10	70905501	70905621	1 +	AGGAGCAGCCTTTCCCACCTGAGCCTCCCAAGGCCTGGGCACCCCGGGTGGGAGCTCTGGCCCCTGTGGCTTTGAAGGAAGATGGACACGGCCTAATTGGTCTCTCTTTGTGGCCCAGTG
chr10	75108110	75108230	1 +	AAGTCAGGGCCGCCCTGACAGTAGAGGCCCTTGTGGGCGGCGTTCAGCACGTGGGTGATGCCCAGCTTCCACAGCTCAAAGCGGTTGTTTGCCGTGGCCCTGGGGAGGGCAGGAAGGGCA
chr10	75108230	75108350	1 +	CTTGATGCCGGCCAAGCCATGGGACCAGGAGGGAGGCTGTGCCTGGCCCCCTGCTGCAGAGGGACCGAGCCATTAGGGTCCAAAGAGAGTCCAACCCCAGCAAGCTCCAAGTGGGGTCTG
chr10	79023516	79023636	1 +	GAACTGGAACCAGAGCCCACTCTCCTGTCCTGTCCAACCGGTCCCAGTGAGAGTGTAAGCTCCCTGGGGGGAGGGGCCATCCAGCAACCCCACATCCACACAACCGTCCACTCCTCTTCT
chr10	86668380	86668500	1 +	TATATTAGCCGTGTGAGTCATGGTGGACCGGCTGGGAGGCGGCAGGCTGGCAGGCACAGTGTAGGGTTACAGTCCATTTATGGGCGCAGCCGAAGGCAGATATCAGTGTCGATGGCATTC
chr10	94368079	94368199	1 +	AAGTGCTGGGATTACAGGCGTAAGCCACTGTGCCTGGCCGAAAGAAGCATTAAATGCCGGGGTGATCAACCCAAAACAATTGTTAGGAGAACTTACCTACAGAGTGCTGTGGCAATCCTC
chr10	101036978	101037098	1 +	GGGGTGTGTGAGGGGACCCTGAGGAGCCGCTGCTCATTCGGGCATTGCAGGTGGGATCCGGGGCCTGTGATCTGACCCCAACCCCCCTCCCTTGCAGAGAGCTGCAGGTGGGCATCCCGG
chr10	113590748	113590868	1 +	CTTGGCAAAGTCCTTCTTGTACTCATTGTCACTCTGGAGCCTGCCAACGTTGAGGAAATGCTTCATCCTTGGGTCATCGTCGACACTGCGGTACCCGATCTGCAGGCCTCGGTCCCGCAG
chr10	127344291	127344411	1 +	CTCTGTAACCCCAGTTTGCATCATGCACCGCTCATGACTCAGTATCAAGAAGCACCATTGTTGCATGGGTTTCCTTCCCCTGTTTGGACACCCGGAGGGTCTTGCTTCGTCTCTTTCTGC
chr10	3514983	3515103	1 -	TAGAACAATAGAAAACCATGCATTTGTTTCCTTGTTTTTTTGAAAGTTCACTGATAACAGAAACATTTAATCCATTAAAACTCCGGGTCTCGGCCCATTCCTGGCTAAGCAAAGCCACCT
chr10	6143849	6143969	1 -	GGTCACCGCCTGACCGACTCCCTATGTGCTTATTAGTGTGTGGGGTCTATGAAAGCAGCCAATTTGTTTTTATTTTGTTCGCTGTTTTCCCGGAGCCTGAAACAGTCTCTCACACACAGC
chr10	6215726	6215846	1 -	CACAGAGTTGCACTAACTGGTCTGGGGTGGGGCCTGGCATCAGGGATTTTAGCATCCCCCAGGAGACTCCAGCATACAGCCGGGGCTGAACACCCTTGCACTAGGGTTTCACAATCAACT
chr10	70905561	70905681	1 -	GGTGTACAGGAATCTGATTCCGACATTGAGAAGCATTGATTGCTGGGCCTCTTCGGGGGCCACTGGGCCACAAAGAGAGACCAATTAGGCCGTGTCCATCTTCCTTCAAAGCCACAGGGG
chr10	75108170	75108290	1 -	TCTGCAGCAGGGGGCCAGGCACAGCCTCCCTCCTGGTCCCATGGCTTGGCCGGCATCAAGTGCCCTTCCTGCCCTCCCCAGGGCCACGGCAAACAACCGCTTTGAGCTGTGGAAGCTGGG
chr10	79023456	79023576	1 -	GCTTACACTCTCACTGGGACCGGTTGGACAGGACAGGAGAGTGGGCTCTGGTTCCAGTTCTGCTTCTGACCTGCTCCTGGCCTTGCTGTTCATCCCTCAGTAAAACTGAGAGCTTAAGCT
chr10	86668320	86668440	1 -	ACTGTGCCTGCCAGCCTGCCGCCTCCCAGCCGGTCCACCATGACTCACACGGCTAATATAGCCCCTGGGGAGGGGTGTCCGGCACCCAGCACCCCCCAGGGGGGAGGAAGGGGAACTGGC
chr10	101036918	101037038	1 -	CGGATCCCACCTGCAATGCCCGAATGAGCAGCGGCTCCTCAGGGTCCCCTCACACACCCCAGGCTCAAAGGCTGGTTCTCCCACCTGAGGATCCCAGGGTCAGACTGAGCCAGGGCCCAG
chr10	113590808	113590928	1 -	TAGGCACCCATGATCTGCCTCTGCTCCTCTGACTTGCAGTTCCGGTACAAAGAGGCTTTCCTGCGGGACCGAGGCCTGCAGATCGGGTACCGCAGTGTCGACGATGACCCAAGGATGAAG
chr10	127344231	127344351	1 -	CAATGGTGCTTCTTGATACTGAGTCATGAGCGGTGCATGATGCAAACTGGGGTTACAGAGCTGGAGGGGCCGGCAAGGATCTCGGCTTTCATGGAGCTTTGGAGAGGTTTATTTACAATG
chr10	8054608	8054728	1 +	TCGCCAGCGCCAGGCTCCTCCCCCCCGGCGCGGATGACACTAGAACCTCCTTAAGTTGCGTCGCGCCACAGCTGTCTGCGAACACTGAGCTGCCTGGCGCCGTCTTGATACTTTCAGAAA
chr10	97850121	97850241	1 +	ACCCAGCCGCCCGCCCGCCCCCGGCCCACCTGAGCCCGGGCCCGCGGCGCCCGCATCAGCACTGCGGACAGCGCCCCGGGCCCCAGCTCGCCGCCACCGCCGCCGCCCACCTGCTCCCGG
chr10	119651302	119651422	1 +	CGAGCGGGCCGAGGCCCCGCCCCCGCTCCTCTGCCCCGCCCGCCGCGATTATAGCCGATGACTCAGGGCGGAGCTCCGCATCCAACCCCGGGCCGCGGCCAACTTCTCTGGACTGGACCA
chr10	15168634	15168754	1 -	GGGCGGGACGGGGCGCGGGCGGGGCGGGGCGGGGCGTAGCGCCCGGGCTCCGACTCCAAGCAGTACGGCGGGAGGCACTAGAGGGAGCTGCGGCCGCTCCGGCCCGGCCCCGAGCACCGC
chr10	60944138	60944258	1 -	CGCCTGGGAGCGGGGTGGGGGCAGGCGAAGGGGAGGGCTGCGGGTGGAAAGGGGCGAGCCCCTCTCGCCCGGGACTGGGAAGAGCGGCCACGGCGCCGGGCGAGGCGGCAGGGCGAGGCA
chr11	33699057	33699177	22 -	TAACTATGAATACATACATAATACTATGTATTCATAGTTAAGAAATCTTAACCGAATACATAGTTAAGAAATCCAGGGGCCGGGTGTGGTGGCTGGCACTTGTAATCTCAGCACTTTGGG
chr11	1244658	1244778	8 +	GGCCACCCCCTCCTCCACCCCAGGAACAGCTCACACTACCAAAGTGCTGACTACCACAACCACGGGCTTCACAGCCACCCCCTCCTCCAGCCCAGGGACGGCACGCACGCTTCCAGTGTG
chr11	1244718	1244838	5 -	GGGATGGAGGAGGGGGTCACCGTGGAACCTCTGGTTGTGGGTGTGGTGGTTGTGCTGATCCACACTGGAAGCGTGCGTGCCGTCCCTGGGCTGGAGGAGGGGGTGGCTGTGAAGCCCGTG
chr11	1229367	1229487	1 +	CAGGCGTGGAAGCAGAGCCCCTCATGCCAGAAGGTCCCACCAGAGGGCCCAGGGTGGGAAGGGCACTGGCTGGGAGGGTGCCGGAAGACCTGCCGATGCGTGGAGGGAGGTAGAGCAGTG
chr11	64341475	64341595	1 +	AGAGCGAGCTGGCCGCTGCCATCCAGGAGGTACTGAGACGGTTCGGCAGCCCAGACTGGTATGGCACCTGGGACGCCCTTGCCACACCGCGGCTTCCACTGAACTGCTCTTCCTGCGCCC
chr11	65969078	65969198	1 +	GATTCAGGACCCGGAGGACAGGGGAGTTGAAAAAGTGAGGGCTGAACCCGGGACGGAGGCCAGGCTTACTGTTGAAGGGCTGGAGAGGACGTATTTGAGGTTTAAGGGCATATGGTCTCT
chr11	68036297	68036417	1 +	ACCACCCGCTATGACATCGACATGACCAAGTGCATCTACTGCGGCTTCTGCCAGGAGGCCTGTCCCGTGGATGCCATCGTCGAGGCACGTGAGGCCCCCGGGTGGGAGGGGGCCTGAGGC
chr11	69071612	69071732	1 +	CTCCCAGGACAGCAGACCCTAAACCCTCTTGAGGGGGAGCTGGGGGCGCCCCCAACACACAGAGGAGAAACGCGGCCCAGCATATTGCGCAGCACGCCCGTCAGACTCCTTCCTGTGCGG
chr11	69105742	69105862	1 +	CAGGGCTCCTCCTTGGCCACCAGCCTGGGTCCCAGGACGCAGGGCCATATGGCAGGTTTAGAAATTAAGCCAGGCCCTGACATTCCTGTGTGCAGCTCCGGAGGCCCCCTCCCCGCCCCG
chr11	70522795	70522915	1 +	CCTCCAACCAGGCGGCATCATTTGAGACTCGTGCAGAAGGGAAGCCGCCCCAAGCCAGCCAGGCATTTGGGCCCCTAAATGCCACAGCTCCTCTCTTAGCGGCCACAGTTGCCCCGGCAA
chr11	70522915	70523035	1 +	CGTGCGGCCGCGGGCAGGCTACCTTCACTGAGGCCTCCCTCCAGACCCGCAGCTCCAATCCACACCCTCTTTGAAAAATGTTTACACACAGTGCCACGAGGTCTCCGGCAGAGGGCTTGC
chr11	70523035	70523155	1 +	GGGTGCAAGGAAACCCACAGGCCCACACCTGCAATGCTGGTGTGGGTGTGGAGGGGCAGCTGCTTGTCTCCTGCTCCTCCCCGAGCATCAAAGCACGCGGGTGGCACAGCAGGGTGTGCT
chr11	70742639	70742759	1 +	GCAGGCCCAGGACGCGGAATGAATGTCAGCACTAATCTGTTTAGGCTCAAAAGGAGGCGGATTCAGAGCTCTCCATGCACAGCCACCCCACTGGGCAGCGTGGCTGACTGGCTGCCGGAG
chr11	71478312	71478432	1 +	ACACCTTTGACAGTGGCCAAATTACACGTGGGAGTTGAACAAACGGGAAATCACGGGTTCTCTTTGAAATTTCCTTCTCCAGGAAGTCCTGACGGCCACGCTGGATCTGGAGGACGTCCG
chr11	71478432	71478552	1 +	GAGCTACAGGGCGGAGATTTCATCTCGAAACCTGGCGGTGAGTGCTCCAGTAGACACCTGTGTGGGATGCTCATCAAAGACGTGGAAAGTGGCCCCATTCGTGCGGGCCTGGTGGAGGCC
chr11	72685905	72686025	1 +	CCCCCACCAAGGCTGGAGGGAGGGGGCCGGAGGGCAATCGGGGAGGGCAATCAGGGCAATCATCTACTGTGGAGTAGAAGGCAGGCACCCAGCCAGGCCCCCAGCCCCCTGCCCAAAGGC
chr11	72742234	72742354	1 +	GGGAGCCCTGGAACTTGCTCACCTGATCCGGCCACCCCTGCTTGCAGCAACAAAAGGTCGTGTTTATGCAGTGCTTACCGTCTACCCAGCACCACACTAAACATATCACATGGATTGCCT
chr11	77150940	77151060	1 +	TCCCTTCATGGATTGGGTTACCCTGGGCACAACACGTGCGCTCAGGATTTCCTCCGATTACCATGGCCAGCTCACAGCCTTGGGCCGGCGGATGCTCTGCTCTTGACTGTCTTGGGCTCG
chr11	86676929	86677049	1 +	CAACCCTGGAGATGAAACCTGCATGCTCCGGTTACCATCTGTGATTGCCTCAGCACTCCTTTTCTTCTCATCCAGCCCTGCAGCACCTGGGAAACCAGTTCTTTATATTAACTTCCTGTT
chr11	117838223	117838343	1 +	TAAGCATCGACATTTGCATCCAAAGGTTCAAGCAGCCGCCTCAGGTTCCAGAGGCTGAGGAGGAGGATAATTTAAATTAAAAACACTTCGGCTGCCTCTGGTATCCTTATCTGCTTCTCT
chr11	118102761	118102881	1 +	ACTGGGTCTTCAGACTCCGGGTTCCTCCTCTTTTACCAGTACATACTGAGCGAGCACTGGAGGGTAAGAGGCAGTTACCAGCCTGTTTCTCCCACACACGTGACCTCTCTTGACTCCGCA
chr11	119822408	119822528	1 +	AAGTGGTAGCTGTTACTACTTTTCCGGTTACTAAGGCTGAAAACCCAAGGGTCATCCCTGATTCCCCCTCCCCTCATTCCAGCACCCTCGCTGCCATCCCATGCAGGTCCCTCCGTTTCT
chr11	120129810	120129930	1 +	GGCCTCCCCGCCCCCACCACCACATTCCTGGACTCTCCAGGCAGGGAGATTCAGAGTTGTTCTCAGTAGCATTTGCCCCACCAGCAAACGGCCGGAAATGCCATAGCATGGAAAATACCA
chr11	126186890	126187010	1 +	GCTCAGTTTGTTTGTTTGAGAGAGGAGCTGGTGGAGACCGTCCGAGGCTGAAGTCCACTACGGCCCCACAGAGCCCCAGCTGCAGGAAGCCAGAGAAAAGAGCGCCATTCCTGCCTCCGT
chr11	133832867	133832987	1 +	TAAGCTCGAAGGAGGCTGACGGGGGAGGGCAGTGGCTCCGGGAGCGAGCGGGGACGGGCGCTGGGCTGGGAGGGGGACGCGGGGCTGCGGGGGATGCGAGGCTGGGGGGAGGAGCTGGGA
chr11	134843806	134843926	1 +	GATGACGGTGTCACATCGTTACAGACAGAATGCCTCAGCGTGCTTCATACTCCTCCATATCTGGTCCCCACCCAAAATATTCTCTGTCCCCTTCGGCCGGCTGCCTGGGCACTGAGTGAT
chr11	1229427	1229547	1 -	TGGATGAACACCAAGCACCTCTGGGCCTCAGTTTCCCCACCATGCCCAGCTGGCTCATGGCACTGCTCTACCTCCCTCCACGCATCGGCAGGTCTTCCGGCACCCTCCCAGCCAGTGCCC
chr11	64341415	64341535	1 -	ACCAGTCTGGGCTGCCGAACCGTCTCAGTACCTCCTGGATGGCAGCGGCCAGCTCGCTCTGGACCTCGAGACTGAGGCCCTGGATGTGGCGGATGAAGAGTTCCCGGTGCTCACACTGAG
chr11	65969018	65969138	1 -	GCCTCCGTCCCGGGTTCAGCCCTCACTTTTTCAACTCCCCTGTCCTCCGGGTCCTGAATCCACTGCAACTGTCCCCACTTTGCCTCCCAGTAGTATCAGAAGCTTCCCTCCCTTGCTCCC
chr11	65969138	65969258	1 -	TCACTTACAGACTGTCTTGGCTGTTTTCCCTATAACAGCACAGCATTCAAGGTGCCTAACAGAGACCATATGCCCTTAAACCTCAAATACGTCCTCTCCAGCCCTTCAACAGTAAGCCTG
chr11	68036357	68036477	1 -	ACTCAAAGTTGGGGCCCTGCAGGTTGAGGTGCAGGGACGGTGGTTAGGCCCTGCTGAGGAGCCTCAGGCCCCCTCCCACCCGGGGGCCTCACGTGCCTCGACGATGGCATCCACGGGACA
chr11	69071672	69071792	1 -	GCCTGGGGGCAGCCCCTCACCCCCCAGGAATGAGAGGATTGGTCAGACTCCCGGGACAGGCCGCACAGGAAGGAGTCTGACGGGCGTGCTGCGCAATATGCTGGGCCGCGTTTCTCCTCT
chr11	69105802	69105922	1 -	CCAAGCACAGGGCAGGCGCTGAGCCCCGGGCTGGCAGAGGTAGGGAGTGGGCTGCAGGCACGGGGCGGGGAGGGGGCCTCCGGAGCTGCACACAGGAATGTCAGGGCCTGGCTTAATTTC
chr11	70522855	70522975	1 -	GATTGGAGCTGCGGGTCTGGAGGGAGGCCTCAGTGAAGGTAGCCTGCCCGCGGCCGCACGTTGCCGGGGCAACTGTGGCCGCTAAGAGAGGAGCTGTGGCATTTAGGGGCCCAAATGCCT
chr11	70522975	70523095	1 -	GCTGCCCCTCCACACCCACACCAGCATTGCAGGTGTGGGCCTGTGGGTTTCCTTGCACCCGCAAGCCCTCTGCCGGAGACCTCGTGGCACTGTGTGTAAACATTTTTCAAAGAGGGTGTG
chr11	70523095	70523215	1 -	TCTGGACAGAGAGGCCTCCCGGTGTGCACACAGCAGCCAGCTGGCCCGGGCAGATGCAGAAGCACACCCTGCTGTGCCACCCGCGTGCTTTGATGCTCGGGGAGGAGCAGGAGACAAGCA
chr11	70742699	70742819	1 -	CCCCCGCCCCCAGCAGGGAGTGGCCATGCCTGCGCTCCAGGCCGCCCCCTTGCCTCTTATCTCCGGCAGCCAGTCAGCCACGCTGCCCAGTGGGGTGGCTGTGCATGGAGAGCTCTGAAT
chr11	71478372	71478492	1 -	CAGGTGTCTACTGGAGCACTCACCGCCAGGTTTCGAGATGAAATCTCCGCCCTGTAGCTCCGGACGTCCTCCAGATCCAGCGTGGCCGTCAGGACTTCCTGGAGAAGGAAATTTCAAAGA
chr11	72685845	72685965	1 -	ATTGCCCTGATTGCCCTCCCCGATTGCCCTCCGGCCCCCTCCCTCCAGCCTTGGTGGGGGCCCTCATAGGCCTCTTTGGTTCACACCATTCAAAGGAGCCCCTTCTGCCTGGCCCTGGAA
chr11	72742174	72742294	1 -	CGACCTTTTGTTGCTGCAAGCAGGGGTGGCCGGATCAGGTGAGCAAGTTCCAGGGCTCCCTGTGGGCCTGCTGGAGAATCGAGAGGGAGACTGAGTCAGGGAGTCTTCCCTAGCTGTTGT
chr11	77150880	77151000	1 -	TAATCGGAGGAAATCCTGAGCGCACGTGTTGTGCCCAGGGTAACCCAATCCATGAAGGGACGGGGGGTTGCCATGGTCAGGGACAGGTTTGGTTTCCGGGTGGGACGATGGCCCAGTTGC
chr11	86676869	86676989	1 -	AGGAGTGCTGAGGCAATCACAGATGGTAACCGGAGCATGCAGGTTTCATCTCCAGGGTTGGAGGAACAAAGGGAAGTGGTTGCACCATCAGAAGCTGGACCTGAGGTGAAAAAGACTTGC
chr11	117838283	117838403	1 -	CTGCGTCTCAGACGAGGCTGTCATACCGGGAATTTCAGTGGGCAGGTGCTCAAGGAAGGGAGAGAAGCAGATAAGGATACCAGAGGCAGCCGAAGTGTTTTTAATTTAAATTATCCTCCT
chr11	118102821	118102941	1 -	CTCAGCTTCCTTGTCTGTAAAGTGGAGATAGTAACACCGGCCCCACCCCCACAAGATGTCTGCGGAGTCAAGAGAGGTCACGTGTGTGGGAGAAACAGGCTGGTAACTGCCTCTTACCCT
chr11	119822468	119822588	1 -	AGGACAGCAGTGCCGGCAAGAGAGGAGAGTCGCATGGGCTGGGGAGGCAGTGCAAGGCTGAGAAACGGAGGGACCTGCATGGGATGGCAGCGAGGGTGCTGGAATGAGGGGAGGGGGAAT
chr11	120129870	120129990	1 -	CAGAGATGGGGCCAAATCTCCATCCTCATCTCCTTAGGTCCTCTTTTCCATCTCTGGTGATGGTATTTTCCATGCTATGGCATTTCCGGCCGTTTGCTGGTGGGGCAAATGCTACTGAGA
chr11	126186830	126186950	1 -	TAGTGGACTTCAGCCTCGGACGGTCTCCACCAGCTCCTCTCTCAAACAAACAAACTGAGCCTGCTCTGCAAATGTTTGATGACCGGTCCCCTCTATACCTCCCTTGCAGCCTCCCCAGGC
chr11	133832807	133832927	1 -	CGCCCGTCCCCGCTCGCTCCCGGAGCCACTGCCCTCCCCCGTCAGCCTCCTTCGAGCTTATTCTCTGGGCCTCTGGACCACAACAAGGTCCGCAGCCCGAAGGTCCCCAACCGGTGGGTT
chr11	134843746	134843866	1 -	ATATGGAGGAGTATGAAGCACGCTGAGGCATTCTGTCTGTAACGATGTGACACCGTCATCATCTTGTGTCGGGTTCTTGCAGAGTAGCCCTGTTTCTGAACAGAGAAAGGTGTCCTGGGA
chr11	8081228	8081348	1 +	GAGGGGCGCGGGACGGTGCGGTCGGCCTCCCCGCCTCCACGCGCGCGCACGACCCGCGCACTCCCGGAGCTTCGCCCATCTCGCCTCGCCGCGCCGCGCAGGCAGCCGCTCGCAGAGCCA
chr11	45921561	45921681	1 +	CAGACAAGGTTCCAGTCCGGTGAGCAGCTTACATTCTGGGAGGGAGACCTGCAATAAACAAGCAAACAACTTCAACTTTCCATGAGTGCTAGCCAGCCCTGGGAGGCTCCGCTGCCAGAA
chr11	60455767	60455887	1 +	AGCCCAAGGTAGCAGAAGCTACTGATTTCCTGTCACCTGATGTCTATCAGCGATTTCATCTTCAGGCCTGGACTACACCACTCACCCTCCCAGTGTGCTTGAGAAACAAACTGCACCCAC
chr11	60971656	60971776	1 +	AGCAGAACAAGCAGGCGTGAGACACTCACAGGTTGGGTTTGATCGCATGCGTGTCGGAGAGGAGAGAGCAGAGAGAGACACAGGAACAAGAACAGCAAAGGGTAGAGCAGACCTGCGCCA
chr11	61102409	61102529	1 +	TGACGCAGGCCCCACACTGCCTGCTCCCCGTCCCACCCCTCCCTGAGCACGCCACCCCGCCCTCTCCCTCTCTGAGAGCGAGATACCCGGCCAGACACCCTCACCTGCGGTGCCCAGCTG
chr11	64591140	64591260	1 +	TCAACGCGGGTTAAACTTTGACCAAGGAAATGATTGCTAAACTCGATTCCATAAGTGTCACCGGTCACACTTTAATTCCAGTCTAAAATTAAAGTCTTCAGTCTCCACATTCCCTACTTT
chr11	67415598	67415718	1 +	GTCCGCCCCGCGCCGCCCCCGCTGGGCACTGGGCATGCCCCAGGCGTTTCTATATAAAGCGGCGCCGCTTGGGCCGGGCGCTGTGCCACTGCCACCGCCGCCGCCGCTGCATCCCGCCCG
chr11	71928976	71929096	1 +	CCGAGCCGCCGATTGGCTAGGAGCACTTGAGCAGCGGAAGCAGCTGGCTCGCGCGGGGACTGCGGTGAGGGGGCGAGCCGTGAAGATGGCGGCAGTGGTGGAGGTGGAGGTTGGAGGTGG
chr11	73647603	73647723	1 +	CTCTCAGGCGCTGCGGGAGGAGAGAAATGCCCCAGGCTCTCCGGGGCACACAAAGCGCAGGCGCAGCGGGTTGGGTGGCAGCAGCATCGAGTAGCGGCCGCTTAGGCAGCAACATCCGCA
chr11	94973631	94973751	1 +	GCAACGACCAATCCGCAGTGGCCGAAGTGGAAGTCGGCGTAACGGCACTAAGGGGCGGGGCCGAAGCGGCCCAGGGGGCGGGCGTTTGAAATCAGTGCCTTAGAGTAGACCCTAAACCTC
chr11	102317404	102317524	1 +	GAGTGCGGAACGCCTGGTACAGATAGGGGTGGGGATTTGGGTGACGCATTTAAAAGACAGCGTGAGACTCGCGCCCTCCGGCACGGAAAAGGCCAGGCGACAGGTGTCGCTTGAAAAGAC
chr11	117986314	117986434	1 +	CGGGGGCGGGGCGTCTGTAGGCCTCGCCCCGCTGACGTCAGCCCTGCGGGGCGCTGGCGGAGCGGGCGGCGGAGCTGTCAGTCCCAGCCCAAGGGTAGCTGGAGGCGCGCAGGCCGGCTC
chr11	118304657	118304777	1 +	TCTGCCTTGAACGTTTCCAAGTGAGGTAAAACCCGCAGGCCCAGAGGCCTCTCTACTTCCTGTGTGGGGTTCAGAAACCCTCCTCCCCTCCCAGCCTCAGGTGCCTGCTTCAGAAAATGG
chr11	441932	442052	1 -	GCTGCAGGACGCTGGAGGAGGAGGAGGGAGGGGCGAGCCCCACGCGGAAGTCAGGTAGGAGCACCCGCCGCTGGCAGCCACTCTCCTGGCCGCCAAACCCCAGCTGGAACTCCGGCCACA
chr11	535525	535645	1 -	GGCCCGATGGCGCGCAGCCAATGGTAGGCCGCGCCTGGCAGACGGACGGGCGCGGGGCGGGGCGTGCGCAGGCCCGCCCGAGTCTCCGCCGCCCGTGCCCTGCGCCCGCAACCCGAGCCG
chr11	60855909	60856029	1 -	CTCCCCCAACCCCACCCCTAAACACACATGCACTGGGGCTGACAGCTATTTCCTCTCTCAGCCTCCCTCTCCCACCTCTGTCTGCCCGCTGCCTCTTGTCTAGCTGCTGTCAGGAGCTGA
chr11	66568519	66568639	1 -	AAGAGAACGCGCAGGCGCCGCAAACCAGCGCCCATTGGTCGGCGTGCCGTCGCCCCGCTGGAGGGAGGACTCAGGCCCCGCTGGCCGCGGGCTCGGTACCCGGTGGGTCGGTGGAGCGTC
chr12	9065222	9065342	42 -	CTCTGAGAGCACAGAAAATGTCCACAGCCGCGGCAAGGTGGCTGCAGCTGCACCCTGGGAGCTCCTGCTCCACCAGTTCGGAAGGGGCGGGGCTCCTGCTTGTCCCTGGCTCACCTGCTC
chr12	38202775	38202895	26 -	GAGAAGGGTACCCATCCCAGACTCAGTCCCCGCACCCAGGGAGTGGGTCAGCTGGAAACCCTACAGGCAGTCACAGCTCTCAGACTCCTTTCTGACAATGTCTATCACTGACTCCATCAG
chr12	38202835	38202955	24 +	GGTTTCCAGCTGACCCACTCCCTGGGTGCGGGGACTGAGTCTGGGATGGGTACCCTTCTCATTAGTAAGATCCGGGAGGAGTATCCAGACAGGATCATAAACCATTCAGCATCCTGCCCA
chr12	9065282	9065402	19 +	TCCCAGGGTGCAGCTGCAGCCACCTTGCCGCGGCTGTGGACATTTTCTGTGCTCTCAGAGGCCCAGCAAAGTCCCCTGCCCACTGCAGGCTCCAGGGTGCCTACTCCGGCTGCCTGGCTT
chr12	92861082	92861202	8 +	AACTGACAAAGAATGGTGAACTGACCATTCTAAGCCCTTCTGCAGGAGAGAGATTTCATGAGAAAACATCATTATAAAGAATTATTATTCTGGCCGGGCACGGTGGCTCACACCTGTAAT
chr12	3077299	3077419	4 +	TCCGCCCCGCCCCTCCCCGCTCCGCCCCCGGGCCGCCCCGCCCCGCAGGCTCGCCATTCCCGGGCAGGCCCCGCCCCCTGTTTCCGCTGGCGGCGGCGGCGGCGGCGGTGCCGGAGCGCG
chr12	14441767	14441887	2 +	CGTGAGCCACCGCGCCCTGCCCAGGATACCAAACTCACCGCACCCGGCCCAGGATACCAAACTCTTATTAGATACATGATTGCAAATATTTTCTCCCGTTCTGTAATTTGTCTACAACTT
chr12	130674710	130674830	2 +	CAAAACCTTCTTATCACCCCAAGCCGAAACCCCATATCCATGACCGGCCGCTCCCCATTCCCCACCCCCGCCCCTGCACCCTCCATCAGCATGCTTTCCGTCTGTGTGGGTTCGCCTGCT
chr12	6914503	6914623	2 +	GGGTCACATGCGCCCGCGCGGCCCTATAGGCGCCTCCTCCGCCCGCCGCCCGGGAGCCGCAGCCGCCGCCGCCACTGCCACTCCCGCTCTCTCAGCGCCGCCGTCGCCACCGCCACCGCC
chr12	6376280	6376400	1 +	AGGGGCCCAGGTGAAGCTGGGGGCTAGGCGGGGCCCTAGGACATTCTGTTCTTTTTACACTGTTGGCTGCCAGGCCAGGAATGTGTAATCGCCCCTGCTGTGGTCACAGAGTTGCAGGA

chr12	11884428	11884548	1	+	CCCTTTTCCTCTGTAGACTGTAGACTGCTTTGGGATTACGTCTATCAGTTGCTTTCTGACAGCCGGTACGAAAACTTCATCCGATGGGAGGACAAAGAATCCAAAATATTCCGGATAGTG
chr12	109246290	109246410	1	+	GAGAGGACCTTCTGTACCTGCGGGCATCCGAGATGGCCCGGGCAGAGGGCATTCCCAAAATTTACGTGGCAGCCAACAGTGGCGCCCGTATTGGCATGGCAGAGGAGATCAAACACATGT
chr12	116497135	116497255	1	+	AGGCACCAGCTCCCGGGGTTCAGAGCCAGAGGAAGCGGATGCACCAGGAACGCTGTCACTTTGATGTGCAGGCAGCGAGGCGGCAGGGCGCGGCTGGGCTGCCCTCAGCTGTCAGGTTGG
chr12	117033660	117033780	1	+	TCCTAGGACCAGGCTGGTCCACCACCAAGCCCCTGCTGATTGCCACATGTGCAAATTCTGCAAGAGGACAGAGACGCCGCCAGTGCCCCGGGAAGTGCGGTGCTCCCCCTACTCAGCTCT
chr12	117054029	117054149	1	+	ACTTAAGCTCCACAGGCCCCTCCTCTTTGGCACACATGACAACTGGCTGTGAAGATTCCTGCGGTACCAGGTCTCTCACCCCAACTCCCGGATCCAACCCTTCCTCATCTATAACCTCCC
chr12	117678258	117678378	1	+	CTTCTAACCCAATTTGTCCAGATCCGGAGCCCAGGCTCTCACAGCTACATGAGGCTCCATCCCACTCTGGTGCCAGAAAGAGGATACTACCCCCACCCCGCCCCCACCAACCCTTGCCAA
chr12	124301408	124301528	1	+	AATGCTGCCAGACAGACTGGGGGCAGCTTTCCCGGAGACAGCTTTCCTGGGGGCAGGTGTGGTCTGTCCTGTCTGCCCTCCAGTGCTCGGCCTCCCTGCGGGGCACGGTACATGGACTGT
chr12	132310269	132310389	1	+	GCATTTCAGTTGGGGTCGGTAACACGCAGAAGTAAAGGAACTGAGGCATGCAAAGGCCAGGACTGTCAGGGACTCTGAGTTCCCTCACCCAGAGGAGCCGGGGCTGAGTGCCAGGAGTGA
chr12	132843589	132843709	1	+	ATGGCCTGACGTCCTGCCGGCTCCTGACTGAGGCCAAATTCTGCTTAGAACATTGAGCAAAGTGCAAACAGGGTGTCTGTAAAGAAAAGAGTGCTGGCCGAGCGTGGTGGCTCATGCCTG
chr12	6376220	6376340	1	-	TGTAAAAAAGAACAGAATGTCCTAGGGCCCCGCCTAGCCCCCAGCTTCACCTGGGCCCCTCCCGGGTCTGGACAAGGTTGGAGGGGGTGGCGAGGAATCAGCAGGAAAGAGGAGGGACCA
chr12	11884368	11884488	1	-	GTCAGAAAGCAACTGATAGACGTAATCCCAAAGCAGTCTACAGTCTACAGAGGAAAAGGGCAAGAAAACACTGTTGAAAATGTTTCTTGTTGAGGCACTAACCAGAAGAATCAAAAAAGA
chr12	49842359	49842479	1	-	GCCAAGGGTGACAGAATCATGCCTGATATTGAGACTCATGTGTGCTATACAGTGCAGGACAGACCCTGGGACCTGCATGTTTATTTCAAAAAAAGTGAGTAGGCCGGGCGCGCTGGCTCA
chr12	109246230	109246350	1	-	TTTTGGGAATGCCCTCTGCCCGGGCCATCTCGGATGCCCGCAGGTACAGAAGGTCCTCTCCAGGGCCAAAGGATCCAATGCGAAAGGTGATGTCATTGCCGATGACGATCACATCCCGTC
chr12	116497195	116497315	1	-	CGCCCAGAGATATCTGGAGGCCTCCGGAGCCTGGCTACTGCGTAGGCAGGGCAGCAAGTGCCAACCTGACAGCTGAGGGCAGCCCAGCCGCGCCCTGCCGCCTCGCTGCCTGCACATCAA
chr12	117033720	117033840	1	-	TTTTGCAAACACCTGCCTTGCAGGCTGTCCTCCCACACAGCGACCTTGGGAAAGCCAGGAAGAGCTGAGTAGGGGGAGCACCGCACTTCCCGGGGCACTGGCGGCGTCTCTGTCCTCTTG
chr12	117054089	117054209	1	-	CGGGCTTGGGTCAGGGGTGCCCCGAGGATCTGGGGAGCAGGGGGCAGCTCTGAGCCACCTGGGAGGTTATAGATGAGGAAGGGTTGGATCCGGGAGTTGGGGTGAGAGACCTGGTACCGC
chr12	117678318	117678438	1	-	TCACCCAGAGAGCCCCGGAATCCTAACTCCTAGTACATGAAGATGTCTGCGATCCAAAGCTTGGCAAGGGTTGGTGGGGGCGGGGTGGGGGTAGTATCCTCTTTCTGGCACCAGAGTGGG
chr12	124301468	124301588	1	-	CAAATATCCCCTCTGGATTCCTGTGCATCCTAAGATACAGATGGCACACCAGGAGTGTCCACAGTCCATGTACCGTGCCCCGCAGGGAGGCCGAGCACTGGAGGGCAGACAGGACAGACC
chr12	130674770	130674890	1	-	GGAAGAGGCCGGACCCGGAAGGCCACGTGTTACAGGATCCCACGTATACGACCCGTCCCGAGCAGGCGAACCCACACAGACGGAAAGCATGCTGATGGAGGGTGCAGGGGCGGGGGTGGG
chr12	132310329	132310449	1	-	CCCGTCCTTCTGGGTGGGGCTGTTGGGTGGGAGGCAGCCTGACCTCACGTGGGTGCGCTCTCACTCCTGGCACTCAGCCCCGGCTCCTCTGGGTGAGGGAACTCAGAGTCCCTGACAGTC
chr12	6444907	6445027	1	+	TGCTGCTATGAGAGAGAAAAAAAAAACAGCCACAATAGAGATTCTGCCTTCAAAGGTTGGCTTGCCACCTGAAGCAGCCACTGCCCAGGGGGTGCAAAGAAGAGACAGCAGCGCCCAGCT
chr12	56521751	56521871	1	+	TAGGACCCAGTGGAAGTGCCTCTGCCTCATTCAGACTCTGTTAACTTCTCTCAGTGACGTAAAGGAGCAGCCCGAGCTCATTCTCTGCCCGCAGCCCCCCTTCATCTCTCTCCTCCTGCT
chr12	57755043	57755163	1	+	CGCCCGCCCCGCCCGCCCGCCACTCCGGGGGGGTCTCCGCCGCCGCCGCCGCCGGAAGGAGCCGCCATTTGCCACCGCCGAGCGCACGGGCCGAGCCAAGCCTGATCCCGGAGCCGGAGG
chr12	108515228	108515348	1	+	GAGGGCTGCGGGCGGTTCAATGGCAAGTCGCCGGGGGCGGGGCCAGAGGCCGGCGGAGAAGGAGGACCCGGGAGCCGGCGGCCCGGAGCTGGGAGCGCGGGGAAGGCGGTTGGGGTTCTG
chr12	121918512	121918632	1	+	ACCGCCCTGCCCTGTCGCTTTAGGGCCTGTCGCTTCCGGCGGTGGCGGTTGCCATGGGGACGGAGCTTGGGTGGCAACCAGAACTAGGGAGCTGGTGGAGAAGGTGGCGGCCGCTGGAAG
chr12	4538425	4538545	1	-	AGAAAAGGATGTGGCGAATCTACGTTCGCGGATCCGCGGTGTGGAAAAAGTATGTCGGCAAGTCAGCTGGTTTCCCAGTGCAGGACGCGCTGACAGCTCGAGTGAGCGGACTGCCCAGGA
chr12	44876274	44876394	1	-	CTCCTTACCCCGCCTCCCCCGGCCCGCCCCTCCCTCCCCGGAGGAGCAGTCTCTCCGCGCGTCTCCCGGAGCTTTCTCCATTGTCTCTGCCTTTACAACAGGTTCGGGCGGCGGGGAAGA
chr12	53207210	53207330	1	-	GATCAGTCACCCCCACCAACCCCAAATCTTCCCCACCCTGGGGAGTGTCACTTCCTCCTCTGCCGTCTCCCAGATCAGTACACAAAGGCTGCTGCTGCCGCCAGAGGAAGGACTGCTCTG
chr13	112013899	112014019	30	+	AGGGTTCAGTCCCGGGAGGGACCAAGCGGGCGGTGCCAGATTTCACCACGCTCCCCAGAAGGGTGCACAAGTTAAAACTTGGGAATTGTTTATTTCTGGAATTTTTTTTAATTTAATATT
chr13	110598187	110598307	9	-	AAGCACATTTTCTTGTACAAAATAGCCTTTCGGTCTATTTAGTGCAGTTTTGTTTTTTGTTTTTTTATTCATTTTAGAGATGAGGTCTTGCTATGTTGGCCGGATTGGTCTTCAACTCTT
chr13	29339581	29339701	5	+	GGGCTGGGGGGTGCCGGGCCTTCCAAAGCCACTGCTTCATGTAGGCCAGGTGAGCCTCAGAAAAGTCCGGCCCAGTGATGCTCAGGAGCGGTGGCCTGTTGGGAAAGTGCCTCCAGGCCT
chr13	20188942	20189062	4	+	CAAATAACACAATTCAGTGACATTCAGCAGGATGCAAATTCCAGACACTGCAATCATGAACACTGTGAAGACAGTCTTCTCCGTGGGCCGGGACACAAAGCAGTCCACAGTGTTGGGACA
chr13	29339899	29340019	4	+	TGGTCCGGGGCCAGCCCAGGTACCAGCTCAAGTAGTTGCCCATGACAGCAATGCAGTAGTCGGGACGTTCTCTTAGAAATTCAGCTTCCAGAAGTTTCCGAAGTCTGCGGCCGGGGCCAA
chr13	90670908	90671028	4	+	GATCCTCCCACCTCTGCCCCCAAAAGTGCTGGGATTGTCGGTGTGAGCCATGGTGCCCGGCAGTTCTGGTGATCTATTGTGTAGTCAGGTGACTACAGCTAATAACAATGTAGGTTTTAT
chr13	29339641	29339761	4	-	CCCTCCTCACCGCTCCTCCCAACTGGGACTATGCCCGTATCCAGAGAGAGATGGTCCCTGAGGCCTGGAGGCACTTTCCCAACAGGCCACCGCTCCTGAGCATCACTGGGCCGGACTTTT
chr13	29339959	29340079	4	-	TTGCGATGCTTTGCGCGCTTTCTGGCGTCCTGATTCCAACGGTCACCAAGCTCAGCACACTTGGCCCCGGCCGCAGACTTCGGAAACTTCTGGAAGCTGAATTTCTAAGAGAACGTCCCG
chr13	110668180	110668300	4	-	AAGTGCTGTGTTTACAGGCGTGAGCCACCGCGCCCGGCTAAGATGTAAAAGTCTTAGAACGTCACACTACAGCGTGTGTTTCTGTGATGCCTGTTTCCCCAGGCTCGAGACCTCCGTGTG
chr13	20189002	20189122	2	-	TTCTATGTCATGTACGACGGCTTCTCCATGCAGCGGCTGGTGAAGTGCAACGCCTGGCCTTGTCCCAACACTGTGGACTGCTTTGTGTCCCGGCCCACGGAGAAGACTGTCTTCACAGTG
chr13	30170866	30170986	2	-	TGCAGGAGCATAGGCACGTGGTGTGGGTGCCCCCGGGAGAGACACCTCACACAGTCAGGAGGGTGCAGGGAAATTTCCTGCGGAGGGGCTGTCTCAAAAGATGGACGGGAATCAGTAGAG
chr13	112013839	112013959	2	-	TTCTGGGGAGCGTGGTGAAATCTGGCACCGCCCGCTTGGTCCCTCCCGGGACTGAACCCTCCCTTCGTCCAGCGTCTCCAGGCTGCGGACGCTCCCCGCCCCTCTTATGGCCTCTTGGTT
chr13	24671671	24671791	1	+	TAGAATTTTCTGGCTAAAGCGATTTTTTGTTTAAAACAACAACAACCTGACTCCTAGACTCATTCAGGTTGACCACCTTAGACAAATCCGGCTCACATGGGCCCTTGGAAGAGAATGCTA
chr13	28618648	28618768	1	+	GCAGGAAGCAATGAGATCCTCGATGTCTCCATGGCCGTTTCATTTGAACACGTAGCTGTGGAAACCGGGTTTTAGGTCGAGTTAATCAGGAGCATCTACGTAGGAGAAAGTTCCCAAGCA
chr13	30107664	30107784	1	+	TGGATGTGTCAGACCATGAGCCTTGGCAGTGGAGAAACCAGGCATCTGCAGGCAGAAGCCCAGCCATAGAATAGCAAGTCACACAGGCCTGTATTGCCCGGCAATGCAACACGTGTAAGT
chr13	30170806	30170926	1	+	ACCTCCCGGCCTTCATACCCACCGTTCCTTCTGACTGGTATAGCCTCTCTGCCTCCCCTTCTCTACTGATTCCCGTCCATCTTTTGAGACAGCCCCTCCGCAGGAAATTTCCCTGCACCC
chr13	47841260	47841380	1	+	TCATCTTCCCCAAGCTCTAGTGGTTGGCCTCCAAAACTCAAGAGACAGTTCCAACATCTACAGCAAGTTGGCGGTGTCCTTGGCTCCCCGGATTATTTTGCAATCTGCTGCTCACACCTC
chr13	60591473	60591593	1	+	AAGGCTGCAGCCAATGTGCAGTCGAAGTGCCTGGCTTGAAAGTGTTCCAGTGCAATGTTTTGTGGGTTTGAGGTTTGTCTTCACTCGTACGCATCGTGCGTGGTAAGTTCCCCGGGGAAG
chr13	99390803	99390923	1	+	GGCCCAGGGAAGCCACTTCTTCCCCTTCCGATCAGCCCTGCCGCATCAGAGACGGCTCTGCTCCCGGGTGGGAGAAGCTCCCGCCATCCTCTGCCTTCCCCTGCCCCTAGACAATCATAT
chr13	109818437	109818557	1	+	GGAGGGTTTAATGGGGTACATGATTTACCAGGCTCAGTCGCACACCTCCTTCCGGGGCTGGACACTGGTGGGGGGGGGGGGGGTCCCAGAGAGGAGTCACTCAGCCAGAGTCATGTGGGA
chr13	110555226	110555346	1	+	ACACCTGCTCTCCCACCACAAACCTCCAACTACTCTAACGCGCCGGAATAGAACTCAAATGAGGCTTGAATTCCTCTTCCACGTGACAACCTTCCAACACTCAAAAACTTCCTGGGACTG
chr13	110557653	110557773	1	+	AACACCCAGTCCCCAGAGACGCAGCTGGAGCTGGATGCCGGCACAGGGAAGTGGCGCAAGTCTGGGCTCCCCGCCGCCTTCCAAGCTGGCTCTTCAAGGGCCAGGTGCTGGGGATGCAAA
chr13	110598247	110598367	1	+	ACAAAAAACAAAACTGCACTAAATAGACCGAAAGGCTATTTTGTACAAGAAAATGTGCTTTAAAAAAATATGTAAGTTTCACCAAAAGAAATTGAGCAGGTCCGGGTGCCTTCCCCGCCA
chr13	112116885	112117005	1	+	CCGGTAAGGAGCCAAGGATGAAGAGGGAGAGGAAGAAAGGAAGAGAAGGGACTACACATTAGAAACGGAGTCACTACAGACGTCAACACTGGGCAAGACGCGTGCCCGTCTCATAGACTT
chr13	112329562	112329682	1	+	TTTGTTCTGCCGGGGCTCAGAGTCTCCTGGGCACACTCCCCCAGCTCCATGCTCCCACTCAGGAGACCATCAGGGGATGACGGGCCAGGGGCAGGGCACGTACACTGCCACCTGGGGCAT
chr13	24671731	24671851	1	-	CTCTGCTCGTTGCTGGGCCAACTATGAAAATAAACACATTCTGATTTTCTCTTTTCACCATAGCATTCTCTTCCAAGGGCCCATGTGAGCCGGATTTGTCTAAGGTGGTCAACCTGAATG
chr13	28618708	28618828	1	-	CGGCAGGACAGCTGAACCCCTACGTGCGCTCGGCCAGCTGCGCCTTCCACTTCGGCATCCTGCTTGGGAACTTTCTCCTACGTAGATGCTCCTGATTAACTCGACCTAAAACCCGGTTTC
chr13	30107724	30107844	1	-	TCTTTACATCTCTGCTGACAGATTTCATCACTGGTGCTGAGTGCAGGGAGTCCCGCAGCCACTTACACGTGTTGCATTGCCGGGCAATACAGGCCTGTGTGACTTGCTATTCTATGGCTG
chr13	47841320	47841440	1	-	TGGCATCATACAGAGAAAAGGAAATGCCGTCTCTCCCTTTCCTCCTGTCAAGACAGCTAAGAGGTGTGAGCAGCAGATTGCAAAATAATCCGGGGAGCCAAGGACACCGCCAACTTGCTG
chr13	60591533	60591653	1	-	GCCTCAGACACACACAATGGAAGATCATCGATAAGTCTAGCGTGCCAAGCCACTGCCTCACTTCCCCGGGGAACTTACCACGCACGATGCGTACGAGTGAAGACAAACCTCAAACCCACA
chr13	99390743	99390863	1	-	CAGAGCCGTCTCTGATGCGGCAGGGCTGATCGGAAGGGGAAGAAGTGGCTTCCCTGGGCCCCCAAGGAGCAAGAAGCCAGTCCCTGGGGCCCGTTGCCACCACCTCCCAGGGCCCTCGCC
chr13	109818377	109818497	1	-	CAGCCCCGGAAGGAGGTGTGCGACTGAGCCTGGTAAATCATGTACCCCATTAAACCCTCCCCAGGATGGGCTCAAAGGGTGGAGACAAGCCCAGGCAGGACCAGTCAGGTGAGACTCCAT
chr13	110555166	110555286	1	-	ATTTGAGTTCTATTCCGGCGCGTTAGAGTAGTTGGAGGTTTGTGGTGGGAGAGCAGGTGTGGCCTGTGTGTAACAGGACGGGCTGCCTCCGAAACTCGTGCTTCCAACACTTACAGTAAT
chr13	110557593	110557713	1	-	CTTGCGCCACTTCCCTGTGCCGGCATCCAGCTCCAGCTGCGTCTCTGGGGACTGGGTGTTGGAGAGAGTGAGTGCATTTTGCATGTGGAATGGATGCACGTCTGTGGGAGCCTGAAGCCA
chr13	112116945	112117065	1	-	AAAGTTGTAGCGGACCAGGGCTGGCTCTACTCCGGCTGAAGTAGCCTGTGGACAGCTGCAAAGTCTATGAGACGGGCACGCGTCTTGCCCAGTGTTGACGTCTGTAGTGACTCCGTTTCT
chr13	112329622	112329742	1	-	CCTGATTCACCTGTAGTCGTTTTCTGGTGCCCCTCATACCTCTGGGGAGCACCGGCCACCATGCCCCAGGTGGCAGTGTACGTGCCCTGCCCCTGGCCCGTCATCCCCTGATGGTCTCCT
chr13	94601777	94601897	1	+	GGCTTATGGCAGAGGAGCCCGCCTCATTGGCTCTCAGGCTCCAGAGCAGCAGGTCTCCGGCGCCCACCCCGCCTCCCCCAGCTGCCGACGTGGGGCGGGCAGCCGCCGGCGGCTGGGAGC
chr13	99258337	99258457	1	-	TGTGAAAGAGAAAAACCACATCCAGGGTAAAGTCATAAGGTGAAAAAGCCTATTTCAGAGAGCACTTCCTGAAAGAGACAAAGCAGCAATTAAAGTCAGCCCAGCACCAACTCCGACGCC
chr13	99307357	99307477	1	-	ACAGAGAAAAAAAAAGTCACCACCATAAAAGGAGGTCTGCACAGCCTCTCTTAAAACAACATGCCACAGTTAAAACTTACTTCAGTTTGGACAACTACTCACAGCTACTACACAGAGACC
chr14	20601676	20601796	17	+	CAAGGATGATTTGCAGACTGGTGAAGAGACTGGGCCCTTCCTGTTTGATTAGGGAACTGGCCGAGGTGCTTGGCTTGGTGGGGGGCGCCGGACGACTGGAGGCCTCATGTGGAACTGGGA
chr14	20601736	20601856	15	-	GTCTGCACCAGTATATACCAGTGCTAGGACCTGCTGTACACTGGTGGGGGACTAGTGGATTCCCAGTTCCACATGAGGCCTCCAGTCGTCCGGCGCCCCCCACCAAGCCAAGCACCTCGG
chr14	72319601	72319721	13	+	AAGTTCTGGGATTACAGGCGTGAGCCACCGCACCCGGCCTGAAGGGGGAAAATCATCACAGATATGAAGATGATTTTGAAGCAGCCAAAGTAAAATAGACACTAGACACTGCCGAACATA
chr14	75233873	75233993	6	-	GGATTACAGGCATGAGCCACCGCACCCGGCCCCATCTCTCTTTCCATAATGTTCTTTCCTCTCTGCCCTTTCTCCTACCCACTTGTCTCCCTTCTTGGCAGCCTAGAGAACTTAAATTCA
chr14	102973915	102974035	4	+	GCAGGAGTCCCAAGAGGTCTTCCATCATCGGCATGAACGTGACCTTACAGAATTCTGCAAAGTCCCGTAAGCCTTTCTCACCCCAAACTGAGCCACCTACCTTGTGCAGCTCCTCCTTCT
chr14	102973855	102973975	4	-	TTGCAGAATTCTGTAAGGTCACGTTCATGCCGATGATGGAAGACCTCTTGGGACTCCTGCCCATGGGCTGTCCCTGCTGCATGCAGGACGCCAGGGCCAAGCCTGGCCCCGGGGCCCCTG
chr14	63315177	63315297	2	+	GTGCTGAGATTACAGGTGTTAGCCACCACGCCCGGCCAGCCTTGCCTTTGACAAAGACCAGAAGAGCTGAATTTGTCCTGAACTGTTTTCTCCTACCTTCCCGTATTTGCTTTAAGTCCT
chr14	63728014	63728134	2	-	GGGTGGGGGCGGGGCTGGGCGGGGCGGGGCGCGGCGCGCGCGGGGCGGGGGCGCGCGGCCTGTGGCGCCGTCACCCGGCAGACTCCGGAGGGTAGAGCGCTGTGCCGGTTCCGCTGCCGC
chr14	64655074	64655194	1	+	GAGAAACTAGGCTGTCGGTGGGACACATGGGTGTGAATCAGCTCTGCTACTTACATGCTCTGTGTGTCTCCGCAGGACACTTAACCTCTTTGAGCCTTACTTTCGTCATCTGGAAATCAA
chr14	64655194	64655314	1	+	GAGGGTTGCCCTAGATAATTCTAAGGACCGGCCCAGCTGAAGGTTTGTGAGTGCATGAGAAGCCTGCGGTGGGTAAGGTTATGGTGTCAGCTTCCACGTGGTCTGCGTATACAGTGAAGC
chr14	95327665	95327785	1	+	TCAGTCAACCCCCAAAATCCTTGGAGAAAATCCATTGCATAGTTTTAAGCTGCTCAGCTCTGTCATGCGGTACTAGCTAACTAGAGCACGATCCTCTCCTCTCCATCTCCACAGCATCTT
chr14	97217751	97217871	1	+	GCGTTTTTGTGCTGCAAACGATTGCATAACTGTCCGGAGAATTGGGTCAATCTCTGGCTTAGTCAAGACCCAACAGTCTTGGTTTAACCGTTTTGTAGTGAGAGGGTTGAATTCTGGCCT
chr14	97217871	97217991	1	+	CTGATATTTTTCCCAGGGCCTGTGGAGGGAGTCACGAAGGTCAGCCCCTCCGGGCTTCCTGTTCACCGAGGGTCTCTACTTAGACTTTTGGCCGGCTCATCAAATGGGGATATGCCCTCA
chr14	100603425	100603545	1	+	CCCCTTCCCCTGCTCAGCCAGGACTCGATGCCAGCAGGCGGCAGCTGCCACTGCTCTCCAGGACCCCTCCCGCCCCTGCTGTACCCGGCTTTCTTCCTCCCTGTTGCTTCCCACATCTTG
chr14	100603545	100603665	1	+	TTGCGGCTTCCTCCTCTCGGAGTGGCGGCCCCTCCCCTGGCCAATCTCCCTGGCTGAGGTCTTGGCATCCTTCCTCTAACCCATGGTGCTTGCCCACAAGTGGCCTTTGTTCCCGGTCCC
chr14	100603665	100603785	1	+	GCCTCTCTATCCTGCCCTTGCTCCTCAAATACCATCTCCAGCCTTCGTCCAGCCCTGCTGGGCCCACACACCTTGCAAGGAGCAGTGGTGGGGACAGTGCAGTCTGTAGCCCTGTGGAAT
chr14	103095313	103095433	1	+	GCGGGTCTCCTGGTCTCCAGGCTCTGTAACTGTCCCTCCGTCATGGCAGGTGTGCCCAGGGCTGGGATCAGGCCCACAGCAGGAGGTGCCGAACATGGTATGGGCTCAGCTGGTCCGGGA
chr14	104101055	104101175	1	+	GGCCCAGGGCCGTGGGGCAGCTCCTGGGCGCAGCACTAAGGCTGGTCTGGGTGGGAGGCTGCCCTGGCCCCAGCCCCCCACCCCTGAGTGTTTCCCACGTGCGTGTGGGTGTGGGAAACT
chr14	104285064	104285184	1	+	AGCTCTGCCCTGTGGGCCCCTCGGCACTCGCATGAAGCCTCTGGGGCCTGGACCACTCCCGTCCTATTGAGGGAGGATGCAGGGTGGAAAGTGCTCCTCCAGCAAGGATGAAGGAAAAGC
chr14	104314700	104314820	1	+	TCAGCTGGACCTGTGGCCTCGGAGGACTCGCTTCCTGGCTCCTGCTCTCTTCTGTGGCCTGTTGGGCTCACTGCTGCAGGCCCAGCGTGGACTCTCACCCAGAGTCAGCGCCCGGTGCCT
chr14	104878237	104878357	1	+	CCACTCCCTAGGACCCCGAGTCCTGGCCCGACCTTGGGACTGTCTGAGCACATGGGTGGGCATGGCTGTGCCTCCCCGGGAAGAAAGAGGCCCCTCCTCTGCCTGCCTCGATGGGCCCTT
chr14	104878357	104878477	1	+	GAGCTGGCACACCTGTTGCTGGGCGTGGACTTCAGCGCTGGGCTCCTGGCTCTTCTGCTCTGTGTTCGCCTTAACACGTGTCCACATTCCAACATGTATGTGCTGGAGCGTGTGCAGCAC
chr14	64655014	64655134	1	-	GAGCATGTAAGTAGCAGAGCTGATTCACACCCATGTGTCCCACCGACAGCCTAGTTTCTCCGGGTTACCACACCGCCTCTCATTGCCGTAAGTCAGCTTCCCTTTACTTATTTGGGAAAC
chr14	64655134	64655254	1	-	TCTCATGCACTCACAAACCTTCAGCTGGGCCGGTCCTTAGAATTATCTAGGGCAACCCTCTTGATTTCCAGATGACGAAAGTAAGGCTCAAAGAGGTTAAGTGTCCTGCGGAGACACACA
chr14	95327725	95327845	1	-	AAGGAAACAGGTAGGTGGTGGTGGAGGGCATCTAAGGGAGAGATGACCATGGCCGGGACCAAGATGCTGTGGAGATGGAGAGGAGAGGATCGTGCTCTAGTTAGCTAGTACCGCATGACA
chr14	97217811	97217931	1	-	AGGAAGCCCGGAGGGGCTGACCTTCGTGACTCCCTCCACAGGCCCTGGGAAAAATATCAGAGGCCAGAATTCAACCCTCTCACTACAAAACGGTTAAACCAAGACTGTTGGGTCTTGACT
chr14	100603365	100603485	1	-	TGGAGAGCAGTGGCAGCTGCCGCCTGCTGGCATCGAGTCCTGGCTGAGCAGGGGAAGGGGTCATCACAGAAACTGAGCCAGCTTTGTCACTCCCTGCTGTGGGTCGTCATCCTCTGGGTG
chr14	100603485	100603605	1	-	ACCTCAGCCAGGGAGATTGGCCAGGGGAGGGGCCGCCACTCCGAGAGGAGGAAGCCGCAACAAGATGTGGGAAGCAACAGGGAGGAAGAAAGCCGGGTACAGCAGGGGCGGGAGGGGTCC
chr14	100603605	100603725	1	-	CAGCAGGGCTGGACGAAGGCTGGAGATGGTATTTGAGGAGCAAGGGCAGGATAGAGAGGCGGGACCGGGAACAAAGGCCACTTGTGGGCAAGCACCATGGGTTAGAGGAAGGATGCCAAG
chr14	103095253	103095373	1	-	CCTGGGCACACCTGCCATGACGGAGGGACAGTTACAGAGCCTGGAGACCAGGAGACCCGCAAGGCAGGGAGTGAGCCTGACTCAGCCCCCAGCCATGGCTAGTACTCGGCACTTTCCCGG
chr14	104100995	104101115	1	-	AGCCTCCCACCCAGACCAGCCTTAGTGCTGCGCCCAGGAGCTGCCCCACGGCCCTGGGCCTGAGGCCGGTGTGTCTTGAGCCTCGTGGCCTGCCCGGGCTTAGCACCCGGTGCTGGCGGA
chr14	104285004	104285124	1	-	GGGAGTGGTCCAGGCCCCAGAGGCTTCATGCGAGTGCCGAGGGGCCCACAGGGCAGAGCTGTCCTTCTGGAAGGTCAGAGACCCAGAAGGACAGACCCGGCTGTAGCATGAATGACCCTG
chr14	104314640	104314760	1	-	AGGCCACAGAAGAGAGCAGGAGCCAGGAAGCGAGTCCTCCGAGGCCACAGGTCCAGCTGACCCCAAGGCAGGGTGCCTGGTGCAGTGACCCTCAGGCTTCACCCACATGCCCCGGTGGCC
chr14	104878177	104878297	1	-	CCCACCCATGTGCTCAGACAGTCCCAAGGTCGGGCCAGGACTCGGGGTCCTAGGGAGTGGTCACCAGTTCCCCAGGCCCCATGTGACCTCAGGCTGGGTGGGTGGGCAAGCAGCAGGTAC
chr14	104878297	104878417	1	-	GAGCAGAAGAGCCAGGAGCCCAGCGCTGAAGTCCACGCCCAGCAACAGGTGTGCCAGCTCAAGGGCCCATCGAGGCAGGCAGAGGAGGGGCCTCTTTCTTCCCGGGGAGGCACAGCCATG
chr14	104878417	104878537	1	-	TCGTGGCTGAGCCACCCGGGCTTGGCCAGCACTAACCTTGAGTGCCTCCTCCGGGACTCGGTGCTGCACACGCTCCAGCACATACATGTTGGAATGTGGACACGTGTTAAGGCGAACACA
chr14	105474742	105474862	1	+	CCCCGCCCCGGCCGCGGAGCCAATGGGCGCGCGGACAGCCGGGCAGGCGGGGCTGGGCGCGGGCGGCGGCGGCCCGGAGGAGAACGGGCGGAGGGCGCGGGCCGACCGGGCGCACCGACC
chr14	21511299	21511419	1	-	ACCTAACGTGGCTCTTTATAGCTTCCAAGAAAGCGCGACACCGGAAATGACTTTTCTGTCTTGCTCAGCTCCAGGGGTCATTTTCCGGTTAGCCTTCGGGGTGTCCGCGTGAGAATTGGC
chr14	24263136	24263256	1	-	TGGCCTCTTCTCTCCGCCCCCTACAGCAGTTTGGCCCCTCCCTCCCACATAAGTCACTTACCAGGTCTGTCCCTGCGGCATCCAGTCTGTGGGTCCTGTCCCATCCATCCTGACCTGTTC
chr14	95714080	95714200	1	-	GGCCGTCCTCCCGCCCCGCCGCTTGGTGGCGGCCGCATGCTGCCCGGATATAAAGGGTCGGCCCCACATCCCAGGGACCAGCGAGCGGCCTTGAGAGGCTCTGGCTCTTGCTTCTTAGGC
chr14	105021031	105021151	1	-	GAGAGCGCAGCGTCGACCCTTTGTGGACGCCGAGTGGCGGTCGCTCGCCCCGCCCCGCGCCGTCGGGCGCTCCTTCCTCAGCGGCGGGAAGCTGGCGGCAGCGGCGGTGGCGGTGGCTGA
chr15	64794838	64794958	18	+	CACGCCCGGCAGCTTGTCCATTTCTATACGGAAGTCAGCTAGGATTGTGTAAGAGATTGCACTGAATCTGTAGATCAATTTGAGGACTATTACTATCCTAACAAATAGTCTCTGAATCCT
chr15	85641073	85641193	3	-	ATTACAGGCGTGAGCCACCTCGCCCGGCCAAAAGACAATATCTTATTTGGTCTAATGCTATTGCTCTCTTGAGGAAGTGTGTATAAAGTAAAATACAGAAACCTGCAAAACAAAGTACCT
chr15	34582824	34582944	3	-	TGCAGGCGCCGGGTTGGAGGCACGCCGCGGACCTGCCCCTCCCGGAGACCTGCCCCGGAAGGGGCAGGGCCCCTTCTCCAGGCCAGGCACTGCCTGGCAAGGCTGCTGGAGGGAGATCTG
chr15	28886080	28886200	2	+	AGAGGCGGCCCTGCGTGCCGTACGCTGCGTCCGGGGCGCGCCCGCCGCTATTCGGGAAGCTATTCAGCTTCCCGGGCTCATTAGCAGTCGCGGTGTGCGGCTCGGCGCGGGCTCACAAAG
chr15	58523112	58523232	1	+	TGCCAAATGAGCGGGCACCTCTATGTTCCAGCAGCCCTCGCTGCCCAGCTTCTGAGCTGCAAGCCAGCTTCCTTCCACAGAATTCTCTGCACCTTGGCTTCCGGTGGCTCCAAGCACTTT

chr15	63105967	63106087	1	+	AAGTGCTCAGATTACAGGCCTGAGCCACCGCTCCCGGCCTGAATCAGTTAACCTTTCTGGGCATTCATATCATTGACTATAAAATGGGGGTAGTGTTAGTTTATGCTTCCCAGATTGCAG
chr15	81002343	81002463	1	+	GCCAGCTCGCAGCCGCGGAAGAGGCTGGTATCCGTCTGCGACCACTGCAAGGGCAAGATGCAGCTGGTGGCTGACCTGCTGCTGCTGTCGAGCGAGGCGCGGCCCGTGCTCTTCGAGGGC
chr15	85770291	85770411	1	+	TACCCAAACTGCCACAGCCAGGATTCTCACATGGGCTGTCCGGCTCTGGAGCCTGATCTCTGTTCAAGGTGACTAATCCCTGCAGGGTTTGCTGTGGACGCCCAAGCAGAGCCTCACGTA
chr15	94317359	94317479	1	+	GCAGGACAGGGTGAGCCGGTAGTTCAGGCTAGGTTCTTCCCATTCCTCCTGGTTATCACCTGCCACTTAAAGCTTTTCTCTCTGCATACGCCTGTGCTATCTGCTTCTGCTTATTTTCAG
chr15	58523052	58523172	1	-	GCAGCTCAGAAGCTGGGCAGCGAGGGCTGCTGGAACATAGAGGTGCCCGCTCATTTGGCAGGGGTGCCCAGAGCGAGAGGAAGTGGGGCTCCTCAGTTAGGAAGCTTTGTCAGACATCCC
chr15	81002283	81002403	1	-	CATCTTGCCCTTGCAGTGGTCGCAGACGGATACCAGCCTCTTCCGCGGCTGCGAGCTGGCCCCGCCGATGGCGCTCGCAGGAGCCGGAGAAGCCGCCTCGCCAGTGGGCTTCCCGGCGCT
chr15	85770351	85770471	1	-	CTAGCCAGTACCGCTTGGAGCCCGGCCCAGGGCAGAGCCTGCTGGGAGCAGGGAAGTGGGTACGTGAGGCTCTGCTTGGGCGTCCACAGCAAACCCTGCAGGGATTAGTCACCTTGAACA
chr15	94317419	94317539	1	-	GAGCTGGATGGGCCAGCACTGTCCTATGCCTTGAGGCTGAGCAATGCCCGGCAAAGGCACCTGAAAATAAGCAGAAGCAGATAGCACAGGCGTATGCAGAGAGAAAAGCTTTAAGTGGCA
chr15	59372830	59372950	1	-	TGACGCTACGAAAACAAACCCTGATTGGTCAGGCCTGAGCTGAGTTCTCATTTATGGACAGATTGCCCGGCCCGAGCCGAGACTCAGCCAGAGGAGTACGGATTAAGTGGCCGAAGAAA
chr15	82952649	82952769	1	-	GGGCGGGGCGGGCACCGCCCCAGCGCGGCCGCCCAGCCCCCGCCCGCCCGCGCCTGGCGGCGGTGGCGGCAGTGGCAGCAGTGGCAGCCGCGCAGCCCCGCGGAATGGAGCGGCGCCGGG
chr15	88913338	88913458	1	-	GGCCAGCTTGGGCGGAGCGCACGGCCAGTGGGAGGTGCTGAGCCGCCTGATTTATTCCGGTCCCAGAGGAGAAGGCGCCAGAACCCCGCGGGGTCTGAGCAGCCCAGCGTGCCCATTCCA
chr16	76048027	76048147	9	+	GATGAGAATACTTTATTTTAATATAGTATAATTATTGATACTTTTATTTATTTACAATTACTGTATAAGAAAACTTTGCCTGGCCGGGCACAGTGGCTCGCGCCTGTAATCCCCAGCACT
chr16	29107625	29107745	6	+	TCTTGGTCACTGAAGGGGCTCGAGAGGCCGCGAGGCGCTGGGGACAGGTCCGGGAGTCAGGCCAGGAAAGTCTCCTCGGAATAAGGGAAGAAAAGGCGCTCTTTTGATGTTATTATTCC
chr16	29107565	29107685	5	-	CTGACTCCCGGACCTGTCCCCAGCGCCTCGCGGCCTCTCGAGCCCCTTCAGTGACCAAGATGCAGAGATCAGGACGCCATTGCACCCACCCCAGGTGCCCGCCTCTAGCTGGCTCCGCCTG
chr16	59532989	59533109	5	-	GGTCCCTAACAGGCTATGGACTGGTAGCGGTCCATGGCCCAGGGGTTGGGGACCCCTGTTTCAGAAGCTATTACACAAAAATAATCAGCCGGGGCTGGTGGCTCTCGCCTGTAATCCGAG
chr16	2135855	2135975	5	-	TGCACCCGCCCCGCCCCCCCTCGCCCCGTCCGCCCCGCGCCGCGCGGGGAGGAGGAGGAGGAGCCGCGGCGGGGCCCGCACTGCAGCGCCAGCGTCCGAGCGGGCGGCCGAGCTCCCGGA
chr16	29127607	29127727	2	+	ATGAAATGCCTGTGGAGGCTGATTTCACCGGAGTCAGGGGAAGTCGGTCTAAGCAAAGAGCAGGGGCAGGGATGAAAATAACAGAACAGTGATCCAGGTAGCAACCGTGTGCCGGGGAGG
chr16	55760645	55760765	2	+	GGCTCCCTGCTCTTGTCCTGGCCACTCTCGCTGCTTCCGCGGCTTGGGGTGAGTCCTTCTGAAGTCAAATATGCGGGCAGCTTTTGAAATCCTTGTTCTGAGGCCGAACTGGGCGCAGAT
chr16	55760765	55760885	2	+	GCGTAGAAAGGCAAAGACACAAAAGGTCCGGCTCCGTGGCGGGGCGCGACCTCCGTACTTGGAATTGGACTTGGAGCAGCTGAGCCCAGCCAGCCTGGCCCGCGCGGAGACACAGGGAGG
chr16	55760885	55761005	2	+	GTGAACATGCTGAGACCGCCCTGCACTGCTTGCCCCAAGAAGGCCGGCAGCCGGCCCACCTCACTCCGCACACAAGAGAAATTTAGGCAGCTCAGTTTATTGTCCCATAATTCGTCCCGT
chr16	84849269	84849389	2	+	GGCCGCTATTCACCCTCCTCGGCCTCCCTCCCTCCTACCTGCCCGTGGCTGCTGCTGTCTCCACTGGTGGGTGAGGGGAGGGGCTGGGACTGAGTGAGCGGTTTCTGCCCTGCAGGTATC
chr16	29127547	29127667	2	-	CTCTTTGCTTAGACCGACTTCCCCTGACTCCGGTGAAATCAGCCTCCAGGCATTTCATCAGCCCTTGTTCGTCCACAACACGGCTAGGCAGGTTGTGCTCAGGGGGTCTGAGGCTTTCA
chr16	55760585	55760705	2	-	AGAAGGACTCACCCCAAGCCGCGGAAGCAGCGAGAGTGGCCAGGACAAGAGCAGGGAGCCACATCCTGGAAGGGCGACAGTTCCGGGGGCCTGCGAGGTCTCCGTGCAGCTCAGAGGGAC
chr16	55760705	55760825	2	-	AAGTACGGAGGTCGCGCCCCGCCACGGAGCCGGACCTTTTGTGTCTTTGCCTTTCTACGCATCTGCGCCCAGTTCGGCCCAGAACAAGGATTTCAAAAAGTGCCCCGCATATTTGACTTC
chr16	55760825	55760945	2	-	GGTGGGCCGGCTGCCGGCCTTCTTGGGGCAAGCAGTGCAGGGCGGTCTCAGCATGTTCACCCTCCCTGTGTCTCCGCGCGGGCCAGGCTGGCTGGGCTCAGCTGCTCCAAGTCCAATTCC
chr16	88909508	88909628	2	-	AGGAAAATAAACAGCTGTTTAAAGCAGTGGCGTCCTCCGTCCCAGCCGCCGTGATGGTCACCCGGGTTGCAGTGGCGTCTTCTGTCCCAGCTGCCGTCATGGTCACCCGGGTTGCAGTGG
chr16	28292445	28292565	2	+	GCGGGCGGCGGCGCGCGAGCCGGAGGGCGGAGCCGCGGGCCGGGCGGGCAGGTGCGCGCTGGCTGGAGGGCGGAGCCGCGATGCCGCGATGGAGCGCAGCCCGGGCGGGCGCCGGGGCCG
chr16	3484802	3484922	1	+	CATGGTCGGGCATCTCTTCCAAGAGTGGCATCGAGTACAGCCGGACCATGTGATGTCGGCTGGGCAGCCGCCACCAGGCCCCACCCTTCGGCCGCCCGCAGAGCCCGCCTTCCTGTCCAT
chr16	11135656	11135776	1	+	CTAATAGAGAAGCCCGTGCAGTAGGTGGGGGAGAGAACAAACCCCATATGCAATCTGCCATTTGACCTGGGCCATGCCTTAGAATGTTCTGTAGGCTCGGGTGGGCCCGCAGCAGGGCA
chr16	14959794	14959914	1	+	AGCCACCATGCCCGGCCAACACGCAACATGTTTAAGACCAAAAGGACTGTTTTGCAATGAAGCAGATGAATCAACCAGTAAGGCCAACCCCTCAAAAAATGTAGCACTGAAGTTTCTTCA
chr16	17134481	17134601	1	+	TTCTCCCATCCGTGTGCAGGGACGTCTCGGCCCGTCGAAGACCCAGGCGGGCAAAGGAGTGGTACAAGGTGAGTGTCACGTCGCTCAGGCTGTGGATGCCGTCAGGCTCATCGTAGACA
chr16	31148573	31148693	1	+	ATGGCGGCCACTGCGCGGGTGTGCGCGCCGTCCAGGGGCCCGTCCTGGGAGTGCACGCCCAGCAGTACCGACCGCGCGGGCTCCAGCGTCCCATTCCTGCGCTCGACCGGGGCA
chr16	68707806	68707926	1	+	GTACCCACTGCCCAGCAAGCGGCAGGGGTGTGGCGGGCCGGGGAGGAATCTGAGAGGGGCGGGGCGGGTCAGGAATGCCTGGGCTCCGTTCCAACTTCTGTCCCCACTGTTGTCCATCCG
chr16	68707926	68708046	1	+	GTAAACCACGGCCAGCCCACAGCTGACAGGGCAGGGCGCTGAGACCTCTGTGTGTCCTCCAGGAACCTGACGACCCAGGCACTCCAGGAAGACGATGCCCACTAATTACAAGAATGATAG
chr16	84344076	84344196	1	+	GTGCCTGGCCTTCTCTTGAGTCTTTGATGCTAGAAGGTGATGCACAGGGCAAGTGATTTAGAGCCTGGCTCCGGACTGAGGCATTCAGCGGCGTGGGTTCAGGCAGCTTCTTTTACCACT
chr16	85360409	85360529	1	+	CTGCCAGCTGCTCCCTGTCAGGCTGCAGCCAAGTCCGGGCAGCTCCTCAGCCAGAGACCCACCAGGAGCATGTCCCGCAGTCAGGCCCCGCCTGGGCAGCCACTGCTGCTCAGAAACGTG
chr16	85782611	85782731	1	+	TCTTCAACTTCTTTAACAAGCCGCTAGTCTTGCTCCATGTCCTCACCACAGCTCTGTGCAATCTGCCATCTAACCCATTCCCTTGCAGAGCAGCACTCCGGAAGTCTCCTGCACCACTGCC
chr16	85848253	85848373	1	+	ACCAGGCAGGGAGAGCCAGTGTCCATGCGGCCTCCGGGTAGTGAGGACGCGAGCTGCACTGTGAGATCCTCTCTGCCTTGTTGTGTGTTTGAAATGTTCGTGCTGAAGTGTTGGGGGGAA
chr16	87808472	87808592	1	+	GGCCACCATGTTGCACAACTGCGTAGGTTCTGCAACATGTTGGCCTCCTTTGGATTGTTGTTGTCTTGAGGATGGTTTTATACAGGCCGGGAGTTGAAATCTCAAAGAGCTACAGGGCC
chr16	88599613	88599733	1	+	GCCCTCCCCAGAAGGACAACTGTGCTGTGTCCGCCCCTCACCCCTTGAGCACTTGCAGCGTGCAGCTCCTGCTCCTGCAGGGCTGCTGCGGTCGGGTGGGACGGCTCCCTTTGTGTTTCC
chr16	88599733	88599853	1	+	TAACAGCGACGCCCGGTATTCTGTTCCATGTTGACTTCTTTCTTCTTACAATGGTAGGTTTTAAAAAAGCAACTATTCGAAAAGAACAGGAGCCTGATTTTGAAGAGAAAAGGTTTACG
chr16	88909568	88909688	1	+	TGACCATCACGGCGGCTGGGACGGAGGAGCGCCACTGCTTTAAACAGCTGTTTATTTTCCTTCAGAATCACACGGTCCCACAGCTTCCTCTGGGAAAGGCACAGATGTGCAAAGAGGAGAC
chr16	88910520	88910640	1	+	CAGCCTCAGTGTCCTCCGGAGCCACCGTCATCTGAAGGCGTGGGGACAGGCAGTGCCCTCCCACCTCAGGAAGAGCTGTGGGGTGAGCTGCGGATGGCGTGAGCAGTGCAGGGCGGCCCT
chr16	89304969	89305089	1	+	GTGGGACCCAAGAGTGAAGCTCTCCAATCGGCCCATGGGCCTGAGCCTCGGGTGCAAAGGAGGTGGCATGTGGGGGCCTGTGCTCCGCCCCTGCTGCCTCTTGCCTGGACGGCGTGCAG
chr16	90031311	90031431	1	+	TCAGCCGCATCCGGGAGGAGCTGGACCGCGAGCGGGAGGAACGAAACTACTTCCAGCTGGAGCGGGACAAGATCCACACCTTCTGGGAGATCACACGGAGGCAGCTGGAGGAGAAGAAGG
chr16	3484862	3484982	1	-	GCAGGCCGACGAGCCCAGTTAGATGGCTGGCAGCTCCTTGCAGAAAACAGAAGGGGTCAGATGGACAGGAAGGCGGGCTCTGCGGGCGGCCGAAGGGTGGGGCCTGGTGGCGGCTGCCCA
chr16	11135716	11135836	1	-	GTGTGGCCAAGCCACCCGCTCTGCCACTGACACTGGCCTGTGCTGTGCTGCCGGCATGGCTGCCCTGCTGCGGGCCCACCCGAGCCTACAGAACATTCTAAGGCATGGCCCAGGTCAAAT
chr16	17134421	17134541	1	-	CTCCTTTGCCCGCCTGGGTCTTCGACGGGCCGAGACGTCCCTGCACACGGATGGGGAGAACAGCTGCGAGCCGGTGAGCCCATATATGGGATGCAGAGAGGAGAGCGAGGGGGAGG
chr16	31148513	31148633	1	-	GGGCGTGCACTCCCAGGACGGGCCCCTGGACGGCGCGCACACCCGCGCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTGGAGCTGGGCGCCGACCTGGCCCTGCTGCGCCT
chr16	68707866	68707986	1	-	GGAGGACACACAGAGGTCTCAGCGCCCTGCCCTGTCAGCTGTGGGCTGGCCGTGGTTTACCGGATGGACAACAGTGGGGACAGAAGTTGGAACGGAGCCCAGGCATTCCTGACCCGCCCC
chr16	84344136	84344256	1	-	GTTTCATCTTTCTCACTTCCAGAGAAGGAAATGGAAGCAACACAGAGAGGTTCACAGAGAAGTGGTAAAAGAAGCTGCCTGAACCCACGCCGCTGAATGCCTCAGTCCGGAGCCAGGCTC
chr16	84849329	84849449	1	-	AGGGGTAGGTGTAGTCCTTCACCTCGTCATACCAGGACTGCACATGGAACCCCGGAGAGCGATACCTGCAGGGCAGAAACCGCTCACTCAGTCCCAGCCCCTCCCCTCACCCACCAGTGG
chr16	85360469	85360589	1	-	AGCGCCCGCCCGCCTGCCGGATGAGAGGTGGCAGGTGTGTAATAAACCATTAGTCACTGTCAGTTTCTGAGCAGCAGTGGCTGCCCAGGCGGGGCCTGACTGCGGGACATGTCCTCTGGT
chr16	85782671	85782791	1	-	CTGAGAGTGGTGGGTTCCCGCTGGGAGGCTTTTGAGGGGGTAGCAGTCTTGGGGCCATCAGGCAGTGGTCAGGAGACTTCCGGAGTGCTGCTCTGCAAGGGAATGGGTTAGATGGCAGAT
chr16	85848313	85848433	1	-	AGACAGACGGCGGGCTGTGTGTAGGGGTGATCGGATATTTATTATCCCACCTGGGACACTTTCCCCCCAACACTTCAGCACGAACATTTCAAACACACAACAAGGCAGAGAGGATCTCAC
chr16	87808532	87808652	1	-	GCCTCTGCATTTAACCATCATTCCCACCTGCCCACTTCACTCATCTCTTTCCTGGGTCTGGGCCCTGTAGCTCTTTGAGATTTCAACTCCCGGCCTGTATAAAAACCATCCTCAAGACAA
chr16	88599673	88599793	1	-	AACCTACCATTGTAAGAAGAAAGAAGTCAACATGGAACAGAATACCGGGCGTCGCTGTTAGGAAACACAAAGGGAGCCGTCCCAACCGACCGCAGCAGCCCTGCAGGAGCAGGAGCTGCA
chr16	88910460	88910580	1	-	GAGGGCACTGCCTGTCCCCACGCCTTCAGATGACGGTGGCTCCGGAGGACACTGAGGCTGGGAGTGTCCGGTCCTCAGTGGGCTGTGCCTTTCCAGGTTTTCTCAGTCACCACGCAGCAA
chr16	89304909	89305029	1	-	CTTTGCACCCGAGGCTCAGGCCCATGGGGCCGATTGGAGAGCTTCACTCTTGGGTCCCACACACGTGGAGATGCACCCGGTGCATGTCCAGCCCTGGGCGAGGTATGGGGCTGCTCACCT
chr16	90031251	90031371	1	-	CCAGCTGGAAGTAGTTTCGTTCCTCCCGCTCGCGGTCCAGCTCCTCCCGGATGCGGCTGACATGCTCCTCCACCTGGCCAGGTGCAGTGGGTCAGGTGAGGCACTGAGCAGGGGCCCATG
chr16	1533587	1533707	1	+	CTGGCTGCCGCGGCAGGGCCGCTATTTGTTGCGGTTGGCTACGCCTTCCAGCTCACCAAAAACAGTCTCAAAAACAACCATTTCCTCTCTGCTGAGAGCCAGGGAAGGCGAGCTCTGCGC
chr16	28553845	28553965	1	+	GCCAAGTGAAAACTACATTTCCCACGGGGCAGCGGGTCACGTCACAGAGGAACGACTACGCATGCGTCAAGGTCCTCCGCGCGCGACTACGCTCATAAAAGGAAAAAAAGCGTGTGCG
chr16	28931896	28932016	1	+	CTGCCTGCCGACCCCCGCAGACACCCATGGTTGAGTGCCCTCCAGGCCCCTGCCTGCCCCCAGCATCCCCTGCGCGAAGCTGGGTGCCCCGGAGAGTCTGACCACCATGCCACCTCCTCGCC
chr16	3577348	3577468	1	-	GGCTGTTGAAATCAGACAGGAAGGAAGAATGAGGTGGAGCCCAGCACAGGAAGAGGTGAGGACCCGGAGCCACAGGGACAGCCGGTGGGCTCGGTGGGGCTGCAGAAGGTCGGGGCTGCA
chr16	67416436	67416556	1	-	GGACCGGCGCGGAGTGACGCAGCGCGGTTTGGCCGCTGTGGGGCGCCGTAGCCCGCGCCGTTGTCAGGGGAACGGGCCCAGCGCCGGACGAGGCCCAGCCAGTCTGGGTCTGGCCTGGCC
chr16	68448465	68448585	1	-	CCGGGTCACCATTGGCTCCGGCGGCGCGAGGGAGGCGGGGTCAGAGGAATGAAGCGCGGAGCTGTTCGCCGCTCCAGGTGCTGAGTCTGAGGGAGGCTCCGGACCCGAGAGCCGCGAGAG
chr16	85751055	85751175	1	-	CTGGCCCGTGCAATCCTGGCGCCCGCGGCCCGGCGGCTGCCGTCAGCGCCGCCCTCTAGGAGCGGGGCGGCGCGGCTGCCCGAGCGCCGGCCGGGCCGGGCCATGACCCCC
chr17	1469382	1469502	4	-	AGGAAGTGGAGTCAGGGAGTCGCAAGCATTGCTCAAAGGGTGTCCGCCTGGAGGGGCATTTACCCCGGTCTACCGTATTTACCGCGTTCTACCGTATTTACCCCGATCTACCGTATTTAC
chr17	55434213	55434333	3	+	TGGAGATAGGTTGCTGGAGTTTGACTATCGATTTAAAACTTCACTTCTCTGTTTTCCACTTTTCTCACCTGTAAAATGGGGGAGGCCGGGCACAGTGGCTCACACCTGTAATCCTCAACAC
chr17	22694539	22694659	2	+	CAGAACCAGTAGCCCAGGAAGCAGGTGCCGCTGGCCACCAGGAGCCCAAGTACCCTCCCCGCACCAGTCACACAGAGACCCGCTGCCAGGCCGGTCAGCGCAGGGCAGGGCCCCAGAAGC
chr17	31709595	31709715	2	+	AAAGAAGATAAAGAAACTCAAGAGCCCATCAGGTGTCCCGCCCCAGGTGCGACGGCCAGGGCCACATCACCGGGTAGTACGCGTCCCACTGTAGCGCCTCCGGGTGCCCCTTGGCAGCC
chr17	22694479	22694599	2	-	GGGGAGGGTACTTGGGCTCCTGGTGGCCAGCGGCACCTGCTTCCTGGGCTACTGGTTCTGGCGAGTGCTGGGGGCACTGGGGGGAGGCTTCGCAGGACTGTGGGGGCCGGGCGGGGAGG
chr17	31709535	31709655	2	-	CTGGCCGTCGCACCTGGGGGCGGGACACCTGATGGGCTCTTGAGTTTCTTTATCTTCTTTGCTCTGTGCTATCCTGATACCACTTTGCTCTCGGGCGACTTGAAAGGCCTAGCACCATCC
chr17	4641637	4641757	2	-	CCCACATTCCGACCCCAAGCGACCTCCGAGAGGGCGGGGTCTCAGGCTGGGTTATTTAGCTCGTCCACCCTTCTCCACCAGAAGGAGCGAAACATCTTTGAGCAAGATGGGTCTCTACCG
chr17	36090102	36090222	2	-	AATTTCCCTCCTCACCCCCAGATTCCATTTCCCCATCCGCCAGGGCTGCCTATAAAGAGGAGAGCTGGTTTCAGACTTCAGAAGGACACGGGCAGCAGACAGTGGTCAGTCCTTTCTTGG
chr17	493878	493998	1	+	GGTAGAGACCCCGGTCCCATATGCAGATTCCCCCAAACCGTTCAGCCACCACCCACCACAATAAGCTGCACCAAAGCTGTCCCAGAGTTCCTGTTCAGCCAATCAAT
chr17	1469442	1469562	1	+	AATGCCCCTCCAGGCGGACACCCTTGAGCAATGCTTGCGACTCCCTGACTCCACTTCCTCATCCTCACCCAGCCCCGCTCTCCGTACCTGCTGCTTCCACTCAGGGCTGATACTCCGGC
chr17	1469562	1469682	1	+	AGTATTTCCACACCATGTTCTTTATGCACAACTCCCGCAGAAGCTCTGAGGCCTAAGGGGAGGAGGAGTGAGGTCAGAGGTCCTGGACACCCTGGGCCCTTCCCTCTGAAGACATCGAACATA
chr17	3545388	3545508	1	+	GAGCCCAAATGGCCTTGCCCAGCCCTCCCGGGAGCCCTCGGAGATGGACACTGTCATTATCACCTACGTTTCACAGATGGTCTCCAGGGAGCTGCGAGTCAAGTGTGAAACTAAAGAAAA
chr17	3641848	3641968	1	+	GTAATGTTTGTAGTCACACTTTGTGGATAAGCAATTTCCGGGAAAGGCAGGTCTTTCAGACCCTGGAACCTGGTGTTTCTTAATACAGACGTCAGAACCCTGTCCCCACCCTGTAGGATC
chr17	4177655	4177775	1	+	AAATGGAGACAAGCCTTGGGAGTCTCTTTGCTTTGGCTAAAACAAGCACCCAGCATCCTGATGCCCCAGCTGCACTGCCGGCCTGACCCGAGCAGTCAAACAAAGGGTTGAGAAACGTGG
chr17	4177775	4177895	1	+	AGAAAGTTTCCTCTTACTGAGCTACGCTCTATACACAATGCGGGAGGGAGCCAACAGCAGGGCCCGGGCTTTGCTCCGCTGATGGAAAGCCAACAGAGCTCAATGAAATCAAAGCACACC
chr17	8889024	8889144	1	+	GCCTGCTCATGTGGGAGAGCTTTGGGGACGGGGTGGGAGCTGCATGGACCCAGGACCGAAAACACAGCTCAGGCAGTGTGGGGCATGGGTGTCACCAGGGCCCGGCTCCTTACCAAAGC
chr17	9105062	9105182	1	+	AGTCCAAGGACAGGTGTTTTGTTTGAGCGTCCATTTCAGAATGAAAGACGTGGTGTTAGCCCCTTTACCAGCAGGGACATTCCCAAAGAATGCTGCCCTCTGACACCTGGCCTTTAGG
chr17	14318297	14318417	1	+	CTGTCATTCTTCCGGGAGAGGCATGTCAGCAGGCGCAGCGGGAGAGGGGATGAGGGAATTGCCACGTGTCCACGGCTCTCTGGCTCAACCAGGCAGGGTTGGGGCAAACCTTCGCCCTCT
chr17	31512648	31512768	1	+	GCCCTGGCAAGTCAGACTGTGCCAGAGACGATGCCCGGTGCTGCCTCCTGAGGATACCACACTGTCCCTTCCCCAAAGGCCCCAAAAGAGCAGACAACAGCCTTTCTGTGCAAACCCTGG
chr17	32183966	32184086	1	+	TGAGCCACTGCGCCCAGCCCCTTTTGTTTTATAGCTAAGAAACACAGTAACTCCTTATTGAAATATCCAAAATTTAATATTTTGCCATAGACATTGAAAAACTAAATTTTTTTGAGATAT
chr17	50612409	50612529	1	+	TGCTGGGTCATCAGGCTGCCCCACGGGACGGCTAAGCCTCCAACACCAGCTCCACTCTCCTTGGCCACCTGTGGCGTCGACCTTCACTCACTCACCCTCTTTCCTTCCACCAGCCGGGGA
chr17	55270908	55271028	1	+	TGGAATTACAGGCGTGAGCCACCGCGCCCGGCCTTGGGTAAATCTTGTGTCTTACGCTTTATAGGATGCTTAGCAGCATCGCGGCCCCTACCTCCTAGTTGCAAGTAGGACCCCCAGTGC
chr17	76521040	76521160	1	+	ACAGAGTGAGACCCGGGGGATGATGTCTCCGTTCTTCCCCCAGGAAATAGTGAAATGGGACCTTGGTACTGGTGCGGTAGTAGGGGGCAGTTTCTGGACCACATGGCCAGGGCTGATCAG
chr17	77258576	77258696	1	+	CCCTCCCACAGGCGCCATATGGCTATTCCCCTCAGAGACGCACCAGGCCAGCCCCACTGCCCTCAGGACCAACCTCCAACTTCTCCTCGGCTTGGGATCTCCGGTTTCTCTTTGTCAA
chr17	79422457	79422577	1	+	CCGGCTGCTGCCCTCTGTGTTTCACCCAGGGCTTCCCGGCCCAGGCTGCCTCCTCTGTCCTCCCGCTCCCTACACACCCCTTCATTTGCGGAAGCCGCCAGGCAGACACTCGGTCTGGGC
chr17	79452913	79453033	1	+	ATCCCGCTCACGGCCCCCGGCCACCTGGACCACGTCTCCCCTCCAACACCCACTGAGACGTGCAGCTTGGAGCACATGGCTTCATCTCTCCAGGTCTCGGTTTACCCATCTGTGGAATG
chr17	79453033	79453153	1	+	GGGGTGATCGCAGGGCCTCCCTCAGGAGATTGCTTTGAGGATCAAATGAGCGAATTTCTGCAGCAGTCCTCAACCTGCAGTCACGGCAGTGTGTCCTTTCTGTAAACCCGGGATGAAATG
chr17	80236406	80236526	1	+	GGGTCCCCTCCATACACATGGGGACCATCGGGGAAACCGTAGGCAGCCGGCGGGGCAGTGATAGACTCACCTCCCTTGTTTCCCTGTGGCCGTCATGGCTGCTGTCCCGCGTCTTAGTGG
chr17	80707827	80707947	1	+	TCTCCTGCAACAGGCCGGTACAAGCAGAGCCTTGACCCAACTGTGGATGAAGTCAAGAAGCTCTGCACGTCCTTACGTCGCAACGCCAAGGAGGAGCGAGTCCTCTTTCACTACAATGG
chr17	80878929	80879049	1	+	TCGGAAGCCCCTTCCTCTAGGGGCCCGTCCCTCCTCTTCCCAGGCCCCGTCCCCCGCCTTGCCCTCTGAAAGTGGTCTTCAGCACCACCCGATAAGCGGTGACTTCTCATCTTAGAAG
chr17	80997647	80997767	1	+	CTGACTCACGTCCCACATAGGCCCTCGCTGCGGGGGCCGCGTCCTGGCCCCAGGCTCACATCCAGGCTCTGAGTCTGTATTCACTCCCCGACACAGGGGTTGTCCTCTCTGTGGGCCCCT
chr17	81071667	81071787	1	+	CGTCCGTCCCTGAGCCTCTGTTTGAGGGACTCACGTCCAGCTCCCGGCAGACTCAGCGCGGGGGTCGGATGCCTTCTCCGCACCATCCCGCACCGCCACGAGCTGCTGTGGCTCACATTC
chr17	81110059	81110179	1	+	CTCTTCCCACACTGAACTCTGGGGAATTGAGTGCAGGGCACAGCCCGGCTCAGCCTGCCCGCTGGTGGGAGCCCCTGGGAAGCTGCGGCGCTCCTTTATCTGATGTGGTTTAGTAAAAGC
chr17	82218666	82218786	1	+	AAGAGAGGACAGAGGCCCGGCCAGGGCTAGAGCATAAACCAGGCTGGTGCTGACCACGGCAGAAGGGCAGAAGGTACCCTCCGGCTGTGCGTGGAGAACGGGCAGCAGGGACGAGGGCCT
chr17	493818	493938	1	-	TTGGTGGGGTGGTGGCTGAACGGTTGGGGGAATCTGCATATGGGACCGGGGTCTCTACCTCAGCTTCTCCGTCAGTGTCAGTGCCGGGGCTGGATTCTCTCCAAGCCCCTCTGATTTCT
chr17	1469502	1469622	1	-	CCCCTTAGGCCTCAGAGCTTCTGCGGGAGTTGTGCATAAAGAACATGGTGTGGAAATACTGCCGGAGTATCAGCCCTGAGTGGAAGCAGCAGGTACGGAGAGCGGGGCTGGGTGAGGATG
chr17	3545328	3545448	1	-	ATAATGACAGTGTCCATCTCCGAGGGCTCCCGGCCAGGGCTGGGCAAGGCCATTTGGGCTCAGAGCTGGCCAGGGTGTGTGCTCAGCATGGGGGCACCCTCTGGGGCCAGGAGGCAGGACA
chr17	3641788	3641908	1	-	TCTGAAAGACCTGCCTTTCCCGGAAATTGCTTATCCACAAAGTGTGACTACAAACATTACTGATTGTTTAACAAACCTGGAAGAGATGATCACGTGACCATGTTTCCTCAGAGATGCAAG
chr17	3641908	3642028	1	-	ACACGCGCGCGCACACTCCCAGGCACACGCACATGCTCCAGCCTCAGTCTTACAAAGTCTGATCCTACAGGGTGGGGACAGGGTTCTGACGTCTGTATTAAGAAACACCAGGTTCCAGGG
chr17	4177715	4177835	1	-	CTGCTGTTGGCTCCCTCCCGCATTGTGTATAGAGCGTAGCTCAGTAAGAGGAAACTTTCTCCACGTTTCTGAACCCTTTGTTTGACTGCTGGGTCAGGCCGGCAGTCGAGCTGGGGCAT
chr17	8888964	8889084	1	-	TCTGGTCCTGGGTCCATGCAGCTCCCACCCCGTCCCCAAAGCTCTCCCACATGAGCAGGCTCTAAGCAGAGCAAGGGGGCAGTGCTAGGAGTCCTGGGCTGGCCCTGAGTCCTGCTGTCT
chr17	9105002	9105122	1	-	TAACACCACGTCTTTTCATTCTGAAATGGACGCTCAAAACAAAACACCTGTCCTTGGACTGCCGGGTCTCTCACGGGCCCCACATGGCCAGCCAGCACGCTGCTCCCCACGGTGAGACCCAGCCA
chr17	14318237	14318357	1	-	AATTCCCTCATCCCCTCTCCCGCTGCGCCTGCTGACATGCCTCTCCCGGAAGAATGACAGGGATCCTCTCTCAGCAGGACTGGTGAAGGGAGAGGAGAGGTGGCAGGGCCCAGCCTGCAG
chr17	31512588	31512708	1	-	GTGGTATCCTCAGGAGGCAGCACCGGGCATCGTCTCTGGCACAGTCTGACTTGCCAGGGCTCTGTCCCTCAAGACCCAGAGCCAGCCCTGAGCTCACAGCTCCCTGTACCCTGGGACACA
chr17	50612349	50612469	1	-	GGAGAGTGGAGCTGGTGTTGGAGGCTTAGCCGTCCCGTGGGGCAGCCTGATGACCCAGCAGCCCCGGTCCTCCCTCATCTGGGAAGCCGGGGTGACCCAGGCTTCTGGTCAGGCCCA
chr17	55434153	55434273	1	-	AGTGGAAAACAGAGAAGTGAAGTTTTAAATCGATAGTCAAACTCCAGCAACCTATCTCCAGAGTCTATGCTCTTAACCACTATACTAAAACATGTTTCCCCGGGGCAGGGCAAGTCAAGG

chr17	77258516	77258636	1 -	GCAGTGGGGCTGGCCTGGTGCGTCTCTGAGGGGAATAGCCATATGGCGCCTGTGGGAGGGGCCCCAGGATTGGGTCCTAGTCTCTCCAGTGTGGACACAGAGCCACGAGGCAGAAAGTAC
chr17	79422517	79422637	1 -	CGACCCAGCATCTGCCCAGCCTGGCCCCGCCCAGCCTGAGGCTGCTGGACCCTGGGCCTTGCCCAGACCGAGTGTCTGCCTGGCGGCTTCCGCAAATGAAGGGGTGTGTAGGGAGCGGGA
chr17	79452973	79453093	1 -	CAGAAATTCGCTCATTTGATCCTCAAAGCAATCTCCTGAGGGAGGCCCTGCGATCACCCCCATTCCACAGATGGGTAAACCGAGACCTGGAGAGATGAAGCCATGTGCTCCAAGCTGCAC
chr17	80236346	80236466	1 -	CACTGCCCCGCCGGCTGCCTACGGTTTCCCCGATGGTCCCCATGTGTATGGAGGGGACCCCCTAGCAGAGCCCAGGGGTTTCCCTGAGTTCAGGGGGCAATGCTGGGAGGAAGTCTGAGG
chr17	80707767	80707887	1 -	TTCTTGACTTCATCCACAGTTGGGTCAAGGCTCTGCTTGTACCGGGCCTGTTGCAGGAGAAGAAATGAAGAAATTTACCACGGACTCCAGGGAATGCTTGGAACTCATCCCCTACCCTTT
chr17	80707887	80708007	1 -	ACACCCACCTTGTTGAAGACCCAGACCTCCCCGTTGACTGTGGGCCGGGGCACCCCGTGGCCATTGTAGTGAAAGAGGACTCGCTCCTCCTTGGCGTTGCGACGTAAGGACGTGCAGAGC
chr17	80878989	80879109	1 -	CACAAGCAGGGCTGCTCCGGGGCGCGCACAGCCGAAACGCAGAACCTGACCCAAGCCAGGCTTCTAAGATGAGAAGTCACCGCTTATCGGGTGGTGCTGAAGACCACTTTCAGAGGGCAA
chr17	80997707	80997827	1 -	CAGCAGGGCTGGGGCAGAGGCCGGCTCTGGGGGCACCATGAGAATTTGGCGGACTGAGGCAGGGGCCCACAGAGAGGACAACCCCTGTGTCGGGGAGTGAATACAGACTCAGAGCCTGGA
chr17	81071727	81071847	1 -	CTACTTGGCGTGGGAACTGCTCCAATTCTCGGCTGCCTCCTGGACAGAGCTCGGATGGCAGAATGTGAGCCACAGCAGCTCGTGGCGGTGCGGGATGGTGCGGAGAAGGCATCCGACCCC
chr17	81110119	81110239	1 -	AGCTGCTTCCCACACAAACACTACCAGCCACGTCCCAGGCCACGGGGAGGTGTGTGGGAGGCTTTTACTAAACCACATCAGATAAAGGAGCGCCGCAGCTTCCCAGGGGCTCCCACCAGC
chr17	82218726	82218846	1 -	TGGAACAGATGCAGGTGAGTGACGGGCTTCGGGAACAGCCAGTGCCACCAGCCTGGCCCCAGGCCCTCGTCCCTGCTGCCCGTTCTCCACGCACAGCCGGAGGGTACCTTCTGCCCTTCT
chr17	2030073	2030193	1 +	CCCGCCCCCGCTGGCCGATCGGCGATCGATCGCAATGTCTGCGCTCTCCGCGTTCTTCCAGCGCTGTCTTTTTAGTACCACATGCGCAGGCAGGTGATGGCGGCGCTGGTCGTATCCGGG
chr17	7435355	7435475	1 +	GAGCTCTGACTGGCGACCCGACCCGGCGGAAACCACCTCGACAGCCTCCAGAAAGGGGCGTGGCTGAAAATGTAGGGGCGTGGCCACGTGGGCATCAGGAAGAAGTAACCTGTTGAATCT
chr17	7572746	7572866	1 +	GGCCGGGGCGGCCAAACCAATGCGATGGCCGGGGCGGAGTCGGGCGCTCTATAAGTTGTCGATAGGCGGGCACTCCGCCCTAGTTTCTAAGGATCATGTCTGCGAGCCAGGATTCCCGGT
chr17	34255205	34255325	1 +	ATCCCTCCTCCTGCTTGACTCCGCCCTCTCTCCCTCTGCCCGCTTTCAATAAGAGGCAGAGACAGCAGCCAGAGGAACCGAGAGGCTGAGACTAACCCAGAAACATCCAATTCTCAAACT
chr17	39962924	39963044	1 +	GGTGGGGTCACTAGGGCAGGCGGGGTCCCCGGAAGCCTCTGTCCCTGCATAAAGCAGCCTGTCCTGGCAAGGGATGGTCATCCTCTCAACCTACAGACCCAGTGAGCCCTAGGCCCTCAC
chr17	35119705	35119825	1 -	TCTGGGCGCGGGAATCCCGGCGGATCCCGGGCGGGCGGATGACCCCCAGCCCTACCCTTGGTGCCGCCTCCTCCTCTCTCCTTTCTCCTCCGGCAGCCAGCGCGCCTGTGTCCTCTCTAG
chr17	41801887	41802007	1 -	AGTGGTTCCAGGGCCCTGACCAGTAGGTGCTCAATAAATGTTTGTTGTTGAATGAGTCATAGTACCCGTGGTCGTCTCCCTGGAGCTCAGTTGTAAGGGTACAGGTCCTTCCCTCCCTCT
chr17	63932290	63932410	1 -	CTCCCCTGGGTCCCAATTTGCATGGCAGGAAGGGGCCTGGTGAGGAAGAGGCGGGGAGGGGACAGGCTGCAGCCGGTGCAGTTACACGTTTTCCTCCAAGGAGCCTCGGACGTTGTCACG
chr18	514482	514602	21 -	GTCCGAGGAGGGGTCCGGAGGTCTGGCCGAGGTCCGAGGAGGGGTCTGGAGGTCTGGCCGAGGTCCGAGGAGGGTCCGGAGGTCTGAAAGCGCAGACTGCAGGGCAGACTACTGCAGGAT
chr18	52665957	52666077	12 +	ATTCTCTAATATGATTGAAAGCATGGTGAAGTATCCATATAAGGAAAGTAAGAAATTCGGCCGGGTGCCGTGACTCATGCCTGTACTTTGAGAGACCTAGGCAGGCAGATCACCAGGTCA
chr18	46149833	46149953	9 +	AGGCTGGTCTCAAATTCCTGGGCTCAAGCGATCCACCCTCCTTGACCTCTCACAGCACCCGGCCCTAAATGAGCATTTATTGAGCAATATCTATTCAACAACAAGTTCTGTACTTGGGCT
chr18	12746924	12747044	4 +	CCGTCTCAAAAAAACAAAACAAAACAAAAAAACAAAAAACAAAAAAAACTGGGAAGATTGTTACTTTACAGGACATGCCCGGCATTCACGTGTGTGGTGGGAAGGGAGAAGTTGTGGAAA
chr18	29179139	29179259	2 +	GTGCTGGGATTATGGGCATGAGCTACGGCGCCCGGCCAGCAATCCTCTTCTTTATTTAGTGTTTGTTGAGTCTCTAAGTTGGGCTCAGTGTTTCTCTTCTATGCACCCATTGCCCTATGA
chr18	514422	514542	1 +	CTCTCTCCCTGGAGGTTCTTCTCTTACTTCCCACCCTCTTTCCTGTTCGTCAGCGCCTAGATCCTGCAGTAGTCTGCCCTGCAGTCTGCGCTTTCAGACCTCCGGACCCTCCTCGGACCT
chr18	8478072	8478192	1 +	GGAGGAGATCCTCAGAGCAGCAGGCCTCCATCCTGGCTGTGCATCAGAGCTCCCGGGGAGCTCTGAAAAACTCTAGGCGTGCCCAACTCCAGCGATTCCGATTTAATTAGACTAGGGTGG
chr18	10127935	10128055	1 +	CCGGACCATGGCAATATGATCATGCACAGCCTCTTATTACATATGGACCTCCCAGGGAGGAAATGACATGTCATGAATATCGAGTGAGTGTGTTTGCACGAGCAATCCCGAATTCCACAG
chr18	13404344	13404464	1 +	AGAGTGGAGTGCCGCGACGGTGTGGCCGCAGCCTGGCTGTGCCTTCACGACGCAGCTGCAATCAGAGGAGCTGTGGGACGCTGTCCCACGTGGACACAGCCCACTCACTGGGTGCTGCTC
chr18	37310864	37310984	1 +	CCAAGGAAGTGGGGGTCTCTCTCCTCCACGCTCACATAGTGGCCGGGCCAGACGGTAGTGACATGGGAGTGGCGATGGGATGGGACACGAGAAGGCCGTGGTGCCTTCTCTCTGTCATTC
chr18	48113843	48113963	1 +	AGGCTACACACTAGTGCACAAGGTGGCTGTGAAAACACCGCTGCACCAGGAGCCTGGGGCCGGCTGTAAAATGCTGGCCAAATCCCCATTCACTCTGTGTCTCCATCTACTTGTCTGAAA
chr18	76412536	76412656	1 +	CCTTAGGAAGACAATGGCCATGGAGACTGACCTCATTTCTTCCTCAAGGACTGCAATGCACTGGGTAATAGAGGAAGGGAGGGGAGGCCGGAGGATAAGGACACACCGTGCCTCCTGATG
chr18	79320199	79320319	1 +	TCGGTGAGCACAGTGCACCTGGACCTGTGTGGGGAACTGAGGTTCTGGGAGGGAAGGAGCCCGGACCTGGGAGTGTTGGTCCCTAGAACGCAGCGGAGGCGCAGTGCGAGTACGTCCTCT
chr18	79404153	79404273	1 +	TGCGTCGGACCAGGGGGAATATTCCAGTACCTCTGAGGAACGATGTCCCAGGTTGGGCCCCGGGCTGGACGAAGGACCCTTATTAAGGCGTTGGCGTGCTTATTTATGGAACATTAAATA
chr18	8478132	8478252	1 -	CAGCCCGGACTGCTTACTCCAATCACCTGGAGGGCTTTAGAAGCCAGCAAGGTCCCAACTCCACCCTAGTCTAATTAAATCGGAATCGCTGGAGTTGGGCACGCCTAGAGTTTTTCAGAG
chr18	10127995	10128115	1 -	ATGAGGCTCAGACCCTCACCCTGAGTAACATGAGCAGCCACAGAGTGGGATCTGGCTGGCCTGTGGAATTCGGGATTGCTCGTGCAAACACACTCACTCGATATTCATGACATGTCATTT
chr18	12746984	12747104	1 -	CCTGGCTGCCCCCATTCACCCTCTCAGGGATGTCATCATTGTGAATGGAGTCCACCTTTCTTTCCACAACTTCTCCCTTCCCACCACACACGTGAATGCCGGGCATGTCCTGTAAAGTAA
chr18	13404404	13404524	1 -	TGCCCGGCCGCATCTTAATATAAATTTTTAACGACAATAAAAGTGCAGCGCCCAGCACAGGAGCAGCACCCAGTGAGTGGGCTGTGTCCACGTGGGACAGCGTCCCACAGCTCCTCTGAT
chr18	37310804	37310924	1 -	CACTACCGTCTGGCCCGGCCACTATGTGAGCGTGGAGGAGAGAGACCCCCACTTCCTTGGGAGATGGGCGAGAGGAGAGAAAGTTCCCAGGCAATCCTCCCAGGGCTAGGTGGTGTCCTC
chr18	48113783	48113903	1 -	GCCCCAGGCTCCTGGTGCAGCGGTGTTTTCACAGCCACCTTGTGCACTAGTGTGTAGCCTGCTTCCTGGAGTGCACCCTGCCGATGGTGGGACAGGCGTACGCCTCGCACAGAGAGCAAG
chr18	52665897	52666017	1 -	CCGAATTTCTTACTTTCCTTATATGGATACTTCACCATGCTTTCAATCATATTAGAGAATTTGATATAAGTGAAGTCTAGAGACATTTTAAAATTGATGGTGAATTAATTTGAGCAAGTG
chr18	76412596	76412716	1 -	CTGTTGGTCACTTTGTCACGTGGGGCCACATCTTGGCAACGACTTGACTTCCTGCTTCCACATCAGGAGGCACGGTGTGTCCTTATCCTCCGGCCTCCCCTCCCTTCCTCTATTACCCAG
chr18	79320259	79320379	1 -	TCCAAAAGGCCCTGCTGACCACCTGATCAGAGTGCTGTGTGCCCCTCCCCTTCCCCTGGCAGAGGACGTACTCGCACTGCGCCTCCGCTGCGTTCTAGGGACCAACACTCCCAGGTCCGG
chr18	79404213	79404333	1 -	GCCAGCGAGAAAGATTTACAAAGGCAAATAGGATGGCCTCGTCACAGCGCAAACAAACGGTATTTAATGTTCCATAAATAAGCACGCCAACGCCTTAATAAGGGTCCTTCGTCCAGCCCG
chr18	70288965	70289085	1 +	GCGGCCGCGCGCCCCTCCTGGAGGAGGAGGAGGAAGGAGGCGGGAGGAGGAGTTGCCGAGAGGAGAAGGCGAGCGCGGCAGTCGCGCCGGCGCTGGGCGAGGAAGCGGAGCCGGGCCGCC
chr18	50287651	50287771	1 -	CTGGTTTGCAGCGGAGACGACGCATGGGGCCTGCGCAATAGGAGTACGCTGCCTGGGAGGCGTGACTAGAAGCGGAAGTAGTTGTGGGCGCCTTTGCAACCGCCTGGGACGCCGCCGAGT
chr19	5277848	5277968	35 -	CCAGGAACTTCCGGAAGCCACTGGGCAGCATGTGCTTTGTTTTTTGTTGCTCCCGTAACCACTGTTGGGCATCAAGATCTGGCCCTTGAACGTTCTGCGAACCCTGTTGTCAATACCTCT
chr19	5277788	5277908	32 +	CGTTCATCCGGCACCAGTCAGACCAATATGTCAAAATTAAGCGTTAACTGGGGGAAACCCAGAGGTATTGACAACAGGGTTCGCAGAACGTTCAAGGGCCAGATCTTGATGCCCAACAGT
chr19	58102095	58102215	7 -	AATTGCTGGGATTACAGGCGTGAACCACTGCGCCCGGCTGAGTATATGGGGTTTTTTAGTAAGCTGCCTAAACAGGGAAAAGTCACCGTCCTTATGGAGCTTCTACTCTAGCTTTTATAC
chr19	39737957	39738077	7 -	GAGGGGCTTGGAATCAGGAATAAAGCCAGAGGCAGGGCTGATAGGGGCCATTTAAATTCTGCAGCTCAGAGATTCACACAGAAGTCTGGACACAATTCAGAAGAGCCACCCAGAAGGAGA
chr19	38184448	38184568	5 -	AGGCTTCCTGGGCTCTGATCCAGGCTGTGTTCCTCACCAGCCCTGTGACTCTGGGCCTCAGCTGCCTCATCTGTAAAAGGGGGAGGACAGGGGCCGGGCGCAGTGGCTCACGCCTGTAAT
chr19	51458413	51458533	5 -	AAGTTCCTCCTCTGAGGAGGTCACTTTTCTGACTTCACCCCCAACCTCCTGCGGGACCTCCCCTAAGTCTTGAGACCTCAGTTTCTGAGAGAAGAACCCTGAGGAACAGACGTTCCCTGG
chr19	57916551	57916671	3 -	GGTCAGAGCCAATGAGCACTCGGAAAGAAGGCATTTCCACGTGTGCACGTAACGTAAGGCTGAGACTTCCGGGGTCTCTAGTAGCGGCTGTGTATCGGTGACGCGGGTGTTTCCCCAGTT
chr19	47726124	47726244	2 +	GCTGGAGGAGCAGGACCTCTTCCGCGACATCCAGGGCCTGCCCCGGCACGCAGCCTTGCGCAAGCTCAACGACCTGGTGAAGAGGGCCCGGCTGGTGCGAGTGAGTAGTCCTGAGGGCTG
chr19	48563242	48563362	2 +	ACAGCTACTACAATGCAAATCATATGATATCCACTCTGTGACCTAGCAATTCTGTTCCTAGTTATTTGCCCAAGAGAAATGAGAACGCCGGTTCCCACAAAGACAGGAACAACTGTGGCA
chr19	660354	660474	1 +	AACGGCCCAGCTGCCTGGGAGAAGCCCTCGTGGGCAGGCACACAGCCCATGGCAGCCAGTCCCCCCTGCGTCAGAGGCAGGCAGGAGCTTCCCGACAGCCAGCCCAGGTGTCTCAGCAGC
chr19	667028	667148	1 +	GGACCTCGACAGGTGTGGGCTTGGTTCCGTGAGCTCTCTTAGCCCCTTTTTCAATTCAGGATCCCGTCCCCGTGAACCCTGGGGGCCTCGGCAAACATGAGACGAGAGGACTCCTAAAGG
chr19	827893	828013	1 +	CTCGAGGGCCGGTGAGTGCCTCTCTGTGCCGGTGGTCCCCCATCTGTGCTAGGGCCCGGCTGCCAGGGCAGAACTCAGACTTAAAGCACAGAGAAGGCAAGCGGCTTGGCCTGGGTCACA
chr19	828013	828133	1 +	CAGCCAGCCCGGCCTGGACGATCCCGCGAAAGGCGTGAGGGCGGACGGTGTGCGGGACTCAGGGGCCCCCTGTCCTCTTAGGGAGTGGGACGATGGGGGAGGGTGGGTCCCCCCGCAGCC
chr19	831349	831469	1 +	TAACAGGCATGAGCCACCGTGCCTGGCTGAGAAACAGTAGCTATCAAACGCCGGCTGTGAGCCACGTCTGTGCTGGGGGTTGGGGACCCAGCAGGCATGGTAGAGCCGGTCACTGAGGGA
chr19	855877	855997	1 +	GGACTTCCCAACCCTGACAGGCGGCGGGCAGGTGGGCAGGGCCTCGCAGTCCAGCTTCCCCACCTTGTCTGCCTCCACAGGGGGACTCCGGCAGCCCCTTGGTCTGCAACGGGCTAATCC
chr19	1012021	1012141	1 +	CCCCACCCGCGCCCTCGCACCCTCGGCCCCGGGGCATGCCTCACCCTTGTTCTCCTCGTTCTCGGCCAGGCCCTTCACGCTGGACATGAGGATGTCATCGTAGCCCAGGAACTCATCCAG
chr19	1154589	1154709	1 +	ACTCCTTTGTGCTGCCCACAGCGCCTTTCCTGGCCTCCCCGGCCCCAACTACAACGATTAAGGTGGGCCCGACAGGGCTGCCCAGGTCACAGGGCAGCCGTAGGACCAGGCACCCAGACT
chr19	1882197	1882317	1 +	CCCATCTCTGCCACCCTATGGGTGACGGGCCGCTGAGGCAAGGACAGAGCTCGAACTGAAGGGACCCACGAGGGACCCGAACAGGCCCCGCTACGTGAGCGTGCACAGGCGCCGGGTCCC
chr19	2634481	2634601	1 +	TCCTGGGCTACAGATGTGGAGGCTGCTGGGTACAGGGAGAGGTTTCTGAGTCCTGGAGACTGTGGCAGAGCCCCTGATTTCGGCACAGCGCCCCGTAATTACTTGCGGGCTGCACACACG
chr19	3189565	3189685	1 +	AGTCCTGTCACGCCAACTGGTGACTTCTCTCAGGATGCCCGGTGCCCTCCATGGCGTCCACCACAAGTGGTCTCAGCCCATTCAGACGCGGGTCTGAGGGAGTTGGTGCTGGTTTCGCCT
chr19	3467900	3468020	1 +	ACATACATCTCTCAATCCAGCTTCCTCCGCATCCTCCCATCTTGCCCCATTTCTGCCACGTCAGACACTTCCTGAGAGTCTCACCTTCAAAATGACACCGCTGCCCATCCATTGCTCAAT
chr19	4735561	4735681	1 +	AAAAAAAATTAAATATTTATTCCCTCAGCATCATATCTACAATAATCCCATTTATTCTCAATGCCACAGTGGCAATTCTTCGATGGATCGGCCAGGGAGATTTGAAGTACCCGGGAAGCC
chr19	5189197	5189317	1 +	TCCACAAGTTTCCCCCATCTACGTTCATCTTCTGCACGGGCTAATTTTATTAAAGTTCCTCAAAGAGAGAATTGTAAATTCATTAGCACGCATGTTAGACCAGACCTTCCTTTACGCCGG
chr19	5332784	5332904	1 +	GGTTTTCTGTTGATCCTGATGTTGGCAGCCCAGCTCTGGGGGCTTTCAGAGAACTCTGACCGCACATCTAAAAAATGCAATTTGTTAGACGCGGTGGCTCACGCCTGTAATCCCGGCACT
chr19	6057712	6057832	1 +	CAATTAATTTCCTCCCTCTGAACAAGAAGGAACAAGCCCGGAGTGCTCTCAGGAGTACCAGTTGCTTCAAAGCCCAGATTCTGTCCTGGTAGCTTGTCTTAACACTCCCAGTGTCATTAG
chr19	8111727	8111847	1 +	CTTGGGCTGCACCGGTGCTCCTGGGAGACGCATTCATCCAGGTCTGCAGGAGATGGAGCCCAGACCCCCCACCCCATGGTGTGTGCATTGGGTGGGCGCAGAAGGGAGAAAGACCCATCA
chr19	11239416	11239536	1 +	CCCAATGCCCCCCACCCACACCTGGCCCTGAGCCCCAGGAAGCGTGATCCCGGCGTGGCCTAGCCGGACATTCGCCTGATGCAACTATCGCACCACTGCCAGGCCCTTGTGCAATGCGGG
chr19	14554022	14554142	1 +	TTGAGCTCAACAGGTGGGCTGTGCGGCACCACATCAGCTCTGCAAGGGGGCCCTGGAGGCCCATGTGTGGTGGGGTATGGCCTGGCTTTCAACATGCACGCGTGGTCTTCTGGGCTCTGG
chr19	17846080	17846200	1 +	GTGCTGGGATTACCGGCGTGAGAAACTGCGCCTGGCCTAATGAGGTTTAAGACAATCAGAGGACTAGGACCCCTAGGACTCAGCTTTCGCAGCTGTGAAATGGGCTGACTCCCCAGCATC
chr19	33392313	33392433	1 +	GCTCTCCACGTAGAGCCTCAGCAGCCCACGGGTGCGCCCGTCCCATCCCCGGACTCTGTGGAATCCCAGCATCAGCCTCTCCTCATGGTAGCTTCCACTGCTGGACTTGGCTTGAGCACC
chr19	35785155	35785275	1 +	CAGACGGCCTCCTGTTTCTCCCCCAAACCGCAGGAGGAAAGGGGAGAGAGGGGGAGAAGCAGCGGAAGCCAGGGGGCAGCAGCTGGAAGACGTTCTTTGCACTGGGCCGGGGCCCCAGTGT
chr19	40733120	40733240	1 +	TCTACATAATTTCCTTTGTCACATCCTCTGTGTGCTCAGGACCTATCTGGAAGAGGAGCTAGTGAAGGCACGGGAACGTCCCCGTCCCCGGAAGGACATGTATGAGAAGATGGTGGCTGT
chr19	45336722	45336842	1 +	TGCTGTGTGATGAGTGTGATCATCCCCATTTTACTAGACGAGGAGACAGAGGCTCAGCCAGAGATCATTGTTCCCCCGGTTTACATGGAACAGAAATGGCAGGGCCAGGATTTAAACCTA
chr19	48061961	48062081	1 +	CCACCCAGGACCGGCCCCAAAGCCCTTCTCGATTACCTCGAAAGGATCTCCGGCACTGAAGTCGAAGGAGAGGATGAGGTGAACCTCCCGCGTCGGGGGCAGCACGAGTGGGAAGGGAGT
chr19	48573255	48573375	1 +	TGGCCACCCACCCGGAGGAGCTCTGTCTGCTGTCCCTGTCCCTGGCCTCTCGCTGGCTTAATTGTCCCTTTCATTCCTCCACTCAAATCGAGCGATATCAGCACGCCAGGCCCTGGACGT
chr19	48573375	48573495	1 +	GTTTTGTGGGAACAAACAGGCCTGTTTGTCTACGTCCCAGGCGTAGAGAAGTTCGTCCCGGGGCCAGATTTGTTTTACAAGGTGGACAGCAGGCACAGGGTACCTGTTTTAGGAATGCGA
chr19	50666829	50666949	1 +	ACCCCCTGCGCTGCCACCACCTTCGGCAGATAGGCTGCTCAGCGTGGAGGCGCTGCTGATGGTCTCCAGTGGGTGGTCACTGCTGCTCCGACTGTCCACCTCCTCGATGCCAGAATCCGT
chr19	51754304	51754424	1 +	TTAGGGTTGACCGGAATGGGAGTATTCCTGCCTATGCTGCAAAAGTCCCTGACTCTTCTGGTAACTGAAACATGAGAAATGGCCTCGGCGAGCAGCACAGCCTCCCAGTAAAGCACTGGA
chr19	53984574	53984694	1 +	AGTGCTAACAGTTCTGGGATGCTGATGTACAAGGTGGGGCTGGGAGATGAGGCCGGGAAAGTAGCCACAAGCTAGAGTGTAAAGGTACCAGGGTGGCCGGGCGCGGTGGCTCATGCCTGT
chr19	55372482	55372602	1 +	GGAGACCCGGGATTCACCACAGAGCAAGCGAGGGGCAGAGGTACCAAGCCATGTCCCCGAGAGCCCCCAGACCTAGATGGCAGGGAAGGACAGGATGGGACTGAGAGCGCGGAGGTGGTG
chr19	660294	660414	1 -	ACTGGCTGCCATGGGCTGTGTGCCTGCCCACGAGGGCTTCTCCCAGGCAGCTGGGCCGTTCCGGGCCTCCTTTGCTGTCCTGGGCTCTGGGATCAGGCTGAGGCCCCGCGCAGCTGGGTC
chr19	660414	660534	1 -	AACGGGGCGTCTCTGCCGCTGGGGAGCTTGCCCGGCGGCTGAGTCAGGGGCGGCACTGCTGCTGCTGAGACACCTGGGCTGGCTGTCGGGAAGCTCCTGCCTGCCTCTGACGCAGGGGGG
chr19	667088	667208	1 -	GGACGTGAGAATGAGCTGTCAACACACCTCTCTGCCCCGGAGGGAGTGGCGCGTGTCATTCCTTTAGGAGTCCTCTCGTCTCATGTTTGCCGAGGCCCCCAGGGTTCACGGGGACGGGAT
chr19	827953	828073	1 -	GAGTCCCGCACACCGTCCGCCCTCACGCCTTTCGCGGGATCGTCCAGGCCGGGCTGGCTGTGTGACCCAGGCCAAGCCGCTTGCCTTCTCTGTGCTTTAAGTCTGAGTTCTGCCCTGGCA
chr19	831409	831529	1 -	AGCTTCCTGGCACCTCCAGGCTGGGCCAGGTGCCCCTCCCCTGGCAATCACACGCCTGAGTCCCTCAGTGACCGGCTCTACCATGCCTGCTGGGTCCCCAACCCCCAGCACAGACGTGGC
chr19	855937	856057	1 -	CAAAGGCATCGGGGTAGAGCCCTGAGGCGCAGCCTCCCCGGACGAAGGAGGCAATTCCGTGGATTAGCCCGTTGCAGACCAAGGGGCTGCCGGAGTCCCCCTGTGGAGGCAGACAAGGTG
chr19	1012081	1012201	1 -	CACCCACCCGCAGACCCCACGCGGGACCAGTGCTTCGGGGACCGCTTCAGCCGCCTGCTGCTGGATGAGTTCCTGGGCTACGATGACATCCTCATGTCCAGCGTGAAGGGCCTGGCCGAG
chr19	1154649	1154769	1 -	TCACACCGGCTGCTGACAAAGCCAGATGTGGGGGAGTCAGCCTGCAGCTCCACTGCTCACAGTCTGGGTGCCTGGTCCTACGGCTGCCCTGTGACCTGGGCAGCCCTGTCGGGCCCACCT
chr19	1882257	1882377	1 -	CTTTGTTTCTAGAGCCTTTGTTTGTTGTATTTCCTCTGTCTCCAGACATCGCAGGCCGGTGGGACCCGGCGCCTGTGCACGCTCACGTAGCGGGGCCTGTTCGGGTCCCTCGTGGGTCCC
chr19	2634541	2634661	1 -	TGAAAACGCTCTGCTCCCGGAAGGTCACAGCTCATTGCTACCACCCTCCCCGAGAGAAAACGTGTGTGCAGCCCGCAAGTAATTACGGGGCGCTGTGCCGAAATCAGGGGCTCTGCCACA
chr19	3189625	3189745	1 -	CCTCGAGGGCCAGGGTCGGGCCGGGTGGCCACAAGCTAGTGTGGACACGGCCCTCTGCGGAGGCGAAACCAGCACCAACTCCCTCAGACCCGCGTCTGAATGGGCTGAGACCACTTGTGG
chr19	3467960	3468080	1 -	CCTCCTCACCTTGCCCTGCCGGGAGGTCAAGGGTGGTGGACTGACCCCACACTCTGTACCATTGAGCAATGGATGGGCAGCGGTGTCATTTTGAAGGTGAGACTCTCAGGAAGTGTCTGA
chr19	4735621	4735741	1 -	TGCAGACAACAGGCATCGTTTCATAAATCAATGAAAATTACAAAGATGTAGTACAATGAGGGCTTCCCGGGTACTTCAAATCTCCCTGGCCGATCCATCGAAGAATTGCCACTGTGGCAT
chr19	5189257	5189377	1 -	TGTTTTAGCATCTTCTGTTTCATTATCATCGGGCTCAGCTGACTCCTAATCTTTTTCTACCCGGCGTAAAGGAAGGTCTGGTCTAACATGCGTGCTAATGAATTTACAATTCTCTCTTTG
chr19	6057652	6057772	1 -	TGGTACTCCTGAGAGCACTCCGGGCTTGTTCCTTCTTGTTCAGAGGGAGGAAATTAATTGCTTTCTTAGGGCAGATGAACTCTGGTACCATCTGGAGGCCAGCGAGTACCAGGAGAGGAG
chr19	8111667	8111787	1 -	GGCTCCATCTCCTGCAGACCTGGATGAATGCGTCTCCCAGGAGCACCGGTGCAGCCCAAGAGGTGACTGTCTCAATGTCCCTGGCTCCTACCGCTGCACCTGCCGCCAGGGCTTTGCCGG
chr19	11239476	11239596	1 -	CCTTTTATGCCTCATACCCCCACTGATCCCCAGTCAATCGTTAACTGGCCGACCTGGTGCCCCGCATTGCACAAGGGCCTGGCAGTGGTGCGATAGTTGCATCAGGCGAATGTCCGGCTA
chr19	14554082	14554202	1 -	GGAGCAGGAGCCATTAGCTCCGTTTCACAGATGAAGAGGCCAAGATCTAAGCAGTAAATCCCAGAGCCCAGAAGACCACGCGTGCATGTTGAAAGCCAGGCCATACCCCACCACACATGG
chr19	33392253	33392373	1 -	CACAGAGTCCGGGGATGGGACGGGCGCACCCGTGGGCTGCTGAGGCTCTACGTGGAGAGCTCTCTAAGGGCCTCCTTCCTAGCGGCCATGCTCCAGAGCCCCACAGAGCCTGTGTGGCCC
chr19	35785095	35785215	1 -	TGCTTCTCCCCTCTCTCCCCTTTCCTCCTGCGGTTTGGGGGAGAAACAGGAGGCCGTCTGAGGAACCAGGCCTCCACCTGCCCCTCGCCACCCCCAGCATCCCACTCACCTTTCCGCAGG
chr19	40733180	40733300	1 -	TAGCGGGGCTTGGTGACTGCACCCTGGGCATGCTCCTCAGGGGTAGGGGCCCCAGGGTCCACAGCCACCATCTTCTCATACATGTCCTTCCGGGGACGGGGACGTTCCCGTGCCTTCACT
chr19	45336662	45336782	1 -	TGGCTGAGCCTCTGTCTCCTCGTCTAGTAAAATGGGGATGATCACACTCATCACACAGCATTGAGGTGAGACTTAAATGAGATAAAGATTGAAAGAAGAAGAAAGTGTTAACTAAGGAAA
chr19	45611757	45611877	1 -	AACAAAAAAACCCACACACACGAAAACGCATAGGTTATCTTTTAGCCCTCTAAATTGAGCATTCATGCCTAAAAAAATAAGGATAATTCTGGCCAGGCCCGGTGGCTCACGCCTGTAATC
chr19	47726184	47726304	1 -	TCAGGGACTCACAGCACTGGTAGGAGAGGACCGAGGAAACCTCCTCCAAGAATGCGCGCCCAGCCCTCAGGACTACTCACTCGCACCAGCCGGGCCCTCTTCACCAGGTCGTTGAGCTTG
chr19	48062021	48062141	1 -	GACAAGATAATGAGCAGCCGGAAGCACCTCCACCTGGTGGATGCTGGTTTAGCCATCAACACTCCCTTCCCACTCGTGCTGCCCCCGACGCGGGAGGTTCACCTCATCCTCTCCTTCGAC
chr19	48563302	48563422	1 -	TCCAGTCCTCTGTTAATGGACACCTCGGCGGTTTCCAGGTCAGGCTATTACTCCCAAAGCTGCCACAGTTGTTCCTGTCTTTGTGGGAACCGGCGTTCTCATTTCTCTTGGGCAAATAAC
chr19	48573315	48573435	1 -	CGGGACGAACTTCTCTACGCCTGGGACGTAGACAAACAGGCCTGTTTGTTCCCACAAAACACGTCCAGGGCCTGGCGTGCTGATATCGCTCGATTTGAGTGGAGGAATGAAAGGGACAAT
chr19	48573435	48573555	1 -	GCCTGAGCGCAGAGCCAGGACCCCCCTGTCCCCCACCCACATGCCTACGTGGCTGCATTCTCGCATTCCTAAAACAGGTACCCTGTGCCTGCTGTCCACCTTGTAAAACAAATCTGGCCC

chr19	50666889	50667009	1 -	CCTGCCCCAGCAGCACCGGCTCCCGCTGCCCCACAGCCTGGCCCGGACCCTCCGCCTGGCACGGATTCTGGCATCGAGGAGGTGGACAGTCGGAGCAGCAGTGACCACCCACTGGAGACC
chr19	51754364	51754484	1 -	GGAGCTAGTGAACAGTAGTCCTGGGATTCTAGTCCAGGCAATCTGGCTTTACCACCTCAGTCCAGTGCTTTACTGGGAGGCTGTGCTGCTCGCCGAGGCCATTTCTCATGTTTCAGTTAC
chr19	55372422	55372542	1 -	TCGGGGACATGGCTTGGTACCTCTGCCCCTCGCTTGCTCTGTGGTGAATCCCGGGTCTCCTCTGCCCCCATGCCTGGGGCTGGCCCACTGTGAGCCTGGGTAGGCGTCGCTGCCTCCCCC
chr19	543973	544093	1 +	GGGCGGGGCTGTGACCGTCACCTCACCTCCCCCACAGGAAGCGCGTGTGGGGAGGCTCGGGGCCGGGGCCAGCACCCACACTGGGTCTCCACAGCGGCATGGAGGCCTGCGTGTCTTCAC
chr19	984266	984386	1 +	CCGCGGGGCCGCCGCTCTGGCCCGCGTGGGGCAGTCGTCCGCGTCTCGCTCATGATGACGCACGTCCGGGGCGGTGGGGAAGGCAAGATGGCGGCGCCCATGGAGGTGGCCGTGTGTACG
chr19	2360178	2360298	1 +	ACCCGGCCCCGCCCCGCCCCTCCCTTCCTCCAGCCCCGGGCCCAGCTCCGGCTTCTGCTCCACTTCGGGGTGGGCGGGATCCGGGCAGTAGCGGTGCAGCCTCGTCGTCCGGAGCGCGGT
chr19	3094282	3094402	1 +	CATGGTGGGCGCGCTTGGCCGCCGGCCCCTCCCATTGGCCGCACCGTCTGCCCGTCGCGGGCTGCGCTCCCAGCCTGCTAGGTTGTCCGGCGCTGTCGCTCGGTTGCGGCGGCTGCGGTT
chr19	16888919	16889039	1 +	TGCATCTTGCTGGCCTGGCACCTGGGTCCCTGGGAGGCGCCACACTGGATATAGCCACGTGGGGCAGCCCGGTCTCCATAACCCACACTCCAGTCCTCCCACGGGCTGGCTGGCAAGCGG
chr19	17523241	17523361	1 +	GCATGGGGGCTGCCCAGCCACGTGCAAGTTTCTGTGGGGGGATCCAGAGGAGGCACCCGGCTGAGCAGGAGATGGGAATTGAAACCTGCGCAGAGGCGGCTGTGCAGGGTGAGAGTGGAG
chr19	35329107	35329227	1 +	CATAGAGAAGCAGGGGGTGTGGCCATGGAGGGGAAACCTCTGTCACCAGAGACTTTACTGTACTTCTCCTTTTGCTCTCAGATGCTGCCAGGGTCCCTGAAGAGGGAAGACACGCGGAAA
chr19	41363867	41363987	1 +	CTCCCCCAGCAAGCTCCATAAGGCGCATGCGTTATGAGTTCAGGTCCGACTTAACCCCGCCTCTAAGCGCAGCGCATGCGTCATTCCTACCTTAGCGCACTTAACGGTTAGGAGAGGAGA
chr19	41877200	41877320	1 +	AGCCCATCTCCGGGGGGCTGGGCAGGAAGTAGGGTGGGGTTTGGGGTAGGGATCTGGTACCCTGGGACTGCTGCAACTCAAACTAACCAACCCACTGGGAGAAGATGCCTGGGGGTCCAG
chr19	44846217	44846337	1 +	GGGGCGGGGTCAGAACGCCAGGAGGGGGCGGGGCCGGAGCCAGGGTCGGCTTGACTCGGGGGAGCAGCGGGTGGATCCTGTGACGTCAGCGGGTTCGAACCGCCGGAGCTGAGCGAGAGG
chr19	50418858	50418978	1 +	GCTTGTGGCCAGCGGGCACCCTCCTCCCCCCGGCAGGGGCTGGGCCAAGATATAAATAGGGTTGGCGGCTGCAGCGGGCGGCAAACAGCCCGCCCGGCACCACCATGCTCGCCCTGGAGG
chr19	53992228	53992348	1 +	CCTCCCCTTGGGAGCTTCCCGGGACCCCAGGTCTTCCTTTTCCGAATCCCAGAGGGTCCCCAAGTCCTCTGTTCTCAAACTCTGAGCCCAAGGGAACCCCGGCCACATCTCCTCCAAACA
chr19	56567415	56567535	1 +	CCTCCGTTCCGGACTACACTTCCCAGGGGCTATTGCAGCGGAGGACACGCCCACTTCCGGAAAGGACCCAAAGCCGGGCGAGTGCACGTCCCGCCGGTTGCTGAGGAGAAGGGAGGTCTG
chr19	1401491	1401611	1 -	CCGGAGCCGCGCGCGCGCGTCCTCTCGCGGGTCCGCCCCCCGGGCCTGTTGGACCCGCCCCCGGCCCACAAGCCCCTGCAGGGAGCGGGCCCGGGCGGCGCGCGATCGAGGTCGGGTCGC
chr19	7702090	7702210	1 -	GCCATGCGTGTAATGTTATCCGGGTGGCAAGCCCATATTTAGGTCTATGAAAATAGAAGCTGTCAGTGGCTCTACTTTCAGAAGAAAGTGTCTCTCTTCCTGCTTAAACCTCTGTCTCTG
chr19	19138437	19138557	1 -	GCTCAAGACACACTGATTGGTCGGACGGGATGCTCGTCAGACCAGAGTCGGGCTCTAATTGGTCGAGTTTCCGCAGAGTGCCCGGAGCCCTAGGCCGGTGGGTGAGTGCACCGCGTTCTC
chr19	51887910	51888030	1 -	TGCATCATAAAGGGACGGCTGGTGCCGTATTCCGTGTCTCCGGAAAGACGCAGTATGGCCCTCGCCGGCCGCCATCCCCGAAACTTGCGAGTGTCGCGTCTGCAGTGTGTGGGGTTCGCG
chr2	241707548	241707668	40 +	TCCCAAAGTGCTGGGATTACAGACGTGAGTACCACACCCGGCCTGGGCACATGTTTTGCAAGACTGAGATAGCTGTGTTTTTTTCCTTAGGTACAGCATCTTGACTAGGGAATACAGAGA
chr2	227667812	227667932	36 -	CATTGCGGTCCGGTCATGGTGCATCTGTCGCTCAACTTGTTCAAGGAGATAGAAATCTCACTCTCTCTTTTTTTCGTTTTTCTTTTGAGACGGAGTCTCACTCTTTTTGCTCAGGCTGGA
chr2	239935879	239935999	15 +	TTTATAAAATACCCGGTCTTGACCGGGTATGTCTTTATTGGCAGCGTGAAAACAGACTAACACACAGGGAAACTGTTGTTTTCAGAAACGCCCTGTGTTGCAATACCTGGAAGGTGCTTC
chr2	24879105	24879225	15 -	GCTGGGATTACAGGCATGAGCCACCGCGCCCGGCCCAGTCTTTCAGTCTTACTGGAACAGCCTGTGGGGTTACTGCAAGGGTGAGGAGCCATGTCAGAGAGGCAGGCGACTTGCTCCAGG
chr2	85393807	85393927	13 -	AATTCTGATCAATTGGCAAGTTGAACTTGCTGATTTGTGCCAAGAACCATACCATAGATACCCCAGCCGGGTGCGGTGGTTCACGCCTATAACCCCAGCACTTTGGGAGGGCAAGACGGG
chr2	25341884	25342004	9 -	GAGAGAGGGAGCGCGACAGCGAGCGGAGGGAGGGAGCGAGCGAGCGAGGCAGGCAGGCGGGCCGGGAGGGAGGGAGGGCGCGCGGGCGGCGGCGGCGGCGAGAGCAGAGGACGAGCCGGG
chr2	128670592	128670712	6 +	GGTAGCATTCCCATTCCACCATAGGCACAGTGACAGGGAGGGCCTGTTAAAACAGAATGTAGAGTCTCATAGAAAATACCAGGCCGGGCGTGGTGGCTCACGCCTCTAATCCCAGCACTT
chr2	94871574	94871694	3 +	GCACCATGGCGCAGACAGTGCCGCCCTGCGAGCTGCCCTGCAAAGAGTACGACGTGGCCCGTAACACGGGCGCCTACACGTCCTCCGGCCTGGCCACCGCCAGCTTCCGCACCTCCAAGT
chr2	94871514	94871634	3 -	GGGCCACGTCGTACTCTTTGCAGGGCAGCTCGCAGGGCGGCACTGTCTGCGCCATGGTGCCTGCCGCCCACCAGGGCCAGGGGAGTGAGGACTGTGTGTGGTCAGCCGGTTGCGGTCAGC
chr2	234098281	234098401	2 +	TATCTCTCTCCTCTTTGTGGCTTACATTATTCCTCCCCACTCTCCTTCCCTCATTAACACACCTTTTTGTTGTTGTTGTTGTTGTCGTCGTTGTTGTTGTTGTTCCGGGCAATATATTGA
chr2	84964150	84964270	2 -	TGTAAGCCACCACGCCCAGCCGGTTTTTTCTTTTGTTTTTCCCTTTTTAACCCCATTCTCTACCTTATGCAACTGGTGCCCTGTGGTCAACTCAGACTTCTCATTCATGCCCTCAGCTCC
chr2	1267625	1267745	1 +	TAGCATTGGGGAATATGTAGCAGTTTATCGGGGGAAAAGAGGAATCTTCAGAAGGTGAGAATCTTTCACCGGAGCTACTGTGTGGAAATGATCGTTCGCACGGAGTCATGCGCTCCGTGG
chr2	1269967	1270087	1 +	CGTGCCATGCTGCCCATGACTGACTTGCCGGATCTTCACAACTCAGCAAAGTGGATGCCCTCAAAGAAGCCCCGGGTGGATGCTTCCTTGTGCAGGGTGGCAAGGTCATGCAAGACCTCT
chr2	2649213	2649333	1 +	AAAGACCTCTCTGTCCAGACGCCCAGACTCCGACGATGCGGACCTGCACTCGGGCTGCCTGCTTCCTCGGTGGTGGGACGTGGGACTCTGCTCCTCCCCACTAGCCTCATTTGGTTTCCA
chr2	3280276	3280396	1 +	AAGTCGGCAAAACCTTAAGGAGGCTCCACGCTCCCTCACGCACACAGAGGAACTCGGACCCGGTCTCCCAACTCCTCGCCCGGCCTCGTTCCCATCCTCCAGGTGCCTCGAGGCGGCATC
chr2	9138749	9138869	1 +	CGCTGTTAGGAAAGGTACCCTCCCCCTCCGGCCCTGCGAAGTCCCCCAAGCTCACAACCAGAAATCCTCAGCCACCAGGCAAGGAGCTGGCCTGTCCTGTCTTCCTGGCTCCTCTCCGCC
chr2	10044528	10044648	1 +	TTTGAGGTGGCCTCGTCTTGTTTGATCTCGGGGAACCTCGGCAGACGGAAAGCTTTGATGCTTTGGTGCATGGCAGATAGAGAGGAAACGTGTATCTTCGTACATTTAAAGTTTCCTTTC
chr2	10432237	10432357	1 +	GGAAAAGGTATTTAGAAAAACAGGAGTTCGGCCTTGGGTTCATCCGTGGCGTGGCCTTCCCCCAGCCGCCTTGCCCTGGGCTGGGCGCCGTTGGGAATCAAACCCACACGCCTGGGGAGC
chr2	10880655	10880775	1 +	TCCAGTGTGTCCTGGTCACATCTGGGCCCGCACCACCTCACAGGCTCCCGGTGCGAAGGAGTGGGCGGCCTTTTCAGATTCGCCAGAGCTGGTTTGCGGAAGCTCCCAGAACAGACCACG
chr2	20670762	20670882	1 +	TGCCTCTTGCTGCGCGCAGTGGCAGGCCCGGTGCCGAGCCCGTTGGCACTGCGGCGGCTGGGCTTCGGCTGGCCGGGCGGAGGGGGCTCTGCGGCAGAGGAGCGCGCGGTGCTAGTCGTC
chr2	28545453	28545573	1 +	GAGAAGCGACGGGTATAACAGGTTAGGGCGAAGGGCACTGGACAGGAGCCAGAAAACCCGGGCTCTGATTTCGGTCCCACTTTCGGTGGTTTCTTGAGGCAAGTCACACGGTCTTTCGGG
chr2	64260509	64260629	1 +	AATCATACTTTAATCTCTCTAAAAATTTAGAGTTCCGGTTGCAAAACTTCCCTTTCTGCAAAGAATGAGTTAAGAATGAGAGGGTCATTGGCCGAGTCATTTTCCCTCTGTGGGCTTAGT
chr2	85711496	85711616	1 +	CCGGAGCCGGAGATGCCGGCCAGAACTCTGGGTTCTCTGGAAGTGGTGGGAGGAAACCCGCAGGAGGGAAGAGGCCATCTCTCCTTTAACTCCTAGGGGAACAGACCGCAGGGGCTGAGG
chr2	85711616	85711736	1 +	GTGCTAGCCCTTTCTGAAGCTGAGAGGGAGCCGGAAAGGAAGGGACTCAGGGGATCTCATGGGAGCCAGAAGGGCCCAGACTTAGGATCCGAAATTGTGCCTATGAGAGTGGTGAGCATT
chr2	96957144	96957264	1 +	CCCCGGCTGACTGCTTCTTAAGAGATCCCCTTGTCACCCGCCTCCATGGCCATGTTTCTGGCTGAATATGGTAAGGTTATTATTGAATGACTGACTAGTGTTTTCCCACTCTTATGTCTG
chr2	111716266	111716386	1 +	AAAGGGCTTCTTCACTCCAAAATGTCAGCGACGTGGCTGAGGATGGAGGTGAACCGCGCAACGGGCATTCCGGGCCCCTCTTGCCAAAATGTCAACAGAGACCCTCATAGACTTTGTTAA
chr2	127051501	127051621	1 +	AGTGCAAGCCCCAGAGTGCCACCCCCAACCCCGCCTCACAGGCCCTGCTCTCTCGGCACCAAGACCTCGCCCAGCCACAGCCACCACCCGCCCACCCTGCTTGACCCGGCAGGTGGCAGG
chr2	127631669	127631789	1 +	CTTCACACTGGCCCTGCAGCACCCGGCCCTCCAGGACGAGGTCTACTGCCAGATCCTGAAGCAGCTGACGCACAACTCCAACAGGTCTGCTGGGGCGGCGGCCAGCCCACGCGGGCACCC
chr2	205806185	205806305	1 +	CTGCCTGGGAAGGGGGGCTCTGGACAGGTGCCTTCCTAAGGAGCCCAAAACACTCAGTGTCTTGGCCTCACTCCTGTGCCCCACCTCTCGCCACTGAGAGGCCCGGTGAGTTCCTGTAGC
chr2	233485751	233485871	1 +	GCCCCACAACTTTACCCAGCTAGATATCGGAAGCCACTCGAACTTTTCGGGAAAGTATTTGGCAATTTCAATCTTCTCCACGGGAAGACGATAGAAATCGGCAACTCTCTGCCTCAGGGA
chr2	239312871	239312991	1 +	CTTCATCTGCAGAGGGAGACCGGGAGCCTCTGAAGACCGCTCCAGCTCTGCACTGTGGGGGCGGCCGGCCAGCAGGCAGGCAATGCTCTCAGGCCCCACGCTCCTCTCACTGGCTGCCGA
chr2	239374018	239374138	1 +	GGTACACAGAAAAACTGAGCCCGGAAGACACAGAGGTAATTCAAGCCCCTCTAAGGAGGGACACTGAGAACAGTGATGCTATGGCGTCCGCAGAACAGGCACCAACGGATGCAAAGCAGA
chr2	239508992	239509112	1 +	ACCACGGGCAGGTGCCCTAACCCAGTCTGTGTTGATTTGGCCAACTAAAGCCACCCTTGATTTCGTCTCATGCTCAGGCTGTGTGAGCTCACCAGCTGCGGGGGTGGAGTCTTCACTTCG
chr2	239935999	239936119	1 +	TCAATACAGACCTTGTTATTACTCCCGGCTCCCCCAGGGCTGGGCAGCCTGAACCAGGTGCTGGGATCCTGCAGTTATTACAAGGGCAGCTGTGGCTCCAGCCCCAGAACTTCTCCTGTT
chr2	240462109	240462229	1 +	CCCGGGCTGAGTCCCCTGCTCTGGTCCAGCTGCCACGGCGGGGGAAACATGGTCCCGATCACGCCCCCTCCCTGTGCGCAGACCACTTCCAGCACCTGCTGAACGACTCGGAGCGGACGC
chr2	240619490	240619610	1 +	AGGACCCTCTGCCTCAGTGGCTCCTGGGCGTGATTAAACTTGCCATTTCCTGGGCCCATCCTAGACAGGCTGCTGCAAGCCAGCCAGGCCGGGATCCTGCTGCCCCGGGGAGGACGTGGG
chr2	240851581	240851701	1 +	GTTGGGGCCACTGATCTGGGCAGAGCCTCGTGGGGTCTCCCAGGGGCTCAGACGTTGGCCAGGACCCCACAGGGAGGATGCTCAGGTCAAAAAGATGCCCGCACTCCGGGCGCTGCCCAG
chr2	240906694	240906814	1 +	GGCTCCCGGGGCACTTTCCACTTGCTCACGTGTTTGCCTTGAGCGTGCAGCCAGTCACGGATGCAAGCAGGCGCGCCTGCATGCACACACAGGCAGCCTTCAGCCAGGAGAGAGAGCCTG
chr2	241200161	241200281	1 +	AGGTTGTGCCAGACGTACCCCCCGAGTACTACTCCTGCCGGTTCAGAGTGAACAAGCTGCCACGGTAAGGCAGGGGCCCTGCCAGTCGGAGGAAAGAACAGGAGTGAGTGGGAGTCGGTG
chr2	241751230	241751350	1 +	CTTGCTCACTTCTAGAGAGTCCGTTTTACGTCCTCATCGAGACTTCAGGCTCCAACGCAGGCCATGACGCTGAGAAGCTGGGCCACTTCCTGGAGCACGCGCTGGGCTCCGGCCTGGTGA
chr2	241768379	241768499	1 +	GCATGCGTGGGCAGCAGGGGGCGTGGGCAGCGGGGGCACGGGCAGGACCACGTGGGCCGTGATCGTGGGTTGCCGAGAGGACCTGAGCGCTGCGGCTCTGCTGAATGGAGCCGGGTCCCT
chr2	1267565	1267685	1 -	TCTCACCTTCTGAAGATTCCTCTTTTCCCCCGATAAACTGCTACATATTCCCCAATGCTATGTCTCAGACACCCGAGCAGGTGTAGGTGAGAAGAGTGTGAGTTGTTCACTTACCCCGGT
chr2	1269907	1270027	1 -	GGGCATCCACTTTGCTGAGTTGTGAAGATCCGGCAAGTCAGTCATGGGCAGCATGGCACGGCCCCAGAAGTTCTTCCCAACAGTGGTCATCACGGCCCCCACAGCCCCACTCTACCCAGT
chr2	2649153	2649273	1 -	AGGCAGCCCGAGTGCAGGTCCGCATCGTCGGAGTCTGGGCGTCTGGACAGAGAGGTCTTTCAGCAGCTCTGCCAACCTCAGCAGCCCACGGGGGCTGGATCCCGGCCGCAGAAGTGAGGG
chr2	3280216	3280336	1 -	GGTCCGAGTTCCTCTGTGTGCGTGAGGGAGCGTGGAGCCTCCTTAAGGTTTTGCCGACTTGTCTGTAGCTGTGGGTAACCACCACGGTGCTTTGCAACCTGTGAGGCTCCGGACTCAGGT
chr2	9138689	9138809	1 -	TGGTTGTGAGCTTGGGGGACTTCGCAGGGCCGGAGGGGGAGGGTACCTTTCCTAACAGCGACACCCTGTGGTGTTGGCCGCTGCAACAGACACTCAGGTGACTTGTCTGTCTCCTTGAGA
chr2	10044468	10044588	1 -	CATCAAAGCTTTCCGTCTGCCGAGGTTCCCCGAGATCAAACAAGACGAGGCCACCTCAAATCCCCGGCCTCTGTCCCGCAGGCTGCGCCACTAAACCCCCTGTGATGTCACAGAACCGGG
chr2	10432177	10432297	1 -	GGAAGGCCACGCCACGGATGAACCCAAGGCCGAACTCCTGTTTTTCTAAATACCTTTTCCGGGGCCCACGAGGTCCCTCTCAGAAGCCTGAAGGTCCTGTGGGTTCTGTCTCCTCTTGGG
chr2	10880595	10880715	1 -	TCCTTCGCACCGGGAGCCTGTGAGGTGGTGCGGGCCCAGATGTGACCAGGACACACTGGACGTTGCTCAGCGGTGGCCTCCACACCAGGTCATGAGGCAGACAGAGTTCCTGGGAGTTTG
chr2	20670702	20670822	1 -	CAGCCGCCGCAGTGCCAACGGGCTCGGCACCGGGCCTGCCACTGCGCGCAGCAAGAGGCAGAACGCGCGGGGGGGGCGCGGTTCACGACGGTGGCGCCTCATGGCGTCCGCCACGTCGAA
chr2	28545393	28545513	1 -	CGGGTTTTCTGGCTCCTGTCCAGTGCCCTTCGCCCTAACCTGTTATACCCGTCGCTTCTCATGGCTGAATTCGGGTCTGCAGGAGCTTCTGATGTGTTCCAGCAGCTGTGCTCGATCCGG
chr2	85711556	85711676	1 -	ATGAGATCCCCTGAGTCCCTTCCTTTCCGGCTCCCTCTCAGCTTCAGAAAGGGCTAGCACCCTCAGCCCCTGCGGTCTGTTCCCCTAGGAGTTAAAGGAGAGATGGCCTCTTCCCTCCTG
chr2	111716206	111716326	1 -	TGCGCGGTTCACCTCCATCCTCAGCCACGTCGCTGACATTTTGGAGTGAAGAAGCCCTTTGGTGAGATGCCAGTCCAATTTGGATTTTGCTCAGTGTTGAGCCTGGGCACCGGGCCCATT
chr2	127051561	127051681	1 -	GGCTGGGACAGATGTGTGTTGCTGTCCCCTGCCATGGACTATCTATAGGTGCAGCAAGATCCTGCCACCTGCCGGGTCAAGCAGGGTGGGCGGGTGGTGGCTGTGGCTGGGCGAGGTCTT
chr2	127631729	127631849	1 -	ACCAGCTGCGGTGTCCTCTCTGAGCCTCGGTCTGGCCTCAGGGGCCGGGATGAGGACTGAGGGTGCCCGCGTGGGCTGGCCGCCGCCCCAGCAGACCTGTTGGAGTTGTGCGTCAGCTGC
chr2	205806245	205806365	1 -	TAACATCGCATTGGCTGGTGAGTGCGCTGGGGTTGGCTCATCCACTTCAGGCTGACATTTGCTACAGGAACTCACCGGGCCTCTCAGTGGCGAGAGGTGGGGCACAGGAGTGAGGCCAAG
chr2	233485811	233485931	1 -	AGGACCTATGCCCCTGCCCTGGACCTGGTGTGGAACGCGGCCCAGGGTGGGACTGCCGGCTCCCTGAGGCAGAGAGTTGCCGATTTCTATCGTCTTCCCGTGGAGAAGATTGAAATTGCC
chr2	234098341	234098461	1 -	CAAAGTCATTTCCAGATGTTAAAGCAGGTTGTCTGATTTGCCGTCTAGTAACCTTTGTTTTCAATATATTGCCCGGAACAACAACAACAACGACGACAACAACAACAACAACAAAAAGGT
chr2	239312931	239313051	1 -	AGGCTGGCCACCTTGACTCCTTGCTCTGCAGGCTGCCCCCGGCACCTCGTCTGCCTCCCGTCGGCAGCCAGTGAGGAGGAGCGTGGGGCCTGAGAGCATTGCCTGCCTGCTGGCCGGCCGC
chr2	239374078	239374198	1 -	CTGTGCAGTTTTGTTCTGCTGTTCACCGGCTGAAGTTCCAGGCCCTGCTGCCTGATCGCCTCTGCTTTGCATCCGTTGGTGCCTGTTCTGCGGACGCCATAGCATCACTGTTCTCAGTGT
chr2	239509052	239509172	1 -	GGTGGCTGCTTCCGGAGACCCACCTGTGTTAAGGGTCACACTGAACCTGCAGGGAATCCTCGAAGTGAAGACTCCACCCCCGCAGCTGGTGAGCTCACACAGCCTGAGCATGAGACGAAA
chr2	239935939	239936059	1 -	CACCTGGTTCAGGCTGCCCAGCCCTGGGGGAGCCGGGAGTAATAACAAGGTCTGTATTGAGAAGCACCTTCCAGGTATTGCAACACAGGGCGTTTCTGAAAACAACAGTTTCCCTGTGTG
chr2	240462049	240462169	1 -	GATCGGGACCATGTTTCCCCCGCCGTGGCAGCTGGACCAGAGCAGGGGACTCAGCCCGGGAGACTCAGCTCTGAGGATACACTCTGAGGACCTCGGAGTCGGACGCCACACTGCAGCGGC
chr2	240619430	240619550	1 -	GATGGGCCCAGGAAATGGCAAGTTTAATCACGCCCAGGAGCCACTGAGGCAGAGGGTCCTTAACCCCAGAAGAAGCACTGTGTGGAGAGTTCTCACTCCCGTTCTTTTGCCCTATCCTGG
chr2	240851521	240851641	1 -	GGCCAACGTCTGAGCCCCTGGGAGACCCCACGAGGCTCTGCCCAGATCAGTGGCCCCAACGCGGCAGCTCAGGCTTGACTTACATATCAGCAGGAAGCCCAGGGGACGGAGCTCCCGGTG
chr2	240906634	240906754	1 -	CCGTGACTGGCTGCACGCTCAAGGCAAACACGTGAGCAAGTGGAAAGTGCCCCGGGAGCCAGGAAGGTGCCTCCTGGCCATCCCCTCTCTTTGCCGCGTCCCTTCCAAAGTGTCCTGGCA
chr2	241200101	241200221	1 -	GCAGCTTGTTCACTCTGAACCGGCAGGAGTAGTACTCGGGGGGTACGTCTGGCACAACCTCCAGCAGGACGTTGGGGATGCCCAGCCATGCCAGCAGGCCGGCCGACCAGTTGGAGGCCT
chr2	241751170	241751290	1 -	CTGCGTTGGAGCCTGAAGTCTCGATGAGGACGTAAAACGGACTCTCTAGAAGTGAGCAAGGAAGGCAGAGTGAGCAGAGGCTCCGGCTGCCAGGGCAAGAATCAGGGCTGCTCGGGCAGA
chr2	241768319	241768439	1 -	ACGGCCCACGTGGTCCTGCCCGTGCCCCCGCTGCCCACGCCCCCTGCTGCCCACGCATGCCCCCCGCTGCCCACGCATGCCCGGGGAACGAGCAGCAAGCAGGCAGAACCACCACCCAGC
chr2	68157808	68157928	1 +	TGCAGGTCCCCGGCCTGTGACGTTTTAGGAAAGGGGCGGAGCTGCAGGGGTGGTTGGCTGAGGCTGGCTTCTGCGTGGTGCAGCTGCGCACGTGTTTCAGCCGGCAGCGCTTTAAGATTT
chr2	97713496	97713616	1 +	TTGAGCACAGCACTTTGTGACTTTGATGTAAACATCAAACACAGCCCCCTTTCCTGTCTTCGCATCCAGGAAATAGGTTAGTTTCAGACAAGCCTGCTTGCCGGAGCTCAGCAGACACCA
chr2	102142666	102142786	1 +	GCGGACTGGCCCAGCCGAGCCGTCTCCGCCCGTTCCCCGCCCCCGCAGCGGCGGGGCTAGAGCCAGAGCCGCGCCCGGCAGTTCCCGGCCGCGAGGGCGGGCGCAGCTTGTGGCCGGCGG
chr2	113127518	113127638	1 +	CAGTGGGGCAGGGTGGCAGACGCCTAGCTTGGGTGAGTGACTATTTCTTTATAAACCACAACTCTGGGCCCGCAATGGCAGTCCACTGCCTTGCTGCAGTCACAGAATGGAAATCTGCAG
chr2	197453472	197453592	1 +	GACCGGAGCCGGGCTCCGGGCCCGACCAGAGGAGGGCGGTGCTGCAGGGCTGGTCCGGGAGGTGACGACCGGCTTCGGAGAGTCTATCATGGCAGCTCGGACTGGTCATACGGCCTTGAG
chr2	203238938	203239058	1 +	GGCCCGTTGGTTTCCGGGTCCCGCGGGGTGCCCCCGCCCACACGCTATGCCTTAAATTGGGCCAGGCTGAGGCGCTGCTGCTGGAGCGGCCGATCCGAGACGTGGCTCCCTGGGCGGCAG
chr2	203936683	203936803	1 +	GGTAAGCGTGACACTACATAAACTCCCAGAAAACCCACTTCCTTTCCAGCAAATAGAAAACAACCGAGAGCCTGAATTCACTGTCAGCTTTGAACACTGAACGCGAGGACTGTTAACTGT
chr2	218125948	218126068	1 +	GTTCAGACAAGTCCGTTGGCGGGGGCTGGGATGCCTGCATCTTCCTTGTTAAAAAAGGAAGTGCAGGTTCAAAACATTCAGAGACAGAAGGTGGATAGACAAATCTCCACCTTCAGACTG
chr2	219461351	219461471	1 +	CAGGCTAGATAGTGCCGCCTCATTGGCCCTGGACCGAGGTCGGGATGTGACTTGTCTGCGGTGTGTGTTCCTCTGCACCAGGCCCAGCTCACCCAAGAAATGGGCGTCCTAGCCATGCTG
chr2	264769	264889	1 -	TGCCCCGCGCGCCTGCGCAGTCCCGCACCAACGCCAACAGGGCAGCGCGTGTGAGAGCCACGCCTGCGCAATCGGCTCCAGTGCGCCTGCGGAGGCGGTCCTATGACGGTAGTAGGACGG
chr2	33599250	33599370	1 -	TCTTGCGCACGCTCCGGACATGCGCAGTGCGGGAGCTGAGGCGCCAGCTGTGGATTTGGAAGTTCCGGGGAAGTCGCGCATGCGCGAGTGTACGCGTTGCCGGCGAAGAGGGGAGCCTGA
chr2	84881043	84881163	1 -	TGCTGCCGGGCTCACCCCAGCCCCGCCCGGAGGCGCCCCGCGGCCCCGGCTAGCCAGGGCGGGCGGCCACCTCTGCCCTACTCCTTCCCTCCGCGTTCCGGGCCTCGGAGCCGCCTTGAG
chr2	162074174	162074294	1 -	CACTCTGCGCCCCGGCTGCCGCCCAGCGCCCTACACCGCCCTCAGGGGGCCCTCGCGGGCTCCCCCGGCCGGGATGCCAGTGCCCCGCGCCACGCGCGCCTGCTCCCGCGCCGCCTGCC
chr2	224765030	224765150	1 -	GGATGTGAAATTATGAAAGTATTTTATTGTTCATAGAAATAAAAAACACAGTTACTTTGCATTTGGTTTCCTGTTGAAGAGTGGGTGAGTTACTGAGAAAAATGGTTCATTGAATATCTT
chr2	234496579	234496699	1 -	GCGGGCGGCGGCGGGCGGGGCCCAGGTGCGCCCGGCCGCGTCGGGCCCGTGACTGCTCGGGGGGCGGCGCCCTCCCGCCGCAGCCGCAGTGGCTGGCGCCGCAGCCAGGAGCCATGGGCA
chr20	56487716	56487836	44 +	CTTATAGTTCTGGAGACTAACGTCCAAAATCAAGGTGTCATCAGGGTTAGTTTCTTCTGAGGGAAGGATCTGGTCCAGGCCTCTCATTGGCTTCTAGACGGCCTTCGCCCTGTTCACATC
chr20	56487776	56487896	39 -	GGACTGGTGTCCTAATAAGGGAAAATGTGGACACAAAGACAGACATGATAGAGGGAAGATGATGTGAACAGGGCGAAGGCCGTCTAGAAGCCAATGAGAGGCCTGGACCAGATCCTTCCC
chr20	1657738	1657858	5 -	CTAGAAGCAGGTTACTGTTGCATTCCATCATAGCCACTTCCTCTTGAATTGAGGGAGGCAGGGCTTGTCTTCTGTCTTCAGAGCAGGGCCTGACATCTCCCCAGAACAGACGTTTGAACA
chr20	1491093	1491213	1 +	ACTACGCTGCTTCTTGGGACACTGGGGGTGCCCTCTGCCGGAGTCAGGCAAATTTTCAGTGGACCCCTCTTTACTCTATCTTCATGGGGTCAAGCTTCTTCAGGCATGGCAGAGCACTTA
chr20	19975322	19975442	1 +	GCATTTCTACTTCCTCCTCCGACTCGCTGGAGTTCGACCGGAGCATGCCTCTGTTTGGCTACGAGGCGGACACCAACAGCAGCCTGGAGGACTACGAGGGGGAAAGTGACCAAGAGACCA
chr20	50284109	50284229	1 +	GTCACACACACAGGGCCACCGATGGCATGGATGCACCCCGGCACATCCTGACTGCGAGGAGTGACTGCTCCTCACACTGCCACTTCCGGGCTGTGTGACTCTGGGCAAGTCACTTCCCCT
chr20	51671168	51671288	1 +	TGGAGCGAACCACGGTCCCGGGGATTTTCGAGTCCCTTCGAATCACCCAGCTGTACACGATCTTGCCCATGTCCAGGTTCACACGCAAACTAGGCACAAAACCAGAGCAAACAGGCTAAC
chr20	54146338	54146458	1 +	ATGCTTGGACTCAACTTCAGAATGTTTCTTGATACTGTGTTTCAGGCAACTGCCACCAATCAATTGGTGTTGGCACAATCCAGAGGACCGCTACCGGTCTCCAGTAGATTTCACCTGGTG
chr20	56958454	56958574	1 +	CTGTTGGGGCCCTACAGCTGCCCGCTGGACCCCAGAATGTGCCTGCACAAACTCCACTCCCGAAATCATCACAGGCCCTCCTTGAACCCGAGCCAGCCGAGGGCCTGGAGAACATTCCGG

chr20	57460352	57460472	1	+	GCACTTCTCCTGGGCTCCTGCGCTCCTGGCGCTGAGGTAAGAGGAGACACACGCAACCTTGCTGGCCTGGCCAGGAGGAGCCCACAGCCGTCATTTCAGACAGAGGAACCTGAGCCGGAC
chr20	57615489	57615609	1	+	GAAGGGACATGCAAAAACTTACCCCGTTGTTGGCTGAACTGAGGGCCAGGGGTCTCTGGAATTGTAGCTGCATGTTGCTGGGGCCTCTCGGCTGCAGAAAGAAAGATGGGTCAGAGGGGT
chr20	60113726	60113846	1	+	TGGGTGATGCTTTTCAGTAGCCTATGGACATGGCACCAAGTGACAATGACTTCCGTGCCTAAGGAGTGTTCTGAATGCAGAACAGGGAGCACCTCCTCCGGGTTGGGAGAGATGCCTCTG
chr20	61349079	61349199	1	+	TCCAGGGTTTTGTGCTTGGAAGATCACACGTATGTCATGGGACAGAGTTCCTGTCTATATGGAACATGGGCCACTTCTCAGGAACCGGCCTGCAGCCCCGATGGACAGGCTGGGTCATCA
chr20	62887791	62887911	1	+	GGGCCCTGTTGGTAAAGCTGGAACTGAGTGGGGTGAACATCTAGGTGGAGAAGGTCACCTGGAACCAGGCCTCCCAGCTGCCCCCCACCGTGATGCTGAGTTACAGAGAGTGCCCCCACT
chr20	63493639	63493759	1	+	GAGGATGCTGAGTCTGGCCAAGGGCCAGGCCAGGGACAGAGCTGGAGGAGCCTCGCCCCACCCTAGCTTCTGGACACCGTGCTGCCTCCGAGCTTGCCCAGCCTTGTCCGGAGCTTCTC
chr20	1491033	1491153	1	-	ACTGAAAATTTGCCTGACTCCGGCAGAGGGCACCCCCAGTGTCCCAAGAAGCAGCGTAGTGAAGTGATAAGCTCCCAGGCTCTGCGCTCACACCCACTGGCTTCCAGCTTGATTGCTCCT
chr20	19975262	19975382	1	-	AGCCAAACAGAGGCATGCTCCGGTCGAACTCCAGCGAGTCGGAGGAGGAAGTAGAAATGCTCATGTCGCTCAGCCGCTGCCGGCCTCCATGGCACGGGGGCCGTGATTCAGAGCTGGGCG
chr20	50284049	50284169	1	-	TCCTCGCAGTCAGGATGTGCCGGGGTGCATCCATGCCATCGGTGGCCCTGTGTGTGTGACGAGGCTGCACGGCCCAAGGGTGGCTCCCAGAAAGCGTGTGTCACCTGCCTTGGTCACAGC
chr20	51671108	51671228	1	-	TCGTGTACAGCTGGGTGATTCGAAGGGACTCGAAAATCCCCGGGACCGTGGTTCGCTCCAGCACGATTCCTGAGCAGCTGGGCAGGATTTCGTACTTACTCACAGACAAGACAGGTGAGC
chr20	54146398	54146518	1	-	CCCTTCATTTATGTATTGTTAATGCTTTTTTTCTGTTATGATTGGCCCAGATCTCTCTACACCAGGTGAAATCTACTGAGAACCGGTAGCGGTCCTCTGGATTGTGCCAACACCAATTG
chr20	56958514	56958634	1	-	TACTGGGATTACAGGCATGAGTCACCGCACCCAGCACCTGAAATTCATTTTGATTTCTGTCCGGAATGTTCTCCAGGCCCTCGGCTGGCTCGGGTTCAAGGAGGGCCTGTGATGATTTCG
chr20	57460412	57460532	1	-	GCTCCACAGGCAGAACAGCCGCTCACCCACAGCAACGGCAGTGTCTGAACCCAGGTTCACGTCCGGCTCAGGTTCCTCTGTCTGAAATGACGGCTGTGGGCTCCTCCTGGCCAGGCCAGC
chr20	57615549	57615669	1	-	TACCCCTAGGGAGCTGCCCACCTTTGTGGGGTGGAGGCCTGGTGCTGTCTTCTGTCCCCCACCCCTCTGACCCATCTTTCTTTCTGCAGCCGAGAGGCCCCAGCAACATGCAGCTACAAT
chr20	60113786	60113906	1	-	ATGGGTTCCAGGAAAGCCCAGTACTGCTATGCACAGAGGCCGATACTGGGCAGGTGGGGGCAGAGGCATCTCTCCCAACCCGGAGGAGGTGCTCCCTGTTCTGCATTCAGAACACTCTT
chr20	61349139	61349259	1	-	AGCCTTGGGTTGGGGCAGGTAGAGCATATGTGGCCCTGCAGGGTCCCCGCTGTCTGTTCCTGATGACCCAGCCTGTCCATCGGGGCTGCAGGCCGGTTCCTGAGAAGTGGCCCATGTTCC
chr20	62887851	62887971	1	-	ATATCTTAATGATTTGTCCACAGAAACACCGGGTTGTCTTCCTCTGCCCCTCTGCCCCGCAGTGGGGGCACTCTCTGTAACTCAGCATCACGGTGGGGGGCAGCTGGGAGGCCTGGTTCC
chr20	63493699	63493819	1	-	CTGTTTGTGGCAGGTGGCCCAGAGGGAGGCTTCATGGGATGGGAGTGGGGGCCACACTAGGAGAAGCTCCGGACAAGGCTGGGCCAAGCTCGGAGGCAGCACGGTGTCCAGAAGCTAGGG
chr20	3470959	3471079	1	+	GCCGGCCCCGCCCACCGCCCCGCTGTGGCCCCTTTGGACCGCACGAGCCACCGTCCGCACAGCCCCGCCCCGCACGGCCAGGCGAAGCGGAGCCGGCCGTGCGGTGTGTGTGTATGTGTT
chr20	41136886	41137006	1	+	GGCGGGACATGTCGGCTGTCCATCAGTGCCCGCGACCAATCCGCAGGCAGCCCCGCCCCCGCCCCTCCCGGGAGAGGGCGCGCGGAGGAACCCGCCGCCGCCGGTGTGAGGCGGCCCGTCC
chr20	50794981	50795101	1	+	GGTCCCGCGGGGCATGCAGCGGACCGGGGGCGGGGCTCCGAGGCCCGGGCGCAACCACGGGCTCCCAGGCAGCCTCCCGCCAGCCGGACCCCGTCGCCCTCCTGATGCTGCTCGTGGACGCT
chr20	62952629	62952749	1	+	GCACCCGAGTGGTATGCCCCGCCCTGCCCCGCCTGCCCGCCTGGTGGCCGTCTGGGGGCGACAAGTCCTGAAGAAACCGAGCGGAAGCGCGCTGGACTGGACTTGGGCTGGT
chr20	35699311	35699431	1	-	CTCAGCTCTACGTCTCTCACGGAAAACGACGGGGAGGGCGCTCGCGGCCCGATGAATCGCTTCCGGAGCGCCGGGCAGCACTTCCGGGAGCCTGGGGCCCAGGACTGCAGCGGCTTCGGA
chr20	52191737	52191857	1	-	GGAGCCGCTGCTGCAAAGCCAGGTTGGGGCGCCGGGCCCGGCCAGCGCCCTCTAGGCAGCGGAAGTGCAGCTTGCTTTACATCCGTCCTCCCCGCCTCGCAGAGTTGGGAGAAGGCAGGG
chr21	13373542	13373662	12	+	AGTCCAGGAAAGGCATATTCATAACCTCAGTACATAAATGGTGCTGAAGAAGAGTCAGGCTATTCCAGGTTCTTCTGTATCTGCTCACCGAGCTGCTCCGAGCCCGGCTTAGAGGACCAG
chr21	13373602	13373722	10	-	GTCACCACCAACTGCAGGGAGGCCAGCCATGGTGCCACAGGCTACAGCCTCCAGTCTGTCCTGGTCCTCTAAGCCGGGCTCGGAGCAGCTCGGTGAGCAGATACAGAAGAACCTGGAATA
chr21	34595460	34595580	1	+	TTTGACCTTTGAGCAAATTACTGGCTCTCTGCTAAGAGTGTACAGACCCATCTATTCATCATAGACTTCACTGTCTGGGAATGAGCCCCGGAGCCCAGGCTCTGCAGGTTGTTGCTGTTA
chr21	34595580	34595700	1	+	CGTAAGCCAGTGCAGGAGCCGTGCTGAGAAAAGGAAACTGCGCAATCTGCTCAGGTTCCCAGGAAGGCCAGGGTCCTTGTCCCACCTGAGGAGCTGACTTCTCAACTGGCAGCAGATTCA
chr21	39010698	39010818	1	+	AAGCCCTCCCAGCTCTGCCTGCTGGCCTCCCAGGCCACGACCACACACACCCTCTCCTGCCACCCCCAGGCCTCCCTCCAGCTCCCCTAGCCAGGCTTCCCTAGCTGGTGTCCCA
chr21	41672433	41672553	1	+	GGAGGGAATGGGGGTGCGGAGCCCTGTGCGCCAGAAACCTTACAGAACCAGCTCCCGGGGGCCTGCGGATTCACCCCAAAGCCAATGAGGCCCTCCTGACCCAAGGGGAAATGGAGAAAC
chr21	41740823	41740943	1	+	CCGCAGGCAGCCAGCTAGGTCTTGCTTCGCCGCAGGAGCGTGGCGGCGGGGCCATGGCCGCCCTGGAACTTGAGGCTCTGCAGGTTGATGTGGGCCCCATGCCTGAGCAGAGTCTCCACC
chr21	44771266	44771386	1	+	TGCAAGTCTGCCTTGTTTGGTACCAGCACAGAGCATCACTGTCACTAAGTGTGCCGGGGGAGAATGCTGAGCTGCTTGGCGGTGTGTGCGCGCCTGTGCGAGGCCAGGTCTCACAGTCCC
chr21	44933673	44933793	1	+	CGTGGAATCGTTGCCAGGTCATGGCTCCCTGCTATCGAACACCGGACATGGGTCGTGTGCTGCACCTGGCAGTTGCAGGACCGACACCCGCAATGCCTTAAGAGGTGATGACTGCCTTCC
chr21	44987837	44987957	1	+	CAGGCCGGAGCCCGTGGGCTGGGACCAGGGCAGAGTCGTAGAAGCTGCACAAAGATGTTTAGGGGCCACATGCTGCCGTGGAGGCCGTGCAATGAAATCGGCCCCATCCAGAGCCCCCGT
chr21	45386467	45386587	1	+	TGGGAACCGGCACTGCAGGGTCAGGTGCATCCCTTTCCATGTGAGCTCCTGGCCAGCCCAGGCAGACAGGGGAGGCCACACAGCTTCCAGGCAGGCAGCGGCTGGGCCTGAGCTGGCCCA
chr21	46120183	46120303	1	+	AGGGGTGATGCTGAAGGGCTGTGTGGTAAAACCCCGGCCACCAGCTCCCCTTGACATCAGGTGAAGGGGCTTCCTCCCAGGAAGTGGACGAGGTCCTACCCACGTGTGGGTGGCCTCAGG
chr21	34595520	34595640	1	-	GGGAACCTGAGCAGATTGCGCAGTTTCCTTTTCTCAGCACGGCTCCTGCACTGGCTTACGTAACAGCAACAACCTGCAGAGCCTGGGCTCCGGGGCTCATTCCCAGACATGAAGTGAAGTCTAT
chr21	39010638	39010758	1	-	AGAGAGGGTGTGTGTGTGGTCGTGGCCTGGGAGGCCAGCAGGCCAGAGCTGGGAGGGCTTCGCACATCTCTCCGGAGCTTGGGTCCATCCTGGAAGCCATGGGGAGGAGCAAGGATTGAA
chr21	41672373	41672493	1	-	CCCCGGGAGCTGGTTCTGTAAGGTTTCTGGCGCACAGGGCTCCGCACCCCCATTCCCTCCTGTAACGCTTGCACTAGCACCCAGTTGCTCGGGTCATCTGGACCAGGTCTGTCTGCTGGA
chr21	41740763	41740883	1	-	CGGCCATGGCCCCGCCGCCACGCTCCTGCGGCGAAGCAAGACCTAGCTGGCTGCCTGCGGAGACCGGGGGTCCACGTGGGGCTCTTGTCCTGTCCTGTGTTCCTCGTGGGGATGGAACGA
chr21	44771326	44771446	1	-	GTGGCGCGATGACCGGGAGCAGTTCTATAAGATTGCCAAGCAGATCGTCCAGAAGTCTCTGGGACTGTGAGACCTGGCCTCGCACAGGCGCGCACACACCGCCAAGCAGCTCAGCATTCT
chr21	44933733	44933853	1	-	GGACTCCACTCAATCCCTCTTCTCCAGGAGCCATGCAAAGTGTCAGCCAGCCAGGCCCCTGGAAGGCAGTCATCACCTCTTAAGGCATTGCGGGTGTCGGTCCTGCAACTGCCAGGTGCA
chr21	44987897	44988017	1	-	CGCCCCGGGGGGGGCCACCTGAGGAGCCCACACAGCCACAGGCCAGTTGTTCTTCCAAGGACGGGGGCTCTGGATGGGGCCGATTTCATTGCACGGCCTCCACGGCAGCATGTGGCCCCT
chr21	45386527	45386647	1	-	GTGTATGTCCCCCAGCCTGGCTGGCCGGACACAGCCGGTGGGACAGGAGCCCGGCAGGTATGGGCCAGCTCAGGCCCAGCCGCTGCCTGCTGGAAGCTGTGTGGCCTCCCCTGTCTGCC
chr21	46120243	46120363	1	-	ACCCATAGCTCCTTCCCGGTGCCTGTAGCTGCCGCTCTGAGCACGGTGTCTCTCGGTCCCCCTGAGGCCACCCACACGTGGGTAGGACCTCGTCCACTTCCTGGGAGGAAGCCCCTTCAC
chr21	33025855	33025975	1	+	CCCGCCCCCGCCCCCGCCACCGCTGCCGCCGTCGCCGCTGCCACCGGGCTATAAAAACCGGCCGAGCCCCTAAAGGTGCGGATGCTTATTATAGATCGACGCGACACACGCCCGGTGC
chr21	42403844	42403964	1	+	TTGAGGTTTTTCTTCACAGCCTCAGCCTTGCCTCTCCCCCTCTTGCTTTATCTCCTCATTTCTGTGTGCAGGCGAGCTTCTTGGCCTAAGGGCAGGAAGAGATGGCAGCGGGGGAGACGC
chr22	46806113	46806233	14	-	ATCAAACATCTGGGTCTCTATACTACGTTTTCCACAGCAGCTCGGCACTGAGCCATGGGGTAAATGTGATAAGAGGGTTGGAGGCCGGGCGCGGTGGCTCACACCTGTAATCCCAGCAC
chr22	49164330	49164450	4	+	GCCCTGGAGACGTGCAGGCTGAGGCACCCCAGGCCGCTGGGAGCCCTGGAGACGTGCAGGCTGAGGCACCCGGGCCGCTGGGAGCCCTGGGGACGTGCAGGCTGAGGCACCCCAGTCCC
chr22	49164390	49164510	3	-	AGCCTCCACCACACAGGAGACAGACAGGAGGTGTCGGAAACGGAGCCAGACAACTGTGTGGGGACTGGGGTGCCTCAGCCTGCACGTCCCCAGGGCTCCCAGCGGCCCGGGGTGCCTCAG
chr22	50460100	50460220	3	-	CAGGGAGGATCAGGGCAGGCGGAGTGGCCCGTGATGACCACGTGTGCCCGGCCTGTGCAGTGTCGGAGGAGCTGGAGCCCAGCACGCTGACCCCGTCCTCAGCCCTGAAGCCCTCCGAC
chr22	30857960	30858080	1	+	CACCTGCCCACTACACTGCAGACAGAAGAGGCGGGAGGGTGTCCGGAGAAAGTATGCCGGGGGAAAGAGAGGATCTTTGCAGGCACTGCGCAGCTAGGCCTCGCCAAGGGGGACCAATCA
chr22	30922668	30922788	1	+	TGGGGCATTGGGGAGGACCCAGAGCTTTCAATAAGGGAAGAAATGATGTGGGGAGGGACAGTAAATCAAAGTAGGGGATTAGGCCGGGCGCTGTGGCTCACGTCTGAATCCCAGCCCTT
chr22	35328296	35328416	1	+	CAAGCCAAGGCCATGAGATGTGAGCAGTCTGGGGACTCAGAAGGCTGAGCAAGGTGGATGCAGGGACAGCTCCCATGCACTGGGCACTTCCCGTGTCCCGGGCTATATGTGGACACTTGG
chr22	35328416	35328536	1	+	TTCACATCGCTCACGTAATCCTGACCACCCCCATTTTCCAGGTCAGGAAATAGGCATAGGGAGATCAGATAACACGTCCAGGGTTATATGGCTGGTAAGTAGCAGAGCTGCGATTTGAAC
chr22	37726402	37726522	1	+	GCCCAGAGACAGCCAGGGCCCCAGGCGCAGTGCAGCAGCGGGGGCCGCACCCACAGCCCTGGCCGTGCAGAGGTGGAGCGCCTCTTCGGGCAAGAGCGCAGGTGAGCCCGGGGGTGGGGT
chr22	44396209	44396329	1	+	GTTGACGAATGGGAGAGGGGATCAGAGGGATCAGCAAGCGAGAAACACTGAAGCCAAACTGACCAGGGACATGAGAGGTCCAAAGAAGAGATGGGAATCCCGGAGTAAGAGACAGGAATC
chr22	44591325	44591445	1	+	AGAAGGGTCCCAGGTGTGGCTGTGACTGCGGGAGCCTCCCTCTGTGAGTGCCAATTCCCTCACCGACTTGGGGTCTCCCAAGAGGCCACCTCACCTGGCCATGCAAGGAGGAAGCAGCAG
chr22	45585364	45585484	1	+	CCTCGTTAAAATTATTACCTCTTAAGGGGTTAAATGTGCGCCGCTGACCGCGTCCTGCAGCCCATGTGGAGAGTTTGGCCCGGGATCAGTACACATTACAAATGAGATTCAGAAATTCCA
chr22	45585484	45585604	1	+	CCTAAAAACAACAGCCGGCCGTCCCTGCCCAACGATGAGTGATTGCCCTGTCCTGGCTTTCCACGGCAAATCCCAGGGATGACGCGCTTTCCTTTTCTGGGAGACACAGCCCTGTCACC
chr22	46097873	46097993	1	+	TTCAGCCACCAGACCTCCTGAGCTGACTTCCTGGTCTCCTTGTGTCTTGCAGAATGTGGCCCCGTCCCAGAGCACCACCCGAGACATCAGGAGCCCATCGTGGGCTAGGGAAGATCCTCC
chr22	46686269	46686389	1	+	AGTCCTGCGGGAGTCCAGGACCGGCCCCTCCTCCACGGATGGCCAGCTTCCTCCTGACTGCCCCCAAGCCCGGCTGTGTTAAGCACTTCGCGTCGATATAAAGCATTGGTATTTGACATT
chr22	46686389	46686509	1	+	TTAACAGTAACAAACTTGCCAGTGCTTTACACACTGCCAGCTTCCAGAGCTTATCATCCGTGCTCCCGAACAGACGCCAAGGTCATGCTCCCAGCCGGATTGTCGTAGCCTCGCCGCCG
chr22	48872957	48873077	1	+	ACGGCCGGGACACCTTCCCTGGGGCGGCTGCTGGCCATCCTGTCTGATGGGCCAGATGTCTCCACCTGCTTGGATTCAGAAATCCCCCGACTCCAAAACGAACCTTTAAGTGTGGCGCA
chr22	49164210	49164330	1	+	GCTTGGAAGCTTCCGGAAGACAGTGAGGGGAAGCCGAAGTGGAAGACCTGGTCAGGGTGTAGCAGAGAAAGGCACAGTGGAGGCGAAGAACGTGGCTACGAGGCTCCCAGGCTGTCTGGGA
chr22	49164450	49164570	1	+	CACACAGTTGTCTGGCTCCGTTTCCGACACCTCCTGTCTGTCTCCTGTGTGGTGGAGGCTTCAGCCCCCAACAGGTGGACGGGGTGCCGGCCAGGGTGCCCACTGCACTGTGGCTTTCAG
chr22	50035059	50035179	1	+	AGAGCTGTTTGAGGGGCTTTTAGAGTTCGGGGGTGCACTCCTGCTGCCCGGATGGATTGGGGGGAAGCCATGCCAGTACCAGCAGCTGCCCCAGGGCCCGCTGGAGCCGTCCTGCGTGGG
chr22	50035179	50035299	1	+	CAGACTCAGAGCTGTGAAGACCTGGTGGGGACCCCATGACGTCCTGACAAGGTGGCTGCAGCACAGGAGTGAGAGCCAGTGGGGCTCCAAGGACGCCAGCCGTGACTCTCACAGCCGGCC
chr22	50035299	50035419	1	+	TGGGCTGGGGTGGGGAAGCCCCTGAAGACACAGGACATCGGGGTTCCATTCACACCTGCTGGGGGCAGCTTGAAGGGAGAAGTGAGGCTGGGGTGTCCCTGACAACATGGGAGGGGCCCC
chr22	50460160	50460280	1	+	TGCACAGGCCGGGCACACGTGGTCATCACGGGGCCACTCCGCCTGCCCTGATCCTCCCTGGCCAATGTCAGCATCCAGAGACCACCAGGACTCCACCCCCACCCCTCCACCTGAGATCT
chr22	30858020	30858140	1	-	ACAAACAAACAAAAAAAAAACAAAGTGAATCACAACCTGATTATCTTGTGATTCTCCCCATGATTGGTCCCCCTTGGCGAGGCCTAGCTGCGCAGTGCCTGCAAAGATCCTCTCTTTCCC
chr22	35328356	35328476	1	-	CCTATGCCTATTTCCTGACCTGGAAAATGGGGGTGGTCAGGATTACGTGAGCGATGTGAACCAAGTGTCCACATATAGCCCGGGACACGGGAAGTGCCCAGTGCATGGGAGCTGTCCCTG
chr22	37726342	37726462	1	-	AGGGCTGTGGGTGCGGCCCCCGCTGCTGCACTGCGCCTGGGGCCCTGGCTGTCTCTGGGCCAGCCTCCTGGGTGGGGGCAGGTCGGCCAGCACAGTGTACTCCTCCCGCTCCAAGTTGTG
chr22	44396149	44396269	1	-	AGTTTGGCTTCAGTGTTTCTCGCTTGCTGATCCCTCTGATCCCCTCTCCCATTCGTCAACTGGTGCGCCCTCATTCCCCTGCGCTCAGCCTCTGTTCTGCCTCCTGGAGGGCCTCCCGGA
chr22	44591265	44591385	1	-	AGGGAATTGGCACTCACAGAGGGAGGCTCCCGCAGTCACAGCCACACCTGGGACCCTTCTGCCACTCCCCAGGCCTAGAAGTCCGGGCTGGGCCCCACTCTAAGTGCTAGTTGACCTTGG
chr22	45585304	45585424	1	-	CTGCAGGACGCGGTCAGCGGCGCACATTTAACCCCTTAAGAGGTAATAATTTTAACGAGGTGATCTGGGCCCTGCTGGCTGGGACAATGGACGGTCTCAAGCCTTGACTGAGGCCTTGCC
chr22	45585424	45585544	1	-	AAGCCAGGACAGGGCAATCACTCATCGTTGGGCAGGGACGGCCGCGCTGTTGTTTTTAGGTGGAATTTCTGAATCTCATTTGTAATGTGTACTGATCCCGGGCCAAACTCTCCACATGGG
chr22	45585544	45585664	1	-	GGAGGCCGGGCCCAGCACCCTGGGAAAGAACTTGGCTGCCAGCCAGGGTGTGGCCCCCGGGGTGACAGGGCTGTGTCTCCCAGAAAAGAGAAAGCGCGTCATCCCTGGGATTTGCCGTGA
chr22	46097933	46098053	1	-	GTGAGTCCTTCCCTGCCCAGGCGGGGAGTAAAGACGCAGCTACCTGGGCCGTTAGGTCCCGGAGGATCTTCCCTAGCCCACGATGGGCTCCTGATGTCTCGGGTGGTGCTCTGTTCTGGGAGCA
chr22	46686329	46686449	1	-	CGGATGATAAGCTCTGGAAGCTGGCAGTGTGTAAAGCACTGGCAAGTTTGTTACTGTTAAAATGTCAAATACCAATGCTTTATATCGACGCGAAGTGCTTAACACAGCCGGGCTTGGGGG
chr22	46686449	46686569	1	-	GGGAGGGGCCTCCACGCCAGCGCCGGGAAGGCTGTGGGGCCTCCACACCTGCCTCATCACGGCGGCGAGGCTACGACAATCCGGCTGGCGTCTGTTCTGGGAGCA
chr22	48873017	48873137	1	-	CGGGCCGTGGTCCCCAAGAAGAGGCAGCTGCTGGGTTTGACGCTTGCTCATTCCGAAAGTTGCGCCACACTTAAAGGTTCGTTTGGAGTCGGGGGGATTTCTGAATCCAAGCAGGTGGA
chr22	49164270	49164390	1	-	CCTGCACGTCTCCAGGGCTCCCAGCGGCCTGGGGTGCCTCAGCCTGCACGTCTCCAGGGCTCCCAGCAGCCTGGTAGCCACGTTCTTCGCCTCCACTGTGCCTTTCTCTGCT
chr22	50034999	50035119	1	-	CCAATCCATCCGGGCAGCAGGAGTGCACCCCCGAACTCTAAAAGCCCCTCAAACAGCTCTCCCCACCCTCTCCTTATTCCCTGTGGTTATGATGATTTCCTGAGTCTAGCCCGTGACTGC
chr22	50035119	50035239	1	-	TGCAGCCACCTTGTCAGGACGTCATGGGGTCCCCACCAGGTCTTCACAGCTCTGAGTCTGCCCACGCAGGACGGCTCCAGCGGGCCCTGGGGCAGCTGCTGGTACTGCATGGCTTCCCC
chr22	50035239	50035359	1	-	AGCAGGTGTGAATGGAACCCCGATGTCCTGTGTCTTCAGGGGCTTCCCCACCCAGCCCAGGCCGGCTGTGAGAGTCACGGCTGGCGTCCTTGGAGCCCCACTGGCTCTCACTCCTGTGC
chr22	17084920	17085040	1	+	GTCCCAGACTAAACTCCTCCCCTCGGCCCGGCCCGCCCCTGGGCCCGGGCTGGAAGCCGGAAGCGAGCAAAGTGGAGCCGACTCGAACTCCACCGCGGAAAAGAAAGCCTCAGAACGTTC
chr22	20394073	20394193	1	+	TGGAGTCTGACGCCTGCGCGGCGCAAACGCTCCCGGGAGGTGTAGTTTGCGCTCATTTCGCGCAGGCGCGCTTTCCCGCAGCGGCCGCCTGCTGCTCTTTGTGGCAGTCGCAGTCCTTTT
chr22	37807858	37807978	1	+	CCTAGCTCCGATTGGCTGCTGGAGCCCGGCCCCCGGCCACGCGACCAGGCTGCGTCCGCGATGCGCACGGCTCCCAGGCAGGCAGGCGCGCTCGGGCGAGGTAGGAGCGATGTGGCCTGG
chr22	37849339	37849459	1	+	AGGCTTCCGGTTTCCCGGCAGGCCCGAGTGGGGCTGAACTTCCGGCCTCAGGACGCAGGCGCGGGCCGCTCATTTCGCTCTTTCCGGCGGTGCTCGCAAGCGAGGCAGCCATGTCTATC
chr22	45310038	45310158	1	+	GCGCAGTCCCCTCCCCGAGAACCATCCCCTTGCCCCGCCCAGCGTCAGGGGTGCGCGGCCGCCGAGAGACCCCGGAGGCGTAGCCGGCTGCGGAGGCGAAGAGGTGGCAGCGCGAGCTGG
chr22	20437784	20437904	1	-	CTGGCCCGGGATCAGGGAGCCGATGTGGAATTTCCTGCCCGGCTCGGCGCCCCTCCTGCCGCCCCCCGCCCGGCCTCGCACTCCGCTTCCGGCCGCTCTCGCTGCGGCCGCACCCGCGCC
chr22	23752683	23752803	1	-	TTCTCTGAGCCTTGCTTCCCCTCTGTAAAATGGGTTAATAATATTCAACATGTCAACAACAGCTATTGTGAGGGTCATAAGATCCTGGCTGAGAAAATGACTGTGGTGGGTCTGGGAGT
chr22	30471941	30472061	1	-	GCCCAGGAGTGGGGGCAAAAGGACCCAGCTGGGTCAGGGCTGACAAACTAGGCTTGGCCTCTTGCCTATAGTGGCCACCACTCCTCAAGCCCCAGCCAGCACCATGAGCGGCCGAGTTGG
chr22	37149875	37149995	1	-	ACCCCAGGCCTTGCCCCTCTATCCTCTGCACAGGAAGTGGGCTGGCTCTGGGCTTTTAGTCTTTGCGGCCCCAGCAGCCAGAGCTCAGCAGGGCCCTGGAGAGATGGCCACGGTCCCAGC
chr22	41926765	41926885	1	-	AGGCGGGGGCGGGGCAGGGCAGAGTGCTCCCCCCGCCCCCCGCTTCCTCCCCGAGGGCCCCGGAGCCCAGCTCAGCCTCAGTCCCCGCAGCTTGTGCGCGGCGTCGGCACCATGAGGGCG
chr22	50244982	50245102	1	-	GCGGCCCAGGCCTCACCAACTTCACGCGCTGCCGGCGTTCCCGTGACGTATTTCCGGCGCGCCCGCCCTAGTGCTCTTCACACTGGCGCGGCTGTGACGCGACGGAGGCGGCGAGAGCGG
chr3	125832482	125832602	15	-	ACCTGAAAATTTTTTTCAAGTGGCGCCCCACTACAATCCGGCCGTTCTTCCGGGGGGGGCCGGAGCAAGCCTGGCTCTCGCCTGGTGGCGTTTCTCACTGGGGCCTCCAAATGTTGTA
chr3	49708234	49708354	14	-	GGAGTATCAGTTTTGCAAGATGAAATGAGTGTGGAGATTGGCTGCACGACAATGTGAATAGACTTAACACTTAAAAATGGCTATGATGGGTGACCGGGCACAGTGGCGCACGCCTGTAAC
chr3	54626219	54626339	8	-	CGCTGCTGGCGCGCACTGTACAGCGGCATCAGCCGCTTGTAGGACATGTCCAGCAGCTGGTCGAGGTCCACGCCACGGTAGGTGAACCTGCGGAAGGTCTGCTTCTTCTGCTCTACTTCT
chr3	54626159	54626279	5	+	TCACGATAACTGCGCAGGCGCGGACCAGAGAGCTCTTTTCTGAGGATCCGGCAAGATGGCAGAAGTAGCAGAAGAAGCAGACCTTCCGCAGGTTCACCTACCGTGGCGTGGACCTGGA
chr3	32511588	32511708	4	+	GTGCTGAGATCACAGGTATGAGCCACCGCGCCCGGCCTCAGTGTAGTTTAATGTGTACTTCTCCCATGAGGAAAGCTGAACATATTTCATATCAAGGGCCATTTTATGTTTTTG
chr3	31670812	31670932	2	-	GTGCCTACGCCCGGTCCATTCTCACCATCCCGTGGGTGGAGCTCGGAGGAAAAGTCAGCATCAACTGTGCCAAGACTGGGTACTCAGCGACAGTGATATTCCACACGAAGCCTTTCTATG
chr3	31670872	31670992	1	+	TGCTGACTTTTCCTCCGAGCCTCCACCCACGGGATGGTGAGAATGGACCGGGCGTAGGCACTAGGCAGGGTGAATACGTACTCCTCCCCGTGTTCCAGGAGCCTCAACACACCTCCAGGGA
chr3	44451275	44451395	1	+	GGCATAAGGCTGGGGTCTTAAGGCCAGGCAGCAAGTACCGGATTGCCCAGCCAGGAAGTCACGTGCTTCTATTTCATAGGGAGGCTCCAGGTGGTCCCCCAGAGCAGAGCTGCTCCTGAG
chr3	52845353	52845473	1	+	GTGGACTGATGTTTGTGGATGATGAAGCAGGACCCAGTCGCTTTGTTTGTCTCCCACCTCCCCACCTCCCATCCCTTACCCAACTCCCCGGGCCATCCCTGATACCTCAGCCTCTTGAGA
chr3	53152256	53152376	1	+	CCCTGCTTTACCCCAGGTGTAGGCAATTAGACAGCAATGAGGTGGCTGCCCACTCCTGTCCATCCTCCCATCACAGACCCTGTGCTCAACCGGCAAGGAAGCCAGGCATCTTCTTCCTCCTC
chr3	58123335	58123455	1	+	AAAGCTGACATTGAAATGCCCTTTGACCCCTCTAAAGTCGTGGCATCGGGGCCAGGTCTCGAGCACGGGAAGGTGGGTGAAGCTGGCCTCCTTAGCGTCGACTGCTCGGAAGCGGGACCG
chr3	63905551	63905671	1	+	AACCCACTAATTGCCCGCTTGTGATTGCTGCTTTGCTGCCACTGCCCCAGAAACCATTTGGAAAAATCCTCATGCTTTTTGAAAATACCGGTTTTCTGAAGAGCTGAAGCCAAGCTCTGGA
chr3	120682159	120682279	1	+	GATATAAAGCCACAATGCTTCTTTCTCCTTCAAACCACTCTTTGGATATTCCGGTTCCCACTGCTTCACTGGTCAGTGCGTCACTCAAACTAGCTGAAAGAATTGTCTAA
chr3	126056119	126056239	1	+	AGGCTAAGGTTCTGACAAACCTCCATCATTCTGCGAATCTCTAATGCTGAGGTCTCAGCGTTGGAGGTCCCTCCTGCCAGCCTCGCTGACACCCGGGACGCCCAAGCAGCAAGGGCAGGT
chr3	194876165	194876285	1	+	TGAACTCTTCGATCCTATCCTTGGACTCCGGTGACATGGGAAATCTTCAGTTCTTTGGTTATTCAGGGAGGGGTACAGATGAGATATGAGGAACACCAGGCTCGCGGGACTGGAGCAGCC
chr3	195258943	195259063	1	+	GTATCAGCATGGTGAATAAACAGGTATGCGCTTTCTAGAGTGACAACAGCAGGGTGTCAGTTCCCAACACACCTATTCCGGTACCATTATTAGCAGCCACCGTTGACCAAGCACCTGCCA

chr3	197533428	197533548	1	+	GCCCAGAAGAAAGGGTTCTGACCATCCAACTGGCTCCCGGGTAGCTGGGCTTCCACTCACCGGCTCCGCCGCACTGGCATAAGTCCGACGGCCAATCGGGATAAAGGAAGTAGAACCAAG
chr3	197547725	197547845	1	+	CCTCCCTGGAGGCCCCTAGCTCACTGGGCCACCCTCCTCTTTGCTCACTGCGTCGCAGCCACCACTGACTCCAAGAACTCCTTGCCCACGTGAGGGCGTTCCTGCCTCAGAGTACCGGCT
chr3	44451215	44451335	1	-	GACTTCCTGGCTGGGCAATCCGGTACTTGCTGCCTGGCCTTAAGACCCCAGCCTTATGCCACACTTCTTGCATTTCCTGTAGTGTTGTCTTTCCACATCTGTCCTCTCATGAGAATCTCC
chr3	52845413	52845533	1	-	GTTTGGGGTGACCCATGCTGGACAGGTAGAGTCCAAATTCCTCCAGAGTCACGTTTCTGCTCTCAAGAGGCTGAGGTATCAGGGATGGCCCGGGGAGTTGGGTAAGGGATGGGAGGTGGG
chr3	53152316	53152436	1	-	GGAGGATGATGAAAGACCCAACGGTCAGTGGTCACATGGACTGACTGATGGAGCAAGGGAGAGGAGGAAGAAGATGCCTGGCTTCCTTGCCGGTTGAGCACAGGGTCTGATGGGAGGATG
chr3	58123395	58123515	1	-	CTGAATACTGACTTCGGCTTTTGTTCCCGAGTCCGAGACAGCTTCCAGGCCCAGGGCCCCCGGTCCCGCTTCCGAGCAGTCGACGCTAAGGAGGCCAGCTTCACCCACCTTCCCGTGCTC
chr3	63905611	63905731	1	-	GAGTAGAAAAGGGGAACCAAAACAAAATTGCTCCTGGTGAGAAATCTGCCTTTCCTGCCTTCCAGAGCTTGCTCCATCTCTTCAGAAAACCGGTATTTTCAAAAAGCATGAGGATTTTTC
chr3	120682219	120682339	1	-	ACCAAAGGCAATTGTGTAACCGGTTAAATAAGCTTGCTGGACTTTGTCCCTGTGTATGAGTTAGACAATTCTTTCAGCTAGTTTGAGTGACGCACTGACCAGTGAAGCGCAGTGAAGCAG
chr3	126056179	126056299	1	-	CACCACAGACAGGGCAGGCTGGAGACATGAGGGGCCTCTACAGTGGGAGGGCAGCCCTCAACCTGCCCTTGCTGCTTGGGCGTCCCGGGTGTCAGCGAGGCTGGCAGGAGGGACCTCCAA
chr3	194876105	194876225	1	-	AACCAAAGAACTGAAGATTTCCCATGTCACCGGAGTCCAAGGATAGGATCGAAGAGTTCACCATAATGCTTAGGTTTCCCCGGCACGCTCCGCTCTTCTCTCAAAAACCAGAAAGGCGCC
chr3	195258883	195259003	1	-	CTGACACCCTGCTGTTGTCACTCTAGAAAGCGCATACCTGTTTATTCACCATGCTGATACCGTTGATTCAGTTGGAGGGCAGTGCAGCTAGCTTGCAAAACAGCTTTCTGGCCAGGTTTA
chr3	195259003	195259123	1	-	GATAGCACAGCTGTGCTGCCGGGATAACAGATGAAATGAGACAGCTCACAGCCTGGCACATGGCAGGTGCTTGGTCAACGGTGGCTGCTAATAATGGTACCGGAATAGGTGTGTTGGGAA
chr3	197533488	197533608	1	-	GTCTGTCTAGTCTGTCCTTGTACTCACGGCTTCCTTTTCTCTTGCAGACGCCCACTATTGCTTGGTTCTACTTCCTTTATCCCGATTGGCCGTCGGACTTATGCCAGTGCGGCGGAGCCG
chr3	197547785	197547905	1	-	TGGGAGCCACTTTAGTGAGGGAGACAGAGGACTCAGCATCCAGGATGAGGGCAGAGCAGGAGCCGGTACTCTGAGGCAGGAACGCCCTCACGTGGGCAAGGAGTTCTTGGAGTCAGTGGT
chr3	32951564	32951684	1	+	ATAACTCGTGCTCACAGGAAGCCACGCACCCTTGAAAGGCACCGGGTCCTTCTTAGCATCGTGCTTCCTGAGCAAGCCTGGCATTGCCTCACAGACCTTCCTCAGAGCCGCTTTCAGAAA
chr3	46242380	46242500	1	+	CTGATGGTATCTCTGTTTCAGGAGTGGTGACGCCTAAGCTATCACTGGACATATCAAGGACTTCACTAAATTAGCAGGTACCACTGGTCTTCTTGTGCTTATCCGGGCAAGAACTTATCG
chr3	46353780	46353900	1	+	TATCATGCAAATTATCACTAGTAGGAGAGCAGAGAGTGGAAATGTTCCAGGTATAAAGACCCACAAGATAAAGAAGCTCAGAGTCGTTAGAAACAGGAGCAGATGTACAGGGTTTGCCTG
chr3	46370866	46370986	1	+	ACTCCACCCTCCTTCAAAAGAAACAGCATTTCCTACTTTTATACTGTCTATATGATTGATTTGCACAGCTCATCTGGCCAGAAGAGCTGAGACATCCGTTCCCCTACAAGAAACTCTCCC
chr3	108822706	108822826	1	+	CCTTCACCACATTTCCTGTTTGTAACTGAAACAAAGTACACACAAAAGATTTTAAGAAACAGAAGAGAAAAGAATCCGAGGCACAGATAAAGATAAGTTTTACTGTCATGCTGCTTTTAA
chr3	191329341	191329461	1	+	CCCGCCCGCCTTTCTGTCTCCTCTCTCCCTCCGTACTGGACGGCCCCGGTCCATTTCCGGGCTCCGGATATTTGGTATCGATTGGGGCCGGGGACGCGGAGCAGGTGGCCGCGGCGGGGC
chr3	3109951	3110071	1	-	TTAACCATTACAGCCGTGATGATGAAAGAGTGAAGAACCGCCTCTAAGTTAAAAAGTGCACCCAGAGATAAGGTTCGTTCTCAATGCCCTGCCGCTGCTTCTCATCGCATGGCCACCGCA
chr3	31981221	31981341	1	-	CCTTCGCCTCCTCCTCCTCTTCCTCCTGTATGAGTCAGGCATTTCCCGGGGATTTGGAGCAGGCACGCGCGGCCCGGGCGTCCGGAGCTGTAGCAGCAGCAGCAGCCGCCGTGCCGGGGC
chr3	46208271	46208391	1	-	ACAGGAAGCTGAGTACTTCCTACTTGGTCAGGATCTTGAAACTTGAATTCATAAAAACCCAGAAAGCCCCAGAAACAAAGACTTCACGGACAAAGTCCCTTGGAACCAGAGTAAGTGTCA
chr3	46693638	46693758	1	-	CGGGGCTGGGCGAAGGGGGCGGGGCTGGCAGGGGGCGGGACTGGCAGGGGGCAGGGTGGGGGTGCGAGCGAGGAGCCGCACAGGCAGTCCCGGCGCGGGGCAACCACAGCGCTCAGGTAA
chr3	49929770	49929890	1	-	CACAATGCACCCCGGGGGCGGGCCGAGTCGGGCTGAGCGGCTGGAGCTGGGCCTTGGCCGCGAGAGGCCGGCGAAAGCTATCTTCCTGCACCGGCGGCCGGGTGAGGGCGGTGGGAGGGA
chr3	124887324	124887444	1	-	GAAGGGGAGGAGAAAGGAGAGGAGGAAAGTGGAGCCTGGCGGGCCGGAGGGAGGAAGGGAAGGGGCGGAGGCCAGGGGCAGAGTGTGCCGGCGCGCGGGGGAGTCTCGGCGCTGGGCGCG
chr3	128123771	128123891	1	-	CGTGAGCCTATGGAGAGCGGAGGTGTTCCCGCTTCCACCAATGGAAAGCCGGTCTAGGCGGGCCTTTGCAAATTGCCCTAGTAACGGCCGCATGGTAACTCAGGCGCCGGGCGCACTGTC
chr3	151384712	151384832	1	-	AATAGAACACATACAAAGGCACTGTTGTTACACAACAAACATCATAGTGCTGAAATGACAAAAATCCAGGGTAGTGATCACAATCAGAAGACAGGAGCTGCAGAACAGAACACTTTCTCA
chr3	171460364	171460484	1	-	GAAGCGGTGATAGACAGTTCTGCGTGGTTCTCCACCCCCACCCTCCCCCTGCTGAGTGGAGGAGTTGATGTGTCTCATTATAACAGCCAATGCAGCCGCCATCCACGCACAAGCAAAGAA
chr4	981739	981859	23	+	GCCACTCCTGACAGCCGTAAGCTGCCCAGCGGCTTCTGATGCAAGAACCAGCAAGAACCTGGCCTTGTGCCGTCCACTCTTTTTTTTTCTTTTTGAGACGGAGTCTCACTCTGTTGCCCA
chr4	178415366	178415486	22	-	AGAAAAAGCACCGTAAGTTCTCACTCCAGTCGGAGTTGAGACTGCCCTGAATAGCCGAATTCGGAGCCCGGCCGCCAGGCTTTCAAGCTGCCCCTGGCTTGAAAGTGGATTTTCATGGAG
chr4	9566842	9566962	16	+	GGGACGTAGTTCCTACCTGGCTTTCCAACAATGTGTAAGCCCGGAATTCTTACATAAGTCCATGGAGAAGGGAAAGGAATGCTGGTAACGACAAGATTGAATTCTCCACCTGCCAGGCAT
chr4	9566902	9567022	16	-	TGTAAGAAATGTCACATTCCTATTTCTGTAACTTCAGTTAAATCTGCTCTGAGTCCCTGGATGCCTGGCAGGTGGAGAATTCAATCTTGTCGTTACCAGCATTCCTTTCCCTTCTCCATG
chr4	8635488	8635608	8	-	ATTACAGGCGTGAGCCACCGCACCTGGCCCGGTTTTCTGGTTTCTAACCCTGGTTGTGTGATGGTGCATAAGTCACTTGACCTGTCTGTGCTTGTGAGATGGAGATAATTCTAATATGTT
chr4	73869313	73869433	4	+	GGGAATTTCCCTGGCCCGGGGGCTCCGGGCTTTCCAGCCCCAACCATGCATAAAAGGGGTTCGCGGATCTCGGAGAGCCACAGAGCCCGGGCCGCAGGCACCTCCTCGCCAGCTCTTCCG
chr4	72533966	72534086	2	-	CAAACTGCTGGGATTACAGGCGTGAGCCCCTGCACCCAGCCGGGGACTGTGATGTTCTATGACAATATCTAAATTTGTCTTCTAATTTGTTTTTATGGACAGTGTCCTTCTGGCCGAGGA
chr4	67545462	67545582	2	-	GCACAGGCCAAGCGTTCTTGTTTGTTGAGGGCGGAGCCAATGGCGGGGGAGTGTTGTTAGCGCGCGCCTTCCGGATCGCAGCTCTCGCGGCAGTCGCCTGAGACTTAAGGTTATTGCTTG
chr4	73998636	73998756	2	-	AGCATCCCAAAGCTTGAGTTTCCTGTCAGTGGGGAGAGATGAGTGTAGATAAAAGGAGTGCAGAAGGCACGAGGAAGCCACAGTGCTCCGGATCCTCCAATCTTCGCTCCTCCAATCTCC
chr4	687296	687416	1	+	CGGGAGGCAGGAGGCCGTGTCACTCAAGGTCAACTTCCATGAGTCGACTGAGCTCCAGGCCACACCCTCGGACACAGCAGCCAGACCCAGGCTCCGCCCGGACAAGGTCTGACTCAGCCC
chr4	1092701	1092821	1	+	GTCACAGAGGCTGCGCTGGGCCAGGTCAGCCCAGGGCCCCAAGGAAGAGCTGCCCGGTGCTCACGCGTGCTTTGCCCGCATCCTGCGAACTGGGAGGCCGCGAAGGCCTGAGAGTCAAGG
chr4	1205080	1205200	1	+	GGGCTCTTGGCTGTGAGGCCTGGCCTGTCCCTGTGGCTAAGGCGGAAGACCCAGCTGTCCCCTCCCTGTGCCCTCGCCACGCCCTCCCCGTAACGCTGACCAGACTTTGCACAGGGCAGG
chr4	1228424	1228544	1	+	GGGAAATTAGCCTGTGGCCCTCAGGCTTGTTCCCCAAGCACCAGCCCGGACACTGGGAGAGGCTACATGAAGGCTTCCCCGCCACGCGCGGCCCCTCAACCTCTGCCCAGGCGTCCTGAG
chr4	1533428	1533548	1	+	CCAGCCCGAAGCCCCTCATCTTCCCACTCAAATGTGTGCTCTTAATTGCAATCAATGCTCAGAAAAGCAATTAGCCCCCGACTGGCCACGCTGGTCATCTCTGATGGCAAGAAGGACTGC
chr4	1533548	1533668	1	+	AGAGGGTCACGCCGATGCGGTGAAGGGGCCGGCAGGGGGCTGTGGGGACAGAGATCCATCAGCCTTCCCACAATTAACGCCGAATCGCCACCCTCACCTCCTAAATTACACCGGCGGCCG
chr4	5731744	5731864	1	+	GCCCAGAGAGGTTCAGTGACTCTGCCAGGGACACACAGCGACCCAGCGTCACCATCGGAGCCCCAGAGGCCTTTGTCACTTCCTGTGCTGTATTGCCCAACACTGGGGTTATGGAGTCAG
chr4	7277951	7278071	1	+	AGGGGAGTGTCTGAGCACGTCTTGGCTTCGCTTGTGGATACCTTGTCATTGGTAGTGGGCCTGATCATTATGCCTGTGACAGATGAAGAAATTGAGGCACAGAGAGGCTCAGCAATTGGC
chr4	7473816	7473936	1	+	AGGCAGGATTGAAGAGGCCTGGCTCTGGCGGGGTCTGGGGGGAGAGGGGTTCCCCATGCCCACTTCACCTCCTTCCAGTGCATTCTGCACACAGCAGCCAGAGGGTGTTTCAAAAGTAGC
chr4	8286764	8286884	1	+	CATCAAGATCCATCCCAAGGTGGGTGGGCGTGGGTGGAGGGGCGGAAGCACCTGGGGCTGGGCATGGTGGCCTCTTCCCAGACGCCGGAACCCAGAGGCAAGCTAGCCCCACCTTCCATC
chr4	10079477	10079597	1	+	TCCAGTTCCCACAGGCTGAGCCGGGACTCGCCCAGAATCCAAGCCTCGGCACCCGCACTGGGCCTTTGCCTCTGGTACATGCAGCAGAGGCTCTGCAGCGGGGGCCTTCCTTCCATCTCC
chr4	108399760	108399880	1	+	CTAATTGCCGGCTACTTGAGATGTGTCCGTCTTAGACACGGGGAGTTGGGAGGCCCACAGTGAGAAGGCAACTAGATAAGTGTTCCAGTGTGGAGCCAGCCAGATGGCTATTAAATGTCT
chr4	152074984	152075104	1	+	CCTCCACGGAGCTGCCCGGTGCCATCCGCGGCTCGTGCAAACACTCTGCTCCAAGATTATGAGCGAGTGACAGCACAGCCTTTCAAGGTGTGCTAAATGAGAAATGTGCAATTTAGGCAG
chr4	687356	687476	1	-	CCGTCCTGCAGAAAAAGGAAGACAGGGCGGCTGTTGCCCAAGCTCCCTGTCCTGTCCCGTGGGCTGAGTCAGACCTTGTCCGGGCGGAGCCTGGGTCTGGCTGCTGTGTCCGAGGGTGTG
chr4	1092761	1092881	1	-	CCGCCTCTCCTGGCCTCTTGGCGAGAGTCCGCGTGAGTGACCTGCATTCTCCCCCGACTGCCTTGACTCTCAGGCCTTCGCGGCCTCCCAGTTCGCAGGATGCGGGCAAAGCACGCGTGA
chr4	1205140	1205260	1	-	GGACCTCAGCCGGGTGCTGTCTCCACCCACAGCCAGTTCCTGTCCATGTGCCCCCAGGGCCCTGCCCTGTGCAAAGTCTGGTCAGCGTTACGGGGAGGGCGTGGCGAGGGCACAGGGAGG
chr4	1228484	1228604	1	-	GACCAGTGCCGGCCTGCAGCCTACATGCGGCTGAGGAGGCTGCGGTGGGAATTGCTGGGACTCAGGACGCCTGGGCAGAGGTTGAGGGGCCGCGCGTGGCGGGGAAGCCTTCATGTAGCC
chr4	1533488	1533608	1	-	GATGGATCTCTGTCCCCACAGCCCCCTGCCGGCCCCTTCACCGCATCGGCGTGACCCTCTGCAGTCCTTCTTGCCATCAGAGATGACCAGCGTGGCCAGTCGGGGGCTAATTGCTTTTCT
chr4	5731684	5731804	1	-	CTCCGATGGTGACGCTGGGTCGCTGTGTGTCCCTGGCAGAGTCACTGAACCTCTCTGGGCCTCTGTTTCCTCCTCTGACAATGATGTGACTCCCGGCCCACTCCAAGAGGACTGGAAGCC
chr4	7277891	7278011	1	-	GCCCACTACCAATGACAAGGTATCCACAAGCGAAGCCAAGACGTGCTCAGACACTCCCCTGTACACCGCAATGTCCAGGGCCAGTGGGTACAGCCTCCCCCGGAGCTGTCCCTGAACTCT
chr4	7473756	7473876	1	-	GGCATGGGGAACCCCTCTCCCCCCAGACCCCGCCAGAGCCAGGCCTCTTCAATCCTGCCTAGCAGTGACTGCACCAGCCTCCGGGTCCCTGGTGACCCCATGCCAGGACCGCGCCCACCC
chr4	8286704	8286824	1	-	CAGCCCCAGGTGCTTCCGCCCCTCCACCCACGCCCACCCACCTTGGGATGGATCTTGATGGTGGCAATGTCCGACTTCTTGTCGATGTCTTTGATGGTGGCCTCATAGGAGTCCCCATTC
chr4	10079537	10079657	1	-	ATGAAGGCCACTGTCTGGGAGCAGTTGAGTAAGTTAGAACCGGAAGAATTGACAAGGAAGGGAGATGGAAGGAAGGCCCCCGCTGCAGAGCCTCTGCTGCATGTACCAGAGGCAAAGGCC
chr4	108399700	108399820	1	-	CTGTGGGCCTCCCAACTCCCCGTGTCTAAGACGGACACATCTCAAGTAGCCGGCAATTAGATTGAAACCTTATATTACTGCTGGCGGAGGCGGCCTAGGAGAAAACGTGAATTGAAATGA
chr4	152074924	152075044	1	-	ATAATCTTGGAGCAGAGTGTTTGCACGAGCCGCGGATGGCACCGGGCAGCTCCGTGGAGGTGTCAAAGCAGCAAAAGGGGACACTTGAGCAGATCAGCTTACTTCACAGAGAGACATCAG
chr4	184932973	184933093	1	-	GCGACAAAGCCAGACTCTGTCGGGAGAAAAAACAAAACAAAACAAAAAAAACCCTCAAAACTAAGGGGCCTGGGGGCTGTGCTGGATACCGGACACAAACAGAAAATTCTGTGGGGTGAG
chr4	54657877	54657997	1	+	GCGCAGAGGGAGGGCGCTGGGAGGAGGGGCTGCTGCTCGCCGCTCGCGGCTCTGGGGGCTCGGCTTTGCCGCGCTCGCTGCACTTGGGCGAGAGCTGGAACGTGGACCAGAGCTCGGATC
chr4	67558647	67558767	1	+	GTGTGTGTGCGTCTGTGTGTGTGTGTGTGTCCTGTTGGTGGTAGTGTTGGTGGTTAAAAAGCAATTTGGGACTTCCTCTTTGAACAGTTGCCTTTTCCTCTCACAGAAGGAAGATTTCATTT
chr4	159267729	159267849	1	+	TAATTCTGTGTTAAGCCTTTTTGAGGGGAGTCTGTGTGCAGTCAGCCATTTTAGCTTTTTTCTTTTTTTTTTTTTTTTCCTCTCCTTTTCTTTTGCCTCTTGTTCTTCAATCTCAGAAAT
chr4	39032350	39032470	1	-	AGTTCAAGACCTTTTTTTTTTTTTAAGTCTTACTCAAAAGGAAGTGAGTATGAGGTGAACTGCATTAACCTAAAGTGCTGCAGAGATAAACTTAAAGCAGGAAGCAACATACCATGAATG
chr4	48134209	48134329	1	-	TCTTCTGAGGTTTTCAGAACAGGAAAATAGGTGGGGTTAACTCTGCCCGTGAGAAACATCTTGAGCGAACTATGATTTCAGTTGAAAGATGTGTTTTTGTGAGTAGAGCACCGCAGAAGA
chr4	48906733	48906853	1	-	TCACCAGCTTAAGTGCTTAGCGGGCAGGCGAGGGGGCGGAGCAAGAGAAGAAAACACAAAGGGCCGGAAGGAAGCCGGGGAGACAGGTGGGGTACTCGGGAAGCTGGAGCGGGCCGGCGG
chr4	170026354	170026474	1	-	CCGCCCGGCGAGCCGCACTGGGCATGCTCGGCCCCGGCCGGCCCAGGCTCCTGTAGGTGGGAAGCTCCGCGCTCCCGGCAGCCGGCGGCGCAGCTCGCAACGCTGTGAGGCGCCGGCGGA
chr5	32203701	32203821	13	+	TGGGATTACAGGCGTGAGCCACTGCGCCCGGCCAGTTTCCCATTTTCTGCCTCTGCCCAGTTCCTCAATGCAATGGATCCAGATGTCTGCCTTATGCAACCACTACCTGGTGACCACTCC
chr5	54392234	54392354	7	-	ATTACAGGCGTGAGCCACTGCGCCCGGCCTGCTGTTTATTTTTTGGTGAAGCACTTTAACATTTAAGCTATATATAGTGAAGACCTGTGAACTTACCACTCCACTTGATTAAAAAAAAAC
chr5	109059010	109059130	7	-	AGTAGATGTTAAACAGCAATATATTGAGAGAAGTAAGTAGAAGGTGGGAAGAGGTTGTTACCAAGGTTTAACTTGAAAATAGCATAAAATTGGCCGGGCATGGTGGCTCACGCCTGTAAT
chr5	3750901	3751021	3	-	CTTACAGACAGGCAGAGAGAAACAAAAGAAACCTTGGATGCATCATGAGCTGGTCCCCCAAGCCTTGAGAAAGCTGTCCACGTCAGACAGGGTCCCGGCTGTGTGTGCCCCATTTGTACC
chr5	177599622	177599742	3	-	CGGCGCTGAGTTCAGCTGACAGCCCGCGCAGGCGTTAGGAGCCGAGCCCTGAAGACAAGTTGACTGAATTTGAAACCCGACTCTGCTTGCCGGGCGCGGTGGCTCACGCCTGTAATCCCA
chr5	434844	434964	1	+	ACCATCCAAGCTCAGATCTGTGTGTCTACGCTCAGATGCGTCGGTGGCTGGGCTGCCCTGCTCCTGGTCAGGCCGGAGCCCGTCCTAAGACACACGCTTTGCAGAGCTGTGCATGCGCAG
chr5	1856742	1856862	1	+	CCTCCGGAGCCCACCCCGGCTCCACCTTGGCTCCCAGGCCGGCACCCCCGGGCTGAGCACAGGGCCAGGGGCAGGCGGGTTCCAGAGGGAGCATTTCCAAGGGAGGAGGAAAACCAAAGT
chr5	3750841	3750961	1	+	GTTCTGTTGCTTCTGATATATACAACCAGGGTGGGCTGCCCACCAGGGTCCCTCAGCTGTGGTACAAATGGGGCACACACAGCCGGGACCCTGTCTGACGTGGACAGCTTTCTCAAGGCT
chr5	4879123	4879243	1	+	GTGGCCTGCTCTTGGCTTTGGGTGGTGACCGGGCTGGGAGGTTGGGCTTCTCCCTGAGATGGTCACTGCGTCAGGTATGAGGATGCCACACAGTCCTGCGCTCAATGGACACGTAACCTT
chr5	33549425	33549545	1	+	CATCAGGCCTCCCTTCCTTCCCCTCAGCCGTGGAGGCGCCAGGCATTCAGTCATAAAGAGGGGTTAGGTCTAGTTCCGGTGAACCCTGCTTTCCCTCCCACACCACAGAGCAGGAGGCAC
chr5	76801558	76801678	1	+	GAGGAAATTGCAAAAGTTTATCTTGTTCCGGAAATATTTTGAAGGTAGAGCCAAAAGGATTTGCTGATGGGTTGGATGGGAGAGAAAGTGAGTAGTCAGGATGACATGCCTTCCAAGCCT
chr5	135825640	135825760	1	+	TTCCTTCATACCCAGGCTGCCTCGGCACACTAGGACCTCATCTCTGGGTCCCCACACTCACTGGCCTGCTGCCCCGTCCTGCAGGTCTCGGCAGAGTTCCCCCGTGACAGTGACCGGGAT
chr5	151567122	151567242	1	+	TGATACAATCTCGTATTTTAGGTTCTGAAGCTCATCCACATCTATGGCTGACATAGTCATTATCGATTTCCCTACTGGCCAGTCTTGGCGGATAGACCCTGTACAGTTGACTTCTTCAAA
chr5	170149555	170149675	1	+	ACTTTATAGATGAGGACGCTGATGTGTTCAGTCACTCGCCTGTTGGCACACATTGGCTAGCAGAGGTGGTCCTGCATCTCTAGTCCCTCGGGACTCAAGCCGGTGCCCTAAACCACCTCA
chr5	173795031	173795151	1	+	GCCCAAGTCAAGGAGTCAGCCTGATCCCCATTCAGGTGCACATTGCCCCGGCGGCCCCCGGCAAATCACTTTCATCTTTGAGCCTCAGTGTCCTCATAACGGGGCTGTTGTGAGCTGTGG
chr5	173795151	173795271	1	+	TGAGCAGCAGGTGATACGGAGCTTGCATTCAGCCCCTGTGAACGACTTGCCGGGACTGCTCTAAGCAGGGACCTCACCACCCTTCCGGGGACATCCTGGAGCAGGAAGGCTCCTGCTGGT
chr5	177386314	177386434	1	+	GGACATGCTCAGCTCGGCCTTCCAGCTGGCTGGAGGTAGGGCCCGGGTGGAGGAGACCTGGGAGGGGTTCCTGAAGGGCCTTGGACAACGCTGGCTCATGCTCCCCAGGGAAGGTGGCTG
chr5	178287019	178287139	1	+	CAGCGAATAATGCCAAGATGCGGGGCTGAACTTTCCAGCGAAAGCCTGTGCTTCCCCAAGATGCTGGACGCCCAAAGGTCCGGGCTGCCGTGTGCAGGAGACGGGAGCCTGACCCTTGCC
chr5	180232661	180232781	1	+	AAGAGGGAATAGGACAGAGAAATGGAACCCAGACCCAGACCCCAGTATCTCAAGAAACATCTTCCTTCTTTCAAGACCTTTGAAAACACAACTGGGCCGGGCGCGGCGGCTCACGCCTGT
chr5	434784	434904	1	-	CAGGGCAGCCCAGCCACCGACGCATCTGAGCGTAGACACACAGATCTGAGCTTGGATGGTGGTCACTGCGCTATGGCAGGAATGTGCACCCCGAAGCTTGGGGCGGGACCAGCGTGGCCA
chr5	1856682	1856802	1	-	GTGCTCAGCCCGGGGGTGCCGGCCTGGGAGCCAAGGTGGAGCCGGGGTGGGCTCCGGAGGACGGACCGCAGAGGTGGGCCGGGAGGCGCTGGCGAGCACGCAGCTCCCTCAGGCTCGTCC
chr5	1856802	1856922	1	-	CTCACCCGGCCCTGGGAGCGGGGGCGTTTCCCCTCTGTCCTTGCCCCCTGCCTGGCAGGCACTTTGGTTTTCCTCCTCCCTTGGAAATGCTCCCTCTGGAACCCGCCTGCCCCTGGCCCT
chr5	4879183	4879303	1	-	CCCCAGCTGCAGCCCACTCCTCAGCCCAGGCGACAATCTGTCGATGTGTCGGCCTCGTGCAAGGTTACGTGTCCATTGAGCGCAGGACTGTGTGGCATCCTCATACCTGACGCAGTGACC
chr5	33549365	33549485	1	-	CTCTTTATGACTGAATGCCTGGCGCCTCCACGGCTGAGGGGAAGGAAGGGAGGCCTGATGCCAATGACTCAGAGATCGCCTTTGATTTTTCTCTCCATACAGTGCTCCAGAAACTGCAGT
chr5	76801498	76801618	1	-	ATCCTTTTGGCTCTACCTTCAAAATATTTCCGGAACAAGATAAACTTTTGCAATTTCCTCTTGCTCCCACCCTCACCCAAAACACCAGCCTCCCTTTCCCAGTTCTCAATAGCCTCTCAG
chr5	135825700	135825820	1	-	GGTTCTGTAGTAATGCACAAATCCTGAGGCATAAAGACCATGGTCCCTGGAGAGAGGGGCATCCCGGTCACTGTCACGGGGGAACTCTGCCGAGACCTGCAGGACGGGGCAGCAGGCCAG
chr5	151567182	151567302	1	-	CGGGAGAAGGAAGTGTCCATTTTTCTTCAGCTCAGGAACTTGAATGACAACCAGCCTATGTTTGAAGAAGTCAACTGTACAGGGTCTATCCGCCAAGACTGGCCAGTAGGGAAATCGATA
chr5	170149615	170149735	1	-	GTTTTACTACAAAACAGCGTGTCCCAATTTCAGGATGCCAATCCCCAGAAATCAGTAGAATGAGGTGGTTTAGGGCACCGGCTTGAGTCCCGAGGGACTAGAGATGCAGGACCACCTCTG
chr5	173795091	173795211	1	-	AGCAGTCCCGGCAAGTCGTTCACAGGGGCTGAATGCAAGCTCCGTATCACCTGCTGCTCACCACAGCTCACAACAGCCCCGTTATGAGGACACTGAGGCTCAAAGATGAAAGTGATTTGC
chr5	174629431	174629551	1	-	CGTGAGCTACCGTGCCCGGCGCCTGTGATATATTTCTAAGCGATCACTGTCCTTCCACTCCCAGCCCACTTCCCATTCCAGGCTATTCTTCACACAACAGCCAGAACTGCTCCTTTTGGA
chr5	177386374	177386494	1	-	TCCCCACCACCAGCCCGGCCACCGGGTTGGACAGGATGGCGTTATCCTTGAAGATGTCACCAGCCACCTTCCCTGGGGAGCATGAGCCAGCGTTGTCCAAGGCCCTTCAGGAACCCCTCC
chr5	178287079	178287199	1	-	CATCCCATGGCACACCTGGGGTTAGGGCCCTGCCGCAGTCCCCAGCTGCTCTTCTGATTAGGCAAGGGTCAGGCTCCCGTCTCCTGCACACGGCAGCCCGGACCTTTGGGCGTCCAGCAT
chr5	111224306	111224426	1	+	CGCCCCCTTCCCCGCCCACCGTCCCTGCGAGCGCGGGCGGCGGCGGTGGGCGTGTGCGCGCGTGAAGGACGCCGCCTCTCTCTCGCTCCTGCGTTCGCAGGCGGCGGCTGGCGGCCGGCT
chr5	132658093	132658213	1	+	GTGCCTGAAAAAGCAGAGACCATGGTGTCAGGCGTCACCACTTGGGCCTATAAAAGCTGCCACAAGACGCCAAGGCCACAAGCCACCCAGCCTATGCATCCGCTCCTCAATCCTCTCCTG
chr5	134114601	134114721	1	+	TCCCGGGAGAGGAGAGGCGGGGCGGACCTGTGTCCCGCCCCCGGCCCGGCCCGCCCCCAGTGCCCGCCCCGCCCCCGGCACTCGGCCGGCGGCGCCTTTGATGTTCCGACCCGCCAGCTC
chr5	149141425	149141545	1	+	AGCCCGGCGGGGCGGGGCCTCGGACACGCGCCGGTGCGTCCAGCAGGTGGCAGCAGCGAGCGGCCGCGCCCCCTGCGCTGCCAACCCGCGAGCCCGCATCATGGATGTCGAGCTCCCCTA
chr5	178113472	178113592	1	+	CCACATCCGGGGGCCGGGGCCGGGCTGTGGGCTTGCCGCGCGCCGGTGAGTCAGGCCGGGTTTTCCCTCCGCCTTTGGGGCAGGCGATCGAGCGCCGCGGAGCGCGTCCCTCCCTCGCCA
chr5	108381369	108381489	1	-	CCGGCGCGCCCGCCCCCGCCGGCCCAGAGGAGGAGCCGCCGCTCTCGCCGCCGCCGCGGGACGGGGCCTACGCTGCCGCCTCCTCCTCTCAGCACCTGGCGCGGCGCTACGCGGCCCTGG
chr5	132543481	132543601	1	-	CATTCTCTATCTGATTGTTAGAAATTATTCATTTCCTCAAAGACAGACAATAAATTGACTGGGGACGCAGTCTTGTACTATGCACTTTCTTTGCCAAAGGCAAACGCAGAACGTTTCAGA
chr5	135578950	135579070	1	-	GGTTCTGCATATTAATGAGCTCGCTCGCTGCGAGGGCAGGAGCGGATTTAAAAGAGGCCAGGGCGGGCGGAGGGAGGCTGTGGAGAGAGCGCGGAGACAAGCGCAGAGCGCAGCGCACGG
chr5	138213282	138213402	1	-	GAGCCGGCCAATGACAGGCAGATATTTTTGGTGCAGATGGGCAGCCAGTATTATCGCCGATGATTGGCTGGAGTGGCCCGAGTCGGGAAAATGGCTGCGAGTACCTCCATGGTCCCGGTG
chr5	179345363	179345483	1	-	CCCGCCCGCCCCTCCGCGCCTCGCCTCCTCCGCCCCGCGCCCTGCGGTGCTGCAGCTGCGGGCGGCTCCAGCTGCCCCCAGATGTGGGCTGGGCGGCTCGCGGGGAACTTTCGCGCCGGC

chr6	150064812	150064932	7	+	GGATTTGTCTCCCCTGCTGTGGGGCAGCCGCTGTGACAGGTCCTGGGGGTAGGAAGGGAGAAGGGGTGCTCCCTGTCCTCAGGGAGCTCACACAGCTGCTGAGGGAAGCAAGGTGACAGC
chr6	150064752	150064872	6	-	CTCCCTTCCTACCCCCAGGACCTGTCACAGCGGCTGCCCCACAGCAGGGGAGACAAATCCTCTGCCTTCCCGGATGACCTGGGGTAGCAGGAGCTAAGGAGCCATCTCCTCAGATTTGGA
chr6	6687156	6687276	4	-	CGGAGGCCCGGGAGGGGCGGGTCTTCCAGCCTGGAGGGTGAGGCCTGGAGTGGGCGGGGCTCCCAGCCAGGAGGGTGAGGACTGGAGTGGGCGGGGCTTCCAGCCAGGAGATGAGGCCTG
chr6	6687216	6687336	2	+	GCCCCGCCCACTCCAGGCCTCACCCTCCAGGCTGGAAGACCCGCCCCTCCCGGGCCTCCGGATCCTGGCTGGGAGCCATCTCTGCCTCCTGCCGCTTCCTGCACTCCTGATCAGGTCAGT
chr6	32637341	32637461	2	+	GCCAAAACCTGACTTGGCAGGGTTTGGTTTGGGTGTCTTCAGATTTCCTTGTCTTGAGGTCCTCACAATTACTCTACAGCTCAGAACACCAACTGCTGAGGCTGCCTTGGGAAGAGGATG
chr6	33075930	33076050	2	+	AGAAGACTACTTGGGTTCATGGTCTCTAATATTTCAAACAGGAGCTCCCTTTAGCGAGTCCTTCTTTTCCTGACTGCAGCTCTTTTCATTTTGCCATCCTTTTCCAGCTCCATGATGGTT
chr6	13711672	13711792	2	-	TTCCCCTCCCGCGCTCCCGCGTCGCCCCCGCCCTCGGCGCCTCGTCCCCGGGCCGCGCGCCCGCGCTCCGGCCAACGTTCTCTCCCGGCCTCCCGGGCCCGCCGCCTACTCCCGCGTCTC
chr6	32666625	32666745	2	-	ATTGGTTCTTTTCCGAGGGACCATCCAATCCTGCCACTCACGGAAACATCCACAGGTTTTTATTCTTTCTGCCAGGTACATCAGATCCATCAGGTCCGAGCTGTGTTGACTACCACTGCT
chr6	14949702	14949822	1	+	AAATTTTAAAAAGAGCTCATGTAGAAGAAAAATGGTGCTGCTCACTGTGAATCTGGGGCATAGCAGTGAGGCGGCAGGGACACTGAGCCCCACAATTCCGCCAGGGCCCTCACCAGTAGG
chr6	34008068	34008188	1	+	CCAGCGGCCTTCCAGTGGATGCCTAGGTCCCGGCCTCTCCACCCTCACTTCACTCCGCCCTCCACCCCAATCCCTCTGTGCTGCTTCACGGGCCTCCTTCAATTTCTTAAACTTGCCAGA
chr6	42966723	42966843	1	+	ACCCACCCATCTACATCCATTTCCTCTTTCCGCCTTTCCGGTGCCCACGTCCTCTTACCCTGAGTTCTTGATCCTGGTGCAGGCTGCCCGGCTGCTGTGGGTCAGAAGGGCATAGAGATC
chr6	56099058	56099178	1	+	TTCAATAGTATCATGTTCAACGTAAATACGTGCTCCTCACATTGAATTATGGTCTACACAGACTTGCCGGTCAGTCTGCCCTTTCTAACATTGTTTCTACGGGAGAATGAATTACAGATT
chr6	136360994	136361114	1	+	GCGGCCGCACCTGCCTCTGGGCGCGCTCTGCCTCCTCCCGCTCGCGCAGCGCCCGCTCCTCCGCCTGCCGCTGCAGCTGCTCCTCCTTCTCCCGGGCCTGCTCGGCTTCCAGCCTGCGCG
chr6	139771793	139771913	1	+	TTGAAATGATCTTTTCTCCTCCGTTCTCCGGTGAACACACACAGGAAACTATGTCTTTTGGTATTTCGTCAGAATATTTGTGTGCTGTTGTAGAAGATTTTGTAGGGCTAAGTGGTTTT
chr6	150301132	150301252	1	+	CCCAAAGAGCATCAAGTTACTGAGCCACCGTCTTTCTGGGGACAAAAAGGTCTCATGTAAAAGAATGAGCTCACACCCGGGTGGGACGTTTTGCAATTTGATGGAGAGGATGTCGAGTAC
chr6	155256650	155256770	1	+	CCCGGGAAATACCCACACCCCGGCTTGGCAGATTTTGCCGACAATCTCATCAAAGAGAGTGACATCCTGAGCGATGAAGATGATGACCACCGTCAGACTGTGAAGCAGGGCAGCCCTACT
chr6	159316186	159316306	1	+	CCCTCTGTAAGGCCTCCTGACCTCAGAGCGGGTGACCGCACGTGGCCTTGCAGTGCAGATAGCTCCACTGTCAAATGCACACAGGTAACCCCGGCCCCTTCCTGGACTCTGGGAGGTTTC
chr6	168995776	168995896	1	+	GGTCCCTCGTGCGGAGGAACAGGAAGTACGCTCATGAGTGAGTACTGCGGATCCACCACACGGGACCTGCCTATGGCACGGGCTGTTCAAGATCACAGGCCTCACAGAAAGCAAGCTGAG
chr6	169072624	169072744	1	+	GTCCTGCCCAGATCCTCTTAGATTCCATGCACAGCGTGCGTCTGTGGGTTTGCTGCTTGGGGTCCACACCACAGACCTCATGAGAGTATCCAGAGGCTGTGGAACAGGGTGTCCCATCGG
chr6	169240405	169240525	1	+	TCCGATGGTGGCCTCTTCCCCCAAGAGCCGTGTTCTGGGGCCTCACCTTGCAGGTACACGTGGTGCAGCTGTCCACCACCCACGTTTCATTTTCCGCAAAGAACCGGCCATCCTGCCAGC
chr6	170023513	170023633	1	+	CCGCTTCCCGCGCGGGCTGAGGAGAGATGGCGCAGAGGCGCTGGGAACCCACGGGCTTCTGAGGAGCGCAGCGGGCACGACGACGGAGCGGAGTCCTGAGGCCACAGCTGAGGAAAGGGT
chr6	170248116	170248236	1	+	CTTCCAACAACGGTCTGTGTGCGGCCCGCGGGGCCAGAGGTCCAGCCAGGGTTTCCGGAGGGCTCCCTGAAGGCTCACAGCTGTGCCTGGCACTGGCCTGCTGCAGACAGCCAGGGTCTT
chr6	6687276	6687396	1	-	CTGTAGGAATGCTGTGGAGCTAACAGTCAGGAAGGACATTTCAGAGGTCTGTGACTGGCCACTGACCTGATCAGGAGTGCAGGAAGCGGCAGGAGGCAGAGATGGCTCCCAGCCAGGATC
chr6	14949762	14949882	1	-	TCAGAATTTGTATATTGCCCCTAAGAGCTCAAACTCCCCCAAACCCAGTACCCGGCTTCACCTACTGGTGAGGGCCCTGGCGGAATTGTGGGGCTCAGTGTCCCTGCCGCCTCACTGCTA
chr6	34008128	34008248	1	-	GAAGGTGTTTCAGGGAAAGGGGATAGCATGTGCTAGGCCCTGGGGTGGGAAGGGGGCTGGTCTGGCAAGTTTAAGAAATTGAAGGAGGCCCGTGAAGCAGCACAGAGGGATTGGGGTGGA
chr6	42966663	42966783	1	-	GGGTAAGAGGACGTGGGCACCGGAAAGGCGGAAAGAGGAAATGGATGTAGATGGGTGGGTGGTGAGGAAGGGAGAAGGGAATGGGACGCTGATGGTGAGGAGGCTTCCCTGTGTTCCTCT
chr6	56098998	56099118	1	-	TGTGTAGACCATAATTCAATGTGAGGAGCACGTATTTACGTTGAACATGATACTATTGAAATATCTTCATAAAACCTAAAAAGATAAAAGAAATATTAAACATAGGCCGGGTGCAGTGGC
chr6	110595358	110595478	1	-	CAGGCATGAGCCATGGTGCCCGGCCAAGCCTTTAATATGCTGATAACATTGTGCATTTCCAGGAAGGTGATATAGTGCAACCTTTCTAAGCTTACTTGGCCAAAGAACTGTTTTTTTCTT
chr6	136360934	136361054	1	-	AGGAGCGGGCGCTGCGCGAGCGGGAGGAGGCAGAGCGCGCCCAGAGGCAGGTGCGGCCGCACCCCACCCTGGCCCCGGCCCCAGTCCCGCAGGGAGACGCCCCAGCCCAGCAGAGGAGGG
chr6	139771733	139771853	1	-	CAAAAGACATAGTTTCCTGTGTGTGTTCACCGGAGAACGGAGGAGAAAAGATCATTTCAAGTAAAGGATGCAGTGTTGACTGAGAGGTGTCGGAGGGTGTGACCTGCTCTCTGCGAAGTC
chr6	150301072	150301192	1	-	TTACATGAGACCTTTTTGTCCCCAGAAAGACGGTGGCTCAGTAACTTGATGCTCTTTGGGATTGTCTAACCTAAATTTGTCTCCTCTTCCCTCTCGGGGGCTGCGTAGATTTTCCCCTAC
chr6	155256590	155256710	1	-	ACTCTCTTTGATGAGATTGTCGGCAAAATCTGCCAAGCCGGGGTGTGGGTATTTCCCGGGAGAAGTGCTCTTGGAGTCCTGCCTGCCCTCAGCCGTGGGGCAGCCGCTGCTCTGGGTGCC
chr6	159316126	159316246	1	-	ATCTGCACTGCAAGGCCACGTGCGGTCACCCGCTCTGAGGTCAGGAGGCCTTACAGAGGGCGGCTGAACCATGTCACGGGCTGCAGCCTCCTGACCTGGCCAGGGACGTGCTGACTCCCG
chr6	168995716	168995836	1	-	TGTGGTGGATCCGCAGTACTCACTCATGAGCGTACTTCCTGTTCCTCCGCACGAGGGACCGGTGTAGTGGGAAGCACCCAGCTCTGGAAACACAGGGATCTTCCTTAGCATCTTGACGTC
chr6	169072564	169072684	1	-	CCAAGCAGCAAACCCACAGACGCACGCTGTGCATGGAATCTAAGAGGATCTGGGCAGGACCCTGGGTGGTCCGGGGCTCCGGGGAGCAGAGGCCACACTGACATTAACTGGGTGAGGATT
chr6	169240345	169240465	1	-	CGTGTACCTGCAAGGTGAGGCCCCAGAACACGGCTCTTGGGGGAAGAGGCCACCATCGGACACTTGGCAGAACCTGACTGCCTGGAAATGCCAGCGTTCAGTGCTGATGTGTGAAACCGG
chr6	170023453	170023573	1	-	AGAAGCCCGTGGGTTCCCAGCGCCTCTGCGCCATCTCTCCTCAGCCCGCGCGGGAAGCGGCGCCGAGCATTGCCCGGCTGGCGAGACCTCCCGTGAGGCGCGAACGCGGCCTGAGGAGAG
chr6	170248056	170248176	1	-	CTCCGGAAACCCTGGCTGGACCTCTGGCCCCGCGGGCCGCACACAGACCGTTGTTGGAAGGCCTCGACTTGACTTCATCTTGGTTTCCTTCTGGTGTACACCGTCATCTCGTTTTTCTTC
chr6	25279018	25279138	1	+	CAGCAGATGGCTCCCGGGCTCTCTCGCGAGCCCGCTCGCCCCCTCTCCAGACGCAGGGCTTTTGCGGTTTGGGAGGGAGGCTGCGAGGAGGGGCGCGGTGCCCGCCGCCGCCACCGCAGC
chr6	36291310	36291430	1	+	CCTTTGCAGATGAGTATCTCAGAGTCCTCAACGTGGGTGTGGCCGAGGTGAAGAAATCCTTCCTGGGGCCCTTGTCCCCGTCCTGTAAGATGGTGCAGATGATGAGGCAGTTTCTGTACC
chr6	44223515	44223635	1	+	GAGGTGGCAGTGGGCGCAGGGCGGGGCGAGCTCAGCGGAGGGCGGGTTTGAATGTGCCCCGGCGGGAGAGGGAAGCTGCAGCGAGAGCGCGCGGATCTCAGCGCGGGAGCAGTGCTTCTG
chr6	52186295	52186415	1	+	AACCCACTGCGACACGCCACGTAAGTGACCACAGAAGGAGAAAAGCCCTATAAAAAGAGAGACGATAGCGCTACATTTTGTCCATCTCATAGCAGGCACAAACTCATCCATCCCCAGTTG
chr6	85450003	85450123	1	+	GAAGGACCCGCCCCGGCCTTGACCCGGGCCCCGCCCCTCCAGCCGGGGCACCGAGCCCCGGCCCTAGCTGCTCGCCCCTACTCGCCGGCACTCGCCCGGCTCGCCCGCTTTCGCACCCAG
chr6	95577456	95577576	1	+	CCGCCCGCTCCGTGACCCCGCCCCCACCCGTCCCGCCCCTGAAAGCGCCCGGAACGCTGTGCGCGCGCCTTCGGGGAGGAGGGGCTGTCTGGGCTCGGGGCGCGGCGGCAGTCAGCTCTA
chr6	96521759	96521879	1	+	CGTCGGGGGCGGAGCCTCTTGTCCCTCTGCGCGGCCCGTTCCGCCTCTCTTCTCCCACCGCCTGTCGGCTGACGTGTCTGCAGTTCCTCCGCGTCTACTGCGAGTCAGGCCGTGATGGCG
chr6	158232176	158232296	1	+	GCGGCGGTGAAGGGAGGCGGAGACTCGGCCGAGACGCGGGGGGAGGCGGCGGCGGCGGCGATGCGGGGCTGCTGGAGGCGGAGAGGCACGGAGGAGCCGCTGGGGCTGCCGCCACGGCCG
chr6	32953057	32953177	1	-	GATTGGTTTAGACAAAATGACAAGGGCACCTATTGGAAATGATCTGGCAAAACATGATCTAAGGCCACCCTCTCGGGGAGGGAGTTGGGGAAGCTGGGTTGGCTGGGTTGGTAGCTCCTA
chr6	88963577	88963697	1	-	CTATCCTTCCGCTGAGCTTCCTCTTCTTTCCCTCTGACCTCGGAAAGGGGGCGGGGCTTTCGGGGGCGGAAGTTGCGGTGCATTGTGGGTTCTCCTGGAGCTGTGGAGTTGATCCTGAAT
chr6	100881288	100881408	1	-	GAGGGCCCGGAGTCGACGAGTCGACGTGCCGACGTTGGCGCTGCAGCGGGGCGGTGACGTGTAGGCCGGCGCCAGCTCCACTCTGTCCCTCCTCGCCGGGTCTGTGCGTCTTTGCGTCTG
chr7	158279808	158279928	47	+	TTCGAGCCCGGCCAGAGCAGACACCGAGGCAGAGAAGGCGCCCAGAGTGAGCGAGGGCTGCTAGCACGTTATCACCTCTCAATGTGGACTTGACCCCACGGTGTGCCAGGTAAAATAAAG
chr7	75912210	75912330	40	+	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAGGCTTCCTTGCCAGTGGGTGTAGCAGAAACGAGAAGTGACATAAACAGTCAGGAAGCCGGCTAGGTGCGGTGGCTCACACCTGTAATCC
chr7	1116295	1116415	40	-	TGCAGTCATGTCATCATCCTGCGTGGGCGTCGGTGATGGAAGCTGTCCCTAGAGCTGTAGTGATGTCATCATCCTGCATGGGCGTTGGTGATGGAAGCCTGTCCGTAGAGCTGTAGTGAT
chr7	1116355	1116475	39	+	CTACAGCTCTAGGGACAGCTTCCATCACCGACGCCCACGCAGGATGATGACATGACTGCAGCTCTACGGACCGGCTTCCATCACCGACGTCCACGCAGGATGATGACATCACTGCAGTTC
chr7	129592861	129592981	33	-	CTCTCAAAGTGCTGAGATTACAGGCCTGAGCCACCACGCCCGGCCAAGAATCAGAATTTACCGGAGCAGAAACCTCTGCAGCCTGGGATAGGAGAACCTCAACTGTAATTGCAGGATTGC
chr7	1994614	1994734	28	-	CCTCTCACTGTGTCCTCACACGGTGGGAGGGGCGAGGGAGCTCTGGGGTCCCTTTTATGAGGGTGCTAATCCCCCCCCCGAGGCTCCGCCCGGTGGCCTCCTCACCTCCCCGGGCTCCCT
chr7	64794348	64794468	23	+	GGACGCCGGGCTGGGAACGGTCCAATCAGGCACCCAGCTGGAGCGGACATGACGTCTTCCGGGAGGCGGCGGGGTCTTTGTCTCGCTGCAGCGGGTGCTGCAGGTCTGGCCTTCACTTTT
chr7	29645770	29645890	18	+	TGGAACGTCTTCAGGGGGTGCCTCCCCTATAAGCCCGCCGTCTGTCCAGGGGAGCCCAGAGCGAGTCCGGTCTTCACCCACTAGCAGATCTCACTGGGGCCTCCAAATGTTGTAACCAAG
chr7	29645710	29645830	13	-	TCTGGGCTCCCCTGGACAGACGGCGGGCTTATAGGGGAGGCACCCCCTGAAGACGTTCCAGGGCCCTGTAGGCCACCGTCTTCTGGAGGGGAACGGATTGACTGCCGTTGTGCCCGGCCA
chr7	5045780	5045900	8	+	CGGAGGCTGACTTCCGGTGCACTCCTGCGCGTGTGCACCTCTCTCTGTGTGCGTGTTCGCGCATGCGCGCCGCCGCTGCACTGCCCTCGCTTCCTGTGCGTCCTCAGGTCACCGCTTGCT
chr7	71174376	71174496	7	+	CCTGGGGCTCTGGGGACCTGTGGGGAAGGTGGTTCTGACAGCAGAAGCCAAATGAAGAAGAGGCTGGTGTGTGTCTCACGTGTCCGTGTGAAGAGACCACTAAACAGGCTTTGTGTGAGC
chr7	28531669	28531789	6	-	CTAAGTGCTGGGATTACAGGCGTGAGCCCCCACGCCCGGCTAGCCTCAGTTTTTAGTTAGGGTCTCCATACCCCTCTCTGTTGGCCTGGTTTCAGAATTCCTATGTAAAGTAAAAGTTTA
chr7	129592801	129592921	5	+	TGAGACTGGGCTCCTTCAGAGTTTTAAACTCACAAACAACTTGTCCATGCTGAGCCTCTAGCAATCCTGCAATTACAGTTGAGGTTCTCCTATCCCAGGCTGCAGAGGTTTCTGCTCCGG
chr7	1492735	1492855	2	+	TTGGACTCGGGCCGAGCCAGTCAAGGCCCGTAGTGGCCTCACTGGTCTCTGGGAACAGGCCATGAGCAGGCCCATGGGGAGTGGGGCGCGGGCTTACCCGGGCGGGAGTGGGGAGTGGGG
chr7	34991978	34992098	2	+	AAAATGGTTAAACATCCTCGTACATGTAAATGCTGGCACGTTTGTTTCGGCAGGAGGGACCTAACTGTGAGACACGTGAGTCAAAGGATGTGAGCTGTGCCCGGAAGCACTGCAGCAGTC
chr7	66503220	66503340	2	+	CCGCTGCCAGCAATGGATGCACCAGCCCCGCCAGGGGTGGCACCATGTGCTCCCCCAGGGCACCTCCGGGCCCCAGCACTCACCATGGGGGGCTTCTGGTACCGACCGTCTTAAGTAGAC
chr7	4116324	4116444	2	-	GGCACACAGAGCGGGTGGCACGTGCAGATGCACTGGGCACGTGCTGGTGCCCTCGGTGTGCTGGGCGCTGCTGGACCCAAGCCCAGGGTGCAGACTCCTCACCCCGGCCTGGCTGTCTCG
chr7	34991918	34992038	2	-	GTCCCTCCTGCCGAAACAAACGTGCCAGCATTTACATGTACGAGGATGTTTAACCATTTTTTATTATAGCAAGAAACTGAAAAATATTTATATGCCCGGTAATATGGAATGGACTAAATA
chr7	66503160	66503280	2	-	CCCTGGGGGAGCACATGGTGCCACCCCTGGCGGGGCTGGTGCATCCATTGCTGGCAGCGGACCCCTCTAGGGGGCCTGGGCTTGTGGCATCTCTGAGGGCCCAGATCGCACAAGGGGACC
chr7	376966	377086	1	+	GCGTCCTACAATGCATTTGAATGTTCAACGCAGCATTCGCCTCTCTGGGCCTCAGTTTCCTCCTCTGTGACTCAGGACAATGGTCCCAGCCCCGTTTCCAGGAAGGCAGAGGACCTTGAG
chr7	1331826	1331946	1	+	AACACGTTCATGCATCTGTTCACTCATTCGCTCACTCTTCATCTCACAGCTATTCTTCGAGTTCTTCCTCGAAGAAGAAGAGCCAGGCACTGTGGCAGGCTGGGCACGCCAGGGAACAAA
chr7	1936588	1936708	1	+	TGACAGGCAGGGGCGCCTGAGGCTGCCCCAAAGGCGCACGGATGGACCTACCCACGGAAGGTCGAGGATGGCAGGGACCGGGGGTGGGGGGTGCCTACCTGCCACCTCCTTGGACGATGG
chr7	2146054	2146174	1	+	GTAGGCTGCTCACAGCGGCACACTACGCCGGCTGATAGGCAACATTCATCTTCTAAAAGCCAAGCTCCTGAAAACAGGCACACGAATGACCCAGCCGTCACTTCAGAAGCTCGGCCTGAG
chr7	4116384	4116504	1	+	CACACCGAGGGCACCAGCACGTGCCCAGTGCATCTGCACGTGCCACCCGCTCTGTGTGCCACAGCGTGGAAGGGCCTGGGAAGCTCTGGATAAAGGCTCCTCTCATCCTTTCTTGCTCAT
chr7	4236005	4236125	1	+	GCCCACAAACCTACTTCTGTCTTTTGGATTTAAAGCACCGTCACCTCCTAAGGAGCCCTGTGAACCTGCATTAGCCAAAGCCGATTCCCTGTTCTTCTTCCCGGTGTGCACACATCCCCT
chr7	4707194	4707314	1	+	CCAAACACTAACGGAGAGGGAAGAGGTGCGGGGAGCTCAGGGCGTTCGGGGTGGTGTTCTGGTGGAGGGGACGCTGGTAAAGAGCAGGTCTGGCTCAGTGCTTATTTCAGGGAAAACTCT
chr7	6648091	6648211	1	+	GGTAAATGCCCGGCTTTGGTGATGCCGACGAGCACCCTCCCAGGTGTAGGGACCTTTGTGCCTCCAGGGCCTGAGGGCCTTGGCACTGCACCAGCCACTGGTGAGCAGGAGGGCACTAGT
chr7	55068675	55068795	1	+	CATGCACAGATGGCTGAAGTATTGAGAACGCTCCAGTGACCGGGAGGCAATAGTCTGTCCACATCTAAGAACACACTTGGAATAACCTTAGAGAAGAGAGAGAGAGAGAGAGAATGCATGGT
chr7	73769097	73769217	1	+	ACGGGGTGGTCAAGTATTGGCGGTCACCCAGGCCCCGTGCTCCAGAAGGGTGAGGTTTCACAGTCCATGCAGGTTGGTCCCTGGGCCCCGAAGTCGACTGCCCGGCCCCGCAAAGCCGTGG
chr7	100985961	100986081	1	+	GGCAGCCCCTGGAGCTCAGCCCCTCCACTTCCATCAGGTTGAACTAGACAAAACTTAGCTCATAAACGAGAGGATTGGGCAAAACCACAAAAGTCCACCGACTTCAAAACAAACATGTGG
chr7	128121576	128121696	1	+	CGGGAGCGAAAAGATAGCTTGGGGAGCAAATGTGGACTCACTGAAATTAAAGTTAAATTGGAATAAATTAAATTAAATGGCAACTTTCCGGTGCTCATCTCTCAGGCCAAATTATTGTGC
chr7	149822066	149822186	1	+	CCGCAGCTGCGGCCCGGGCCTGGCCTCTCGCTCTGGGTCCTGCCCCTGCCTGATGGCCAAGGCCGACCCCACCTGCAACAGCACCTTCCTCCACCTGGACACCCAGGGCTGCTACTCAGG
chr7	158252920	158253040	1	+	CCTTAATCTTCCCTCACCCTTGGGCTGGCGGAGTGAGAGTCCCTGTGGCCCGAGGTTCCTCCTGTCATGCCCACGGCACTCAGAACTGAGGCTGGCATGCGGAGGGTGTGGTTTCCCCGG
chr7	376906	377026	1	-	GGAAACTGAGGCCCAGAGAGGCGAATGCTGCGTTGAACATTCAAATGCATTGTAGGACGCCCTGGGTGTGTCCGCCGGGAGCTGCCGCCCCGCCCACCACCCTTGCACCTCGGGGCCTGG
chr7	1331766	1331886	1	-	TCGAAGAATAGCTGTGAGATGAAGAGTGAGCGAATGAGTGAACAGATGCATGAACGTGTTCAGGGCACCGGGTGGCTTCTTAGCCACAGCTGCAGATGGGTGTGGGTTTGCCTGCGGGGC
chr7	1492675	1492795	1	-	GCCTGTTCCCAGAGACCAGTGAGGCCACTACGGGCCTTGACTGGCTCGGCCCGAGTCCAACCGTTACCTGGGTTTGAGTGGGCTGTTTCCCCGTTGTCTTCCCCGGTGTCTCCAGCTCAG
chr7	1936528	1936648	1	-	CTTCCGTGGGTAGGTCCATCCGTGCGCCTTTGGGGCAGCCTCAGGCGCCCCTGCCTGTCATCCCCAGAGGGTTTGTCCTCCCCTGTGGGCAGCCGGGTCTGGTGGTTGCTGGGGCAGAGC
chr7	2145994	2146114	1	-	GCTTTTAGAAGATGAATGTTGCCTATCAGCCGGCGTAGTGTGCCGCTGTGAGCAGCCTACACCACGCAGTCTTGATGCACTTCCTGGGTGTTGTGTAACTTTCCTTCTCTGCTGATCTGA
chr7	4235945	4236065	1	-	CAGGGCTCCTTAGGAGGTGACGGTGCTTTAAATCCAAAAGACAGAAGTAGGTTTGTGGGCTGCGCATTTGGTACTCCATGCGGCAAGTCTGACGCATGCCACACTTACACCACCGGGCAA
chr7	4707134	4707254	1	-	AGAACACCACCCCGAACGCCCTGAGCTCCCCGCACCTCTTCCCTCTCCGTTAGTGTTTGGGCAATGTCTGTGTCCACCGCACCAGGGGTGGTAACAAAGAGGGCAACGTAACATCATGGG
chr7	6648031	6648151	1	-	CACAAAGGTCCCTACACCTGGGAGGGTGCTCGTCGGCATCACCAAAGCCGGGCATTTACCCAGAATCCCACCAACACAACTGCAGGCTCTCCAGCTTCTGTCCCCAGGCCCTGGTTTAAC
chr7	55068615	55068735	1	-	GGACAGACTATTGCCTCCCGGTCACTGGAGCGTTCTCAATACTTCAGCCATCTGTGCATGATGGGTACAGTAGGAATTGAATTGTGCCAGTTGGTAACGGCTTCAGTAAGGGCTGCAGAG
chr7	71174316	71174436	1	-	CTTCTTCATTTGGCTTCTGCTGTCAGAACCACCTTCCCCACAGGTCCCCAGAGCCCCAGGCCGGCCTAACCATGTGCAGACCCCTGACATCTCACACCCCAGTGCCAATGTGCGGTCATG
chr7	73769157	73769277	1	-	CCAGCCCACCCCCAGAAGCCAGGAAGCCCCCGCGCTGGACTGGGGCAGCTTCCCCAGCAGCCACGGCTTTGCGGGCCGGGCAGTCGACTTCGGGGCCCAGGGACCAACCTGCATGGACTG
chr7	128121636	128121756	1	-	AGCCGCCAGGAAGTGCCAGAATCCACCGCCAAAGCCCTCTCCTCTGCAGCCAGAAACGCTGCACAATAATTTGGCCTGAGAGATGAGCACCGGAAAGTTGCCATTTAATTTAATTTATTC
chr7	149822006	149822126	1	-	TTGGCCATCAGGCAGGGGCAGGACCCAGAGCGAGAGGCCAGGCCCGGGCCGCAGCTGCGGGAACAGGGCCCCCACGGGCCCCAGGAGCAGGCCTCCAGCAGCCCTGGGCAAGGCTGCTGC
chr7	158252860	158252980	1	-	AGGAACCTCGGGCCACAGGGACTCTCACTCCGCCAGCCCAAGGGTGAGGGAAGATTAAGGTCTCCTTTGAGAAACCAGGCTCTGCTTTGTGATATGGGGTCGTTTTCCGGCATGTTAATC
chr7	100049694	100049814	1	+	CACAGAGAGGACCTCCCGAATTTCTAGAGGGGCCGCTACGGCCCCGCACTACTTTTCCGCGGGGGCGGGGCTATGACGCACTTCCGGGTGCGCGGTCCCGAGGTACGCGGTGCGGTCTCC
chr7	134779554	134779674	1	+	ATAGGGGATATGTGTTCACTTAGCATGGACTTCTGGGAGGGGCCAAGGAAGGGCGGTCTGGAGTTTTATTGAATAGAGCAGTGTGTATTCGGCTGCCTGCCTGCCCGCCTGCTTGCTCTC
chr7	149873896	149874016	1	+	GCGCGGCGGGCTGGATCAGGAGATGCGCGTGCGCGGCCCGGCCCGGCTGATCGCTTCGGGTGCTCGACTCCTGTTGCGCATGCTCAGCGCGCTGCCCGGCTGGGGACCCGCGCACCTGCA
chr7	3043826	3043946	1	-	TAGTCTCATTTCCTGTCGGGTTTTGCATTTCCCTCCCCCGCCCCTCCCAGCCTATGACATACTTTCTCTCCTTTTTTCTCTCCTGCCTCCTCTGGCCTTCGGACTCCTGCCCGCGCCGCC
chr7	113087683	113087803	1	-	TGGCCTGAGTTCCCCTGAATGTCACAATCTCACCACCCAGCAATGAGGTATTTTACTGCTGTCTCAAGATCAGATTATTACTGTAGAGAAGATTTTTATTTTTTGTTTCATTAACAGATT
chr7	130668696	130668816	1	-	GGGGAGGGCGGGCCTTGGCCCCGAGTGAAGGCGCGGCGGCCCAACCGGCGTGAGAGCGCGGGGCCGGCCTTCCTGCAGCCTCTTCCGCTCGCCGGCTGCGGCGCCTGGGACGGTTGCGGT
chr7	134459059	134459179	1	-	GCGCAGCGGCGCGCCAACCGCAGGCGCCCTTTCTGCCGACCTCACGGGCTATTTAAAGGTACGCGCCGCGGCCAAGGCCGCACCGTACTGGGCGGGGGTCTGGGGAGCGCAGCAGCCATG
chr7	143408815	143408935	1	-	AGGTGAGGCCGGGACTCCGCCCCCGGCGCTGGCCCCGCCCCCCGCCCCCGCCCGGCCCGCCCGGCTCTCCTAGTCCCTTGCAACCTGGCGCTGCCATCCGGGCCACTGTCCCAGGTCCCG
chr8	29711148	29711268	7	-	AGTGCTGGGATCACAGGCATGAGCCACCGCACCCGGCATAGACCTATTCTTTAGAGGAAACTGTCAGTGATAGTTTCACAAAGAAGCCAATTGTCTATAAAAATGCAGTGCACACTGCCT
chr8	11849248	11849368	2	-	TTCAAGACCAGTCTGGCCAACGTAGCAAGACCCCATTTCTACCAAAGAAAATAAAAGCTGAGTTTGAGCCCCAGGAGCGTCCCCTGGTGTTGAGAGATCAGTTGCCTACAAGGTCTGAGG
chr8	133461866	133461986	2	-	CTACCACCCAGCCTTCATCAAGTATGTCTTTGACAACTGGCTGCAAGGGCACGGGCGATACCCATCTACCGGCATCCTCTCGGTCATCTTCTCAATGCATGTCTGCGATGAGGTATGCCA
chr8	144398533	144398653	2	-	CTTTGGCCCTGACAGGAGGACAATCCCAAGGGGGAGGGCACAGAGCAGGAACCCAGCACCACCCCTGAAGCAGACGACGACGGCCGCAGACACGGATTCCTGATTCTGAGCCGGGAAGAC
chr8	6936067	6936187	1	+	GCAGTTCCCAACACGAAGTTCTGTTCGCCGGCAGAATACTAATCTGCAAGAGCAGACCATGCCCCTTGTTGAGCCTGGGAACACAGAGGAAGCATGAGAAATTAAGCACCAAGGTCAGCG
chr8	20912879	20912999	1	+	CATGCATCCCCGGCCCCCCAGCCCACTAGGTTCTGATTCTTCAGCCTGCCCTATGACAGCACAGGTTCTCATTGCTCAGCCTGCAGGGCGTGACCCTGGACCCTCCTCATACTAGGTGAC
chr8	21350522	21350642	1	+	AGGTTGCTTCAGTGTCTCCCCTGGATCCCAGGTTCAAGGCAGACCCGGCCAAGGCCAAGGCCAGACCCATTTAACTTTCAGATCCTTCCCACTCCCCACGCTCTGGACCAAGAGAACAAG
chr8	28029357	28029477	1	+	CTTTCATCCGCTCACACGCTTTTTTGCCCGTGATCTGAGCTGCCTCTGGCAAAAATGATAGCCACAGTCACACCAAGACAAGGACCTGCTTAGAAATCTTTGGCACCATGGCCGGGCATG
chr8	48544873	48544993	1	+	CATGAGCACACAGATGTTTTCACACCCCAGATGGTAGCCGGTGTTTCAGGAAGCTGTCCTTTTGACACCGCATCACCAGGAAAACCCTAGGAGGTTAACGATATCATAGAGGCAACTTTG

chr8	60714928	60715048	1	+	GCATGAGGGCGCAGGCGCCATAGTGGGGAGGGGCAGGAGGGAATATTCTGCCGGCAGCCACAAGAATAGGAAAGAGAAATACTCTGTCCGAATGGTTTGTTTTTTTGTGTTGGTGGGATT
chr8	100894745	100894865	1	+	GGAATTATTTTCCCTCTCTCTGCCTGCCAGGAGGTGAACCTTTGCAATTCTCCCAAAGCAAGGGTTTAAATGGATGATCTGATCAGACCGAGCACAGTAGGAAGGCTAAAATCCGGGTTC
chr8	133461806	133461926	1	+	GGCCTCTCTTGGGAACACAGGACGGTGAGCTTCGAGGCAGCCCTGTGGGCAGGGGGAGGGTGGCATACCTCATCGCAGACATGCATTGAGAAGATGACCGAGAGGATGCCGGTAGATGGG
chr8	140350865	140350985	1	+	ACAGGAGCAACAAAACAGGATCTGATTTGCAATTTAAACAGTAACTGTGAGGGGTGTCCGGAGAATGAAGCAATGGGAGGCTGGAGTGGAGCAAGGGAGAGGGGCAGGAGGCTCCAGAGG
chr8	140350985	140351105	1	+	AGATGACGGCAAATTAAACAGAACGAAGGCAGTCAGGGCGAGAAAGCAGAAGCAGGCTGGCTGGGCCTCTCAACGAATCCAAGGTGCAGAGGGGAGAGGATGGCAGAAAAGGTGATTCCA
chr8	142017038	142017158	1	+	GGCCTTCTCTGATGGCACTGCTGCTCCCTGGAACCAGGGTGGCATCCTCGCTTGGCACAGCTGGCCCTCGGGGCTGCCCAGGCCTGCCCGGGTCCCATGTGGCAGGAGGGACTCGGAGCA
chr8	142017158	142017278	1	+	GGCACATGGGCCAGGGGCAGGAAGGTGTCGGGCCAGGCCAGCCAAATGCAGGCAGGCAAGGGGCCGCCACAGGGACACAGGTGGCAGCGTGAGTGCTCCCCCAGAGCCGGAGAAGGGGTT
chr8	142670299	142670419	1	+	CCTTTCATGACAGTGAACCCTGCGCTGAAGGCGTTGGGGCTCCTGCAGTTCTGGGGCAGCCACAGGCGCCCAGGGTTTCGTGCCGATCAGCCCAGGACGGTCTTCCCGGTGCAGTTTCTG
chr8	142765495	142765615	1	+	CTGAGACACGCTTTCTGGCCATGCCCATTTTTGCCTCTGGGTACTGAGTGGGACCTGTTAGACCCCCGGGACTGGATTCTGGTGGCTGCGATGATGGGGCCGTTCCTGCCTCCACAGGGA
chr8	143310343	143310463	1	+	TCCATCACAGCAAAAGACCAGCCGGGATCAAAGGTGGAAGCTCAGCCCCACCCCAGCTGCCAAGTCAGATACAGAGGAGGGCCGTGGGCGGAGGGTGAGCAGCCCGTCAGGACCTGACTC
chr8	144398473	144398593	1	+	CCCGCAGGGGACCCCAGCCCCAGGTCCCAGGTCCCAGGCCCTGCCCCTCACCATGGTGGAGTCTTCCCGGCTCAGAATCAGGAATCCGTGTCTGCGGCCGTCGTCGTCTGCTTCAGGGGT
chr8	6936007	6936127	1	-	ATGGTCTGCTCTTGCAGATTAGTATTCTGCCGGCGAACAGAACTTCGTGTTGGGAACTGCCTCATTGGTGGTGTGAGTTTCACATACTGCTGCACGCGTGTCGATTAACGTTCTGCTGTC
chr8	20912939	20913059	1	-	GCCAGGAGAAGCCGGAGCACTGGGGTGAGGCGGGGGACCAATCACCTATCCCCCAGCTGCGTCACCTAGTATGAGGAGGGTCCAGGGTCACGCCCTGCAGGCTGAGCAATGAGAACCTGT
chr8	21350582	21350702	1	-	TACAGCAATGTAAATGCAGCAGGCTTGCTTCCTTTCCCATGTAGGTGAACCTGCGGGGCTCTTGTTCTCTTGGTCCAGAGCGTGGGGAGTGGGAAGGATCTGAAAGTTAAATGGGTCTGG
chr8	28029297	28029417	1	-	TATCATTTTTGCCAGAGGCAGCTCAGATCACGGGCAAAAAAGCGTGTGAGCGGATGAAAGATGCCATCAGAAGAGGAGTGGACCGGCAGGTGGCTGAGGGCATGTTTGAAAGGGCCCAGG
chr8	48544933	48545053	1	-	GTCCCCACACCTGAGCATTGGTACAATGGCCTGGTGCCCTTGAAATTGCAGAGCTACTCCCAAAGTTGCCTCTATGATATCGTTAACCTCCTAGGGTTTTCCTGGTGATGCGGTGTCAAA
chr8	60714988	60715108	1	-	AACTCTAATGTCTTTCTCCAATCACATTTCTCACTGATCAAGAAGAGCCATGCATTGAGCAATCCCACCAACACAAAAAAACAAACCATTCGGACAGAGTATTTCTCTTTCCTATTCTTG
chr8	100894805	100894925	1	-	AAGGTCACACCATTAATAACCAGCCAAGTTGGAATTTGGAATTGGATCTGCCAGATTCCAGAACCCGGATTTTAGCCTTCCTACTGTGCTCGGTCTGATCAGATCATCCATTTAAACCCT
chr8	140350925	140351045	1	-	CCAGCCTGCTTCTGCTTTCTCGCCCTGACTGCCTTCGTTCTGTTTAATTTGCCGTCATCTCCTCTGGAGCCTCCTGCCCCTCTCCCTTGCTCCACTCCAGCCTCCCATTGCTTCATTCTC
chr8	142016978	142017098	1	-	CTGTGCCAAGCGAGGATGCCACCCTGGTTCCAGGGAGCAGCAGTGCCATCAGAGAAGGCCCTGCAGGCTGTCGGCCCCCCGGGTCACAGCAGCTTGTTCTGGCAGCCCCTCCTCCCCCGG
chr8	142017098	142017218	1	-	CTTGCCTGCCTGCATTTGGCTGGCCTGGCCCGACACCTTCCTGCCCCTGGCCCATGTGCCTGCTCCGAGTCCCTCCTGCCACATGGGACCCGGGCAGGCCTGGGCAGCCCCGAGGGCCAG
chr8	142670239	142670359	1	-	GCTGCCCCAGAACTGCAGGAGCCCCAACGCCTTCAGCGCAGGGTTCACTGTCATGAAAGGAATGTGACGCCCTGCGCCCATTCTACAGATGGAGAGAGCAGGGCGGAGCCCGGGGCCCAG
chr8	142670359	142670479	1	-	CAAGCAGGCGGGCTGAGCACTGGTCCTGGTGACCGGAAGGCAGCACTGCCCTCCCCGCATCAGAAACTGCACCGGGAAGACCGTCCTGGGCTGATCGGCACGAAACCCTGGGCGCCTGTG
chr8	142765555	142765675	1	-	ACATTCTTTAATTTCTTTTAATTCCTGTTCCACCACATCCTGGTCGCCCTTGCCCTGGGCTCCCTGTGGAGGCAGGAACGGCCCCATCATCGCAGCCACCAGAATCCAGTCCCGGGGGTC
chr8	143310403	143310523	1	-	CTGCCCTCATCCTGTTTGGGCCGGCCTCAGTCTGTTGTGTCGAGCATCTCACCCTCCTGCGAGTCAGGTCCTGACGGGCTGCTCACCCTCCGCCCACGGCCCTCCTCTGTATCTGACTTG
chr8	11501615	11501735	1	+	TACAAATAATAACAAAATATGCAATAGTCTCTGTCCTAAATACCGCAGAGGTGATTGAGTCTCATAGAAAGCTCTCGTGACTTTGCACTGTCATATCCGTAGCCAAGCATTGGTTGCAGC
chr8	28093066	28093186	1	+	GTGCACGTCGGCTTCCGGGAAGAGCTTTACGATACATTGACCGACATTTTACGACAGGCGGGATTGTTTTGTGGCTGTCAGCTTTCCCCGTGGTCTGAGTTTGTGGCTGCATTTTTATCT
chr8	28317189	28317309	1	+	TGTCATGGAGGTGGGCAGGGAAGGGGAGGGCTGTGCGTGGGGGAGAGGATATATATGCTGGTGTGGCTGAGAAAGCGGAACCGAGCCTCGCATCCATCGGAGGGAGCCGGGGACTGACAG
chr8	39913814	39913934	1	+	TCACTGCCCCTGTGATAAACTGTGGTCACTGGCTGTGGCAGCAACTATTATAAGATGCTCTGAAAACTCTTCAGACACTGAGGGGCACCAGAGGAGCAGACTACAAGAATGGCACACGCT
chr8	85177116	85177236	1	+	CTGCCATTTAAACTCAGGTCCCCACCCCTCGCAGCCCCTTCTCCTCGTTTCCACCCCTCCCCCCTCGGTCGTGGGCCTCATTCACGCTTCCCCGGGCTTGGGGAGGGGGCGGAGGCCCGG
chr8	94719820	94719940	1	+	GGTTCCCGGGCCGCCTGCGGGGACGCGGTTGGCGGCGACACCGGAGGGGGGTGGGTCAGGAAGTGGGGGCGCGGCGGCCAGGAGCGGGCCCCCGGAGGCCGAGGGGTTCGGCGACGCGGA
chr8	21913649	21913769	1	-	CCGCAGGGCCTATCAGCCTGTCGTCATCGAGCAGACTAGAATAGTATAGAAAACCCTAGGCAGAGAGGAAATGAACTTCAGAGAAGGGAAACACACGGCTAAGAAGAGAGAGGCAAGGGC
chr8	53251608	53251728	1	-	CGAGCTCTCCGCCCGCAGGCCCCCAGCGCCCAGCCGCGTCCCGGCTGCGTCCCGCCGGTCCCGCCCCGCCCCGCCCCGCAGAGCCGCCGCCAGTAGTGGGAGACGTGCGCTGAGAGGCGG
chr8	141001188	141001308	1	-	CGCGCGCGGGCCCGCGCCGACGCAGCACGGCCTCGAGGGCGCGAGCCCGCGCCGCCGCCGCCGCCGCCGGTCCCGGACCACTGTGAGCCCGCGGCGTGAGGCGTGGGAGGAAGCGCGGCT
chr9	63814974	63815094	17	+	CGGGGCAAAGCAGAGCCTTCTTGCCCCTTTGGCCATGGCGGGTCCCCGTCAGAACAAGCGACGATGGTGTGAGCATTGTGAGAAAAAGGGCCCGTGGGGCTGGGCCGGCCGTTCGCCCCT
chr9	63814914	63815034	17	-	CGCTTGTTCTGACGGGGACCCGCCATGGCCAAAGGGGCAAGAAGGCTCTGCTTTGCCCCGCCCTGGCACTAGAGCCCCGGCAGCCTCATCCTGAGAAAGAGGGGCTGACGGACACCCAGA
chr9	100410477	100410597	5	-	GGTTTCTGTTCTCATTGTTCAGCTTCACAACCACTTTATTTCTAGAACATATGGTCTCTAACTCATTAAGAAATAGCCGAACTGACCGGGTGCGGTGGCTCACGCCTGTAATTCTGGCAC
chr9	134690634	134690754	2	-	CGAGGCAGGGCACCACGCTGCGGAGGAGGGTCCCATCCTTGTCCCCACCAGCAGCCACATACCGGGGGCAGACCCAGGCTAGCCCAGAGGGTCCCATCCCTGTCCCCACCAGCGGCCACA
chr9	446187	446307	1	+	TTCTGTCCTTGGGGGTGGAGAGGAGGAACTTCTGCTGGCCACATTCTCCCCTGCATCTGTAGCTTTTCTGCACTGGGCAGGGCGGTGCCGGCACGCCGTGTTCCTGCATGCCCCTCCATT
chr9	34400554	34400674	1	+	GAGGCCGGGGCTTGGGAGTTCATGGCTTCGCTGGGGTGGGGCCAAGCCCCTGGCTTTGTGATCCCCCCACTCGTTAATGTTGACCTCCCTGCCGTCCAGTCTTCTCTCTTGGCCAGCCCT
chr9	87551786	87551906	1	+	GCCGGAGAGAGTCACCGTAGAGCCCAGGAGGAGAGACCCGAAGATAAGCATCACCCTGTGCTGTCATCTCTGAGGGGCGGGCGCTGCTGATAGACACGTGAAAGTCTAGCCTGCAGCAGA
chr9	89656118	89656238	1	+	CCTGAGTGTGGAGTCATCCAGAGGGCTGGCTGCTGGGTCGAAGCACATTCTCTGACCTGGCTGGAGCTCAGGTCCGGTCACAGGCTGGGTCACCTTGGCCTTTTGTCCTCTCAGCATGGA
chr9	108615972	108616092	1	+	TACCGGACATCCAACTGTTATACACCTTGGCACTGGATTTGCTCCACTTGTTGTAAGCACCACAAGGTTTTTAGTATTGTGTAACAAGACCTTAACAGAGTATCGGATACACTGACTATG
chr9	108616092	108616212	1	+	TTATATTAGTACCCGGAGAAGTGGAAAGATTCTAAAAATCATAACATAAAAAAAGAAGTGAAGGAAGTGGGCTTGAAGAAGACTCAAGGAAGACATAGTAGCTCTTAGTCATATTAAAAA
chr9	111687661	111687781	1	+	CTAAAACAAAGACATATTGCCTGGTTTCCGTGTACCTTGTATCCATCTTTGTGGTGAGAGTGTATACAATTCTGTCCGGTTTTTCTTCTTCTTCTTTTTTTTTTTCTTTTTTCTTTTCCA
chr9	119360974	119361094	1	+	CTATCCCAAGATGGCCCCAACTTCCCGGTATACAACTCCGCACCCTGTGAGAAAACCTCTGCAAACTGAGAACAAAATTTGTTCAGAATGATATATTTTGTGTCCTCACCAGGCTCTCCA
chr9	124096381	124096501	1	+	AGGACTTGCCCAACAACACTCCACTTCCCGGGGCTCCAAAACCTCTGCCATTTCCTCCCGTGAGATCAGCCTTTGGAGCAGTCTCTAGGGATGTGCCACAGGATTCTGCACTGTTTTTTC
chr9	124369645	124369765	1	+	CATTTCCCTTCCCAGCTGTCCCAACTTCCAGGACTGCACGACTGAGAGGCAGAGCAGGGGCCCCCGTGCCTCTGGACTTAACATTCCTGTCCGGAATGGTCTCCTTCTCTTCTGCCTCCC
chr9	126420942	126421062	1	+	CCCTCCAGCAGTCTCTTCCTTTTCGGAAATGTCCGGGTGTGGCCACAGGTTAGGCTCCTGAGCTATTGCAACACAGCCCCCAGTTGTCCCACCAAGAGGTTTTGTTGTTTTTTTCCCCCA
chr9	129100918	129101038	1	+	CAGGGCCCAACACCTGGCCCACTTTAGACACAGGAAACCGAAGCCCAGGGGTCACATGGGAGCTGGTGTGGCAGCCGGGGAACCCACACAGGTGGTCTGACTTTGGGGTCAATGCCCCTG
chr9	132197892	132198012	1	+	GGCCGCGCAGAGGCTTCCCAGGCCATCCCGAGCATCCAGCACCCACCCTTCCCTTCTCCTCTCCCCGCTGCAGGAGAATCCCTACCTATGCAGCAACGAGTGTGACGCCTCCAACCCGGA
chr9	133574926	133575046	1	+	TCTGGGGCCTCCACAGACCCCCCTCCTGCGGGGCACGCTGGCCTAAGAGACGTGGCACTGAGCCTCGGCTGTCGAGAGGGGACTTCCCACGGCCCGTGGACCTTTGTGCTCCTGGGGCAG
chr9	133708260	133708380	1	+	CCCAGCAGGAGCTGTAGGGGCGTTACCTCGTGCAGCGGGTCTCTCCTCATGTTGCGCCCGGCCAGCGGCTCATCGTGGGGGAAGACGACGGAGTAGTTCTTGGCGTAGGACTCATGGCTT
chr9	133960181	133960301	1	+	CAGTCCAGCGGATCCCAGCAAGACAACGCGTTCCCAAAGGCATCGCTGCAGGTGCACTGTGAGGTCAGGGCGCCCTCCGGGACCAAGCTGGGCCAGAAAGTTCTTATCTGTGGGGGTTTT
chr9	134282304	134282424	1	+	CCGATGGCTCACGGCCGCCCTGAGCCAGCGGGTTCTGCCCTCACCCTGCCTAGGGCTCCTGCCTTGAGGCTGCCTCCAGCAGGGCCCTGAGTACAGGAATCGGAGGGATCCACAGACACA
chr9	134333456	134333576	1	+	ATGGGTGTCGGCGCAGACTGCTGCCGTGCGTGCGGGGTCTGGAGCCTCTGGCGCTGAGGGGAGGGGAGAGTGAGTTGGGCCTGGGCCAGGCCGTGTGTAAATCCTCCAGCCGCCATGGAT
chr9	134373264	134373384	1	+	ATGGCAGTAACAGGAAGGGCATGGCCACCGAGACGCACTGAGTTATGGGCACCTGCCGTCTGCCAGGAACTGTGGTCCACGCCCGACTGTCTTTAACAGCTCTGTGCCTGCTGCTGTGTG
chr9	134416367	134416487	1	+	TGGTGCAGATCCTGCTGCCTGCAAGCATCGCTCTATTTTGTCATAATGCTCGGCTTCTGGTTCCCCCCGAGTGGCTGCTTCCTGGGACAGATTGAAAGGCATCTCGGTGCCCTGCATGGG
chr9	134481931	134482051	1	+	AGTGCCGTGGGCCTCCCCAGCTTGGCTGCGTGTGGCAGCAAATCCAGCCAGGCGGTCCTCAGCAAGAGAGACATCACAATCTCACAGGTGGTCAGTGCCGGAGGGATGCCTTCCACCTTT
chr9	134690694	134690814	1	+	ATGTGGCTGCTGGTGGGGACAAGGATGGGACCCTCCTCCGCAGCGTGGTGCCCTGCCTCGCCCAGCACGCGGCTCTAAGCTGGTCCTGGGGCTCTTCTGAGTGCCCAGGATTCACAGTGG
chr9	136522689	136522809	1	+	CCCGACACCACACGCAGTCTGGGGAACTCGCCATCCCGCCTTCCCAACTCCCCGCCATGGGCCCTCCCAGGGCTGCCCCTACACCAGGCGCCCCGTTCCCACCCCCTGGGCCTGGCAGCC
chr9	136600099	136600219	1	+	CCGCAGTAACACAAAGAAAACTTTGTCCCGGCAGCCGGTCCCCAGGGCCTCCCGTCCATGTGCAGAGCAGGACTCCGGGCCAGCGGCACAGGGCTGTGCCATTGAGGCAGCTCAGGGTCT
chr9	137041310	137041430	1	+	TCTCCCTCCCAGATTGCCATGGTGACAGCGCGGGCGCTTCCTGTGAGGGGCAGTGCTTCCCGGAAAGTGGAGGCAGGGCAAGGGAGGAGGCGCTAGGGAAACGTCCAAAGACCGGGCACG
chr9	446247	446367	1	-	AAGGGGGAAAAGGCACGGAGGGAGAAGATGAGCTATTCTGCAAACGGCCATCCCTGACGCAATGGAGGGGCATGCAGGAACACGGCGTGCCGGCACCGCCCTGCCCAGTGCAGAAAAGCT
chr9	34400494	34400614	1	-	CACAAAGCCAGGGGCTTGGCCCCACCCCAGCGAAGCCATGAACTCCCAAGCCCCGGCCTCAGCCTAACCAGGAAAGGGGCTCGGAGGGAGAAAGGCCCAGGGCAGTGGGGACGGGTCCCA
chr9	87551726	87551846	1	-	CACAGGGTGATGCTTATCTTCGGGTCTCTCCTCCTGGGCTCTACGGTGACTCTCTCCGGCTTGGTTACAGCTTCTCCATGTTGCTGTATCAGGACCTGCACTTCCCTGAGAGAGTTCATG
chr9	89656058	89656178	1	-	CCAGGTCAGAGAATGTGCTTCGACCCAGCAGCCAGCCCTCTGGATGACTCCACACTCAGGGCCTGGAAAGTGAAACCGCTTGCGGAAGGCAGTGGAGGTGCAGCATCGCTTTCACTCCGG
chr9	100332444	100332564	1	-	CAGGCGTGAGCCACTGCGCCCGGCCTGTTTGAGCAATATTATAATTACCTATACTACCTTTACTGGAAGTTAAAGTTTCATCAGAGATCTGCCTTCCTCCTAGAATTGTTGGTTGGTAT
chr9	108616032	108616152	1	-	CACTTCTTTTTTTATGTTATGATTTTTAGAATCTTTCCACTTCTCCGGGTACTAATATAACATAGTCAGTGTATCCGATACTCTGTTAAGGTCTTGTTACACAATACTAAAAACCTTGTG
chr9	111687601	111687721	1	-	CTCTCACCACAAAGATGGATACAAGGTACACGGAAACCAGGCAATATGTCTTTGTTTTAGGTTCAAAGTCTGTCAAAATGAGCCTCTAACTTATATCCTAATTAATGAGGACTTATTGGA
chr9	119360914	119361034	1	-	AGAGGTTTTCTCACAGGGTGCGGAGTTGTATACCGGGAAGTTGGGGCCATCTTGGGATAGCTAGGAGACTGTATTCCCTCAAGGGTGGCAGGTAGATTGATAAGGTAATTAACAAAAGCA
chr9	124096321	124096441	1	-	CGGGAGGAAATGGCAGAGGTTTTGGAGCCCCGGGAAGTGGAGTGTTGTTGGGCAAGTCCTTTCCCTTCTCTGAGGCTCGGTCCCCTGGTTTATAAAATGTGAATAAGAATTATGTTTAAT
chr9	124369585	124369705	1	-	CCCCTGCTCTGCCTCTCAGTCGTGCAGTCCTGGAAGTTGGGACAGCTGGGAAGGGAAATGGCAGACAGTGTCTAAAGTTGTCTGGGCGGTCATTTCCCGAGTCAGTGTGGCCTTTTAATT
chr9	126420882	126421002	1	-	CAGGAGCCTAACCTGTGGCCACACCCGGACATTTCCGAAAAGGAAGAGACTGCTGGAGGGAACACTTATCACATAAAGTAAGTGGTCAATTACTAGGTGCCTTTTTCACACAGCACATGT
chr9	129100858	129100978	1	-	CCCATGTGACCCCTGGGCTTCGGTTTCCTGTGTCTAAAGTGGGCCAGGTGTTGGGCCCTGCCTCGAGGAGTGCTGTGGGCCTGCAGGGTCCTGTTGAGTTCGAAGCTCTGAACCCACACC
chr9	132197832	132197952	1	-	AGGAGAAGGGAAGGGTGGGTGCTGGATGCTCGGGATGGCCTGGGAAGCCTCTGCGCGGCCTAGCCCCTGCCTGCGAACCGAGAAACCTGCTCTGTGGCTACAGGGCCTGTGCTCCGGTGC
chr9	133574866	133574986	1	-	CAGTGCCACGTCTCTTAGGCCAGCGTGCCCCGCAGGAGGGGGGTCTGTGGAGGCCCCAGAAGCTGCAGCAGCCCCAGGAGGGGCGCTTGGTCTTCATCTGGAAGGGGCTGCAGCTGCCGG
chr9	133708200	133708320	1	-	CGGGCGCAACATGAGGAGAGACCCGCTGCACGAGGTAACGCCCCTACAGCTCCTGCTGGGGACTGGCAGCGAGGGTCTGGGACGTCCTCAGGGCAGCGGAGTGACAGAAATGCAAGGTGT
chr9	133960121	133960241	1	-	ACAGTGCACCTGCAGCGATGCCTTTGGGAACGCGTTGTCTTGCTGGGATCCGCTGGACTGTCGGCCCCAGCTTGGTTCATTTGCTGCTTTTTCACAGTTCTTTCTCCTGATAGAGAGTGG
chr9	134282244	134282364	1	-	AGGAGCCCTAGGCAGGGTGAGGGCAGAACCCGCTGGCTCAGGGCGGCCGTGAGCCATCGGGAGGCACTCAGGAGCACGCAGGGAGCCAGGCCCCGGCTAAGCCAAGCCGCGGCTCAAATG
chr9	134333396	134333516	1	-	CCCTCAGCGCCAGAGGCTCCAGACCCCGCACGCACGGCAGCAGTCTGCGCCGACACCCATCACCCCCAGCCCTGGCCCCGGGTACAGCTGGGGAAACCGAGGCCCAGCTGGAAATTACTA
chr9	134373204	134373324	1	-	GACGGCAGGTGCCCATAACTCAGTGCGTCTCGGTGGCCATGCCCTTCCTGTTACTGCCATTCCTAGCCCAAGAACAGCACCAAAGGCTGGTCTCTGGGACCCGAGTCCTTCATCCCACCC
chr9	134416307	134416427	1	-	CCAGAAGCCGAGCATTATGACAAAATAGAGCGATGCTTGCAGGCAGCAGGATCTGCACCAGGCATGGGCTCCGGTCAGCTGACTCTCATCAGCCCTGGGGGTGGGCGCTCAGCAAAGGGG
chr9	134481871	134481991	1	-	GAGGACCGCCTGGCTGGATTTGCTGCCACACGCAGCCAAGCTGGGGAGGCCCACGGCACTGGACTGAGGACAGCCTCCAGCTAATACCCAGCTAGGAGCTGAGATGACCTCCGGCCAACA
chr9	136522629	136522749	1	-	CCATGGCGGGGAGTTGGGAAGGCGGGATGGCGAGTTCCCCAGACTGCGTGTGGTGTCGGGGGGACGCGTCTGGAGCGGGGTGTGCGCTGGGAGGAGGCTTGCACAGGGTCCAGGTGCCAG
chr9	136600039	136600159	1	-	CATGGACGGGAGGCCCTGGGGACCGGCTGCCGGGACAAAGTTTTCTTTGTGTTACTGCGGCTGGCCCCCCTGCCAGAGTGAAGGCGGCTGAATGGGGCCCTGGGAGGCAGCCCCCACCCT
chr9	137041250	137041370	1	-	GGAAGCACTGCCCCTCACAGGAAGCGCCCGCGCTGTCACCATGGCAATCTGGGAGGGAGAGGGCCTCCAGGCGTGTACCCAGTCCTCAGGCTCCTGGGAGGAACCTGCCAGAAGCGGGGA
chr9	78297047	78297167	1	+	AGCGCAGGGCCTGCGACAGCACGGGCCAATGGGGCGCCGACTCGGCGCAGGAACAAGGCGGGGGTTCGGGGCCGGCTGCAGACTCTCACCGCAGCGGCCAGGAACGCCAGCCGTTCACGC
chr9	132978659	132978779	1	+	TGAAAATCAGGGAGGGGAACAGAAGAGGAAAAACACACAGAGAGACAGAGCAAAAAGGAGAAGTATCTATTTGTGCAAAGAGTCACACAGTTGACAGAGTGGAGGCCAGTCCCGAGAGAG
chr9	136952193	136952313	1	+	GAGGAGGGAGGCAGAGGGGCACACCCCCTTGGGAGGGGCACCTGCTGGGTATGTGCATGAAGAGGTGGGTCTCTGGGTCACCTGCCCATGGCCACTTCCTTCTCTCTGTCCCTGTGGGCC
chr9	136977424	136977544	1	+	GAGTGTTCAGTGGGCTGTCCCCGGGCCCTGGGTGGAGGCCAAGCCTGGCCCATAAATAGGGGTCTCCTCAGTGCCCTCCGCTCCTCCTGCACACCTCCCTCGCTCTCCCACACCACTGGC
chr9	35609919	35610039	1	-	AGCGGATAGGGGCGGCCCGGAGCCAGCCAGGCAGTTTTATTGAAATCTTTTTAAATAATTGCACGTGTTAGTCTCATGTGTCAGCAATGCTGTGTCTGGTTCAGTGATCCCCACGGGAAC
chr9	35650890	35651010	1	-	CACAGGGCGGGGTCTTTGTTCTTTTTTTCATCCCTCCCCTCCCCCTTCCTCCCCGGAAACCAGAGACTTTGCCACCACCAGTATTGGGGATGCTGAGCTGCGGGGTACGGGCCTGAGGAG
chr9	96619802	96619922	1	-	GTCTCCGTGACGTCACGCCGCATTGGCCAATGAAAGGCCTCAGTCTGCGGGCCCCGAGGAGGGTTGTGGGCCCTTTTTTGTGAATGAAGCGCCACGGAACAGCCCTCCTGGGGTCCCCAC
chr9	137459293	137459413	1	-	TGACGTCACGGTAGGTGGGGCCGACCGCCCCTCTGGGCCCGCCCGGGCCCTGACGTCACGATGGGCGGGGCCGGCCCTCGGTTCGGGCAGCGCTCTCCCGGGAGCGGCGGCACGCGCGGA
chrX	103376458	103376578	3	+	GGGGGGCGAGCTCGGTGGTGACGCGCGGCCCTCACGTGACCCAGAGCTGCAGAGCGACGCAGCCTTCGGTGCAGTCGTCACTCGCGTCTGGCTACCAGCTCCCCGCTGCCCTGAGCTCGG
chrX	47445819	47445939	2	-	TTTTGCCTGTTTTGTATTTTATATAAATTGAGTCAATTATATATCATATAATTGAGCCATATACTCTTTAGCATCTGTCTTCTGTCATTCACATTATGTATGTGAGAGTCATCCATATGT
chrX	118727528	118727648	1	+	GCGCCGGCCCCCAGCCTCCAGGGCGGCGGAGCCGGGAAGTGGAAGAGGGAGCGAAGGAGGCGGGGACTGCCAAGGCTCCAGCCCGGCCGGGCTCCGAGGCGAGAGGCTGCATGGAGTGGC
chrX	71618470	71618590	1	-	AGAGGTAACTCCCTGGAAGAGGCTGCTGCTGAGAACTGCCTGAAACTCCCACTTCCTCTGTGACTGCAGGTTTCCAACCACAAGCACCAAAGCAGAGGGGCAGGCAGCACACCACCCAGC
chrX	78139600	78139720	1	-	CCGCCTTCCGTTTCCCTCCTCCCGCTCCCCGCAGGGGTGGAGCCTGAGCGAGGAGCCCGCGAGCTCTCCTCTCTCCTCTGTCTCCGCGGATGACGAGTGGCTGGATAACATGGAGTCGGG
chrX	79367290	79367410	1	-	AGGCACCTCCCTGGGCCCGCCCACGGTCTCCCCCCAGTTTGGGACTGCGTCATAAGTATCCCAGACCTCGGCTTGCAGTAGTGTTAGACTGAAGATAAAGTAAGTGCTGTTTGGGCTAAC
chrX	141177059	141177179	1	-	GGAGCTTGCGTAGCCTCCCGGACCCCGGCGCACACCGCCCCCCGCCCCCCGCCCCTGGCCACCAAGCGCCTCCGTGGACACGCACTTCCTGCGAGGGCTCCGTGCGCACCTTGGCCGAGC

Table S7 Genotype association with race group and disease status

Site	Contingency table_race	p_value_race	p_adj_race	Contingency table_disease	p_value_disease	p_adj_disease
chr1:1206612	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr1:1755633	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 59, 'CT': 1}}	0.47244094	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 67, 'CT': 1}}	1	1
chr1:1947645	{'African_American': {'CC': 43, 'CT': 18, 'TT': 2}, 'Not_African_American': {'CT': 25, 'TT': 17, 'CC': 12}}	1.0633E-07	1.3717E-05	{'ARMB': {'CC': 27, 'CT': 20, 'TT': 5}, 'APMB': {'CC': 28, 'CT': 23, 'TT': 14}}	0.232685078	1
chr1:2425928	{'African_American': {'CC': 66}, 'Not_African_American': {'CC': 57, 'CT': 1}}	0.46774194	0.90275544	{'ARMB': {'CC': 57, 'CT': 1}, 'APMB': {'CC': 66}}	0.467741935	1
chr1:2425979	{'African_American': {'CC': 50, 'TT': 5, 'CT': 3}, 'Not_African_American': {'CC': 61}}	0.00244413	0.06305862	{'ARMB': {'CC': 47, 'TT': 4, 'CT': 2}, 'APMB': {'CC': 64, 'CT': 1, 'TT': 1}}	0.230055514	1
chr1:2426036	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 60}}	1	1	{'ARMB': {'CC': 57, 'CT': 1}, 'APMB': {'CC': 69}}	0.456692913	1
chr1:2590917	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr1:2590953	{'African_American': {'GG': 53, 'AG': 11}, 'Not_African_American': {'GG': 30, 'AG': 18, 'AA': 8}}	0.00016273	0.0083971	{'ARMB': {'GG': 40, 'AG': 13, 'AA': 2}, 'APMB': {'GG': 43, 'AG': 16, 'AA': 6}}	0.482105981	1
chr1:3167258	{'African_American': {'GG': 65, 'AG': 2}, 'Not_African_American': {'GG': 61}}	0.49717028	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 67, 'AG': 2}}	0.49913878	1
chr1:3167371	{'African_American': {'CC': 62, 'CT': 3}, 'Not_African_American': {'CC': 57, 'CT': 3}}	1	1	{'ARMB': {'CC': 56, 'CT': 2}, 'APMB': {'CC': 63, 'CT': 4}}	0.684870029	1
chr1:3556710	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr1:3947941	{'African_American': {'GG': 62, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 66}}	0.467741935	1
chr1:3947989	{'African_American': {'AA': 66, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 59}, 'APMB': {'AA': 68, 'AG': 1}}	1	1
chr1:3948000	{'African_American': {'CC': 66}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.48031496	0.90275544	{'ARMB': {'CC': 57, 'CT': 1}, 'APMB': {'CC': 69}}	0.456692913	1
chr1:3948021	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr1:4058749	{'African_American': {'AA': 63}, 'Not_African_American': {'AA': 60, 'AG': 1}}	0.49193548	0.90275544	{'ARMB': {'AA': 55, 'AG': 1}, 'APMB': {'AA': 68}}	0.451612903	1
chr1:4058949	{'African_American': {'GG': 63}, 'Not_African_American': {'GG': 59, 'AG': 1}}	0.48780488	0.90275544	{'ARMB': {'GG': 56}, 'APMB': {'GG': 66, 'AG': 1}}	1	1
chr1:5503351	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr1:5503359	{'African_American': {'AA': 55, 'CC': 1}, 'Not_African_American': {'AA': 61}}	0.47863248	0.90275544	{'ARMB': {'AA': 54}, 'APMB': {'AA': 62, 'CC': 1}}	1	1
chr1:5503393	{'African_American': {'AA': 67}, 'Not_African_American': {'AA': 59, 'AG': 1}}	0.47244094	0.90275544	{'ARMB': {'AA': 58}, 'APMB': {'AA': 68, 'AG': 1}}	1	1
chr1:5503406	{'African_American': {'AA': 62, 'CC': 2}, 'Not_African_American': {'AA': 60}}	0.49645948	0.90275544	{'ARMB': {'AA': 57}, 'APMB': {'AA': 65, 'CC': 2}}	0.499213218	1
chr1:5503412	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 58, 'AA': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr1:5651315	{'African_American': {'CC': 64, 'CT': 1}, 'Not_African_American': {'CC': 59, 'CT': 1}}	1	1	{'ARMB': {'CC': 56, 'CT': 2}, 'APMB': {'CC': 67}}	0.213290323	1
chr1:5651322	{'African_American': {'AA': 57, 'CC': 1}, 'Not_African_American': {'AA': 61}}	0.48739496	0.90275544	{'ARMB': {'AA': 56, 'CC': 1}, 'APMB': {'AA': 62}}	0.478991597	1
chr1:5651350	{'African_American': {'GG': 63, 'AG': 2}, 'Not_African_American': {'GG': 59, 'AG': 1}}	1	1	{'ARMB': {'GG': 56, 'AG': 1}, 'APMB': {'GG': 66, 'AG': 2}}	1	1
chr1:9233320	{'African_American': {'GG': 64, 'AG': 2}, 'Not_African_American': {'GG': 61}}	0.4968129	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr1:10642683	{'African_American': {'GG': 62, 'AG': 4}, 'Not_African_American': {'GG': 61}}	0.12023416	0.81817066	{'ARMB': {'GG': 57, 'AG': 2}, 'APMB': {'GG': 66, 'AG': 2}}	1	1
chr1:10642757	{'African_American': {'GG': 58, 'AG': 6}, 'Not_African_American': {'GG': 41, 'AG': 13, 'AA': 3}}	0.01131093	0.16835887	{'ARMB': {'GG': 39, 'AG': 14, 'AA': 2}, 'APMB': {'GG': 60, 'AG': 5, 'AA': 1}}	0.012944885	1
chr1:11964094	{'African_American': {'TT': 65}, 'Not_African_American': {'TT': 58, 'CT': 1}}	0.47580645	0.90275544	{'ARMB': {'TT': 59}, 'APMB': {'TT': 64, 'CT': 1}}	1	1
chr1:12035077	{'African_American': {'CC': 61, 'CT': 4}, 'Not_African_American': {'CC': 61}}	0.1197802	0.81817066	{'ARMB': {'CC': 57, 'CT': 1}, 'APMB': {'CC': 65, 'CT': 3}}	0.623789892	1
chr1:14949963	{'African_American': {'CC': 65, 'CT': 2}, 'Not_African_American': {'CC': 61}}	0.49717028	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 67, 'CT': 2}}	0.49913878	1
chr1:14950030	{'African_American': {'TT': 54, 'CT': 10}, 'Not_African_American': {'TT': 48, 'CT': 7, 'CC': 1}}	0.60103653	1	{'ARMB': {'TT': 46, 'CT': 8, 'CC': 1}, 'APMB': {'TT': 56, 'CT': 9}}	0.786437201	1
chr1:17394880	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr1:17394911	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 55, 'CT': 2}}	0.59362384	1	{'ARMB': {'CC': 58}, 'APMB': {'CC': 63, 'CT': 3}}	0.247049567	1
chr1:19920383	{'African_American': {'CC': 58, 'CT': 7, 'TT': 1}, 'Not_African_American': {'CC': 52, 'CT': 6, 'TT': 1}}	1	1	{'ARMB': {'CC': 56, 'CT': 3}, 'APMB': {'CC': 54, 'CT': 10, 'TT': 2}}	0.059432617	1
chr1:19920451	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'CT': 1}}	1	1
chr1:20409984	{'African_American': {'TT': 66}, 'Not_African_American': {'TT': 59, 'CT': 1}}	0.47619048	0.90275544	{'ARMB': {'TT': 58}, 'APMB': {'TT': 67, 'CT': 1}}	1	1
chr1:20409995	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 68}}	0.464566929	1
chr1:20410040	{'African_American': {'GG': 61, 'AG': 3, 'AA': 1}, 'Not_African_American': {'GG': 61}}	0.2447619	0.90275544	{'ARMB': {'GG': 55, 'AG': 2, 'AA': 1}, 'APMB': {'GG': 67, 'AG': 1}}	0.40598404	1
chr1:22001714	{'African_American': {'GG': 48, 'AG': 7, 'AA': 5}, 'Not_African_American': {'GG': 58}}	0.00026854	0.01222668	{'ARMB': {'GG': 52, 'AA': 3, 'AG': 1}, 'APMB': {'GG': 54, 'AG': 6, 'AA': 2}}	0.164137795	1
chr1:22001817	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'CT': 1}}	1	1
chr1:23559546	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 59, 'AG': 1}}	0.47244094	0.90275544	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 69}}	0.456692913	1
chr1:26282856	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr1:38836233	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr1:42036013	{'African_American': {'AA': 65}, 'Not_African_American': {'AA': 59, 'AG': 1}}	0.48	0.90275544	{'ARMB': {'AA': 59}, 'APMB': {'AA': 65, 'AG': 1}}	1	1
chr1:53071632	{'African_American': {'AA': 66, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 59}, 'APMB': {'AA': 68, 'AG': 1}}	1	1
chr1:58814457	{'African_American': {'GG': 63, 'AG': 3}, 'Not_African_American': {'GG': 61}}	0.24521935	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 66, 'AG': 2}}	1	1
chr1:77351121	{'African_American': {'CC': 55, 'CT': 11}, 'Not_African_American': {'CC': 41, 'CT': 9, 'TT': 3}}	0.18342587	0.90275544	{'ARMB': {'CC': 41, 'CT': 13, 'TT': 1}, 'APMB': {'CC': 55, 'CT': 7, 'TT': 2}}	0.15732937	1
chr1:77351129	{'African_American': {'CC': 63, 'CT': 4}, 'Not_African_American': {'CC': 57, 'CT': 2}}	0.68379816	1	{'ARMB': {'CC': 56, 'CT': 2}, 'APMB': {'CC': 64, 'CT': 4}}	0.686024351	1
chr1:89088805	{'African_American': {'TT': 66, 'CT': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'CT': 1}}	1	1
chr1:116982887	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr1:116982906	{'African_American': {'AA': 65, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 57, 'AG': 1}, 'APMB': {'AA': 69}}	0.456692913	1
chr1:154321061	{'African_American': {'TT': 66, 'AA': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'AA': 1}}	1	1
chr1:154321155	{'African_American': {'CC': 66, 'GG': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'GG': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr1:163885674	{'African_American': {'TT': 37, 'CT': 16, 'CC': 8}, 'Not_African_American': {'TT': 25, 'CT': 19, 'CC': 11}}	0.25431068	0.90275544	{'ARMB': {'TT': 32, 'CT': 18, 'CC': 5}, 'APMB': {'TT': 30, 'CT': 17, 'CC': 14}}	0.143170203	1
chr1:177964370	{'African_American': {'CC': 59, 'CT': 7}, 'Not_African_American': {'CC': 35, 'CT': 17, 'TT': 1}}	0.00355201	0.07610248	{'ARMB': {'CC': 47, 'CT': 9}, 'APMB': {'CC': 47, 'CT': 15, 'TT': 1}}	0.3626157	1
chr1:200916181	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr1:201889751	{'African_American': {'AA': 64, 'AG': 2}, 'Not_African_American': {'AA': 61}}	0.4968129	0.90275544	{'ARMB': {'AA': 56, 'AG': 2}, 'APMB': {'AA': 69}}	0.206599175	1
chr1:206797125	{'African_American': {'CC': 62, 'CT': 3}, 'Not_African_American': {'CC': 55, 'CT': 2}}	1	1	{'ARMB': {'CC': 54, 'CT': 3}, 'APMB': {'CC': 63, 'CT': 2}}	0.663688787	1
chr1:228211004	{'African_American': {'TT': 64}, 'Not_African_American': {'TT': 56, 'CT': 1}}	0.47107438	0.90275544	{'ARMB': {'TT': 53}, 'APMB': {'TT': 67, 'CT': 1}}	1	1
chr1:228211011	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr1:228211012	{'African_American': {'CC': 62, 'CT': 1}, 'Not_African_American': {'CC': 54}}	1	1	{'ARMB': {'CC': 58}, 'APMB': {'CC': 58, 'CT': 1}}	1	1
chr1:232531693	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 60, 'CT': 1}}	1	1	{'ARMB': {'CC': 56, 'CT': 2}, 'APMB': {'CC': 69}}	0.206599175	1
chr1:232531865	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr10:3514933	{'African_American': {'CC': 55, 'CT': 7}, 'Not_African_American': {'CC': 47, 'CT': 9, 'TT': 1}}	0.50518176	0.91357636	{'ARMB': {'CC': 43, 'CT': 10}, 'APMB': {'CC': 59, 'CT': 6, 'TT': 1}}	0.175862898	1
chr10:3515072	{'African_American': {'AA': 66, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 59}, 'APMB': {'AA': 68, 'AG': 1}}	1	1
chr10:6215680	{'African_American': {'AA': 58, 'AG': 3}, 'Not_African_American': {'AA': 60}}	0.24380165	0.90275544	{'ARMB': {'AA': 52, 'AG': 2}, 'APMB': {'AA': 66, 'AG': 1}}	0.585408709	1
chr10:8054672	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'AA': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr10:34815327	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr10:60944248	{'African_American': {'GG': 66}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.48031496	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr10:60944256	{'African_American': {'GG': 64, 'AG': 2}, 'Not_African_American': {'GG': 61}}	0.4968129	0.90275544	{'ARMB': {'GG': 58}, 'APMB': {'GG': 67, 'AG': 2}}	0.499812523	1
chr10:70905567	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr10:75108121	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 67, 'CT': 1}}	1	1
chr10:75108169	{'African_American': {'TT': 66, 'CT': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'CT': 1}}	1	1
chr10:10103700	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr10:11359083	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr10:11965131	{'African_American': {'CC': 60, 'CT': 2}, 'Not_African_American': {'CC': 60}}	0.49600325	0.90275544	{'ARMB': {'CC': 54, 'CT': 1}, 'APMB': {'CC': 66, 'CT': 1}}	1	1
chr10:11965140	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 60}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 68}}	0.464566929	1
chr11:441948	{'African_American': {'AA': 63, 'AG': 2}, 'Not_African_American': {'AA': 59, 'AG': 2}}	1	1	{'ARMB': {'AA': 56, 'AG': 2}, 'APMB': {'AA': 66, 'AG': 2}}	1	1
chr11:441987	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr11:535603	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 54, 'AG': 2, 'AA': 1}}	0.40554892	0.90275544	{'ARMB': {'GG': 56, 'AG': 2}, 'APMB': {'GG': 64, 'AA': 1, 'AG': 1}}	0.787815079	1
chr11:1229429	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr11:1229449	{'African_American': {'CC': 63, 'CT': 1}, 'Not_African_American': {'CC': 50, 'CT': 5}}	0.09411947	0.81817066	{'ARMB': {'CC': 56}, 'APMB': {'CC': 57, 'CT': 6}}	0.028936838	1
chr11:1244733	{'African_American': {'CC': 55, 'CT': 8}, 'Not_African_American': {'CC': 59}}	0.00632509	0.10642654	{'ARMB': {'CC': 51, 'CT': 6}, 'APMB': {'CC': 63, 'CT': 2}}	0.144406244	1
chr11:1244812	{'African_American': {'TT': 65, 'CC': 1}, 'Not_African_American': {'TT': 59}}	1	1	{'ARMB': {'TT': 58, 'CC': 1}, 'APMB': {'TT': 66}}	0.472	1
chr11:1244817	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr11:33699077	{'African_American': {'AA': 67}, 'Not_African_American': {'AA': 59, 'AG': 1}}	0.47244094	0.90275544	{'ARMB': {'AA': 59}, 'APMB': {'AA': 67, 'AG': 1}}	1	1
chr11:45921578	{'African_American': {'CC': 65}, 'Not_African_American': {'CC': 49, 'CT': 5, 'TT': 2}}	0.00367305	0.07610248	{'ARMB': {'CC': 54, 'CT': 1}, 'APMB': {'CC': 60, 'CT': 4, 'TT': 2}}	0.331275823	1
chr11:60455790	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'AA': 1}}	1	1
chr11:60971685	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'AA': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr11:61102415	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'AA': 1}}	1	1
chr11:61102442	{'African_American': {'CC': 66, 'AA': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'AA': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr11:61102443	{'African_American': {'CC': 65, 'GG': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'GG': 1}, 'APMB': {'CC': 68}}	0.464566929	1
chr11:65969132	{'African_American': {'CC': 62, 'CT': 3}, 'Not_African_American': {'CC': 60}}	0.24516129	0.90275544	{'ARMB': {'CC': 56, 'CT': 1}, 'APMB': {'CC': 66, 'CT': 2}}	1	1
chr11:66568589	{'African_American': {'GG': 64, 'AG': 1}, 'Not_African_American': {'GG': 59, 'AG': 1}}	1	1	{'ARMB': {'GG': 57}, 'APMB': {'GG': 66, 'AG': 2}}	0.499870968	1
chr11:67415703	{'African_American': {'CC': 66, 'GG': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'GG': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr11:68036449	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 59, 'CT': 1}}	0.47244094	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 68}}	0.464566929	1
chr11:69071645	{'African_American': {'GG': 58, 'AG': 4}, 'Not_African_American': {'GG': 61}}	0.11892764	0.81817066	{'ARMB': {'GG': 55, 'AG': 1}, 'APMB': {'GG': 64, 'AG': 3}}	0.62495002	1

chr11:69071686	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr11:69071712	{'African_American': {'GG': 62, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 66}}	0.467741935	1
chr11:69105842	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 57, 'AG': 2}}	0.21726984	0.90275544	{'ARMB': {'GG': 55, 'AG': 2}, 'APMB': {'GG': 69}}	0.202666667	1
chr11:70522825	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr11:70522964	{'African_American': {'GG': 64, 'AG': 3}, 'Not_African_American': {'GG': 48, 'AG': 7}}	0.18251075	0.90275544	{'ARMB': {'GG': 52, 'AG': 4}, 'APMB': {'GG': 60, 'AG': 6}}	0.752307228	1
chr11:71478390	{'African_American': {'CC': 47, 'CT': 17}, 'Not_African_American': {'CC': 53, 'CT': 6}}	0.02217203	0.28601914	{'ARMB': {'CC': 44, 'CT': 12}, 'APMB': {'CC': 56, 'CT': 11}}	0.495910618	1
chr11:71929024	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 56, 'CT': 1}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 64, 'CT': 1}}	1	1
chr11:73647665	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'GG': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'GG': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr11:73647667	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'GG': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'GG': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr11:77150940	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr11:86676953	{'African_American': {'TT': 58, 'CT': 3, 'CC': 2}, 'Not_African_American': {'TT': 54, 'CT': 5, 'CC': 1}}	0.61007271	1	{'ARMB': {'TT': 52, 'CT': 3, 'CC': 3}, 'APMB': {'TT': 60, 'CT': 5}}	0.162485812	1
chr11:86677022	{'African_American': {'AA': 65, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 59}, 'APMB': {'AA': 67, 'AG': 1}}	1	1
chr11:94973701	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr11:10231750	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'GG': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'GG': 1}}	1	1
chr11:11783824	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr11:11783837	{'African_American': {'GG': 62, 'AG': 3}, 'Not_African_American': {'GG': 61}}	0.2447619	0.90275544	{'ARMB': {'GG': 57, 'AG': 2}, 'APMB': {'GG': 66, 'AG': 1}}	0.599235023	1
chr11:11798635	{'African_American': {'TT': 59, 'CT': 5}, 'Not_African_American': {'TT': 60}}	0.05812135	0.56650187	{'ARMB': {'TT': 56, 'CT': 2}, 'APMB': {'TT': 63, 'CT': 3}}	1	1
chr11:12012990	{'African_American': {'CC': 65, 'CT': 2}, 'Not_African_American': {'CC': 61}}	0.49717028	0.90275544	{'ARMB': {'CC': 57, 'CT': 2}, 'APMB': {'CC': 69}}	0.21050689	1
chr11:12618693	{'African_American': {'CC': 65, 'CT': 2}, 'Not_African_American': {'CC': 60, 'CT': 1}}	1	1	{'ARMB': {'CC': 57, 'CT': 2}, 'APMB': {'CC': 68, 'CT': 1}}	0.594540917	1
chr11:13383281	{'African_American': {'CC': 62}, 'Not_African_American': {'CC': 57, 'CT': 1}}	0.48333333	0.90275544	{'ARMB': {'CC': 57}, 'APMB': {'CC': 62, 'CT': 1}}	1	1
chr11:13383284	{'African_American': {'CC': 63}, 'Not_African_American': {'CC': 58, 'TT': 1}}	0.48360656	0.90275544	{'ARMB': {'CC': 57, 'TT': 1}, 'APMB': {'CC': 64}}	0.475409836	1
chr11:13383287	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 57, 'CT': 1}}	1	1	{'ARMB': {'CC': 57, 'CT': 1}, 'APMB': {'CC': 65, 'CT': 1}}	1	1
chr12:3077309	{'African_American': {'CC': 63, 'AA': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 56}, 'APMB': {'CC': 68, 'AA': 1}}	1	1
chr12:3077315	{'African_American': {'CC': 65, 'AA': 1}, 'Not_African_American': {'CC': 57}}	1	1	{'ARMB': {'CC': 56}, 'APMB': {'CC': 66, 'AA': 1}}	1	1
chr12:6376267	{'African_American': {'TT': 64, 'CT': 2}, 'Not_African_American': {'TT': 61}}	0.4968129	0.90275544	{'ARMB': {'TT': 57, 'CT': 2}, 'APMB': {'TT': 68}}	0.213848269	1
chr12:6445019	{'African_American': {'CC': 57, 'CT': 4}, 'Not_African_American': {'CC': 59, 'CT': 1}}	0.3645392	0.90275544	{'ARMB': {'CC': 52, 'CT': 3}, 'APMB': {'CC': 64, 'CT': 2}}	0.658168352	1
chr12:56521840	{'African_American': {'CC': 55, 'CT': 5}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.11415679	0.81817066	{'ARMB': {'CC': 55, 'CT': 2}, 'APMB': {'CC': 60, 'CT': 4}}	0.682803531	1
chr12:57755077	{'African_American': {'TT': 66, 'GG': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 58, 'GG': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr12:92861118	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'GG': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'GG': 1}}	1	1
chr12:10924632	{'African_American': {'GG': 52, 'AG': 7}, 'Not_African_American': {'GG': 55, 'AG': 2}}	0.16295309	0.90275544	{'ARMB': {'GG': 47, 'AG': 6}, 'APMB': {'GG': 60, 'AG': 3}}	0.297013789	1
chr12:11649728	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 59, 'AG': 1}}	0.47244094	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 68}}	0.464566929	1
chr12:11703373	{'African_American': {'CC': 56, 'CT': 9}, 'Not_African_American': {'CC': 61}}	0.00299449	0.0678263	{'ARMB': {'CC': 51, 'CT': 7}, 'APMB': {'CC': 66, 'CT': 2}}	0.079187926	1
chr12:11703374	{'African_American': {'CC': 64, 'CT': 2}, 'Not_African_American': {'CC': 61}}	0.4968129	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 67, 'CT': 1}}	1	1
chr12:11705420	{'African_American': {'GG': 59, 'AG': 3, 'AA': 1}, 'Not_African_American': {'GG': 61}}	0.17954562	0.90275544	{'ARMB': {'GG': 54, 'AG': 2, 'AA': 1}, 'APMB': {'GG': 66, 'AG': 1}}	0.405548924	1
chr12:11767835	{'African_American': {'GG': 61, 'AG': 3}, 'Not_African_American': {'GG': 36, 'AG': 12, 'AA': 5}}	0.00018264	0.008835	{'ARMB': {'GG': 41, 'AG': 9, 'AA': 3}, 'APMB': {'GG': 56, 'AG': 6, 'AA': 2}}	0.387207843	1
chr12:11767842	{'African_American': {'GG': 58, 'AG': 4}, 'Not_African_American': {'GG': 61}}	0.11892764	0.81817066	{'ARMB': {'GG': 53, 'AG': 2}, 'APMB': {'GG': 66, 'AG': 2}}	1	1
chr12:12191851	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 60}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 67, 'CT': 1}}	1	1
chr12:12191857	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 59, 'CT': 1}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 66, 'CT': 1}}	1	1
chr12:12430150	{'African_American': {'GG': 63, 'AG': 3}, 'Not_African_American': {'GG': 61}}	0.24521935	0.90275544	{'ARMB': {'GG': 56, 'AG': 3}, 'APMB': {'GG': 68}}	0.097514811	1
chr12:12430154	{'African_American': {'GG': 48, 'AG': 10, 'AA': 1}, 'Not_African_American': {'GG': 45, 'AG': 12}}	0.63986491	1	{'ARMB': {'GG': 43, 'AG': 12}, 'APMB': {'GG': 50, 'AG': 10, 'AA': 1}}	0.636271685	1
chr12:13231036	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr12:13231044	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 60}}	1	1	{'ARMB': {'CC': 58}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr13:28618813	{'African_American': {'CC': 63, 'CT': 3}, 'Not_African_American': {'CC': 61}}	0.24521935	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 66, 'CT': 2}}	1	1
chr13:29339999	{'African_American': {'GG': 65, 'AG': 2}, 'Not_African_American': {'GG': 36, 'AG': 12, 'AA': 5}}	2.3946E-05	0.00142569	{'ARMB': {'GG': 42, 'AG': 8, 'AA': 3}, 'APMB': {'GG': 59, 'AG': 6, 'AA': 2}}	0.411788408	1
chr13:30107674	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 68}}	0.464566929	1
chr13:30107790	{'African_American': {'CC': 63, 'CT': 3}, 'Not_African_American': {'CC': 61}}	0.24521935	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 66, 'CT': 2}}	1	1
chr13:30170953	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr13:47841332	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 60, 'CT': 1}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr13:47841352	{'African_American': {'AA': 65, 'AG': 2}, 'Not_African_American': {'AA': 61}}	0.49717028	0.90275544	{'ARMB': {'AA': 59}, 'APMB': {'AA': 67, 'AG': 2}}	0.49913878	1
chr13:60591615	{'African_American': {'TT': 65, 'CT': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 58}, 'APMB': {'TT': 68, 'CT': 1}}	1	1
chr13:94601862	{'African_American': {'CC': 62, 'CT': 2, 'TT': 1}, 'Not_African_American': {'CC': 60, 'TT': 1}}	0.74647134	1	{'ARMB': {'CC': 54, 'CT': 2, 'TT': 1}, 'APMB': {'CC': 68, 'TT': 1}}	0.452239631	1
chr13:99390746	{'African_American': {'CC': 62, 'CT': 1}, 'Not_African_American': {'CC': 57}}	1	1	{'ARMB': {'CC': 54}, 'APMB': {'CC': 65, 'CT': 1}}	1	1
chr13:11066821	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr13:11066827	{'African_American': {'GG': 66}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.48031496	0.90275544	{'ARMB': {'GG': 58}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr13:11201385	{'African_American': {'CC': 63}, 'Not_African_American': {'CC': 57, 'CT': 1}}	0.47933884	0.90275544	{'ARMB': {'CC': 56, 'CT': 1}, 'APMB': {'CC': 64}}	0.47107438	1
chr13:11201387	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr13:11211689	{'African_American': {'AA': 56, 'AG': 7, 'GG': 1}, 'Not_African_American': {'AA': 59}}	0.00910096	0.14360948	{'ARMB': {'AA': 51, 'AG': 3, 'GG': 1}, 'APMB': {'AA': 64, 'AG': 4}}	0.834034826	1
chr13:11211696	{'African_American': {'CC': 64, 'TT': 1}, 'Not_African_American': {'CC': 41, 'TT': 12}}	0.00049741	0.01904412	{'ARMB': {'CC': 47, 'TT': 6}, 'APMB': {'CC': 58, 'TT': 7}}	1	1
chr13:11211697	{'African_American': {'CC': 65, 'TT': 1}, 'Not_African_American': {'CC': 44, 'TT': 12}}	0.00053893	0.01904412	{'ARMB': {'CC': 49, 'TT': 6}, 'APMB': {'CC': 60, 'TT': 7}}	1	1
chr13:11211698	{'African_American': {'CC': 65, 'TT': 1}, 'Not_African_American': {'CC': 44, 'TT': 11}}	0.00113288	0.03507406	{'ARMB': {'CC': 49, 'TT': 6}, 'APMB': {'CC': 60, 'TT': 6}}	0.768512602	1
chr13:11211699	{'African_American': {'CC': 64, 'TT': 1}, 'Not_African_American': {'CC': 45, 'TT': 11}}	0.00121885	0.03628417	{'ARMB': {'CC': 50, 'TT': 6}, 'APMB': {'CC': 59, 'TT': 6}}	1	1
chr13:11211705	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr13:11232968	{'African_American': {'AA': 67}, 'Not_African_American': {'AA': 59, 'AG': 1}}	0.47244094	0.90275544	{'ARMB': {'AA': 59}, 'APMB': {'AA': 67, 'AG': 1}}	1	1
chr13:11232972	{'African_American': {'CC': 57, 'CT': 1}, 'Not_African_American': {'CC': 61}}	0.48739496	0.90275544	{'ARMB': {'CC': 53, 'CT': 1}, 'APMB': {'CC': 65}}	0.453781513	1
chr14:20601703	{'African_American': {'AA': 66, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 59}, 'APMB': {'AA': 68, 'AG': 1}}	1	1
chr14:21511397	{'African_American': {'AA': 65, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 57, 'AG': 1}, 'APMB': {'AA': 69}}	0.456692913	1
chr14:63315203	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'AA': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr14:63315213	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'AA': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr14:64655015	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr14:75233967	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr14:95327733	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr14:97217853	{'African_American': {'GG': 60, 'AG': 5, 'AA': 1}, 'Not_African_American': {'GG': 61}}	0.05855316	0.56650187	{'ARMB': {'GG': 54, 'AG': 4}, 'APMB': {'GG': 67, 'AA': 1, 'AG': 1}}	0.177378532	1
chr14:10060356	{'African_American': {'GG': 44, 'TT': 16}, 'Not_African_American': {'GG': 37, 'TT': 24}}	0.17665912	0.90275544	{'ARMB': {'GG': 34, 'TT': 21}, 'APMB': {'GG': 47, 'TT': 19}}	0.333030321	1
chr14:10309526	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'TT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'TT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr14:10309531	{'African_American': {'GG': 51, 'AG': 8}, 'Not_African_American': {'GG': 59, 'AG': 1}}	0.01658306	0.22621947	{'ARMB': {'GG': 50, 'AG': 5}, 'APMB': {'GG': 60, 'AG': 4}}	0.731153399	1
chr14:10309535	{'African_American': {'GG': 54, 'AG': 7}, 'Not_African_American': {'GG': 59, 'AG': 1}}	0.061393	0.5866442	{'ARMB': {'GG': 49, 'AG': 6}, 'APMB': {'GG': 64, 'AG': 2}}	0.139339497	1
chr14:10410117	{'African_American': {'CC': 58, 'AA': 2}, 'Not_African_American': {'CC': 59}}	0.49579832	0.90275544	{'ARMB': {'CC': 52, 'AA': 1}, 'APMB': {'CC': 65, 'AA': 1}}	1	1
chr14:10428501	{'African_American': {'CC': 63, 'CT': 1}, 'Not_African_American': {'CC': 60}}	1	1	{'ARMB': {'CC': 58}, 'APMB': {'CC': 65, 'CT': 1}}	1	1
chr14:10428508	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr14:10431472	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr14:10431472	{'African_American': {'CC': 58, 'CT': 6}, 'Not_African_American': {'CC': 41, 'CT': 11, 'TT': 6}}	0.00445491	0.08145506	{'ARMB': {'CC': 40, 'CT': 12, 'TT': 5}, 'APMB': {'CC': 59, 'CT': 5, 'TT': 1}}	0.011325174	1
chr14:10431475	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr14:10431480	{'African_American': {'GG': 63}, 'Not_African_American': {'GG': 59, 'AG': 1}}	0.48780488	0.90275544	{'ARMB': {'GG': 55}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr14:10431481	{'African_American': {'CC': 47, 'CT': 12, 'TT': 3}, 'Not_African_American': {'CC': 35, 'CT': 14, 'TT': 7}}	0.21276186	0.90275544	{'ARMB': {'CC': 37, 'CT': 14, 'TT': 5}, 'APMB': {'CC': 45, 'CT': 12, 'TT': 5}}	0.793384179	1
chr14:10487842	{'African_American': {'CC': 46, 'CT': 17}, 'Not_African_American': {'TT': 23, 'CT': 17, 'CC': 13}}	4.4366E-11	1.717E-08	{'ARMB': {'CC': 21, 'CT': 19, 'TT': 13}, 'APMB': {'CC': 38, 'CT': 15, 'TT': 10}}	0.094232723	1
chr14:10487848	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 56, 'AG': 2}}	0.21329032	0.90275544	{'ARMB': {'GG': 55, 'AG': 2}, 'APMB': {'GG': 68}}	0.205935484	1
chr15:81002335	{'African_American': {'AA': 62, 'AG': 4}, 'Not_African_American': {'AA': 61}}	0.12023416	0.81817066	{'ARMB': {'AA': 55, 'AG': 3}, 'APMB': {'AA': 68, 'AG': 1}}	0.330716886	1
chr15:82952716	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr15:94317481	{'African_American': {'TT': 57, 'CT': 5}, 'Not_African_American': {'TT': 61}}	0.05748169	0.56650187	{'ARMB': {'TT': 53, 'CT': 4}, 'APMB': {'TT': 65, 'CT': 1}}	0.18139696	1
chr16:1533598	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr16:3484909	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr16:3484915	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 59, 'CT': 1}}	0.47244094	0.90275544	{'ARMB': {'CC': 57, 'CT': 1}, 'APMB': {'CC': 69}}	0.456692913	1
chr16:3484934	{'African_American': {'TT': 65, 'CT': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 57, 'CT': 1}, 'APMB': {'TT': 69}}	0.456692913	1
chr16:11135793	{'African_American': {'AA': 66, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 59}, 'APMB': {'AA': 68, 'AG': 1}}	1	1
chr16:14959878	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'AA': 1}}	1	1
chr16:17134595	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 69}}	0.456692913	1
chr16:28553875	{'African_American': {'CC': 62, 'CT': 1}, 'Not_African_American': {'CC': 60}}	1	1	{'ARMB': {'CC': 57}, 'APMB': {'CC': 65, 'CT': 1}}	1	1
chr16:28931996	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'GG': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'GG': 1}}	1	1
chr16:29127569	{'African_American': {'GG': 63, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 56}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr16:55760618	{'African_American': {'CC': 66}, 'Not_African_American': {'CC': 57, 'CT': 3}}	0.10513057	0.81817066	{'ARMB': {'CC': 57, 'CT': 1}, 'APMB': {'CC': 66, 'CT': 2}}	1	1

chr16:55760650	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr16:55760753	{'African_American': {'AA': 60, 'AG': 4}, 'Not_African_American': {'AA': 59, 'AG': 2}}	0.68032252	1	{'ARMB': {'AA': 56, 'AG': 2}, 'APMB': {'AA': 63, 'AG': 4}}	0.684870029	1
chr16:55760806	{'African_American': {'GG': 56, 'AG': 11}, 'Not_African_American': {'GG': 34, 'AG': 18, 'AA': 6}}	0.00095867	0.03091726	{'ARMB': {'GG': 47, 'AG': 9, 'AA': 2}, 'APMB': {'GG': 43, 'AG': 20, 'AA': 4}}	0.100027185	1
chr16:55760829	{'African_American': {'AA': 66, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 59}, 'APMB': {'AA': 68, 'AG': 1}}	1	1
chr16:55760853	{'African_American': {'AA': 60, 'AG': 5}, 'Not_African_American': {'AA': 59, 'AG': 1}}	0.20962115	0.90275544	{'ARMB': {'AA': 56, 'AG': 1}, 'APMB': {'AA': 63, 'AG': 5}}	0.218444235	1
chr16:55760909	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 57, 'CT': 1}, 'APMB': {'CC': 69}}	0.456692913	1
chr16:59533042	{'African_American': {'GG': 53, 'AA': 3}, 'Not_African_American': {'GG': 61}}	0.1065621	0.81817066	{'ARMB': {'GG': 51, 'AA': 3}, 'APMB': {'GG': 63}}	0.095352324	1
chr16:59533053	{'African_American': {'AA': 63, 'GG': 1, 'AG': 1}, 'Not_African_American': {'AA': 60, 'GG': 1}}	1	1	{'ARMB': {'AA': 56, 'GG': 1, 'AG': 1}, 'APMB': {'AA': 67, 'GG': 1}}	0.729392729	1
chr16:68707872	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 69}}	0.456692913	1
chr16:68707925	{'African_American': {'CC': 65, 'CT': 2}, 'Not_African_American': {'CC': 61}}	0.49717028	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 67, 'CT': 2}}	0.49913878	1
chr16:76048043	{'African_American': {'TT': 66, 'GG': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 58, 'GG': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr16:84344220	{'African_American': {'CC': 64, 'CT': 3}, 'Not_African_American': {'CC': 58, 'CT': 2}}	1	1	{'ARMB': {'CC': 56, 'CT': 3}, 'APMB': {'CC': 66, 'CT': 2}}	0.662715347	1
chr16:85360587	{'African_American': {'GG': 48, 'AG': 7, 'AA': 2}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.01078941	0.16374513	{'ARMB': {'GG': 51, 'AG': 4}, 'APMB': {'GG': 57, 'AG': 4, 'AA': 2}}	0.639290392	1
chr16:87808602	{'African_American': {'GG': 62, 'AG': 3}, 'Not_African_American': {'GG': 59, 'AG': 1}}	0.62011582	1	{'ARMB': {'GG': 57, 'AG': 2}, 'APMB': {'GG': 64, 'AG': 2}}	1	1
chr16:88599640	{'African_American': {'GG': 60, 'AG': 3}, 'Not_African_American': {'GG': 43, 'AG': 12, 'AA': 3}}	0.00299137	0.0678263	{'ARMB': {'GG': 45, 'AG': 9, 'AA': 1}, 'APMB': {'GG': 58, 'AG': 6, 'AA': 2}}	0.454605774	1
chr16:88909531	{'African_American': {'GG': 60, 'CC': 3}, 'Not_African_American': {'GG': 52, 'CC': 3}}	1	1	{'ARMB': {'GG': 52, 'CC': 4}, 'APMB': {'GG': 60, 'CC': 2}}	0.421132653	1
chr16:88909671	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 60, 'AG': 1}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr16:88910612	{'African_American': {'GG': 64, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr16:90031340	{'African_American': {'CC': 51, 'CT': 8, 'TT': 1}, 'Not_African_American': {'CC': 52, 'CT': 5}}	0.55977562	1	{'ARMB': {'CC': 44, 'CT': 8, 'TT': 1}, 'APMB': {'CC': 59, 'CT': 5}}	0.185518779	1
chr17:1469676	{'African_American': {'GG': 59, 'AG': 1}, 'Not_African_American': {'GG': 54, 'AG': 2, 'AA': 1}}	0.42163534	0.90275544	{'ARMB': {'GG': 51, 'AG': 1}, 'APMB': {'GG': 62, 'AG': 2, 'AA': 1}}	1	1
chr17:2030143	{'African_American': {'TT': 66, 'GG': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'GG': 1}}	1	1
chr17:3641939	{'African_American': {'GG': 61, 'AG': 3}, 'Not_African_American': {'GG': 61}}	0.2443871	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 64, 'AG': 2}}	1	1
chr17:4177816	{'African_American': {'CC': 65, 'CT': 2}, 'Not_African_American': {'CC': 61}}	0.49717028	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr17:4177895	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr17:9105136	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr17:14318263	{'African_American': {'CC': 60, 'CT': 2}, 'Not_African_American': {'CC': 47, 'CT': 7}}	0.07969857	0.73436535	{'ARMB': {'CC': 49, 'CT': 3}, 'APMB': {'CC': 58, 'CT': 6}}	0.72924257	1
chr17:22694621	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 57, 'AA': 1, 'AG': 1}}	0.21726984	0.90275544	{'ARMB': {'GG': 57, 'AA': 1}, 'APMB': {'GG': 67, 'AG': 1}}	0.710730159	1
chr17:22694649	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 58, 'AA': 1, 'AG': 1}}	0.22122235	0.90275544	{'ARMB': {'GG': 58, 'AA': 1}, 'APMB': {'GG': 67, 'AG': 1}}	0.715285589	1
chr17:31512642	{'African_American': {'GG': 62, 'AG': 1}, 'Not_African_American': {'GG': 60, 'AG': 1}}	1	1	{'ARMB': {'GG': 56}, 'APMB': {'GG': 66, 'AG': 2}}	0.500655652	1
chr17:31709570	{'African_American': {'AA': 66, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 59}, 'APMB': {'AA': 68, 'AG': 1}}	1	1
chr17:31709686	{'African_American': {'CC': 60, 'CT': 5, 'TT': 1}, 'Not_African_American': {'CC': 46, 'CT': 7, 'TT': 1}}	0.68569841	1	{'ARMB': {'CC': 48, 'CT': 7}, 'APMB': {'CC': 58, 'CT': 5, 'TT': 2}}	0.476695861	1
chr17:32183977	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'AA': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr17:32183979	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'AA': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr17:34255217	{'African_American': {'TT': 65, 'CT': 1}, 'Not_African_American': {'TT': 60}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 66, 'CT': 1}}	1	1
chr17:39963039	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'AA': 1}}	1	1
chr17:50612526	{'African_American': {'GG': 62, 'AA': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 57, 'AA': 1}, 'APMB': {'GG': 66}}	0.467741935	1
chr17:76521074	{'African_American': {'CC': 66, 'AA': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'AA': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr17:77258551	{'African_American': {'GG': 63, 'AG': 3}, 'Not_African_American': {'GG': 61}}	0.24521935	0.90275544	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 67, 'AG': 2}}	1	1
chr17:77258626	{'African_American': {'AA': 62, 'AG': 4}, 'Not_African_American': {'AA': 61}}	0.12023416	0.81817066	{'ARMB': {'AA': 58, 'AG': 1}, 'APMB': {'AA': 65, 'AG': 3}}	0.622854434	1
chr17:79452925	{'African_American': {'GG': 60, 'AG': 1}, 'Not_African_American': {'GG': 58}}	1	1	{'ARMB': {'GG': 55, 'AG': 1}, 'APMB': {'GG': 63}}	0.470588235	1
chr17:79452932	{'African_American': {'CC': 60, 'CT': 5}, 'Not_African_American': {'CC': 59, 'CT': 2}}	0.44142375	0.90275544	{'ARMB': {'CC': 56, 'CT': 3}, 'APMB': {'CC': 63, 'CT': 4}}	1	1
chr17:79452948	{'African_American': {'GG': 63}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.49193548	0.90275544	{'ARMB': {'GG': 57}, 'APMB': {'GG': 66, 'AG': 1}}	1	1
chr17:79453006	{'African_American': {'GG': 60, 'AA': 3, 'AG': 2}, 'Not_African_American': {'GG': 61}}	0.12156282	0.81817066	{'ARMB': {'GG': 57, 'AA': 1, 'AG': 1}, 'APMB': {'GG': 64, 'AA': 2, 'AG': 1}}	1	1
chr17:79453020	{'African_American': {'CC': 65, 'CT': 2}, 'Not_African_American': {'CC': 60, 'CT': 1}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 67, 'CT': 2}}	1	1
chr17:79453117	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 68}}	0.464566929	1
chr17:80236435	{'African_American': {'CC': 51, 'CT': 11}, 'Not_African_American': {'CC': 55, 'CT': 4}}	0.09714154	0.81817066	{'ARMB': {'CC': 44, 'CT': 9}, 'APMB': {'CC': 62, 'CT': 6}}	0.265846749	1
chr17:80236497	{'African_American': {'CC': 64, 'CT': 2}, 'Not_African_American': {'CC': 61}}	0.4968129	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 67, 'CT': 1}}	1	1
chr17:80707826	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr17:80879029	{'African_American': {'GG': 53, 'AG': 8, 'AA': 3}, 'Not_African_American': {'GG': 34, 'AG': 14, 'AA': 5}}	0.07319765	0.69091441	{'ARMB': {'GG': 40, 'AG': 11, 'AA': 1}, 'APMB': {'GG': 47, 'AG': 11, 'AA': 7}}	0.17226299	1
chr17:80879072	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 59, 'AG': 1}}	0.47244094	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr17:81071668	{'African_American': {'CC': 54, 'CT': 4}, 'Not_African_American': {'CC': 61}}	0.05342946	0.55139198	{'ARMB': {'CC': 52, 'CT': 3}, 'APMB': {'CC': 63, 'CT': 1}}	0.334410561	1
chr17:81071673	{'African_American': {'GG': 66}, 'Not_African_American': {'GG': 58, 'AG': 1}}	0.472	0.90275544	{'ARMB': {'GG': 58}, 'APMB': {'GG': 66, 'AG': 1}}	1	1
chr17:81071766	{'African_American': {'CC': 60, 'CT': 2, 'TT': 1}, 'Not_African_American': {'CC': 57, 'CT': 4}}	0.43583481	0.90275544	{'ARMB': {'CC': 53, 'CT': 4, 'TT': 1}, 'APMB': {'CC': 64, 'CT': 2}}	0.306476513	1
chr17:81071796	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr17:81110092	{'African_American': {'GG': 64, 'TT': 1}, 'Not_African_American': {'GG': 57}}	1	1	{'ARMB': {'GG': 54, 'TT': 1}, 'APMB': {'GG': 67}}	0.450819672	1
chr17:81110218	{'African_American': {'AA': 63, 'AG': 2}, 'Not_African_American': {'AA': 61}}	0.49650794	0.90275544	{'ARMB': {'AA': 58}, 'APMB': {'AA': 66, 'AG': 2}}	0.499174603	1
chr17:82218731	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr17:82218823	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 58, 'CT': 3}}	0.10542627	0.81817066	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 67, 'CT': 2}}	1	1
chr18:514471	{'African_American': {'GG': 59, 'AG': 2}, 'Not_African_American': {'GG': 56, 'AG': 3}}	0.67688357	1	{'ARMB': {'GG': 53, 'AG': 2}, 'APMB': {'GG': 62, 'AG': 3}}	1	1
chr18:514558	{'African_American': {'AA': 60, 'AG': 2, 'GG': 1}, 'Not_African_American': {'AA': 55, 'GG': 1}}	0.74749492	1	{'ARMB': {'AA': 52, 'GG': 2, 'AG': 1}, 'APMB': {'AA': 63, 'AG': 1}}	0.460081295	1
chr18:10128035	{'African_American': {'AA': 34, 'AG': 23, 'GG': 3}, 'Not_African_American': {'AA': 24, 'AG': 19, 'GG': 13}}	0.01706695	0.22775554	{'ARMB': {'AA': 21, 'AG': 20, 'GG': 10}, 'APMB': {'AA': 37, 'AG': 22, 'GG': 6}}	0.149525925	1
chr18:29179170	{'African_American': {'CC': 66, 'AA': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'AA': 1}}	1	1
chr18:29179190	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 58, 'AA': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr18:37310893	{'African_American': {'CC': 56, 'CT': 8, 'TT': 1}, 'Not_African_American': {'CC': 43, 'CT': 9, 'TT': 4}}	0.22342402	0.90275544	{'ARMB': {'CC': 42, 'CT': 11, 'TT': 3}, 'APMB': {'CC': 57, 'CT': 6, 'TT': 2}}	0.186505844	1
chr18:37310916	{'African_American': {'AA': 66, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 59}, 'APMB': {'AA': 68, 'AG': 1}}	1	1
chr18:46149862	{'African_American': {'CC': 56, 'CT': 3, 'TT': 1}, 'Not_African_American': {'CC': 61}}	0.05739982	0.56650187	{'ARMB': {'CC': 54, 'CT': 1, 'TT': 1}, 'APMB': {'CC': 63, 'CT': 2}}	0.7840528	1
chr18:48113788	{'African_American': {'CC': 64}, 'Not_African_American': {'CC': 58, 'CT': 1}}	0.4796748	0.90275544	{'ARMB': {'CC': 55, 'CT': 1}, 'APMB': {'CC': 67}}	0.455284553	1
chr18:48113883	{'African_American': {'GG': 61, 'AG': 3, 'AA': 1}, 'Not_African_American': {'GG': 49, 'AG': 7}}	0.18458792	0.90275544	{'ARMB': {'GG': 47, 'AG': 7}, 'APMB': {'GG': 63, 'AG': 3, 'AA': 1}}	0.143008087	1
chr18:70288978	{'African_American': {'CC': 66, 'GG': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'GG': 1}}	1	1
chr18:79404224	{'African_American': {'GG': 62, 'AG': 4}, 'Not_African_American': {'GG': 61}}	0.12023416	0.81817066	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 66, 'AG': 3}}	0.624762582	1
chr19:544037	{'African_American': {'CC': 55, 'CT': 8}, 'Not_African_American': {'CC': 58, 'CT': 1}}	0.03315963	0.38306793	{'ARMB': {'CC': 49, 'CT': 5}, 'APMB': {'CC': 64, 'CT': 4}}	0.507115127	1
chr19:660448	{'African_American': {'GG': 64, 'AG': 3}, 'Not_African_American': {'GG': 61}}	0.24575541	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 66, 'AG': 3}}	0.248708169	1
chr19:660455	{'African_American': {'AA': 66, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 59}, 'APMB': {'AA': 68, 'AG': 1}}	1	1
chr19:667131	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr19:827957	{'African_American': {'CC': 59, 'CT': 3, 'TT': 1}, 'Not_African_American': {'CC': 61}}	0.17954562	0.90275544	{'ARMB': {'CC': 55, 'CT': 2, 'TT': 1}, 'APMB': {'CC': 65, 'CT': 1}}	0.409860689	1
chr19:828032	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 60, 'CT': 1}}	1	1	{'ARMB': {'CC': 58}, 'APMB': {'CC': 67, 'CT': 2}}	0.499812523	1
chr19:828105	{'African_American': {'GG': 58, 'AG': 5, 'AA': 1}, 'Not_African_American': {'GG': 61}}	0.04134999	0.47066016	{'ARMB': {'GG': 54, 'AA': 1, 'AG': 1}, 'APMB': {'GG': 65, 'AG': 4}}	0.266873567	1
chr19:831398	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr19:831402	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 57, 'AG': 2, 'AA': 1}}	0.41494886	0.90275544	{'ARMB': {'GG': 55, 'AG': 2, 'AA': 1}, 'APMB': {'GG': 67, 'AG': 1}}	0.40598404	1
chr19:856015	{'African_American': {'GG': 59, 'AG': 6}, 'Not_African_American': {'GG': 61}}	0.02804464	0.33555035	{'ARMB': {'GG': 56, 'AG': 3}, 'APMB': {'GG': 64, 'AG': 3}}	1	1
chr19:1012052	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr19:1012121	{'African_American': {'GG': 57, 'AG': 6}, 'Not_African_American': {'GG': 48, 'AG': 9}}	0.40872747	0.90275544	{'ARMB': {'GG': 44, 'AG': 7}, 'APMB': {'GG': 61, 'AG': 8}}	0.784245118	1
chr19:1012158	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 67, 'CT': 1}}	1	1
chr19:1012192	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr19:1154629	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr19:1882286	{'African_American': {'CC': 62, 'CT': 4}, 'Not_African_American': {'CC': 60}}	0.12072534	0.81817066	{'ARMB': {'CC': 54, 'CT': 4}, 'APMB': {'CC': 68}}	0.042388321	1
chr19:2360198	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr19:2360201	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr19:2634588	{'African_American': {'GG': 64, 'AG': 3}, 'Not_African_American': {'GG': 61}}	0.24575541	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 67, 'AG': 2}}	1	1
chr19:2634611	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr19:2634629	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr19:3094361	{'African_American': {'TT': 66, 'GG': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 58, 'GG': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr19:3189721	{'African_American': {'CC': 64, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 67}}	0.468253968	1
chr19:3468000	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr19:5189286	{'African_American': {'CC': 62, 'CT': 3}, 'Not_African_American': {'CC': 47, 'TT': 3, 'CT': 1}}	0.09957215	0.81817066	{'ARMB': {'CC': 46, 'CT': 3, 'TT': 3}, 'APMB': {'CC': 63, 'CT': 1}}	0.059651723	1
chr19:5189289	{'African_American': {'AA': 41, 'AG': 16, 'GG': 6}, 'Not_African_American': {'AA': 58}}	7.5619E-08	1.1706E-05	{'ARMB': {'AA': 48, 'AG': 8, 'GG': 1}, 'APMB': {'AA': 51, 'AG': 8, 'GG': 5}}	0.351277321	1
chr19:7702190	{'African_American': {'GG': 62, 'AG': 3}, 'Not_African_American': {'GG': 61}}	0.2447619	0.90275544	{'ARMB': {'GG': 57}, 'APMB': {'GG': 66, 'AG': 3}}	0.250857143	1
chr19:8111712	{'African_American': {'AA': 66, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 58, 'AG': 1}, 'APMB': {'AA': 69}}	0.4609375	1
chr19:11239513	{'African_American': {'TT': 58, 'CT': 6, 'CC': 1}, 'Not_African_American': {'TT': 60}}	0.01940386	0.25455235	{'ARMB': {'TT': 54, 'CT': 2, 'CC': 1}, 'APMB': {'TT': 64, 'CT': 4}}	0.538350713	1
chr19:14554047	{'African_American': {'GG': 63, 'AG': 2}, 'Not_African_American': {'GG': 59, 'AG': 1}}	1	1	{'ARMB': {'GG': 55, 'AG': 2}, 'APMB': {'GG': 67, 'AG': 1}}	0.591357986	1

chr19:17846109	{'African_American': {'CC': 60, 'CT': 3}, 'Not_African_American': {'CC': 61}}	0.24409913	0.90275544	{'ARMB': {'CC': 55, 'CT': 1}, 'APMB': {'CC': 66, 'CT': 2}}	1	1
chr19:17846133	{'African_American': {'CC': 66, 'GG': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'GG': 1}}	1	1
chr19:17846168	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 59, 'CT': 2}}	0.22514764	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 67, 'CT': 2}}	0.49913878	1
chr19:35785100	{'African_American': {'CC': 60, 'CT': 1}, 'Not_African_American': {'CC': 57, 'CT': 3}}	0.3645392	0.90275544	{'ARMB': {'CC': 53, 'CT': 2}, 'APMB': {'CC': 64, 'CT': 2}}	1	1
chr19:40733137	{'African_American': {'TT': 63, 'CT': 3}, 'Not_African_American': {'TT': 61}}	0.24521935	0.90275544	{'ARMB': {'TT': 58, 'CT': 1}, 'APMB': {'TT': 66, 'CT': 2}}	1	1
chr19:40733204	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr19:41363968	{'African_American': {'TT': 66, 'CT': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'CT': 1}}	1	1
chr19:41877253	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'GG': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'GG': 1}}	1	1
chr19:41877254	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'AA': 1}}	1	1
chr19:45336792	{'African_American': {'GG': 61, 'AG': 1}, 'Not_African_American': {'GG': 57, 'AG': 2}}	0.61258073	1	{'ARMB': {'GG': 53, 'AG': 2}, 'APMB': {'GG': 65, 'AG': 1}}	0.590336134	1
chr19:45611770	{'African_American': {'GG': 65, 'AG': 2}, 'Not_African_American': {'GG': 61}}	0.49717028	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 67, 'AG': 2}}	0.49913878	1
chr19:47726147	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr19:47726256	{'African_American': {'TT': 64, 'CT': 1}, 'Not_African_American': {'TT': 60, 'CT': 1}}	1	1	{'ARMB': {'TT': 58}, 'APMB': {'TT': 66, 'CT': 2}}	0.499174603	1
chr19:47726274	{'African_American': {'GG': 61, 'AG': 3}, 'Not_African_American': {'GG': 61}}	0.2443871	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 64, 'AG': 2}}	1	1
chr19:48573374	{'African_American': {'GG': 63, 'AG': 2}, 'Not_African_American': {'GG': 61}}	0.49650794	0.90275544	{'ARMB': {'GG': 56, 'AG': 1}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr19:48573430	{'African_American': {'GG': 36, 'AG': 23, 'AA': 6}, 'Not_African_American': {'AG': 23, 'AA': 17, 'GG': 15}}	0.00131117	0.03758674	{'ARMB': {'GG': 21, 'AG': 20, 'AA': 15}, 'APMB': {'GG': 30, 'AG': 26, 'AA': 8}}	0.139028507	1
chr19:50418966	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'AA': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr19:53984660	{'African_American': {'TT': 66, 'AA': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'AA': 1}}	1	1
chr19:53992231	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'AA': 1}}	1	1
chr19:53992266	{'African_American': {'TT': 66, 'AA': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 58, 'AA': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr19:53992268	{'African_American': {'TT': 66, 'AA': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 58, 'AA': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr19:53992271	{'African_American': {'CC': 66, 'AA': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'AA': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr19:55372491	{'African_American': {'GG': 65}, 'Not_African_American': {'GG': 58, 'AG': 1}}	0.47580645	0.90275544	{'ARMB': {'GG': 58}, 'APMB': {'GG': 65, 'AG': 1}}	1	1
chr19:55372541	{'African_American': {'GG': 60, 'AG': 4, 'AA': 1}, 'Not_African_American': {'GG': 61}}	0.1197802	0.81817066	{'ARMB': {'GG': 55, 'AG': 3, 'AA': 1}, 'APMB': {'GG': 66, 'AG': 1}}	0.221936581	1
chr19:55372592	{'African_American': {'CC': 53, 'CT': 6, 'TT': 2}, 'Not_African_American': {'CC': 57, 'CT': 2}}	0.1373195	0.90275544	{'ARMB': {'CC': 53, 'CT': 3}, 'APMB': {'CC': 57, 'CT': 5, 'TT': 2}}	0.560186876	1
chr19:56567435	{'African_American': {'TT': 66, 'GG': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'GG': 1}}	1	1
chr19:58102129	{'African_American': {'GG': 60, 'AG': 3}, 'Not_African_American': {'GG': 61}}	0.24409913	0.90275544	{'ARMB': {'GG': 56, 'AG': 1}, 'APMB': {'GG': 65, 'AG': 2}}	1	1
chr2:1267742	{'African_American': {'GG': 61, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 57}, 'APMB': {'GG': 65, 'AG': 1}}	1	1
chr2:2649253	{'African_American': {'GG': 44, 'AG': 11, 'AA': 4}, 'Not_African_American': {'GG': 60}}	9.6385E-06	0.0006782	{'ARMB': {'GG': 54, 'AG': 4, 'AA': 1}, 'APMB': {'GG': 50, 'AG': 7, 'AA': 3}}	0.37503724	1
chr2:3280281	{'African_American': {'CC': 64, 'CT': 2}, 'Not_African_American': {'CC': 51, 'TT': 2, 'CT': 1}}	0.40072639	0.90275544	{'ARMB': {'CC': 53, 'CT': 1, 'TT': 1}, 'APMB': {'CC': 62, 'CT': 2, 'TT': 1}}	1	1
chr2:9138786	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 57, 'CT': 1}, 'APMB': {'CC': 69}}	0.456692913	1
chr2:9138787	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr2:9138856	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 60}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr2:9138866	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr2:10044557	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 58, 'CT': 3}}	0.10542627	0.81817066	{'ARMB': {'CC': 56, 'CT': 3}, 'APMB': {'CC': 69}}	0.095229307	1
chr2:10880683	{'African_American': {'CC': 35, 'CT': 17, 'TT': 8}, 'Not_African_American': {'CC': 45, 'CT': 12}}	0.0037363	0.07610248	{'ARMB': {'CC': 43, 'CT': 8, 'TT': 2}, 'APMB': {'CC': 37, 'CT': 21, 'TT': 6}}	0.024934583	1
chr2:10880691	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 53, 'CT': 8}}	0.01350296	0.19002349	{'ARMB': {'CC': 53, 'CT': 6}, 'APMB': {'CC': 66, 'CT': 3}}	0.30020089	1
chr2:20670811	{'African_American': {'CC': 56, 'CT': 7}, 'Not_African_American': {'CC': 61}}	0.01314566	0.19002349	{'ARMB': {'CC': 54, 'CT': 3}, 'APMB': {'CC': 63, 'CT': 4}}	1	1
chr2:28545560	{'African_American': {'CC': 51, 'CT': 10, 'TT': 1}, 'Not_African_American': {'CC': 37, 'CT': 12, 'TT': 5}}	0.11298269	0.81817066	{'ARMB': {'CC': 39, 'CT': 13}, 'APMB': {'CC': 49, 'CT': 9, 'TT': 6}}	0.027223145	1
chr2:68157811	{'African_American': {'CC': 66}, 'Not_African_American': {'CC': 57, 'GG': 1}}	0.46774194	0.90275544	{'ARMB': {'CC': 57}, 'APMB': {'CC': 66, 'GG': 1}}	1	1
chr2:68157903	{'African_American': {'TT': 66, 'AA': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'AA': 1}}	1	1
chr2:68157913	{'African_American': {'CC': 66, 'AA': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'AA': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr2:68157920	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 58, 'AA': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr2:94871585	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr2:94871641	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 59, 'CT': 2}}	0.22514764	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr2:94871670	{'African_American': {'AA': 66, 'AG': 1}, 'Not_African_American': {'AA': 60}}	1	1	{'ARMB': {'AA': 57, 'AG': 1}, 'APMB': {'AA': 69}}	0.456692913	1
chr2:97713531	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 58, 'CT': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr2:111716374	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 58, 'CT': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr2:127631769	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 60, 'AG': 1}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr2:128670620	{'African_American': {'CC': 66, 'AA': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'AA': 1}}	1	1
chr2:128670681	{'African_American': {'CC': 64, 'CT': 2}, 'Not_African_American': {'CC': 61}}	0.4968129	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 67, 'CT': 1}}	1	1
chr2:203239044	{'African_American': {'CC': 47, 'CT': 15, 'TT': 2}, 'Not_African_American': {'CC': 61}}	7.4123E-06	0.00057371	{'ARMB': {'CC': 48, 'CT': 9, 'TT': 1}, 'APMB': {'CC': 60, 'CT': 6, 'TT': 1}}	0.578427981	1
chr2:219461456	{'African_American': {'CC': 62, 'CT': 3}, 'Not_African_American': {'CC': 61}}	0.2447619	0.90275544	{'ARMB': {'CC': 55, 'CT': 2}, 'APMB': {'CC': 68, 'CT': 1}}	0.589179724	1
chr2:227667927	{'African_American': {'GG': 55, 'AG': 9}, 'Not_African_American': {'GG': 61}}	0.00293535	0.0678263	{'ARMB': {'GG': 55, 'AG': 3}, 'APMB': {'GG': 61, 'AG': 6}}	0.502327144	1
chr2:233485922	{'African_American': {'CC': 53, 'CT': 5, 'TT': 3}, 'Not_African_American': {'CC': 59, 'CT': 1}}	0.04711107	0.4995064	{'ARMB': {'CC': 50, 'CT': 3, 'TT': 3}, 'APMB': {'CC': 62, 'CT': 3}}	0.198946691	1
chr2:234098456	{'African_American': {'AA': 62, 'AG': 1}, 'Not_African_American': {'AA': 60}}	1	1	{'ARMB': {'AA': 58}, 'APMB': {'AA': 64, 'AG': 1}}	1	1
chr2:234496610	{'African_American': {'AA': 66, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 59}, 'APMB': {'AA': 68, 'AG': 1}}	1	1
chr2:239312972	{'African_American': {'CC': 37, 'CT': 13, 'TT': 8}, 'Not_African_American': {'CC': 54, 'CT': 3, 'TT': 1}}	0.00048731	0.01904412	{'ARMB': {'CC': 44, 'CT': 4, 'TT': 3}, 'APMB': {'CC': 47, 'CT': 12, 'TT': 6}}	0.184685449	1
chr2:239374108	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr2:239509067	{'African_American': {'CC': 36, 'CT': 19, 'TT': 2}, 'Not_African_American': {'CC': 59, 'CT': 2}}	6.5006E-06	0.00055905	{'ARMB': {'CC': 44, 'CT': 11, 'TT': 1}, 'APMB': {'CC': 51, 'CT': 10, 'TT': 1}}	0.817675944	1
chr2:239935894	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 57, 'AG': 1}}	0.464	0.90275544	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 67}}	0.464	1
chr2:239936025	{'African_American': {'CC': 58, 'CT': 6}, 'Not_African_American': {'CC': 61}}	0.02782139	0.33555035	{'ARMB': {'CC': 53, 'CT': 4}, 'APMB': {'CC': 66, 'CT': 2}}	0.41028065	1
chr2:240462070	{'African_American': {'GG': 54, 'AG': 7, 'AA': 1}, 'Not_African_American': {'GG': 60}}	0.0092771	0.14360948	{'ARMB': {'GG': 55, 'AG': 3, 'AA': 1}, 'APMB': {'GG': 59, 'AG': 4}}	0.851682931	1
chr2:240619475	{'African_American': {'GG': 62, 'AG': 3}, 'Not_African_American': {'GG': 61}}	0.2447619	0.90275544	{'ARMB': {'GG': 57, 'AG': 2}, 'APMB': {'GG': 66, 'AG': 1}}	0.599235023	1
chr2:240851586	{'African_American': {'GG': 56, 'AG': 8}, 'Not_African_American': {'GG': 41, 'AG': 13, 'AA': 1}}	0.11688783	0.81817066	{'ARMB': {'GG': 44, 'AG': 9}, 'APMB': {'GG': 53, 'AG': 12, 'AA': 1}}	1	1
chr2:240851632	{'African_American': {'GG': 56, 'AG': 7, 'AA': 2}, 'Not_African_American': {'GG': 61}}	0.00452528	0.08145506	{'ARMB': {'GG': 56, 'AG': 2, 'AA': 1}, 'APMB': {'GG': 61, 'AG': 5, 'AA': 1}}	0.722238382	1
chr2:240851678	{'African_American': {'GG': 63, 'AG': 1}, 'Not_African_American': {'GG': 60, 'AG': 1}}	1	1	{'ARMB': {'GG': 56, 'AG': 1}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr2:240851681	{'African_American': {'CC': 65, 'CT': 2}, 'Not_African_American': {'CC': 61}}	0.49717028	0.90275544	{'ARMB': {'CC': 57, 'CT': 2}, 'APMB': {'CC': 69}}	0.21050689	1
chr2:240851686	{'African_American': {'TT': 58, 'CT': 3}, 'Not_African_American': {'TT': 60, 'CT': 1}}	0.61872352	1	{'ARMB': {'TT': 54, 'CT': 2}, 'APMB': {'TT': 64, 'CT': 2}}	1	1
chr2:240906693	{'African_American': {'CC': 64, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 57, 'CT': 1}, 'APMB': {'CC': 68}}	0.46031746	1
chr2:240906766	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr2:241200185	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 59, 'AG': 2}}	0.22514764	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr2:241200201	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr2:241751311	{'African_American': {'GG': 66}, 'Not_African_American': {'GG': 58, 'AG': 2}}	0.2247619	0.90275544	{'ARMB': {'GG': 56, 'AG': 2}, 'APMB': {'GG': 68}}	0.209904762	1
chr2:241751314	{'African_American': {'CC': 62, 'CT': 4}, 'Not_African_American': {'CC': 60}}	0.12072534	0.81817066	{'ARMB': {'CC': 57, 'CT': 2}, 'APMB': {'CC': 65, 'CT': 2}}	1	1
chr2:241768396	{'African_American': {'GG': 62, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 66}}	0.467741935	1
chr2:241768492	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 60}}	1	1	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 69}}	0.456692913	1
chr20:3470999	{'African_American': {'CC': 48, 'CT': 7}, 'Not_African_American': {'CC': 61}}	0.0043521	0.08145506	{'ARMB': {'CC': 50, 'CT': 4}, 'APMB': {'CC': 59, 'CT': 3}}	0.703248452	1
chr20:3471024	{'African_American': {'CC': 66, 'GG': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'GG': 1}}	1	1
chr20:41136905	{'African_American': {'TT': 66, 'AA': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 58, 'AA': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr20:56487729	{'African_American': {'GG': 62, 'AG': 4}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.36695816	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 64, 'AG': 4}}	0.371424056	1
chr20:56487815	{'African_American': {'CC': 61, 'CT': 3}, 'Not_African_American': {'CC': 33, 'CT': 15, 'TT': 7}}	2.5077E-06	0.00024262	{'ARMB': {'CC': 36, 'CT': 11, 'TT': 6}, 'APMB': {'CC': 58, 'CT': 7, 'TT': 1}}	0.015213696	1
chr20:57615669	{'African_American': {'AA': 65, 'AG': 2}, 'Not_African_American': {'AA': 61}}	0.49717028	0.90275544	{'ARMB': {'AA': 59}, 'APMB': {'AA': 67, 'AG': 2}}	0.49913878	1
chr20:61349131	{'African_American': {'TT': 56, 'CT': 5, 'CC': 1}, 'Not_African_American': {'TT': 60, 'CT': 1}}	0.15958753	0.90275544	{'ARMB': {'TT': 53, 'CT': 3, 'CC': 1}, 'APMB': {'TT': 63, 'CT': 3}}	0.830337058	1
chr20:61349181	{'African_American': {'TT': 50, 'CT': 10, 'CC': 2}, 'Not_African_American': {'TT': 39, 'CT': 17}}	0.07465146	0.69614736	{'ARMB': {'TT': 45, 'CT': 10}, 'APMB': {'TT': 44, 'CT': 17, 'CC': 2}}	0.197593863	1
chr20:62952746	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr21:13373561	{'African_American': {'TT': 66, 'AA': 1}, 'Not_African_American': {'TT': 59}}	1	1	{'ARMB': {'TT': 56, 'AA': 1}, 'APMB': {'TT': 69}}	0.452380952	1
chr21:13373562	{'African_American': {'CC': 63, 'AA': 1}, 'Not_African_American': {'CC': 59}}	1	1	{'ARMB': {'CC': 56, 'AA': 1}, 'APMB': {'CC': 66}}	0.463414634	1
chr21:13373564	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 58, 'AA': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr21:13373568	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 59}}	1	1	{'ARMB': {'CC': 58}, 'APMB': {'CC': 66, 'CT': 1}}	1	1
chr21:13373570	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 59, 'AA': 1}}	0.47244094	0.90275544	{'ARMB': {'CC': 58, 'AA': 1}, 'APMB': {'CC': 68}}	0.464566929	1
chr21:13373603	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 58, 'AA': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr21:13373608	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'GG': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'GG': 1}}	1	1
chr21:13373648	{'African_American': {'GG': 62, 'AA': 1}, 'Not_African_American': {'GG': 53}}	1	1	{'ARMB': {'GG': 51, 'AA': 1}, 'APMB': {'GG': 64}}	0.448275862	1
chr21:13373653	{'African_American': {'AA': 64}, 'Not_African_American': {'AA': 55, 'AG': 1}}	0.46666667	0.90275544	{'ARMB': {'AA': 55}, 'APMB': {'AA': 64, 'AG': 1}}	1	1
chr21:13373660	{'African_American': {'CC': 65}, 'Not_African_American': {'CC': 57, 'GG': 1}}	0.47154472	0.90275544	{'ARMB': {'CC': 58}, 'APMB': {'CC': 64, 'GG': 1}}	1	1
chr21:13373679	{'African_American': {'TT': 65, 'CT': 1}, 'Not_African_American': {'TT': 59}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 65, 'CT': 1}}	1	1
chr21:13373686	{'African_American': {'TT': 63}, 'Not_African_American': {'TT': 55, 'CT': 1}}	0.47058824	0.90275544	{'ARMB': {'TT': 54}, 'APMB': {'TT': 64, 'CT': 1}}	1	1
chr21:39010689	{'African_American': {'GG': 59, 'AG': 4}, 'Not_African_American': {'GG': 49, 'AG': 7, 'AA': 1}}	0.2733999	0.90275544	{'ARMB': {'GG': 45, 'AG': 6, 'AA': 1}, 'APMB': {'GG': 63, 'AG': 5}}	0.345641889	1
chr21:41672523	{'African_American': {'GG': 61, 'AG': 2}, 'Not_African_American': {'GG': 50, 'AA': 2, 'AG': 2}}	0.37043937	0.90275544	{'ARMB': {'GG': 49, 'AA': 2, 'AG': 2}, 'APMB': {'GG': 62, 'AG': 2}}	0.364676173	1

chr21:44771365	{'African_American': {'CC': 62, 'CT': 4}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.36695816	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 64, 'CT': 4}}	0.371424056	1
chr21:44933675	{'African_American': {'GG': 59, 'AG': 1}, 'Not_African_American': {'GG': 61}}	0.49586777	0.90275544	{'ARMB': {'GG': 54, 'AG': 1}, 'APMB': {'GG': 66}}	0.454545455	1
chr21:44933682	{'African_American': {'CC': 48, 'CT': 14}, 'Not_African_American': {'CC': 54, 'CT': 5}}	0.0449688	0.49301959	{'ARMB': {'CC': 52, 'CT': 5}, 'APMB': {'CC': 50, 'CT': 14}}	0.077888592	1
chr21:44933723	{'African_American': {'GG': 63, 'AG': 2}, 'Not_African_American': {'GG': 61}}	0.49650794	0.90275544	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr21:44933758	{'African_American': {'CC': 63, 'CT': 2}, 'Not_African_American': {'CC': 61}}	0.49650794	0.90275544	{'ARMB': {'CC': 57, 'CT': 1}, 'APMB': {'CC': 67, 'CT': 1}}	1	1
chr21:44933763	{'African_American': {'GG': 45, 'AG': 15, 'AA': 2}, 'Not_African_American': {'GG': 41, 'AG': 9, 'AA': 4}}	0.45795352	0.90275544	{'ARMB': {'GG': 44, 'AG': 8, 'AA': 3}, 'APMB': {'GG': 42, 'AG': 16, 'AA': 3}}	0.319328029	1
chr21:44933828	{'African_American': {'TT': 66}, 'Not_African_American': {'TT': 54, 'CT': 4}}	0.04522531	0.49301959	{'ARMB': {'TT': 58, 'CT': 1}, 'APMB': {'TT': 62, 'CT': 3}}	0.620639081	1
chr21:44987924	{'African_American': {'GG': 40, 'AG': 18, 'AA': 2}, 'Not_African_American': {'GG': 60}}	2.8456E-07	3.1464E-05	{'ARMB': {'GG': 47, 'AG': 8}, 'APMB': {'GG': 53, 'AG': 10, 'AA': 2}}	0.654064529	1
chr21:45386476	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr21:45386548	{'African_American': {'CC': 61, 'GG': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 54, 'GG': 1}, 'APMB': {'CC': 68}}	0.447154472	1
chr22:30472059	{'African_American': {'GG': 63, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 67}}	0.464	1
chr22:30858019	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 55, 'AG': 4}}	0.1849029	0.90275544	{'ARMB': {'GG': 56, 'AG': 2}, 'APMB': {'GG': 65, 'AG': 3}}	1	1
chr22:35328430	{'African_American': {'CC': 65, 'CT': 2}, 'Not_African_American': {'CC': 61}}	0.49717028	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 67, 'CT': 2}}	0.49913878	1
chr22:37807865	{'African_American': {'TT': 57, 'CT': 5}, 'Not_African_American': {'TT': 61}}	0.05748169	0.56650187	{'ARMB': {'TT': 55, 'CT': 1}, 'APMB': {'TT': 63, 'CT': 4}}	0.3749167	1
chr22:37849451	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'GG': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'GG': 1}}	1	1
chr22:41926850	{'African_American': {'GG': 64, 'TT': 1}, 'Not_African_American': {'GG': 56}}	1	1	{'ARMB': {'GG': 55}, 'APMB': {'GG': 65, 'TT': 1}}	1	1
chr22:41926853	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 58, 'AG': 2}}	0.22122235	0.90275544	{'ARMB': {'GG': 57, 'AG': 2}, 'APMB': {'GG': 68}}	0.213848269	1
chr22:41926882	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 59, 'AG': 1}}	0.47244094	0.90275544	{'ARMB': {'GG': 58}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr22:44396152	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 58}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 64, 'CT': 1}}	1	1
chr22:44396163	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 59}}	1	1	{'ARMB': {'CC': 57, 'CT': 1}, 'APMB': {'CC': 67}}	0.464	1
chr22:44396200	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr22:45585333	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr22:45585404	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr22:45585446	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr22:45585506	{'African_American': {'GG': 62, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 56, 'AG': 1}, 'APMB': {'GG': 67}}	0.459677419	1
chr22:46686548	{'African_American': {'CC': 47, 'CT': 12}, 'Not_African_American': {'CC': 58, 'CT': 2}}	0.00432903	0.08145506	{'ARMB': {'CC': 51, 'CT': 5}, 'APMB': {'CC': 54, 'CT': 9}}	0.407124958	1
chr22:48872959	{'African_American': {'CC': 61, 'CT': 5}, 'Not_African_American': {'CC': 59, 'CT': 1}}	0.21067311	0.90275544	{'ARMB': {'CC': 56, 'CT': 3}, 'APMB': {'CC': 64, 'CT': 3}}	1	1
chr22:48873131	{'African_American': {'CC': 59, 'CT': 1}, 'Not_African_American': {'CC': 61}}	0.49586777	0.90275544	{'ARMB': {'CC': 55, 'CT': 1}, 'APMB': {'CC': 65}}	0.462809917	1
chr22:49164342	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr22:49164403	{'African_American': {'GG': 60, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 64}}	0.475409836	1
chr22:50035094	{'African_American': {'GG': 60, 'AG': 6}, 'Not_African_American': {'GG': 60}}	0.02861282	0.33555035	{'ARMB': {'GG': 55, 'AG': 4}, 'APMB': {'GG': 65, 'AG': 2}}	0.417522922	1
chr22:50035296	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr22:50035352	{'African_American': {'CC': 61, 'CT': 6}, 'Not_African_American': {'CC': 55, 'CT': 2}}	0.2860987	0.90275544	{'ARMB': {'CC': 53, 'CT': 3}, 'APMB': {'CC': 63, 'CT': 5}}	0.728298948	1
chr22:50460235	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr3:3109990	{'African_American': {'GG': 56, 'AG': 6}, 'Not_African_American': {'GG': 60}}	0.02759406	0.33555035	{'ARMB': {'GG': 55, 'AG': 2}, 'APMB': {'GG': 61, 'AG': 4}}	0.683809971	1
chr3:3109996	{'African_American': {'GG': 63, 'AG': 2}, 'Not_African_American': {'GG': 61}}	0.49650794	0.90275544	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr3:31981244	{'African_American': {'TT': 63, 'CT': 1}, 'Not_African_American': {'TT': 59, 'CT': 1}}	1	1	{'ARMB': {'TT': 54, 'CT': 2}, 'APMB': {'TT': 68}}	0.201940729	1
chr3:32511621	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr3:46208383	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 60}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 67}}	0.468253968	1
chr3:46370968	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'GG': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'GG': 1}}	1	1
chr3:49708248	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr3:49929805	{'African_American': {'GG': 66}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.48031496	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr3:52845481	{'African_American': {'CT': 27, 'TT': 25, 'CC': 10}, 'Not_African_American': {'TT': 58}}	1.9885E-14	1.5391E-11	{'ARMB': {'TT': 41, 'CT': 8, 'CC': 6}, 'APMB': {'TT': 42, 'CT': 19, 'CC': 4}}	0.128520674	1
chr3:52845525	{'African_American': {'AA': 61, 'AG': 1}, 'Not_African_American': {'AA': 55}}	1	1	{'ARMB': {'AA': 52}, 'APMB': {'AA': 64, 'AG': 1}}	1	1
chr3:53152345	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr3:53152416	{'African_American': {'TT': 55, 'CT': 9}, 'Not_African_American': {'TT': 61}}	0.00293535	0.0678263	{'ARMB': {'TT': 51, 'CT': 7}, 'APMB': {'TT': 65, 'CT': 2}}	0.080111055	1
chr3:53152429	{'African_American': {'CC': 63, 'CT': 2}, 'Not_African_American': {'CC': 60, 'CT': 1}}	1	1	{'ARMB': {'CC': 56, 'CT': 1}, 'APMB': {'CC': 67, 'CT': 2}}	1	1
chr3:58123501	{'African_American': {'GG': 57, 'AG': 9}, 'Not_African_American': {'GG': 61}}	0.00306708	0.0678263	{'ARMB': {'GG': 53, 'AG': 5}, 'APMB': {'GG': 65, 'AG': 4}}	0.730952027	1
chr3:63905612	{'African_American': {'GG': 60, 'AG': 6}, 'Not_African_American': {'GG': 61}}	0.02831755	0.33555035	{'ARMB': {'GG': 55, 'AG': 4}, 'APMB': {'GG': 66, 'AG': 2}}	0.415281114	1
chr3:108822716	{'African_American': {'CC': 66}, 'Not_African_American': {'CC': 59, 'GG': 1}}	0.47619048	0.90275544	{'ARMB': {'CC': 57, 'GG': 1}, 'APMB': {'CC': 68}}	0.46031746	1
chr3:108822794	{'African_American': {'TT': 65, 'CT': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 58}, 'APMB': {'TT': 68, 'CT': 1}}	1	1
chr3:120682219	{'African_American': {'AA': 66, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 58, 'AG': 1}, 'APMB': {'AA': 69}}	0.4609375	1
chr3:120682223	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr3:120682318	{'African_American': {'CC': 65, 'CT': 2}, 'Not_African_American': {'CC': 59, 'CT': 2}}	1	1	{'ARMB': {'CC': 57, 'CT': 2}, 'APMB': {'CC': 67, 'CT': 2}}	1	1
chr3:125832562	{'African_American': {'GG': 52, 'AG': 9}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.01665957	0.22621947	{'ARMB': {'GG': 50, 'AG': 6}, 'APMB': {'GG': 62, 'AG': 4}}	0.510171666	1
chr3:126056179	{'African_American': {'GG': 62, 'AG': 3}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.61970702	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 64, 'AG': 3}}	0.622042786	1
chr3:126056218	{'African_American': {'CC': 60, 'CT': 4}, 'Not_African_American': {'CC': 44, 'CT': 10}}	0.04871276	0.50950909	{'ARMB': {'CC': 51, 'CT': 4}, 'APMB': {'CC': 53, 'CT': 10}}	0.167602294	1
chr3:191329453	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 59, 'CT': 1}}	0.47244094	0.90275544	{'ARMB': {'CC': 58}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr3:194876195	{'African_American': {'GG': 55, 'AG': 10}, 'Not_African_American': {'GG': 61}}	0.00139725	0.03862405	{'ARMB': {'GG': 53, 'AG': 5}, 'APMB': {'GG': 63, 'AG': 5}}	1	1
chr3:197533514	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr3:197547814	{'African_American': {'CC': 30, 'CT': 27, 'TT': 3}, 'Not_African_American': {'CC': 49, 'CT': 9, 'TT': 2}}	0.00038366	0.01649722	{'ARMB': {'CC': 43, 'CT': 12, 'TT': 1}, 'APMB': {'CC': 36, 'CT': 24, 'TT': 4}}	0.059291535	1
chr3:197547856	{'African_American': {'CC': 50, 'CT': 11, 'TT': 2}, 'Not_African_American': {'CC': 58, 'CT': 2}}	0.00684432	0.11271291	{'ARMB': {'CC': 53, 'CT': 3, 'TT': 1}, 'APMB': {'CC': 55, 'CT': 10, 'TT': 1}}	0.136561472	1
chr4:981746	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr4:981776	{'African_American': {'TT': 66, 'GG': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'GG': 1}}	1	1
chr4:981788	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'AA': 1}}	1	1
chr4:981797	{'African_American': {'CC': 66, 'AA': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'AA': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr4:981823	{'African_American': {'TT': 66, 'GG': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'GG': 1}}	1	1
chr4:981826	{'African_American': {'TT': 66, 'GG': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 58, 'GG': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr4:1092766	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr4:1092801	{'African_American': {'AG': 27, 'GG': 20, 'AA': 17}, 'Not_African_American': {'GG': 49, 'AG': 6, 'AA': 1}}	4.4007E-10	1.1354E-07	{'ARMB': {'GG': 27, 'AG': 17, 'AA': 8}, 'APMB': {'GG': 42, 'AG': 16, 'AA': 10}}	0.485653505	1
chr4:1092827	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 58, 'AG': 2}}	0.22122235	0.90275544	{'ARMB': {'GG': 56, 'AG': 2}, 'APMB': {'GG': 69}}	0.206599175	1
chr4:1205170	{'African_American': {'GG': 63, 'AG': 3}, 'Not_African_American': {'GG': 61}}	0.24521935	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 65, 'AG': 3}}	0.247844019	1
chr4:1533498	{'African_American': {'AA': 66, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 59}, 'APMB': {'AA': 68, 'AG': 1}}	1	1
chr4:1533661	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 59, 'AG': 1}}	0.47244094	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 68}}	0.464566929	1
chr4:1533663	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr4:5731792	{'African_American': {'GG': 64, 'AG': 3}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.62072272	1	{'ARMB': {'GG': 55, 'AG': 4}, 'APMB': {'GG': 69}}	0.04266273	1
chr4:5731801	{'African_American': {'GG': 61, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 65}}	0.471544715	1
chr4:5731811	{'African_American': {'AA': 63, 'AG': 2}, 'Not_African_American': {'AA': 51, 'AG': 1}}	1	1	{'ARMB': {'AA': 54, 'AG': 2}, 'APMB': {'AA': 60, 'AG': 1}}	0.606043132	1
chr4:5731839	{'African_American': {'GG': 65}, 'Not_African_American': {'GG': 59, 'AG': 1}}	0.48	0.90275544	{'ARMB': {'GG': 58}, 'APMB': {'GG': 66, 'AG': 1}}	1	1
chr4:7277944	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 53, 'CT': 3, 'TT': 1}}	0.04210632	0.47232312	{'ARMB': {'CC': 55, 'CT': 2, 'TT': 1}, 'APMB': {'CC': 65, 'CT': 1}}	0.409860689	1
chr4:7473855	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr4:8286717	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr4:8635503	{'African_American': {'AA': 62, 'AG': 3}, 'Not_African_American': {'AA': 60}}	0.24516129	0.90275544	{'ARMB': {'AA': 56, 'AG': 1}, 'APMB': {'AA': 66, 'AG': 2}}	1	1
chr4:9566848	{'African_American': {'GG': 65}, 'Not_African_American': {'GG': 59, 'AG': 1}}	0.48	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 66}}	0.472	1
chr4:73869391	{'African_American': {'CC': 56, 'CT': 2}, 'Not_African_American': {'CC': 57, 'CT': 4}}	0.67997902	1	{'ARMB': {'CC': 53, 'CT': 2}, 'APMB': {'CC': 60, 'CT': 4}}	0.685008368	1
chr4:108399770	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr4:159267797	{'African_American': {'TT': 66, 'AA': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 58, 'AA': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr4:178415404	{'African_American': {'AA': 59, 'GG': 1, 'AG': 1}, 'Not_African_American': {'AA': 60}}	1	1	{'ARMB': {'AA': 56, 'GG': 1}, 'APMB': {'AA': 63, 'AG': 1}}	0.72231405	1
chr5:3750985	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr5:4879235	{'African_American': {'CC': 51, 'CT': 11}, 'Not_African_American': {'CC': 59, 'CT': 1}}	0.00426055	0.08145506	{'ARMB': {'CC': 52, 'CT': 4}, 'APMB': {'CC': 58, 'CT': 8}}	0.543548422	1
chr5:4879236	{'African_American': {'GG': 66}, 'Not_African_American': {'GG': 58, 'AG': 3}}	0.10795651	0.81817066	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 66, 'AG': 2}}	1	1
chr5:32203752	{'African_American': {'CC': 66, 'GG': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'GG': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr5:32203821	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 67, 'CT': 1}}	1	1
chr5:54392346	{'African_American': {'GG': 64, 'AG': 2}, 'Not_African_American': {'GG': 61}}	0.4968129	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr5:76801588	{'African_American': {'GG': 65, 'AG': 2}, 'Not_African_American': {'GG': 61}}	0.49717028	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr5:111224329	{'African_American': {'CC': 66, 'AA': 1}, 'Not_African_American': {'CC': 60}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 67, 'AA': 1}}	1	1
chr5:132658121	{'African_American': {'TT': 66, 'AA': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'AA': 1}}	1	1
chr5:135825653	{'African_American': {'CC': 58, 'GG': 1}, 'Not_African_American': {'CC': 60}}	0.49579832	0.90275544	{'ARMB': {'CC': 57, 'GG': 1}, 'APMB': {'CC': 61}}	0.487394958	1
chr5:135825716	{'African_American': {'GG': 63, 'AG': 2, 'AA': 1}, 'Not_African_American': {'GG': 41, 'AG': 11}}	0.00236135	0.06302363	{'ARMB': {'GG': 48, 'AG': 9, 'AA': 1}, 'APMB': {'GG': 56, 'AG': 4}}	0.10993394	1
chr5:135825729	{'African_American': {'CC': 43, 'CT': 14, 'TT': 3}, 'Not_African_American': {'CC': 42, 'CT': 13, 'TT': 1}}	0.81260059	1	{'ARMB': {'CC': 38, 'CT': 13, 'TT': 1}, 'APMB': {'CC': 47, 'CT': 14, 'TT': 3}}	0.762766737	1

chr5:135825756	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr5:138213299	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
chr5:149141544	{'African_American': {'TT': 66, 'GG': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'GG': 1}}	1	1
chr5:170149611	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 58}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 65, 'AG': 1}}	1	1
chr5:170149645	{'African_American': {'GG': 47, 'AG': 17}, 'Not_African_American': {'GG': 33, 'AG': 20, 'AA': 2}}	0.11723872	0.81817066	{'ARMB': {'GG': 28, 'AG': 23, 'AA': 2}, 'APMB': {'GG': 52, 'AG': 14}}	0.003110806	1
chr5:173795109	{'African_American': {'TT': 57, 'CT': 7}, 'Not_African_American': {'TT': 61}}	0.01326158	0.19002349	{'ARMB': {'TT': 54, 'CT': 3}, 'APMB': {'TT': 64, 'CT': 4}}	1	1
chr5:173795253	{'African_American': {'CC': 64, 'CT': 2}, 'Not_African_American': {'CC': 61}}	0.4968129	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 67, 'CT': 1}}	1	1
chr5:177386403	{'African_American': {'CC': 60, 'CT': 3}, 'Not_African_American': {'CC': 36, 'TT': 9, 'CT': 8}}	9.3795E-05	0.0051855	{'ARMB': {'CC': 47, 'CT': 5, 'TT': 1}, 'APMB': {'CC': 49, 'TT': 8, 'CT': 6}}	0.090910121	1
chr5:177386404	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr5:177599665	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 60, 'AG': 1}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 67, 'AG': 2}}	0.49913878	1
chr5:178287030	{'African_American': {'TT': 65, 'CT': 2}, 'Not_African_American': {'TT': 61}}	0.49717028	0.90275544	{'ARMB': {'TT': 59}, 'APMB': {'TT': 67, 'CT': 2}}	0.49913878	1
chr5:178287108	{'African_American': {'CT': 28, 'CC': 24, 'TT': 10}, 'Not_African_American': {'TT': 31, 'CT': 18, 'CC': 7}}	1.1892E-05	0.00076704	{'ARMB': {'TT': 23, 'CT': 20, 'CC': 11}, 'APMB': {'CT': 26, 'CC': 20, 'TT': 18}}	0.220197747	1
chr5:178287122	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr6:13711789	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 58, 'AG': 2}}	0.60206974	1	{'ARMB': {'GG': 56, 'AG': 2}, 'APMB': {'GG': 68, 'AG': 1}}	0.591847019	1
chr6:14949717	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr6:14949830	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr6:25279039	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'AA': 1}}	1	1
chr6:25279045	{'African_American': {'CC': 66, 'AA': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'AA': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr6:32666627	{'African_American': {'GG': 62, 'AA': 1}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.74390244	1	{'ARMB': {'GG': 55, 'AA': 1, 'AG': 1}, 'APMB': {'GG': 67}}	0.209284028	1
chr6:33075962	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'GG': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'GG': 1}}	1	1
chr6:33076025	{'African_American': {'CC': 66, 'GG': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'GG': 1}}	1	1
chr6:42966673	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 59, 'CT': 1}}	0.47244094	0.90275544	{'ARMB': {'CC': 58}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr6:42966785	{'African_American': {'GG': 64, 'AG': 1}, 'Not_African_American': {'GG': 58, 'AG': 1}}	1	1	{'ARMB': {'GG': 58}, 'APMB': {'GG': 64, 'AG': 2}}	0.498033045	1
chr6:42966786	{'African_American': {'AA': 65, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 57, 'AG': 1}, 'APMB': {'AA': 69}}	0.456692913	1
chr6:42966787	{'African_American': {'GG': 64, 'AG': 1}, 'Not_African_American': {'GG': 58}}	1	1	{'ARMB': {'GG': 57}, 'APMB': {'GG': 65, 'AG': 1}}	1	1
chr6:42966792	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'AA': 1}}	1	1
chr6:42966793	{'African_American': {'GG': 64, 'AG': 1}, 'Not_African_American': {'GG': 57}}	1	1	{'ARMB': {'GG': 55, 'AG': 1}, 'APMB': {'GG': 66}}	0.459016393	1
chr6:42966801	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'AA': 1}}	1	1
chr6:42966806	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 58, 'AG': 1}}	1	1	{'ARMB': {'GG': 56, 'AG': 1}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr6:42966817	{'African_American': {'GG': 60, 'AG': 1}, 'Not_African_American': {'GG': 58}}	1	1	{'ARMB': {'GG': 55}, 'APMB': {'GG': 63, 'AG': 1}}	1	1
chr6:42966824	{'African_American': {'GG': 59, 'AA': 1}, 'Not_African_American': {'GG': 56}}	1	1	{'ARMB': {'GG': 54}, 'APMB': {'GG': 61, 'AA': 1}}	1	1
chr6:42966825	{'African_American': {'TT': 66, 'AA': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'AA': 1}}	1	1
chr6:42966834	{'African_American': {'CC': 66, 'GG': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'GG': 1}}	1	1
chr6:56099008	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 59, 'CT': 1}}	0.47244094	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 67, 'CT': 1}}	1	1
chr6:56099165	{'African_American': {'AA': 67}, 'Not_African_American': {'AA': 58, 'AG': 1}}	0.46825397	0.90275544	{'ARMB': {'AA': 58, 'AG': 1}, 'APMB': {'AA': 67}}	0.468253968	1
chr6:85450023	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 58, 'AA': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr6:85450061	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 58, 'CT': 2}}	0.22122235	0.90275544	{'ARMB': {'CC': 57, 'CT': 1}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr6:85450121	{'African_American': {'CC': 66, 'GG': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'GG': 1}}	1	1
chr6:88963603	{'African_American': {'GG': 65, 'AG': 2}, 'Not_African_American': {'GG': 61}}	0.49717028	0.90275544	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr6:96521782	{'African_American': {'CC': 66, 'AA': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'AA': 1}}	1	1
chr6:96521784	{'African_American': {'CC': 66, 'AA': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'AA': 1}}	1	1
chr6:100881320	{'African_American': {'GG': 60, 'AG': 4}, 'Not_African_American': {'GG': 61}}	0.11940834	0.81817066	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 64, 'AG': 3}}	0.622882924	1
chr6:136360972	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 56, 'CT': 1}}	0.45967742	0.90275544	{'ARMB': {'TT': 56, 'CT': 1}, 'APMB': {'TT': 67}}	0.459677419	1
chr6:136360994	{'African_American': {'TT': 66, 'CT': 1}, 'Not_African_American': {'TT': 55}}	1	1	{'ARMB': {'TT': 54, 'CT': 1}, 'APMB': {'TT': 67}}	0.450819672	1
chr6:136361049	{'African_American': {'GG': 66}, 'Not_African_American': {'GG': 58, 'AG': 1}}	0.472	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 65, 'AG': 1}}	1	1
chr6:136361091	{'African_American': {'CC': 66, 'AA': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'AA': 1}}	1	1
chr6:136361094	{'African_American': {'GG': 60, 'AA': 1, 'AG': 1}, 'Not_African_American': {'GG': 55}}	1	1	{'ARMB': {'GG': 55, 'AG': 1}, 'APMB': {'GG': 60, 'AA': 1}}	0.730327144	1
chr6:136361096	{'African_American': {'TT': 66, 'AA': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'AA': 1}}	1	1
chr6:136361102	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'GG': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'GG': 1}}	1	1
chr6:136361111	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'GG': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'GG': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr6:136361113	{'African_American': {'CC': 66}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.48031496	0.90275544	{'ARMB': {'CC': 58, 'AA': 1}, 'APMB': {'CC': 68}}	0.464566929	1
chr6:139771739	{'African_American': {'CC': 63, 'CT': 1}, 'Not_African_American': {'CC': 59}}	1	1	{'ARMB': {'CC': 56}, 'APMB': {'CC': 66, 'CT': 1}}	1	1
chr6:139771752	{'African_American': {'TT': 61, 'CT': 1}, 'Not_African_American': {'TT': 59}}	1	1	{'ARMB': {'TT': 55}, 'APMB': {'TT': 65, 'CT': 1}}	1	1
chr6:139771753	{'African_American': {'CC': 65}, 'Not_African_American': {'CC': 59, 'CT': 1}}	0.48	0.90275544	{'ARMB': {'CC': 57}, 'APMB': {'CC': 67, 'CT': 1}}	1	1
chr6:139771878	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr6:139771908	{'African_American': {'GG': 62}, 'Not_African_American': {'GG': 57, 'AG': 1}}	0.48333333	0.90275544	{'ARMB': {'GG': 54, 'AG': 1}, 'APMB': {'GG': 65}}	0.458333333	1
chr6:150064928	{'African_American': {'AA': 66}, 'Not_African_American': {'AA': 60, 'AG': 1}}	0.48031496	0.90275544	{'ARMB': {'AA': 59}, 'APMB': {'AA': 67, 'AG': 1}}	1	1
chr6:150301084	{'African_American': {'TT': 63}, 'Not_African_American': {'TT': 57, 'CT': 1}}	0.47933884	0.90275544	{'ARMB': {'TT': 55, 'CT': 1}, 'APMB': {'TT': 65}}	0.462809917	1
chr6:150301093	{'African_American': {'CC': 64, 'CT': 1}, 'Not_African_American': {'CC': 56}}	1	1	{'ARMB': {'CC': 53}, 'APMB': {'CC': 67, 'CT': 1}}	1	1
chr6:155256739	{'African_American': {'AA': 63, 'GG': 1}, 'Not_African_American': {'AA': 60}}	1	1	{'ARMB': {'AA': 57}, 'APMB': {'AA': 66, 'GG': 1}}	1	1
chr6:155256752	{'African_American': {'GG': 62}, 'Not_African_American': {'GG': 58, 'AG': 1}}	0.48760331	0.90275544	{'ARMB': {'GG': 57}, 'APMB': {'GG': 63, 'AG': 1}}	1	1
chr6:155256754	{'African_American': {'AA': 61, 'AG': 1}, 'Not_African_American': {'AA': 59}}	1	1	{'ARMB': {'AA': 57}, 'APMB': {'AA': 63, 'AG': 1}}	1	1
chr6:155256767	{'African_American': {'TT': 66, 'GG': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 58, 'GG': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr6:159316147	{'African_American': {'GG': 61, 'AG': 2, 'AA': 1}, 'Not_African_American': {'GG': 61}}	0.49625806	0.90275544	{'ARMB': {'GG': 56, 'AA': 1}, 'APMB': {'GG': 66, 'AG': 2}}	0.342149489	1
chr6:159316164	{'African_American': {'GG': 62, 'CC': 2}, 'Not_African_American': {'GG': 49, 'CC': 4}}	0.40798953	0.90275544	{'ARMB': {'GG': 47, 'CC': 4}, 'APMB': {'GG': 64, 'CC': 2}}	0.401498599	1
chr6:159316167	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 60}}	1	1	{'ARMB': {'CC': 57, 'CT': 1}, 'APMB': {'CC': 68}}	0.46031746	1
chr6:159316298	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 60}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 66, 'AG': 1}}	1	1
chr6:159316301	{'African_American': {'GG': 65}, 'Not_African_American': {'GG': 56, 'AA': 1}}	0.46721311	0.90275544	{'ARMB': {'GG': 56}, 'APMB': {'GG': 65, 'AA': 1}}	1	1
chr6:168995812	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr6:168995860	{'African_American': {'TT': 63, 'CT': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 57}, 'APMB': {'TT': 67, 'CT': 1}}	1	1
chr6:169072569	{'African_American': {'CC': 66, 'TT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'TT': 1}}	1	1
chr6:169072575	{'African_American': {'CC': 66, 'TT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'TT': 1}}	1	1
chr6:169072588	{'African_American': {'TT': 66, 'CC': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'CC': 1}}	1	1
chr6:169072699	{'African_American': {'AA': 67}, 'Not_African_American': {'AA': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'AA': 59}, 'APMB': {'AA': 68, 'AG': 1}}	1	1
chr6:169240429	{'African_American': {'AA': 58, 'AG': 2}, 'Not_African_American': {'AA': 61}}	0.24380165	0.90275544	{'ARMB': {'AA': 57, 'AG': 1}, 'APMB': {'AA': 62, 'AG': 1}}	1	1
chr6:169240512	{'African_American': {'GG': 58}, 'Not_African_American': {'GG': 58, 'AG': 1}}	1	1	{'ARMB': {'GG': 54, 'AG': 1}, 'APMB': {'GG': 62}}	0.47008547	1
chr6:169240524	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 60}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr6:170023459	{'African_American': {'CC': 63}, 'Not_African_American': {'CC': 58, 'CT': 1}}	0.48360656	0.90275544	{'ARMB': {'CC': 55, 'CT': 1}, 'APMB': {'CC': 66}}	0.459016393	1
chr6:170023465	{'African_American': {'CC': 63}, 'Not_African_American': {'CC': 58, 'CT': 1}}	0.48360656	0.90275544	{'ARMB': {'CC': 56, 'CT': 1}, 'APMB': {'CC': 65}}	0.467213115	1
chr6:170023526	{'African_American': {'CC': 63, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 65, 'CT': 1}}	1	1
chr6:170023606	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr6:170023624	{'African_American': {'AA': 65, 'AG': 1}, 'Not_African_American': {'AA': 60}}	1	1	{'ARMB': {'AA': 58, 'AG': 1}, 'APMB': {'AA': 67}}	0.468253968	1
chr6:170248094	{'African_American': {'CC': 64}, 'Not_African_American': {'CC': 56, 'CT': 1}}	0.47107438	0.90275544	{'ARMB': {'CC': 56}, 'APMB': {'CC': 64, 'CT': 1}}	1	1
chr6:170248100	{'African_American': {'TT': 66}, 'Not_African_American': {'TT': 56, 'CC': 1}}	0.46341463	0.90275544	{'ARMB': {'TT': 57}, 'APMB': {'TT': 65, 'CC': 1}}	1	1
chr6:170248190	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 57, 'TT': 2}}	0.22077419	0.90275544	{'ARMB': {'CC': 54, 'TT': 2, 'CT': 1}, 'APMB': {'CC': 68}}	0.092084972	1
chr7:376941	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr7:377077	{'African_American': {'GG': 63, 'AG': 1}, 'Not_African_American': {'GG': 60}}	1	1	{'ARMB': {'GG': 56}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr7:377084	{'African_American': {'GG': 66}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.48031496	0.90275544	{'ARMB': {'GG': 58}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr7:377085	{'African_American': {'AA': 66}, 'Not_African_American': {'AA': 60, 'AG': 1}}	0.48031496	0.90275544	{'ARMB': {'AA': 57, 'AG': 1}, 'APMB': {'AA': 69}}	0.456692913	1
chr7:1116393	{'African_American': {'CC': 62, 'CT': 1, 'TT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 57}, 'APMB': {'CC': 66, 'CT': 1, 'TT': 1}}	1	1
chr7:1116469	{'African_American': {'GG': 59, 'AG': 1}, 'Not_African_American': {'GG': 61}}	0.49586777	0.90275544	{'ARMB': {'GG': 54}, 'APMB': {'GG': 66, 'AG': 1}}	1	1
chr7:1331771	{'African_American': {'CC': 60}, 'Not_African_American': {'CC': 60, 'TT': 1}}	1	1	{'ARMB': {'CC': 54, 'TT': 1}, 'APMB': {'CC': 66}}	0.454545455	1
chr7:1331795	{'African_American': {'CC': 65}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.48412698	0.90275544	{'ARMB': {'CC': 56, 'CT': 1}, 'APMB': {'CC': 69}}	0.452380952	1
chr7:1331798	{'African_American': {'CC': 65, 'CT': 2}, 'Not_African_American': {'CC': 59}}	0.49803175	0.90275544	{'ARMB': {'CC': 57, 'CT': 2}, 'APMB': {'CC': 67}}	0.217269841	1
chr7:1331942	{'African_American': {'AA': 66}, 'Not_African_American': {'AA': 58, 'AG': 1}}	0.472	0.90275544	{'ARMB': {'AA': 56, 'AG': 1}, 'APMB': {'AA': 68}}	0.456	1
chr7:1492734	{'African_American': {'GG': 52, 'AG': 6, 'AA': 2}, 'Not_African_American': {'GG': 59}}	0.00609006	0.10642654	{'ARMB': {'GG': 49, 'AA': 2, 'AG': 2}, 'APMB': {'GG': 62, 'AG': 4}}	0.304424233	1
chr7:1492748	{'African_American': {'CC': 45, 'CT': 9, 'TT': 3}, 'Not_African_American': {'CC': 59, 'CT': 2}}	0.00619603	0.10642654	{'ARMB': {'CC': 44, 'CT': 4, 'TT': 3}, 'APMB': {'CC': 60, 'CT': 7}}	0.137226375	1
chr7:1492772	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr7:1492817	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'CT': 1}}	1	1
chr7:1492840	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 60}}	1	1	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 68}}	0.46031746	1

chr7:1936548	{'African_American': {'CC': 66}, 'Not_African_American': {'CC': 59, 'CT': 1}}	0.47619048	0.90275544	{'ARMB': {'CC': 57}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr7:1936558	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 59, 'CT': 1}}	0.47244094	0.90275544	{'ARMB': {'TT': 57, 'CT': 1}, 'APMB': {'TT': 69}}	0.456692913	1
chr7:1936623	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr7:1936665	{'African_American': {'AA': 65, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 58}, 'APMB': {'AA': 68, 'AG': 1}}	1	1
chr7:2146074	{'African_American': {'AA': 65, 'AG': 1}, 'Not_African_American': {'AA': 61}}	1	1	{'ARMB': {'AA': 57, 'AG': 1}, 'APMB': {'AA': 69}}	0.456692913	1
chr7:3043904	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr7:4116340	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr7:4116379	{'African_American': {'GG': 59, 'AG': 4, 'AA': 1}, 'Not_African_American': {'GG': 52, 'AG': 5}}	0.85955813	1	{'ARMB': {'GG': 50, 'AG': 3, 'AA': 1}, 'APMB': {'GG': 61, 'AG': 6}}	0.489600109	1
chr7:4116390	{'African_American': {'CC': 66}, 'Not_African_American': {'CC': 56, 'CT': 1}}	0.46341463	0.90275544	{'ARMB': {'CC': 55}, 'APMB': {'CC': 67, 'CT': 1}}	1	1
chr7:4116443	{'African_American': {'CC': 61, 'TT': 1}, 'Not_African_American': {'CC': 60}}	1	1	{'ARMB': {'CC': 57}, 'APMB': {'CC': 64, 'TT': 1}}	1	1
chr7:4116446	{'African_American': {'CC': 61, 'TT': 1}, 'Not_African_American': {'CC': 60}}	1	1	{'ARMB': {'CC': 57}, 'APMB': {'CC': 64, 'TT': 1}}	1	1
chr7:4235954	{'African_American': {'TT': 65}, 'Not_African_American': {'TT': 60, 'CT': 1}}	0.48412698	0.90275544	{'ARMB': {'TT': 58}, 'APMB': {'TT': 67, 'CT': 1}}	1	1
chr7:4235957	{'African_American': {'TT': 66}, 'Not_African_American': {'TT': 59, 'CT': 1}}	0.47619048	0.90275544	{'ARMB': {'TT': 58}, 'APMB': {'TT': 67, 'CT': 1}}	1	1
chr7:4236078	{'African_American': {'AA': 67}, 'Not_African_American': {'AA': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'AA': 58, 'AG': 1}, 'APMB': {'AA': 69}}	0.4609375	1
chr7:4236091	{'African_American': {'TT': 66, 'AA': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'AA': 1}}	1	1
chr7:4236109	{'African_American': {'GG': 66}, 'Not_African_American': {'GG': 56, 'AG': 2}}	0.21675846	0.90275544	{'ARMB': {'GG': 56, 'AG': 1}, 'APMB': {'GG': 66, 'AG': 1}}	1	1
chr7:4236115	{'African_American': {'AA': 66, 'GG': 1}, 'Not_African_American': {'AA': 58}}	1	1	{'ARMB': {'AA': 58}, 'APMB': {'AA': 66, 'GG': 1}}	1	1
chr7:4236119	{'African_American': {'AA': 67}, 'Not_African_American': {'AA': 58, 'GG': 1}}	0.46825397	0.90275544	{'ARMB': {'AA': 58}, 'APMB': {'AA': 67, 'GG': 1}}	1	1
chr7:4707144	{'African_American': {'TT': 65}, 'Not_African_American': {'TT': 59, 'CT': 1}}	0.48	0.90275544	{'ARMB': {'TT': 58}, 'APMB': {'TT': 66, 'CT': 1}}	1	1
chr7:4707147	{'African_American': {'CC': 63, 'CT': 2}, 'Not_African_American': {'CC': 58}}	0.49753432	0.90275544	{'ARMB': {'CC': 56}, 'APMB': {'CC': 65, 'CT': 2}}	0.49993336	1
chr7:4707152	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 58, 'CT': 1}}	1	1	{'ARMB': {'CC': 57, 'CT': 1}, 'APMB': {'CC': 66, 'CT': 1}}	1	1
chr7:4707153	{'African_American': {'CC': 63}, 'Not_African_American': {'CC': 57, 'CT': 1}}	0.47933884	0.90275544	{'ARMB': {'CC': 55, 'CT': 1}, 'APMB': {'CC': 65}}	0.462809917	1
chr7:4707154	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 56}}	1	1	{'ARMB': {'CC': 56, 'CT': 1}, 'APMB': {'CC': 65}}	0.467213115	1
chr7:4707174	{'African_American': {'TT': 66, 'CT': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'CT': 1}}	1	1
chr7:5045837	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'AA': 1}}	1	1
chr7:5045838	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 59, 'GG': 1}}	0.47244094	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 67, 'GG': 1}}	1	1
chr7:5045865	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'AA': 1}}	1	1
chr7:5045900	{'African_American': {'TT': 66, 'AA': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 58, 'AA': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr7:6648198	{'African_American': {'AA': 65, 'AG': 1}, 'Not_African_American': {'AA': 60}}	1	1	{'ARMB': {'AA': 59}, 'APMB': {'AA': 66, 'AG': 1}}	1	1
chr7:29645711	{'African_American': {'TT': 66, 'CT': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 58, 'CT': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr7:29645806	{'African_American': {'CC': 52, 'CT': 5, 'TT': 2}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.0461109	0.49569219	{'ARMB': {'CC': 56, 'CT': 1, 'TT': 1}, 'APMB': {'CC': 56, 'CT': 5, 'TT': 1}}	0.257232637	1
chr7:29645809	{'African_American': {'CC': 42, 'CT': 12, 'TT': 7}, 'Not_African_American': {'CC': 53, 'CT': 4, 'TT': 1}}	0.00750113	0.12095571	{'ARMB': {'CC': 48, 'CT': 6, 'TT': 2}, 'APMB': {'CC': 47, 'CT': 10, 'TT': 6}}	0.291204604	1
chr7:29645810	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr7:55068619	{'African_American': {'TT': 66, 'CT': 1}, 'Not_African_American': {'TT': 57}}	1	1	{'ARMB': {'TT': 58}, 'APMB': {'TT': 65, 'CT': 1}}	1	1
chr7:55068646	{'African_American': {'CC': 65}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.48412698	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 67}}	0.468253968	1
chr7:55068682	{'African_American': {'CC': 63}, 'Not_African_American': {'CC': 58, 'CT': 1}}	0.48360656	0.90275544	{'ARMB': {'CC': 57}, 'APMB': {'CC': 64, 'CT': 1}}	1	1
chr7:55068713	{'African_American': {'GG': 60, 'AG': 2}, 'Not_African_American': {'GG': 61}}	0.49593496	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 62, 'AG': 2}}	0.496734639	1
chr7:64794466	{'African_American': {'TT': 66, 'AA': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'AA': 1}}	1	1
chr7:66503301	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr7:71174462	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 59}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 67}}	0.468253968	1
chr7:75912253	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'AA': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr7:75912290	{'African_American': {'TT': 66, 'GG': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'GG': 1}}	1	1
chr7:75912291	{'African_American': {'CC': 66, 'GG': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'GG': 1}}	1	1
chr7:128121707	{'African_American': {'GG': 59, 'AG': 4}, 'Not_African_American': {'GG': 61}}	0.11912271	0.81817066	{'ARMB': {'GG': 54, 'AG': 2}, 'APMB': {'GG': 66, 'AG': 2}}	1	1
chr7:128121729	{'African_American': {'CC': 63, 'CT': 1}, 'Not_African_American': {'CC': 60}}	1	1	{'ARMB': {'CC': 57, 'CT': 1}, 'APMB': {'CC': 66}}	0.467741935	1
chr7:129592812	{'African_American': {'CC': 57, 'CT': 4}, 'Not_African_American': {'CC': 61}}	0.1188277	0.81817066	{'ARMB': {'CC': 53, 'CT': 2}, 'APMB': {'CC': 65, 'CT': 2}}	1	1
chr7:129592860	{'African_American': {'TT': 62, 'CT': 1, 'CC': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 56, 'CT': 1}, 'APMB': {'TT': 67, 'CC': 1}}	0.706064516	1
chr7:129592940	{'African_American': {'CC': 63, 'CT': 4}, 'Not_African_American': {'CC': 61}}	0.12076631	0.81817066	{'ARMB': {'CC': 57, 'CT': 2}, 'APMB': {'CC': 67, 'CT': 2}}	1	1
chr7:129592945	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr7:134779647	{'African_American': {'CC': 66, 'AA': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'AA': 1}}	1	1
chr7:143408852	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr7:149822008	{'African_American': {'CC': 62, 'CT': 1}, 'Not_African_American': {'CC': 55}}	1	1	{'ARMB': {'CC': 56, 'CT': 1}, 'APMB': {'CC': 61}}	0.483050847	1
chr7:149822141	{'African_American': {'GG': 67}, 'Not_African_American': {'GG': 59, 'AG': 1}}	0.47244094	0.90275544	{'ARMB': {'GG': 59}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr7:149873920	{'African_American': {'TT': 66, 'AA': 1}, 'Not_African_American': {'TT': 61}}	1	1	{'ARMB': {'TT': 59}, 'APMB': {'TT': 68, 'AA': 1}}	1	1
chr7:158252872	{'African_American': {'CC': 62, 'CT': 1}, 'Not_African_American': {'CC': 57, 'CT': 1}}	1	1	{'ARMB': {'CC': 55}, 'APMB': {'CC': 64, 'CT': 2}}	0.5	1
chr7:158252987	{'African_American': {'AA': 67}, 'Not_African_American': {'AA': 60, 'AG': 1}}	0.4765625	0.90275544	{'ARMB': {'AA': 59}, 'APMB': {'AA': 68, 'AG': 1}}	1	1
chr7:158279860	{'African_American': {'CC': 55, 'CT': 5, 'TT': 1}, 'Not_African_American': {'CC': 61}}	0.02747342	0.33555035	{'ARMB': {'CC': 54, 'CT': 2, 'TT': 1}, 'APMB': {'CC': 62, 'CT': 3}}	0.821783802	1
chr8:11501656	{'African_American': {'TT': 67}, 'Not_African_American': {'TT': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'TT': 58, 'AA': 1}, 'APMB': {'TT': 69}}	0.4609375	1
chr8:11501659	{'African_American': {'CC': 49, 'CT': 7, 'TT': 3}, 'Not_African_American': {'CC': 61}}	0.00054131	0.01904412	{'ARMB': {'CC': 50, 'CT': 6, 'TT': 1}, 'APMB': {'CC': 60, 'TT': 2, 'CT': 1}}	0.080995041	1
chr8:28029316	{'African_American': {'TT': 65, 'CT': 1}, 'Not_African_American': {'TT': 60}}	1	1	{'ARMB': {'TT': 56, 'CT': 1}, 'APMB': {'TT': 69}}	0.452380952	1
chr8:28029459	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 59, 'AG': 1}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 65, 'AG': 2}}	0.498031746	1
chr8:28029460	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 60}}	1	1	{'ARMB': {'GG': 58}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr8:28029467	{'African_American': {'GG': 54, 'AG': 3}, 'Not_African_American': {'GG': 61}}	0.1096225	0.81817066	{'ARMB': {'GG': 55, 'AG': 1}, 'APMB': {'GG': 60, 'AG': 2}}	1	1
chr8:28029468	{'African_American': {'GG': 54, 'AG': 2}, 'Not_African_American': {'GG': 60}}	0.23088456	0.90275544	{'ARMB': {'GG': 56, 'AG': 1}, 'APMB': {'GG': 58, 'AG': 1}}	1	1
chr8:28317297	{'African_American': {'CC': 66, 'GG': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'GG': 1}}	1	1
chr8:29711230	{'African_American': {'AA': 66}, 'Not_African_American': {'AA': 60, 'AG': 1}}	0.48031496	0.90275544	{'ARMB': {'AA': 58}, 'APMB': {'AA': 68, 'AG': 1}}	1	1
chr8:39913834	{'African_American': {'CC': 60, 'CT': 4}, 'Not_African_American': {'CC': 61}}	0.11940834	0.81817066	{'ARMB': {'CC': 55, 'CT': 1}, 'APMB': {'CC': 66, 'CT': 3}}	0.627210793	1
chr8:60714930	{'African_American': {'CC': 64}, 'Not_African_American': {'CC': 56, 'CT': 1}}	0.47107438	0.90275544	{'ARMB': {'CC': 54, 'CT': 1}, 'APMB': {'CC': 66}}	0.454545455	1
chr8:85177144	{'African_American': {'CC': 66, 'AG': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'AG': 1}}	1	1
chr8:94719844	{'African_American': {'CC': 66, 'GG': 1}, 'Not_African_American': {'CC': 60}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 67, 'GG': 1}}	1	1
chr8:94719846	{'African_American': {'CC': 66, 'GG': 1}, 'Not_African_American': {'CC': 60}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 67, 'GG': 1}}	1	1
chr8:94719877	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'GG': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'GG': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr8:133461935	{'African_American': {'GG': 64, 'AG': 2}, 'Not_African_American': {'GG': 61}}	0.4968129	0.90275544	{'ARMB': {'GG': 58}, 'APMB': {'GG': 67, 'AG': 2}}	0.499812523	1
chr8:133461984	{'African_American': {'TT': 64}, 'Not_African_American': {'TT': 58, 'CT': 1}}	0.4796748	0.90275544	{'ARMB': {'TT': 57}, 'APMB': {'TT': 65, 'CT': 1}}	1	1
chr8:140350873	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 58}}	1	1	{'ARMB': {'CC': 56}, 'APMB': {'CC': 67, 'CT': 1}}	1	1
chr8:140350901	{'African_American': {'AA': 66}, 'Not_African_American': {'AA': 58, 'TT': 2}}	0.2247619	0.90275544	{'ARMB': {'AA': 57, 'TT': 1}, 'APMB': {'AA': 67, 'TT': 1}}	1	1
chr8:140350968	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr8:140351024	{'African_American': {'CC': 62, 'CT': 2}, 'Not_African_American': {'CC': 59, 'CT': 2}}	1	1	{'ARMB': {'CC': 56, 'CT': 2}, 'APMB': {'CC': 65, 'CT': 2}}	1	1
chr8:142016979	{'African_American': {'CC': 63, 'TT': 1}, 'Not_African_American': {'CC': 60}}	1	1	{'ARMB': {'CC': 55, 'TT': 1}, 'APMB': {'CC': 68}}	0.451612903	1
chr8:142017040	{'African_American': {'GG': 55, 'AG': 7}, 'Not_African_American': {'GG': 53, 'AG': 4, 'AA': 1}}	0.44094599	0.90275544	{'ARMB': {'GG': 52, 'AG': 4}, 'APMB': {'GG': 56, 'AG': 7, 'AA': 1}}	0.637810736	1
chr8:142017153	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 59}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr8:142670253	{'African_American': {'TT': 62, 'CT': 1}, 'Not_African_American': {'TT': 60}}	1	1	{'ARMB': {'TT': 56, 'CT': 1}, 'APMB': {'TT': 66}}	0.463414634	1
chr9:34400530	{'African_American': {'TT': 65}, 'Not_African_American': {'TT': 59, 'CT': 1}}	0.48	0.90275544	{'ARMB': {'TT': 58}, 'APMB': {'TT': 66, 'CT': 1}}	1	1
chr9:34400627	{'African_American': {'GG': 65, 'AG': 1}, 'Not_African_American': {'GG': 57}}	1	1	{'ARMB': {'GG': 55}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
chr9:34400638	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'GG': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'GG': 1}}	1	1
chr9:34400645	{'African_American': {'GG': 66}, 'Not_African_American': {'GG': 57, 'AG': 1}}	0.46774194	0.90275544	{'ARMB': {'GG': 58}, 'APMB': {'GG': 65, 'AG': 1}}	1	1
chr9:34400648	{'African_American': {'GG': 64, 'AG': 1}, 'Not_African_American': {'GG': 58}}	1	1	{'ARMB': {'GG': 56, 'AG': 1}, 'APMB': {'GG': 66}}	0.463414634	1
chr9:34400670	{'African_American': {'GG': 63, 'AG': 1}, 'Not_African_American': {'GG': 54}}	1	1	{'ARMB': {'GG': 53}, 'APMB': {'GG': 64, 'AG': 1}}	1	1
chr9:35651010	{'African_American': {'GG': 66}, 'Not_African_American': {'GG': 59, 'AG': 1}}	0.47619048	0.90275544	{'ARMB': {'GG': 57}, 'APMB': {'GG': 68, 'AG': 1}}	1	1
chr9:87551727	{'African_American': {'CC': 64}, 'Not_African_American': {'CC': 54, 'CT': 1}}	0.46218487	0.90275544	{'ARMB': {'CC': 55}, 'APMB': {'CC': 63, 'CT': 1}}	1	1
chr9:87551803	{'African_American': {'GG': 58, 'AG': 4}, 'Not_African_American': {'GG': 61}}	0.11892764	0.81817066	{'ARMB': {'GG': 55, 'AG': 2}, 'APMB': {'GG': 64, 'AG': 2}}	1	1
chr9:89656065	{'African_American': {'TT': 63}, 'Not_African_American': {'TT': 57, 'CT': 1}}	0.47933884	0.90275544	{'ARMB': {'TT': 55}, 'APMB': {'TT': 65, 'CT': 1}}	1	1
chr9:89656101	{'African_American': {'CC': 60, 'CT': 2}, 'Not_African_American': {'CC': 61}}	0.49593496	0.90275544	{'ARMB': {'CC': 56}, 'APMB': {'CC': 65, 'CT': 2}}	0.49993336	1
chr9:89656113	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
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chr9:108615987	{'African_American': {'CC': 65, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 68}}	0.464566929	1
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chr9:134282254	{'African_American': {'CC': 62}, 'Not_African_American': {'CC': 59, 'TT': 1}}	0.49180328	0.90275544	{'ARMB': {'CC': 56}, 'APMB': {'CC': 65, 'TT': 1}}	1	1
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chr9:134282387	{'African_American': {'GG': 60, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 56, 'AG': 1}, 'APMB': {'GG': 65}}	0.467213115	1
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chr9:134282395	{'African_American': {'GG': 63, 'AG': 2}, 'Not_African_American': {'GG': 61}}	0.49650794	0.90275544	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 67, 'AG': 1}}	1	1
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chr9:134373222	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'CT': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr9:134373223	{'African_American': {'GG': 64, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 57, 'AG': 1}, 'APMB': {'GG': 68}}	0.46031746	1
chr9:134373227	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 60}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 68}}	0.464566929	1
chr9:134373236	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 69}}	0.4609375	1
chr9:134373293	{'African_American': {'CC': 66, 'CT': 1}, 'Not_African_American': {'CC': 61}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'CT': 1}}	1	1
chr9:134373321	{'African_American': {'CC': 61, 'CT': 3}, 'Not_African_American': {'CC': 61}}	0.2443871	0.90275544	{'ARMB': {'CC': 57, 'CT': 2}, 'APMB': {'CC': 65, 'CT': 1}}	0.601715185	1
chr9:134416325	{'African_American': {'CC': 64, 'CT': 1}, 'Not_African_American': {'CC': 60}}	1	1	{'ARMB': {'CC': 59}, 'APMB': {'CC': 65, 'CT': 1}}	1	1
chr9:134416483	{'African_American': {'AA': 62, 'AG': 1}, 'Not_African_American': {'AA': 55}}	1	1	{'ARMB': {'AA': 56}, 'APMB': {'AA': 61, 'AG': 1}}	1	1
chr9:134481969	{'African_American': {'GG': 57, 'AG': 4}, 'Not_African_American': {'GG': 61}}	0.1188277	0.81817066	{'ARMB': {'GG': 52, 'AG': 2}, 'APMB': {'GG': 66, 'AG': 2}}	1	1
chr9:134482040	{'African_American': {'CC': 67}, 'Not_African_American': {'CC': 60, 'AA': 1}}	0.4765625	0.90275544	{'ARMB': {'CC': 59}, 'APMB': {'CC': 68, 'AA': 1}}	1	1
chr9:134690653	{'African_American': {'CC': 63}, 'Not_African_American': {'CC': 56, 'CT': 1}}	0.475	0.90275544	{'ARMB': {'CC': 55, 'CT': 1}, 'APMB': {'CC': 64}}	0.466666667	1
chr9:134690734	{'African_American': {'GG': 34, 'AG': 19, 'AA': 8}, 'Not_African_American': {'AA': 31, 'AG': 18, 'GG': 6}}	2.683E-08	5.1917E-06	{'ARMB': {'AA': 22, 'AG': 21, 'GG': 11}, 'APMB': {'GG': 29, 'AA': 17, 'AG': 16}}	0.011616841	1
chr9:134690739	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 61}}	1	1	{'ARMB': {'GG': 58, 'AG': 1}, 'APMB': {'GG': 69}}	0.4609375	1
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chr9:136522665	{'African_American': {'GG': 66, 'AG': 1}, 'Not_African_American': {'GG': 56, 'AG': 2}}	0.59641857	1	{'ARMB': {'GG': 55, 'AG': 2}, 'APMB': {'GG': 67, 'AG': 1}}	0.591357986	1
chr9:136522702	{'African_American': {'CC': 66}, 'Not_African_American': {'CC': 59, 'CT': 2}}	0.22872141	0.90275544	{'ARMB': {'CC': 58, 'CT': 1}, 'APMB': {'CC': 67, 'CT': 1}}	1	1
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chr9:137041311	{'African_American': {'TT': 65}, 'Not_African_American': {'TT': 58, 'CT': 1}}	0.47580645	0.90275544	{'ARMB': {'TT': 55}, 'APMB': {'TT': 68, 'CT': 1}}	1	1
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