Supporting Information Appendix

SI Materials and Methods

Construction of dexamethasone inducible MET1 silencing lines.

DNA fragments including two different regions of *MET1* gene (Fig. S2) were amplified from *Arabidopsis thaliana* genomic DNA by PCR using the following primers*:* FWDAttB1dxRNAimet1α (5´-GGGG-ACA-AGT-TTG-TAC-AAA-AAA-GCA-GGC-TAA-gcc-cta-cat-ctc-aag-aag-tct-cctca-3´), REVAttB2dxRNAimet1α (5´-GGG-GAC-CAC-TTT-GTA-CAA-GAA-AGC-TGG-GTA-aga-cat-cat-tgc-ttg-cttg-tat-aat-gag-3´), FWDAttB1dxRNAimet1β (5´-GGGG-ACA-AGT-TTG-TAC-AAA-AAA-GCA-GGC-TAA-tcc-tca-aca-cca-acc-cta-gata-3´) and REVAttB2dxRNAimet1β (5´-GGG-GAC-CAC-TTT-GTA-CAA-GAA-AGC-TGG-GTA-tca-atc-cga-ata-cgg-aat-atac-3´). The respective purified PCR products were cloned in pDONR221 and transferred into pOpOff2Hyg with a CaMV 35S-LhGR cassette on the same T-DNA, a GUS reporter gene fused to the RNAi construct was also present in the T-DNA to allow monitoring of the dexamethasone inducible expression, as well as a hygromycin resistance construct as a selectable marker gene (1). The resultant vectors were used for Agrobacterium-mediated transformation of Arabidopsis ecotype Col0 plants as previously reported (2). Transgenic plants carriyng these constructions were selected in Hygromycin containing selective media; plants with 3:1 segregation rates corresponding to single insertions were selected to produce homozygous lines.

Handling of DNA methylation and demethylation mutants

F1 ddc and rdd plants were utilized in all experiments to avoid possible transgenerational epigenetic effects such as those reported for *ddc* in which widespread transposon activation (3). Homozygous *ddc* triple mutants with the reported curled leaf phenotype where genotyped; *rdd* triple mutants were also genotyped before experiments. Homozygous Inducible RNAi lines were used for all experiments, to induce *MET1* silencing in solid MS media seeds were grown in MS with 10 µM dexamethasone. Dexamethasone was reapplied every 4 days directly to seedlings with a previously sterilized small brush. In liquid medium, seedlings where germinated in MS with 10 µM dexamethasone and dexamethasone was reapplied every 4 days. To avoid unwanted cumulative DNA methylation alterations due loss of MET1 we did not further propagated RNAimet1 plants that were in any moment induced with dexamethasone.

Isolation of Plant Nuclei

Plant nuclei were purified as previously described (4) with the following modifications: enough fresh MEB buffer (1M 2-methyl-2,4-pentadienol, 2% PVP-10, 10 mM PIPES-KOH, 10 mM Sodium Metabisulfite, 10 mM MgCl2, 200 mM L-Lysine, 6 mM EGTA, 0.5% Triton X-100) was added to moisten 10 g of frozen tissue powder, to homogenize 1 extra volume of MEB buffer was added and then vortex thoroughly. The sample was filtered through 3 layers of Polyester/Nylon cloth (Reusable wipes, Scotch Brite), 2 layers of HydroKnit (Kimberly-Clark), and one layer of 60 µm Nylon NET Filter (Millipore) and centrifuged at 8500 rpm for 5 minutes at 4ºC. The supernatant was discarded and the nuclei pellet was carefully resuspended in 30 mL of MEB buffer until pellet is completely resuspended, and then centrifuged at 8500 for 5 minutes. These washes were repeated three more times. After the washes, nuclei pellet was used for DNA isolation using the CTAB DNA extraction protocol. Typically DNA yields ranged between 5-10 μg from 10 g of tissue.

MethylC-Seq library construction and sequencing

DNA was fragmented to 100-300 bp using a Sonicator (Covaris), then DNA fragments were blunt ended and, a dA 3′-end addition was performed prior to sequencing adapter ligation. Illumina methylated adapters were used according to the manufacturer's instructions (Illumina). The bisulfite conversion of arabidopsis DNA was carried out using ZYMO EZ DNA Methylation-Gold kit and amplified by 12 cycles of PCR. High-throughput pair-end sequencing was carried out using the Illumina Genetic Analyzer (GA2) according to manufacturer instructions. Raw GA sequencing data were processed by Illumina base-calling pipeline (SolexaPipeline-1.0).

Processing of MethylC-Seq Reads and Identification of Methylated Cytosine Positions

Pair end reads generated by Illumina sequencing were aligned to the Col-0 TAIR10 Arabidopsis thaliana genome, as well as the cI857 Sam7 Lambda genome (48,502 bases) using SOAP2 software. MethylC-Seq reads for each biological replicate were processed and aligned independently as previously reported (5). Identification of methylated cytosine positions for each biological replicate was performed independently as described previously (6). The bisulfite conversion rates in all cases were greater than 99.6% (Table S1).

Identifying Differentially Methylated Cytosines

For all positions considered to contain methylated cytosines (see previous paragraph) we performed the following analyses: The contingency table formed by the counts of methylated and non-methylated cytosines was evaluated for the significance of treatments by the F test, formed by the likelihood ratio tests between and within treatments. If the P-value of the F test was $\alpha \leq 0.05$ and the data were not sparse (less than 5 zeroes in the contingency table), then a logistic model including all factors (P, O, T) and their interactions was fitted ("full" or "saturated" model). With this model we evaluated if at least one of the factors or interactions was significantly affecting the proportion of methylation and determine a factorial DmCs when the model was significant at $P \leq 0.05$ (Fig. S13). We also fitted logistic models varying a single factor (P, O or T) while the other two remained constant; for example, varying P (HP or LP) in O = root at time = 7 dat. These 3*2*2=12 models were fitted relaxing the stringency of the F test to $\alpha \leq 0.10$, and only when the data were not sparse (Fig. S14). If the P-value for one of these models is $P \leq 0.05$, we have evidence of DmCs for the single factor tested when the other two are at fixed values.

Identification and construction of Differentially Methylated Regions

Differentially methylated Regions (DMRs) were defined as regions in the Arabidopsis genome where DmC density was higher than genome wide DmC density. DMRs are defined for each phosphate contrast (Tables S8 and S9), and thus contain DmCs defined by the corresponding model, where the F test has $\alpha \leq 0.1$ and the P value of the model was $\alpha \leq 0.05$ (see previous paragraph). Two parameters determine a DMR, the minimum number of DmCs that the DMR must contain, fixed here to four, and the maximum distance between neighboring DmCs within the DMR. To determine the maximum distance between neighboring DmCs, we calculated the number of DMRs that will be obtained as function of this distance, d*. The maximum number of DMRs for each contrast was obtained between 800 and 1300 bp, but for the majority of the cases the value of d* which resulted in more DMRs was 1000 bp (Fig. S15). Thus, DMRs in Table S9 are defined as regions in the genome where there are at least 4 DmCs with a maximum distance between neighboring DmCs of 1000 bp.

Mapping and Processing of mRNA-Seq Reads

RNA-Seq reads generated with the Illumina analysis pipeline (fastQ format) were assessed the quality with FastQC (version 0.10.1) and processed using Perl scripts to remove reads that contained adapter sequences and low quality reads. The paired-end clean reads were aligned to the Arabidopsis thaliana TAIR10 reference sequence using Bowtie2 v2.1.0 (7). The raw counts, per gene were estimated by HTseq v0.5.4 (8). The data were normalized in edgeR v3.9.16 (9) using the trimmed mean of M values (TMM) method. Only genes with ≥ 5 reads in total, across all samples, were included in the final analysis. The normalized raw counts per gene were used to identify genes that were differentially expressed between samples using edgeR package using a 5% FDR cutoff.

Analysis of association between differential methylation and differential expression

To obtain a correlation between methylation changes and differential expression of PSR genes, we first associated DmCs and DMRs to genomic regions using TAIR 10 Annotation. DMRs mapped to genomic regions were filtered in function of methylation direction (hypermethylation, hypomethylation) to select only loci with consistent methylation change marks. As we also mapped DmCs that did not score for our arbitrary minimun DmC number for DMR construction, we determined more astringent handling of these DmCs, these DmCs were filtered 1) by using a more astringent F-Test P-value ($\alpha \leq 0.05$) than those used to generate DMRs ($\alpha \leq 0.1$), 2) Scoring only DmCs with the same methylation direction in case of overlapping with DMRs or loci with assigned DMRs.

Once DMRs and DmCs were mapped to specific loci, we searched for loci that were associated with both differential methylation changes and differential expression in the same phosphate contrasts. Loci identified this approach were subjected to a detailed analysis to categorized genomic region in which the methylation changes occurred, level and direction of differential expression change (upregulated, downregulated) and the direction of methylation change (hypermethylation, hypomethylation) (Tables S4 and S5).

Functional categories enrichment

Gene lists were generated with the resulting Arabidopsis thaliana IDs from the association analysis described above. These lists were processed in MySQL to eliminate repetitive *loci*, and then analyzed in the webtool VirtualPlant 1.3 (http://virtualplant.bio.nyu.edu/cgi-bin/vpweb/) (10) using the BioMaps tool ($P \leq 0.01$) for find enrichment of functional categories. In this way groups of genes that are significantly over-represented were identified. In each case, the hypergeometric distribution was used to assess overrepresentation. To select the functional categories that were significant and over-represented we use a cut point in a normalized frequency (NF=Relative frequency of set/Relative frequency of reference) that was greater than or equal to 1.5 Fold (Table S3).

Sequencing Datasets Visualization using the EPIC-CoGe Genome Browser.

Whole genome methyl cytosine positions (mCs) profiling for all phosphate treatments, DMRs and DmCs mapped to the TAIR10 reference sequence, gene models, and functional genomic elements were visualized using the EPIC-CoGe genome browser (11). All these datasets can be viewed in the EPIC-CoGe browser at: https://goo.gl/iP6zER

Supplementary Definitions and Abbreviations

Methylation context: Methylation context refers to the specific sequence context in which a methylated cytosine is located, in plants this DNA methylation modification is applied in three different sequence contexts (CG, CHG and CHH, where H= A, C or T), context also can be defined as CG context (CG) and non-CG context (CHG and CHH).

Methylation change: Methylation change is defined as any change in the DNA methylation status of a specific cytosine position or a genomic region, namely changes in the methylation levels. These DNA methylation changes can be classified in function of the direction of the methylation change as either the result of an increase (hypermethylation) or a decrease (hypomethylation) of DNA methylation levels.

Differentially methylated cytosine (DmC): A differentially methylated cytosine is a cytosine position in which a significant DNA methylation change occurred in response to an environmental or developmental factor. DmCs can be further classified in function of the methylation context (DmCGs, DmCHGs and DmCHHs) or in function of the methylation change direction (hyper-DmCs and hypo-DmCs).

Differentially methylated region (DMR): A differentially methylated region is defined as a cluster of DmCs in which methylation patterns are significantly affected in response to environmental or developmental factors. DMRs can be classified in function of the methylation change direction (hyper-DmCs and hypo-DmCs).

Gene-related differential methylation: Gene-related differential methylation refers to changes in methylation patterns that occur inside features as upstream, gene body and downstream regions associated to a specific gene. Transposable elements adjacent to or within genes are also considered as Gene-Related (GR-TEs).

Low phosphate differentially methylated DEGs (Pi-methDEGs): Low phosphate differentially methylated DEGs are referred as Low Pi starvation responsive genes that are differentially methylated in response to LP conditions, these Pi-methDEGs can present overlap with DMRs or individual DmCs within Gene-related regions.

P factor DmCs (Pf-DmCs): P factor DmCs are exceptionally significant DmCs strongly associated to DNA methylation in response to changes in the phosphate status, these Pf-DmCs are the result of the analysis of a complete 2 x 2 x 2 factorial experiment.

P factor differentially methylated DEGs (Pf-methDEGs): P factor differentially methylated DEGs are defined as Pi-methDEGs that overlap with at least one Pf-DmC.

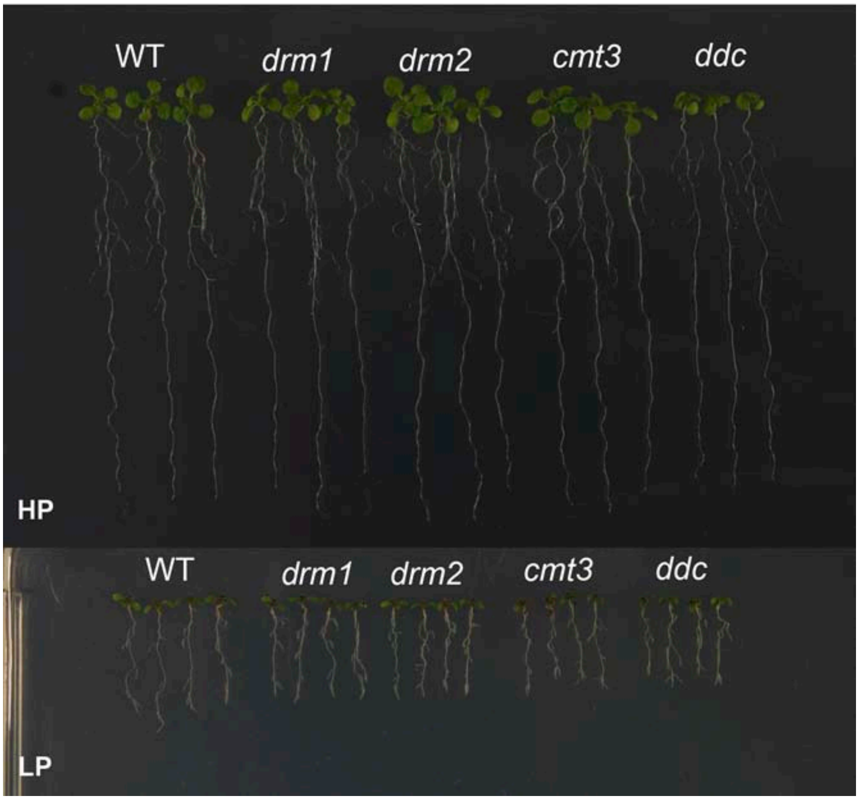

Fig. S1. Arabidopsis non-CG methylation mutants show alterations in the root responses to low Pi availability. Seedlings were grown for 14 d on medium with 1 mM Pi (HP) and 5 µM Pi (LP). Seedlings growing in 1 mM Pi (HP) are shown in the upper panel and seedling growing the 5 µM Pi (LP) are shown in the lower panel.

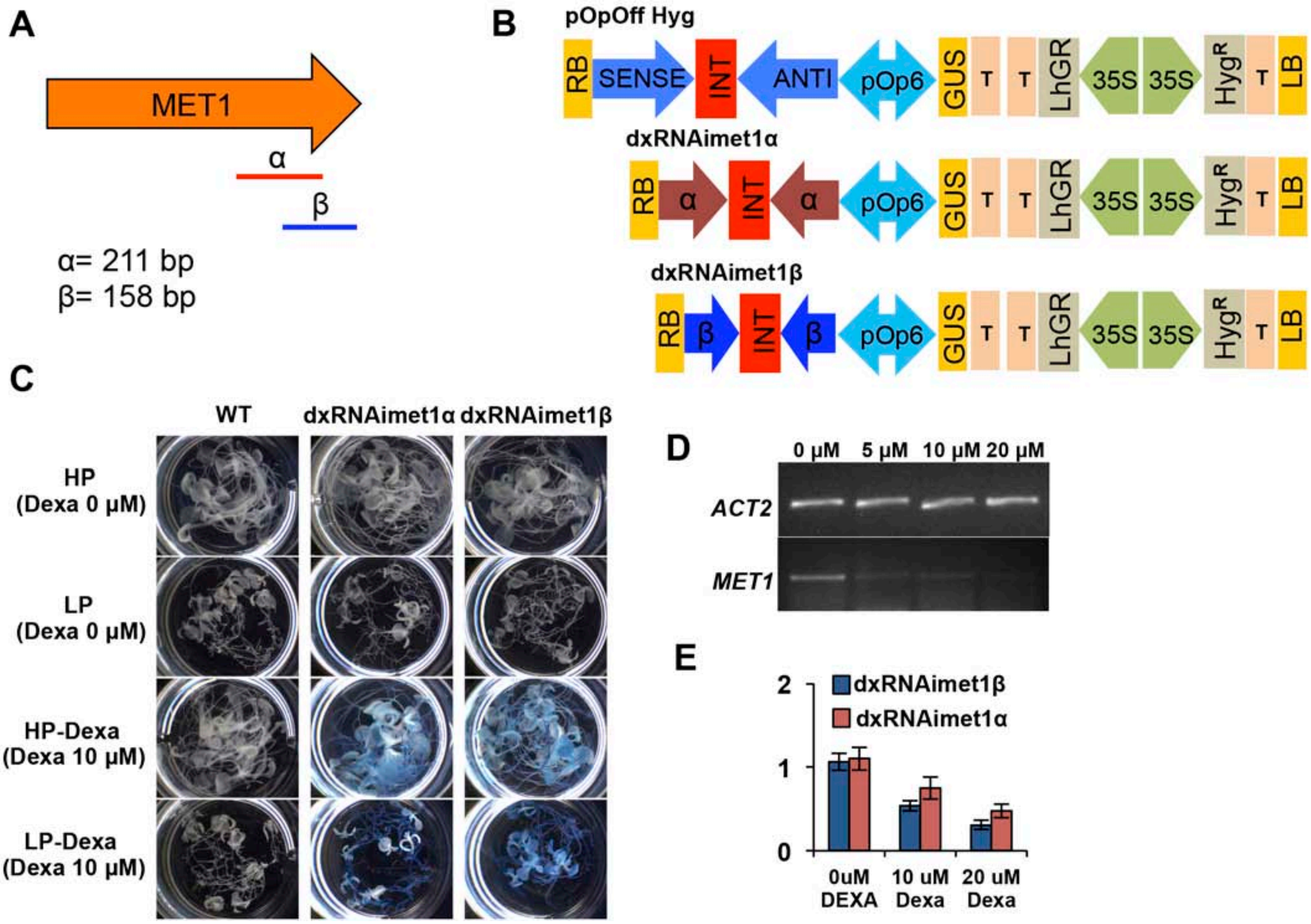

Fig. S2. Design and characterization of dxRNAiMET1 inducible mutants. A) Relative position and fragment size of α and β versions of *MET1* RNAi. B) Backbone of original pOpOff Hyg vector and dxRNAimet1α and dxRNAimet1β constructs. C) Analysis of GUS reporter gene induction; Seedlings were grown for 14 d on liquid MS medium with 1 mM Pi (HP) and 5 μM Pi (LP) in hydroponics systems, for induction of GUS reporter gene 10 μM dexamethasone was supplied to both phosphate treatments (HP-Dexa, LP-Dexa). D) RT-PCR of *MET1* transcript in dxRNAimet1β mutant RNA supplied with different dexamethasone concentrations (0, 5, 10 and 20 μM), *ACT2* was used as internal control. E) qRT-PCR of MET1 transcript in dxRNAimet1α and dxRNAimet1β mutants induced with 0,10 and 20 μM dexamethasone.

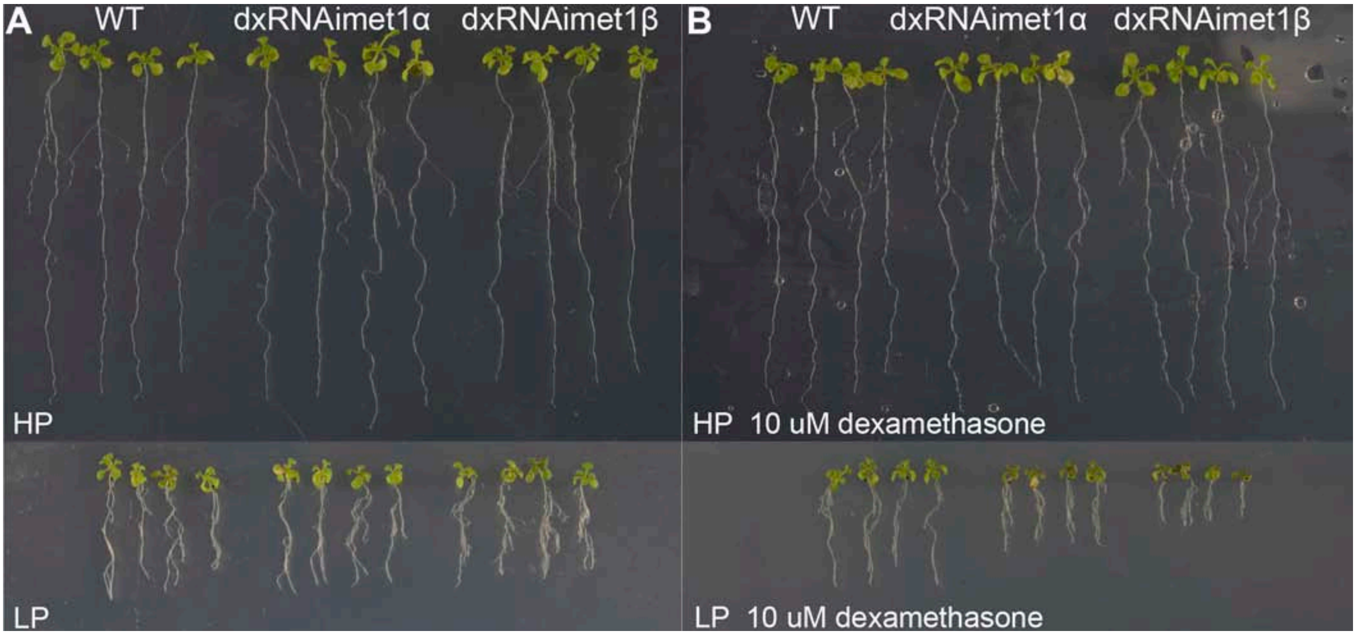

Fig. S3. Arabidopsis dxRNAiMET1 lines show alterations in Pi starvation morphologic responses. A) Seedlings were grown for 14 d on MS medium with 1 mM Pi (HP) and 5 µM Pi (LP). B) Seedlings were grown for 14 d on MS medium with 10 µM dexamethasone and 1 mM Pi (HP-dexa) and 5 µM Pi (LP-dexa), 10µM dexamethasone was resupplied every 4 days. The phenotypes of the RNAi lines and WT controls are shown in 1 mM Pi (HP) is shown in the upper picture of each panel and the phenotypes of seedlings grown in 5 µM Pi (LP) are shown in the lower picture of each panel.

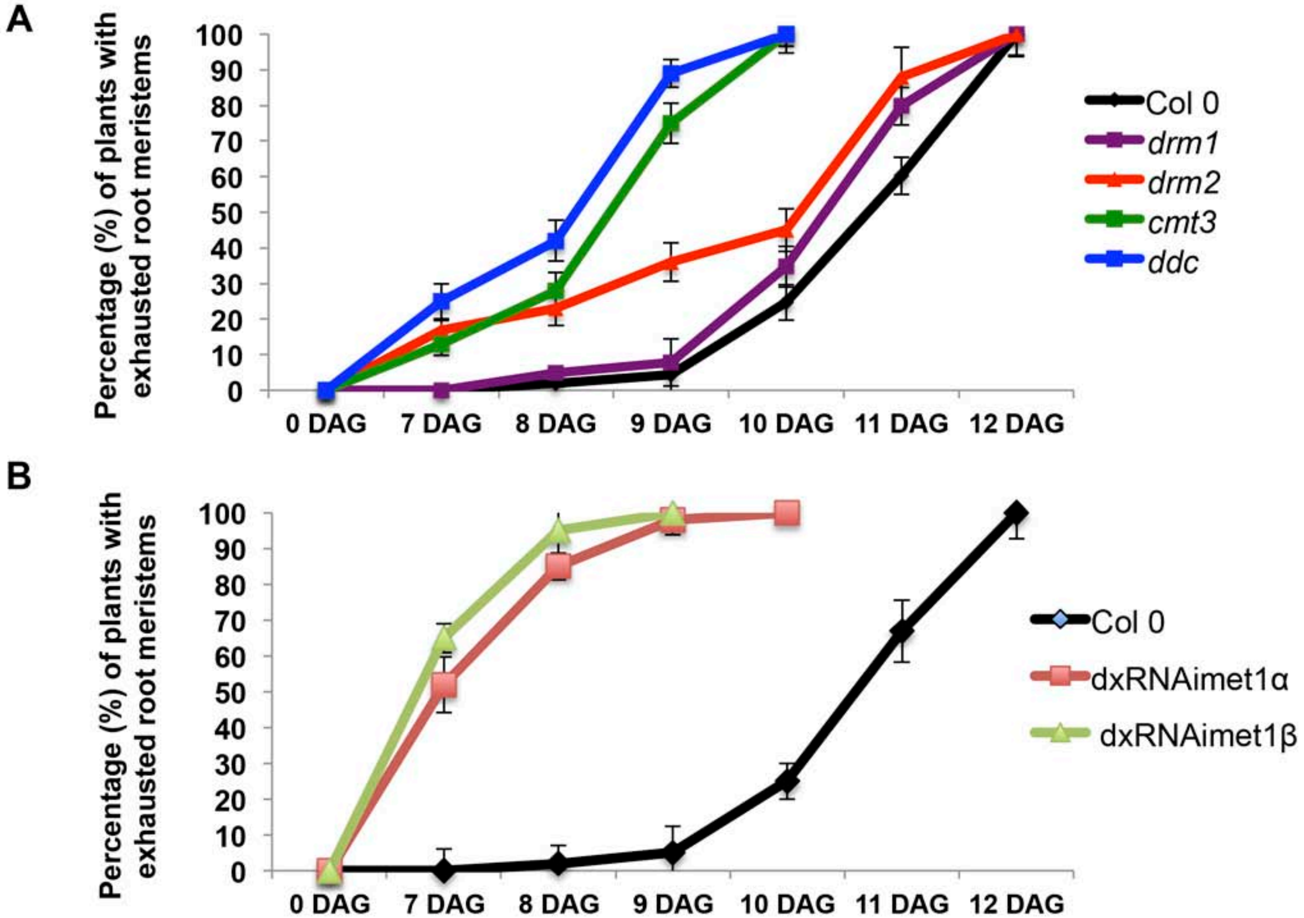

Fig. S4. DNA methylation mutants show premature meristem exhaustion in –Pi. A) Quantitative analysis of root meristem exhaustion events in non-CpG DNA methylation mutants (*drm1, drm2, cmt3* and *ddc*) grown under phosphate starvation. B) Quantitative analysis of root meristem exhaustion events in dxRNAimet1 inducible mutants grown under phosphate starvation in the presence of 10 μM dexamethasone. We established meristem exhaustion event supported on cell parameters such as the development of root hairs, cell disorganization and differentiated protoxylem in the primary root meristem. Values are the mean ± SD from six biological replicates (N = 20, with two technical replicates each).

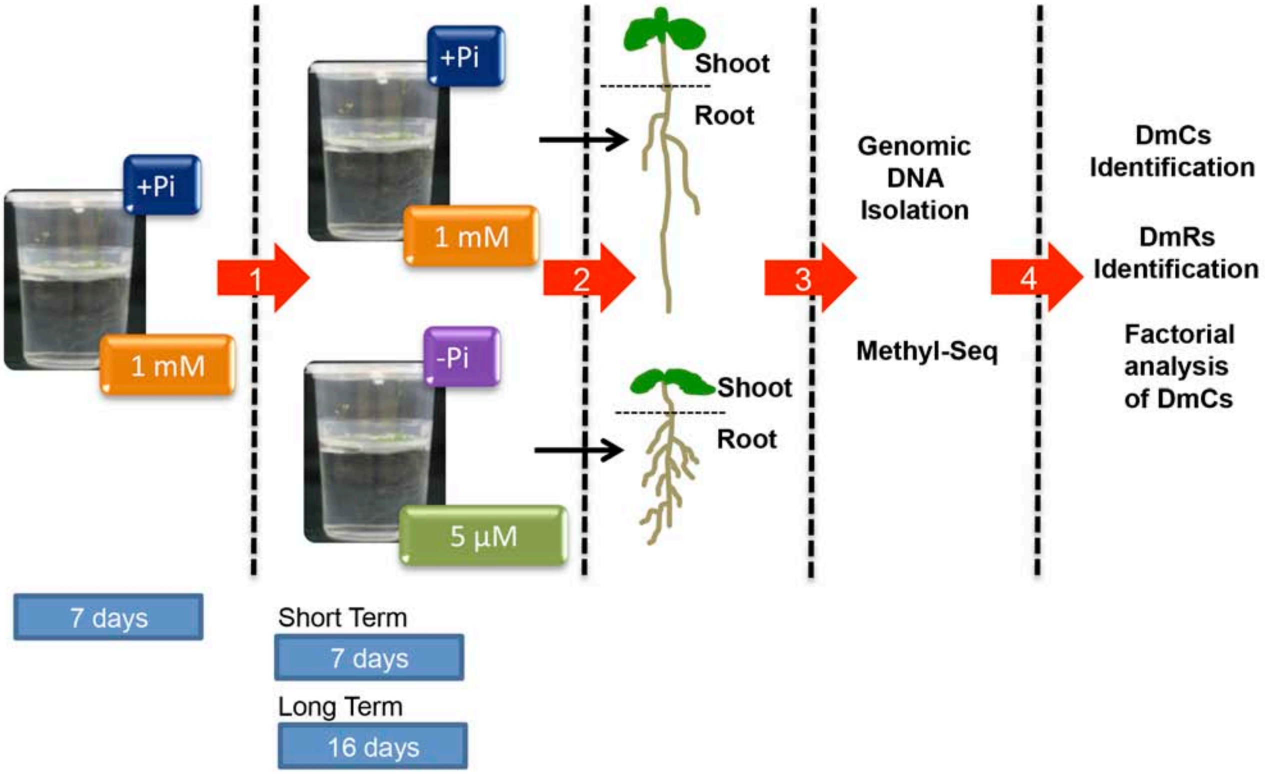

Fig. S5. General approach used to identify Pi Starvation-induced genome-wide changes in cytosine methylation. Plants were grown initially for 7 days in HP hydroponic medium. 1) Plants were transferred to fresh HP or LP media for 7 days or 17 days. 2) HP and LP treated seedlings were collected and shoot and root organs were separated for DNA Isolation. 3) High-throughput sequencing of bisulfite-treated genomic DNA was performed. 4) Methyl-Seq reads were mapped and whole genome mC profiling was calculated, differential methylation (DmC) levels were determined at each methylcytosine for each phosphate contrast (LP vs HP, e.g. $-Pi_t$ Shoot 7 dat. VS $+Pi_t$ Shoot 7 dat), DMRs were calculated for either hypermethylated or hypomethylated DmCs sets and finally a factorial analysis of DmCs was performed.

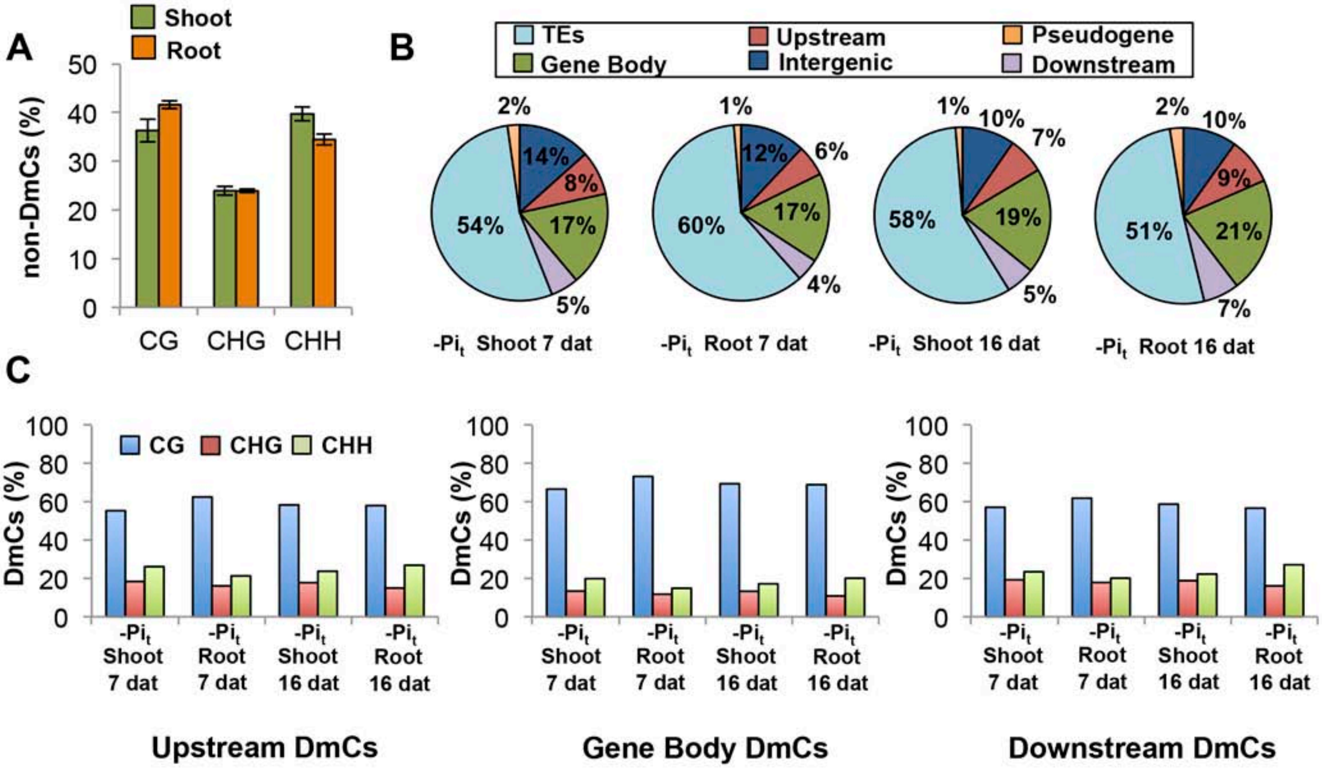

Fig. S6. Detailed methylation Context Cut-off and Distribution among genomic features of Gene Related DmCs. A) Context Cut-off of root and shoot libraries. B) Mapping of DmCs to genomic features by phosphate contrast. C) Methylation context distribution of Gene Related DmCs (upstream, gene body and downstream regions) by phosphate contrast.

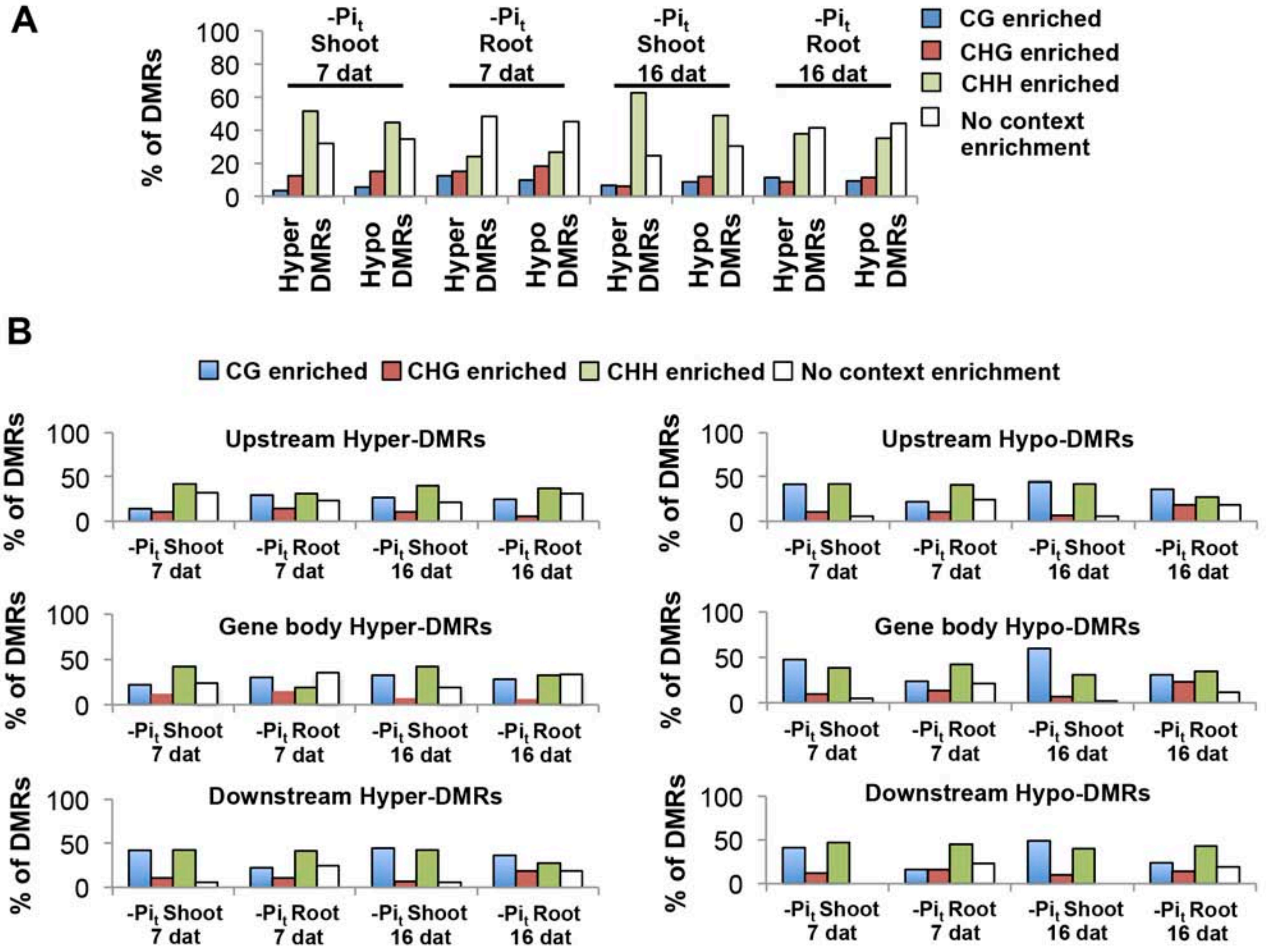

Fig. S7. Detailed Analysis of DMR methylation context enrichment. A) Context enrichment of total Hyper and Hypo DMRs for each individual phosphate contrast. B) Context enrichment of Gene Related hypomethylated and hypermethylated DMRs, in upstream, gene body and downstream regions by phosphate contrast.

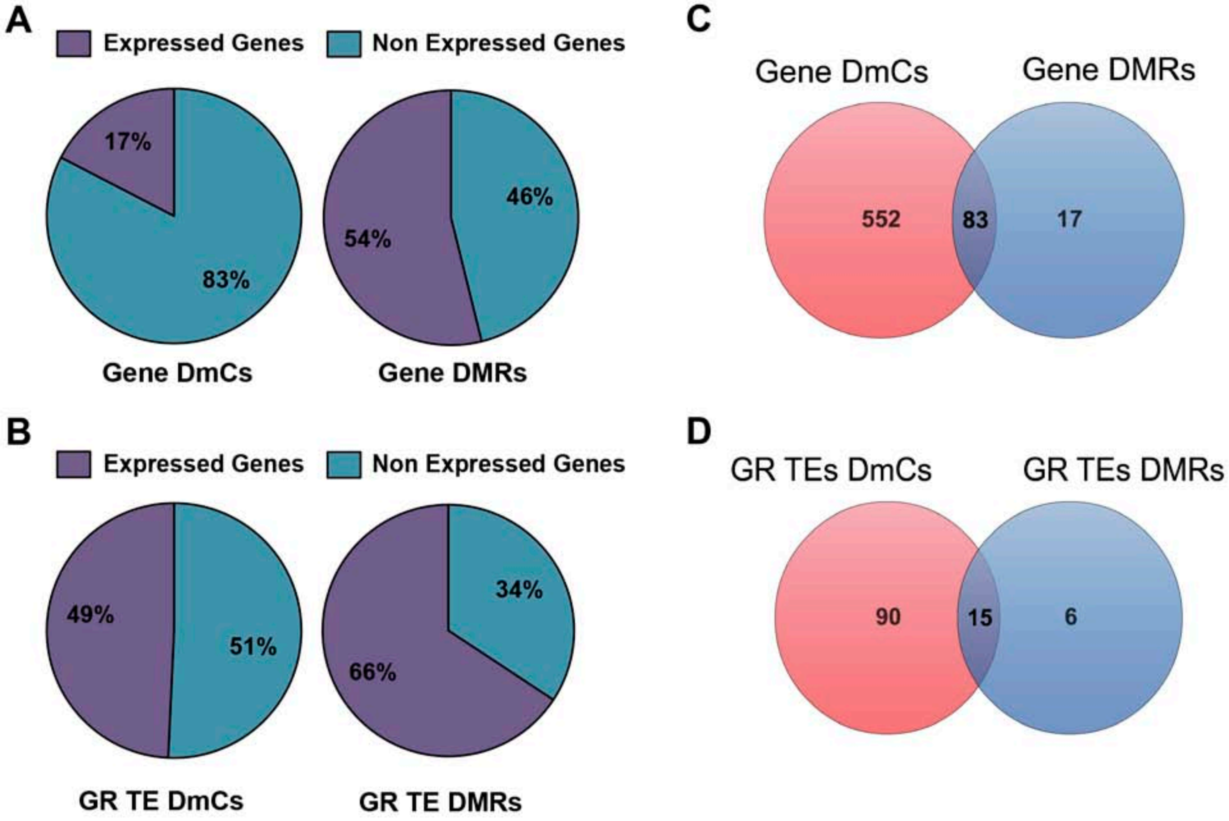

Fig. S8. Distribution of DmCs and DMRs between Expressed and Non-Expressed Genes. A) Percent cut-off of Genic DmCs and DMRs among Expressed genes and Non-Expressed Genes. B) Percent cut-off of Gene Related Transposable Elements (GR TEs) DmCs and DMRs between Expressed genes and Non-Expressed. C) Venn Diagram showing de distribution of differentially methylated loci between Gene DmCs and DMRs. D) Venn Diagram showing de distribution of differentially methylated loci between GR TEs DmCs and DMRs.

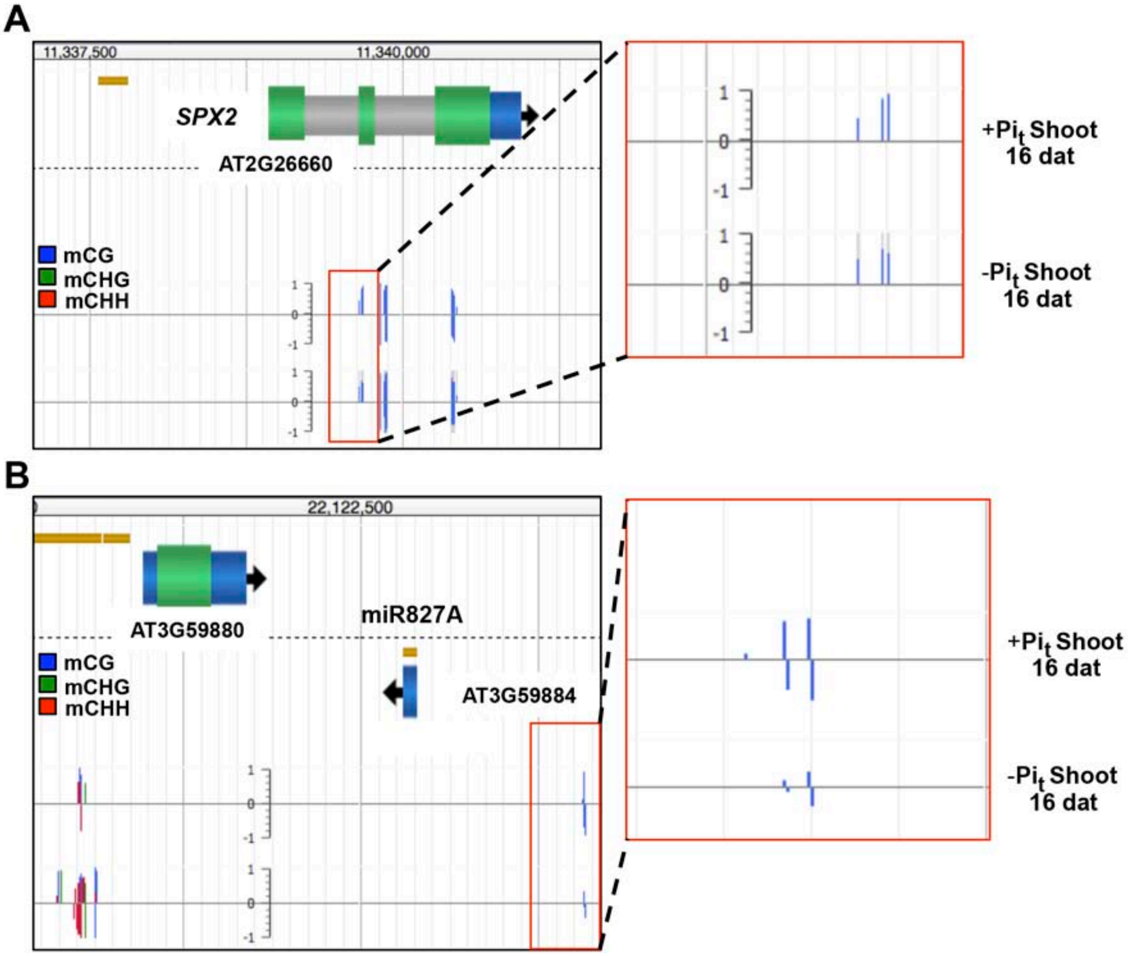

Fig. S9. Genome browser visualization of methylation profiling of Arabidopsis *SPX2* and miRNA827A genes. A) Genome browser screen shot from Arabidopsis *SPX2* locus, DNA methylation patterns during HP (+Pi$_t$ Shoot 16 dat) and LP (-Pi$_t$ Shoot 16 dat) conditions, zoom of differentially methylated zone is displayed on the right. A) Genome browser screen shot from Arabidopsis miR827A locus, DNA methylation patterns during HP (+Pi$_t$ Shoot 16 dat) and LP (-Pi$_t$ Shoot 16 dat) conditions, zoom of differentially methylated zone is displayed on the right.

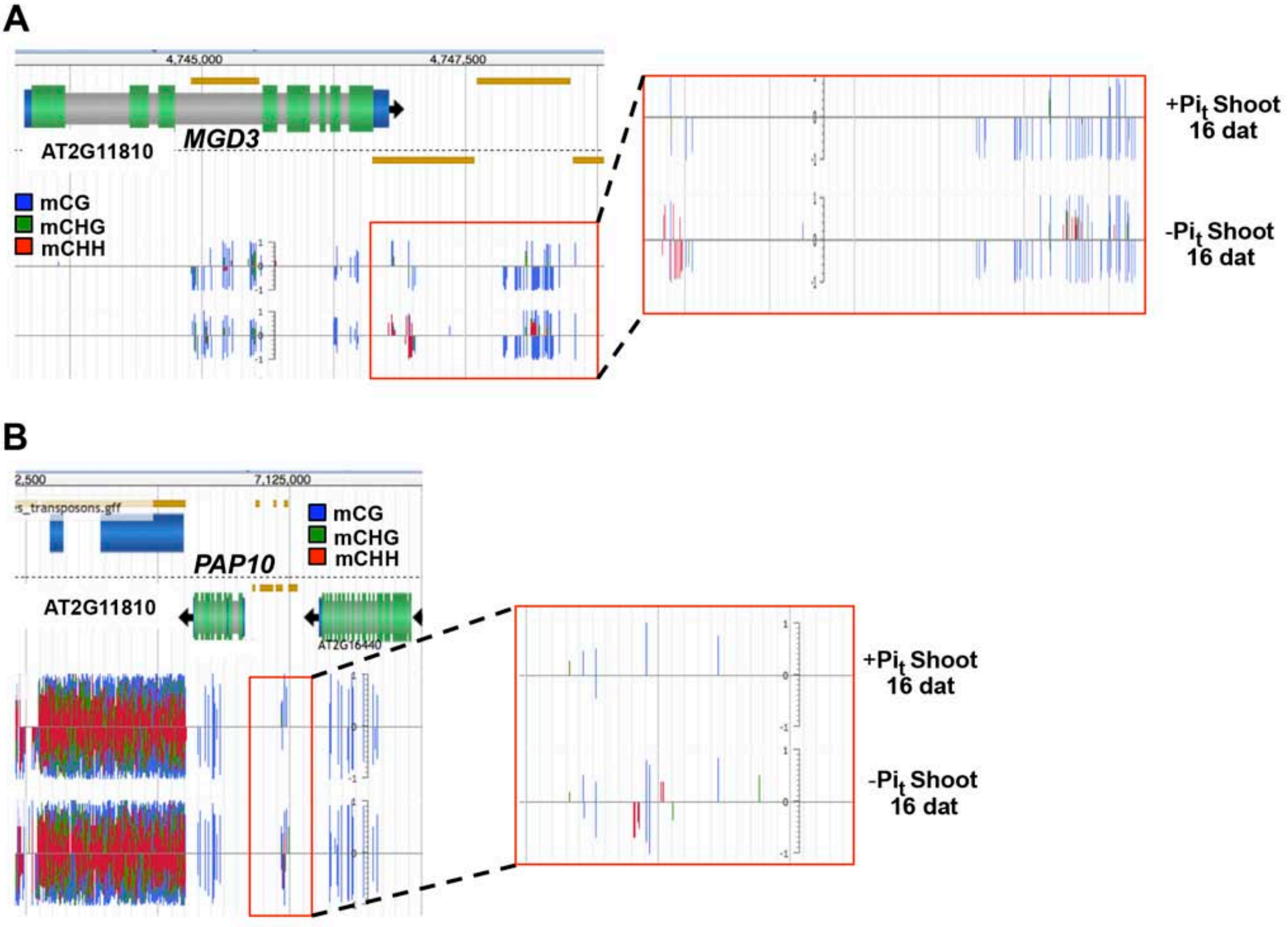

Fig. S10. Genome browser visualization of methylation profiling of Arabidopsis *MGD3* and *PAP10* genes. A) Genome browser screen shot from Arabidopsis *MGD3* locus, DNA methylation patterns during HP (+Pi$_t$ Shoot 16 dat) and LP (-Pi$_t$ Shoot 16 dat) conditions, zoom of differentially methylated zone is displayed on the right. A) Genome browser screen shot from Arabidopsis *PAP10* locus, DNA methylation patterns during HP (+Pi$_t$ Shoot 16 dat) and LP (-Pi$_t$ Shoot 16 dat) conditions, zoom of differentially methylated zone is displayed on the right.

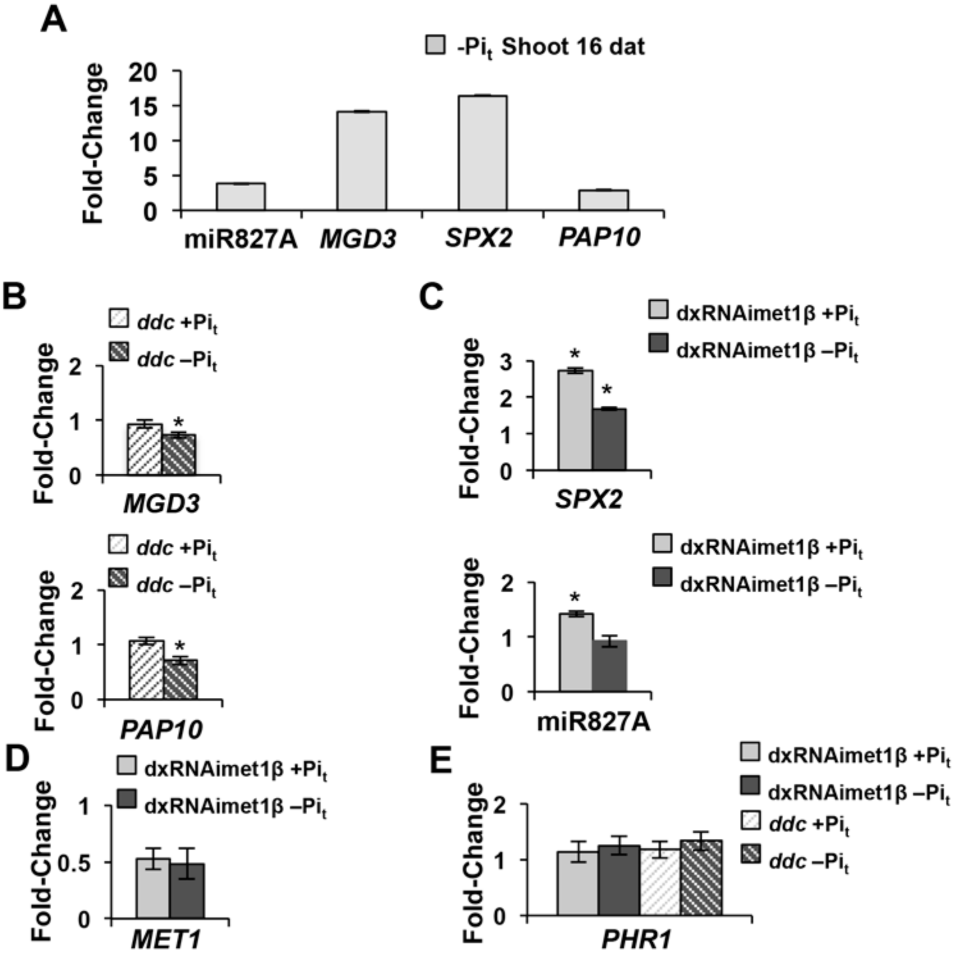

Fig. S11. Expression analysis of PSR genes targeted by DNA methylation changes. A) Real-time PCR analysis of *miR827A*, *MGD3*, *SPX2* and *PAP10* in the shoot of Col 0 seedlings grown in liquid MS under HP (+Pi_t Shoot 16 dat) and LP (-Pi_t Shoot 16 dat) conditions, *AtACT2,* At5g55840 and AT3G53090 were used as internal controls; HP values were used as calibrator samples. B) Real-time PCR analysis of *MGD3* and *PAP10* in the shoot of *ddc* triple mutants seedlings grown in liquid MS under HP (+Pi_t Shoot 16 dat) and LP (-Pi_t Shoot 16 dat) conditions. C) Real-time PCR analysis of miR827A and *SPX2* in shoot of dxRNAimet1β seedlings grown in liquid MS under HP-dexa (+Pi_t Shoot 16 dat, 10 uM dexamethasone) and LP-dexa (-Pi_t Shoot 16 dat, 10 uM dexamethasone) conditions. D) Real-time PCR analysis is shown for *MET1* in shoot of dxRNAimet1β seedlings grown in liquid MS under HP-dexa (+Pi_t Shoot 16 dat, 10 uM dexamethasone) and LP dexa (-Pi_t Shoot 16 dat, 10 uM dexamethasone) conditions. E) Real-time PCR analysis is shown for *PHR1* in shoot of dxRNAimet1β seedlings grown in liquid MS under HP-dexa (+Pi_t Shoot 16 dat, 10 uM dexamethasone) and LP-dexa (-Pi_t Shoot 16 dat, 10 uM dexamethasone) and *ddc* triple mutants in LP (-Pi_t Shoot 16 dat) and HP (+Pi_t Shoot 16 dat) conditions. In all cases dexamethasone was resupplied every 4 days into the hydroponic system and *AtACT2,* At5g55840 and AT3G53090 were used as internal controls; (B to E) WT respective values for each phosphate treatment (HP, LP) were used as calibrator samples for the respective treatments.

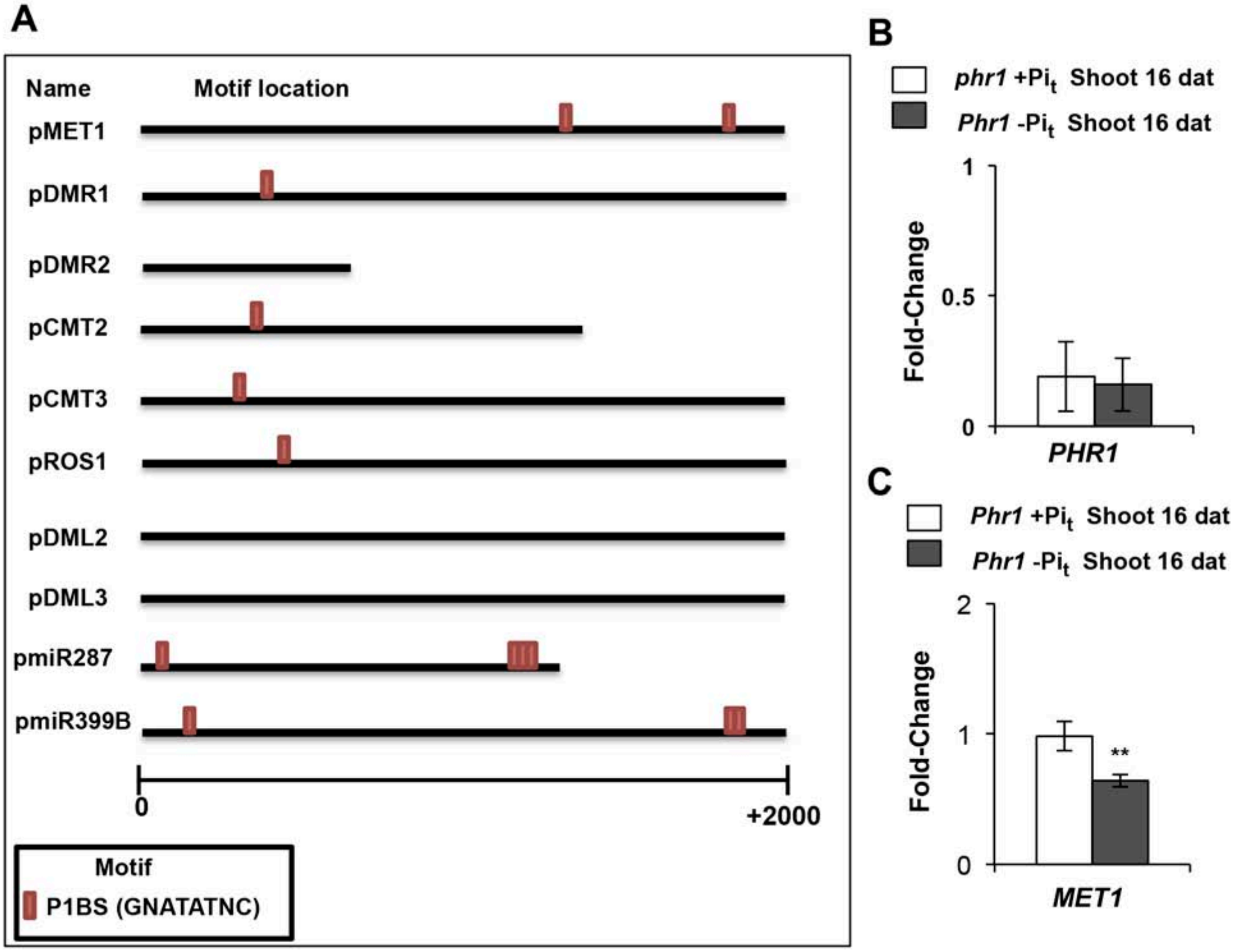

Fig. S12. Expression of *MET1* is regulated by PHR1. A) Analysis of the presence of P1BS motifs in a 2000 bp upstream region from the transcription start site (TSS) of DNA methyltransferases and demethylases; promoter regions of miR399B and miR827A were used as reference for the presence of P1BS in upstream regions, analysis was performed using the PLACE database (Red boxes indicate relative position of P1BS motifs from TSS (0) to 2000 bp upstream (+2000). B) Real-time PCR analysis of *PHR1* in the shoot of *phr1* seedlings grown in liquid MS under HP (+Pi$_t$ Shoot 16 dat) and LP (-Pi$_t$ Shoot 16 dat) conditions. C) Real-time PCR analysis of *MET1* in the shoot of *phr1* seedlings grown in liquid MS under HP (+Pi$_t$ Shoot 16 dat) and LP (-Pi$_t$ Shoot 16 dat) conditions; notice that the level of expression of *MET1* is reduced by 40% in *phr1* respect to that found in the WT. *AtACT2,* At5g55840 and AT3G53090 were used as internal controls, and HP respective values for each phosphate treatment (HP, LP) were used as calibrator samples.

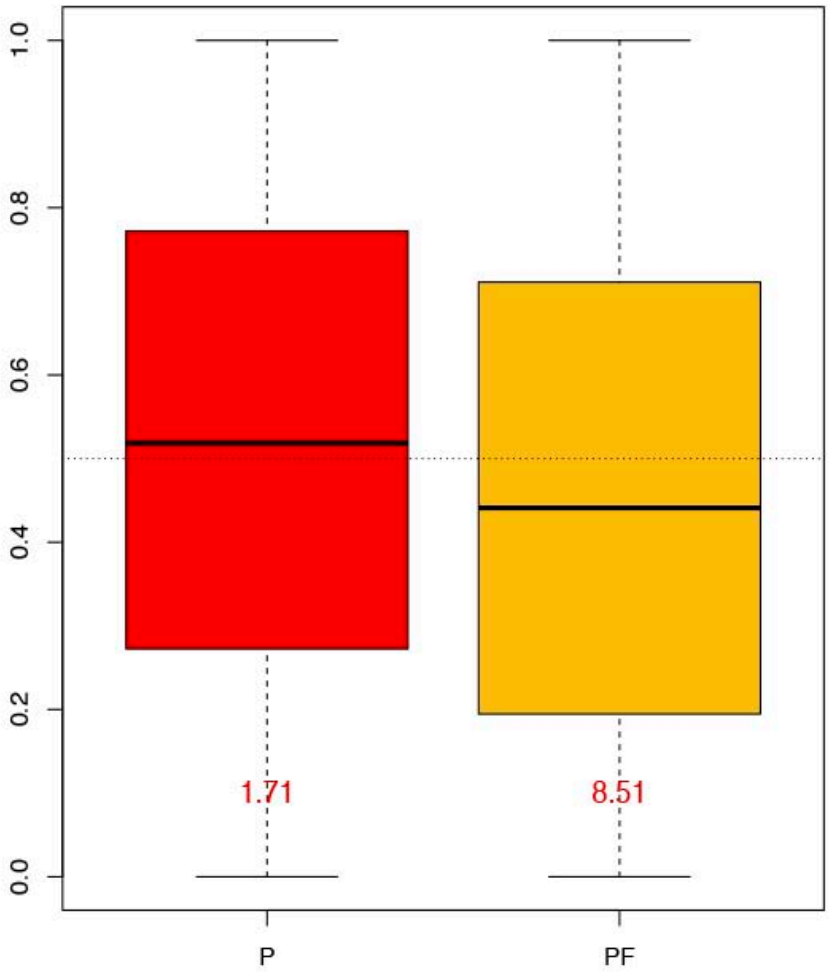

Figure S13. Boxplot for the probabilities of the tests on the parameter "P" (phosphorous) of the full model and the F-test (PF) for the 5,867,837 positions found to be methylated in all five chromosomes. The numbers in red are the percentages of significant tests in each distribution at α = 0.05.

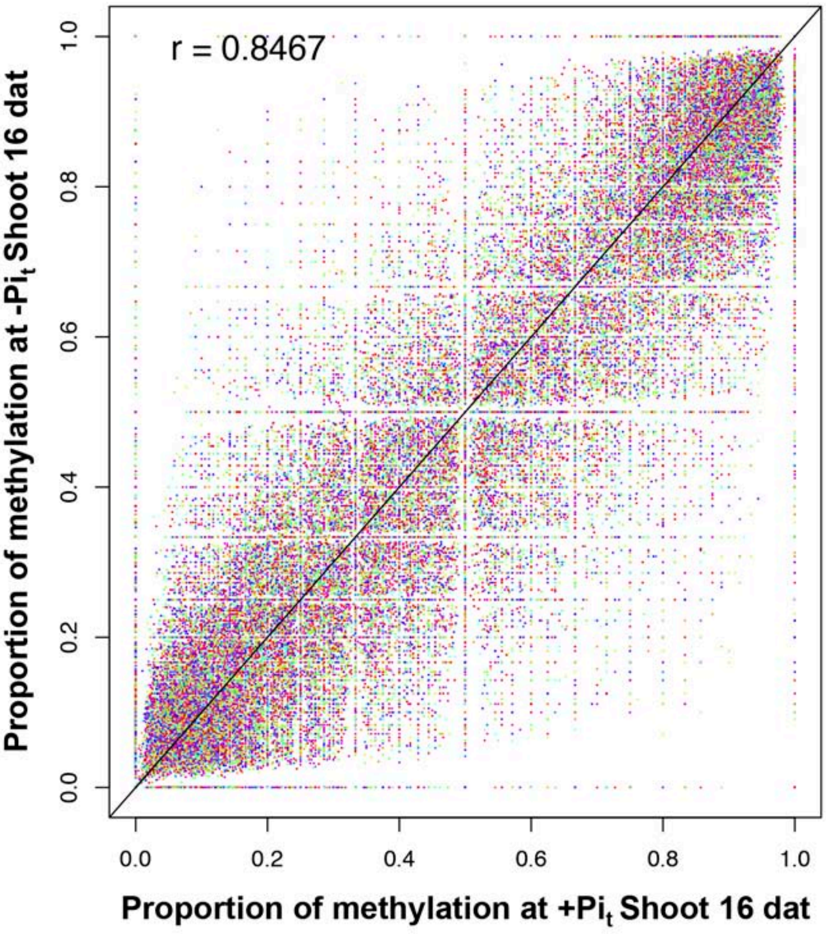

Fig. S14. Scatterplot for the estimated proportion of methylation (PM) for 100,000 positions, which are a random sample of the estimated 1,191,764 methylated cytocines. The proportion of methylation is shown as points for the treatments +Pi$_t$ Shoot 16 dat (X axis) and -Pi$_t$ Shoot 16 dat (Y axis). The estimated correlation between the values in the full set was r = 0.8467, r2 = 0.7168

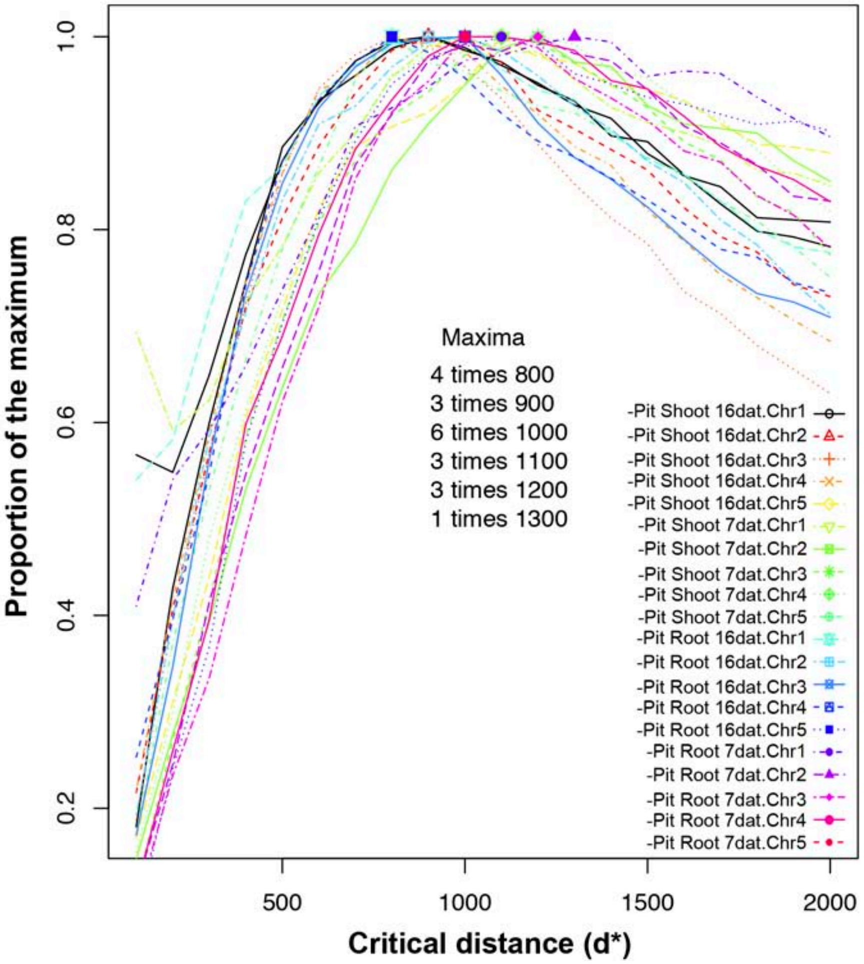

Fig. S15. Estimation of the optimum critic distance (d*) between DmCs that generates the maximum number of DMRs.

TABLE S1. Details of Methyl-Seq Libraries. Only reads mapping to Arabidopsis thaliana nuclear genome or phage Lambda genome are included in this analysis.

HIGH Pi LIBRARIES	**+Pi Shoot 7 d.a.t. rep 1**	**+Pi Shoot 7 d.a.t. rep2**	**+Pi Root 7 d.a.t. rep1**	**+Pi Root 7 d.a.t. rep2**	**+Pi Shoot 16 d.a.t. rep1**	**+Pi Shoot 16 d.a.t. rep2**	**+Pi Root 16 d.a.t. rep1**	**+Pi Root 16 d.a.t. rep2**
Reads (mapped and Non-clonal)	25270793.18	31917362.96	28232152.9	25535392.41	29777020.66	28593900.17	27528487.47	31567351.04
Total bases mapped	2274371386	2872562667	2540893761	2298185317	2679931859	2573451015	2477563872	2841061594
Lambda Cytosine Non-conversion/E	0.22%	0.21%	0.28%	0.21%	0.26%	0.23%	0.25%	0.28%
% Genome Covered (at least 1 read	95.2	92.8	94.12	94.39	93.1	92.3	94.2	94.15
% Genomic Cytosines (at least 1 rea	91.24	94.83	94.64	93.81	92.04	90.01	94.85	96.84
% Mappable Cytosines Covered (at	93.7	96.65	96.5	95.66	94.46	92.45	96.63	97.63
Average Read Depth at Cytosines	8.17	9.99	8.97	8.24	8.68	8.84	8.8	10.15
Average Read Depth at Methylcytos	17.79	18.69	18.55	20.34	18.36	19.34	18.27	19.55
Number of nuclear Methylcytosines	2980982	3306687	2916656	2702174	3445532	3355061	3046141	3281528
Context:								
mCG (% of mC)	1288761 (43.23%)	1421450 (42.98%)	1365729 (46.82%)	1246458 (46.12%)	1359664 (39.46%)	1289981 (38.44%)	1364883 (44.8%)	1435887 (43.75%)
mCHG (% of mC)	709206 (23.79%)	773265 (23.39%)	727081 (24.93%)	688159 (25.48%)	797893 (23.16%)	783625 (23.36%)	744070 (24.43%)	792829 (24.17%)
mCHH (% mC)	983015 (32.98%)	1111981 (33.63%)	823846 (28.25%)	767557 (28.4%)	1287975 (37.38%)	1281455 (38.2%)	937188 (30.77%)	1052812 (32.08%)
% Genome methylated	6.95%	7.71%	6.80%	6.30%	8.04%	7.83%	7.10%	7.65%

LOW Pi LiBRARIES	**-Pi Shoot 7 d.a.t. rep1**	**-Pi Shoot 7 d.a.t. rep2**	**-Pi Root 7 d.a.t. rep1**	**-Pi Root 7 d.a.t. rep2**	**-Pi Shoot 16 d.a.t. rep1**	**-Pi Shoot 16 d.a.t. rep2**	**-Pi Root 16 d.a.t. rep1**	**-Pi Root 16 d.a.t. rep2**
Reads (mapped and Non-clonal)	29160717.39	23710551.58	28761991.72	29309702.21	32043716.57	32744720	31062117.82	35006451.47
Total bases mapped	2624464565	2133949642	2588579254	2637873199	2883934491	2947024800	2795590604	3150580632
Lambda Cytosine Non-conversion/E	0.23%	0.24%	0.21%	0.23%	0.30%	0.32%	0.25%	0.21%
% Genome Covered (at least 1 read	93.7	92.1	92.8	95.3	93.4	95.1	92.5	92.2
% Genomic Cytosines (at least 1 rea	94.28	90.51	94.43	94.11	94.96	96.08	91.39	91.09
% Mappable Cytosines Covered (at	96.19	93.1	96.33	96.66	96.78	97.63	93.91	93.87
Average Read Depth at Cytosines	9.31	7.69	9.28	9.45	10.18	10.19	10.24	11.59
Average Read Depth at Methylcytos	17.86	17.4	18.73	20.08	19.38	18.71	21.67	24.23
Number of nuclear Methylcytosines	3283241	3066983	2979224	3009773	3771690	3618308	3334243	3411372
Context:								
mCG (% of mC)	1391530 (42.38%)	1276730 (41.62%)	1373719 (46.1%)	1364087 (45.32%)	1461364 (38.74%)	1464186 (40.46%)	1385494 (41.55%)	1397878 (40.97%)
mCHG (% of mC)	766382 (23.34%9	727270 (23.72%)	742871 (24.95%)	752425 (25%)	844573 (22.4%)	816646 (22.58%)	799461 (23.98%)	814762 (23.89%)
mCHH (% mC)	1125329 (34.28%)	1062983 (34.66%)	862634 (28.95%)	893261 (29.68%)	1465753 (38.86%)	1337476 (36.96%)	1149288 (34.47%)	1198732 (35.14%)
% Genome methylated	7.66%	7.15%	6.95%	7.02%	8.80%	8.44%	7.78%	7.96%

Table S2. Differentially expressed genes targeted by differential methylation (Pi-methDEGs) representative of GO enriched categories. Arabidopsis Locus ID and Gene Descriptions of Pi-methDEGs are shown.

Locus ID	Gene Description
AT4G13390	EXTENSIN 12 (*EXT12*) $^{\text{Hypo, Down}}$
AT1G08430	ALUMINUM-ACTIVATED MALATE TRANSPORTER 1 (*ALMT1*) $^{\text{Hyper,Down}}$
AT1G20840	TONOPLAST MONOSACCHARIDE TRANSPORTER1 (*TMT1*) $^{\text{Hyper,Down}}$
AT1G52940	PURPLE ACID PHOSPHATASE 5 (*PAP5*) $^{\text{Hypo, Up}}$
AT2G11810	MONOGALACTOSYL DIACYLGLYCEROL SYNTHASE 3 (*MGD3*) $^{\text{Hyper,Up}}$
AT1G21250	CELL WALL-ASSOCIATED KINASE (*WAK1*) $^{\text{Hypo, Up}}$
AT1G35625	RING/U-BOX SUPERFAMILY PROTEIN $^{\text{Hypo,Up}}$

$^{\text{Up}}$ Upregulated $^{\text{Down}}$ Downregulated
$^{\text{Hypo}}$ Hypo-methylated $^{\text{Hyper}}$ Hyper-methylated

Table S3. GO enrichment analysis of diferentially methylated PSR genes (Pi-methDEGs) and Pi Factor diferentially methylated PSR genes (Pf-methDEGs). (VirtualPlant 1.3).

	Category	Count	% of total	P-value	Normed Frequency (Fold-Change)
Pi-methDEGs					
Pi-methDEGs Short Term	Receptor enzyme mediated signalling	14	1.2	0.000547	4.41
Pi-methDEGs Long Term	Glycolipid metabolism	5	1.3	0.00062	13
	Transported compounds (substrates)	61	16	1.84e-05	2.05
	Phosphate metabolism	56	14.7	0.00062	2
Pi-methDEGs Short Term ∩ Long Term	Glycolipid metabolism	3	6.1	0.000666	61
Pi-methDEGs Root	Transmembrane signal transduction	18	6.5	1.13e-05	4.64
	Phosphate metabolism	37	13.5	0.00329	1.95
Pi-methDEGs Shoot	Glycolipid metabolism	4	1.2	0.00597	12
	Cellular sensing and response to external stimulus	37	10.7	0.00597	1.94
	Phosphate metabolism	52	15.1	0.00121	1.91
Pi-methDEGs Root ∩ Shoot	Protein/peptide degradation	5	16.6	0.03	4.3
	Cell wall	3	10	0.03	8.7
Pf-methDEgs	METABOLISM	74	35.7	0.000125	1.72
	Phosphate metabolism	36	17.4	0.00109	2.2

Table S4. Phosphate Starvation responsive genes targeted by differential methylation (Pi-methDEGs). Locus ID of Pi-methDEGs is shown. Hypermethylated and Hypomethylated DEGs are listed as Upregulated or Downregulated. Each particular LP contrast is showed by separated.

-Pi$_t$ Shoot 7 dat

Hypermethylated		Hypomethylated	
Upregulated	**Downregulated**	**UpRegulated**	**Downregulated**
AT5G41750	AT1G68440	AT2G18150	AT1G74290
AT1G58280	AT5G18030	AT3G47480	AT1G12020
AT2G18530	AT3G46240	AT1G61370	AT2G15020
AT5G37840	AT1G29450	AT2G17500	AT5G15360
AT1G61480	AT3G51870	AT2G04495	AT2G26215
AT1G54095	AT3G09162	AT1G03940	AT5G59070
AT4G04990	AT4G34730	AT5G35050	AT3G01345
AT4G14090	AT1G63540	AT4G00500	AT5G13770
AT3G17190	AT5G66520	AT4G10500	AT5G67385
AT4G15270	AT5G10340	AT2G04400	AT1G67900
AT2G04100	AT5G37130	AT1G02470	AT5G24155
AT1G64610	AT1G49990	AT4G33770	AT3G26490
AT3G14205	AT3G54770	AT3G03790	AT2G16270
AT5G07570	AT3G48420	AT2G38250	AT5G38000
AT1G66360	AT4G20362	AT1G74270	AT4G38340
AT5G38910	AT3G54580	AT4G15540	AT3G21870
AT5G67340	AT2G04795	AT3G25610	AT2G24720
AT3G28210	AT2G25900	AT3G09830	AT5G09660
AT1G32960	AT4G17460	AT4G38560	AT2G33770
AT1G72330	AT1G08430	AT1G49800	AT2G18470
AT2G47000	AT4G26320	AT1G26380	AT3G02850
AT1G79400	AT3G18290	AT4G20210	AT1G65730
AT1G62540	AT4G37610	AT1G08310	
AT1G74590	AT4G35090	AT4G22470	
AT3G09270	AT4G27030	AT4G21390	
AT2G34600	AT4G09600	AT3G57240	
AT5G27600	AT2G17780	AT2G05710	
AT2G11810	AT1G32450	AT4G04610	
AT4G37670	AT2G39730	AT3G59140	
AT2G16430	AT4G07400	AT4G23700	
	AT5G13740	AT1G21250	
		AT4G04490	
		AT2G39770	
		AT4G15200	
		AT3G47420	
		AT1G17420	
		AT3G59884	
		AT5G20410	
		AT3G61990	
		AT3G20660	
		AT5G39050	
		AT1G53310	
		AT3G26840	
		AT3G08720	
		AT2G26660	
		AT4G08390	
		AT1G66570	
		AT4G33030	
		AT3G56040	
		AT2G36750	
		AT1G21240	
		AT1G80840	

-Pi$_t$ Root 7 dat

Hypermethylated		Downmethylated	
Upregulated	**Downregulated**	**Upregulated**	**Downregulated**
AT5G20790	AT2G35920	AT2G16676	AT4G16900
AT1G54095	AT2G15980	AT4G27850	AT2G17033
AT3G04050	AT3G53360	AT1G21930	AT2G03140
AT4G03140	AT3G27870	AT1G70130	AT1G02890
AT4G15990	AT3G55160	AT2G20320	AT4G26680
AT2G20560	AT2G17525	AT4G28930	AT1G66180
AT1G71140	AT1G72180	AT5G47980	AT5G19740
AT2G34210	AT1G21630	AT5G52700	AT3G50370
AT1G61610	AT5G46460	AT1G08590	AT3G63070
AT1G72890	AT1G50180	AT2G16230	AT5G13770
AT3G28930	AT3G28690	AT4G22217	AT1G17450
AT1G67980	AT1G17600	AT2G07678	AT5G10800
AT4G39640	AT2G07676	AT5G27950	AT1G64310
AT1G54030	AT3G09162	AT2G14290	AT3G24190
AT1G06160	AT4G00910	AT2G22770	AT4G02660
AT4G01470	AT1G63540	AT3G05690	AT1G62310
	AT2G17930	AT4G09030	AT2G32240
	AT5G41780	AT2G22470	AT5G46450
	AT2G22070	AT5G25250	AT1G26270
	AT1G16800	AT2G47275	AT5G02860
	AT3G47110	AT1G31885	AT1G27180
	AT3G18840	AT3G54700	AT3G22275
	AT1G03540	AT2G26560	AT1G35660
	AT1G79710	AT1G11180	AT1G52320
	AT3G05340	AT1G22150	AT2G31970
	AT4G17140	AT4G23920	AT1G76990
	AT1G53800	AT2G26660	AT5G40820
	AT1G74580		AT4G01820
	AT2G07751		AT1G30410
	AT5G24350		AT1G19220
	AT5G37130		AT2G28470
	AT4G16920		AT4G19020
	AT4G31210		AT3G05680
	AT1G73710		AT3G04340
	AT4G19530		AT5G19820
	AT5G20610		AT5G64390
	AT1G67120		AT1G50840
	AT5G14880		AT5G02310
	AT1G22060		AT4G11110
	AT2G25730		AT1G04110
	AT3G14460		AT1G12280
	AT3G11964		AT4G16890
	AT3G06530		AT1G70320
	AT4G20362		
	AT4G05631		
	AT5G59650		
	AT3G54580		
	AT4G36140		
	AT2G07673		
	AT2G15900		
	AT5G05400		
	AT2G01910		
	AT1G24706		
	AT4G18600		
	AT3G47930		
	AT1G80070		
	AT3G02260		
	AT2G01950		
	AT1G06490		
	AT2G22125		
	AT4G00450		
	AT3G27170		

AT2G18760
AT4G09680
AT1G01040
AT5G13010
AT5G46330
AT3G14270
AT5G47820
AT3G07160
AT2G31960
AT1G16710
AT5G13530
AT4G08480
AT4G14760
AT4G02710
AT4G32850
AT1G79280
AT4G30710
AT1G67500
AT3G27670
AT1G02500
AT2G38440
AT3G26030
AT4G15180
AT5G42400
AT4G16340
AT1G55860
AT3G06290

-Pi$_t$ Shoot 16 dat

Hypermethylated		**Hypomethylated**	
Upregulated	**Downregulated**	**Upregulated**	**Downregulated**
AT1G67520	AT1G12730	AT1G36622	AT2G47020
AT5G41750	AT4G03100	AT2G45920	AT2G32500
AT4G20460	AT5G14120	AT2G18150	AT1G29560
AT2G38823	AT1G57770	AT1G61370	AT5G28415
AT1G21940	AT5G26730	AT2G04495	AT5G26670
AT4G23000	AT1G19720	AT5G15480	AT5G51150
AT4G09780	AT5G15780	AT4G01700	AT2G21045
AT1G68850	AT1G24160	AT1G26390	AT4G21250
AT5G39110	AT3G44755	AT2G18690	AT1G66180
AT4G04990	AT1G34047	AT2G42980	AT1G68400
AT3G59570	AT5G14020	AT4G01350	AT5G49152
AT5G24200	AT2G30600	AT3G49980	AT5G28262
AT5G41280	AT4G20430	AT4G00500	AT1G63100
AT2G43880	AT4G36470	AT4G10500	AT5G17165
AT4G10260	AT5G44410	AT3G14470	AT4G16008
AT2G41730	AT2G05540	AT2G14878	AT5G19740
AT3G45330	AT3G09080	AT1G26410	AT3G52490
AT2G15780	AT2G14760	AT1G21529	AT2G15880
AT1G69790	AT5G06670	AT3G22850	AT5G57100
AT3G43110	AT2G25160	AT2G04400	AT3G53680
AT2G05580	AT5G28840	AT1G61360	AT1G30870
AT2G02720	AT3G49290	AT5G35425	AT3G04450
AT5G52710	AT2G14170	AT1G02470	AT4G28410
AT3G28210	AT1G20650	AT4G33770	AT5G28630
AT1G32960	AT4G26320	AT5G25260	AT5G13770
AT4G12120	AT3G21090	AT4G14368	AT4G01330
AT4G08870	AT3G18290	AT5G63680	AT5G27890
AT1G02520	AT4G37610	AT5G45720	AT3G46600
AT2G14580	AT5G57180	AT3G03790	AT5G35170
AT3G03640	AT5G37630	AT3G14700	AT5G04960
AT3G21520	AT5G06640	AT5G45000	AT2G15960

AT1G54040
AT1G62540
AT2G26150
AT2G11810
AT1G01010
AT1G62580
AT2G22860
AT1G07390
AT3G11570

AT2G24980
AT3G60530
AT3G47340
AT5G54280
AT1G60800
AT4G16370
AT1G34355
AT5G01180
AT5G04230
AT1G32060
AT5G52920
AT2G01918
AT1G67710
AT3G10710
AT3G13065
AT5G63920
AT1G70290
AT5G01360
AT5G13740

AT3G43250
AT1G13340
AT1G62760
AT2G36724
AT2G18720
AT5G58620
AT5G23950
AT3G15518
AT5G15070
AT3G19970
AT1G26420
AT4G38560
AT1G63530
AT3G29970
AT5G17390
AT4G32250
AT1G28180
AT5G25930
AT4G36430
AT1G13470
AT4G39675
AT5G53048
AT1G35625
AT1G26380
AT5G55410
AT3G63380
AT2G15830
AT5G14550
AT4G10720
AT5G26690
AT1G61550
AT2G16870
AT3G10320
AT2G04070
AT4G15120
AT5G53110
AT1G08310
AT1G55790
AT1G32950
AT1G43910
AT3G62590
AT3G21700
AT3G48300
AT4G37370
AT4G39980
AT3G51970
AT1G17290
AT5G20960
AT4G09030
AT2G22470
AT3G59140
AT3G13100
AT5G13320
AT1G61810
AT5G17860
AT5G58940
AT4G23700
AT1G29230
AT1G21250
AT1G01340
AT3G17690
AT4G04490
AT4G04510
AT4G04540
AT2G39770
AT2G04040

AT2G05632
AT1G78020
AT1G33640
AT3G16180
AT3G18845
AT1G67870
AT5G37010
AT3G01310
AT3G22142
AT5G07570
AT1G09460
AT1G50732
AT1G52870
AT4G20820
AT1G74770
AT2G16140
AT5G44530
AT1G61760
AT3G07070
AT3G22150
AT1G64720
AT1G20080
AT5G28080
AT5G36120
AT3G48290
AT3G26310
AT3G14630
AT1G24540
AT1G49720
AT3G25690
AT5G52100
AT3G42670
AT2G28190
AT4G08920
AT2G26760
AT3G01480
AT4G14140
AT4G05520
AT4G13390
AT1G50240
AT4G04330
AT3G54590
AT4G16480
AT1G05360
AT2G46740
AT4G10340
AT4G25560
AT5G35407
AT3G60840
AT2G01530
AT3G08500
AT1G70760
AT2G23050
AT2G34710
AT2G33770
AT5G26570
AT1G61520
AT3G55980
AT5G63780
AT1G53160
AT2G29630
AT5G46700
AT5G55820

		AT4G25640	
		AT4G34200	
		AT4G00900	
		AT1G70140	
		AT5G39190	
		AT3G47420	
		AT4G28490	
		AT4G37680	
		AT1G51760	
		AT1G51800	
		AT3G45140	
		AT2G36530	
		AT3G59884	
		AT2G25680	
		AT5G20410	
		AT2G19900	
		AT2G22560	
		AT1G37130	
		AT3G61990	
		AT2G40180	
		AT5G43350	
		AT1G53310	
		AT5G56630	
		AT3G05630	
		AT2G26010	
		AT2G18660	
		AT1G52940	
		AT3G53620	
		AT3G26090	
		AT4G21470	
		AT1G12210	
		AT3G08720	
		AT2G26660	
		AT5G66760	
		AT3G43190	
		AT4G02050	
		AT4G33030	
		AT1G74100	
		AT5G54810	
		AT3G56040	
		AT3G53150	
		AT1G24100	
		AT1G05620	
		AT5G24380	

-Pi$_t$ Root 16 dat

Hypermehylated		Hypomethylated	
Upregulated	Downregulated	Upregulated	Downregulated
AT4G16900	AT4G03380	AT5G02180	AT5G44578
AT4G13690	AT3G45070	AT2G47950	AT4G08300
AT4G37710	AT1G43140	AT2G18690	AT5G25040
AT3G23450	AT1G12730	AT2G22930	AT1G50050
AT5G26270	AT2G34100	AT4G00500	AT4G18250
AT4G23000	AT2G10560	AT4G08450	AT4G15590
AT1G63750	AT2G07676	AT1G21529	AT5G52790
AT5G26280	AT2G07687	AT2G36730	AT4G04930
AT1G67000	AT3G46490	AT4G33770	AT2G28470
AT5G39110	AT2G07675	AT4G02320	AT4G13390
AT1G26250	AT2G07722	AT4G05140	AT3G17320
AT4G04990	AT4G08290	AT5G14120	AT5G24920
AT2G07698	AT2G05790	AT3G26614	AT5G55250
AT1G45015	AT2G07751	AT1G63540	AT3G58810

AT2G41730
AT5G42930
AT1G20390
AT2G12200
AT1G26240
AT2G07671
AT2G15220
AT5G27845
AT1G32970
AT5G57610
AT3G45720
AT5G38910
AT5G67340
AT4G10060
AT1G57630
AT4G39210
AT1G12240
AT1G32200
AT1G68050
AT2G29940
AT2G46530
AT1G47960
AT4G23600
AT1G62560
AT5G14780
AT2G32400
AT1G30560
AT2G05520
AT1G55020
AT3G14720
AT5G22300
AT1G20860
AT2G05620
AT3G09910
AT1G11720
AT5G20280
AT3G54670
AT1G30530
AT2G07682
AT2G07777
AT2G19660
AT2G07721
AT1G47400
AT4G22460
AT1G34047
AT1G36240
AT3G14730
AT5G45230
AT2G34290
AT3G54580
AT2G07673
AT1G44835
AT4G19980
AT1G44030
AT2G28250
AT2G02120
AT5G06905
AT2G13540
AT3G21090
AT4G21760
AT5G45380
AT1G48300
AT3G42640
AT4G30110
AT1G71920
AT4G18120
AT2G16640
AT4G37590
AT5G04950
AT1G08090
AT1G74260
AT1G62280
AT1G20840
AT5G40850
AT1G16160
AT5G45105
AT3G30340
AT3G44510
AT1G33030
AT5G64000
AT4G39980
AT5G05730
AT2G04040
AT3G11670
AT1G78360
AT3G47420
AT3G46330
AT3G59884
AT1G63020
AT1G16370
AT1G73220
AT1G21230
AT2G26660
AT1G30510
AT3G48260

Table S5. List of differentially methylated PSR genes (Pi-methDEGs). Locus ID and gene description of Pi-methDEGs is shown. Pi-methDEGs are arranged by methylation direction (Hypermethylation, Hypomethylation) and by expression (Upregulated, Downregulated).

Hypermethylated

Upregulated

Locus ID	Gene Description
AT4G16900	Disease resistance protein (TIR-NBS-LRR class) family
AT1G67520	lectin protein kinase family protein
AT5G41750	Disease resistance protein (TIR-NBS-LRR class) family
AT4G13690	unknown protein
AT4G37710	VQ motif-containing protein
AT3G23450	unknown protein
AT5G26270	unknown protein
AT1G58280	Phosphoglycerate mutase family protein
AT2G18530	Protein kinase superfamily protein
AT5G37840	unknown protein
AT4G20460	NAD(P)-binding Rossmann-fold superfamily protein
AT2G38823	unknown protein
AT1G21940	unknown protein
AT1G61480	S-locus lectin protein kinase family protein
AT4G23000	Calcineurin-like metallo-phosphoesterase superfamily protein
AT1G63750	Disease resistance protein (TIR-NBS-LRR class) family
AT5G26280	TRAF-like family protein
AT4G09780	TRAF-like family protein
AT1G67000	Protein kinase superfamily protein
AT1G68850	Peroxidase superfamily protein
AT5G20790	unknown protein
AT1G54095	Protein of unknown function (DUF1677)
AT5G39110	RmlC-like cupins superfamily protein
AT1G26250	Proline-rich extensin-like family protein
AT4G04990	Protein of unknown function (DUF761)
AT4G14090	Anthocyanidin 5-O-glucosyltransferase
AT3G17190	unknown protein
AT4G15270	glucosyltransferase-related
AT3G04050	Pyruvate kinase family protein
AT3G59570	Ypt/Rab-GAP domain of gyp1p superfamily protein
AT5G24200	alpha/beta-Hydrolases superfamily protein
AT4G03140	NAD(P)-binding Rossmann-fold superfamily protein
AT2G07698	ATPase, F1 complex, alpha subunit protein
AT1G45015	MD-2-related lipid recognition domain-containing protein
AT5G41280	Receptor-like protein kinase-related family protein
AT2G43880	Pectin lyase-like superfamily protein
AT4G10260	pfkB-like carbohydrate kinase family protein
AT4G15990	unknown protein
AT2G41730	unknown protein
AT5G42930	alpha/beta-Hydrolases superfamily protein
AT1G20390	transposable element gene
AT2G12200	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT3G45330	Concanavalin A-like lectin protein kinase family protein
AT1G26240	Proline-rich extensin-like family protein
AT2G07671	ATP synthase subunit C family protein
AT2G15780	Cupredoxin superfamily protein
AT2G04100	MATE efflux family protein
AT2G15220	Plant basic secretory protein (BSP) family protein

AT1G64610	Transducin/WD40 repeat-like superfamily protein
AT5G27845	transposable element gene
AT2G20560	DNAJ heat shock family protein
AT1G32970	Subtilisin-like serine endopeptidase family protein
AT1G71140	MATE efflux family protein
AT2G34210	Transcription elongation factor Spt5
AT1G69790	Protein kinase superfamily protein
AT3G14205	Phosphoinositide phosphatase family protein
AT5G07570	glycine/proline-rich protein
AT5G57610	Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain
AT1G61610	S-locus lectin protein kinase family protein
AT3G43110	unknown protein
AT2G05580	Glycine-rich protein family
AT1G66360	Calcium-dependent lipid-binding (CaLB domain) family protein
AT3G45720	Major facilitator superfamily protein
AT2G02720	Pectate lyase family protein
AT5G38910	RmlC-like cupins superfamily protein
AT5G67340	ARM repeat superfamily protein
AT5G52710	Copper transport protein family
AT4G10060	Beta-glucosidase, GBA2 type family protein
AT1G57630	Toll-Interleukin-Resistance (TIR) domain family protein
AT1G72890	Disease resistance protein (TIR-NBS class)
AT4G39210	(APL3)
AT1G12240	(ATBETAFRUCT4)
AT1G32200	(ATS1)
AT3G28210	(PMZ)
AT1G32960	(SBT3.3)
AT4G12120	(SEC1B)
AT1G68050	FLAVIN-BINDING, KELCH REPEAT, F BOX 1 (FKF1)
AT1G72330	ALANINE AMINOTRANSFERASE 2 (ALAAT2)
AT4G08870	ARGININE AMIDOHYDROLASE 2 (ARGAH2)
AT1G02520	ATP-BINDING CASSETTE B11 (ABCB11)
AT2G47000	ATP-BINDING CASSETTE B4 (ABCB4)
AT2G29940	ATP-BINDING CASSETTE G31 (ABCG31)
AT2G46530	AUXIN RESPONSE FACTOR 11 (ARF11)
AT3G28930	AVRRPT2-INDUCED GENE 2 (AIG2)
AT2G14580	BASIC PATHOGENESIS-RELATED PROTEIN 1 (PRB1)
AT3G03640	BETA GLUCOSIDASE 25 (BGLU25)
AT1G67980	CAFFEOYL-COA 3-O-METHYLTRANSFERASE (CCOAMT)
AT1G79400	CATION/H+ EXCHANGER 2 (CHX2)
AT1G47960	CELL WALL / VACUOLAR INHIBITOR OF FRUCTOSIDASE 1 (C/VIF1)
AT4G23600	CORONATINE INDUCED 1 (CORI3)
AT3G21520	DUF679 DOMAIN MEMBRANE PROTEIN 1 (DMP1)
AT1G54040	EPITHIOSPECIFIER PROTEIN (ESP)
AT1G62540	FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 2 (FMO GS-OX2)
AT1G62560	FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 3 (FMO GS-OX3)
AT5G14780	FORMATE DEHYDROGENASE (FDH)
AT4G39640	GAMMA-GLUTAMYL TRANSPEPTIDASE 1 (GGT1)
AT2G32400	GLUTAMATE RECEPTOR 5 (GLR5)
AT1G74590	GLUTATHIONE S-TRANSFERASE TAU 10 (GSTU10)
AT3G09270	GLUTATHIONE S-TRANSFERASE TAU 8 (GSTU8)
AT1G30560	GLYCEROL-3-PHOSPHATE PERMEASE 3 (G3Pp3)
AT2G05520	GLYCINE-RICH PROTEIN 3 (GRP-3)
AT2G26150	HEAT SHOCK TRANSCRIPTION FACTOR A2 (HSFA2)
AT2G34600	JASMONATE-ZIM-DOMAIN PROTEIN 7 (JAZ7)
AT1G55020	LIPOXYGENASE 1 (LOX1)
AT5G27600	LONG-CHAIN ACYL-COA SYNTHETASE 7 (LACS7)
AT3G14720	MAP KINASE 19 (MPK19)

AT1G54030	MODIFIED VACUOLE PHENOTYPE 1 (MVP1)
AT2G11810	MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE TYPE C (MGDC)
AT4G37670	N-ACETYL-L-GLUTAMATE SYNTHASE 2 (NAGS2)
AT1G01010	NAC DOMAIN CONTAINING PROTEIN 1 (NAC001)
AT1G62580	NITRIC OXIDE-DEPENDENT GUANYLATE CYCLASE 1 (NOGC1)
AT5G22300	NITRILASE 4 (NIT4)
AT1G06160	OCTADECANOID-RESPONSIVE ARABIDOPSIS AP2/ERF 59 (ORA59)
AT1G20860	PHOSPHATE TRANSPORTER 1;8 (PHT1;8)
AT2G22860	PHYTOSULFOKINE 2 PRECURSOR (PSK2)
AT2G05620	PROTON GRADIENT REGULATION 5 (PGR5)
AT2G16430	PURPLE ACID PHOSPHATASE 10 (PAP10)
AT3G09910	RAB GTPASE HOMOLOG C2B (RABC2b)
AT1G07390	RECEPTOR LIKE PROTEIN 1 (RLP1)
AT1G11720	STARCH SYNTHASE 3 (SS3)
AT5G20280	SUCROSE PHOSPHATE SYNTHASE 1F (SPS1F)
AT3G54670	TITAN8 (TTN8)
AT4G01470	TONOPLAST INTRINSIC PROTEIN 1;3 (TIP1;3)
AT3G11570	TRICHOME BIREFRINGENCE-LIKE 8 (TBL8)
AT1G30530	UDP-GLUCOSYL TRANSFERASE 78D1 (UGT78D1)
AT4G25960	ATP-BINDING CASSETTE B2 (ABCB2)
AT2G04460	transposable element gene

Hypermethylated

Downregulated

Locus ID	**Gene Description**
AT1G68440	unknown protein
AT2G35920	RNA helicase family protein
AT4G03380	unknown protein
AT2G15980	Tetratricopeptide repeat (TPR)-like superfamily protein
AT3G53360	Tetratricopeptide repeat (TPR)-like superfamily protein
AT3G27870	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein
AT3G45070	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT1G43140	Cullin family protein
AT1G12730	GPI transamidase subunit PIG-U
AT4G03100	Rho GTPase activating protein with PAK-box/P21-Rho-binding domain
AT5G14120	Major facilitator superfamily protein
AT3G55160	unknown protein
AT5G18030	SAUR-like auxin-responsive protein family
AT2G17525	Pentatricopeptide repeat (PPR) superfamily protein
AT1G72180	Leucine-rich receptor-like protein kinase family protein
AT1G21630	Calcium-binding EF hand family protein
AT5G46460	Pentatricopeptide repeat (PPR) superfamily protein
AT3G46240	unknown protein
AT1G29450	SAUR-like auxin-responsive protein family
AT1G50180	NB-ARC domain-containing disease resistance protein
AT2G34100	unknown protein
AT1G57770	FAD/NAD(P)-binding oxidoreductase family protein
AT2G10560	unknown protein
AT5G26730	Fasciclin-like arabinogalactan family protein
AT3G51870	Mitochondrial substrate carrier family protein
AT3G28690	Protein kinase superfamily protein
AT1G17600	Disease resistance protein (TIR-NBS-LRR class) family
AT1G19720	Pentatricopeptide repeat (PPR-like) superfamily protein

AT2G07676	unknown protein
AT3G09162	unknown protein
AT4G34730	ribosome-binding factor A family protein
AT4G00910	Aluminium activated malate transporter family protein
AT2G07687	Cytochrome c oxidase, subunit II
AT1G63540	hydroxyproline-rich glycoprotein family protein
AT2G17930	Phosphatidylinositol 3- and 4-kinase family protein with FAT domain
AT5G15780	Pollen Ole e 1 allergen and extensin family protein
AT5G41780	myosin heavy chain-related
AT5G66520	Tetratricopeptide repeat (TPR)-like superfamily protein
AT2G22070	pentatricopeptide (PPR) repeat-containing protein
AT1G16800	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT3G47110	Leucine-rich repeat protein kinase family protein
AT3G46490	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT3G18840	Tetratricopeptide repeat (TPR)-like superfamily protein
AT1G03540	Pentatricopeptide repeat (PPR-like) superfamily protein
AT1G79710	Major facilitator superfamily protein
AT3G05340	Tetratricopeptide repeat (TPR)-like superfamily protein
AT2G07675	Ribosomal protein S12/S23 family protein
AT2G07722	unknown protein
AT4G08290	nodulin MtN21-like transporter family protein
AT5G10340	F-box family protein; CONTAINS InterPro DOMAIN/s
AT4G17140	pleckstrin homology (PH) domain-containing protein
AT1G24160	unknown protein
AT1G53800	unknown protein
AT1G74580	Pentatricopeptide repeat (PPR) superfamily protein
AT2G05790	O-Glycosyl hydrolases family 17 protein
AT2G07751	NADH:ubiquinone/plastoquinone oxidoreductase, chain 3 protein
AT5G24350	unknown protein
AT5G37130	Protein prenylyltransferase superfamily protein
AT4G16920	Disease resistance protein (TIR-NBS-LRR class) family
AT2G07682	transposable element gene
AT3G44755	unknown protein
AT2G07777	ATP synthase 9 mitochondria
AT4G31210	DNA topoisomerase, type IA, core
AT1G73710	Pentatricopeptide repeat (PPR) superfamily protein
AT4G19530	Encodes a TIR-NB-LRR resistance protein
AT2G19660	Cysteine/Histidine-rich C1 domain family protein
AT2G07721	unknown protein
AT1G47400	unknown protein
AT4G22460	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT1G34047	Encodes a defensin-like (DEFL) family protein
AT1G49990	F-box family protein
AT5G20610	unknown protein
AT1G36240	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein
AT3G14730	Pentatricopeptide repeat (PPR) superfamily protein
AT1G67120	nucleoside-triphosphatase
AT3G54770	RNA-binding (RRM/RBD/RNP motifs) family protein
AT5G14880	Potassium transporter family protein
AT5G14020	Endosomal targeting BRO1-like domain-containing protein
AT2G30600	BTB/POZ domain-containing protein
AT1G22060	unknown protein
AT4G20430	Subtilase family protein
AT4G36470	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT5G44410	FAD-binding Berberine family protein
AT5G45230	Disease resistance protein (TIR-NBS-LRR class) family
AT2G25730	unknown protein
AT3G14460	LRR and NB-ARC domains-containing disease resistance protein

AT3G11964	RNA binding protein
AT2G05540	Glycine-rich protein family
AT3G06530	ARM repeat superfamily protein
AT3G48420	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
AT2G34290	Protein kinase superfamily protein
AT3G09080	Transducin/WD40 repeat-like superfamily protein
AT4G20362	Potential natural antisense gene
AT4G05631	unknown protein
AT5G59650	Leucine-rich repeat protein kinase family protein
AT3G54580	Proline-rich extensin-like family protein
AT2G04795	unknown protein
AT4G36140	disease resistance protein (TIR-NBS-LRR class)
AT2G14760	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT5G06670	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT2G07673	unknown protein
AT2G15900	Phox-associated domain
AT1G44835	YbaK/aminoacyl-tRNA synthetase-associated domain
AT4G19980	unknown protein
AT5G05400	LRR and NB-ARC domains-containing disease resistance protein
AT1G44030	Cysteine/Histidine-rich C1 domain family protein
AT2G25900	A. THALIANA TANDEM ZINC FINGER PROTEIN 1 (ATCTH)
AT2G01910	(ATMAP65-6)
AT4G17460	(HAT1)
AT2G28250	(NCRK)
AT2G02120	(PDF2.1)
AT1G24706	(THO2)
AT4G18600	(WAVE5)
AT5G06905	CYTOCHROME P450, FAMILY 712, SUBFAMILY A, POLYPEPTIDE 2 (CYP712A2)
AT2G25160	CYTOCHROME P450, FAMILY 82, SUBFAMILY F, POLYPEPTIDE 1 (CYP82F1)
AT5G28840	GDP-D-MANNOSE 3',5'-EPIMERASE (GME)
AT3G47930	L-GALACTONO-1,4-LACTONE DEHYDROGENASE (GLDH)
AT2G13540	ABA HYPERSENSITIVE 1 (ABH1)
AT3G49290	ABL INTERACTOR-LIKE PROTEIN 2 (ABIL2)
AT1G80070	ABNORMAL SUSPENSOR 2 (SUS2)
AT2G14170	ALDEHYDE DEHYDROGENASE 6B2 (ALDH6B2)
AT1G20650	ALTERED SEED GERMINATION 5 (ASG5)
AT1G08430	ALUMINUM-ACTIVATED MALATE TRANSPORTER 1 (ALMT1)
AT4G26320	ARABINOGALACTAN PROTEIN 13 (AGP13)
AT1G64950	CYTOCHROME P450, FAMILY 89, SUBFAMILY A, POLYPEPTIDE 5 (CYP89A5)
AT3G21090	ATP-BINDING CASSETTE G15 (ABCG15)
AT4G21760	BETA-GLUCOSIDASE 47 (BGLU47)
AT3G02260	BIG (BIG)
AT2G01950	BRI1-LIKE 2 (BRL2)
AT3G18290	BRUTUS (BTS)
AT4G37610	BTB AND TAZ DOMAIN PROTEIN 5 (bt5)
AT1G06490	CALLOSE SYNTHASE 7 (CalS7)
AT4G35090	CATALASE 2 (CAT2)
AT2G22125	CELLULOSE SYNTHASE-INTERACTIVE PROTEIN 1 (CSI1)
AT4G00450	CENTER CITY (CCT)
AT3G27170	CHLORIDE CHANNEL B (CLC-B)
AT5G57180	CHLOROPLAST IMPORT APPARATUS 2 (CIA2)
AT2G18760	CHROMATIN REMODELING 8 (CHR8)
AT4G09680	CONSERVED TELOMERE MAINTENANCE COMPONENT 1 (CTC1)
AT5G45380	DEGRADATION OF UREA 3 (DUR3)
AT1G48300	DIACYLGLYCEROL ACYLTRANSFERASE 3 (DGAT3)
AT1G01040	DICER-LIKE 1 (DCL1)
AT5G37630	EMBRYO DEFECTIVE 2656 (EMB2656)
AT5G13010	EMBRYO DEFECTIVE 3011 (EMB3011)

AT5G06640	EXTENSIN 10 (EXT10)
AT2G24980	EXTENSIN 6 (EXT6)
AT4G27030	FATTY ACID DESATURASE A (FADA)
AT5G46330	FLAGELLIN-SENSITIVE 2 (FLS2)
AT3G14270	FORMS APLOID AND BINUCLEATE CELLS 1B (FAB1B)
AT5G47820	FRAGILE FIBER 1 (FRA1)
AT4G09600	GAST1 PROTEIN HOMOLOG 3 (GASA3)
AT3G60530	GATA TRANSCRIPTION FACTOR 4 (GATA4)
AT3G07160	GLUCAN SYNTHASE-LIKE 10 (GSL10)
AT2G31960	GLUCAN SYNTHASE-LIKE 3 (GSL03)
AT3G47340	GLUTAMINE-DEPENDENT ASPARAGINE SYNTHASE 1 (ASN1)
AT3G42640	H(+)-ATPASE 8 (HA8)
AT4G30110	HEAVY METAL ATPASE 2 (HMA2)
AT1G71920	HISTIDINE BIOSYNTHESIS 6B (HISN6B)
AT1G16710	HISTONE ACETYLTRANSFERASE OF THE CBP FAMILY 12 (HAC12)
AT5G13530	KEEP ON GOING (KEG)
AT4G18120	MEI2-LIKE 3 (ML3)
AT2G17780	MID1-COMPLEMENTING ACTIVITY 2 (MCA2)
AT4G08480	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 9 (MAPKKK9)
AT2G16640	MULTIMERIC TRANSLOCON COMPLEX IN THE OUTER ENVELOPE MEMBRANE 132 (TOC132)
AT5G54280	MYOSIN 2 (ATM2)
AT4G37590	NAKED PINS IN YUC MUTANTS 5 (NPY5)
AT4G14760	NETWORKED 1B (NET1B)
AT4G02710	NETWORKED 1C (NET1C)
AT5G04950	NICOTIANAMINE SYNTHASE 1 (NAS1)
AT1G32450	NITRATE TRANSPORTER 1.5 (NRT1.5)
AT1G08090	NITRATE TRANSPORTER 2:1 (NRT2:1)
AT1G60800	NSP-INTERACTING KINASE 3 (NIK3)
AT4G32850	NUCLEAR POLY(A) POLYMERASE (nPAP)
AT1G79280	NUCLEAR PORE ANCHOR (NUA)
AT4G16370	OLIGOPEPTIDE TRANSPORTER (OPT3)
AT1G34355	PARALLEL SPINDLE 1 (PS1)
AT5G01180	PEPTIDE TRANSPORTER 5 (PTR5)
AT5G04230	PHENYL ALANINE AMMONIA-LYASE 3 (PAL3)
AT1G32060	PHOSPHORIBULOKINASE (PRK)
AT5G52920	PLASTIDIC PYRUVATE KINASE BETA SUBUNIT 1 (PKP-BETA1)
AT2G01918	PSBQ-LIKE 3 (PQL3)
AT1G74260	PURINE BIOSYNTHESIS 4 (PUR4)
AT4G30710	QWRF DOMAIN CONTAINING 8 (QWRF8)
AT1G67500	RECOVERY PROTEIN 3 (REV3)
AT1G67710	RESPONSE REGULATOR 11 (ARR11)
AT3G27670	RESURRECTION1 (RST1)
AT3G10710	ROOT HAIR SPECIFIC 12 (RHS12)
AT2G39730	RUBISCO ACTIVASE (RCA)
AT1G02500	S-ADENOSYLMETHIONINE SYNTHETASE 1 (SAM1)
AT2G38440	SCAR HOMOLOG 2 (SCAR2)
AT3G26030	SERINE/THREONINE PROTEIN PHOSPHATASE 2A 55 KDA REGULATORY SUBUNIT B PRIME DELTA
AT4G15180	SET DOMAIN PROTEIN 2 (SDG2)
AT5G42400	SET DOMAIN PROTEIN 25 (SDG25)
AT1G62280	SLAC1 HOMOLOGUE 1 (SLAH1)
AT4G16340	SPIKE1 (SPK1)
AT3G13065	STRUBBELIG-RECEPTOR FAMILY 4 (SRF4)
AT1G20840	TONOPLAST MONOSACCHARIDE TRANSPORTER1 (TMT1)
AT5G63920	TOPOISOMERASE 3ALPHA (TOP3A)
AT1G70290	TREHALOSE-6-PHOSPHATASE SYNTHASE S8 (TPS8)
AT5G01360	TRICHOME BIREFRINGENCE-LIKE 3 (TBL3)

AT1G55860	UBIQUITIN-PROTEIN LIGASE 1 (UPL1)
AT5G40850	UROPHORPHYRIN METHYLASE 1 (UPM1)
AT4G07400	VIER F-BOX PROTEINE 3 (VFB3)
AT1G16160	WALL ASSOCIATED KINASE-LIKE 5 (WAKL5)
AT3G06290	YEAST SAC3 HOMOLOG B (SAC3B)
AT5G13740	ZINC INDUCED FACILITATOR 1 (ZIF1)
AT5G45105	ZINC TRANSPORTER 8 PRECURSOR (ZIP8)

Hypomethylated

Upregulated

Locus ID	**Gene Description**
AT1G36622	unknown protein
AT5G02180	Transmembrane amino acid transporter family protein
AT2G45920	U-box domain-containing protein
AT2G18150	Peroxidase superfamily protein
AT3G47480	Calcium-binding EF-hand family protein
AT2G16676	unknown protein
AT4G27850	Glycine-rich protein family
AT1G61370	S-locus lectin protein kinase family protein
AT2G17500	Auxin efflux carrier family protein
AT2G04495	unknown protein
AT2G47950	unknown protein
AT5G15480	C2H2-type zinc finger family protein
AT4G01700	Chitinase family protein
AT1G21930	unknown protein
AT1G26390	FAD-binding Berberine family protein
AT2G18690	unknown protein
AT1G03940	HXXXD-type acyl-transferase family protein
AT1G70130	Concanavalin A-like lectin protein kinase family protein
AT2G20320	DENN (AEX-3) domain-containing protein
AT5G35050	Domain of unknown function DUF1985
AT2G42980	Eukaryotic aspartyl protease family protein
AT4G01350	Cysteine/Histidine-rich C1 domain family protein
AT2G22930	UDP-Glycosyltransferase superfamily protein
AT3G49980	F-box and associated interaction domains-containing protein
AT4G00500	alpha/beta-Hydrolases superfamily protein
AT4G08450	Disease resistance protein (TIR-NBS-LRR class) family
AT4G28930	unknown protein
AT4G10500	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT3G14470	NB-ARC domain-containing disease resistance protein
AT5G47980	HXXXD-type acyl-transferase family protein
AT2G14878	other RNA
AT1G26410	FAD-binding Berberine family protein
AT1G21529	other RNA
AT3G22850	Aluminium induced protein with YGL and LRDR motifs
AT2G36730	Pentatricopeptide repeat (PPR) superfamily protein
AT2G04400	Aldolase-type TIM barrel family protein
AT1G61360	S-locus lectin protein kinase family protein
AT5G35425	transposable element gene
AT1G02470	Polyketide cyclase/dehydrase and lipid transport superfamily protein
AT4G33770	Inositol 1,3,4-trisphosphate 5/6-kinase family protein
AT5G25260	SPFH/Band 7/PHB domain-containing membrane-associated protein family
AT4G14368	Regulator of chromosome condensation (RCC1) family protein
AT5G63680	Pyruvate kinase family protein

AT5G52700	Copper transport protein family
AT5G45720	AAA-type ATPase family protein
AT3G03790	ankyrin repeat family protein / regulator of chromosome condensation (RCC1) family protein
AT4G02320	Plant invertase/pectin methylesterase inhibitor superfamily
AT2G38250	Homeodomain-like superfamily protein
AT1G74270	Ribosomal protein L35Ae family protein
AT3G14700	SART-1 family
AT5G45000	Disease resistance protein (TIR-NBS-LRR class) family
AT3G43250	Family of unknown function (DUF572)
AT1G13340	Regulator of Vps4 activity in the MVB pathway protein
AT1G62760	Plant invertase/pectin methylesterase inhibitor superfamily protein
AT4G05140	Nucleoside transporter family protein
AT2G36724	unknown protein
AT2G18720	Translation elongation factor EF1A/initiation factor IF2gamma family protein
AT5G14120	Major facilitator superfamily protein
AT4G15540	nodulin MtN21-like transporter family protein
AT5G58620	zinc finger (CCCH-type) family protein
AT1G08590	similar to CLV1-like leucine rich repeat transmembrane receptor-like protein kinase
AT3G25610	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein
AT5G23950	Calcium-dependent lipid-binding (CaLB domain) family protein
AT3G09830	Protein kinase superfamily protein
AT3G15518	unknown protein
AT5G15070	Phosphoglycerate mutase-like family protein
AT3G19970	alpha/beta-Hydrolases superfamily protein
AT3G26614	transposable element gene; non-LTR retrotransposon family (LINE)
AT1G26420	FAD-binding Berberine family protein
AT1G63540	hydroxyproline-rich glycoprotein family protein
AT4G38560	Arabidopsis phospholipase-like protein (PEARLI 4) family
AT2G16230	O-Glycosyl hydrolases family 17 protein
AT3G30340	nodulin MtN21-like transporter family protein
AT1G63530	hydroxyproline-rich glycoprotein family protein
AT3G29970	B12D protein
AT4G22217	Encodes a defensin-like (DEFL) family protein
AT5G17390	Adenine nucleotide alpha hydrolases-like superfamily protein
AT1G49800	unknown protein
AT4G32250	Protein kinase superfamily protein
AT1G28180	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT5G25930	Protein kinase family protein with leucine-rich repeat domain
AT4G36430	Peroxidase superfamily protein
AT3G44510	alpha/beta-Hydrolases superfamily protein
AT1G13470	Protein of unknown function (DUF1262)
AT4G39675	unknown protein
AT5G53048	Potential natural antisense gene
AT1G33030	O-methyltransferase family protein
AT1G35625	RING/U-box superfamily protein
AT1G26380	FAD-binding Berberine family protein
AT2G07678	unknown protein
AT5G27950	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT5G55410	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT3G63380	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein
AT2G15830	unknown protein
AT5G14550	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein
AT4G10720	Ankyrin repeat family protein
AT5G26690	Heavy metal transport/detoxification superfamily protein
AT4G20210	Terpenoid cyclases/Protein prenyltransferases superfamily protein
AT1G61550	S-locus lectin protein kinase family protein
AT2G16870	Disease resistance protein (TIR-NBS-LRR class) family

AT3G10320	Glycosyltransferase family 61 protein
AT2G04070	MATE efflux family protein
AT4G15120	VQ motif-containing protein
AT2G14290	Protein of unknown function
AT5G53110	RING/U-box superfamily protein
AT1G08310	alpha/beta-Hydrolases superfamily protein
AT1G55790	Heavy metal transport/detoxification protein
AT1G32950	Subtilase family protein
AT1G43910	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT3G62590	alpha/beta-Hydrolases superfamily protein
AT4G22470	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
AT4G21390	(B120)
AT2G22770	(NAI1)
AT5G64000	(SAL2)
AT3G21700	(SGP2)
AT3G57240	BETA-1,3-GLUCANASE 3 (BG3)
AT3G48300	CYTOCHROME P450, FAMILY 71, SUBFAMILY A, POLYPEPTIDE 23 (CYP71A23)
AT4G37370	CYTOCHROME P450, FAMILY 81, SUBFAMILY D, POLYPEPTIDE 8 (CYP81D8)
AT3G56000	CELLULOSE SYNTHASE LIKE A14 (CSLA14)
AT3G05690	NUCLEAR FACTOR Y, SUBUNIT A2 (NF-YA2)
AT4G39980	3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE 1 (DHS1)
AT2G05710	ACONITASE 3 (ACO3)
AT3G51970	ACYL-COA STEROL ACYL TRANSFERASE 1 (ASAT1)
AT1G17290	ALANINE AMINOTRANSFERAS (AlaAT1)
AT5G20960	ALDEHYDE OXIDASE 1 (AO1)
AT5G05730	ANTHRANILATE SYNTHASE ALPHA SUBUNIT 1 (ASA1)
AT4G04610	APS REDUCTASE 1 (APR1)
AT4G09030	ARABINOGALACTAN PROTEIN 10 (AGP10)
AT2G22470	ARABINOGALACTAN PROTEIN 2 (AGP2)
AT3G59140	ATP-BINDING CASSETTE C10 (ABCC10)
AT3G13100	ATP-BINDING CASSETTE C7 (ABCC7)
AT5G13320	AVRPPHB SUSCEPTIBLE 3 (PBS3)
AT1G61810	BETA-GLUCOSIDASE 45 (BGLU45)
AT5G17860	CALCIUM EXCHANGER 7 (CAX7)
AT5G58940	CALMODULIN-BINDING RECEPTOR-LIKE CYTOPLASMIC KINASE 1 (CRCK1)
AT4G23700	CATION/H+ EXCHANGER 17 (CHX17)
AT1G29230	CBL-INTERACTING PROTEIN KINASE 18 (CIPK18)
AT1G21250	CELL WALL-ASSOCIATED KINASE (WAK1)
AT1G01340	CYCLIC NUCLEOTIDE GATED CHANNEL 10 (CNGC10)
AT3G17690	CYCLIC NUCLEOTIDE GATED CHANNEL 19 (CNGC19)
AT4G04490	CYSTEINE-RICH RLK (RECEPTOR-LIKE PROTEIN KINASE) 36 (CRK36)
AT4G04510	CYSTEINE-RICH RLK (RECEPTOR-LIKE PROTEIN KINASE) 38 (CRK38)
AT4G04540	CYSTEINE-RICH RLK (RECEPTOR-LIKE PROTEIN KINASE) 39 (CRK39)
AT2G39770	CYTOKINESIS DEFECTIVE 1 (CYT1)
AT2G04040	DETOXIFICATION 1 (DTX1)
AT4G25640	DETOXIFYING EFFLUX CARRIER 35 (DTX35)
AT3G11670	DIGALACTOSYL DIACYLGLYCEROL DEFICIENT 1 (DGD1)
AT4G34200	EMBRYO SAC DEVELOPMENT ARREST 9 (EDA9)
AT4G00900	ER-TYPE CA2+-ATPASE 2 (ECA2)
AT5G25250	FLOTILLIN 1 (FLOT1)
AT4G15200	FORMIN 3 (FH3)
AT1G70140	FORMIN 8 (FH8)
AT5G39190	GERMIN-LIKE PROTEIN 2 (GER2)
AT1G78360	GLUTATHIONE S-TRANSFERASE TAU 21 (GSTU21)
AT3G47420	GLYCEROL-3-PHOSPHATE PERMEASE 1 (G3Pp1)
AT4G28490	HAESA (HAE)
AT4G37680	HEPTAHELICAL PROTEIN 4 (HHP4)
AT1G51760	IAA-ALANINE RESISTANT 3 (IAR3)

AT1G51800	IMPAIRED OOMYCETE SUSCEPTIBILITY 1 (IOS1)
AT3G45140	LIPOXYGENASE 2 (LOX2)
AT1G17420	LIPOXYGENASE 3 (LOX3)
AT2G36530	LOW EXPRESSION OF OSMOTICALLY RESPONSIVE GENES 2 (LOS2)
AT3G46330	MATERNAL EFFECT EMBRYO ARREST 39 (MEE39)
AT2G47275	MICRORNA403 (MIR403)
AT3G59884	MICRORNA827A (MIR827A)
AT2G25680	MOLYBDATE TRANSPORTER 1 (MOT1)
AT5G20410	MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE 2 (MGD2)
AT2G19900	NADP-MALIC ENZYME 1 (NADP-ME1)
AT2G22560	NETWORKED 2D (NET2D)
AT1G37130	NITRATE REDUCTASE 2 (NIA2)
AT1G31885	NOD26-LIKE INTRINSIC PROTEIN 3;1 (NIP3;1)
AT1G63020	NUCLEAR RNA POLYMERASE D1A (NRPD1A)
AT3G61990	O-MTASE FAMILY 3 PROTEIN (OMTF3)
AT1G16370	ORGANIC CATION/CARNITINE TRANSPORTER 6 (OCT6)
AT1G73220	ORGANIC CATION/CARNITINE TRANSPORTER1 (OCT1)
AT3G20660	ORGANIC CATION/CARNITINE TRANSPORTER4 (OCT4)
AT5G39050	PHENOLIC GLUCOSIDE MALONYLTRANSFERASE 1 (PMAT1)
AT2G40180	PHOSPHATASE 2C5 (PP2C5)
AT5G43350	PHOSPHATE TRANSPORTER 1;1 (PHT1;1)
AT3G54700	PHOSPHATE TRANSPORTER 1;7 (PHT1;7)
AT1G53310	PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PPC1)
AT5G56630	PHOSPHOFRUCTOKINASE 7 (PFK7)
AT2G26560	PHOSPHOLIPASE A 2A (PLA2A)
AT3G05630	PHOSPHOLIPASE D P2 (PLDP2)
AT3G26840	PHYTYL ESTER SYNTHASE 2 (PES2)
AT2G26010	PLANT DEFENSIN 1.3 (PDF1.3)
AT2G18660	PLANT NATRIURETIC PEPTIDE A (PNP-A)
AT1G52940	PURPLE ACID PHOSPHATASE 5 (PAP5)
AT3G53620	PYROPHOSPHORYLASE 4 (PPa4)
AT3G26090	REGULATOR OF G-PROTEIN SIGNALING 1 (RGS1)
AT4G21470	RIBOFLAVIN KINASE/FMN HYDROLASE (FMN/FHY)
AT1G12210	RPS5-LIKE 1 (RFL1)
AT1G11180	SECRETORY CARRIER MEMBRANE PROTEIN 2 (SCAMP2)
AT3G08720	SERINE/THREONINE PROTEIN KINASE 2 (S6K2)
AT2G26660	SPX DOMAIN GENE 2 (SPX2)
AT4G08390	STROMAL ASCORBATE PEROXIDASE (SAPX)
AT5G66760	SUCCINATE DEHYDROGENASE 1-1 (SDH1-1)
AT3G43190	SUCROSE SYNTHASE 4 (SUS4)
AT1G66570	SUCROSE-PROTON SYMPORTER 7 (SUC7)
AT4G02050	SUGAR TRANSPORTER PROTEIN 7 (STP7)
AT1G22150	SULFATE TRANSPORTER 1;3 (SULTR1;3)
AT4G33030	SULFOQUINOVOSYLDIACYLGLYCEROL 1 (SQD1)
AT1G74100	SULFOTRANSFERASE 16 (SOT16)
AT5G54810	TRYPTOPHAN SYNTHASE BETA-SUBUNIT 1 (TSB1)
AT4G23920	UDP-D-GLUCOSE/UDP-D-GALACTOSE 4-EPIMERASE 2 (UGE2)
AT3G56040	UDP-GLUCOSE PYROPHOSPHORYLASE 3 (UGP3)
AT2G36750	UDP-GLUCOSYL TRANSFERASE 73C1 (UGT73C1)
AT3G53150	UDP-GLUCOSYL TRANSFERASE 73D1 (UGT73D1)
AT1G24100	UDP-GLUCOSYL TRANSFERASE 74B1 (UGT74B1)
AT1G05620	URIDINE-RIBOHYDROLASE 2 (URH2)
AT1G21240	WALL ASSOCIATED KINASE 3 (WAK3)
AT1G21230	WALL ASSOCIATED KINASE 5 (WAK5)
AT1G80840	WRKY DNA-BINDING PROTEIN 40 (WRKY40)
AT5G24380	YELLOW STRIPE LIKE 2 (YSL2)

Hypomethylated

Downregulated

Locus ID	Gene Description
AT2G47020	Peptide chain release factor 1
AT2G32500	Stress responsive alpha-beta barrel domain protein
AT1G74290	alpha/beta-Hydrolases superfamily protein
AT4G16900	Disease resistance protein (TIR-NBS-LRR class) family
AT2G17033	pentatricopeptide (PPR) repeat-containing protein
AT1G29560	Zinc finger C-x8-C-x5-C-x3-H type family protein
AT2G03140	alpha/beta-Hydrolases superfamily protein
AT5G28415	transposable element gene
AT1G02890	AAA-type ATPase family protein
AT1G12020	unknown protein
AT4G26680	Tetratricopeptide repeat (TPR)-like superfamily protein
AT5G44578	unknown protein
AT5G26670	Pectinacetylesterase family protein
AT4G08300	nodulin MtN21-like transporter family protein
AT5G51150	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein
AT2G15020	unknown protein
AT2G21045	Rhodanese/Cell cycle control phosphatase superfamily protein
AT4G21250	Sulfite exporter TauE/SafE family protein
AT1G66180	Putative aspartyl protease (ASP)
AT1G68400	leucine-rich repeat transmembrane protein kinase family protein
AT5G49152	Potential natural antisense gene
AT5G28262	Unknown gene
AT1G63100	GRAS family transcription factor
AT5G17165	unknown protein
AT4G16008	unknown protein
AT5G25040	Major facilitator superfamily protein
AT5G15360	unknown protein
AT5G19740	Peptidase M28 family protein
AT3G52490	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein
AT1G50050	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein
AT3G50370	unknown protein
AT2G26215	transposable element gene
AT2G15880	Leucine-rich repeat (LRR) family protein
AT3G63070	Tudor/PWWP/MBT domain-containing protein
AT5G57100	Nucleotide/sugar transporter family protein
AT3G53680	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain
AT1G30870	Peroxidase superfamily protein
AT3G04450	Homeodomain-like superfamily protein
AT4G28410	Tyrosine transaminase family protein
AT5G28630	glycine-rich protein
AT5G59070	UDP-Glycosyltransferase superfamily protein
AT3G01345	Expressed protein
AT5G13770	Pentatricopeptide repeat (PPR-like) superfamily protein
AT5G67385	Phototropic-responsive NPH3 family protein
AT4G01330	Protein kinase superfamily protein
AT1G67900	Phototropic-responsive NPH3 family protein
AT5G24155	FAD/NAD(P)-binding oxidoreductase family protein
AT5G27890	myosin heavy chain-related protein
AT4G18250	receptor serine/threonine kinase, putative

AT3G46600	GRAS family transcription factor
AT5G35170	adenylate kinase family protein
AT5G04960	Plant invertase/pectin methylesterase inhibitor superfamily
AT3G26490	Phototropic-responsive NPH3 family protein
AT1G17450	B-block binding subunit of TFIIIC
AT2G15960	unknown protein
AT5G10800	RNA recognition motif (RRM)-containing protein
AT2G05632	unknown protein
AT1G78020	Protein of unknown function (DUF581)
AT1G33640	unknown protein
AT1G64310	Tetratricopeptide repeat (TPR)-like superfamily protein
AT3G24190	Protein kinase superfamily protein
AT4G02660	Beige/BEACH domain ;WD domain, G-beta repeat protein
AT1G62310	transcription factor jumonji (jmjC) domain-containing protein
AT2G16270	unknown protein
AT3G16180	Major facilitator superfamily protein
AT3G18845	Encodes a Protease inhibitor/seed storage/LTP family protein [pseudogene]
AT1G67870	glycine-rich protein
AT5G38000	Zinc-binding dehydrogenase family protein
AT5G37010	unknown protein
AT2G32240	Protein coding
AT3G01310	Phosphoglycerate mutase-like family protein
AT4G38340	Plant regulator RWP-RK family protein
AT5G46450	Disease resistance protein (TIR-NBS-LRR class) family
AT3G22142	Encodes a Protease inhibitor/seed storage/LTP family protein
AT1G26270	Phosphatidylinositol 3- and 4-kinase family protein
AT5G07570	glycine/proline-rich protein
AT1G09460	Carbohydrate-binding X8 domain superfamily protein
AT5G02860	Pentatricopeptide repeat (PPR) superfamily protein
AT4G15590	transposable element gene
AT1G50732	unknown protein.
AT5G52790	Protein coding
AT1G52870	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein
AT4G20820	FAD-binding Berberine family protein
AT1G74770	zinc ion binding protein
AT1G27180	disease resistance protein (TIR-NBS-LRR class), putative
AT2G16140	transposable element gene
AT5G44530	Subtilase family protein
AT1G61760	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
AT3G07070	Protein kinase superfamily protein
AT3G22275	unknown protein
AT1G35660	unknown protein
AT1G52320	unknown protein
AT3G22150	Tetratricopeptide repeat (TPR)-like superfamily protein
AT1G64720	membrane related protein CP5 (CP5)
AT4G04930	(DES-1-LIKE)
AT2G31970	(RAD50)
AT1G20080	(SYTB)
AT5G28080	(WNK9)
AT5G36120	COFACTOR ASSEMBLY, COMPLEX C (B6F) (CCB3)
AT3G48290	CYTOCHROME P450, FAMILY 71, SUBFAMILY A, POLYPEPTIDE 24 (CYP71A24)
AT3G26310	CYTOCHROME P450, FAMILY 71, SUBFAMILY B, POLYPEPTIDE 35 (CYP71B35)
AT3G14630	CYTOCHROME P450, FAMILY 72, SUBFAMILY A, POLYPEPTIDE 9 (CYP72A9)
AT1G24540	CYTOCHROME P450, FAMILY 86, SUBFAMILY C, POLYPEPTIDE 1 (CYP86C1)
AT1G49720	ABSCISIC ACID RESPONSIVE ELEMENT-BINDING FACTOR 1 (ABF1)
AT1G76990	ACT DOMAIN REPEAT 3 (ACR3)
AT5G40820	ATAXIA TELANGIECTASIA-MUTATED AND RAD3-RELATED (ATR)
AT4G01820	ATP-BINDING CASSETTE B3 (ABCB3)

AT1G30410	ATP-BINDING CASSETTE C12 (ABCC12)
AT1G19220	AUXIN RESPONSE FACTOR 19 (ARF19)
AT2G28470	BETA-GALACTOSIDASE 8 (BGAL8)
AT3G25690	CHLOROPLAST UNUSUAL POSITIONING 1 (CHUP1)
AT5G52100	CHLORORESPIRATION REDUCTION 1 (crr1)
AT3G42670	CHROMATIN REMODELING 38 (CHR38)
AT4G19020	CHROMOMETHYLASE 2 (CMT2)
AT2G28190	COPPER/ZINC SUPEROXIDE DISMUTASE 2 (CSD2)
AT4G08920	CRYPTOCHROME 1 (CRY1)
AT2G26760	CYCLIN B1;4 (CYCB1;4)
AT3G21870	CYCLIN P2;1 (CYCP2;1)
AT3G01480	CYCLOPHILIN 38 (CYP38)
AT4G14140	DNA METHYLTRANSFERASE 2 (DMT2)
AT3G05680	EMBRYO DEFECTIVE 2016 (EMB2016)
AT3G04340	EMBRYO DEFECTIVE 2458 (emb2458)
AT5G19820	EMBRYO DEFECTIVE 2734 (emb2734)
AT4G05520	EPS15 HOMOLOGY DOMAIN 2 (EHD2)
AT4G13390	EXTENSIN 12 (EXT12)
AT3G17320	F-BOX OVEREXPRESSED/OPPRESSED ABA SIGNALING 1 (FOA1)
AT1G50240	FUSED (FU)
AT2G24720	GLUTAMATE RECEPTOR 2.2 (GLR2.2)
AT5G24920	GLUTAMINE DUMPER 5 (GDU5)
AT4G04330	HOMOLOGUE OF CYANOBACTERIAL RBCX 1 (RbcX1)
AT5G64390	HUA ENHANCER 4 (HEN4)
AT3G54590	HYDROXYPROLINE-RICH GLYCOPROTEIN (HRGP1)
AT5G55250	IAA CARBOXYLMETHYLTRANSFERASE 1 (IAMT1)
AT4G16480	INOSITOL TRANSPORTER 4 (INT4)
AT1G05360	KILLING ME SLOWLY 2 (KMS2)
AT2G46740	L -GULONO-1,4-LACTONE (L -GULL) OXIDASE 5 (GULLO5)
AT4G10340	LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM II 5 (LHCB5)
AT4G25560	LONG AFTER FAR-RED LIGHT 1 (LAF1)
AT3G58810	METAL TOLERANCE PROTEIN A2 (MTPA2)
AT5G35407	MICRORNA396B (MIR396B)
AT3G60840	MICROTUBULE-ASSOCIATED PROTEIN 65-4 (MAP65-4)
AT2G01530	MLP-LIKE PROTEIN 329 (MLP329)
AT3G08500	MYB DOMAIN PROTEIN 83 (MYB83)
AT1G70760	NADH DEHYDROGENASE-LIKE COMPLEX L (NdhL)
AT2G23050	NAKED PINS IN YUC MUTANTS 4 (NPY4)
AT5G09660	PEROXISOMAL NAD-MALATE DEHYDROGENASE 2 (PMDH2)
AT2G34710	PHABULOSA (PHB)
AT2G33770	PHOSPHATE 2 (PHO2)
AT5G26570	PHOSPHOGLUCAN WATER DIKINASE (PWD)
AT1G61520	PHOTOSYSTEM I LIGHT HARVESTING COMPLEX GENE 3 (LHCA3)
AT1G50840	POLYMERASE GAMMA 2 (POLGAMMA2)
AT2G18470	PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASE 4 (PERK4)
AT5G02310	PROTEOLYSIS 6 (PRT6)
AT1G30510	ROOT FNR 2 (RFNR2)
AT3G55980	SALT-INDUCIBLE ZINC FINGER 1 (SZF1)
AT5G63780	SHOOT APICAL MERISTEM ARREST 1 (SHA1)
AT4G11110	SPA1-RELATED 2 (SPA2)
AT1G53160	SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 4 (SPL4)
AT3G02850	STELAR K+ OUTWARD RECTIFIER (SKOR)
AT1G04110	STOMATAL DENSITY AND DISTRIBUTION 1 (SDD1)
AT1G12280	SUPPRESSOR OF MKK1 MKK2 2 (SUMM2)
AT4G16890	SUPPRESSOR OF NPR1-1, CONSTITUTIVE 1 (SNC1)
AT2G29630	THIAMINC (THIC)
AT5G46700	TORNADO 2 (TRN2)
AT1G70320	UBIQUITIN-PROTEIN LIGASE 2 (UPL2)

AT3G48260	WITH NO LYSINE (K) KINASE 3 (WNK3)
AT5G55820	WYRD (WYR)
AT1G65730	YELLOW STRIPE LIKE 7 (YSL7)

Table S6. Representative Pi starvation genes targeted by P factor DmCs (Pf-methDEGs). Arabidopsis Locus ID and Gene Descriptions of Pf-methDEGs are shown.

Locus ID	**Gene Description**
AT3G47420	PHOSPHATE STARVATION-INDUCED GENE 3 (*PS3*) $^{\text{Hypo, Up}}$
AT1G67710	RESPONSE REGULATOR 11 (*ARR11*) $^{\text{Hyper, Down}}$
AT3G59884	MICRORNA827A (MIR827A) $^{\text{Hypo, Up}}$
AT5G20410	MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE 2 (*MGD2*) $^{\text{Hypo, Up}}$
AT2G26660	SPX DOMAIN GENE 2 (*SPX2*) $^{\text{Hypo, Up}}$
AT2G16430	PURPLE ACID PHOSPHATASE 10 (*PAP10*) $^{\text{Hyper, Up}}$
AT4G33030	SULFOQUINOVOSYLDIACYLGLYCEROL 1 (*SQD1*) $^{\text{Hypo, Up}}$
AT3G11670	DIGALACTOSYL DIACYLGLYCEROL DEFICIENT 1 (*DGD1*) $^{\text{Hypo, Up}}$

$^{\text{Up}}$ Upregulated $^{\text{Down}}$ Downregulated
$^{\text{Hypo}}$ Hypo-methylated $^{\text{Hyper}}$ Hyper-methylated

Table S7. List of P factor differentially methylated DEGs (Pf-methDEGs).

Locus ID	**Gene Description**
AT2G47020	Peptide chain release factor 1
AT2G38250	Homeodomain-like superfamily protein
AT1G68440	unknown protein
AT1G74290	alpha/beta-Hydrolases superfamily protein
AT1G74270	Ribosomal protein L35Ae family protein
AT1G36622	unknown protein
AT2G15980	Tetratricopeptide repeat (TPR)-like superfamily protein
AT5G41750	Disease resistance protein (TIR-NBS-LRR class) family
AT3G27870	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein
AT1G29560	Zinc finger C-x8-C-x5-C-x3-H type family protein
AT3G23450	unknown protein
AT1G12020	unknown protein
AT5G26270	unknown protein
AT1G58280	Phosphoglycerate mutase family protein
AT1G12730	GPI transamidase subunit PIG-U
AT2G18150	Peroxidase superfamily protein
AT3G55160	unknown protein
AT2G18530	Protein kinase superfamily protein
AT3G47480	Calcium-binding EF-hand family protein
AT2G15020	unknown protein
AT3G46240	Receptor protein kinase-related protein
AT4G21250	Sulfite exporter TauE/SafE family protein
AT2G34100	unknown protein
AT1G68400	leucine-rich repeat transmembrane protein kinase family protein
AT1G61370	S-locus lectin protein kinase family protein
AT5G28262	Unknown gene
AT1G61480	S-locus lectin protein kinase family protein
AT3G51870	Mitochondrial substrate carrier family protein
AT3G28690	Protein kinase superfamily protein
AT1G19720	Pentatricopeptide repeat (PPR-like) superfamily protein
AT2G07676	unknown protein
AT5G15360	unknown protein
AT5G19740	Peptidase M28 family protein
AT2G07687	Cytochrome c oxidase, subunit III
AT1G63540	hydroxyproline-rich glycoprotein family protein
AT3G50370	unknown protein
AT5G15780	Pollen Ole e 1 allergen and extensin family protein
AT4G38560	Arabidopsis phospholipase-like protein (PEARLI 4) family
AT2G26215	Transposable element gene
AT3G47110	Leucine-rich repeat protein kinase family protein
AT2G15880	Leucine-rich repeat (LRR) family protein
AT3G18840	Tetratricopeptide repeat (TPR)-like superfamily protein
AT2G16230	O-Glycosyl hydrolases family 17 protein

AT3G04450	Homeodomain-like superfamily protein
AT4G14090	Anthocyanidin 5-O-glucosyltransferase, glucosylates the 5-position of the flavonoid A-ring.
AT3G17190	unknown protein
AT3G05340	Tetratricopeptide repeat (TPR)-like superfamily protein
AT2G07675	Ribosomal protein S12/S23 family protein
AT2G07722	unknown protein
AT1G03940	HXXXD-type acyl-transferase family protein
AT5G10340	F-box family protein
AT5G59070	UDP-Glycosyltransferase superfamily protein
AT3G01345	Expressed protein
AT4G17140	pleckstrin homology (PH) domain-containing protein
AT5G13770	Pentatricopeptide repeat (PPR-like) superfamily protein
AT5G67385	Phototropic-responsive NPH3 family protein
AT4G03140	NAD(P)-binding Rossmann-fold superfamily protein
AT2G05790	O-Glycosyl hydrolases family 17 protein
AT2G07751	NADH:ubiquinone/plastoquinone oxidoreductase, chain 3 protein
AT1G67900	Phototropic-responsive NPH3 family protein
AT5G25930	Protein kinase family protein with leucine-rich repeat domain
AT5G24155	FAD/NAD(P)-binding oxidoreductase family protein
AT2G07698	ATPase, F1 complex, alpha subunit protein
AT4G01350	Cysteine/Histidine-rich C1 domain family protein
AT5G04960	Plant invertase/pectin methylesterase inhibitor superfamily
AT4G00500	alpha/beta-Hydrolases superfamily protein
AT2G07682	gypsy-like retrotransposon family
AT4G08450	Disease resistance protein (TIR-NBS-LRR class) family
AT2G07777	ATP synthase 9 mitochondrial
AT4G39675	unknown protein
AT1G20390	gypsy-like retrotransposon family
AT2G07721	unknown protein
AT1G35625	RING/U-box superfamily protein
AT1G62310	transcription factor jumonji (jmjC) domain-containing protein
AT2G07678	unknown protein
AT1G26380	FAD-binding Berberine family protein
AT2G16270	unknown protein
AT2G07671	ATP synthase subunit C family protein
AT5G27950	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT1G49990	F-box family protein
AT2G04100	MATE efflux family protein
AT1G64610	Transducin/WD40 repeat-like superfamily protein
AT1G67870	glycine-rich protein
AT3G14730	Pentatricopeptide repeat (PPR) superfamily protein
AT1G61550	S-locus lectin protein kinase family protein
AT2G36730	Pentatricopeptide repeat (PPR) superfamily protein
AT2G20560	DNAJ heat shock family protein
AT3G22142	Encodes a Protease inhibitor/seed storage/LTP family protein
AT5G07570	glycine/proline-rich protein

AT5G02860	Pentatricopeptide repeat (PPR) superfamily protein
AT2G04400	Aldolase-type TIM barrel family protein
AT3G14460	LRR and NB-ARC domains-containing disease resistance protein
AT1G08310	alpha/beta-Hydrolases superfamily protein
AT3G09080	Transducin/WD40 repeat-like superfamily protein
AT1G27180	disease resistance protein (TIR-NBS-LRR class), putative
AT5G25260	SPFH/Band 7/PHB domain-containing membrane-associated protein family
AT5G63680	Pyruvate kinase family protein
AT5G52700	Copper transport protein family
AT5G45720	AAA-type ATPase family protein
AT3G54580	Proline-rich extensin-like family protein
AT2G02720	Pectate lyase family protein
AT4G22470	protease inhibitor/seed storage/lipid transfer protein (LTP) family protei
AT5G67340	ARM repeat superfamily protein
AT2G07673	unknown protein
AT5G05400	LRR and NB-ARC domains-containing disease resistance protein
AT3G03790	ankyrin repeat family protein / regulator of chromosome condensation (RCC1) family protein
AT2G25900	(ATCTH)
AT4G21390	(B120)
AT4G17460	(HAT1)
AT1G32960	(SBT3.3)
AT1G24706	(THO2)
AT1G68050	FLAVIN-BINDING, KELCH REPEAT, F BOX 1 (FKF1)
AT3G05690	NUCLEAR FACTOR Y, SUBUNIT A2 (NF-YA2)
AT2G13540	ABA HYPERSENSITIVE 1 (ABH1)
AT2G05710	ACONITASE 3 (ACO3)
AT3G51970	ACYL-COA STEROL ACYL TRANSFERASE 1 (ASAT1)
AT1G72330	ALANINE AMINOTRANSFERASE 2 (ALAAT2)
AT2G14170	ALDEHYDE DEHYDROGENASE 6B2 (ALDH6B2)
AT3G25610	AMINOPHOSPHOLIPID ATPASE10 (ALA10)
AT4G04610	APS REDUCTASE 1 (APR1)
AT4G08870	ARGININE AMIDOHYDROLASE 2 (ARGAH2)
AT5G40820	ATAXIA TELANGIECTASIA-MUTATED AND RAD3-RELATED (ATR)
AT4G01820	ATP-BINDING CASSETTE B3 (ABCB3)
AT2G47000	ATP-BINDING CASSETTE B4 (ABCB4)
AT3G59140	ATP-BINDING CASSETTE C10 (ABCC10)
AT1G30410	ATP-BINDING CASSETTE C12 (ABCC12)
AT2G29940	ATP-BINDING CASSETTE G31 (ABCG31)
AT2G46530	AUXIN RESPONSE FACTOR 11 (ARF11)
AT3G57240	BETA-1,3-GLUCANASE 3 (BG3)
AT2G01950	BRI1-LIKE 2 (BRL2)
AT3G18290	BRUTUS (BTS)
AT4G37610	BTB AND TAZ DOMAIN PROTEIN 5 (bt5)
AT1G06490	CALLOSE SYNTHASE 7 (CalS7)
AT4G35090	CATALASE 2 (CAT2)
AT4G23700	CATION/H+ EXCHANGER 17 (CHX17)

AT1G79400	CATION/H+ EXCHANGER 2 (CHX2)
AT1G47960	CELL WALL / VACUOLAR INHIBITOR OF FRUCTOSIDASE 1 (C/VIF1)
AT1G21250	CELL WALL-ASSOCIATED KINASE 1 (WAK1)
AT4G00450	CENTER CITY (CCT)
AT5G66520	CHLOROPLAST RNA EDITING FACTOR 7 (CREF7)
AT3G25690	CHLOROPLAST UNUSUAL POSITIONING 1 (CHUP1)
AT2G18760	CHROMATIN REMODELING 8 (CHR8)
AT2G26760	CYCLIN B1;4 (CYCB1;4)
AT3G21870	CYCLIN P2;1 (CYCP2;1)
AT4G04490	CYSTEINE-RICH RLK (RECEPTOR-LIKE PROTEIN KINASE) 36 (CRK36)
AT4G04510	CYSTEINE-RICH RLK (RECEPTOR-LIKE PROTEIN KINASE) 38 (CRK38)
AT2G39770	CYTOKINESIS DEFECTIVE 1 (CYT1)
AT1G01040	DICER-LIKE 1 (DCL1)
AT3G11670	DIGALACTOSYL DIACYLGLYCEROL DEFICIENT 1 (DGD1)
AT4G10500	DMR6-LIKE OXYGENASE 1 (DLO1)
AT4G14140	DNA METHYLTRANSFERASE 2 (DMT2)
AT5G37630	EMBRYO DEFECTIVE 2656 (EMB2656)
AT4G34200	EMBRYO SAC DEVELOPMENT ARREST 9 (EDA9)
AT4G13390	EXTENSIN 12 (EXT12)
AT4G27030	FATTY ACID DESATURASE A (FADA)
AT4G15200	FORMIN 3 (FH3)
AT2G24720	GLUTAMATE RECEPTOR 2.2 (GLR2.2)
AT1G74590	GLUTATHIONE S-TRANSFERASE TAU 10 (GSTU10)
AT3G09270	GLUTATHIONE S-TRANSFERASE TAU 8 (GSTU8)
AT3G47420	GLYCEROL-3-PHOSPHATE PERMEASE 1 (G3Pp1)
AT1G71920	HISTIDINE BIOSYNTHESIS 6B (HISN6B)
AT4G33770	INOSITOL 1,3,4-TRISPHOSPHATE 5/6 KINASE 2 (ITPK2)
AT5G13530	KEEP ON GOING (KEG)
AT3G45330	L-TYPE LECTIN RECEPTOR KINASE I.1 (LECRK-I.1)
AT1G70130	L-TYPE LECTIN RECEPTOR KINASE V.2 (LECRK-V.2)
AT3G45140	LIPOXYGENASE 2 (LOX2)
AT1G17420	LIPOXYGENASE 3 (LOX3)
AT3G59884	MICRORNA827A (MIR827A)
AT3G60840	MICROTUBULE-ASSOCIATED PROTEIN 65-4 (MAP65-4)
AT2G17780	MID1-COMPLEMENTING ACTIVITY 2 (MCA2)
AT4G08480	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 9 (MAPKKK9)
AT5G20410	MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE 2 (MGD2)
AT5G54280	MYOSIN 2 (ATM2)
AT4G37670	N-ACETYL-L-GLUTAMATE SYNTHASE 2 (NAGS2)
AT2G19900	NADP-MALIC ENZYME 1 (NADP-ME1)
AT4G37590	NAKED PINS IN YUC MUTANTS 5 (NPY5)
AT4G14760	NETWORKED 1B (NET1B)
AT4G02710	NETWORKED 1C (NET1C)
AT2G22560	NETWORKED 2D (NET2D)
AT4G38340	NIN-LIKE PROTEIN 3 (NLP3)
AT3G16180	NITRATE TRANSPORTER 1.12 (NRT1.12)

AT1G62580	NITRIC OXIDE-DEPENDENT GUANYLATE CYCLASE 1 (NOGC1)
AT5G22300	NITRILASE 4 (NIT4)
AT1G32450	NRT1/ PTR FAMILY 7.3 (NPF7.3)
AT5G01180	NRT1/ PTR FAMILY 8.2 (NPF8.2)
AT1G63020	NUCLEAR RNA POLYMERASE D1A (NRPD1A)
AT3G61990	O-MTASE FAMILY 3 PROTEIN (OMTF3)
AT1G16370	ORGANIC CATION/CARNITINE TRANSPORTER 6 (OCT6)
AT1G73220	ORGANIC CATION/CARNITINE TRANSPORTER1 (OCT1)
AT3G20660	ORGANIC CATION/CARNITINE TRANSPORTER4 (OCT4)
AT3G09830	PATTERN-TRIGGERED IMMUNITY (PTI) COMPROMISED RECEPTOR-LIKE CYTOPLASMIC KINASE 1 (PCRK1)
AT5G09660	PEROXISOMAL NAD-MALATE DEHYDROGENASE 2 (PMDH2)
AT5G04230	PHENYL ALANINE AMMONIA-LYASE 3 (PAL3)
AT2G33770	PHOSPHATE 2 (PHO2)
AT1G53310	PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PPC1)
AT3G26840	PHYTYL ESTER SYNTHASE 2 (PES2)
AT2G17500	PIN-LIKES 5 (PILS5)
AT1G74260	PURINE BIOSYNTHESIS 4 (PUR4)
AT2G16430	PURPLE ACID PHOSPHATASE 10 (PAP10)
AT1G08590	PXY-LIKE1 (PXL1)
AT3G53620	PYROPHOSPHORYLASE 4 (PPa4)
AT4G30710	QWRF DOMAIN CONTAINING 8 (QWRF8)
AT1G07390	RECEPTOR LIKE PROTEIN 1 (RLP1)
AT1G67500	RECOVERY PROTEIN 3 (REV3)
AT1G67710	RESPONSE REGULATOR 11 (ARR11)
AT1G30510	ROOT FNR 2 (RFNR2)
AT2G39730	RUBISCO ACTIVASE (RCA)
AT1G02500	S-ADENOSYLMETHIONINE SYNTHETASE 1 (SAM1)
AT2G38440	SCAR HOMOLOG 2 (SCAR2)
AT3G08720	SERINE/THREONINE PROTEIN KINASE 2 (S6K2)
AT1G62280	SLAC1 HOMOLOGUE 1 (SLAH1)
AT1G29450	SMALL AUXIN UPREGULATED RNA 64 (SAUR64)
AT4G11110	SPA1-RELATED 2 (SPA2)
AT4G16340	SPIKE1 (SPK1)
AT2G26660	SPX DOMAIN GENE 2 (SPX2)
AT3G02850	STELAR K+ OUTWARD RECTIFIER (SKOR)
AT4G08390	STROMAL ASCORBATE PEROXIDASE (SAPX)
AT1G66570	SUCROSE-PROTON SYMPORTER 7 (SUC7)
AT4G33030	SULFOQUINOVOSYLDIACYLGLYCEROL 1 (SQD1)
AT3G14205	SUPPRESSOR OF ACTIN 2 (SAC2)
AT5G58620	TANDEM ZINC FINGER PROTEIN 9 (TZF9)
AT1G20840	TONOPLAST MONOSACCHARIDE TRANSPORTER1 (TMT1)
AT1G55860	UBIQUITIN-PROTEIN LIGASE 1 (UPL1)
AT1G70320	UBIQUITIN-PROTEIN LIGASE 2 (UPL2)
AT3G56040	UDP-GLUCOSE PYROPHOSPHORYLASE 3 (UGP3)
AT2G36750	UDP-GLUCOSYL TRANSFERASE 73C1 (UGT73C1)
AT1G24100	UDP-GLUCOSYL TRANSFERASE 74B1 (UGT74B1)

AT1G30530	UDP-GLUCOSYL TRANSFERASE 78D1 (UGT78D1)
AT4G15540	USUALLY MULTIPLE ACIDS MOVE IN AND OUT TRANSPORTERS 38 (UMAMIT38)
AT4G07400	VIER F-BOX PROTEINE 3 (VFB3)
AT1G21240	WALL ASSOCIATED KINASE 3 (WAK3)
AT1G21230	WALL ASSOCIATED KINASE 5 (WAK5)
AT1G80840	WRKY DNA-BINDING PROTEIN 40 (WRKY40)
AT1G65730	YELLOW STRIPE LIKE 7 (YSL7)
AT5G13740	ZINC INDUCED FACILITATOR 1 (ZIF1)

Table S8. Global statistics for DMRs in all phosphate treatments for each chromosome.

Treatment	Total DmCs	Total DMRs	DmCs in DMRs	% of Orphan DmCs	Average DmCs in DMR	Min. DMR lenght	Max. DMR lenght	Total lenght DMRs	Average DMR lenght
-Pit Shoot 7 dat									
Chr1	5035	316	2565	49	8	4	12016	677156	2143
Chr2	9454	382	7275	23	19	27	120607	897704	2350
Chr3	6034	399	3416	43	9	19	11081	785636	1969
Chr4	4879	360	2786	43	8	31	9049	682089	1895
Chr5	5393	369	3034	44	8	21	12062	795618	2156
-Pit Root 7 dat									
Chr1	4392	283	2012	54	7	43	11998	546110	1930
Chr2	6010	357	3784	37	11	21	41255	797689	2234
Chr3	5313	396	2900	45	7	47	11820	766423	1935
Chr4	4350	346	2420	44	7	68	7340	692735	2002
Chr5	4978	351	2598	48	7	33	12036	703869	2005
-Pit Shoot 16 dat									
Chr1	6633	432	3789	43	9	9	13070	906415	2098
Chr2	15222	489	12781	16	26	32	120794	1193179	2440
Chr3	8199	564	5498	33	10	17	13730	1200930	2129
Chr4	6371	469	4303	32	9	13	14357	1057663	2255
Chr5	7435	502	4755	36	9	12	16698	1112910	2217
-Pit Root 16 dat									
Chr1	6559	429	3702	44	9	12	16716	902107	2103
Chr2	9840	504	7348	25	15	28	55297	1139108	2260
Chr3	8101	542	5343	34	10	10	9451	1123677	2073
Chr4	6366	447	4202	34	9	37	12215	1006861	2252
Chr5	7436	469	4611	38	10	16	12126	1038047	2213

Table S9. List of DMRs identified in this study. DMRs are separated by methylation direction (Hyper-DMRs, Hypo-DMRs) and phosphate contrast.

-Pit Shoot 7dat (Hyper-DMRs)

Chromosome	Start	End	number of DMCs	DMR lenght	P-value
Chr1	1445307	1446088	4	782	8.76E-07
Chr1	4333883	4334405	4	523	2.18E-07
Chr1	5692819	5695942	8	3124	7.27E-12
Chr1	7353082	7365097	67	12016	3.49E-59
Chr1	7430057	7431111	5	1055	1.35103E-05
Chr1	8453534	8457498	12	3965	6.12E-16
Chr1	8729357	8731382	7	2026	7.82E-10
Chr1	9304834	9305582	5	749	1.29788E-06
Chr1	9371813	9373167	6	1355	1.37E-10
Chr1	9575338	9576849	5	1512	1.96038E-06
Chr1	10358486	10360322	9	1837	1.35E-13
Chr1	10699884	10701325	5	1442	6.09E-07
Chr1	11306271	11309658	8	3388	5.79E-07
Chr1	11834700	11836671	6	1972	2.29E-09
Chr1	11896003	11897129	5	1127	8.58E-10
Chr1	11957967	11958015	5	49	1.54E-09
Chr1	12406357	12411126	12	4770	1.45E-13
Chr1	12670322	12671594	5	1273	1.31E-08
Chr1	12679126	12680579	5	1454	2.37892E-06
Chr1	12681691	12684590	10	2900	7.48E-16
Chr1	12822344	12823143	5	800	9.26E-07
Chr1	12998945	13001231	6	2287	7.46E-08
Chr1	13002709	13004176	5	1468	2.17E-09
Chr1	13020144	13022138	4	1995	6.79036E-06
Chr1	13101704	13102219	5	516	4.81E-08
Chr1	13127010	13127535	4	526	3.15687E-06
Chr1	13295625	13296371	4	747	1.87E-07
Chr1	13326679	13327757	6	1079	1.73513E-06
Chr1	13399389	13400182	5	794	5.18194E-06
Chr1	13491560	13492253	4	694	3.74716E-05
Chr1	13517848	13519668	6	1821	2.28E-11
Chr1	13560480	13562545	9	2066	2.12E-13
Chr1	13575088	13575855	4	768	1.79941E-06
Chr1	13625112	13627712	7	2601	7.53534E-06
Chr1	13647905	13652024	12	4120	3.80E-15
Chr1	13678792	13680494	4	1703	6.70305E-06
Chr1	13694115	13694986	5	872	1.34E-09
Chr1	13768779	13771263	7	2485	1.19578E-06
Chr1	13772972	13776119	11	3148	1.52E-14
Chr1	13779089	13781173	8	2085	2.51E-09
Chr1	13784335	13785251	4	917	6.08496E-06
Chr1	13794675	13796207	4	1533	3.94727E-05
Chr1	13798950	13801634	11	2685	8.88E-14
Chr1	13820653	13821426	4	774	2.15937E-06
Chr1	13825397	13827470	5	2074	2.19E-07
Chr1	13828823	13829978	7	1156	4.42E-10
Chr1	13888716	13890817	8	2102	7.39E-09
Chr1	13945306	13947688	7	2383	1.20E-09
Chr1	13956709	13959114	7	2406	2.11E-08
Chr1	14061975	14063193	5	1219	6.80174E-05
Chr1	14078061	14079118	5	1058	2.10E-10
Chr1	14085677	14087356	4	1680	5.25148E-06
Chr1	14089011	14090199	7	1189	3.30E-11
Chr1	14109634	14113484	10	3851	2.82E-13
Chr1	14119445	14124397	13	4953	8.28E-11
Chr1	14125700	14127241	4	1542	3.91234E-05
Chr1	14178284	14180047	4	1764	7.10678E-05

Chr1	14198860	14200667	6	1808	4.40208E-06
Chr1	14221585	14223996	10	2412	8.86E-15
Chr1	14229582	14231246	9	1665	5.57E-11
Chr1	14234747	14237562	7	2816	1.45E-10
Chr1	14246524	14249946	9	3423	3.32E-11
Chr1	14251114	14252210	6	1097	2.19048E-06
Chr1	14253754	14256188	10	2435	4.06E-12
Chr1	14258042	14258686	4	645	2.59E-08
Chr1	14259756	14260708	4	953	1.83346E-05
Chr1	14269329	14272443	10	3115	7.52E-12
Chr1	14275455	14276239	5	785	1.73497E-06
Chr1	14281386	14282717	4	1332	1.77585E-06
Chr1	14327213	14329580	8	2368	1.12E-09
Chr1	14338381	14340183	4	1803	8.49126E-06
Chr1	14442847	14448348	13	5502	5.61E-17
Chr1	14450874	14452438	8	1565	1.70E-08
Chr1	14471075	14471283	4	209	6.25E-07
Chr1	14482610	14483703	4	1094	2.51875E-05
Chr1	14492371	14494602	5	2232	2.21866E-06
Chr1	14503043	14504505	4	1463	1.2005E-05
Chr1	14509595	14510547	6	953	4.45E-07
Chr1	14539692	14540565	4	874	3.93E-07
Chr1	14585692	14587929	6	2238	3.66E-10
Chr1	14589568	14594186	9	4619	2.85E-09
Chr1	14598926	14599958	6	1033	2.58E-13
Chr1	14715193	14717457	5	2265	2.11076E-06
Chr1	14895771	14897040	5	1270	8.74172E-05
Chr1	15053565	15055492	5	1928	4.77E-09
Chr1	15079479	15080215	5	737	5.84E-09
Chr1	15081239	15085774	63	4536	1.31E-45
Chr1	15137264	15138823	4	1560	7.68E-08
Chr1	15152092	15154614	6	2523	2.63E-08
Chr1	15161683	15162819	4	1137	1.74234E-06
Chr1	15185050	15186089	6	1040	6.40E-08
Chr1	15187802	15189499	5	1698	5.79E-07
Chr1	15421685	15423304	6	1620	2.44E-08
Chr1	15437418	15438790	7	1373	5.92E-11
Chr1	15445538	15448696	9	3159	2.77E-12
Chr1	15451068	15451658	4	591	1.17E-07
Chr1	15489276	15491658	8	2383	1.45E-09
Chr1	15500426	15500758	4	333	5.91424E-06
Chr1	15505075	15507229	7	2155	1.85E-10
Chr1	15513217	15513389	4	173	6.11358E-06
Chr1	15535001	15537074	6	2074	1.69E-07
Chr1	15539278	15540667	7	1390	3.39E-09
Chr1	15542339	15544613	13	2275	3.02E-16
Chr1	15546629	15549744	8	3116	8.92E-13
Chr1	15554351	15557384	9	3034	4.64E-10
Chr1	15558685	15561479	6	2795	5.06E-07
Chr1	15564568	15571358	18	6791	1.40E-20
Chr1	15575189	15577762	6	2574	3.02E-07
Chr1	15611506	15613800	4	2295	0.000604706
Chr1	15617030	15618951	5	1922	4.27225E-06
Chr1	15670308	15671638	4	1331	9.38E-08
Chr1	15681400	15683139	4	1740	7.40107E-05
Chr1	15700271	15702382	9	2112	1.74E-11
Chr1	15707524	15712728	12	5205	6.39E-13
Chr1	15752401	15752922	4	522	1.75938E-06
Chr1	15784039	15786305	6	2267	2.98E-09
Chr1	15790286	15791687	7	1402	6.59E-10
Chr1	15800805	15801852	4	1048	6.51E-07
Chr1	15878223	15879167	4	945	1.90926E-06
Chr1	15951261	15951688	5	428	7.1306E-05

Chr1	16027189	16028743	4	1555	3.2345E-06
Chr1	16097625	16098417	6	793	4.06E-08
Chr1	16101338	16103270	8	1933	1.23E-11
Chr1	16112513	16113252	4	740	5.2332E-06
Chr1	16114656	16114659	4	4	6.34E-07
Chr1	16119211	16122455	8	3245	6.36E-10
Chr1	16198752	16199982	6	1231	4.83E-13
Chr1	16281942	16284313	5	2372	3.14E-09
Chr1	16313036	16314338	5	1303	1.99E-08
Chr1	16377273	16379267	6	1995	4.88E-10
Chr1	16384023	16385008	6	986	8.71E-10
Chr1	16391079	16392464	4	1386	1.07474E-05
Chr1	16510079	16518764	35	8686	2.52E-40
Chr1	16521008	16524632	21	3625	1.87E-20
Chr1	16526666	16528030	5	1365	7.1845E-06
Chr1	16570445	16574090	10	3646	1.76E-12
Chr1	16588179	16588667	6	489	1.59E-08
Chr1	16626958	16633386	13	6429	1.77E-20
Chr1	16635181	16637285	6	2105	4.10E-09
Chr1	16645875	16645928	8	54	5.42E-11
Chr1	16676000	16678574	6	2575	2.78E-07
Chr1	16692450	16694048	5	1599	8.06427E-06
Chr1	16697377	16698518	4	1142	3.05286E-06
Chr1	16742958	16745151	4	2194	3.31E-08
Chr1	17027071	17028370	5	1300	1.34E-08
Chr1	17029413	17030005	5	593	2.40E-07
Chr1	17037213	17039065	5	1853	2.13E-07
Chr1	17046979	17049133	10	2155	8.71E-14
Chr1	17257178	17258795	4	1618	1.27849E-05
Chr1	17260124	17261946	5	1823	9.16E-07
Chr1	17522885	17524605	4	1721	3.27926E-05
Chr1	17534902	17535715	5	814	6.87E-08
Chr1	17677525	17680457	7	2933	1.43E-07
Chr1	17689724	17690567	7	844	3.69E-10
Chr1	18013919	18015226	4	1308	3.21678E-06
Chr1	18192350	18192447	4	98	1.15936E-05
Chr1	18380378	18381062	4	685	4.83316E-05
Chr1	18969656	18970977	5	1322	1.63766E-05
Chr1	19388261	19388355	4	95	4.19E-08
Chr1	19732842	19733758	4	917	1.6701E-06
Chr1	20320078	20320362	6	285	4.63E-08
Chr1	21454629	21456571	5	1943	4.57E-07
Chr1	21526210	21526857	4	648	1.78376E-06
Chr1	21746248	21748782	7	2535	2.65E-08
Chr1	23567602	23568891	4	1290	6.30955E-05
Chr1	23926856	23928665	8	1810	4.02E-10
Chr1	24273022	24276391	85	3370	2.75E-122
Chr1	25660100	25660462	4	363	3.76138E-06
Chr1	26369339	26371085	7	1747	1.86E-09
Chr1	26712307	26712322	4	16	6.77E-08
Chr2	1111	3715	141	2605	1.49E-157
Chr2	5389	5969	42	581	9.36E-84
Chr2	9912	12274	39	2363	3.96E-58
Chr2	247644	248902	4	1259	4.52E-10
Chr2	373138	373918	4	781	2.15494E-06
Chr2	1435108	1435312	4	205	0.000134855
Chr2	1507021	1510588	8	3568	6.87E-11
Chr2	1548922	1549851	6	930	5.40E-15
Chr2	1784161	1787020	9	2860	6.06E-11
Chr2	1830676	1832707	6	2032	1.02E-11
Chr2	1996272	1997415	4	1144	8.82E-08
Chr2	2036754	2037707	6	954	4.62E-09
Chr2	2378132	2381186	7	3055	1.35E-08

Chr2	2401274	2401820	8	547	4.74E-10
Chr2	2438323	2439357	5	1035	2.16453E-06
Chr2	2448017	2451423	10	3407	3.03E-12
Chr2	2463972	2467024	9	3053	6.87E-15
Chr2	2490313	2491327	5	1015	3.24792E-05
Chr2	2492952	2493682	4	731	1.9357E-05
Chr2	2499896	2500528	4	633	1.08E-07
Chr2	2504989	2506996	7	2008	2.74E-11
Chr2	2510836	2512807	4	1972	1.84429E-06
Chr2	2591920	2592613	5	694	6.30E-08
Chr2	2724641	2727039	7	2399	5.61E-10
Chr2	2776269	2777956	5	1688	2.23E-08
Chr2	2830204	2831068	4	865	4.42466E-05
Chr2	2844846	2845415	4	570	1.01832E-06
Chr2	3077195	3078791	5	1597	3.09E-09
Chr2	3084519	3086759	4	2241	9.91E-07
Chr2	3088433	3089004	4	572	1.45184E-05
Chr2	3103109	3104364	5	1256	9.91E-09
Chr2	3163072	3164332	5	1261	7.29E-09
Chr2	3226693	3228456	5	1764	1.93536E-06
Chr2	3240802	3242201	22	1400	1.11E-24
Chr2	3247282	3258599	400	11318	0
Chr2	3259768	3367888	3153	108121	0
Chr2	3375058	3379192	74	4135	2.53E-95
Chr2	3381751	3382080	8	330	1.42E-09
Chr2	3392907	3395318	41	2412	4.52E-62
Chr2	3396335	3397388	49	1054	1.21E-84
Chr2	3398713	3400886	15	2174	7.58E-22
Chr2	3404815	3406660	12	1846	1.38E-16
Chr2	3412683	3412972	11	290	1.41E-17
Chr2	3418666	3418799	11	134	3.04E-14
Chr2	3428957	3429853	6	897	3.47E-08
Chr2	3431505	3431627	5	123	3.36E-07
Chr2	3434038	3434495	10	458	8.42E-16
Chr2	3438177	3438891	21	715	8.35E-28
Chr2	3442815	3442977	4	163	1.09238E-05
Chr2	3459027	3461940	35	2914	2.02E-47
Chr2	3463389	3465432	10	2044	3.93E-12
Chr2	3468287	3468594	11	308	1.08E-11
Chr2	3474764	3476303	13	1540	3.20E-16
Chr2	3478472	3478500	5	29	4.13E-08
Chr2	3482618	3482640	4	23	4.61E-08
Chr2	3483951	3485008	4	1058	5.1772E-06
Chr2	3486063	3493596	171	7534	9.27E-245
Chr2	3496915	3502005	51	5091	1.13E-79
Chr2	3509149	3510674	33	1526	1.16E-37
Chr2	3521440	3522204	4	765	4.05074E-06
Chr2	3536658	3538231	6	1574	1.39E-08
Chr2	3542361	3543175	4	815	2.74E-07
Chr2	3548189	3549789	7	1601	3.18E-08
Chr2	3555038	3555985	6	948	8.02E-09
Chr2	3566238	3569306	6	3069	0.000216461
Chr2	3605702	3607567	55	1866	5.97E-42
Chr2	3614967	3628073	285	13107	8.70E-193
Chr2	3663077	3664163	4	1087	7.37467E-05
Chr2	3724763	3725895	5	1133	5.35126E-06
Chr2	3732328	3735155	6	2828	1.73E-07
Chr2	3742418	3743514	6	1097	1.22E-09
Chr2	3764842	3766037	4	1196	2.41991E-05
Chr2	3786560	3787481	6	922	7.27E-08
Chr2	3825978	3827644	5	1667	5.95096E-06
Chr2	3840073	3841170	5	1098	7.65E-07
Chr2	3858051	3859893	5	1843	1.17E-07

Chr2	3861540	3863223	5	1684	7.69E-07
Chr2	3880221	3881990	6	1770	4.28E-08
Chr2	3885361	3889623	10	4263	2.28E-12
Chr2	3891340	3893275	7	1936	9.61E-09
Chr2	3914772	3916181	4	1410	2.20545E-06
Chr2	3923424	3924167	4	744	1.24901E-05
Chr2	3948531	3949199	4	669	1.96E-07
Chr2	3950778	3953751	9	2974	5.47E-10
Chr2	3971190	3975357	11	4168	2.75E-16
Chr2	4009172	4009831	5	660	6.55E-07
Chr2	4011374	4012154	4	781	5.93381E-05
Chr2	4051408	4053390	4	1983	3.25236E-05
Chr2	4095034	4096261	5	1228	1.13442E-06
Chr2	4121668	4123597	4	1930	6.84E-07
Chr2	4130175	4131831	5	1657	0.000289925
Chr2	4166618	4168815	7	2198	1.39E-07
Chr2	4182474	4185280	8	2807	1.60E-10
Chr2	4188345	4193291	13	4947	2.06E-17
Chr2	4212882	4214337	4	1456	9.19E-07
Chr2	4241732	4241991	5	260	3.52503E-07
Chr2	4258683	4260678	5	1996	2.02E-07
Chr2	4276556	4277445	4	890	8.67E-07
Chr2	4289935	4291499	4	1565	1.16E-07
Chr2	4311381	4311935	7	555	3.70E-09
Chr2	4388886	4390835	5	1950	1.72487E-05
Chr2	4391931	4393466	6	1536	5.18211E-06
Chr2	4395726	4401642	16	5917	1.51E-24
Chr2	4463726	4464296	4	571	6.15E-08
Chr2	4490933	4492185	5	1253	8.84941E-07
Chr2	4517501	4520240	6	2740	1.97E-07
Chr2	4533048	4534178	5	1131	4.9114E-05
Chr2	4578153	4580779	5	2627	5.23E-07
Chr2	4596923	4599545	6	2623	5.18E-09
Chr2	4606993	4607304	4	312	9.41E-07
Chr2	4674902	4678217	6	3316	1.35992E-05
Chr2	4695731	4698180	7	2450	2.39E-09
Chr2	4705203	4707100	8	1898	1.33E-13
Chr2	4710804	4714196	13	3393	2.76E-15
Chr2	4718005	4720849	8	2845	6.32E-13
Chr2	4731152	4733137	8	1986	8.78E-13
Chr2	4734505	4736675	8	2171	7.50E-09
Chr2	4779386	4782015	6	2630	2.83E-08
Chr2	4815635	4817080	4	1446	3.49144E-06
Chr2	4907285	4908850	7	1566	2.18E-10
Chr2	4975598	4980298	13	4701	1.26E-16
Chr2	4988571	4989584	4	1014	3.01766E-05
Chr2	4994029	4996404	6	2376	2.80E-08
Chr2	5036483	5036656	4	174	2.24058E-05
Chr2	5046219	5046398	4	180	1.01E-07
Chr2	5052356	5052468	4	113	1.50E-09
Chr2	5087914	5088974	4	1061	1.10E-07
Chr2	5093613	5095024	6	1412	1.40E-07
Chr2	5100686	5104626	11	3941	4.03E-11
Chr2	5128989	5129640	4	652	6.51211E-06
Chr2	5254101	5256880	9	2780	2.84E-11
Chr2	5299300	5302095	6	2796	3.42E-08
Chr2	5309632	5311218	4	1587	6.89444E-06
Chr2	5328647	5330113	4	1467	6.01E-08
Chr2	5332522	5336127	10	3606	5.24E-11
Chr2	5359501	5359753	4	253	6.1092E-05
Chr2	5360903	5362012	4	1110	2.16E-09
Chr2	5374857	5376783	4	1927	6.86E-07
Chr2	5379895	5381972	5	2078	6.61E-09

Chr2	5475157	5477997	7	2841	7.12E-09
Chr2	5494984	5497811	8	2828	1.44E-10
Chr2	5518435	5520288	5	1854	6.90E-08
Chr2	5571945	5575451	9	3507	8.21E-11
Chr2	5576931	5578545	5	1615	7.2084E-06
Chr2	5600886	5602081	7	1196	5.94E-10
Chr2	5603531	5605850	6	2320	7.99E-08
Chr2	5621965	5625203	7	3239	2.45E-10
Chr2	5628368	5630346	5	1979	3.60588E-05
Chr2	5780819	5782101	6	1283	2.17E-07
Chr2	5783475	5784959	4	1485	3.0984E-06
Chr2	5808320	5809188	4	869	1.08347E-05
Chr2	5887087	5888556	4	1470	0.000333543
Chr2	5900931	5904112	13	3182	3.10E-14
Chr2	5985841	5988646	6	2806	3.31E-09
Chr2	5991322	5992726	4	1405	1.6011E-05
Chr2	6127024	6127531	4	508	1.53678E-05
Chr2	6267966	6268883	5	918	2.24593E-06
Chr2	6344028	6344373	4	346	1.72263E-05
Chr2	6424873	6426259	4	1387	2.6776E-06
Chr2	6434077	6434512	4	436	1.67627E-06
Chr2	6461768	6463343	4	1576	6.82673E-06
Chr2	6526003	6528078	8	2076	3.47E-10
Chr2	6623513	6626133	5	2621	4.62E-07
Chr2	6701109	6702578	4	1470	8.88E-07
Chr2	6718679	6719951	4	1273	3.12676E-06
Chr2	6720965	6722144	4	1180	5.25275E-06
Chr2	6724641	6725732	5	1092	9.4824E-06
Chr2	6769095	6772297	7	3203	2.49E-10
Chr2	6784950	6786748	6	1799	8.67E-08
Chr2	6881439	6883440	4	2002	1.33916E-05
Chr2	6892293	6892863	4	571	2.86465E-06
Chr2	6941811	6943870	6	2060	5.94E-09
Chr2	6971511	6972905	7	1395	5.16159E-05
Chr2	7009436	7009974	7	539	3.40E-12
Chr2	7011557	7013450	6	1894	8.42E-11
Chr2	7080760	7080786	5	27	6.54E-11
Chr2	7115228	7116835	6	1608	1.71E-08
Chr2	7118012	7119887	5	1876	2.20E-08
Chr2	7190804	7191451	4	648	0.002318163
Chr2	7224410	7226745	6	2336	6.26E-10
Chr2	7233341	7237806	9	4466	3.34E-14
Chr2	7780055	7781560	6	1506	4.71E-12
Chr2	7956210	7956377	6	168	9.41E-11
Chr2	8563257	8563801	5	545	0.000295475
Chr2	8564826	8566532	4	1707	6.38049E-06
Chr2	8818007	8820159	5	2153	7.03E-07
Chr2	9123171	9124967	6	1797	6.46E-10
Chr2	9189714	9192248	8	2535	1.83E-09
Chr2	9195171	9195302	4	132	3.08985E-06
Chr2	10003408	10005425	10	2018	1.15E-12
Chr2	10356729	10357898	5	1170	1.70E-07
Chr2	10592290	10593825	4	1536	1.25E-07
Chr2	10602492	10603991	5	1500	1.69986E-05
Chr2	10606918	10607753	4	836	7.08E-07
Chr2	10875741	10877849	7	2109	2.31E-07
Chr2	11867212	11867687	4	476	8.35131E-07
Chr2	13223842	13225106	4	1265	0.000466516
Chr2	13421995	13423424	5	1430	1.65E-07
Chr2	16150572	16150850	4	279	1.64E-08
Chr2	17338114	17341232	8	3119	3.31E-08
Chr2	18652299	18655482	6	3184	1.18E-09
Chr3	2808603	2811380	8	2778	4.32E-13

Chr3	3538202	3539032	4	831	8.44147E-06
Chr3	5278382	5280927	6	2546	6.37E-07
Chr3	5862114	5862292	7	179	5.27E-10
Chr3	5954908	5955291	4	384	3.38812E-05
Chr3	8343639	8343828	4	190	5.08541E-05
Chr3	8597952	8597970	5	19	7.15E-15
Chr3	8843020	8843143	4	124	1.03E-07
Chr3	8854960	8856963	8	2004	1.39E-13
Chr3	9615411	9616710	5	1300	1.59E-09
Chr3	9787032	9788260	6	1229	8.84E-09
Chr3	9808394	9809081	5	688	4.92446E-07
Chr3	10342459	10345250	7	2792	7.48E-10
Chr3	10918581	10920476	7	1896	4.55E-12
Chr3	11065861	11068156	6	2296	1.18601E-06
Chr3	11098889	11099637	6	749	1.06E-08
Chr3	11119239	11120549	4	1311	2.80531E-05
Chr3	11329914	11333740	10	3827	1.57E-13
Chr3	11407677	11409983	5	2307	1.94E-07
Chr3	11421064	11423384	5	2321	4.20939E-06
Chr3	11495256	11496770	5	1515	1.36E-07
Chr3	11579940	11583604	11	3665	5.58E-16
Chr3	11659887	11660479	5	593	3.99525E-06
Chr3	11721071	11721901	4	831	4.23165E-05
Chr3	11833422	11834204	5	783	4.47969E-06
Chr3	11875330	11876561	7	1232	2.46E-10
Chr3	12017065	12017954	4	890	1.47866E-06
Chr3	12024415	12025613	4	1199	7.21669E-06
Chr3	12029230	12031083	6	1854	6.54E-07
Chr3	12044861	12047953	7	3093	9.29E-10
Chr3	12108828	12109788	4	961	3.1649E-06
Chr3	12192921	12195089	8	2169	6.39E-07
Chr3	12207501	12209913	6	2413	2.68E-08
Chr3	12217157	12217402	6	246	1.14E-10
Chr3	12221511	12223124	4	1614	2.92464E-05
Chr3	12230325	12231959	4	1635	3.40001E-06
Chr3	12250911	12252062	4	1152	1.73462E-05
Chr3	12293548	12296350	6	2803	1.18E-09
Chr3	12305434	12307007	5	1574	5.44E-10
Chr3	12335725	12337275	5	1551	1.04938E-06
Chr3	12345211	12346936	5	1726	2.09341E-07
Chr3	12478671	12480218	4	1548	4.31E-07
Chr3	12482020	12483890	6	1871	7.27E-08
Chr3	12496449	12497072	7	624	3.90E-08
Chr3	12500469	12502149	8	1681	8.25E-10
Chr3	12506118	12507288	4	1171	9.07E-08
Chr3	12509377	12510766	5	1390	2.76E-08
Chr3	12518303	12519205	4	903	0.000575024
Chr3	12538623	12541688	8	3066	1.70E-09
Chr3	12543019	12544780	7	1762	2.72E-09
Chr3	12555436	12556928	5	1493	1.64E-07
Chr3	12567933	12569356	4	1424	7.27261E-06
Chr3	12577527	12579390	7	1864	9.07E-11
Chr3	12676433	12677508	4	1076	3.47E-08
Chr3	12689152	12691340	6	2189	2.62E-07
Chr3	12699708	12701783	6	2076	2.57E-09
Chr3	12719498	12723046	6	3549	8.16E-10
Chr3	12750086	12751375	6	1290	1.21E-07
Chr3	12856816	12858723	6	1908	1.47039E-06
Chr3	12920787	12922545	6	1759	1.64E-08
Chr3	12926006	12927245	5	1240	6.21E-07
Chr3	12983372	12986127	8	2756	4.82E-10
Chr3	13087298	13088388	7	1091	7.23484E-06
Chr3	13102073	13103773	5	1701	3.45E-07

Chr3	13114216	13115082	4	867	1.30961E-05
Chr3	13118019	13120882	10	2864	2.16E-10
Chr3	13163509	13164275	5	767	2.59E-08
Chr3	13170261	13171995	8	1735	3.41E-13
Chr3	13188524	13191796	8	3273	1.84249E-06
Chr3	13194377	13195411	4	1035	4.42E-07
Chr3	13196965	13198149	4	1185	7.74178E-05
Chr3	13214777	13216389	4	1613	2.15E-07
Chr3	13247515	13248765	5	1251	2.28E-07
Chr3	13343485	13347103	7	3619	1.11E-09
Chr3	13409297	13410636	4	1340	2.36978E-05
Chr3	13412177	13412508	5	332	4.62E-08
Chr3	13416641	13418489	5	1849	6.48E-07
Chr3	13427479	13428310	4	832	5.73E-09
Chr3	13440487	13442664	13	2178	3.54E-20
Chr3	13444561	13446346	6	1786	4.29E-08
Chr3	13477678	13480572	7	2895	5.26E-11
Chr3	13513114	13514054	4	941	6.05043E-05
Chr3	13516940	13518065	4	1126	2.53094E-05
Chr3	13550547	13551402	5	856	7.78234E-06
Chr3	13582350	13584006	7	1657	3.44E-08
Chr3	13586076	13587770	28	1695	6.91E-27
Chr3	13588852	13593601	229	4750	2.27E-196
Chr3	13596765	13598609	5	1845	0.001401172
Chr3	13603831	13605645	6	1815	1.79E-09
Chr3	13607578	13608497	4	920	1.78048E-05
Chr3	13617496	13620045	5	2550	1.92E-07
Chr3	13625329	13627002	4	1674	9.30515E-05
Chr3	13637076	13639778	5	2703	7.01E-09
Chr3	13654171	13656727	8	2557	3.43E-11
Chr3	13678167	13678796	4	630	5.98994E-06
Chr3	13707427	13707684	9	258	3.62E-14
Chr3	13802409	13807380	15	4972	2.15E-22
Chr3	13815531	13817014	4	1484	1.90411E-05
Chr3	13831170	13833530	7	2361	1.44E-10
Chr3	13874667	13876695	6	2029	7.99E-08
Chr3	13888051	13889295	4	1245	1.90977E-06
Chr3	13895313	13896906	4	1594	0.002443173
Chr3	13907571	13908012	5	442	1.53081E-06
Chr3	13909147	13911370	4	2224	5.94494E-06
Chr3	13919703	13921596	4	1894	0.001029968
Chr3	13934922	13935673	4	752	5.68E-07
Chr3	13970047	13971866	5	1820	1.90E-10
Chr3	13986353	13987138	4	786	3.06352E-06
Chr3	14005488	14007289	6	1802	2.52615E-05
Chr3	14026980	14027793	4	814	1.57855E-05
Chr3	14034423	14035948	5	1526	2.74725E-06
Chr3	14065993	14066834	4	842	1.35936E-05
Chr3	14072897	14074394	4	1498	1.46496E-06
Chr3	14098403	14099284	7	882	1.94E-15
Chr3	14113587	14114513	5	927	3.69E-07
Chr3	14122331	14124090	5	1760	1.07343E-07
Chr3	14158747	14161679	10	2933	9.36E-15
Chr3	14167604	14168226	6	623	2.08E-10
Chr3	14171695	14172192	4	498	8.79E-08
Chr3	14173265	14173919	4	655	0.0001344
Chr3	14180358	14181497	8	1140	4.06E-07
Chr3	14186050	14186581	4	532	8.73661E-05
Chr3	14188574	14189275	4	702	0.000740843
Chr3	14194191	14204060	388	9870	0
Chr3	14205332	14208508	16	3177	7.03E-17
Chr3	14214302	14215925	10	1624	1.32E-15
Chr3	14217707	14218677	4	971	0.000114748

Chr3	14221667	14224971	12	3305	1.83E-11
Chr3	14248479	14250393	4	1915	0.000217329
Chr3	14256123	14258291	9	2169	4.67E-10
Chr3	14277776	14278920	4	1145	0.000146373
Chr3	14342318	14344181	7	1864	5.50E-10
Chr3	14345522	14346218	6	697	2.18E-08
Chr3	14392795	14393357	4	563	0.000171421
Chr3	14412762	14415674	9	2913	2.92E-10
Chr3	14433797	14438988	9	5192	5.28E-14
Chr3	14454356	14455492	4	1137	1.88E-08
Chr3	14464144	14466022	5	1879	1.81E-07
Chr3	14507507	14508093	4	587	2.06917E-06
Chr3	14513209	14514412	5	1204	1.49E-10
Chr3	14551918	14553197	4	1280	2.71359E-05
Chr3	14556428	14558166	6	1739	4.52E-11
Chr3	14574851	14575967	5	1117	2.64027E-05
Chr3	14579712	14581550	6	1839	3.97E-09
Chr3	14624455	14625788	5	1334	4.32E-08
Chr3	14715054	14717240	4	2187	2.02082E-06
Chr3	14770596	14773148	5	2553	5.71E-07
Chr3	14774307	14775674	6	1368	5.26E-12
Chr3	14793822	14796759	6	2938	1.92E-07
Chr3	14801013	14803116	5	2104	1.41711E-06
Chr3	14815306	14815642	4	337	9.79E-08
Chr3	14819289	14820470	4	1182	3.12856E-06
Chr3	14823373	14824309	5	937	4.08E-08
Chr3	14825621	14827627	6	2007	4.74E-07
Chr3	14849639	14850766	4	1128	3.69E-08
Chr3	14978593	14983420	15	4828	9.53E-17
Chr3	14985575	14987232	8	1658	4.75E-08
Chr3	15033149	15034595	6	1447	4.26E-08
Chr3	15083352	15085326	7	1975	1.67E-11
Chr3	15098068	15100054	4	1987	2.83942E-05
Chr3	15108548	15109659	5	1112	6.73E-07
Chr3	15115602	15117954	7	2353	1.44E-08
Chr3	15120046	15122752	10	2707	1.67E-15
Chr3	15136919	15138361	6	1443	1.21E-07
Chr3	15148098	15149088	4	991	1.07692E-06
Chr3	15255192	15256190	6	999	1.14E-08
Chr3	15257446	15259050	4	1605	9.38E-09
Chr3	15280197	15281221	4	1025	1.54957E-06
Chr3	15381077	15383001	8	1925	7.87E-10
Chr3	15459335	15462450	11	3116	7.95E-13
Chr3	15494136	15495263	4	1128	4.96304E-06
Chr3	15497064	15498128	5	1065	2.43E-09
Chr3	15542435	15543494	5	1060	6.18629E-06
Chr3	15574688	15575748	6	1061	2.01318E-06
Chr3	15580217	15581604	4	1388	4.03841E-06
Chr3	15690170	15691081	4	912	7.34E-07
Chr3	15692606	15693944	4	1339	1.6559E-05
Chr3	15714886	15716576	7	1691	5.62E-07
Chr3	15718450	15720027	8	1578	1.18E-11
Chr3	15722152	15723653	4	1502	3.12417E-06
Chr3	15810043	15810339	4	297	1.42E-07
Chr3	15847418	15849240	4	1823	0.000131901
Chr3	16340056	16341771	6	1716	2.77E-10
Chr3	16590007	16591745	5	1739	5.69E-07
Chr3	16601596	16604013	4	2418	1.99118E-07
Chr3	16810616	16812712	5	2097	4.48E-07
Chr3	16957543	16959452	7	1910	1.74E-10
Chr3	17058827	17058849	4	23	2.00E-10
Chr3	17431414	17431854	4	441	1.44762E-06
Chr3	17979125	17979950	5	826	4.63E-09

Chr3	18791259	18792809	6	1551	5.63E-10
Chr3	18794210	18794992	5	783	7.64949E-07
Chr3	18860144	18861107	4	964	5.86201E-06
Chr3	19243037	19243582	4	546	9.49789E-06
Chr3	20202088	20203509	5	1422	0.013074487
Chr3	21324188	21325958	4	1771	1.21035E-06
Chr3	22370259	22370293	4	35	7.69251E-06
Chr3	23204156	23205360	7	1205	4.69E-08
Chr4	631300	632262	4	963	1.21053E-05
Chr4	635205	636829	4	1625	2.20E-07
Chr4	782598	783526	4	929	2.04121E-05
Chr4	862911	864329	4	1419	2.12279E-05
Chr4	1019737	1020670	4	934	3.16804E-05
Chr4	1063657	1063934	6	278	3.91E-12
Chr4	1665796	1669899	11	4104	1.31E-11
Chr4	1673811	1676660	10	2850	1.28E-12
Chr4	1677941	1679270	6	1330	4.29E-11
Chr4	1686951	1689180	4	2230	2.99967E-06
Chr4	1695602	1696940	8	1339	9.22E-09
Chr4	1763559	1764625	4	1067	4.20E-07
Chr4	1797305	1800298	11	2994	1.68E-09
Chr4	1808012	1809386	5	1375	1.46E-07
Chr4	1816084	1817666	4	1583	9.80E-07
Chr4	1830234	1831767	4	1534	0.000235059
Chr4	1936948	1937682	4	735	3.77061E-06
Chr4	1944313	1945800	5	1488	2.82539E-06
Chr4	1947165	1948552	5	1388	3.90E-08
Chr4	1949765	1951502	4	1738	9.3326E-06
Chr4	1977450	1978395	4	946	9.68E-07
Chr4	2000012	2001972	6	1961	2.41E-07
Chr4	2006197	2007341	6	1145	1.74E-08
Chr4	2013521	2014178	4	658	9.29E-07
Chr4	2040737	2042120	5	1384	1.07054E-06
Chr4	2048669	2050121	4	1453	7.59981E-05
Chr4	2142788	2143026	5	239	2.35E-07
Chr4	2160859	2162104	4	1246	2.59902E-06
Chr4	2247297	2248145	4	849	2.45E-07
Chr4	2282413	2283463	4	1051	5.69457E-05
Chr4	2284514	2285574	5	1061	2.59E-08
Chr4	2287008	2288001	6	994	9.41E-11
Chr4	2358462	2358673	4	212	2.45446E-06
Chr4	2360026	2361216	6	1191	4.30E-08
Chr4	2597829	2601870	12	4042	1.27E-17
Chr4	2708603	2708965	4	363	1.84694E-06
Chr4	2832474	2834132	8	1659	9.65E-11
Chr4	2881356	2882808	4	1453	4.41145E-05
Chr4	2887215	2889640	6	2426	3.84E-08
Chr4	2893985	2895234	4	1250	1.08E-08
Chr4	2897835	2900579	6	2745	1.31075E-06
Chr4	2953430	2953946	4	517	1.37622E-06
Chr4	2963340	2964223	5	884	2.51E-07
Chr4	2968784	2969485	5	702	1.80579E-05
Chr4	2980622	2981598	4	977	4.16788E-05
Chr4	3003175	3004112	4	938	0.000162813
Chr4	3010509	3012683	7	2175	1.50E-08
Chr4	3018739	3022561	7	3823	3.39E-11
Chr4	3044496	3045226	5	731	1.69131E-05
Chr4	3054362	3056928	13	2567	2.53E-08
Chr4	3079416	3081531	9	2116	6.66E-10
Chr4	3090740	3092367	6	1628	2.40E-07
Chr4	3099110	3099370	4	261	1.31483E-05
Chr4	3102623	3105194	10	2572	4.63E-16
Chr4	3157175	3158769	5	1595	3.16138E-06

Chr4	3164509	3165643	4	1135	7.76E-07
Chr4	3178270	3179121	4	852	1.76E-07
Chr4	3180310	3181116	4	807	3.01E-07
Chr4	3182512	3183929	5	1418	6.53E-07
Chr4	3264342	3266037	4	1696	8.29958E-06
Chr4	3270346	3273346	10	3001	8.44E-15
Chr4	3274605	3276983	11	2379	6.11E-14
Chr4	3351698	3353190	4	1493	5.84571E-05
Chr4	3374482	3377739	9	3258	5.75E-13
Chr4	3383864	3384566	4	703	2.33323E-05
Chr4	3385798	3388085	7	2288	4.24E-09
Chr4	3411389	3413392	4	2004	6.25118E-06
Chr4	3436088	3438934	8	2847	1.21E-11
Chr4	3467095	3469818	9	2724	5.71E-13
Chr4	3480220	3482095	8	1876	2.19E-10
Chr4	3483375	3485084	5	1710	2.5038E-05
Chr4	3488638	3490609	8	1972	3.21E-09
Chr4	3493368	3494962	8	1595	5.50E-07
Chr4	3498526	3500152	6	1627	1.24E-07
Chr4	3588337	3589931	5	1595	9.85E-09
Chr4	3618660	3619500	4	841	3.44E-07
Chr4	3624612	3625669	6	1058	1.26E-12
Chr4	3628278	3629546	5	1269	6.12E-10
Chr4	3631009	3631244	4	236	1.81227E-06
Chr4	3634393	3635580	5	1188	1.37E-07
Chr4	3649793	3651458	4	1666	1.17E-08
Chr4	3693978	3694529	4	552	6.21982E-05
Chr4	3695683	3696137	4	455	0.000345529
Chr4	3698830	3700922	4	2093	4.25E-07
Chr4	3715874	3716971	4	1098	2.14E-08
Chr4	3736056	3737094	6	1039	6.68E-07
Chr4	3739664	3743723	12	4060	3.46E-13
Chr4	3749265	3751519	4	2255	4.97618E-05
Chr4	3755078	3756531	5	1454	6.41372E-06
Chr4	3784808	3789640	9	4833	1.52E-09
Chr4	3839241	3840777	5	1537	4.42E-07
Chr4	3864710	3865661	5	952	1.54546E-06
Chr4	3871660	3873786	10	2127	8.22E-14
Chr4	3908969	3910623	6	1655	1.0973E-07
Chr4	3915552	3916483	4	932	1.10403E-05
Chr4	3934701	3937033	5	2333	5.49E-07
Chr4	3942460	3943611	4	1152	1.3193E-05
Chr4	3950572	3955925	246	5354	2.19E-167
Chr4	3964615	3966875	16	2261	2.18E-10
Chr4	3968310	3969524	9	1215	8.77E-12
Chr4	3977700	3980451	25	2752	1.77E-27
Chr4	3982400	3983540	11	1141	3.41E-11
Chr4	3989538	3990859	4	1322	2.07E-07
Chr4	3992559	3992802	5	244	1.27E-08
Chr4	3994093	3995564	11	1472	2.31E-11
Chr4	3999914	4000477	7	564	1.53E-07
Chr4	4003709	4004228	12	520	7.69E-13
Chr4	4007195	4007362	8	168	1.49E-09
Chr4	4008777	4011483	10	2707	3.49E-11
Chr4	4016285	4016403	4	119	8.26E-09
Chr4	4024336	4026357	6	2022	5.86E-07
Chr4	4037521	4038571	5	1051	2.21E-09
Chr4	4101794	4103010	4	1217	9.42E-08
Chr4	4159425	4160926	5	1502	4.10284E-06
Chr4	4183547	4185654	7	2108	8.81E-10
Chr4	4239848	4243251	17	3404	2.42E-17
Chr4	4249564	4250784	4	1221	6.65E-07
Chr4	4269539	4270047	6	509	4.66E-09

Chr4	4278509	4283186	13	4678	2.28E-15
Chr4	4304087	4305534	6	1448	1.12E-09
Chr4	4360495	4362001	5	1507	9.39E-08
Chr4	4386847	4388680	6	1834	6.27E-07
Chr4	4391737	4394485	8	2749	1.07E-11
Chr4	4400192	4401278	5	1087	8.47E-09
Chr4	4405013	4405901	5	889	1.72E-09
Chr4	4425622	4427061	5	1440	1.03E-07
Chr4	4440701	4441912	6	1212	1.31552E-06
Chr4	4451884	4453493	4	1610	1.70E-08
Chr4	4489139	4491955	5	2817	9.29E-08
Chr4	4530543	4531902	5	1360	4.17E-08
Chr4	4543286	4544517	4	1232	1.04693E-06
Chr4	4559972	4561094	5	1123	9.54E-08
Chr4	4564112	4565319	7	1208	1.01E-07
Chr4	4609301	4609627	4	327	4.17309E-06
Chr4	4646774	4648181	4	1408	1.08497E-06
Chr4	4681051	4682269	4	1219	0.000290705
Chr4	4710407	4712030	5	1624	6.09732E-06
Chr4	4726524	4727905	4	1382	3.93133E-06
Chr4	4731557	4734440	10	2884	1.33E-11
Chr4	4739634	4740566	4	933	0.000138967
Chr4	4744353	4745648	4	1296	7.64E-07
Chr4	4746987	4748972	4	1986	6.21624E-06
Chr4	4758543	4761710	8	3168	3.08E-13
Chr4	4770291	4772394	6	2104	2.97E-09
Chr4	4775904	4779141	10	3238	3.11E-14
Chr4	4835486	4836913	4	1428	6.01202E-06
Chr4	4926309	4927499	4	1191	4.35192E-05
Chr4	4933249	4933944	5	696	1.24E-07
Chr4	4945645	4946560	4	916	3.79E-07
Chr4	4958954	4959755	5	802	1.75963E-05
Chr4	4961702	4962543	4	842	1.89046E-06
Chr4	4965810	4966106	4	297	5.83E-08
Chr4	5022695	5024463	9	1769	2.36E-11
Chr4	5039879	5040532	4	654	0.000101327
Chr4	5042441	5045198	9	2758	1.31E-13
Chr4	5049132	5051892	7	2761	7.87E-10
Chr4	5060383	5061800	5	1418	2.36978E-06
Chr4	5069701	5072010	4	2310	4.88E-07
Chr4	5076671	5078945	7	2275	1.32E-09
Chr4	5090702	5092627	5	1926	3.48E-07
Chr4	5100972	5101317	5	346	6.84E-07
Chr4	5307054	5308270	5	1217	6.17262E-06
Chr4	5348408	5348906	4	499	9.8041E-07
Chr4	5528302	5530014	4	1713	1.51028E-05
Chr4	5532656	5534023	8	1368	2.31E-14
Chr4	5666456	5667496	4	1041	5.72846E-06
Chr4	5939681	5940635	4	955	3.17E-07
Chr4	5954515	5956010	5	1496	7.30E-11
Chr4	5966478	5967343	4	866	1.04907E-06
Chr4	5987651	5988436	4	786	2.50486E-05
Chr4	6068499	6072148	7	3650	4.81E-10
Chr4	6529484	6529801	5	318	6.73484E-07
Chr4	6531848	6536557	11	4710	1.14E-10
Chr4	6654061	6655935	6	1875	2.64E-09
Chr4	6723506	6724941	5	1436	1.21E-08
Chr4	6726044	6727535	4	1492	7.89E-07
Chr4	6730348	6730378	4	31	2.66091E-06
Chr4	7688170	7688682	5	513	2.01E-09
Chr4	8318216	8318582	4	367	8.67638E-05
Chr4	8900939	8902682	6	1744	2.67E-07
Chr4	8905697	8906424	4	728	2.31271E-05

Chr4	9735323	9737742	6	2420	3.58E-09
Chr4	9955990	9957015	4	1026	0.00010837
Chr4	10992973	10995146	4	2174	8.36269E-06
Chr4	10996219	10997948	7	1730	5.21E-10
Chr4	11037398	11039430	6	2033	4.27E-07
Chr4	11363413	11364365	4	953	6.75E-07
Chr4	11366214	11367922	8	1709	3.28E-10
Chr4	11820227	11821370	4	1144	1.63578E-05
Chr4	13572245	13572745	4	501	2.62859E-05
Chr4	13627248	13628949	7	1702	4.74E-11
Chr4	13630630	13631928	6	1299	4.63E-07
Chr4	13887279	13888105	4	827	1.72083E-06
Chr4	14283523	14284784	5	1262	2.524E-05
Chr4	15554684	15555108	4	425	1.52E-07
Chr4	17714562	17715757	4	1196	3.6103E-05
Chr5	64895	69541	20	4647	5.90E-27
Chr5	137079	138792	5	1714	1.42155E-06
Chr5	2257869	2259789	10	1921	1.00E-14
Chr5	2392045	2395622	13	3578	1.98E-10
Chr5	3253169	3253271	8	103	7.50E-13
Chr5	4324247	4325423	5	1177	3.49E-07
Chr5	5218548	5220608	9	2061	1.25E-11
Chr5	6207791	6209091	5	1301	3.27437E-06
Chr5	6405363	6406434	4	1072	4.20E-07
Chr5	6630872	6633406	9	2535	3.72E-08
Chr5	7027636	7028616	6	981	2.89E-07
Chr5	8313343	8313400	4	58	1.72E-07
Chr5	8549745	8550752	4	1008	3.36461E-06
Chr5	8573327	8574528	6	1202	8.95E-11
Chr5	8576140	8577067	5	928	7.55E-08
Chr5	8716378	8717272	4	895	3.84713E-05
Chr5	9412940	9416716	7	3777	4.17E-10
Chr5	9711193	9713515	5	2323	8.05E-07
Chr5	9892089	9893318	4	1230	4.8029E-06
Chr5	9927887	9929295	7	1409	1.53E-12
Chr5	9996749	9998364	5	1616	2.25167E-06
Chr5	10060969	10061973	4	1005	3.18237E-06
Chr5	10094828	10096188	5	1361	1.81E-07
Chr5	10097611	10099827	7	2217	2.92E-11
Chr5	10101962	10106880	10	4919	7.97E-10
Chr5	10256431	10260491	9	4061	1.09E-11
Chr5	10350636	10352082	5	1447	1.15E-08
Chr5	10364478	10366234	5	1757	1.13E-09
Chr5	10583814	10584332	4	519	2.25177E-06
Chr5	10589989	10591210	5	1222	8.04652E-07
Chr5	10605433	10607380	6	1948	2.26E-10
Chr5	10626413	10627266	4	854	1.94577E-06
Chr5	10711015	10712607	4	1593	4.07479E-05
Chr5	10811075	10813158	4	2084	1.28242E-05
Chr5	10903293	10904116	6	824	6.84E-07
Chr5	10958431	10959525	4	1095	1.93136E-05
Chr5	11044137	11044333	4	197	2.72E-08
Chr5	11047264	11048193	4	930	7.38E-07
Chr5	11079058	11080292	5	1235	5.81382E-07
Chr5	11086882	11087704	4	823	4.00E-08
Chr5	11103112	11104193	5	1082	2.33256E-05
Chr5	11128165	11129365	5	1201	1.07E-10
Chr5	11137021	11138323	4	1303	6.69254E-05
Chr5	11139615	11141360	5	1746	5.119E-05
Chr5	11145102	11146594	6	1493	4.10E-08
Chr5	11172214	11174725	5	2512	5.84056E-06
Chr5	11178944	11182327	11	3384	1.26E-14
Chr5	11184800	11188238	41	3439	2.14E-31

Chr5	11207708	11210395	7	2688	1.81E-08
Chr5	11315891	11316857	4	967	4.49E-08
Chr5	11319244	11320194	4	951	4.71011E-06
Chr5	11326382	11328328	5	1947	9.73E-08
Chr5	11335134	11336907	4	1774	3.83E-07
Chr5	11352606	11354262	5	1657	5.26E-07
Chr5	11391670	11392735	5	1066	4.78E-07
Chr5	11398380	11399815	7	1436	1.03E-07
Chr5	11421479	11424535	8	3057	2.37E-10
Chr5	11432181	11434032	5	1852	1.57E-08
Chr5	11460509	11463018	7	2510	5.63E-07
Chr5	11475204	11479887	12	4684	1.96E-14
Chr5	11481755	11483360	4	1606	7.48E-08
Chr5	11507021	11509831	5	2811	2.80E-11
Chr5	11563605	11565882	6	2278	1.90643E-06
Chr5	11569535	11572058	9	2524	1.28E-12
Chr5	11578137	11579796	5	1660	5.04E-07
Chr5	11599985	11602039	4	2055	3.27468E-06
Chr5	11646669	11649583	6	2915	1.62E-08
Chr5	11651133	11652563	5	1431	2.66E-07
Chr5	11653812	11655850	4	2039	2.67661E-05
Chr5	11690188	11691006	6	819	5.37E-08
Chr5	11701507	11710254	55	8748	5.27E-39
Chr5	11722873	11724238	13	1366	6.43E-11
Chr5	11726122	11736280	114	10159	3.40E-88
Chr5	11750489	11751916	4	1428	3.28664E-06
Chr5	11755813	11757241	7	1429	1.33594E-06
Chr5	11762695	11765507	7	2813	2.66E-08
Chr5	11771290	11772295	5	1006	1.57E-07
Chr5	11776107	11778999	7	2893	1.67E-07
Chr5	11782792	11785351	7	2560	1.04E-10
Chr5	11787883	11790091	8	2209	1.59271E-05
Chr5	11793993	11796956	8	2964	7.56E-07
Chr5	11803773	11805395	5	1623	1.20E-07
Chr5	11806643	11810776	8	4134	3.85E-11
Chr5	11813799	11815026	4	1228	7.79226E-06
Chr5	11833457	11836225	6	2769	7.59E-07
Chr5	11842073	11843745	15	1673	1.39E-17
Chr5	11868432	11869447	5	1016	2.30937E-06
Chr5	11912408	11915506	10	3099	1.09E-11
Chr5	11916871	11919460	4	2590	3.94797E-06
Chr5	11921375	11923101	4	1727	1.10801E-05
Chr5	11936319	11944506	68	8188	2.73E-52
Chr5	11973082	11974655	4	1574	6.97986E-06
Chr5	11980254	11982382	5	2129	2.50E-11
Chr5	11986504	11987822	6	1319	6.43E-07
Chr5	12007653	12009897	7	2245	8.99E-11
Chr5	12011003	12011846	4	844	3.10911E-05
Chr5	12019272	12021272	7	2001	2.02E-10
Chr5	12029560	12031301	8	1742	6.75E-11
Chr5	12032948	12034990	7	2043	6.04E-11
Chr5	12037262	12040679	8	3418	9.13E-09
Chr5	12041825	12043495	4	1671	1.04092E-06
Chr5	12044614	12046315	6	1702	1.6404E-05
Chr5	12101285	12104350	6	3066	9.51E-08
Chr5	12110338	12112538	7	2201	6.21E-10
Chr5	12116407	12117256	5	850	1.0223E-05
Chr5	12125032	12128376	13	3345	5.24E-17
Chr5	12134036	12136515	7	2480	6.18E-10
Chr5	12142934	12148284	14	5351	5.66E-14
Chr5	12153783	12156186	6	2404	2.18E-08
Chr5	12160316	12164175	8	3860	7.98E-11
Chr5	12174792	12175964	5	1173	1.77E-09

Chr5	12192223	12193368	4	1146	1.58844E-06
Chr5	12226858	12229799	8	2942	3.02E-11
Chr5	12236212	12239558	9	3347	9.85E-15
Chr5	12240752	12242274	5	1523	4.40E-09
Chr5	12246171	12246797	5	627	5.40479E-07
Chr5	12318312	12320943	5	2632	1.94E-07
Chr5	12327428	12329932	7	2505	1.03E-10
Chr5	12342476	12344803	8	2328	1.59E-08
Chr5	12346449	12348863	9	2415	7.50E-11
Chr5	12366838	12368170	6	1333	4.10E-07
Chr5	12369534	12370318	4	785	1.38389E-05
Chr5	12398451	12399369	11	919	5.10E-15
Chr5	12430779	12431925	6	1147	3.68649E-07
Chr5	12471055	12472537	5	1483	6.56E-07
Chr5	12506191	12508554	4	2364	4.91678E-05
Chr5	12511026	12512412	4	1387	6.09793E-06
Chr5	12517217	12519694	6	2478	1.70E-09
Chr5	12523310	12524220	8	911	1.08E-10
Chr5	12529805	12532836	9	3032	2.02E-09
Chr5	12534220	12536287	8	2068	1.93E-11
Chr5	12578381	12581778	9	3398	6.92E-13
Chr5	12609812	12611488	4	1677	3.81E-07
Chr5	12636918	12637823	6	906	5.98E-09
Chr5	12645266	12647755	7	2490	1.72E-09
Chr5	12650276	12651051	4	776	6.60183E-06
Chr5	12714278	12716468	4	2191	6.08899E-05
Chr5	12744506	12746783	7	2278	1.56E-07
Chr5	12752526	12754111	5	1586	4.92E-08
Chr5	12756160	12758896	7	2737	4.27E-10
Chr5	12760674	12762695	11	2022	2.22E-18
Chr5	12767730	12769116	6	1387	2.45E-08
Chr5	12770423	12772448	4	2026	2.42E-07
Chr5	12916654	12917582	4	929	7.16E-08
Chr5	12936690	12937277	5	588	5.26E-08
Chr5	12946594	12947219	5	626	1.06E-09
Chr5	12969023	12971229	5	2207	1.37E-08
Chr5	13002978	13003905	4	928	1.41E-07
Chr5	13022384	13026314	10	3931	2.12E-12
Chr5	13030322	13031442	4	1121	2.12379E-06
Chr5	13033896	13036669	8	2774	3.15E-08
Chr5	13089714	13090177	4	464	5.35617E-05
Chr5	13130687	13133202	6	2516	4.23E-08
Chr5	13158496	13159976	4	1481	4.00E-07
Chr5	13181691	13182955	4	1265	3.05134E-05
Chr5	13187634	13188579	4	946	1.17274E-06
Chr5	13282274	13284040	5	1767	6.82E-08
Chr5	13295141	13297208	4	2068	5.45395E-06
Chr5	13300031	13302402	7	2372	5.45E-10
Chr5	13323739	13324464	4	726	6.47468E-05
Chr5	13372938	13374776	7	1839	1.48E-11
Chr5	13496036	13497208	4	1173	8.28E-08
Chr5	13887996	13889618	5	1623	2.60E-11
Chr5	13929264	13930663	4	1400	3.59E-08
Chr5	13961919	13963717	9	1799	4.86E-13
Chr5	13969228	13969739	5	512	2.21E-09
Chr5	14206637	14207158	4	522	1.78086E-06
Chr5	14256542	14257725	12	1184	6.04E-14
Chr5	14259633	14262578	11	2946	2.31E-18
Chr5	14271315	14272422	4	1108	1.75E-08
Chr5	14573999	14574989	4	991	1.41936E-06
Chr5	14589737	14589768	4	32	5.96E-07
Chr5	14680453	14681112	4	660	1.19001E-06
Chr5	14828380	14829407	4	1028	6.46E-09

Chr5	14832440	14834144	5	1705	9.31E-07
Chr5	15238199	15239883	6	1685	2.95E-08
Chr5	15353064	15353455	4	392	7.39E-07
Chr5	15495315	15496099	7	785	3.43E-09
Chr5	15649596	15650419	4	824	1.45866E-06
Chr5	15947311	15948027	5	717	1.39E-07
Chr5	16033725	16033745	6	21	8.28E-13
Chr5	16699263	16700914	6	1652	2.21E-09
Chr5	16970709	16971023	4	315	3.58E-08
Chr5	17598115	17599110	6	996	4.58E-09
Chr5	17602464	17604580	7	2117	3.33E-10
Chr5	18144786	18146442	6	1657	3.57E-07
Chr5	18170435	18171923	5	1489	6.67E-07
Chr5	18473862	18475139	5	1278	6.62394E-06
Chr5	18625048	18625337	4	290	7.56E-07
Chr5	18937950	18938828	6	879	3.55E-07
Chr5	19192318	19194076	4	1759	2.06008E-05
Chr5	19360369	19363263	8	2895	2.10E-11
Chr5	20803534	20804070	4	537	2.28E-09
Chr5	21545678	21547119	5	1442	1.64E-08
Chr5	21689740	21690568	7	829	7.87E-11
Chr5	22614756	22616982	7	2227	5.42E-08
Chr5	26069849	26070816	4	968	1.06381E-06
Chr5	26209923	26210219	7	297	3.65E-11

-Pit Shoot 7dat (Hypo-DMRs)

Chromosome	Start	End	number of DMCs	DMR lenght	P-value
Chr1	4331464	4333344	4	1881	0.000300095
Chr1	7355052	7357260	9	2209	2.98E-11
Chr1	7360580	7362579	6	2000	3.14436E-05
Chr1	8865040	8865096	4	57	4.17384E-06
Chr1	10723623	10724736	5	1114	3.33E-08
Chr1	12855916	12857007	4	1092	4.02E-07
Chr1	13100598	13102038	4	1441	3.69615E-06
Chr1	13187148	13188767	5	1620	7.38313E-06
Chr1	13442458	13442995	5	538	2.87E-09
Chr1	13514503	13515434	4	932	0.000118154
Chr1	13941767	13945017	7	3251	1.04E-09
Chr1	13957440	13958507	4	1068	3.49737E-06
Chr1	14092814	14094304	5	1491	3.09884E-06
Chr1	14198403	14199846	6	1444	2.09E-08
Chr1	14220395	14221326	4	932	3.27728E-05
Chr1	14223049	14223741	5	693	1.21E-07
Chr1	14234472	14236651	4	2180	0.000722846
Chr1	14242631	14245306	6	2676	1.80E-07
Chr1	14247868	14249348	6	1481	1.22E-07
Chr1	14320637	14320789	4	153	1.36E-08
Chr1	14325093	14325921	4	829	2.41E-07
Chr1	14498206	14498727	4	522	1.99E-07
Chr1	14542984	14544176	4	1193	1.73E-07
Chr1	14582820	14584698	6	1879	5.74E-09
Chr1	14715836	14717015	4	1180	2.33744E-06
Chr1	15154572	15156544	6	1973	5.92E-09
Chr1	15180791	15182731	7	1941	3.21E-12
Chr1	15496702	15498322	4	1621	9.95E-08
Chr1	15503769	15505408	6	1640	4.14351E-06
Chr1	15515692	15518601	5	2910	1.24E-07
Chr1	15611572	15613299	4	1728	2.85422E-06
Chr1	15671920	15672462	4	543	1.81139E-05
Chr1	15711135	15712770	5	1636	3.93715E-06
Chr1	15766249	15767392	4	1144	0.000223252
Chr1	15874926	15876555	4	1630	2.85E-09

Chr1	16015386	16017948	5	2563	2.30246E-05
Chr1	16094413	16098359	7	3947	4.79E-10
Chr1	16111179	16111315	4	137	0.000345396
Chr1	16117487	16118626	4	1140	1.63E-07
Chr1	16122308	16124581	6	2274	1.55E-09
Chr1	16312030	16314312	4	2283	1.54717E-05
Chr1	16318233	16319247	5	1015	2.1877E-06
Chr1	16509935	16513548	7	3614	3.04E-09
Chr1	16517771	16519743	5	1973	1.93539E-05
Chr1	16630181	16630982	4	802	4.12E-07
Chr1	16634524	16636234	4	1711	9.76766E-06
Chr1	16680017	16681141	4	1125	2.86563E-06
Chr1	17027821	17030201	6	2381	1.28E-08
Chr1	17255440	17257122	6	1683	3.48E-07
Chr1	19424903	19424931	4	29	3.48E-07
Chr1	19887137	19887261	4	125	1.16E-10
Chr1	20314728	20315215	4	488	2.37703E-05
Chr1	26343557	26343851	4	295	7.20368E-06
Chr1	27635711	27636487	5	777	1.38E-08
Chr2	9710	11137	8	1428	4.48E-12
Chr2	373581	374783	5	1203	3.13257E-06
Chr2	375880	376421	4	542	3.62E-07
Chr2	2398334	2400356	4	2023	4.3746E-06
Chr2	2468132	2469483	5	1352	6.43E-07
Chr2	2622773	2623308	4	536	1.54659E-05
Chr2	2676874	2681341	8	4468	2.18E-08
Chr2	2825402	2826896	4	1495	9.71353E-05
Chr2	2878536	2879443	4	908	1.72986E-05
Chr2	3076557	3077625	4	1069	1.22445E-06
Chr2	3082631	3083445	5	815	7.59E-10
Chr2	3098846	3100459	4	1614	8.47E-07
Chr2	3230953	3232313	4	1361	7.41E-07
Chr2	3550698	3551941	5	1244	2.56E-07
Chr2	3615456	3616749	4	1294	0.000847242
Chr2	3620562	3621415	4	854	0.001578697
Chr2	3640357	3640899	4	543	8.30078E-07
Chr2	3643196	3644541	5	1346	1.21E-07
Chr2	3681282	3681637	4	356	1.41972E-05
Chr2	3821866	3823286	4	1421	2.99321E-05
Chr2	3858690	3861695	7	3006	5.86E-09
Chr2	3879915	3881098	4	1184	5.11E-08
Chr2	3888237	3889355	5	1119	3.22E-08
Chr2	3905312	3907080	4	1769	3.72839E-06
Chr2	3920285	3921904	4	1620	4.66507E-05
Chr2	3951608	3952717	5	1110	4.41017E-05
Chr2	4125238	4126316	4	1079	2.02636E-06
Chr2	4171250	4172646	5	1397	4.44E-07
Chr2	4238706	4240524	4	1819	3.01129E-06
Chr2	4256951	4259718	7	2768	2.47E-12
Chr2	4289962	4290789	5	828	2.50311E-05
Chr2	4368819	4370764	5	1946	1.49E-08
Chr2	4563469	4564337	4	869	2.15457E-06
Chr2	4712622	4713106	4	485	0.000367025
Chr2	4952271	4953520	4	1250	1.37225E-05
Chr2	4974800	4976556	4	1757	6.36024E-06
Chr2	4981688	4984385	4	2698	1.50E-07
Chr2	5100300	5101886	4	1587	1.10E-07
Chr2	5135613	5137794	6	2182	3.31E-09
Chr2	5332615	5334406	7	1792	3.81E-07
Chr2	5352914	5353428	4	515	2.30925E-06
Chr2	5369389	5370413	4	1025	2.34933E-05
Chr2	5563534	5565524	4	1991	9.00527E-05
Chr2	5598865	5600373	6	1509	1.29E-08

Chr2	5616418	5617786	4	1369	1.91382E-06
Chr2	5797492	5800115	4	2624	4.56756E-06
Chr2	5893173	5895370	6	2198	2.42E-10
Chr2	6027657	6029013	4	1357	3.01E-07
Chr2	6266095	6268053	4	1959	5.51186E-06
Chr2	6343268	6343788	4	521	3.50245E-05
Chr2	6435708	6436459	4	752	4.35E-08
Chr2	6507670	6509573	6	1904	1.24E-10
Chr2	6788837	6789342	4	506	2.41272E-06
Chr2	6837495	6838423	5	929	5.81E-07
Chr2	7225041	7226925	5	1885	4.68868E-06
Chr2	8818263	8820142	4	1880	1.88305E-05
Chr2	8995532	8995881	4	350	5.60E-07
Chr2	9188372	9190402	4	2031	1.99306E-06
Chr2	10604385	10605493	5	1109	2.48148E-05
Chr2	10814594	10815192	7	599	4.75E-09
Chr2	13223271	13224544	6	1274	1.36E-07
Chr2	15405297	15405909	6	613	2.00E-14
Chr2	15411378	15411631	4	254	2.76E-08
Chr2	17337752	17338225	5	474	6.82229E-06
Chr3	1555774	1558761	6	2988	4.15E-09
Chr3	1963676	1964604	5	929	4.04E-08
Chr3	1968901	1970421	9	1521	2.94E-14
Chr3	3809823	3810727	5	905	1.61E-08
Chr3	9785746	9786581	4	836	6.53E-08
Chr3	10106549	10107771	4	1223	1.9567E-05
Chr3	10634531	10634629	4	99	1.6123E-05
Chr3	10920102	10921079	4	978	1.3536E-05
Chr3	10970598	10972984	5	2387	0.000668079
Chr3	11145014	11147236	5	2223	3.80E-08
Chr3	11492242	11493109	6	868	8.28675E-07
Chr3	11681017	11682434	5	1418	9.36E-08
Chr3	11874636	11876793	5	2158	1.62E-08
Chr3	12102494	12103667	5	1174	4.38E-08
Chr3	12195295	12197961	6	2667	9.84E-09
Chr3	12203088	12203668	4	581	1.13176E-05
Chr3	12205213	12207293	9	2081	1.80E-10
Chr3	12220600	12222265	4	1666	3.48E-07
Chr3	12291294	12292280	4	987	2.44694E-05
Chr3	12402781	12403477	5	697	7.98185E-06
Chr3	12441569	12442897	5	1329	2.42436E-05
Chr3	12463427	12465030	6	1604	8.81697E-06
Chr3	12525880	12526882	4	1003	9.87559E-05
Chr3	12533700	12535025	6	1326	7.69E-10
Chr3	12556044	12557202	4	1159	9.33108E-06
Chr3	12723521	12724325	4	805	1.38829E-05
Chr3	12965819	12966912	11	1094	3.53E-12
Chr3	13169542	13170553	4	1012	0.000567459
Chr3	13362750	13366521	8	3772	1.90E-10
Chr3	13467978	13469133	6	1156	1.31E-07
Chr3	13515836	13517420	6	1585	4.05E-08
Chr3	13636486	13639538	7	3053	7.92E-13
Chr3	13706114	13707200	9	1087	2.77E-16
Chr3	13709806	13711098	6	1293	2.90205E-06
Chr3	13714104	13714669	4	566	5.62077E-06
Chr3	13813953	13815886	4	1934	0.001005696
Chr3	13826921	13828121	4	1201	1.14E-07
Chr3	13831010	13833248	4	2239	2.40144E-05
Chr3	13865830	13866789	4	960	5.51298E-05
Chr3	13881037	13882169	4	1133	0.003462901
Chr3	14078489	14080462	5	1974	5.26E-07
Chr3	14151822	14153315	5	1494	6.13E-08
Chr3	14172711	14173291	5	581	9.65065E-05

Chr3	14185764	14187177	8	1414	6.61E-09
Chr3	14190824	14190914	4	91	7.00E-07
Chr3	14205692	14208913	11	3222	1.72E-11
Chr3	14211248	14215110	11	3863	1.67E-09
Chr3	14357741	14359201	4	1461	4.25895E-06
Chr3	14410129	14411621	4	1493	1.48619E-05
Chr3	14420451	14420963	4	513	1.58316E-05
Chr3	14426722	14428060	5	1339	6.43E-08
Chr3	14557000	14558052	4	1053	4.72603E-05
Chr3	14579204	14579494	4	291	3.99307E-06
Chr3	14769734	14771373	4	1640	2.93915E-06
Chr3	14846753	14848435	4	1683	1.92937E-06
Chr3	14862393	14863185	5	793	1.09548E-05
Chr3	15114733	15117220	5	2488	2.01E-09
Chr3	15119701	15121368	7	1668	1.12E-13
Chr3	15134379	15135430	4	1052	0.00221785
Chr3	15153760	15155590	4	1831	8.18E-08
Chr3	15251098	15252931	4	1834	1.63519E-06
Chr3	15305405	15306457	6	1053	3.44E-08
Chr3	15330054	15331418	9	1365	1.11E-11
Chr3	15443691	15445506	6	1816	4.79E-07
Chr3	15496998	15497769	5	772	2.07491E-06
Chr3	15581640	15582182	4	543	1.31193E-06
Chr3	15719135	15720282	4	1148	2.58571E-05
Chr3	15963412	15964267	4	856	4.15908E-06
Chr3	15998931	15999516	4	586	3.92E-07
Chr3	16437687	16438622	4	936	8.98E-07
Chr3	16640190	16640910	4	721	7.76702E-06
Chr3	16809536	16810827	5	1292	7.07E-07
Chr3	16812289	16813768	6	1480	1.91E-08
Chr3	16957477	16960445	6	2969	1.36E-08
Chr3	17472718	17472785	4	68	6.35E-09
Chr3	18793023	18794690	5	1668	1.45099E-06
Chr3	22232642	22233732	4	1091	6.0564E-05
Chr3	23108942	23110173	5	1232	9.78E-08
Chr4	226396	226550	4	155	3.55E-09
Chr4	330736	331272	4	537	0.000503862
Chr4	1230859	1230879	4	21	4.46E-09
Chr4	1694171	1696023	4	1853	8.82956E-05
Chr4	1763473	1765492	5	2020	7.99E-08
Chr4	1812283	1812948	5	666	4.14E-08
Chr4	1986512	1988789	5	2278	8.94E-09
Chr4	2013487	2014736	4	1250	8.76E-08
Chr4	2141084	2141929	4	846	8.00886E-07
Chr4	2197566	2199298	4	1733	5.37438E-06
Chr4	2202129	2202849	4	721	0.000219421
Chr4	2284887	2287724	6	2838	1.80E-09
Chr4	2353758	2354955	4	1198	0.000148306
Chr4	2834722	2835561	4	840	0.000231095
Chr4	2854256	2855894	4	1639	3.08284E-05
Chr4	3016930	3018323	4	1394	4.71E-08
Chr4	3030585	3032193	4	1609	2.62053E-05
Chr4	3040767	3042287	4	1521	0.000110302
Chr4	3054479	3056242	9	1764	8.20405E-06
Chr4	3139805	3140480	4	676	1.85E-07
Chr4	3180691	3182755	5	2065	5.95E-08
Chr4	3187405	3188530	4	1126	3.6706E-06
Chr4	3224031	3225274	4	1244	6.45055E-07
Chr4	3494225	3495308	4	1084	7.85662E-06
Chr4	3538726	3540074	5	1349	1.72E-07
Chr4	3554175	3555009	4	835	5.31825E-06
Chr4	3566215	3567449	5	1235	7.49E-10
Chr4	3691942	3693729	8	1788	6.30E-10

Chr4	3740951	3743125	5	2175	0.00010464
Chr4	3776872	3779244	5	2373	8.54974E-07
Chr4	3795778	3796935	4	1158	6.73E-08
Chr4	3846379	3846560	4	182	3.80827E-05
Chr4	3849459	3850723	4	1265	1.18556E-05
Chr4	3871695	3872309	4	615	0.000842282
Chr4	3911709	3913591	4	1883	3.66228E-05
Chr4	3927341	3929869	6	2529	1.54E-09
Chr4	3954031	3955233	5	1203	1.13128E-05
Chr4	3963594	3966798	6	3205	2.96755E-05
Chr4	3968069	3969249	5	1181	0.000171015
Chr4	3974079	3975065	5	987	2.20E-09
Chr4	3979281	3980385	4	1105	6.41991E-05
Chr4	3994607	3996253	5	1647	3.43163E-05
Chr4	4110581	4112485	4	1905	7.43696E-05
Chr4	4181506	4184017	6	2512	5.42E-09
Chr4	4212106	4213228	4	1123	1.83476E-06
Chr4	4214388	4215291	4	904	4.64E-07
Chr4	4306993	4307669	5	677	2.50924E-06
Chr4	4348640	4350322	4	1683	0.000222957
Chr4	4427710	4428179	4	470	3.17048E-05
Chr4	4437840	4441795	8	3956	1.11E-08
Chr4	4601235	4601659	5	425	3.93E-07
Chr4	4753773	4755583	4	1811	6.82527E-06
Chr4	4763049	4763976	5	928	4.73E-09
Chr4	4770093	4771546	4	1454	1.466E-06
Chr4	5044201	5044360	4	160	5.32901E-05
Chr4	5062279	5063786	6	1508	1.77E-10
Chr4	5065053	5065845	5	793	4.04E-10
Chr4	5069017	5070078	4	1062	1.23946E-06
Chr4	5081271	5083125	6	1855	2.67E-08
Chr4	5116472	5117731	4	1260	1.00642E-05
Chr4	5489575	5490542	5	968	2.73E-08
Chr4	5534279	5536150	5	1872	1.53E-07
Chr4	5955409	5957803	5	2395	3.24001E-05
Chr4	6726826	6729006	6	2181	1.37E-09
Chr4	6919275	6919832	4	558	5.62169E-05
Chr4	10993608	10995061	5	1454	2.65613E-05
Chr4	11036787	11038308	4	1522	0.000659936
Chr4	14146220	14146674	5	455	9.23E-09
Chr5	2394285	2395916	5	1632	2.13322E-05
Chr5	2401826	2402038	4	213	2.98484E-06
Chr5	3899070	3900107	4	1038	2.87E-07
Chr5	9093207	9094448	5	1242	9.89E-07
Chr5	10736158	10737449	5	1292	6.69E-07
Chr5	10838180	10839291	4	1112	1.57803E-06
Chr5	10887172	10891040	10	3869	7.82E-14
Chr5	10994325	10995144	4	820	9.70091E-05
Chr5	11161317	11162778	7	1462	1.26E-07
Chr5	11184699	11188654	16	3956	7.66E-08
Chr5	11206908	11209387	8	2480	3.43E-10
Chr5	11343565	11344646	4	1082	9.40766E-06
Chr5	11363320	11365816	6	2497	1.32E-07
Chr5	11429226	11430862	5	1637	6.03E-08
Chr5	11460646	11462462	6	1817	3.83E-10
Chr5	11472747	11473618	4	872	3.63967E-06
Chr5	11474715	11475787	4	1073	4.67E-07
Chr5	11508428	11509886	5	1459	6.63E-10
Chr5	11590735	11591605	4	871	2.12E-08
Chr5	11642192	11644701	5	2510	1.57665E-06
Chr5	11649220	11650642	5	1423	3.01164E-06
Chr5	11700106	11700631	4	526	3.4119E-06
Chr5	11702274	11702862	4	589	0.004682368

Chr5	11727723	11728774	4	1052	0.000726177
Chr5	11737004	11738183	4	1180	1.2583E-05
Chr5	11751709	11753285	6	1577	7.84E-07
Chr5	11783237	11784749	4	1513	4.50206E-06
Chr5	11937662	11939508	10	1847	1.02E-10
Chr5	11941041	11942247	4	1207	0.002540336
Chr5	12009302	12011390	8	2089	2.55E-07
Chr5	12014020	12015107	4	1088	1.17702E-05
Chr5	12022550	12024538	6	1989	2.77E-08
Chr5	12028884	12030013	5	1130	1.38E-07
Chr5	12039331	12039966	4	636	0.000160615
Chr5	12051498	12052567	4	1070	8.06817E-06
Chr5	12109205	12110103	4	899	1.03536E-05
Chr5	12118934	12121101	4	2168	3.13E-07
Chr5	12153060	12155297	7	2238	7.18E-11
Chr5	12190091	12191964	4	1874	2.69E-07
Chr5	12234617	12235366	4	750	4.65E-07
Chr5	12317554	12318773	4	1220	3.4131E-06
Chr5	12326280	12328754	5	2475	1.12E-08
Chr5	12403796	12404738	4	943	6.38534E-06
Chr5	12458576	12462732	7	4157	1.92E-09
Chr5	12473705	12474448	4	744	4.25E-07
Chr5	12502530	12503764	4	1235	6.551E-06
Chr5	12528981	12530193	4	1213	0.000371285
Chr5	12572168	12574273	6	2106	1.35E-07
Chr5	12641714	12643040	4	1327	3.12682E-05
Chr5	12762824	12763852	4	1029	2.35E-08
Chr5	12946730	12948182	4	1453	3.03445E-06
Chr5	12951796	12953234	4	1439	3.40E-07
Chr5	12954318	12955721	4	1404	9.82464E-06
Chr5	12998507	13001032	7	2526	2.96E-09
Chr5	13002467	13004082	4	1616	6.50191E-06
Chr5	13023428	13025611	4	2184	1.40864E-05
Chr5	13122094	13123205	4	1112	1.94E-07
Chr5	13135266	13136452	4	1187	2.34E-07
Chr5	13185417	13186387	4	971	4.05887E-05
Chr5	13259458	13261200	7	1743	2.00E-09
Chr5	13296920	13298102	4	1183	2.23198E-06
Chr5	13324903	13325962	4	1060	4.32E-08
Chr5	13398671	13401907	7	3237	1.28E-08
Chr5	13529325	13530897	6	1573	1.10916E-08
Chr5	13966378	13967874	5	1497	1.96E-08
Chr5	14172970	14174010	4	1041	2.50013E-05
Chr5	15354515	15355887	4	1373	8.89998E-06
Chr5	15561859	15562091	8	233	2.33E-13
Chr5	15841031	15841196	4	166	2.4573E-06
Chr5	16470846	16471462	4	617	2.44985E-06
Chr5	16702892	16704623	5	1732	4.41465E-07
Chr5	18196366	18197835	5	1470	4.64E-08
Chr5	19891228	19892180	5	953	1.34233E-06
Chr5	21167611	21168442	4	832	1.55044E-05

-Pit Root 7dat (Hyper-DMRs)

Chromosome	Start	End	number of DMCs	DMR lenght	P-value
Chr1	5694500	5695522	5	1023	1.63554E-06
Chr1	6590349	6591039	5	691	7.38E-07
Chr1	7069397	7069777	4	381	1.28222E-06
Chr1	7353322	7355168	9	1847	1.01E-07
Chr1	7358200	7365105	25	6906	6.33E-21
Chr1	8731206	8732783	6	1578	2.57E-09
Chr1	8928203	8930006	5	1804	4.15E-08
Chr1	9371307	9372664	4	1358	0.000232174

Chr1	9678242	9679633	5	1392	3.02532E-06
Chr1	13005187	13006465	4	1279	3.90464E-05
Chr1	13099961	13101629	4	1669	2.07059E-05
Chr1	13299251	13299993	4	743	3.35912E-07
Chr1	13328799	13330714	7	1916	1.15E-09
Chr1	13335202	13336520	4	1319	2.62E-07
Chr1	13391839	13393325	4	1487	3.05768E-06
Chr1	13493078	13494473	4	1396	1.10822E-05
Chr1	13652115	13653922	4	1808	4.13655E-06
Chr1	13661124	13662559	6	1436	1.22E-07
Chr1	13794104	13795567	5	1464	9.68314E-06
Chr1	13828763	13831820	6	3058	1.51E-07
Chr1	13862742	13863592	4	851	2.69853E-05
Chr1	13884748	13885708	4	961	1.14553E-06
Chr1	13924409	13925092	4	684	1.12698E-06
Chr1	13942856	13944088	5	1233	1.55E-07
Chr1	13948865	13949748	4	884	5.1178E-05
Chr1	13956360	13957440	4	1081	1.90524E-06
Chr1	14044951	14045914	4	964	0.000301473
Chr1	14081655	14082144	4	490	0.000285338
Chr1	14083264	14085747	4	2484	1.99877E-05
Chr1	14105244	14105752	4	509	5.53926E-05
Chr1	14183116	14183541	4	426	3.68283E-05
Chr1	14189649	14190753	5	1105	0.001213201
Chr1	14193656	14195245	4	1590	2.02852E-06
Chr1	14199458	14202183	6	2726	4.27E-09
Chr1	14221929	14223664	6	1736	7.07E-09
Chr1	14229360	14231203	5	1844	1.48E-07
Chr1	14233971	14236792	9	2822	1.50E-10
Chr1	14241842	14243112	6	1271	7.05E-08
Chr1	14253270	14254409	4	1140	1.58611E-05
Chr1	14269329	14270183	6	855	1.55162E-06
Chr1	14271393	14272487	4	1095	4.39E-07
Chr1	14321437	14322807	5	1371	3.3022E-06
Chr1	14334366	14335925	5	1560	5.7398E-06
Chr1	14387385	14389465	6	2081	2.21E-07
Chr1	14466739	14467154	4	416	0.00023684
Chr1	14582344	14582615	4	272	4.82106E-06
Chr1	14600759	14604031	9	3273	5.75E-10
Chr1	14849454	14851195	7	1742	2.24E-10
Chr1	15067271	15068324	7	1054	1.21E-08
Chr1	15073101	15073626	5	526	8.46593E-06
Chr1	15081492	15085829	30	4338	1.53E-27
Chr1	15151078	15152573	4	1496	1.44406E-05
Chr1	15156864	15158355	6	1492	1.94E-07
Chr1	15200051	15201180	5	1130	1.76499E-05
Chr1	15442312	15444207	4	1896	1.4715E-05
Chr1	15464877	15465043	4	167	5.31781E-05
Chr1	15500787	15501779	4	993	6.31E-09
Chr1	15506338	15507693	6	1356	4.23E-09
Chr1	15510196	15511551	4	1356	3.94E-07
Chr1	15538187	15541750	10	3564	9.14E-14
Chr1	15560880	15562219	4	1340	9.17311E-05
Chr1	15573317	15575471	8	2155	9.33E-15
Chr1	15639389	15640681	4	1293	2.48953E-06
Chr1	15667252	15669102	5	1851	4.32E-09
Chr1	15671023	15671626	4	604	5.77E-07
Chr1	15687140	15688753	4	1614	3.13084E-05
Chr1	15698954	15700145	5	1192	4.52915E-06
Chr1	15712329	15715809	11	3481	7.36E-16
Chr1	15738285	15739099	4	815	5.08766E-06
Chr1	15956648	15958077	4	1430	2.98634E-06
Chr1	16015804	16017868	5	2065	7.77734E-07

Chr1	16094864	16097549	7	2686	3.62E-10
Chr1	16102961	16105058	4	2098	4.59124E-06
Chr1	16369874	16371755	5	1882	2.71898E-06
Chr1	16391898	16392918	4	1021	1.29337E-05
Chr1	16491491	16491818	4	328	5.77E-07
Chr1	16513359	16514985	9	1627	4.44E-10
Chr1	16523619	16524601	5	983	8.48E-08
Chr1	16526521	16528402	5	1882	5.45E-08
Chr1	16538829	16539336	4	508	3.92E-07
Chr1	16626998	16628678	5	1681	4.90E-08
Chr1	16635151	16636839	6	1689	8.70E-09
Chr1	16694729	16695434	4	706	5.14113E-06
Chr1	17027895	17029372	7	1478	4.02E-09
Chr1	17036626	17039000	7	2375	1.31E-08
Chr1	18002440	18003975	6	1536	1.59E-07
Chr1	19336964	19337651	4	688	2.59792E-05
Chr1	20085286	20088597	8	3312	4.57E-12
Chr1	20709996	20710643	5	648	1.96E-07
Chr1	21747900	21750374	7	2475	2.98E-09
Chr1	21751552	21752647	7	1096	3.97E-10
Chr1	24273579	24275839	39	2261	4.30E-50
Chr1	26366858	26368261	4	1404	2.29E-08
Chr2	1247	3743	87	2497	1.48E-174
Chr2	5552	5915	7	364	5.54E-07
Chr2	8552	12512	8	3961	0.000931465
Chr2	17636	18621	5	986	7.35E-10
Chr2	47098	47690	7	593	6.02E-08
Chr2	303346	303396	5	51	5.72E-11
Chr2	375999	377963	9	1965	5.89E-12
Chr2	821730	822102	4	373	1.02227E-05
Chr2	1784044	1786839	7	2796	5.96E-08
Chr2	1907987	1909469	4	1483	3.24144E-05
Chr2	1910589	1911759	4	1171	4.1679E-05
Chr2	2079823	2080322	6	500	1.25552E-07
Chr2	2202822	2205615	9	2794	5.28E-12
Chr2	2377724	2381774	10	4051	3.07E-12
Chr2	2392029	2394844	10	2816	1.79E-16
Chr2	2401452	2404121	7	2670	1.44749E-06
Chr2	2407004	2409049	6	2046	1.58631E-05
Chr2	2448912	2449391	4	480	7.92943E-05
Chr2	2450497	2452175	5	1679	1.24E-07
Chr2	2466610	2467331	4	722	1.06138E-05
Chr2	2505143	2506798	4	1656	3.78791E-06
Chr2	2576951	2578930	4	1980	2.65739E-05
Chr2	2644766	2645791	4	1026	4.44998E-06
Chr2	2692064	2694955	5	2892	2.72589E-05
Chr2	2707925	2708582	6	658	2.34E-07
Chr2	2717674	2718486	4	813	0.000773636
Chr2	2742122	2743321	4	1200	4.11488E-05
Chr2	2746394	2747099	4	706	2.42442E-05
Chr2	2856465	2857015	6	551	3.99E-09
Chr2	3084132	3085576	5	1445	9.07E-07
Chr2	3093456	3095017	6	1562	2.74E-09
Chr2	3101408	3103870	7	2463	2.78E-10
Chr2	3160728	3162188	4	1461	1.33032E-06
Chr2	3226869	3228120	4	1252	1.04891E-05
Chr2	3240687	3242048	21	1362	2.07E-20
Chr2	3247282	3247952	13	671	1.44E-19
Chr2	3249266	3253259	39	3994	9.34E-48
Chr2	3254818	3259190	29	4373	1.46E-27
Chr2	3260253	3263946	49	3694	3.07E-68
Chr2	3265366	3280730	160	15365	1.56E-193
Chr2	3282238	3283522	6	1285	1.03E-07

Chr2	3285308	3306620	212	21313	7.93E-242
Chr2	3307632	3338270	271	30639	2.97E-308
Chr2	3339836	3344762	66	4927	8.86E-67
Chr2	3346256	3352004	57	5749	3.16E-64
Chr2	3353458	3355862	22	2405	8.15E-27
Chr2	3356904	3359550	20	2647	3.21E-25
Chr2	3360814	3367952	99	7139	1.53E-112
Chr2	3377482	3379110	10	1629	6.53E-15
Chr2	3393393	3393848	10	456	2.87E-13
Chr2	3398749	3398880	11	132	1.50E-16
Chr2	3431385	3431570	4	186	2.31614E-06
Chr2	3455834	3455904	4	71	1.1508E-06
Chr2	3459037	3461024	10	1988	9.80E-12
Chr2	3485144	3486571	9	1428	1.49E-13
Chr2	3487585	3489119	9	1535	2.30E-13
Chr2	3490190	3490453	5	264	2.41E-07
Chr2	3491597	3493336	14	1740	1.58E-19
Chr2	3497893	3500110	8	2218	1.98E-10
Chr2	3543017	3543786	5	770	3.13E-11
Chr2	3548487	3550185	4	1699	1.6208E-06
Chr2	3605740	3607297	14	1558	3.18E-08
Chr2	3615021	3627437	86	12417	3.49E-78
Chr2	3687348	3689525	5	2178	8.54E-10
Chr2	3728437	3730241	5	1805	7.24E-07
Chr2	3764978	3765549	4	572	1.08065E-06
Chr2	3786566	3787241	5	676	1.05882E-06
Chr2	3817148	3817209	4	62	8.71175E-06
Chr2	3821818	3823175	4	1358	1.21559E-06
Chr2	3881193	3883872	6	2680	4.86E-09
Chr2	3886480	3887908	5	1429	3.18E-07
Chr2	3905756	3907826	4	2071	1.14918E-05
Chr2	3951451	3953104	11	1654	2.00E-12
Chr2	3968177	3970190	7	2014	3.29E-07
Chr2	4007571	4008529	6	959	2.23E-08
Chr2	4010944	4012485	4	1542	4.32351E-05
Chr2	4041984	4043057	4	1074	2.82724E-05
Chr2	4051527	4052105	4	579	1.85567E-06
Chr2	4054753	4055691	4	939	2.93317E-06
Chr2	4090991	4093136	6	2146	1.51E-08
Chr2	4129916	4130148	6	233	5.00E-09
Chr2	4200905	4201994	4	1090	9.42E-08
Chr2	4234049	4235049	4	1001	0.000112808
Chr2	4238359	4241010	9	2652	2.38E-09
Chr2	4504310	4505757	5	1448	1.50E-08
Chr2	4519289	4520240	4	952	9.29611E-05
Chr2	4627597	4629130	4	1534	3.31843E-06
Chr2	4688149	4689565	6	1417	2.29E-07
Chr2	4722411	4724105	5	1695	2.13671E-06
Chr2	4728568	4729075	4	508	1.48064E-06
Chr2	4734125	4736192	4	2068	9.19E-09
Chr2	4808417	4809174	4	758	2.57627E-05
Chr2	4813616	4817263	9	3648	5.40E-12
Chr2	4844011	4844487	13	477	6.05E-19
Chr2	4849542	4852578	7	3037	1.67E-09
Chr2	4951972	4953408	5	1437	2.11E-08
Chr2	4978562	4980670	4	2109	0.000522976
Chr2	4983931	4987379	9	3449	2.01E-11
Chr2	4990136	4991801	4	1666	8.20891E-06
Chr2	5041248	5043432	5	2185	8.99E-07
Chr2	5044774	5047711	7	2938	7.03E-08
Chr2	5100872	5102680	6	1809	6.25E-08
Chr2	5103728	5105024	6	1297	5.58E-11
Chr2	5134905	5136629	4	1725	0.000194024

Chr2	5253362	5254863	5	1502	2.25E-09
Chr2	5277398	5279953	6	2556	1.58E-09
Chr2	5280965	5282751	6	1787	1.12E-09
Chr2	5287307	5289241	6	1935	4.55E-08
Chr2	5301997	5303345	5	1349	4.42E-13
Chr2	5310956	5311924	4	969	6.2175E-06
Chr2	5334917	5336443	7	1527	1.47E-08
Chr2	5369042	5370187	5	1146	2.10E-08
Chr2	5377037	5378454	5	1418	2.48E-07
Chr2	5379723	5380858	6	1136	3.70E-11
Chr2	5384248	5385076	4	829	7.05E-08
Chr2	5530430	5532246	6	1817	1.60553E-06
Chr2	5566580	5567809	11	1230	9.78E-15
Chr2	5573123	5575060	6	1938	5.25E-10
Chr2	5579462	5580504	4	1043	3.66075E-06
Chr2	5850238	5851309	4	1072	1.52905E-05
Chr2	5984154	5985232	4	1079	1.83356E-06
Chr2	6008464	6010382	4	1919	5.84E-10
Chr2	6027881	6030044	6	2164	4.58E-07
Chr2	6116290	6118558	7	2269	1.05E-07
Chr2	6120246	6120291	5	46	2.01E-07
Chr2	6462451	6463067	4	617	1.66884E-06
Chr2	6555452	6557523	5	2072	7.44E-09
Chr2	6702022	6703275	4	1254	1.2081E-06
Chr2	6942884	6943449	5	566	5.71E-08
Chr2	6975105	6975389	4	285	0.000130141
Chr2	7009288	7011746	7	2459	1.36E-07
Chr2	7173681	7175389	4	1709	0.000298909
Chr2	7227279	7228161	5	883	5.96E-10
Chr2	7778442	7780331	5	1890	1.05E-09
Chr2	8819108	8820400	5	1293	7.54E-07
Chr2	8911389	8911509	4	121	1.54E-08
Chr2	9122904	9123922	5	1019	6.21E-08
Chr2	9528992	9529356	4	365	2.15E-08
Chr2	10408819	10409601	5	783	6.45E-10
Chr2	11867364	11867899	4	536	4.11049E-06
Chr2	17339210	17340084	6	875	1.32517E-05
Chr2	18165845	18166069	5	225	9.24E-08
Chr2	18651522	18653327	6	1806	1.77E-09
Chr3	2810702	2813255	5	2554	5.42E-07
Chr3	3664368	3664444	4	77	5.34E-07
Chr3	7949389	7950126	5	738	9.08E-08
Chr3	9185383	9187118	4	1736	1.0307E-06
Chr3	9310344	9311902	4	1559	3.19E-07
Chr3	9617771	9619606	5	1836	1.85E-08
Chr3	9708245	9708578	4	334	4.54E-07
Chr3	10110348	10111930	5	1583	7.2076E-06
Chr3	10167298	10168340	4	1043	1.31383E-05
Chr3	10339745	10341317	6	1573	1.87E-09
Chr3	10478832	10479743	4	912	7.51E-07
Chr3	10559175	10561317	5	2143	1.92E-08
Chr3	11018200	11018750	4	551	3.11E-07
Chr3	11059797	11060778	4	982	2.39442E-06
Chr3	11065625	11066566	4	942	4.70418E-05
Chr3	11330457	11331657	5	1201	3.54E-07
Chr3	11356740	11357659	4	920	2.21801E-06
Chr3	11416296	11417633	5	1338	4.98E-09
Chr3	11548954	11550250	5	1297	2.28E-07
Chr3	11575569	11576801	4	1233	0.000112206
Chr3	11581957	11582658	4	702	2.15E-07
Chr3	11632466	11633335	4	870	6.92948E-05
Chr3	11636756	11637799	5	1044	1.40E-07
Chr3	11721877	11721923	5	47	8.48E-12

Chr3	12037282	12040950	9	3669	2.97E-14
Chr3	12051350	12052445	5	1096	3.52938E-06
Chr3	12070657	12071801	4	1145	2.33653E-06
Chr3	12178105	12180589	9	2485	4.14E-14
Chr3	12192921	12194863	5	1943	2.73E-08
Chr3	12202598	12204280	5	1683	1.43E-07
Chr3	12209248	12210630	5	1383	8.78E-08
Chr3	12251716	12253234	6	1519	1.05E-08
Chr3	12283894	12284936	4	1043	1.67237E-05
Chr3	12288531	12290146	5	1616	5.83339E-07
Chr3	12324966	12326886	4	1921	1.22061E-06
Chr3	12334807	12335488	4	682	4.27E-07
Chr3	12382064	12384248	4	2185	5.297E-06
Chr3	12402486	12403698	6	1213	4.49E-08
Chr3	12427047	12428899	5	1853	1.22651E-06
Chr3	12440082	12443293	7	3212	1.18E-09
Chr3	12467786	12470723	7	2938	2.92E-10
Chr3	12494402	12495161	4	760	4.80E-07
Chr3	12499959	12502064	5	2106	2.36E-07
Chr3	12532559	12534472	5	1914	1.41E-07
Chr3	12679206	12680575	4	1370	0.00013369
Chr3	13084897	13088388	10	3492	1.10E-11
Chr3	13099028	13100760	4	1733	0.00023208
Chr3	13113803	13115424	4	1622	9.37E-07
Chr3	13144484	13144968	4	485	0.001051588
Chr3	13246541	13248752	5	2212	4.32E-10
Chr3	13285484	13286687	6	1204	8.29E-09
Chr3	13408288	13410583	9	2296	6.99E-16
Chr3	13468712	13470397	4	1686	6.19289E-06
Chr3	13476492	13477793	4	1302	0.002753498
Chr3	13547845	13550464	5	2620	1.35E-07
Chr3	13574947	13577276	6	2330	9.60E-08
Chr3	13580344	13582484	7	2141	1.06E-08
Chr3	13586196	13587693	13	1498	6.12E-10
Chr3	13588954	13592267	39	3314	8.01E-34
Chr3	13608292	13611440	8	3149	1.55E-11
Chr3	13625151	13626130	4	980	1.85019E-05
Chr3	13636205	13637314	7	1110	1.74E-12
Chr3	13663914	13667115	8	3202	1.87E-07
Chr3	13675149	13676292	6	1144	5.52E-07
Chr3	13712225	13712397	4	173	1.0535E-06
Chr3	13813360	13814609	5	1250	3.29931E-06
Chr3	13826502	13827885	7	1384	1.43E-08
Chr3	13829266	13834644	15	5379	7.95E-16
Chr3	13901794	13904565	5	2772	8.41E-09
Chr3	13911109	13911839	4	731	3.71821E-06
Chr3	13996822	13998620	5	1799	8.39E-08
Chr3	13999772	14001583	9	1812	2.06E-12
Chr3	14037536	14038798	5	1263	1.04E-07
Chr3	14122003	14123093	5	1091	3.85E-08
Chr3	14156827	14157095	4	269	1.14407E-06
Chr3	14172047	14173296	7	1250	5.60018E-05
Chr3	14180470	14181737	11	1268	1.22E-11
Chr3	14190459	14190945	4	487	0.000240295
Chr3	14195461	14203872	160	8412	2.08E-213
Chr3	14207719	14208627	4	909	2.20458E-05
Chr3	14212836	14213619	4	784	1.86042E-05
Chr3	14217754	14218658	4	905	0.000273013
Chr3	14221744	14222214	5	471	1.65865E-06
Chr3	14254732	14256239	4	1508	1.12685E-06
Chr3	14257468	14259589	4	2122	4.66E-07
Chr3	14344012	14344087	4	76	2.33713E-06
Chr3	14374337	14375237	4	901	2.25276E-06

Chr3	14410493	14411160	4	668	1.02977E-06
Chr3	14434199	14436751	5	2553	1.54367E-06
Chr3	14548914	14550517	7	1604	7.75196E-06
Chr3	14552245	14553458	4	1214	3.97848E-05
Chr3	14555113	14556817	4	1705	1.74018E-07
Chr3	14565026	14568426	8	3401	5.16E-12
Chr3	14739447	14741622	5	2176	2.84006E-06
Chr3	14795899	14798559	10	2661	5.05E-12
Chr3	14799573	14800534	4	962	0.000118256
Chr3	14803718	14805850	4	2133	4.12248E-06
Chr3	14830120	14830530	4	411	1.73776E-05
Chr3	14849700	14850752	7	1053	7.57E-09
Chr3	14857297	14858169	4	873	4.57955E-06
Chr3	15041081	15042602	4	1522	1.26861E-05
Chr3	15056926	15057567	4	642	2.83799E-06
Chr3	15114042	15115184	4	1143	4.48E-07
Chr3	15144162	15145709	5	1548	1.94E-07
Chr3	15246014	15246408	4	395	4.30775E-06
Chr3	15262655	15264002	6	1348	4.17E-10
Chr3	15304034	15305747	6	1714	7.42525E-05
Chr3	15328363	15329142	5	780	1.72656E-08
Chr3	15376791	15377291	5	501	2.01757E-06
Chr3	15411041	15411562	4	522	1.70845E-06
Chr3	15441380	15442428	4	1049	5.72021E-06
Chr3	15461675	15463424	4	1750	1.0241E-05
Chr3	15465698	15467050	6	1353	2.83E-09
Chr3	15497751	15498840	4	1090	4.61381E-06
Chr3	15533866	15535028	4	1163	5.72204E-06
Chr3	15574153	15575627	4	1475	4.8672E-05
Chr3	15580772	15582898	8	2127	6.20E-09
Chr3	15711388	15712384	4	997	1.1425E-05
Chr3	15719319	15719977	4	659	7.53346E-05
Chr3	15933496	15933868	4	373	9.7493E-06
Chr3	16337417	16337950	4	534	0.000111421
Chr3	16339477	16339885	4	409	3.22E-08
Chr3	16959029	16960496	4	1468	8.7519E-05
Chr3	17683391	17684026	5	636	8.89E-08
Chr3	17978925	17980950	6	2026	1.83E-07
Chr3	20202657	20203400	6	744	2.97E-08
Chr3	20306930	20307538	4	609	2.00915E-06
Chr3	21326230	21329116	6	2887	2.66E-11
Chr3	23111574	23113756	4	2183	0.000123466
Chr4	1673480	1675746	8	2267	1.62E-11
Chr4	1685052	1685591	6	540	2.26E-08
Chr4	1688732	1689546	5	815	7.49783E-06
Chr4	1692587	1694716	4	2130	7.46234E-05
Chr4	1787881	1788761	4	881	5.36E-08
Chr4	1799515	1800690	4	1176	2.91E-08
Chr4	1804827	1806279	4	1453	9.97219E-06
Chr4	1822043	1823289	4	1247	1.07E-08
Chr4	1855442	1856233	4	792	2.29195E-05
Chr4	1937009	1938192	4	1184	5.1998E-06
Chr4	1948394	1949765	4	1372	1.84471E-06
Chr4	2003469	2006857	10	3389	2.71E-11
Chr4	2206915	2208317	4	1403	1.80767E-05
Chr4	2212297	2214011	5	1715	2.55E-07
Chr4	2270656	2272525	6	1870	5.57249E-07
Chr4	2284525	2286192	4	1668	1.36045E-06
Chr4	2357830	2358073	4	244	7.96096E-06
Chr4	2599333	2601902	6	2570	1.84897E-06
Chr4	2705767	2707787	4	2021	8.45719E-05
Chr4	2762597	2763510	4	914	3.32701E-05
Chr4	2785290	2786245	4	956	1.00E-06

Chr4	2830239	2832086	6	1848	6.18E-09
Chr4	2837381	2839349	6	1969	6.93E-10
Chr4	2852217	2854211	5	1995	4.14135E-06
Chr4	2894860	2896133	5	1274	1.63998E-06
Chr4	3009813	3012865	7	3053	5.52E-09
Chr4	3054384	3055369	6	986	3.78297E-06
Chr4	3061186	3061339	5	154	1.20404E-06
Chr4	3085933	3086979	4	1047	1.46647E-05
Chr4	3091549	3091590	4	42	1.64E-10
Chr4	3095278	3096848	4	1571	2.35884E-07
Chr4	3106781	3108406	5	1626	1.37E-08
Chr4	3109431	3111355	5	1925	6.43E-09
Chr4	3134556	3137029	8	2474	2.32E-13
Chr4	3139391	3140800	4	1410	2.18064E-05
Chr4	3175179	3175961	4	783	6.26E-08
Chr4	3180350	3181087	4	738	0.000474792
Chr4	3349415	3350347	4	933	1.76565E-06
Chr4	3364968	3365682	4	715	1.47023E-06
Chr4	3408663	3409910	4	1248	5.55229E-05
Chr4	3482169	3482994	5	826	4.44E-07
Chr4	3500255	3500860	5	606	1.0523E-05
Chr4	3561301	3563123	5	1823	4.18E-07
Chr4	3620590	3623264	7	2675	1.48711E-06
Chr4	3624345	3625036	4	692	0.000140404
Chr4	3626791	3627599	4	809	1.97742E-05
Chr4	3633610	3634821	4	1212	1.08385E-06
Chr4	3677505	3679345	6	1841	2.27E-07
Chr4	3683372	3684295	4	924	2.26E-07
Chr4	3698566	3699884	6	1319	6.74E-08
Chr4	3738363	3739483	4	1121	8.49E-08
Chr4	3740672	3741183	4	512	1.04E-08
Chr4	3777924	3779394	4	1471	1.51984E-06
Chr4	3784477	3786064	4	1588	1.97655E-05
Chr4	3795868	3796870	4	1003	3.18E-07
Chr4	3839413	3840813	7	1401	1.49467E-07
Chr4	3844144	3845891	4	1748	0.000123769
Chr4	3871992	3873400	4	1409	2.54E-07
Chr4	3903089	3904808	5	1720	1.07673E-06
Chr4	3913937	3915490	6	1554	1.02E-09
Chr4	3933819	3934503	4	685	1.24767E-06
Chr4	3946579	3947142	5	564	1.01705E-06
Chr4	3950538	3955910	56	5373	2.85E-75
Chr4	3959213	3961629	7	2417	7.66E-10
Chr4	3966407	3969592	9	3186	1.07E-11
Chr4	3977492	3978906	12	1415	1.61E-13
Chr4	3992525	3996580	16	4056	1.84E-16
Chr4	3998201	3998381	4	181	6.97E-07
Chr4	4019727	4020157	4	431	2.32E-07
Chr4	4023291	4024706	4	1416	8.3411E-07
Chr4	4041084	4042513	7	1430	1.31E-08
Chr4	4067919	4069452	5	1534	1.95E-07
Chr4	4160068	4160878	5	811	2.92389E-05
Chr4	4240980	4243201	5	2222	8.32322E-06
Chr4	4244221	4246201	4	1981	6.66E-08
Chr4	4249146	4249572	4	427	9.47348E-06
Chr4	4277487	4279435	7	1949	1.80E-08
Chr4	4286768	4287617	6	850	5.74E-11
Chr4	4289151	4290141	8	991	1.82E-09
Chr4	4294758	4295998	5	1241	9.09E-07
Chr4	4306678	4307048	4	371	1.49974E-05
Chr4	4326928	4327967	5	1040	4.27E-10
Chr4	4384736	4386663	4	1928	1.42506E-06
Chr4	4412706	4413439	4	734	5.06E-08

Chr4	4599191	4601821	6	2631	3.49E-08
Chr4	4680920	4683037	4	2118	6.95E-07
Chr4	4720605	4721502	4	898	5.60423E-05
Chr4	4724074	4725135	4	1062	2.47E-07
Chr4	4777623	4778463	5	841	2.53035E-06
Chr4	4853708	4854813	7	1106	2.64E-11
Chr4	4975041	4975108	4	68	1.59E-07
Chr4	4997103	4998246	4	1144	8.92417E-06
Chr4	5039810	5042296	5	2487	1.99E-07
Chr4	5046745	5049517	5	2773	1.54E-08
Chr4	5059831	5062249	6	2419	8.78E-08
Chr4	5064923	5067074	4	2152	2.82622E-07
Chr4	5069755	5070883	5	1129	4.41E-10
Chr4	5074025	5077555	9	3531	6.57E-12
Chr4	5530406	5531118	4	713	1.17E-08
Chr4	5583551	5584673	4	1123	2.68466E-06
Chr4	5688660	5689859	4	1200	7.88E-07
Chr4	5940636	5941110	5	475	7.80E-07
Chr4	5955403	5955923	5	521	5.90E-08
Chr4	5957115	5959669	5	2555	2.50E-08
Chr4	5966883	5969351	7	2469	4.60E-12
Chr4	6467932	6469399	8	1468	5.11E-12
Chr4	8903315	8904201	4	887	0.00010328
Chr4	9509839	9510917	4	1079	1.23E-07
Chr4	10051545	10053110	4	1566	8.48E-07
Chr4	11036787	11037505	5	719	1.89E-07
Chr4	13329548	13332295	9	2748	1.23E-08
Chr4	14967496	14967810	4	315	4.71697E-06
Chr4	17712661	17714101	4	1441	1.01302E-06
Chr5	2259797	2260526	4	730	6.20E-07
Chr5	3253162	3253235	4	74	1.41926E-06
Chr5	4320399	4321242	4	844	3.18794E-07
Chr5	5644133	5645567	4	1435	1.84E-07
Chr5	6437297	6438383	4	1087	1.32413E-06
Chr5	6631672	6632575	4	904	1.05678E-05
Chr5	7038383	7039171	4	789	7.76736E-06
Chr5	9206908	9207228	4	321	4.10183E-05
Chr5	9996723	9998301	4	1579	7.73E-07
Chr5	10052027	10054365	5	2339	4.49E-08
Chr5	10098006	10099931	4	1926	2.39869E-06
Chr5	10106448	10107241	4	794	2.3277E-06
Chr5	10144730	10147469	6	2740	2.1743E-07
Chr5	10258988	10260229	4	1242	6.26514E-05
Chr5	10363754	10364717	4	964	6.47E-07
Chr5	10365819	10367269	6	1451	1.29E-09
Chr5	10557904	10558783	4	880	2.69663E-06
Chr5	10592186	10594359	5	2174	5.22E-07
Chr5	10888099	10888366	4	268	6.35E-08
Chr5	10976277	10977532	4	1256	2.99716E-05
Chr5	11079617	11081417	5	1801	6.93038E-05
Chr5	11135814	11138001	4	2188	7.43E-07
Chr5	11175716	11176304	4	589	3.51698E-06
Chr5	11184651	11186219	21	1569	1.37E-12
Chr5	11187788	11188495	5	708	1.0299E-05
Chr5	11212940	11214329	7	1390	4.18E-10
Chr5	11295197	11296767	7	1571	2.61E-07
Chr5	11328415	11328823	4	409	9.06E-07
Chr5	11341207	11342799	4	1593	8.86005E-05
Chr5	11373659	11374974	4	1316	2.94E-08
Chr5	11394485	11395826	4	1342	0.000105862
Chr5	11407477	11409027	5	1551	1.43865E-06
Chr5	11429190	11430364	4	1175	2.41601E-05
Chr5	11438492	11439317	5	826	1.00373E-07

Chr5	11478511	11480280	7	1770	1.09E-08
Chr5	11505383	11506267	5	885	2.39E-08
Chr5	11535891	11537222	4	1332	7.92913E-06
Chr5	11572388	11573135	5	748	2.67E-08
Chr5	11592910	11594987	5	2078	5.42E-09
Chr5	11602174	11603576	5	1403	6.65E-09
Chr5	11701665	11704223	15	2559	1.82E-10
Chr5	11705352	11709217	15	3866	2.42E-18
Chr5	11711005	11712175	4	1171	5.10702E-06
Chr5	11723431	11724855	13	1425	5.03E-08
Chr5	11726439	11729412	22	2974	1.57E-15
Chr5	11730691	11738141	30	7451	2.82E-21
Chr5	11763400	11766653	8	3254	3.27E-08
Chr5	11768047	11770062	8	2016	9.37E-10
Chr5	11771857	11772332	4	476	7.85774E-06
Chr5	11833285	11835498	6	2214	3.15E-07
Chr5	11842699	11843823	6	1125	7.56327E-05
Chr5	11847045	11847698	4	654	4.66399E-05
Chr5	11912596	11913604	5	1009	2.60E-08
Chr5	11936485	11937697	7	1213	9.03E-07
Chr5	11939288	11944595	26	5308	8.14E-27
Chr5	11952502	11952756	4	255	2.26196E-06
Chr5	11990523	11993066	12	2544	1.51E-07
Chr5	11994970	11996157	4	1188	7.23E-07
Chr5	12001740	12003413	4	1674	1.99837E-05
Chr5	12012703	12014664	4	1962	6.41092E-05
Chr5	12019620	12022411	7	2792	6.82E-10
Chr5	12036605	12041730	14	5126	3.01E-15
Chr5	12073443	12075192	5	1750	1.25E-07
Chr5	12110338	12113056	5	2719	3.75E-08
Chr5	12114123	12116614	5	2492	3.69E-08
Chr5	12123515	12126532	11	3018	8.26E-11
Chr5	12143433	12144412	6	980	3.48E-08
Chr5	12146672	12148503	12	1832	4.22E-12
Chr5	12210861	12210895	4	35	5.72E-07
Chr5	12223170	12224088	4	919	3.51927E-06
Chr5	12226048	12227252	5	1205	1.73E-09
Chr5	12245592	12250616	9	5025	1.44E-09
Chr5	12263827	12264066	5	240	9.55E-09
Chr5	12293147	12294036	4	890	2.43882E-06
Chr5	12326741	12328057	4	1317	9.51917E-06
Chr5	12348352	12349621	5	1270	1.42E-08
Chr5	12362061	12363402	4	1342	0.000117623
Chr5	12375594	12377193	6	1600	6.44E-07
Chr5	12431053	12431962	4	910	3.35239E-05
Chr5	12458275	12460608	6	2334	1.38E-07
Chr5	12574268	12577144	7	2877	3.91E-12
Chr5	12581583	12582524	5	942	5.69E-07
Chr5	12611312	12612489	4	1178	1.13E-07
Chr5	12614009	12614965	4	957	9.6744E-05
Chr5	12744142	12745033	4	892	2.095E-05
Chr5	12754016	12755026	4	1011	0.000190239
Chr5	12757140	12757959	5	820	1.06E-07
Chr5	12770914	12773803	6	2890	5.63E-08
Chr5	12967726	12968663	4	938	0.000113146
Chr5	12998064	12999241	5	1178	2.12E-07
Chr5	13071723	13072188	4	466	0.000510951
Chr5	13173435	13174299	5	865	1.71576E-06
Chr5	13254807	13255138	4	332	5.94253E-07
Chr5	13309044	13310850	4	1807	4.02E-08
Chr5	13401009	13401548	4	540	8.51E-08
Chr5	13846043	13847280	4	1238	1.18922E-06
Chr5	13884311	13885210	4	900	7.47189E-05

Chr5	14267933	14269345	4	1413	2.58E-08
Chr5	14702654	14703779	5	1126	1.17184E-05
Chr5	15337178	15338499	4	1322	6.71E-07
Chr5	17093222	17095321	6	2100	5.97E-12
Chr5	17603745	17604305	4	561	2.37089E-06
Chr5	18472099	18473360	6	1262	1.32E-09
Chr5	19360756	19362585	6	1830	2.57E-10
Chr5	22615209	22615411	4	203	7.75E-07
Chr5	24722999	24723680	5	682	5.31E-08
Chr5	25282679	25283572	5	894	5.33E-07

-Pit Root 7dat (Hypo-DMRs)

Chromosome	Start	End	number of DMCs	DMR lenght	P-value
Chr1	2719399	2720580	5	1182	3.77E-07
Chr1	6273963	6275024	4	1062	0.000243688
Chr1	7068092	7070951	6	2860	4.10E-09
Chr1	7353108	7357715	15	4608	1.24E-15
Chr1	7362656	7365072	10	2417	2.76E-13
Chr1	8729700	8731065	5	1366	1.44373E-06
Chr1	8790318	8791385	4	1068	0.000271185
Chr1	8928521	8929144	5	624	6.21E-07
Chr1	8931577	8932596	4	1020	1.80175E-05
Chr1	9372060	9373271	4	1212	1.38861E-05
Chr1	9687265	9687706	4	442	8.36021E-06
Chr1	10357469	10359127	5	1659	3.10503E-05
Chr1	10699157	10700480	6	1324	2.18E-08
Chr1	12016205	12017206	4	1002	1.91305E-05
Chr1	12408004	12409648	5	1645	2.70E-07
Chr1	12569097	12570592	4	1496	2.18281E-06
Chr1	12671445	12672024	4	580	0.000291127
Chr1	12678082	12679494	6	1413	7.39E-07
Chr1	13003305	13003834	6	530	5.21E-08
Chr1	13381807	13382582	4	776	7.38171E-05
Chr1	13560150	13561369	4	1220	1.1596E-05
Chr1	13579013	13579967	4	955	0.00038736
Chr1	13605328	13606257	4	930	7.39426E-06
Chr1	13631872	13634292	6	2421	7.83E-08
Chr1	13678615	13681440	6	2826	1.19E-10
Chr1	13690565	13692610	6	2046	5.82E-08
Chr1	13773717	13774625	5	909	8.03475E-06
Chr1	13787826	13789458	5	1633	3.75E-10
Chr1	13821470	13823284	5	1815	5.09994E-06
Chr1	13917849	13919888	7	2040	2.05E-08
Chr1	13954173	13956087	7	1915	1.75E-09
Chr1	13960203	13960985	5	783	2.70E-09
Chr1	14087004	14089128	5	2125	7.88004E-06
Chr1	14119851	14123062	5	3212	3.26E-08
Chr1	14133649	14133737	5	89	2.58E-09
Chr1	14182626	14183608	5	983	8.45E-07
Chr1	14198383	14200128	5	1746	4.2543E-06
Chr1	14224428	14226025	4	1598	5.4148E-05
Chr1	14231298	14232498	4	1201	2.44105E-06
Chr1	14259243	14260559	4	1317	1.17E-07
Chr1	14261858	14262799	4	942	1.23816E-06
Chr1	14273436	14274574	4	1139	1.33058E-05
Chr1	14316434	14316903	5	470	1.26E-09
Chr1	14336333	14338381	5	2049	5.88E-08
Chr1	14449978	14451141	4	1164	3.09169E-05
Chr1	14454817	14455678	4	862	1.60393E-05
Chr1	14462559	14464242	4	1684	2.41621E-05
Chr1	14471243	14472002	5	760	1.58E-08
Chr1	14486384	14488133	4	1750	2.05232E-06

Chr1	14490418	14491173	4	756	6.54E-08
Chr1	14493523	14495341	5	1819	2.85184E-06
Chr1	14502883	14503779	6	897	4.02E-08
Chr1	14541042	14545440	10	4399	2.35E-13
Chr1	14600776	14601593	4	818	6.30E-10
Chr1	14850596	14851806	4	1211	6.66202E-06
Chr1	15074428	15076458	9	2031	1.26E-13
Chr1	15082202	15085683	11	3482	2.09E-09
Chr1	15179446	15180545	4	1100	1.41225E-06
Chr1	15191637	15193328	6	1692	6.55922E-06
Chr1	15205150	15207646	6	2497	3.05E-08
Chr1	15214605	15216866	5	2262	1.20E-07
Chr1	15446589	15446787	4	199	2.47286E-05
Chr1	15503388	15505819	6	2432	2.86E-11
Chr1	15507040	15508404	4	1365	1.44448E-06
Chr1	15516162	15516939	4	778	0.000525576
Chr1	15522462	15524068	6	1607	1.69E-07
Chr1	15550183	15551765	4	1583	2.7446E-06
Chr1	15559532	15561341	4	1810	2.58499E-05
Chr1	15678165	15679074	5	910	1.65E-07
Chr1	15705407	15708484	9	3078	2.63E-17
Chr1	15709969	15711626	5	1658	2.96E-07
Chr1	15869643	15870373	4	731	2.66932E-05
Chr1	16046139	16047884	4	1746	1.53E-07
Chr1	16102169	16102848	5	680	3.48893E-06
Chr1	16107738	16108789	5	1052	1.25E-08
Chr1	16122385	16124106	5	1722	5.47E-08
Chr1	16382161	16384082	6	1922	3.55E-08
Chr1	16510381	16511404	4	1024	0.000107294
Chr1	16513427	16514395	6	969	0.000363995
Chr1	16517543	16519027	5	1485	2.14059E-06
Chr1	16522407	16525151	9	2745	6.34E-10
Chr1	16526901	16528138	6	1238	7.94E-07
Chr1	16627426	16628052	5	627	7.10E-08
Chr1	16676462	16677741	4	1280	3.41443E-05
Chr1	17034844	17035685	5	842	3.57E-07
Chr1	17036834	17037532	4	699	1.0185E-05
Chr1	17044785	17045441	4	657	1.13204E-06
Chr1	17256104	17257237	4	1134	2.05E-07
Chr1	17258354	17259785	4	1432	7.68E-07
Chr1	17530826	17531667	4	842	2.14857E-06
Chr1	17532932	17534479	6	1548	3.53E-09
Chr1	18111252	18111294	5	43	3.65E-08
Chr1	18180462	18181413	4	952	9.35415E-05
Chr1	18967004	18967699	5	696	1.41E-07
Chr1	22696756	22697952	5	1197	0.00076923
Chr2	2714	3671	6	958	3.09E-07
Chr2	9579	11391	7	1813	0.031335111
Chr2	13089	16032	7	2944	3.27E-09
Chr2	29024	30106	5	1083	3.78E-08
Chr2	39802	42264	8	2463	2.00E-07
Chr2	529990	531544	6	1555	6.06E-09
Chr2	536289	536927	4	639	5.37629E-05
Chr2	1420916	1421814	4	899	6.06938E-05
Chr2	1511121	1512953	5	1833	6.93E-09
Chr2	1649476	1649618	4	143	2.73983E-05
Chr2	1884655	1886247	6	1593	4.90E-08
Chr2	1906744	1909610	6	2867	2.5652E-06
Chr2	2401493	2403392	4	1900	1.45186E-06
Chr2	2420889	2422434	4	1546	6.30469E-06
Chr2	2476956	2478123	4	1168	0.000467908
Chr2	2482270	2483951	7	1682	9.58E-09
Chr2	2486849	2490373	11	3525	8.81E-12

Chr2	2491532	2491858	4	327	4.91231E-06
Chr2	2595807	2597249	5	1443	1.15E-07
Chr2	2647059	2648461	4	1403	2.53511E-05
Chr2	2649634	2649793	4	160	1.25E-07
Chr2	2749552	2751319	4	1768	1.56581E-05
Chr2	2770612	2771314	5	703	1.86E-08
Chr2	2972137	2973951	4	1815	9.24E-07
Chr2	3071640	3072248	5	609	2.55801E-06
Chr2	3089439	3090364	4	926	7.66478E-05
Chr2	3098262	3100332	5	2071	4.19333E-06
Chr2	3247456	3248583	6	1128	5.76E-07
Chr2	3267897	3268490	5	594	3.58E-08
Chr2	3276302	3276530	5	229	1.39E-07
Chr2	3278981	3289374	34	10394	1.64E-38
Chr2	3291298	3291933	4	636	2.48225E-05
Chr2	3310454	3311930	4	1477	0.000132593
Chr2	3352872	3353110	4	239	6.04647E-06
Chr2	3357514	3359249	6	1736	1.05E-08
Chr2	3458956	3459428	4	473	2.64171E-06
Chr2	3551971	3553406	4	1436	2.30333E-06
Chr2	3565030	3567833	6	2804	1.1526E-06
Chr2	3600843	3601700	4	858	5.96678E-05
Chr2	3606487	3607140	6	654	3.55E-07
Chr2	3615020	3615119	5	100	5.04E-08
Chr2	3616851	3624539	28	7689	2.02E-25
Chr2	3625600	3626958	8	1359	0.000502076
Chr2	3635918	3636990	4	1073	0.000517677
Chr2	3677183	3678330	4	1148	1.89E-07
Chr2	3682703	3684863	5	2161	6.84E-09
Chr2	3732431	3733388	4	958	1.53142E-05
Chr2	3758383	3761511	11	3129	4.52E-15
Chr2	3763973	3766199	9	2227	1.03E-12
Chr2	3821669	3823869	5	2201	6.76E-10
Chr2	3836538	3838581	4	2044	1.27E-08
Chr2	3847864	3848237	4	374	4.33514E-06
Chr2	3871530	3873990	6	2461	4.82E-09
Chr2	3878062	3879446	5	1385	5.21E-08
Chr2	3885364	3888273	8	2910	1.67E-09
Chr2	3897431	3899513	4	2083	1.41015E-06
Chr2	3946317	3947498	5	1182	2.05809E-06
Chr2	3950877	3952840	7	1964	1.92E-07
Chr2	3974182	3975357	4	1176	2.07E-07
Chr2	3992996	3994013	4	1018	1.03493E-05
Chr2	4124778	4125938	4	1161	1.77088E-06
Chr2	4151417	4152661	4	1245	6.41032E-07
Chr2	4173255	4175429	5	2175	6.61E-07
Chr2	4192899	4193077	4	179	5.00E-07
Chr2	4208004	4209446	7	1443	1.60E-10
Chr2	4277407	4278053	5	647	1.24E-08
Chr2	4288732	4291392	8	2661	2.93E-10
Chr2	4383936	4385742	6	1807	7.02E-11
Chr2	4396489	4398209	6	1721	1.92E-07
Chr2	4461661	4465523	8	3863	1.91E-11
Chr2	4492668	4495726	9	3059	2.95E-15
Chr2	4595951	4599315	8	3365	1.21E-09
Chr2	4693844	4694615	6	772	1.39E-09
Chr2	4699272	4701774	8	2503	4.44E-10
Chr2	4716111	4717607	4	1497	3.33997E-06
Chr2	4727882	4728473	4	592	0.000100139
Chr2	4779736	4780126	5	391	1.06E-09
Chr2	4782449	4783298	6	850	1.05363E-06
Chr2	4816914	4818314	6	1401	2.26E-10
Chr2	4850535	4853850	8	3316	6.82E-10

Chr2	4855804	4856625	4	822	1.06178E-05
Chr2	4901296	4902483	4	1188	0.000168068
Chr2	4907635	4908811	4	1177	2.92753E-06
Chr2	4983102	4983874	4	773	1.53795E-06
Chr2	4988171	4989525	5	1355	2.64E-07
Chr2	4992386	4994038	6	1653	3.69E-08
Chr2	5090797	5093735	9	2939	1.58E-12
Chr2	5232947	5235337	5	2391	3.57E-08
Chr2	5329976	5331080	4	1105	0.000164206
Chr2	5340148	5340570	4	423	3.45303E-06
Chr2	5367546	5368486	5	941	2.20687E-06
Chr2	5443805	5445280	4	1476	1.20925E-06
Chr2	5472820	5473814	4	995	0.000161893
Chr2	5477692	5479772	5	2081	1.54843E-06
Chr2	5570595	5571904	5	1310	1.10E-07
Chr2	5602345	5604405	4	2061	6.43908E-06
Chr2	5626782	5628509	4	1728	8.04855E-06
Chr2	5635655	5636483	4	829	6.31441E-06
Chr2	5729492	5730976	4	1485	2.86E-07
Chr2	5786728	5787650	4	923	5.8686E-06
Chr2	5848639	5850780	6	2142	2.74E-07
Chr2	5995016	5997638	5	2623	4.04E-07
Chr2	6222032	6223093	4	1062	2.69975E-05
Chr2	6436924	6437521	4	598	2.21E-07
Chr2	6623501	6624132	4	632	9.6402E-06
Chr2	6719678	6720925	5	1248	1.29E-08
Chr2	6770052	6772310	5	2259	6.23E-07
Chr2	6781657	6783257	5	1601	2.89E-07
Chr2	6846619	6846959	5	341	5.11E-09
Chr2	6936090	6937748	4	1659	8.14986E-06
Chr2	6954626	6956171	5	1546	4.23E-07
Chr2	7015608	7016870	5	1263	1.02E-07
Chr2	7226122	7227240	5	1119	4.01E-08
Chr2	7230698	7231765	5	1068	2.50604E-07
Chr2	9194013	9195123	4	1111	0.000116797
Chr2	9692155	9692175	6	21	3.00E-14
Chr2	10598287	10599639	4	1353	2.4673E-05
Chr2	10875725	10877209	6	1485	1.08904E-07
Chr2	12452751	12453923	4	1173	1.24E-07
Chr2	18703085	18703179	5	95	1.68E-08
Chr3	6470650	6470976	4	327	9.21E-07
Chr3	8101233	8101571	4	339	9.16829E-06
Chr3	9692664	9695345	6	2682	5.69E-09
Chr3	10342724	10343601	4	878	2.22E-09
Chr3	10480434	10481933	8	1500	1.22E-08
Chr3	11145066	11146851	4	1786	1.97733E-06
Chr3	11174476	11175408	4	933	3.66E-08
Chr3	11356397	11356413	4	17	1.12E-09
Chr3	11417117	11419292	4	2176	3.24761E-07
Chr3	11579452	11580235	4	784	1.78E-07
Chr3	11583233	11584387	5	1155	3.20E-09
Chr3	11634342	11635210	4	869	2.92557E-06
Chr3	11636246	11639250	7	3005	4.02E-09
Chr3	11685014	11686798	7	1785	9.78E-11
Chr3	11881306	11882520	4	1215	6.09E-08
Chr3	12026033	12027294	5	1262	2.39E-07
Chr3	12028784	12029541	4	758	3.57E-07
Chr3	12033468	12034048	4	581	2.62E-07
Chr3	12044489	12046920	6	2432	8.39E-08
Chr3	12069155	12070530	5	1376	5.74E-08
Chr3	12180868	12182595	4	1728	1.83672E-05
Chr3	12199567	12200661	4	1095	0.000384517
Chr3	12202117	12204810	6	2694	7.91E-10

Chr3	12293304	12294434	4	1131	0.000239854
Chr3	12395647	12396995	6	1349	5.70E-07
Chr3	12484938	12485577	4	640	2.28566E-06
Chr3	12493258	12494939	5	1682	2.47E-07
Chr3	12496546	12499095	8	2550	2.70E-10
Chr3	12528707	12531872	6	3166	1.33E-08
Chr3	12534351	12536291	6	1941	1.07E-07
Chr3	12539196	12540441	5	1246	2.98474E-06
Chr3	12652536	12653498	4	963	4.77411E-06
Chr3	12700924	12701557	4	634	1.74355E-06
Chr3	12749385	12750997	5	1613	7.93E-08
Chr3	12762829	12765693	6	2865	1.6157E-06
Chr3	12826152	12827509	4	1358	4.04E-07
Chr3	12862570	12864134	4	1565	8.87E-07
Chr3	12939261	12941244	5	1984	4.851E-06
Chr3	12944298	12945884	7	1587	1.11E-09
Chr3	12961553	12964962	11	3410	1.06E-14
Chr3	13025330	13026327	4	998	3.43834E-06
Chr3	13112931	13114591	4	1661	4.33861E-06
Chr3	13122499	13123773	4	1275	1.71634E-05
Chr3	13150569	13151463	4	895	3.16E-07
Chr3	13160008	13162274	6	2267	3.66E-11
Chr3	13189672	13191972	7	2301	5.71E-10
Chr3	13196176	13197341	6	1166	2.75E-07
Chr3	13316736	13320420	7	3685	9.31E-09
Chr3	13321828	13323204	4	1377	5.12301E-06
Chr3	13361236	13364440	6	3205	6.02E-09
Chr3	13366987	13368707	5	1721	6.11E-10
Chr3	13406630	13406912	4	283	1.3403E-06
Chr3	13410523	13412548	5	2026	1.97E-07
Chr3	13423906	13425370	4	1465	3.82253E-06
Chr3	13444148	13446292	7	2145	1.98567E-07
Chr3	13467893	13469336	6	1444	1.30E-07
Chr3	13476614	13477917	4	1304	1.03E-07
Chr3	13587020	13587696	5	677	0.000555821
Chr3	13588831	13592567	22	3737	5.01E-11
Chr3	13604895	13606199	6	1305	2.10E-10
Chr3	13616967	13619680	7	2714	3.85E-10
Chr3	13645960	13647186	5	1227	6.33E-07
Chr3	13648382	13649619	4	1238	2.00319E-06
Chr3	13661035	13661536	4	502	2.50625E-05
Chr3	13663080	13663565	5	486	5.19045E-06
Chr3	13673381	13675687	6	2307	1.69E-08
Chr3	13678014	13678719	5	706	4.58E-09
Chr3	13801618	13802298	4	681	2.13932E-05
Chr3	13813502	13816425	7	2924	1.29E-11
Chr3	13872340	13873295	5	956	8.17178E-06
Chr3	13879598	13879876	5	279	2.79E-07
Chr3	13887649	13888580	4	932	1.0332E-05
Chr3	13893175	13894425	6	1251	1.81E-09
Chr3	13909858	13911641	4	1784	1.27099E-05
Chr3	13950479	13951509	5	1031	4.66E-08
Chr3	13979523	13980866	4	1344	1.05044E-06
Chr3	14005725	14006847	7	1123	3.74689E-07
Chr3	14009031	14009305	4	275	1.01E-07
Chr3	14116393	14117244	4	852	2.84186E-05
Chr3	14194883	14198373	17	3491	6.84E-10
Chr3	14199603	14199988	4	386	6.97E-07
Chr3	14203000	14204013	10	1014	3.72E-18
Chr3	14206919	14208858	9	1940	1.31739E-06
Chr3	14212517	14212730	5	214	0.004716606
Chr3	14213929	14216439	7	2511	2.38E-10
Chr3	14223171	14224129	9	959	2.72556E-06

Chr3	14246959	14250014	6	3056	2.71593E-06
Chr3	14330575	14331787	4	1213	9.99E-08
Chr3	14431389	14434952	6	3564	1.12E-08
Chr3	14504715	14506132	4	1418	3.93361E-06
Chr3	14529171	14530701	4	1531	2.1765E-05
Chr3	14552389	14554624	7	2236	2.15E-10
Chr3	14556254	14557112	4	859	6.50411E-05
Chr3	14619987	14621657	6	1671	1.17E-07
Chr3	14633289	14635327	5	2039	4.35E-07
Chr3	14657288	14658191	4	904	1.2122E-05
Chr3	14729930	14731688	7	1759	1.93E-10
Chr3	14796558	14798096	6	1539	2.91E-08
Chr3	14820174	14823067	6	2894	2.34E-08
Chr3	14824426	14827122	6	2697	9.84359E-07
Chr3	14954677	14955557	4	881	7.04403E-06
Chr3	14977526	14978593	4	1068	3.71971E-05
Chr3	14997540	14998438	4	899	4.21E-07
Chr3	15032469	15033476	5	1008	1.74E-07
Chr3	15045749	15046865	4	1117	7.1068E-07
Chr3	15101630	15103123	4	1494	1.34724E-05
Chr3	15119675	15122758	9	3084	2.26E-12
Chr3	15147159	15148837	6	1679	1.51E-09
Chr3	15248835	15250641	4	1807	1.27966E-05
Chr3	15257615	15258117	8	503	1.22E-10
Chr3	15261045	15261935	4	891	5.15865E-07
Chr3	15327100	15328151	4	1052	6.15E-07
Chr3	15379379	15380124	5	746	9.72E-07
Chr3	15422633	15424612	4	1980	8.34E-07
Chr3	15489825	15492003	4	2179	4.28E-08
Chr3	15540970	15543403	5	2434	1.65966E-07
Chr3	15591638	15593714	4	2077	0.000430403
Chr3	15716030	15717440	8	1411	5.89E-09
Chr3	16691988	16693105	4	1118	0.000532208
Chr3	18792205	18794297	5	2093	2.34394E-06
Chr3	22233097	22234436	4	1340	1.32E-08
Chr3	23108975	23110240	4	1266	1.13207E-06
Chr4	632097	635880	9	3784	1.91E-12
Chr4	655207	655943	4	737	4.62836E-06
Chr4	1097945	1099690	5	1746	6.37E-07
Chr4	1668208	1670162	5	1955	1.04769E-05
Chr4	1689339	1690339	9	1001	9.10E-11
Chr4	1764802	1766616	5	1815	1.17659E-07
Chr4	1807830	1809410	4	1581	5.99E-07
Chr4	1827824	1828634	4	811	2.19741E-06
Chr4	1858329	1859422	5	1094	3.79E-10
Chr4	1945158	1946674	7	1517	1.03E-07
Chr4	1950589	1953491	7	2903	2.61E-10
Chr4	1969458	1970996	6	1539	1.81E-08
Chr4	2043898	2044660	6	763	4.40E-09
Chr4	2159581	2161265	4	1685	2.34352E-06
Chr4	2195393	2198151	6	2759	1.35649E-05
Chr4	2245732	2247821	5	2090	7.88E-08
Chr4	2281047	2283242	5	2196	1.78684E-06
Chr4	2643699	2644120	4	422	1.48262E-05
Chr4	2645159	2647255	4	2097	6.64E-07
Chr4	2830896	2833040	6	2145	4.17E-09
Chr4	2882963	2886834	8	3872	2.32E-11
Chr4	2910953	2912120	6	1168	8.29971E-06
Chr4	2915449	2916545	5	1097	0.000134229
Chr4	2974229	2975970	6	1742	1.45E-08
Chr4	3005154	3006341	4	1188	5.04E-07
Chr4	3015514	3016902	4	1389	8.0723E-06
Chr4	3031416	3034214	7	2799	9.05E-07

Chr4	3037107	3038081	4	975	3.92864E-05
Chr4	3061041	3062277	4	1237	2.87465E-06
Chr4	3067407	3069792	5	2386	8.04139E-06
Chr4	3092236	3093572	7	1337	4.67E-11
Chr4	3180224	3183348	8	3125	6.09E-11
Chr4	3189067	3190532	4	1466	2.77581E-05
Chr4	3264901	3266191	5	1291	2.30E-07
Chr4	3287227	3288901	4	1675	3.18033E-06
Chr4	3318365	3319223	6	859	1.23287E-07
Chr4	3375123	3376488	4	1366	0.000231128
Chr4	3397499	3398545	6	1047	2.10084E-06
Chr4	3401290	3403433	6	2144	3.85E-08
Chr4	3408698	3409374	4	677	2.42834E-06
Chr4	3411127	3411975	4	849	0.000906672
Chr4	3457981	3459088	4	1108	6.05E-08
Chr4	3461772	3461999	4	228	1.1542E-06
Chr4	3468608	3470062	6	1455	2.40367E-05
Chr4	3495224	3496865	6	1642	4.58E-10
Chr4	3568801	3570301	6	1501	4.20759E-07
Chr4	3580869	3584534	9	3666	4.13E-09
Chr4	3585620	3588977	7	3358	3.33E-10
Chr4	3594955	3595542	4	588	1.32107E-05
Chr4	3596577	3598202	5	1626	1.87E-07
Chr4	3626845	3627924	5	1080	7.10516E-06
Chr4	3676525	3677469	5	945	7.0913E-07
Chr4	3693750	3694575	6	826	1.67E-10
Chr4	3706658	3708708	8	2051	2.22E-10
Chr4	3744975	3747837	5	2863	3.62598E-06
Chr4	3756785	3758270	4	1486	1.32752E-06
Chr4	3782128	3782680	4	553	7.09E-07
Chr4	3786816	3787700	4	885	8.07E-07
Chr4	3796930	3797777	4	848	9.40681E-05
Chr4	3878787	3880281	4	1495	1.94875E-06
Chr4	3881499	3883376	4	1878	1.30233E-06
Chr4	3931849	3934278	6	2430	1.45E-07
Chr4	3947779	3948278	4	500	6.38E-07
Chr4	3950612	3953717	26	3106	4.12E-30
Chr4	3954748	3955925	4	1178	4.54E-07
Chr4	3963594	3966645	11	3052	2.44917E-06
Chr4	3977729	3979632	7	1904	0.00148965
Chr4	3992710	3996755	17	4046	9.01E-15
Chr4	4029383	4030359	4	977	4.28505E-05
Chr4	4181697	4185386	7	3690	1.20E-08
Chr4	4240741	4243753	8	3013	1.07E-13
Chr4	4307143	4307951	4	809	0.000119233
Chr4	4365406	4366548	5	1143	2.19744E-05
Chr4	4388680	4390421	4	1742	1.05914E-05
Chr4	4392919	4394903	8	1985	3.72E-07
Chr4	4409558	4411917	8	2360	6.05E-12
Chr4	4432950	4434343	4	1394	4.17697E-05
Chr4	4438461	4440025	4	1565	2.53E-07
Chr4	4489994	4490174	4	181	1.73E-07
Chr4	4491356	4492825	4	1470	0.000348197
Chr4	4528486	4530467	4	1982	1.17682E-06
Chr4	4599532	4601296	5	1765	2.26E-07
Chr4	4701485	4702062	4	578	5.72676E-06
Chr4	4704313	4705602	5	1290	6.72E-07
Chr4	4711076	4712998	4	1923	3.44337E-05
Chr4	4752593	4754055	6	1463	4.50E-10
Chr4	4760577	4761369	4	793	2.64E-07
Chr4	4778663	4779517	5	855	0.000166908
Chr4	4900256	4902906	4	2651	3.19378E-06
Chr4	4959193	4961504	7	2312	2.12E-09

Chr4	4965560	4968442	7	2883	5.26E-09
Chr4	4982747	4983299	6	553	5.03E-09
Chr4	5015101	5016225	4	1125	9.06E-08
Chr4	5023205	5025576	5	2372	7.11E-08
Chr4	5041629	5043142	5	1514	8.45635E-06
Chr4	5049354	5050720	5	1367	6.81871E-05
Chr4	5055109	5055972	7	864	3.44E-09
Chr4	5058508	5060870	6	2363	1.73E-10
Chr4	5076736	5078032	4	1297	1.41042E-06
Chr4	5080790	5081496	4	707	1.408E-05
Chr4	5307042	5308827	6	1786	1.23E-07
Chr4	5941456	5943178	4	1723	1.77621E-05
Chr4	6131370	6132155	4	786	6.47537E-05
Chr4	6332404	6333233	4	830	2.17659E-05
Chr4	6917152	6918424	4	1273	2.3181E-05
Chr4	8318205	8318677	6	473	6.28E-10
Chr4	9489100	9489837	4	738	2.69525E-06
Chr4	9733111	9734294	5	1184	2.57E-07
Chr4	10993713	10995146	5	1434	6.61642E-06
Chr4	11366136	11366841	4	706	7.40E-07
Chr4	13329274	13330468	6	1195	4.15E-08
Chr4	13628045	13629303	4	1259	6.16456E-06
Chr5	136671	138020	4	1350	7.89E-08
Chr5	2260550	2262472	4	1923	0.000131935
Chr5	4320868	4324850	9	3983	2.52E-09
Chr5	7037180	7038845	5	1666	1.02E-08
Chr5	8573987	8574967	4	981	2.10491E-06
Chr5	9093185	9094174	4	990	4.70E-08
Chr5	9183147	9185799	7	2653	1.20E-08
Chr5	9413560	9415073	5	1514	5.49296E-06
Chr5	9564752	9568438	8	3687	1.81E-11
Chr5	9892884	9894395	4	1512	2.1852E-06
Chr5	9906758	9907966	4	1209	4.09863E-05
Chr5	9925343	9927482	7	2140	7.91E-09
Chr5	9982586	9983423	4	838	1.55421E-05
Chr5	10054483	10056222	4	1740	8.11789E-06
Chr5	10157532	10158164	4	633	4.87664E-06
Chr5	10352097	10353580	5	1484	1.25E-09
Chr5	10359950	10362762	11	2813	3.52E-12
Chr5	10364658	10365303	4	646	3.67E-08
Chr5	10577045	10578326	4	1282	9.84957E-07
Chr5	10624307	10626545	5	2239	4.0695E-05
Chr5	10729323	10729896	4	574	4.89593E-07
Chr5	10739635	10741850	4	2216	6.8267E-05
Chr5	10972104	10972800	4	697	1.33E-07
Chr5	11056169	11057824	5	1656	4.30893E-06
Chr5	11082049	11083114	5	1066	5.15E-08
Chr5	11087736	11089308	5	1573	2.45951E-06
Chr5	11101038	11103159	4	2122	1.3363E-05
Chr5	11139512	11141039	4	1528	2.58435E-05
Chr5	11151189	11153526	7	2338	2.71E-09
Chr5	11181307	11183651	7	2345	6.67891E-05
Chr5	11185246	11186349	4	1104	0.061883927
Chr5	11188360	11188740	9	381	7.77511E-06
Chr5	11208938	11209178	4	241	9.81E-07
Chr5	11211547	11212919	11	1373	3.69E-12
Chr5	11347620	11350364	7	2745	1.54E-09
Chr5	11352033	11353255	7	1223	1.00781E-07
Chr5	11355255	11356966	4	1712	3.56386E-05
Chr5	11358844	11359904	4	1061	1.01438E-06
Chr5	11369196	11369973	5	778	2.15568E-06
Chr5	11402694	11403196	4	503	1.859E-05
Chr5	11410187	11414390	8	4204	1.93E-09

Chr5	11429402	11430161	5	760	8.04E-07
Chr5	11529652	11530645	4	994	5.69008E-06
Chr5	11549272	11549829	4	558	9.04791E-06
Chr5	11589490	11590864	5	1375	1.31E-08
Chr5	11593121	11594393	4	1273	4.28585E-05
Chr5	11703087	11703692	5	606	2.45304E-06
Chr5	11704745	11708854	12	4110	1.30E-07
Chr5	11722642	11724812	8	2171	4.19E-07
Chr5	11727456	11731445	12	3990	0.478063695
Chr5	11735268	11736342	6	1075	7.05E-10
Chr5	11749554	11751320	5	1767	6.05E-07
Chr5	11773797	11774988	4	1192	1.52191E-05
Chr5	11787657	11788948	4	1292	2.9599E-06
Chr5	11804831	11807446	5	2616	3.92E-07
Chr5	11842610	11843429	4	820	5.17E-07
Chr5	11908176	11909143	4	968	4.29715E-06
Chr5	11910237	11912171	4	1935	4.63661E-06
Chr5	11918662	11922210	7	3549	3.64E-09
Chr5	11923421	11923967	4	547	3.85E-07
Chr5	11936602	11939872	24	3271	1.08E-22
Chr5	11941321	11942680	10	1360	4.18E-13
Chr5	11980009	11980609	4	601	1.18068E-06
Chr5	11984673	11987458	12	2786	2.51E-14
Chr5	11997692	11999126	6	1435	1.78E-09
Chr5	12008215	12011177	10	2963	2.58E-13
Chr5	12013512	12015101	5	1590	8.05E-09
Chr5	12034696	12035206	5	511	4.68E-08
Chr5	12040023	12041365	9	1343	6.18E-10
Chr5	12102997	12104363	6	1367	1.21692E-06
Chr5	12124711	12126592	7	1882	3.73E-10
Chr5	12130495	12133315	10	2821	3.75E-10
Chr5	12155645	12156186	4	542	8.22E-07
Chr5	12158737	12160436	6	1700	3.25E-08
Chr5	12166679	12168459	4	1781	9.50601E-05
Chr5	12174932	12175488	5	557	2.00E-07
Chr5	12213328	12215854	5	2527	9.66E-08
Chr5	12222743	12223779	4	1037	1.04E-07
Chr5	12233191	12236588	11	3398	1.41E-15
Chr5	12237870	12239916	7	2047	5.06E-09
Chr5	12242824	12244418	6	1595	1.24E-08
Chr5	12255097	12256290	5	1194	2.10E-07
Chr5	12290697	12292383	4	1687	4.68434E-06
Chr5	12319420	12320849	4	1430	4.08E-07
Chr5	12340512	12341867	4	1356	5.93926E-06
Chr5	12347728	12348766	5	1039	3.27783E-06
Chr5	12366632	12367522	4	891	7.27265E-06
Chr5	12398893	12399412	6	520	2.96E-07
Chr5	12406830	12408688	5	1859	7.51E-08
Chr5	12427465	12428913	5	1449	2.25172E-05
Chr5	12460700	12462618	4	1919	9.99E-07
Chr5	12471081	12475623	11	4543	8.54E-16
Chr5	12515059	12517525	8	2467	3.16E-11
Chr5	12612518	12612562	4	45	4.07006E-06
Chr5	12633409	12634037	4	629	1.95069E-05
Chr5	12640645	12642060	5	1416	4.18168E-05
Chr5	12711232	12713598	4	2367	1.81078E-05
Chr5	12715279	12716784	5	1506	1.26891E-05
Chr5	12775046	12777551	9	2506	8.68E-11
Chr5	12784496	12786153	5	1658	1.73E-08
Chr5	12792796	12795160	6	2365	1.79916E-07
Chr5	12916904	12917716	4	813	2.3333E-05
Chr5	12948010	12949475	6	1466	4.7124E-07
Chr5	12954953	12956287	4	1335	3.25E-07

Chr5	12969539	12971052	4	1514	1.31392E-06
Chr5	12972522	12974071	4	1550	0.000133768
Chr5	13015805	13017399	4	1595	2.90E-08
Chr5	13030396	13032607	4	2212	0.009583002
Chr5	13162147	13164562	5	2416	1.91E-11
Chr5	13289417	13291553	4	2137	1.41706E-05
Chr5	13326130	13327366	4	1237	1.50691E-06
Chr5	13374902	13375798	4	897	3.37662E-06
Chr5	13737041	13737869	4	829	1.59412E-05
Chr5	13888151	13889914	4	1764	8.71E-07
Chr5	14253440	14253624	5	185	2.27431E-05
Chr5	14381687	14382502	5	816	1.56E-09
Chr5	14576964	14578592	5	1629	1.57E-07
Chr5	15637677	15638289	4	613	6.25098E-07
Chr5	15646619	15648619	4	2001	0.000355547
Chr5	15926072	15927262	6	1191	7.27E-09
Chr5	16261249	16261405	4	157	6.60043E-05
Chr5	17443006	17445388	5	2383	3.35706E-06
Chr5	19361508	19362793	4	1286	2.01927E-05
Chr5	21168967	21169614	5	648	1.54063E-06

-Pit Shoot 16 dat (Hyper-DMRs)

Chromosome	Start	End	number of DMCs	DMR lenght	P-value
Chr1	1211865	1212769	4	905	3.16E-09
Chr1	4333119	4334436	4	1318	3.27554E-06
Chr1	6590998	6593230	7	2233	4.30E-09
Chr1	6658336	6659229	4	894	4.88896E-06
Chr1	7358648	7360096	5	1449	0.000396044
Chr1	7361145	7363508	5	2364	0.002797563
Chr1	7430464	7431925	4	1462	3.36952E-05
Chr1	8458478	8459555	4	1078	3.4937E-05
Chr1	8644321	8645675	5	1355	1.24641E-06
Chr1	8729113	8732424	12	3312	8.13E-19
Chr1	8929448	8930630	4	1183	2.40066E-06
Chr1	9686846	9687810	4	965	2.07579E-05
Chr1	10359130	10361787	15	2658	3.36E-20
Chr1	10697740	10700392	4	2653	2.55661E-05
Chr1	11302930	11303224	4	295	3.62479E-05
Chr1	11304842	11306271	5	1430	2.66E-08
Chr1	11505076	11508096	6	3021	1.79E-07
Chr1	12175592	12176336	4	745	2.05963E-05
Chr1	12402715	12403421	4	707	0.000126042
Chr1	12856230	12858099	7	1870	2.64E-09
Chr1	12860890	12861146	4	257	9.42074E-06
Chr1	13648345	13650503	4	2159	6.1722E-06
Chr1	13830638	13832884	5	2247	2.57E-08
Chr1	13885395	13887535	7	2141	1.96E-09
Chr1	13956654	13957540	5	887	7.38E-08
Chr1	14089816	14091031	5	1216	9.71E-07
Chr1	14125700	14127674	5	1975	8.0478E-06
Chr1	14228150	14229851	5	1702	3.1614E-06
Chr1	14259288	14260219	4	932	3.80E-07
Chr1	14261916	14264612	5	2697	3.80722E-07
Chr1	14269356	14270030	6	675	4.15E-10
Chr1	14324596	14325421	4	826	2.25171E-05
Chr1	14493392	14496609	6	3218	5.48219E-06
Chr1	14508655	14510103	5	1449	7.04E-08
Chr1	14544849	14545558	5	710	3.06E-08
Chr1	15081309	15085481	42	4173	2.41E-51
Chr1	15436467	15440262	11	3796	1.82E-11
Chr1	15492999	15493526	4	528	3.24054E-05
Chr1	15497779	15500218	7	2440	1.53E-11

Chr1	15509514	15509657	4	144	7.54901E-06
Chr1	15533717	15534935	6	1219	9.51E-09
Chr1	15539772	15540663	6	892	3.52E-12
Chr1	15697817	15699761	9	1945	7.58E-14
Chr1	15707520	15708344	4	825	1.15818E-05
Chr1	15802891	15804772	4	1882	2.34051E-05
Chr1	16378674	16379995	4	1322	1.35147E-05
Chr1	16513019	16514853	10	1835	2.46E-12
Chr1	16526291	16530372	12	4082	7.39E-16
Chr1	16632286	16634038	8	1753	1.67E-13
Chr1	16635151	16636545	6	1395	8.83E-08
Chr1	16674931	16676346	4	1416	1.24543E-05
Chr1	16726910	16728426	4	1517	3.10479E-05
Chr1	16732628	16733705	4	1078	1.29E-08
Chr1	16959353	16961218	4	1866	2.37671E-05
Chr1	17028098	17029748	5	1651	1.42E-07
Chr1	17036106	17040220	9	4115	2.74E-09
Chr1	17677306	17679249	4	1944	2.50895E-05
Chr1	17680354	17681250	4	897	5.77409E-06
Chr1	18158498	18159468	4	971	8.51E-08
Chr1	18969049	18969760	4	712	7.87E-07
Chr1	20086086	20087825	5	1740	2.53E-08
Chr1	21751173	21751957	4	785	6.49208E-05
Chr1	24272882	24275823	139	2942	2.21E-224
Chr1	24526905	24528168	5	1264	6.89709E-06
Chr1	26360727	26361120	6	394	1.34E-09
Chr1	26371026	26371617	5	592	5.38E-09
Chr2	1229	3722	84	2494	2.99E-177
Chr2	5537	5981	14	445	6.02E-16
Chr2	9594	10571	42	978	9.53E-70
Chr2	39645	40088	6	444	3.13E-07
Chr2	43405	44434	4	1030	3.98E-08
Chr2	47118	48312	6	1195	3.71E-10
Chr2	362455	362519	4	65	2.24764E-06
Chr2	375292	375976	6	685	2.71746E-06
Chr2	822876	824402	4	1527	9.55E-07
Chr2	1263936	1263970	4	35	2.61864E-06
Chr2	1548702	1549094	6	393	6.78E-12
Chr2	1761941	1764376	5	2436	9.53E-08
Chr2	2036017	2037702	5	1686	8.61E-07
Chr2	2466794	2468172	4	1379	6.18E-07
Chr2	2489981	2492334	5	2354	4.89E-08
Chr2	2509896	2511048	4	1153	3.52509E-06
Chr2	2708073	2709522	4	1450	5.37E-07
Chr2	2805875	2807936	6	2062	2.65E-08
Chr2	2832894	2834332	4	1439	2.13406E-05
Chr2	3078385	3080276	4	1892	3.28586E-05
Chr2	3087078	3088045	4	968	2.05076E-06
Chr2	3097760	3098516	5	757	6.65E-07
Chr2	3161107	3162245	5	1139	5.08033E-05
Chr2	3163646	3166069	4	2424	6.74942E-06
Chr2	3240754	3242210	74	1457	2.10E-139
Chr2	3245294	3245499	14	206	7.33E-23
Chr2	3247280	3367914	7284	120635	0
Chr2	3375070	3379103	103	4034	1.13E-157
Chr2	3381730	3382098	30	369	1.14E-69
Chr2	3389197	3389545	6	349	4.80E-12
Chr2	3393395	3400972	220	7578	0
Chr2	3404754	3406630	29	1877	6.59E-49
Chr2	3411078	3411276	5	199	1.34E-08
Chr2	3412612	3412877	15	266	1.93E-21
Chr2	3418590	3418799	16	210	5.21E-23
Chr2	3428917	3429171	11	255	1.27E-22

Chr2	3431386	3431579	6	194	2.56E-08
Chr2	3434012	3434416	13	405	2.38E-17
Chr2	3438292	3439777	54	1486	5.77E-139
Chr2	3447423	3447643	13	221	5.24E-23
Chr2	3451820	3452101	7	282	9.19E-11
Chr2	3453832	3454208	12	377	6.88E-21
Chr2	3455789	3456075	12	287	3.93E-19
Chr2	3457914	3461256	81	3343	5.95E-165
Chr2	3462992	3465642	52	2651	1.65E-116
Chr2	3468270	3469482	26	1213	5.71E-46
Chr2	3471459	3471655	10	197	2.44E-12
Chr2	3474764	3476303	34	1540	1.02E-61
Chr2	3478009	3478522	30	514	1.40E-63
Chr2	3482443	3482674	5	232	7.12E-07
Chr2	3483767	3485127	26	1361	1.06E-37
Chr2	3486361	3487585	22	1225	1.83E-33
Chr2	3488724	3493588	127	4865	9.15E-234
Chr2	3495332	3502057	95	6726	4.13E-153
Chr2	3509226	3509734	31	509	3.43E-49
Chr2	3519665	3520673	4	1009	2.87999E-06
Chr2	3547437	3549156	4	1720	4.93571E-05
Chr2	3550866	3551789	5	924	0.000268106
Chr2	3605800	3607322	19	1523	9.15E-21
Chr2	3615092	3623604	91	8513	7.59E-80
Chr2	3624611	3628052	39	3442	3.84E-55
Chr2	3689138	3690266	4	1129	1.37262E-06
Chr2	3830681	3831709	4	1029	1.76172E-06
Chr2	3843434	3845009	4	1576	2.7452E-06
Chr2	3859091	3861826	6	2736	9.22E-07
Chr2	3871208	3872247	5	1040	1.18E-08
Chr2	3877959	3880951	7	2993	1.01E-09
Chr2	3922365	3923807	5	1443	1.57E-10
Chr2	4054851	4056664	5	1814	7.69586E-06
Chr2	4124726	4127009	4	2284	5.16E-08
Chr2	4189661	4190381	4	721	1.1656E-06
Chr2	4209044	4210227	4	1184	0.000189553
Chr2	4236897	4240861	7	3965	8.05E-07
Chr2	4311645	4311886	4	242	5.74553E-06
Chr2	4387980	4389833	5	1854	9.06054E-05
Chr2	4582050	4582618	4	569	2.41915E-05
Chr2	4679232	4681674	5	2443	1.84E-08
Chr2	4692227	4692828	4	602	3.35316E-06
Chr2	4694879	4695639	5	761	7.87E-08
Chr2	4710872	4714196	9	3325	7.57E-11
Chr2	4722411	4723465	4	1055	9.04E-07
Chr2	4726753	4728418	4	1666	0.000112574
Chr2	4730551	4731361	4	811	3.65E-07
Chr2	4733091	4736675	12	3585	5.76E-16
Chr2	4739703	4740479	6	777	8.45E-10
Chr2	4844008	4844137	14	130	1.99E-38
Chr2	4897103	4898106	4	1004	1.41E-07
Chr2	4977971	4979253	4	1283	5.46949E-05
Chr2	4988167	4989925	4	1759	0.000127979
Chr2	5085567	5087836	7	2270	7.16E-08
Chr2	5104371	5106266	6	1896	3.12982E-06
Chr2	5202794	5203795	4	1002	3.56921E-05
Chr2	5209349	5210849	5	1501	2.70893E-06
Chr2	5302571	5304457	4	1887	0.000136065
Chr2	5310700	5310995	4	296	1.04624E-05
Chr2	5333306	5335483	5	2178	4.86E-08
Chr2	5371076	5372622	5	1547	2.73031E-06
Chr2	5454656	5456286	4	1631	2.05E-07
Chr2	5531399	5532163	4	765	2.98266E-05

Chr2	5810940	5813305	6	2366	9.92E-08
Chr2	5847818	5848911	6	1094	2.85E-09
Chr2	5880315	5882609	8	2295	1.40E-12
Chr2	6112370	6113125	7	756	8.17E-11
Chr2	6228694	6229819	7	1126	2.50E-09
Chr2	6529782	6532075	6	2294	3.11E-07
Chr2	6555167	6557019	5	1853	4.26E-07
Chr2	6701109	6703432	5	2324	6.18E-07
Chr2	6704564	6706677	6	2114	9.04E-09
Chr2	6767033	6768924	4	1892	5.01824E-06
Chr2	6971179	6972751	4	1573	5.22148E-06
Chr2	7005780	7006904	5	1125	2.47E-07
Chr2	7226083	7228723	6	2641	5.35E-07
Chr2	8565071	8566532	6	1462	1.37856E-06
Chr2	9122587	9125209	8	2623	1.31E-07
Chr2	10001895	10003424	5	1530	1.68E-08
Chr2	10592479	10593305	4	827	9.44841E-06
Chr2	12450107	12451254	4	1148	1.25E-09
Chr2	12810650	12810774	4	125	5.89166E-06
Chr2	18651868	18654517	6	2650	3.10452E-07
Chr3	2809255	2810716	6	1462	6.17E-10
Chr3	5278527	5280623	7	2097	3.89E-07
Chr3	6275067	6275585	4	519	7.32E-10
Chr3	7104162	7104241	4	80	7.58E-08
Chr3	8537525	8538225	4	701	1.94385E-06
Chr3	9016237	9016985	4	749	1.44253E-05
Chr3	9239060	9240694	6	1635	3.19E-10
Chr3	9695345	9697373	6	2029	1.25E-07
Chr3	9785700	9788265	6	2566	1.01E-09
Chr3	10339890	10341737	8	1848	1.60E-09
Chr3	10342788	10345250	7	2463	3.39E-10
Chr3	10480437	10481801	4	1365	1.87058E-05
Chr3	10970345	10972925	7	2581	4.75E-08
Chr3	11056579	11056866	4	288	5.57E-07
Chr3	11495282	11496681	4	1400	3.22E-07
Chr3	11687506	11688265	4	760	3.1036E-06
Chr3	11872172	11874053	6	1882	8.58E-09
Chr3	12033083	12035210	5	2128	2.68E-07
Chr3	12068888	12069892	4	1005	3.51E-08
Chr3	12194790	12195473	4	684	8.48251E-07
Chr3	12222725	12223696	4	972	1.70E-07
Chr3	12288905	12291223	5	2319	5.47E-07
Chr3	12306034	12307899	4	1866	1.54802E-06
Chr3	12402654	12403438	4	785	0.000163995
Chr3	12404559	12405624	4	1066	4.47E-07
Chr3	12500587	12502218	6	1632	3.28E-08
Chr3	12544974	12545519	4	546	1.98E-08
Chr3	12952065	12954026	4	1962	7.64005E-06
Chr3	12986005	12987851	5	1847	8.21E-07
Chr3	13117459	13119461	7	2003	4.39E-08
Chr3	13160738	13161397	4	660	6.10E-09
Chr3	13191522	13192440	4	919	6.87E-09
Chr3	13407713	13410462	5	2750	9.15E-08
Chr3	13414722	13417379	4	2658	1.06209E-06
Chr3	13447925	13448672	6	748	1.33E-09
Chr3	13587086	13587773	13	688	7.01E-26
Chr3	13588800	13592495	125	3696	3.62E-178
Chr3	13630848	13633664	6	2817	2.39817E-06
Chr3	13641556	13643741	5	2186	1.99E-07
Chr3	13801985	13804385	5	2401	6.94E-07
Chr3	13809357	13811115	4	1759	3.02464E-06
Chr3	13821085	13822606	5	1522	6.33E-10
Chr3	13877366	13879041	5	1676	1.26718E-06

Chr3	13889137	13891666	6	2530	3.36E-08
Chr3	13894569	13898018	6	3450	3.44E-09
Chr3	13909054	13909907	4	854	1.36826E-06
Chr3	13951119	13953397	7	2279	5.60E-11
Chr3	14033235	14033477	5	243	1.78E-07
Chr3	14106499	14108458	4	1960	4.31477E-05
Chr3	14162519	14163791	4	1273	4.72E-07
Chr3	14165593	14167815	7	2223	8.10E-10
Chr3	14194635	14197485	111	2851	1.38E-120
Chr3	14199391	14204031	127	4641	3.39E-216
Chr3	14236414	14238269	7	1856	3.79E-12
Chr3	14249075	14249483	4	409	1.39603E-06
Chr3	14256311	14257635	6	1325	6.94E-07
Chr3	14391870	14393453	4	1584	0.000190138
Chr3	14409890	14411814	4	1925	4.79082E-05
Chr3	14431934	14434176	6	2243	4.63E-07
Chr3	14638614	14640046	4	1433	2.71165E-05
Chr3	15043420	15044634	5	1215	7.84E-08
Chr3	15137943	15138863	4	921	1.12703E-05
Chr3	15143903	15146269	5	2367	2.61E-08
Chr3	15154775	15155053	4	279	1.97161E-06
Chr3	15229831	15230546	4	716	2.73322E-05
Chr3	15255680	15257011	6	1332	1.17E-10
Chr3	15309306	15311894	9	2589	1.73E-14
Chr3	15374980	15377230	5	2251	1.14E-09
Chr3	15535989	15537784	5	1796	4.95E-08
Chr3	15543431	15544426	4	996	1.65344E-06
Chr3	15574854	15576492	5	1639	1.66693E-06
Chr3	15584317	15587651	13	3335	3.92E-16
Chr3	15719293	15719986	5	694	6.12092E-06
Chr3	15724081	15726173	6	2093	2.23E-08
Chr3	15922924	15923895	4	972	2.14477E-05
Chr3	16641811	16642856	4	1046	8.63525E-06
Chr3	20308994	20309351	4	358	0.000134826
Chr3	21322737	21324425	9	1689	1.23E-10
Chr3	23110014	23110960	4	947	0.00014976
Chr4	413752	414314	11	563	9.39E-16
Chr4	635857	636858	5	1002	3.48E-07
Chr4	1675143	1678403	5	3261	1.62E-09
Chr4	1826172	1827540	6	1369	9.11E-10
Chr4	1829523	1830693	4	1171	4.31E-07
Chr4	1936988	1937710	4	723	1.79217E-05
Chr4	1951043	1953009	6	1967	1.17E-08
Chr4	1990373	1992090	4	1718	1.04E-07
Chr4	2016083	2018030	7	1948	6.04E-08
Chr4	2195315	2196596	5	1282	3.44585E-05
Chr4	2200091	2203086	8	2996	8.60E-13
Chr4	2212736	2213994	6	1259	3.56E-10
Chr4	2275292	2276284	6	993	3.63E-07
Chr4	2280437	2285735	13	5299	1.10E-16
Chr4	2287731	2288334	4	604	0.000400844
Chr4	2304930	2305859	4	930	5.97797E-06
Chr4	2597477	2598559	4	1083	0.000964097
Chr4	2707085	2708753	5	1669	2.79434E-06
Chr4	2857089	2858356	4	1268	2.50E-07
Chr4	3019567	3020997	6	1431	1.69E-08
Chr4	3071284	3072522	5	1239	2.09223E-05
Chr4	3078674	3080446	4	1773	3.58674E-05
Chr4	3155203	3156053	4	851	3.59739E-05
Chr4	3181581	3183973	5	2393	1.81245E-05
Chr4	3290610	3291118	4	509	7.63E-07
Chr4	3367607	3368536	4	930	3.24225E-06
Chr4	3462827	3465257	6	2431	2.70E-08

Chr4	3546773	3548025	4	1253	1.70367E-06
Chr4	3551466	3552975	4	1510	3.005E-05
Chr4	3619500	3622940	9	3441	3.32E-10
Chr4	3627355	3628112	4	758	3.13618E-06
Chr4	3676947	3678252	5	1306	7.53E-08
Chr4	3712492	3714190	5	1699	6.26E-07
Chr4	3776813	3777590	4	778	2.29976E-05
Chr4	3920992	3922194	4	1203	6.47202E-05
Chr4	3950074	3955903	120	5830	1.07E-139
Chr4	3965385	3966790	5	1406	2.89111E-05
Chr4	3968149	3969441	5	1293	1.34E-07
Chr4	3992253	3992962	5	710	2.26203E-06
Chr4	4241098	4243270	5	2173	3.49124E-05
Chr4	4249779	4251135	4	1357	7.03556E-07
Chr4	4387528	4390255	6	2728	1.30E-09
Chr4	4437162	4440425	5	3264	2.66827E-06
Chr4	4600333	4601555	4	1223	9.41042E-06
Chr4	4730270	4730479	4	210	0.00011449
Chr4	4731634	4734037	9	2404	1.15E-10
Chr4	4899575	4900062	4	488	1.88814E-05
Chr4	4961185	4965949	12	4765	1.78E-15
Chr4	5014747	5016492	5	1746	1.32826E-05
Chr4	5026759	5029160	5	2402	1.18E-07
Chr4	5054146	5056569	6	2424	6.78E-09
Chr4	5069864	5070694	4	831	1.10756E-06
Chr4	5073268	5075612	7	2345	6.01E-09
Chr4	5399052	5401895	6	2844	2.71E-08
Chr4	5521738	5523324	6	1587	2.57E-07
Chr4	5622855	5625009	5	2155	9.66437E-06
Chr4	5627329	5629022	4	1694	4.94501E-06
Chr4	5647058	5647128	4	71	5.87E-07
Chr4	5822387	5823161	4	775	1.85E-09
Chr4	5966464	5967604	5	1141	1.24178E-05
Chr4	6130158	6132414	6	2257	3.90E-10
Chr4	6652699	6654087	5	1389	3.79661E-06
Chr4	6723455	6724722	10	1268	1.18E-11
Chr4	6727699	6729747	8	2049	3.94E-14
Chr4	7390161	7390954	4	794	8.70E-07
Chr4	7688192	7688559	4	368	1.18E-08
Chr4	8901251	8903385	5	2135	1.67E-08
Chr4	9484424	9485331	4	908	4.13098E-05
Chr4	9491628	9491940	4	313	2.33086E-05
Chr4	11037510	11040617	8	3108	1.58E-11
Chr4	17712917	17714568	7	1652	8.63E-09
Chr5	65503	66385	4	883	1.96837E-05
Chr5	724923	726354	4	1432	1.85E-07
Chr5	2040059	2040175	4	117	4.96128E-06
Chr5	2258120	2262558	12	4439	1.02E-15
Chr5	3253148	3253276	23	129	7.71E-43
Chr5	4324081	4325638	4	1558	6.9593E-06
Chr5	5008048	5008343	4	296	3.50343E-06
Chr5	6208714	6208881	4	168	0.000110144
Chr5	7027636	7028655	5	1020	1.43E-07
Chr5	9250695	9253590	6	2896	2.4521E-06
Chr5	9412260	9412897	4	638	5.98E-07
Chr5	9925797	9927234	7	1438	3.00E-12
Chr5	9982017	9983146	4	1130	4.6004E-05
Chr5	10049683	10050919	5	1237	4.56E-09
Chr5	10054792	10055966	4	1175	1.14036E-06
Chr5	10105789	10106785	4	997	3.85003E-06
Chr5	10518377	10519011	4	635	0.000856418
Chr5	10739116	10740540	5	1425	1.10227E-05
Chr5	10885035	10887052	4	2018	1.28E-08

Chr5	11070697	11072199	4	1503	4.32919E-06
Chr5	11100550	11103234	7	2685	3.98E-11
Chr5	11154233	11154617	4	385	2.06682E-05
Chr5	11328351	11328583	4	233	1.43058E-06
Chr5	11342995	11344277	4	1283	2.82E-09
Chr5	11397789	11398790	4	1002	4.80E-07
Chr5	11559553	11560647	4	1095	2.62182E-05
Chr5	11582099	11582704	4	606	2.56213E-06
Chr5	11626393	11627859	4	1467	5.17609E-05
Chr5	11658802	11660431	4	1630	1.4237E-05
Chr5	11701698	11704122	10	2425	5.04E-10
Chr5	11706034	11709953	13	3920	7.69E-14
Chr5	11723414	11724979	10	1566	1.10E-12
Chr5	11726216	11736116	75	9901	4.91E-86
Chr5	11749690	11751269	5	1580	2.01167E-06
Chr5	11753621	11754837	5	1217	0.002872112
Chr5	11764999	11765921	12	923	1.46E-29
Chr5	11768934	11770801	7	1868	1.93E-07
Chr5	11796417	11797877	5	1461	0.000961448
Chr5	11904330	11904906	4	577	2.69E-07
Chr5	11919038	11920542	5	1505	1.33778E-05
Chr5	11935843	11937823	6	1981	3.29931E-06
Chr5	11939401	11940635	8	1235	2.87E-13
Chr5	11982451	11983712	6	1262	1.27E-09
Chr5	11993085	11995390	7	2306	2.39E-10
Chr5	12000700	12001981	4	1282	5.95447E-05
Chr5	12006927	12007994	4	1068	1.08089E-06
Chr5	12048660	12050517	4	1858	1.76644E-07
Chr5	12228155	12230044	6	1890	4.75E-08
Chr5	12289242	12291543	8	2302	3.68E-07
Chr5	12402337	12404221	5	1885	7.88244E-07
Chr5	12431925	12432856	4	932	1.04048E-05
Chr5	12610433	12611992	4	1560	2.11E-08
Chr5	12742197	12742381	5	185	4.95342E-07
Chr5	12747457	12748479	6	1023	1.75601E-06
Chr5	12770478	12772952	7	2475	1.76E-09
Chr5	12969819	12970391	4	573	7.8795E-05
Chr5	12977652	12980305	7	2654	1.95E-10
Chr5	13023996	13025582	4	1587	0.001260716
Chr5	13282340	13283956	4	1617	4.97424E-05
Chr5	13538190	13539372	5	1183	1.29398E-06
Chr5	13847297	13848176	4	880	8.47E-07
Chr5	14038311	14038888	4	578	6.79043E-06
Chr5	14702397	14703779	4	1383	3.63754E-06
Chr5	15239782	15240321	4	540	6.93E-07
Chr5	15241515	15243006	4	1492	2.64006E-05
Chr5	15353375	15356882	6	3508	2.69E-08
Chr5	15493104	15494980	4	1877	6.16333E-06
Chr5	15925443	15926778	4	1336	7.94796E-06
Chr5	17601048	17603089	5	2042	8.67E-07
Chr5	18491034	18493041	4	2008	5.30278E-05
Chr5	19359938	19361884	6	1947	6.18E-09
Chr5	21172759	21172804	4	46	7.70E-18
Chr5	21689891	21691711	7	1821	3.49E-11

-Pit Shoot 16 dat (Hypo-DMRs)

Chromosome	Start	End	number of DMCs	DMR lenght	P-value
Chr1	76910	77399	4	490	5.51E-08
Chr1	789649	789666	4	18	2.59E-07
Chr1	2342395	2342850	10	456	3.58E-25
Chr1	2719344	2720761	8	1418	7.01E-16
Chr1	3819733	3820601	11	869	5.60E-16

Chr1	4093309	4093982	4	674	5.63E-08
Chr1	4176483	4177330	4	848	7.40518E-06
Chr1	4329878	4330265	4	388	6.03E-07
Chr1	4570623	4570854	4	232	1.53928E-06
Chr1	5694636	5695795	5	1160	3.99E-08
Chr1	5913446	5914785	4	1340	2.94E-07
Chr1	6589065	6589731	4	667	1.97494E-06
Chr1	7065987	7067941	4	1955	1.00821E-05
Chr1	7353082	7365034	66	11953	3.93E-65
Chr1	7440786	7441206	6	421	4.89E-13
Chr1	7972206	7973255	6	1050	3.95932E-06
Chr1	8458595	8459553	4	959	1.90E-07
Chr1	8461027	8461402	5	376	2.59E-07
Chr1	8526022	8526223	5	202	3.72E-16
Chr1	8790575	8792576	10	2002	1.97E-14
Chr1	8929168	8929812	4	645	5.4577E-06
Chr1	9677175	9677557	5	383	5.54169E-06
Chr1	10215778	10216025	5	248	6.64E-07
Chr1	10698542	10700241	5	1700	1.22E-08
Chr1	10807547	10807620	4	74	1.32E-16
Chr1	11561005	11561145	4	141	4.33E-08
Chr1	11807669	11807817	5	149	3.13E-08
Chr1	11888680	11890223	6	1544	3.22E-07
Chr1	11900871	11901620	4	750	2.72E-07
Chr1	12140114	12141704	4	1591	2.3936E-06
Chr1	12404985	12406765	5	1781	2.69349E-06
Chr1	12408438	12410067	7	1630	1.89E-11
Chr1	12679962	12680618	4	657	7.18E-09
Chr1	12681646	12682721	4	1076	1.75428E-06
Chr1	12715307	12716582	4	1276	1.45913E-05
Chr1	12807396	12809095	4	1700	1.32892E-05
Chr1	12820558	12822767	5	2210	7.22E-07
Chr1	12830652	12832040	4	1389	8.27E-07
Chr1	13001178	13001797	5	620	1.44E-08
Chr1	13008603	13011834	8	3232	1.37E-12
Chr1	13019749	13020684	4	936	1.25E-07
Chr1	13098962	13100197	6	1236	4.01E-09
Chr1	13127047	13127791	4	745	1.13125E-05
Chr1	13173865	13176528	5	2664	8.72E-08
Chr1	13185173	13187206	5	2034	4.13514E-06
Chr1	13188514	13190176	4	1663	9.96097E-06
Chr1	13233376	13234058	4	683	1.11E-07
Chr1	13266986	13268326	7	1341	2.40E-13
Chr1	13295954	13297109	4	1156	2.08E-07
Chr1	13326998	13328454	4	1457	8.88427E-05
Chr1	13335365	13336438	4	1074	5.80388E-06
Chr1	13375839	13376825	4	987	0.000360447
Chr1	13381570	13384070	6	2501	1.86E-10
Chr1	13399812	13401005	5	1194	9.36E-08
Chr1	13493017	13494804	5	1788	1.29E-07
Chr1	13505552	13506871	4	1320	2.43124E-05
Chr1	13512504	13514293	8	1790	8.73E-13
Chr1	13561224	13563768	8	2545	1.63E-11
Chr1	13574374	13575998	7	1625	1.86E-09
Chr1	13595263	13596532	7	1270	3.38E-09
Chr1	13630060	13631552	6	1493	5.48E-08
Chr1	13644196	13645189	4	994	1.99218E-06
Chr1	13649914	13650981	6	1068	3.37E-07
Chr1	13652284	13654171	5	1888	1.34E-08
Chr1	13662475	13664026	5	1552	1.04472E-06
Chr1	13690631	13692981	6	2351	4.64E-09
Chr1	13711486	13712876	6	1391	3.38E-08
Chr1	13723880	13725024	4	1145	8.67E-07

Chr1	13751455	13752859	5	1405	4.83E-07
Chr1	13769145	13771058	10	1914	1.86E-10
Chr1	13772108	13775305	10	3198	2.26E-08
Chr1	13787913	13790027	8	2115	7.11E-11
Chr1	13796396	13799214	8	2819	1.17E-13
Chr1	13823413	13824513	5	1101	2.23617E-07
Chr1	13828634	13830128	7	1495	1.02904E-06
Chr1	13832768	13836422	16	3655	2.40E-20
Chr1	13840540	13842501	6	1962	1.33E-10
Chr1	13845046	13847192	4	2147	8.10605E-06
Chr1	13871458	13872995	4	1538	2.18E-08
Chr1	13888282	13889335	6	1054	1.05E-08
Chr1	13919271	13922326	11	3056	6.83E-16
Chr1	13945222	13947955	6	2734	3.41E-08
Chr1	13950595	13953025	6	2431	1.53E-08
Chr1	13954743	13956010	9	1268	1.35E-08
Chr1	13957563	13960695	7	3133	1.45E-09
Chr1	13970023	13972508	8	2486	4.17E-11
Chr1	13977640	13978491	4	852	1.89828E-05
Chr1	14035394	14037114	5	1721	2.96017E-06
Chr1	14053326	14054551	6	1226	9.20E-10
Chr1	14059161	14060296	5	1136	4.21E-08
Chr1	14071943	14073235	4	1293	6.68689E-06
Chr1	14077111	14080382	9	3272	1.86E-10
Chr1	14088457	14093110	11	4654	7.96E-15
Chr1	14104845	14106081	8	1237	6.28E-12
Chr1	14109400	14112126	7	2727	4.87E-07
Chr1	14122088	14122903	7	816	1.62E-07
Chr1	14124276	14125756	4	1481	7.17015E-07
Chr1	14139598	14140419	4	822	4.30918E-06
Chr1	14143856	14145999	7	2144	2.05E-09
Chr1	14181616	14182841	4	1226	2.37858E-06
Chr1	14199604	14201578	8	1975	3.16E-10
Chr1	14203016	14204576	4	1561	0.000940535
Chr1	14208830	14213389	11	4560	1.86E-12
Chr1	14215813	14216607	4	795	3.89232E-06
Chr1	14221689	14224470	9	2782	3.89E-12
Chr1	14225892	14227169	4	1278	2.02064E-06
Chr1	14228253	14229687	8	1435	8.84E-09
Chr1	14233853	14234172	4	320	7.53E-08
Chr1	14235208	14237204	9	1997	8.69E-13
Chr1	14239739	14241594	5	1856	2.44E-10
Chr1	14247016	14248278	14	1263	1.44E-16
Chr1	14250200	14250997	6	798	4.27E-10
Chr1	14252847	14255227	7	2381	8.93E-09
Chr1	14259166	14260186	7	1021	1.24E-09
Chr1	14267211	14270510	12	3300	5.34E-11
Chr1	14271589	14272846	5	1258	2.90072E-06
Chr1	14275072	14276468	4	1397	0.000497763
Chr1	14279510	14280496	4	987	1.092E-05
Chr1	14310667	14314441	9	3775	6.75E-11
Chr1	14315630	14318668	16	3039	9.51E-17
Chr1	14321559	14323430	5	1872	5.61E-09
Chr1	14328220	14329198	5	979	5.79E-07
Chr1	14387385	14389570	5	2186	1.54E-07
Chr1	14433114	14434760	6	1647	7.81E-10
Chr1	14450447	14451735	6	1289	1.92E-08
Chr1	14457165	14460139	6	2975	3.23E-08
Chr1	14474159	14474310	4	152	4.1183E-06
Chr1	14479398	14481089	5	1692	3.97E-10
Chr1	14486088	14488724	6	2637	1.31E-07
Chr1	14491693	14494545	7	2853	2.39E-09
Chr1	14495763	14497339	7	1577	1.52E-07

Chr1	14500262	14507663	22	7402	5.89E-31
Chr1	14539579	14540847	5	1269	1.3185E-05
Chr1	14542074	14545363	11	3290	7.40E-14
Chr1	14582192	14584968	11	2777	4.93E-11
Chr1	14587274	14588212	4	939	5.85554E-06
Chr1	14590153	14590501	6	349	2.00E-10
Chr1	14597497	14603563	11	6067	5.51E-15
Chr1	14609511	14610114	4	604	2.97595E-05
Chr1	14670726	14672266	5	1541	1.40E-07
Chr1	14683734	14683973	4	240	7.77E-07
Chr1	14715265	14716298	4	1034	1.46838E-05
Chr1	14721244	14722344	19	1101	1.65E-30
Chr1	14812743	14814262	5	1520	1.79E-07
Chr1	14837259	14838395	5	1137	4.50E-07
Chr1	14846157	14850623	15	4467	4.55E-16
Chr1	14887203	14887742	4	540	5.30694E-07
Chr1	14893255	14894981	4	1727	0.000541765
Chr1	14896548	14897514	4	967	8.29E-08
Chr1	15007078	15008528	5	1451	7.27E-10
Chr1	15045982	15047252	4	1271	0.004099481
Chr1	15060197	15061191	4	995	7.81E-07
Chr1	15063758	15075231	37	11474	7.78E-43
Chr1	15079461	15084916	42	5456	9.12E-180
Chr1	15092203	15095647	14	3445	6.07E-11
Chr1	15103707	15104592	4	886	2.20611E-06
Chr1	15136068	15136955	4	888	0.000303963
Chr1	15138275	15138976	4	702	2.90E-08
Chr1	15140022	15140382	4	361	0.000122879
Chr1	15141650	15142349	4	700	4.22E-08
Chr1	15144668	15145071	4	404	8.5428E-06
Chr1	15147686	15148851	5	1166	1.79E-09
Chr1	15153561	15157968	13	4408	1.98E-14
Chr1	15163943	15164958	4	1016	9.59E-09
Chr1	15184453	15185902	7	1450	1.28E-07
Chr1	15188654	15190866	8	2213	7.48E-12
Chr1	15200339	15201306	9	968	3.23E-09
Chr1	15208530	15208707	4	178	5.26E-09
Chr1	15413817	15413909	4	93	7.08E-07
Chr1	15417715	15421256	10	3542	8.22E-11
Chr1	15426925	15428039	4	1115	8.09885E-06
Chr1	15437559	15439278	7	1720	1.64E-10
Chr1	15444920	15453022	21	8103	5.87E-25
Chr1	15485973	15487650	5	1678	1.60E-08
Chr1	15488741	15490565	9	1825	5.15E-09
Chr1	15492383	15493748	8	1366	1.86E-09
Chr1	15503911	15507059	11	3149	1.75E-15
Chr1	15510820	15511388	4	569	2.70E-07
Chr1	15532593	15535186	8	2594	6.32E-14
Chr1	15536455	15537158	5	704	1.20251E-05
Chr1	15541695	15542600	4	906	5.60541E-05
Chr1	15543619	15545259	7	1641	6.32E-10
Chr1	15551326	15552964	6	1639	1.49777E-05
Chr1	15556910	15562166	18	5257	3.94E-22
Chr1	15564188	15565351	4	1164	7.15E-07
Chr1	15566641	15572303	19	5663	1.29E-23
Chr1	15633220	15634993	5	1774	4.85E-08
Chr1	15654321	15656718	5	2398	5.33757E-06
Chr1	15670745	15672756	8	2012	3.95E-10
Chr1	15677065	15678061	4	997	2.75381E-06
Chr1	15683276	15684357	6	1082	1.26E-11
Chr1	15685483	15687140	5	1658	2.03E-07
Chr1	15690859	15692323	6	1465	4.16562E-07
Chr1	15694612	15696106	4	1495	0.000376934

Chr1	15697176	15703147	20	5972	2.29E-27
Chr1	15704303	15706065	5	1763	1.37E-07
Chr1	15707084	15708623	5	1540	7.64E-07
Chr1	15717028	15717766	5	739	1.51E-07
Chr1	15735393	15736383	4	991	1.21346E-05
Chr1	15757035	15758383	7	1349	5.22E-09
Chr1	15759488	15760107	6	620	1.94E-08
Chr1	15804821	15805319	5	499	6.39981E-05
Chr1	15812968	15814160	4	1193	8.02327E-05
Chr1	15822375	15825320	10	2946	9.40E-14
Chr1	15831971	15833334	4	1364	1.00E-08
Chr1	15845629	15846928	5	1300	2.28E-07
Chr1	15851886	15852861	7	976	1.68E-11
Chr1	15872777	15873774	4	998	2.5294E-06
Chr1	15876094	15878262	8	2169	8.77E-11
Chr1	15935662	15935688	6	27	2.66E-14
Chr1	15950686	15952380	4	1695	1.79766E-06
Chr1	16016607	16018775	6	2169	8.46E-10
Chr1	16046993	16049409	9	2417	1.86E-12
Chr1	16079058	16080057	4	1000	4.59E-07
Chr1	16093818	16095025	7	1208	8.65E-10
Chr1	16098111	16104976	29	6866	8.78E-31
Chr1	16110011	16114203	13	4193	5.77E-20
Chr1	16116515	16117957	6	1443	8.62E-13
Chr1	16119378	16121155	7	1778	1.75E-10
Chr1	16122445	16125286	8	2842	1.44E-12
Chr1	16196112	16197459	4	1348	1.0303E-07
Chr1	16198494	16200125	6	1632	3.03E-08
Chr1	16201230	16203460	5	2231	2.64E-09
Chr1	16207622	16208902	5	1281	2.34E-08
Chr1	16238423	16239902	4	1480	3.64E-07
Chr1	16298803	16299891	5	1089	1.05E-07
Chr1	16317987	16320122	4	2136	0.000835308
Chr1	16321127	16322276	4	1150	7.86213E-06
Chr1	16329491	16331674	8	2184	2.26E-11
Chr1	16368579	16369385	4	807	1.01609E-06
Chr1	16370676	16372270	4	1595	1.32507E-05
Chr1	16373664	16377688	10	4025	6.62E-13
Chr1	16384716	16386307	6	1592	3.65E-09
Chr1	16489019	16491321	9	2303	1.20E-12
Chr1	16495847	16496389	4	543	1.20E-09
Chr1	16503603	16504502	5	900	1.96E-08
Chr1	16507054	16510317	10	3264	3.33725E-06
Chr1	16511402	16514550	11	3149	5.02E-17
Chr1	16520045	16524030	15	3986	6.13E-15
Chr1	16525110	16532930	22	7821	1.97E-23
Chr1	16538551	16538611	5	61	3.19E-09
Chr1	16572156	16573142	4	987	3.42E-07
Chr1	16584802	16586997	7	2196	4.31E-09
Chr1	16605809	16607066	4	1258	1.65998E-06
Chr1	16629623	16631111	4	1489	0.000311544
Chr1	16633842	16637030	8	3189	1.13E-12
Chr1	16656167	16657039	6	873	2.41E-14
Chr1	16679696	16681986	8	2291	2.43E-09
Chr1	16743220	16743927	6	708	1.79E-08
Chr1	17023477	17025950	7	2474	1.20E-09
Chr1	17036037	17037990	4	1954	0.000701323
Chr1	17039653	17041025	4	1373	4.16E-07
Chr1	17044897	17046175	7	1279	2.46E-11
Chr1	17047191	17049187	8	1997	5.13E-08
Chr1	17257963	17260427	10	2465	4.41E-18
Chr1	17261889	17265081	9	3193	1.46E-11
Chr1	17341824	17342801	4	978	2.8759E-05

Chr1	17361873	17363435	5	1563	6.25E-08
Chr1	17489200	17489993	4	794	5.36E-07
Chr1	17676635	17678192	6	1558	4.87E-07
Chr1	17842344	17844528	9	2185	2.07E-12
Chr1	18297509	18297687	5	179	2.88E-09
Chr1	18338680	18339913	8	1234	1.52E-12
Chr1	18643946	18644079	4	134	2.88E-07
Chr1	19336379	19338732	9	2354	1.15E-11
Chr1	19344640	19345557	7	918	2.45E-10
Chr1	19714603	19714838	4	236	2.25E-07
Chr1	19727903	19728973	4	1071	1.32E-07
Chr1	19885420	19887261	6	1842	2.16E-23
Chr1	19904214	19904497	5	284	5.10E-09
Chr1	19963195	19964071	5	877	2.99E-08
Chr1	20086568	20088191	4	1624	3.01481E-06
Chr1	20317031	20318549	6	1519	4.17E-08
Chr1	20412357	20412504	7	148	2.59E-10
Chr1	20685688	20685800	4	113	1.99001E-06
Chr1	21453103	21453391	4	289	1.31E-07
Chr1	21691696	21692418	4	723	2.22564E-06
Chr1	21747456	21753122	22	5667	7.03E-31
Chr1	21860568	21860624	4	57	1.23018E-05
Chr1	22644357	22644936	9	580	2.26E-19
Chr1	22662791	22663114	5	324	2.90E-08
Chr1	22697561	22699358	8	1798	1.77E-10
Chr1	23355979	23356814	5	836	1.95E-07
Chr1	23805873	23806063	5	191	3.29E-09
Chr1	24275851	24277431	5	1581	1.27552E-05
Chr1	25159700	25160064	4	365	8.70E-07
Chr1	26367310	26368405	4	1096	2.08E-07
Chr1	26940007	26940065	4	59	6.39E-10
Chr1	27515040	27515145	4	106	3.74E-07
Chr1	27863736	27864613	6	878	1.44E-10
Chr1	28910203	28910847	4	645	8.40E-07
Chr1	29476766	29477922	5	1157	1.39016E-05
Chr1	29589827	29590036	4	210	1.40E-07
Chr1	29611703	29611711	4	9	1.11E-07
Chr1	30385021	30385206	4	186	1.39E-10
Chr2	1267	3783	92	2517	2.98E-243
Chr2	5416	5997	16	582	2.13E-22
Chr2	9621	11209	30	1589	6.49E-176
Chr2	39262	40919	6	1658	1.03127E-05
Chr2	303259	303404	8	146	2.30E-14
Chr2	373272	379543	17	6272	2.99E-24
Chr2	533222	534841	6	1620	5.19E-09
Chr2	567150	569435	4	2286	9.21E-07
Chr2	585037	586010	5	974	3.41E-10
Chr2	819943	820084	4	142	3.85E-07
Chr2	1228906	1232077	8	3172	1.91E-12
Chr2	1335666	1335926	4	261	1.69E-09
Chr2	1828438	1829605	5	1168	5.77E-08
Chr2	1883355	1884405	5	1051	3.07E-07
Chr2	1889447	1890175	4	729	8.53584E-06
Chr2	2036499	2038659	7	2161	5.35E-09
Chr2	2077394	2078286	7	893	2.70E-10
Chr2	2091814	2092662	4	849	5.58055E-06
Chr2	2187773	2189482	7	1710	5.35E-10
Chr2	2278580	2279947	8	1368	5.25E-12
Chr2	2302620	2304782	6	2163	1.38E-07
Chr2	2326026	2326457	4	432	4.79676E-05
Chr2	2373448	2374254	4	807	9.46447E-06
Chr2	2375804	2376678	4	875	0.000131401
Chr2	2380287	2382109	7	1823	1.45E-12

Chr2	2384271	2385147	4	877	1.49295E-06
Chr2	2401267	2403371	6	2105	5.01E-11
Chr2	2406212	2406951	5	740	1.03E-09
Chr2	2448030	2454034	14	6005	3.33E-20
Chr2	2464937	2465941	6	1005	4.25E-07
Chr2	2474826	2476745	4	1920	0.000332279
Chr2	2487824	2489669	8	1846	5.40E-09
Chr2	2491164	2494270	11	3107	7.33E-15
Chr2	2495788	2501618	18	5831	9.51E-18
Chr2	2504846	2507777	11	2932	2.93E-12
Chr2	2528371	2529758	6	1388	4.34E-09
Chr2	2532304	2533933	7	1630	5.22E-11
Chr2	2576371	2578057	4	1687	3.53E-07
Chr2	2592015	2593944	4	1930	7.72E-09
Chr2	2602858	2605019	8	2162	5.89E-12
Chr2	2622199	2625838	9	3640	7.92E-15
Chr2	2626891	2627563	4	673	1.53021E-06
Chr2	2647712	2649634	6	1923	2.16E-08
Chr2	2666829	2669972	6	3144	3.77E-09
Chr2	2677359	2677442	4	84	1.16166E-05
Chr2	2683758	2686889	9	3132	1.92E-12
Chr2	2699724	2700530	4	807	5.65E-10
Chr2	2703433	2704990	5	1558	2.16E-08
Chr2	2711947	2713983	7	2037	3.55E-10
Chr2	2718037	2720414	6	2378	4.06067E-06
Chr2	2741778	2743279	5	1502	3.30623E-06
Chr2	2768941	2770846	4	1906	2.16E-07
Chr2	2796788	2798860	4	2073	1.64301E-06
Chr2	2800074	2801910	4	1837	3.22968E-06
Chr2	2809048	2810098	7	1051	4.27E-09
Chr2	2824327	2826896	7	2570	1.37E-10
Chr2	2879281	2881993	8	2713	7.45E-11
Chr2	2902394	2904683	5	2290	4.29873E-06
Chr2	3057779	3061164	6	3386	1.99E-10
Chr2	3065335	3067222	4	1888	1.66883E-05
Chr2	3075581	3077503	5	1923	7.51E-08
Chr2	3080180	3081560	4	1381	1.78382E-05
Chr2	3084179	3086278	4	2100	8.43947E-05
Chr2	3091057	3093167	8	2111	3.20E-11
Chr2	3098565	3102569	10	4005	6.13E-14
Chr2	3104364	3105500	4	1137	1.04129E-05
Chr2	3120121	3124812	10	4692	2.00E-13
Chr2	3154345	3155632	4	1288	1.78E-08
Chr2	3161765	3163582	4	1818	1.98381E-05
Chr2	3215285	3216927	4	1643	5.96994E-07
Chr2	3247334	3248181	4	848	1.73271E-05
Chr2	3283492	3283791	8	300	2.14E-12
Chr2	3286874	3287448	7	575	1.14E-12
Chr2	3544082	3545299	5	1218	1.64E-07
Chr2	3548837	3551971	10	3135	2.09E-13
Chr2	3554334	3556733	7	2400	2.12E-12
Chr2	3559025	3559774	4	750	7.37506E-06
Chr2	3570057	3571508	4	1452	4.64608E-05
Chr2	3584757	3586820	6	2064	1.54E-08
Chr2	3605330	3607324	28	1995	3.97E-67
Chr2	3614983	3617225	22	2243	5.52E-49
Chr2	3618462	3627836	83	9375	4.43E-74
Chr2	3638541	3642045	8	3505	4.11E-12
Chr2	3643808	3644731	8	924	1.54E-10
Chr2	3687901	3689420	12	1520	2.08E-12
Chr2	3732945	3735141	9	2197	8.24E-13
Chr2	3752269	3753348	5	1080	2.31311E-06
Chr2	3754795	3754971	4	177	7.84605E-06

Chr2	3768670	3772281	14	3612	3.09E-17
Chr2	3790500	3791370	6	871	4.29E-07
Chr2	3826208	3827525	4	1318	1.77703E-06
Chr2	3835826	3839740	14	3915	1.14E-19
Chr2	3855497	3857542	6	2046	3.46E-10
Chr2	3865410	3865441	4	32	4.52E-07
Chr2	3869192	3870448	5	1257	2.81E-09
Chr2	3876109	3881054	12	4946	1.40E-15
Chr2	3883481	3890823	16	7343	9.45E-23
Chr2	3899941	3901837	10	1897	3.83E-13
Chr2	3923809	3924937	5	1129	2.1597E-06
Chr2	3942664	3944293	5	1630	1.32E-07
Chr2	3946622	3949759	20	3138	6.75E-21
Chr2	3950919	3954740	19	3822	1.20E-20
Chr2	3955882	3956716	7	835	9.67E-09
Chr2	3958378	3959919	8	1542	2.30E-11
Chr2	3963653	3967252	15	3600	2.94E-23
Chr2	3968482	3971871	12	3390	1.29E-16
Chr2	3973581	3976044	5	2464	1.35E-07
Chr2	3982784	3985169	8	2386	1.37E-10
Chr2	4009430	4011313	6	1884	2.16503E-06
Chr2	4061496	4062267	4	772	0.000660383
Chr2	4111453	4113228	5	1776	6.94E-10
Chr2	4114591	4115452	4	862	3.2882E-05
Chr2	4129028	4132603	9	3576	2.89873E-05
Chr2	4151541	4156575	12	5035	5.24E-16
Chr2	4165667	4166395	5	729	1.71E-07
Chr2	4167587	4168206	5	620	1.01E-08
Chr2	4173007	4180026	24	7020	2.71E-36
Chr2	4181388	4183387	5	2000	1.06E-07
Chr2	4184849	4185485	4	637	3.82366E-06
Chr2	4188066	4190388	10	2323	3.35E-13
Chr2	4191531	4193372	12	1842	3.95E-16
Chr2	4198618	4201903	11	3286	3.48E-13
Chr2	4204501	4206339	6	1839	1.16E-10
Chr2	4238559	4240138	6	1580	7.76E-09
Chr2	4241282	4242119	9	838	8.32E-22
Chr2	4250678	4251775	4	1098	2.67842E-06
Chr2	4253731	4254903	5	1173	1.83E-07
Chr2	4256777	4259143	7	2367	5.51E-10
Chr2	4260362	4261608	4	1247	2.78272E-05
Chr2	4278031	4281854	19	3824	2.00E-22
Chr2	4284308	4285536	4	1229	1.79E-08
Chr2	4286542	4288032	4	1491	1.40436E-06
Chr2	4289536	4293776	13	4241	3.99E-17
Chr2	4311272	4311957	7	686	7.72E-08
Chr2	4367903	4369991	9	2089	1.73E-14
Chr2	4378060	4380014	8	1955	8.15E-09
Chr2	4386375	4387213	4	839	1.66261E-05
Chr2	4392334	4395085	8	2752	3.65E-11
Chr2	4396430	4398621	10	2192	4.76E-09
Chr2	4400050	4403825	10	3776	4.18E-13
Chr2	4408334	4410360	4	2027	2.56E-07
Chr2	4412893	4413502	5	610	1.04787E-06
Chr2	4452528	4453847	4	1320	1.89258E-06
Chr2	4465331	4467006	8	1676	1.08E-13
Chr2	4494607	4495875	6	1269	2.40E-08
Chr2	4515584	4517761	4	2178	5.26E-07
Chr2	4519463	4520247	6	785	1.03E-07
Chr2	4522859	4523115	4	257	3.29004E-06
Chr2	4533059	4534022	4	964	2.03E-07
Chr2	4561111	4561555	4	445	4.04E-09
Chr2	4569903	4570841	4	939	6.03572E-06

Chr2	4572441	4579022	20	6582	2.23E-25
Chr2	4580262	4582650	11	2389	6.55E-15
Chr2	4595268	4597474	6	2207	3.69E-09
Chr2	4605180	4606293	4	1114	1.29E-07
Chr2	4612157	4613865	5	1709	9.54E-07
Chr2	4616770	4617681	4	912	1.89135E-05
Chr2	4676804	4677742	4	939	2.90E-07
Chr2	4703879	4707660	7	3782	1.21901E-06
Chr2	4778285	4779134	4	850	2.59204E-06
Chr2	4780169	4784318	8	4150	4.96E-14
Chr2	4808244	4808785	4	542	1.09055E-06
Chr2	4812090	4814008	7	1919	2.62E-10
Chr2	4818828	4820230	5	1403	2.72718E-06
Chr2	4835998	4836651	4	654	3.16E-07
Chr2	4840663	4842040	4	1378	5.66E-07
Chr2	4846252	4847525	4	1274	4.22868E-06
Chr2	4853150	4854216	4	1067	0.001592927
Chr2	4863437	4864738	5	1302	6.22E-08
Chr2	4895287	4895560	4	274	5.84E-07
Chr2	4901051	4902248	5	1198	1.22972E-05
Chr2	4904313	4905294	4	982	3.67E-07
Chr2	4906312	4908376	9	2065	1.79E-08
Chr2	4927057	4928239	5	1183	1.94E-07
Chr2	4934847	4936940	6	2094	2.59E-07
Chr2	4953292	4954491	5	1200	1.83E-10
Chr2	4985991	4989364	9	3374	2.02E-17
Chr2	4993000	4994621	5	1622	2.13E-07
Chr2	4999851	5002112	8	2262	8.69E-12
Chr2	5041850	5044530	6	2681	2.77E-10
Chr2	5045759	5047744	7	1986	1.61E-08
Chr2	5058322	5058740	4	419	0.000105136
Chr2	5080609	5081718	4	1110	9.91242E-06
Chr2	5088888	5092006	11	3119	2.86E-15
Chr2	5119656	5119920	5	265	8.34E-07
Chr2	5122504	5123504	4	1001	6.46135E-06
Chr2	5127236	5129445	11	2210	1.52E-15
Chr2	5135259	5136043	5	785	4.18E-07
Chr2	5137628	5139112	6	1485	6.20E-11
Chr2	5182995	5184343	4	1349	1.83E-07
Chr2	5187431	5187957	4	527	7.91E-07
Chr2	5200097	5201038	4	942	0.000365708
Chr2	5217562	5219046	7	1485	2.05E-15
Chr2	5235082	5237594	4	2513	5.33E-07
Chr2	5241648	5243245	6	1598	2.54E-08
Chr2	5244641	5245779	5	1139	1.61314E-05
Chr2	5250473	5251720	5	1248	4.17144E-07
Chr2	5253148	5255557	8	2410	1.51E-11
Chr2	5261961	5263880	4	1920	1.23E-08
Chr2	5277578	5283111	13	5534	7.44E-17
Chr2	5300318	5301352	5	1035	5.24267E-06
Chr2	5302563	5303214	4	652	1.73223E-06
Chr2	5328342	5329965	6	1624	1.63431E-05
Chr2	5333633	5335149	4	1517	2.28E-07
Chr2	5338833	5340079	4	1247	2.68776E-06
Chr2	5342943	5344767	5	1825	1.84E-08
Chr2	5356475	5358508	5	2034	5.62E-08
Chr2	5364098	5365146	4	1049	6.5312E-07
Chr2	5368185	5369853	6	1669	1.01E-09
Chr2	5379358	5381349	6	1992	3.27E-09
Chr2	5441247	5442180	4	934	2.31725E-06
Chr2	5469764	5475767	14	6004	1.36E-12
Chr2	5494919	5497336	9	2418	2.00E-11
Chr2	5560217	5565224	16	5008	1.40E-16

Chr2	5566942	5567811	5	870	5.87E-07
Chr2	5569397	5571031	5	1635	1.29E-09
Chr2	5573457	5575045	9	1589	1.22E-12
Chr2	5582205	5583269	4	1065	2.86E-09
Chr2	5589995	5590034	4	40	3.29E-09
Chr2	5598755	5602489	21	3735	2.88E-21
Chr2	5612308	5614127	6	1820	1.33E-08
Chr2	5624646	5626247	5	1602	2.81621E-05
Chr2	5630332	5631392	4	1061	5.5813E-05
Chr2	5635776	5636709	4	934	5.75725E-06
Chr2	5780676	5782573	4	1898	1.51809E-05
Chr2	5810587	5811830	4	1244	3.70954E-06
Chr2	5817046	5818694	4	1649	1.51192E-06
Chr2	5848341	5849429	4	1089	4.87E-09
Chr2	5894505	5895806	5	1302	2.81E-11
Chr2	5897715	5898463	4	749	2.37E-08
Chr2	5901069	5905107	8	4039	7.78E-08
Chr2	5982538	5985135	6	2598	5.45E-08
Chr2	5991145	5994306	7	3162	5.51E-08
Chr2	5999134	6000356	5	1223	3.71E-07
Chr2	6027074	6028679	5	1606	5.61E-08
Chr2	6076436	6080371	8	3936	3.96E-13
Chr2	6095913	6097997	5	2085	1.15284E-06
Chr2	6107141	6109159	7	2019	7.72E-09
Chr2	6111849	6112690	4	842	9.94E-07
Chr2	6119430	6121100	5	1671	2.92E-07
Chr2	6124277	6125866	7	1590	7.86E-12
Chr2	6133956	6134742	4	787	1.13E-07
Chr2	6160570	6162093	7	1524	2.14E-14
Chr2	6255811	6256816	6	1006	4.61E-09
Chr2	6258763	6259635	5	873	2.59E-07
Chr2	6265535	6268840	9	3306	5.42E-11
Chr2	6314908	6315283	7	376	6.07E-19
Chr2	6390451	6391806	8	1356	2.68E-12
Chr2	6507723	6509128	12	1406	5.70E-21
Chr2	6528671	6530134	4	1464	0.000231744
Chr2	6548684	6549513	4	830	1.16E-08
Chr2	6770028	6770962	4	935	1.40E-07
Chr2	6838445	6843341	14	4897	1.08E-18
Chr2	6845767	6846187	4	421	7.01205E-07
Chr2	6881439	6883902	6	2464	5.23E-10
Chr2	6892303	6893097	16	795	4.40E-20
Chr2	6942769	6945540	13	2772	3.62E-14
Chr2	6971571	6972753	5	1183	3.30382E-06
Chr2	6975039	6977587	4	2549	0.000113212
Chr2	7005293	7005328	4	36	1.02994E-05
Chr2	7007589	7010133	7	2545	2.06E-11
Chr2	7013313	7019020	12	5708	7.52E-18
Chr2	7067434	7067734	4	301	7.06E-08
Chr2	7151115	7151994	5	880	3.66816E-06
Chr2	7159929	7160083	4	155	3.14144E-06
Chr2	7190949	7191426	16	478	1.12E-35
Chr2	7230538	7233318	9	2781	5.03E-13
Chr2	8040017	8040487	5	471	1.57E-10
Chr2	8562293	8563770	6	1478	6.37E-08
Chr2	8565273	8566249	4	977	8.37E-07
Chr2	8575163	8575259	4	97	4.06E-07
Chr2	8819364	8820624	4	1261	4.48E-07
Chr2	8911214	8911467	6	254	1.72E-09
Chr2	8948405	8948654	5	250	8.16587E-06
Chr2	8995306	8998072	6	2767	2.61E-09
Chr2	9123247	9125004	5	1758	1.5012E-06
Chr2	9189820	9190854	6	1035	3.01E-08

Chr2	9653347	9654688	5	1342	2.09E-07
Chr2	10597555	10599989	4	2435	5.28E-08
Chr2	10604511	10605493	4	983	5.16531E-06
Chr2	10607708	10608434	4	727	3.19E-07
Chr2	10875711	10876923	9	1213	5.20E-12
Chr2	10877941	10880145	7	2205	1.85E-09
Chr2	11325397	11327089	5	1693	2.22E-07
Chr2	11546883	11547705	5	823	2.08813E-06
Chr2	11952697	11953102	4	406	8.70756E-06
Chr2	12450695	12451984	4	1290	9.60354E-05
Chr2	12472630	12473239	4	610	0.001252191
Chr2	14281732	14281814	4	83	5.96E-11
Chr2	14472494	14472942	4	449	3.15135E-06
Chr2	15405297	15405909	8	613	1.17E-29
Chr2	15815267	15815464	4	198	3.75E-09
Chr2	16589812	16590637	13	826	7.97E-28
Chr2	17338114	17341476	13	3363	9.92E-18
Chr2	17363451	17363679	4	229	2.45E-08
Chr2	17492226	17492579	7	354	7.39E-09
Chr2	18296060	18296385	5	326	4.53E-10
Chr2	19320214	19320769	14	556	6.26E-30
Chr3	347471	348173	10	703	7.38E-28
Chr3	382003	382140	4	138	3.44E-08
Chr3	932800	932935	5	136	1.14E-09
Chr3	1555487	1556836	9	1350	1.45E-08
Chr3	1559935	1560668	10	734	1.08E-12
Chr3	1675177	1675326	4	150	1.09355E-06
Chr3	1962150	1967839	13	5690	1.31E-13
Chr3	2138501	2138933	4	433	6.52619E-06
Chr3	2814210	2817116	9	2907	5.08E-09
Chr3	4913512	4914279	13	768	2.35E-26
Chr3	4925515	4925685	6	171	1.25E-09
Chr3	5027680	5028526	6	847	1.62E-10
Chr3	5249414	5249973	4	560	1.21E-08
Chr3	5930635	5930653	5	19	3.03E-12
Chr3	5955253	5955349	6	97	1.03E-08
Chr3	6091378	6091869	6	492	8.80E-14
Chr3	6470637	6470798	5	162	9.41E-10
Chr3	7040452	7041361	4	910	3.808E-06
Chr3	7803966	7805872	4	1907	8.23394E-06
Chr3	8097042	8097214	6	173	4.07E-09
Chr3	8256006	8256246	4	241	4.48623E-06
Chr3	8385091	8386603	4	1513	5.85964E-05
Chr3	8541399	8542862	4	1464	1.01233E-06
Chr3	9618391	9620477	7	2087	3.34E-11
Chr3	9692533	9694267	5	1735	8.27E-09
Chr3	9852215	9852528	4	314	0.001700148
Chr3	10108635	10110549	7	1915	6.17E-11
Chr3	10478473	10480087	4	1615	2.6863E-05
Chr3	10481124	10483118	5	1995	7.96E-07
Chr3	10514139	10514939	6	801	7.79E-08
Chr3	10587840	10587856	6	17	9.48E-10
Chr3	10849339	10849559	4	221	8.93E-07
Chr3	10885158	10887265	6	2108	5.16E-09
Chr3	10919158	10920027	5	870	2.67E-08
Chr3	11079226	11079270	4	45	3.84375E-07
Chr3	11117273	11117763	6	491	6.44E-09
Chr3	11119151	11120363	6	1213	5.74E-09
Chr3	11177367	11179836	5	2470	7.51E-08
Chr3	11354615	11356330	4	1716	8.49E-07
Chr3	11387803	11389211	5	1409	3.54628E-06
Chr3	11414006	11415518	5	1513	2.56396E-06
Chr3	11473639	11474562	5	924	1.06444E-05

Chr3	11491594	11493287	5	1694	1.58811E-06
Chr3	11495789	11496948	5	1160	3.21E-07
Chr3	11563587	11565773	7	2187	1.01E-11
Chr3	11575027	11576434	5	1408	6.39E-07
Chr3	11579940	11581128	7	1189	6.84E-09
Chr3	11583394	11583697	4	304	4.94E-07
Chr3	11633454	11636733	13	3280	1.06E-14
Chr3	11658389	11658408	4	20	1.09083E-06
Chr3	11681555	11682235	4	681	1.10737E-05
Chr3	11700708	11701770	5	1063	1.20108E-06
Chr3	11871897	11876013	8	4117	6.93E-13
Chr3	11880224	11883428	7	3205	2.32E-10
Chr3	11942919	11944150	5	1232	2.98E-10
Chr3	12000614	12001923	4	1310	5.27E-07
Chr3	12004331	12008271	7	3941	1.15E-08
Chr3	12024045	12026777	6	2733	2.31E-10
Chr3	12028056	12030775	6	2720	1.96E-09
Chr3	12031890	12034463	10	2574	3.78E-12
Chr3	12037854	12042698	11	4845	1.05E-21
Chr3	12048384	12049791	4	1408	2.36235E-05
Chr3	12052908	12054172	7	1265	1.90E-11
Chr3	12069456	12070682	6	1227	3.38E-09
Chr3	12095583	12096707	4	1125	1.76219E-06
Chr3	12173023	12174681	4	1659	2.02811E-05
Chr3	12175744	12176741	4	998	1.49523E-07
Chr3	12183724	12184457	5	734	5.39E-08
Chr3	12189797	12195179	13	5383	4.08E-14
Chr3	12204685	12207994	10	3310	1.09E-12
Chr3	12210977	12212613	7	1637	7.36E-08
Chr3	12220547	12222721	10	2175	9.82E-10
Chr3	12224257	12225786	6	1530	4.39E-09
Chr3	12227111	12229063	5	1953	6.1317E-08
Chr3	12250548	12251716	5	1169	1.07164E-05
Chr3	12253234	12254537	7	1304	4.66E-07
Chr3	12285033	12286255	5	1223	2.00E-07
Chr3	12294771	12296350	6	1580	6.39E-08
Chr3	12313508	12314335	8	828	6.16E-11
Chr3	12321513	12323087	5	1575	2.45016E-06
Chr3	12325387	12325771	4	385	3.37615E-06
Chr3	12329068	12333442	10	4375	6.02E-14
Chr3	12388829	12390615	4	1787	8.27E-07
Chr3	12395499	12396595	4	1097	0.000353362
Chr3	12401767	12403698	10	1932	1.15E-15
Chr3	12405138	12406183	8	1046	2.09E-10
Chr3	12426758	12428821	6	2064	1.29E-09
Chr3	12430674	12432705	5	2032	1.52273E-05
Chr3	12434251	12435839	7	1589	1.87E-09
Chr3	12444733	12447790	6	3058	8.38E-07
Chr3	12461543	12465363	14	3821	8.72E-14
Chr3	12473662	12474447	6	786	4.70E-08
Chr3	12479988	12482480	6	2493	5.86E-12
Chr3	12484871	12485090	4	220	3.98E-08
Chr3	12515248	12516479	5	1232	3.88742E-05
Chr3	12519664	12522030	12	2367	3.23E-14
Chr3	12524425	12525988	4	1564	6.71E-08
Chr3	12538900	12539256	5	357	2.57676E-07
Chr3	12540628	12541139	5	512	1.03E-08
Chr3	12542850	12544390	4	1541	2.03352E-05
Chr3	12545413	12546974	5	1562	8.51E-07
Chr3	12548098	12549176	4	1079	2.87799E-05
Chr3	12550610	12552567	4	1958	2.64935E-05
Chr3	12556773	12557894	7	1122	4.12E-09
Chr3	12560319	12561688	5	1370	1.57E-07

Chr3	12576643	12577608	4	966	4.95633E-06
Chr3	12580896	12582257	6	1362	6.86E-08
Chr3	12602886	12604716	4	1831	2.35197E-06
Chr3	12698490	12699688	4	1199	3.57909E-06
Chr3	12701623	12703690	7	2068	2.37E-09
Chr3	12716234	12718460	7	2227	2.52E-10
Chr3	12764636	12765399	4	764	2.80E-07
Chr3	12781674	12783385	4	1712	7.02967E-05
Chr3	12799696	12801962	5	2267	2.43E-07
Chr3	12824796	12828016	8	3221	3.19E-14
Chr3	12839096	12841378	5	2283	2.15026E-06
Chr3	12856005	12858377	5	2373	1.45E-08
Chr3	12922426	12923500	4	1075	7.22763E-05
Chr3	12925087	12928445	6	3359	5.14E-10
Chr3	12935100	12936474	5	1375	1.58704E-06
Chr3	12937558	12939265	6	1708	4.54E-10
Chr3	12944037	12946776	6	2740	2.98E-10
Chr3	12949417	12950850	5	1434	5.60E-09
Chr3	12958092	12958607	4	516	1.71787E-05
Chr3	12984783	12987929	9	3147	5.67E-10
Chr3	12989058	12990452	4	1395	4.06322E-07
Chr3	12992122	12993296	4	1175	1.69E-08
Chr3	13017209	13018879	4	1671	1.23218E-06
Chr3	13025223	13025642	4	420	3.49E-07
Chr3	13084874	13086597	4	1724	4.66729E-06
Chr3	13087971	13090717	7	2747	1.94E-09
Chr3	13092576	13092832	4	257	3.42539E-06
Chr3	13097386	13101155	13	3770	2.22E-17
Chr3	13113371	13116958	8	3588	2.49E-11
Chr3	13148649	13149876	5	1228	8.11E-10
Chr3	13175518	13176461	4	944	3.69E-08
Chr3	13190569	13193093	9	2525	3.10E-15
Chr3	13194200	13195471	4	1272	4.36637E-05
Chr3	13205371	13206396	4	1026	6.59028E-06
Chr3	13214296	13215590	5	1295	9.67E-08
Chr3	13244741	13246056	4	1316	3.28E-07
Chr3	13285492	13287182	5	1691	4.02E-08
Chr3	13322301	13323928	4	1628	3.69771E-06
Chr3	13333522	13334008	4	487	6.92E-07
Chr3	13353307	13354392	4	1086	4.39654E-06
Chr3	13364005	13367540	11	3536	4.16E-12
Chr3	13381494	13383394	5	1901	6.49697E-06
Chr3	13389907	13390038	4	132	5.57024E-06
Chr3	13405056	13407229	7	2174	1.45E-11
Chr3	13409665	13412899	9	3235	1.21E-10
Chr3	13415472	13416685	7	1214	9.21E-12
Chr3	13417878	13421522	13	3645	6.31E-18
Chr3	13425331	13426420	4	1090	1.30308E-06
Chr3	13429518	13431040	4	1523	9.73251E-05
Chr3	13435469	13437041	6	1573	1.28E-09
Chr3	13438694	13441389	8	2696	1.39E-11
Chr3	13445736	13447976	13	2241	2.70E-16
Chr3	13456169	13458077	6	1909	1.48E-09
Chr3	13468346	13470145	5	1800	1.57346E-06
Chr3	13477081	13479216	10	2136	2.16E-14
Chr3	13515946	13516705	4	760	5.92947E-06
Chr3	13523750	13524115	4	366	1.73986E-06
Chr3	13550848	13551583	5	736	1.06E-07
Chr3	13554922	13556249	4	1328	2.02136E-05
Chr3	13559722	13565880	14	6159	2.25E-18
Chr3	13571502	13572646	5	1145	3.67E-08
Chr3	13576590	13577545	6	956	1.30E-09
Chr3	13579111	13581463	5	2353	3.58E-09

Chr3	13586110	13587734	13	1625	5.19E-08
Chr3	13588831	13592511	52	3681	4.26E-197
Chr3	13593549	13599066	26	5518	7.20E-22
Chr3	13600252	13601481	4	1230	1.42687E-05
Chr3	13608671	13610133	5	1463	4.37946E-06
Chr3	13612949	13613925	4	977	4.11215E-05
Chr3	13618073	13619060	4	988	4.49E-07
Chr3	13620585	13623036	13	2452	5.32E-19
Chr3	13624604	13626505	5	1902	1.07E-09
Chr3	13638370	13639980	8	1611	2.74E-09
Chr3	13644759	13649589	14	4831	3.93E-18
Chr3	13652338	13656759	12	4422	2.30E-13
Chr3	13659867	13662482	6	2616	2.00341E-06
Chr3	13664697	13668136	7	3440	1.75E-10
Chr3	13678167	13679204	5	1038	5.58E-08
Chr3	13681836	13685510	13	3675	1.68E-15
Chr3	13693221	13693430	5	210	3.29E-07
Chr3	13699364	13700400	6	1037	2.26E-10
Chr3	13705945	13708533	13	2589	1.02E-10
Chr3	13709626	13710963	20	1338	2.56E-23
Chr3	13712323	13713405	6	1083	3.47E-07
Chr3	13737030	13737750	6	721	3.21E-08
Chr3	13738916	13741644	6	2729	9.92E-09
Chr3	13742736	13744017	5	1282	2.52309E-06
Chr3	13746328	13746889	5	562	2.75E-09
Chr3	13750219	13751164	4	946	9.00678E-05
Chr3	13756148	13756930	6	783	2.66502E-06
Chr3	13770891	13772265	6	1375	5.0875E-06
Chr3	13779140	13779951	6	812	2.62E-07
Chr3	13794126	13795804	6	1679	6.21E-08
Chr3	13803495	13805718	8	2224	3.59E-10
Chr3	13809422	13811162	11	1741	4.43E-10
Chr3	13812240	13816708	52	4469	1.61E-45
Chr3	13819052	13822262	10	3211	1.66E-13
Chr3	13826465	13835215	22	8751	1.30E-23
Chr3	13838858	13840776	17	1919	1.53E-19
Chr3	13853827	13853982	19	156	4.31E-27
Chr3	13865851	13866789	4	939	1.36606E-05
Chr3	13869862	13871817	7	1956	2.22E-09
Chr3	13893596	13895142	4	1547	2.55118E-06
Chr3	13899687	13902879	6	3193	3.88E-07
Chr3	13928406	13930622	6	2217	3.94E-08
Chr3	13937125	13939708	8	2584	8.37E-13
Chr3	13946672	13947598	4	927	1.81E-08
Chr3	13950092	13951970	8	1879	2.56E-08
Chr3	13964539	13966633	5	2095	4.8446E-06
Chr3	13970000	13970986	5	987	5.50578E-06
Chr3	13973093	13974570	4	1478	5.08E-07
Chr3	13980477	13983718	8	3242	2.02E-13
Chr3	13998324	14000386	7	2063	6.61E-09
Chr3	14011620	14012749	5	1130	6.69E-07
Chr3	14025863	14026813	5	951	1.58E-08
Chr3	14033536	14035274	6	1739	4.59E-10
Chr3	14066513	14069368	8	2856	1.44E-12
Chr3	14106479	14107836	8	1358	5.52E-13
Chr3	14124955	14125874	4	920	2.52833E-05
Chr3	14149529	14150387	5	859	2.74E-08
Chr3	14158443	14160165	5	1723	4.35E-07
Chr3	14163030	14163727	4	698	7.40561E-05
Chr3	14165372	14168968	11	3597	5.91E-12
Chr3	14171864	14174072	14	2209	5.59E-15
Chr3	14179381	14181621	31	2241	2.72E-32
Chr3	14185627	14187188	37	1562	2.72E-47

Chr3	14190210	14190851	7	642	5.09E-09
Chr3	14195608	14199834	158	4227	0
Chr3	14200860	14204077	199	3218	0
Chr3	14205291	14208913	113	3623	1.73E-98
Chr3	14210218	14217107	51	6890	3.72E-45
Chr3	14218290	14220561	19	2272	3.09E-25
Chr3	14221790	14225908	41	4119	5.01E-34
Chr3	14241346	14246039	14	4694	9.40E-23
Chr3	14250042	14251502	5	1461	3.14967E-06
Chr3	14258247	14259149	6	903	1.47E-08
Chr3	14262153	14263466	7	1314	1.42E-11
Chr3	14293065	14293754	4	690	6.99091E-06
Chr3	14337270	14337958	4	689	8.16E-08
Chr3	14339081	14339249	4	169	0.000174524
Chr3	14365982	14366839	4	858	4.35504E-05
Chr3	14375530	14377934	5	2405	6.67E-07
Chr3	14389443	14390366	5	924	3.27E-08
Chr3	14393077	14394535	5	1459	8.79E-07
Chr3	14409884	14413215	10	3332	4.48E-14
Chr3	14422019	14424616	5	2598	8.01E-08
Chr3	14426289	14430502	9	4214	2.00E-10
Chr3	14435315	14437137	5	1823	3.65141E-06
Chr3	14438643	14442126	10	3484	8.62E-11
Chr3	14449200	14450584	6	1385	6.44E-08
Chr3	14467161	14467690	4	530	4.92E-07
Chr3	14485557	14487172	6	1616	5.56E-08
Chr3	14494790	14496807	6	2018	9.83E-12
Chr3	14498984	14501812	6	2829	3.70E-09
Chr3	14521095	14522936	4	1842	1.61E-07
Chr3	14541044	14541483	6	440	8.06E-09
Chr3	14544371	14545605	5	1235	6.60945E-06
Chr3	14546672	14551571	20	4900	6.35E-21
Chr3	14552636	14553290	4	655	4.90825E-06
Chr3	14556072	14558618	8	2547	2.03E-09
Chr3	14564672	14569250	12	4579	3.13E-10
Chr3	14579834	14583003	7	3170	1.02E-10
Chr3	14616549	14617500	4	952	7.61E-08
Chr3	14620790	14623006	5	2217	5.84E-08
Chr3	14638157	14638772	6	616	2.47E-08
Chr3	14642579	14644247	4	1669	6.18E-07
Chr3	14657352	14659258	6	1907	1.45E-07
Chr3	14661445	14662386	7	942	1.42E-10
Chr3	14702267	14703101	6	835	1.91E-11
Chr3	14706488	14713281	13	6794	2.82E-17
Chr3	14715856	14719252	9	3397	1.71E-13
Chr3	14729221	14731223	6	2003	6.05E-11
Chr3	14739409	14740058	5	650	1.00976E-05
Chr3	14742843	14744785	6	1943	6.44E-11
Chr3	14762324	14762981	4	658	1.40301E-06
Chr3	14774593	14775636	5	1044	1.13916E-07
Chr3	14781948	14783048	8	1101	1.25E-11
Chr3	14786483	14787227	4	745	5.28E-08
Chr3	14788867	14789319	4	453	4.90054E-06
Chr3	14794816	14798777	16	3962	1.69E-22
Chr3	14820532	14823724	7	3193	1.78E-08
Chr3	14828381	14830244	5	1864	7.74E-08
Chr3	14838465	14841388	11	2924	4.92E-12
Chr3	14847098	14847839	4	742	2.07025E-06
Chr3	14861359	14863638	13	2280	2.90E-18
Chr3	14871828	14872143	4	316	5.67712E-06
Chr3	14894200	14894827	4	628	1.65472E-06
Chr3	14924377	14925409	4	1033	6.12E-07
Chr3	14977304	14979476	6	2173	4.61E-07

Chr3	14980960	14982717	6	1758	7.14E-08
Chr3	14984924	14986751	7	1828	4.65E-12
Chr3	15000579	15002672	5	2094	5.16928E-06
Chr3	15035270	15036913	8	1644	7.64E-14
Chr3	15042568	15043947	4	1380	7.65262E-05
Chr3	15045256	15047627	10	2372	2.10E-13
Chr3	15056281	15058450	5	2170	5.78E-07
Chr3	15064531	15066084	4	1554	0.000417032
Chr3	15105545	15110280	11	4736	2.05E-12
Chr3	15113926	15115110	5	1185	2.80E-07
Chr3	15127885	15128524	4	640	6.4433E-05
Chr3	15137479	15140729	10	3251	6.88E-17
Chr3	15141985	15148877	19	6893	9.50E-25
Chr3	15154301	15155358	5	1058	5.92E-09
Chr3	15161204	15162611	5	1408	4.88E-07
Chr3	15251027	15251718	7	692	2.95E-10
Chr3	15252861	15254260	9	1400	6.18E-11
Chr3	15258605	15259636	4	1032	8.04011E-05
Chr3	15261117	15261434	4	318	6.63099E-06
Chr3	15263340	15264289	4	950	1.09025E-05
Chr3	15300592	15304789	13	4198	1.53E-18
Chr3	15305971	15306214	4	244	8.17E-07
Chr3	15318173	15320205	4	2033	7.33056E-05
Chr3	15325157	15325721	4	565	2.85795E-06
Chr3	15328151	15328806	4	656	3.2714E-06
Chr3	15331009	15331399	6	391	3.15E-08
Chr3	15364320	15365410	5	1091	1.41E-09
Chr3	15374907	15377816	8	2910	3.42E-10
Chr3	15385899	15386985	4	1087	3.25054E-05
Chr3	15412090	15412964	4	875	1.23E-08
Chr3	15444731	15446198	4	1468	9.02053E-05
Chr3	15459694	15460709	4	1016	1.76646E-06
Chr3	15461872	15464273	7	2402	3.55E-09
Chr3	15479065	15480801	5	1737	3.06E-08
Chr3	15488338	15489825	4	1488	3.77E-07
Chr3	15496421	15499217	6	2797	5.01008E-06
Chr3	15501160	15501376	4	217	3.34765E-05
Chr3	15507917	15509035	6	1119	3.50E-08
Chr3	15528248	15530828	4	2581	1.19004E-06
Chr3	15534682	15535798	5	1117	1.61733E-05
Chr3	15549176	15550897	4	1722	7.83E-07
Chr3	15572965	15573636	4	672	3.76904E-06
Chr3	15580810	15583139	8	2330	9.83E-09
Chr3	15589156	15594008	12	4853	9.40E-13
Chr3	15595630	15596593	6	964	6.52092E-06
Chr3	15621687	15623052	4	1366	3.87408E-06
Chr3	15635166	15636231	4	1066	2.04465E-05
Chr3	15688007	15688400	5	394	3.33962E-06
Chr3	15693103	15694100	5	998	1.14E-07
Chr3	15715934	15720116	22	4183	1.32E-25
Chr3	15848553	15851643	9	3091	6.48E-11
Chr3	15915906	15916169	4	264	4.49471E-06
Chr3	15962732	15964955	4	2224	4.60E-07
Chr3	15997858	15999463	4	1606	0.000165325
Chr3	16011239	16011372	7	134	9.90E-11
Chr3	16070792	16071652	5	861	2.24E-07
Chr3	16159022	16161672	8	2651	5.20E-10
Chr3	16248674	16249113	4	440	1.57352E-06
Chr3	16526176	16528996	20	2821	4.92E-27
Chr3	16590407	16591795	9	1389	1.25E-10
Chr3	16594744	16595875	5	1132	1.07772E-05
Chr3	16694843	16696964	7	2122	1.80E-11
Chr3	16829952	16830803	4	852	3.83027E-06

Chr3	16958918	16961570	5	2653	2.16E-07
Chr3	17057063	17057952	4	890	5.92337E-05
Chr3	17430571	17433026	6	2456	6.67E-08
Chr3	17472698	17472821	4	124	3.49398E-05
Chr3	17981442	17983845	6	2404	1.66E-09
Chr3	18359732	18360709	4	978	1.8127E-06
Chr3	18794155	18795384	9	1230	1.95E-12
Chr3	18860986	18861144	4	159	9.70E-07
Chr3	20304738	20305822	5	1085	1.15E-07
Chr3	20485236	20486002	4	767	8.59E-09
Chr3	22124066	22124633	4	568	6.18E-26
Chr3	22696991	22697028	4	38	1.82E-08
Chr3	23108925	23109685	4	761	3.32866E-07
Chr3	23376255	23376312	5	58	4.03E-09
Chr3	23408999	23410006	6	1008	3.37E-10
Chr4	226396	226695	5	300	9.13E-26
Chr4	331390	331641	8	252	3.69E-14
Chr4	631203	633109	9	1907	3.95E-11
Chr4	634170	636827	10	2658	1.82E-12
Chr4	782475	783256	4	782	4.12543E-06
Chr4	861949	863637	5	1689	8.05E-08
Chr4	1230840	1232543	9	1704	6.96E-13
Chr4	1314673	1315537	5	865	4.41E-08
Chr4	1455391	1456361	4	971	1.27054E-05
Chr4	1593053	1594335	4	1283	8.10278E-06
Chr4	1596236	1597117	6	882	1.48E-08
Chr4	1620082	1620552	4	471	5.48E-08
Chr4	1621934	1622825	4	892	2.4196E-06
Chr4	1668952	1669868	5	917	3.99749E-06
Chr4	1673775	1675203	6	1429	7.90E-07
Chr4	1676441	1677949	4	1509	4.19281E-06
Chr4	1682344	1685373	7	3030	1.61E-09
Chr4	1686546	1687654	4	1109	4.41111E-05
Chr4	1691803	1694252	11	2450	8.58E-14
Chr4	1696183	1698643	9	2461	1.27E-12
Chr4	1787533	1789015	6	1483	4.65E-07
Chr4	1792128	1792609	5	482	1.36726E-06
Chr4	1796373	1797315	5	943	1.70E-07
Chr4	1798402	1798701	4	300	3.12433E-06
Chr4	1803351	1806775	13	3425	2.85E-20
Chr4	1815752	1817679	6	1928	9.79E-10
Chr4	1825192	1826642	5	1451	4.22E-07
Chr4	1844512	1845939	4	1428	2.24E-09
Chr4	1859718	1860795	7	1078	8.87E-11
Chr4	1914851	1916204	4	1354	1.3626E-06
Chr4	1918561	1919867	4	1307	5.40372E-06
Chr4	1921300	1924617	11	3318	3.36E-15
Chr4	1936824	1938395	6	1572	1.78E-08
Chr4	1950995	1951955	4	961	6.40E-07
Chr4	1953265	1954698	5	1434	4.69E-08
Chr4	1978624	1981131	5	2508	7.60885E-06
Chr4	2000903	2002273	4	1371	8.62E-07
Chr4	2004058	2007486	10	3429	2.05E-13
Chr4	2013686	2014130	4	445	4.70991E-05
Chr4	2018192	2020230	7	2039	1.57E-10
Chr4	2041083	2042699	5	1617	0.000303966
Chr4	2068521	2071347	6	2827	1.08E-07
Chr4	2117615	2117631	4	17	1.30E-10
Chr4	2139485	2142835	10	3351	1.20133E-08
Chr4	2191520	2193761	4	2242	1.80E-07
Chr4	2202187	2203366	4	1180	4.60537E-05
Chr4	2233659	2233858	5	200	4.86E-09
Chr4	2245593	2246793	4	1201	9.54316E-05

Chr4	2249662	2250303	4	642	3.48E-08
Chr4	2255050	2257612	5	2563	1.53E-08
Chr4	2273436	2273774	4	339	7.83029E-06
Chr4	2280464	2282115	7	1652	2.79E-08
Chr4	2287511	2288654	10	1144	1.29E-12
Chr4	2292276	2292649	4	374	2.49532E-05
Chr4	2303836	2305449	5	1614	1.66E-07
Chr4	2326012	2326451	15	440	3.06E-44
Chr4	2348285	2348720	4	436	1.30081E-06
Chr4	2361815	2364505	8	2691	1.04E-09
Chr4	2533934	2534389	6	456	4.60E-12
Chr4	2597078	2598883	8	1806	4.66E-09
Chr4	2643722	2644868	5	1147	2.33928E-05
Chr4	2709178	2710820	5	1643	4.37925E-06
Chr4	2834132	2837197	7	3066	4.50E-11
Chr4	2865826	2866362	4	537	8.34298E-06
Chr4	2869009	2869921	4	913	3.06412E-05
Chr4	2870977	2871991	5	1015	6.04E-07
Chr4	2873517	2875023	6	1507	9.44E-09
Chr4	2878602	2881572	11	2971	1.43E-13
Chr4	2890251	2891878	5	1628	1.87E-07
Chr4	2893048	2893644	5	597	1.67E-07
Chr4	2898899	2899859	4	961	7.22E-08
Chr4	2910753	2912910	5	2158	1.59E-07
Chr4	2915436	2916621	4	1186	1.20E-08
Chr4	2920475	2920862	6	388	2.65E-08
Chr4	2967071	2970140	11	3070	1.92E-17
Chr4	2973187	2976066	9	2880	2.49E-12
Chr4	3017183	3019017	5	1835	3.79E-09
Chr4	3023424	3024963	5	1540	5.16357E-06
Chr4	3047624	3049145	4	1522	1.82E-09
Chr4	3054346	3056871	71	2526	9.39E-58
Chr4	3061072	3062411	21	1340	1.60E-24
Chr4	3071425	3072008	4	584	3.07E-07
Chr4	3074454	3075952	4	1499	3.80432E-06
Chr4	3079750	3083476	14	3727	7.16E-19
Chr4	3086182	3087335	4	1154	4.9576E-07
Chr4	3088854	3093950	15	5097	2.12E-20
Chr4	3095278	3096417	5	1140	1.69E-08
Chr4	3102582	3102719	4	138	8.78163E-06
Chr4	3109376	3110869	5	1494	1.24E-09
Chr4	3116918	3118359	6	1442	1.47E-08
Chr4	3126393	3127989	5	1597	1.22E-07
Chr4	3135134	3137828	7	2695	1.61E-10
Chr4	3156701	3160061	8	3361	2.42E-10
Chr4	3164129	3166655	9	2527	4.18E-13
Chr4	3176982	3178081	4	1100	1.15491E-06
Chr4	3180224	3181553	4	1330	4.93072E-06
Chr4	3187405	3189117	5	1713	4.94326E-06
Chr4	3263894	3265783	6	1890	8.24E-10
Chr4	3268420	3269239	6	820	2.05E-10
Chr4	3270340	3272808	14	2469	1.12E-21
Chr4	3275656	3280911	16	5256	8.37E-19
Chr4	3288901	3290317	4	1417	1.48489E-05
Chr4	3317941	3319451	6	1511	7.54524E-06
Chr4	3341512	3343570	6	2059	2.23043E-06
Chr4	3349415	3351566	7	2152	1.25E-08
Chr4	3353603	3354473	4	871	1.11035E-05
Chr4	3364497	3367314	7	2818	3.65E-08
Chr4	3372957	3373620	4	664	5.26894E-06
Chr4	3383053	3384422	5	1370	2.69E-07
Chr4	3386340	3388783	6	2444	6.04E-07
Chr4	3389967	3391315	5	1349	4.92E-08

Chr4	3396577	3398234	4	1658	0.018321304
Chr4	3416354	3417452	5	1099	2.06989E-06
Chr4	3431945	3433094	5	1150	7.26E-10
Chr4	3434144	3435446	7	1303	5.41E-10
Chr4	3470321	3470774	4	454	6.66E-08
Chr4	3487900	3490362	7	2463	6.05E-08
Chr4	3491678	3500751	24	9074	8.01E-29
Chr4	3507529	3510090	5	2562	4.93E-10
Chr4	3540754	3542771	9	2018	2.48E-12
Chr4	3548643	3550607	10	1965	1.64E-14
Chr4	3562243	3563725	5	1483	5.5446E-06
Chr4	3566085	3566531	4	447	0.000139521
Chr4	3570943	3572007	4	1065	2.22221E-05
Chr4	3584421	3586508	9	2088	8.70E-13
Chr4	3588095	3588977	4	883	1.39601E-05
Chr4	3593527	3595542	8	2016	4.12E-13
Chr4	3599311	3601412	8	2102	4.89E-12
Chr4	3602678	3603711	4	1034	1.39E-08
Chr4	3616681	3620609	10	3929	7.64E-15
Chr4	3624232	3627736	9	3505	2.46E-08
Chr4	3629744	3631361	5	1618	1.46043E-06
Chr4	3632648	3635989	12	3342	9.55E-18
Chr4	3638412	3640618	6	2207	1.06E-07
Chr4	3641745	3643792	6	2048	2.52E-08
Chr4	3648578	3651195	6	2618	2.10E-08
Chr4	3661214	3661998	7	785	5.34E-08
Chr4	3689750	3690520	4	771	9.64E-08
Chr4	3694354	3696007	11	1654	7.54E-14
Chr4	3703264	3704121	6	858	3.60E-08
Chr4	3709150	3711354	5	2205	5.06E-08
Chr4	3712850	3713301	5	452	7.54E-07
Chr4	3715919	3716447	4	529	2.75E-07
Chr4	3737094	3742497	27	5404	4.09E-25
Chr4	3747144	3749265	9	2122	2.39E-09
Chr4	3778893	3781211	5	2319	4.09E-08
Chr4	3790729	3793264	6	2536	4.88E-08
Chr4	3832451	3834525	4	2075	1.9999E-05
Chr4	3840472	3841049	4	578	1.99003E-05
Chr4	3847704	3852380	13	4677	6.68E-17
Chr4	3865125	3866307	4	1183	1.01446E-05
Chr4	3871587	3872088	5	502	0.000135159
Chr4	3873377	3873847	4	471	3.80E-07
Chr4	3882336	3884978	9	2643	7.20E-12
Chr4	3906235	3908800	10	2566	4.78E-14
Chr4	3913197	3915626	10	2430	9.29E-16
Chr4	3923469	3927512	10	4044	7.27E-16
Chr4	3929439	3931396	4	1958	6.36E-08
Chr4	3935915	3938759	8	2845	6.66E-13
Chr4	3943570	3946860	5	3291	5.11E-07
Chr4	3949129	3955922	86	6794	5.13E-88
Chr4	3957097	3958489	5	1393	9.51E-07
Chr4	3960764	3968629	36	7866	7.12E-37
Chr4	3977492	3979981	21	2490	5.37E-15
Chr4	3982343	3983571	14	1229	1.78E-11
Chr4	3987384	3988674	8	1291	1.06E-11
Chr4	3992490	3996193	29	3704	5.28E-26
Chr4	3998149	3998361	5	213	0.000137615
Chr4	4000106	4000821	9	716	4.17E-09
Chr4	4003309	4004102	8	794	0.018720822
Chr4	4007092	4007365	7	274	1.94E-12
Chr4	4008403	4012337	28	3935	1.34E-22
Chr4	4015549	4018867	8	3319	1.28E-09
Chr4	4023142	4024373	4	1232	7.14084E-05

Chr4	4026160	4028630	8	2471	3.72E-10
Chr4	4036070	4037399	7	1330	1.59E-10
Chr4	4041581	4044364	7	2784	5.21E-08
Chr4	4047738	4049835	9	2098	1.46E-12
Chr4	4053650	4054455	7	806	8.82E-11
Chr4	4061753	4063595	6	1843	7.80E-09
Chr4	4064735	4065703	4	969	1.02E-07
Chr4	4100062	4101379	4	1318	5.94371E-05
Chr4	4111748	4114571	8	2824	2.39E-12
Chr4	4124732	4126007	6	1276	8.59E-08
Chr4	4135623	4137690	8	2068	4.66E-13
Chr4	4158296	4161303	10	3008	1.59E-12
Chr4	4174678	4175462	4	785	3.20E-07
Chr4	4177755	4178698	5	944	2.21E-07
Chr4	4179928	4181276	5	1349	2.70E-07
Chr4	4182506	4186822	16	4317	2.79E-18
Chr4	4212111	4213869	5	1759	4.64966E-06
Chr4	4236437	4239676	12	3240	1.24E-13
Chr4	4241749	4248076	20	6328	3.50E-21
Chr4	4249275	4250825	4	1551	4.93618E-06
Chr4	4260118	4263607	9	3490	5.29E-11
Chr4	4276341	4282451	20	6111	8.91E-26
Chr4	4287107	4288515	9	1409	6.18E-13
Chr4	4289827	4293279	8	3453	4.33E-11
Chr4	4294324	4298282	8	3959	2.13E-09
Chr4	4303917	4305534	7	1618	5.46E-08
Chr4	4308409	4309620	5	1212	1.09E-08
Chr4	4321968	4322366	4	399	3.14674E-05
Chr4	4326803	4328161	4	1359	3.45854E-06
Chr4	4340056	4341315	7	1260	5.68E-14
Chr4	4346679	4348078	5	1400	6.23E-08
Chr4	4350141	4354240	8	4100	1.87E-12
Chr4	4355432	4357494	5	2063	1.35631E-05
Chr4	4358830	4362012	6	3183	1.33E-07
Chr4	4365313	4366510	4	1198	9.71662E-07
Chr4	4380990	4382075	5	1086	8.3252E-05
Chr4	4386922	4388066	5	1145	2.21E-07
Chr4	4389462	4390784	5	1323	1.80E-08
Chr4	4392037	4393477	6	1441	3.06E-08
Chr4	4401338	4403565	6	2228	1.33E-10
Chr4	4406894	4407793	4	900	3.08E-08
Chr4	4409472	4410663	7	1192	1.53E-10
Chr4	4414714	4416188	4	1475	5.88E-09
Chr4	4418333	4421697	7	3365	2.43E-11
Chr4	4423049	4427106	14	4058	5.30E-21
Chr4	4429130	4429504	4	375	2.5826E-05
Chr4	4431233	4436002	13	4770	7.23E-17
Chr4	4438345	4442065	11	3721	4.65E-16
Chr4	4450513	4452322	5	1810	5.38499E-06
Chr4	4454686	4455353	4	668	2.82261E-06
Chr4	4487112	4488076	5	965	2.34E-09
Chr4	4505885	4507524	6	1640	8.95E-08
Chr4	4514969	4517625	11	2657	3.33E-12
Chr4	4524633	4525397	4	765	4.58E-07
Chr4	4527279	4528220	4	942	8.27E-07
Chr4	4543867	4545935	6	2069	1.20E-10
Chr4	4553198	4556252	8	3055	3.14E-10
Chr4	4558096	4560772	7	2677	1.77672E-08
Chr4	4563633	4564462	7	830	7.84E-08
Chr4	4565914	4572238	17	6325	1.94E-24
Chr4	4645552	4647274	5	1723	5.27E-07
Chr4	4710081	4712171	7	2091	3.06E-08
Chr4	4720499	4721263	5	765	7.19E-09

Chr4	4722914	4726441	11	3528	7.95E-11
Chr4	4731063	4732277	6	1215	3.98E-10
Chr4	4735325	4735998	5	674	1.10E-09
Chr4	4744279	4748969	11	4691	2.33E-18
Chr4	4750222	4751872	5	1651	3.74E-08
Chr4	4752886	4754067	5	1182	3.70749E-06
Chr4	4758711	4761585	13	2875	1.39E-19
Chr4	4762791	4768931	17	6141	2.53E-18
Chr4	4770469	4772091	6	1623	1.85E-08
Chr4	4774708	4778578	10	3871	2.16E-13
Chr4	4780632	4782600	11	1969	3.77E-13
Chr4	4785515	4787509	5	1995	2.97E-07
Chr4	4832069	4833649	6	1581	1.79E-08
Chr4	4835740	4837885	5	2146	4.87E-07
Chr4	4852807	4854285	4	1479	1.41826E-05
Chr4	4856285	4858814	9	2530	4.96E-18
Chr4	4900567	4901346	5	780	3.5524E-06
Chr4	4924925	4926793	7	1869	1.99E-11
Chr4	4932639	4935487	9	2849	1.09E-14
Chr4	4958580	4964495	21	5916	4.34E-25
Chr4	4997173	4998491	4	1319	3.58289E-06
Chr4	5003717	5006021	6	2305	8.08E-10
Chr4	5014862	5018840	9	3979	1.00E-11
Chr4	5021850	5022868	5	1019	1.74E-08
Chr4	5024584	5027438	9	2855	4.27E-08
Chr4	5042911	5049487	24	6577	6.78E-27
Chr4	5054070	5055289	5	1220	1.02366E-05
Chr4	5056941	5059091	6	2151	6.42E-07
Chr4	5060527	5068426	24	7900	2.09E-20
Chr4	5069696	5071246	9	1551	2.30E-10
Chr4	5074223	5081206	33	6984	6.46E-39
Chr4	5082566	5083639	8	1074	9.70E-11
Chr4	5091294	5092317	4	1024	5.13E-07
Chr4	5100627	5102024	4	1398	2.07E-07
Chr4	5103047	5105218	9	2172	1.31E-11
Chr4	5129293	5132350	11	3058	2.33E-15
Chr4	5137289	5139439	5	2151	2.51809E-06
Chr4	5307176	5308700	4	1525	1.6749E-06
Chr4	5402703	5403039	4	337	8.06E-08
Chr4	5489932	5490172	6	241	2.32E-09
Chr4	5509535	5511540	6	2006	7.87E-09
Chr4	5521238	5523524	8	2287	4.38E-13
Chr4	5525255	5527596	4	2342	1.28769E-06
Chr4	5533945	5535328	5	1384	5.37E-08
Chr4	5570632	5571156	4	525	8.08358E-05
Chr4	5638951	5639329	5	379	2.06E-14
Chr4	5915514	5916997	4	1484	1.55379E-05
Chr4	5940635	5943372	6	2738	1.22E-07
Chr4	5968687	5970203	4	1517	1.58E-08
Chr4	6057992	6059073	4	1082	2.25E-08
Chr4	6070200	6071706	6	1507	5.77E-08
Chr4	6126480	6128745	5	2266	6.78E-08
Chr4	6314947	6315823	4	877	7.42E-12
Chr4	6467219	6468573	5	1355	3.20E-11
Chr4	6529676	6532217	4	2542	0.000389207
Chr4	6536289	6536819	4	531	9.81E-09
Chr4	6651627	6653748	4	2122	2.96E-09
Chr4	6723516	6724876	4	1361	1.51636E-06
Chr4	6915220	6918455	6	3236	8.75E-10
Chr4	7089631	7089807	4	177	1.12789E-07
Chr4	7132003	7132447	4	445	1.61E-08
Chr4	7687935	7688381	8	447	5.07E-19
Chr4	7784284	7785034	5	751	1.15185E-06

Chr4	8044896	8045021	4	126	1.79E-15
Chr4	8367389	8368422	4	1034	5.18E-09
Chr4	8904948	8906200	5	1253	8.63E-09
Chr4	9022496	9022656	4	161	2.49951E-06
Chr4	9733152	9734415	6	1264	3.39E-11
Chr4	9902331	9902343	4	13	1.0963E-06
Chr4	10053433	10054541	5	1109	1.56E-11
Chr4	10173087	10173720	5	634	3.00E-08
Chr4	10544793	10545611	4	819	6.42E-08
Chr4	10648472	10649077	5	606	1.67E-08
Chr4	10994804	10995932	4	1129	6.67377E-06
Chr4	11040989	11042270	4	1282	6.54E-09
Chr4	11137402	11137612	4	211	7.61E-07
Chr4	11173387	11173887	6	501	1.00E-08
Chr4	11208587	11209799	5	1213	2.56696E-06
Chr4	11347897	11349545	7	1649	3.2021E-07
Chr4	11657497	11657830	7	334	1.27E-17
Chr4	11822433	11824777	8	2345	1.17E-11
Chr4	12368111	12369093	4	983	2.04387E-06
Chr4	12570156	12571370	4	1215	0.000483324
Chr4	13328284	13329548	4	1265	5.1559E-05
Chr4	13627248	13629436	10	2189	2.60E-16
Chr4	13630514	13630742	5	229	1.02E-07
Chr4	14146220	14147007	13	788	4.43E-13
Chr4	14282360	14283038	4	679	1.95621E-05
Chr4	14682487	14683398	4	912	7.87828E-06
Chr4	15391053	15392000	5	948	6.58E-12
Chr4	16111535	16111746	8	212	4.74E-17
Chr4	16325609	16325973	4	365	3.42E-08
Chr4	16374536	16375298	5	763	2.68E-11
Chr4	16442224	16442389	4	166	6.5484E-06
Chr4	18026164	18027126	10	963	4.69E-16
Chr5	64895	66433	11	1539	1.49E-12
Chr5	68603	69591	7	989	1.44E-09
Chr5	2393392	2394755	7	1364	2.30072E-06
Chr5	2401733	2402463	7	731	1.90E-11
Chr5	3249104	3249875	13	772	6.64E-19
Chr5	3253146	3253246	5	101	1.53E-20
Chr5	4988071	4988565	4	495	0.000111793
Chr5	5391290	5391749	4	460	4.68471E-06
Chr5	5644859	5646630	5	1772	6.88E-08
Chr5	5855579	5856518	4	940	6.43659E-06
Chr5	6210981	6212229	6	1249	2.5422E-06
Chr5	6632791	6633391	4	601	2.42858E-06
Chr5	6897604	6897753	4	150	6.14E-08
Chr5	7027902	7028400	4	499	9.58E-08
Chr5	7030274	7031962	5	1689	7.97E-07
Chr5	7236340	7236857	4	518	9.50203E-05
Chr5	7378007	7378181	4	175	4.7759E-07
Chr5	8549731	8550473	4	743	8.65E-07
Chr5	8572382	8574574	12	2193	1.49E-14
Chr5	8718504	8720874	6	2371	1.7194E-05
Chr5	8930733	8931943	4	1211	9.8385E-06
Chr5	8952476	8952615	4	140	5.01042E-05
Chr5	9186222	9188883	6	2662	6.76E-08
Chr5	9273782	9275003	5	1222	1.49E-08
Chr5	9414877	9416372	4	1496	1.18436E-05
Chr5	9755905	9756904	6	1000	3.97E-09
Chr5	9829106	9829764	4	659	1.15648E-05
Chr5	9891346	9892447	4	1102	1.42296E-06
Chr5	9904656	9906604	5	1949	2.0955E-06
Chr5	9926264	9929112	10	2849	8.50E-14
Chr5	9949570	9954897	13	5328	3.16E-17

Chr5	9980861	9982086	4	1226	6.72E-09
Chr5	9996002	9998926	7	2925	3.68E-11
Chr5	10095327	10098111	8	2785	5.80E-11
Chr5	10105235	10105818	4	584	0.000157007
Chr5	10126846	10127150	4	305	2.693E-05
Chr5	10140833	10141348	4	516	7.54E-08
Chr5	10199932	10203981	8	4050	8.91E-11
Chr5	10256038	10257849	7	1812	1.93E-09
Chr5	10351608	10354237	7	2630	5.13E-08
Chr5	10355254	10356317	4	1064	9.63055E-06
Chr5	10360199	10361421	5	1223	7.95E-09
Chr5	10372695	10374119	4	1425	1.7484E-05
Chr5	10410970	10411158	4	189	4.02E-07
Chr5	10413571	10414238	4	668	0.000118311
Chr5	10514190	10515605	5	1416	8.33826E-06
Chr5	10548011	10551067	7	3057	8.67E-11
Chr5	10552954	10554149	5	1196	4.28E-09
Chr5	10578837	10580009	4	1173	5.26E-07
Chr5	10587938	10590486	7	2549	3.73E-09
Chr5	10592366	10595822	8	3457	6.51E-10
Chr5	10623061	10624407	4	1347	7.29033E-05
Chr5	10634663	10635295	5	633	3.87E-10
Chr5	10685373	10686504	4	1132	1.97385E-06
Chr5	10738661	10739583	4	923	1.52793E-05
Chr5	10742540	10746299	11	3760	1.22E-15
Chr5	10765410	10769466	14	4057	3.88E-20
Chr5	10778309	10779533	4	1225	0.000251707
Chr5	10789921	10791862	4	1942	0.000240982
Chr5	10795127	10795469	4	343	1.58E-07
Chr5	10846736	10848325	4	1590	1.82782E-07
Chr5	10889645	10891381	5	1737	8.51476E-06
Chr5	10902934	10904533	5	1600	1.82E-07
Chr5	11050255	11052025	5	1771	0.000751352
Chr5	11056490	11058583	6	2094	8.84E-09
Chr5	11067781	11068312	4	532	0.000170705
Chr5	11101698	11104605	5	2908	1.21E-07
Chr5	11122246	11123419	6	1174	7.89E-09
Chr5	11141639	11142296	4	658	2.85E-08
Chr5	11145146	11146649	4	1504	8.98468E-06
Chr5	11161242	11162145	5	904	9.00E-07
Chr5	11167087	11168205	4	1119	4.80E-08
Chr5	11180040	11181340	8	1301	5.96E-09
Chr5	11184744	11188843	289	4100	0
Chr5	11206710	11208044	8	1335	1.47E-10
Chr5	11214769	11215535	6	767	1.34893E-06
Chr5	11219440	11220614	5	1175	1.34E-09
Chr5	11298987	11300120	4	1134	1.08632E-05
Chr5	11318988	11321449	7	2462	3.75E-08
Chr5	11324088	11324609	6	522	3.21E-07
Chr5	11335784	11340568	12	4785	8.21E-16
Chr5	11349469	11350951	6	1483	1.18E-07
Chr5	11352005	11353131	5	1127	1.53E-07
Chr5	11356468	11359341	10	2874	6.05E-13
Chr5	11363476	11366914	10	3439	9.06E-16
Chr5	11396671	11404413	21	7743	1.32E-21
Chr5	11407828	11409173	4	1346	0.000270868
Chr5	11411117	11412187	4	1071	8.1147E-05
Chr5	11430314	11431245	4	932	5.03152E-06
Chr5	11435723	11438198	8	2476	3.40E-14
Chr5	11454528	11455935	5	1408	1.0224E-06
Chr5	11466800	11469072	6	2273	8.40E-09
Chr5	11475464	11477250	10	1787	1.01E-14
Chr5	11478653	11479413	4	761	6.82047E-05

Chr5	11499390	11500558	5	1169	6.89E-07
Chr5	11520078	11521727	5	1650	5.54E-08
Chr5	11568560	11569236	4	677	2.50E-08
Chr5	11573182	11573708	4	527	7.8084E-06
Chr5	11578029	11579968	6	1940	8.17E-08
Chr5	11582266	11583631	4	1366	2.35431E-06
Chr5	11584908	11587110	7	2203	9.48E-09
Chr5	11593029	11593297	4	269	6.67E-08
Chr5	11624423	11624749	4	327	5.84E-07
Chr5	11630506	11632198	5	1693	1.67409E-06
Chr5	11642687	11644675	4	1989	1.28917E-05
Chr5	11650324	11652579	6	2256	4.35807E-06
Chr5	11687927	11688209	4	283	2.54E-07
Chr5	11692891	11693781	4	891	0.000554744
Chr5	11697749	11699201	5	1453	8.54E-07
Chr5	11700504	11705352	46	4849	9.04E-35
Chr5	11707038	11711067	16	4030	1.48E-12
Chr5	11723350	11725006	14	1657	1.33E-15
Chr5	11726094	11729764	44	3671	4.52E-120
Chr5	11730770	11735114	24	4345	2.09E-31
Chr5	11737277	11739332	8	2056	1.06E-08
Chr5	11742649	11744458	8	1810	3.39E-13
Chr5	11751241	11752878	10	1638	9.27E-14
Chr5	11754476	11755546	6	1071	0.000141691
Chr5	11757038	11757770	4	733	7.58E-08
Chr5	11765754	11766176	5	423	3.61E-08
Chr5	11767982	11768492	4	511	1.63075E-06
Chr5	11771745	11773019	5	1275	6.91181E-06
Chr5	11776581	11778901	12	2321	2.14E-19
Chr5	11782543	11784749	12	2207	7.35E-18
Chr5	11787922	11789429	7	1508	5.65E-08
Chr5	11799039	11807426	20	8388	1.81E-18
Chr5	11821953	11825732	9	3780	1.80E-11
Chr5	11833139	11835056	11	1918	9.70E-13
Chr5	11842588	11845483	8	2896	3.26E-08
Chr5	11850506	11852886	5	2381	3.57E-07
Chr5	11868763	11869675	4	913	0.00021503
Chr5	11897382	11899393	8	2012	8.96E-12
Chr5	11903854	11904626	4	773	2.72E-07
Chr5	11906488	11908725	4	2238	5.30865E-05
Chr5	11911311	11914325	11	3015	3.85E-18
Chr5	11915730	11917173	4	1444	1.71906E-06
Chr5	11918185	11919261	4	1077	2.69069E-06
Chr5	11935192	11943120	101	7929	1.16E-93
Chr5	11944290	11945683	9	1394	6.12E-12
Chr5	11952258	11955025	8	2768	5.92E-10
Chr5	11971056	11971871	4	816	5.64E-07
Chr5	11972915	11973125	4	211	1.03925E-05
Chr5	11974798	11976997	9	2200	1.38E-11
Chr5	11979755	11995032	77	15278	8.01E-67
Chr5	11997692	11998163	7	472	4.50E-08
Chr5	11999473	12001309	4	1837	2.39688E-05
Chr5	12002464	12003787	5	1324	2.20056E-07
Chr5	12007525	12008835	4	1311	1.89416E-06
Chr5	12009852	12015198	20	5347	4.85E-20
Chr5	12018060	12020470	10	2411	4.30E-16
Chr5	12021926	12025405	18	3480	1.48E-26
Chr5	12027766	12029606	5	1841	5.42992E-06
Chr5	12030655	12031617	5	963	2.27277E-06
Chr5	12034527	12043190	26	8664	3.68E-26
Chr5	12044672	12045748	7	1077	2.36E-09
Chr5	12052454	12055408	9	2955	3.09E-08
Chr5	12056963	12059723	9	2761	5.17E-14

Chr5	12061878	12062947	6	1070	1.01E-07
Chr5	12063948	12065509	5	1562	0.000468256
Chr5	12069629	12076439	15	6811	1.60E-15
Chr5	12103724	12104567	6	844	3.98E-10
Chr5	12105989	12112753	23	6765	9.63E-27
Chr5	12124261	12125470	8	1210	1.14E-11
Chr5	12127294	12127609	4	316	1.21814E-06
Chr5	12137083	12139308	10	2226	7.86E-11
Chr5	12140496	12142934	9	2439	5.13E-10
Chr5	12145638	12150092	16	4455	9.01E-19
Chr5	12154263	12157330	10	3068	2.61E-11
Chr5	12159327	12159661	4	335	0.000162582
Chr5	12161518	12163954	9	2437	3.24E-08
Chr5	12165539	12170076	16	4538	3.18E-17
Chr5	12175167	12180477	18	5311	6.58E-23
Chr5	12199412	12201860	4	2449	4.18128E-06
Chr5	12210929	12212089	5	1161	2.61052E-06
Chr5	12213525	12213905	4	381	1.37715E-05
Chr5	12214928	12219342	9	4415	3.32E-11
Chr5	12221366	12226868	17	5503	2.51E-27
Chr5	12228410	12235570	24	7161	3.45E-28
Chr5	12237542	12239258	7	1717	6.58E-11
Chr5	12245716	12246698	4	983	3.62375E-06
Chr5	12255628	12256848	6	1221	2.53E-09
Chr5	12265284	12266838	4	1555	2.54E-09
Chr5	12270422	12272077	5	1656	2.55E-07
Chr5	12284998	12287349	8	2352	6.31E-17
Chr5	12296766	12300516	9	3751	7.65E-15
Chr5	12311790	12316142	12	4353	1.99E-12
Chr5	12320245	12322696	7	2452	4.20E-09
Chr5	12327012	12328130	8	1119	1.24E-09
Chr5	12329193	12330149	7	957	7.74E-10
Chr5	12333415	12335226	4	1812	3.52E-07
Chr5	12342321	12349089	17	6769	2.56E-23
Chr5	12353013	12353156	4	144	5.64E-08
Chr5	12357881	12358628	4	748	3.2887E-06
Chr5	12360568	12363717	9	3150	3.75E-08
Chr5	12368658	12374065	14	5408	4.59E-14
Chr5	12380018	12381500	4	1483	9.38E-08
Chr5	12382691	12383972	5	1282	3.29309E-07
Chr5	12387199	12390669	8	3471	1.93E-07
Chr5	12396836	12400255	9	3420	9.56E-12
Chr5	12403526	12404409	5	884	8.00E-08
Chr5	12407210	12407807	4	598	4.79418E-05
Chr5	12409163	12411603	9	2441	6.94E-09
Chr5	12412875	12414637	5	1763	4.43E-07
Chr5	12428555	12431594	10	3040	4.55E-11
Chr5	12469264	12470426	4	1163	2.79635E-05
Chr5	12471706	12472666	4	961	5.12573E-06
Chr5	12473669	12476909	14	3241	2.09E-15
Chr5	12479548	12481130	5	1583	5.66711E-05
Chr5	12488818	12489702	5	885	9.50E-07
Chr5	12500618	12504835	17	4218	3.74E-18
Chr5	12512847	12513449	4	603	3.70395E-06
Chr5	12518354	12518835	4	482	7.42604E-06
Chr5	12520167	12523079	10	2913	7.43E-11
Chr5	12524406	12526007	4	1602	5.70179E-05
Chr5	12530340	12536279	21	5940	8.64E-25
Chr5	12566796	12566807	4	12	6.32E-07
Chr5	12573230	12575380	6	2151	5.89E-10
Chr5	12579521	12580445	5	925	7.13E-07
Chr5	12610391	12613067	8	2677	1.46E-14
Chr5	12614081	12615701	6	1621	2.64444E-06

Chr5	12621748	12622658	4	911	9.41E-07
Chr5	12623741	12625651	5	1911	4.19E-07
Chr5	12633044	12633506	4	463	5.45014E-06
Chr5	12635123	12636929	7	1807	1.21887E-06
Chr5	12641731	12643765	6	2035	1.65E-08
Chr5	12645923	12646770	4	848	1.00E-06
Chr5	12649867	12650806	6	940	9.90E-07
Chr5	12711006	12712588	8	1583	2.91E-10
Chr5	12713864	12714043	4	180	1.19264E-06
Chr5	12715279	12717117	8	1839	4.05E-10
Chr5	12740617	12741648	5	1032	1.76E-08
Chr5	12746349	12748263	5	1915	5.15E-07
Chr5	12755774	12758165	8	2392	8.50E-11
Chr5	12759287	12760086	5	800	1.81405E-06
Chr5	12770229	12770914	4	686	0.000213362
Chr5	12774195	12775054	5	860	5.29E-07
Chr5	12785843	12789903	9	4061	1.81E-13
Chr5	12792982	12795160	8	2179	3.85E-11
Chr5	12809414	12809444	5	31	1.80543E-05
Chr5	12810864	12811099	8	236	2.28E-07
Chr5	12924373	12925888	8	1516	9.48E-08
Chr5	12927911	12928875	4	965	5.02075E-06
Chr5	12936116	12937321	4	1206	2.80427E-06
Chr5	12940931	12943384	8	2454	2.17E-11
Chr5	12945984	12947198	5	1215	1.93E-08
Chr5	12948597	12950009	4	1413	9.06E-07
Chr5	12953355	12954658	4	1304	2.0677E-06
Chr5	12956804	12957896	5	1093	1.06E-11
Chr5	12967254	12970789	12	3536	3.44E-13
Chr5	12972549	12974491	11	1943	2.51E-14
Chr5	12983492	12985173	5	1682	9.69224E-05
Chr5	12997614	13000977	16	3364	3.30E-20
Chr5	13011625	13012687	4	1063	5.50417E-07
Chr5	13021007	13024918	13	3912	2.51E-17
Chr5	13028666	13029102	5	437	2.51E-07
Chr5	13035121	13037924	9	2804	1.95E-11
Chr5	13039771	13043253	7	3483	5.58E-09
Chr5	13073054	13074511	6	1458	3.69E-08
Chr5	13115220	13117071	4	1852	2.18E-07
Chr5	13118611	13118886	4	276	0.00017288
Chr5	13120512	13120611	4	100	3.92625E-06
Chr5	13123581	13125127	4	1547	8.79111E-06
Chr5	13142097	13143387	4	1291	3.23E-07
Chr5	13145136	13146456	7	1321	5.24E-12
Chr5	13148937	13150928	4	1992	9.68E-08
Chr5	13160318	13161880	5	1563	8.52E-07
Chr5	13170235	13175774	18	5540	9.38E-23
Chr5	13188330	13188946	4	617	1.45455E-06
Chr5	13262456	13264611	5	2156	4.23E-08
Chr5	13285520	13287372	6	1853	5.80E-07
Chr5	13290097	13292559	5	2463	7.34E-07
Chr5	13295304	13297776	9	2473	3.40E-10
Chr5	13300803	13302017	5	1215	1.45E-09
Chr5	13303394	13304959	6	1566	3.38E-09
Chr5	13316440	13319609	7	3170	7.27E-11
Chr5	13320801	13321207	5	407	6.31E-08
Chr5	13324067	13326845	11	2779	5.33E-20
Chr5	13334060	13335239	9	1180	2.13E-13
Chr5	13338682	13339874	6	1193	7.13E-09
Chr5	13373637	13378196	11	4560	1.29E-11
Chr5	13379209	13382536	11	3328	2.29E-16
Chr5	13394587	13396743	6	2157	4.41E-10
Chr5	13397947	13400883	8	2937	5.40E-13

Chr5	13403527	13404481	4	955	1.43287E-06
Chr5	13405517	13406584	9	1068	4.05E-10
Chr5	13409847	13412337	13	2491	3.98E-17
Chr5	13536022	13540126	10	4105	3.05E-10
Chr5	13782204	13783067	4	864	1.89333E-05
Chr5	13790118	13791829	4	1712	2.6765E-06
Chr5	13794090	13795289	4	1200	1.86282E-05
Chr5	13822641	13823755	4	1115	9.23141E-06
Chr5	13851774	13851822	6	49	2.05E-09
Chr5	13926427	13929666	7	3240	5.81E-09
Chr5	13961352	13962979	4	1628	1.85345E-05
Chr5	13965212	13967421	8	2210	1.18E-10
Chr5	13997504	13999246	10	1743	7.15E-15
Chr5	14085952	14087772	6	1821	7.04E-08
Chr5	14204573	14205245	4	673	6.87238E-06
Chr5	14380695	14382968	10	2274	1.31E-14
Chr5	14610784	14611192	4	409	1.0863E-05
Chr5	14678662	14680936	6	2275	4.24E-09
Chr5	14962302	14962871	5	570	1.28E-08
Chr5	15235763	15236688	4	926	1.76E-08
Chr5	15337315	15337719	5	405	3.21009E-06
Chr5	15339106	15339691	4	586	1.79E-08
Chr5	15385833	15386805	9	973	5.32E-12
Chr5	15498110	15498242	4	133	1.70899E-06
Chr5	15647729	15648787	5	1059	1.06545E-06
Chr5	16262007	16262447	4	441	2.16519E-05
Chr5	16470318	16471618	4	1301	3.29E-07
Chr5	17094036	17095163	5	1128	2.52443E-06
Chr5	17252267	17254218	4	1952	3.0791E-06
Chr5	17707407	17708241	5	835	8.69E-09
Chr5	18015989	18016382	4	394	8.17739E-06
Chr5	18193958	18196111	6	2154	4.15E-07
Chr5	18427561	18428692	4	1132	2.05288E-06
Chr5	18477091	18477847	6	757	7.38E-07
Chr5	18545316	18546100	4	785	5.52739E-06
Chr5	19313953	19314254	4	302	6.57441E-06
Chr5	19360177	19362114	4	1938	0.000469681
Chr5	20034619	20034663	4	45	2.27919E-06
Chr5	21161913	21162768	4	856	7.82711E-06
Chr5	21166433	21167161	4	729	2.36908E-06
Chr5	21922854	21923003	4	150	3.89E-07
Chr5	22004054	22005916	4	1863	2.16542E-05
Chr5	22262709	22262887	4	179	1.88101E-06
Chr5	22616122	22618012	5	1891	2.86E-08
Chr5	22640527	22640841	4	315	8.63E-07
Chr5	23025228	23026341	6	1114	2.46E-09
Chr5	23240795	23241308	4	514	8.8831E-06
Chr5	23914404	23915147	4	744	1.35695E-06
Chr5	23987006	23987165	5	160	3.74E-10
Chr5	24453946	24454566	4	621	1.60E-11
Chr5	25957491	25958221	6	731	4.04E-17

-Pit Root 16 dat (Hyper-DMRs)

Chromosome	Start	End	number of DMCs	DMR lenght	P-value
Chr1	238792	239290	4	499	5.67E-07
Chr1	1430333	1430886	7	554	2.71E-11
Chr1	1613561	1614545	4	985	9.19E-08
Chr1	1956070	1957540	4	1471	2.74E-07
Chr1	4093264	4093435	5	172	1.47E-09
Chr1	4329989	4330346	5	358	5.62E-08
Chr1	4331680	4334412	11	2733	1.40E-13
Chr1	4682909	4684386	4	1478	1.19E-07

Chr1	5099169	5099593	4	425	2.88E-08
Chr1	5693082	5694742	7	1661	1.23E-08
Chr1	5915156	5916324	7	1169	1.38029E-06
Chr1	6009775	6010296	4	522	8.86307E-05
Chr1	6011922	6012881	5	960	2.70E-07
Chr1	6274780	6276410	5	1631	7.63496E-06
Chr1	7066276	7070951	13	4676	2.53E-13
Chr1	7246413	7246596	4	184	1.35706E-06
Chr1	7352971	7365148	111	12178	5.17E-116
Chr1	7717592	7718037	4	446	9.00E-07
Chr1	7969605	7970909	5	1305	4.92395E-06
Chr1	7972152	7973402	8	1251	4.18E-08
Chr1	7985244	7986420	4	1177	7.88E-07
Chr1	8453552	8457085	10	3534	7.28E-10
Chr1	8728696	8728976	4	281	3.98386E-06
Chr1	8732188	8733509	5	1322	2.22299E-06
Chr1	8928107	8929336	7	1230	6.10E-09
Chr1	8930484	8932657	15	2174	4.82E-19
Chr1	9174546	9176291	6	1746	7.45E-07
Chr1	9368701	9370605	5	1905	6.32E-07
Chr1	9574332	9576863	5	2532	1.24E-08
Chr1	9579809	9580488	4	680	3.56E-07
Chr1	9678078	9679469	7	1392	2.01E-11
Chr1	9681043	9682632	4	1590	1.02511E-06
Chr1	9683831	9685473	7	1643	2.47E-08
Chr1	9686869	9688245	7	1377	4.72E-10
Chr1	10153655	10154544	6	890	3.17E-08
Chr1	10357623	10360112	8	2490	7.49E-11
Chr1	10362094	10362725	5	632	1.32E-08
Chr1	10533540	10534474	5	935	1.80E-07
Chr1	10697059	10700810	17	3752	9.07E-21
Chr1	10965121	10965958	4	838	0.000290119
Chr1	11304834	11306396	7	1563	8.33E-09
Chr1	11308298	11309572	7	1275	8.22E-09
Chr1	11506307	11508078	6	1772	2.26E-08
Chr1	11511276	11512182	4	907	7.65E-07
Chr1	11899343	11901620	6	2278	8.87527E-06
Chr1	12139093	12140277	7	1185	2.17E-09
Chr1	12141691	12143048	4	1358	8.41865E-06
Chr1	12173833	12176861	6	3029	1.26964E-06
Chr1	12376854	12377690	5	837	0.000130826
Chr1	12406263	12410067	16	3805	1.18E-23
Chr1	12627843	12628523	4	681	3.06819E-06
Chr1	12665797	12667916	6	2120	1.73E-07
Chr1	12671338	12672768	6	1431	2.16E-07
Chr1	12682680	12683297	5	618	6.99E-08
Chr1	12715398	12717065	4	1668	1.86417E-07
Chr1	12820285	12823689	8	3405	8.07E-14
Chr1	12847563	12849409	5	1847	4.87E-07
Chr1	12859998	12861773	5	1776	1.99102E-06
Chr1	13002556	13003785	10	1230	9.31E-11
Chr1	13011691	13012967	4	1277	4.30468E-06
Chr1	13019672	13022624	8	2953	2.09E-08
Chr1	13174379	13174890	4	512	1.89E-08
Chr1	13177548	13179040	4	1493	9.03E-07
Chr1	13264005	13267118	9	3114	4.74E-11
Chr1	13295418	13296574	4	1157	0.000683804
Chr1	13299251	13299902	6	652	1.23774E-06
Chr1	13372484	13373688	5	1205	1.87885E-07
Chr1	13376013	13377005	4	993	1.24021E-05
Chr1	13381564	13383182	5	1619	1.97E-07
Chr1	13411303	13412852	5	1550	7.50E-08
Chr1	13440864	13442940	6	2077	4.31E-07

Chr1	13446855	13448092	4	1238	2.82667E-05
Chr1	13494423	13494810	5	388	2.71E-08
Chr1	13518599	13519196	4	598	3.15233E-05
Chr1	13575075	13575729	5	655	1.18E-09
Chr1	13579759	13581351	5	1593	8.56E-07
Chr1	13594002	13594647	4	646	8.0277E-05
Chr1	13613927	13615341	5	1415	7.08E-12
Chr1	13643832	13646181	7	2350	1.54E-10
Chr1	13652467	13653592	4	1126	3.37633E-06
Chr1	13662566	13664354	7	1789	9.23E-10
Chr1	13681348	13682540	5	1193	3.08565E-05
Chr1	13691812	13693683	4	1872	2.4966E-05
Chr1	13705403	13706147	4	745	0.000268155
Chr1	13710956	13712047	6	1092	3.20E-10
Chr1	13720514	13721570	4	1057	4.77029E-06
Chr1	13726613	13727034	4	422	1.35121E-06
Chr1	13764193	13765767	4	1575	3.29E-09
Chr1	13773811	13774411	6	601	1.29E-08
Chr1	13777757	13779476	5	1720	7.09E-08
Chr1	13781223	13782617	6	1395	4.13E-08
Chr1	13783727	13784629	5	903	6.40241E-06
Chr1	13789052	13792502	13	3451	3.24E-19
Chr1	13805449	13806554	4	1106	5.89535E-05
Chr1	13826134	13827464	10	1331	2.52E-14
Chr1	13828568	13831796	13	3229	2.27E-13
Chr1	13841370	13842253	4	884	6.27E-07
Chr1	13916748	13919186	5	2439	1.95E-07
Chr1	13922987	13925092	8	2106	6.18E-09
Chr1	13942137	13946133	11	3997	2.17E-15
Chr1	13951171	13951574	4	404	4.92E-07
Chr1	13956676	13962761	16	6086	2.49E-15
Chr1	13970077	13971685	6	1609	2.91E-10
Chr1	13977918	13978491	4	574	1.35E-08
Chr1	14022927	14023824	5	898	3.07E-10
Chr1	14059627	14061784	5	2158	1.02162E-05
Chr1	14070195	14073845	8	3651	1.45E-12
Chr1	14083748	14085747	8	2000	1.43E-09
Chr1	14086961	14089421	5	2461	3.65038E-06
Chr1	14098717	14100625	4	1909	1.64E-09
Chr1	14102369	14104974	9	2606	1.41E-10
Chr1	14120077	14121951	5	1875	5.05113E-06
Chr1	14125887	14127764	6	1878	4.24E-09
Chr1	14128998	14132353	10	3356	5.05E-15
Chr1	14180945	14185447	10	4503	1.92E-12
Chr1	14193560	14194894	5	1335	4.84E-08
Chr1	14197403	14199218	5	1816	2.32E-08
Chr1	14200288	14202696	6	2409	2.4499E-05
Chr1	14211197	14216457	15	5261	1.62E-15
Chr1	14222557	14223664	5	1108	2.10E-07
Chr1	14225589	14226535	5	947	1.71E-07
Chr1	14235408	14237204	5	1797	2.59E-07
Chr1	14238306	14240108	4	1803	0.000410326
Chr1	14243468	14244459	5	992	1.69851E-05
Chr1	14245902	14246244	4	343	1.0962E-05
Chr1	14247405	14248280	4	876	0.000142823
Chr1	14249749	14251382	8	1634	1.79E-09
Chr1	14253165	14255227	9	2063	1.39E-10
Chr1	14259288	14261706	5	2419	2.87946E-06
Chr1	14269443	14271212	6	1770	3.90E-09
Chr1	14286287	14287453	6	1167	4.67E-08
Chr1	14313193	14314292	5	1100	7.77E-08
Chr1	14316475	14317931	6	1457	3.95E-09
Chr1	14328220	14329802	5	1583	4.54762E-05

Chr1	14335793	14336239	5	447	1.70296E-06
Chr1	14388222	14389570	5	1349	1.12E-08
Chr1	14431304	14433554	8	2251	1.73E-08
Chr1	14434580	14435797	8	1218	3.26E-12
Chr1	14437847	14440136	8	2290	1.55E-09
Chr1	14441995	14445609	9	3615	1.21E-12
Chr1	14454432	14455412	5	981	5.76E-09
Chr1	14458415	14459418	5	1004	7.93E-09
Chr1	14469510	14470240	5	731	4.98824E-06
Chr1	14476823	14479697	7	2875	3.35E-09
Chr1	14481018	14483636	9	2619	3.46E-13
Chr1	14488520	14489379	5	860	1.08234E-06
Chr1	14493948	14495078	8	1131	3.15E-10
Chr1	14496262	14497075	4	814	1.24188E-06
Chr1	14500341	14503255	12	2915	2.25E-14
Chr1	14505304	14506354	4	1051	5.77E-08
Chr1	14509623	14511167	8	1545	1.75421E-05
Chr1	14539113	14540667	6	1555	6.47E-09
Chr1	14582592	14585037	8	2446	1.87E-08
Chr1	14588626	14589047	4	422	1.0433E-06
Chr1	14590198	14591458	6	1261	1.37E-09
Chr1	14600789	14602650	8	1862	5.63E-09
Chr1	14720903	14722057	4	1155	1.82415E-06
Chr1	14837442	14840211	6	2770	1.21E-08
Chr1	14841675	14842512	4	838	9.55571E-06
Chr1	14849233	14850194	5	962	8.37E-07
Chr1	15052068	15052272	4	205	0.000822771
Chr1	15060128	15061114	5	987	1.10E-07
Chr1	15067428	15068806	7	1379	8.62E-10
Chr1	15073247	15074617	7	1371	6.73E-09
Chr1	15076388	15080298	14	3911	3.89E-17
Chr1	15081503	15086007	114	4505	3.71E-112
Chr1	15094112	15095482	6	1371	1.50E-08
Chr1	15096491	15097216	5	726	2.63481E-06
Chr1	15099160	15103406	20	4247	4.30E-16
Chr1	15135923	15139000	13	3078	1.06E-14
Chr1	15141903	15142815	4	913	3.36959E-05
Chr1	15151171	15152345	4	1175	0.000154763
Chr1	15153569	15154303	8	735	2.52E-13
Chr1	15156700	15157123	4	424	7.72E-07
Chr1	15158360	15164955	18	6596	1.03E-17
Chr1	15179618	15183342	12	3725	2.97E-14
Chr1	15186188	15187624	6	1437	1.80E-09
Chr1	15198113	15199182	6	1070	7.13E-09
Chr1	15416871	15417659	4	789	0.000112154
Chr1	15424493	15426705	4	2213	1.80901E-05
Chr1	15429077	15430340	4	1264	2.83685E-05
Chr1	15432430	15433377	4	948	2.19E-07
Chr1	15436732	15438174	10	1443	5.42E-12
Chr1	15445363	15446595	7	1233	1.39E-09
Chr1	15448696	15453635	13	4940	2.17E-15
Chr1	15488741	15490727	7	1987	2.05E-09
Chr1	15492199	15496334	14	4136	9.25E-15
Chr1	15498434	15501451	9	3018	1.02E-11
Chr1	15502899	15504015	5	1117	8.03E-07
Chr1	15505854	15511672	21	5819	2.78E-27
Chr1	15533131	15533486	4	356	1.60488E-06
Chr1	15534627	15535932	4	1306	1.3076E-05
Chr1	15538681	15540877	5	2197	7.47327E-05
Chr1	15542174	15544885	8	2712	5.43E-11
Chr1	15546505	15549738	9	3234	4.08E-13
Chr1	15550796	15551976	5	1181	0.000283566
Chr1	15555925	15557926	11	2002	5.54E-13

Chr1	15559858	15560613	4	756	3.22E-07
Chr1	15561735	15564016	7	2282	5.13E-12
Chr1	15565391	15569420	10	4030	1.47E-10
Chr1	15573902	15574534	5	633	1.00031E-06
Chr1	15578718	15582747	6	4030	1.75E-09
Chr1	15591386	15591997	4	612	9.34E-09
Chr1	15593307	15594696	6	1390	0.00023149
Chr1	15611034	15612320	5	1287	3.50E-08
Chr1	15618623	15620732	7	2110	5.64E-10
Chr1	15624886	15626134	4	1249	6.34E-07
Chr1	15638081	15640313	9	2233	1.57E-11
Chr1	15671129	15674116	12	2988	1.85E-15
Chr1	15677195	15679882	9	2688	6.15E-11
Chr1	15682526	15685444	8	2919	8.72E-10
Chr1	15697587	15701408	10	3822	4.59E-10
Chr1	15703147	15706783	9	3637	1.30E-11
Chr1	15708630	15709545	4	916	0.000175028
Chr1	15711508	15711788	4	281	1.00069E-05
Chr1	15713056	15715575	9	2520	2.53E-10
Chr1	15801346	15804760	12	3415	1.52E-13
Chr1	15817659	15818513	4	855	2.79544E-07
Chr1	15854470	15855456	7	987	1.67E-10
Chr1	15870416	15873810	8	3395	3.24E-09
Chr1	15876333	15877475	4	1143	2.19904E-06
Chr1	16006145	16007628	4	1484	0.000316162
Chr1	16093656	16097009	7	3354	1.36E-10
Chr1	16098380	16100040	4	1661	1.27365E-06
Chr1	16101965	16105166	14	3202	4.55E-16
Chr1	16107759	16109496	5	1738	5.95622E-07
Chr1	16117806	16119587	5	1782	6.07241E-05
Chr1	16122688	16124066	7	1379	1.52E-08
Chr1	16177316	16178418	6	1103	5.11E-09
Chr1	16189355	16190870	4	1516	3.08431E-05
Chr1	16198276	16199069	4	794	2.56E-07
Chr1	16200300	16202400	5	2101	4.52E-08
Chr1	16240127	16240403	4	277	0.000214161
Chr1	16319612	16321138	7	1527	3.15E-10
Chr1	16335910	16337575	5	1666	2.10E-08
Chr1	16368434	16369810	4	1377	3.4337E-05
Chr1	16377392	16379222	7	1831	6.81347E-07
Chr1	16381154	16381688	5	535	1.50696E-06
Chr1	16383040	16384267	4	1228	6.20E-08
Chr1	16431027	16431831	4	805	2.10818E-06
Chr1	16488936	16491435	9	2500	6.78E-10
Chr1	16510103	16511404	11	1302	4.34E-10
Chr1	16512836	16515003	10	2168	7.69E-11
Chr1	16516028	16529551	61	13524	1.71E-59
Chr1	16557179	16558724	4	1546	2.88104E-06
Chr1	16585633	16586513	5	881	5.45E-11
Chr1	16610106	16610794	5	689	1.49294E-06
Chr1	16626519	16628131	6	1613	9.23E-09
Chr1	16661170	16663941	8	2772	2.15E-10
Chr1	16676000	16677027	5	1028	1.62E-07
Chr1	16678031	16679586	5	1556	1.19E-08
Chr1	16680904	16682476	4	1573	2.76E-08
Chr1	16695928	16698586	7	2659	5.51E-13
Chr1	16711771	16712746	6	976	9.79E-10
Chr1	16718374	16718525	7	152	3.09E-11
Chr1	16726639	16729974	7	3336	1.54E-07
Chr1	16942838	16943670	4	833	1.0664E-05
Chr1	16944742	16946107	5	1366	2.34E-08
Chr1	16959321	16960463	4	1143	7.00408E-06
Chr1	17028035	17028969	5	935	4.63E-08

Chr1	17036510	17042493	19	5984	8.38E-22
Chr1	17047131	17048473	5	1343	6.41E-08
Chr1	17072439	17073532	4	1094	9.49E-08
Chr1	17256033	17259387	8	3355	6.83E-11
Chr1	17260608	17263497	8	2890	2.01E-10
Chr1	17305750	17305782	5	33	2.88E-09
Chr1	17363492	17365843	7	2352	1.41E-09
Chr1	17521786	17525095	16	3310	4.40E-18
Chr1	17608513	17608910	5	398	2.01E-09
Chr1	17677306	17678578	6	1273	1.15618E-05
Chr1	17680788	17681756	4	969	0.000207093
Chr1	17842365	17845158	9	2794	1.28E-12
Chr1	17846632	17846695	5	64	3.47E-07
Chr1	18380329	18380962	4	634	3.21E-09
Chr1	18790120	18790164	5	45	1.80E-08
Chr1	18894703	18894945	4	243	7.79952E-06
Chr1	18965091	18967490	7	2400	1.35E-07
Chr1	18969416	18969928	4	513	0.000627102
Chr1	19336334	19339109	12	2776	3.85E-13
Chr1	19342526	19343980	4	1455	1.52805E-05
Chr1	19345245	19345428	4	184	4.74548E-06
Chr1	20087166	20088880	4	1715	0.000108414
Chr1	20313844	20315876	6	2033	3.33E-11
Chr1	20317869	20319482	4	1614	6.04E-08
Chr1	21245872	21248829	11	2958	7.41E-17
Chr1	21748605	21753429	21	4825	9.23E-26
Chr1	22084923	22085562	4	640	1.93894E-06
Chr1	22100994	22103409	5	2416	3.32322E-06
Chr1	22694186	22696674	10	2489	1.07E-09
Chr1	23240308	23240349	4	42	3.11393E-06
Chr1	23280611	23281130	4	520	1.01541E-05
Chr1	23651611	23651935	4	325	1.2693E-06
Chr1	23711314	23711413	4	100	7.08E-07
Chr1	23927035	23928172	5	1138	9.82251E-06
Chr1	24272882	24275686	100	2805	3.16E-132
Chr1	24456852	24458056	4	1205	1.33E-07
Chr1	25145949	25146687	4	739	1.73521E-05
Chr1	25159339	25163315	12	3977	1.75E-11
Chr1	26367395	26371098	14	3704	5.10E-18
Chr1	27068247	27068673	4	427	3.87E-08
Chr1	27923740	27924566	5	827	1.46E-16
Chr1	29379410	29380457	4	1048	0.000105314
Chr1	29474607	29478335	8	3729	3.32E-08
Chr2	1092	3775	174	2684	8e-323
Chr2	5458	6203	45	746	9.38E-70
Chr2	9478	13032	81	3555	4.76E-189
Chr2	39314	40830	7	1517	2.68E-09
Chr2	43405	45396	6	1992	6.39E-08
Chr2	65168	66825	5	1658	8.76E-09
Chr2	254259	254445	4	187	3.68077E-07
Chr2	374844	377902	8	3059	2.37E-12
Chr2	532154	536825	15	4672	3.90E-16
Chr2	567836	568689	4	854	2.76446E-06
Chr2	573000	574846	5	1847	1.28E-07
Chr2	823369	824775	6	1407	8.89E-12
Chr2	926796	927895	5	1100	9.77E-08
Chr2	1402373	1403426	4	1054	3.52E-07
Chr2	1486305	1487045	4	741	1.8825E-05
Chr2	1741892	1742164	4	273	4.03165E-06
Chr2	1883430	1884500	7	1071	2.61E-09
Chr2	1956074	1958411	4	2338	4.72E-07
Chr2	2003343	2005179	7	1837	2.47E-10
Chr2	2036668	2038659	6	1992	1.18E-12

Chr2	2041903	2043603	4	1701	7.07E-07
Chr2	2051419	2052668	4	1250	2.41E-07
Chr2	2059118	2060118	4	1001	1.20252E-05
Chr2	2074755	2075400	4	646	5.15724E-06
Chr2	2079218	2080103	5	886	1.78811E-05
Chr2	2082175	2082296	4	122	2.78E-08
Chr2	2104528	2105695	4	1168	3.99454E-06
Chr2	2112296	2112661	4	366	9.24599E-06
Chr2	2113726	2114685	5	960	2.16E-11
Chr2	2148780	2148953	4	174	0.00016956
Chr2	2202210	2204006	4	1797	0.000144828
Chr2	2278500	2279170	4	671	4.06377E-05
Chr2	2302788	2305507	6	2720	5.52E-09
Chr2	2367432	2368250	5	819	1.53E-07
Chr2	2376017	2380820	19	4804	3.63E-27
Chr2	2386845	2387916	4	1072	7.1541E-06
Chr2	2392354	2392751	4	398	8.89E-08
Chr2	2397048	2400578	7	3531	5.63E-10
Chr2	2404593	2408292	8	3700	2.82E-10
Chr2	2418190	2420276	4	2087	5.01464E-05
Chr2	2440110	2441875	5	1766	3.29E-08
Chr2	2464727	2465673	4	947	5.79E-07
Chr2	2482016	2483232	5	1217	1.32E-09
Chr2	2489339	2491771	8	2433	3.12E-09
Chr2	2493103	2493752	5	650	1.80E-07
Chr2	2499714	2500681	5	968	1.44E-07
Chr2	2507971	2511453	10	3483	4.51E-12
Chr2	2531502	2534029	5	2528	8.93E-07
Chr2	2564344	2565586	4	1243	6.80494E-06
Chr2	2576516	2577471	7	956	1.84E-11
Chr2	2603075	2604375	4	1301	3.5133E-06
Chr2	2617545	2619210	4	1666	5.28395E-05
Chr2	2623387	2625692	12	2306	2.41E-15
Chr2	2644766	2645911	5	1146	1.49E-08
Chr2	2648173	2650597	5	2425	2.44E-08
Chr2	2664889	2665313	4	425	2.74926E-05
Chr2	2684047	2685568	5	1522	1.77233E-06
Chr2	2692025	2693213	6	1189	4.45E-09
Chr2	2711808	2712196	5	389	8.32E-11
Chr2	2717823	2719945	7	2123	9.50E-11
Chr2	2745411	2749503	7	4093	3.24E-09
Chr2	2751109	2751827	4	719	1.43131E-06
Chr2	2771036	2772107	4	1072	6.54643E-05
Chr2	2790418	2790520	5	103	6.51E-10
Chr2	2797467	2799122	5	1656	6.25E-07
Chr2	2805399	2805568	4	170	3.56E-07
Chr2	2808660	2809633	4	974	5.92146E-05
Chr2	2817485	2819159	6	1675	6.74976E-05
Chr2	2829257	2830575	4	1319	2.71597E-06
Chr2	2835295	2835636	4	342	3.06E-07
Chr2	2855293	2857236	6	1944	4.47E-10
Chr2	2878764	2882400	13	3637	7.04E-14
Chr2	2902343	2903652	5	1310	4.84E-07
Chr2	2932488	2933998	5	1511	5.03E-08
Chr2	3001418	3001632	4	215	5.49E-08
Chr2	3060891	3061843	4	953	1.43863E-06
Chr2	3066196	3066674	7	479	7.47E-12
Chr2	3077625	3078907	6	1283	2.79E-07
Chr2	3082177	3085328	9	3152	4.25E-13
Chr2	3086759	3088782	9	2024	8.83E-12
Chr2	3090707	3091556	8	850	2.78E-11
Chr2	3100315	3102057	8	1743	1.68E-10
Chr2	3103141	3104280	8	1140	7.47E-10

Chr2	3105839	3107025	4	1187	1.13991E-06
Chr2	3214294	3215580	4	1287	6.16E-07
Chr2	3225754	3227643	7	1890	1.64259E-06
Chr2	3230953	3232550	5	1598	3.12E-07
Chr2	3240761	3242111	12	1351	2.50E-14
Chr2	3244750	3244955	6	206	1.73E-10
Chr2	3247284	3261949	226	14666	7.40E-248
Chr2	3263055	3297655	827	34601	0
Chr2	3299936	3311541	177	11606	7.71E-201
Chr2	3312666	3320504	148	7839	1.22E-175
Chr2	3321815	3367962	1022	46148	0
Chr2	3376890	3379027	26	2138	1.00E-31
Chr2	3381715	3382098	16	384	1.39E-25
Chr2	3398412	3400702	18	2291	1.90E-18
Chr2	3406484	3406677	4	194	1.67025E-05
Chr2	3408872	3409047	5	176	1.65E-10
Chr2	3423567	3423721	5	155	1.04E-07
Chr2	3434179	3434541	11	363	8.01E-16
Chr2	3438177	3438833	8	657	4.04E-09
Chr2	3447446	3447618	9	173	7.12E-14
Chr2	3454064	3454220	5	157	2.49678E-06
Chr2	3458864	3461297	25	2434	8.88E-19
Chr2	3463348	3465339	10	1992	5.55E-12
Chr2	3466829	3467147	8	319	1.30E-11
Chr2	3468234	3469262	8	1029	2.20E-11
Chr2	3475753	3476445	15	693	9.44E-21
Chr2	3478235	3478396	5	162	2.82E-10
Chr2	3483901	3486697	19	2797	2.47E-21
Chr2	3487727	3489221	12	1495	5.99E-15
Chr2	3490388	3491210	5	823	2.28154E-06
Chr2	3492258	3493588	16	1331	3.87E-14
Chr2	3498065	3498514	6	450	9.86E-09
Chr2	3509175	3509621	10	447	4.02E-12
Chr2	3520749	3522332	6	1584	2.45E-08
Chr2	3536862	3539380	8	2519	1.91E-11
Chr2	3542739	3545922	6	3184	3.45E-07
Chr2	3547942	3552241	17	4300	1.54E-16
Chr2	3554917	3556710	5	1794	2.92E-08
Chr2	3564986	3565483	4	498	1.18E-08
Chr2	3605525	3607555	61	2031	8.86E-88
Chr2	3614958	3628039	505	13082	0
Chr2	3640045	3645305	13	5261	1.88E-15
Chr2	3656712	3656866	4	155	3.00E-08
Chr2	3662341	3663077	4	737	0.000241634
Chr2	3681903	3683425	4	1523	5.30293E-06
Chr2	3686830	3688434	7	1605	1.99E-08
Chr2	3710541	3711271	4	731	3.43881E-06
Chr2	3713224	3714820	4	1597	4.84E-09
Chr2	3717874	3718327	7	454	5.76916E-06
Chr2	3721722	3723868	5	2147	3.10352E-05
Chr2	3737318	3738201	5	884	3.91E-07
Chr2	3739780	3741238	4	1459	3.33E-07
Chr2	3752637	3753017	4	381	4.11E-08
Chr2	3760335	3762249	5	1915	5.41277E-06
Chr2	3763873	3768979	18	5107	7.47E-21
Chr2	3770435	3771561	5	1127	4.45E-08
Chr2	3822066	3823394	4	1329	8.73E-07
Chr2	3849308	3853284	13	3977	3.46E-15
Chr2	3857480	3865140	25	7661	2.52E-28
Chr2	3867787	3870218	6	2432	5.02E-09
Chr2	3871232	3873478	9	2247	1.13E-10
Chr2	3878875	3880221	5	1347	3.11E-07
Chr2	3883687	3887715	10	4029	1.72E-12

Chr2	3919898	3922484	10	2587	3.23E-15
Chr2	3943328	3944931	4	1604	1.96E-08
Chr2	3948619	3949370	6	752	9.59E-10
Chr2	3950926	3953162	13	2237	4.17E-14
Chr2	3955930	3956501	4	572	0.000137906
Chr2	3961723	3963460	6	1738	8.90E-08
Chr2	3973827	3975466	9	1640	5.24E-12
Chr2	3980712	3981484	4	773	1.57E-08
Chr2	3983960	3985171	4	1212	1.80809E-06
Chr2	3994571	3995560	4	990	1.17E-07
Chr2	4008460	4009799	5	1340	1.22E-08
Chr2	4014447	4016074	5	1628	1.45929E-06
Chr2	4050880	4052987	7	2108	3.86E-09
Chr2	4055409	4057039	4	1631	1.70079E-06
Chr2	4064276	4065170	5	895	5.21854E-06
Chr2	4091879	4096305	15	4427	2.46E-20
Chr2	4110572	4112711	6	2140	2.70185E-06
Chr2	4116804	4120091	9	3288	8.70E-13
Chr2	4121540	4123329	5	1790	1.97E-07
Chr2	4124726	4125884	4	1159	0.000157956
Chr2	4130122	4131811	12	1690	1.92E-21
Chr2	4171733	4172245	4	513	2.88E-07
Chr2	4176355	4176925	4	571	1.31729E-05
Chr2	4182314	4187064	16	4751	1.45E-21
Chr2	4201239	4201994	4	756	1.24212E-05
Chr2	4218436	4220409	4	1974	5.20913E-06
Chr2	4228870	4230162	5	1293	1.51E-08
Chr2	4238581	4240230	11	1650	1.15E-15
Chr2	4241541	4242842	6	1302	4.30409E-07
Chr2	4253093	4254307	6	1215	1.29E-10
Chr2	4258194	4261230	9	3037	1.79E-12
Chr2	4276637	4278833	7	2197	1.25E-10
Chr2	4280315	4280618	5	304	1.3637E-06
Chr2	4284306	4285502	6	1197	5.39E-10
Chr2	4288379	4294770	23	6392	2.90E-30
Chr2	4369351	4370476	4	1126	6.96E-07
Chr2	4375509	4376991	4	1483	5.57533E-06
Chr2	4378769	4387677	21	8909	9.52E-27
Chr2	4392809	4396430	12	3622	2.90E-15
Chr2	4398351	4402794	11	4444	7.88E-18
Chr2	4405181	4406517	5	1337	2.96E-09
Chr2	4408125	4410429	4	2305	2.24531E-06
Chr2	4468156	4469865	4	1710	1.79E-07
Chr2	4490187	4493174	11	2988	8.08E-13
Chr2	4494240	4494721	4	482	4.23859E-06
Chr2	4495949	4497568	8	1620	3.62E-08
Chr2	4510454	4511793	4	1340	4.5196E-06
Chr2	4519754	4522859	11	3106	7.35E-11
Chr2	4532227	4533257	4	1031	7.65164E-06
Chr2	4565733	4567297	4	1565	6.51E-07
Chr2	4570130	4570862	6	733	3.31E-08
Chr2	4572805	4574271	4	1467	5.96663E-06
Chr2	4579001	4582222	13	3222	1.79E-15
Chr2	4597385	4599984	7	2600	1.34E-10
Chr2	4613162	4615348	4	2187	1.87976E-05
Chr2	4641605	4643585	7	1981	2.24E-09
Chr2	4658147	4661050	6	2904	9.61E-10
Chr2	4670940	4671493	4	554	1.04687E-05
Chr2	4676599	4676686	4	88	0.000883773
Chr2	4681726	4683797	5	2072	3.97E-10
Chr2	4688149	4689628	7	1480	1.01E-07
Chr2	4695802	4697707	6	1906	1.50E-09
Chr2	4698788	4700671	6	1884	1.44E-08

Chr2	4704654	4707660	10	3007	5.63E-13
Chr2	4710923	4712685	8	1763	6.71E-10
Chr2	4715133	4718467	11	3335	5.57E-13
Chr2	4720410	4723530	11	3121	5.87E-12
Chr2	4726116	4728418	7	2303	3.89E-08
Chr2	4730827	4732873	6	2047	9.59E-09
Chr2	4734505	4735318	4	814	3.65842E-05
Chr2	4738127	4739356	6	1230	3.11E-11
Chr2	4808187	4809887	5	1701	1.23951E-05
Chr2	4812717	4818233	16	5517	1.26E-22
Chr2	4825531	4826227	4	697	1.61347E-06
Chr2	4834668	4835217	5	550	7.58E-09
Chr2	4840286	4841790	11	1505	1.13E-13
Chr2	4843768	4844235	5	468	3.80E-09
Chr2	4852614	4854870	6	2257	4.37E-07
Chr2	4878139	4878495	4	357	3.3948E-05
Chr2	4894948	4895967	6	1020	1.02E-08
Chr2	4900701	4905153	14	4453	7.66E-15
Chr2	4908108	4908843	8	736	9.19E-09
Chr2	4927144	4930048	8	2905	4.31E-09
Chr2	4935780	4936757	6	978	9.77669E-06
Chr2	4951061	4953408	5	2348	1.47719E-07
Chr2	4973921	4976346	6	2426	7.09E-08
Chr2	4978465	4980016	11	1552	1.05E-13
Chr2	4982268	4983475	5	1208	3.87786E-06
Chr2	4984772	4986430	5	1659	1.69459E-06
Chr2	4990447	4992605	6	2159	3.78663E-06
Chr2	4997617	5001354	11	3738	2.66E-17
Chr2	5023099	5024689	5	1591	7.32E-09
Chr2	5033491	5036937	9	3447	1.91E-09
Chr2	5038592	5040268	5	1677	3.16E-08
Chr2	5058428	5059804	5	1377	6.66109E-05
Chr2	5085932	5086849	5	918	3.75E-08
Chr2	5088633	5090549	6	1917	3.21E-07
Chr2	5092398	5093372	4	975	0.00026037
Chr2	5099753	5102154	10	2402	6.41E-12
Chr2	5103554	5106032	7	2479	2.07E-07
Chr2	5122454	5124751	6	2298	3.00E-08
Chr2	5129139	5129711	5	573	3.01E-09
Chr2	5130825	5134420	12	3596	8.76E-13
Chr2	5138567	5140274	5	1708	6.54865E-06
Chr2	5173066	5174352	4	1287	1.49274E-05
Chr2	5176075	5177544	6	1470	1.03E-07
Chr2	5183359	5184632	5	1274	6.43E-07
Chr2	5191608	5192256	5	649	3.36702E-06
Chr2	5233947	5237165	12	3219	1.73E-14
Chr2	5252539	5253914	7	1376	3.53E-07
Chr2	5256434	5257168	4	735	3.82906E-05
Chr2	5279410	5281830	7	2421	6.41E-12
Chr2	5284195	5285120	4	926	5.32015E-06
Chr2	5297749	5299151	5	1403	9.85296E-06
Chr2	5301132	5302095	4	964	1.81045E-06
Chr2	5325044	5326798	4	1755	1.4758E-06
Chr2	5327987	5332781	9	4795	1.22E-08
Chr2	5339411	5341201	5	1791	3.02809E-06
Chr2	5357416	5362317	10	4902	1.50E-13
Chr2	5363455	5364077	4	623	4.13E-07
Chr2	5365136	5367649	7	2514	1.21E-09
Chr2	5369428	5372130	8	2703	3.24E-09
Chr2	5379507	5382684	6	3178	3.45E-08
Chr2	5386926	5389406	9	2481	6.37E-10
Chr2	5443170	5443921	5	752	1.91E-08
Chr2	5469891	5470861	4	971	1.82E-07

Chr2	5472265	5472781	4	517	1.84314E-05
Chr2	5478221	5479481	5	1261	7.08017E-07
Chr2	5487569	5488882	5	1314	2.74E-08
Chr2	5497016	5498324	6	1309	1.85E-07
Chr2	5524182	5524844	5	663	6.083E-06
Chr2	5529914	5533610	11	3697	3.18E-13
Chr2	5559665	5562390	9	2726	5.01E-12
Chr2	5563408	5564486	4	1079	1.11605E-05
Chr2	5566770	5568096	10	1327	1.54E-15
Chr2	5570306	5571911	6	1606	4.01E-08
Chr2	5573225	5575846	12	2622	1.19E-14
Chr2	5600506	5603032	7	2527	4.09E-10
Chr2	5604257	5605974	8	1718	4.83E-13
Chr2	5619043	5620552	8	1510	3.49E-10
Chr2	5621621	5623057	4	1437	6.17E-07
Chr2	5632716	5636861	10	4146	1.41E-14
Chr2	5658642	5660022	4	1381	5.19E-07
Chr2	5712190	5713670	9	1481	8.82E-13
Chr2	5778463	5780313	5	1851	1.85365E-05
Chr2	5784622	5785738	5	1117	3.23E-07
Chr2	5809919	5811853	5	1935	2.12E-08
Chr2	5826404	5826830	4	427	7.29E-11
Chr2	5829572	5830529	4	958	3.09118E-06
Chr2	5884587	5885721	5	1135	0.000129968
Chr2	5895473	5897059	6	1587	8.16E-13
Chr2	5902212	5903856	6	1645	2.15E-07
Chr2	5984168	5985715	4	1548	0.000529613
Chr2	5986776	5988912	9	2137	2.24E-12
Chr2	5991814	5993642	7	1829	5.89E-10
Chr2	5995708	5995997	4	290	1.26621E-06
Chr2	5999307	6000396	6	1090	4.23E-08
Chr2	6007779	6009174	4	1396	2.06192E-06
Chr2	6010858	6011903	5	1046	1.61E-10
Chr2	6026994	6028102	6	1109	1.02488E-05
Chr2	6073346	6074909	4	1564	4.39349E-06
Chr2	6080660	6081826	4	1167	2.65393E-06
Chr2	6114228	6115270	4	1043	6.53548E-06
Chr2	6116273	6119541	8	3269	8.93E-12
Chr2	6122047	6123262	5	1216	6.16E-07
Chr2	6231953	6234493	6	2541	1.09E-09
Chr2	6259140	6261606	6	2467	7.30E-08
Chr2	6264164	6264789	6	626	3.68113E-07
Chr2	6266095	6267228	5	1134	8.79822E-07
Chr2	6330569	6332062	4	1494	3.55E-10
Chr2	6341537	6342894	6	1358	2.49E-12
Chr2	6424355	6425847	4	1493	1.24841E-06
Chr2	6433565	6435818	7	2254	3.64E-10
Chr2	6458749	6461664	10	2916	1.59E-14
Chr2	6479653	6480509	4	857	0.00031433
Chr2	6510264	6510459	4	196	4.71335E-06
Chr2	6552470	6554243	7	1774	5.50E-07
Chr2	6606854	6607877	4	1024	7.23E-09
Chr2	6619598	6620444	6	847	3.64E-09
Chr2	6622089	6623041	4	953	6.65656E-06
Chr2	6701826	6703452	9	1627	2.06E-12
Chr2	6717665	6721771	13	4107	9.17E-18
Chr2	6727430	6729042	6	1613	1.61E-09
Chr2	6767466	6768689	4	1224	9.27452E-06
Chr2	6769772	6771806	6	2035	4.40E-09
Chr2	6837577	6838084	7	508	1.09E-09
Chr2	6841862	6843804	9	1943	9.19E-16
Chr2	6845187	6847381	6	2195	4.69E-10
Chr2	6881967	6882936	4	970	0.000820213

Chr2	6911452	6912290	4	839	2.24939E-05
Chr2	6953418	6955294	6	1877	1.06E-08
Chr2	6957152	6958403	4	1252	0.000988117
Chr2	6974501	6976413	5	1913	1.23E-07
Chr2	7005315	7006296	4	982	2.93E-07
Chr2	7008879	7010049	5	1171	1.22643E-06
Chr2	7011588	7012361	4	774	3.35182E-05
Chr2	7015630	7016701	6	1072	5.59E-09
Chr2	7173312	7175451	4	2140	4.80657E-06
Chr2	7190949	7192163	30	1215	8.87E-39
Chr2	7211593	7213545	4	1953	2.72631E-06
Chr2	7230514	7233052	10	2539	1.31E-14
Chr2	7235813	7236983	5	1171	2.68098E-06
Chr2	7581441	7583636	5	2196	5.08E-08
Chr2	7720792	7721517	4	726	2.22505E-07
Chr2	7779993	7781934	6	1942	1.47046E-06
Chr2	8061358	8061438	5	81	3.15E-09
Chr2	8076297	8077520	5	1224	2.89871E-06
Chr2	8199899	8200218	9	320	1.21E-14
Chr2	8271461	8272600	4	1140	3.39638E-05
Chr2	8555231	8555811	7	581	1.20E-12
Chr2	8562270	8563871	10	1602	8.42E-14
Chr2	8565555	8566886	7	1332	4.11E-07
Chr2	8816720	8819944	10	3225	4.26E-12
Chr2	8911389	8911416	6	28	5.09E-10
Chr2	9122097	9125094	8	2998	4.25E-11
Chr2	9189506	9190854	5	1349	1.12467E-06
Chr2	9654249	9654854	4	606	0.000747162
Chr2	10408325	10408950	4	626	2.10025E-05
Chr2	10435219	10437245	8	2027	1.14E-12
Chr2	10593209	10593926	4	718	8.37636E-06
Chr2	10595266	10596328	7	1063	1.46E-10
Chr2	10606726	10608954	8	2229	4.88E-09
Chr2	10874917	10878671	9	3755	2.34E-08
Chr2	12449413	12450838	5	1426	1.29396E-06
Chr2	12657121	12658304	4	1184	0.000788224
Chr2	13223293	13225978	11	2686	8.04E-13
Chr2	13421969	13424352	8	2384	4.51E-13
Chr2	14404548	14405775	4	1228	4.45503E-06
Chr2	14410530	14412242	4	1713	1.47E-07
Chr2	14472547	14473085	5	539	7.25E-07
Chr2	16008587	16009307	4	721	1.37E-07
Chr2	17338114	17338342	4	229	6.88E-08
Chr2	17339450	17341137	11	1688	6.37E-12
Chr2	18398801	18398832	8	32	2.95E-14
Chr2	18651523	18652291	5	769	2.09E-07
Chr2	19320214	19320769	8	556	3.32E-14
Chr3	381814	383044	5	1231	2.86E-13
Chr3	1560027	1560546	9	520	4.35E-13
Chr3	1963577	1964029	5	453	1.15E-08
Chr3	1966566	1967848	4	1283	2.802E-06
Chr3	2720862	2721867	4	1006	0.000141384
Chr3	2808974	2809966	4	993	4.00E-08
Chr3	2814009	2814946	4	938	2.80107E-06
Chr3	3807086	3808197	6	1112	1.36E-08
Chr3	3809514	3810332	4	819	2.18351E-05
Chr3	4928288	4929257	6	970	1.45E-08
Chr3	4948628	4950224	5	1597	3.64E-07
Chr3	5279033	5281803	10	2771	6.94E-11
Chr3	5283973	5286574	11	2602	7.86E-11
Chr3	7708789	7708831	5	43	2.85E-10
Chr3	7805841	7807074	4	1234	4.61E-07
Chr3	8101281	8101613	4	333	1.13E-07

Chr3	8411145	8411775	4	631	1.8853E-05
Chr3	8541030	8542691	5	1662	6.47E-07
Chr3	8846084	8847657	4	1574	1.04E-07
Chr3	8977348	8977997	5	650	2.21E-09
Chr3	9012012	9014407	7	2396	1.48E-11
Chr3	9226796	9227685	6	890	1.43E-11
Chr3	9230264	9231807	4	1544	8.40607E-06
Chr3	9379227	9381420	7	2194	1.64E-13
Chr3	9389168	9389537	6	370	5.47E-08
Chr3	9391240	9392505	4	1266	2.22119E-06
Chr3	9615681	9616602	7	922	9.83E-10
Chr3	9664863	9665185	4	323	3.24473E-06
Chr3	9692341	9696983	12	4643	8.12E-16
Chr3	10222707	10223909	4	1203	3.59667E-06
Chr3	10340862	10343747	12	2886	2.50E-16
Chr3	10478619	10480152	8	1534	4.25E-09
Chr3	10481253	10483338	7	2086	3.29E-08
Chr3	10530876	10531486	4	611	7.76109E-06
Chr3	10847632	10847655	4	24	1.65E-07
Chr3	10919405	10921079	7	1675	3.56E-10
Chr3	10927780	10929461	8	1682	1.32E-10
Chr3	10932031	10932839	4	809	2.34E-07
Chr3	11117938	11120531	8	2594	4.83E-12
Chr3	11142675	11144011	7	1337	1.48E-09
Chr3	11330331	11333119	12	2789	1.72E-12
Chr3	11334966	11335491	4	526	1.71103E-06
Chr3	11338913	11341304	5	2392	1.62E-08
Chr3	11349058	11350824	7	1767	5.25E-10
Chr3	11355624	11356704	6	1081	1.23247E-07
Chr3	11393280	11393657	4	378	5.46401E-05
Chr3	11407689	11409164	9	1476	2.04E-12
Chr3	11421914	11422151	4	238	3.16E-07
Chr3	11491566	11493616	6	2051	7.63E-08
Chr3	11567615	11568195	4	581	9.90E-07
Chr3	11569475	11570888	4	1414	0.031601117
Chr3	11575269	11577671	6	2403	1.37687E-06
Chr3	11635147	11638389	13	3243	9.02E-15
Chr3	11657136	11658402	6	1267	1.68684E-06
Chr3	11660307	11660422	4	116	1.92468E-06
Chr3	11666305	11666941	4	637	3.98372E-05
Chr3	11680394	11681537	6	1144	9.56E-08
Chr3	11688073	11688645	4	573	2.93778E-06
Chr3	11862374	11862786	4	413	1.94879E-06
Chr3	11870746	11872910	8	2165	8.90E-09
Chr3	11874932	11876592	4	1661	0.001856367
Chr3	11883910	11884893	4	984	1.93E-07
Chr3	11933145	11935443	4	2299	1.44595E-06
Chr3	11936468	11937877	4	1410	1.57484E-05
Chr3	11940264	11940702	5	439	1.78E-10
Chr3	11942961	11943684	6	724	9.93E-09
Chr3	12002811	12003220	5	410	7.91E-08
Chr3	12022015	12023977	7	1963	3.18E-11
Chr3	12025376	12026976	4	1601	4.13184E-05
Chr3	12033323	12034772	8	1450	7.67E-13
Chr3	12037282	12041910	17	4629	1.07E-23
Chr3	12044488	12045325	5	838	1.75923E-06
Chr3	12046740	12048842	4	2103	2.53212E-06
Chr3	12051918	12052602	6	685	1.27938E-06
Chr3	12058916	12059750	7	835	6.41E-08
Chr3	12067209	12067325	4	117	1.40725E-06
Chr3	12069155	12070155	4	1001	2.29E-10
Chr3	12106117	12106938	4	822	0.00037679
Chr3	12155858	12157034	5	1177	1.61215E-05

Chr3	12173420	12175538	4	2119	1.80162E-06
Chr3	12187471	12187821	7	351	5.10E-12
Chr3	12190180	12193162	8	2983	3.66E-10
Chr3	12196230	12197476	5	1247	2.90E-08
Chr3	12198548	12200436	4	1889	2.02601E-06
Chr3	12202044	12204151	8	2108	2.60E-10
Chr3	12205213	12206207	6	995	4.72E-08
Chr3	12211121	12211784	5	664	2.02E-07
Chr3	12215971	12217153	7	1183	1.64E-09
Chr3	12219013	12222721	9	3709	3.52E-11
Chr3	12250322	12253227	8	2906	1.85E-12
Chr3	12254243	12254880	5	638	8.72E-07
Chr3	12283493	12285581	6	2089	9.20E-10
Chr3	12290490	12293758	8	3269	9.13E-09
Chr3	12319314	12321320	7	2007	1.18E-10
Chr3	12322617	12325951	6	3335	1.05E-09
Chr3	12345921	12347894	5	1974	7.29017E-06
Chr3	12373594	12374182	4	589	2.64E-07
Chr3	12377515	12378444	5	930	2.95867E-05
Chr3	12396134	12397688	5	1555	8.99661E-07
Chr3	12402213	12403435	6	1223	5.86E-11
Chr3	12405594	12411799	15	6206	1.91E-18
Chr3	12427091	12428663	5	1573	2.58E-10
Chr3	12434253	12435528	4	1276	1.84232E-06
Chr3	12437314	12437779	4	466	7.95E-07
Chr3	12441206	12442646	6	1441	2.68E-08
Chr3	12462934	12465632	6	2699	6.23348E-05
Chr3	12469039	12470592	4	1554	1.97E-08
Chr3	12473706	12473766	5	61	2.63E-08
Chr3	12475562	12478637	10	3076	1.90E-12
Chr3	12482947	12484173	5	1227	2.45784E-05
Chr3	12489707	12490384	4	678	0.003480453
Chr3	12492082	12492962	4	881	1.16269E-06
Chr3	12496449	12498941	10	2493	1.68E-11
Chr3	12502240	12503337	5	1098	7.27E-08
Chr3	12510632	12512035	4	1404	1.33144E-06
Chr3	12515128	12517324	4	2197	0.000112421
Chr3	12521682	12523100	5	1419	2.52785E-05
Chr3	12532665	12534569	4	1905	1.60E-08
Chr3	12539196	12541395	13	2200	1.77E-21
Chr3	12546229	12546958	4	730	0.000428626
Chr3	12548023	12549139	5	1117	3.80377E-06
Chr3	12552111	12553580	6	1470	5.05E-08
Chr3	12564237	12564589	4	353	9.19085E-06
Chr3	12565691	12565935	4	245	7.85355E-06
Chr3	12576012	12578244	5	2233	6.44363E-05
Chr3	12582551	12584035	5	1485	1.05E-07
Chr3	12585974	12588775	8	2802	6.19E-07
Chr3	12616234	12618553	5	2320	1.10E-08
Chr3	12634754	12636487	5	1734	1.10E-10
Chr3	12675408	12677586	5	2179	8.72E-08
Chr3	12686572	12688089	5	1518	0.000107341
Chr3	12698509	12699271	5	763	1.82879E-05
Chr3	12706273	12707463	8	1191	5.34E-10
Chr3	12710549	12712182	5	1634	4.78E-07
Chr3	12715874	12718516	4	2643	7.11321E-06
Chr3	12722629	12724545	7	1917	8.07E-12
Chr3	12747115	12748893	6	1779	1.03748E-06
Chr3	12750367	12751576	7	1210	3.68E-09
Chr3	12800438	12804253	7	3816	2.30E-11
Chr3	12819552	12821523	9	1972	6.32E-12
Chr3	12827391	12830870	10	3480	5.53E-12
Chr3	12853812	12855749	4	1938	4.30269E-06

Chr3	12856803	12857538	6	736	2.03E-14
Chr3	12858576	12859994	5	1419	4.78E-07
Chr3	12862268	12863731	5	1464	2.67E-08
Chr3	12931875	12933608	6	1734	4.12E-08
Chr3	12935100	12935848	4	749	7.26E-07
Chr3	12944166	12947929	14	3764	2.77E-17
Chr3	12962454	12966165	13	3712	2.79E-15
Chr3	12972723	12973215	4	493	2.78E-07
Chr3	12983389	12985004	9	1616	2.03E-13
Chr3	13015878	13017889	6	2012	5.55E-09
Chr3	13055884	13057499	4	1616	4.25E-07
Chr3	13086774	13091077	13	4304	3.09E-16
Chr3	13119365	13120136	6	772	8.97E-07
Chr3	13123366	13124015	8	650	1.45E-12
Chr3	13144323	13144593	4	271	2.56E-07
Chr3	13150999	13152067	4	1069	1.84016E-06
Chr3	13157820	13160993	8	3174	3.95E-08
Chr3	13162236	13163410	4	1175	9.69E-07
Chr3	13190076	13190852	10	777	1.66E-11
Chr3	13191989	13192762	5	774	3.46E-07
Chr3	13200178	13200464	4	287	8.17E-07
Chr3	13203597	13206198	10	2602	3.49E-13
Chr3	13239925	13242121	8	2197	6.04E-09
Chr3	13248937	13250133	6	1197	4.17E-10
Chr3	13254544	13256219	4	1676	2.63107E-05
Chr3	13276336	13277893	6	1558	3.20E-09
Chr3	13322227	13323204	4	978	1.77811E-06
Chr3	13341857	13342668	4	812	2.83E-07
Chr3	13355582	13357656	6	2075	1.22E-07
Chr3	13365577	13367802	7	2226	6.45E-10
Chr3	13380731	13382856	5	2126	6.65E-08
Chr3	13385262	13386919	4	1658	7.97274E-06
Chr3	13401252	13404354	7	3103	2.42E-09
Chr3	13407229	13411598	17	4370	1.88E-24
Chr3	13418225	13421729	10	3505	1.19E-14
Chr3	13436757	13437535	5	779	7.58E-07
Chr3	13441239	13441633	5	395	1.85E-08
Chr3	13444161	13444647	4	487	3.39622E-06
Chr3	13456485	13457661	4	1177	3.7051E-05
Chr3	13477403	13479216	5	1814	3.97E-08
Chr3	13514215	13519527	12	5313	7.38E-18
Chr3	13520540	13521915	4	1376	2.41536E-06
Chr3	13545389	13548003	6	2615	1.29E-09
Chr3	13555639	13556772	4	1134	0.000119524
Chr3	13563953	13564668	4	716	1.12057E-06
Chr3	13576194	13576981	5	788	1.11E-07
Chr3	13585742	13587760	51	2019	4.83E-80
Chr3	13588842	13592561	391	3720	0
Chr3	13594128	13596341	6	2214	4.61E-08
Chr3	13602820	13604238	6	1419	4.08E-08
Chr3	13608517	13613253	14	4737	8.03E-13
Chr3	13615340	13616385	5	1046	3.95E-10
Chr3	13617496	13619129	4	1634	1.32419E-06
Chr3	13620870	13622987	9	2118	1.42E-13
Chr3	13625550	13626130	4	581	7.30E-07
Chr3	13628898	13630057	4	1160	1.70E-08
Chr3	13633523	13633664	5	142	3.59E-07
Chr3	13636301	13641396	14	5096	1.20E-16
Chr3	13642643	13644759	8	2117	5.44E-12
Chr3	13649619	13651732	7	2114	1.58E-08
Chr3	13653974	13657052	14	3079	5.39E-16
Chr3	13671729	13673268	7	1540	1.26E-07
Chr3	13675625	13676208	4	584	3.33825E-05

Chr3	13678336	13678539	5	204	9.68E-11
Chr3	13682793	13682946	4	154	0.007521476
Chr3	13707164	13707654	5	491	5.25E-08
Chr3	13709824	13711098	5	1275	0.000450167
Chr3	13712276	13712429	4	154	1.57E-07
Chr3	13771490	13771816	4	327	3.35399E-06
Chr3	13777651	13778958	4	1308	6.31185E-06
Chr3	13801937	13805613	12	3677	1.04E-17
Chr3	13809434	13809644	4	211	6.21814E-06
Chr3	13813067	13816289	12	3223	2.79E-10
Chr3	13819190	13820791	6	1602	3.84E-09
Chr3	13829266	13829758	4	493	0.000173629
Chr3	13838959	13839685	5	727	4.1564E-08
Chr3	13853883	13854054	6	172	4.81E-08
Chr3	13872986	13874190	4	1205	5.02119E-06
Chr3	13875627	13876260	5	634	4.16E-07
Chr3	13886703	13890146	17	3444	3.19E-24
Chr3	13891150	13891847	5	698	1.02E-07
Chr3	13904654	13905034	5	381	4.19E-07
Chr3	13906075	13907948	6	1874	2.35E-09
Chr3	13920979	13921747	8	769	6.58E-14
Chr3	13925802	13930438	14	4637	1.48E-17
Chr3	13944787	13945704	4	918	1.02541E-06
Chr3	13948953	13950655	4	1703	1.86E-09
Chr3	13952645	13954707	9	2063	9.76E-12
Chr3	13956424	13959498	8	3075	1.55E-11
Chr3	13967307	13968830	9	1524	3.13E-14
Chr3	13970464	13973291	7	2828	1.02E-07
Chr3	13978570	13979624	4	1055	6.54E-07
Chr3	13993291	13993792	4	502	3.41131E-05
Chr3	13997474	13999473	6	2000	6.82E-10
Chr3	14011418	14014151	7	2734	2.44111E-06
Chr3	14045120	14045611	4	492	3.43149E-06
Chr3	14077499	14080496	11	2998	1.44E-15
Chr3	14107297	14108151	4	855	0.000128475
Chr3	14123949	14124655	4	707	6.85556E-06
Chr3	14157098	14157283	5	186	2.59E-08
Chr3	14164433	14166479	10	2047	7.83E-12
Chr3	14168796	14171313	9	2518	2.28E-10
Chr3	14172762	14172933	4	172	5.23767E-05
Chr3	14180460	14181737	9	1278	3.21E-09
Chr3	14185759	14186147	4	389	0.000143103
Chr3	14190029	14190796	6	768	3.18849E-06
Chr3	14195440	14204046	647	8607	0
Chr3	14205335	14208552	50	3218	1.46E-39
Chr3	14210218	14213723	19	3506	4.78E-13
Chr3	14214864	14215933	9	1070	5.13E-11
Chr3	14222483	14225129	16	2647	2.49E-19
Chr3	14245304	14247826	7	2523	1.55E-11
Chr3	14251246	14252236	4	991	0.000128228
Chr3	14253600	14258113	12	4514	1.30E-13
Chr3	14271489	14273891	5	2403	2.29E-07
Chr3	14293110	14294338	4	1229	1.71202E-06
Chr3	14341151	14343600	7	2450	2.71E-08
Chr3	14345507	14346636	4	1130	1.49E-07
Chr3	14375237	14376641	5	1405	2.58E-08
Chr3	14388424	14389849	5	1426	4.61772E-07
Chr3	14390909	14392918	6	2010	8.86E-09
Chr3	14411234	14413015	6	1782	7.07E-08
Chr3	14420903	14423962	9	3060	2.93E-11
Chr3	14428409	14428977	5	569	1.21153E-05
Chr3	14438988	14440629	5	1642	1.11E-08
Chr3	14442521	14443690	5	1170	7.97E-08

Chr3	14513058	14513905	4	848	6.38E-09
Chr3	14543175	14545665	9	2491	7.83E-12
Chr3	14546800	14548516	9	1717	3.29E-15
Chr3	14549895	14550705	4	811	1.66257E-06
Chr3	14554503	14558420	16	3918	6.70E-18
Chr3	14565168	14570327	15	5160	9.39E-19
Chr3	14582619	14583580	5	962	5.35E-09
Chr3	14616356	14619452	10	3097	3.41E-10
Chr3	14620530	14621767	7	1238	1.84E-10
Chr3	14629700	14630506	4	807	8.72891E-06
Chr3	14657360	14658750	7	1391	1.12E-09
Chr3	14660152	14660365	4	214	1.96146E-06
Chr3	14691112	14691887	5	776	2.46159E-06
Chr3	14701858	14702812	5	955	1.04E-09
Chr3	14706488	14706736	4	249	9.78E-07
Chr3	14707770	14710741	7	2972	2.59E-08
Chr3	14717056	14718951	8	1896	2.68E-10
Chr3	14729221	14731901	8	2681	6.19E-09
Chr3	14778572	14781152	8	2581	3.94E-13
Chr3	14785660	14786897	4	1238	4.11105E-05
Chr3	14795786	14797742	11	1957	1.39E-16
Chr3	14805217	14809633	13	4417	5.04E-20
Chr3	14821996	14823166	5	1171	4.55E-07
Chr3	14838058	14839674	4	1617	3.21E-07
Chr3	14848956	14849846	4	891	3.88E-08
Chr3	14872053	14872948	4	896	3.83486E-06
Chr3	14932374	14934859	5	2486	3.44E-08
Chr3	14969897	14971129	5	1233	7.69E-07
Chr3	15032015	15034405	8	2391	8.70E-09
Chr3	15041680	15043336	6	1657	2.12E-07
Chr3	15046583	15048085	4	1503	4.97E-07
Chr3	15053942	15056035	7	2094	3.19E-08
Chr3	15062456	15063998	5	1543	1.08E-07
Chr3	15067749	15070375	8	2627	3.12E-09
Chr3	15072517	15073787	6	1271	7.93E-07
Chr3	15099668	15100072	5	405	8.20E-09
Chr3	15106514	15108548	9	2035	2.91E-11
Chr3	15113481	15114338	7	858	5.02E-10
Chr3	15120745	15122756	8	2012	4.64E-09
Chr3	15124291	15125230	5	940	6.85E-09
Chr3	15138730	15141000	8	2271	9.04E-11
Chr3	15144958	15145628	4	671	1.90E-08
Chr3	15148601	15151868	6	3268	2.33E-07
Chr3	15153588	15154025	4	438	2.19925E-05
Chr3	15162054	15163739	4	1686	1.6775E-06
Chr3	15246507	15248446	10	1940	4.06E-11
Chr3	15252201	15254633	14	2433	6.26E-20
Chr3	15255795	15257649	4	1855	1.94611E-06
Chr3	15258799	15260407	4	1609	1.1917E-05
Chr3	15262886	15263814	4	929	9.07498E-06
Chr3	15266639	15267437	5	799	2.73482E-06
Chr3	15298919	15300959	4	2041	3.68609E-06
Chr3	15305330	15307573	6	2244	1.17E-07
Chr3	15324363	15326269	5	1907	6.70E-07
Chr3	15328423	15329009	6	587	4.22E-08
Chr3	15330054	15331274	4	1221	2.94825E-06
Chr3	15360475	15362145	5	1671	6.08E-07
Chr3	15374716	15377939	12	3224	9.78E-17
Chr3	15382556	15384381	5	1826	9.49017E-07
Chr3	15388641	15390615	5	1975	7.67662E-06
Chr3	15415519	15417019	5	1501	1.46789E-06
Chr3	15420627	15421394	4	768	2.2076E-06
Chr3	15458987	15464407	19	5421	2.69E-26

Chr3	15531853	15534045	6	2193	9.60E-10
Chr3	15537404	15539068	4	1665	1.15331E-05
Chr3	15543184	15545575	5	2392	2.16E-08
Chr3	15546798	15548475	10	1678	8.23E-14
Chr3	15578323	15579563	5	1241	6.02E-08
Chr3	15581001	15585781	14	4781	9.33E-20
Chr3	15587113	15589039	6	1927	1.34E-07
Chr3	15590549	15591815	6	1267	1.29081E-05
Chr3	15595665	15597052	5	1388	4.26E-07
Chr3	15631152	15631871	4	720	1.76969E-05
Chr3	15691393	15692596	6	1204	2.26859E-07
Chr3	15712429	15713851	5	1423	1.30E-10
Chr3	15714905	15716909	11	2005	1.08E-13
Chr3	15719977	15721919	7	1943	9.69E-10
Chr3	15851331	15852258	4	928	1.43E-08
Chr3	15918949	15919773	4	825	3.23E-08
Chr3	16178320	16180394	6	2075	1.30E-10
Chr3	16331032	16332134	4	1103	1.41573E-06
Chr3	16337039	16339878	6	2840	7.11E-07
Chr3	16499753	16501220	4	1468	3.86789E-06
Chr3	16590350	16592886	10	2537	7.18E-13
Chr3	16601892	16603161	4	1270	1.02274E-06
Chr3	16669941	16670316	4	376	1.84691E-06
Chr3	16693707	16697892	11	4186	4.72E-11
Chr3	16812010	16813266	7	1257	3.84E-09
Chr3	16961484	16962341	4	858	5.13E-07
Chr3	17099932	17100945	4	1014	1.64069E-05
Chr3	17112798	17112998	4	201	1.77771E-05
Chr3	17117416	17117425	4	10	6.51E-10
Chr3	17394004	17394776	4	773	2.72E-09
Chr3	17404773	17406012	5	1240	1.36268E-06
Chr3	17978597	17983189	16	4593	2.90E-22
Chr3	18062394	18063074	4	681	4.53276E-06
Chr3	18791300	18792344	6	1045	7.70E-12
Chr3	18794012	18795748	12	1737	5.90E-13
Chr3	18885825	18886783	5	959	3.40E-10
Chr3	20202207	20203486	6	1280	1.19E-08
Chr3	20233785	20234795	7	1011	1.27E-09
Chr3	20306009	20308188	9	2180	1.11E-12
Chr3	20726305	20728354	12	2050	2.77E-16
Chr3	21326230	21326753	4	524	4.68553E-06
Chr3	22233376	22234436	4	1061	0.000569034
Chr3	22696225	22697528	5	1304	1.55774E-05
Chr3	23108943	23111991	12	3049	6.17E-17
Chr3	23115061	23115755	4	695	1.15113E-06
Chr4	49442	52862	10	3421	5.21E-16
Chr4	631745	634317	10	2573	1.59E-11
Chr4	725645	725681	8	37	2.06E-13
Chr4	862997	864578	6	1582	1.52E-08
Chr4	1063647	1064040	5	394	1.47E-08
Chr4	1313173	1315184	8	2012	1.83E-08
Chr4	1453309	1454985	4	1677	2.13395E-05
Chr4	1487137	1488595	5	1459	3.24E-08
Chr4	1565753	1566483	4	731	2.30E-08
Chr4	1618775	1620169	4	1395	0.009405277
Chr4	1623841	1624901	5	1061	3.65E-09
Chr4	1650869	1651613	4	745	1.78197E-06
Chr4	1667015	1669191	6	2177	1.18851E-05
Chr4	1674166	1676430	8	2265	7.84E-10
Chr4	1683932	1685444	6	1513	1.64E-08
Chr4	1690166	1690521	4	356	1.08856E-06
Chr4	1692898	1698582	17	5685	1.32E-14
Chr4	1752322	1753553	4	1232	1.03037E-05

Chr4	1787907	1790185	9	2279	6.91E-12
Chr4	1791497	1792418	4	922	5.89309E-07
Chr4	1793799	1795120	6	1322	3.75E-07
Chr4	1798528	1801552	9	3025	6.71E-11
Chr4	1807830	1811417	10	3588	2.31E-15
Chr4	1829254	1833683	14	4430	8.30E-18
Chr4	1836603	1838225	4	1623	1.43E-08
Chr4	1856051	1857770	7	1720	5.62E-08
Chr4	1870878	1872421	4	1544	1.73139E-06
Chr4	1905850	1908161	7	2312	1.99E-10
Chr4	1921200	1922260	4	1061	0.000549895
Chr4	1945524	1946495	4	972	3.85212E-06
Chr4	1950306	1954960	12	4655	1.20E-15
Chr4	1977555	1979066	6	1512	1.54483E-06
Chr4	1988366	1990938	7	2573	9.81E-07
Chr4	2003992	2005353	5	1362	1.29E-09
Chr4	2006455	2007425	6	971	1.09E-09
Chr4	2008546	2010426	4	1881	1.63487E-06
Chr4	2048396	2049059	6	664	6.17E-08
Chr4	2072815	2074275	6	1461	1.95E-09
Chr4	2090875	2092469	4	1595	3.89E-07
Chr4	2143168	2144641	4	1474	2.11E-07
Chr4	2198404	2200350	5	1947	0.00058985
Chr4	2212232	2214024	4	1793	1.50E-08
Chr4	2247817	2249539	5	1723	1.22257E-05
Chr4	2271002	2272488	5	1487	9.45E-07
Chr4	2273591	2274903	4	1313	7.19E-07
Chr4	2281950	2283011	5	1062	2.39471E-06
Chr4	2284225	2285182	6	958	3.53E-07
Chr4	2288054	2288799	7	746	3.47E-09
Chr4	2305008	2307528	6	2521	8.91E-09
Chr4	2597354	2602212	14	4859	1.13E-17
Chr4	2644188	2648033	11	3846	4.02E-16
Chr4	2701753	2702980	4	1228	1.28352E-05
Chr4	2707170	2708569	5	1400	8.94E-07
Chr4	2709968	2713019	9	3052	1.67E-12
Chr4	2812056	2813695	8	1640	1.89E-09
Chr4	2830698	2831973	4	1276	7.56E-07
Chr4	2833134	2835033	8	1900	2.98E-12
Chr4	2850622	2852055	5	1434	1.77E-09
Chr4	2872085	2874632	7	2548	7.90E-09
Chr4	2885719	2888604	8	2886	2.91E-13
Chr4	2892681	2894100	5	1420	2.80E-07
Chr4	2895785	2897695	6	1911	2.56479E-06
Chr4	2902128	2902550	4	423	6.23469E-06
Chr4	2911955	2916280	12	4326	3.09E-15
Chr4	2921731	2921909	4	179	8.70E-08
Chr4	2953593	2954102	4	510	8.76E-08
Chr4	2968584	2970061	6	1478	5.32E-11
Chr4	2973755	2976209	6	2455	2.70E-07
Chr4	2977284	2980149	5	2866	3.70174E-06
Chr4	2981632	2985483	9	3852	5.94E-11
Chr4	3007076	3008024	5	949	4.50E-08
Chr4	3009398	3013988	9	4591	1.04E-12
Chr4	3015262	3017354	11	2093	8.00E-15
Chr4	3019655	3020622	8	968	7.10E-11
Chr4	3023235	3023866	4	632	3.52819E-05
Chr4	3029268	3029667	5	400	1.64E-08
Chr4	3031235	3031784	4	550	0.000109244
Chr4	3039626	3040791	4	1166	7.14262E-06
Chr4	3046032	3050310	13	4279	1.49E-12
Chr4	3054405	3056714	30	2310	1.30E-13
Chr4	3061193	3061530	6	338	2.00E-08

Chr4	3068498	3070352	7	1855	8.63E-11
Chr4	3071496	3073962	7	2467	3.04E-08
Chr4	3076069	3078739	10	2671	7.70E-16
Chr4	3080131	3082530	6	2400	6.31E-07
Chr4	3091508	3094377	6	2870	2.44525E-06
Chr4	3097939	3099095	4	1157	2.42795E-06
Chr4	3100602	3101723	4	1122	4.55E-07
Chr4	3106101	3106764	5	664	1.37E-07
Chr4	3110140	3110844	5	705	6.25E-08
Chr4	3127596	3131273	8	3678	7.94E-08
Chr4	3136054	3138228	9	2175	1.34E-11
Chr4	3139957	3140093	4	137	5.54E-07
Chr4	3157209	3159362	4	2154	3.54964E-06
Chr4	3180498	3184600	11	4103	1.37E-13
Chr4	3186097	3186996	7	900	1.89E-08
Chr4	3263358	3265783	8	2426	2.53E-10
Chr4	3267773	3269189	4	1417	4.55E-07
Chr4	3270403	3273247	9	2845	3.38E-10
Chr4	3276605	3279487	10	2883	1.17E-09
Chr4	3286520	3287367	5	848	1.83E-08
Chr4	3288841	3290484	6	1644	1.06E-09
Chr4	3304227	3305389	5	1163	3.92E-07
Chr4	3313057	3313847	4	791	1.54256E-05
Chr4	3317248	3318553	4	1306	1.47E-09
Chr4	3321433	3322852	6	1420	1.98E-07
Chr4	3339899	3341761	5	1863	1.09073E-06
Chr4	3347784	3350422	5	2639	1.41E-08
Chr4	3352644	3354119	4	1476	1.24E-08
Chr4	3399859	3402706	8	2848	1.86E-09
Chr4	3403848	3404994	4	1147	8.69185E-06
Chr4	3432957	3434860	5	1904	6.91E-09
Chr4	3456833	3457641	4	809	1.70E-07
Chr4	3458707	3461716	7	3010	6.79E-10
Chr4	3464160	3465459	6	1300	1.00E-09
Chr4	3477407	3479064	4	1658	2.2518E-05
Chr4	3486603	3489690	7	3088	1.84E-12
Chr4	3490721	3493321	10	2601	7.31E-13
Chr4	3494993	3497061	11	2069	7.04E-14
Chr4	3499859	3502295	8	2437	5.97E-09
Chr4	3504310	3506077	5	1768	2.94E-09
Chr4	3540689	3543520	13	2832	1.82E-18
Chr4	3544581	3548025	15	3445	1.73E-14
Chr4	3550923	3552289	6	1367	2.37E-08
Chr4	3556089	3558779	11	2691	1.27E-13
Chr4	3567867	3569724	4	1858	6.32E-07
Chr4	3573873	3575458	8	1586	2.91E-09
Chr4	3584089	3588730	12	4642	1.30E-11
Chr4	3591155	3593463	9	2309	9.69E-12
Chr4	3595173	3597045	6	1873	6.47E-09
Chr4	3603067	3606061	7	2995	6.11E-09
Chr4	3618995	3620791	5	1797	1.14E-09
Chr4	3624294	3625419	5	1126	1.81E-08
Chr4	3628548	3632354	15	3807	3.74E-15
Chr4	3676151	3679112	11	2962	1.36E-13
Chr4	3680446	3682524	7	2079	1.14E-07
Chr4	3683533	3685119	4	1587	3.47949E-06
Chr4	3686628	3688089	5	1462	1.68E-07
Chr4	3697180	3697977	6	798	3.50E-09
Chr4	3706742	3707994	7	1253	5.66E-09
Chr4	3716528	3718483	5	1956	1.46536E-05
Chr4	3723343	3724599	4	1257	1.33664E-05
Chr4	3728568	3729493	4	926	3.40E-07
Chr4	3736257	3737094	7	838	5.12E-10

Chr4	3742535	3745386	8	2852	5.65E-11
Chr4	3786425	3793354	23	6930	3.87E-29
Chr4	3814816	3815970	4	1155	2.8125E-06
Chr4	3820205	3821721	4	1517	3.0983E-06
Chr4	3825391	3826188	4	798	5.43606E-06
Chr4	3838832	3840751	6	1920	1.39E-07
Chr4	3844289	3845036	5	748	5.33E-08
Chr4	3847858	3850845	12	2988	6.11E-12
Chr4	3858790	3859882	4	1093	7.32E-08
Chr4	3864486	3865862	7	1377	1.04E-09
Chr4	3871897	3872106	6	210	3.44E-08
Chr4	3873533	3875138	4	1606	6.33337E-06
Chr4	3881382	3882518	5	1137	5.38E-11
Chr4	3906722	3908431	7	1710	5.12E-10
Chr4	3911585	3912983	5	1399	3.67974E-07
Chr4	3915204	3917428	11	2225	1.16E-16
Chr4	3921772	3922988	4	1217	3.73611E-05
Chr4	3925084	3928115	8	3032	6.79E-11
Chr4	3933819	3934803	5	985	1.83E-07
Chr4	3936205	3938712	4	2508	7.14983E-05
Chr4	3941634	3942761	4	1128	0.000234486
Chr4	3946968	3948232	6	1265	1.79E-10
Chr4	3950508	3955923	368	5416	0
Chr4	3959213	3966793	79	7581	1.04E-74
Chr4	3967943	3969327	20	1385	3.90E-24
Chr4	3973432	3975031	7	1600	1.43E-07
Chr4	3977492	3980545	52	3054	3.30E-50
Chr4	3982483	3983676	8	1194	2.17972E-07
Chr4	3987312	3987767	7	456	3.68E-07
Chr4	3994140	3996301	25	2162	4.42E-30
Chr4	3999872	4000727	7	856	1.66E-08
Chr4	4002028	4002250	11	223	4.45E-16
Chr4	4003847	4004200	6	354	1.57206E-06
Chr4	4005670	4007377	25	1708	8.00E-16
Chr4	4008775	4011630	35	2856	5.64E-28
Chr4	4018867	4019878	4	1012	6.41601E-07
Chr4	4023756	4025958	5	2203	8.73E-08
Chr4	4034012	4037571	13	3560	1.77E-13
Chr4	4045396	4047296	9	1901	1.02E-11
Chr4	4062384	4063056	6	673	6.13E-09
Chr4	4065504	4069079	11	3576	1.22E-21
Chr4	4110262	4112149	5	1888	7.82E-08
Chr4	4160302	4161929	4	1628	2.55309E-05
Chr4	4180605	4183670	8	3066	1.30E-09
Chr4	4214910	4216620	5	1711	1.46E-07
Chr4	4239790	4243332	16	3543	9.54E-16
Chr4	4244757	4246056	6	1300	4.68E-08
Chr4	4249137	4249821	5	685	1.29971E-06
Chr4	4257365	4260311	6	2947	9.04E-11
Chr4	4268939	4270988	8	2050	4.28E-10
Chr4	4274037	4277437	12	3401	1.58E-18
Chr4	4278597	4280956	7	2360	1.46E-09
Chr4	4282321	4284497	7	2177	2.37E-08
Chr4	4288105	4289130	7	1026	2.90E-12
Chr4	4300666	4303000	6	2335	1.04E-12
Chr4	4304645	4307213	12	2569	2.05E-16
Chr4	4337340	4338928	4	1589	0.001196851
Chr4	4354305	4356584	4	2280	4.9015E-06
Chr4	4360897	4366139	16	5243	2.27E-16
Chr4	4371250	4373137	6	1888	1.42E-10
Chr4	4383250	4387154	11	3905	1.78E-11
Chr4	4390069	4391494	4	1426	0.001067544
Chr4	4392712	4393843	8	1132	9.95E-10

Chr4	4402205	4403679	5	1475	1.81988E-06
Chr4	4406979	4407853	5	875	1.57E-07
Chr4	4409085	4411507	12	2423	2.59E-15
Chr4	4418319	4419371	5	1053	1.10232E-06
Chr4	4422840	4428033	9	5194	6.77E-13
Chr4	4477882	4479267	4	1386	2.95226E-05
Chr4	4487608	4488117	6	510	3.00E-09
Chr4	4511530	4513136	7	1607	2.38E-09
Chr4	4515380	4516365	6	986	3.80E-09
Chr4	4521785	4523598	4	1814	0.002877655
Chr4	4540590	4543471	10	2882	1.79E-12
Chr4	4552319	4556632	17	4314	6.29E-21
Chr4	4560330	4562547	11	2218	4.11E-13
Chr4	4568758	4569823	6	1066	6.23E-08
Chr4	4600811	4603311	10	2501	7.99E-13
Chr4	4651978	4654758	6	2781	5.24E-11
Chr4	4678241	4682703	12	4463	4.61E-15
Chr4	4708801	4710701	5	1901	6.266E-06
Chr4	4717689	4718668	4	980	1.81514E-05
Chr4	4722784	4727411	16	4628	1.79E-17
Chr4	4735322	4737268	6	1947	7.20E-07
Chr4	4742843	4745992	9	3150	6.57E-09
Chr4	4760313	4761369	10	1057	1.52E-16
Chr4	4762603	4764872	13	2270	1.75E-14
Chr4	4774343	4775107	5	765	2.81E-07
Chr4	4776421	4781354	19	4934	3.25E-18
Chr4	4831742	4832974	4	1233	8.1797E-06
Chr4	4855855	4856792	5	938	1.26964E-05
Chr4	4858244	4859252	4	1009	6.09534E-05
Chr4	4894999	4897578	5	2580	4.54E-08
Chr4	4946040	4947031	5	992	7.1544E-06
Chr4	4962618	4964861	9	2244	2.61E-13
Chr4	4987675	4989522	8	1848	4.34E-11
Chr4	5003657	5003748	4	92	6.77E-07
Chr4	5007717	5011199	10	3483	1.33E-14
Chr4	5016499	5018370	7	1872	5.60E-11
Chr4	5021603	5022358	4	756	5.9905E-05
Chr4	5039810	5041297	5	1488	7.54111E-06
Chr4	5044158	5048882	15	4725	5.49E-18
Chr4	5049892	5051200	4	1309	2.74E-07
Chr4	5053626	5056569	7	2944	1.04004E-05
Chr4	5062237	5063534	7	1298	3.32E-10
Chr4	5064698	5065563	4	866	4.37147E-05
Chr4	5067897	5071289	12	3393	6.66E-12
Chr4	5074528	5077575	14	3048	6.27E-18
Chr4	5083475	5083832	4	358	5.20765E-06
Chr4	5098223	5102962	9	4740	3.79E-14
Chr4	5107315	5108078	4	764	3.73428E-06
Chr4	5126823	5127790	4	968	9.54386E-06
Chr4	5128893	5131606	8	2714	1.38E-09
Chr4	5303637	5307176	9	3540	6.77E-13
Chr4	5335019	5335880	4	862	1.99548E-06
Chr4	5347981	5350477	8	2497	4.03E-13
Chr4	5399067	5401742	8	2676	2.08E-11
Chr4	5487782	5490277	7	2496	9.66E-09
Chr4	5493314	5493639	4	326	8.97881E-05
Chr4	5520877	5522536	9	1660	3.07E-11
Chr4	5527789	5529025	4	1237	2.99E-07
Chr4	5573184	5573425	4	242	2.92E-07
Chr4	5584088	5585409	6	1322	2.63E-07
Chr4	5595681	5596189	4	509	3.64E-07
Chr4	5697727	5697837	4	111	3.51658E-06
Chr4	5767537	5769034	4	1498	4.78815E-06

Chr4	5821522	5825295	11	3774	4.06E-10
Chr4	5826474	5827120	4	647	5.29083E-06
Chr4	5939681	5941110	6	1430	3.98E-09
Chr4	5946628	5946764	4	137	4.46616E-06
Chr4	5966717	5968057	6	1341	1.61E-08
Chr4	6014748	6015356	4	609	3.07E-07
Chr4	6468286	6468972	4	687	3.23259E-05
Chr4	6470912	6472891	5	1980	4.13064E-06
Chr4	6533842	6534520	4	679	6.13E-07
Chr4	6724209	6724947	4	739	0.000270524
Chr4	6727605	6728487	5	883	9.85E-09
Chr4	6918560	6919249	6	690	2.71E-12
Chr4	7357289	7358913	4	1625	0.000486599
Chr4	7525927	7526431	4	505	6.27207E-06
Chr4	8317590	8319642	8	2053	2.43E-11
Chr4	8903639	8904140	4	502	7.60E-10
Chr4	9069240	9070418	4	1179	3.7431E-06
Chr4	9486162	9488257	5	2096	9.63E-09
Chr4	9489408	9491543	4	2136	5.87255E-07
Chr4	9511364	9513423	5	2060	3.76E-07
Chr4	9732710	9733983	6	1274	5.14E-07
Chr4	9909366	9909768	4	403	1.63E-07
Chr4	10036864	10037804	4	941	1.81912E-06
Chr4	10544476	10545571	4	1096	4.92926E-05
Chr4	10993951	10996711	12	2761	4.18E-17
Chr4	11040074	11041188	4	1115	8.30256E-06
Chr4	11091416	11093331	7	1916	2.18E-11
Chr4	11137610	11139223	5	1614	9.07E-09
Chr4	11415889	11416112	4	224	1.16616E-06
Chr4	11822550	11823162	4	613	8.79818E-05
Chr4	11836903	11838285	9	1383	1.21E-13
Chr4	11845061	11846309	4	1249	4.69318E-06
Chr4	13329783	13331843	8	2061	9.78E-10
Chr4	13628323	13631492	12	3170	1.95E-15
Chr4	14787621	14787956	4	336	2.99E-08
Chr4	16081712	16082380	4	669	3.92222E-06
Chr4	17664070	17664176	4	107	5.84716E-06
Chr4	17713016	17714670	6	1655	3.80E-08
Chr4	17715863	17716954	4	1092	8.88508E-06
Chr5	65136	69114	19	3979	6.53E-15
Chr5	743930	744733	4	804	3.34465E-06
Chr5	2106298	2107666	4	1369	6.9487E-05
Chr5	2260865	2262238	5	1374	0.002236739
Chr5	2347215	2348190	5	976	5.42E-10
Chr5	2391925	2394972	9	3048	2.33E-12
Chr5	2442626	2443233	7	608	6.61479E-06
Chr5	3253146	3253245	16	100	4.12E-25
Chr5	3904877	3905560	7	684	1.96E-08
Chr5	3908197	3910412	4	2216	3.73455E-05
Chr5	4321082	4322082	5	1001	1.56E-07
Chr5	4324350	4325576	7	1227	5.68753E-07
Chr5	5112193	5113519	5	1327	1.29465E-06
Chr5	5217538	5220188	9	2651	1.06E-10
Chr5	5644119	5645788	7	1670	4.58E-10
Chr5	6207035	6208380	4	1346	2.00832E-05
Chr5	6211487	6212321	4	835	4.13508E-05
Chr5	6349307	6350245	4	939	1.4837E-06
Chr5	6406923	6407725	4	803	3.36015E-05
Chr5	6632180	6633226	5	1047	1.03497E-06
Chr5	7027938	7030231	7	2294	6.74E-09
Chr5	7031761	7032972	5	1212	1.78236E-05
Chr5	7036699	7037005	5	307	9.38E-09
Chr5	7412854	7412907	4	54	9.92207E-06

Chr5	7414910	7416040	5	1131	1.13E-10
Chr5	7824202	7824516	6	315	2.90E-07
Chr5	8292916	8293257	4	342	3.88E-12
Chr5	8549786	8550509	6	724	2.11E-09
Chr5	8572162	8574440	8	2279	2.23E-11
Chr5	8613927	8614577	4	651	1.48042E-06
Chr5	8666437	8667114	6	678	8.46E-09
Chr5	8721664	8723250	6	1587	7.70E-11
Chr5	8919038	8919100	4	63	6.76E-07
Chr5	9091486	9093336	5	1851	6.07E-09
Chr5	9184876	9185647	5	772	1.79E-09
Chr5	9186777	9188373	8	1597	5.95E-09
Chr5	9251639	9253330	4	1692	3.15515E-05
Chr5	9561474	9565132	9	3659	7.49E-15
Chr5	9567518	9568250	7	733	2.30E-12
Chr5	9710806	9711799	4	994	0.000121974
Chr5	9906775	9909493	10	2719	3.29E-10
Chr5	9925169	9928595	18	3427	2.70E-20
Chr5	9949546	9952725	12	3180	1.52E-19
Chr5	9979037	9980012	5	976	3.55E-07
Chr5	9981558	9982543	4	986	9.25608E-06
Chr5	9996993	9998258	4	1266	0.000150948
Chr5	10051295	10053664	8	2370	5.06E-10
Chr5	10054912	10056251	5	1340	2.87E-08
Chr5	10095891	10099603	8	3713	3.18E-12
Chr5	10103829	10106598	10	2770	1.06E-14
Chr5	10139930	10141550	5	1621	5.85E-08
Chr5	10170566	10171775	4	1210	0.000146865
Chr5	10359820	10363210	9	3391	6.21E-12
Chr5	10367403	10368350	5	948	3.17E-10
Chr5	10463841	10464128	4	288	4.03016E-06
Chr5	10497654	10498616	4	963	3.48352E-05
Chr5	10573309	10575559	5	2251	2.04235E-05
Chr5	10577110	10578062	5	953	1.32E-07
Chr5	10579783	10580801	4	1019	9.57301E-06
Chr5	10582872	10584764	8	1893	3.14E-10
Chr5	10591472	10595971	12	4500	2.63E-15
Chr5	10626413	10627108	5	696	1.22E-09
Chr5	10632847	10632943	4	97	5.28E-07
Chr5	10725080	10726764	4	1685	6.30017E-06
Chr5	10728248	10729912	7	1665	1.86E-08
Chr5	10730932	10733249	9	2318	1.51E-12
Chr5	10743623	10745579	6	1957	2.99E-09
Chr5	10756183	10756797	4	615	8.24109E-06
Chr5	10767764	10769713	6	1950	1.39449E-06
Chr5	10795491	10795729	4	239	3.54004E-05
Chr5	10888358	10888907	4	550	2.08E-08
Chr5	10890270	10890512	4	243	2.33469E-06
Chr5	10942101	10943200	4	1100	1.56E-09
Chr5	10948455	10949554	6	1100	1.82E-09
Chr5	10974438	10975829	4	1392	3.94E-07
Chr5	11037810	11039673	4	1864	0.002704158
Chr5	11079058	11081661	9	2604	1.12E-10
Chr5	11089718	11092353	10	2636	1.97E-13
Chr5	11099287	11101491	7	2205	1.89E-09
Chr5	11105001	11109398	10	4398	3.69E-13
Chr5	11110710	11114819	12	4110	1.05E-15
Chr5	11127756	11129608	5	1853	1.37E-08
Chr5	11156506	11159128	5	2623	3.45148E-06
Chr5	11161268	11163144	5	1877	7.11E-08
Chr5	11169981	11170617	4	637	2.832E-06
Chr5	11178756	11182322	31	3567	5.46E-35
Chr5	11184651	11188882	182	4232	2.33E-198

Chr5	11194946	11198591	10	3646	3.49E-14
Chr5	11206996	11209509	9	2514	4.19E-12
Chr5	11214848	11217535	10	2688	1.05E-11
Chr5	11223797	11224837	5	1041	3.63574E-07
Chr5	11315891	11318613	6	2723	1.76E-08
Chr5	11324436	11325292	4	857	1.35754E-05
Chr5	11327363	11328762	11	1400	6.42E-09
Chr5	11335731	11337159	4	1429	0.000211989
Chr5	11338236	11339616	5	1381	1.48E-08
Chr5	11343146	11347168	12	4023	1.32E-12
Chr5	11348493	11352954	12	4462	4.49E-10
Chr5	11364986	11366356	6	1371	6.39E-09
Chr5	11369529	11370610	7	1082	2.09E-10
Chr5	11390943	11392579	6	1637	3.49E-07
Chr5	11393698	11395979	7	2282	2.76E-09
Chr5	11397962	11400251	8	2290	1.14E-09
Chr5	11408625	11412188	8	3564	9.94E-11
Chr5	11413691	11415596	4	1906	2.5517E-06
Chr5	11422233	11423751	6	1519	1.04E-09
Chr5	11430161	11433271	13	3111	1.45E-16
Chr5	11434897	11437609	9	2713	1.61E-12
Chr5	11439139	11440946	6	1808	6.12E-10
Chr5	11448822	11450433	4	1612	7.62E-08
Chr5	11453150	11456164	12	3015	5.79E-14
Chr5	11466143	11467286	5	1144	1.13E-08
Chr5	11474673	11478653	12	3981	2.70E-17
Chr5	11484593	11485337	5	745	1.73E-07
Chr5	11505625	11509205	10	3581	5.03E-12
Chr5	11510246	11511300	5	1055	1.25E-07
Chr5	11518485	11519714	4	1230	1.06351E-06
Chr5	11529641	11536341	18	6701	3.79E-17
Chr5	11578538	11580543	15	2006	6.58E-21
Chr5	11581650	11582946	5	1297	2.66E-07
Chr5	11585668	11586965	5	1298	2.74E-07
Chr5	11590446	11592299	7	1854	6.65E-11
Chr5	11593317	11594544	8	1228	5.00E-09
Chr5	11601721	11604066	8	2346	2.02E-07
Chr5	11626131	11628953	11	2823	2.77E-13
Chr5	11632950	11634314	4	1365	5.40291E-06
Chr5	11642419	11644804	8	2386	2.82E-08
Chr5	11645898	11646982	5	1085	4.98E-08
Chr5	11649339	11650324	5	986	1.42895E-06
Chr5	11651356	11652774	7	1419	1.18E-12
Chr5	11656742	11658089	5	1348	7.11E-10
Chr5	11660352	11661636	4	1285	2.84766E-06
Chr5	11667471	11668184	9	714	1.53E-15
Chr5	11690117	11690960	11	844	1.84E-10
Chr5	11693775	11695296	5	1522	1.03971E-05
Chr5	11697788	11698397	5	610	3.26E-07
Chr5	11701557	11705627	78	4071	2.04E-82
Chr5	11706790	11710957	32	4168	7.20E-28
Chr5	11722873	11724699	48	1827	6.83E-36
Chr5	11726080	11738205	242	12126	1.08E-260
Chr5	11741713	11743740	6	2028	6.61E-09
Chr5	11747420	11752187	14	4768	2.11E-16
Chr5	11754352	11754866	4	515	0.000104716
Chr5	11766281	11769368	8	3088	4.75E-10
Chr5	11771075	11773039	6	1965	2.66E-11
Chr5	11775546	11779062	12	3517	2.35E-15
Chr5	11782806	11784963	7	2158	5.47E-08
Chr5	11788568	11789252	12	685	7.21E-22
Chr5	11795337	11796905	12	1569	9.05E-20
Chr5	11798119	11799356	9	1238	3.36E-08

Chr5	11806578	11810180	11	3603	1.09E-15
Chr5	11813810	11815238	6	1429	6.08E-10
Chr5	11822758	11825086	7	2329	8.67E-11
Chr5	11830916	11831148	8	233	5.97E-11
Chr5	11832353	11836261	13	3909	7.86E-16
Chr5	11837571	11838164	5	594	9.00131E-06
Chr5	11842107	11844841	19	2735	3.29E-18
Chr5	11846457	11848832	7	2376	7.71E-11
Chr5	11906764	11911203	9	4440	6.67E-11
Chr5	11912482	11914372	8	1891	4.79E-11
Chr5	11915684	11918152	9	2469	1.40E-12
Chr5	11920377	11925945	16	5569	1.08E-17
Chr5	11935228	11944611	112	9384	1.04E-91
Chr5	11962892	11964777	6	1886	1.26E-09
Chr5	11976843	11977959	8	1117	5.20E-14
Chr5	11985453	11991161	41	5709	2.02E-35
Chr5	11997663	12003520	13	5858	2.65E-18
Chr5	12010414	12012043	4	1630	3.42521E-05
Chr5	12016528	12017867	7	1340	2.00E-10
Chr5	12025861	12032244	15	6384	8.26E-11
Chr5	12034345	12035782	8	1438	6.72E-12
Chr5	12039798	12041776	10	1979	5.19E-11
Chr5	12046484	12048241	4	1758	8.09E-10
Chr5	12049273	12053802	11	4530	3.60E-15
Chr5	12062578	12065117	9	2540	5.27E-08
Chr5	12066190	12067442	4	1253	7.51E-07
Chr5	12071950	12073929	4	1980	0.000487245
Chr5	12096526	12098604	7	2079	9.86E-07
Chr5	12099657	12100705	5	1049	0.000178767
Chr5	12106150	12108786	14	2637	6.69E-16
Chr5	12109955	12111942	6	1988	2.02E-08
Chr5	12116623	12117689	5	1067	9.27E-08
Chr5	12122768	12123203	4	436	8.34E-07
Chr5	12124711	12125423	6	713	5.77909E-06
Chr5	12128317	12129415	4	1099	1.30837E-06
Chr5	12136766	12138891	6	2126	3.77E-09
Chr5	12141392	12146637	14	5246	2.17E-20
Chr5	12147706	12151688	11	3983	1.43E-15
Chr5	12153496	12155804	5	2309	9.49E-08
Chr5	12159601	12162957	12	3357	4.45E-18
Chr5	12165808	12167515	8	1708	3.11E-09
Chr5	12173788	12175911	8	2124	1.57351E-06
Chr5	12177421	12178269	4	849	1.36926E-05
Chr5	12184833	12186239	4	1407	2.75131E-06
Chr5	12194555	12196690	6	2136	1.58206E-06
Chr5	12204558	12205003	4	446	7.11E-07
Chr5	12206281	12207426	5	1146	1.54826E-06
Chr5	12214928	12217220	11	2293	1.58E-10
Chr5	12234270	12234819	6	550	2.53E-09
Chr5	12237580	12239048	4	1469	3.05428E-06
Chr5	12242911	12244743	6	1833	2.96283E-06
Chr5	12245854	12249106	9	3253	1.07E-09
Chr5	12265585	12267513	6	1929	1.93E-09
Chr5	12269782	12271504	5	1723	3.65E-07
Chr5	12287938	12291279	12	3342	1.80E-11
Chr5	12292893	12293870	4	978	3.22087E-06
Chr5	12296319	12297306	4	988	5.47E-08
Chr5	12298711	12299299	7	589	1.52E-11
Chr5	12328175	12328821	4	647	0.001213519
Chr5	12341545	12342259	5	715	2.76E-09
Chr5	12343704	12345462	7	1759	1.29E-10
Chr5	12347147	12349733	18	2587	6.14E-24
Chr5	12367327	12369884	6	2558	1.51E-07

Chr5	12382449	12383214	4	766	4.67E-08
Chr5	12387351	12388388	4	1038	3.64447E-05
Chr5	12396797	12400409	11	3613	5.60E-12
Chr5	12410089	12410926	5	838	8.66327E-06
Chr5	12428199	12431962	20	3764	5.03E-23
Chr5	12456030	12456854	4	825	2.96E-08
Chr5	12458055	12459718	5	1664	2.90859E-06
Chr5	12468712	12471081	8	2370	1.51E-08
Chr5	12517506	12518131	4	626	1.36885E-05
Chr5	12520186	12520816	5	631	7.97E-07
Chr5	12527233	12529285	7	2053	7.93E-11
Chr5	12533731	12535587	8	1857	4.05E-11
Chr5	12571191	12576500	15	5310	3.77E-20
Chr5	12579907	12581398	4	1492	8.75629E-07
Chr5	12609753	12611088	4	1336	7.54E-07
Chr5	12612532	12613835	9	1304	3.58E-10
Chr5	12625832	12630263	13	4432	1.83E-13
Chr5	12631412	12633409	9	1998	1.57E-12
Chr5	12637640	12638635	4	996	3.6528E-06
Chr5	12646765	12647385	4	621	5.5211E-06
Chr5	12649310	12650752	4	1443	2.59545E-06
Chr5	12712468	12714451	5	1984	0.000169071
Chr5	12715509	12715875	4	367	1.29229E-05
Chr5	12737164	12738869	6	1706	2.29436E-06
Chr5	12745992	12748825	13	2834	3.33E-17
Chr5	12752765	12753949	5	1185	2.23152E-06
Chr5	12756229	12764500	25	8272	9.77E-31
Chr5	12767268	12768849	6	1582	2.39E-09
Chr5	12771442	12773565	4	2124	2.77499E-06
Chr5	12774751	12776738	5	1988	6.46932E-05
Chr5	12792793	12794649	6	1857	1.98E-07
Chr5	12810870	12811099	16	230	3.55E-19
Chr5	12920451	12922010	5	1560	2.80471E-06
Chr5	12927908	12930238	6	2331	1.30414E-06
Chr5	12936579	12939031	4	2453	3.24597E-06
Chr5	12945984	12948278	5	2295	6.21E-07
Chr5	12949514	12950851	7	1338	2.95E-07
Chr5	12972723	12976007	8	3285	1.98E-12
Chr5	12985114	12986992	5	1879	1.32E-08
Chr5	12992344	12994136	8	1793	8.24E-12
Chr5	13000225	13001384	6	1160	1.75E-10
Chr5	13011100	13013710	7	2611	1.56E-09
Chr5	13017771	13019627	6	1857	7.02E-09
Chr5	13022478	13026368	13	3891	8.22E-18
Chr5	13032944	13035546	7	2603	6.81E-12
Chr5	13070684	13072059	4	1376	5.72E-07
Chr5	13073153	13074872	5	1720	2.46E-07
Chr5	13120136	13121561	7	1426	1.38E-10
Chr5	13128223	13133053	14	4831	1.69E-16
Chr5	13144563	13145269	5	707	9.60E-07
Chr5	13147942	13149724	6	1783	1.52E-07
Chr5	13163225	13165950	8	2726	2.29E-09
Chr5	13167275	13168132	5	858	7.31E-07
Chr5	13171558	13173488	6	1931	1.21E-07
Chr5	13185604	13186519	4	916	5.40E-07
Chr5	13229240	13230244	5	1005	6.23969E-05
Chr5	13254040	13254752	4	713	3.38646E-05
Chr5	13257176	13257949	4	774	1.24E-07
Chr5	13262487	13263740	4	1254	0.000161638
Chr5	13282420	13283118	5	699	2.35E-07
Chr5	13287372	13289170	4	1799	9.10011E-06
Chr5	13290494	13293792	9	3299	1.34E-08
Chr5	13302432	13303582	5	1151	2.5199E-06

Chr5	13320867	13321975	4	1109	1.70522E-05
Chr5	13326017	13328720	12	2704	2.35E-12
Chr5	13335957	13336791	4	835	1.27958E-05
Chr5	13377368	13378930	5	1563	1.62712E-05
Chr5	13381403	13382930	6	1528	5.25E-07
Chr5	13396454	13397966	7	1513	7.93E-11
Chr5	13404749	13410064	19	5316	2.38E-25
Chr5	13528546	13530220	5	1675	1.47E-09
Chr5	13536761	13538306	7	1546	5.00E-08
Chr5	13641620	13642289	4	670	1.29E-07
Chr5	13656642	13657008	4	367	9.66388E-06
Chr5	13717819	13718661	7	843	5.10E-12
Chr5	13782761	13784101	4	1341	3.88497E-05
Chr5	13835401	13837256	4	1856	0.000119275
Chr5	13845912	13848259	7	2348	4.77E-09
Chr5	13887325	13888901	5	1577	9.74E-07
Chr5	13925910	13926241	4	332	2.10628E-06
Chr5	13998883	13999263	4	381	1.52027E-06
Chr5	14200247	14200816	4	570	1.50326E-06
Chr5	14204309	14206338	4	2030	1.87948E-06
Chr5	14256520	14257914	9	1395	4.78E-14
Chr5	14259868	14261190	4	1323	6.57228E-06
Chr5	14270413	14272576	5	2164	4.44743E-08
Chr5	14577588	14578659	4	1072	4.5922E-05
Chr5	14678272	14681092	8	2821	3.09E-09
Chr5	14831562	14832753	4	1192	2.18022E-05
Chr5	14834085	14834124	4	40	7.05E-08
Chr5	15101615	15101886	6	272	2.30E-08
Chr5	15234575	15236881	5	2307	1.07619E-05
Chr5	15353026	15354533	5	1508	1.80E-07
Chr5	15357040	15358235	5	1196	2.40E-08
Chr5	15360143	15361057	5	915	2.20E-09
Chr5	15493492	15498216	19	4725	1.41E-22
Chr5	15646283	15648855	8	2573	7.13E-14
Chr5	15720542	15721372	5	831	1.31E-07
Chr5	15919179	15919703	4	525	5.28172E-05
Chr5	15924655	15926750	6	2096	1.21717E-06
Chr5	16700397	16701580	5	1184	4.71795E-07
Chr5	16703194	16705769	8	2576	2.18E-08
Chr5	17085751	17086476	4	726	9.45701E-05
Chr5	17253156	17254556	6	1401	2.66E-07
Chr5	17305056	17306134	4	1079	6.88399E-06
Chr5	17441015	17444846	13	3832	4.67E-16
Chr5	17597753	17599446	5	1694	4.83E-07
Chr5	17602128	17604547	6	2420	7.07E-08
Chr5	17740306	17742520	4	2215	1.18E-08
Chr5	17890139	17890530	5	392	5.11E-08
Chr5	18171382	18171600	4	219	2.24E-07
Chr5	18195233	18197152	5	1920	1.39E-08
Chr5	18473360	18474706	7	1347	3.14E-09
Chr5	18476018	18477651	6	1634	1.90E-08
Chr5	18480116	18480685	6	570	1.77E-09
Chr5	18493272	18495197	8	1926	5.87E-11
Chr5	19189395	19193340	7	3946	1.28E-10
Chr5	19358620	19364537	18	5918	8.19E-23
Chr5	20048435	20048702	4	268	2.13E-07
Chr5	20209083	20209274	4	192	9.41E-07
Chr5	20426819	20427468	8	650	1.72E-12
Chr5	21544616	21545607	4	992	1.15357E-05
Chr5	21689891	21690668	5	778	3.18665E-06
Chr5	22616970	22618241	5	1272	7.17933E-07
Chr5	24966579	24966594	4	16	7.97E-07

-Pit Root 16 dat (Hypo-DMRs)

Chromosome	Start	End	number of DMCs	DMR lenght	P-value
Chr1	2415419	2415896	4	478	3.72E-08
Chr1	7070852	7073346	4	2495	6.12149E-06
Chr1	7355539	7356850	4	1312	2.87179E-06
Chr1	7362422	7362813	5	392	7.79873E-06
Chr1	9577875	9578816	4	942	9.37E-07
Chr1	9685190	9687048	5	1859	2.97475E-05
Chr1	9689322	9691202	5	1881	0.000155207
Chr1	10361729	10362786	4	1058	6.68571E-05
Chr1	11065062	11066277	4	1216	1.6224E-05
Chr1	11508359	11510057	7	1699	2.65E-10
Chr1	12669255	12671187	5	1933	3.9457E-06
Chr1	13010666	13012451	5	1786	1.54E-07
Chr1	13336520	13339605	8	3086	1.13E-07
Chr1	13394355	13395249	6	895	6.92E-10
Chr1	13560278	13561414	4	1137	4.78129E-05
Chr1	13722287	13723172	5	886	7.73441E-06
Chr1	13796186	13798872	6	2687	3.35E-10
Chr1	13884075	13884921	4	847	2.81282E-05
Chr1	13923240	13924806	4	1567	9.73776E-06
Chr1	14083855	14084967	4	1113	7.63E-08
Chr1	14086457	14087861	4	1405	6.58E-07
Chr1	14089998	14091503	6	1506	5.32E-07
Chr1	14196988	14197775	4	788	3.3682E-05
Chr1	14201295	14202801	4	1507	7.30248E-06
Chr1	14218829	14220426	5	1598	1.25E-07
Chr1	14316542	14318876	6	2335	8.20E-07
Chr1	14325421	14326526	4	1106	3.49674E-06
Chr1	14475910	14476920	4	1011	1.29342E-06
Chr1	14497405	14498425	4	1021	1.55549E-06
Chr1	14582615	14582876	5	262	4.27E-07
Chr1	15493134	15495521	5	2388	3.32E-07
Chr1	15496830	15499997	8	3168	9.41E-10
Chr1	15517201	15519431	6	2231	2.61E-11
Chr1	15542721	15544765	4	2045	4.58252E-06
Chr1	15555533	15557634	5	2102	9.08E-07
Chr1	15567330	15569702	5	2373	6.09621E-06
Chr1	15709806	15711345	4	1540	0.000112894
Chr1	15801640	15803459	4	1820	2.09751E-06
Chr1	15996346	15996357	4	12	9.66E-07
Chr1	16016949	16018252	4	1304	1.75221E-05
Chr1	16046683	16048579	7	1897	8.58E-10
Chr1	16382348	16385159	4	2812	6.92814E-05
Chr1	16521839	16522813	4	975	4.84655E-06
Chr1	16530773	16531553	4	781	3.17709E-05
Chr1	16627076	16628880	6	1805	5.46E-09
Chr1	16633299	16635547	9	2249	2.75E-11
Chr1	18969556	18970861	4	1306	5.81107E-06
Chr1	19344695	19345539	4	845	3.21875E-05
Chr1	20089621	20090508	6	888	5.27205E-06
Chr1	21369215	21369424	4	210	1.62779E-05
Chr1	22102764	22104457	5	1694	0.000115054
Chr1	23358207	23359811	4	1605	1.80658E-06
Chr1	23568588	23569292	4	705	3.07045E-05
Chr1	24457216	24457562	4	347	0.000382234
Chr1	26368164	26369857	5	1694	3.23E-10
Chr1	29476498	29477730	4	1233	8.66096E-05
Chr2	1451	3445	16	1995	2.54E-13
Chr2	9696	10305	10	610	1.77E-20
Chr2	376154	376700	4	547	9.07236E-06
Chr2	821157	822296	4	1140	8.34337E-06

Chr2	1403239	1404077	4	839	2.44023E-06
Chr2	1760837	1761941	4	1105	3.79027E-06
Chr2	2506613	2507292	4	680	1.63E-08
Chr2	2508312	2511215	5	2904	4.07E-08
Chr2	2576106	2576260	4	155	8.38E-07
Chr2	2683751	2684575	4	825	4.04771E-06
Chr2	2804785	2807166	6	2382	4.25298E-06
Chr2	2813085	2815214	5	2130	4.71E-08
Chr2	2932509	2934385	4	1877	1.22832E-05
Chr2	3232462	3233337	4	876	5.61656E-05
Chr2	3269270	3269284	4	15	2.73E-09
Chr2	3294675	3296407	9	1733	1.09E-10
Chr2	3299704	3300764	4	1061	9.62121E-05
Chr2	3313177	3315389	7	2213	5.81E-07
Chr2	3319030	3321462	7	2433	1.08E-09
Chr2	3339993	3341120	6	1128	3.50911E-06
Chr2	3350957	3352758	7	1802	4.46E-09
Chr2	3395112	3395163	4	52	8.30315E-06
Chr2	3396470	3397102	6	633	1.03E-08
Chr2	3464517	3465573	4	1057	9.44406E-06
Chr2	4229280	4230936	4	1657	5.10E-10
Chr2	4280870	4281432	4	563	1.53731E-06
Chr2	4463313	4463430	4	118	6.21E-07
Chr2	4491690	4493286	8	1597	8.08E-14
Chr2	4711522	4712111	5	590	1.06E-08
Chr2	4850571	4851990	4	1420	0.000168712
Chr2	4903309	4904446	4	1138	4.32389E-06
Chr2	4980466	4981107	4	642	2.92707E-06
Chr2	4983852	4983931	4	80	6.86383E-06
Chr2	5121928	5124459	4	2532	5.26924E-05
Chr2	5128129	5130036	7	1908	7.30E-09
Chr2	5134819	5136151	4	1333	3.22792E-06
Chr2	5286986	5288772	5	1787	1.07E-07
Chr2	5328871	5330166	4	1296	8.54771E-06
Chr2	5365861	5368200	7	2340	1.29E-07
Chr2	5375883	5377910	8	2028	1.81E-10
Chr2	5560760	5561797	4	1038	5.03E-07
Chr2	5621786	5622643	4	858	0.000286249
Chr2	5628072	5629733	4	1662	5.81765E-05
Chr2	5880606	5882398	5	1793	7.91494E-06
Chr2	5984217	5985968	4	1752	0.000150758
Chr2	6112803	6112871	4	69	3.34E-08
Chr2	6334459	6335573	4	1115	6.23405E-06
Chr2	6552301	6553261	4	961	1.10864E-06
Chr2	6554675	6555599	4	925	1.81906E-05
Chr2	6725397	6726422	5	1026	1.03E-08
Chr2	6885245	6885416	4	172	6.39313E-05
Chr2	7117555	7118484	5	930	2.71E-08
Chr2	9123768	9124090	5	323	1.67E-07
Chr2	9191574	9194080	6	2507	3.08124E-06
Chr2	12450138	12451518	5	1381	1.98947E-05
Chr2	15405297	15405764	4	468	1.35E-07
Chr2	17500130	17500312	4	183	2.57343E-06
Chr3	5278318	5278562	4	245	1.26887E-05
Chr3	5280802	5282332	5	1531	2.42815E-05
Chr3	9786507	9787776	4	1270	1.85635E-06
Chr3	11018987	11020354	4	1368	4.87962E-06
Chr3	11055028	11055071	4	44	7.56772E-05
Chr3	11685090	11687101	5	2012	7.09E-07
Chr3	11876353	11877111	4	759	1.34E-07
Chr3	11942069	11943546	4	1478	9.95E-09
Chr3	12003094	12004871	4	1778	2.81325E-05
Chr3	12026138	12029904	8	3767	7.20E-13

Chr3	12072074	12072815	4	742	2.23116E-06
Chr3	12096330	12096885	4	556	3.62287E-06
Chr3	12380597	12383321	6	2725	1.30E-08
Chr3	12482011	12483714	5	1704	8.75482E-06
Chr3	12496358	12497668	4	1311	2.58E-08
Chr3	12570295	12570995	4	701	9.43E-07
Chr3	12842404	12843991	4	1588	0.000256117
Chr3	12935345	12937245	4	1901	2.55184E-06
Chr3	12948115	12948694	5	580	1.01E-07
Chr3	13411676	13412606	5	931	1.45E-07
Chr3	13414418	13416049	6	1632	3.02E-08
Chr3	13442532	13443419	6	888	3.06566E-06
Chr3	13467913	13469024	5	1112	8.63E-07
Chr3	13603987	13605343	7	1357	3.89E-08
Chr3	13628010	13628799	5	790	6.98967E-05
Chr3	13644346	13645346	6	1001	7.87E-07
Chr3	13828856	13829423	4	568	1.21959E-05
Chr3	13884418	13886186	7	1769	1.58E-09
Chr3	13887442	13890441	6	3000	2.91E-08
Chr3	13969351	13971520	6	2170	2.8127E-06
Chr3	13976572	13977896	4	1325	1.36885E-05
Chr3	14004972	14005819	4	848	1.5784E-05
Chr3	14041031	14041731	4	701	1.93E-08
Chr3	14119470	14122003	5	2534	9.50E-12
Chr3	14160532	14161873	4	1342	0.000209404
Chr3	14162881	14165403	7	2523	3.79E-11
Chr3	14194733	14196839	11	2107	2.38E-13
Chr3	14201448	14202143	6	696	1.32E-10
Chr3	14221738	14223168	6	1431	4.95E-10
Chr3	14247537	14248197	4	661	1.62123E-05
Chr3	14262374	14264562	5	2189	1.93E-07
Chr3	14349647	14351057	4	1411	0.000140406
Chr3	14544290	14547265	6	2976	3.88E-08
Chr3	14567901	14569182	4	1282	4.20E-07
Chr3	14574020	14574884	4	865	9.00207E-05
Chr3	14719540	14720799	4	1260	1.07256E-06
Chr3	14764846	14766964	6	2119	7.18E-07
Chr3	14976896	14978117	4	1222	5.46828E-05
Chr3	15032450	15033089	4	640	0.00010033
Chr3	15044613	15046073	4	1461	7.85327E-05
Chr3	15119083	15122622	8	3540	1.12E-10
Chr3	15147058	15148553	5	1496	7.92936E-06
Chr3	15154170	15155826	7	1657	1.13E-08
Chr3	15257979	15259566	4	1588	7.65126E-05
Chr3	15310159	15311197	5	1039	4.57343E-06
Chr3	15319480	15321481	6	2002	1.76E-09
Chr3	15715569	15717360	4	1792	2.30E-07
Chr3	17472744	17472791	6	48	2.99E-09
Chr3	18791813	18792596	4	784	3.63522E-06
Chr3	22232641	22232690	4	50	1.50E-07
Chr3	23111385	23112553	7	1169	1.46E-10
Chr4	413805	414280	5	476	1.60E-08
Chr4	1677473	1678679	4	1207	8.58E-07
Chr4	1761338	1762321	4	984	7.69E-08
Chr4	1795166	1800705	13	5540	7.87E-14
Chr4	1850621	1851572	4	952	5.70E-07
Chr4	1920190	1921912	5	1723	7.45658E-06
Chr4	2144028	2144710	4	683	1.36173E-05
Chr4	2174590	2176217	4	1628	1.39478E-06
Chr4	2207805	2209209	4	1405	3.21E-07
Chr4	2270719	2271565	4	847	5.77385E-06
Chr4	2915635	2916017	7	383	1.84E-09
Chr4	2959557	2961118	4	1562	2.36134E-06

Chr4	3061830	3062432	4	603	1.68892E-06
Chr4	3090584	3091429	5	846	1.84E-07
Chr4	3105861	3107684	4	1824	0.000225807
Chr4	3382489	3384245	6	1757	4.11173E-06
Chr4	3465663	3465892	5	230	6.29E-07
Chr4	3486217	3487357	4	1141	9.99109E-07
Chr4	3683384	3685570	5	2187	2.96772E-06
Chr4	3691942	3692330	4	389	5.47988E-06
Chr4	3695350	3696422	4	1073	6.35351E-06
Chr4	3703259	3704314	4	1056	1.26501E-06
Chr4	3710433	3712492	4	2060	3.66E-07
Chr4	3785629	3787037	4	1409	4.54519E-06
Chr4	3858609	3859938	4	1330	9.11503E-07
Chr4	4186101	4188142	5	2042	3.96E-08
Chr4	4244221	4244945	4	725	5.40654E-06
Chr4	4245976	4247108	4	1133	0.000146683
Chr4	4318677	4320004	4	1328	1.03773E-05
Chr4	4487700	4491040	6	3341	2.88E-07
Chr4	4555269	4557945	4	2677	5.06477E-06
Chr4	4560230	4560796	4	567	2.65E-07
Chr4	4564694	4566537	4	1844	1.61303E-05
Chr4	4709680	4711404	4	1725	1.47113E-06
Chr4	4719827	4721064	6	1238	5.17E-08
Chr4	4764958	4765312	4	355	2.02E-08
Chr4	4775426	4776391	4	966	2.05598E-06
Chr4	4934877	4935148	4	272	0.000103867
Chr4	5039255	5040845	4	1591	0.000183727
Chr4	5065865	5067189	4	1325	6.78E-07
Chr4	5204710	5206389	5	1680	2.97E-10
Chr4	5400887	5401482	4	596	3.58834E-06
Chr4	5510075	5510543	4	469	1.31E-08
Chr4	5591933	5593374	4	1442	5.57E-07
Chr4	5968650	5969468	4	819	5.83133E-06
Chr4	6650782	6651625	8	844	4.44E-09
Chr4	8900417	8901655	4	1239	6.20348E-06
Chr4	9509207	9509985	4	779	1.68E-07
Chr4	11036101	11039550	13	3450	5.76E-15
Chr4	13329095	13331676	7	2582	5.43E-08
Chr5	68081	69274	4	1194	7.40491E-06
Chr5	2036593	2037500	10	908	3.13E-11
Chr5	2374091	2375752	5	1662	1.20E-08
Chr5	2393547	2396039	6	2493	3.30E-08
Chr5	3253183	3253260	4	78	0.010457351
Chr5	7027719	7029131	4	1413	6.06248E-06
Chr5	8622173	8623566	5	1394	6.69E-09
Chr5	9904566	9905353	4	788	3.40251E-06
Chr5	10098793	10100846	4	2054	1.59679E-05
Chr5	10379015	10379905	4	891	1.25516E-06
Chr5	10583291	10583777	4	487	9.77E-07
Chr5	10811826	10812455	4	630	0.000116283
Chr5	10957581	10959444	5	1864	1.78E-08
Chr5	11044680	11046869	6	2190	1.97E-07
Chr5	11077864	11081771	10	3908	3.28E-12
Chr5	11139315	11140147	5	833	3.11E-09
Chr5	11151977	11152173	4	197	5.05E-07
Chr5	11166438	11166464	4	27	1.63E-07
Chr5	11171447	11172624	5	1178	4.97406E-05
Chr5	11184856	11186019	6	1164	2.18158E-06
Chr5	11198434	11199142	4	709	9.6534E-06
Chr5	11391493	11392542	4	1050	6.20212E-05
Chr5	11574951	11576014	5	1064	2.32E-08
Chr5	11649276	11650870	5	1595	1.07421E-05
Chr5	11708060	11709078	6	1019	8.40E-10

Chr5	11906679	11908548	8	1870	2.84E-09
Chr5	11939794	11942938	5	3145	4.55E-09
Chr5	12009082	12011591	6	2510	3.59095E-06
Chr5	12147203	12147875	4	673	2.17482E-05
Chr5	12154171	12155200	4	1030	3.51472E-05
Chr5	12241737	12243878	5	2142	3.20833E-06
Chr5	12326891	12327492	6	602	5.93E-07
Chr5	12368980	12370270	4	1291	1.12178E-05
Chr5	12515260	12516331	5	1072	5.75E-08
Chr5	12628865	12630048	5	1184	3.49248E-06
Chr5	12762111	12762764	10	654	1.96E-12
Chr5	12901605	12902548	4	944	2.07E-07
Chr5	12925480	12927522	5	2043	2.30553E-06
Chr5	12946403	12948062	4	1660	2.03763E-05
Chr5	13002554	13005144	8	2591	1.06E-12
Chr5	13173852	13175383	4	1532	1.01E-08
Chr5	13348160	13349574	6	1415	9.32E-07
Chr5	13374304	13375702	4	1399	0.000137944
Chr5	14089567	14089707	4	141	1.91E-07
Chr5	14147887	14148871	4	985	3.6923E-05
Chr5	14558411	14559651	4	1241	1.85E-07
Chr5	15357992	15359690	5	1699	1.28E-07
Chr5	15921883	15924323	7	2441	9.23E-10
Chr5	16702932	16704894	5	1963	1.18201E-06
Chr5	17597710	17599669	4	1960	3.68E-07
Chr5	19891078	19892230	5	1153	9.77E-08

Supporting References

1. Wielopolska A, Townley H, Moore I, Waterhouse P, & Helliwell C (2005) A high-throughput inducible RNAi vector for plants. *Plant biotechnology journal* 3(6):583-590.
2. Martinez-Trujillo M, Limones-Briones V, Cabrera-Ponce J, & Herrera-Estrella L (2004) Improving transformation efficiency ofArabidopsis thaliana by modifying the floral dip method. *Plant Mol Biol Rep* 22(1):63-70.
3. Henderson IR & Jacobsen SE (2008) Tandem repeats upstream of the Arabidopsis endogene SDC recruit non-CG DNA methylation and initiate siRNA spreading. *Genes & development* 22(12):1597-1606.
4. Peterson D, Boehm K, & Stack S (1997) Isolation of milligram quantities of nuclear DNA from tomato (Lycopersicon esculentum), A plant containing high levels of polyphenolic compounds. *Plant Mol Biol Rep* 15(2):148-153.
5. Xiang H*, et al.* (2010) Single base-resolution methylome of the silkworm reveals a sparse epigenomic map. *Nature biotechnology* 28(5):516-520.
6. Lister R*, et al.* (2009) Human DNA methylomes at base resolution show widespread epigenomic differences. *Nature* 462(7271):315-322.
7. Langmead B & Salzberg SL (2012) Fast gapped-read alignment with Bowtie 2. *Nat Meth* 9(4):357-359.
8. Anders S, Pyl PT, & Huber W (2015) HTSeq—a Python framework to work with high-throughput sequencing data. *Bioinformatics* 31(2):166-169.
9. Robinson MD, McCarthy DJ, & Smyth GK (2010) edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. *Bioinformatics* 26(1):139-140.
10. Katari MS*, et al.* (2010) VirtualPlant: a software platform to support systems biology research. *Plant physiology* 152(2):500-515.
11. Lyons E & Freeling M (2008) How to usefully compare homologous plant genes and chromosomes as DNA sequences. *The Plant Journal* 53(4):661-673.