**Supplementary table 1:** Plasma samples from 22 Caucasian individuals.

|  |  |  |
| --- | --- | --- |
|  | **Cases** | **Controls** |
| Diagnosis | Alzheimer' s Disease | Healthy Donor |
| Gender | 5 females; 3 males | 8 females; 6 males |
| Age | 75.2 +/- 9.8 | 59.7 +/- 11.2 |
| MMSE Score | 23.3 +/- 3.4 | 28.8 +/- 0.7 |

**Supplementary table 2 :** Custom gene panel of our targeted bisulfite sequencing protocol. DMCs and/or DMRs were identified in the literature from brain, blood or plasma samples of AD compared to control and were identified in brain-specific.

|  |  |  |  |
| --- | --- | --- | --- |
| **Study** | **Sample** | **Methylated gene** | **Reference** |
| Alzheimer's disease | Cortex | *TNFA* | [1] |
| Alzheimer's disease | Frontal cortex | *TMEM59* | [2] |
| Alzheimer's disease | Frontal cortex | *BDNF, COX2, CREB1, NFKB, SYP* | [3] |
| Alzheimer's disease | Frontal cortex | *SORBS3, SPTBN4, DUSP22, QSCN6* | [4] |
| Alzheimer's disease | Hippocampus | *APOE* | [5, 6] |
| Alzheimer's disease | Hippocampus | *GPM6B* | [7] |
| Alzheimer's disease | Pre-frontal cortex | *ABCA7, ANK1, BIN1, C10orf105, CDH23, IER3, RHBDF2, TREM2* | [8] |
| Alzheimer's disease | Pre-frontal cortex | *NGFR* | [9] |
| Alzheimer's disease | Pre-frontal cortex | *ANK1, MIR486, RHBDF2* | [10] |
| Alzheimer's disease | Pyramidal layers in frontal cortex | *MBP* | [11] |
| Alzheimer's disease | Superior temporal gyrus | *TREM2* | [12] |
| Alzheimer's disease | Superior temporal gyrus | *AGPAT1, B3GALT4, CMYA5, DUSP6, ELOVL1, FBRSL1, FLOT1, HLA-J, KIF25, KLK7, MOV10L1, NAV2, NRG2, PPT2, PPT2-EGFL8, PRDM16, PRRT1, RIBC2, RNF39, RNF5P1, TAP2, TBX15, TNXB, TRIM40, TRIM6, VAX2, ZNF177, ZNF559-ZNF177, ZNRD1-AS1* | [13] |
| Alzheimer's disease | Temporal cortex | *APP, MAPT* | [14] |
| Alzheimer's disease | Temporal lobe cortex | *S100A2, SORBS3* | [15] |
| Alzheimer's disease | Plasma | *LHX2* | [16] |
| Alzheimer's disease | Leucocytes | *FAAH* | [17] |
| Alzheimer's disease | Leucocytes | *ALOX5, SIRT1* | [18] |
| Alzheimer's disease | Leucocytes | *SCNA* | [19] |
| Alzheimer's disease | Lymphocytes | *APP, PS1* | [20] |
| Alzheimer's disease | Lymphocytes | *DR4* | [21] |
| Alzheimer's disease | Mononuclear cells | *ALOX5* | [22] |
| Alzheimer's disease | Mononuclear cells | *BDNF* | [23] |
| Alzheimer's disease | Whole Blood | *DUSP22, FLOT1, B3GALT4, DRD4* | [24] |
| Alzheimer's disease | Whole Blood | *PIN1* | [25] |
| Alzheimer's disease | Whole Blood | *BDNF* | [26] |
| Alzheimer's disease | Whole Blood | *DRD4* | [27] |
| Alzheimer's disease | Whole Blood | *OPRD1* | [28] |
| Alzheimer's disease | Whole Blood | *CNPY1* | [29] |
| Alzheimer's disease | Whole Blood | *DAPK1, GAS1, NDUFS5* | [10] |
| Alzheimer's disease | Whole Blood | *HMOX1* | [30] |
| Brain-specific | Frontal Cortex | *EOMES, SLITRK1, GRM4, SHANK3, JAKMIP1, PPP2R2B, SLITRK1, CACNA1A, SLIT1, BMP4, NUMBL, PCDH9* | [31] |
| Brain-specific | Frontal Cortex | *KIF19* | [32] |

**Supplementary table 3 :** Tissue specificity of genes (RNA and protein expression) in the targeted-bisulfite capture gene panel according to the Protein Atlas Database. Genes with an "enriched" expression in a tissue show at least four-fold higher mRNA level compared to any other tissue. Genes with an "enhanced" expression mean that there is at least four-fold higher mRNA level in a tissue compared to the average level in all other tissues.

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene** | **Tissue specificity  (RNA expression)** | **Brain specificity  (RNA expression)** | **Reliabilty  (protein expression)** |
| *MBP* | Tissue enriched (brain) | Low human brain regional specificity | Enhanced |
| *CACNA1A* | Tissue enriched (brain) | Human brain regional enriched (cerebellum) | Enhanced |
| *OPRD1* | Tissue enriched (brain) | Low human brain regional specificity | Approved |
| *PPP2R2B* | Tissue enriched (brain) | Low human brain regional specificity | Approved |
| *GRM4* | Tissue enriched (brain) | Human brain regional enriched (cerebellum) | Enhanced |
| *PRRT1* | Tissue enriched (brain) | Low human brain regional specificity | Enhanced |
| *CRTC1* | Tissue enhanced (brain) | Low human brain regional specificity | Enhanced |
| *SPTBN4* | Tissue enhanced (brain) | Low human brain regional specificity | Enhanced |
| *SLIT1* | Tissue enhanced (brain) | Low human brain regional specificity |  |
| *SHANK3* | Tissue enhanced (brain) | Low human brain regional specificity | Enhanced |
| *SLITRK1* | Tissue enhanced (brain) | Low human brain regional specificity | Enhanced |
| *ELOVL1* | Tissue enhanced (brain) | Low human brain regional specificity | Supported |
| *SNCA* | Group enriched (blood, bone marrow, brain) | Low human brain regional specificity | Enhanced |
| *PCDH9* | Group enriched (blood, brain) | Low human brain regional specificity |  |
| *CNPY1* | Group enriched (brain, pancreas) | Human brain regional enriched (cerebellum) | Uncertain |
| *LHX2* | Group enriched (brain, retina) | Group enriched (amygdala, basal ganglia, cerebral cortex, hippocampal formation, olfactory human brain regional) |  |
| *MAPT* | Group enriched (brain, skeletal muscle) | Low human brain regional specificity | Enhanced |
| *JAKMIP1* | Tissue enhanced (blood, brain) | Low human brain regional specificity | Uncertain |
| *EOMES* | Tissue enhanced (blood, brain, lymphoid tissue) | Human brain regional enriched (cerebellum) | Uncertain |
| *TNF* | Tissue enhanced (bone marrow, lymphoid tissue) | Low human brain regional specificity | Supported |
| *KIF19* | Tissue enhanced (brain, fallopian tube) | Low human brain regional specificity | Enhanced |
| *RIBC2* | Tissue enhanced (brain, fallopian tube, testis) |  | Approved |
| *C10orf105* | Tissue enhanced (brain, lymphoid tissue) | Low human brain regional specificity | Pending |
| *VAX2* | Tissue enhanced (brain, retina) | Human brain regional enhanced (cerebellum) |  |
| *BDNF* | Tissue enhanced (brain, smooth muscle) | Low human brain regional specificity | Enhanced |
| *KIF25* | Tissue enhanced (adipose tissue, brain) |  | Uncertain |
| *TREM2* | Tissue enhanced (adipose tissue, brain, lung) | Low human brain regional specificity | Approved |
| *PTGS2* | Group enriched (ductus deferens, seminal vesicle) | Low human brain regional specificity | Enhanced |
| *KLK7* | Group enriched (esophagus, skin, tongue) | Low human brain regional specificity | Enhanced |
| *S100A2* | Group enriched (esophagus, tongue) | Not detected in human brain | Enhanced |
| *TRIM40* | Group enriched (intestine, placenta) | Not detected in human brain | Uncertain |
| *ANK1* | Group enriched (skeletal muscle, tongue) | Human brain regional enhanced (cerebellum) | Supported |
| *ALOX5* | Tissue enhanced (blood, bone marrow, lymphoid tissue) | Low human brain regional specificity | Enhanced |
| *DUSP6* | Tissue enhanced (blood) | Low human brain regional specificity | Approved |
| *RNF39* | Tissue enhanced (esophagus, skin) | Not detected in human brain | Uncertain |
| *TBX15* | Tissue enhanced (liver, skeletal muscle, tongue) | Low human brain regional specificity | Uncertain |
| *CMYA5* | Cell type enriched (Cardiomyocytes) | Not detected in human brain | Enhanced |
| *DRD4* | Tissue enriched (retina) | Low human brain regional specificity |  |
| *BIN1* | Tissue enriched (skeletal muscle) | Low human brain regional specificity | Enhanced |
| *MOV10L1* | Tissue enriched (testis) | Low human brain regional specificity | Approved |
| *GAS1* | Tissue enhanced (endometrium) | Low human brain regional specificity | Approved |
| *NAV2* | Tissue enhanced (heart muscle) | Tissue enhanced (heart muscle) | Approved |
| *TRIM6* | Tissue enhanced (kidney) | Low human brain regional specificity | Uncertain |
| *HMOX1* | Tissue enhanced (lymphoid tissue) | Low human brain regional specificity | Enhanced |
| *QSOX1* | Tissue enhanced (placenta) | Low human brain regional specificity |  |
| *DAPK1* | Tissue enhanced (placenta) | Low human brain regional specificity | Approved |
| *CDH23* | Tissue enhanced (retina) | Low human brain regional specificity | Approved |
| *BMP4* | Tissue enhanced (retina) | Low human brain regional specificity | Uncertain |
| *IER3* | Tissue enhanced (seminal vesicle) | Low human brain regional specificity | Approved |
| *ZNF177* | Tissue enhanced (testis) | Low human brain regional specificity | Uncertain |
| *FBRSL1* | Low tissue specificity | Low human brain regional specificity | Enhanced |
| *DUSP22* | Low tissue specificity | Low human brain regional specificity | Approved |
| *TNXB* | Low tissue specificity | Human brain regional enhanced (cerebellum) |  |
| *NUMBL* | Low tissue specificity | Low human brain regional specificity | Approved |
| *APP* | Low tissue specificity | Low human brain regional specificity | Enhanced |
| *FAAH* | Low tissue specificity | Low human brain regional specificity | Approved |
| *ZNRD1-AS1* | Low tissue specificity | Low human brain regional specificity | Supported |
| *PRDM16* | Low tissue specificity | Low human brain regional specificity |  |
| *RHBDF2* | Low tissue specificity | Low human brain regional specificity | Uncertain |
| *TAP2* | Low tissue specificity | Low human brain regional specificity | Approved |
| *ABCA7* | Low tissue specificity | Low human brain regional specificity | Enhanced |
| *HLA-J* | Low tissue specificity | Low human brain regional specificity |  |
| *B3GALT4* | Low tissue specificity | Low human brain regional specificity | Approved |
| *NDUFS5* | Low tissue specificity | Low human brain regional specificity | Supported |
| *NGFR* | Low tissue specificity | Low human brain regional specificity | Enhanced |
| *NFKB1* | Low tissue specificity | Low human brain regional specificity | Enhanced |
| *PSEN1* | Low tissue specificity | Low human brain regional specificity | Approved |
| *AGPAT1* | Low tissue specificity | Low human brain regional specificity | Approved |
| *CREB1* | Low tissue specificity | Low human brain regional specificity | Supported |
| *FLOT1* | Low tissue specificity | Low human brain regional specificity | Enhanced |
| *SORBS3* | Low tissue specificity | Low human brain regional specificity | Approved |
| *MIR486* |  |  |  |
| *PPT2-EGFL8* |  |  |  |
| *RNF5P1* |  |  |  |

**Supplementary table 4 :** 632 DMCs in ccfDNA from plasma (q-value ≤0.05, Methylation change >5%)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **CpG coordinate** | **Gene** | **Gene  annotation** | **CpG  site** | **DMC  (%)** | **q-value** | **Mean case  Methylation (%)** | **Mean control  Methylation (%)** |
| chr19:1052085 | ABCA7 | promoter | shores | 6.35 | 7.20E-10 | 92.43+/-4.37 | 88.75+/-12.53 |
| chr19:1052005 | ABCA7 | exon, CDS | shores | -9.50 | 2.63E-04 | 53.6+/-35.63 | 70.5+/-28.79 |
| chr19:1039774 | ABCA7 | promoter | islands | 8.36 | 2.28E-02 | 25.28+/-7.81 | 21.67+/-11.07 |
| chr19:1047323 | ABCA7 | exon | islands | 10.42 | 3.62E-02 | 50.99+/-10.73 | 41.27+/-12.28 |
| chr6:32138008 | AGPAT1/PPT2-EGFL8 | exon/intron | shelves | -5.31 | 9.47E-03 | 84.91+/-3.73 | 88.01+/-4.01 |
| chr10:45941405 | ALOX5 | exon, UTR | shores | 8.92 | 1.04E-47 | 89.85+/-4.39 | 81.48+/-16.5 |
| chr10:45941051 | ALOX5 | exon, CDS | shores | 7.32 | 2.48E-03 | 79.02+/-7.05 | 76.4+/-6.09 |
| chr10:45868339 | ALOX5 | promoter | shores | 5.94 | 5.52E-03 | 70.43+/-9.59 | 68.21+/-7.31 |
| chr10:45920551 | ALOX5 | exon | shelves | 10.21 | 2.93E-02 | 31.12+/-14.43 | 24.9+/-10.4 |
| chr8:41554011 | ANK1 | promoter | inter | 6.68 | 4.29E-22 | 98.02+/-1.15 | 93.63+/-12.54 |
| chr8:41547841 | ANK1 | promoter | inter | -9.12 | 2.80E-17 | 86.11+/-20.46 | 94.76+/-2.56 |
| chr8:41518719 | ANK1 | exon | inter | -16.99 | 6.13E-05 | 35.96+/-7.61 | 47.05+/-10.63 |
| chr8:41563684 | ANK1 | exon, CDS | inter | -12.78 | 3.82E-04 | 72.99+/-35.52 | 76.64+/-23.19 |
| chr8:41529993 | ANK1 | exon, UTR | inter | 5.50 | 4.47E-03 | 94.34+/-3.42 | 87.62+/-12.55 |
| chr8:41518715 | ANK1 | exon | inter | -12.40 | 1.09E-02 | 23.33+/-8.91 | 31.54+/-9.98 |
| chr8:41517216 | ANK1/MIR486 | intron/promoter | inter | -17.08 | 6.54E-07 | 85.93+/-17.17 | 93.26+/-5.63 |
| chr8:41516990 | ANK1/MIR486 | intron/promoter | inter | 13.45 | 5.10E-03 | 74.72+/-22.49 | 71.4+/-35.89 |
| chr21:27253112 | APP | exon, UTR | inter | 5.64 | 4.31E-30 | 97.73+/-1.07 | 91.8+/-13.11 |
| chr21:27440461 | APP | exon, first\_exon | inter | -8.38 | 3.15E-04 | 43.51+/-7.55 | 46.94+/-8.66 |
| chr21:27425720 | APP | intron | inter | -5.97 | 3.92E-04 | 71.73+/-8.46 | 72.17+/-7.82 |
| chr21:27423439 | APP | exon | inter | -8.87 | 4.20E-04 | 71.2+/-11.58 | 71.76+/-10.89 |
| chr21:27512686 | APP | intron | inter | 11.23 | 4.90E-03 | 49.37+/-10.35 | 46.34+/-13.17 |
| chr21:27440539 | APP | exon, first\_exon | inter | -5.28 | 9.95E-03 | 40.56+/-6.92 | 42.85+/-7.66 |
| chr21:27423455 | APP | exon | inter | -6.30 | 1.20E-02 | 78.08+/-11.18 | 77.24+/-9.41 |
| chr21:27512770 | APP | intron | inter | 5.28 | 2.72E-02 | 67.72+/-4.63 | 64.27+/-6.3 |
| chr21:27423344 | APP | exon | inter | -7.06 | 4.41E-02 | 79.6+/-7.69 | 82.86+/-6.93 |
| chr6:33243552 | B3GALT4 | promoter | shores | 5.74 | 3.17E-14 | 94.02+/-2.97 | 89.84+/-13.25 |
| chr6:33245541 | B3GALT4 | exon, CDS, first\_exon | islands | -5.91 | 6.57E-04 | 2.2+/-1.98 | 12.02+/-9.86 |
| chr6:33252335 | B3GALT4 | exon | inter | -13.76 | 1.49E-03 | 74.25+/-23.68 | 83.51+/-22.84 |
| chr11:27679916 | BDNF | exon, CDS | inter | 16.42 | 1.85E-10 | 84.1+/-18.3 | 64.94+/-27.65 |
| chr11:27742151 | BDNF | intron | islands | 5.00 | 2.28E-02 | 17.64+/-9.56 | 9.46+/-3.76 |
| chr2:127813826 | BIN1 | intron | inter | 7.42 | 1.84E-18 | 94.79+/-4.33 | 90.57+/-12.38 |
| chr2:127821206 | BIN1 | exon | shelves | 5.61 | 1.26E-07 | 97.58+/-2.09 | 89.43+/-24.97 |
| chr2:127808075 | BIN1 | exon | inter | 6.84 | 3.40E-05 | 44.22+/-11.06 | 40.74+/-9.94 |
| chr14:54418410 | BMP4 | exon, UTR, first\_exon | shores | 25.36 | 1.81E-30 | 58.97+/-31.19 | 59.44+/-35.62 |
| chr10:73472449 | C10orf105/CDH23 | exon, UTR/exon, first\_exon | inter | 13.11 | 1.05E-05 | 35+/-7.77 | 32.96+/-12.17 |
| chr10:73472462 | C10orf105/CDH23 | exon, UTR/exon, first\_exon | inter | 11.96 | 5.23E-04 | 39.08+/-9.06 | 37.13+/-12.8 |
| chr10:73472442 | C10orf105/CDH23 | exon, UTR/exon, first\_exon | inter | 13.28 | 1.90E-03 | 45.63+/-12.92 | 49.28+/-16.36 |
| chr10:73472468 | C10orf105/CDH23 | exon, UTR/exon, first\_exon | inter | 11.42 | 3.59E-03 | 50.66+/-13.47 | 53.21+/-12.06 |
| chr10:73472882 | C10orf105/CDH23 | exon, UTR/intron | inter | 8.38 | 9.68E-15 | 28.26+/-23.9 | 29.72+/-15.45 |
| chr10:73473376 | C10orf105/CDH23 | exon, UTR/intron | inter | 8.71 | 6.31E-03 | 33.05+/-9.33 | 32.91+/-12.24 |
| chr10:73472628 | C10orf105/CDH23 | exon, UTR/intron | inter | 10.19 | 1.72E-02 | 60.08+/-15.03 | 54.79+/-14.98 |
| chr10:73472315 | C10orf105/CDH23 | exon, UTR/promoter | inter | 6.15 | 3.62E-02 | 55.3+/-8.34 | 55.14+/-12.77 |
| chr10:73483850 | C10orf105/CDH23 | intron/exon | inter | 7.63 | 1.38E-13 | 81.85+/-11.26 | 79.39+/-11.92 |
| chr10:73483838 | C10orf105/CDH23 | intron/exon | inter | 8.18 | 5.54E-06 | 63.54+/-11.15 | 58.32+/-13.9 |
| chr10:73483828 | C10orf105/CDH23 | intron/exon | inter | 5.49 | 2.15E-04 | 55.9+/-9.59 | 54.33+/-14.09 |
| chr10:73499071 | C10orf105/CDH23 | promoter/intron | inter | 6.30 | 2.26E-28 | 92.99+/-14.24 | 88.35+/-18.4 |
| chr10:73498867 | C10orf105/CDH23 | promoter/intron | inter | 10.92 | 1.77E-04 | 74.26+/-6.21 | 73.08+/-13.24 |
| chr10:73498845 | C10orf105/CDH23 | promoter/intron | inter | 11.52 | 8.26E-04 | 56.44+/-9.94 | 57.78+/-17.13 |
| chr10:73498857 | C10orf105/CDH23 | promoter/intron | inter | 13.04 | 2.30E-03 | 62.68+/-7.92 | 59.99+/-17.06 |
| chr10:73498713 | C10orf105/CDH23 | promoter/intron | inter | 12.43 | 2.61E-03 | 60.68+/-8.52 | 57.47+/-16.38 |
| chr10:73498901 | C10orf105/CDH23 | promoter/intron | inter | 8.02 | 1.07E-02 | 70.16+/-8.73 | 69.88+/-11.13 |
| chr10:73498756 | C10orf105/CDH23 | promoter/intron | inter | 10.70 | 2.93E-02 | 72.75+/-6.01 | 72.19+/-15.27 |
| chr10:73498683 | C10orf105/CDH23 | promoter/intron | inter | 6.83 | 3.58E-02 | 80.73+/-10.05 | 81.51+/-9.73 |
| chr19:13445144 | CACNA1A | exon | inter | -30.21 | 7.89E-30 | 19.4+/-23.16 | 42.19+/-26.75 |
| chr19:13734776 | CACNA1A | exon, UTR, first\_exon | inter | 12.57 | 1.26E-10 | 34.7+/-14.47 | 24.89+/-15.34 |
| chr19:13409407 | CACNA1A | exon, CDS | shores | -13.51 | 1.41E-08 | 18.52+/-17.94 | 30.45+/-18.86 |
| chr19:13734794 | CACNA1A | exon, UTR, first\_exon | inter | 10.84 | 3.69E-08 | 68.61+/-7.98 | 57.97+/-18.22 |
| chr19:13409394 | CACNA1A | exon, CDS | shores | -15.14 | 6.36E-08 | 30.3+/-14.3 | 41.96+/-21.19 |
| chr19:13409376 | CACNA1A | exon, CDS | shores | -14.12 | 9.46E-07 | 28.9+/-20.67 | 37.78+/-17.39 |
| chr19:13318556 | CACNA1A | exon, UTR | islands | 14.07 | 6.63E-06 | 69.31+/-17.08 | 53.04+/-17.5 |
| chr19:13409367 | CACNA1A | exon, CDS | shores | -12.98 | 1.49E-05 | 26.18+/-17.59 | 36.26+/-19.43 |
| chr19:13734720 | CACNA1A | exon, UTR, first\_exon | inter | 6.71 | 3.50E-05 | 63.34+/-15.6 | 59.41+/-13.27 |
| chr19:13409411 | CACNA1A | exon, CDS | shores | -10.40 | 4.59E-05 | 24.7+/-17.18 | 27.99+/-15.43 |
| chr19:13409398 | CACNA1A | exon, CDS | shores | -12.20 | 6.59E-05 | 27.42+/-20.63 | 34.9+/-20.91 |
| chr19:13409396 | CACNA1A | exon, CDS | shores | -11.95 | 2.37E-04 | 26.3+/-21.88 | 34.18+/-18.1 |
| chr19:13629888 | CACNA1A | exon, UTR | inter | 5.03 | 2.44E-04 | 89.45+/-8.28 | 85.67+/-14.7 |
| chr19:13734744 | CACNA1A | exon, UTR, first\_exon | inter | 7.43 | 4.57E-04 | 56.56+/-17.23 | 50.16+/-15.71 |
| chr19:13409931 | CACNA1A | exon, CDS | islands | -9.47 | 5.84E-04 | 59.52+/-18.08 | 61.9+/-15.44 |
| chr19:13409614 | CACNA1A | exon, CDS | islands | -9.63 | 8.35E-04 | 7.89+/-8.18 | 16.27+/-14.27 |
| chr19:13735370 | CACNA1A | promoter | inter | 6.58 | 9.98E-04 | 43.7+/-12.16 | 38.42+/-7.82 |
| chr19:13409914 | CACNA1A | exon, CDS | islands | -9.73 | 1.13E-03 | 46.65+/-18.01 | 50.87+/-16.87 |
| chr19:13409606 | CACNA1A | exon, CDS | islands | -10.41 | 2.57E-03 | 10.84+/-7.66 | 21.14+/-17.15 |
| chr19:13409859 | CACNA1A | exon, CDS | islands | -13.17 | 3.22E-03 | 39.46+/-21.06 | 46.86+/-20.29 |
| chr19:13410050 | CACNA1A | exon, CDS | islands | -7.46 | 6.03E-03 | 81.65+/-10.94 | 84.07+/-6.38 |
| chr19:13409884 | CACNA1A | exon, CDS | islands | -10.77 | 6.38E-03 | 46.61+/-18.27 | 52.48+/-18.78 |
| chr19:13409769 | CACNA1A | exon, CDS | islands | -10.66 | 6.82E-03 | 36.92+/-17.84 | 44.96+/-21.14 |
| chr19:13319579 | CACNA1A | exon, CDS | islands | 9.56 | 8.28E-03 | 53.38+/-19.88 | 47.7+/-16.16 |
| chr19:13409825 | CACNA1A | exon, CDS | islands | -8.38 | 9.50E-03 | 27.19+/-18.15 | 32.31+/-18.46 |
| chr19:13409887 | CACNA1A | exon, CDS | islands | -8.70 | 1.37E-02 | 45.47+/-19.58 | 47.94+/-17.43 |
| chr19:13409889 | CACNA1A | exon, CDS | islands | -10.32 | 1.62E-02 | 42.89+/-19.73 | 48.28+/-19.62 |
| chr19:13734725 | CACNA1A | exon, UTR, first\_exon | inter | 6.95 | 1.72E-02 | 62.02+/-22.18 | 52.44+/-15.09 |
| chr19:13409851 | CACNA1A | exon, CDS | islands | -8.02 | 1.90E-02 | 31.5+/-20.19 | 33.73+/-14.77 |
| chr19:13409755 | CACNA1A | exon, CDS | islands | -9.07 | 2.37E-02 | 48.73+/-22.92 | 50.52+/-15.91 |
| chr19:13409734 | CACNA1A | exon, CDS | islands | -12.49 | 2.40E-02 | 39.15+/-23.8 | 46.75+/-15.48 |
| chr19:13409422 | CACNA1A | exon, CDS | shores | -9.80 | 2.42E-02 | 28.9+/-16.03 | 33.71+/-19.83 |
| chr19:13318560 | CACNA1A | exon, UTR | islands | 7.01 | 3.06E-02 | 71.04+/-19.62 | 65.35+/-13.62 |
| chr19:13409822 | CACNA1A | exon, CDS | islands | -8.43 | 3.39E-02 | 26.72+/-19.52 | 31.43+/-17.74 |
| chr19:13409830 | CACNA1A | exon, CDS | islands | -7.93 | 3.45E-02 | 34.39+/-23.03 | 38.92+/-20.38 |
| chr19:13409445 | CACNA1A | exon, CDS | shores | -10.23 | 4.22E-02 | 29.12+/-21.08 | 35.84+/-20.7 |
| chr19:13409808 | CACNA1A | exon, CDS | islands | -8.64 | 4.71E-02 | 31.89+/-17.56 | 37.09+/-18.72 |
| chr10:73406598 | CDH23 | intron | inter | 28.57 | 5.98E-108 | 87.67+/-16.94 | 59.01+/-36.79 |
| chr10:73377069 | CDH23 | exon, first\_exon | inter | 18.82 | 3.68E-88 | 95.15+/-1.59 | 81.93+/-25.86 |
| chr10:73537448 | CDH23 | exon, CDS | shelves | -24.18 | 9.46E-81 | 83.02+/-23.88 | 96.63+/-2.76 |
| chr10:73199595 | CDH23 | exon, CDS, first\_exon | inter | 14.84 | 5.24E-51 | 94.54+/-5.01 | 79.62+/-28.6 |
| chr10:73569749 | CDH23 | exon | shelves | -15.54 | 2.87E-22 | 72.92+/-23.06 | 74.99+/-22.29 |
| chr10:73406636 | CDH23 | intron | inter | -6.26 | 6.40E-20 | 67.29+/-34.44 | 83.24+/-13.87 |
| chr10:73558885 | CDH23 | exon | inter | 16.36 | 3.84E-13 | 76.89+/-35.34 | 66.7+/-28.93 |
| chr10:73562743 | CDH23 | exon | shelves | 17.56 | 2.96E-11 | 77.84+/-35.25 | 64.26+/-29.57 |
| chr10:73553177 | CDH23 | exon, CDS | inter | 5.25 | 2.17E-08 | 95.05+/-2.82 | 92.48+/-11.48 |
| chr10:73407465 | CDH23 | intron | inter | -16.41 | 4.80E-06 | 45.95+/-22.78 | 45.13+/-19.17 |
| chr10:73537978 | CDH23 | exon, CDS | inter | 17.36 | 7.35E-06 | 82.96+/-32.9 | 74.84+/-26.49 |
| chr10:73558952 | CDH23 | exon | inter | 10.40 | 5.23E-04 | 75.74+/-35.05 | 72.32+/-23.93 |
| chr10:73544085 | CDH23 | exon, CDS | inter | 15.88 | 1.14E-02 | 88.49+/-19.93 | 79.6+/-21.58 |
| chr10:73434858 | CDH23 | intron | inter | 5.66 | 2.72E-02 | 61.16+/-6.44 | 60.27+/-7.86 |
| chr10:73565942 | CDH23 | exon | shores | -8.69 | 2.72E-02 | 65.25+/-10.25 | 66.64+/-8.11 |
| chr10:73468940 | CDH23 | exon, CDS | inter | 5.95 | 2.80E-02 | 68.48+/-8.51 | 65.55+/-6.99 |
| chr10:73553201 | CDH23 | exon, CDS | inter | -5.31 | 3.50E-02 | 80.14+/-10.2 | 85.23+/-4.57 |
| chr5:79096052 | CMYA5 | exon | inter | -16.68 | 6.98E-31 | 75.83+/-21.97 | 87.68+/-13.8 |
| chr5:79095417 | CMYA5 | exon | inter | -8.78 | 6.70E-25 | 84.17+/-19.81 | 94.95+/-2.37 |
| chr5:79095720 | CMYA5 | exon | inter | -9.57 | 3.05E-19 | 75.59+/-22.57 | 79.74+/-21.22 |
| chr5:79033390 | CMYA5 | promoter | inter | -12.26 | 8.39E-17 | 88.68+/-16.71 | 91.82+/-13.34 |
| chr5:79031557 | CMYA5 | exon, CDS | inter | -13.97 | 1.60E-11 | 81.17+/-20.09 | 87.81+/-11.14 |
| chr5:79089265 | CMYA5 | exon | inter | -11.33 | 4.44E-05 | 58.65+/-11.58 | 62.73+/-9.25 |
| chr5:79031476 | CMYA5 | exon, CDS | inter | -6.42 | 1.02E-03 | 57.99+/-8.92 | 64.5+/-3.76 |
| chr7:155327438 | CNPY1 | promoter | shores | 6.15 | 5.59E-15 | 87.86+/-9.15 | 86.6+/-18.03 |
| chr7:155294179 | CNPY1 | exon, UTR | inter | -8.37 | 2.79E-11 | 84.1+/-8.98 | 87.12+/-2.47 |
| chr7:155294416 | CNPY1 | exon, UTR | inter | -14.47 | 3.43E-10 | 34.51+/-17.24 | 43.76+/-7.41 |
| chr7:155294422 | CNPY1 | exon, UTR | inter | -14.12 | 2.06E-09 | 38.69+/-16 | 44.39+/-12.62 |
| chr7:155294428 | CNPY1 | exon, UTR | inter | -11.12 | 4.67E-08 | 62.63+/-15.84 | 63.26+/-13.45 |
| chr7:155294404 | CNPY1 | exon, UTR | inter | -9.31 | 1.21E-07 | 23.14+/-10.84 | 28.93+/-11.89 |
| chr7:155294998 | CNPY1 | exon, UTR | inter | -5.36 | 2.69E-05 | 22.88+/-10.09 | 26.8+/-10.79 |
| chr7:155266930 | CNPY1 | exon, UTR | inter | -9.08 | 3.74E-04 | 46.4+/-15.21 | 59.44+/-10.69 |
| chr7:155327298 | CNPY1 | promoter | shores | -6.96 | 1.53E-03 | 50.12+/-12.25 | 55.52+/-14.35 |
| chr7:155295755 | CNPY1 | exon, UTR | inter | -5.56 | 3.25E-03 | 18.04+/-8.2 | 23.71+/-8.94 |
| chr7:155294003 | CNPY1 | exon, UTR | inter | -8.04 | 3.35E-03 | 72.35+/-14.34 | 78+/-4.27 |
| chr7:155327051 | CNPY1 | promoter | shores | -5.44 | 6.63E-03 | 21.08+/-14.71 | 22.15+/-10.96 |
| chr7:155295743 | CNPY1 | exon, UTR | inter | -5.12 | 1.16E-02 | 14.48+/-6.42 | 18.64+/-7.52 |
| chr2:208463292 | CREB1 | intron | inter | 5.38 | 2.83E-28 | 98.92+/-0.94 | 93.92+/-13.84 |
| chr19:18889034 | CRTC1 | exon, UTR | shores | -14.51 | 1.53E-09 | 69.52+/-13.87 | 74.13+/-14.11 |
| chr19:18889003 | CRTC1 | exon, UTR | shores | -15.07 | 5.24E-06 | 60.91+/-13.79 | 65.45+/-14.5 |
| chr19:18892227 | CRTC1 | exon, UTR | shelves | 5.75 | 1.16E-05 | 94.55+/-3.9 | 90.71+/-11.69 |
| chr19:18888942 | CRTC1 | exon, UTR | islands | -12.42 | 2.23E-05 | 76.51+/-15.69 | 80.43+/-14.03 |
| chr19:18888931 | CRTC1 | exon, UTR | islands | -15.56 | 4.74E-05 | 65.93+/-16.82 | 70.96+/-17.47 |
| chr19:18888855 | CRTC1 | exon, UTR | islands | -14.82 | 5.79E-05 | 64.02+/-19.02 | 67.25+/-14.15 |
| chr19:18888968 | CRTC1 | exon, UTR | islands | -11.98 | 7.91E-05 | 76.88+/-17.02 | 77.8+/-12.96 |
| chr19:18888759 | CRTC1 | exon, UTR | islands | -14.40 | 1.36E-04 | 65.54+/-21.15 | 68.77+/-13.73 |
| chr19:18888276 | CRTC1 | exon, UTR | islands | -18.45 | 1.36E-04 | 67.71+/-21.72 | 68.14+/-17.33 |
| chr19:18888806 | CRTC1 | exon, UTR | islands | -11.52 | 1.50E-04 | 68.21+/-17.34 | 68.63+/-14.08 |
| chr19:18888915 | CRTC1 | exon, UTR | islands | -13.32 | 1.77E-04 | 67.09+/-14.81 | 71.53+/-13.45 |
| chr19:18793853 | CRTC1 | promoter | shores | -6.07 | 3.17E-04 | 12.84+/-4.36 | 19.65+/-6.79 |
| chr19:18888884 | CRTC1 | exon, UTR | islands | -13.84 | 3.26E-04 | 66.8+/-18.08 | 66.63+/-18.8 |
| chr19:18888590 | CRTC1 | exon, UTR | islands | -13.05 | 3.70E-04 | 77.01+/-17.08 | 83.28+/-10.43 |
| chr19:18888966 | CRTC1 | exon, UTR | islands | -13.08 | 5.35E-04 | 62.39+/-21.43 | 63.12+/-15.74 |
| chr19:18888962 | CRTC1 | exon, UTR | islands | -13.53 | 1.13E-03 | 65.7+/-18.95 | 67.57+/-14.95 |
| chr19:18888637 | CRTC1 | exon, UTR | islands | -13.57 | 1.55E-03 | 60.95+/-22.74 | 60.67+/-18.76 |
| chr19:18888900 | CRTC1 | exon, UTR | islands | -10.02 | 2.06E-03 | 81.55+/-14.84 | 83.44+/-12.43 |
| chr19:18888668 | CRTC1 | exon, UTR | islands | -12.38 | 3.14E-03 | 57.5+/-21.49 | 59.38+/-13.6 |
| chr19:18888280 | CRTC1 | exon, UTR | islands | -15.76 | 3.59E-03 | 74.26+/-16.74 | 76.34+/-14.58 |
| chr19:18888246 | CRTC1 | exon, UTR | islands | -16.03 | 3.64E-03 | 68.53+/-22.02 | 67.98+/-14.52 |
| chr19:18888799 | CRTC1 | exon, UTR | islands | -13.99 | 3.81E-03 | 66.9+/-16.92 | 71.93+/-13.14 |
| chr19:18888227 | CRTC1 | exon, UTR | islands | -15.04 | 4.01E-03 | 72.97+/-22.88 | 71.4+/-15.07 |
| chr19:18888952 | CRTC1 | exon, UTR | islands | -10.96 | 1.89E-02 | 70.61+/-18.06 | 68.72+/-15.9 |
| chr19:18888230 | CRTC1 | exon, UTR | islands | -11.90 | 1.89E-02 | 83.02+/-11.33 | 87.4+/-9.58 |
| chr19:18888815 | CRTC1 | exon, UTR | islands | -10.33 | 3.50E-02 | 78.93+/-15 | 80.23+/-12.22 |
| chr19:18888865 | CRTC1 | exon, UTR | islands | -9.25 | 3.63E-02 | 80.14+/-14.21 | 81.73+/-10.79 |
| chr19:18888840 | CRTC1 | exon, UTR | islands | -9.42 | 3.63E-02 | 82.6+/-13.59 | 82.83+/-11.98 |
| chr19:18888599 | CRTC1 | exon, UTR | islands | -11.78 | 3.94E-02 | 72.77+/-17.45 | 78.64+/-13.49 |
| chr19:18889147 | CRTC1 | exon, UTR | shores | -7.27 | 4.19E-02 | 76.6+/-11.39 | 78.26+/-10.73 |
| chr19:18888252 | CRTC1 | exon, UTR | islands | -11.83 | 4.71E-02 | 79.69+/-16.39 | 77.91+/-15.82 |
| chr19:18888694 | CRTC1 | exon, UTR | islands | -10.06 | 4.74E-02 | 73.49+/-15.72 | 77.89+/-11.72 |
| chr9:90321583 | DAPK1 | exon, UTR | shores | -18.24 | 8.64E-24 | 48.79+/-27.11 | 50.27+/-39.65 |
| chr9:90262234 | DAPK1 | promoter | inter | 5.32 | 2.04E-20 | 94.74+/-4.24 | 92.02+/-13.15 |
| chr9:90321115 | DAPK1 | exon, UTR | shores | 5.24 | 2.02E-08 | 81.42+/-2.33 | 76.97+/-12.74 |
| chr9:90315135 | DAPK1 | exon, UTR | inter | 6.13 | 1.38E-02 | 82.16+/-3.34 | 79.47+/-6.8 |
| chr11:636199 | DRD4 | promoter | shores | 22.13 | 3.78E-18 | 34.44+/-30.58 | 23.49+/-23.79 |
| chr11:636508 | DRD4 | promoter | islands | -9.54 | 1.72E-02 | 51.63+/-14.5 | 54.62+/-13.82 |
| chr11:639444 | DRD4 | exon | islands | -12.91 | 2.68E-02 | 52.41+/-14.64 | 58.67+/-16.55 |
| chr11:636923 | DRD4 | promoter | islands | -5.09 | 4.49E-02 | 10.95+/-2.47 | 13.83+/-8.44 |
| chr6:311938 | DUSP22 | exon, CDS | inter | -10.96 | 2.05E-16 | 15.43+/-12.43 | 22.86+/-11.87 |
| chr6:351093 | DUSP22 | exon, UTR | inter | 8.17 | 2.22E-10 | 85.26+/-7.7 | 78.33+/-8.22 |
| chr6:311892 | DUSP22 | exon, CDS | inter | -9.26 | 5.22E-08 | 30.78+/-17.31 | 34.94+/-15.57 |
| chr6:311890 | DUSP22 | exon, CDS | inter | -8.97 | 2.62E-07 | 24.61+/-15.68 | 30.69+/-14.7 |
| chr6:291504 | DUSP22 | promoter | shores | 5.33 | 2.10E-06 | 42.92+/-12.47 | 39.01+/-10.47 |
| chr6:338023 | DUSP22 | exon, first\_exon | inter | -7.26 | 4.46E-06 | 32.08+/-12.14 | 40.77+/-13.05 |
| chr6:349848 | DUSP22 | intron | inter | 5.05 | 9.21E-06 | 93.16+/-3.59 | 89.21+/-5.28 |
| chr6:292399 | DUSP22 | exon, UTR, first\_exon | islands | 19.21 | 1.02E-05 | 53.98+/-26.36 | 37.2+/-18.14 |
| chr6:291533 | DUSP22 | promoter | shores | 6.61 | 6.36E-05 | 36.24+/-13.85 | 29.67+/-12.55 |
| chr6:292311 | DUSP22 | exon, UTR, first\_exon | islands | 16.41 | 1.95E-04 | 48.73+/-23.1 | 39+/-19.41 |
| chr6:291634 | DUSP22 | exon, UTR, first\_exon | shores | 6.74 | 2.38E-03 | 47.47+/-16.68 | 36.69+/-17.26 |
| chr6:292371 | DUSP22 | promoter | islands | 15.08 | 7.72E-03 | 49.22+/-23.08 | 37.53+/-17.72 |
| chr6:292440 | DUSP22 | promoter | islands | 15.77 | 1.04E-02 | 46.06+/-22.97 | 35.99+/-19.83 |
| chr6:291687 | DUSP22 | exon, UTR, first\_exon | shores | 9.29 | 1.33E-02 | 41.41+/-18.45 | 33.47+/-16.83 |
| chr6:292385 | DUSP22 | exon, UTR, first\_exon | islands | 11.90 | 1.44E-02 | 53.48+/-27.2 | 46.02+/-22.12 |
| chr6:292355 | DUSP22 | promoter | islands | 11.81 | 1.64E-02 | 57.48+/-25.01 | 47.01+/-22.1 |
| chr6:292304 | DUSP22 | exon, UTR, first\_exon | islands | 10.23 | 1.86E-02 | 56.18+/-26.87 | 51.01+/-22.36 |
| chr6:292389 | DUSP22 | exon, UTR, first\_exon | islands | 13.86 | 2.17E-02 | 51.09+/-24.95 | 39.9+/-18.96 |
| chr6:292314 | DUSP22 | exon, UTR, first\_exon | islands | 9.59 | 2.56E-02 | 54.75+/-25.82 | 49.74+/-22.64 |
| chr6:292329 | DUSP22 | exon, UTR, first\_exon | islands | 12.24 | 2.78E-02 | 54.22+/-25.43 | 43.07+/-21.91 |
| chr6:292291 | DUSP22 | exon, UTR, first\_exon | islands | 10.44 | 4.75E-02 | 56.79+/-26.88 | 48.02+/-22.64 |
| chr1:43834757 | ELOVL1 | promoter | shores | 5.04 | 1.53E-03 | 70.68+/-9.18 | 66.63+/-8.4 |
| chr3:27759159 | EOMES | exon, CDS | shelves | 5.75 | 7.91E-07 | 89.33+/-5.78 | 83.27+/-7.5 |
| chr3:27760901 | EOMES | exon | shores | 5.90 | 3.34E-02 | 52.9+/-8.3 | 48.35+/-10.99 |
| chr1:46859774 | FAAH | promoter | islands | 12.98 | 3.11E-06 | 63.99+/-13.03 | 59.24+/-9.49 |
| chr1:46858748 | FAAH | promoter | shores | -17.18 | 1.97E-04 | 60.3+/-42.29 | 69.14+/-30.72 |
| chr1:46859671 | FAAH | promoter | shores | 6.39 | 1.29E-03 | 75.38+/-9.77 | 73.49+/-7.76 |
| chr12:133064919 | FBRSL1 | promoter | shores | -6.01 | 2.60E-04 | 12.3+/-4.17 | 19.79+/-8.95 |
| chr12:133065155 | FBRSL1 | promoter | shores | -6.13 | 7.19E-04 | 4.7+/-2.86 | 11.59+/-9.14 |
| chr12:133065223 | FBRSL1 | promoter | shores | -5.24 | 2.76E-04 | 1.29+/-1.26 | 8.96+/-7.86 |
| chr12:133083889 | FBRSL1 | exon | inter | -5.19 | 2.78E-02 | 21.58+/-8.88 | 26.18+/-9.55 |
| chr12:133084873 | FBRSL1 | exon | inter | -5.31 | 8.10E-05 | 89.36+/-8.27 | 92.37+/-5.24 |
| chr12:133085873 | FBRSL1 | exon | inter | -9.31 | 1.86E-19 | 90.73+/-13.34 | 94.5+/-8.77 |
| chr12:133085876 | FBRSL1 | exon | inter | -7.94 | 2.51E-12 | 91.09+/-10.47 | 95.56+/-6.74 |
| chr12:133085885 | FBRSL1 | exon | inter | -7.69 | 6.73E-15 | 92.55+/-12.2 | 95.21+/-5.9 |
| chr12:133086073 | FBRSL1 | exon | inter | -5.33 | 5.79E-09 | 93.4+/-10.91 | 94.5+/-9.69 |
| chr12:133086133 | FBRSL1 | exon | inter | -6.24 | 1.80E-10 | 93.37+/-8.38 | 95.89+/-7 |
| chr12:133086139 | FBRSL1 | exon | inter | -7.00 | 2.18E-12 | 91.95+/-10.35 | 93.75+/-8.6 |
| chr12:133086155 | FBRSL1 | exon | inter | -7.99 | 4.43E-11 | 91.36+/-10.23 | 96.12+/-5.69 |
| chr12:133086169 | FBRSL1 | exon | inter | -9.55 | 3.85E-13 | 90.54+/-10.65 | 95.04+/-7.45 |
| chr12:133086172 | FBRSL1 | exon | inter | -6.52 | 8.91E-09 | 92.66+/-9.11 | 95.78+/-7.2 |
| chr12:133086178 | FBRSL1 | exon | inter | -8.21 | 1.93E-09 | 92.2+/-11.04 | 95.1+/-7.51 |
| chr12:133086196 | FBRSL1 | exon | inter | -9.44 | 2.16E-11 | 90.6+/-11.35 | 94.59+/-7.65 |
| chr12:133086235 | FBRSL1 | exon | inter | -8.02 | 5.10E-10 | 91.04+/-10.63 | 93.18+/-8.62 |
| chr12:133086259 | FBRSL1 | exon | inter | -8.77 | 1.86E-10 | 91.8+/-9.54 | 95.82+/-4.64 |
| chr12:133086268 | FBRSL1 | exon | inter | -7.39 | 2.81E-10 | 93.79+/-9.29 | 96.88+/-5.05 |
| chr12:133086298 | FBRSL1 | exon | inter | -5.12 | 5.64E-10 | 94.62+/-8.06 | 94.48+/-9.84 |
| chr12:133086304 | FBRSL1 | exon | inter | -6.06 | 6.19E-07 | 90.93+/-9.69 | 91.27+/-10.37 |
| chr12:133086313 | FBRSL1 | exon | inter | -6.23 | 1.47E-05 | 91.25+/-7.63 | 94.76+/-4 |
| chr12:133086317 | FBRSL1 | exon | inter | -7.88 | 5.36E-09 | 89.89+/-9.09 | 92.07+/-9.82 |
| chr12:133086376 | FBRSL1 | exon | inter | -6.65 | 9.12E-08 | 88.23+/-7.72 | 89.5+/-10.74 |
| chr12:133086389 | FBRSL1 | exon | inter | -6.18 | 4.77E-07 | 91.17+/-9.09 | 91.95+/-8.64 |
| chr12:133086409 | FBRSL1 | exon | inter | -6.65 | 2.73E-06 | 90+/-8.91 | 92.54+/-8.36 |
| chr12:133086422 | FBRSL1 | exon | inter | -7.22 | 6.63E-06 | 87.25+/-12.72 | 87.2+/-9.09 |
| chr12:133086424 | FBRSL1 | exon | inter | -7.47 | 4.22E-08 | 87.76+/-10.39 | 90.86+/-8.44 |
| chr12:133086442 | FBRSL1 | exon | inter | -9.37 | 3.53E-13 | 86.94+/-12.92 | 91.17+/-6.64 |
| chr12:133086448 | FBRSL1 | exon | inter | -8.55 | 1.38E-12 | 89.26+/-13.39 | 91.42+/-6.77 |
| chr12:133086451 | FBRSL1 | exon | inter | -6.37 | 4.20E-05 | 83.97+/-12 | 83.31+/-10.85 |
| chr12:133086454 | FBRSL1 | exon | inter | -5.76 | 2.63E-05 | 86.14+/-13.43 | 85.9+/-10.17 |
| chr12:133086459 | FBRSL1 | exon | inter | -6.73 | 5.30E-10 | 90.78+/-12.02 | 93.63+/-8.18 |
| chr12:133086493 | FBRSL1 | exon | inter | -7.78 | 4.04E-09 | 87.29+/-13.62 | 88.28+/-10.26 |
| chr12:133086496 | FBRSL1 | exon | inter | -8.01 | 2.68E-13 | 88.76+/-12.2 | 91.45+/-14.27 |
| chr12:133086532 | FBRSL1 | exon | inter | -7.91 | 1.70E-08 | 87.21+/-10.99 | 91.23+/-10.15 |
| chr12:133086559 | FBRSL1 | exon | inter | -6.48 | 2.18E-08 | 91.86+/-10.49 | 94.09+/-9.52 |
| chr12:133086565 | FBRSL1 | exon | inter | -8.25 | 1.06E-14 | 90.94+/-11.64 | 94.3+/-9.33 |
| chr12:133086568 | FBRSL1 | exon | inter | -6.57 | 5.33E-10 | 92.35+/-9.47 | 95.21+/-9.59 |
| chr12:133086572 | FBRSL1 | exon | inter | -6.10 | 5.31E-08 | 91+/-9.01 | 93.85+/-9.39 |
| chr12:133086580 | FBRSL1 | exon | inter | -5.61 | 7.25E-11 | 93.1+/-11.26 | 94.99+/-8.46 |
| chr12:133086624 | FBRSL1 | exon | inter | -5.54 | 5.80E-05 | 91.34+/-9 | 93.66+/-7.33 |
| chr12:133086635 | FBRSL1 | exon | inter | -5.13 | 7.89E-07 | 92.56+/-8.32 | 94.9+/-6.86 |
| chr12:133086653 | FBRSL1 | exon | inter | -8.19 | 1.51E-14 | 90.84+/-12.43 | 94.74+/-7.47 |
| chr12:133086658 | FBRSL1 | exon | inter | -5.12 | 1.35E-07 | 92.17+/-9.64 | 93.03+/-8.99 |
| chr12:133086662 | FBRSL1 | exon | inter | -6.69 | 6.09E-08 | 87.76+/-11.13 | 90.7+/-8.51 |
| chr12:133086680 | FBRSL1 | exon | inter | -5.87 | 9.26E-11 | 91.31+/-9.88 | 95.07+/-6.92 |
| chr12:133086715 | FBRSL1 | exon | inter | -5.95 | 5.35E-10 | 90.35+/-8.16 | 94.09+/-7.28 |
| chr12:133086754 | FBRSL1 | exon | inter | -6.23 | 3.04E-09 | 90.32+/-8.04 | 95.34+/-6.61 |
| chr12:133086758 | FBRSL1 | exon | inter | -6.15 | 9.16E-11 | 92.35+/-9.91 | 95.07+/-7.57 |
| chr12:133086794 | FBRSL1 | exon | inter | -8.56 | 6.98E-16 | 87.81+/-11.75 | 93.07+/-9.97 |
| chr12:133086850 | FBRSL1 | exon | inter | -6.60 | 9.81E-08 | 91.66+/-9.06 | 93.61+/-7.56 |
| chr12:133086880 | FBRSL1 | exon | inter | -9.08 | 4.79E-19 | 90.89+/-11.55 | 95.99+/-7.7 |
| chr12:133086883 | FBRSL1 | exon | inter | -8.36 | 7.99E-16 | 91.65+/-12.33 | 94.67+/-6.86 |
| chr12:133086905 | FBRSL1 | exon | inter | -6.38 | 2.03E-13 | 93.28+/-9.96 | 95.79+/-5.6 |
| chr12:133086990 | FBRSL1 | exon | inter | -7.05 | 1.50E-12 | 91.19+/-9.7 | 95.69+/-5.83 |
| chr12:133102350 | FBRSL1 | exon, CDS | islands | 6.14 | 9.51E-12 | 97.56+/-1.76 | 94.57+/-12.81 |
| chr12:133148752 | FBRSL1 | exon, first\_exon | islands | 5.19 | 2.00E-02 | 81.34+/-5.39 | 75+/-9.79 |
| chr12:133160467 | FBRSL1 | exon, UTR | islands | 20.23 | 3.38E-63 | 92.84+/-7.79 | 78.33+/-30.24 |
| chr6:30708274 | FLOT1 | exon, CDS | shelves | 5.24 | 3.48E-15 | 94.64+/-4.79 | 91.84+/-12.69 |
| chr9:89559401 | GAS1 | exon, UTR, first\_exon | shores | 6.81 | 2.12E-04 | 56.57+/-16.12 | 49.41+/-10.36 |
| chr9:89560072 | GAS1 | exon, UTR, first\_exon | shores | -5.23 | 8.99E-03 | 60.98+/-12.12 | 63.82+/-7.8 |
| chr6:34029204 | GRM4 | exon | inter | 27.63 | 1.69E-104 | 47.81+/-39 | 30.71+/-29.05 |
| chr6:34026938 | GRM4 | exon | shelves | 23.61 | 3.68E-81 | 18.1+/-23.71 | 2.63+/-7.08 |
| chr6:34029047 | GRM4 | exon | inter | 26.58 | 4.85E-53 | 51.35+/-39.31 | 41.02+/-32.54 |
| chr6:34123877 | GRM4 | promoter | shores | -16.78 | 8.48E-37 | 38.61+/-34.89 | 55.54+/-34.94 |
| chr6:34123390 | GRM4 | exon, UTR, first\_exon | shores | -14.08 | 5.08E-18 | 47.38+/-37.77 | 60.54+/-35.68 |
| chr6:34028509 | GRM4 | exon | inter | 5.89 | 7.59E-16 | 94.11+/-3.41 | 90.84+/-12.89 |
| chr6:34124369 | GRM4 | promoter | shores | -9.94 | 2.40E-10 | 32.45+/-27.38 | 40.86+/-28.05 |
| chr6:34030821 | GRM4 | intron | inter | -5.74 | 3.29E-07 | 57.89+/-10.55 | 59.81+/-10.45 |
| chr6:34028093 | GRM4 | exon | shelves | -7.88 | 3.73E-06 | 86.94+/-17.63 | 90.56+/-10.55 |
| chr6:34078484 | GRM4 | intron | inter | -5.88 | 9.25E-06 | 89.35+/-10.71 | 94.82+/-3.13 |
| chr6:34024399 | GRM4 | exon | islands | 7.59 | 2.14E-05 | 54.19+/-16.26 | 51.92+/-11.53 |
| chr6:34078462 | GRM4 | intron | inter | 20.51 | 4.85E-05 | 31.57+/-26.98 | 24.14+/-26.5 |
| chr6:34123489 | GRM4 | promoter | shores | -9.00 | 4.86E-04 | 38.91+/-31.9 | 48.41+/-26.32 |
| chr6:34124380 | GRM4 | promoter | shores | 5.88 | 8.23E-04 | 61.66+/-7.24 | 55.77+/-10.06 |
| chr6:34023353 | GRM4 | exon | shores | -5.79 | 9.38E-04 | 11.55+/-4.35 | 15.85+/-5.56 |
| chr6:34024336 | GRM4 | exon | islands | 5.64 | 9.36E-03 | 47.53+/-9.91 | 42.08+/-13.7 |
| chr6:34024362 | GRM4 | exon | islands | 5.77 | 9.91E-03 | 87.38+/-7.3 | 79.3+/-9.98 |
| chr6:34024312 | GRM4 | exon | islands | 11.24 | 1.04E-02 | 58.18+/-9.3 | 41.44+/-15.08 |
| chr6:34123333 | GRM4 | exon, UTR, first\_exon | shores | -8.52 | 1.11E-02 | 54.22+/-10.26 | 62.5+/-7.75 |
| chr6:34023694 | GRM4 | exon | shores | -6.36 | 1.62E-02 | 72.3+/-6.25 | 77.37+/-7.98 |
| chr6:34024076 | GRM4 | exon | shores | 7.69 | 2.17E-02 | 51.64+/-4.37 | 43.36+/-15.41 |
| chr6:29975328 | HLA-J/ZNRD1-AS1 | exon/intron | islands | -6.17 | 7.20E-10 | 7.82+/-5 | 11.19+/-12.14 |
| chr6:29974065 | HLA-J/ZNRD1-AS1 | promoter/intron | shores | -5.94 | 1.41E-07 | 14.82+/-11.65 | 18.88+/-11.35 |
| chr6:29974022 | HLA-J/ZNRD1-AS1 | promoter/intron | shores | -7.41 | 5.51E-06 | 32.68+/-15.76 | 33.68+/-14.67 |
| chr6:29973407 | HLA-J/ZNRD1-AS1 | promoter/intron | shores | 8.22 | 3.52E-02 | 70.66+/-6.26 | 66.81+/-9.42 |
| chr22:35782831 | HMOX1 | promoter | inter | 7.48 | 3.77E-26 | 98.13+/-1.53 | 93.99+/-14.49 |
| chr22:35782911 | HMOX1 | promoter | inter | 7.77 | 1.91E-18 | 91.33+/-2.46 | 86.58+/-14.49 |
| chr22:35774876 | HMOX1 | promoter | shelves | 6.12 | 1.64E-16 | 81.87+/-6.47 | 80.27+/-16.28 |
| chr22:35777184 | HMOX1 | exon, first\_exon | islands | 8.15 | 1.70E-05 | 8.05+/-19.82 | 0.17+/-0.55 |
| chr6:30713295 | IER3 | promoter | shores | -23.48 | 4.49E-72 | 73.05+/-24.04 | 83.49+/-21.64 |
| chr6:30712839 | IER3 | promoter | shores | -9.18 | 2.24E-02 | 75.86+/-15.16 | 85.11+/-3.99 |
| chr4:6051617 | JAKMIP1 | intron | inter | -5.76 | 4.33E-05 | 75.22+/-5.62 | 77.5+/-4.41 |
| chr4:6107546 | JAKMIP1 | intron | islands | -7.76 | 5.23E-04 | 67.46+/-15.08 | 73.79+/-9.71 |
| chr4:6114676 | JAKMIP1 | intron | islands | 13.58 | 5.65E-04 | 96.65+/-2.43 | 93.46+/-14.08 |
| chr4:6052355 | JAKMIP1 | exon, CDS | inter | 5.99 | 1.85E-02 | 75.31+/-9.17 | 71.71+/-11.57 |
| chr4:6107226 | JAKMIP1 | intron | islands | 11.79 | 2.97E-02 | 60.69+/-9.43 | 53.93+/-12.27 |
| chr4:6107280 | JAKMIP1 | intron | islands | 7.73 | 3.18E-02 | 54.43+/-7.93 | 50.59+/-10.97 |
| chr17:72351374 | KIF19 | exon, CDS | shores | 7.16 | 2.78E-13 | 94.42+/-2.86 | 91.06+/-12.06 |
| chr17:72351406 | KIF19 | exon, CDS | shores | 19.37 | 7.05E-11 | 55.1+/-21.91 | 41.34+/-34.04 |
| chr17:72345115 | KIF19 | exon, first\_exon | shelves | -12.11 | 6.36E-08 | 27.29+/-19.32 | 35.91+/-21.09 |
| chr17:72321958 | KIF19 | promoter | islands | 8.49 | 1.07E-06 | 44.56+/-14.77 | 39.08+/-11.75 |
| chr17:72349067 | KIF19 | exon, CDS | shores | -12.74 | 4.44E-06 | 42.09+/-32.43 | 52.99+/-32.08 |
| chr17:72321961 | KIF19 | promoter | islands | 6.74 | 5.09E-04 | 37.53+/-6.25 | 31.66+/-11.62 |
| chr17:72348242 | KIF19 | exon, CDS | islands | 5.89 | 6.30E-04 | 6.96+/-5.34 | 4.58+/-4.2 |
| chr17:72321956 | KIF19 | promoter | islands | 5.26 | 1.22E-03 | 14.77+/-5.46 | 9.77+/-5.5 |
| chr17:72321949 | KIF19 | promoter | islands | 6.57 | 1.42E-03 | 35.49+/-12.55 | 34.28+/-8.98 |
| chr17:72348228 | KIF19 | exon, CDS | islands | 10.65 | 2.06E-03 | 27.76+/-8.61 | 20.94+/-9.8 |
| chr17:72343968 | KIF19 | promoter | shelves | -9.89 | 6.36E-03 | 71.6+/-9.17 | 70.82+/-11.51 |
| chr17:72348239 | KIF19 | exon, CDS | islands | 10.13 | 6.97E-03 | 23.77+/-7.74 | 17.29+/-11.74 |
| chr17:72343981 | KIF19 | promoter | shelves | -7.50 | 8.26E-03 | 64.08+/-11.79 | 60.53+/-10.21 |
| chr17:72348210 | KIF19 | exon, CDS | islands | 6.12 | 1.37E-02 | 14.15+/-9.48 | 7.91+/-3.97 |
| chr17:72343951 | KIF19 | promoter | shelves | -7.83 | 2.63E-02 | 75.35+/-11.66 | 70.83+/-12.33 |
| chr6:168431480 | KIF25 | exon, first\_exon | inter | -15.47 | 2.69E-33 | 87.41+/-17.22 | 94.17+/-2.32 |
| chr6:168399879 | KIF25 | exon, UTR, first\_exon | shelves | 5.33 | 3.53E-28 | 68.17+/-23.94 | 58.95+/-33.45 |
| chr6:168440826 | KIF25 | exon, CDS | inter | -13.28 | 5.01E-18 | 88.03+/-15.16 | 89.69+/-14.87 |
| chr19:51480510 | KLK7 | exon, UTR | inter | 6.64 | 4.52E-48 | 93.73+/-1.01 | 87+/-16.61 |
| chr19:51480312 | KLK7 | exon, UTR | inter | -6.58 | 1.73E-22 | 78.69+/-18.19 | 84.94+/-12.58 |
| chr19:51487478 | KLK7 | promoter | inter | 8.57 | 2.57E-08 | 26.08+/-6.85 | 19.06+/-9.44 |
| chr19:51487506 | KLK7 | promoter | inter | 11.11 | 8.75E-08 | 31.1+/-14.33 | 20.39+/-10.1 |
| chr19:51487209 | KLK7 | exon, first\_exon | inter | 12.09 | 1.68E-04 | 32.46+/-21.04 | 20.09+/-12.48 |
| chr19:51485352 | KLK7 | exon | inter | -7.15 | 1.28E-03 | 87.87+/-13.81 | 93.81+/-2.77 |
| chr19:51485078 | KLK7 | exon, UTR | inter | 5.42 | 2.35E-03 | 94.6+/-3.17 | 89.21+/-5.83 |
| chr19:51483506 | KLK7 | exon, CDS | inter | -7.59 | 3.18E-03 | 57.34+/-13.64 | 60.8+/-13.93 |
| chr19:51483154 | KLK7 | exon, CDS | inter | 5.98 | 6.95E-03 | 67.97+/-17.32 | 61.48+/-13.65 |
| chr19:51487220 | KLK7 | exon, first\_exon | inter | 7.43 | 3.02E-02 | 23.8+/-17.27 | 14.73+/-9.02 |
| chr9:126777471 | LHX2 | promoter | islands | 5.83 | 2.10E-02 | 23.82+/-11.37 | 12.81+/-7.08 |
| chr9:126762837 | LHX2 | promoter | shores | 5.20 | 2.27E-02 | 15.33+/-12.25 | 11.96+/-9.86 |
| chr9:126777422 | LHX2 | promoter | islands | 6.16 | 2.86E-02 | 27.12+/-11.81 | 23.21+/-13.25 |
| chr9:126777465 | LHX2 | promoter | islands | 6.16 | 2.89E-02 | 25.64+/-9.54 | 17.12+/-5.06 |
| chr9:126795162 | LHX2 | exon, UTR | inter | 5.31 | 3.57E-02 | 86.16+/-9.16 | 81.34+/-6.73 |
| chr17:43971230 | MAPT | promoter | shores | -6.71 | 1.59E-03 | 56.53+/-13.45 | 63.13+/-8.02 |
| chr17:44050822 | MAPT | exon, UTR, first\_exon | inter | 15.44 | 4.81E-07 | 76.65+/-29.12 | 68.89+/-24.86 |
| chr17:44051923 | MAPT | promoter | inter | 17.19 | 2.04E-04 | 75.73+/-33.42 | 65.52+/-31.53 |
| chr17:44052493 | MAPT | promoter | inter | 8.23 | 7.59E-03 | 71.85+/-3.35 | 67.81+/-7.36 |
| chr17:44054236 | MAPT | exon, first\_exon | inter | 18.99 | 4.04E-08 | 75.92+/-34.14 | 68.06+/-30.92 |
| chr17:44054466 | MAPT | exon, first\_exon | inter | -6.01 | 3.51E-03 | 81.13+/-9.78 | 81.69+/-7.55 |
| chr17:44054508 | MAPT | exon, first\_exon | inter | -6.12 | 1.97E-02 | 78.9+/-9.49 | 81.3+/-8.64 |
| chr17:44054839 | MAPT | exon, first\_exon | inter | -7.77 | 2.80E-03 | 44.97+/-12.01 | 43.33+/-9.53 |
| chr17:44056832 | MAPT | exon, first\_exon | shelves | 17.35 | 6.07E-05 | 60.86+/-27.14 | 49.3+/-25.46 |
| chr17:44057594 | MAPT | exon, first\_exon | shelves | 20.24 | 1.26E-04 | 71.95+/-36.84 | 65.32+/-33.47 |
| chr17:44060247 | MAPT | exon, first\_exon | islands | 19.83 | 5.60E-07 | 73.75+/-31.99 | 64.6+/-32.16 |
| chr17:44061022 | MAPT | exon, first\_exon | shores | 18.96 | 1.53E-04 | 68.37+/-29.25 | 58.76+/-27.6 |
| chr17:44061260 | MAPT | exon, first\_exon | shores | -6.18 | 1.73E-04 | 66.56+/-12.24 | 67.76+/-11.54 |
| chr17:44061278 | MAPT | exon, first\_exon | shores | 13.42 | 4.30E-03 | 62.64+/-29.84 | 55.08+/-28.29 |
| chr17:44068923 | MAPT | exon, CDS | inter | 19.31 | 5.01E-06 | 71.88+/-33.95 | 66.2+/-34.74 |
| chr17:44068927 | MAPT | exon, CDS | inter | 5.21 | 3.94E-17 | 95.33+/-1.3 | 92.01+/-12.38 |
| chr17:44073988 | MAPT | exon, CDS | inter | -5.12 | 4.83E-02 | 84.72+/-5.52 | 90.03+/-5.9 |
| chr17:44102000 | MAPT | exon, UTR | inter | 13.50 | 1.95E-02 | 86.49+/-7.8 | 84.3+/-15.12 |
| chr17:44102584 | MAPT | exon, UTR | inter | 7.23 | 2.17E-24 | 94.76+/-6.5 | 93.11+/-11.75 |
| chr17:44103258 | MAPT | exon, UTR | inter | 9.86 | 7.51E-03 | 83.64+/-4.71 | 77.15+/-7.27 |
| chr17:44103553 | MAPT | exon, UTR | inter | 13.70 | 2.43E-04 | 53.51+/-13.74 | 47.98+/-16.14 |
| chr17:44103658 | MAPT | exon, UTR | inter | 15.19 | 4.02E-02 | 53.22+/-8.9 | 48.5+/-16.68 |
| chr17:44103671 | MAPT | exon, UTR | inter | 15.23 | 2.92E-02 | 56.93+/-9.48 | 51.85+/-16.73 |
| chr17:44103786 | MAPT | exon, UTR | inter | 14.48 | 4.23E-02 | 65.2+/-9.56 | 61.67+/-19.66 |
| chr17:44103815 | MAPT | exon, UTR | inter | 15.14 | 2.74E-02 | 54.05+/-7.82 | 48.4+/-16.83 |
| chr17:44103914 | MAPT | exon, UTR | inter | 12.63 | 1.53E-04 | 37.28+/-11.79 | 35.79+/-14.41 |
| chr17:44103957 | MAPT | exon, UTR | inter | 17.88 | 4.23E-04 | 56.62+/-10.35 | 52.64+/-16.13 |
| chr17:44103975 | MAPT | exon, UTR | inter | 17.01 | 1.87E-03 | 72.02+/-10.81 | 72.65+/-18.55 |
| chr17:44103999 | MAPT | exon, UTR | inter | 15.39 | 2.29E-03 | 54.58+/-7.29 | 55.15+/-17.34 |
| chr17:44104179 | MAPT | exon, UTR | inter | 10.66 | 4.83E-03 | 49.36+/-12.12 | 51.81+/-15.26 |
| chr17:44104319 | MAPT | exon, UTR | inter | 7.60 | 4.02E-03 | 23.95+/-9.31 | 25.05+/-10.81 |
| chr17:44104393 | MAPT | exon, UTR | inter | 10.14 | 4.67E-03 | 31.21+/-10.01 | 29.36+/-12.11 |
| chr17:44104586 | MAPT | exon, UTR | inter | 13.65 | 7.53E-08 | 31.19+/-11.87 | 28.11+/-10.5 |
| chr17:44104686 | MAPT | exon, UTR | inter | 18.63 | 2.36E-12 | 60.58+/-7.48 | 50.07+/-13.11 |
| chr17:44105229 | MAPT | exon, UTR | inter | 12.28 | 5.24E-03 | 53.2+/-5.61 | 46.24+/-10 |
| chr18:74693395 | MBP | intron | shores | 8.04 | 5.76E-73 | 83.01+/-22.38 | 79.75+/-29.1 |
| chr18:74702863 | MBP | intron | inter | -19.51 | 9.29E-61 | 21.76+/-23.24 | 35.15+/-29.03 |
| chr18:74695777 | MBP | intron | inter | 8.88 | 1.12E-43 | 7.3+/-20.35 | 0.19+/-0.61 |
| chr18:74697407 | MBP | intron | inter | -17.30 | 1.08E-39 | 63.02+/-35.64 | 84.93+/-19.7 |
| chr18:74701983 | MBP | exon, CDS | inter | 5.84 | 1.85E-38 | 84.37+/-18.84 | 82.74+/-21.26 |
| chr18:74699134 | MBP | intron | inter | 12.39 | 1.94E-33 | 80.48+/-8.44 | 68.82+/-29.07 |
| chr18:74696525 | MBP | intron | inter | -17.73 | 3.18E-28 | 64.69+/-35.84 | 86.64+/-20.5 |
| chr18:74694543 | MBP | exon, UTR | shelves | -5.57 | 7.92E-25 | 91.02+/-17.17 | 94.99+/-2.51 |
| chr18:74727631 | MBP | exon, UTR | inter | -5.37 | 6.56E-19 | 38.59+/-22.63 | 48.4+/-16.78 |
| chr18:74799373 | MBP | intron | islands | 18.43 | 5.86E-18 | 84.29+/-7.75 | 68.58+/-15.18 |
| chr18:74799394 | MBP | intron | islands | 19.02 | 1.36E-17 | 87.92+/-5.44 | 70.91+/-16.57 |
| chr18:74799500 | MBP | intron | islands | 19.74 | 2.21E-16 | 92.87+/-5.03 | 78.55+/-15.08 |
| chr18:74799492 | MBP | intron | islands | 17.66 | 2.46E-15 | 94.42+/-3.8 | 81.83+/-13.54 |
| chr18:74695143 | MBP | intron | shelves | 6.17 | 3.72E-15 | 30.11+/-14.34 | 22.62+/-13.12 |
| chr18:74725348 | MBP | exon, UTR | inter | 9.01 | 2.25E-13 | 86.85+/-12.05 | 76.3+/-26.54 |
| chr18:74799551 | MBP | intron | islands | 18.23 | 2.68E-13 | 93.53+/-4.18 | 81.05+/-10.92 |
| chr18:74799371 | MBP | intron | islands | 17.57 | 1.92E-12 | 67.7+/-7.81 | 56.23+/-14.37 |
| chr18:74799488 | MBP | intron | islands | 18.15 | 2.36E-12 | 89.84+/-8.81 | 77.06+/-14.75 |
| chr18:74799495 | MBP | intron | islands | 18.03 | 2.80E-11 | 90+/-6.57 | 77.11+/-13.99 |
| chr18:74799413 | MBP | intron | islands | 17.25 | 2.96E-11 | 85.83+/-7.3 | 70.74+/-16.59 |
| chr18:74799490 | MBP | intron | islands | 16.15 | 2.35E-10 | 88.86+/-5.85 | 79.04+/-13.09 |
| chr18:74799320 | MBP | intron | islands | 12.51 | 6.43E-10 | 74.05+/-6.57 | 63.81+/-13.38 |
| chr18:74799549 | MBP | intron | islands | 15.30 | 1.21E-09 | 90.65+/-9.6 | 80.13+/-12.08 |
| chr18:74799575 | MBP | intron | islands | 18.66 | 2.73E-09 | 89.23+/-7.16 | 78.28+/-12.71 |
| chr18:74799572 | MBP | intron | islands | 17.29 | 8.58E-09 | 89.61+/-6.62 | 76.89+/-13.94 |
| chr18:74702851 | MBP | intron | inter | -9.07 | 1.33E-08 | 68.03+/-10.35 | 75.22+/-10.97 |
| chr18:74799556 | MBP | intron | islands | 16.58 | 4.26E-08 | 91.52+/-6.39 | 80.94+/-12.31 |
| chr18:74799411 | MBP | intron | islands | 16.69 | 3.35E-07 | 64.02+/-22.42 | 46.68+/-22.72 |
| chr18:74695205 | MBP | intron | shelves | 6.07 | 2.10E-06 | 83.73+/-11.93 | 80.44+/-7.11 |
| chr18:74817167 | MBP | exon, CDS | inter | -7.04 | 1.19E-05 | 59.6+/-10.18 | 66.07+/-9.29 |
| chr18:74728823 | MBP | exon, CDS | inter | -8.09 | 1.64E-05 | 86.35+/-23.19 | 98.52+/-1.11 |
| chr18:74698585 | MBP | intron | inter | 14.87 | 4.55E-04 | 61.45+/-5.62 | 53.67+/-13.48 |
| chr18:74692795 | MBP | intron | shores | -5.17 | 5.99E-03 | 81.68+/-16.02 | 92.12+/-3.66 |
| chr18:74726214 | MBP | exon, UTR | inter | -7.15 | 1.37E-02 | 85.42+/-22.01 | 95.79+/-4.43 |
| chr18:74807414 | MBP | intron | shelves | 9.71 | 1.85E-02 | 44.6+/-11.35 | 44.13+/-14.97 |
| chr18:74698603 | MBP | intron | inter | 6.26 | 2.20E-02 | 89.25+/-4.37 | 84.71+/-5.43 |
| chr18:74695224 | MBP | intron | shelves | 5.39 | 2.53E-02 | 68.54+/-13.77 | 68.46+/-9.66 |
| chr18:74700602 | MBP | intron | inter | -5.61 | 4.11E-02 | 81.23+/-2.02 | 85.36+/-4.3 |
| chr18:74722006 | MBP | intron | inter | -10.24 | 4.77E-02 | 82.56+/-21.4 | 83.1+/-27.11 |
| chr22:50527817 | MOV10L1 | promoter | shores | -9.26 | 3.69E-08 | 76.55+/-34.72 | 70.75+/-31.37 |
| chr22:50528054 | MOV10L1 | promoter | shores | -7.57 | 2.98E-04 | 76.7+/-12.92 | 77.15+/-7.66 |
| chr22:50528251 | MOV10L1 | promoter | islands | 6.10 | 1.64E-02 | 17.06+/-13.23 | 7.51+/-5.86 |
| chr22:50528450 | MOV10L1 | exon, UTR, first\_exon | islands | 10.53 | 3.37E-04 | 78.14+/-14.47 | 66.62+/-13.85 |
| chr22:50528459 | MOV10L1 | promoter | islands | 6.71 | 4.67E-03 | 52.02+/-18.56 | 44.65+/-13.06 |
| chr22:50528669 | MOV10L1 | promoter | islands | 7.08 | 2.59E-02 | 60.65+/-16.91 | 59.6+/-10.12 |
| chr22:50529071 | MOV10L1 | intron | islands | -15.10 | 2.34E-43 | 92.06+/-18.63 | 97.76+/-2.63 |
| chr22:50546666 | MOV10L1 | exon, CDS | inter | -14.83 | 2.63E-14 | 77.59+/-34.83 | 74.52+/-29.43 |
| chr22:50572472 | MOV10L1 | exon, UTR | inter | -10.39 | 1.23E-12 | 74.66+/-32.54 | 71.39+/-28.28 |
| chr22:50582550 | MOV10L1 | exon, CDS | inter | -8.35 | 1.78E-08 | 79.45+/-32.55 | 77.94+/-23.06 |
| chr22:50582666 | MOV10L1 | exon, CDS | inter | 5.32 | 2.95E-02 | 66.22+/-8.16 | 61.4+/-9.68 |
| chr22:50584129 | MOV10L1 | promoter | inter | 5.80 | 5.44E-11 | 91.46+/-3.15 | 87.28+/-11.42 |
| chr22:50585393 | MOV10L1 | promoter | inter | 7.09 | 6.11E-04 | 85.21+/-7.7 | 80.21+/-5.89 |
| chr22:50585400 | MOV10L1 | exon, UTR, first\_exon | inter | 6.42 | 3.02E-03 | 82.91+/-7.41 | 77.86+/-6.89 |
| chr22:50585413 | MOV10L1 | exon, UTR, first\_exon | inter | 6.16 | 2.87E-03 | 84.41+/-5.62 | 78.99+/-7.08 |
| chr22:50585427 | MOV10L1 | exon, UTR, first\_exon | inter | 9.89 | 7.21E-09 | 79.29+/-9.28 | 73.44+/-6.66 |
| chr22:50585490 | MOV10L1 | exon, UTR, first\_exon | inter | 8.56 | 3.00E-04 | 73.75+/-8.92 | 67.47+/-6.24 |
| chr22:50587951 | MOV10L1 | exon, UTR, first\_exon | inter | 10.59 | 2.60E-05 | 69.43+/-8.5 | 60.92+/-13.57 |
| chr22:50588008 | MOV10L1 | exon, UTR, first\_exon | inter | 5.17 | 1.34E-02 | 71.69+/-4.17 | 68.79+/-7.71 |
| chr22:50596654 | MOV10L1 | exon, CDS | inter | -5.68 | 8.66E-10 | 85.53+/-16 | 89.27+/-5.99 |
| chr11:19901631 | NAV2 | exon, CDS | inter | -9.70 | 3.58E-40 | 47.91+/-24.9 | 56.78+/-31.85 |
| chr11:20044114 | NAV2 | exon, UTR, first\_exon | inter | 7.42 | 2.55E-36 | 93.17+/-3.21 | 84.7+/-15.43 |
| chr11:20101704 | NAV2 | exon, CDS | inter | 15.73 | 3.70E-20 | 15.95+/-19.93 | 8.94+/-17.11 |
| chr11:20139843 | NAV2 | exon | inter | 6.55 | 5.16E-19 | 95.74+/-2.7 | 91.6+/-12.68 |
| chr11:20112491 | NAV2 | exon, CDS | inter | -10.98 | 2.14E-12 | 40.42+/-38.02 | 54.11+/-35.29 |
| chr11:19955322 | NAV2 | exon, CDS | inter | -5.03 | 1.16E-09 | 88.41+/-13.99 | 94.44+/-2.11 |
| chr11:19371522 | NAV2 | promoter | shelves | 9.55 | 1.87E-09 | 71.86+/-9.86 | 65.69+/-8.45 |
| chr11:19371067 | NAV2 | promoter | shelves | 6.31 | 2.69E-09 | 81.52+/-12.2 | 76.79+/-10.1 |
| chr11:19371465 | NAV2 | promoter | shelves | -5.89 | 1.89E-02 | 57.07+/-12.87 | 59.83+/-8.26 |
| chr1:39491459 | NDUFS5 | promoter | inter | -8.87 | 3.23E-04 | 35.42+/-8.8 | 42.06+/-7.33 |
| chr1:39491348 | NDUFS5 | promoter | inter | -8.92 | 2.09E-02 | 48.86+/-8.47 | 58.67+/-8.59 |
| chr1:39500094 | NDUFS5 | exon, CDS | inter | 5.92 | 4.43E-02 | 60.85+/-10.38 | 55.74+/-11.15 |
| chr4:103458876 | NFKB1 | exon, first\_exon | inter | 33.60 | 1.80E-107 | 59.51+/-30.64 | 28.54+/-36.15 |
| chr4:103514605 | NFKB1 | exon, first\_exon | inter | -12.49 | 1.36E-03 | 44.45+/-7.27 | 50.12+/-13.57 |
| chr17:47587819 | NGFR | exon, CDS | shelves | 13.05 | 1.77E-19 | 86.05+/-21.32 | 75.26+/-21.97 |
| chr17:47583677 | NGFR | exon, UTR | islands | -5.50 | 1.06E-04 | 85.15+/-7.62 | 85.29+/-4.66 |
| chr17:47589394 | NGFR | exon, CDS | shores | -11.42 | 3.17E-02 | 66.13+/-6.82 | 71.68+/-10.25 |
| chr19:41190874 | NUMBL | exon, first\_exon | shores | -16.71 | 5.25E-44 | 56.45+/-33.79 | 84.22+/-23.15 |
| chr19:41191584 | NUMBL | exon, first\_exon | shores | -14.04 | 5.15E-33 | 76.96+/-19.29 | 85.78+/-4.64 |
| chr19:41197662 | NUMBL | promoter | shores | -9.70 | 3.33E-07 | 57.76+/-9.43 | 60.11+/-11.69 |
| chr19:41197525 | NUMBL | promoter | shores | -6.67 | 2.50E-05 | 62.08+/-10.72 | 61.51+/-18.11 |
| chr19:41197589 | NUMBL | promoter | shores | -7.09 | 5.06E-05 | 67.96+/-9.54 | 68.46+/-10.85 |
| chr19:41197652 | NUMBL | promoter | shores | -8.73 | 5.34E-05 | 37.16+/-11.39 | 39.98+/-9.51 |
| chr19:41197737 | NUMBL | promoter | shores | -10.22 | 9.68E-05 | 65.54+/-10.97 | 66.75+/-9.4 |
| chr19:41197703 | NUMBL | promoter | shores | -7.78 | 1.27E-04 | 76.52+/-11.48 | 76.44+/-5.79 |
| chr19:41197598 | NUMBL | promoter | shores | -5.66 | 1.65E-04 | 26.76+/-8.5 | 28.39+/-7.73 |
| chr19:41195526 | NUMBL | intron | shores | 9.69 | 6.84E-04 | 46.29+/-11.94 | 43.33+/-15.55 |
| chr19:41197723 | NUMBL | promoter | shores | -6.93 | 8.43E-03 | 72.12+/-6.31 | 74.16+/-8 |
| chr19:41197384 | NUMBL | promoter | shores | -5.01 | 4.07E-02 | 35.88+/-7.91 | 40.36+/-17.82 |
| chr1:29190137 | OPRD1 | exon, UTR | shores | 47.85 | 4.34E-125 | 50.42+/-36.14 | 23.36+/-34.02 |
| chr1:29138162 | OPRD1 | promoter | shores | 8.72 | 2.73E-03 | 80.29+/-7.56 | 70.24+/-9.97 |
| chr1:29189836 | OPRD1 | exon, UTR | islands | -7.66 | 4.30E-03 | 76.88+/-10.99 | 83.15+/-8.87 |
| chr1:29189818 | OPRD1 | exon, UTR | islands | -8.50 | 1.76E-02 | 80.47+/-13.27 | 90.46+/-6.49 |
| chr1:29138200 | OPRD1 | promoter | shores | -6.41 | 4.22E-02 | 82.98+/-11.87 | 84.97+/-8.76 |
| chr13:66877393 | PCDH9 | exon, UTR | inter | -11.41 | 3.45E-09 | 72.48+/-13.15 | 77.35+/-4.58 |
| chr13:67802512 | PCDH9 | exon, CDS | shelves | -6.19 | 5.70E-08 | 73.25+/-9.48 | 78.78+/-7.51 |
| chr13:67801122 | PCDH9 | exon, CDS | shelves | -10.45 | 4.21E-05 | 43.29+/-12.01 | 46.35+/-9.74 |
| chr13:67799686 | PCDH9 | exon, CDS | inter | -6.51 | 1.31E-04 | 44.92+/-14.53 | 51.54+/-8.58 |
| chr13:67799701 | PCDH9 | exon, CDS | inter | -6.20 | 1.35E-04 | 71.75+/-9.12 | 73.82+/-6.23 |
| chr13:67801043 | PCDH9 | exon, CDS | shelves | -8.17 | 3.48E-04 | 61.75+/-13.12 | 63.27+/-8.42 |
| chr13:67801551 | PCDH9 | exon, CDS | shelves | -5.01 | 8.02E-04 | 78.81+/-8.48 | 79.29+/-9.13 |
| chr13:67801125 | PCDH9 | exon, CDS | shelves | -6.98 | 9.40E-03 | 28.9+/-14.07 | 33.39+/-10.14 |
| chr13:67802655 | PCDH9 | exon, UTR | shores | -5.21 | 3.66E-02 | 57.59+/-12.23 | 58.52+/-7.84 |
| chr13:67802395 | PCDH9 | exon, CDS | shelves | -5.20 | 4.36E-02 | 48.01+/-13.94 | 52.05+/-7.59 |
| chr5:146434146 | PPP2R2B | intron | inter | 24.35 | 1.98E-46 | 74.18+/-27.88 | 50.9+/-28.76 |
| chr5:146435481 | PPP2R2B | intron | inter | 6.06 | 1.57E-08 | 50.44+/-17.55 | 47.08+/-12.2 |
| chr5:146435620 | PPP2R2B | intron | inter | 5.22 | 3.14E-03 | 26.01+/-19.62 | 20.17+/-7.86 |
| chr1:3352502 | PRDM16 | exon, UTR | shores | -20.05 | 1.50E-26 | 4.94+/-10.2 | 26.2+/-34.86 |
| chr1:3354708 | PRDM16 | exon, UTR | shelves | -5.38 | 4.42E-26 | 88.78+/-17.76 | 94.93+/-1.35 |
| chr1:3352174 | PRDM16 | exon, UTR | shores | -6.03 | 8.05E-23 | 89.64+/-16.13 | 94.48+/-2.6 |
| chr1:3352202 | PRDM16 | exon, UTR | shores | -5.79 | 5.44E-18 | 85.06+/-16.66 | 90.63+/-4.49 |
| chr1:3352328 | PRDM16 | exon, UTR | shores | -7.21 | 4.33E-10 | 78.81+/-15.88 | 87.25+/-3.94 |
| chr1:3352865 | PRDM16 | exon, UTR | shores | -9.89 | 1.18E-04 | 82.43+/-22.54 | 91.87+/-12.2 |
| chr1:3154621 | PRDM16 | exon, first\_exon | shores | 9.63 | 1.22E-03 | 83.75+/-20.23 | 77.6+/-24.02 |
| chr1:3319386 | PRDM16 | exon, CDS | shores | 11.39 | 5.93E-03 | 94.93+/-2.38 | 89.63+/-11.56 |
| chr1:3103106 | PRDM16 | intron | islands | -5.48 | 2.08E-02 | 85.75+/-4.16 | 87.98+/-4.64 |
| chr6:32117171 | PRRT1 | exon, CDS | islands | 6.13 | 3.51E-02 | 56.29+/-16.21 | 46.6+/-11.33 |
| chr6:32117154 | PRRT1 | exon, CDS | islands | 6.19 | 3.86E-02 | 54.27+/-8.92 | 50.72+/-13.84 |
| chr14:73612768 | PSEN1 | promoter | inter | 5.58 | 5.53E-20 | 95.89+/-4.06 | 93.3+/-15.06 |
| chr14:73688842 | PSEN1 | exon, UTR | inter | 6.93 | 1.40E-04 | 41.91+/-11.61 | 40.47+/-7.59 |
| chr1:186650441 | PTGS2 | promoter | shores | -5.15 | 1.50E-03 | 10.93+/-3.68 | 16.27+/-5.53 |
| chr1:180144484 | QSOX1 | exon, CDS | inter | -32.29 | 6.16E-110 | 72.84+/-35.28 | 88.8+/-15.24 |
| chr1:180168817 | QSOX1 | exon, UTR | inter | 6.89 | 5.66E-29 | 96.62+/-1.15 | 91.94+/-13.05 |
| chr1:180165741 | QSOX1 | promoter | inter | 5.10 | 4.31E-11 | 93.83+/-5.27 | 91.21+/-10.19 |
| chr1:180158797 | QSOX1 | exon, CDS | inter | 8.29 | 2.30E-03 | 72.44+/-8.5 | 68.91+/-10.77 |
| chr1:180165488 | QSOX1 | promoter | inter | 9.87 | 8.62E-03 | 73.22+/-10.71 | 68.32+/-12.45 |
| chr17:74472997 | RHBDF2 | exon | shelves | -7.43 | 5.47E-29 | 91.19+/-15.88 | 96.46+/-2.38 |
| chr17:74477691 | RHBDF2 | intron | shelves | -25.13 | 1.69E-24 | 30.72+/-23.03 | 46.44+/-17.94 |
| chr17:74477620 | RHBDF2 | exon, UTR | shelves | 16.26 | 5.86E-18 | 63.2+/-9.43 | 49.99+/-22.09 |
| chr17:74467016 | RHBDF2 | exon, UTR | shores | 11.38 | 2.63E-16 | 83.99+/-13.91 | 76.69+/-25 |
| chr17:74475023 | RHBDF2 | exon | shores | 7.91 | 1.51E-07 | 21.76+/-23.23 | 11.23+/-19.38 |
| chr17:74483966 | RHBDF2 | exon | inter | -8.69 | 3.25E-03 | 68.98+/-7.95 | 73.55+/-7.99 |
| chr17:74498833 | RHBDF2 | promoter | shores | 10.11 | 4.44E-03 | 51.8+/-13.55 | 51.89+/-16.88 |
| chr17:74469757 | RHBDF2 | promoter | shores | -7.65 | 1.91E-02 | 74.04+/-5.98 | 77.53+/-10.11 |
| chr22:45821909 | RIBC2 | exon | inter | -26.42 | 2.37E-79 | 62.44+/-40.5 | 83.47+/-21.97 |
| chr22:45821934 | RIBC2 | exon | inter | -27.00 | 2.35E-77 | 62.89+/-40.65 | 83.52+/-20.81 |
| chr22:45813686 | RIBC2 | promoter | shelves | -27.02 | 2.74E-65 | 57.61+/-44.69 | 83.13+/-19.57 |
| chr22:45809250 | RIBC2 | promoter | islands | 7.71 | 5.14E-04 | 48.03+/-11.7 | 35.11+/-12.24 |
| chr22:45809257 | RIBC2 | promoter | islands | 11.93 | 1.59E-03 | 53.91+/-12.85 | 37.34+/-11.82 |
| chr22:45821956 | RIBC2 | exon | inter | 10.22 | 4.56E-03 | 68.49+/-41.68 | 68.29+/-28.06 |
| chr22:45809299 | RIBC2 | promoter | islands | -5.20 | 1.09E-02 | 69.02+/-6.62 | 73.03+/-12.1 |
| chr22:45809290 | RIBC2 | promoter | islands | -5.11 | 1.73E-02 | 45.97+/-13.13 | 50.24+/-10.67 |
| chr6:30044002 | RNF39 | promoter | shores | -7.04 | 2.71E-03 | 45.25+/-13.91 | 47.44+/-10.26 |
| chr6:30043877 | RNF39 | promoter | shores | -5.88 | 8.73E-03 | 57.36+/-12.22 | 59.18+/-7.89 |
| chr6:30044986 | RNF39 | promoter | shores | 12.60 | 2.39E-02 | 57.9+/-13.17 | 47.04+/-17.64 |
| chr6:30044091 | RNF39 | promoter | shores | -6.68 | 2.43E-02 | 59.83+/-8.27 | 63.69+/-7.57 |
| chr8:38458370 | RNF5P1 | exon, first\_exon | inter | 9.45 | 1.07E-29 | 81.32+/-17.7 | 65.12+/-21.37 |
| chr1:153540764 | S100A2 | promoter | inter | -6.20 | 7.08E-04 | 73.91+/-5.63 | 80.72+/-5.91 |
| chr22:51153370 | SHANK3 | exon, CDS | inter | 6.15 | 2.47E-09 | 98.95+/-0.8 | 91.7+/-17.35 |
| chr22:51170685 | SHANK3 | exon, UTR | shores | 5.55 | 1.67E-03 | 73.31+/-8.1 | 70.59+/-11.32 |
| chr22:51170762 | SHANK3 | exon, UTR | shores | 7.07 | 2.58E-02 | 60.6+/-9.02 | 51.63+/-11.43 |
| chr22:51170777 | SHANK3 | exon, UTR | shores | 6.01 | 2.88E-02 | 74.4+/-5.62 | 66.49+/-6.83 |
| chr22:51170756 | SHANK3 | exon, UTR | shores | 5.66 | 4.22E-02 | 83.5+/-4.64 | 79.14+/-8.98 |
| chr10:98924599 | SLIT1 | exon | inter | -6.22 | 6.25E-24 | 91.62+/-16.38 | 97.05+/-3.76 |
| chr10:98817715 | SLIT1 | exon, UTR | inter | 7.23 | 3.05E-05 | 52.48+/-13.27 | 48.2+/-6.02 |
| chr10:98917644 | SLIT1 | exon | inter | -8.16 | 1.09E-04 | 42.49+/-5.47 | 51.84+/-7.89 |
| chr10:98917635 | SLIT1 | exon | inter | -9.39 | 1.37E-04 | 53.12+/-4.89 | 59.56+/-6.59 |
| chr10:98917281 | SLIT1 | exon | inter | -5.62 | 5.63E-04 | 80.98+/-4.68 | 86.21+/-3.61 |
| chr10:98917565 | SLIT1 | intron | inter | -9.36 | 6.06E-04 | 46.57+/-4.03 | 53.12+/-8.09 |
| chr10:98946589 | SLIT1 | promoter | shores | 6.56 | 6.48E-03 | 52.15+/-8.45 | 44.67+/-9.97 |
| chr10:98823962 | SLIT1 | exon, CDS | inter | -5.48 | 1.30E-02 | 63.52+/-6.28 | 69.59+/-10.86 |
| chr10:98917613 | SLIT1 | exon | inter | -6.64 | 4.26E-02 | 62.1+/-7.43 | 66.17+/-7.22 |
| chr13:84457671 | SLITRK1 | promoter | shelves | -5.97 | 6.55E-15 | 10.35+/-4.07 | 15.27+/-11.7 |
| chr13:84452522 | SLITRK1 | exon, first\_exon, UTR | shores | -5.88 | 8.22E-07 | 61.37+/-11.68 | 63.06+/-14.25 |
| chr13:84454251 | SLITRK1 | exon, first\_exon, CDS | shores | -5.69 | 3.23E-05 | 7.48+/-5.31 | 12.29+/-9.22 |
| chr4:90646676 | SNCA | exon, UTR | inter | 6.15 | 2.71E-12 | 96.33+/-2.19 | 91.07+/-13.83 |
| chr8:22432297 | SORBS3 | exon, CDS | shelves | 5.54 | 1.87E-02 | 49.28+/-13.43 | 43.46+/-11.94 |
| chr19:41012190 | SPTBN4 | exon, CDS | inter | -24.66 | 2.44E-27 | 42.64+/-25.31 | 47.9+/-12.3 |
| chr19:41009787 | SPTBN4 | exon, CDS | inter | 8.70 | 2.71E-18 | 91.34+/-3.36 | 83.67+/-10.71 |
| chr19:41062006 | SPTBN4 | exon, CDS | shores | 6.49 | 3.39E-10 | 90.43+/-7.89 | 84.59+/-10 |
| chr19:41060957 | SPTBN4 | exon | shores | -10.91 | 1.53E-09 | 44.57+/-10.68 | 55.22+/-8.42 |
| chr19:41008826 | SPTBN4 | exon, CDS | inter | 8.23 | 2.87E-09 | 60.18+/-12.04 | 54.26+/-12.48 |
| chr19:41060622 | SPTBN4 | exon | shores | 7.18 | 6.20E-07 | 79.82+/-6.92 | 75.99+/-10.62 |
| chr19:41008730 | SPTBN4 | exon, CDS | inter | 7.39 | 1.55E-06 | 57.97+/-9.17 | 48.53+/-8.32 |
| chr19:40996006 | SPTBN4 | exon, CDS | islands | 7.19 | 2.92E-06 | 89.87+/-3.55 | 81.88+/-8.18 |
| chr19:41008715 | SPTBN4 | exon, CDS | inter | 6.49 | 1.09E-05 | 78.29+/-8.74 | 69.22+/-9.77 |
| chr19:41081449 | SPTBN4 | exon | shores | -5.59 | 7.67E-05 | 87.45+/-7.59 | 85.5+/-15.15 |
| chr19:41025975 | SPTBN4 | exon, CDS | islands | 11.35 | 2.62E-03 | 42.71+/-16.62 | 35.27+/-12.6 |
| chr19:41038578 | SPTBN4 | exon | shelves | -6.29 | 3.48E-03 | 87.8+/-6.62 | 93.26+/-4.85 |
| chr19:41077529 | SPTBN4 | promoter | shelves | -6.20 | 4.16E-03 | 86.91+/-12.27 | 93.4+/-3.64 |
| chr19:41019435 | SPTBN4 | exon, CDS, first\_exon | islands | -7.08 | 4.36E-03 | 68.49+/-7.98 | 76.28+/-9.21 |
| chr19:40996026 | SPTBN4 | exon, CDS | islands | 5.89 | 5.64E-03 | 70.93+/-11.92 | 62.01+/-11.4 |
| chr19:41008745 | SPTBN4 | exon, CDS | inter | 5.97 | 6.38E-03 | 40.18+/-11.66 | 33.27+/-7.31 |
| chr19:40995994 | SPTBN4 | exon, CDS | islands | 5.28 | 8.14E-03 | 78.8+/-4.98 | 73.99+/-11.08 |
| chr19:41026029 | SPTBN4 | exon, CDS | islands | -7.65 | 8.51E-03 | 69.22+/-12.74 | 76.69+/-8.96 |
| chr19:41019099 | SPTBN4 | exon, CDS, first\_exon | islands | 8.07 | 1.02E-02 | 21.93+/-10.13 | 20.33+/-10.56 |
| chr19:41019259 | SPTBN4 | exon, CDS, first\_exon | islands | 8.89 | 1.18E-02 | 24.12+/-11.71 | 24.29+/-6.37 |
| chr19:41019369 | SPTBN4 | exon, CDS, first\_exon | islands | -6.86 | 4.73E-02 | 54.39+/-13.09 | 64.38+/-8.65 |
| chr19:41019193 | SPTBN4 | exon, CDS, first\_exon | islands | 9.20 | 4.77E-02 | 38.33+/-10.78 | 32.54+/-11.94 |
| chr6:32795705 | TAP2 | exon, UTR | inter | -37.10 | 1.11E-135 | 60.92+/-24.77 | 90.26+/-13.6 |
| chr6:32795981 | TAP2 | exon, UTR | inter | 8.12 | 2.69E-39 | 91.58+/-4.38 | 85.61+/-17.44 |
| chr6:32800412 | TAP2 | exon, first\_exon | inter | -5.20 | 5.15E-05 | 59.09+/-21.08 | 63.68+/-15.16 |
| chr6:32798547 | TAP2 | promoter | inter | 6.86 | 5.04E-04 | 95.46+/-1.74 | 87.71+/-16.54 |
| chr6:32796056 | TAP2 | exon, UTR | inter | 11.53 | 2.35E-03 | 79.81+/-35.22 | 78.48+/-30.7 |
| chr6:32794178 | TAP2 | exon, UTR | inter | -6.38 | 1.78E-02 | 65.42+/-7.23 | 69.81+/-4.92 |
| chr6:32800427 | TAP2 | exon, first\_exon | inter | -5.37 | 3.32E-02 | 89.44+/-22.34 | 97.24+/-1.87 |
| chr6:32796792 | TAP2 | exon | inter | 7.29 | 3.91E-02 | 93.77+/-8.35 | 87.15+/-22.54 |
| chr1:119426303 | TBX15 | exon, UTR | inter | 5.50 | 5.91E-05 | 73.79+/-10.36 | 69.31+/-10.42 |
| chr1:119533482 | TBX15 | promoter | shores | 6.60 | 8.36E-04 | 56.07+/-11.8 | 45.56+/-9.54 |
| chr6:31542882 | TNF | promoter | inter | -9.80 | 4.71E-03 | 51.49+/-8.28 | 58.25+/-11.89 |
| chr6:31545721 | TNF | exon, UTR | shelves | -7.48 | 1.26E-02 | 69.42+/-9.49 | 66.37+/-11.15 |
| chr6:31543100 | TNF | promoter | inter | 11.03 | 1.78E-02 | 86.03+/-15.36 | 78.14+/-19.43 |
| chr6:32029204 | TNXB | exon, CDS | inter | -18.56 | 2.06E-16 | 85.11+/-20.62 | 85.64+/-20.25 |
| chr6:32032628 | TNXB | exon, CDS | inter | -5.78 | 3.22E-11 | 92.44+/-11.78 | 96.93+/-1.94 |
| chr6:32064268 | TNXB | exon | islands | 12.81 | 9.69E-08 | 29.71+/-16.1 | 18.7+/-6.76 |
| chr6:32064098 | TNXB | exon | islands | 18.06 | 5.94E-07 | 46.24+/-18.5 | 33.58+/-11.58 |
| chr6:32064246 | TNXB | exon | islands | 11.29 | 2.57E-06 | 46.74+/-19.36 | 43.26+/-12.39 |
| chr6:32016405 | TNXB | exon, CDS | inter | -8.19 | 5.64E-06 | 30.05+/-13.62 | 29.36+/-7.48 |
| chr6:32035694 | TNXB | exon, CDS | inter | -12.20 | 6.37E-05 | 85.4+/-19.69 | 85+/-19.18 |
| chr6:32064258 | TNXB | exon | islands | 10.29 | 1.50E-04 | 38.53+/-17.07 | 33.51+/-11.66 |
| chr6:32016394 | TNXB | exon, CDS | inter | -8.97 | 1.51E-04 | 25.3+/-9.62 | 29.83+/-10.12 |
| chr6:32064024 | TNXB | exon | islands | 16.45 | 2.12E-04 | 44.94+/-19.34 | 31.49+/-14.55 |
| chr6:32049423 | TNXB | exon, CDS | shelves | 26.15 | 2.14E-04 | 75.03+/-30.76 | 69.81+/-32.07 |
| chr6:32064239 | TNXB | exon | islands | 10.26 | 2.61E-04 | 47.94+/-21.74 | 47.85+/-16.57 |
| chr6:32017242 | TNXB | exon, CDS | inter | 6.78 | 2.67E-04 | 81.93+/-29.22 | 84.93+/-26.1 |
| chr6:32064334 | TNXB | exon | islands | 10.00 | 3.17E-04 | 24.58+/-14.4 | 18.08+/-7.43 |
| chr6:32064125 | TNXB | exon | islands | 14.28 | 3.27E-04 | 41.21+/-17.46 | 30.97+/-11.21 |
| chr6:32064339 | TNXB | exon | islands | 10.96 | 8.86E-04 | 31.22+/-15.62 | 24.79+/-11.29 |
| chr6:32015651 | TNXB | exon, CDS | inter | 5.76 | 9.62E-04 | 88.12+/-4.84 | 78.95+/-7.68 |
| chr6:32064345 | TNXB | exon | islands | 10.03 | 1.35E-03 | 22.08+/-11.04 | 14.93+/-8.43 |
| chr6:32016360 | TNXB | exon, CDS | inter | -6.94 | 2.35E-03 | 31.38+/-13.6 | 33.43+/-12.09 |
| chr6:32013855 | TNXB | intron | inter | -10.57 | 2.51E-03 | 71.58+/-7.22 | 74.89+/-17.23 |
| chr6:32061084 | TNXB | exon, CDS | shelves | -8.03 | 3.65E-03 | 59.81+/-8.19 | 64.98+/-7.96 |
| chr6:32016378 | TNXB | exon, CDS | inter | -7.78 | 4.30E-03 | 49.87+/-11.86 | 51.02+/-10.53 |
| chr6:32064660 | TNXB | exon | islands | 11.98 | 5.97E-03 | 25.42+/-14.39 | 14.84+/-8.44 |
| chr6:32016372 | TNXB | exon, CDS | inter | -6.48 | 6.48E-03 | 39.82+/-13.57 | 39.65+/-11.18 |
| chr6:32016426 | TNXB | exon, CDS | inter | -7.80 | 1.01E-02 | 62.71+/-13.61 | 62.69+/-8.9 |
| chr6:32064305 | TNXB | exon | islands | 5.69 | 1.01E-02 | 15.82+/-9.79 | 15.26+/-7.39 |
| chr6:32064153 | TNXB | exon | islands | 11.98 | 1.08E-02 | 63.32+/-17.29 | 53.46+/-12.39 |
| chr6:32064639 | TNXB | exon | islands | 9.37 | 1.17E-02 | 26.79+/-16.45 | 19.87+/-6.13 |
| chr6:32013845 | TNXB | intron | inter | -9.91 | 1.20E-02 | 73.91+/-6.39 | 76.13+/-14.24 |
| chr6:32064320 | TNXB | exon | islands | 8.07 | 1.22E-02 | 15.67+/-12.94 | 8.4+/-4.84 |
| chr6:32064255 | TNXB | exon | islands | 7.71 | 1.26E-02 | 23.92+/-9.77 | 22.09+/-8.39 |
| chr6:32064318 | TNXB | exon | islands | 10.63 | 1.42E-02 | 28.78+/-19.81 | 20.2+/-8.03 |
| chr6:32082822 | TNXB | exon, UTR, first\_exon | inter | -6.88 | 2.16E-02 | 77.54+/-9.47 | 74.69+/-10.26 |
| chr6:32064117 | TNXB | exon | islands | 12.42 | 2.28E-02 | 39.59+/-21.71 | 24.42+/-11.62 |
| chr6:32064123 | TNXB | exon | islands | 12.00 | 2.75E-02 | 37.87+/-7.77 | 27.93+/-11.57 |
| chr6:32064732 | TNXB | exon | islands | 9.88 | 4.02E-02 | 26.85+/-20.11 | 18.12+/-9.36 |
| chr6:32064332 | TNXB | exon | islands | 6.41 | 4.21E-02 | 18.19+/-7.11 | 15.47+/-6.45 |
| chr6:32082841 | TNXB | exon, UTR, first\_exon | inter | -7.32 | 4.30E-02 | 69.02+/-9.9 | 67.9+/-9.9 |
| chr6:32064377 | TNXB | exon | islands | 9.06 | 4.54E-02 | 19.78+/-14.28 | 13.12+/-7.67 |
| chr6:41130871 | TREM2 | exon, UTR, first\_exon | inter | 7.03 | 2.57E-03 | 21.23+/-6.61 | 17.59+/-10.03 |
| chr6:41129207 | TREM2 | exon, CDS | inter | -9.44 | 1.32E-02 | 67.81+/-14.17 | 63.83+/-13.8 |
| chr6:41129194 | TREM2 | exon, CDS | inter | -10.41 | 1.51E-02 | 67.98+/-9.62 | 67.87+/-13.34 |
| chr6:41131011 | TREM2 | promoter | inter | 9.72 | 1.73E-02 | 36.41+/-16.1 | 35.73+/-9.36 |
| chr6:30103745 | TRIM40 | promoter | inter | 26.27 | 1.58E-40 | 89.98+/-11.52 | 71.28+/-22.47 |
| chr6:30116341 | TRIM40 | exon, UTR | inter | 25.14 | 4.92E-38 | 90.88+/-7.87 | 71.76+/-21.24 |
| chr6:30114955 | TRIM40 | exon, CDS | inter | 26.62 | 9.26E-29 | 91.5+/-5.61 | 69.98+/-25.79 |
| chr6:30103840 | TRIM40 | promoter | inter | 22.82 | 6.25E-28 | 81.92+/-18.45 | 65.82+/-20.78 |
| chr6:30104295 | TRIM40 | promoter | inter | -9.26 | 1.17E-02 | 54.57+/-14.16 | 55.07+/-12.47 |
| chr6:30104807 | TRIM40 | exon, UTR, first\_exon | inter | 7.69 | 1.59E-02 | 48.17+/-18.45 | 34.46+/-13.11 |
| chr6:30103699 | TRIM40 | promoter | inter | -8.72 | 2.97E-02 | 34.17+/-10.56 | 32.03+/-11.08 |
| chr11:5617200 | TRIM6 | promoter | inter | 6.02 | 6.09E-08 | 66.21+/-16.11 | 57.07+/-15.96 |
| chr11:5617202 | TRIM6 | promoter | inter | 6.74 | 8.81E-08 | 89.72+/-6.52 | 79.34+/-9.2 |
| chr11:5617162 | TRIM6 | promoter | inter | 7.51 | 1.36E-04 | 80.42+/-14.22 | 71.74+/-14.87 |
| chr11:5617146 | TRIM6 | promoter | inter | 7.23 | 8.35E-03 | 74.28+/-15.53 | 67.98+/-12.38 |
| chr2:71126346 | VAX2 | promoter | shores | 9.49 | 2.61E-07 | 25.51+/-10.63 | 14.5+/-3.58 |
| chr19:9489132 | ZNF177 | intron | inter | 23.14 | 2.65E-22 | 51.57+/-27.32 | 28.06+/-37.67 |
| chr19:9492141 | ZNF177 | intron | inter | 23.00 | 2.16E-17 | 51.56+/-26.05 | 27.58+/-38.33 |
| chr19:9490814 | ZNF177 | exon, CDS | inter | 22.99 | 2.57E-07 | 46.68+/-27.42 | 27.6+/-39.71 |
| chr19:9434101 | ZNF177 | promoter | shores | 9.25 | 1.95E-02 | 83.68+/-13.25 | 80.49+/-13.13 |
| chr19:9473818 | ZNF177 | exon, UTR, first\_exon | islands | 5.15 | 2.61E-02 | 10.69+/-3.92 | 5.99+/-5.97 |
| chr6:30022577 | ZNRD1-AS1 | exon | inter | 13.05 | 3.71E-29 | 94.49+/-1.76 | 83.42+/-19.8 |
| chr6:30023868 | ZNRD1-AS1 | exon | inter | -10.85 | 8.47E-20 | 38.18+/-22.68 | 46.37+/-25.76 |
| chr6:30002859 | ZNRD1-AS1 | exon | inter | 13.20 | 1.07E-18 | 96.1+/-3.2 | 85.28+/-21.1 |
| chr6:29988641 | ZNRD1-AS1 | intron | inter | -6.23 | 7.35E-17 | 52.18+/-19.08 | 67.04+/-15.57 |
| chr6:29969794 | ZNRD1-AS1 | exon | inter | 10.86 | 8.68E-10 | 85.61+/-7.07 | 78.14+/-8.87 |
| chr6:29984251 | ZNRD1-AS1 | exon | inter | 15.08 | 6.63E-06 | 87.22+/-16.29 | 69.97+/-23.21 |
| chr6:30002723 | ZNRD1-AS1 | exon | inter | 14.53 | 1.41E-04 | 66.35+/-5.22 | 62.27+/-15.61 |
| chr6:30024677 | ZNRD1-AS1 | exon | inter | 12.94 | 3.06E-02 | 79.93+/-21.42 | 67.24+/-24.15 |

**Supplementary table 5:** 22 CpG segments and 2 DMRs identified in our plasma study of Alzheimer’s disease. The longest transcript is bold, a slash indicates that two genes overlap the segment and an asterisk indicates that this segment overlapped partially region identified. The two segments of *DUP22* gene overlap two DMRs: chr6:291686-293332 identified in the superior temporal gyrus [13] and chr6:291687-292823 identified in the hippocampus, entorhinal cortex, dorsolateral prefrontal cortex and cerebellum [33][.](#_bookmark53) The CpG segment and the DMR of the *MBP* gene overlap two DMRs identified on cortical pyramidal layers (chr18:74799500-74799572) [11] and on the pre-frontal cortex (chr18:74799495-74799572)[34][.](#_bookmark51)

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Chromosomal  region** | **Gene** | **Region  annotation** | **CpG  site** | **Mean Methylation  variation (%)** | **Mean case  Methylation (%)** | **Mean control  Methylation (%)** | **CpGs** | **Length  (bp)** | **Analysis** |
| chr8:41583290-41585437 | *ANK1* | **exon, intron** | islands | 4.79 | 38.76 +/-11.76 | 37.76 +/-8.82 | 22 | 2148 | Segment |
| chr8:41518645-41519053 | *ANK1* | exon, **intron** | inter | -6.03 | 53.36 +/-3.46 | 54.95 +/-5.69 | 11 | 409 | Segment |
| chr10:73498516-73499071 | *C10orf105/CDH23* | **promoter/intron** | inter | 6.89 | 74.94 +/-5.1 | 74.72 +/-8.95 | 15 | 556 | Segment |
| chr10:73472315-73472882 | *C10orf105/CDH23* | **exon/exon**, promoter, **intron** | inter | 6.25 | 48.79 +/-7.5 | 49.77 +/-5.88 | 14 | 568 | Segment |
| chr6:292165-304636 \* | *DUSP22* | **exon**, promoter, **intron** | islands | 10.54 | 50.95 +/-21.78 | 44.49 +/-18.91 | 36 | 12472 | Segment |
| chr6:290180-292163 \* | *DUSP22* | **exon, promoter**, intron | islands | 4.11 | 53.79 +/-13.8 | 52.1 +/-10.58 | 26 | 1984 | Segment |
| chr12:133084805-133087421 | *FBRSL1* | **exon, intron** | inter | -5.47 | 90.82 +/-8.19 | 92.74 +/-6.44 | 92 | 2617 | Segment |
| chr6:32063949-32064764 | *TNXB* | **exon** | islands | 7.70 | 29.83 +/-13.59 | 23.78 +/-6.12 | 87 | 816 | Segment |
| chr19:13409367-13409931 | *CACNA1A* | **exon** | islands | -9.02 | 34.45 +/-17.28 | 38.86 +/-15.76 | 43 | 565 | Segment |
| chr19:18888093-18889147 | *CRTC1* | **exon** | islands | -11.95 | 73.18 +/-15.23 | 75.3 +/-11.47 | 40 | 1055 | Segment |
| chr17:44103258-44105340 | *MAPT* | **exon** | inter | 9.90 | 50.17 +/-5.19 | 48.86 +/-10.65 | 31 | 2083 | Segment |
| chr13:67800487-67802706 | *PCDH9* | **exon**, promoter | shores | -4.10 | 67.13 +/-8.22 | 68.57 +/-5.56 | 26 | 2220 | Segment |
| chr22:50582666-50588008 | *MOV10L1* | **exon**, promoter, **intron** | inter | 4.13 | 69.88 +/-2 | 66.68 +/-2.64 | 18 | 5343 | Segment |
| chr18:74799320-74807414\* | *MBP* | exon, promoter, **intron** | islands | 16.34 | 82.25 +/-4.72 | 70.64 +/-11.78 | 17 | 8095 | Segment |
| chr7:155266903-155294428 | *CNPY1* | **exon, intron** | islands | -6.18 | 60.14 +/-6.11 | 62.86 +/-3.7 | 13 | 27526 | Segment |
| chr19:41197384-41197984 | *NUMBL* | **promoter** | shores | -6.10 | 65.13 +/-5.21 | 66.76 +/-6.02 | 13 | 601 | Segment |
| chr4:6107207-6107320 | *JAKMIP1* | exon, intron | islands | 8.34 | 61.65 +/-6.89 | 57.76 +/-11.34 | 12 | 114 | Segment |
| chr1:29189738-29189864 | *OPRD1* | **exon** | islands | -4.55 | 85.06 +/-9.12 | 90.17 +/-4.73 | 12 | 127 | Segment |
| chr10:45919511-45923837 | *ALOX5* | **exon,** promoter, **intron** | islands | 4.66 | 52.97 +/-6.46 | 49.73 +/-6.63 | 10 | 4327 | Segment |
| chr21:27372461-27423473 | *APP* | **exon**, promoter, i**ntron** | inter | -3.08 | 75.54 +/-7.62 | 74.95 +/-6.74 | 10 | 51013 | Segment |
| chr1:46859479-46859780 | *FAAH* | **promoter** | islands | 5.02 | 60.78 +/-5.64 | 58.7 +/-6.04 | 10 | 302 | Segment |
| chr5:146434146-146460640 | *PPP2R2B* | **exon**, promoter, **intron** | inter | 4.55 | 61.51 +/-6.3 | 57.34 +/-5.05 | 10 | 26495 | Segment |
| chr18:74799371-74799575\* | *MBP* | **intron,** promoter | islands | 6,19 | 86.69 +/-5.14 | 73.6 +/-12.3 | 15 | 205 | DMR |
| chr12:133085873-133086836 | *FBRSL1* | **intron, exon** | inter | -5,01 | 90.93 +/-9.24 | 92.99 +/-7.21 | 61 | 964 | DMR |

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