**Supplementary Table 11 Ranked list and probes differentially methylated between low-immune and high-immune low-grade glioma sub-groups.**

**Supplementary Table 11b List of probes differentially methylated (DMPs) between low-immune and high-immune low-grade glioma sub-groups.**

| Probes | Gene Symbols | fold change | p-value | q-value |
|---|---|---|---|---|
| cg01644338 | PKD2L2 | 3.4425 | 8.66E-03 | 7.21E-01 |
| cg03062002 | CCR10 | 3.2922 | 4.33E-03 | 7.05E-01 |
| cg03748376 | OR2L13 | 3.1255 | 4.33E-03 | 7.05E-01 |
| cg04514123 | SYNGR3 | 3.0994 | 4.33E-03 | 7.05E-01 |
| cg13719746 | ANP32B | 3.0911 | 8.66E-03 | 7.21E-01 |
| cg13495235 | C9orf24 | 3.0635 | 8.66E-03 | 7.21E-01 |
| cg18765439 | EHBP1L1 | 3.0121 | 4.33E-03 | 7.05E-01 |
| cg06330157 | PKD2L2 | 2.9896 | 8.66E-03 | 7.21E-01 |
| cg22865720 | PRKCZ | 2.9562 | 4.33E-03 | 7.05E-01 |
| cg23342521 | C9orf40 | 2.8916 | 4.33E-03 | 7.05E-01 |
| cg13123656 | TFAM | 2.8241 | 4.33E-03 | 7.05E-01 |
| cg20460852 | TNFRSF10A | 2.7913 | 4.33E-03 | 7.05E-01 |
| cg08944170 | OR2L13 | 2.7838 | 4.33E-03 | 7.05E-01 |
| cg05499621 | C9orf40 | 2.7695 | 8.66E-03 | 7.21E-01 |
| cg12319602 | | 2.7461 | 4.33E-03 | 7.05E-01 |
| cg11503425 | RNF149 | 2.7184 | 8.66E-03 | 7.21E-01 |
| cg20507276 | OR2L13 | 2.7034 | 4.33E-03 | 7.05E-01 |
| cg07444487 | ATE1 | 2.6460 | 4.33E-03 | 7.05E-01 |
| cg13912930 | C9orf24 | 2.6455 | 8.66E-03 | 7.21E-01 |
| cg13536409 | NCAPG2 | 2.6434 | 4.33E-03 | 7.05E-01 |
| cg20007021 | LTB4R2 | 2.6169 | 4.33E-03 | 7.05E-01 |
| cg16470877 | | 2.4735 | 4.33E-03 | 7.05E-01 |
| cg13372456 | GALNT10 | 2.3871 | 8.66E-03 | 7.21E-01 |
| cg09792714 | C9orf24 | 2.3869 | 8.66E-03 | 7.21E-01 |
| cg26490949 | ZMYM2 | 2.3572 | 4.33E-03 | 7.05E-01 |
| cg25209674 | FAM160B1 | 2.3426 | 4.33E-03 | 7.05E-01 |
| cg16662989 | RPL26L1 | 2.3193 | 4.33E-03 | 7.05E-01 |
| cg00994643 | TNFRSF10A | 2.3129 | 4.33E-03 | 7.05E-01 |
| cg00990613 | TNFRSF10A | 2.3119 | 4.33E-03 | 7.05E-01 |
| cg05054145 | MYD88 | 2.2948 | 4.33E-03 | 7.05E-01 |
| cg00092518 | PHF11 | 2.2910 | 4.33E-03 | 7.05E-01 |
| cg15469871 | | 2.2822 | 8.66E-03 | 7.21E-01 |
| cg23193410 | RPL26L1 | 2.2187 | 4.33E-03 | 7.05E-01 |
| cg27209387 | | 2.1879 | 4.33E-03 | 7.05E-01 |
| cg10474712 | | 2.1713 | 4.33E-03 | 7.05E-01 |
| cg01709619 | | 2.1427 | 8.66E-03 | 7.21E-01 |
| cg19033712 | MAPKAPK2 | 2.1221 | 4.33E-03 | 7.05E-01 |
| cg22480558 | TNIP1 | 2.1121 | 8.66E-03 | 7.21E-01 |
| cg05169846 | CACNA2D4 | 2.1087 | 8.66E-03 | 7.21E-01 |
| cg00785941 | OR2L13 | 2.0844 | 4.33E-03 | 7.05E-01 |
| cg12221087 | RNF213 | 2.0823 | 4.33E-03 | 7.05E-01 |
| cg11915218 | | 2.0783 | 4.33E-03 | 7.05E-01 |
| cg06079710 | RNLS | 2.0763 | 4.33E-03 | 7.05E-01 |
| cg14919554 | | 2.0757 | 8.66E-03 | 7.21E-01 |
| cg25095814 | CASP8 | 2.0676 | 4.33E-03 | 7.05E-01 |
| cg06876103 | | 2.0351 | 8.66E-03 | 7.21E-01 |
| cg11018337 | GATA3 | 2.0284 | 4.33E-03 | 7.05E-01 |
| cg24884145 | RPL26L1 | 2.0244 | 4.33E-03 | 7.05E-01 |
| cg11942971 | | 1.9613 | 4.33E-03 | 7.05E-01 |
| cg10077672 | | 1.9603 | 4.33E-03 | 7.05E-01 |
| cg10575376 | DNAH10 | 1.9524 | 8.66E-03 | 7.21E-01 |
| cg24368167 | ACAA1 | 1.9521 | 8.66E-03 | 7.21E-01 |
| cg24183793 | NCAPG2 | 1.9399 | 4.33E-03 | 7.05E-01 |
| cg06916446 | | 1.9375 | 4.33E-03 | 7.05E-01 |
| cg22215678 | SNRPD1 | 1.9248 | 8.66E-03 | 7.21E-01 |
| cg22319311 | TSPYL5 | 1.9210 | 8.66E-03 | 7.21E-01 |
| cg08549335 | ZNRF2 | 1.9189 | 8.66E-03 | 7.21E-01 |
| cg01013370 | HMHA1 | 1.9127 | 8.66E-03 | 7.21E-01 |
| cg18580322 | G2E3 | 1.9018 | 4.33E-03 | 7.05E-01 |
| cg22991152 | MAPKAPK3 | 1.8970 | 8.66E-03 | 7.21E-01 |
| cg24320043 | RNF41 | 1.8970 | 4.33E-03 | 7.05E-01 |
| cg17034030 | ACAA1 | 1.8876 | 8.66E-03 | 7.21E-01 |
| cg01214340 | PHF11 | 1.8674 | 4.33E-03 | 7.05E-01 |
| cg14106085 | FOXD2 | 1.8503 | 8.66E-03 | 7.21E-01 |
| cg23816490 | | 1.8465 | 4.33E-03 | 7.05E-01 |
| cg08798295 | ARPC1B | 1.8448 | 4.33E-03 | 7.05E-01 |
| cg16189596 | PLIN3 | 1.8447 | 8.66E-03 | 7.21E-01 |
| cg08485187 | DNMT3A | 1.8375 | 8.66E-03 | 7.21E-01 |
| cg18963906 | RNLS | 1.8355 | 4.33E-03 | 7.05E-01 |
| cg03719155 | ACP5 | 1.8322 | 8.66E-03 | 7.21E-01 |
| cg08055087 | RREB1 | 1.8293 | 4.33E-03 | 7.05E-01 |
| cg13975303 | | 1.8277 | 8.66E-03 | 7.21E-01 |
| cg05636131 | ZNF398 | 1.8264 | 4.33E-03 | 7.05E-01 |
| cg03437172 | NFRKB | 1.7968 | 8.66E-03 | 7.21E-01 |
| cg27587125 | | 1.7866 | 8.66E-03 | 7.21E-01 |
| cg00544436 | HMGA1 | 1.7685 | 8.66E-03 | 7.21E-01 |
| cg04114405 | SECISBP2L | 1.7682 | 4.33E-03 | 7.05E-01 |
| cg12889538 | PRKAG2 | 1.7600 | 4.33E-03 | 7.05E-01 |
| cg02270689 | | 1.7493 | 8.66E-03 | 7.21E-01 |
| cg05105924 | PRDM8 | 1.7064 | 4.33E-03 | 7.05E-01 |
| cg10332787 | | 1.6812 | 4.33E-03 | 7.05E-01 |
| cg27543700 | C1orf101 | 1.6798 | 4.33E-03 | 7.05E-01 |
| cg02930432 | RASSF1 | 1.6709 | 4.33E-03 | 7.05E-01 |
| cg12143784 | | 1.6596 | 4.33E-03 | 7.05E-01 |
| cg06527318 | | 1.6500 | 4.33E-03 | 7.05E-01 |
| cg18696576 | HMGA1 | 1.6450 | 4.33E-03 | 7.05E-01 |
| cg05247391 | XKR9 | 1.6437 | 4.33E-03 | 7.05E-01 |
| cg04466840 | RGS14 | 1.6419 | 8.66E-03 | 7.21E-01 |
| cg13543854 | GATA3 | 1.6404 | 4.33E-03 | 7.05E-01 |
| cg07997682 | | 1.6384 | 4.33E-03 | 7.05E-01 |
| cg03673190 | VWA5A | 1.6369 | 8.66E-03 | 7.21E-01 |
| cg22720029 | | 1.6202 | 4.33E-03 | 7.05E-01 |
| cg02291020 | ANXA11 | 1.6025 | 4.33E-03 | 7.05E-01 |
| cg13043150 | ARPC1B | 1.5914 | 4.33E-03 | 7.05E-01 |
| cg04380519 | LIMD2 | 1.5657 | 4.33E-03 | 7.05E-01 |
| cg20434529 | OR2L13 | 1.5599 | 8.66E-03 | 7.21E-01 |
| cg20839149 | SH2D2A | 1.5580 | 8.66E-03 | 7.21E-01 |
| cg25801292 | KEAP1 | 1.5538 | 4.33E-03 | 7.05E-01 |
| cg22310062 | ESCO1 | 1.5477 | 8.66E-03 | 7.21E-01 |
| cg07599979 | DSCR9 | 1.5471 | 4.33E-03 | 7.05E-01 |
| cg10039080 | EIF2AK3 | 1.5433 | 4.33E-03 | 7.05E-01 |
| cg00598414 | RASGRP2 | 1.5422 | 8.66E-03 | 7.21E-01 |
| cg03140118 | ZC3H12A | 1.5391 | 8.66E-03 | 7.21E-01 |
| cg19688118 | CCDC112 | 1.5305 | 4.33E-03 | 7.05E-01 |
| cg01140661 | | 1.5288 | 8.66E-03 | 7.21E-01 |
| cg06386249 | MRPL51 | 1.5256 | 4.33E-03 | 7.05E-01 |
| cg25902146 | CD48 | 1.5046 | 8.66E-03 | 7.21E-01 |
| cg09015090 | TIPARP | 1.4981 | 8.66E-03 | 7.21E-01 |
| cg00277263 | | 1.4813 | 8.66E-03 | 7.21E-01 |
| cg20569758 | PTER | 1.4737 | 8.66E-03 | 7.21E-01 |
| cg21283926 | | 1.4691 | 4.33E-03 | 7.05E-01 |
| cg11670109 | FAM188B | 1.4654 | 8.66E-03 | 7.21E-01 |
| cg09305680 | UTP23 | 1.4654 | 4.33E-03 | 7.05E-01 |
| cg14466451 | CSK | 1.4580 | 4.33E-03 | 7.05E-01 |
| cg15427004 | ACAA1 | 1.4557 | 4.33E-03 | 7.05E-01 |
| cg18356159 | PLIN3 | 1.4527 | 4.33E-03 | 7.05E-01 |
| cg14638209 | | 1.4513 | 4.33E-03 | 7.05E-01 |
| cg14399884 | | 1.4488 | 4.33E-03 | 7.05E-01 |
| cg25133192 | DHX9 | 1.4447 | 8.66E-03 | 7.21E-01 |
| cg19897172 | | 1.4404 | 8.66E-03 | 7.21E-01 |
| cg27529014 | | 1.4319 | 8.66E-03 | 7.21E-01 |
| cg17908846 | ZNF341 | 1.4267 | 8.66E-03 | 7.21E-01 |
| cg12726743 | CAMK2G | 1.4229 | 4.33E-03 | 7.05E-01 |
| cg09489048 | PPP1CA | 1.4218 | 8.66E-03 | 7.21E-01 |
| cg00186701 | TSPYL5 | 1.4154 | 8.66E-03 | 7.21E-01 |
| cg17569543 | | 1.4129 | 8.66E-03 | 7.21E-01 |
| cg20862047 | LHPP | 1.4057 | 4.33E-03 | 7.05E-01 |
| cg10521147 | | 1.3978 | 8.66E-03 | 7.21E-01 |
| cg00446123 | LIME1 | 1.3958 | 8.66E-03 | 7.21E-01 |
| cg26115276 | RUFY1 | 1.3732 | 8.66E-03 | 7.21E-01 |
| cg03799957 | VDAC3 | 1.3719 | 8.66E-03 | 7.21E-01 |
| cg01768686 | SPNS3 | 1.3653 | 4.33E-03 | 7.05E-01 |
| cg13275679 | HN1 | 1.3605 | 4.33E-03 | 7.05E-01 |
| cg11370586 | RGS14 | 1.3581 | 8.66E-03 | 7.21E-01 |
| cg07420027 | IL12A | 1.3460 | 4.33E-03 | 7.05E-01 |
| cg02997560 | | 1.3455 | 4.33E-03 | 7.05E-01 |
| cg16391973 | UBLCP1 | 1.3405 | 8.66E-03 | 7.21E-01 |
| cg06183333 | TAOK3 | 1.3397 | 4.33E-03 | 7.05E-01 |
| cg08438690 | PPM1M | 1.3363 | 4.33E-03 | 7.05E-01 |
| cg20880234 | ZMYM2 | 1.3362 | 8.66E-03 | 7.21E-01 |
| cg05475934 | APBB1IP | 1.3342 | 4.33E-03 | 7.05E-01 |
| cg11075316 | TRIM59 | 1.3334 | 8.66E-03 | 7.21E-01 |
| cg18739405 | KIAA1731 | 1.3323 | 8.66E-03 | 7.21E-01 |
| cg08987387 | HDAC4 | 1.3278 | 4.33E-03 | 7.05E-01 |
| cg12682251 | MYBBP1A | 1.3219 | 4.33E-03 | 7.05E-01 |
| cg20912449 | NT5C2 | 1.3154 | 8.66E-03 | 7.21E-01 |
| cg19467930 | C2CD5 | 1.3142 | 8.66E-03 | 7.21E-01 |
| cg04858230 | FAM160B1 | 1.3104 | 8.66E-03 | 7.21E-01 |
| cg16091269 | | 1.3061 | 8.66E-03 | 7.21E-01 |
| cg15572779 | | 1.3048 | 4.33E-03 | 7.05E-01 |
| cg13331936 | | 1.3009 | 4.33E-03 | 7.05E-01 |
| cg12681001 | TNF | 1.2987 | 4.33E-03 | 7.05E-01 |
| cg27278086 | ARHGAP25 | 1.2958 | 8.66E-03 | 7.21E-01 |
| cg02662589 | ESCO1 | 1.2897 | 8.66E-03 | 7.21E-01 |
| cg06346081 | PPCS | 1.2873 | 8.66E-03 | 7.21E-01 |
| cg23199648 | PLXNC1 | 1.2828 | 4.33E-03 | 7.05E-01 |
| cg10177231 | ADM | 1.2792 | 8.66E-03 | 7.21E-01 |
| cg14971823 | MYO15B | 1.2693 | 4.33E-03 | 7.05E-01 |
| cg24150051 | CAPN2 | 1.2685 | 4.33E-03 | 7.05E-01 |
| cg27208307 | SRGN | 1.2651 | 4.33E-03 | 7.05E-01 |
| cg13622808 | | 1.2590 | 8.66E-03 | 7.21E-01 |
| cg16470716 | | 1.2567 | 8.66E-03 | 7.21E-01 |
| cg00690143 | FAM188B | 1.2565 | 8.66E-03 | 7.21E-01 |
| cg12536660 | MICAL2 | 1.2555 | 8.66E-03 | 7.21E-01 |
| cg19611817 | | 1.2527 | 8.66E-03 | 7.21E-01 |
| cg26632656 | COL9A2 | 1.2437 | 8.66E-03 | 7.21E-01 |
| cg27152619 | PHPT1 | 1.2373 | 4.33E-03 | 7.05E-01 |
| cg22038059 | C19orf60 | 1.2349 | 8.66E-03 | 7.21E-01 |
| cg22813622 | FANCI | 1.2324 | 8.66E-03 | 7.21E-01 |
| cg10364301 | | 1.2276 | 4.33E-03 | 7.05E-01 |
| cg23912114 | TROAP | 1.2232 | 4.33E-03 | 7.05E-01 |
| cg23384786 | IMPA1 | 1.2189 | 4.33E-03 | 7.05E-01 |
| cg02273647 | | 1.2160 | 4.33E-03 | 7.05E-01 |
| cg14524442 | VAV1 | 1.2153 | 4.33E-03 | 7.05E-01 |
| cg10636246 | AIM2 | 1.2105 | 4.33E-03 | 7.05E-01 |
| cg23866762 | SETMAR | 1.2073 | 4.33E-03 | 7.05E-01 |
| cg16133940 | CTBS | 1.2058 | 4.33E-03 | 7.05E-01 |
| cg25120928 | C17orf82 | 1.2015 | 4.33E-03 | 7.05E-01 |
| cg22514963 | RND1 | 1.1941 | 8.66E-03 | 7.21E-01 |
| cg12892033 | XRCC3 | 1.1851 | 4.33E-03 | 7.05E-01 |
| cg07314523 | AFMID | 1.1807 | 4.33E-03 | 7.05E-01 |
| cg24175777 | | 1.1783 | 4.33E-03 | 7.05E-01 |
| cg22833204 | STAT1 | 1.1731 | 8.66E-03 | 7.21E-01 |
| cg04167833 | LCP2 | 1.1601 | 4.33E-03 | 7.05E-01 |
| cg24384195 | PIK3CG | 1.1578 | 4.33E-03 | 7.05E-01 |
| cg11036886 | | 1.1514 | 8.66E-03 | 7.21E-01 |
| cg10714639 | HMHA1 | 1.1500 | 4.33E-03 | 7.05E-01 |
| cg00931692 | AFTPH | 1.1500 | 4.33E-03 | 7.05E-01 |
| cg24525763 | | 1.1388 | 4.33E-03 | 7.05E-01 |
| cg12112434 | | 1.1342 | 4.33E-03 | 7.05E-01 |
| cg12325285 | IER3 | 1.1314 | 8.66E-03 | 7.21E-01 |
| cg07283011 | RYK | 1.1307 | 4.33E-03 | 7.05E-01 |
| cg21614638 | DAPP1 | 1.1250 | 4.33E-03 | 7.05E-01 |
| cg16124337 | UBE2J1 | 1.1248 | 4.33E-03 | 7.05E-01 |
| cg05407909 | STX2 | 1.1218 | 4.33E-03 | 7.05E-01 |
| cg14593183 | ZMYM5 | 1.1180 | 4.33E-03 | 7.05E-01 |
| cg02805871 | SLC16A13 | 1.1174 | 8.66E-03 | 7.21E-01 |
| cg21180072 | IL15 | 1.1146 | 8.66E-03 | 7.21E-01 |
| cg14972271 | CAPN2 | 1.1075 | 4.33E-03 | 7.05E-01 |
| cg04270048 | TP53INP2 | 1.1033 | 4.33E-03 | 7.05E-01 |
| cg02711608 | SLC1A5 | 1.1030 | 8.66E-03 | 7.21E-01 |
| cg01743395 | HIST1H2BB | 1.0976 | 8.66E-03 | 7.21E-01 |
| cg07695256 | GALC | 1.0955 | 4.33E-03 | 7.05E-01 |
| cg08291430 | N6AMT1 | 1.0921 | 8.66E-03 | 7.21E-01 |
| cg22973115 | N6AMT1 | 1.0878 | 4.33E-03 | 7.05E-01 |
| cg02821484 | NT5C3A | 1.0866 | 8.66E-03 | 7.21E-01 |
| cg03299331 | | 1.0836 | 4.33E-03 | 7.05E-01 |
| cg04565255 | CLN5 | 1.0731 | 4.33E-03 | 7.05E-01 |
| cg17540096 | ADARB1 | 1.0688 | 8.66E-03 | 7.21E-01 |
| cg21234812 | UBE2Z | 1.0681 | 4.33E-03 | 7.05E-01 |
| cg02795076 | | 1.0656 | 8.66E-03 | 7.21E-01 |
| cg22444610 | KCTD18 | 1.0611 | 4.33E-03 | 7.05E-01 |
| cg08818984 | NR3C1 | 1.0573 | 8.66E-03 | 7.21E-01 |
| cg00041401 | PTPN22 | 1.0557 | 4.33E-03 | 7.05E-01 |
| cg20352798 | ZP3 | 1.0511 | 4.33E-03 | 7.05E-01 |
| cg26271170 | CNDP2 | 1.0503 | 4.33E-03 | 7.05E-01 |
| cg15881332 | PIK3CG | 1.0458 | 4.33E-03 | 7.05E-01 |
| cg04393278 | EHD4 | 1.0448 | 4.33E-03 | 7.05E-01 |
| cg00240653 | | 1.0447 | 8.66E-03 | 7.21E-01 |
| cg24573743 | ANKRD53 | 1.0392 | 4.33E-03 | 7.05E-01 |
| cg11075751 | CDKN2A | 1.0370 | 4.33E-03 | 7.05E-01 |
| cg14558275 | PIK3CG | 1.0364 | 4.33E-03 | 7.05E-01 |
| cg21561142 | DEK | 1.0316 | 4.33E-03 | 7.05E-01 |
| cg16626504 | | 1.0311 | 4.33E-03 | 7.05E-01 |
| cg06812977 | RNLS | 1.0284 | 4.33E-03 | 7.05E-01 |
| cg06645648 | | 1.0275 | 4.33E-03 | 7.05E-01 |
| cg23594990 | KIAA1731 | 1.0239 | 8.66E-03 | 7.21E-01 |
| cg09386807 | RASSF1 | 1.0179 | 4.33E-03 | 7.05E-01 |
| cg18257485 | NOP14 | 1.0089 | 4.33E-03 | 7.05E-01 |
| cg14750332 | GPD2 | -1.0152 | 4.33E-03 | 7.05E-01 |
| cg09378425 | REPIN1 | -1.0832 | 8.66E-03 | 7.21E-01 |
| cg16310192 | ETV6 | -1.0956 | 8.66E-03 | 7.21E-01 |
| cg21784940 | REPIN1 | -1.1044 | 4.33E-03 | 7.05E-01 |
| cg23966068 | HMGN1 | -1.1101 | 8.66E-03 | 7.21E-01 |
| cg22905282 | PYROXD2 | -1.1117 | 4.33E-03 | 7.05E-01 |
| cg12950181 | FAM172A | -1.1273 | 4.33E-03 | 7.05E-01 |
| cg25299176 | YWHAE | -1.1280 | 4.33E-03 | 7.05E-01 |
| cg20778468 | OAZ3 | -1.1912 | 4.33E-03 | 7.05E-01 |
| cg09183316 | CTDSP2 | -1.2100 | 4.33E-03 | 7.05E-01 |
| cg15330017 | HADH | -1.2102 | 4.33E-03 | 7.05E-01 |
| cg13266292 | RPS15 | -1.2126 | 4.33E-03 | 7.05E-01 |
| cg23966224 | | -1.2129 | 8.66E-03 | 7.21E-01 |
| cg24928023 | AGPAT3 | -1.2294 | 8.66E-03 | 7.21E-01 |
| cg24453664 | CD59 | -1.2460 | 8.66E-03 | 7.21E-01 |
| cg27577972 | TUFT1 | -1.2476 | 4.33E-03 | 7.05E-01 |
| cg01870865 | TREX1 | -1.2543 | 4.33E-03 | 7.05E-01 |
| cg21235119 | SETD1B | -1.2844 | 4.33E-03 | 7.05E-01 |
| cg18747378 | HLA-C | -1.3123 | 4.33E-03 | 7.05E-01 |
| cg17524265 | NAPRT1 | -1.3663 | 4.33E-03 | 7.05E-01 |
| cg24793920 | GADD45G | -1.4078 | 8.66E-03 | 7.21E-01 |
| cg10743544 | FMNL3 | -1.4960 | 8.66E-03 | 7.21E-01 |
| cg25498107 | DNAJC17 | -1.6142 | 8.66E-03 | 7.21E-01 |
| cg05384724 | TCTN2 | -1.6423 | 4.33E-03 | 7.05E-01 |
| cg01891969 | | -1.7421 | 4.33E-03 | 7.05E-01 |
| cg18020334 | HLA-C | -1.7653 | 8.66E-03 | 7.21E-01 |
| cg03859732 | VPS39 | -1.8555 | 4.33E-03 | 7.05E-01 |
| cg12981099 | PA2G4 | -1.8594 | 4.33E-03 | 7.05E-01 |
| cg13793166 | PHF19 | -3.2878 | 4.33E-03 | 7.05E-01 |
| cg23758822 | | -3.5488 | 4.33E-03 | 7.05E-01 |