**Supplemental Table 2: Top DMRs differentiating septic and non-septic critically ill patients ranked by effect size.**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Ilumina ID** | **Gene** | **Coordinate** | **Gene Location** | **UCSC CpG Island** | **Relation to**  **CpG Island** | **Beta diff DMR** | **FDR pval DMR** | **Beta diff CpG Site** | **FDR pval CpG site** |
| cg22259797 | C2CD2L | 118986860 | Body |  | OpenSea | 0.101 | 0.000 | 0.123 | 0.017 |
| cg05875700 | ERICH1 | 638208 | Body | chr8:637393-638251 | Island | 0.072 | 0.129 | 0.116 | 0.010 |
| cg15982117 | HLA-DRB1 | 32552106 | Body | chr6:32551851-32552331 | Island | -0.083 | 0.000 | -0.108 | 0.078 |
| cg04546413 |  | 29218101 |  | chr19:29218001-29218733 | Island | -0.065 | 0.002 | -0.107 | 0.006 |
| cg20228731 | FLJ43663 | 130646051 | Body |  | OpenSea | -0.089 | 0.000 | -0.105 | 0.001 |
| cg15602423 | HLA-DRB1 | 32552095 | Body | chr6:32551851-32552331 | Island | -0.083 | 0.000 | -0.102 | 0.052 |
| cg02003183 | CDC42BPB | 103415882 | Body |  | OpenSea | 0.076 | 0.000 | 0.101 | 0.002 |
| cg15145296 |  | 125709740 |  | chr3:125709066-125709452 | S\_Shore | 0.045 | 0.000 | 0.099 | 0.002 |
| cg03876548 | HCG4P6 | 29893605 | TSS200 | chr6:29894140-29895117 | N\_Shore | -0.061 | 0.000 | -0.095 | 0.010 |
| cg13498757 |  | 152161927 |  | chr1:152161321-152161928 | Island | -0.038 | 0.019 | -0.091 | 0.004 |
| cg25350011 | ANGPT2 | 6419483 | Body |  | OpenSea | -0.055 | 0.000 | -0.090 | 0.011 |
| cg10975897 | JARID2 | 15504844 | Body |  | OpenSea | 0.068 | 0.019 | 0.089 | 0.000 |
| cg13401893 | RNF39 | 30039432 | Body | chr6:30038881-30039477 | Island | -0.054 | 0.002 | -0.089 | 0.018 |
| cg11771383 | INPP5A | 134362126 | Body | chr10:134360859-134361084 | S\_Shore | 0.087 | 0.000 | 0.088 | 0.001 |
| cg12754571 | LOC148824 | 247694271 | TSS200 | chr1:247694035-247694501 | Island | 0.066 | 0.001 | 0.088 | 0.012 |
| cg05090695 | CDKN1C | 2907670 | TSS1500 | chr11:2907308-2907675 | Island | -0.054 | 0.082 | -0.088 | 0.000 |
| cg01874867 | PON1 | 94954059 | TSS200 | chr7:94953769-94953971 | S\_Shore | 0.046 | 0.000 | 0.087 | 0.000 |
| cg09279736 | RNF39 | 30039403 | Body | chr6:30038881-30039477 | Island | -0.054 | 0.002 | -0.087 | 0.001 |
| cg04036920 | C11orf41 | 33562503 | TSS1500 |  | OpenSea | 0.074 | 0.013 | 0.085 | 0.000 |
| cg20052079 | JARID2 | 15504923 | Body |  | OpenSea | 0.068 | 0.019 | 0.082 | 0.000 |

HUGO, Human Genome Organization; FDR, false discovery rate; Adj., adjusted; Chr, chromosome; UCSC, University of California, Santa Cruz genome browser; TSS200, within 200 base pairs of a transcription start site; TSS1500, within 1,500 base pairs of a transcription start site; Δβ, difference in beta values between cases and controls (positive value indicates hypermethylation of cases while negative values indicate hypomethylation); NA, methylation probes with no associated gene symbol; P values are derived from linear models including age, sex and cell proportions as covariates.