**Supplementary file 1. “R” packages used in the analysis.**

R version 3.6.1 (2019-07-05)

Platform: x86\_64-pc-linux-gnu (64-bit)

Running under: Ubuntu 18.04.3 LTS

attached base packages:

[1] grid stats4 parallel stats graphics grDevices utils datasets methods

[10] base

other attached packages:

[1] pander\_0.6.3

[2] SmartSVA\_0.1.3

[3] RSpectra\_0.15-0

[4] isva\_1.9

[5] JADE\_2.0-2

[6] fastICA\_1.2-2

[7] qvalue\_2.16.0

[8] sva\_3.32.1

[9] genefilter\_1.66.0

[10] mgcv\_1.8-30

[11] nlme\_3.1-142

[12] ellipse\_0.4.1

[13] Cairo\_1.5-10

[14] reshape\_0.8.8

[15] svd\_0.5

[16] lumi\_2.36.0

[17] preprocessCore\_1.46.0

[18] fields\_9.9

[19] maps\_3.3.0

[20] spam\_2.4-0

[21] dotCall64\_1.0-0

[22] affy\_1.62.0

[23] vsn\_3.52.0

[24] limma\_3.40.6

[25] doParallel\_1.0.15

[26] minfiData\_0.30.0

[27] IlluminaHumanMethylation450kanno.ilmn12.hg19\_0.6.0

[28] IlluminaHumanMethylation450kmanifest\_0.4.0

[29] MEAL\_1.14.0

[30] MethylAid\_1.18.0

[31] org.Hs.eg.db\_3.8.2

[32] AnnotationDbi\_1.46.1

[33] clusterProfiler\_3.12.0

[34] MultiDataSet\_1.12.0

[35] psych\_1.8.12

[36] doBy\_4.6-3

[37] plyr\_1.8.4

[38] gmodels\_2.18.1

[39] haven\_2.2.0

[40] quadprog\_1.5-7

[41] GEOquery\_2.52.0

[42] ggpmisc\_0.3.1

[43] minfi\_1.30.0

[44] bumphunter\_1.26.0

[45] locfit\_1.5-9.1

[46] iterators\_1.0.12

[47] foreach\_1.4.7

[48] Biostrings\_2.52.0

[49] XVector\_0.24.0

[50] SummarizedExperiment\_1.14.1

[51] DelayedArray\_0.10.0

[52] BiocParallel\_1.18.1

[53] matrixStats\_0.55.0

[54] Biobase\_2.44.0

[55] GenomicRanges\_1.36.1

[56] GenomeInfoDb\_1.20.0

[57] IRanges\_2.18.3

[58] S4Vectors\_0.22.1

[59] BiocGenerics\_0.30.0

[60] methylclock\_0.5.0

[61] GAprediction\_1.10.0

[62] forcats\_0.4.0

[63] stringr\_1.4.0

[64] dplyr\_0.8.3

[65] purrr\_0.3.3

[66] readr\_1.3.1

[67] tidyr\_1.0.0

[68] tibble\_2.1.3

[69] ggplot2\_3.2.1

[70] tidyverse\_1.2.1

[71] missMethyl 1.24.0

[72] missMethyl 1.24.0