

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Bonferroni significant CpGs detected in NTR and replication results in other twin cohorts

File Name: Supplementary Data 2

Description: Sensitivity analyses

File Name: Supplementary Data 3

Description: Genome-wide summary statistics from the EWAS meta-analysis

File Name: Supplementary Data 4

Description: Transcription factor binding motif enrichment analysis results for MZ-hypomethylated sites

File Name: Supplementary Data 5

Description: Pathway enrichment analysis results for transcription factors whose motifs are enriched among MZ-hypomethylated sites

File Name: Supplementary Data 6

Description: Pathway enrichment analysis results for nearest genes of MZ-hypomethylated sites

File Name: Supplementary Data 7

Description: Transcription factor binding motif enrichment analysis results for MZ-hypermethylated sites

File Name: Supplementary Data 8

Description: Pathway enrichment analysis results for transcription factors whose motifs are enriched among MZ-hypermethylated sites

File Name: Supplementary Data 9

Description: Pathway enrichment analysis results for nearest genes of MZ-hypermethylated sites

File Name: Supplementary Data 10

Description: mQTLs for MZ-hypomethylated sites

File Name: Supplementary Data 11

Description: mQTLs for MZ-hypermethylated sites

File Name: Supplementary Data 12

Description: Elastic net regression model results

File Name: Supplementary Data 13

Description: Weights from the elastic net regression model trained on meta-analysis significant probes to predict zygoty

File Name: Supplementary Data 14

Description: Weights from the elastic net regression model trained on meta-analysis significant probes to distinguish MZ twins from DZ twins and non-twins