Contribution of Age, Brain Region, Mood Disorder Pathology, and Interindividual Factors on the Methylome of Human Microglia

Supplement 1
Figure S1: Methylation data quality control. (A) Detection p-value. Bar graph showing the proportion of probes with poor quality (detect p>0.0005) probes for each biological sample. All samples had high quality data, with at least 99% of probes passing criteria; (B) Sex prediction. Plot demonstrates consistency for predicted and reported sex, using Chromosome X and Y median intensity; (C) Genotype consistency check with samples from different regions of the same individual. The dendrogram shows clustering of each individual’s samples by genotypes derived from the 59 SNP probes for samples. The y-axis shows Euclidean distance.
Figure S2: QQ plot of p-values of comparison between Mood disorder and control in the model including all sample specimens. The calculated Lambda = 1.458, which was used to adjust for Type-1 Error inflation in the cross-tissue analysis.
Supplementary figure 3

Figure S3: QQ plots of p-values of comparison between Mood disorder and control in the region-specific models. Lambdas for MFG, STG and SVZ are acceptable.
Figures S4: Bar plot showing contribution of different factors to DNA methylation variability (M-value matrix was not adjusted for age and sex) in top 20 principal components, using paired samples for which DNA methylation data is available for two brain regions (i.e., MFG & STG, MFG & SVZ, and STG & SVZ respectively).
Figure S5: Examples of differentially methylated regions (DMRs) that were found significant after correcting for multiple testing in the cross-region analysis comparing individuals diagnosed with combined mood disorders and controls, showing their mean methylation M-values across CpG sites on the y-axis, with control groups in blue and mood disorder in red.
Figure S6: Region-specific differentially methylated regions (DMRs) that were found in comparative analysis, showing control groups in blue and mood disorder in red, with mean methylation M-values across CpG sites on the y-axis.
Supplementary figure 7

Figure S7: Scatter plot of methylation difference (in M-value) on x-axis and gene expression difference (in logFC) on y-axis of 35 DMRs with associated expressed genes. Promoter DMRs are highlighted in red and labelled with the annotated gene names.
Figure S8: Genome browser showing the region of DMR annotated with gene HRH1. Tracks from top to bottom shown: 1, Ensemble gene annotation; 2, CpG island nearby; 3, Region of the DMR; 4, $-\log_{10}(p\text{-value})$ of each CpG probe; 5, adjusted (for age and sex) M-value of each CpG of each sample, with smoothed lines and confident interval, points are coloured into two diagnosis groups.
Data Access:

DNA Methylation data is available on GEO (Gene Expression Omnibus) with accession number GSE191200 and RNA-seq data is available with accession number ng00105.