

Description of Additional supplementary files

Supplementary Data1: Participant characteristics in the overall sample and by sex.

Supplementary Data2: GWAS Catalog lookup of variants in linkage disequilibrium with genome-wide significant SNPs.

Supplementary Data3: Results of multitrait analysis of genome-wide association studies (MTAG).

Supplementary Data4: SuSiE fine-mapping results. Supplementary Data5: Sensitivity analyses for genome-wide significant loci. Supplementary Data6: Sex-stratified GWAS results.

Supplementary Data7: MAGMA gene-set enrichment analysis results.

Supplementary Data8: Exploratory cell-type enrichment analysis using FUMA.

Supplementary Data9: Gene-based association results obtained using MAGMA.

Supplementary Data10: Prioritized genes identified by functional mapping.

Supplementary Data11: GWAS–eQTL colocalization results ($PP.H4 \geq 75\%$).

Supplementary Data12: Brain-specific eQTL evidence for genes associated with sleep traits.

Supplementary Data13: Bidirectional two-sample Mendelian randomization results.

Supplementary Data14: Definitions considered for exclusions in the sensitivity analyses.

Supplementary Data15: List of genes tested in the GWAS–eQTL colocalization analysis.

Supplementary Data16: List of tissues tested in the GWAS–eQTL colocalization analysis.

Supplementary Data17: List of instrumental variables used in Mendelian randomization analyses.