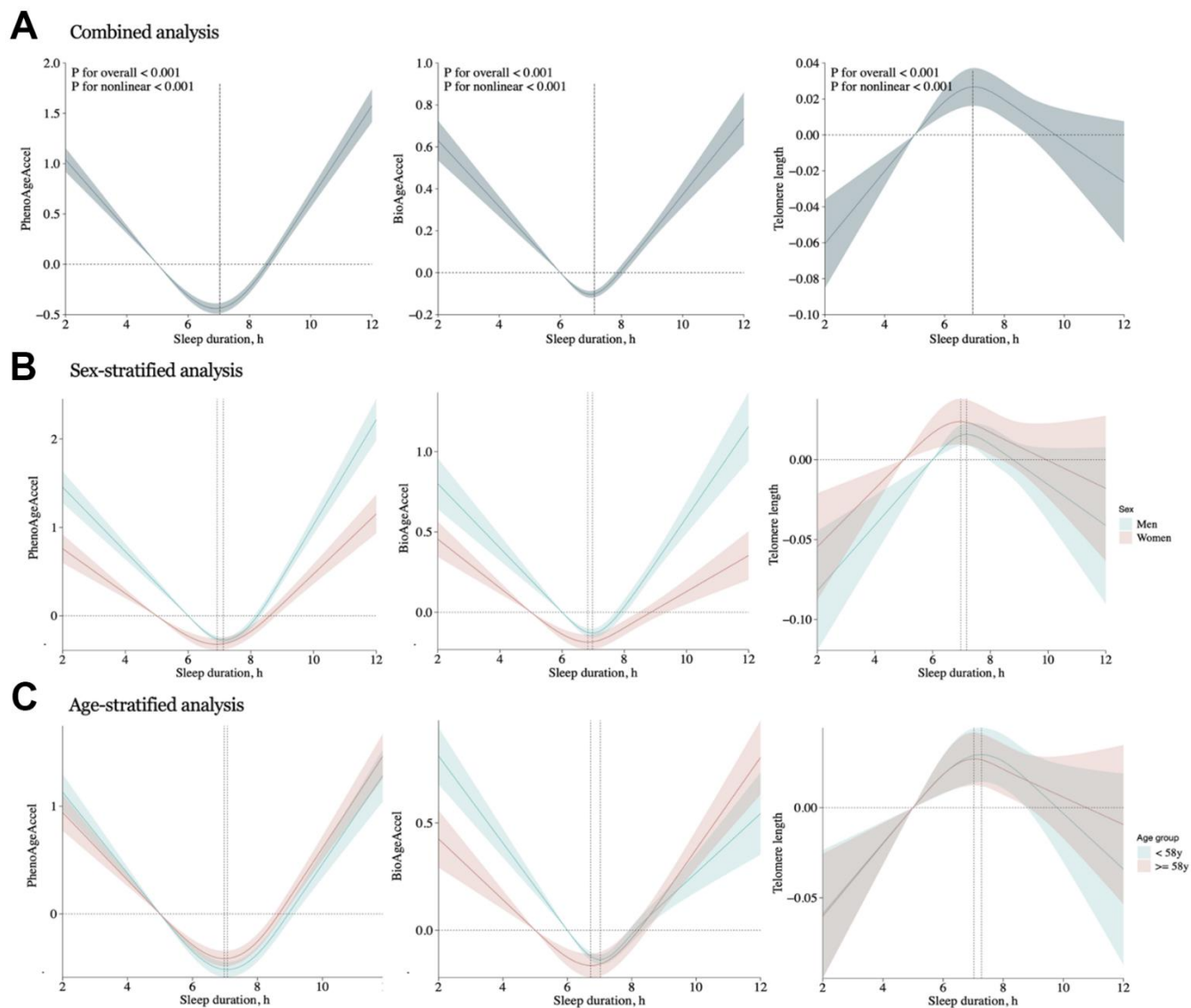
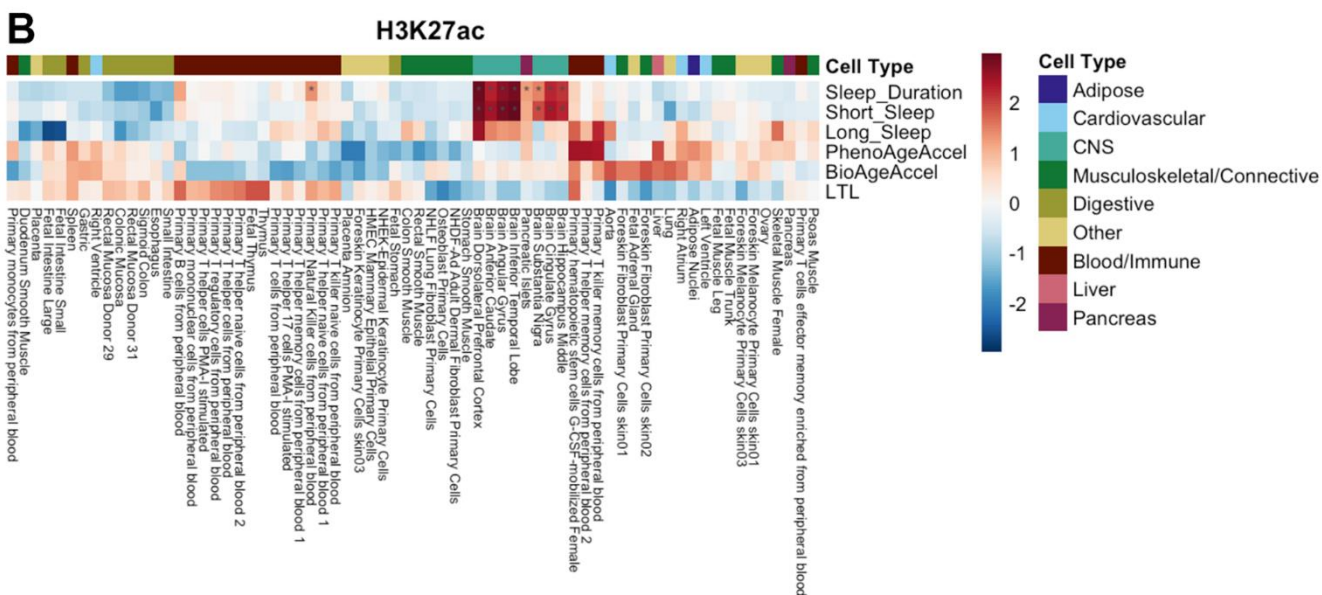
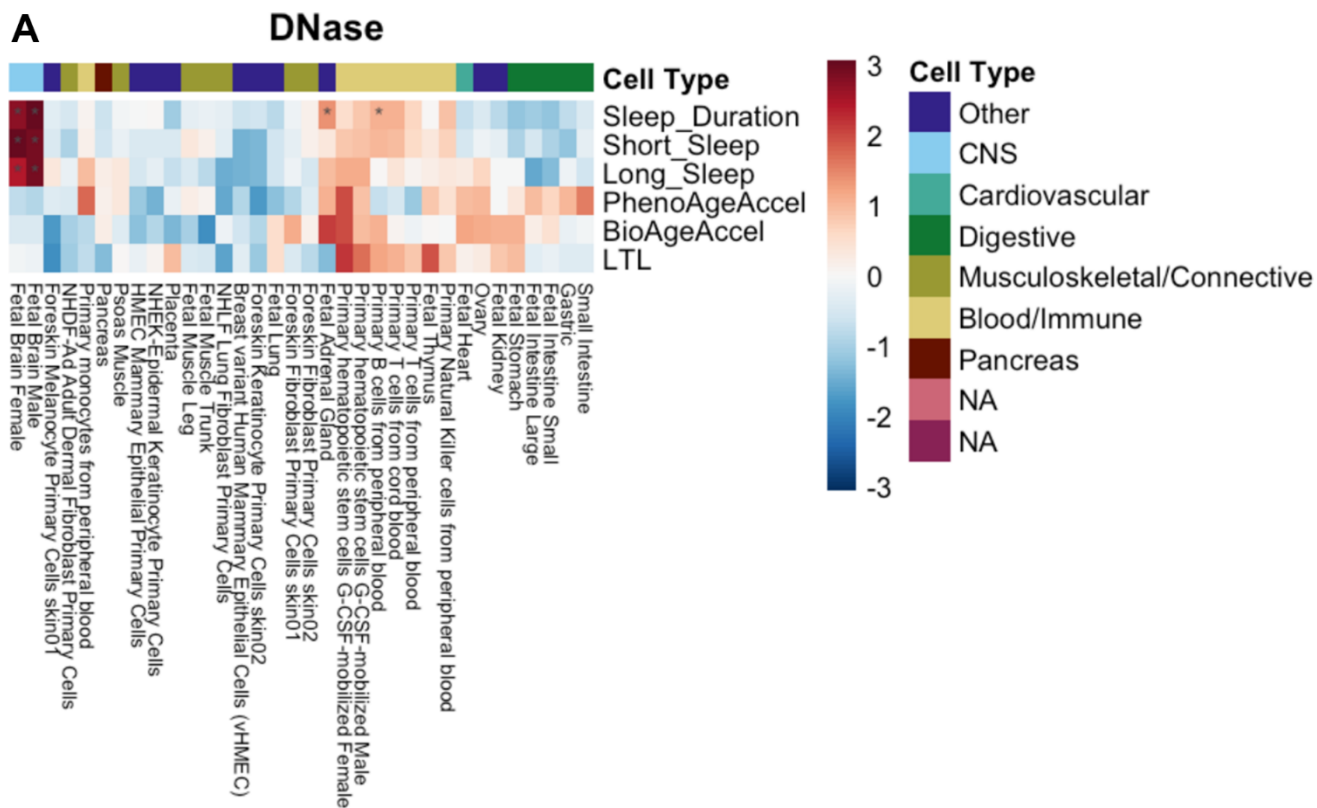
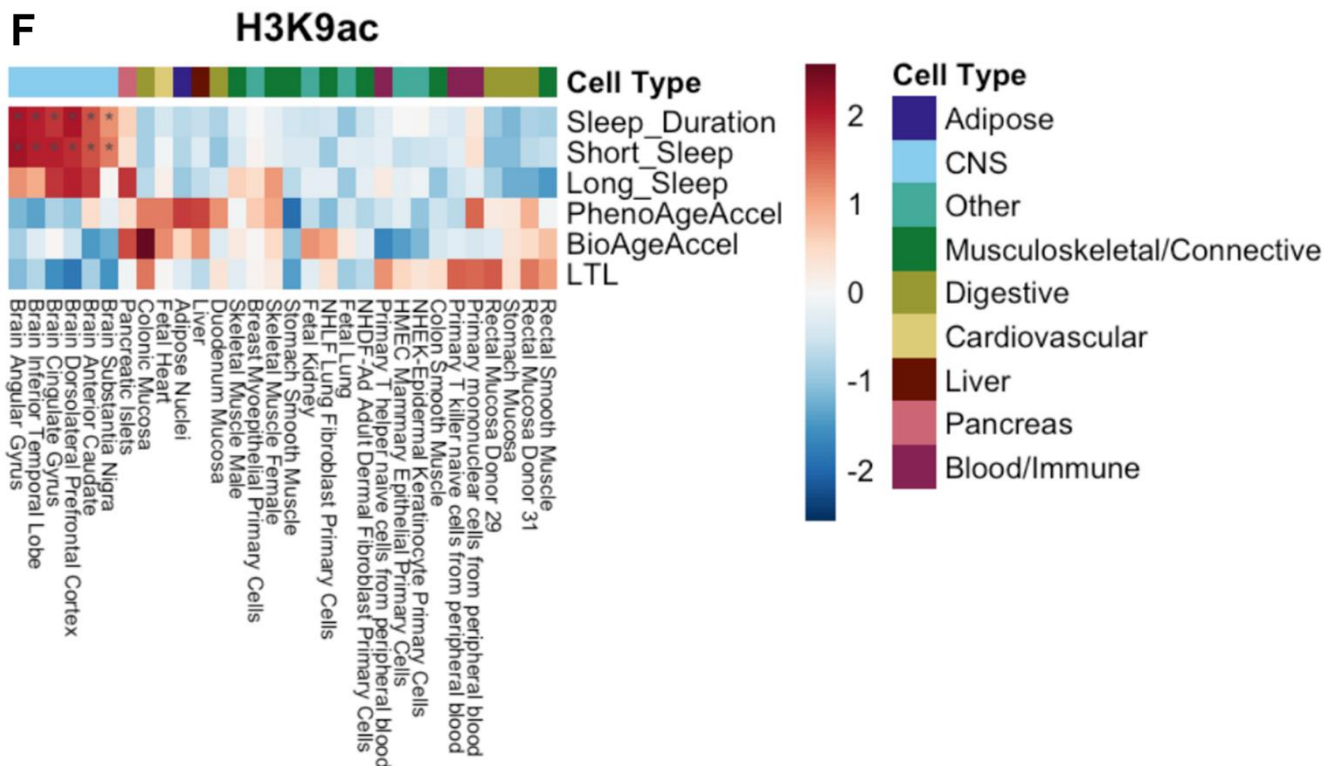


SUPPLEMENTARY FIGURES



Supplementary Figure 1. Results of restricted cubic spline regressions of PhenoAge acceleration (PhenoAgeAccel), BioAge acceleration (BioAgeAccel), and leukocyte telomere length on sleep duration. Models adjusted for, where appropriate, age at baseline, sex, the top five genetic principal components, educational qualifications, body mass index, smoking history, drinking history, physical activity status, leucocyte count (for telomere length as an outcome), and histories of cardiovascular diseases, hypertension, and diabetes mellitus. (A) Combined analysis, (B) Sex-stratified analysis, (C) Age-stratified analysis.





Supplementary Figure 2. Clustering of cell-type-specific annotation for sleep duration phenotypes and biological age measurements over histone marks. Each colored square reflects the z-score, scaled by traits. Red indicates enrichment, blue indicates depletion. Deeper color represents stronger magnitude of effects. Asterisks represent statistical significance withstanding correction (FDR-adjusted P -value < 0.05). (A). DNase, (B). H3K27ac, (C). H3K36me3, (D). H3K4me1, (E). H3K4me3, and (F). H3K9ac. PhenoAgeAccel: PhenoAge acceleration; BioAgeAccel: BioAge acceleration; LTL: leucocyte telomere length.