

**Supplementary Figure S1. Distribution of mortality and anti-mortality CpGs.** With the CpG index (sorted by FDR) on the x-axis and the  $-\log(\text{FDR})$  of the overall mortality association post-CpG removal on the y-axis, the distribution of CpG-level effects is visualized. DNA methylation sites that improve or worsen the mortality association when removed were dubbed anti-mortality CpGs or mortality CpGs, respectively.

**Supplementary Figure S2. Enrichment results for the top 250 annotated mortality CpGs.** For the top 250 mortality CpGs with gene annotations, a network topology-based enrichment analysis was performed using WebGestalt. The top 15 Gene Ontology processes are visualized and sorted by  $-\log(\text{FDR})$ .

**Supplementary Figure S3. Enrichment results for the top 250 annotated anti-mortality CpGs.** For the top 250 anti-mortality CpGs with gene annotations, a network topology-based enrichment analysis was performed using WebGestalt. The top 15 Gene Ontology processes are visualized and sorted by  $-\log(\text{FDR})$ .