

Supplemental Tables

Supplemental Table S1: Sample design, biological information, and quality metrics.

Supplemental Table S2: Accession numbers of reanalyzed publicly available datasets.

Supplemental Table S3: Performance of machine-learning models.

Supplemental Table S4: Genes with significant tissue-independent transcriptional changes with aging as called by DESeq2 with FDR < 5%.

Supplemental Table S5: Functional annotation analysis information (IPA and KEGG)

Supplemental Table S6: Analysis of repeat element transcriptional and chromatin remodeling with mouse aging.

Supplemental Table S7: Detailed results of CIBERSORT RNA deconvolution algorithm.