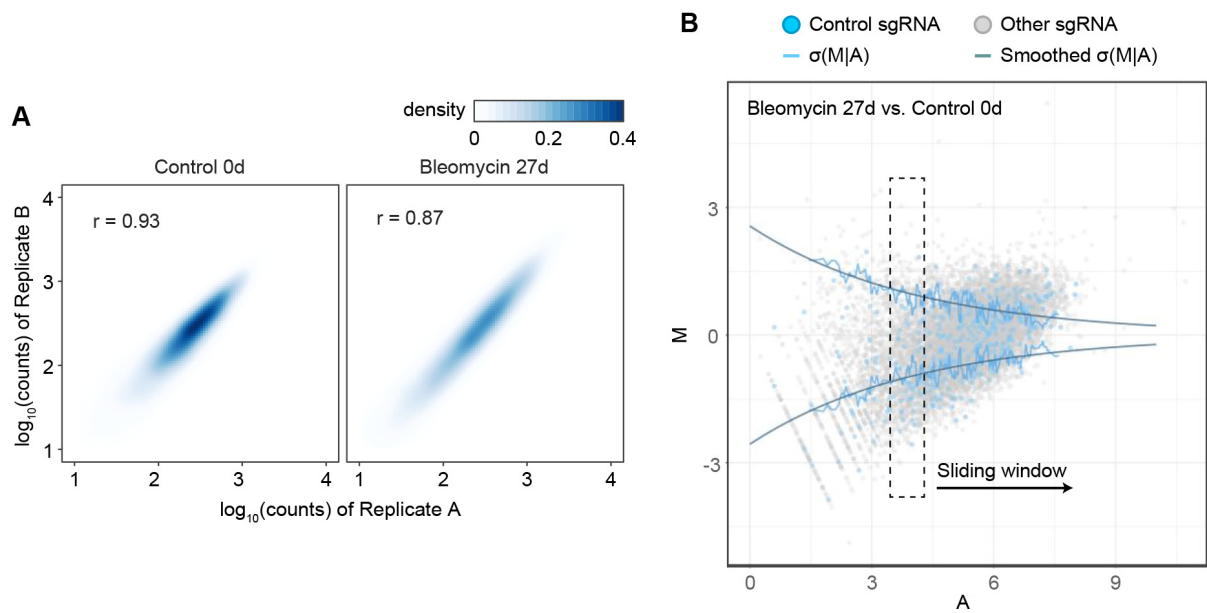
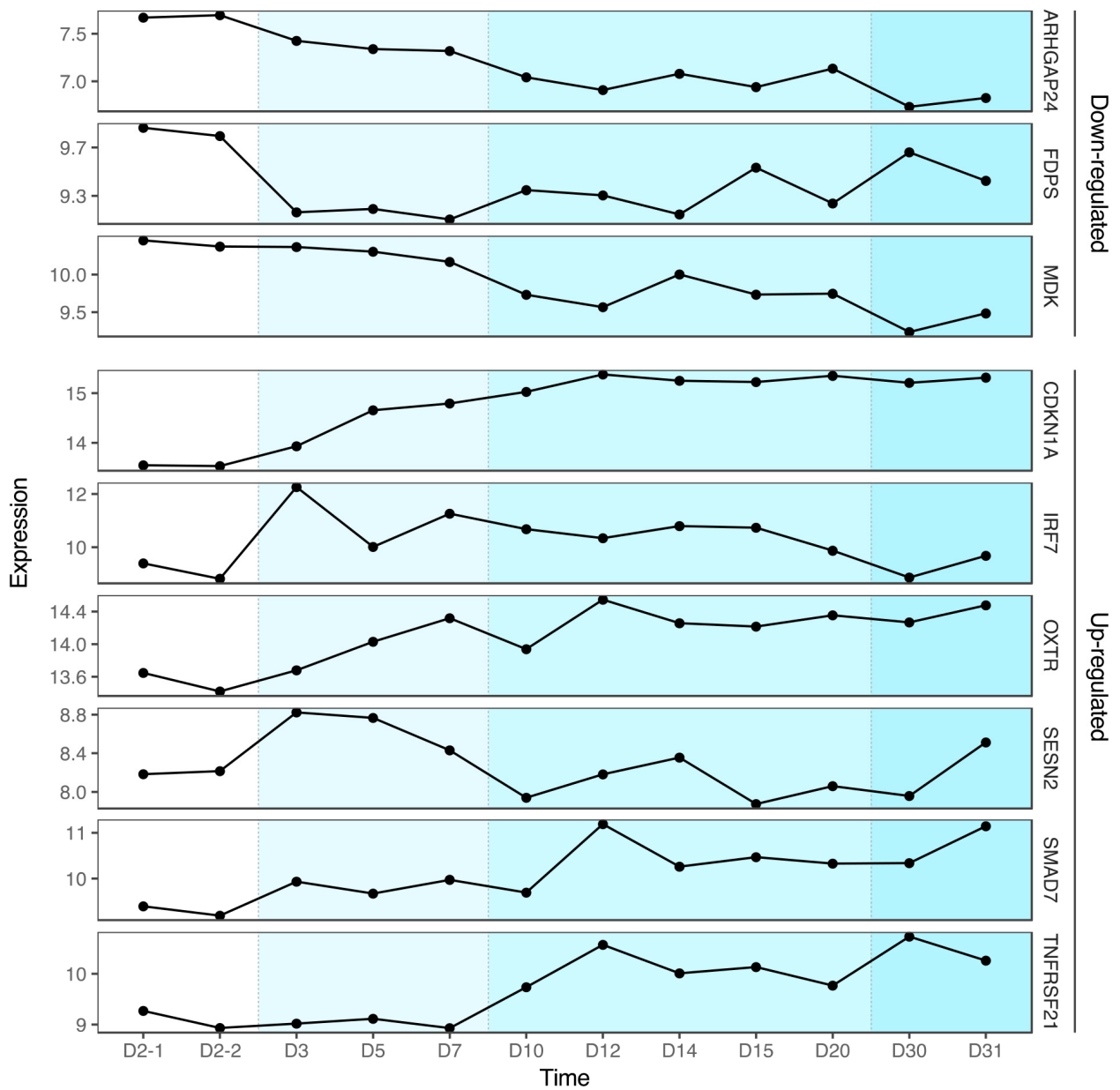


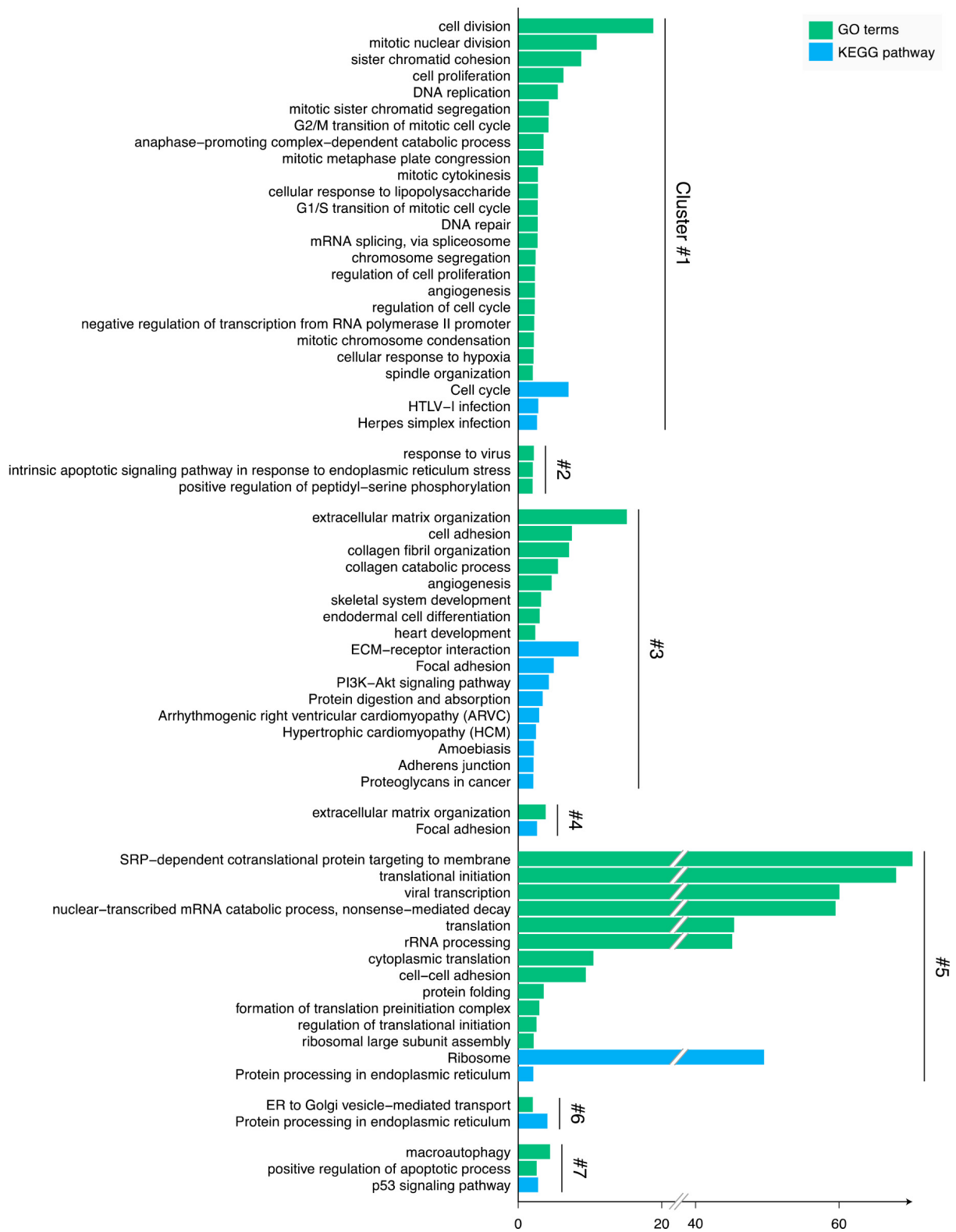
SUPPLEMENTARY FIGURES



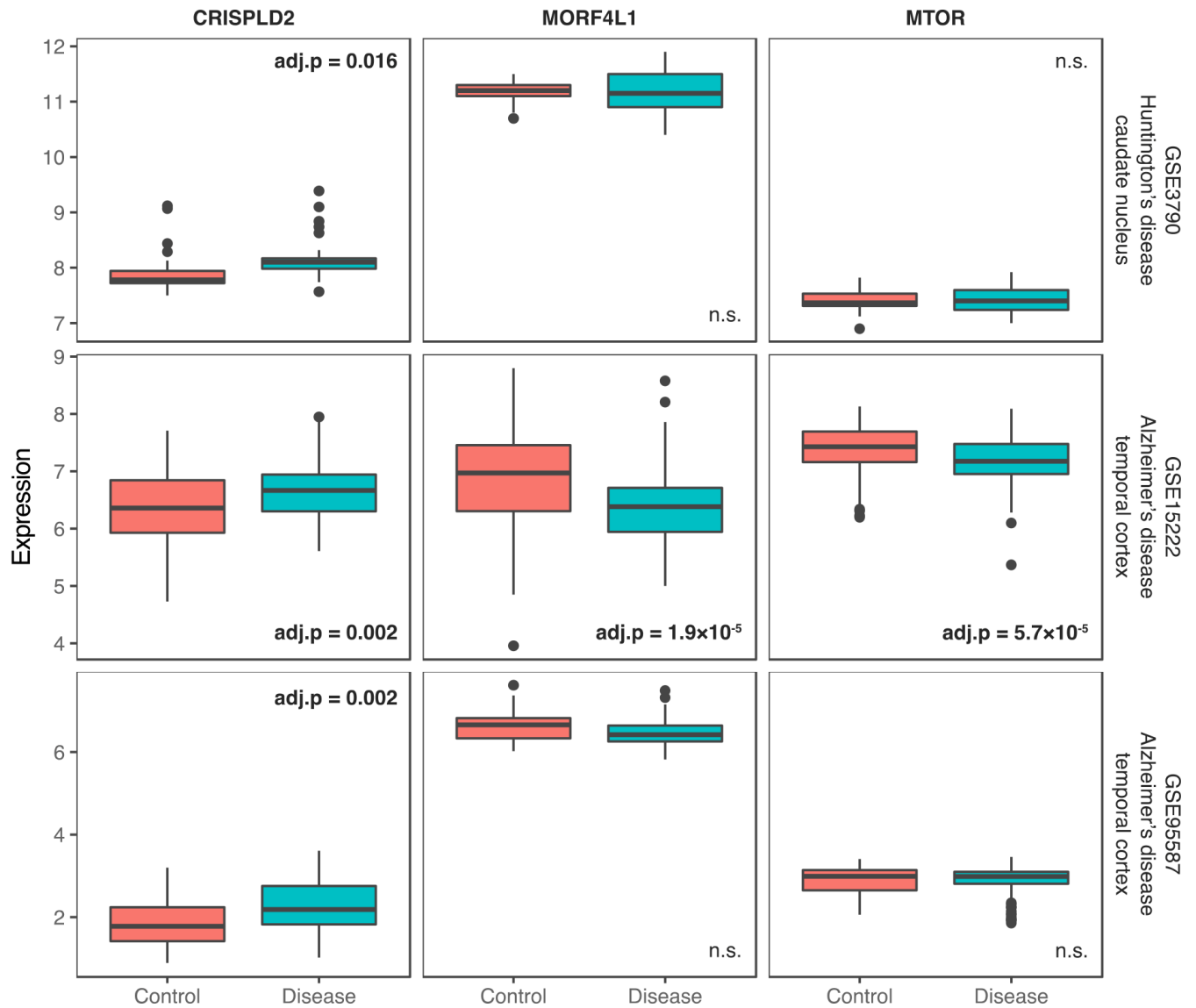
Supplementary Figure 1. The large-scale CRISPR knockout screen and analysis. (A) Replicates of CRISPR screen samples showed high correlation. Pearson correlations (r) were given. (B) M-A plot methods for scoring and identifying candidate senescence bypass genes.



Supplementary Figure 2. Expressions of the candidate bypass genes during senescence. The time-series gene expression data are from dataset GSE41714 (replicative senescence, human diploid fibroblasts). Colors represent groups for differential analysis. Only genes with differential expression (adjust *p*-value < 0.05) were shown.



Supplementary Figure 4. KEGG pathway and GO enrichment results of genes in each cluster in transcriptome data. Terms with adjusted p -value < 0.01 were shown.



Supplementary Figure 5. Expressions of *CRISPLD2*, *MORF4L1*, and *MTOR* in Alzheimer's disease and Huntington's disease patient tissues in previous studies. Data and statistics were obtained from The Myeloid Landscape (<http://research-pub.gene.com/BrainMyeloidLandscape>).