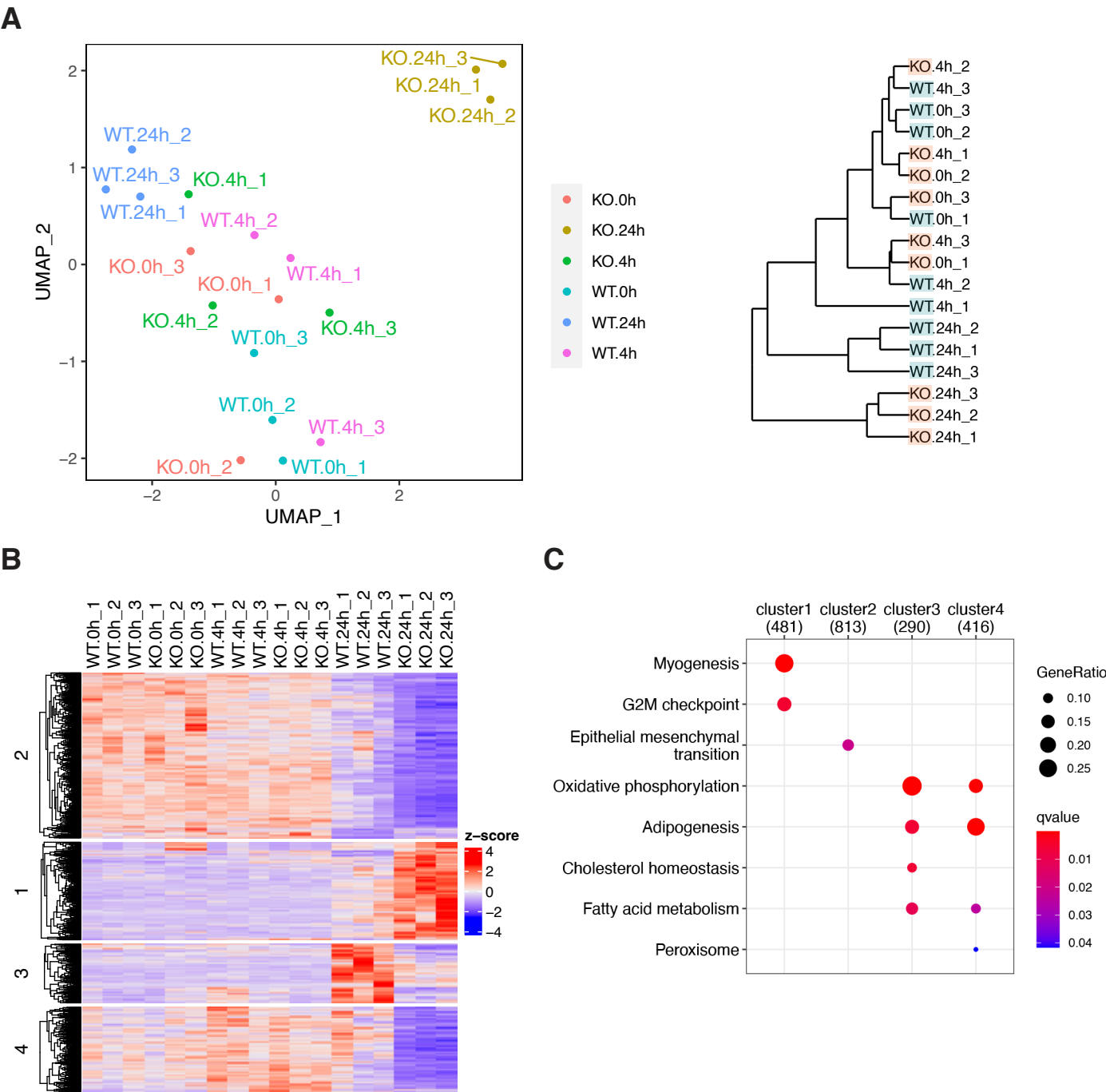




Supplemental figure S2. Analyses of transcriptomic dynamics in iWAT upon cold exposure in *Neat1* KO mice using RNAseqChef. (A) Uniform Manifold Approximation and Projection (UMAP) and hierarchical clustering of RNA-Seq data from iWAT at 0h, 4h, and 24h following cold exposure. UMAP analysis was conducted with a neighbor setting of 5. Early time points (0h, 4h) show overlapping distributions of WT and KO samples, with distinct segregation emerging at 24h. (B) K-means clustering heatmap of RNA-Seq data, with the analysis specifying 4 distinct clusters to categorize gene expression patterns. (C) Enrichment analysis based on the K-means clustering in (B), utilizing a fold change cutoff derived from the differential expression between WT and KO samples at 24h post-exposure. Molecular Signatures Database (MSigDB) was used to detect enrichment genes.