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Supplemental information

Single-cell multi-omics identify novel regulators required for osteoclastogenesis during aging

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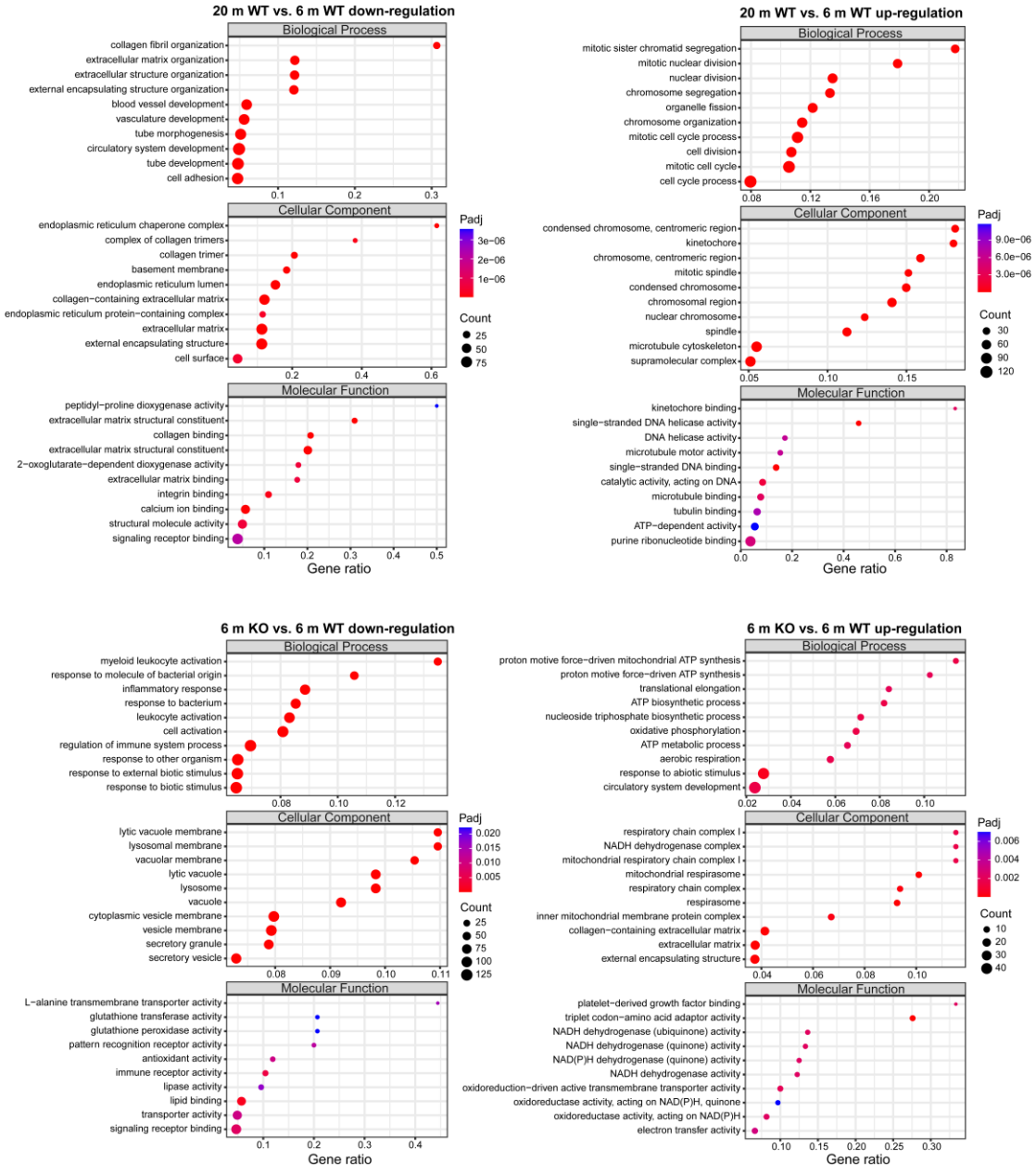
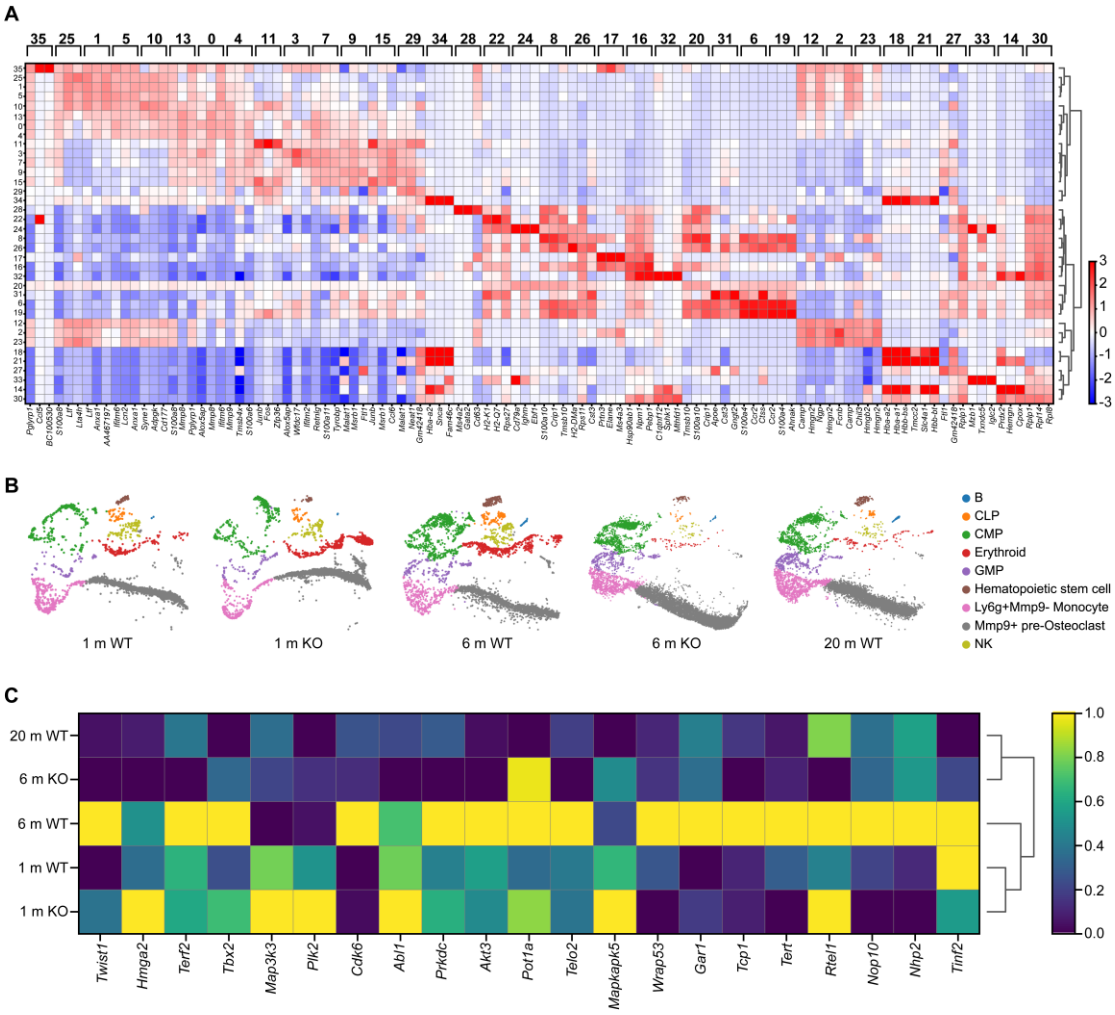
Figure S1. GO enrichment analysis through comparing 6 m and 20 m WT (top) or 6 m KO group (bottom), Related to Figure 1.



Dotplots of GO enrichment results. Each category (Biological Process, Molecular Function, or Cellular Component) shows top 10 GO terms.

Figure S2. Gene expression of critical genes in different cell populations, Related to Figure 2.

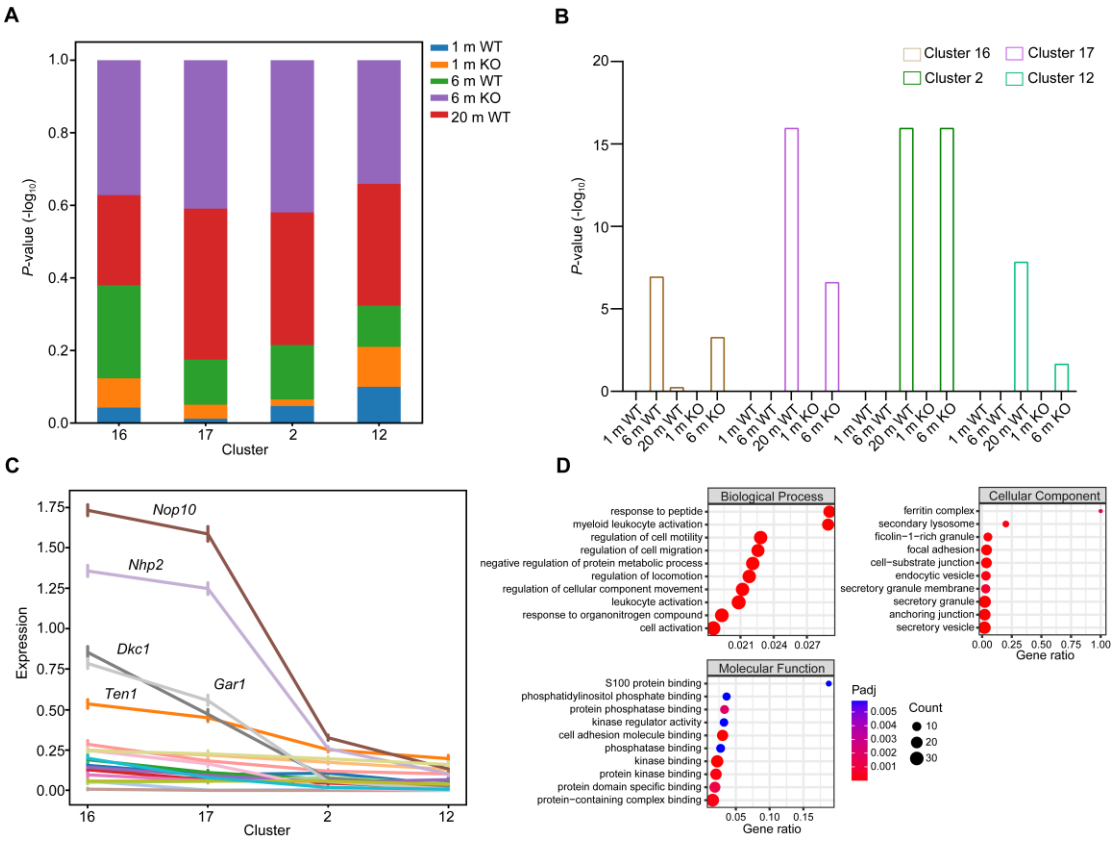


(A) The signature genes for each of the clusters.

(B) UMAP plots of each ageing group.

(C) *Terc*-associated genes expression across different age groups.

Figure S3. The cell composition of cell clusters in the osteoclast committed trajectory (16→17→2→12), Related to Figure 4 and Figure 5.



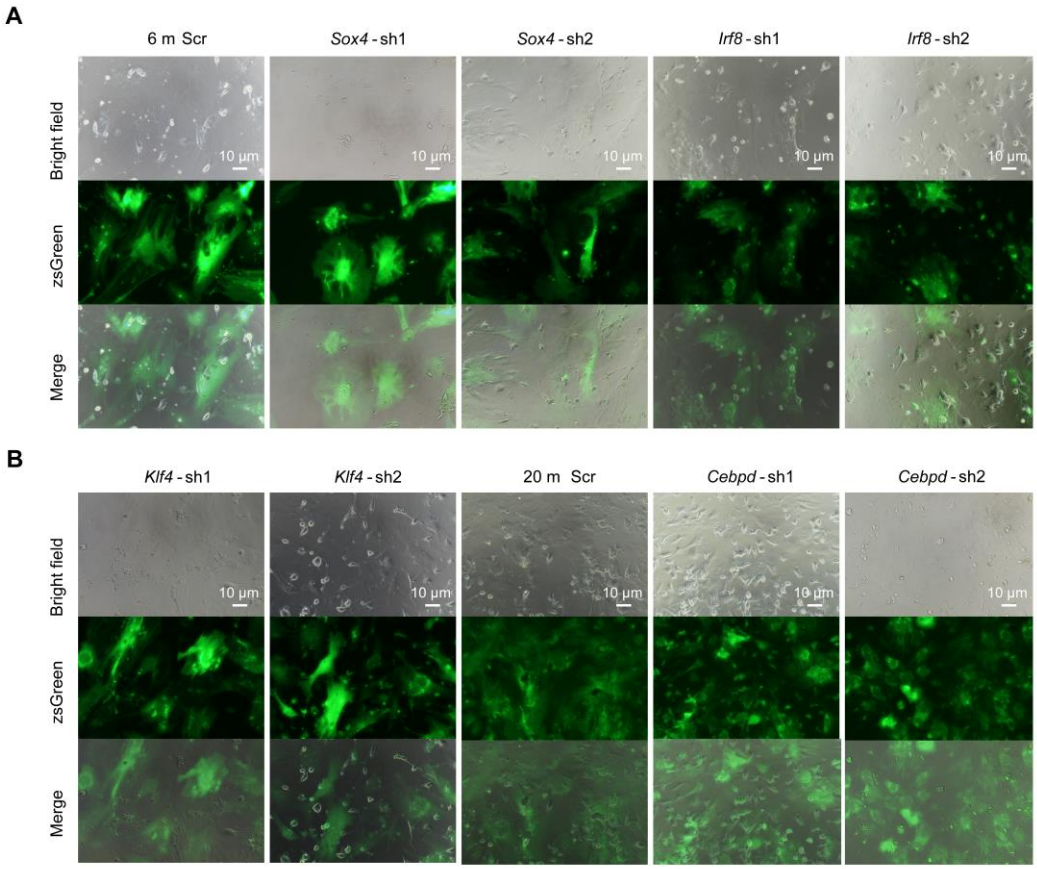
(A) The aged cells (20 m WT and 6 m KO) are dominating this osteoclast committed trajectory, which accounts for more than over 60% of cells in all clusters of this trajectory.

(B) shows that cluster 17, 2, and 12 are all significantly enriched with aged cells (20 m WT and 6 m KO) while the starting cluster (16) is significantly enriched with the adult cells (6 m WT).

(C) The expression of *Terc* relevant genes are generally decreasing along with the osteoclast committed trajectory.

(D) GO enrichment analysis of DEGs in Figure 5C.

Figure S4. shRNA-lentivirus infection of in-vitro cultured BMMs, Related to Figure 7.



The lentivirus vectors with reporter of zsGreen infected in vitro culture BMMs harvested from mice bone marrow.