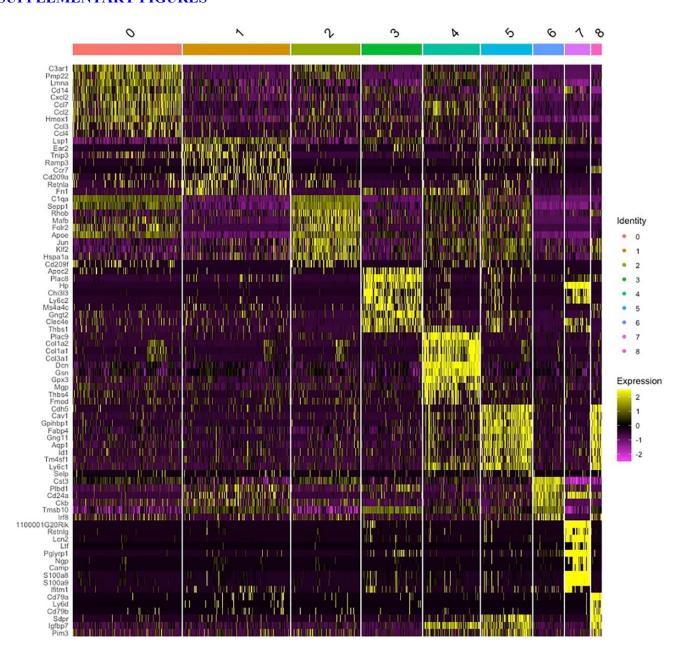
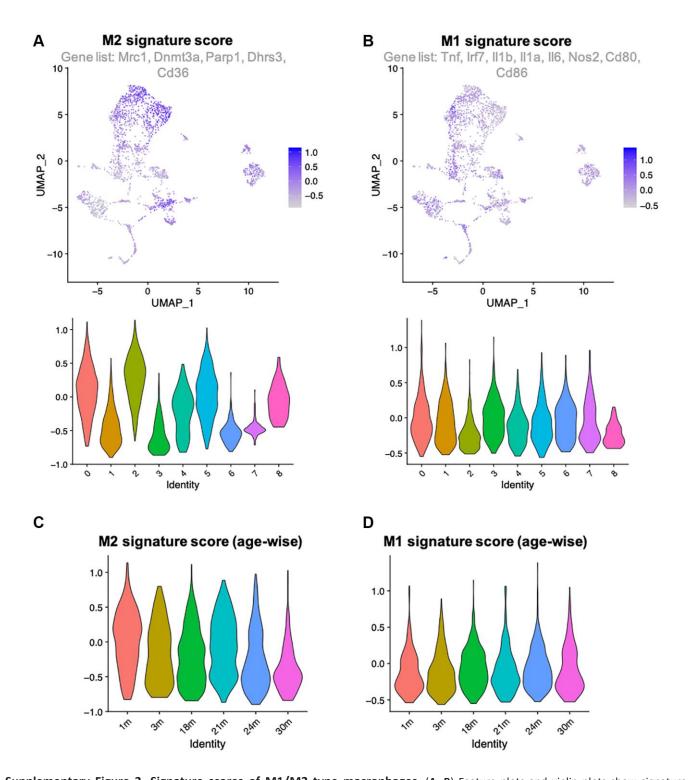
SUPPLEMENTARY FIGURES

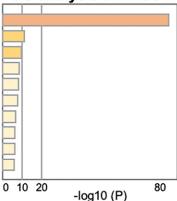


Supplementary Figure 1. Heatmap of unsupervised clustering analysis featuring the top 10 discriminative genes per cluster. Marker genes (defined by log2 fold change) of macrophage subcluster 0 to 8.



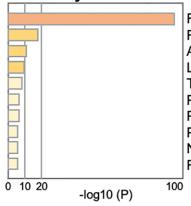
Supplementary Figure 2. Signature scores of M1/M2 type macrophages. (A, B) Feature plots and violin plots show signature scores of M2-type or M1-type macrophage marker genes. (C, D) Violin plots show age-wise signature scores of M2-type or M1-type macrophage marker genes. Plots were generated using AddModuleScore function in R. Genes that were included as each signature score analysis are also indicated.

GO analysis of DEGs in c1



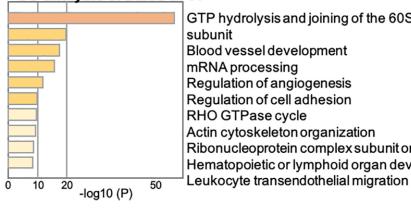
Formation of a pool of free 40S subunits Positive regulation of leukocyte cell-cell adhesion Intestinal immune network for IgA production C-type lectin reveptors (CLRs) Lymphocyte activation Negative regulation of immune system process Positive regulation of cell migration IL-3, IL-5 and GM-CSF signaling Regulation of cytokine production Regulation of leukocyte apoptotic process

GO analysis of DEGs in c6



Formation of a pool of free 40S subunits Ribosome biogenesis Antigen processing and presentation Leukocyte activation Translation factors Protein folding Positive regulation of T cell activation Positive regulation of cell death Negative regulation of immune system process Response to interferon-gamma

GO analysis of DEGs in c8



GTP hydrolysis and joining of the 60S ribosomal subunit Blood vessel development mRNA processing Regulation of angiogenesis Regulation of cell adhesion RHO GTPase cycle Actin cytoskeleton organization Ribonucleoprotein complex subunit organization Hematopoietic or lymphoid organ development

Supplementary Figure 3. Genetic characteristics of macrophage subclusters specifically low in middle-aged skeletal muscle tissue. GO analysis of DEGs in subclusters 1, 6, and 8. The top 10 most significant GO terms are listed and the X-axis is shown as Log p-value (-log10 (P)). Biological terms associated with ribosomal subunits were found to be strikingly increased in all three subclusters.