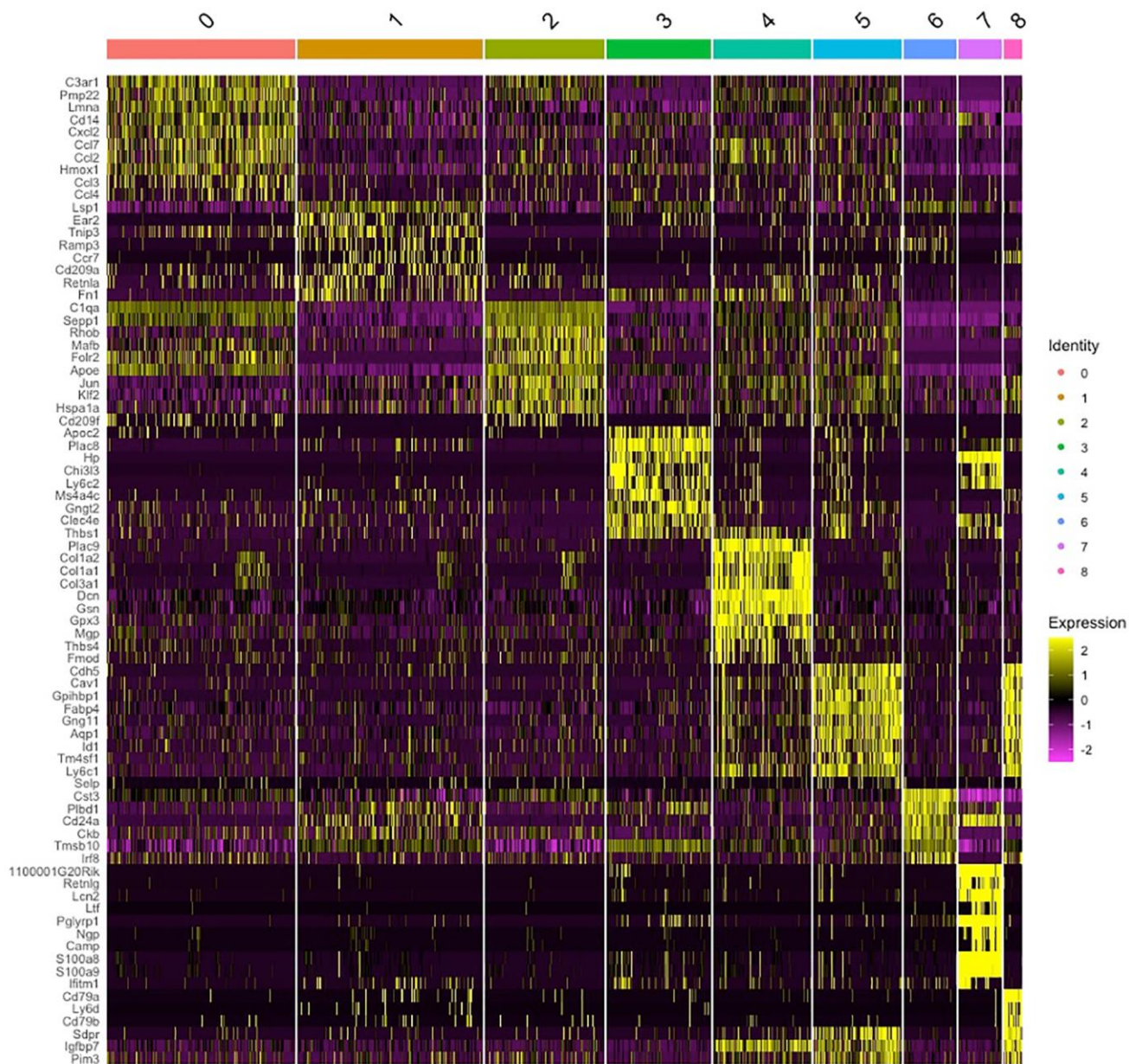
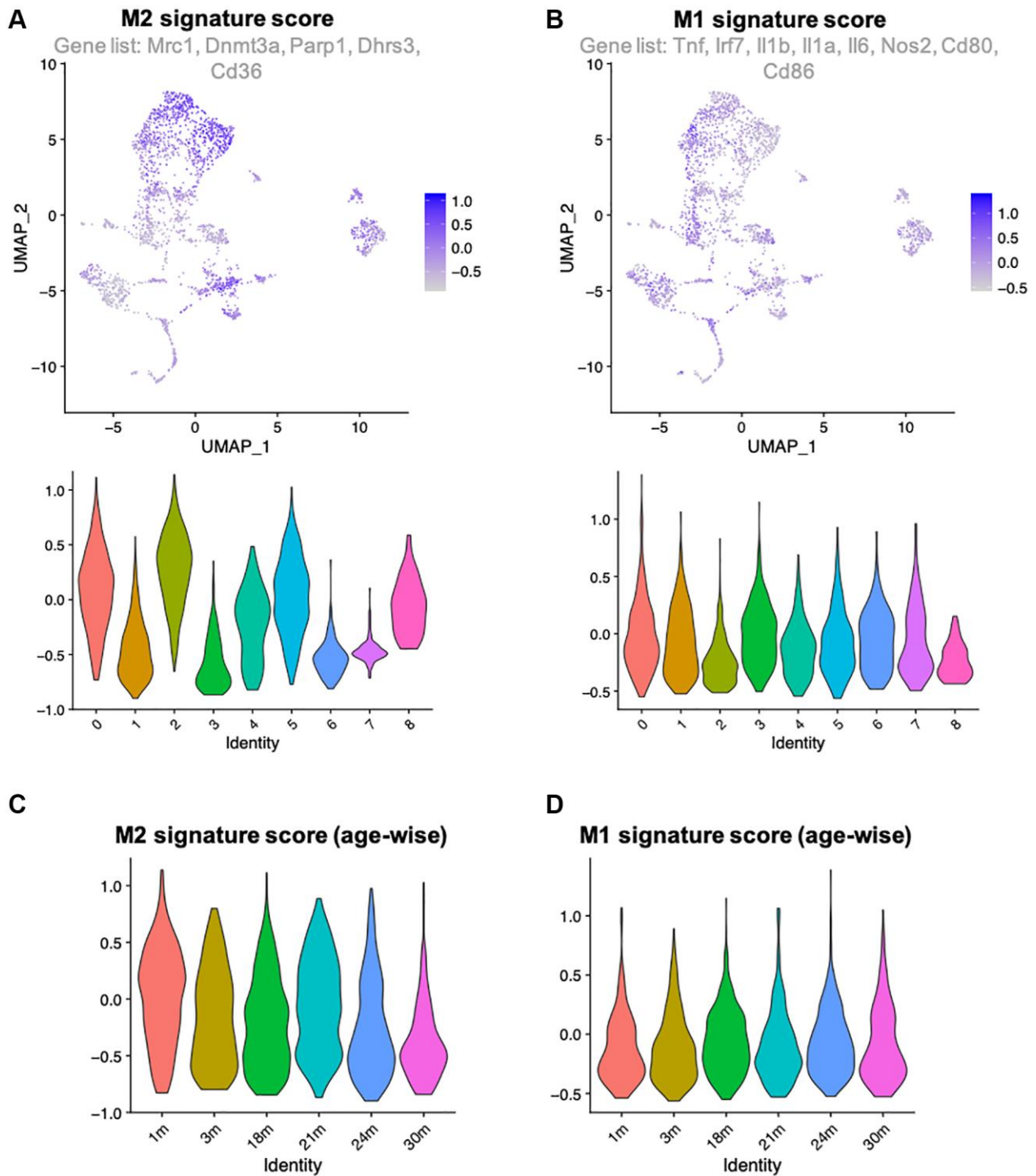


SUPPLEMENTARY FIGURES

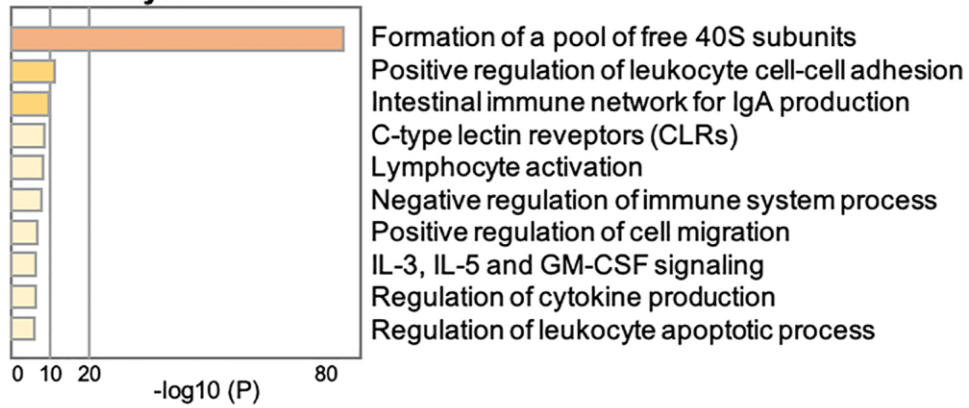


Supplementary Figure 1. Heatmap of unsupervised clustering analysis featuring the top 10 discriminative genes per cluster. Marker genes (defined by log₂ fold change) of macrophage subcluster 0 to 8.

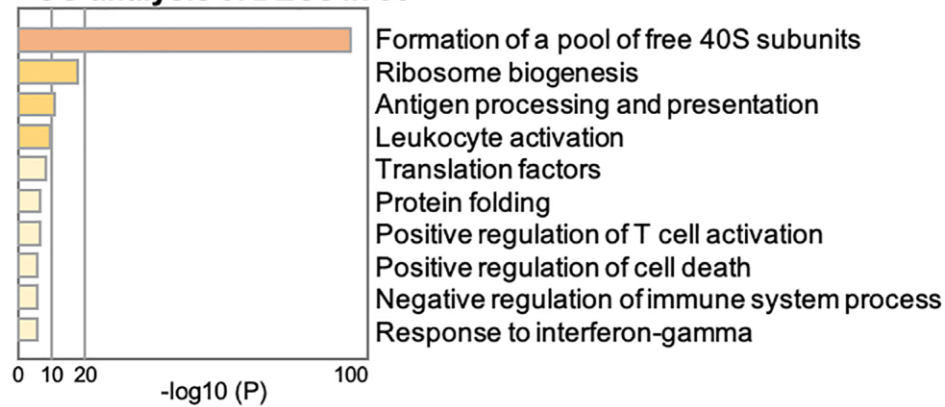


Supplementary Figure 2. Signature scores of M1/M2 type macrophages. (A, B) Feature plots and violin plots show signature scores of M2-type or M1-type macrophage marker genes. (C, D) Violin plots show age-wise signature scores of M2-type or M1-type macrophage marker genes. Plots were generated using `AddModuleScore`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

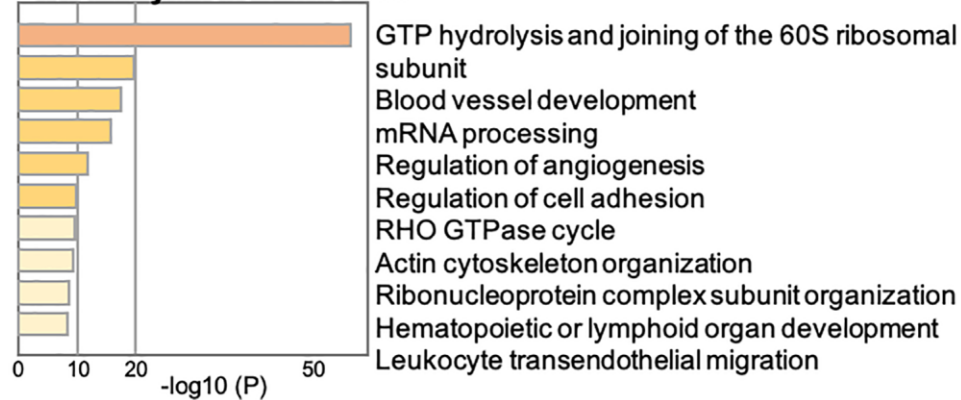
GO analysis of DEGs in c1



GO analysis of DEGs in c6



GO analysis of DEGs in c8



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 ($-\log_{10}(P)$). Biological terms associated with ribosomal subunits were found to be strikingly increased in all three subclusters.