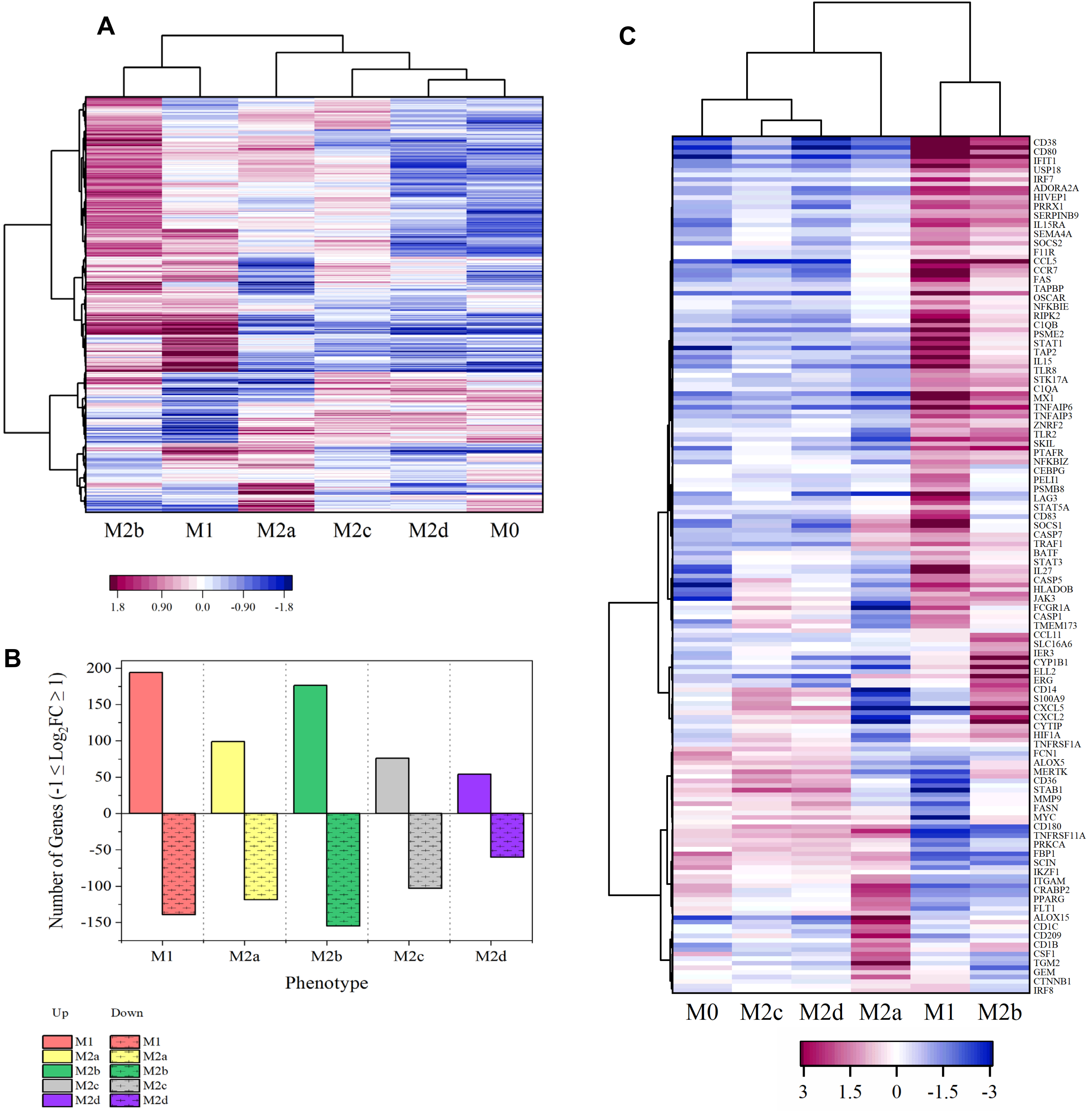

**Supplemental Figure 2: Global Transcriptomics Differentiates the MΦ Functional Phenotypes from the Parent, Resting M0 Phenotype.** Hierarchical cluster analysis performed on the normalized expression data identified differences in the transcriptional profiles of the polarized MΦ phenotypes relative to the M0 parent MΦ. Distance measure is by Pearson correlation with clustering determined using the Ward algorithm. Heatmap scale (-1.8 to 1.8) is colored from blue to red **(A).** The fold change for each gene was calculated relative to the M0 phenotype and the number of up- and down-regulated genes (-1≤ $\text{Log}_2\text{FC}$ ≥1) graphed in **(B).** Gene set enrichment analysis (GSEA) of the global myeloid gene expression revealed 189 significantly differentially expressed genes (SDEGs) identified using a one-way ANOVA with an adjusted p-value (FDR) cutoff of 0.05. Hierarchical cluster analysis was performed on this data using a distance measure calculated using Pearson correlation with clustering determined using the Ward algorithm. Heatmap scale (-1.8 to 1.8) is colored from blue to red **(C).**