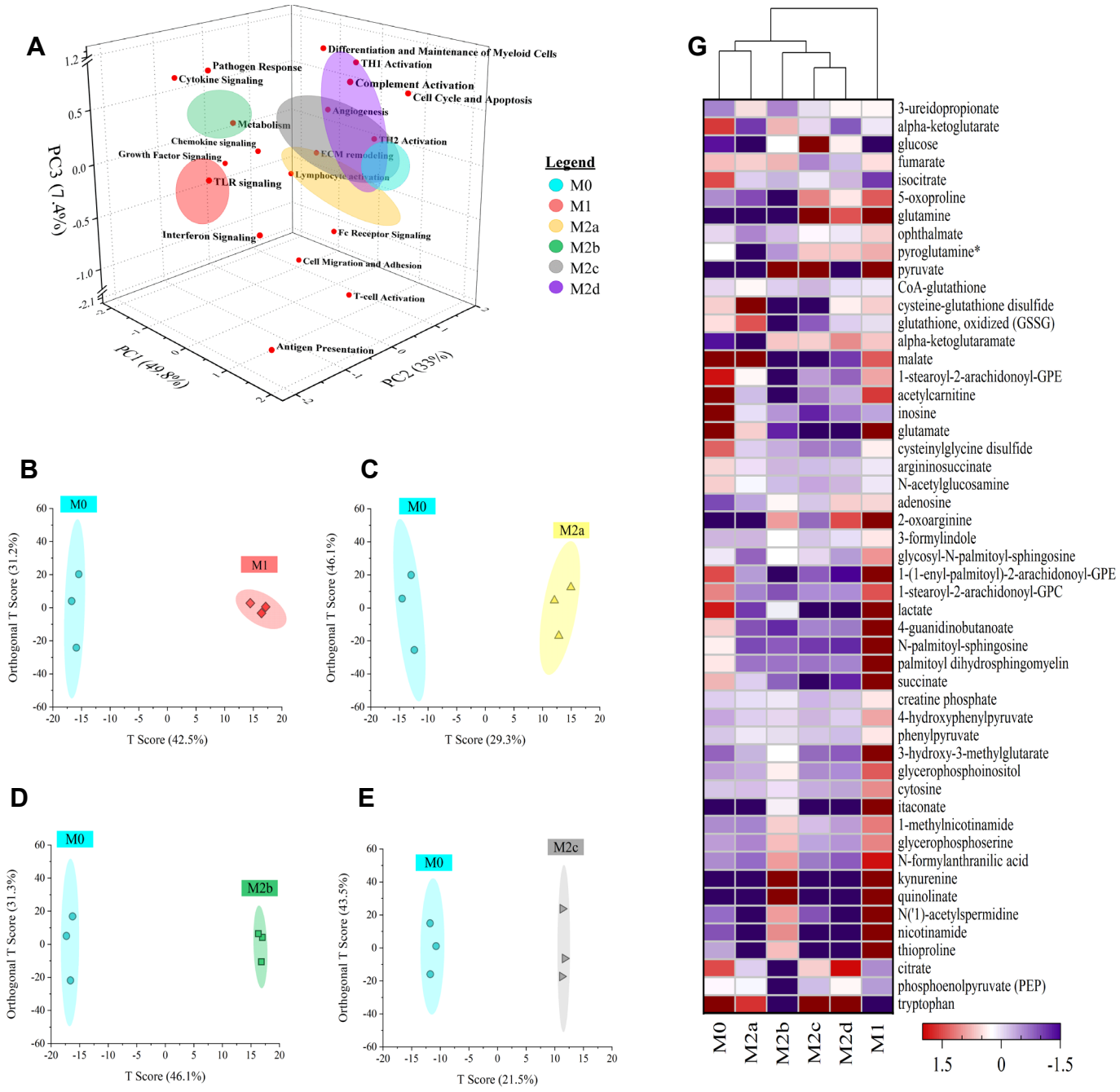

Supplemental Figure 3: MΦ Polarization into Functional Phenotypes Activates Distinct Gene Expression Profiles and Metabolic Differences Relative to the Parent, Resting MΦ Phenotype (M0). Principal component analysis (PCA) 3D loadings plot utilizes red dots to depict the PC1 (x-axis), PC2 (y-axis) and PC3 (z-axis) loadings for each of the 19 Nanostring identified pathways while the colored ellipses denote the 3D representation of the linear combination of the three principal components for each polarized phenotype and the M0 parent cells **(A)**. Orthogonal Projections to Latent Structures Discriminant Analysis (OPLSDA) clustering scores plots with 2D T-scores are depicted for The M0 parent cells (cyan) versus M1 MΦs (IFN-γ/LPS treated shown in red) **(B)**, M2a MΦs (IL-4/IL-13 treated, shown in yellow) **(C)**, M2b MΦs (IC/LPS treated, shown in green) **(D)**, M2c MΦs (IL-10 treated, shown in gray) **(E)**, and M2d MΦs (IL-6/LIF treated, shown in purple) **(F).** Global metabolomics profile of the parent, resting MΦ phenotype (M0) and five polarized MΦ phenotypes identified 498 compounds of known identity, normalized to cell count. Hierarchical cluster analysis was performed on the top 50 significantly differentiated metabolites identified using a one-way ANOVA with an adjusted p-value (FDR) cutoff of 0.05 using a distance measure calculated using Pearson correlation with clustering determined using the Ward algorithm. Heatmap scale (-1 to 1) is colored from purple to red **(G).**