Yang FF, et al. Figure S3

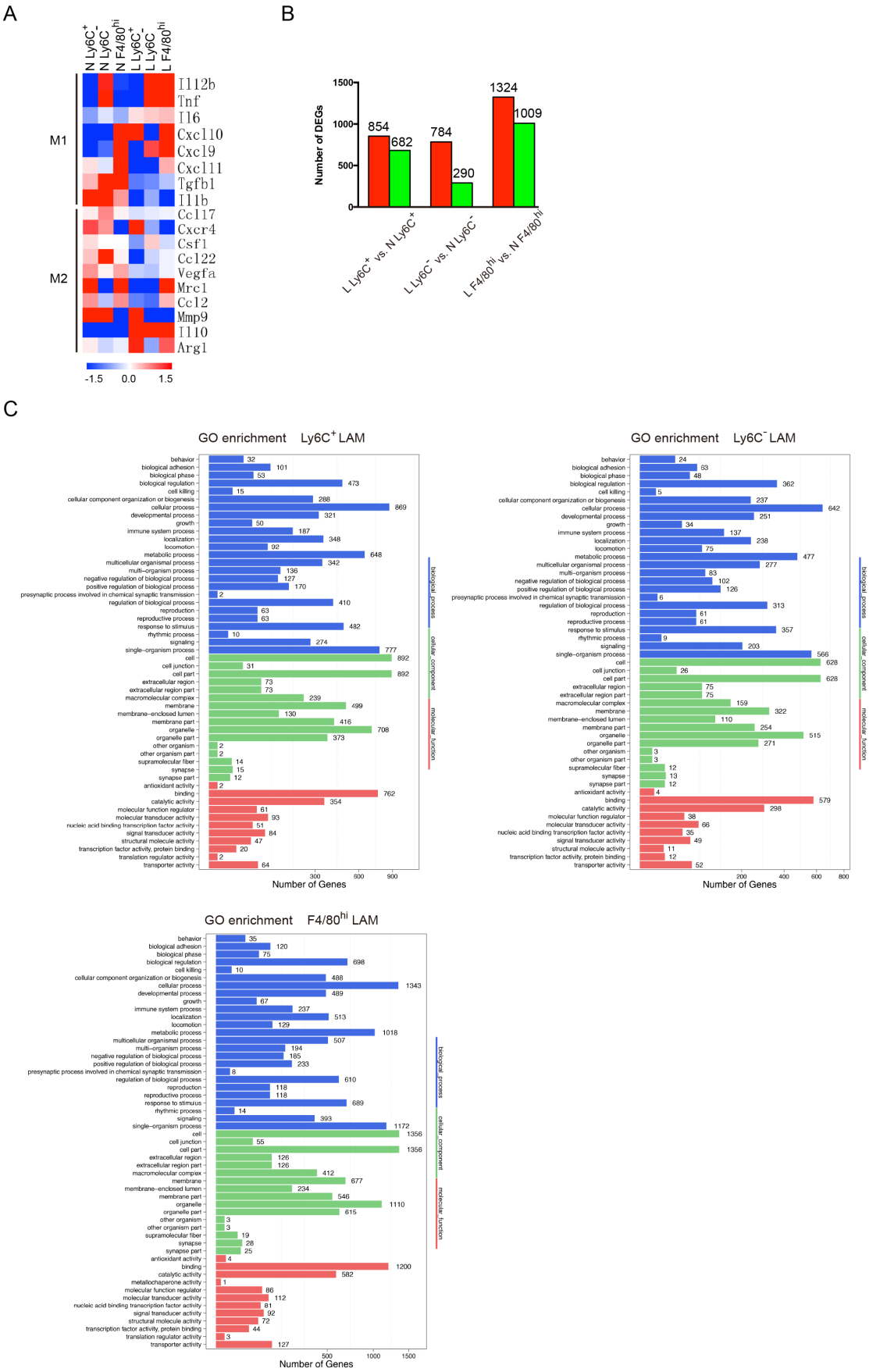

Figure S3. RNA-seq analysis of SP normal macrophage and LAM subsets.

(A) The profile of M1/M2 phenotype-associated genes in normal macrophage and LAM subsets is shown. (B) Counts of DEGs (LAM subsets vs. normal controls, red for upregulation and green for downregulation) are plotted. (C) The DEGs (LAM subsets vs. normal controls) were subjected to GO analysis using DAVID bioinformatics resources. Each bar represents a significantly functional annotation ($P<0.05$).