Figure S1. Characterization of MPs in PTC-M tissue. (A) Heatmap of the top differentially expressed genes of MPs between PTC-M and NT tissues. (B) Gene Ontology annotation and (C) Kyoto Encyclopedia of Genes and Genomes analysis of up-regulated genes of MPs in PTC-M tissue. PTC-M, metastatic papillary thyroid cancer; NT, non-tumor; MP, mononuclear phagocyte; BP, biological process; CC, cellular component; MF, molecular function.

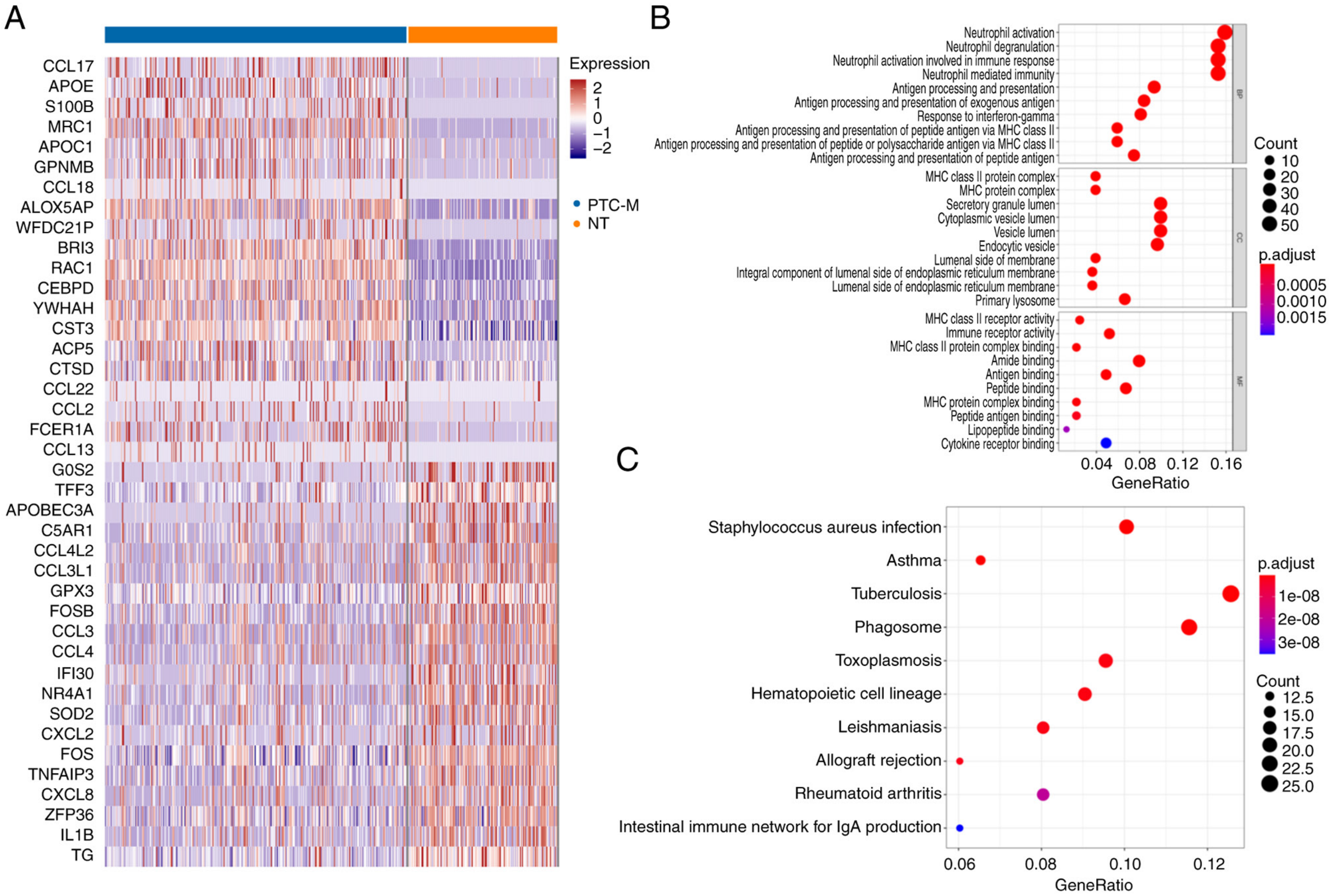

Figure S2. Comparison of Macrophage c1 and c3. (A) GO annotation and (B) KEGG analysis of upregulated genes in Macrophage c1 cluster. (C) GO annotation and (D) KEGG analysis of upregulated genes in Macrophage c3 cluster. GO, Gene Ontology; BP, biological process; CC, cellular component; MF, molecular function; KEGG, Kyoto Encyclopedia of Genes and Genomes.