Supplementary material

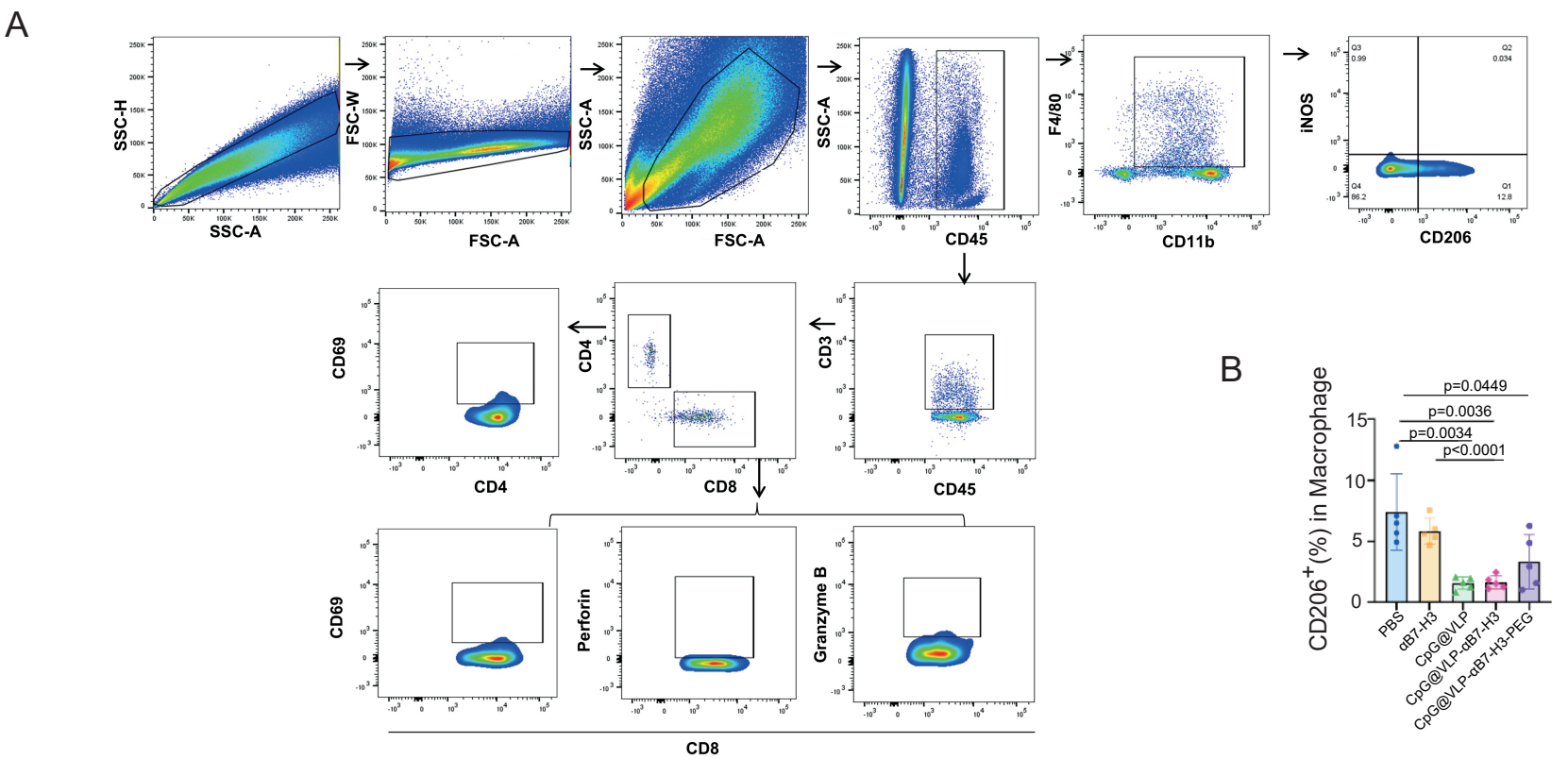

Figure S1 Tumor immune microenvironment remodeling after treatment with VLP nanovaccines.

(A) Flow cytometry gating strategy for tumor microenvironment. (B) The infiltration percentage $CD206^+$ in macrophages at tumor tissue in each treatment group was measured by flow cytometry (n = 5). Data were expressed as the mean ± SD, and differences between two groups were tested using an unpaired, two-tailed Student's t-test. p values less than 0.05 were considered significant, with the corresponding value number specified. (C) GO enrichment scatter plot for upregulated transcriptome genes treated with CpG@VLP-αB7-H3 vs CpG@VLP in $CD45^+$ cells sorting from tumor tissue (n = 3). Genes with an adjusted p value less than 0.05 were identified as differentially expressed genes (DEGs). For GO enrichment analysis of the upregulated DEGs, GO terms with a p value less than 0.05 were considered significantly enriched.

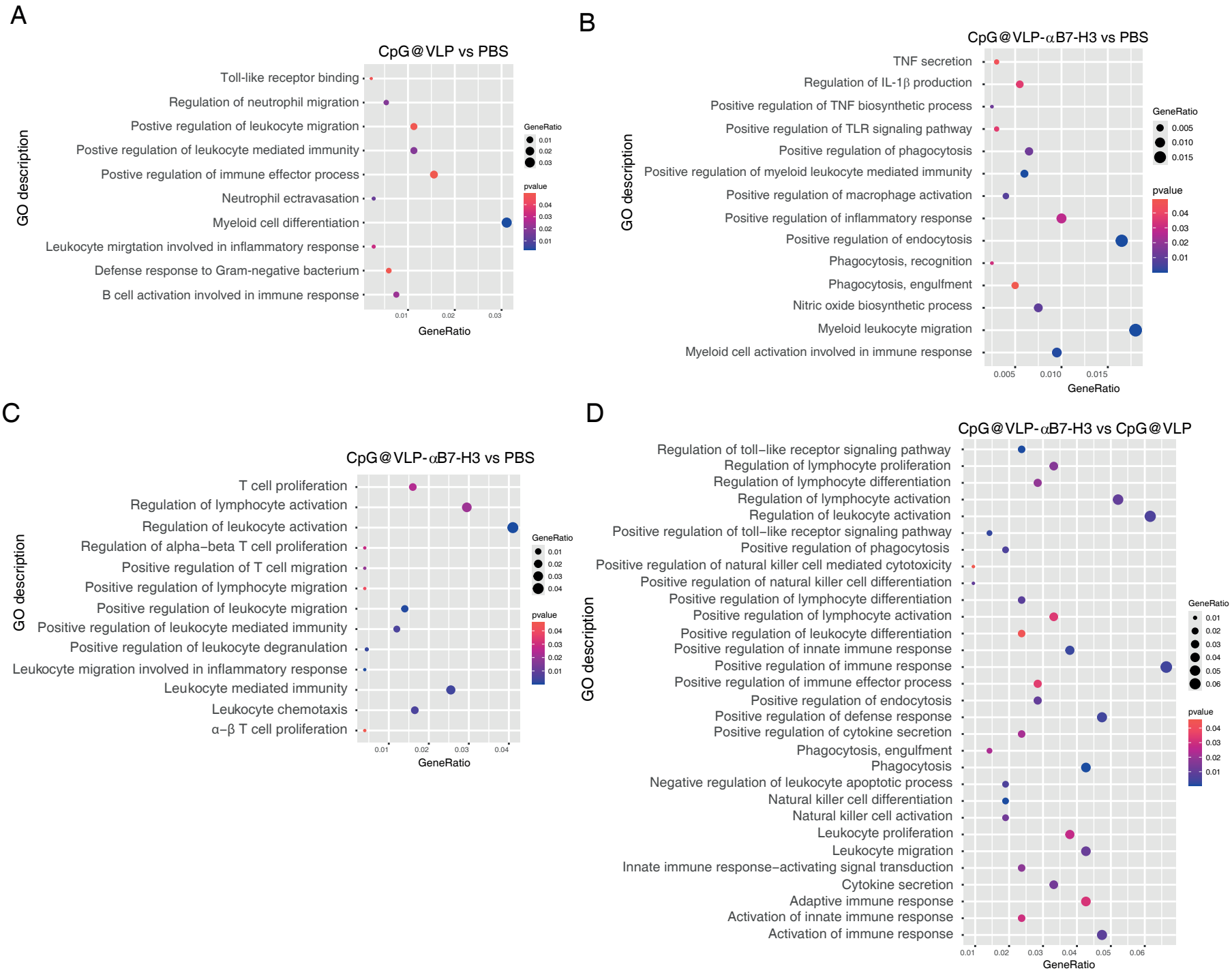

Figure S2 GO enrichment scatter plot for upregulated transcriptome genes treated with VLP nanovaccine in splenocytes.

(A) Myeloid cell differentiation of CpG@VLP vs PBS. (B) M1-like macrophage characteristics of CpG@VLP-αB7-H3 vs PBS. (C) T cell activation characteristics of CpG@VLP-αB7-H3 vs PBS. (D) Leukocyte activation and positive regulation of the immune response of CpG@VLP-αB7-H3 vs CpG@VLP. Genes with an adjusted p value less than 0.05 were identified as differentially expressed genes (DEGs). For GO enrichment analysis of the upregulated DEGs, GO terms with a p value less than 0.05 were considered significantly enriched (n = 3).