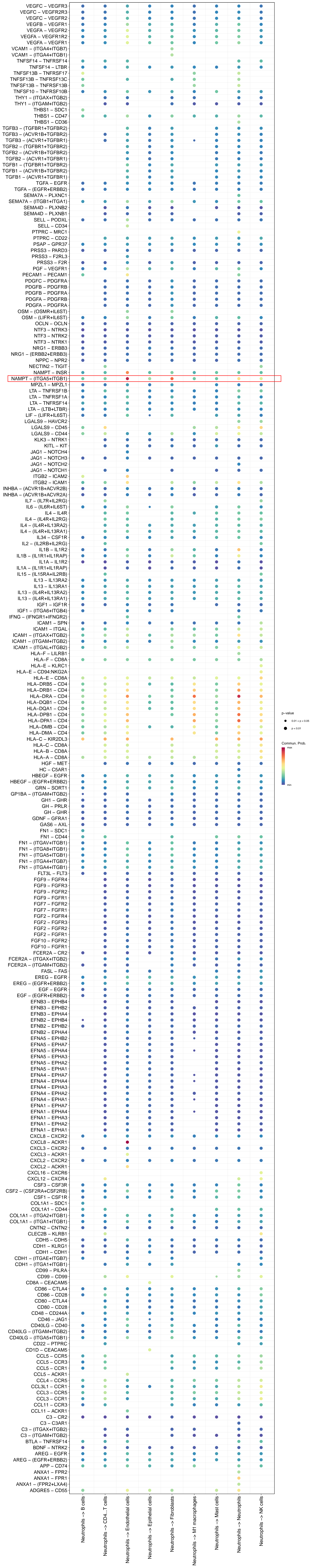


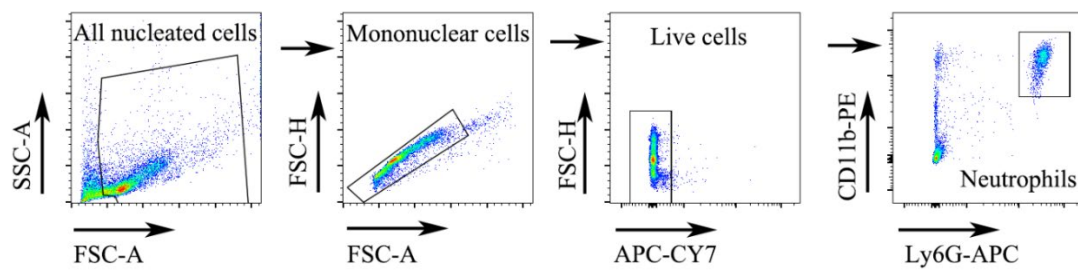
Supplementary Figure 1. Workflow of the study.

A schematic overview of the study design integrating single-cell RNA sequencing analysis, computational algorithms (Augur and CellChat), and in vivo validation experiments. The workflow includes data preprocessing and differential gene expression analysis, identification of disease-relevant immune cell populations, exploration of intercellular communication networks, and validation in DSS-induced colitis mouse models using FACS, H&E, IHC, and ELISA.



Supplementary Figure 2. Communication Network between Neutrophils and Other Cell Types.

Dot heatmap based on the ligand-receptor probability matrix, dot color indicates the probability of communication (commun.prob), and dot size indicates the average expression level of the corresponding gene combinations in the paired cells. The red box indicates the pathway analyzed in this study.



Supplementary Figure 3. Flow Cytometry Gating Strategy.

To analyze peripheral blood neutrophils, the following gating strategy was employed. First, a gate was set on all nucleated cells based on FSC-A and SSC-A to exclude cell debris and aggregates. Subsequently, live cells were selected from the nucleated population using a viability dye (Zombie NIR™, APC-CY7). Finally, neutrophils were identified as the population that was double-positive for Ly6G (APC) and CD11b (PE) within the live cells.