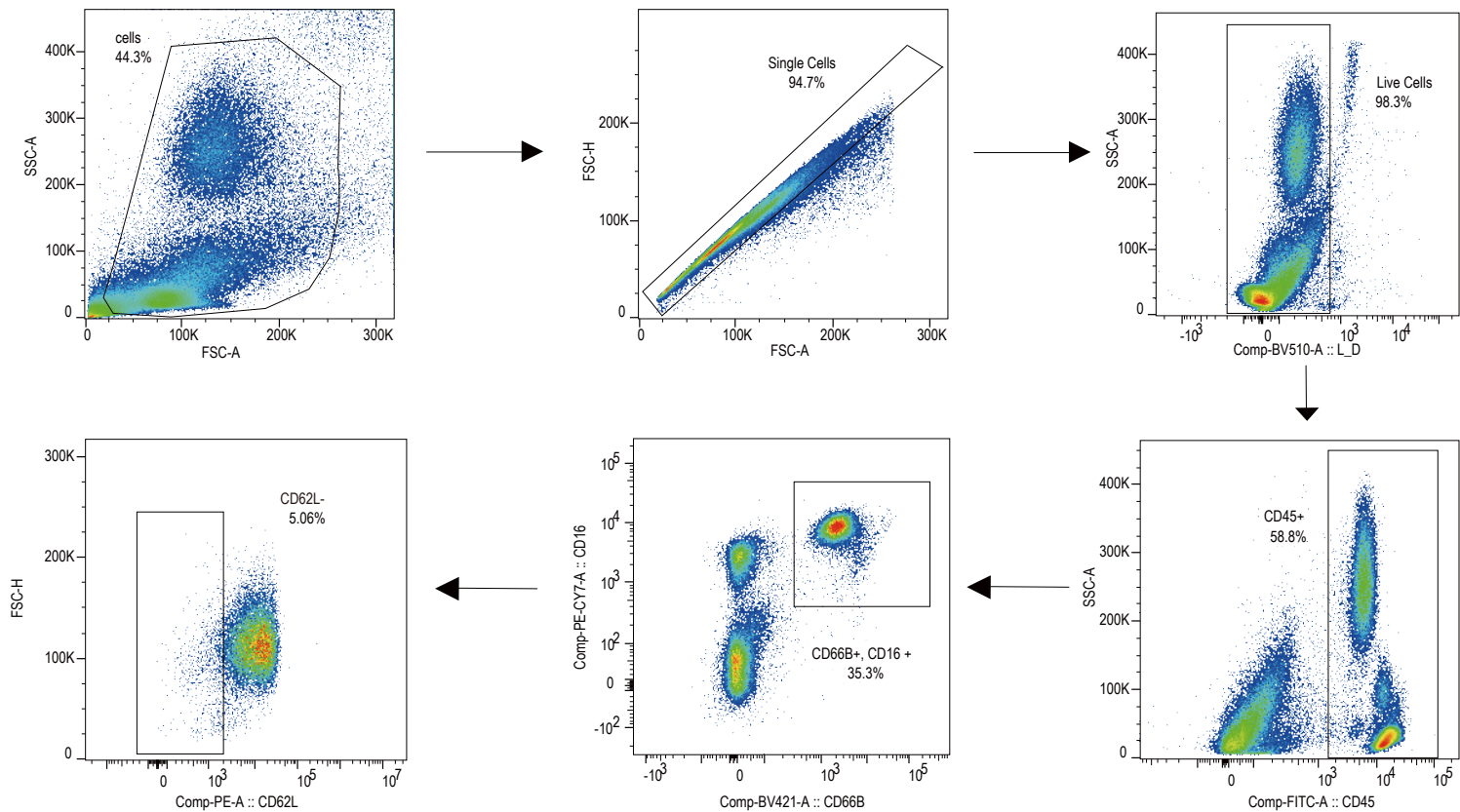
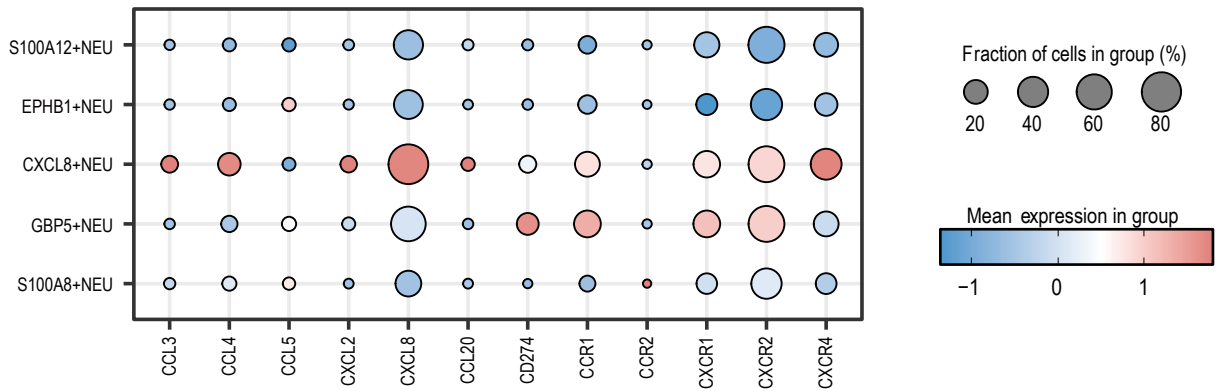


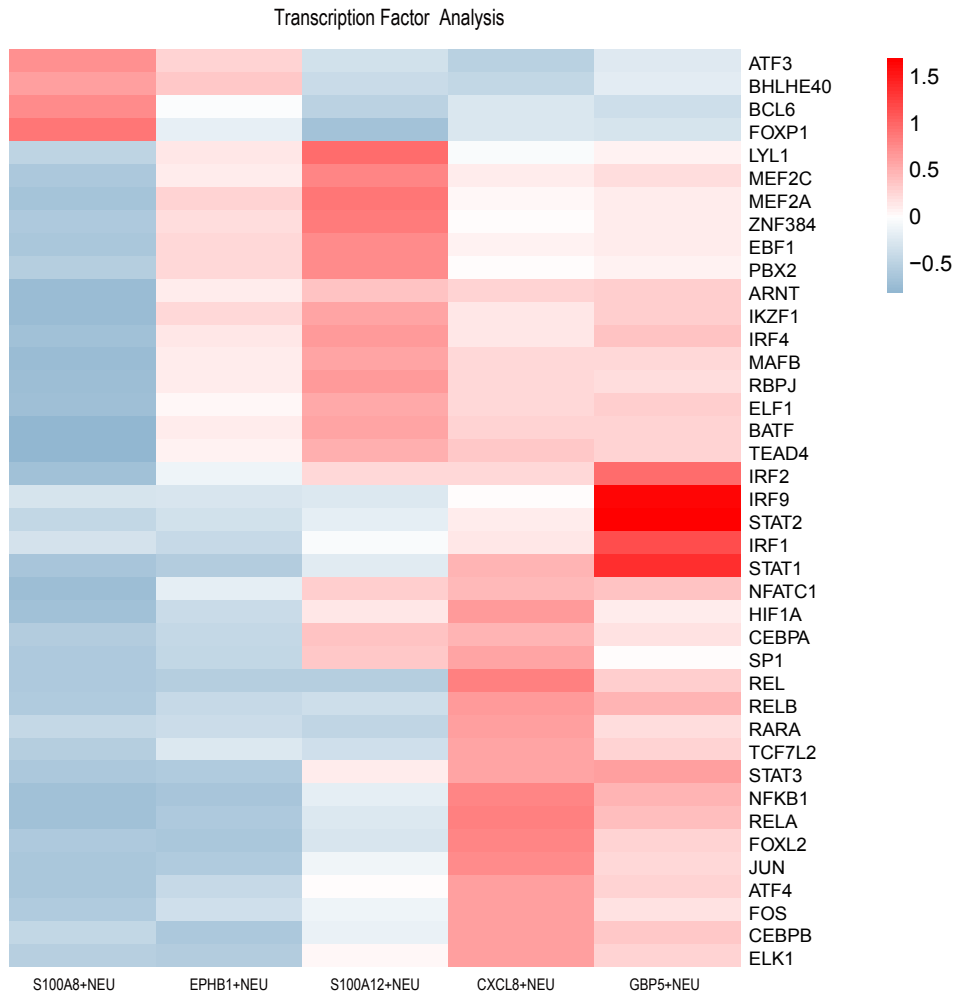
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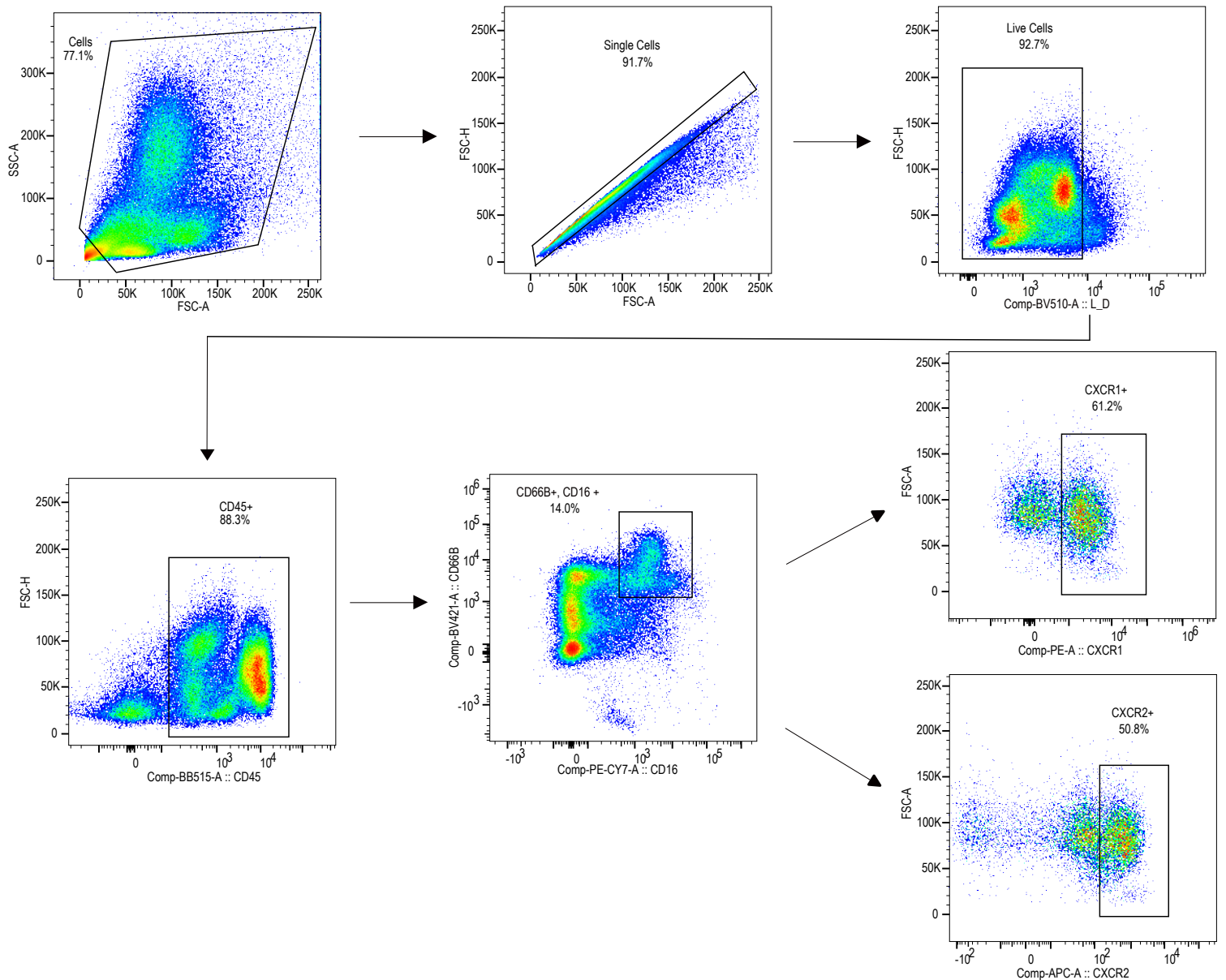


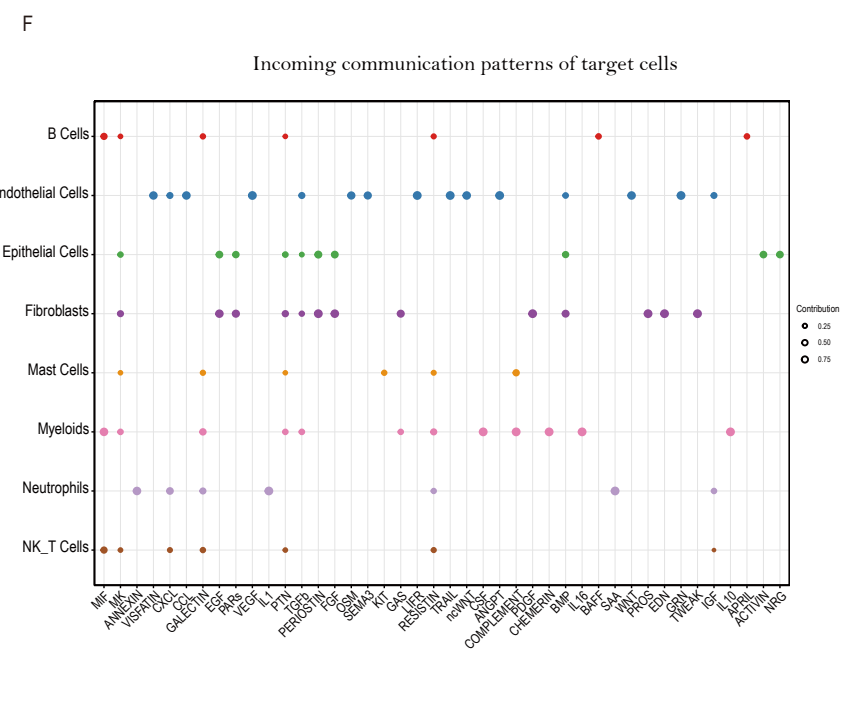
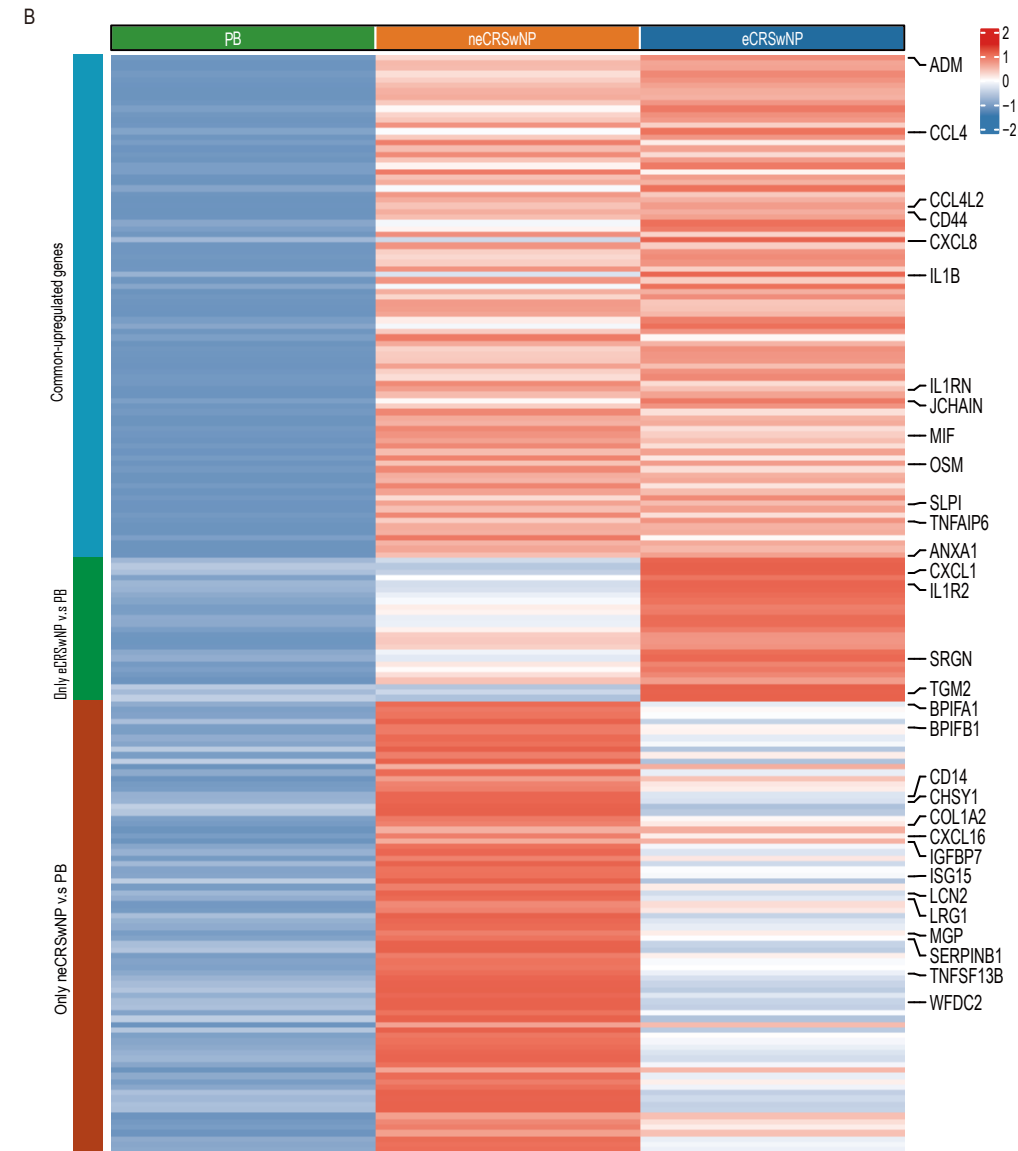
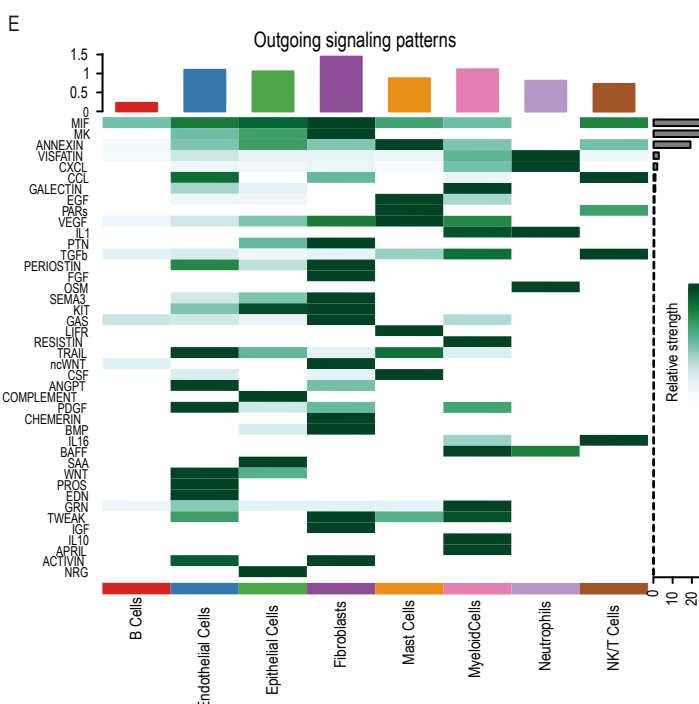
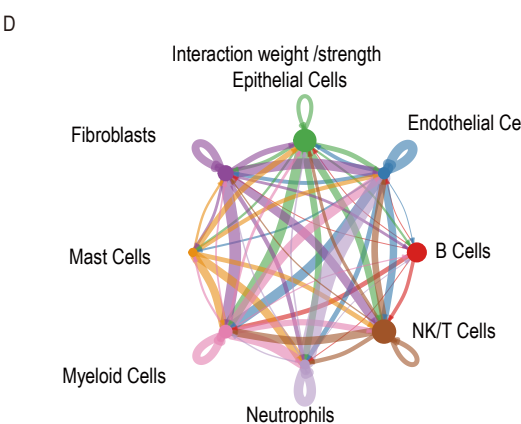
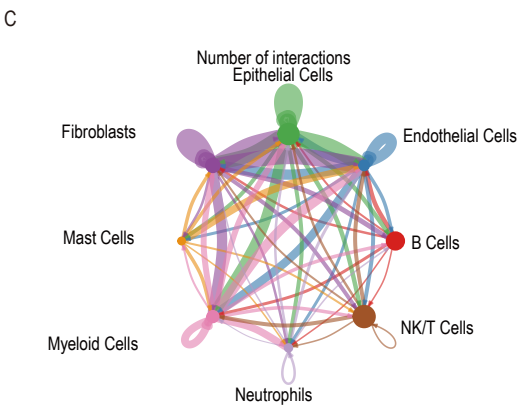
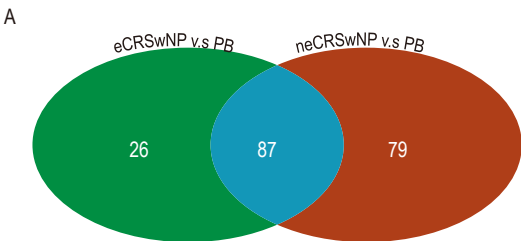
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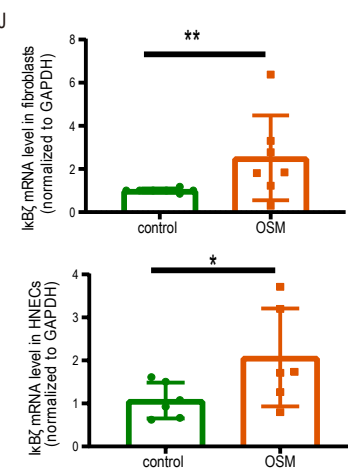
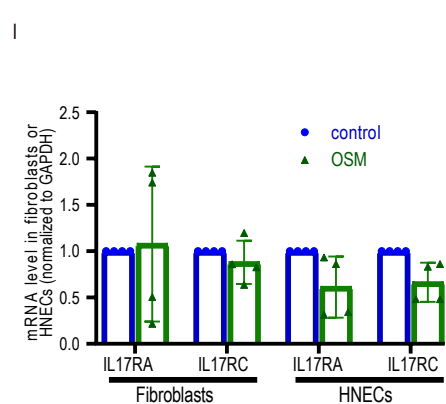
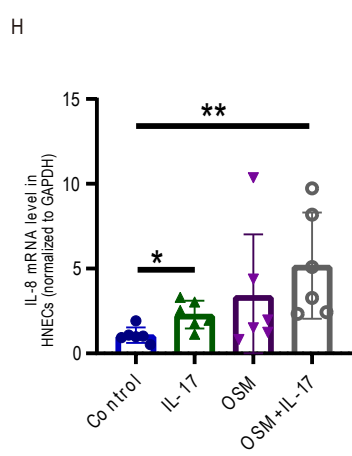
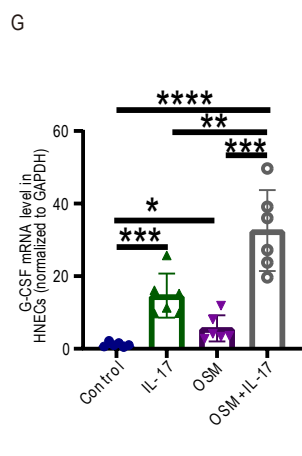
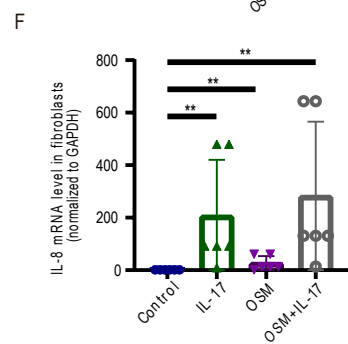
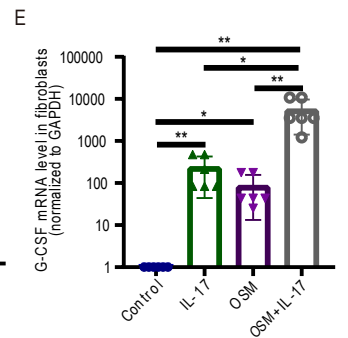
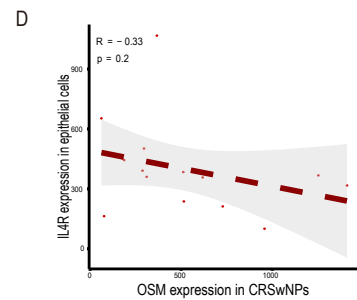
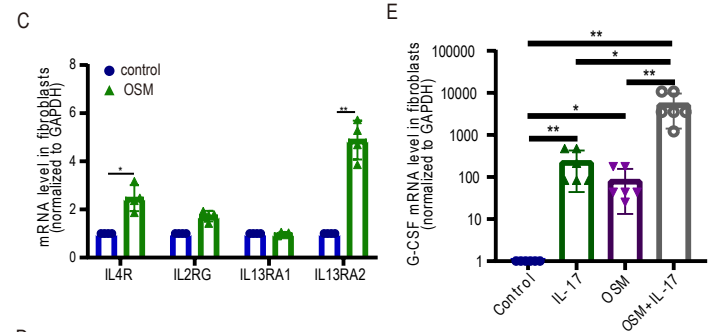
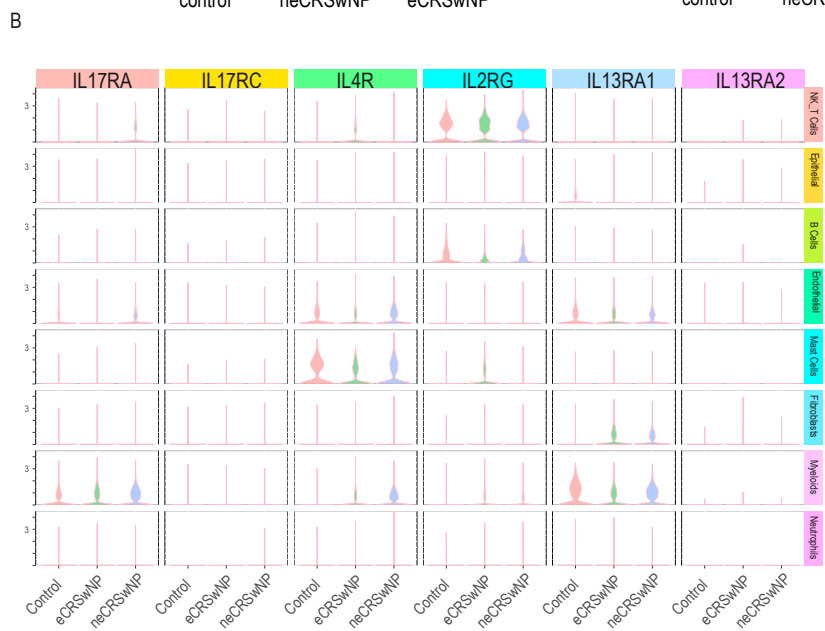
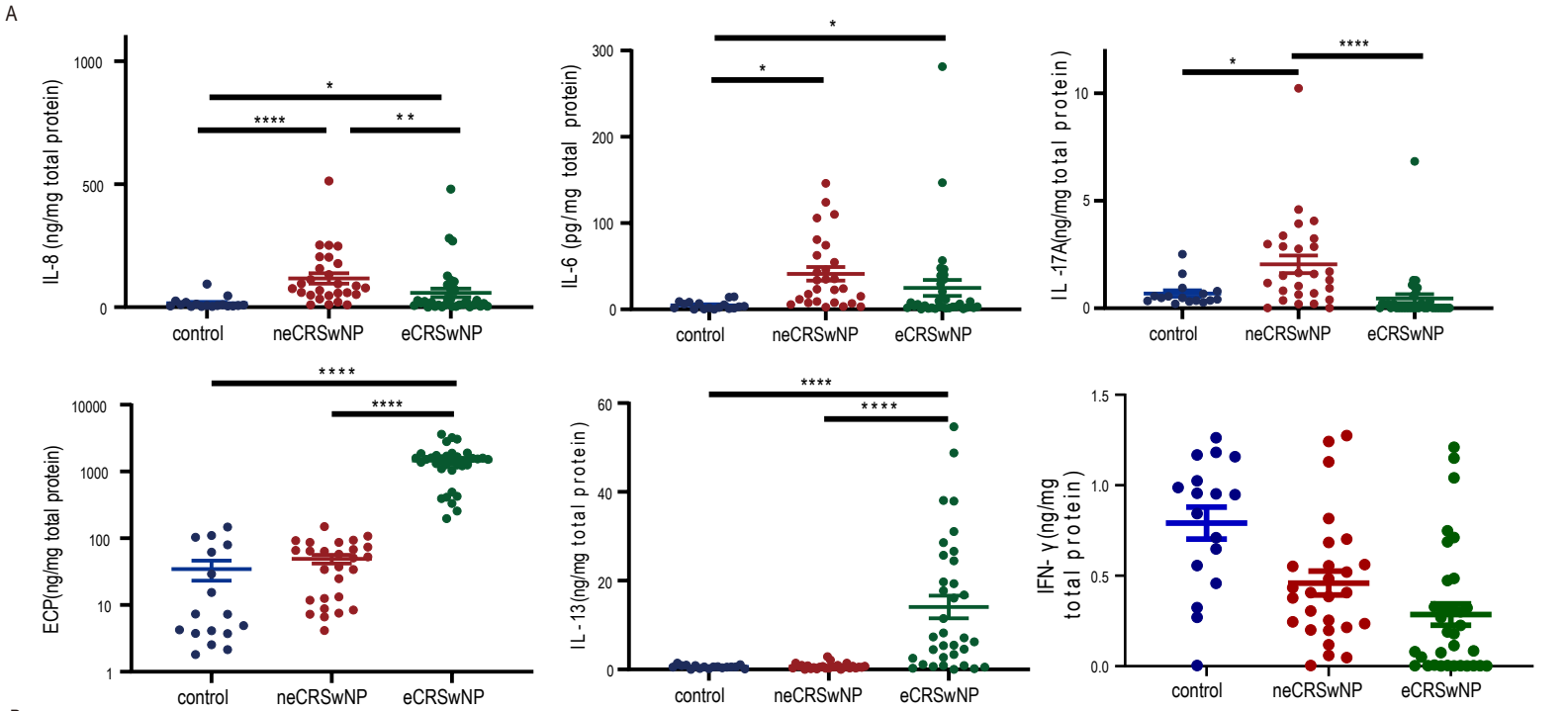


B









Supplemental material

Supplemental Figure Legends

Supplemental Figure 1. (A) Violin plots showing the number of genes and counts and the percentage of mitochondrial and ribosomal genes. (B) UMAP plot displaying the distribution of the samples before and after removing the batch effects. (C) Heatmap visualizing marker gene expression of each cell type. (D) Core network showing the protein–protein interaction (PPI) network for upregulated genes in the neCRSwNP neutrophils compared to the PB neutrophils. The PPI network of significantly upregulated genes (p value < 0.05 and $FC \geq 2$) was constructed utilizing the STRING database, including 123 nodes and 598 edges. (E) The core network showing the PPI network for genes upregulated in eCRSwNP neutrophils compared to PB neutrophils. The PPI network of significantly upregulated genes (p value < 0.05 and $FC \geq 2$) was constructed utilizing the STRING database and included 80 nodes and 384 edges. (F) The bar and GSEA plots showing the results of GO, KEGG, and GSEA pathway enrichment in the neCRSwNP neutrophils compared to the PB neutrophils. (G) The bar plots showing the results of GO, KEGG, and GSEA pathway enrichment in the eCRSwNP neutrophils compared to the PB neutrophils.

Supplemental Figure 2. (A) A representative cell sorting strategy showing activated neutrophils within the live $CD45^+CD66B^+CD16^+CD62L^-$ population.

Supplemental Figure 3. (A) Dot plot depicting the gene expression levels of chemokines and chemokine receptors in different neutrophil subsets. (B) Heatmap

visualizing transcription factor analysis of DEGs in different neutrophil subsets.

Supplemental Figure 4. (A) A representative cell sorting strategy showing CXCR1+ or CXCR2+ neutrophils within the live CD45+CD66B+CD16+ population.

Supplemental Figure 5. (A) Venn diagram showing upregulated genes in the neCRSwNP and eCRSwNP neutrophils compared to the PB neutrophils. (B) Heatmap showing 87 common upregulated genes (including 12 cytokines/chemokines) in the neCRSwNP and eCRSwNP neutrophils. (C) Network graphs showing the number of CellChat interactions. (D) Network graphs showing the CellChat interaction weights. (E) Heatmap visualizing outgoing signaling patterns of CellChat. (F) Heatmap visualizing incoming communication patterns of CellChat target cells.

Supplemental Figure 6. (A) Scatter dot plot depicting the protein levels of ECP, IL-13, IL-8, and G-CSF in tissue homogenates from the control UT (n = 17), neCRSwNP (n = 27), and eCRSwNP (n = 34) groups. (B) Violin plots showing the expression levels of IL-13 receptors and IL-17 receptors. (C) Histogram displaying IL-13 receptor mRNA levels (IL4R, IL2RG, IL13RA1, and IL13RA2) in epithelial cells after 12 h of stimulation with OSM (n = 4). (D) Scatter plot displaying the correlation between the IL4R expression level in epithelial cells and the OSM total expression level in the scRNA-sequencing data of polyp samples. (E-F) Histogram displaying the G-CSF and IL-8 mRNA expression levels after 12 h of stimulation with OSM and IL-17A in fibroblasts (n = 6). (G-H) Histogram displaying the G-CSF and IL-8 mRNA expression levels after 12 h of stimulation with OSM and IL-17A in HNECs (n = 6). (I) Histogram displaying the IL-17 receptor mRNA levels (IL17RA and IL17RC) in fibroblasts (n =

4) and HNECs (n = 4). * p<0.05, ** p<0.01, *** p<0.001, **** p<0.001.

Supplemental Tables

Supplemental Table 1 Characteristics of the subjects

Supplemental Table 2 Filtered genes in scRNA-sequencing

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Supplemental Table 11 The Kyoto encyclopedia of genes and genomes (KEGG) enrichment analysis of neutrophils between the eCRSwNP and the PB group

Supplemental Table 12 The gene set enrichment analysis (GSEA) of neutrophils between the eCRSwNP and the PB group

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Supplemental Table 20 The differential gene expression among groups in GBP5+ neutrophils

**Supplemental Table 21 The differential gene expression among groups in
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**Supplemental Table 22 The differential gene expression among groups in
EPHB1+ neutrophils**

**Supplemental Table 23 The differential gene expression among groups in
S100A12+ neutrophils**