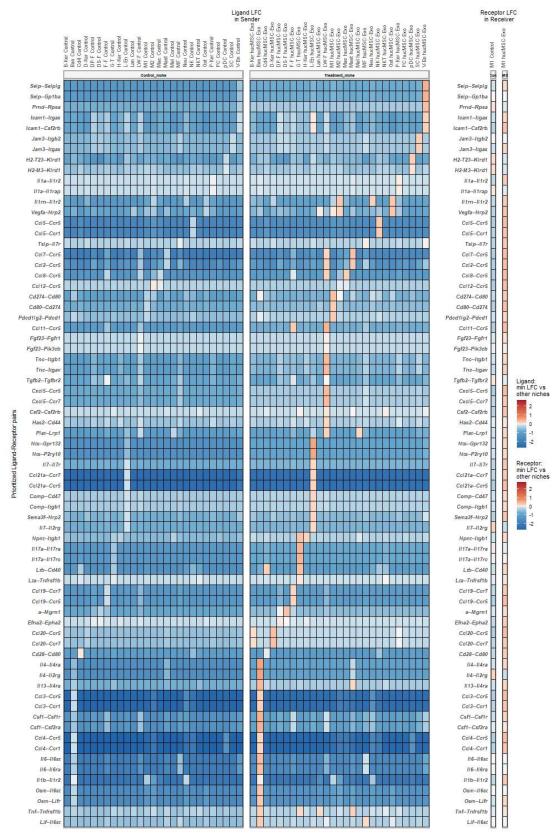


Supplementary Figure 1

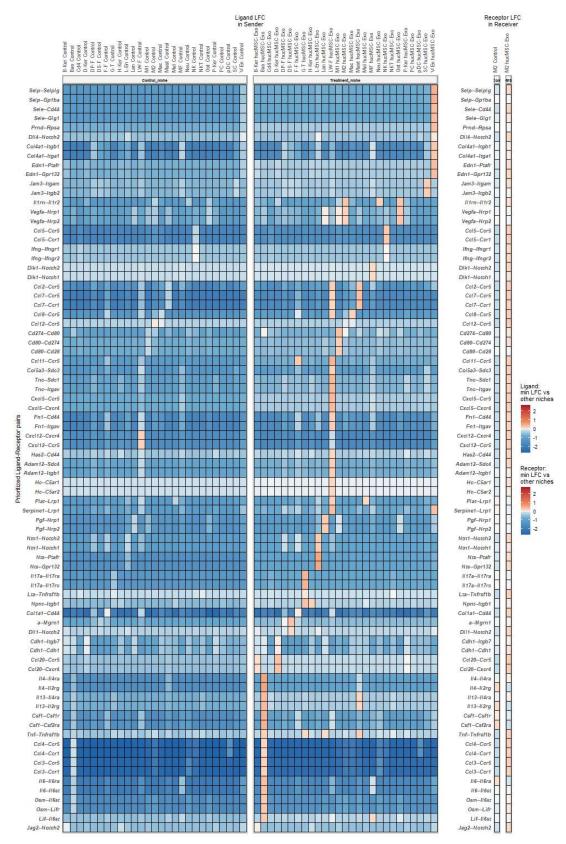
- a) Heatmap of top expressed genes in neutrophil subtypes
- b) Heatmap of Gene Set Enrichment Analysis (GSEA) of genes expressed by neutrophils
- c) Heatmap of Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis of genes

- expressed by neutrophils
- d) Stacked violin plot of relevant differentially expressed genes (DEGs) of neutrophils following hucMSC-Exosomes exposure
- e) Stacked violin plot of relevant differentially expressed genes (DEGs) of macrophages following hucMSC-Exosomes exposure
- f) Combined 2D scatterplot based on UMAP reduction of macrophage coordinates
- g) Scatterplot based on UMAP reduction of macrophages; cells are colored based on gene expression.



Supplementary Figure 2

Heatmap illustrating ligand-receptor expression comparison between the control group and the hucMSC-Exosomes treatment group for M1 macrophages (receiver).



Supplementary Figure 3

Heatmap illustrating ligand-receptor expression comparison between the control group and the hucMSC-Exosomes treatment group for M2 macrophages (receiver).