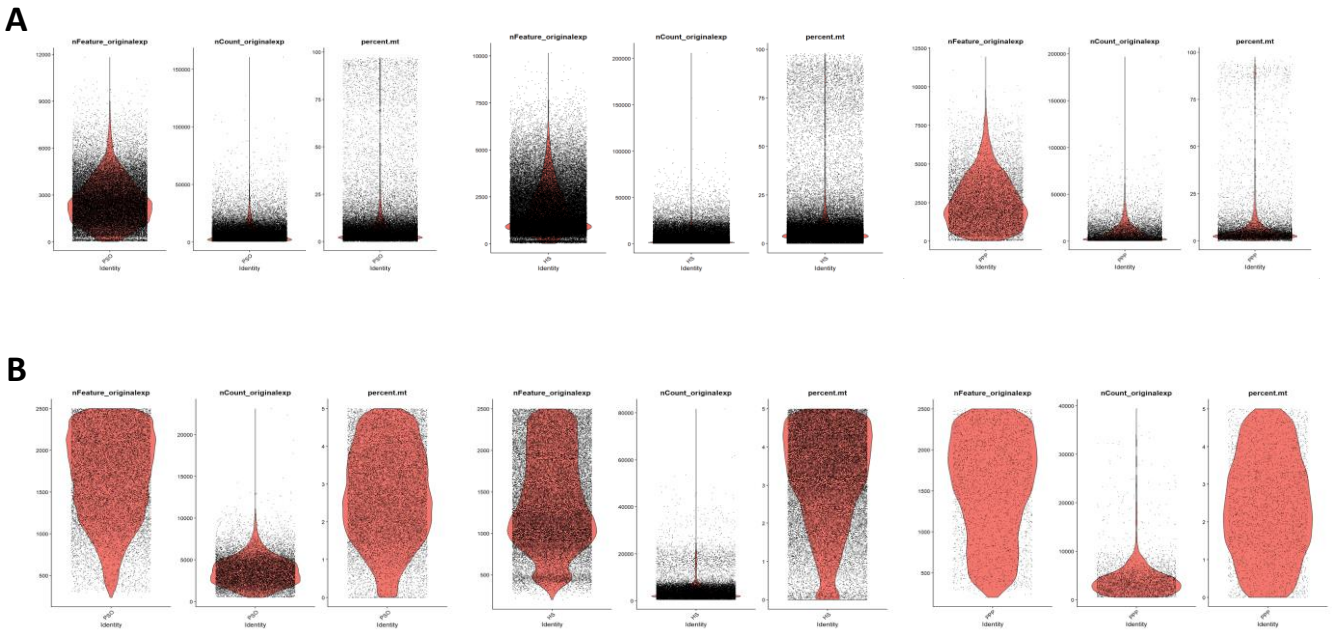
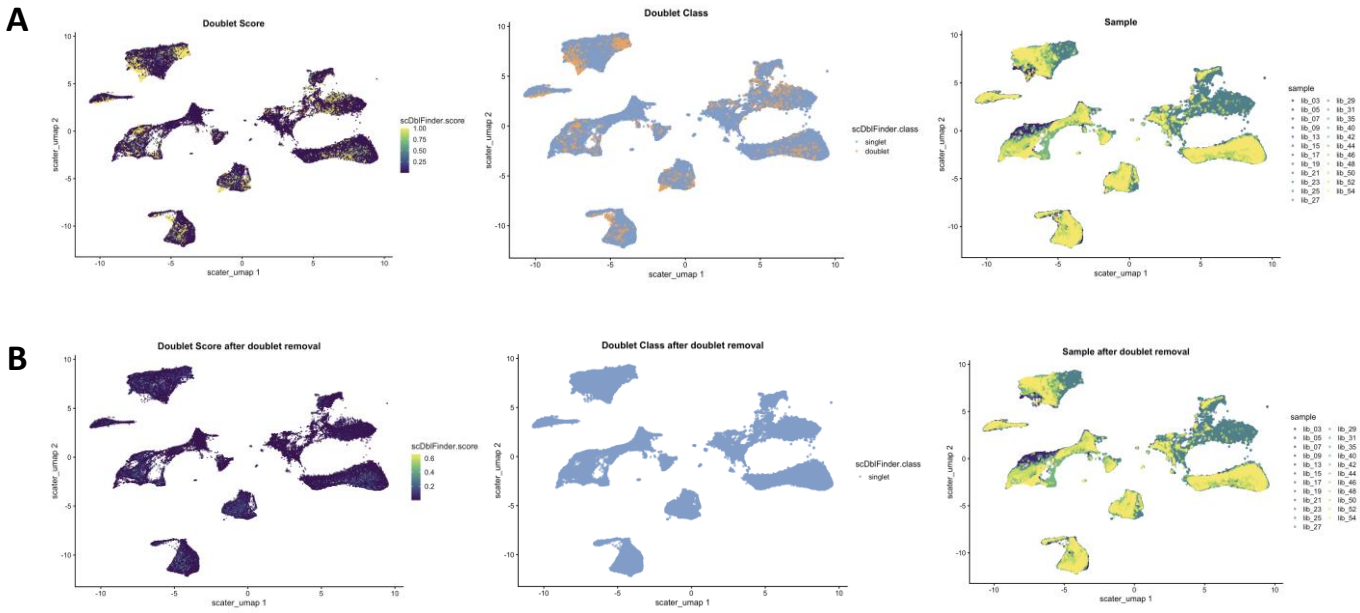
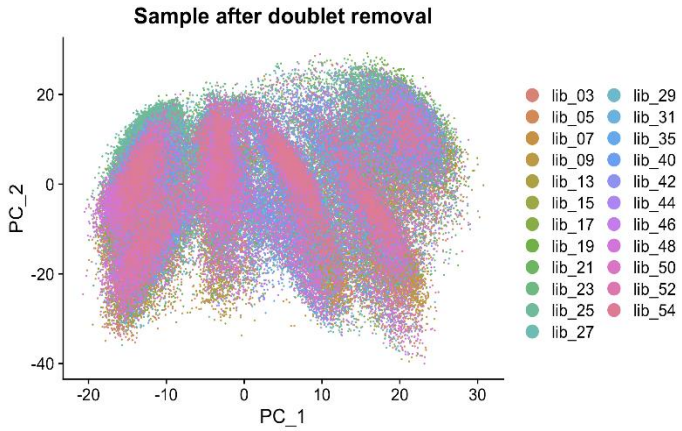


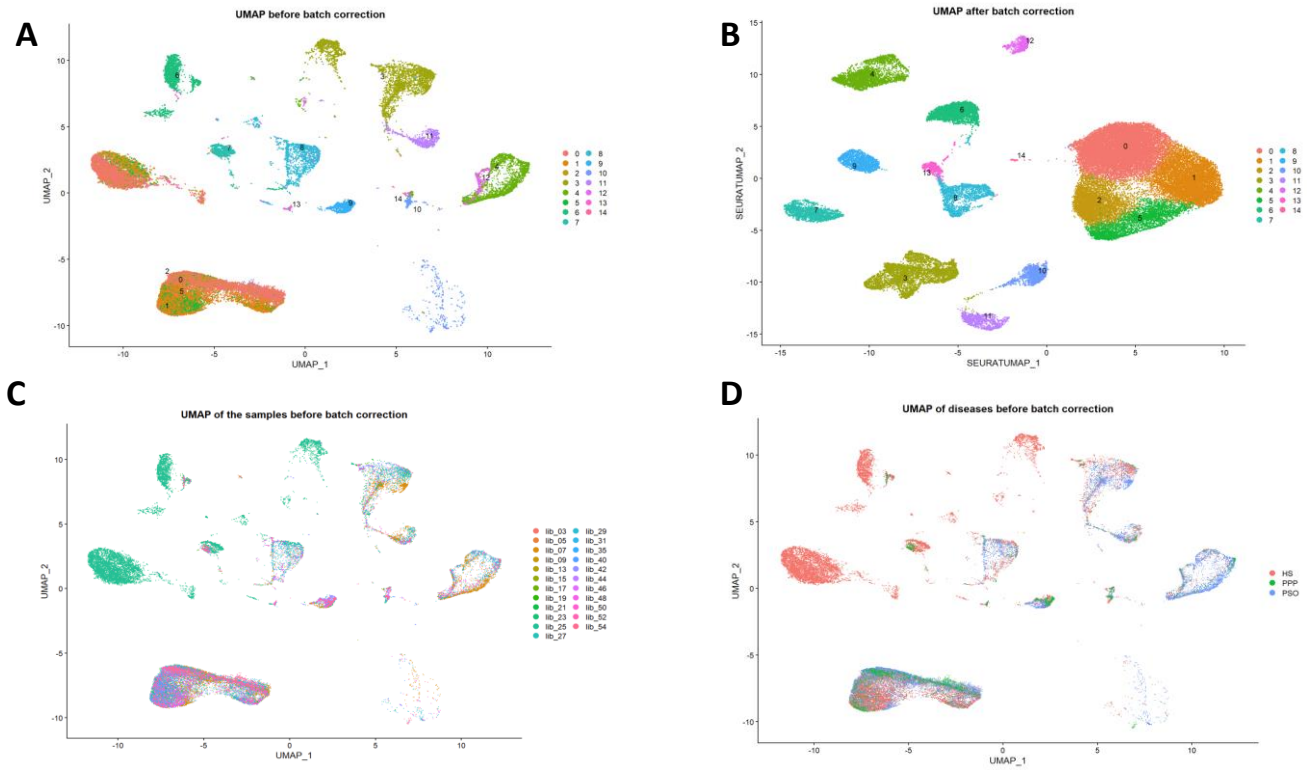
Supplementary Figure 1. Violin plots illustrating the distribution of key quality control metrics across different samples and condition. The plots depict three metrics for each condition: nFeature_originalexp (the number of detected features per cell), nCount_originalexp (the number of counts per cell), and percent.mt (the percentage of mitochondrial genes expressed per cell). Violin plots representing three different types of conditions/samples in the dataset. Each violin plot shows the distribution of the respective metric across all cells in each condition before quality control and removal of low-quality cells. Black dots represent individual cell data points, while the red outline indicates the distribution curve **(A).** The same set of samples/conditions is shown after quality control and filteringquality cells, with the same quality control metrics presented. The percent.mt violin plots reveal the proportion of mitochondrial gene expression, which is a key indicator of cell quality, with higher percentages often reflecting lower cell quality or stress **(B).**



Supplementary Figure 2. UMAP plots displaying the identification and removal of doublets in scRNA-seq data. Left Panel (Doublet Score): UMAP plot showing the distribution of cells colored by their doublet scores as calculated by scDblFinder. The score ranges from low (purple) to high (yellow-green), indicating the likelihood that a given cell is a doublet. Middle Panel (Doublet Class): UMAP plot categorizing cells as either singlets (blue) or doublets (orange) based on their doublet classification. Right Panel (Sample): UMAP plot showing the distribution of cells across different samples before doublet removal. Each color represents a different sample, providing a visual overview of the sample composition in the dataset **(A).** Left Panel (Doublet Score after Doublet Removal): UMAP plot displaying the doublet scores of cells after the removal of identified doublets. The remaining cells, mostly singlets, show generally lower doublet scores. Middle Panel (Doublet Class after Doublet Removal): UMAP plot highlighting the cells classified as singlets (blue) after the doublet removal process. All identified doublets have been excluded, leaving a dataset of high-confidence singlets. Right Panel (Sample after Doublet Removal): UMAP plot illustrating the distribution of singlet cells across the various samples post-doublet removal. The samples are represented by different colors, showing how the sample composition has been refined after filtering out doublets **(B).**



Supplementary Figure 3. The PCA (Principal Component Analysis) plot visualizes the distribution of cells in a scRNA-seq dataset after the removal of doublets. The axes represent the first two principal components (PC1 and PC2), which capture the greatest variance in the dataset. PC1 explains 26.64% of the variability, while PC2 accounts for 14.17% (data not shown). These components are linear combinations of the original gene expression data that reduce the dimensionality of the dataset while preserving as much variability as possible. The points on the plot represent individual cells, with each point colored according to the library (or batch) from which the cell originated. The clustering pattern indicates the degree of similarity between cells based on their gene expression profiles. In this plot, the cells do not cluster tightly based on the library, suggesting that the variability is more likely due to biological differences rather than batch effects or technical noise.

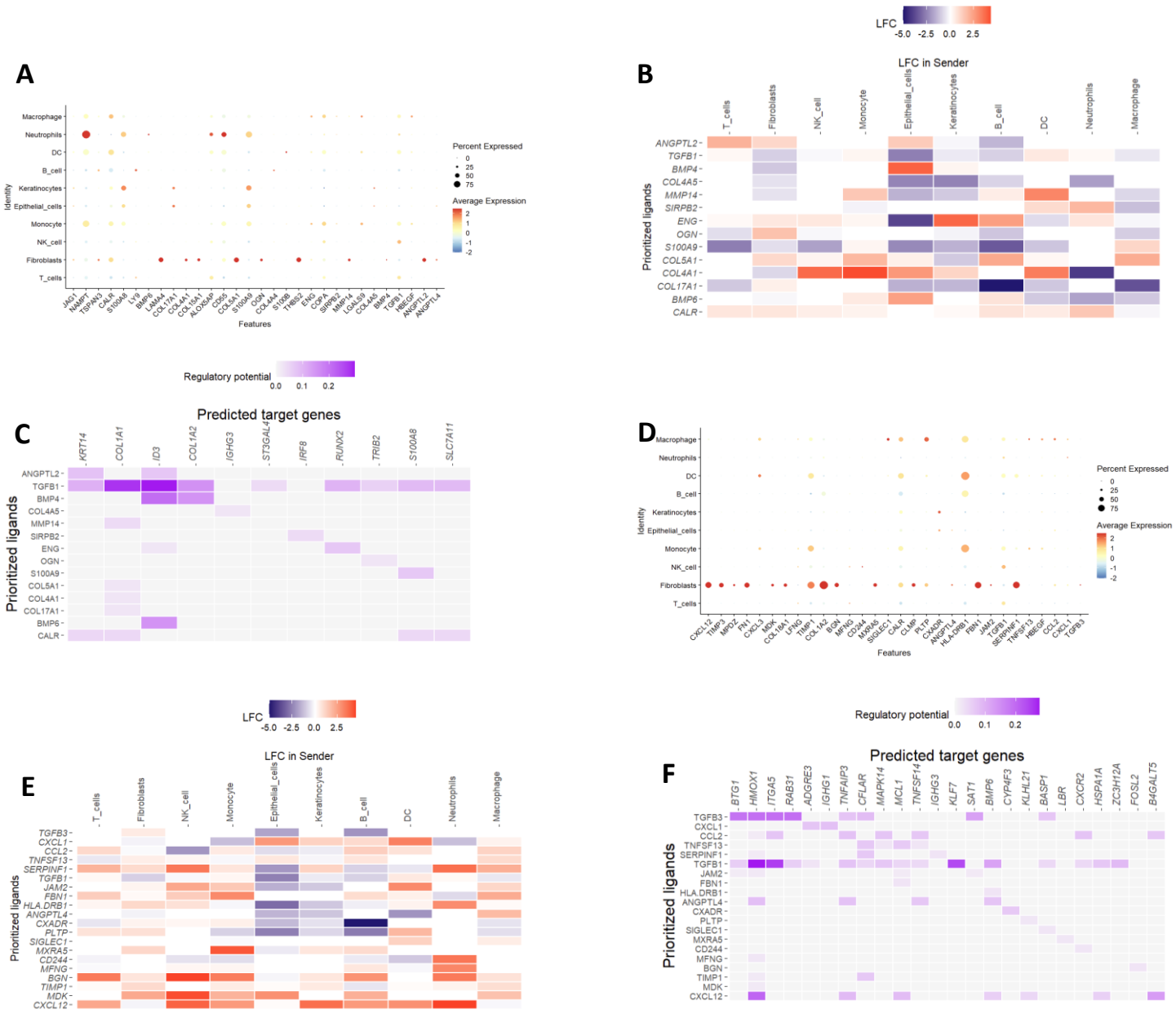


Supplementary Figure 4. UMAP visualization of scRNA-seq data before and after batch correction. UMAP before batch correction: UMAP plot showing the distribution of cells across different batches before the application of batch correction. Each color represents a different batch, with distinct clusters forming based primarily on batch effects rather than biological differences. The presence of batch-specific clustering indicates that the dataset is significantly affected by technical variations, which could confound downstream analyses **(A).** UMAP after batch correction: UMAP plot illustrating the distribution of cells after the application of batch correction. The cells are colored by the same batch as in the left panel. Post-correction, cells from different batches are more integrated, forming clusters based on their biological similarities rather than batch-specific technical artifacts. This integration demonstrates the effectiveness of the batch correction process in mitigating batch effects and improving the accuracy of the clustering results **(B).** UMAP of the samples before batch correction: UMAP plot displaying the distribution of cells from different samples before batch correction. Each color represents a different sample, identified by unique sample IDs. The distinct clustering of cells from the same sample indicates the presence of batch effects, as cells are grouped together based on their sample of origin rather than biological characteristics. This suggests that technical variations between samples are driving the clustering patterns **(C).** UMAP of diseases before batch correction: UMAP plot showing the distribution of cells colored by disease type (HS, PPP, and PSO) before batch correction. The colors represent cells from HS (red), PPP (green), and PSO (blue). The lack of clear separation between cells from different diseases and the overlap of clusters suggest that the dataset is influenced by batch effects, which could obscure true biological differences between the disease states **(D).**

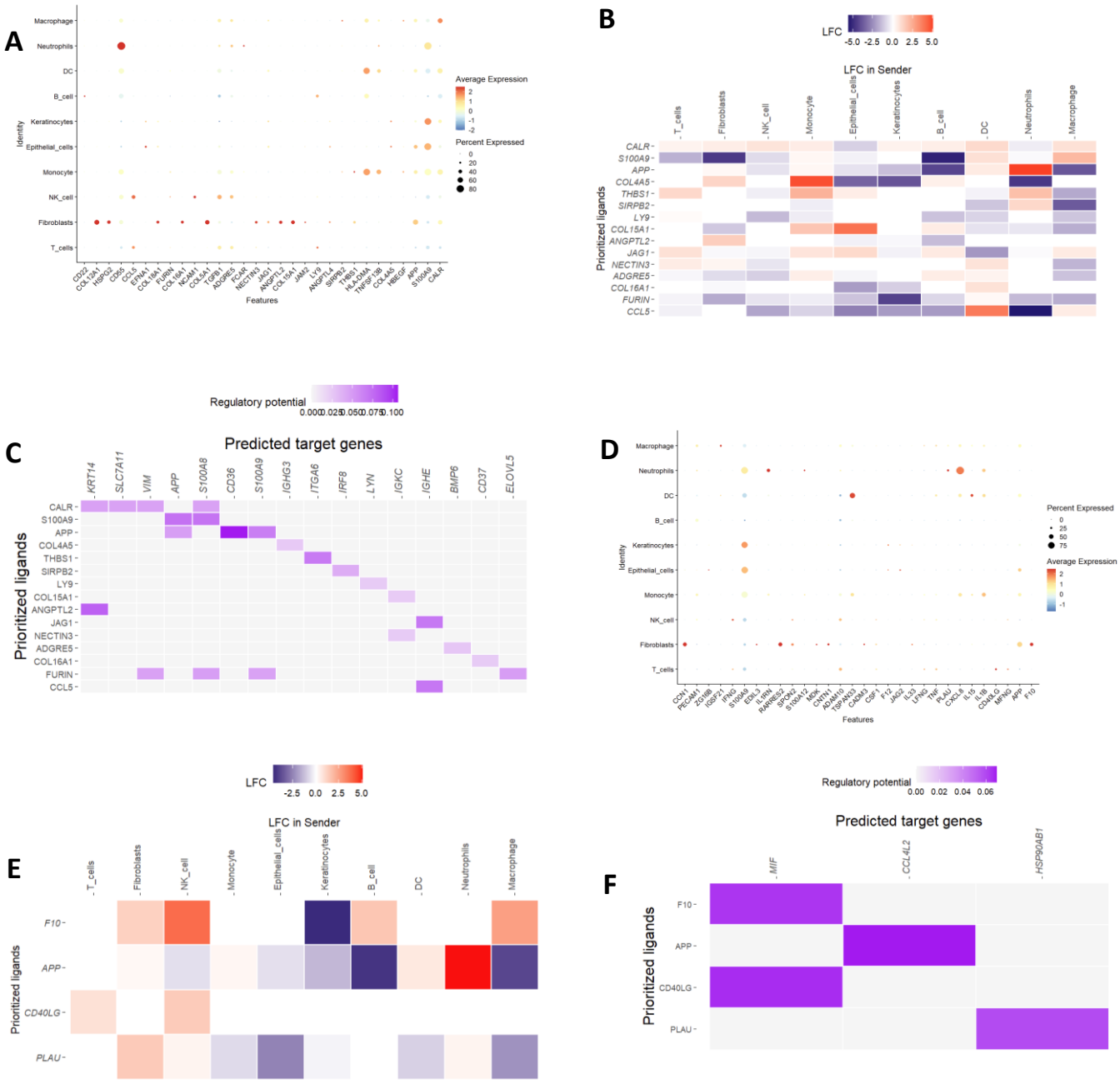
Supplementary Table 1. Differentially expressed features or cluster biomarkers.

p_val	avg_log2FC	pct.1	pct.2	p_val_adj	cluster	gene
0.00	6.861	0.334	0.003	0.00	B_cell	PAX5
0.00	6.507	0.35	0.006	0.00	B_cell	FCRL1
0.00	6.475	0.812	0.011	0.00	B_cell	CD79A
0.00	6.377	0.601	0.021	0.00	B_cell	BANK1
0.00	6.282	0.649	0.167	0.00	B_cell	IGLC1
0.00	6.006	0.847	0.322	0.00	B_cell	IGLC3
0.00	6.004	0.371	0.044	0.00	B_cell	IGHG4
0.00	5.881	0.755	0.212	0.00	B_cell	IGHG1
0.00	5.834	0.984	0.474	0.00	B_cell	IGKC
0.00	5.773	0.914	0.375	0.00	B_cell	IGLC2
0.00	7.556	0.325	0.015	0.00	Epithelial_cells	CALML5
0.00	7.489	0.454	0.012	0.00	Epithelial_cells	SBSN
0.00	7.303	0.679	0.068	0.00	Epithelial_cells	KRTDAP
0.00	7.060	0.761	0.112	0.00	Epithelial_cells	KRT1
0.00	7.054	0.685	0.054	0.00	Epithelial_cells	DMKN
0.00	6.943	0.424	0.03	0.00	Epithelial_cells	KRT6A
0.00	6.804	0.682	0.019	0.00	Epithelial_cells	DSG1
0.00	6.776	0.511	0.085	0.00	Epithelial_cells	S100A7
0.00	6.772	0.442	0.034	0.00	Epithelial_cells	KRT16
0.00	6.771	0.79	0.043	0.00	Epithelial_cells	LGALS7B
0.00	5.651	0.652	0.018	0.00	Fibroblasts	ABCA8
0.00	5.592	0.854	0.066	0.00	Fibroblasts	APOD
0.00	5.567	0.278	0.009	0.00	Fibroblasts	C7
0.00	5.377	0.719	0.027	0.00	Fibroblasts	SLIT2
0.00	5.281	0.51	0.017	0.00	Fibroblasts	ABCA9
0.00	5.058	0.556	0.027	0.00	Fibroblasts	ABCA10
0.00	5.043	0.523	0.015	0.00	Fibroblasts	ADH1B
0.00	4.985	0.308	0.009	0.00	Fibroblasts	TMEM132C
0.00	4.915	0.872	0.093	0.00	Fibroblasts	APOE
0.00	4.836	0.672	0.032	0.00	Fibroblasts	NOVA1
0.00	6.353	0.384	0.021	0.00	Keratinocytes	KRT15
0.00	5.009	0.283	0.022	0.00	Keratinocytes	COL17A1
0.00	4.948	0.854	0.239	0.00	Keratinocytes	KRT14
0.00	4.936	0.797	0.131	0.00	Keratinocytes	KRT5
0.00	4.935	0.639	0.086	0.00	Keratinocytes	S100A2
0.00	4.589	0.358	0.031	0.00	Keratinocytes	DSC3
0.00	4.376	0.377	0.033	0.00	Keratinocytes	MIR205HG
0.00	4.348	0.594	0.059	0.00	Keratinocytes	SFN
0.00	4.344	0.265	0.028	0.00	Keratinocytes	DAPL1
0.00	4.191	0.429	0.039	0.00	Keratinocytes	S100A14
0.00	8.195	0.369	0.001	0.00	Macrophage	LILRB5
0.00	7.476	0.649	0.007	0.00	Macrophage	CD163
0.00	7.418	0.321	0.002	0.00	Macrophage	SIGLEC1
0.00	7.233	0.581	0.007	0.00	Macrophage	FOLR2
0.00	7.176	0.718	0.012	0.00	Macrophage	C1QB

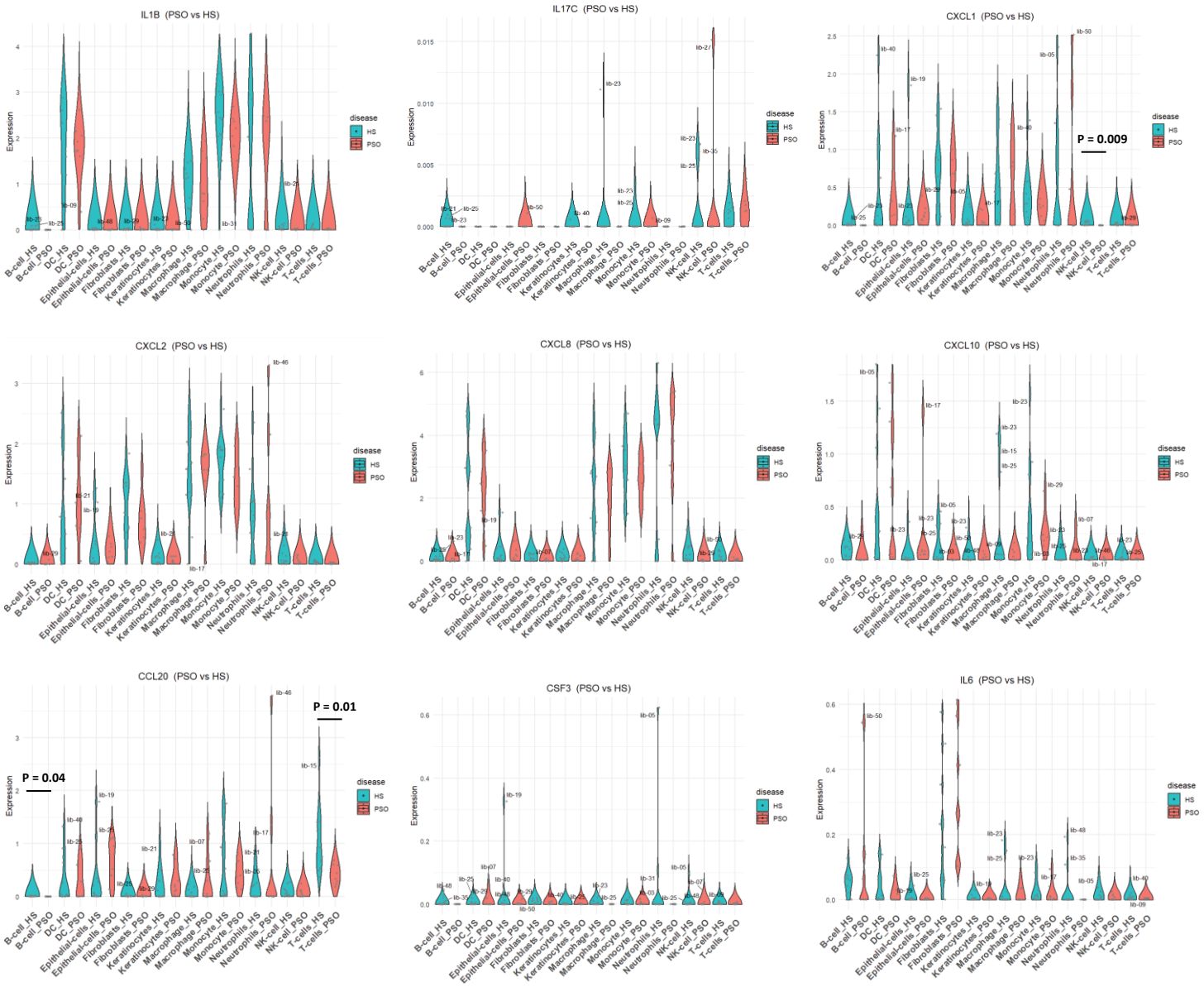
p_val	avg_log2FC	pct.1	pct.2	p_val_adj	cluster	gene
0.00	7.052	0.668	0.009	0.00	Macrophage	C1QC
0.00	7.027	0.595	0.007	0.00	Macrophage	MS4A4A
0.00	7.023	0.811	0.018	0.00	Macrophage	C1QA
0.00	6.804	0.25	0.005	0.00	Macrophage	MARCO
0.00	6.629	0.806	0.029	0.00	Macrophage	F13A1
0.00	6.726	0.348	0.004	0.00	Monocyte/DC	CD1C
0.00	6.643	0.604	0.01	0.00	Monocyte/DC	CLEC10A
0.00	6.594	0.554	0.008	0.00	Monocyte/DC	LGALS2
0.00	6.454	0.505	0.009	0.00	Monocyte/DC	AC020656.1
0.00	6.420	0.941	0.068	0.00	Monocyte/DC	LYZ
0.00	6.111	0.422	0.007	0.00	Monocyte/DC	FCN1
0.00	5.941	0.55	0.009	0.00	Monocyte/DC	CSF2RA
0.00	5.924	0.366	0.006	0.00	Monocyte/DC	CFP
0.00	5.889	0.477	0.009	0.00	Monocyte/DC	RTN1
0.00	5.858	0.69	0.029	0.00	Monocyte/DC	CPVL
0.00	8.474	0.663	0.008	0.00	Neutrophils	AQP9
0.00	8.459	0.289	0.003	0.00	Neutrophils	FCGR3B
0.00	8.380	0.26	0.007	0.00	Neutrophils	PROK2
0.00	8.258	0.347	0.005	0.00	Neutrophils	AC005050.3
0.00	8.071	0.276	0.006	0.00	Neutrophils	PI3
0.00	7.629	0.426	0.012	0.00	Neutrophils	CSF3R
0.00	7.475	0.289	0.006	0.00	Neutrophils	TREM1
0.00	7.258	0.279	0.008	0.00	Neutrophils	KCNJ15
0.00	6.877	0.524	0.038	0.00	Neutrophils	LUCAT1
0.00	6.706	0.355	0.013	0.00	Neutrophils	SERPINA1
0.00	6.623	0.385	0.008	0.00	NK_cells	KLRF1
0.00	5.926	0.395	0.012	0.00	NK_cells	NCAM1
0.00	5.804	0.433	0.011	0.00	NK_cells	KLRC1
0.00	5.030	0.693	0.062	0.00	NK_cells	GNLY
0.00	4.971	0.628	0.026	0.00	NK_cells	TRDC
0.00	4.837	0.715	0.047	0.00	NK_cells	KLRD1
0.00	4.770	0.631	0.028	0.00	NK_cells	XCL1
0.00	4.766	0.613	0.033	0.00	NK_cells	XCL2
0.00	4.542	0.315	0.015	0.00	NK_cells	KLRC2
0.00	4.147	0.262	0.015	0.00	NK_cells	KLRC3
0.00	4.609	0.413	0.02	0.00	T_cells	CD28
0.00	4.537	0.588	0.042	0.00	T_cells	CAMK4
0.00	4.303	0.43	0.028	0.00	T_cells	ICOS
0.00	4.238	0.561	0.044	0.00	T_cells	THEMIS
0.00	4.096	0.756	0.074	0.00	T_cells	BCL11B
0.00	3.874	0.548	0.042	0.00	T_cells	CD3G
0.00	3.788	0.254	0.024	0.00	T_cells	PBX4
0.00	3.762	0.268	0.02	0.00	T_cells	TRAT1
0.00	3.729	0.691	0.068	0.00	T_cells	CD3D
0.00	3.689	0.338	0.026	0.00	T_cells	CD6



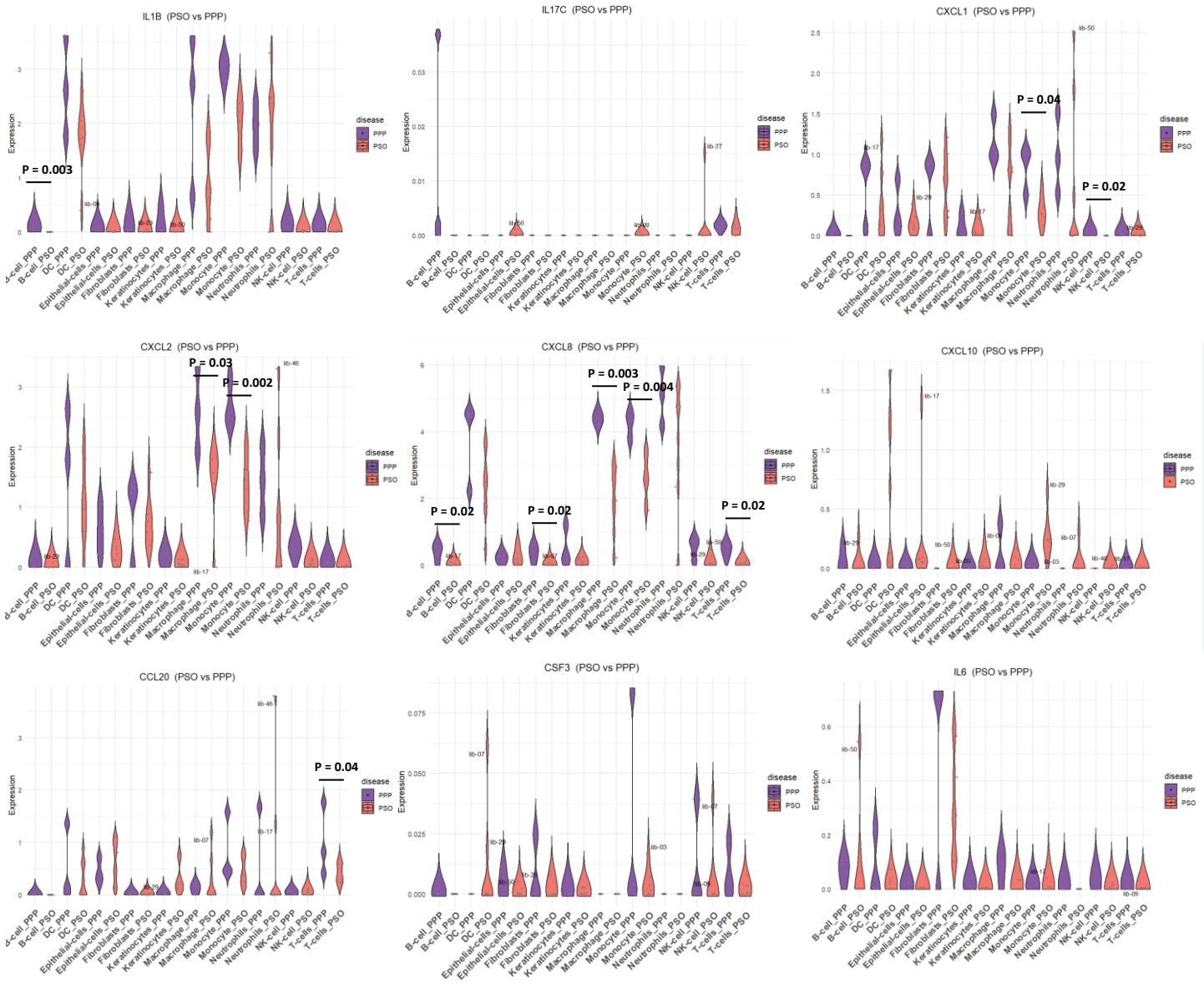
Supplementary Figure 5. Analysis of ligand-receptor interactions and predicted target genes across various cell types (PSO vs HS). Dot plot visualizing the expression levels of top-ranked ligands, with B cells defined as receiver cells, across different sender cell types, measured as average expression (color gradient) and percent expressed (dot size). Each column represents a gene, and each row represents a cell type, including macrophages, neutrophils, DCs, B cells, keratinocytes, epithelial cells, monocytes, NK cells, fibroblasts, and T cells. The color intensity indicates the level of gene expression, with blue representing lower expression and red representing higher expression. Larger dots indicate a higher percentage of cells expressing the gene within that cell type **(A).** Heatmap showing log fold change (LFC) of prioritized ligands across various cell types identified as sender cells. The color gradient represents the LFC, with blue indicating downregulation and red indicating upregulation. The rows correspond to specific ligands, while the columns represent different sender cell types **(B).** Heatmap of predicted ligand-target interactions. The heatmap displays the regulatory potential of prioritized ligands (y-axis) on predicted target genes in B cells (x-axis). The intensity of the purple shading represents the level of regulatory potential, with darker shades indicating higher potential **(C).** Dot plot visualizing the expression levels of top-ranked ligands, with neutrophils defined as receiver cells, across different sender cell types, measured as average expression (color gradient) and percent expressed (dot size). Each column represents a gene, and each row represents a cell type, including macrophages, neutrophils, DCs, B cells, keratinocytes, epithelial cells, monocytes, NK cells, fibroblasts, and T cells. The color intensity indicates the level of gene expression, with blue representing lower expression and red representing higher expression. Larger dots indicate a higher percentage of cells expressing the gene within that cell type **(D).** Heatmap showing log fold change (LFC) of prioritized ligands across various cell types identified as sender cells. The color gradient represents the LFC, with blue indicating downregulation and red indicating upregulation. The rows correspond to specific ligands, while the columns represent different sender cell types **(E).** Heatmap of predicted ligand-target interactions. The heatmap displays the regulatory potential of prioritized ligands (y-axis) on predicted target genes in neutrophiles (x-axis). The intensity of the purple shading represents the level of regulatory potential, with darker shades indicating higher potential **(F).**



Supplementary Figure 6. Analysis of ligand-receptor interactions and predicted target genes across various cell types (PSO vs PPP). Dot plot visualizing the expression levels of top-ranked ligands, with B cells defined as receiver cells, across different sender cell types, measured as average expression (color gradient) and percent expressed (dot size). Each column represents a gene, and each row represents a cell type, including macrophages, neutrophils, DCs, B cells, keratinocytes, epithelial cells, monocytes, NK cells, fibroblasts, and T cells. The color intensity indicates the level of gene expression, with blue representing lower expression and red representing higher expression. Larger dots indicate a higher percentage of cells expressing the gene within that cell type **(A).** Heatmap showing log fold change (LFC) of prioritized ligands across various cell types identified as sender cells. The color gradient represents the LFC, with blue indicating downregulation and red indicating upregulation. The rows correspond to specific ligands, while the columns represent different sender cell types **(B).** Heatmap of predicted ligand-target interactions. The heatmap displays the regulatory potential of prioritized ligands (y-axis) on predicted target genes in B cells (x-axis). The intensity of the purple shading represents the level of regulatory potential, with darker shades indicating higher potential **(C).** Dot plot visualizing the expression levels of top-ranked ligands, with neutrophils defined as receiver cells, across different sender cell types, measured as average expression (color gradient) and percent expressed (dot size). Each column represents a gene, and each row represents a cell type, including macrophages, neutrophils, DCs, B cells, keratinocytes, epithelial cells, monocytes, NK cells, fibroblasts, and T cells. The color intensity indicates the level of gene expression, with blue representing lower expression and red representing higher expression. Larger dots indicate a higher percentage of cells expressing the gene within that cell type **(D).** Heatmap showing log fold change (LFC) of prioritized ligands across various cell types identified as sender cells. The color gradient represents the LFC, with blue indicating downregulation and red indicating upregulation. The rows correspond to specific ligands, while the columns represent different sender cell types **(E).** Heatmap of predicted ligand-target interactions. The heatmap displays the regulatory potential of prioritized ligands (y-axis) on predicted target genes in neutrophiles (x-axis). The intensity of the purple shading represents the level of regulatory potential, with darker shades indicating higher potential **(F).**



Supplementary Figure 7. Differential expression gene analysis (PSO vs HS). Violin plots illustrating the differential expression of various cytokines and chemokines in PSO and HS samples across multiple cell types. The cytokines analyzed include *IL1B*, *IL17C*, *CXCL1*, *CXCL2*, *CXCL8*, *CXCL10*, *CCL20*, *CSF3*, and *IL6*. Each plot compares the expression levels between PSO (red) and HS (blue) across specific cell types, such as B cells, T cells, DCs, macrophages, monocytes, fibroblasts, and others. The y-axis represents the expression levels, while the x-axis shows the different cell types analyzed.



Supplementary Figure 8. Differential expression gene analysis (PSO vs PPP). Violin plots illustrating the differential expression of various cytokines and chemokines in PSO and HS samples across multiple cell types. The cytokines analyzed include *IL1B*, *IL17C*, *CXCL1*, *CXCL2*, *CXCL8*, *CXCL10*, *CCL20*, *CSF3*, and *IL6*. Each plot compares the expression levels between PSO (red) and PPP (purple) across specific cell types, such as B cells, T cells, DCs, macrophages, monocytes, fibroblasts, and others. The y-axis represents the expression levels, while the x-axis shows the different cell types analyzed.