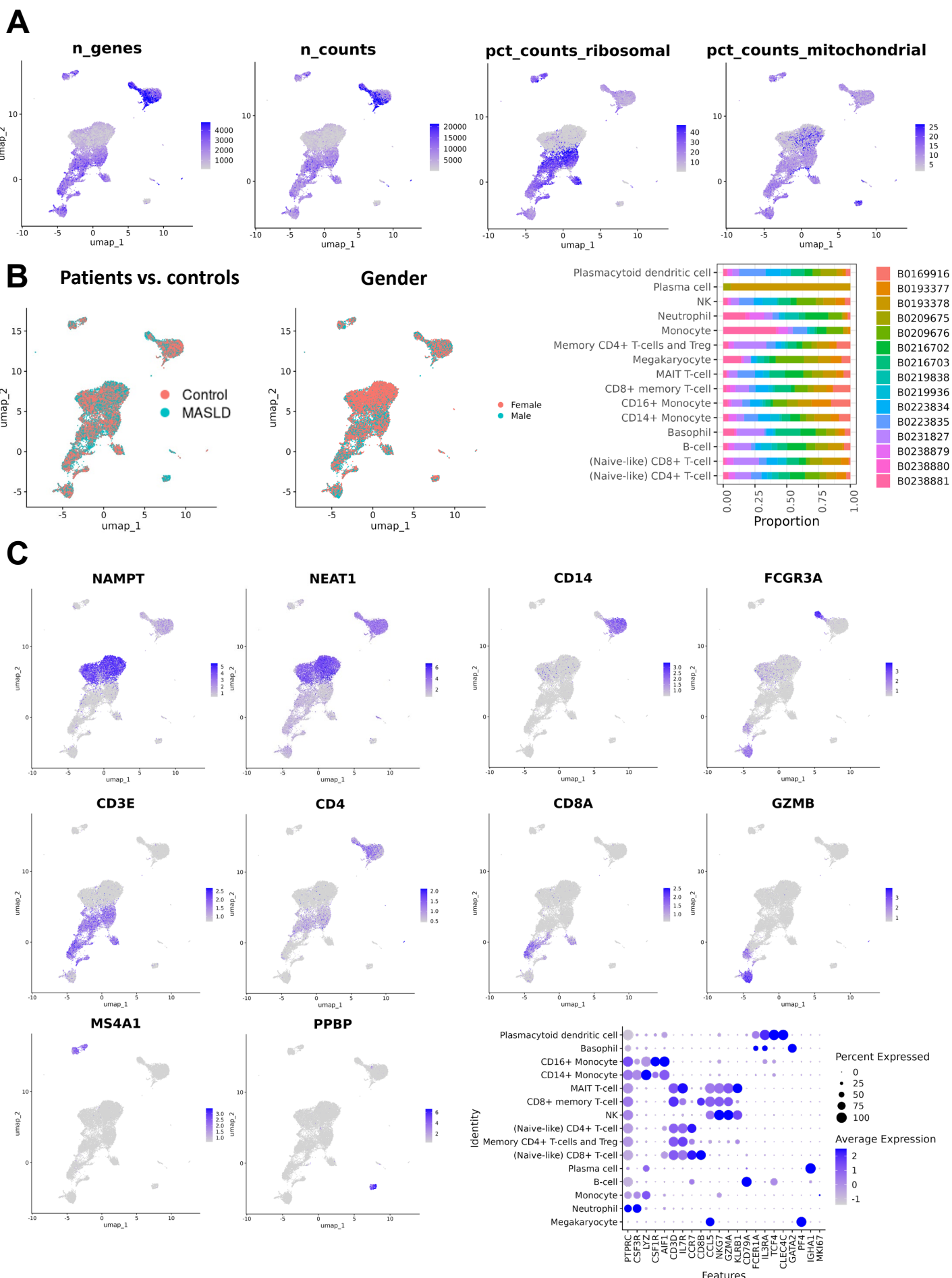
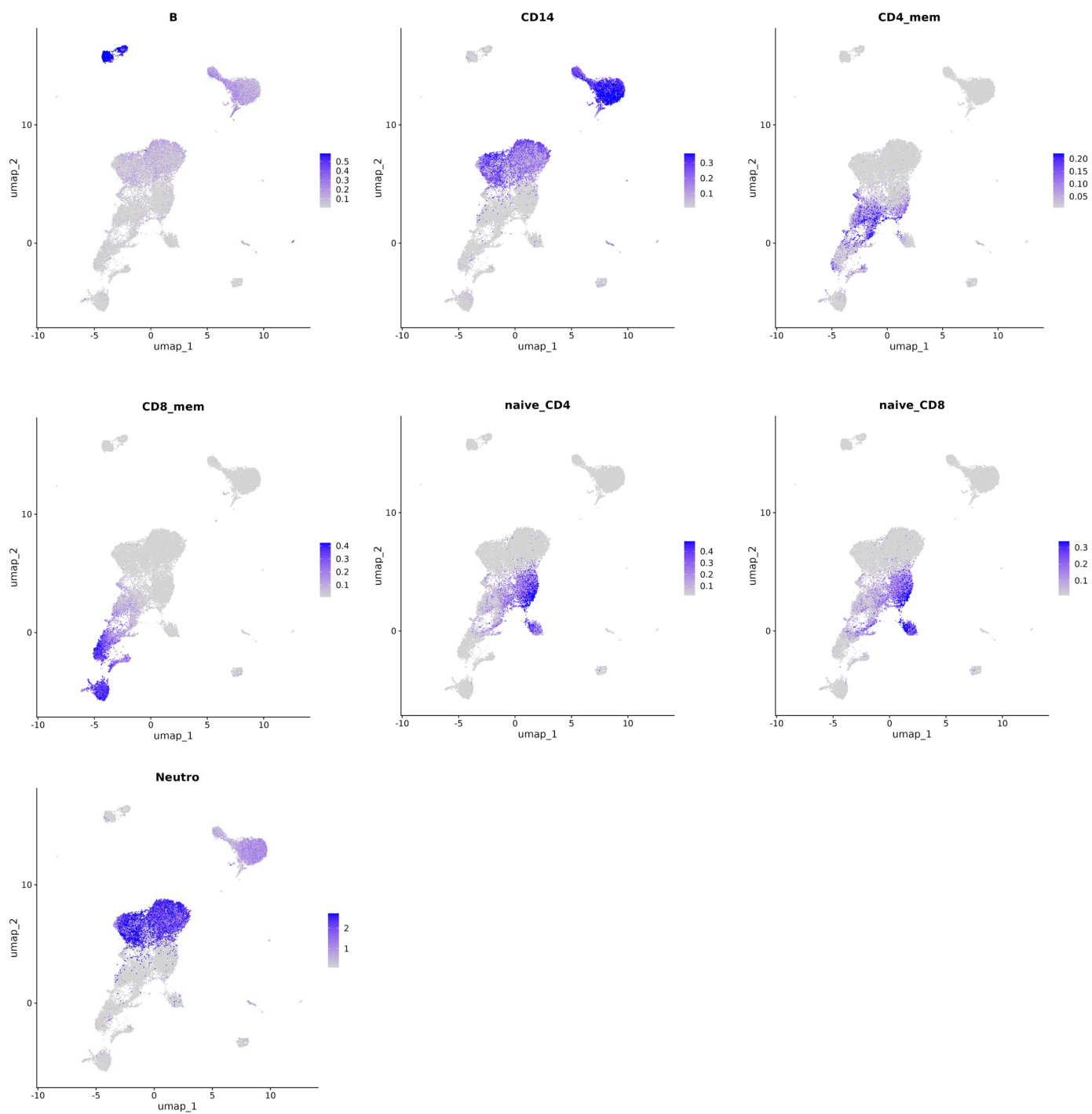




Supp. Fig. 1. (A) UMAP plots showing main quality control features. **(B)** UMAP plots showing integration across health and disease, gender and individual samples. **(C)** Feature plots of markers for major cell populations. **(D)** Dotplot with selected cell type markers.

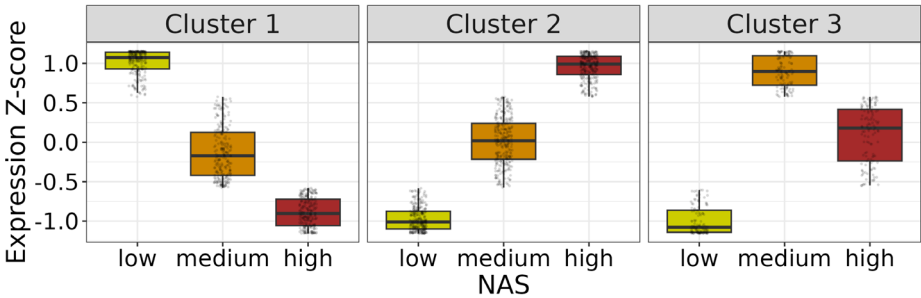
SDC, Figure 2



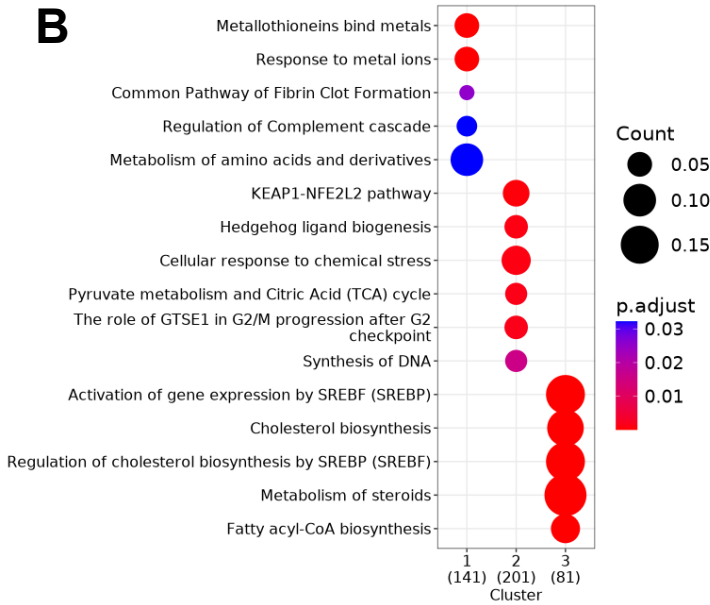
Supp. Fig. 2. Aggregated cell type specificity scores per major cell type population used for enrichment analysis in figure 2B projected onto the UMAP embedding.

SDC, Figure 3

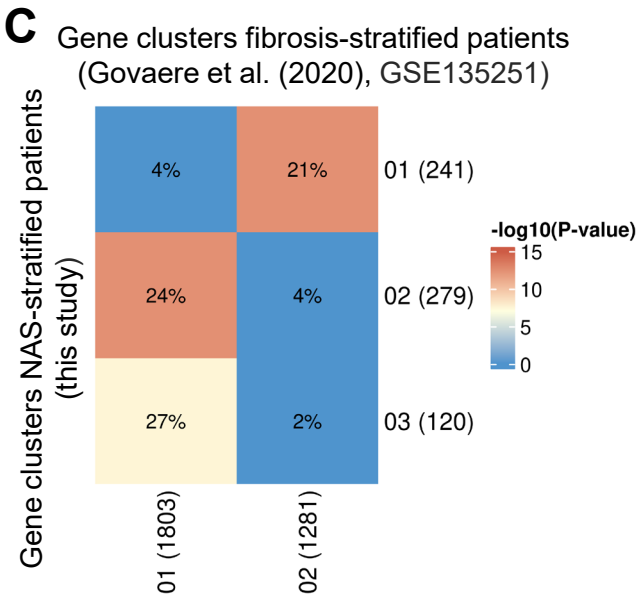
A



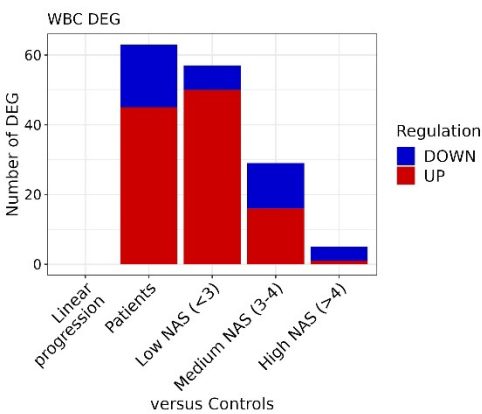
B



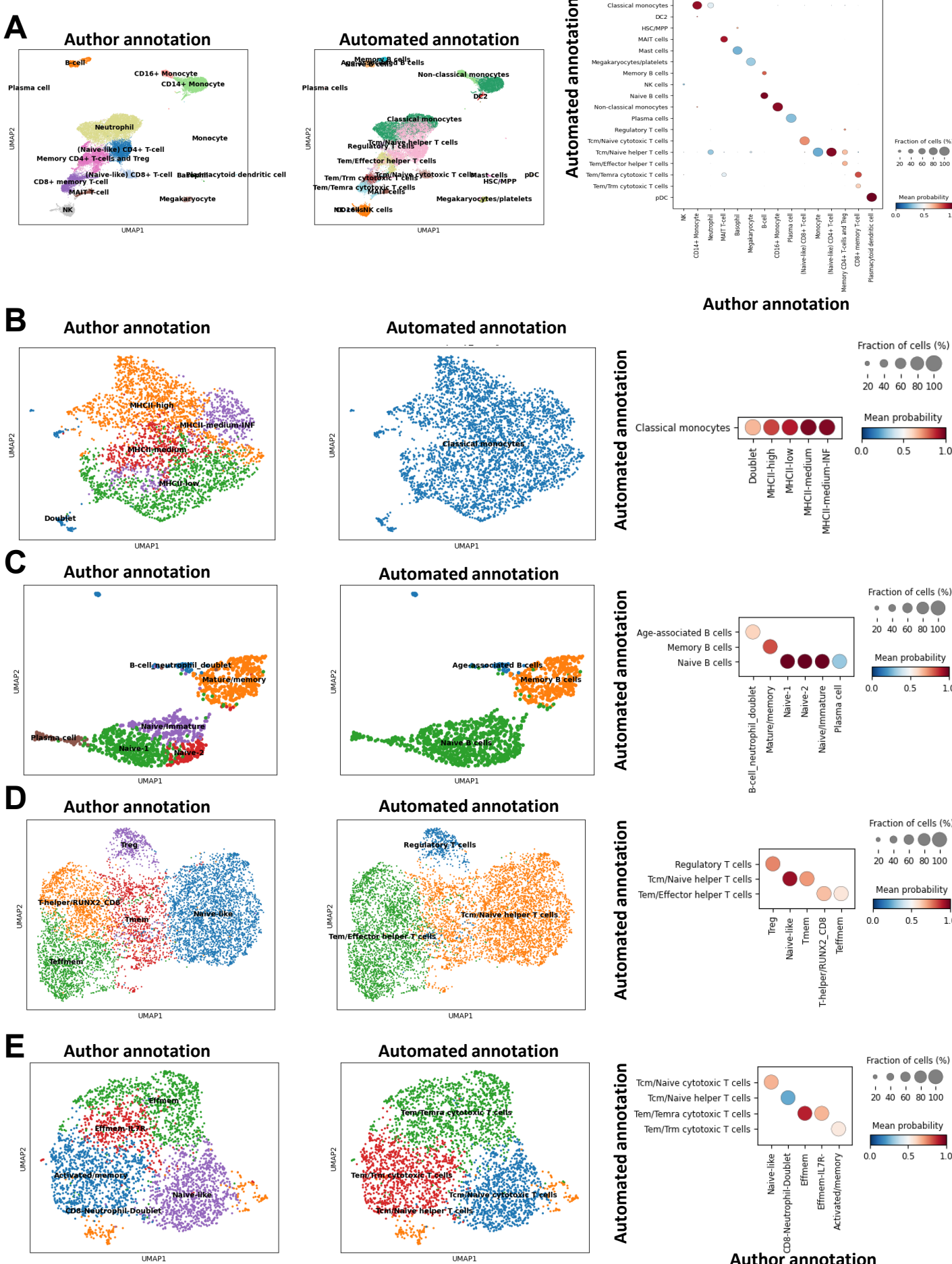
C



D

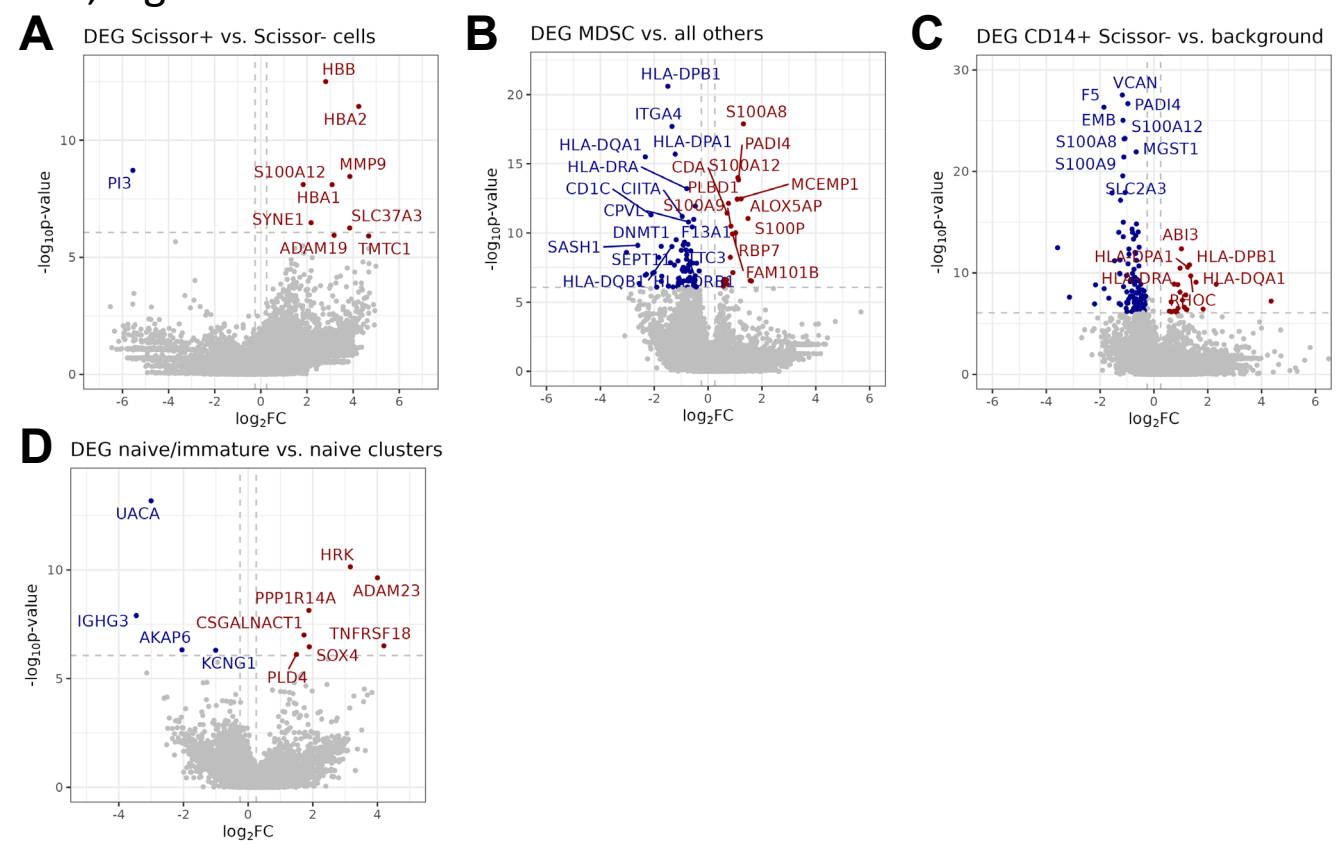


Supp. Fig. 3. Hierarchical cluster analysis of liver bulk DEG and white blood cell DE analysis results. (A) Z-score-normalized gene expression of the top three gene clusters identified by hierarchical clustering from liver bulk DE results (pairwise comparison against low NAS). (B) Reactome enrichment plot of the top three gene clusters from NAS-stratified patients as shown in (A). Numbers in brackets indicate the number of genes per cluster that could be mapped. (C) Pairwise enrichment of gene clusters derived from liver RNAseq from fibrosis-stratified patients (GSE135251) as performed by Sauer et al.¹⁷ and liver RNAseq from NAS-stratified patients. Percentage of overlap between genes in NAS-stratified and fibrosis-stratified clusters shown. Numbers in brackets indicate the number of genes per cluster. (D) Number of up/downregulated DEG in white blood cells bulk RNAseq in a linear disease progression model (FDR<0.1, $|\beta|>1$) and two-group comparisons against healthy controls ($p_{adj}<0.05$, $|\log_{2}FC|>0.25$).

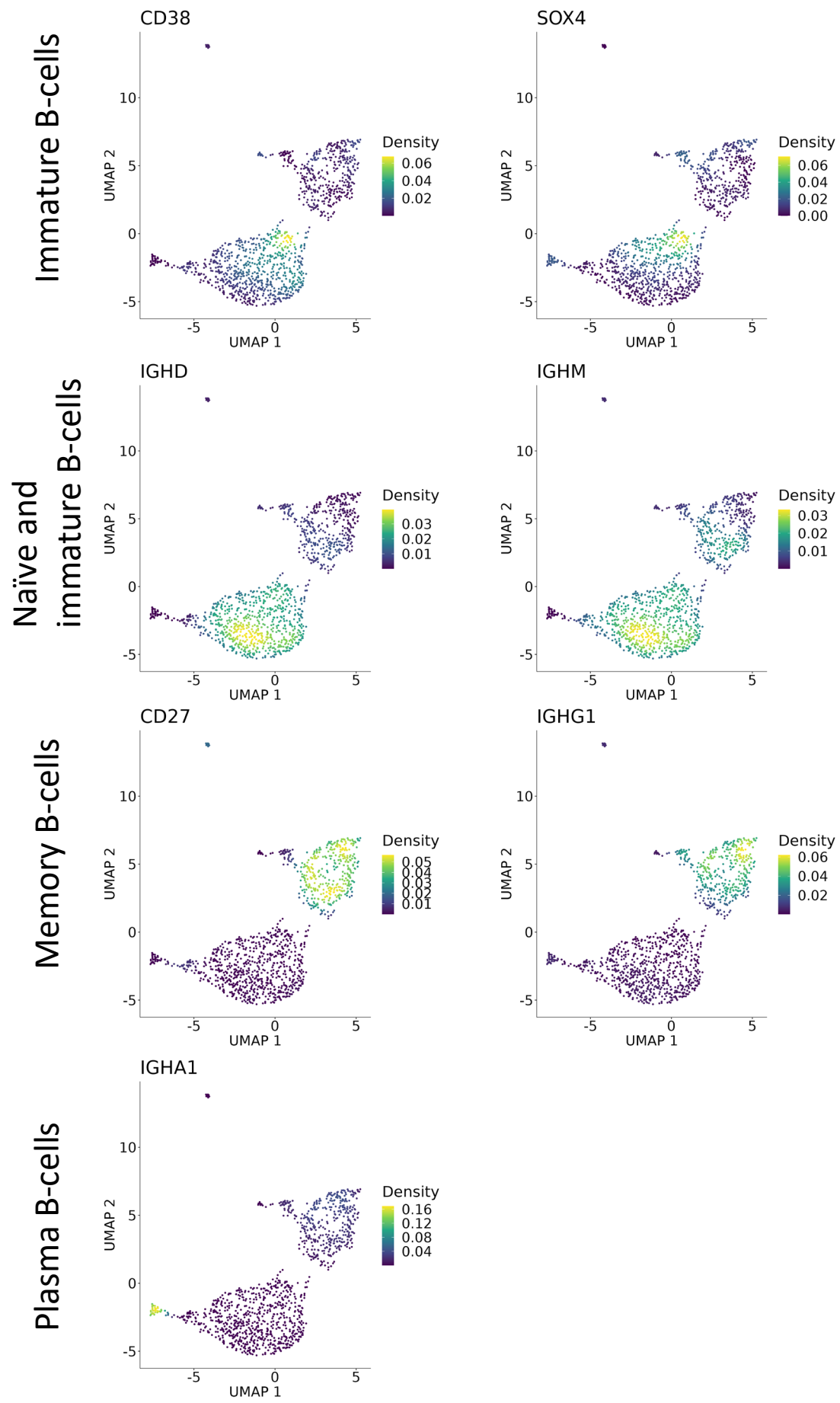


Supp. Fig. 4. Comparison of manual author annotations with automated annotation (CellTypist) for **(A)** the full dataset (note that neutrophils were not in the prediction model), **(B)** CD14+ monocytes, **(C)** B-cells, **(D)** CD4+ T-cells and **(E)** CD8+ T-cells.

SDC, Figure 5



Supp. Fig. 5. Volcano plot of pseudobulk DE testing of **(A)** Scissor+ vs. Scissor- neutrophils, **(B)** MDSC vs. all other CD14+ monocytes, **(C)** Scissor- vs. background CD14+ monocytes and **(D)** naïve/immature vs. naïve B-cell clusters.



Supp. Fig. 6. Density plots of B-cell subpopulation markers.