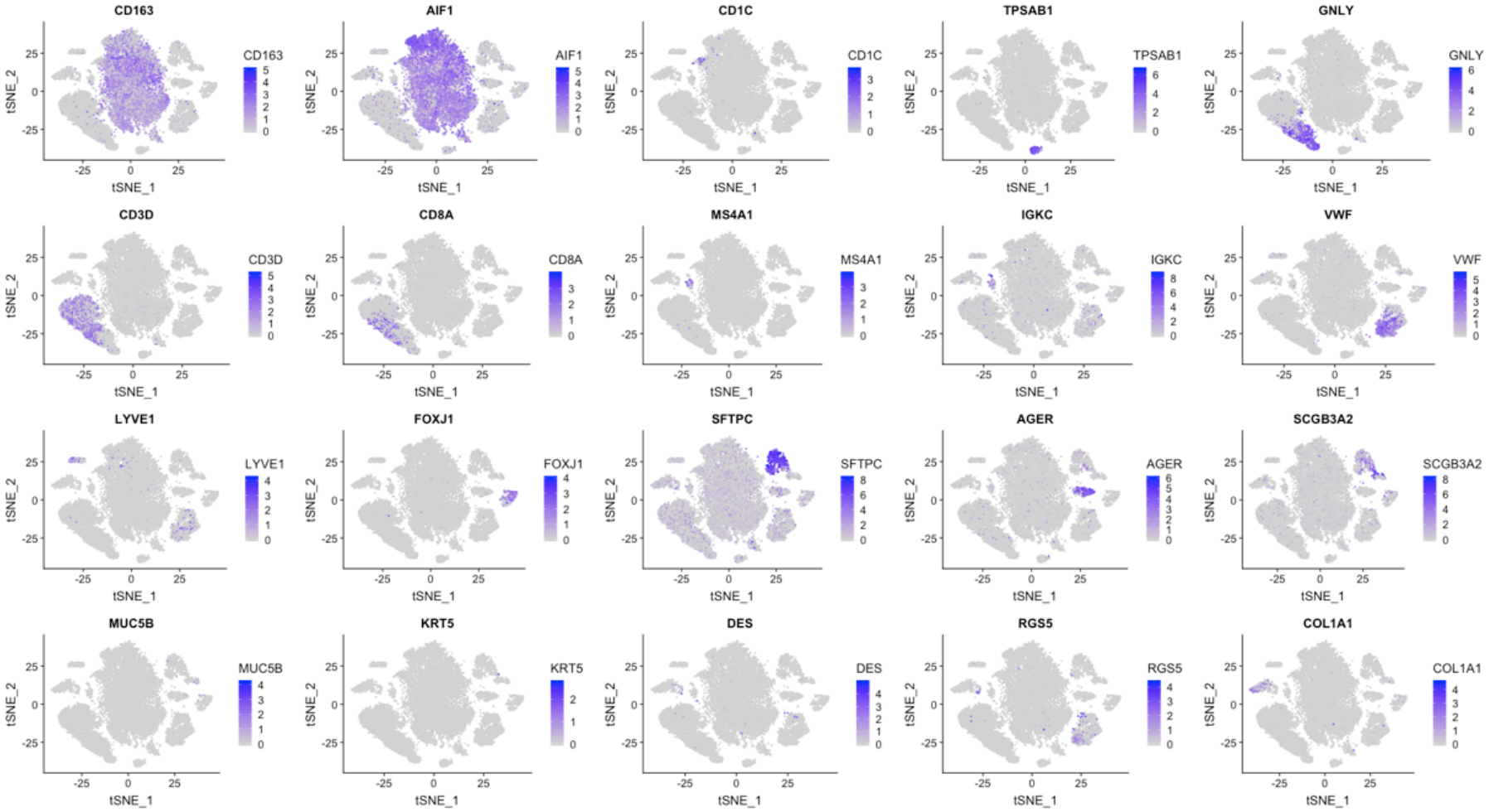

CD163
AIF1
CD1C
TPSAB1
GNLY
CD3D
CD8A
MS4A1
IGKC
VWF
LYVE1
FOXJ1
SFTPC
AGER
SCGB3A2
MUC5B
KRT5
DES
RGS5
COL1A1
tSNE_1
tSNE_2

Figure S1. Club cells, expressed the marker *SCGB1A1* (cluster 12), alveolar type I (AT1) cells expressed *AGER* (cluster 8), alveolar type II cells (AT2) expressed *SFTPC* (cluster 6), and ciliated cells expressed *FOXJ1* (cluster 9). *KRT5* expressing basal airway cells, and *MUC5B* expressing goblet cells were not found in discrete clusters. The rare cells expressing KRT5 (basal cells) and MUC5B (goblet cells) are seen clearly upon reclustering of our combined IPF/control data, Figure 2D and Figure S15. Fibroblasts expressing *COL1A1* and smooth muscle cells expressing *DES* (cluster 7). Endothelial cells, expressing *VWF*, and lymphatic endothelial cells, expressing *LYVE1*, clustered in two distinct adjacent groups (clusters 4 and 11, respectively). Cells with pericyte markers *RGS5* were also distributed in cluster 4. Macrophages, identified by *AIF1* and *CD163* expression, were found in six different clusters, (clusters 0, 1, 3, 14 and 18). A small subset of *CD1C*-expressing dendritic cells were found in cluster 10. *TPSAB1*, a marker of mast cells, was expressed by cells in cluster 13. T lymphocytes, including *CD3* and *CD8A* positive cells, clustered together in cluster 2, while B lymphocyte lineage were marked with *MS4A1*/*CD20* cluster 15, including high expression of immunoglobulin genes (IGKC), and MZB1, a plasma cell marker. NK cells, expressing *GNLY*, were found in cluster 5.

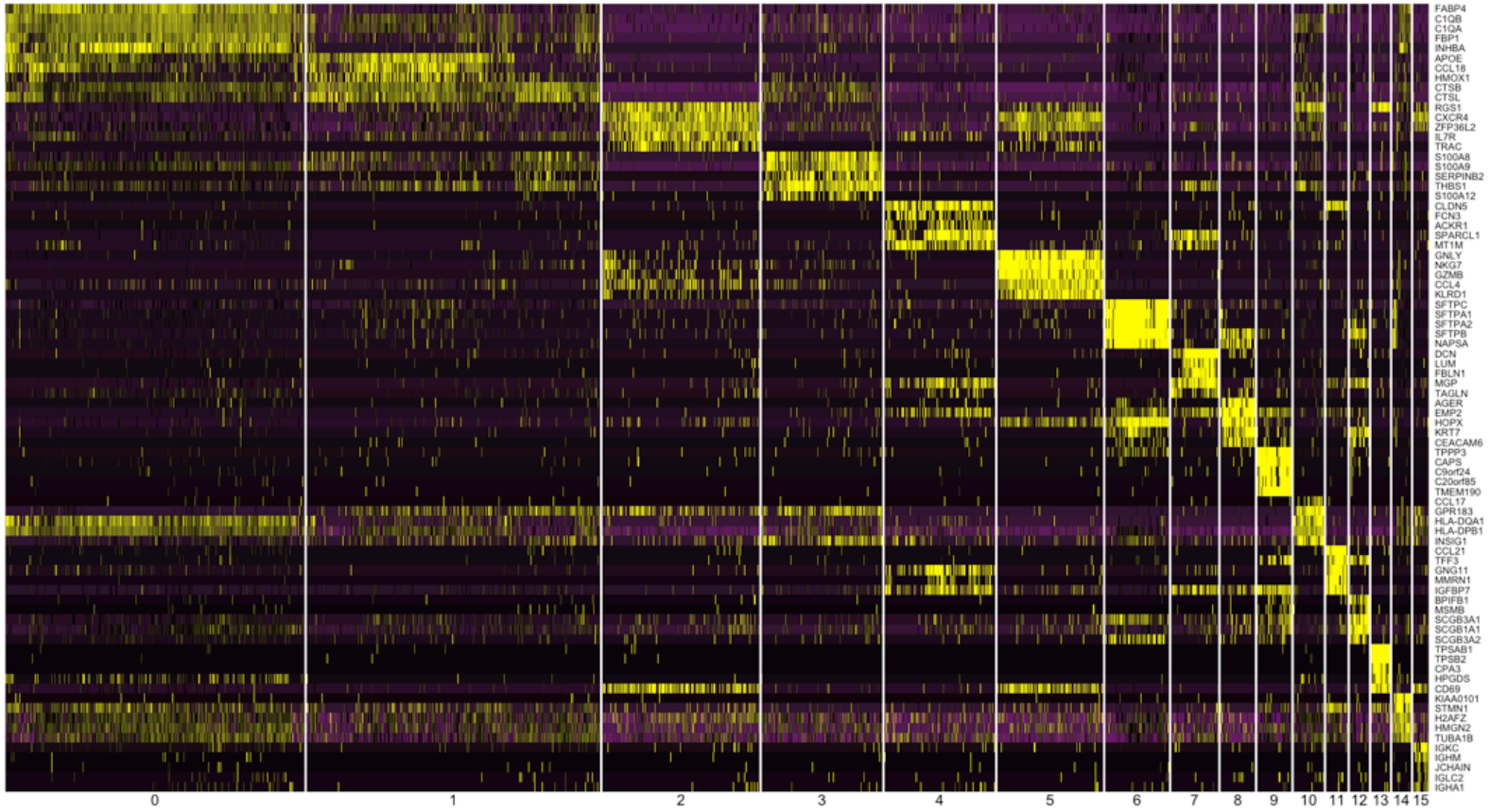


Figure S2. Clustering of top differentially expressed genes from scRNA-seq of normal lungs

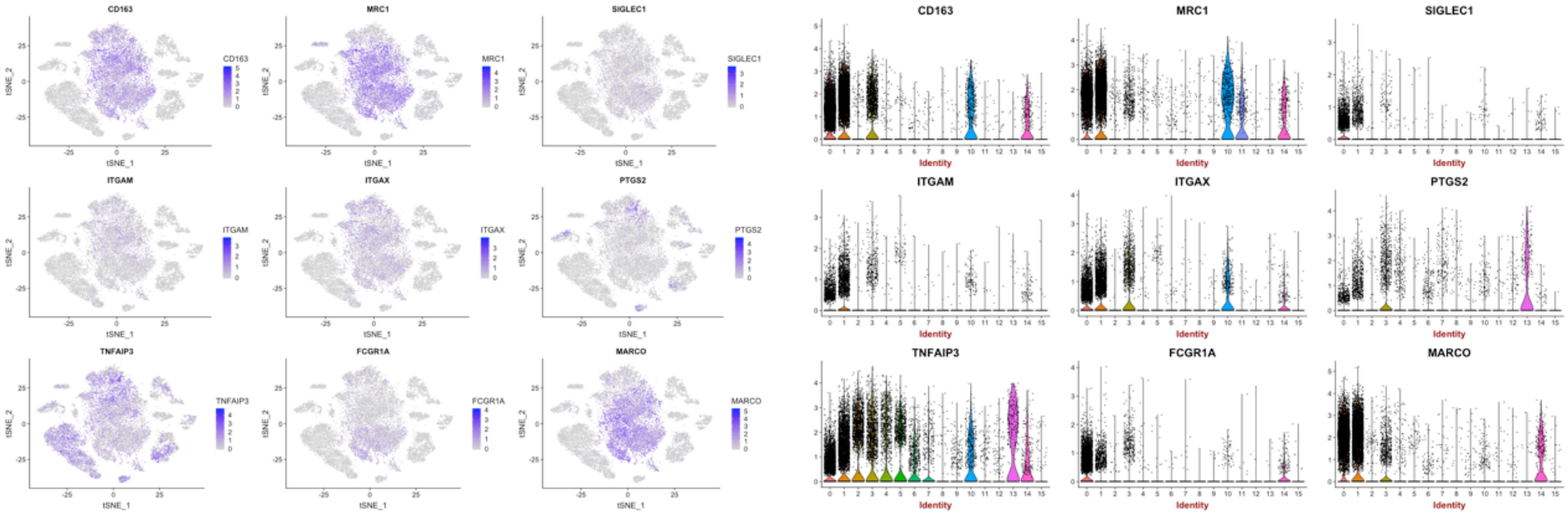


Figure S3. Macrophage marker expression in scRNA-seq clusters from normal lungs. Feature plots (panel A) and Violin plots (panel B) show macrophage markers expressed by all macrophage/monocyte/DC populations (clusters 0, 1, 3, 10 and 14; CD163, ITGAX/CD11c) or restricted mainly to macrophage populations (clusters 0, 1 and 14; MRC1/CD206, SIGLEC1/CD169, ITGAM/CD11b, FCGR1A/CD64, MARCO)

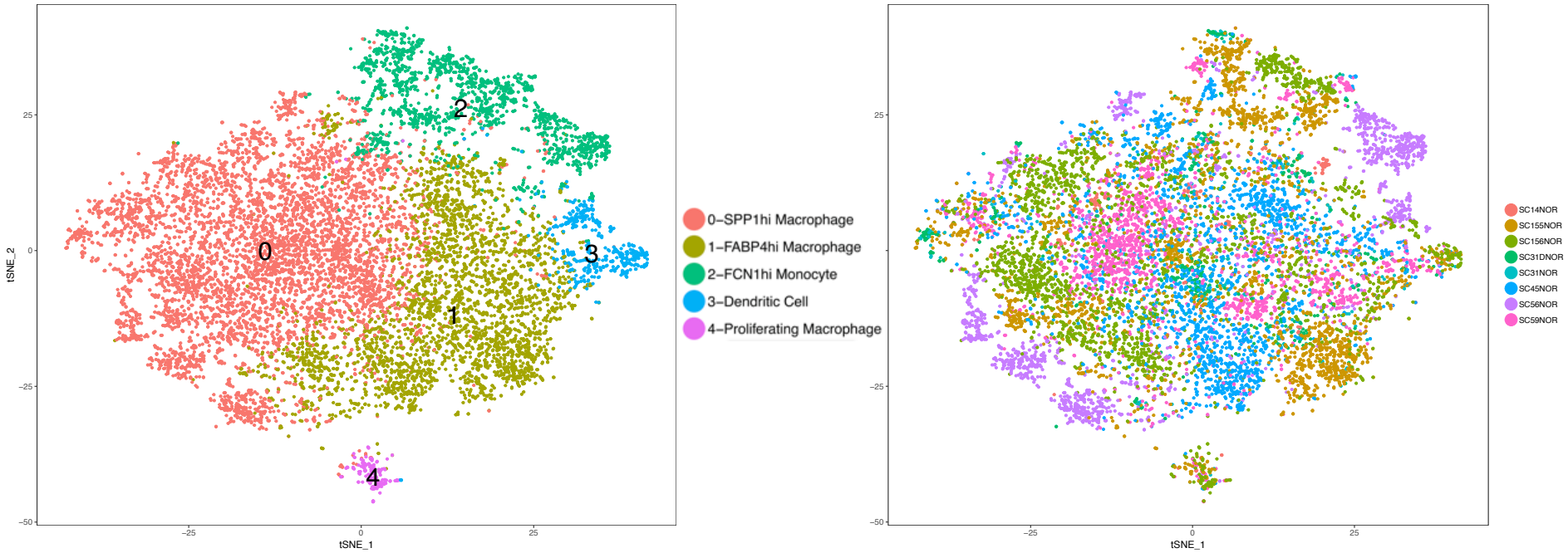


Figure S4 Reclustering of macrophages from healthy lungs, cells colored by cluster (panel A) and by subject (panel B).

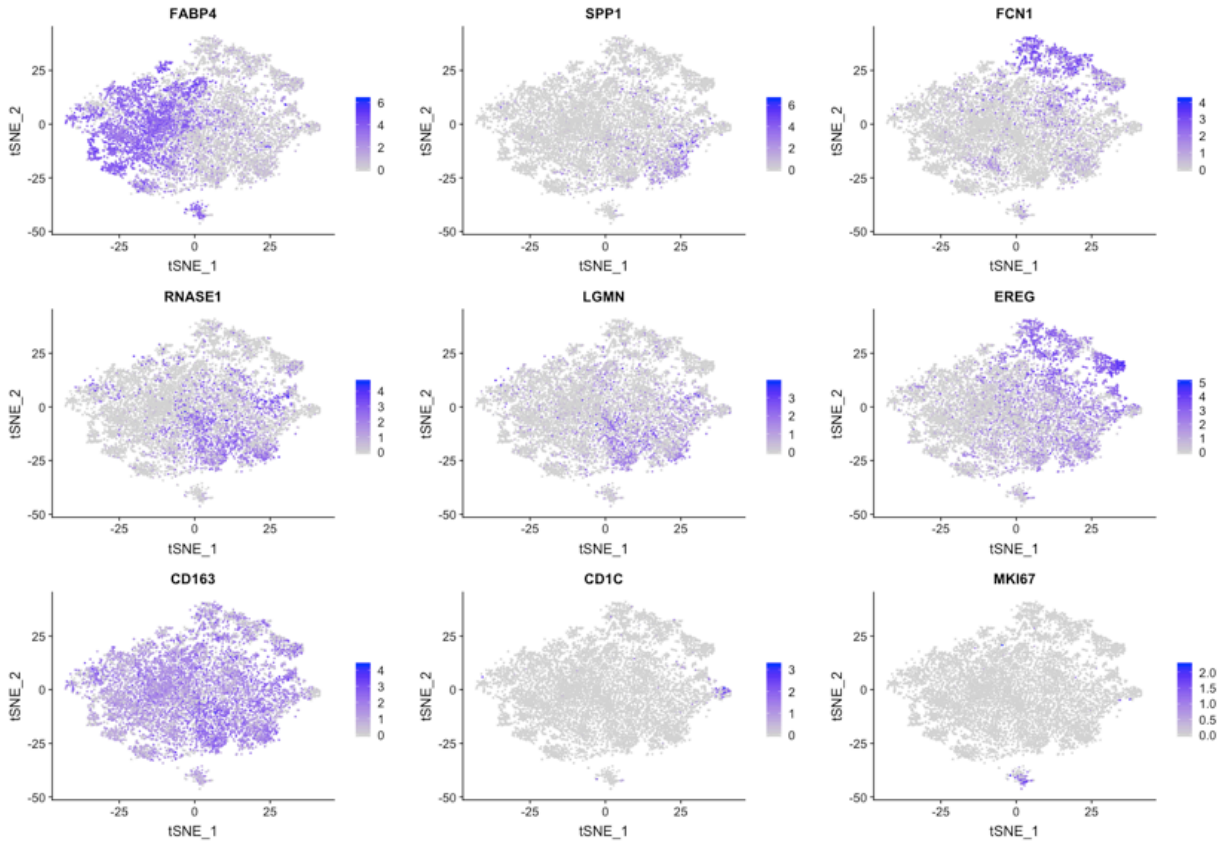


Figure S5 Reclustering of macrophages from healthy lungs, cells colored by gene expression (purple = high expression grey = low), showing FABP4 highly expressed by FABP4^{hi} macrophages; SPP1, LGMN and RNASE1 more highly expressed by SPP1^{hi} macrophages; CD163 and CD1C showing reciprocal expression in all macrophages and dendritic cells, respectively and FCN1 and EREG expressed more highly by FCN1^{hi} macrophages).

Figure S6 Breakout panels showing individual florescent channels and merged images staining from Figure 1E

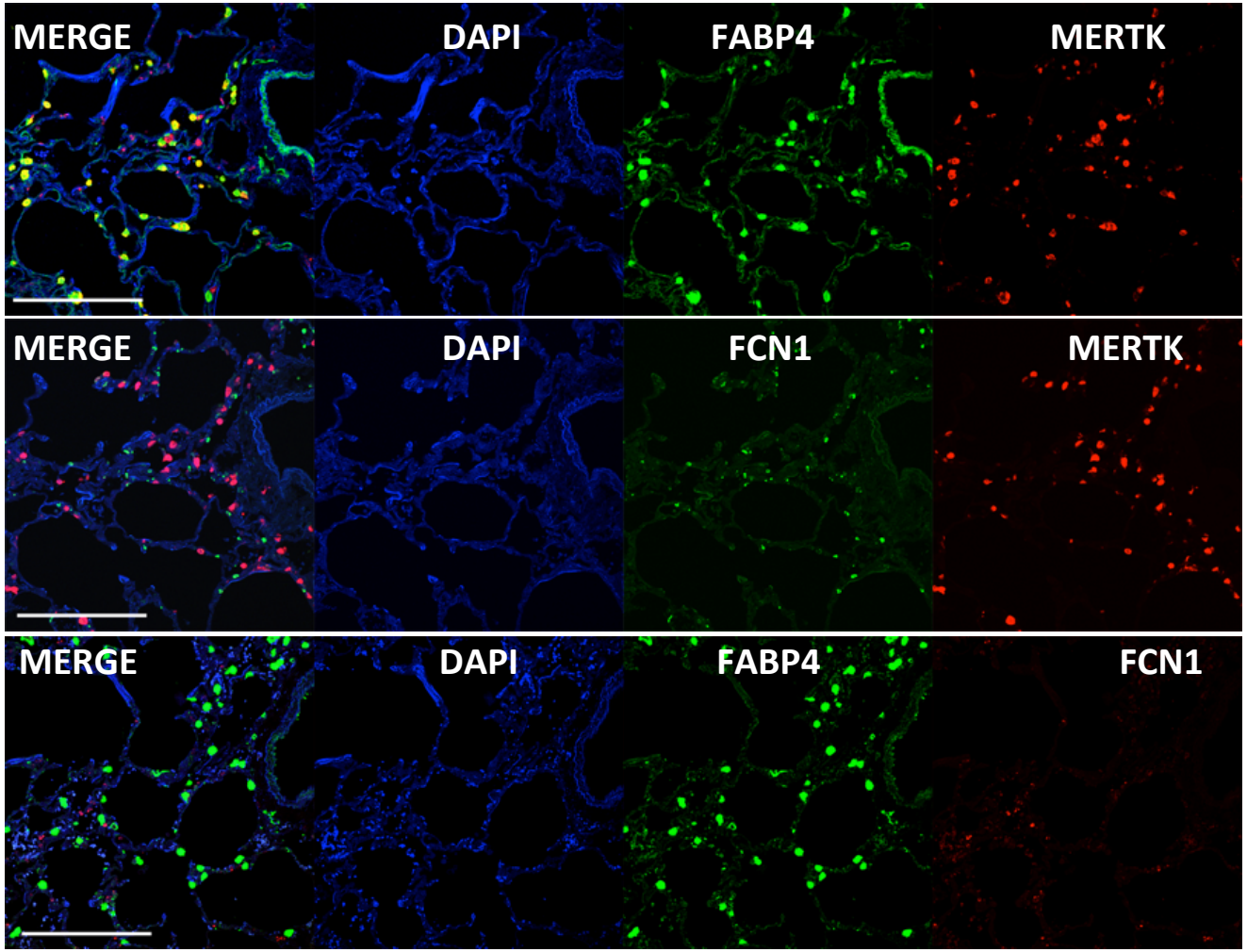
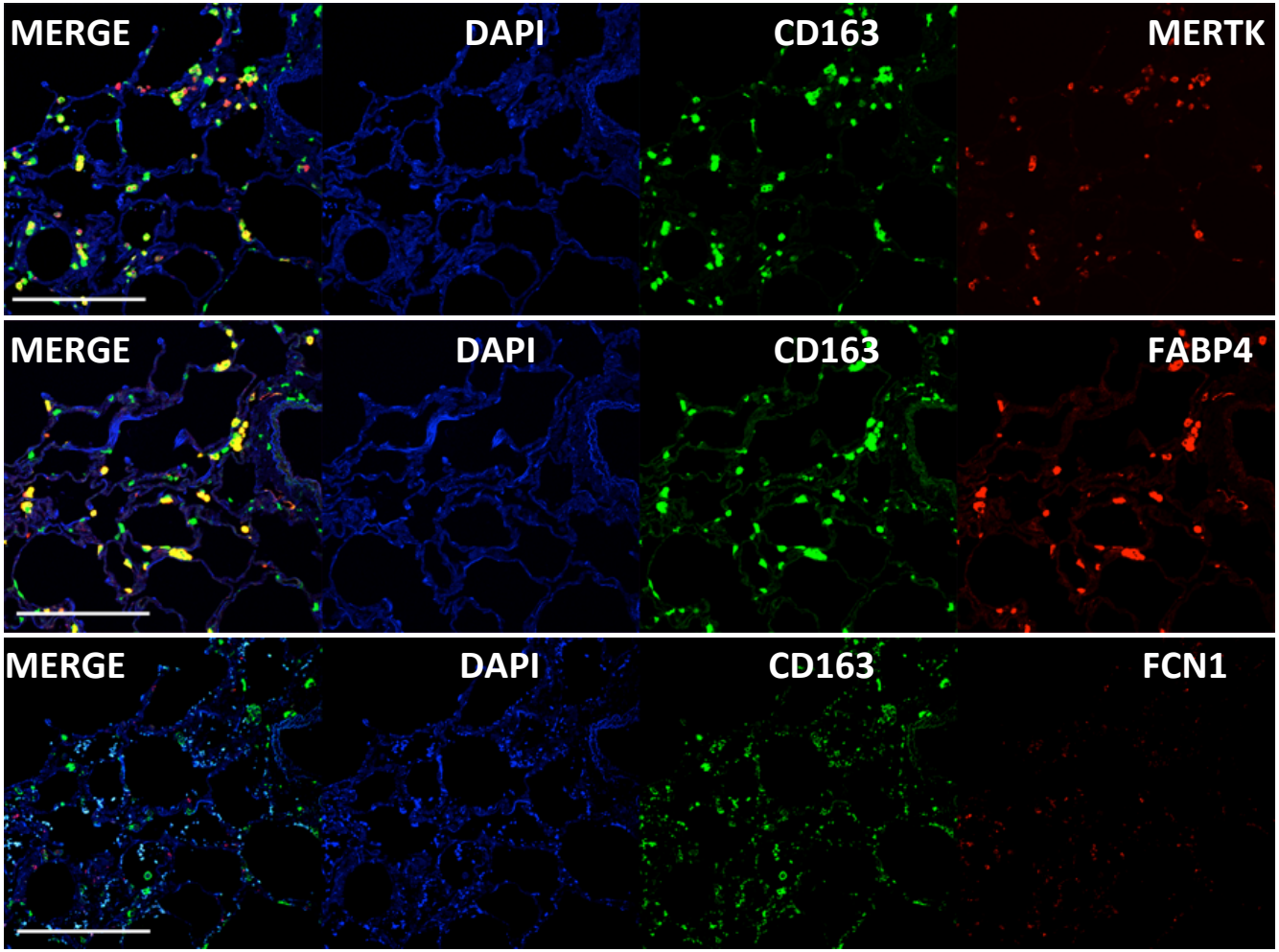


Figure S6 Breakout panels showing individual florescent channels and merged images staining from Figure 1E



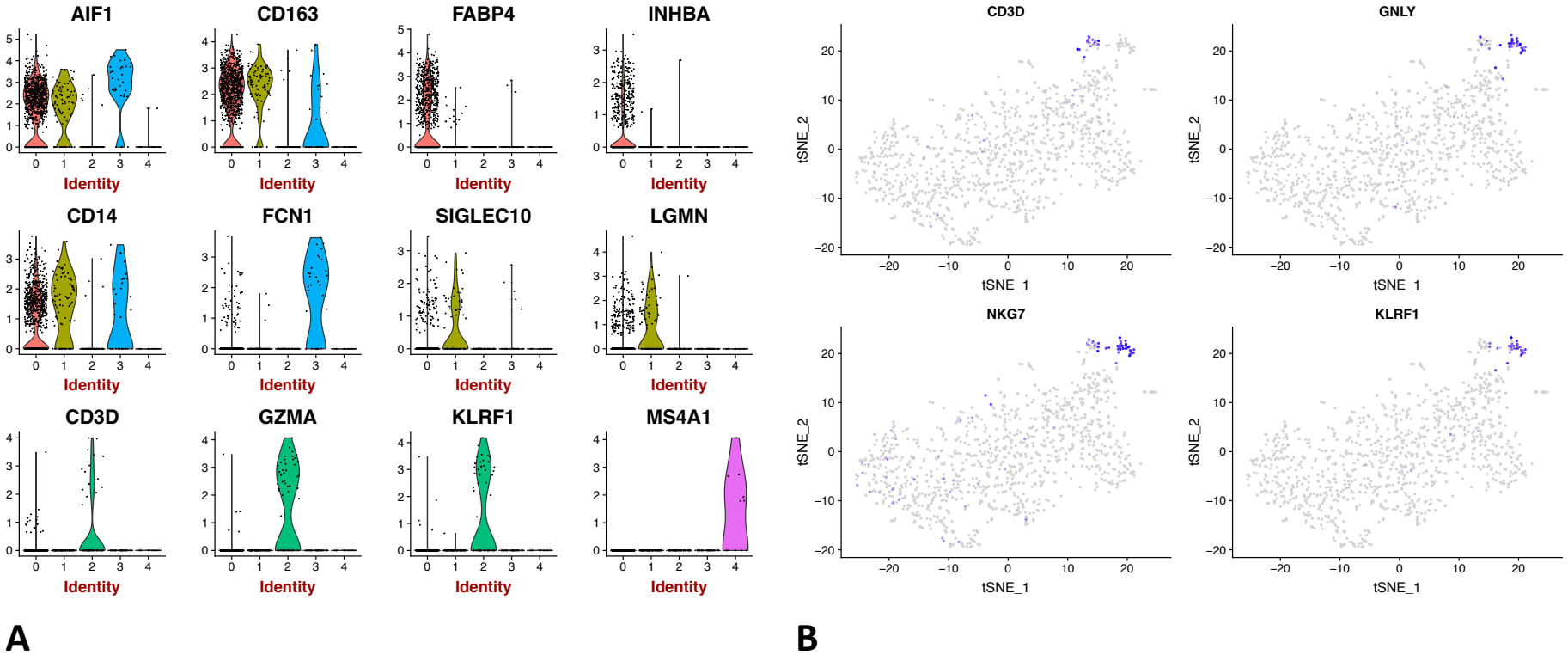


Figure S7. Marker gene expression by cell clusters in healthy bronchoalveolar lavage (panel A) Cluster 2 includes subclusters of T cells (*CD3D*) and NK cells (*KLRF1, GNLY* and *NKG7*; panel B).

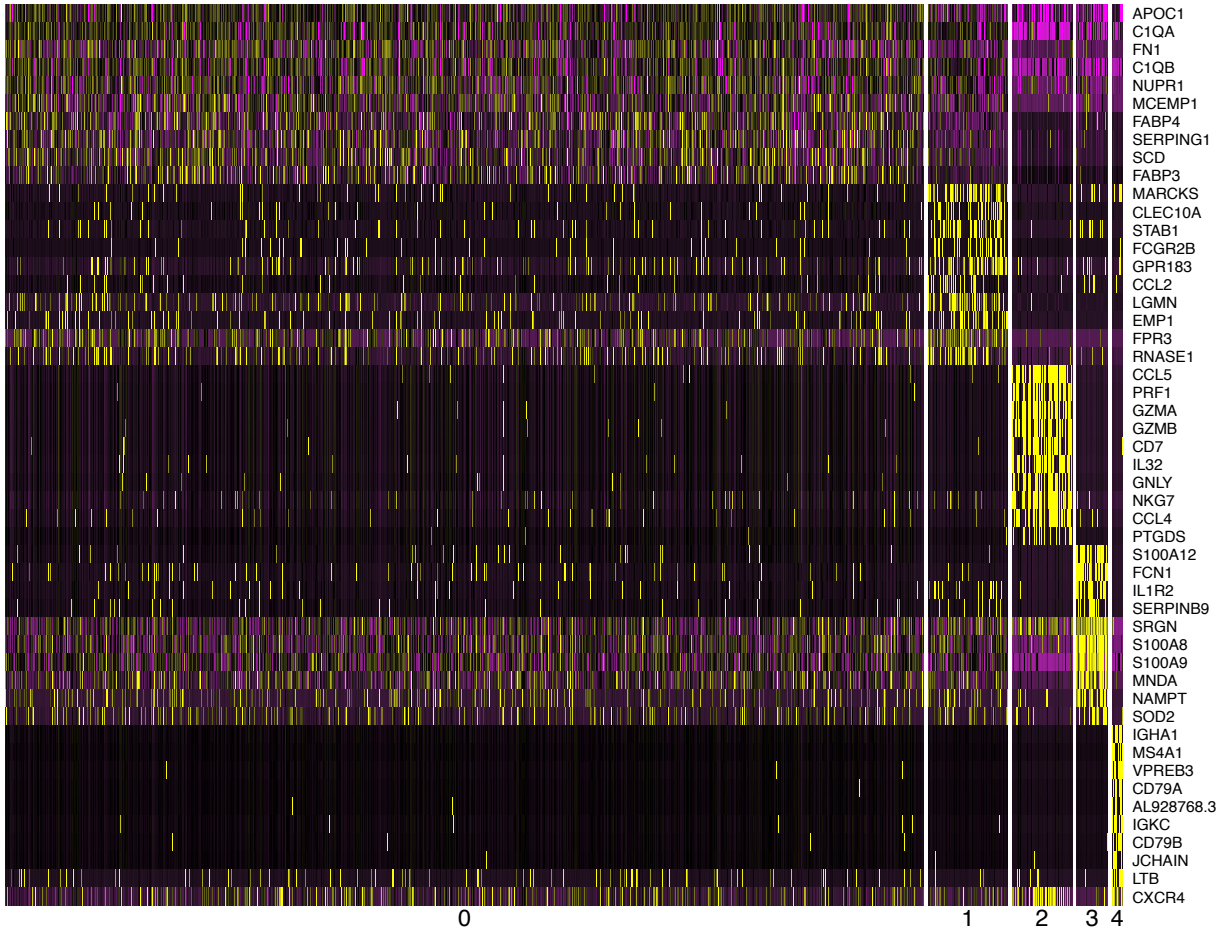


Figure S8. 10 top differentially expressed genes from scRNA-seq data of healthy bronchoalveolar lavage fluid

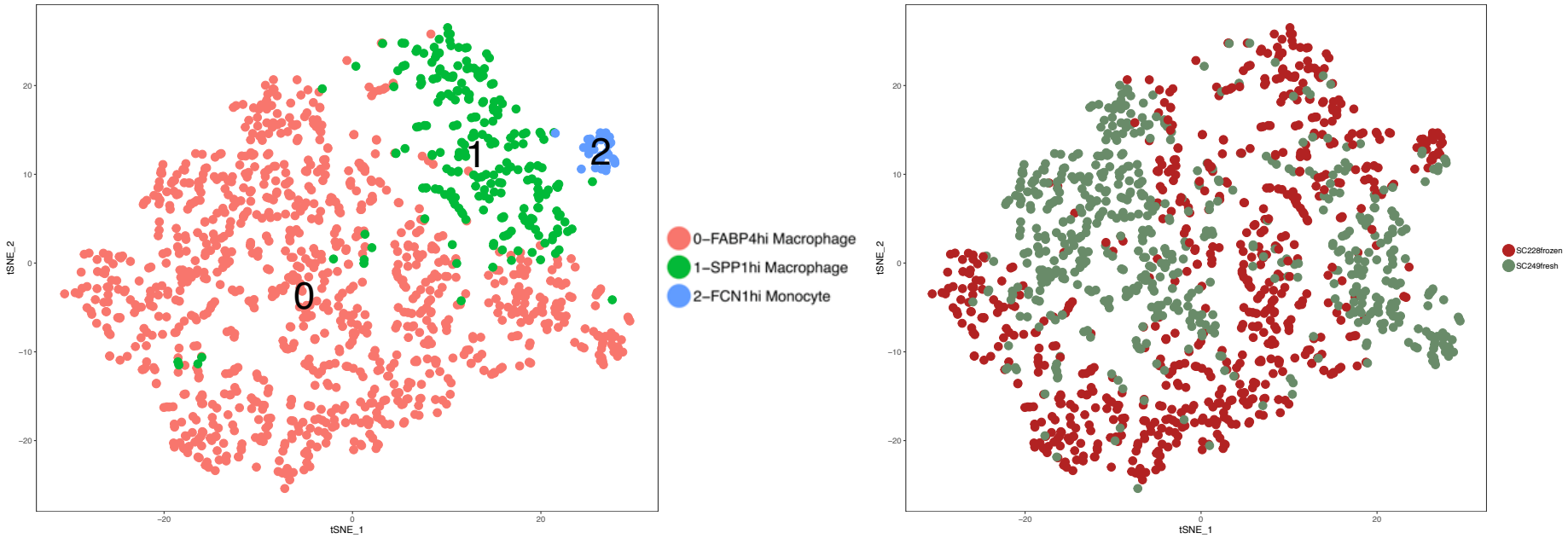


Figure S9. T-SNE plot recluster of macrophages from combined healthy lung BAL (SC228NORbal) and BAL with brushings (SC249NORbal), showing cells colored by cluster assignment (panel A) or by subject (panel B)

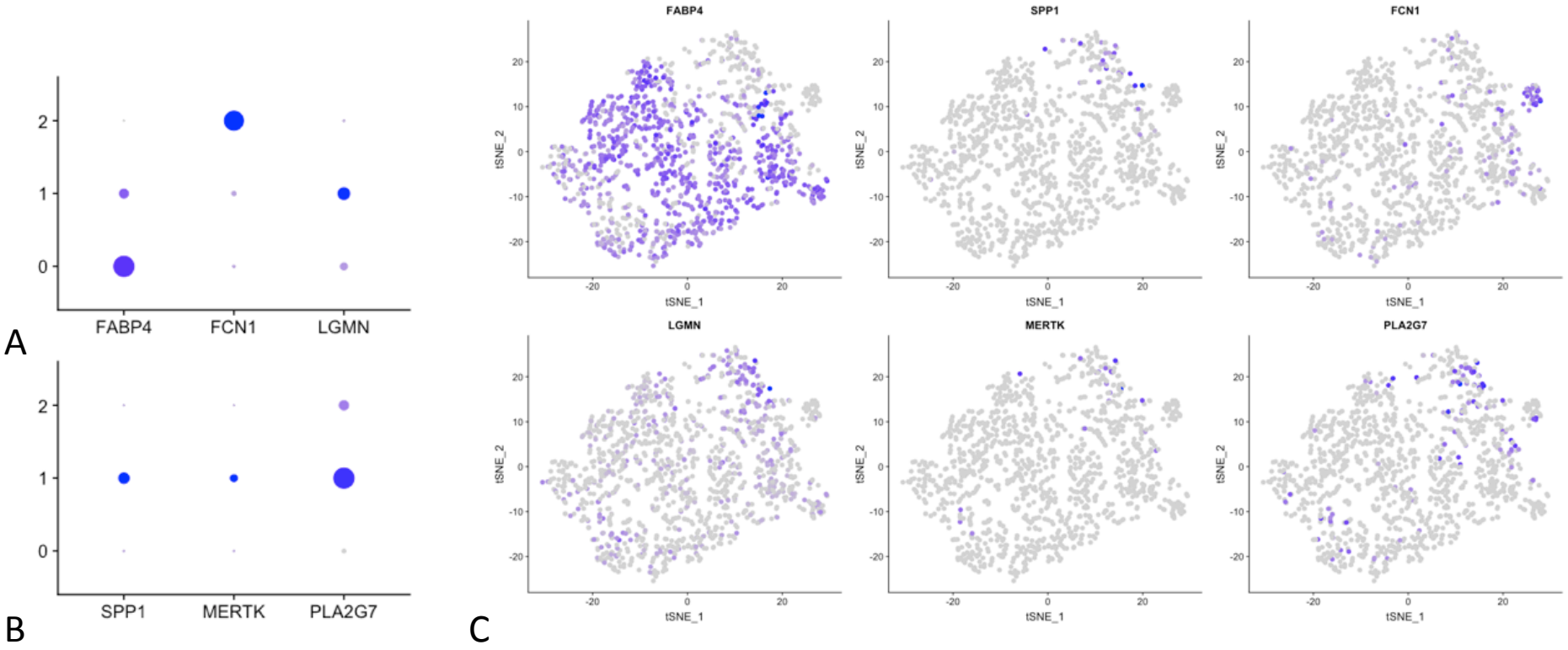
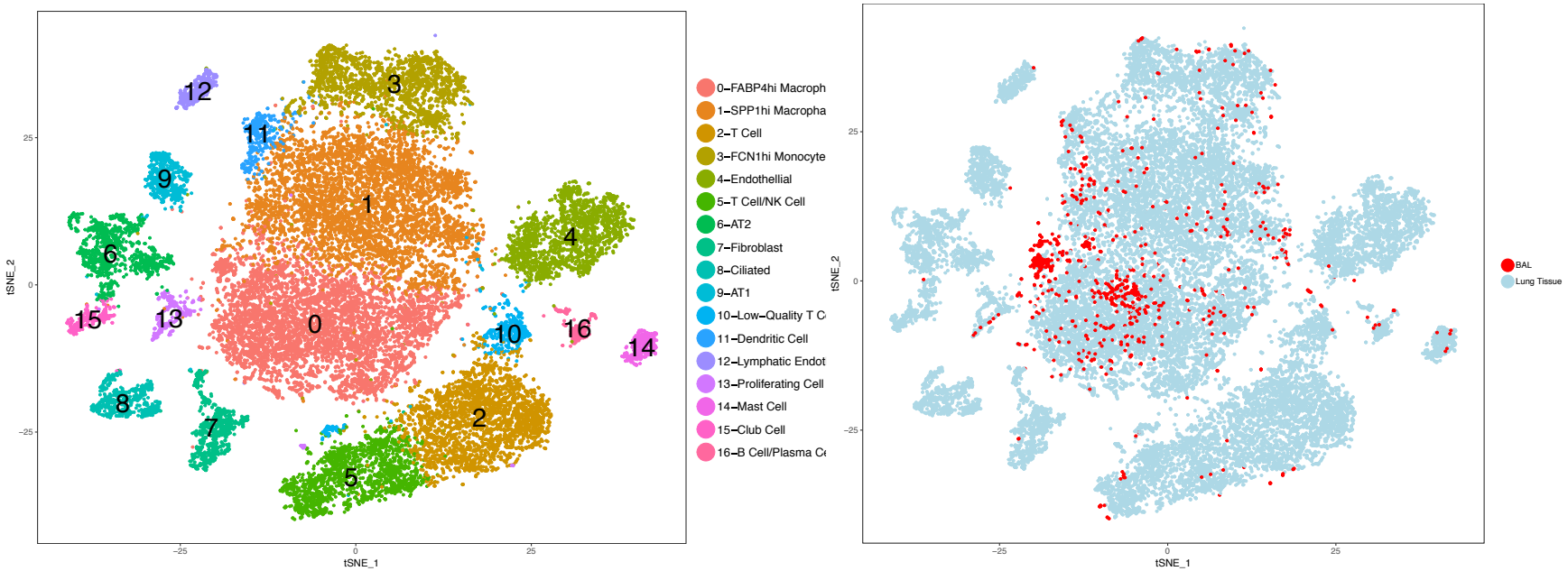


Figure S10. Dot plots (panels A and B) and feature plots (panel C) showing expression of marker genes for FAPB4^{hi} (FABP4), SPP1^{hi} (SPP1, MERTK and PLA2G7) and FCN1^{hi} (FCN1) macrophages in BAL from two healthy control lungs



A **B**

Figure S11. T-SNE plot of combined healthy lung tissues (SC14NOR, SC155NOR, SC156NOR, SC31NOR, SC31DNOR, SC45NOR, SC56NOR, SC59NOR), and healthy bronchoalveolar lavage fluid (SC228NORbal), showing cells colored by cluster assignment (panel A) or by subject (panel B).

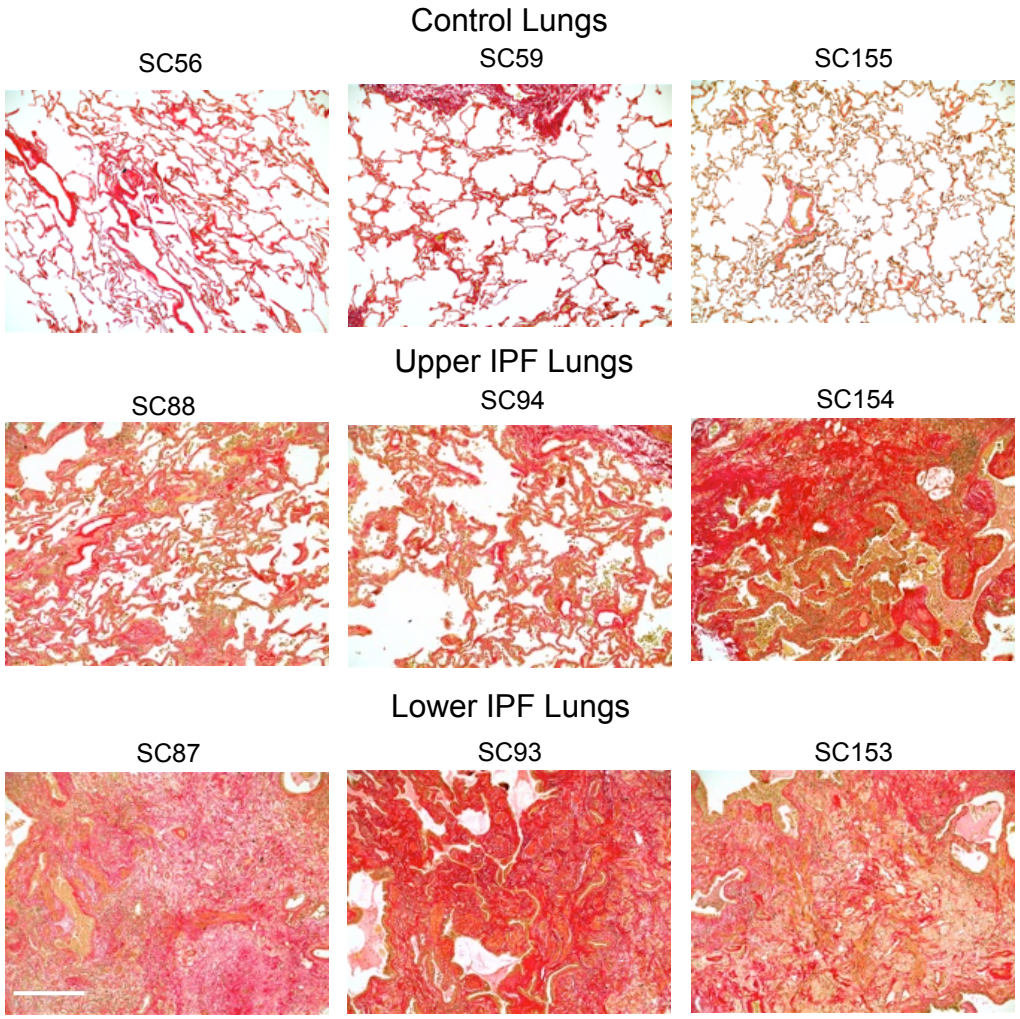


Figure S12A. Picro Sirius Red staining of control lung, and upper and lower lobe IPF lung tissues. Collagen staining (red) is seen in alveolar septa of control lungs, and densely and most prominently in lower lobes of fibrotic IPF tissues. (Scale bar = 400µm)

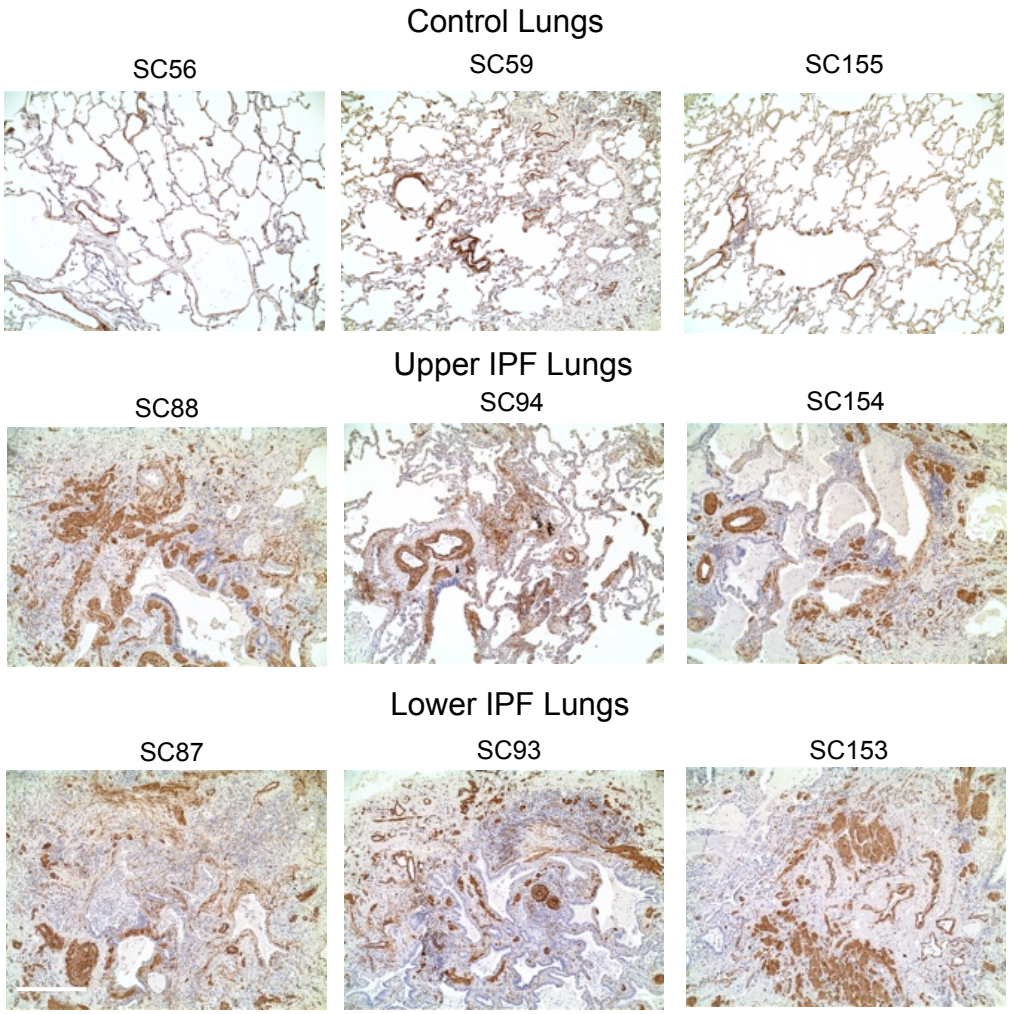


Figure S12B. Smooth muscle actin staining by immunohistochemistry of control lung, and upper and lower lobe IPF lung tissues. Perivascular smooth muscle/ pericyte staining is seen in control lungs, and in addition staining of myofibroblasts is seen most prominently in lower lobes of IPF tissues (brown stain; scale bar = 400µm)

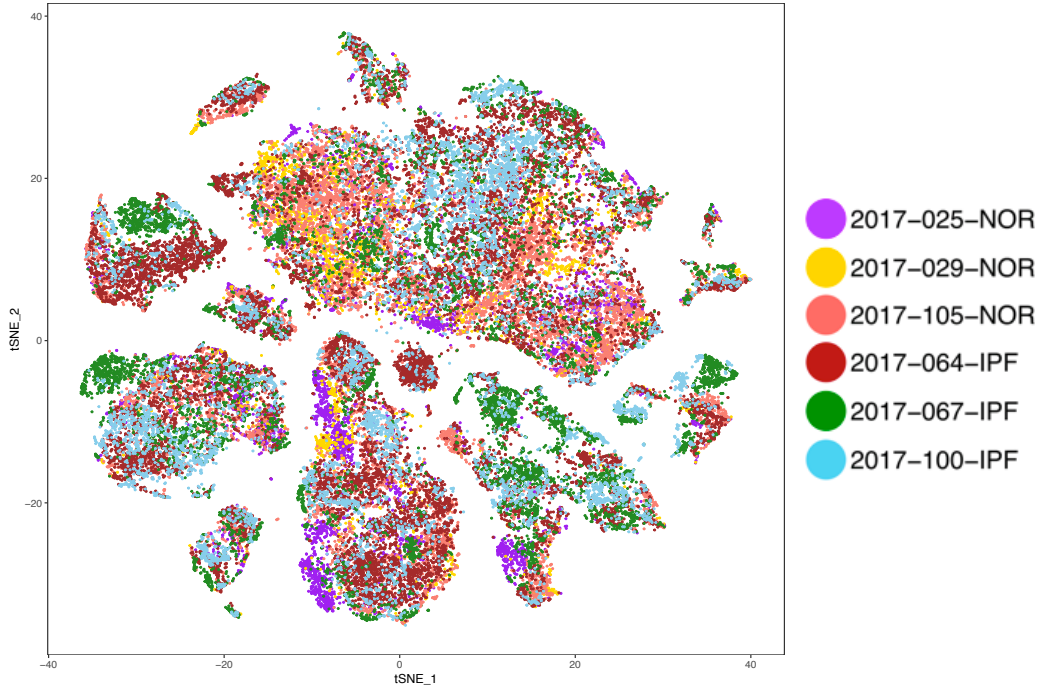


Figure S13. Combined analysis of healthy and IPF lungs, cells colored by subject

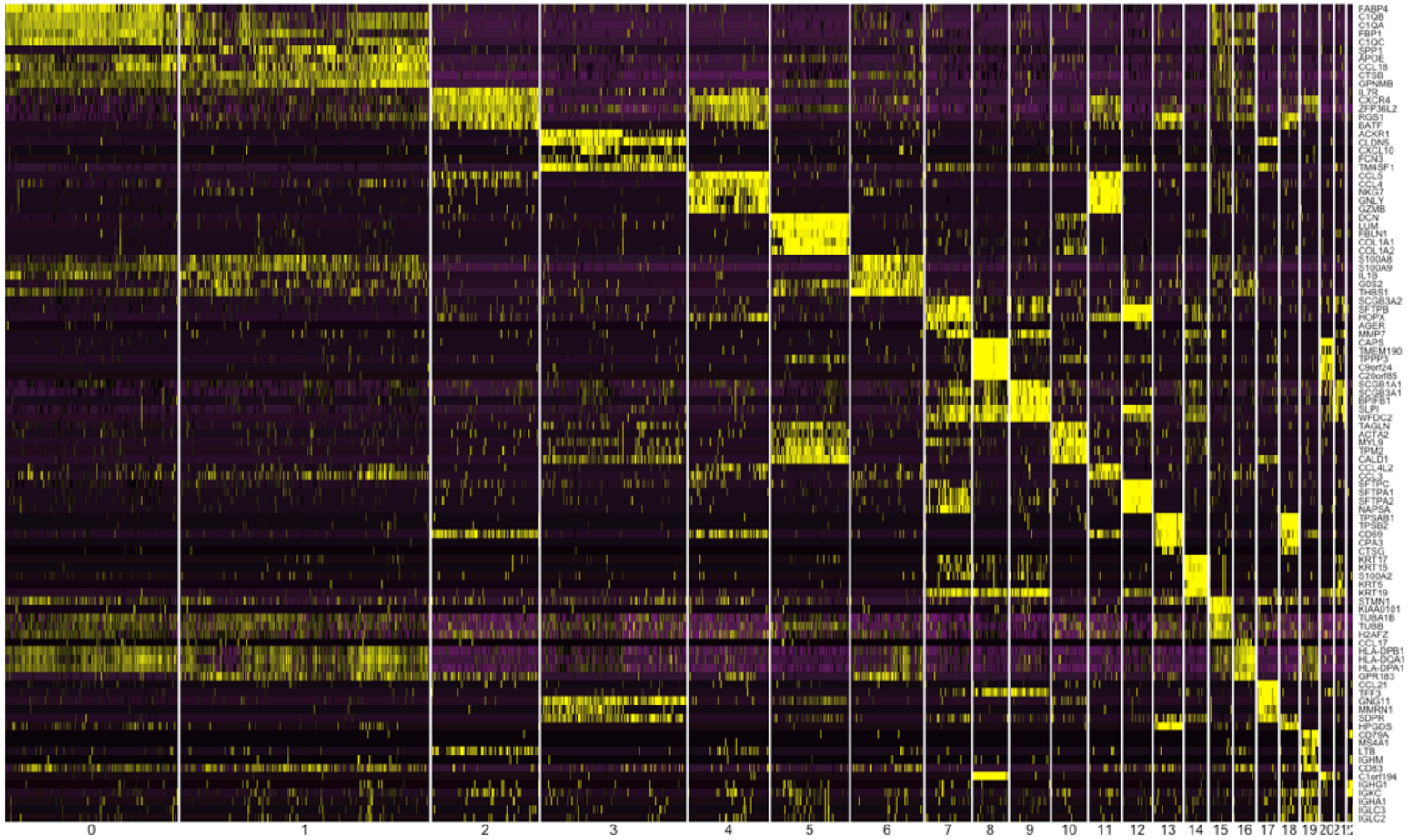


Figure S14. Clustering of top five differentially expressed genes from scRNA-seq of IPF and normal lungs

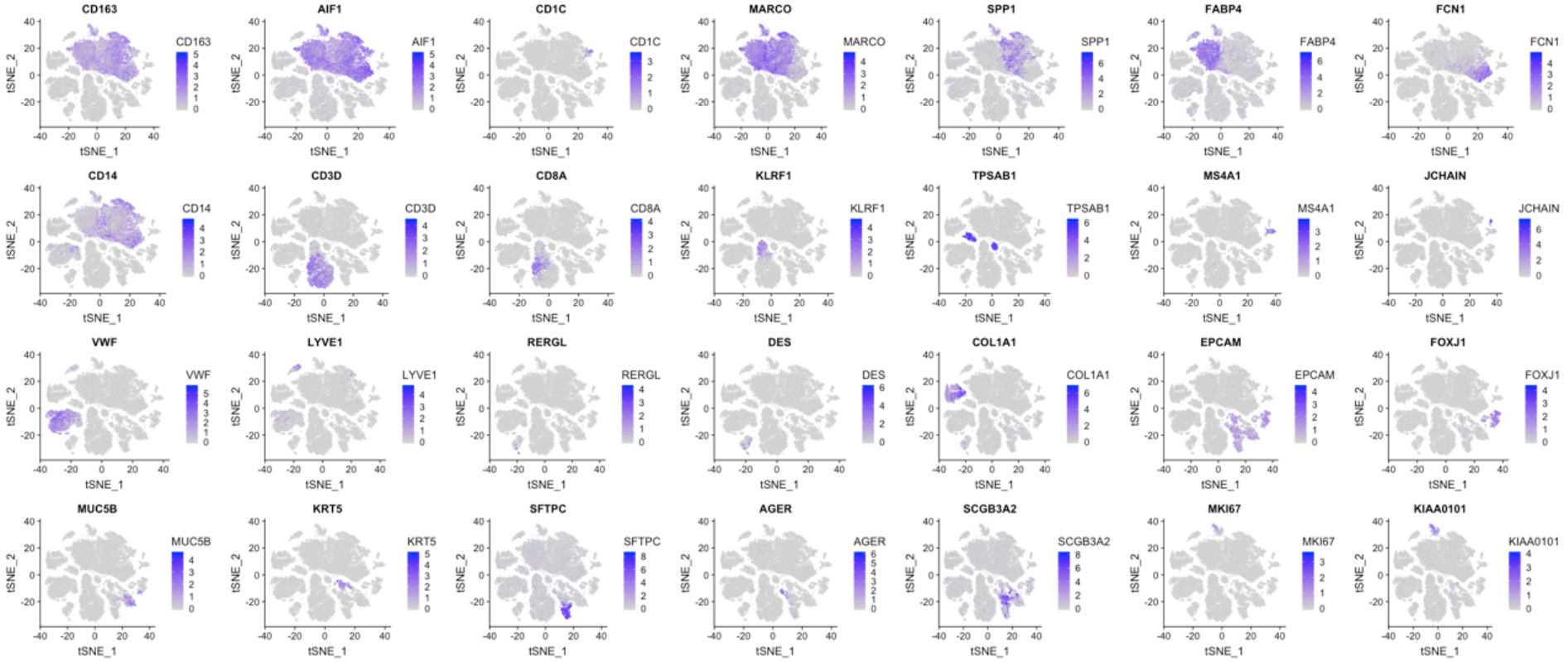


Figure S15. Feature plots of marker genes expressed from scRNA-seq of IPF and normal lungs

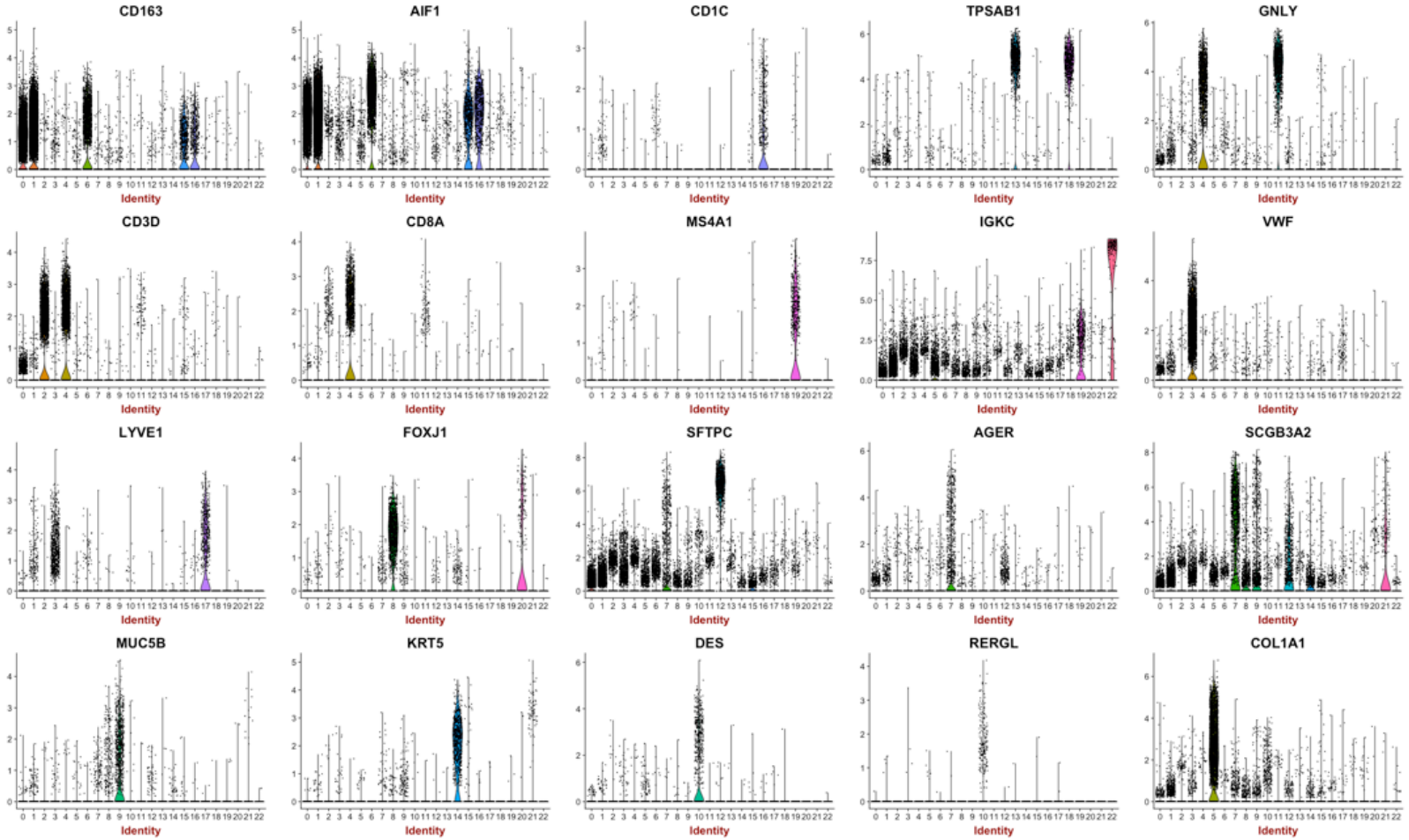


Figure S16. Violin plots of marker genes expressed from scRNA-seq of IPF and normal lungs

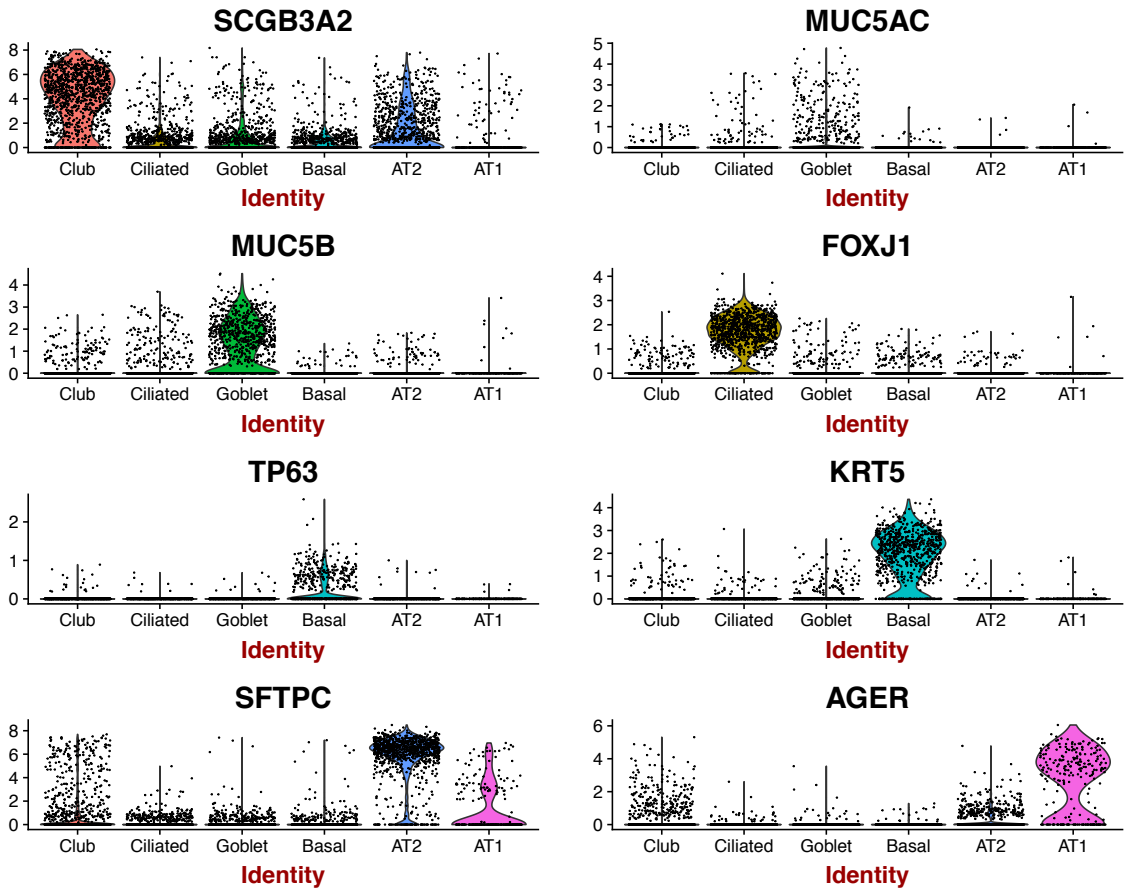
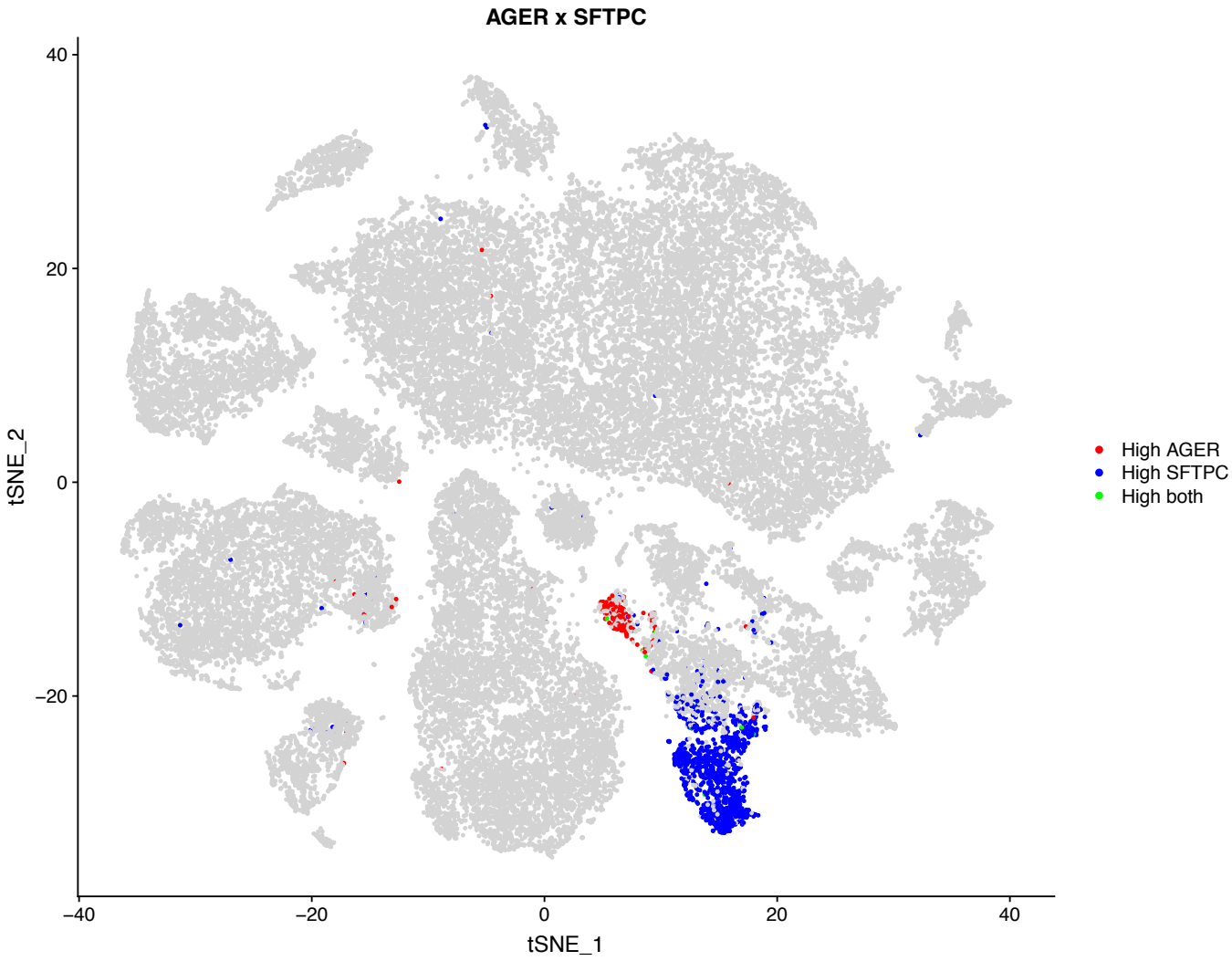


Figure S17. Violin plots of marker genes expressed from scRNA-seq of combined IPF and normal lungs in epithelial cell subclusters

Figure S18.Markers of AT1 and AT2 cells show distinct expression. Expression of high levels of AT1 marker AGER and AT2 marker SFTPC are larger confined to specific cell subsets with only very few cells expressing high levels of both. These cells may represent doublets or rare bipolar cells.



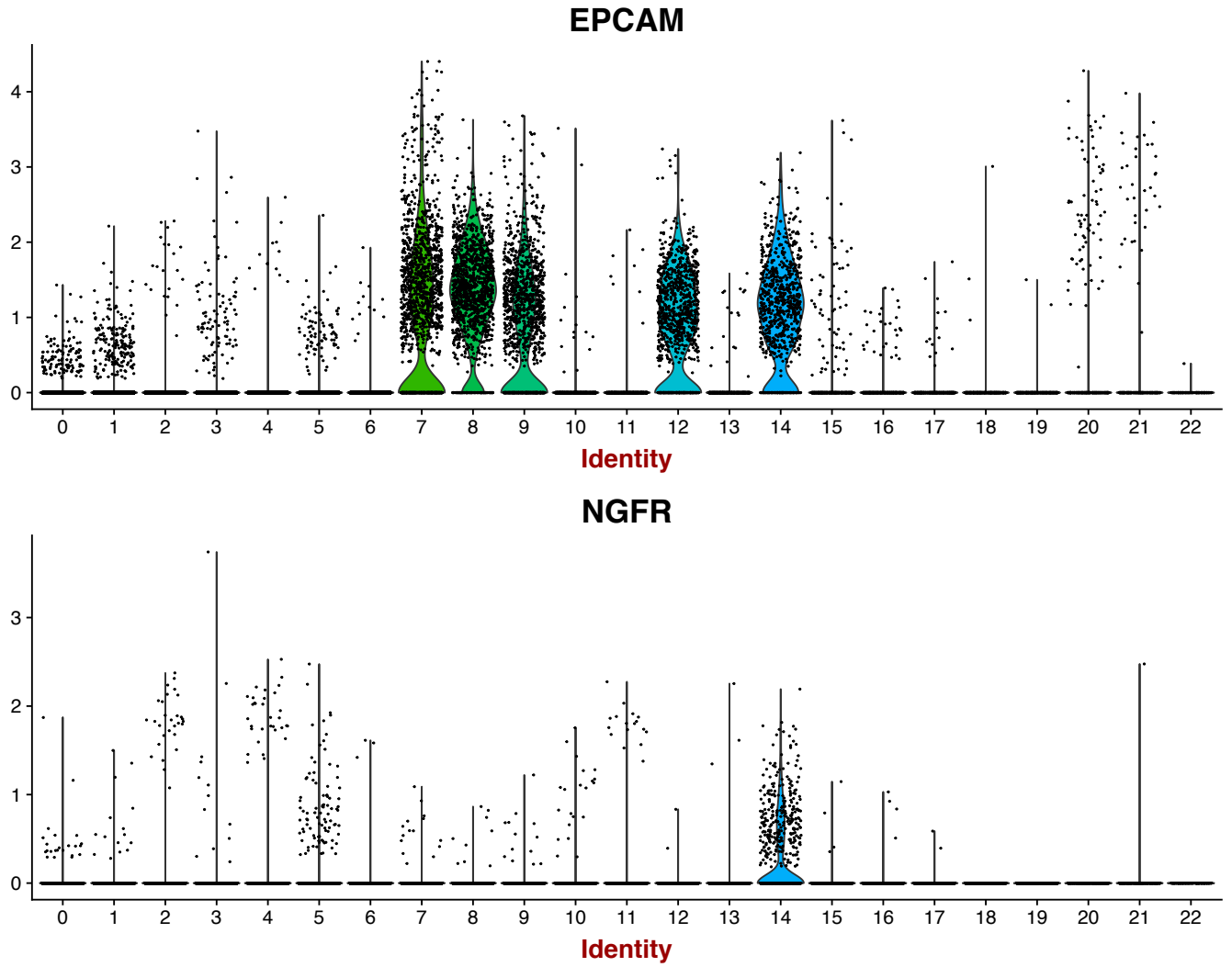
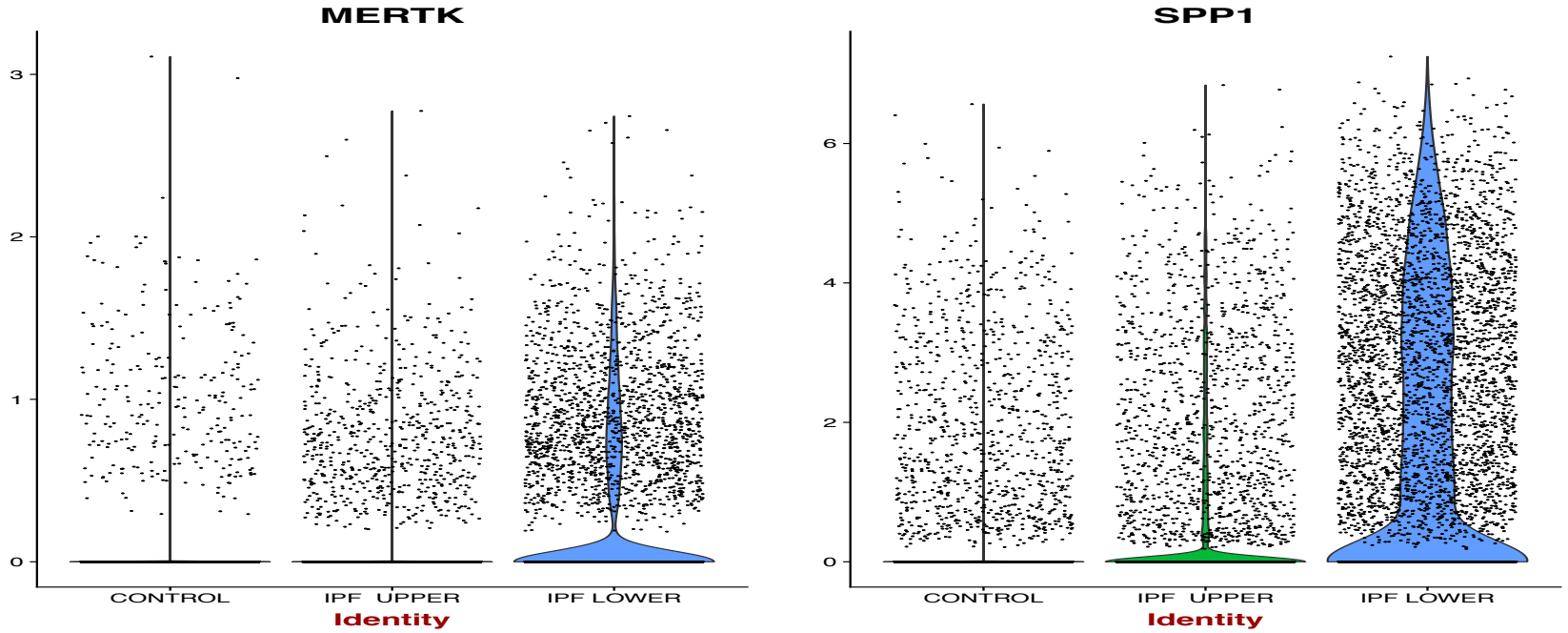


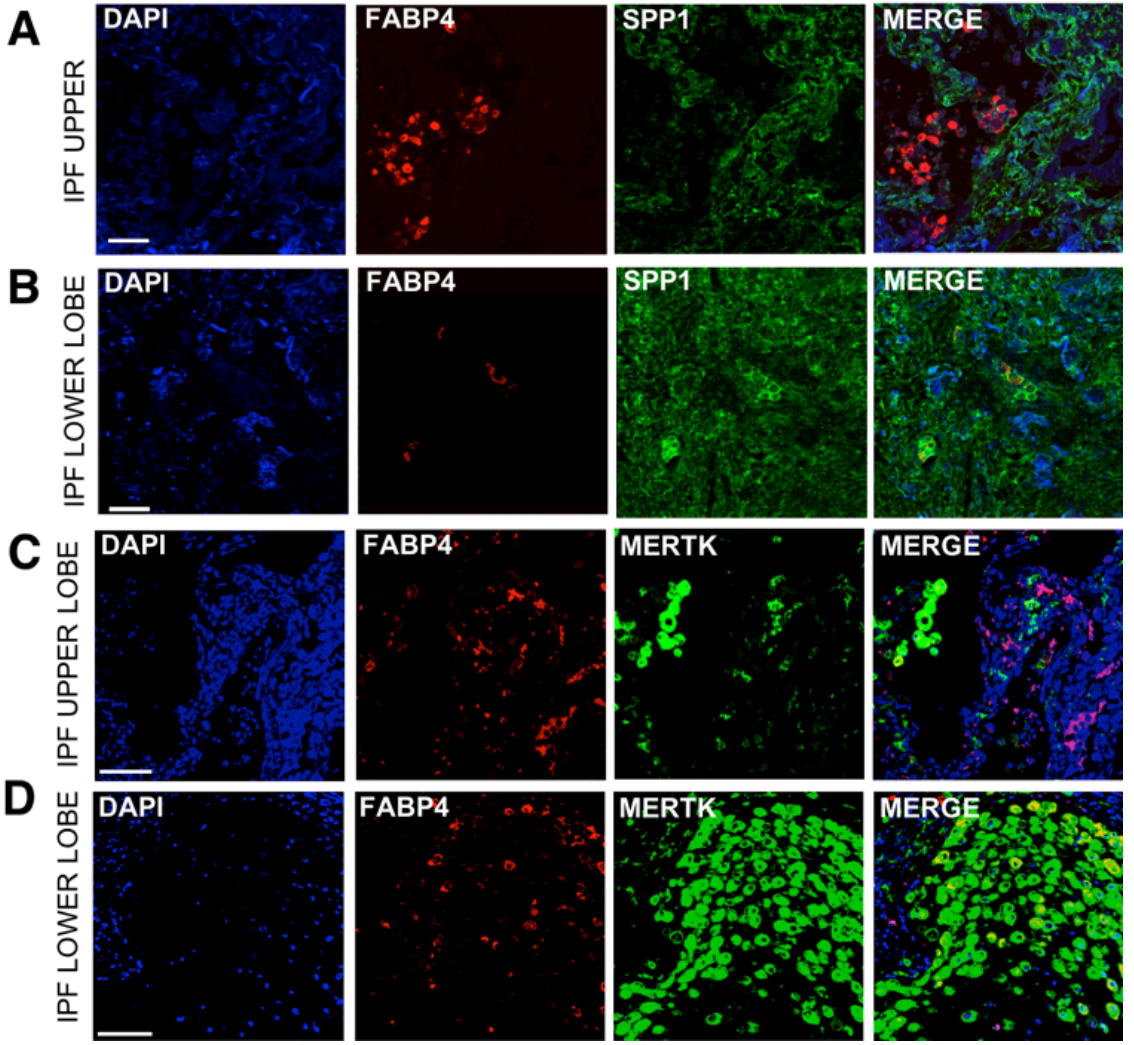
Figure S19.EPCAM and NGFR as markers of epithelial cells. EPCAM is expressed among all epithelial cell types, including, goblet (cluster 9), club and AT1 (cluster 7), ciliated (cluster 8), basal (cluster 14), and AT2 (cluster 12) while NGFR expression is elevated in basal cells (cluster 14).



MERTK gene expression				SPP1 gene expression			
Comparison	Z score	P-value	adjusted P-value	Comparison	Z score	P-value	adjusted P-value
CONTROL - IPF UPPER	-18.37804898	9.85E-76	9.85E-76	CONTROL - IPF UPPER	-19.91341385	1.56E-88	1.56E-88
CONTROL - IPF LOWER	-45.57615762	0	0	CONTROL - IPF LOWER	-67.75375612	0	0
IPF UPPER - IPF LOWER	-21.81872933	7.70E-106	1.16E-105	IPF UPPER - IPF LOWER	-39.18994918	0	0

Figure S20: MERTK and SPP1 gene expression is highly statistically significantly upregulated in IPF, comparing either upper or lower lobes with healthy controls or comparing IPF lower lobes with upper lobes

Figure S21: IF staining of idiopathic pulmonary fibrosis in upper and lower lung tissues. (a) Double IF staining of IPF upper lobe major lung macrophage population SPP1 (green) co-stained with FABP4 (red). (b) Double IF staining of IPF lower lobe major lung macrophage population SPP1 (green) co-stained with FABP4 (red). (c) Double IF staining of IPF upper lobe major lung macrophage population MERTK (green) co-stained with FABP4 (red). (d) Double IF staining in IPF lower lobe of major lung macrophage population MERTK (green) co-stained with FABP4 (red) MERTK is notably expanded in lower lobe as compared to upper lobe. For all panels, nuclei are counterstained with DAPI (blue). Scale bar = 100 µm. IF, immunofluorescence. IPF, idiopathic pulmonary fibrosis.



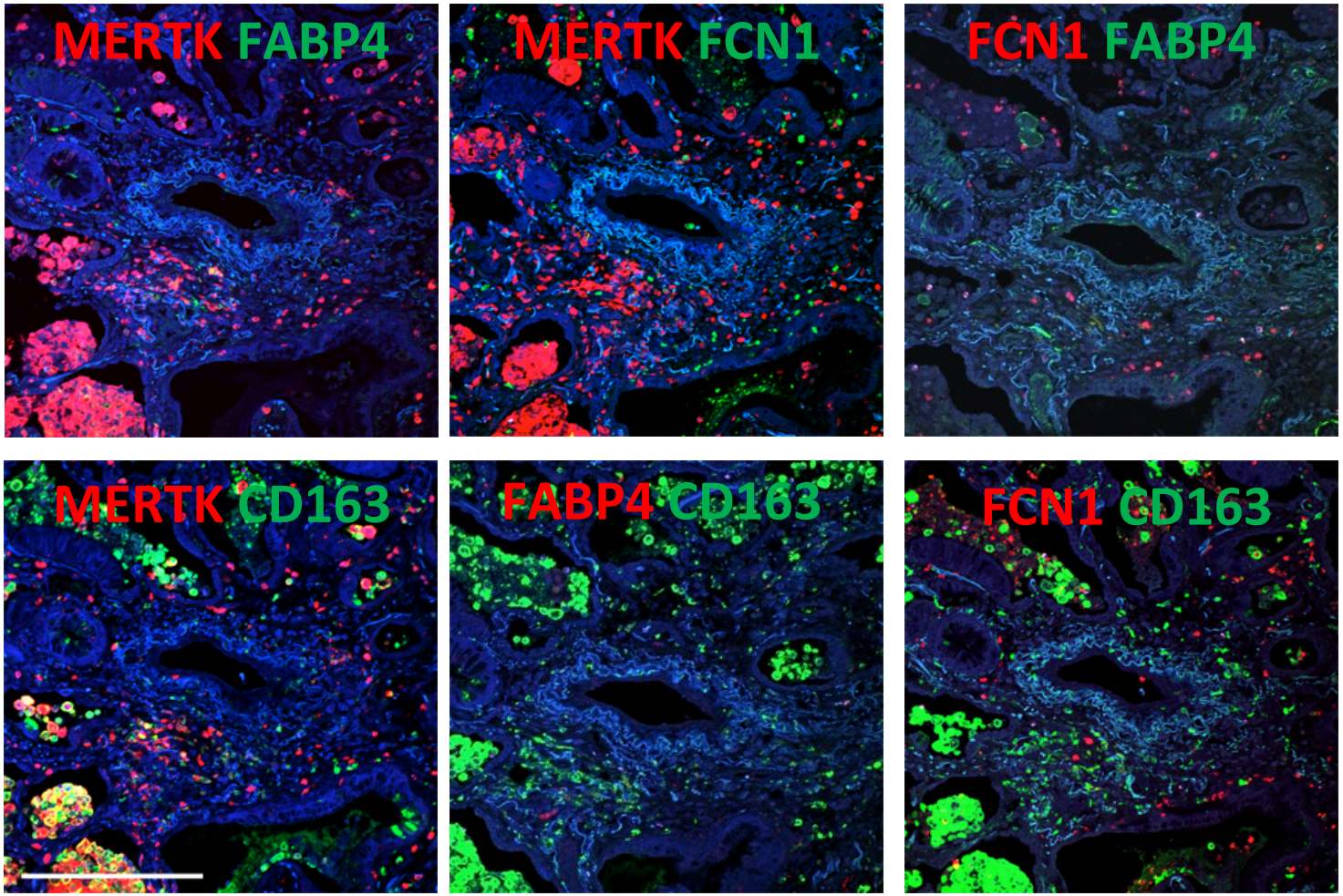


Figure S22: IF staining of serial sections of idiopathic pulmonary fibrosis lower lobe lung tissues, staining with combinations of MERTK, FABP4, FCN1 and CD163 as indicated. For all panels, nuclei are counterstained with DAPI (blue). Scale bar = 500 µm. IF, Immunofluorescence.

Figure S22: Merged and breakout micrographs of IF staining of serial sections of idiopathic pulmonary fibrosis lower lobe lung tissues, staining with combinations of FABP4 x MERTK; FCN1 x MERTK; and FABP4 x FCN1, as indicated. For all panels, nuclei are counterstained with DAPI (blue). Scale bar = 500 µm.

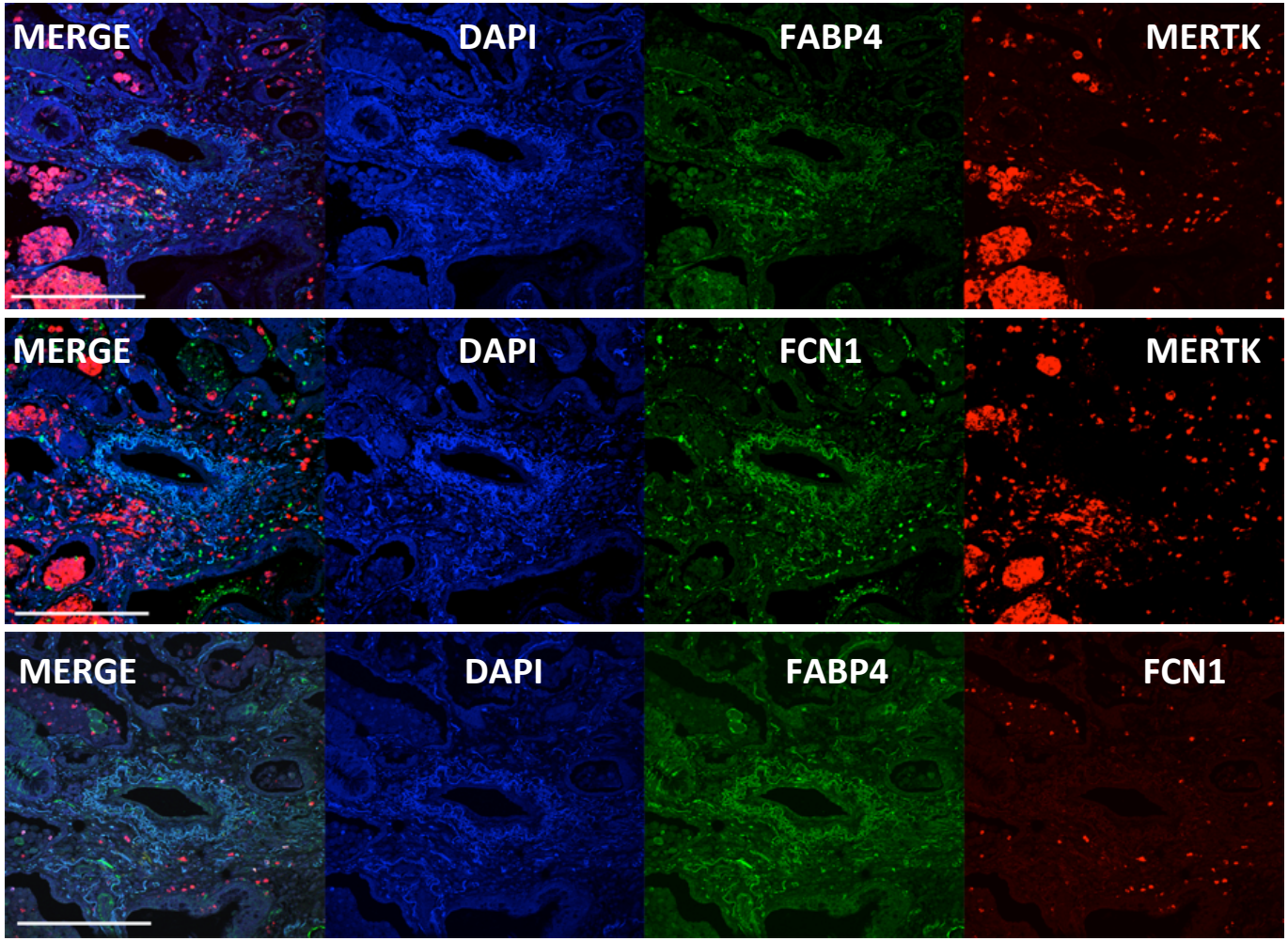


Figure S22: Merged and breakout micrographs of IF staining of serial sections of idiopathic pulmonary fibrosis lower lobe lung tissues, staining with combinations of MERTK x CD163; FABP4 x CD163; and FCN1 x CD163, as indicated. For all panels, nuclei are counterstained with DAPI (blue). Scale bar = 500 µm.

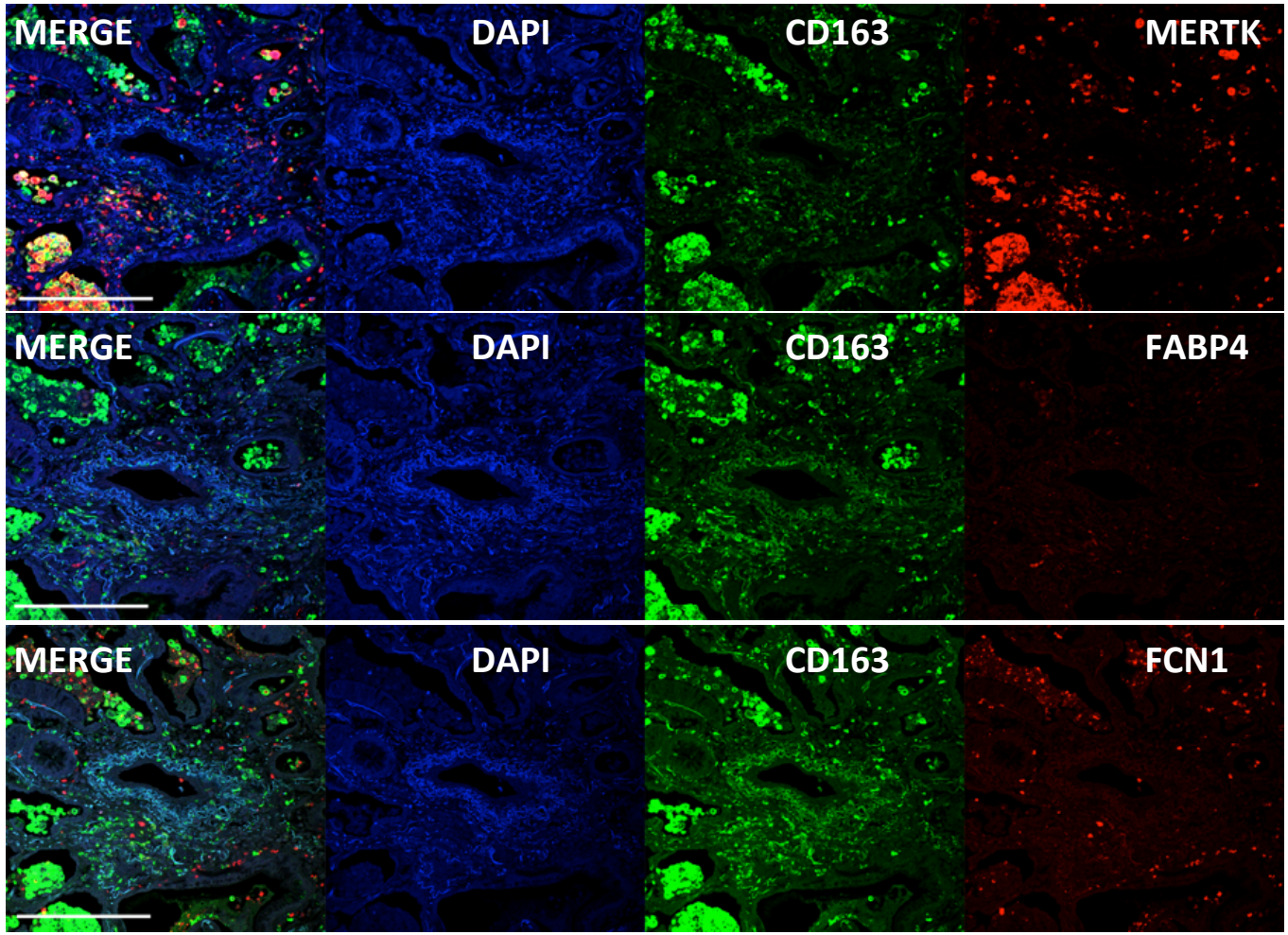
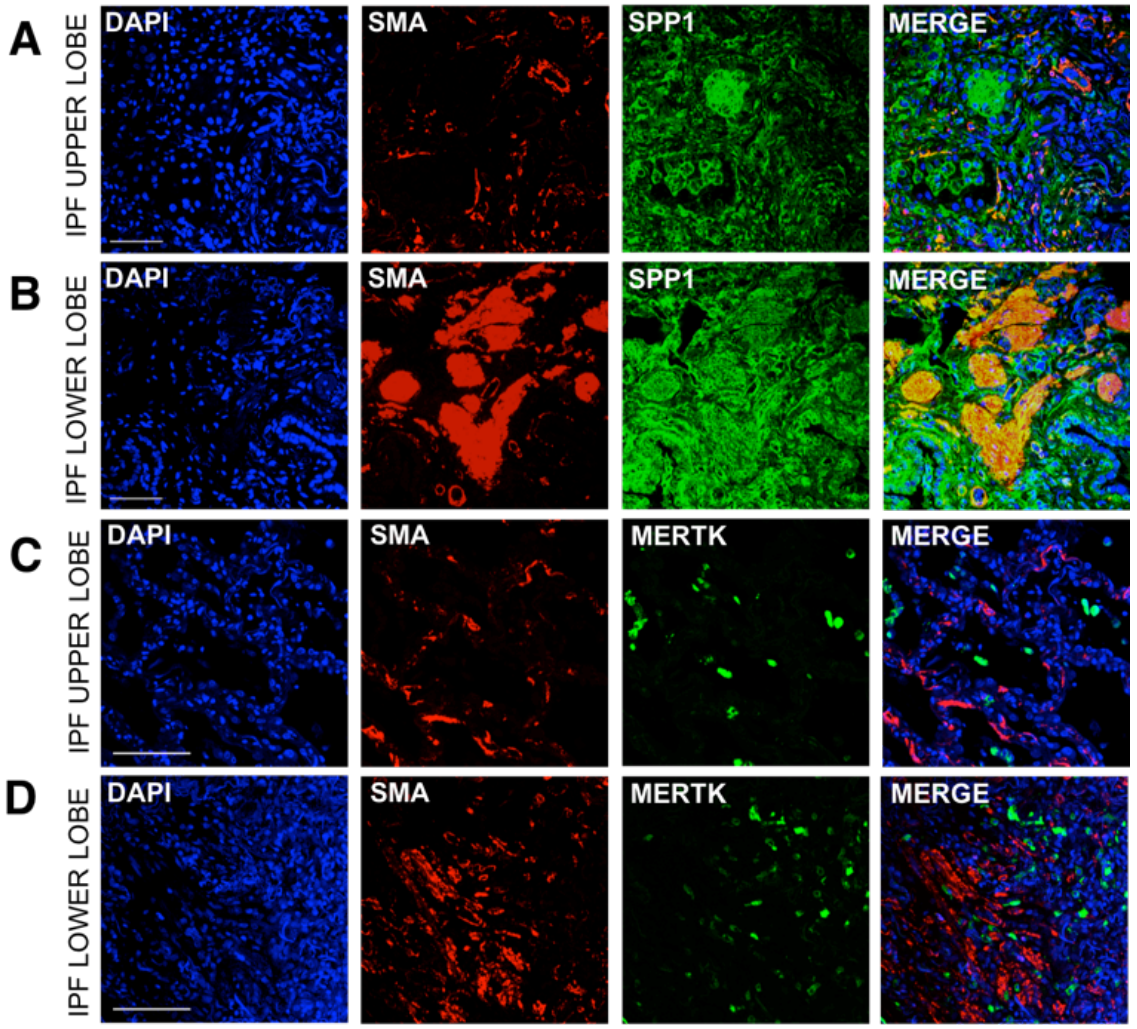


Figure S23: IF staining of SMA in both upper and lower lung tissues of idiopathic pulmonary fibrosis. (a) Double IF staining of IPF upper lobe major lung macrophage population SPP1 (green) costained with SMA (red). (b) Double IF staining of IPF lower lobe major lung macrophage population SPP1 (green) co-stained with SMA (red) dense regions of SMA indicate fibroblastic foci. (c) Double IF staining of IPF upper lobe major lung macrophage population MERTK (green) co-stained with SMA (red). (d) Double IF staining in IPF lower lobe of major lung macrophage population MERTK (green) co-stained with SMA (red) For all panels, nuclei are counterstained with DAPI (blue). Scale bar = 100 µm. IF, immunofluorescence. IPF, idiopathic pulmonary fibrosis. SMA, smooth muscle actin.



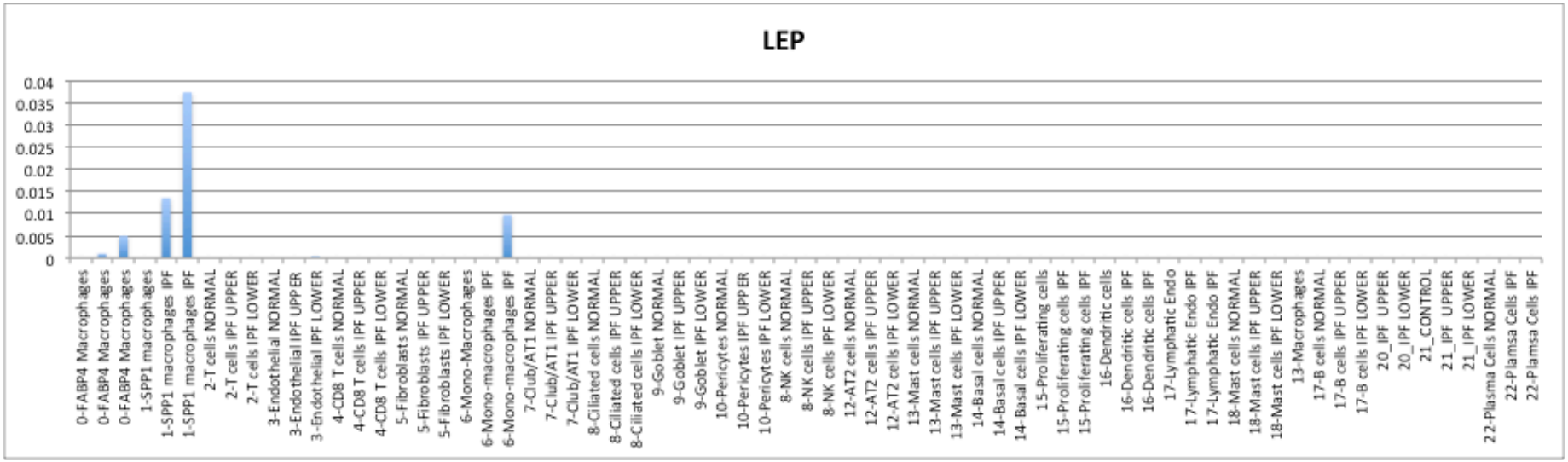
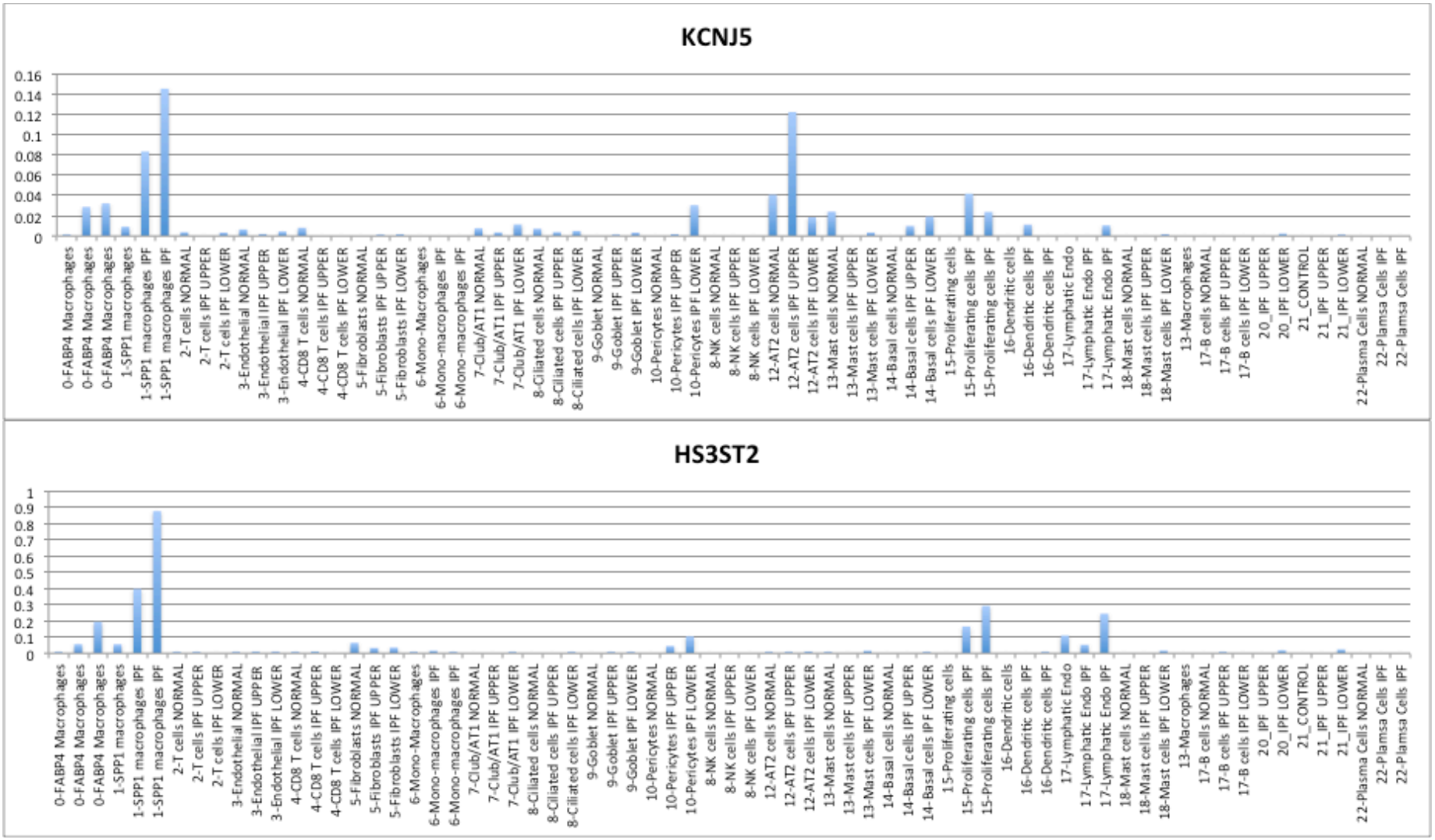


Figure S24. Genes selectively upregulated in lower lobes of IPF compared to healthy control lungs in SPP1^{hi} macrophages: LEP (nd), KCNJ5 (15.76-fold), HS3ST2 (15.58-fold), SPP1 (7.56-fold), SIGLEC15 (7.43-fold), ATP6V0D2 (7.12-fold), LGMN (6.07-fold), MERTK (4.96-fold), MMP9 (3.81-fold), and CD209 (1.86-fold).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0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0-FABP4 Macrophages
0-FABP4 Macrophages
0-FABP4 Macrophages
1-SPP1 macrophages
1-SPP1 macrophages IPF
1-SPP1 macrophages IPF
2-T cells NORMAL
2-T cells IPF UPPER
2-T cells IPF LOWER
3-Endothelial NORMAL
3-Endothelial IPF UPPER
3-Endothelial IPF LOWER
4-CD8 T cells NORMAL
4-CD8 T cells IPF UPPER
4-CD8 T cells IPF LOWER
5-Fibroblasts NORMAL
5-Fibroblasts IPF UPPER
5-Fibroblasts IPF LOWER
6-Mono-Macrophages
6-Mono-macrophages IPF
6-Mono-macrophages IPF
7-Club/AT1 NORMAL
7-Club/AT1 IPF UPPER
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8-Ciliated cells IPF UPPER
8-Ciliated cells IPF LOWER
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13-Mast cells IPF UPPER
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14-Basal cells IPF LOWER
15-Proliferating cells
15-Proliferating cells IPF
15-Proliferating cells IPF
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16-Dendritic cells IPF
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20_IPF UPPER
20_IPF LOWER
21_CONTROL
21_IPF UPPER
21_IPF LOWER
22-Plasma Cells NORMAL
22-Plamsa Cells IPF
22-Plamsa Cells IPF
HS3ST2
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0-FABP4 Macrophages
0-FABP4 Macrophages
0-FABP4 Macrophages
1-SPP1 macrophages
1-SPP1 macrophages IPF
1-SPP1 macrophages IPF
2-T cells NORMAL
2-T cells IPF UPPER
2-T cells IPF LOWER
3-Endothelial NORMAL
3-Endothelial IPF UPPER
3-Endothelial IPF LOWER
4-CD8 T cells NORMAL
4-CD8 T cells IPF UPPER
4-CD8 T cells IPF LOWER
5-Fibroblasts NORMAL
5-Fibroblasts IPF UPPER
5-Fibroblasts IPF LOWER
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6-Mono-macrophages IPF
6-Mono-macrophages IPF
7-Club/AT1 NORMAL
7-Club/AT1 IPF UPPER
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8-Ciliated cells IPF UPPER
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16-Dendritic cells IPF
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17-Lymphatic Endo IPF
17-Lymphatic Endo IPF
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18-Mast cells IPF UPPER
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13-Macrophages
17-B cells NORMAL
17-B cells IPF UPPER
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20_IPF UPPER
20_IPF LOWER
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21_IPF LOWER
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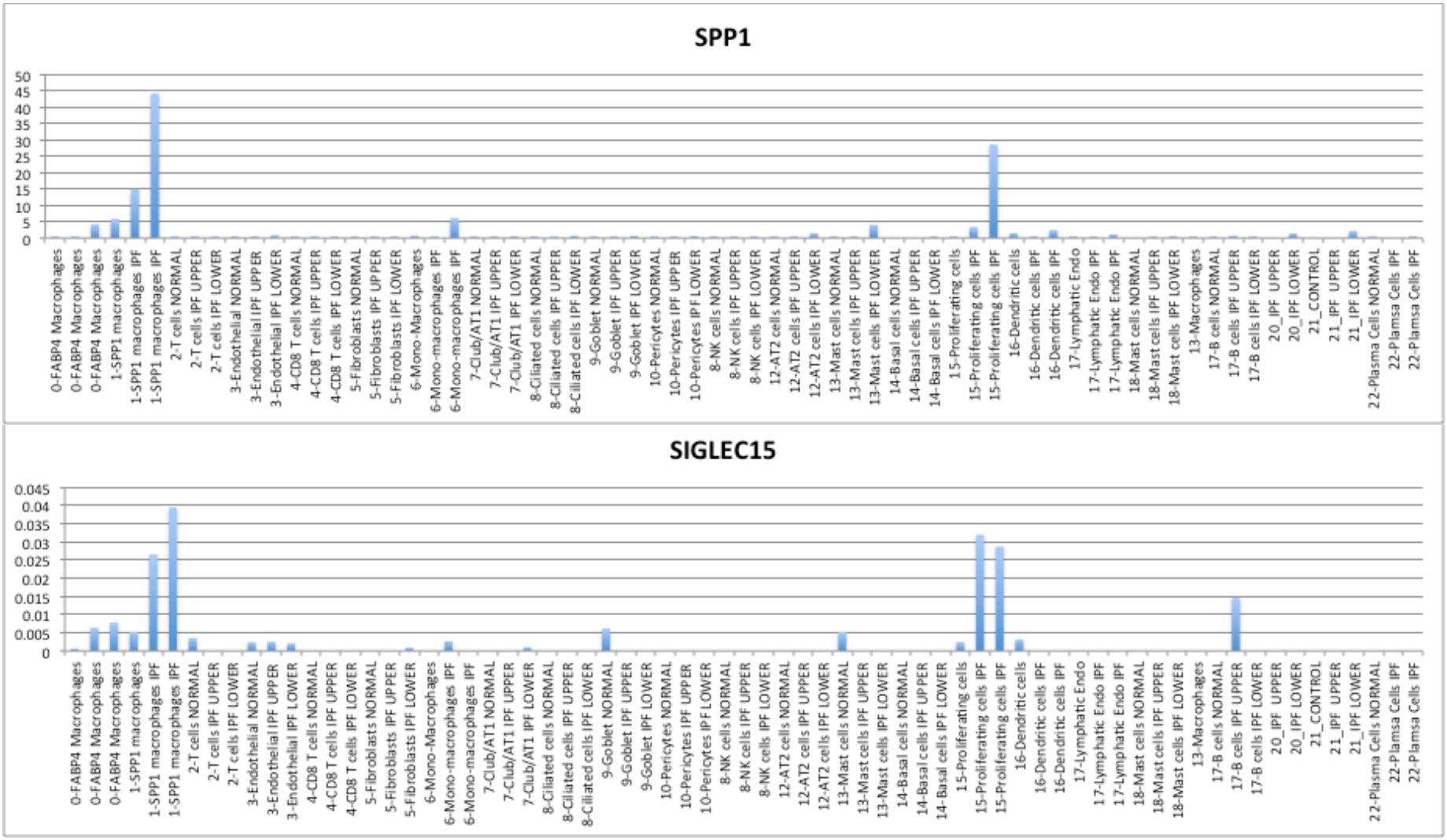
22-Plamsa Cells IPF
22-Plamsa Cells IPF


SPP1
50
45
40
35
30
25
20
15
10
5
0
0-FABP4 Macrophages
0-FABP4 Macrophages
0-FABP4 Macrophages
1-SPP1 macrophages
1-SPP1 macrophages IPF
1-SPP1 macrophages IPF
2-T cells NORMAL
2-T cells IPF UPPER
2-T cells IPF LOWER
3-Endothelial NORMAL
3-Endothelial IPF UPPER
3-Endothelial IPF LOWER
4-CD8 T cells NORMAL
4-CD8 T cells IPF UPPER
4-CD8 T cells IPF LOWER
5-Fibroblasts NORMAL
5-Fibroblasts IPF UPPER
5-Fibroblasts IPF LOWER
6-Mono-Macrophages
6-Mono-macrophages IPF
6-Mono-macrophages IPF
7-Club/AT1 NORMAL
7-Club/AT1 IPF UPPER
7-Club/AT1 IPF LOWER
8-Ciliated cells NORMAL
8-Ciliated cells IPF UPPER
8-Ciliated cells IPF LOWER
9-Goblet NORMAL
9-Goblet IPF UPPER
9-Goblet IPF LOWER
10-Pericytes NORMAL
10-Pericytes IPF UPPER
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8-NK cells NORMAL
8-NK cells IPF UPPER
8-NK cells IPF LOWER
12-AT2 cells NORMAL
12-AT2 cells IPF UPPER
12-AT2 cells IPF LOWER
13-Mast cells NORMAL
13-Mast cells IPF UPPER
13-Mast cells IPF LOWER
14-Basal cells NORMAL
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14-Basal cells IPF LOWER
15-Proliferating cells
15-Proliferating cells IPF
15-Proliferating cells IPF
16-Dendritic cells
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17-Lymphatic Endo
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18-Mast cells NORMAL
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18-Mast cells IPF LOWER
13-Macrophages
17-B cells NORMAL
17-B cells IPF UPPER
17-B cells IPF LOWER
20_IPF UPPER
20_IPF LOWER
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21_IPF UPPER
21_IPF LOWER
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22-Plamsa Cells IPF
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SIGLEC15
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0-FABP4 Macrophages
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4-CD8 T cells IPF LOWER
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6-Mono-Macrophages
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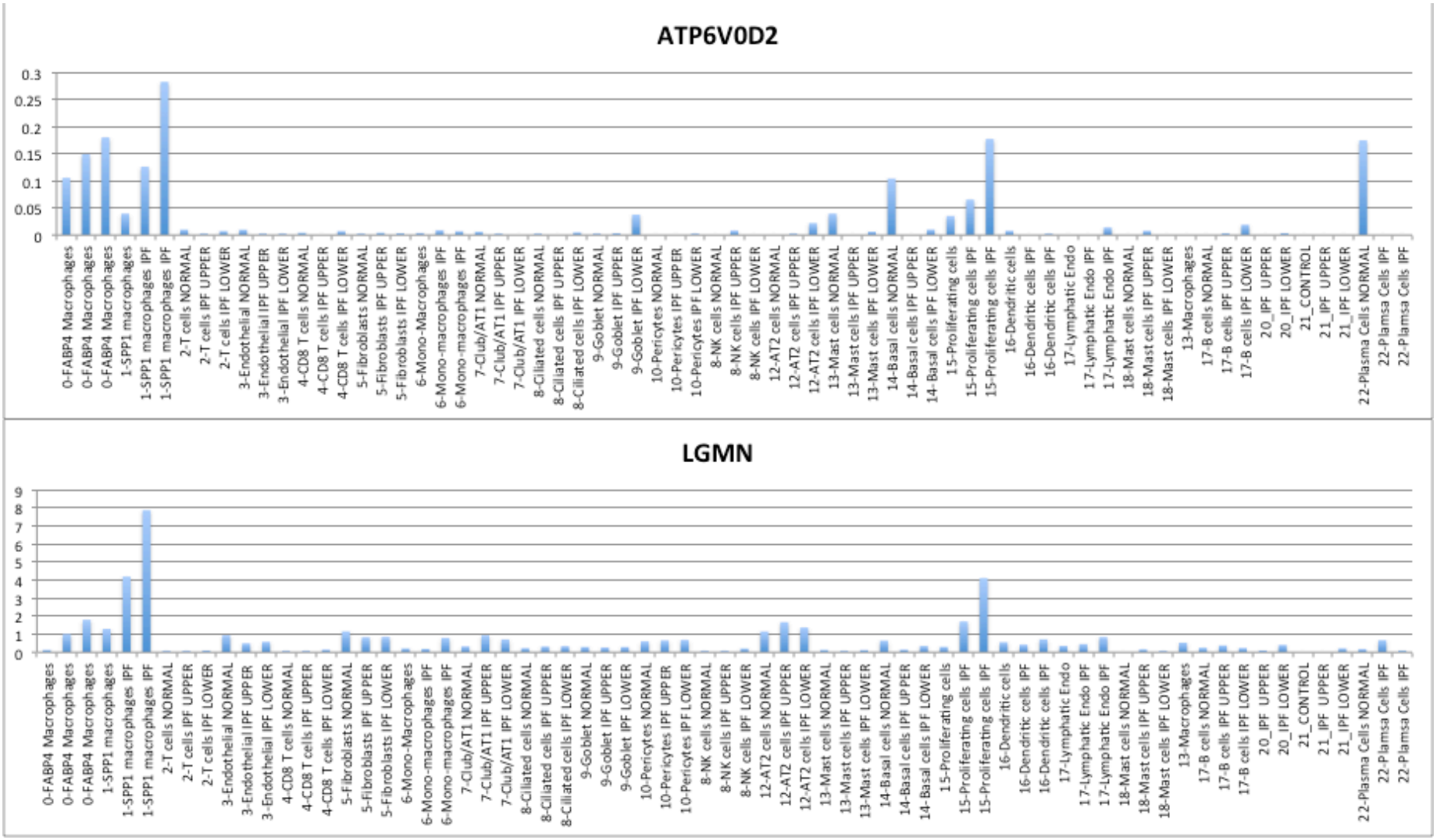
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4-CD8 T cells IPF LOWER
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5-Fibroblasts IPF LOWER
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7-Club/AT1 IPF LOWER
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17-Lymphatic Endo IPF
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18-Mast cells IPF LOWER
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22-Plamsa Cells IPF
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8-Ciliated cells IPF LOWER
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9-Goblet IPF LOWER
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10-Pericytes IPF UPPER
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8-NK cells IPF UPPER
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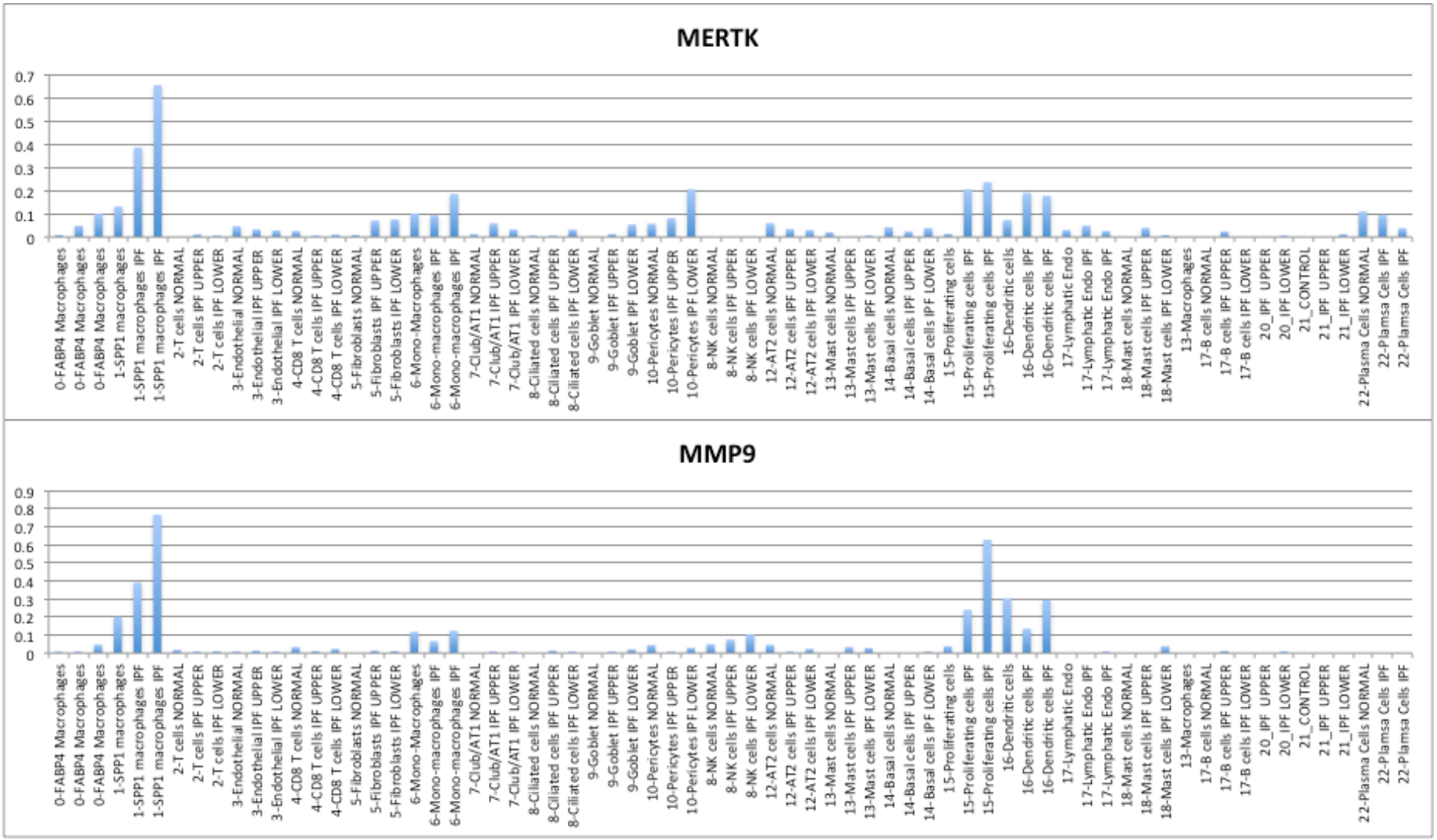
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1-SPP1 macrophages IPF
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2-T cells IPF UPPER
2-T cells IPF LOWER
3-Endothelial NORMAL
3-Endothelial IPF UPPER
3-Endothelial IPF LOWER
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4-CD8 T cells IPF UPPER
4-CD8 T cells IPF LOWER
5-Fibroblasts NORMAL
5-Fibroblasts IPF UPPER
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7-Club/AT1 IPF UPPER
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8-Ciliated cells IPF UPPER
8-Ciliated cells IPF LOWER
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9-Goblet IPF UPPER
9-Goblet IPF LOWER
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17-Lymphatic Endo IPF
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18-Mast cells IPF LOWER
13-Macrophages
17-B cells NORMAL
17-B cells IPF UPPER
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21_IPF UPPER
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22-Plamsa Cells IPF
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0.7
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0.4
0.3
0.2
0.1
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0-FABP4 Macrophages
0-FABP4 Macrophages
1-SPP1 macrophages
1-SPP1 macrophages IPF
1-SPP1 macrophages IPF
2-T cells NORMAL
2-T cells IPF UPPER
2-T cells IPF LOWER
3-Endothelial NORMAL
3-Endothelial IPF UPPER
3-Endothelial IPF LOWER
4-CD8 T cells NORMAL
4-CD8 T cells IPF UPPER
4-CD8 T cells IPF LOWER
5-Fibroblasts NORMAL
5-Fibroblasts IPF UPPER
5-Fibroblasts IPF LOWER
6-Mono-Macrophages
6-Mono-macrophages IPF
6-Mono-macrophages IPF
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7-Club/AT1 IPF UPPER
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14-Basal cells IPF LOWER
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17-Lymphatic Endo IPF
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17-B cells IPF LOWER
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21_IPF UPPER
21_IPF LOWER
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22-Plamsa Cells IPF
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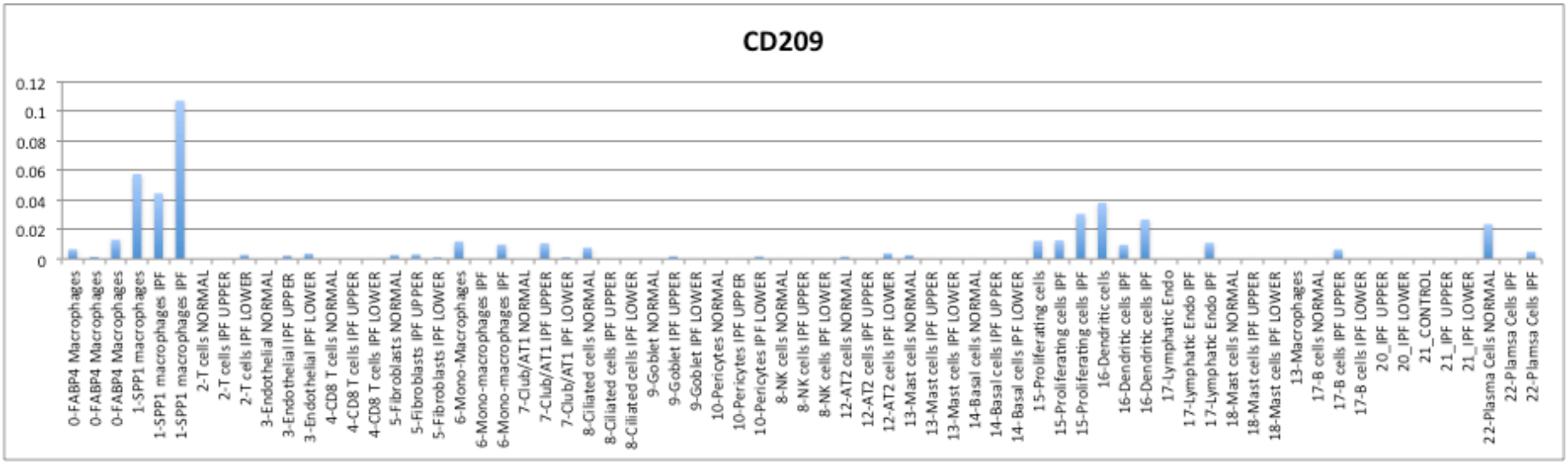
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0-FABP4 Macrophages
1-SPP1 macrophages
1-SPP1 macrophages IPF
1-SPP1 macrophages IPF
2-T cells NORMAL
2-T cells IPF UPPER
2-T cells IPF LOWER
3-Endothelial NORMAL
3-Endothelial IPF UPPER
3-Endothelial IPF LOWER
4-CD8 T cells NORMAL
4-CD8 T cells IPF UPPER
4-CD8 T cells IPF LOWER
5-Fibroblasts NORMAL
5-Fibroblasts IPF UPPER
5-Fibroblasts IPF LOWER
6-Mono-Macrophages
6-Mono-macrophages IPF
6-Mono-macrophages IPF
7-Club/AT1 NORMAL
7-Club/AT1 IPF UPPER
7-Club/AT1 IPF LOWER
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8-Ciliated cells IPF UPPER
8-Ciliated cells IPF LOWER
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9-Goblet IPF UPPER
9-Goblet IPF LOWER
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10-Pericytes IPF UPPER
10-Pericytes IPF LOWER
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8-NK cells IPF UPPER
8-NK cells IPF LOWER
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12-AT2 cells IPF UPPER
12-AT2 cells IPF LOWER
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13-Mast cells IPF UPPER
13-Mast cells IPF LOWER
14-Basal cells NORMAL
14-Basal cells IPF UPPER
14-Basal cells IPF LOWER
15-Proliferating cells
15-Proliferating cells IPF
15-Proliferating cells IPF
16-Dendritic cells
16-Dendritic cells IPF
16-Dendritic cells IPF
17-Lymphatic Endo
17-Lymphatic Endo IPF
17-Lymphatic Endo IPF
18-Mast cells NORMAL
18-Mast cells IPF UPPER
18-Mast cells IPF LOWER
13-Macrophages
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17-B cells IPF UPPER
17-B cells IPF LOWER
20_IPF UPPER
20_IPF LOWER
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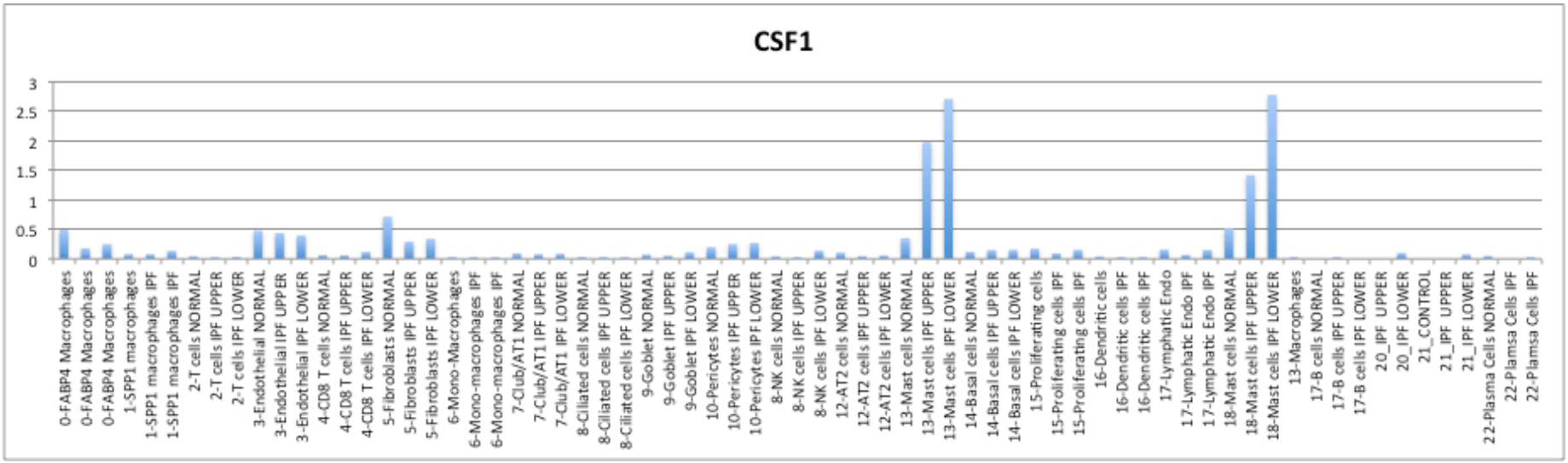
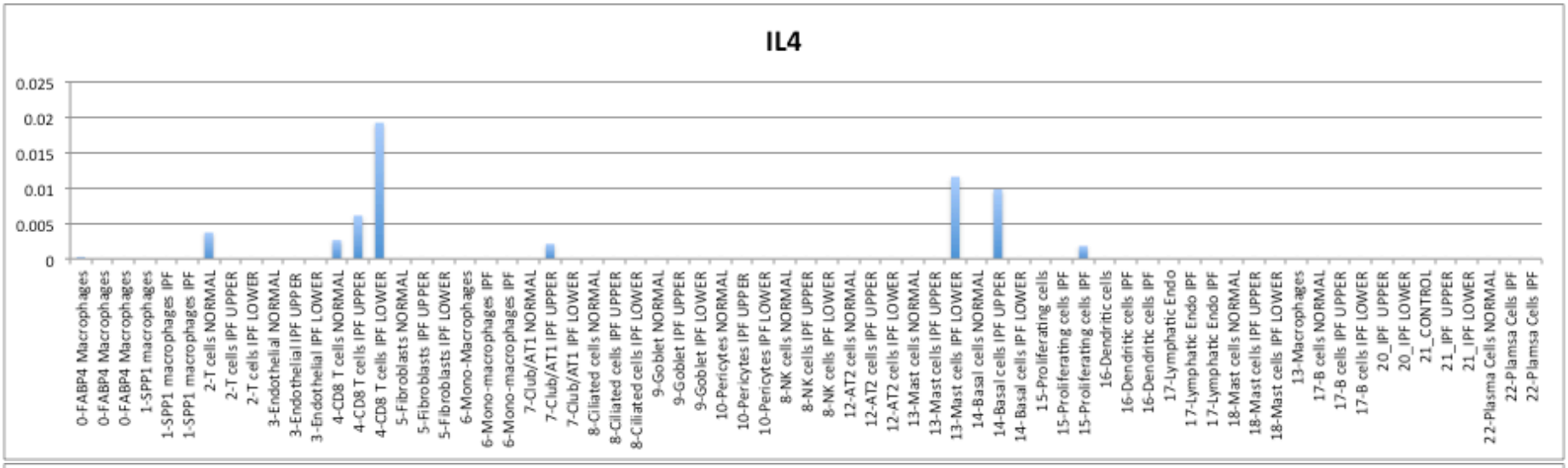


Figure S25. IL4, IL13 and CSF1 expression by cell subsets.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1-SPP1 macrophages IPF
1-SPP1 macrophages IPF
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2-T cells IPF UPPER
2-T cells IPF LOWER
3-Endothelial NORMAL
3-Endothelial IPF UPPER
3-Endothelial IPF LOWER
4-CD8 T cells NORMAL
4-CD8 T cells IPF UPPER
4-CD8 T cells IPF LOWER
5-Fibroblasts NORMAL
5-Fibroblasts IPF UPPER
5-Fibroblasts IPF LOWER
6-Mono-Macrophages
6-Mono-macrophages IPF
6-Mono-macrophages IPF
7-Club/AT1 NORMAL
7-Club/AT1 IPF UPPER
7-Club/AT1 IPF LOWER
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8-Ciliated cells IPF LOWER
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9-Goblet IPF UPPER
9-Goblet IPF LOWER
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10-Pericytes IPF UPPER
10-Pericytes IPF LOWER
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8-NK cells IPF UPPER
8-NK cells IPF LOWER
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12-AT2 cells IPF UPPER
12-AT2 cells IPF LOWER
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14-Basal cells NORMAL
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15-Proliferating cells
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16-Dendritic cells
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17-Lymphatic Endo
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17-Lymphatic Endo IPF
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18-Mast cells IPF UPPER
18-Mast cells IPF LOWER
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17-B cells IPF UPPER
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20_IPF UPPER
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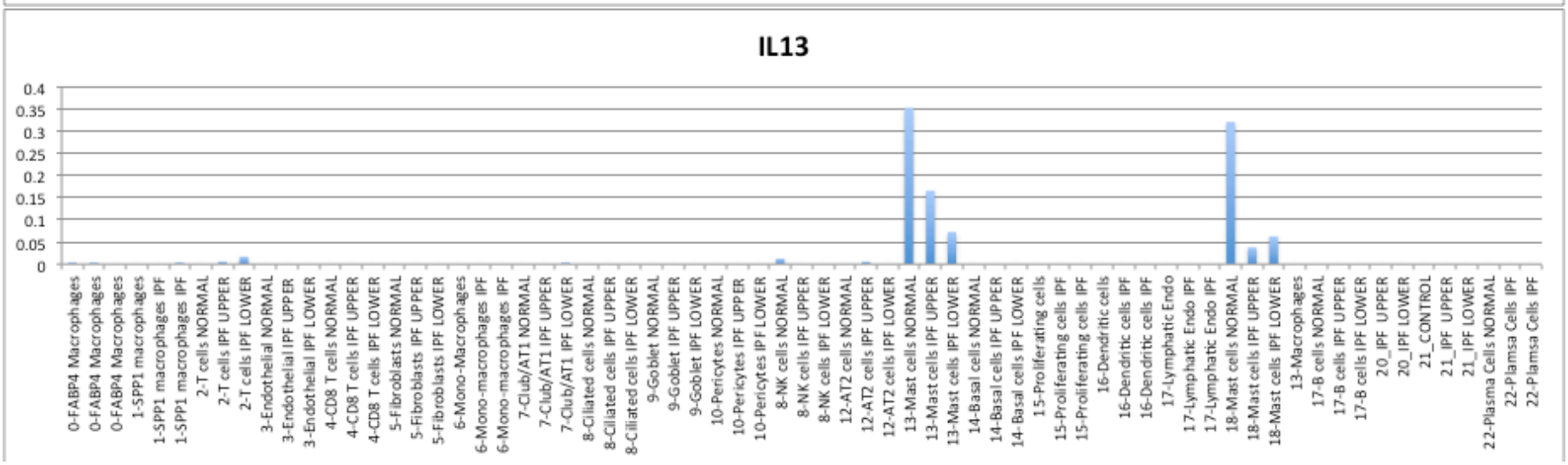
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0-FABP4 Macrophages
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1-SPP1 macrophages IPF
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2-T cells NORMAL
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5-Fibroblasts NORMAL
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7-Club/AT1 IPF LOWER
8-Ciliated cells NORMAL
8-Ciliated cells IPF UPPER
8-Ciliated cells IPF LOWER
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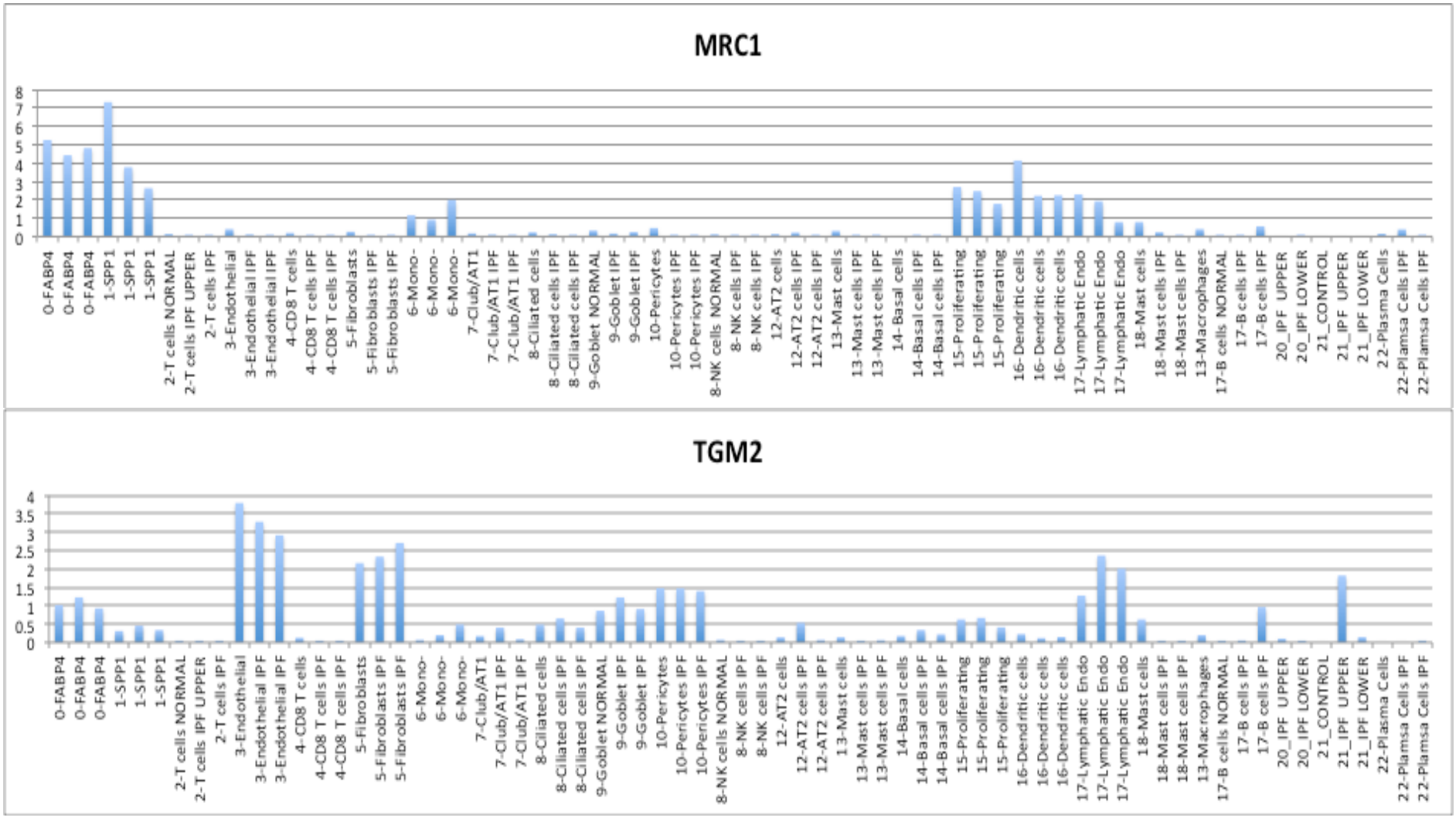
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1-SPP1
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3-Endothelial IPF
3-Endothelial IPF
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4-CD8 T cells IPF
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5-Fibroblasts IPF
5-Fibroblasts IPF
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6-Mono-
6-Mono-
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7-Club/AT1 IPF
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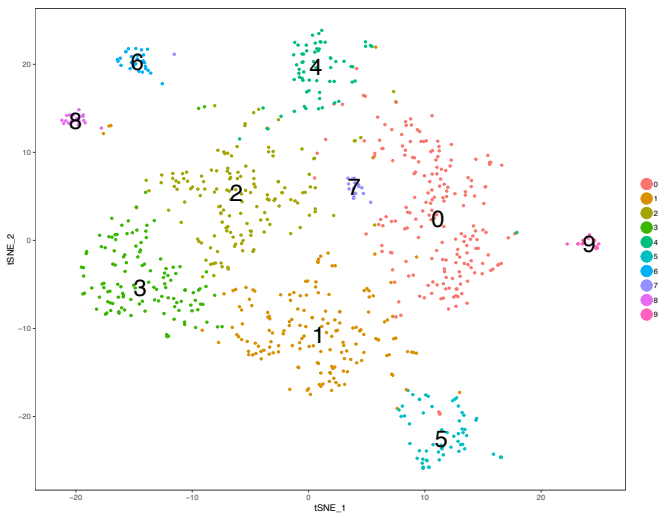
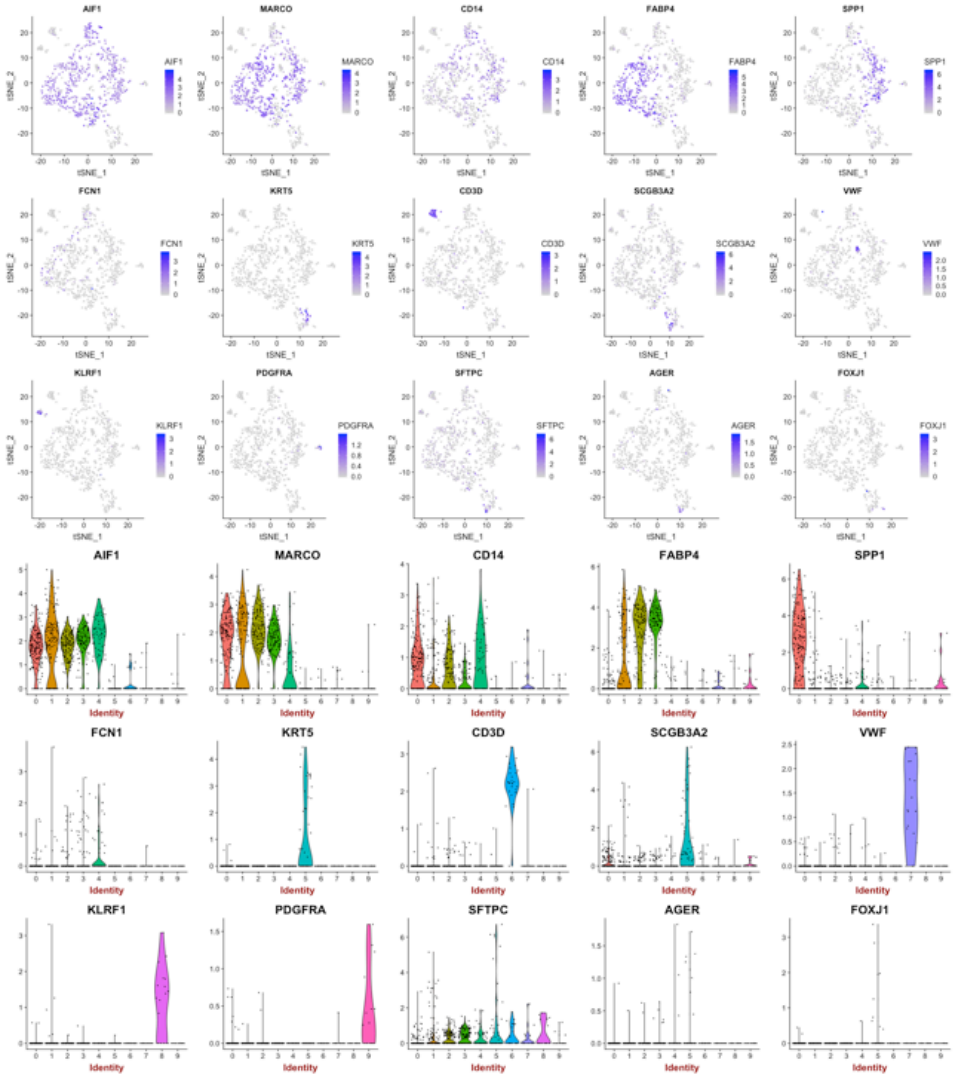
17-B cells IPF
20_IPF UPPER
20_IPF LOWER
21_CONTROL
21_IPF UPPER
21_IPF LOWER
22-Plasma Cells
22-Plamsa Cells IPF
22-Plamsa Cells IPF
TGM2
0-FABP4
0-FABP4
0-FABP4
1-SPP1
1-SPP1
1-SPP1
2-T cells NORMAL
2-T cells IPF UPPER
2-T cells IPF
3-Endothelial
3-Endothelial IPF
3-Endothelial IPF
4-CD8 T cells
4-CD8 T cells IPF
4-CD8 T cells IPF
5-Fibroblasts
5-Fibroblasts IPF
5-Fibroblasts IPF
6-Mono-
6-Mono-
6-Mono-
7-Club/AT1
7-Club/AT1 IPF
7-Club/AT1 IPF
8-Ciliated cells
8-Ciliated cells IPF
8-Ciliated cells IPF
9-Goblet NORMAL
9-Goblet IPF
9-Goblet IPF
10-Pericytes
10-Pericytes IPF
10-Pericytes IPF
8-NK cells NORMAL
8-NK cells IPF
8-NK cells IPF
12-AT2 cells
12-AT2 cells IPF
12-AT2 cells IPF
13-Mast cells
13-Mast cells IPF
13-Mast cells IPF
14-Basal cells
14-Basal cells IPF
14-Basal cells IPF
15-Proliferating
15-Proliferating
15-Proliferating
16-Dendritic cells
16-Dendritic cells
16-Dendritic cells
17-Lymphatic Endo
17-Lymphatic Endo
17-Lymphatic Endo
18-Mast cells
18-Mast cells IPF
18-Mast cells IPF
13-Macrophages
17-B cells NORMAL
17-B cells IPF
17-B cells IPF
20_IPF UPPER
20_IPF LOWER
21_CONTROL
21_IPF UPPER
21_IPF LOWER
22-Plasma Cells
22-Plamsa Cells IPF
22-Plamsa Cells IPF



A



B

C

Figure S26. T-SNE reclustering of proliferating cells panel A, from cluster 15, Figure 2A) include SPP1^{hi} (cluster 0), FABP4^{hi} (clusters 1 and 2) and FCN1^{hi} (subcluster 4), macrophages, basal (KRT5) and club cells (SCGB3A, cluster 5), T cells (CD3D, cluster 6), endothelial cells (VWF, cluster 7), NK cells (KLRF1, cluster 8) and fibroblasts (PDGFRA, cluster 9; panels B and C). Further subclustering of proliferating epithelial cells shows rare proliferating AT2 cells (SFTPC, clusters 1 and2), AT1 cells (AGER, cluster 2) and ciliated cells (FOXJ1; panels D and E).

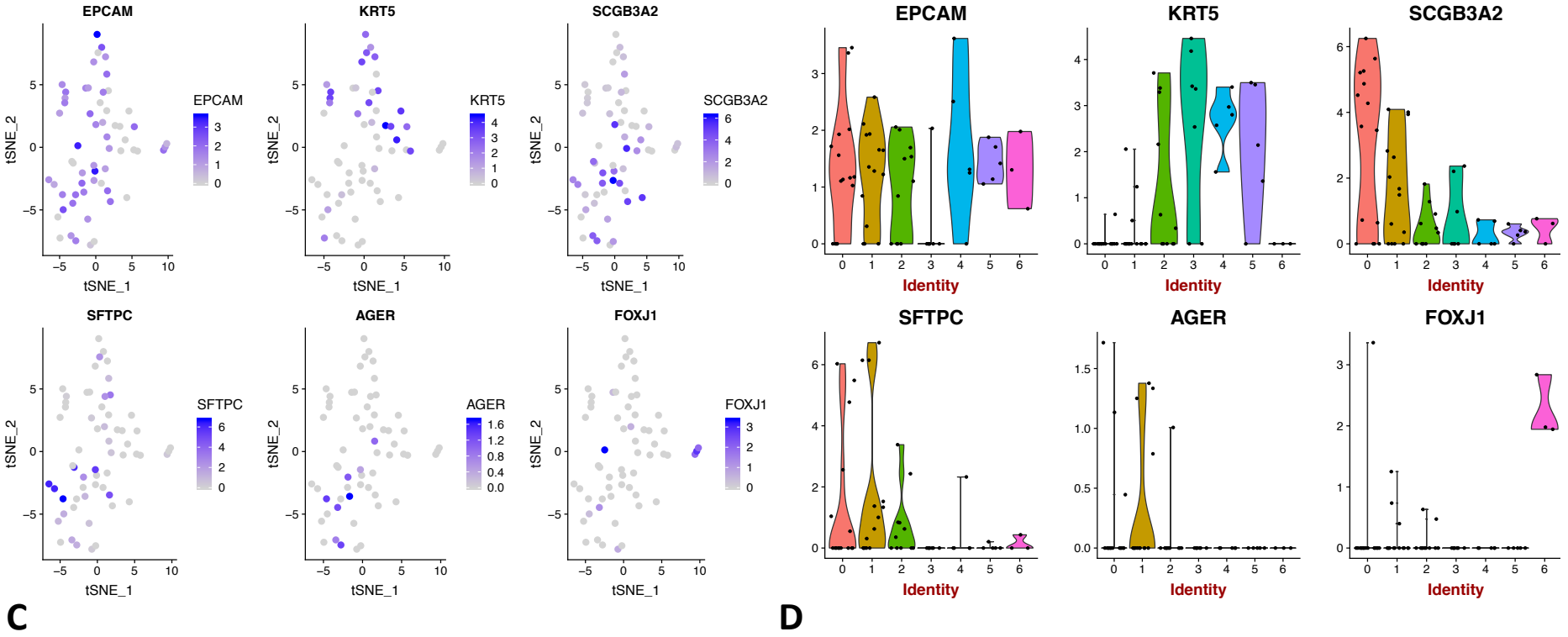


Figure S27. Reclustering of proliferating epithelial cells showed groups of proliferating basal cells (*KRT5*), club cells (*SCGBA2*), AT1 (*AGER*), AT2 (*SFTPC*), ciliated cells (*FOXJ1*).

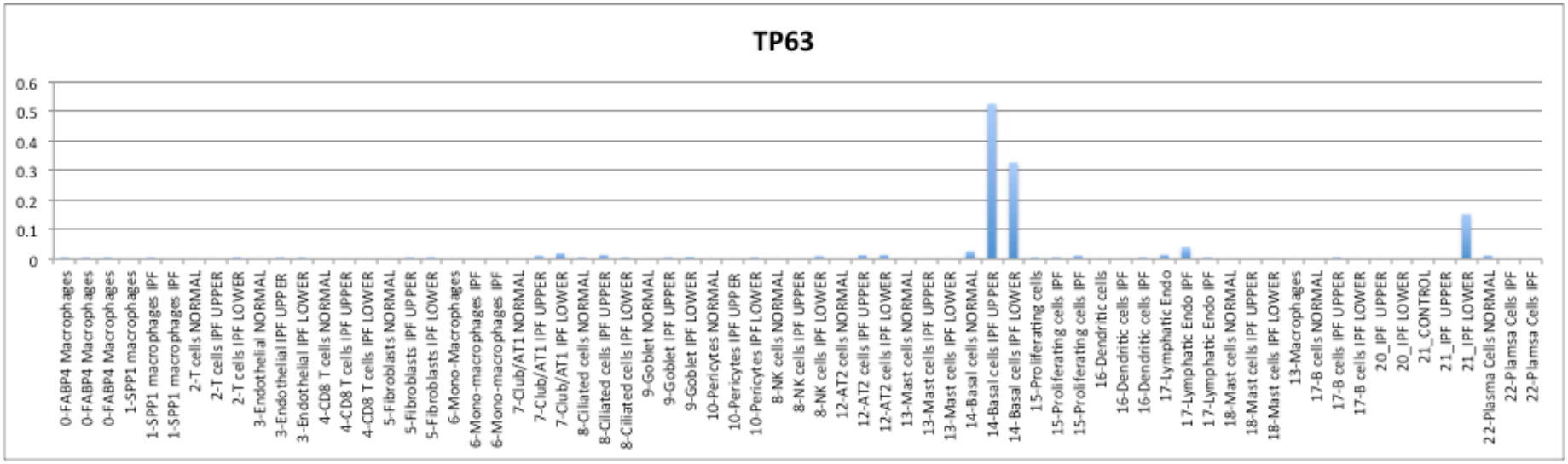
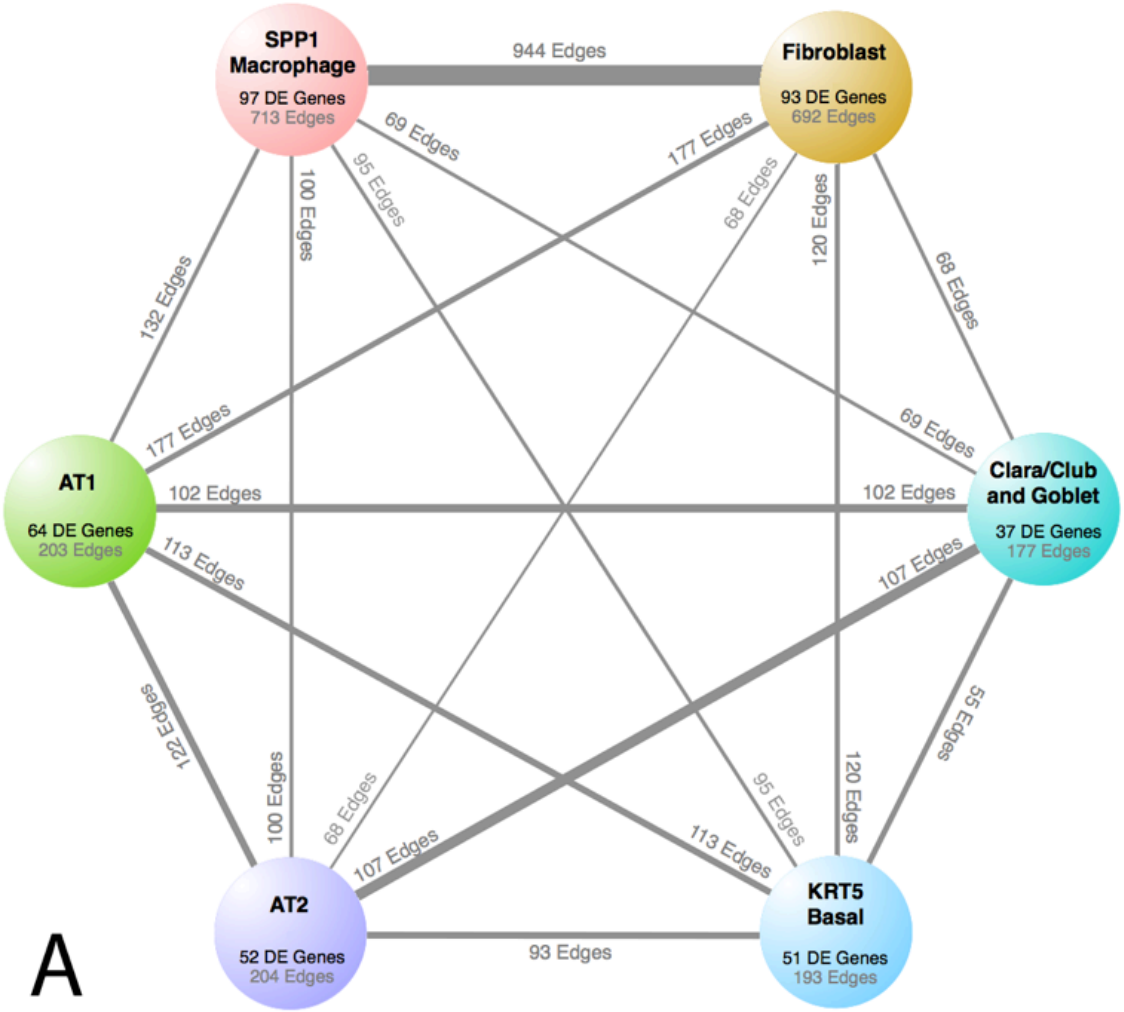


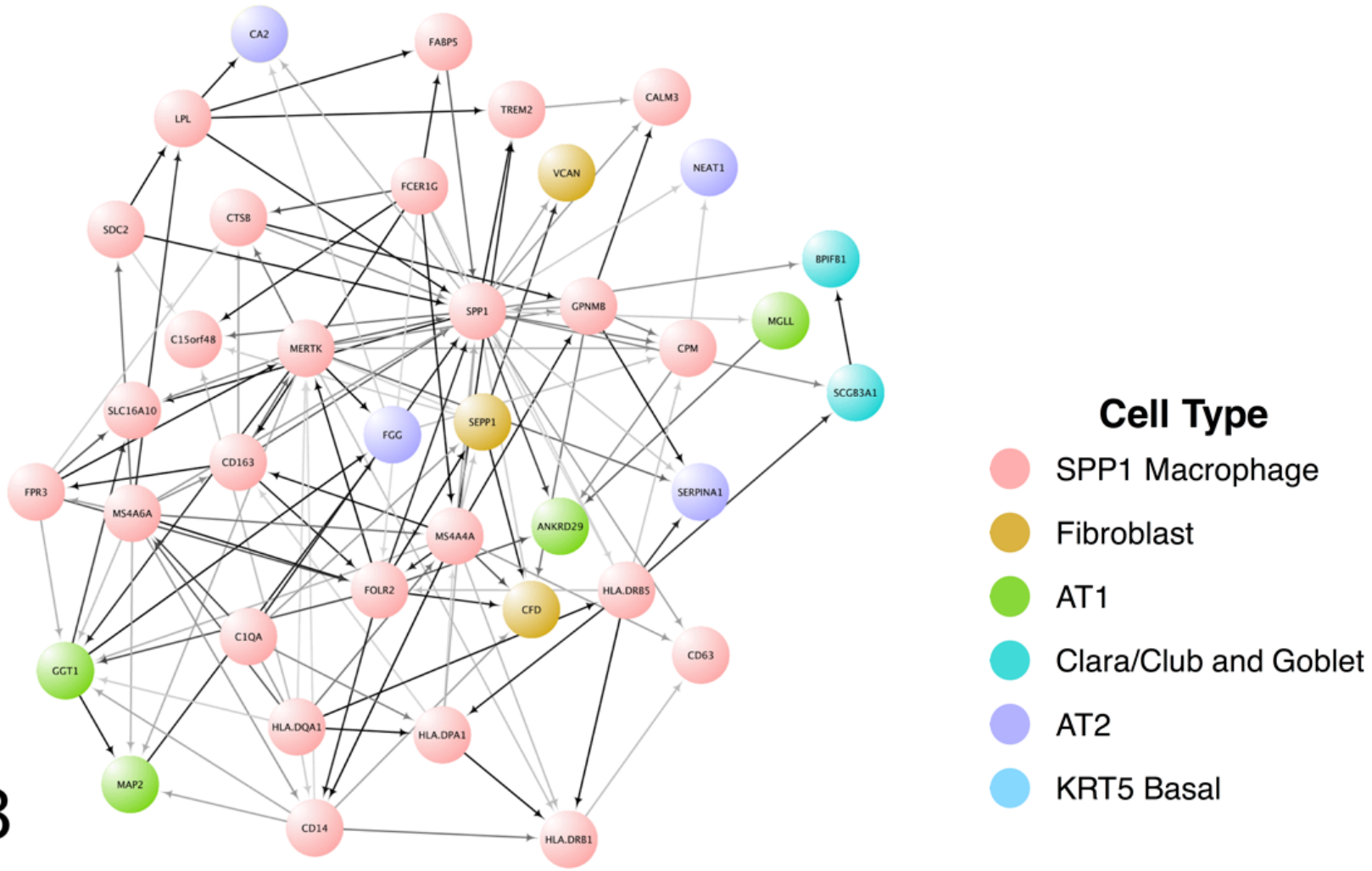
Figure S28. Basal cells in IPF lungs show highly upregulated expression of TP63

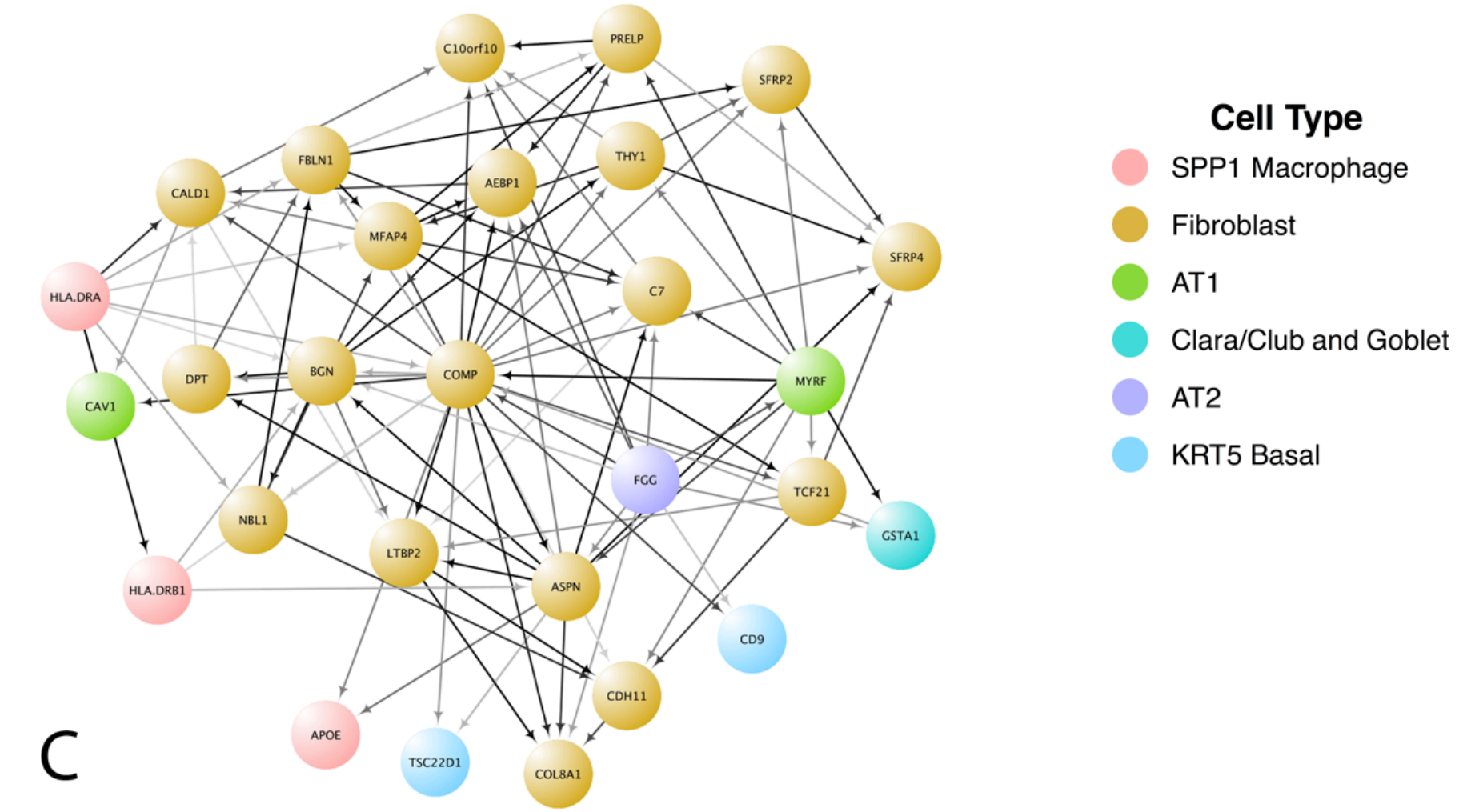
Figure S29. Causal network analysis of IPF and control lung gene expression. In summary (panel A) nodes represent the collection of genes that were differentially expressed in a given cell type. Each node is labeled with the number of differentially expressed (DE) genes that node represents as well as the number of edges among the genes represented by that node. Lines connecting nodes in this figure represent the set edges that connect pairs of genes that were differentially expressed in different cell types. These are labeled with the number of edges in the network that span the two cell types, and the line weights are proportional to the percentage of edges that appear in the network relative to the total number of possible edges. Subnetworks highlight the first neighbors of MERTK and SPP1 (panel B) and COMP (panel C). Node colors indicate the cell type in which in the gene is DE, and darker colored edges correspond to more stable connections.



Cell Type

- SPP1 Macrophage
- Fibroblast
- AT1
- Clara/Club and Goblet
- AT2
- KRT5 Basal


B
CA2
FABP5
LPL
TREM2
CALM3
VCAN
NEAT1
FCER1G
CTSB
SDC2
BPIFB1
SPP1
GPNMB
MGLL
C15orf48
MERTK
CPM
SCGB3A1
SLC16A10
FGG
SEPP1
CD163
FPR3
SERPINA1
MS4A6A
ANKRD29
MS4A4A
FOLR2
HLA.DRB5
CFD
C1QA
CD63
GGT1
HLA.DQA1
HLA.DPA1
MAP2
CD14
HLA.DRB1
Cell Type
SPP1 Macrophage
Fibroblast
AT1
Clara/Club and Goblet
AT2
KRT5 Basal


C10orf10
PRELP
SFRP2
FBLN1
THY1
CALD1
AEBP1
MFAP4
SFRP4
HLA.DRA
C7
DPT
BGN
COMP
MYRF
CAV1
FGG
TCF21
NBL1
GSTA1
LTBP2
HLA.DRB1
ASPN
CD9
CDH11
APOE
TSC22D1
COL8A1
C
Cell Type
SPP1 Macrophage
Fibroblast
AT1
Clara/Club and Goblet
AT2
KRT5 Basal