Supplementary Data

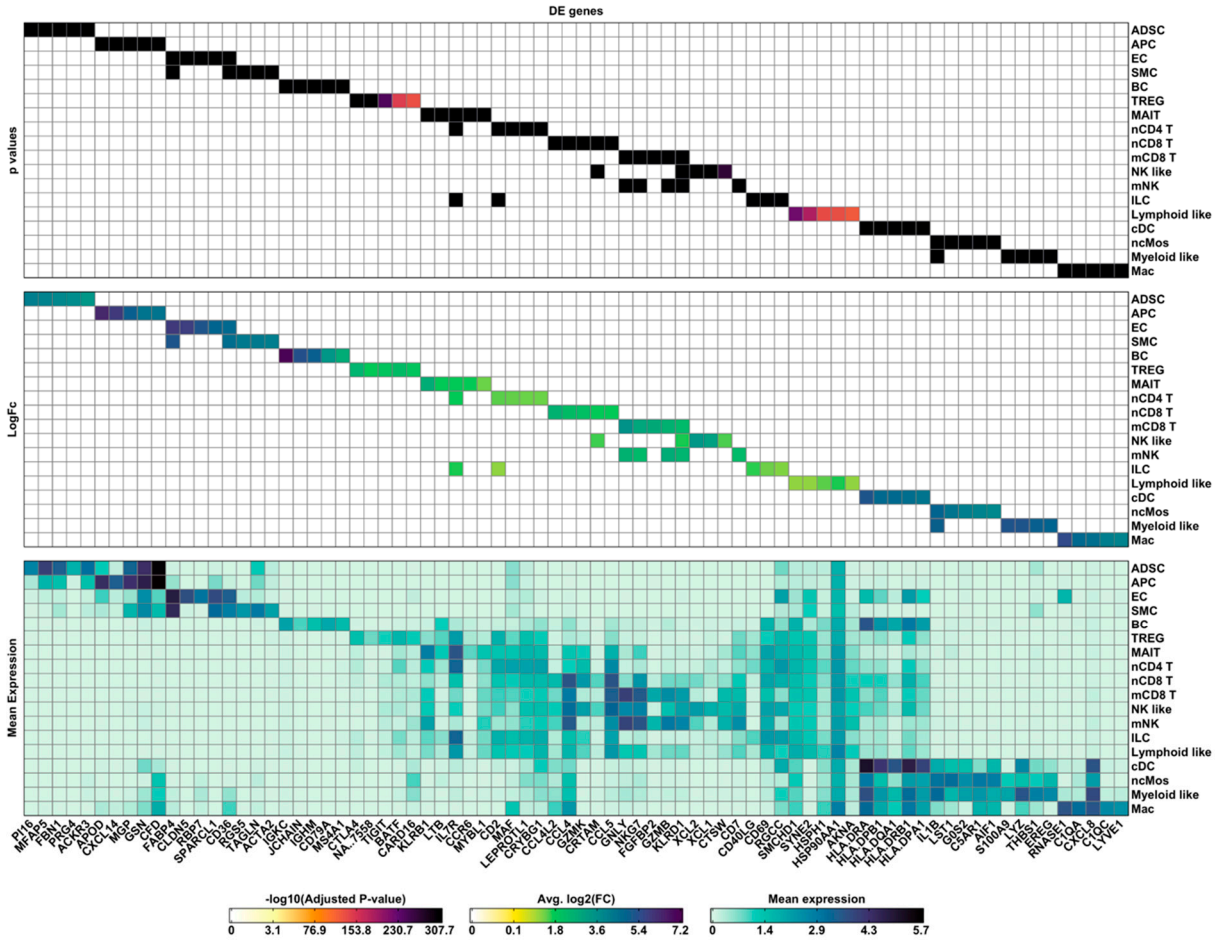


Figure S1. Differentially expressed genes (DEGs) support the clustering of the stromal vascular fraction (SVF). A three-section heatmap showing the top 5 marker genes for each cluster and their mean expression (*bottom*), the associated logFC value (*middle)* and the associated p-value (*top*). These DEGs support the clustering seen in Figure 1.

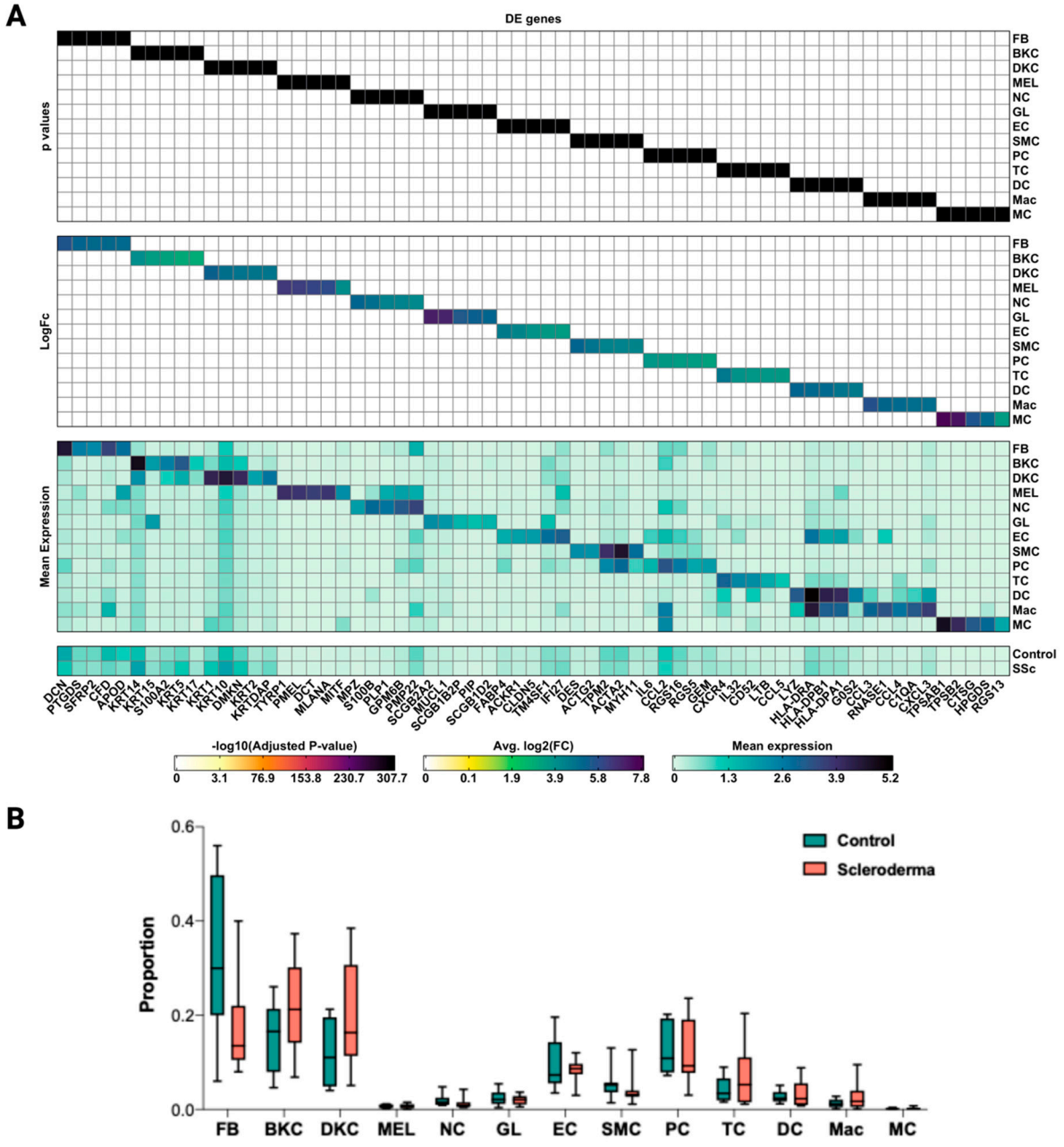


Figure S2. Differentially expressed genes (DEGs) support the clustering of control and scleroderma skin biopsies. (A) A three-section heatmap showing the top 5 marker genes for each cluster with their mean expression per cluster and compared between control and scleroderma (*bottom*), the associated logFC value (*middle)* and the associated p-value (*top*). These DEGs support the clustering seen in Figure 3. **(B)** Boxplots showing the proportion of cells derived from the skin of scleroderma (n = 12) and control (n = 10) for each cell type. * indicates significance ($p < 0.05$). Multiple unpaired t-tests were used for analysis.

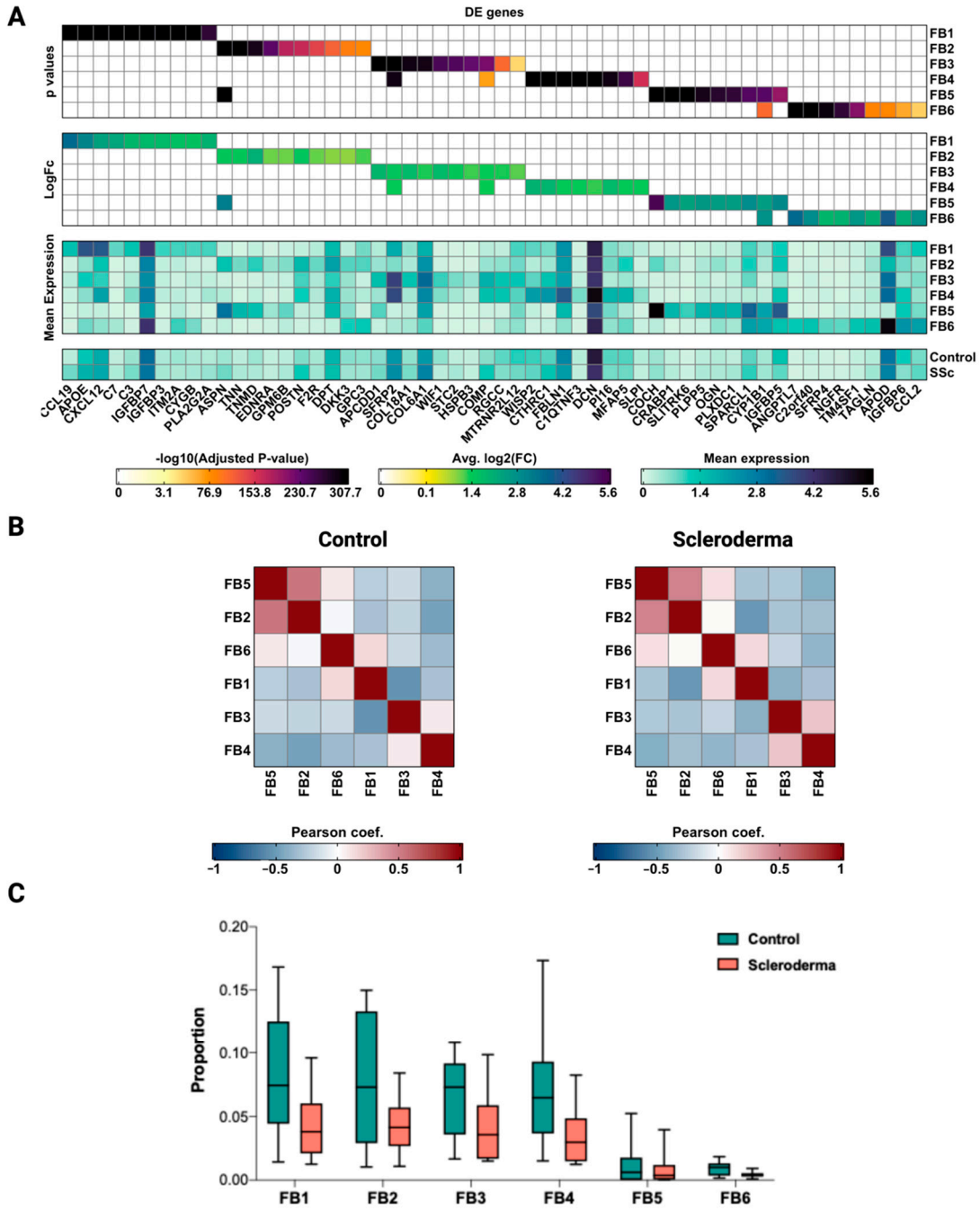


Figure S3. Marker genes of fibroblast subsets and further evidence for sub-clustering approach. (A) A three-section heatmap showing the top 5 marker genes for each cluster with their mean expression per cluster and compared between control and scleroderma (*bottom*), the associated logFC value (*middle)* and the associated p-value (*top*). These DEGs support the

clustering seen in Figure 4. **(B)** Correlation matrices based on Pearson's product-moment correlation coefficient (r) exploring the overlap of highly variable genes between the clusters. Red colour indicates maximum overlap. Blue colour indicates minimum overlap. **(C)** Boxplots showing the proportion of cells derived from the skin of scleroderma (n = 12) and control (n = 10) for each cell type. * indicates signficance ($p < 0.05$). Multiple unpaired t-tests were used for analysis.

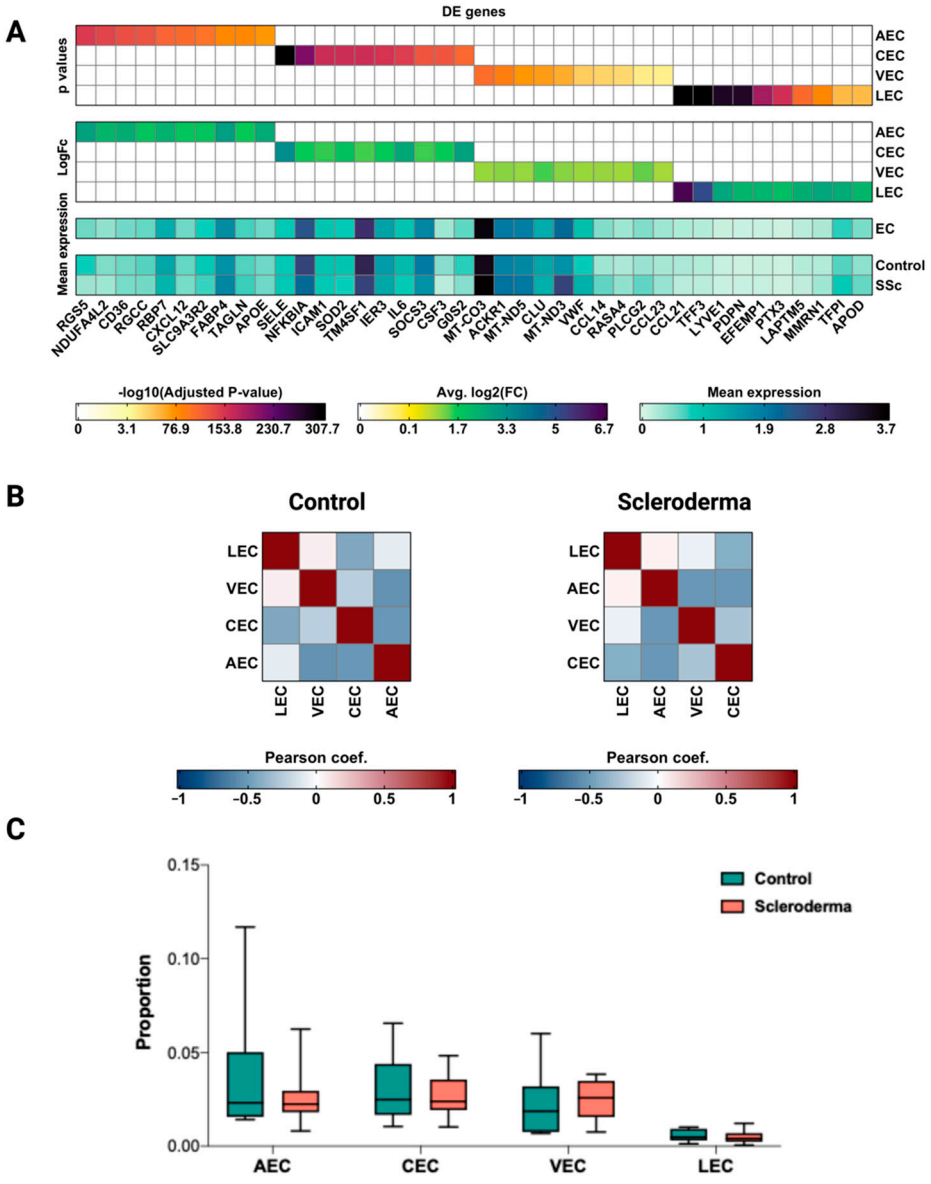


Figure S4. Differentially expressed genes of endothelial subsets and further evidence for sub-clustering approach. (A) A three-section heatmap showing the top 5 marker genes for each cluster with their mean expression per cluster and compared between control and scleroderma (*bottom*), the associated logFC value (*middle)* and the associated p-value (*top*). These DEGs support the clustering seen in Figure 5. **(B)** Correlation matrices based on Pearson's product-moment correlation coefficient (r) exploring the overlap of highly variable genes between the clusters. Red colour indicates maximum overlap. Blue colour indicates minimum overlap. **(C)** Boxplots showing the proportion of cells derived from the skin of scleroderma (n = 12) and control (n = 10) for each cell type. * indicates signficance ($p < 0.05$). Multiple unpaired t-tests were used for analysis.

	No change		Additional (+)		Missing (-)	
FB1	CCN2|EGFR CCN1|ITGB5 CCN2|LRP1	FNDC5|ITGB5 PTHLH|RAMP2	TNFSF9|HLA-DPA1 CCN1|CAV1	CCN1|ITGAV FNDC5|ITGAV	SERPINE1|ITGB5	
FB2	DKK1|KREMEN1 CCN1|ITGB5 CCN2|LRP1	FNDC5|ITGB5 PTHLH|RAMP2	CD55|ADGRE2 VEGFD|NRP2 RARRES1|NRP2 CCN1|CAV1	TNXB|SDC1 FGF2|SDC1 CCN1|ITGAV FNDC5|ITGAV		
FB3	CCN1|ITGB5 CCN2|LRP1	FNDC5|ITGB5	CCN1|CAV1		SERPINE1|ITGB5 DKK1|KREMEN1	
FB4	DKK1|KREMEN1 CCN2|EGFR CCN1|ITGB5	CCN2|LRP1 FNDC5|ITGB5 CXCL12|ACKR3	CCN1|CAV1 CCN1|ITGAV	FNDC5|ITGAV ADM|ACKR3	CSF1|SIRPA SERPINE1|ITGB5	PTHLH|RAMP2
FB5	RARRES1|NRP VEGFD|NRP2 DKK1|KREMEN1 PTHLH|PTH1R	TNXB|SDC1 FGF2|SDC1 PTHLH|RAMP2			VEGFA|NRP2 BMP7|PTPRK COL6A6|SDC1	HSPG2|SDC1 MYOC|FZD1 SERPINE1|ITGB5
FB6	RARRES|NRP2 VEGFD|NRP2 LAMC1|ITGA6 ADAM9|ITGA6 CCN2|EGFR	LAMB2|ITGA6 FN1|ITGA6 CCN2|LRP1 PTHLH|RAMP2	WNT11|FZD2 THBS1|ITGA6	THBS2|ITGA6	VEGFA|NRP2 JAG1|NOTCH3	CCN2|LRP6 MYOC|FZD1

Figure S5. Differences in interactions between control and scleroderma fibroblasts. Table showing the analysis of comparing Figure 6A,B, which display the top 25 interactions between ADSCs (ligands) and fibroblast subsets (receptors). Interactions are shown as "Ligand | Receptor". "No change" indicates that the pair appears in the equivalent control as well as the

scleroderma subset. “Additional (+)” indicates that the pair only appears in the scleroderma subset. “Missing (-)” indicates that the pair only appears in the control subset.

	No change		Additional (+)		Missing (-)	
AEC	THBS2|CD36 COL1A1|CD36 PRG4|CD44 COL6A6|CD44 VCAN|CD44 COL14A1|CD44	HAS2|CD44 C3|CD81 ANOS1|FGFR1 GPC3|CD81 MMP2|FGFR1	COL1A2|CD36 TNFSF4|TNFRSF4	PTHLH|ADRB2 LAMA2|CD44	THBS2|NOTCH3 COL6A3|CD44 COL1A1|CD44	COL6A2|CD44 VEGFA|CD44
CEC	VEGFD|NRP2 THBS2|CD36 COL1A1|CD36 VCAN|SELP	C3|CD81 GPC3|CD81 ANOS1|FGFR1 MMP2|FGFR1	COL1A2|CD36 PTHLH|ADRB2 PRG4|CD44 COL14A1|CD44 COL6A6|CD44	LAMA2|CD44 VCAN|CD44 HAS2|CD44 ANOS1|FGFR1	RARRES1|NRP2	VEGFA|NRP2
VEC	VEGFD|NRP2 VCAN|SELP	C3|CD81 GPC3|CD81	PRG4|CD44 COL14A1|CD44 COL6A6|CD44	LAMA2|CD44 VCAN|CD44 HAS2|CD44	RARRES1|NRP2	VEGFA|NRP2
LEC	VEGFD|NRP2 C3|CD81 ANOS1|FGFR1	GPC3|CD81 MMP2|FGFR1	NTN1|UNC5B COL1A1|FLT4 COL1A2|FLT4 TNFSF4|TNFRSF4 PRG4|CD44	COL14A1|CD44 COL6A6|CD44 LAMA2|CD44 HAS2|CD44	RARRES1|NRP2 VEGFA|NRP2 THBS2|CD36	COL1A1|CD36 VCAN|SELP

Figure S6. Differences in interactions between control and scleroderma endothelial cells. Table showing the analysis of comparing Figure 6A,B, which display the top 25 interactions between ADSCs (ligands) and endothelial cell subsets (receptors). Interactions are shown as “Ligand | Receptor”. “No change” indicates that the pair appears in the equivalent control as well as the scleroderma subset. “Additional (+)” indicates that the pair only appears in the scleroderma subset. “Missing (-)” indicates that the pair only appears in the control subset.

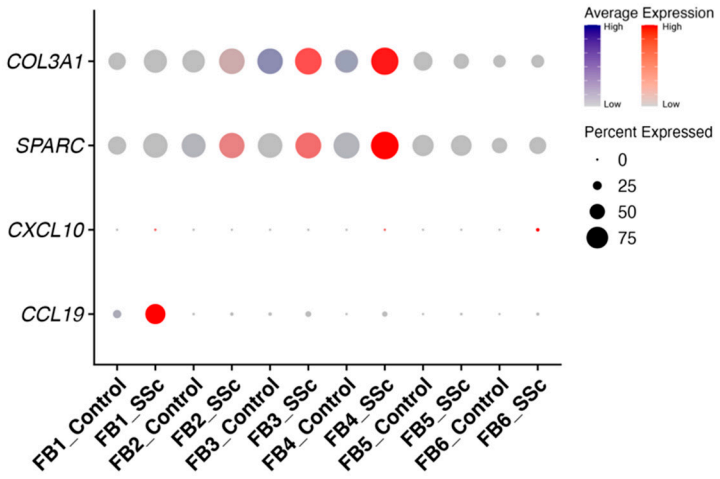


Figure S7. Expression of proinflammatory markers in fibroblasts. Dot plot of genes associated with a proinflammatory phenotype by Korsunsky, *et al.* [9]. Colour intensity implies level of expression and dot size indicates the percentage of the cluster expressing the gene (blue = control; red = scleroderma).