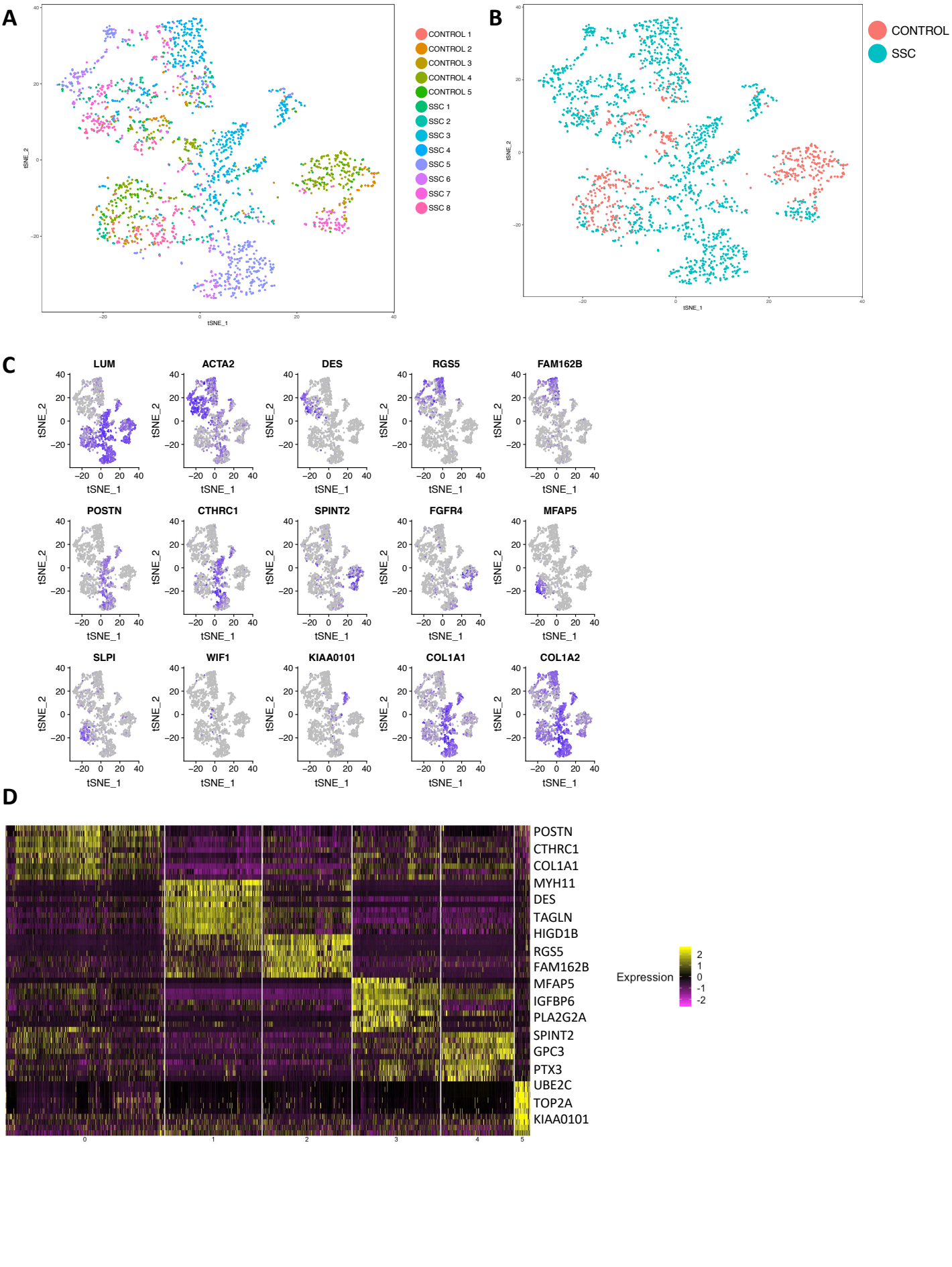
A
CONTROL 1
CONTROL 2
CONTROL 3
CONTROL 4
CONTROL 5
SSC 1
SSC 2
SSC 3
SSC 4
SSC 5
SSC 6
SSC 7
SSC 8
tSNE_1
tSNE_2
B
CONTROL
SSC
C
LUM
ACTA2
DES
RGS5
FAM162B
POSTN
CTHRC1
SPINT2
FGFR4
MFAP5
SLPI
WIF1
KIAA0101
COL1A1
COL1A2
D
POSTN
CTHRC1
COL1A1
MYH11
DES
TAGLN
HIGD1B
RGS5
FAM162B
MFAP5
IGFBP6
PLA2G2A
SPINT2
GPC3
PTX3
UBE2C
TOP2A
KIAA0101
Expression

Supplemental Figure 5

Single-cell RNA-sequencing of human healthy control and SSc-ILD mesenchymal cell populations. (A) t-SNE plot of mesenchymal cells colored according to sample of origin. (B) t-SNE plot of mesenchymal cell populations colored according to disease status. (C) Feature plots demonstrating gene expression of the identified mesenchymal cell types: all fibroblasts (*LUM*),smooth muscle (*DES, ACTA2*), pericytes (*RGS5, FAM162B,ACTA2*), myofibroblast (*ACTA2, POSTN, CTHRC1*), SPINT2^{hi} fibroblast (*SPINT2, FGFR4*), MFAP5^{hi} fibroblast (*MFAP5, SLPI*), WIF1^{hi} fibroblast (*WIF1),* proliferating myofibroblast (*KIAA0101,POSTN, CTHRC1, ACTA2*). (D) Heat map of scaled gene expression data for the top 10 differentially expressed genes identifying each cluster (0-myofibroblast, 1-smooth muscle, 2-pericyte, 3-MFAP5 ^{hi} fibroblast, 4-SPINT2 ^{hi} fibroblast, 5- proliferating myofibroblast), with selected genes listed.