



**Supplementary Fig. S1.**

(A) Hierarchical clustering dendrogram of the samples. The clinical traits were shown at the bottom.

(B) Histogram of k and Scale-free topology.

(C) Clustering of the module eigengenes: cut height =0.40.

**Supplementary Table S1.** Summary of 6 selected genome-wide gene expression datasets involving SSc patients.

GSE number	Samples (control vs SSc)	Platform	Platform version
GSE58095	43 vs. 59	GPL10558	Illumina HumanHT-12 V4.0 expression beadchip
GSE76885	18 vs. 66	GPL6480	Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Probe Name version)
GSE45485	20 vs. 33	GPL6480	Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Probe Name version)
GSE125362	4 vs. 8	GPL6480	Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Probe Name version)
GSE32413	8 vs. 29	GPL4133	Agilent-014850 Whole Human Genome Microarray 4x44K G4112F (Feature Number version)
GSE95065	15 vs. 18	GPL23080	[HG-U133A_2] Affymetrix Human Genome U133A 2.0 Array (HGU133A2 Hs ENTREZG 19.0.0)

SSc: systemic sclerosis.

**Supplementary Table S2.** GO enrichment analysis of genes in the key module.

Term ID	Term	Count	P value	Term name
<i>lightgreen module</i>				
GO:0007155	BP	77	6.22E-29	cell adhesion
GO:0007165	BP	73	1.08E-05	signal transduction
GO:0006955	BP	59	2.62E-18	immune response
GO:0030198	BP	46	1.95E-23	extracellular matrix organization
GO:0006954	BP	45	1.79E-11	inflammatory response
GO:0043547	BP	42	3.22E-05	positive regulation of GTPase activity
GO:0006508	BP	37	1.15E-04	proteolysis
GO:0008284	BP	35	1.37E-04	positive regulation of cell proliferation
GO:0001525	BP	27	2.39E-07	angiogenesis
GO:0007267	BP	26	8.95E-06	cell-cell signaling
GO:0005886	CC	209	2.66E-08	plasma membrane
GO:0070062	CC	186	6.74E-18	extracellular exosome
GO:0005576	CC	131	2.85E-19	extracellular region
GO:0005615	CC	129	3.91E-25	extracellular space
GO:0016020	CC	108	6.30E-04	membrane
GO:0005887	CC	88	4.99E-07	integral component of plasma membrane
GO:0031012	CC	58	7.39E-26	extracellular matrix
GO:0009986	CC	56	3.72E-12	cell surface
GO:0005925	CC	53	3.34E-16	focal adhesion
GO:0005578	CC	44	1.03E-16	proteinaceous extracellular matrix
GO:0005509	MF	54	1.07E-06	calcium ion binding
GO:0042803	MF	45	9.40E-04	protein homodimerization activity
GO:0005102	MF	32	7.21E-06	receptor binding
GO:0003779	MF	26	3.71E-05	actin binding
GO:0004252	MF	25	2.54E-05	serine-type endopeptidase activity
GO:0008201	MF	22	4.33E-07	heparin binding
GO:0004872	MF	21	1.57E-04	receptor activity
GO:0005201	MF	20	1.98E-12	extracellular matrix structural constituent
GO:0051015	MF	20	3.61E-07	actin filament binding
GO:0005178	MF	19	4.82E-08	integrin binding

GO: gene ontology; BP: biological process; CC: cellular component; MF: molecular function.

**Supplementary Table S3.** KEGG pathway analysis of genes in the key module.

Term ID	Count	P value	Term name
hsa04510	37	2.24E-12	Focal adhesion
hsa04151	31	5.66E-04	PI3K-Akt signaling pathway
hsa04062	27	3.38E-07	Chemokine signaling pathway
hsa04514	26	5.26E-09	Cell adhesion molecules (CAMs)
hsa04145	26	1.68E-08	Phagosome
hsa04512	25	4.67E-13	ECM-receptor interaction
hsa04060	25	3.31E-04	Cytokine-cytokine receptor interaction
hsa05152	23	1.93E-05	Tuberculosis
hsa05166	23	0.003219	HTLV-I infection
hsa05150	21	8.47E-14	Staphylococcus aureus infection
hsa04670	20	1.06E-06	Leukocyte transendothelial migration
hsa05140	19	1.92E-09	Leishmaniasis
hsa04611	19	2.61E-05	Platelet activation
hsa04640	18	3.40E-07	Hematopoietic cell lineage
hsa04974	18	4.04E-07	Protein digestion and absorption
hsa05323	18	4.04E-07	Rheumatoid arthritis
hsa05146	16	9.57E-05	Amoebiasis
hsa05145	16	1.47E-04	Toxoplasmosis
hsa05322	15	0.003439	Systemic lupus erythematosus
hsa04612	14	3.77E-05	Antigen processing and presentation

KEGG: Kyoto Encyclopedia of Genes and Genomes.