

Supplementary information for:
Single-cell analysis reveals immune cell abnormalities underlying the clinical heterogeneity of patients with systemic sclerosis

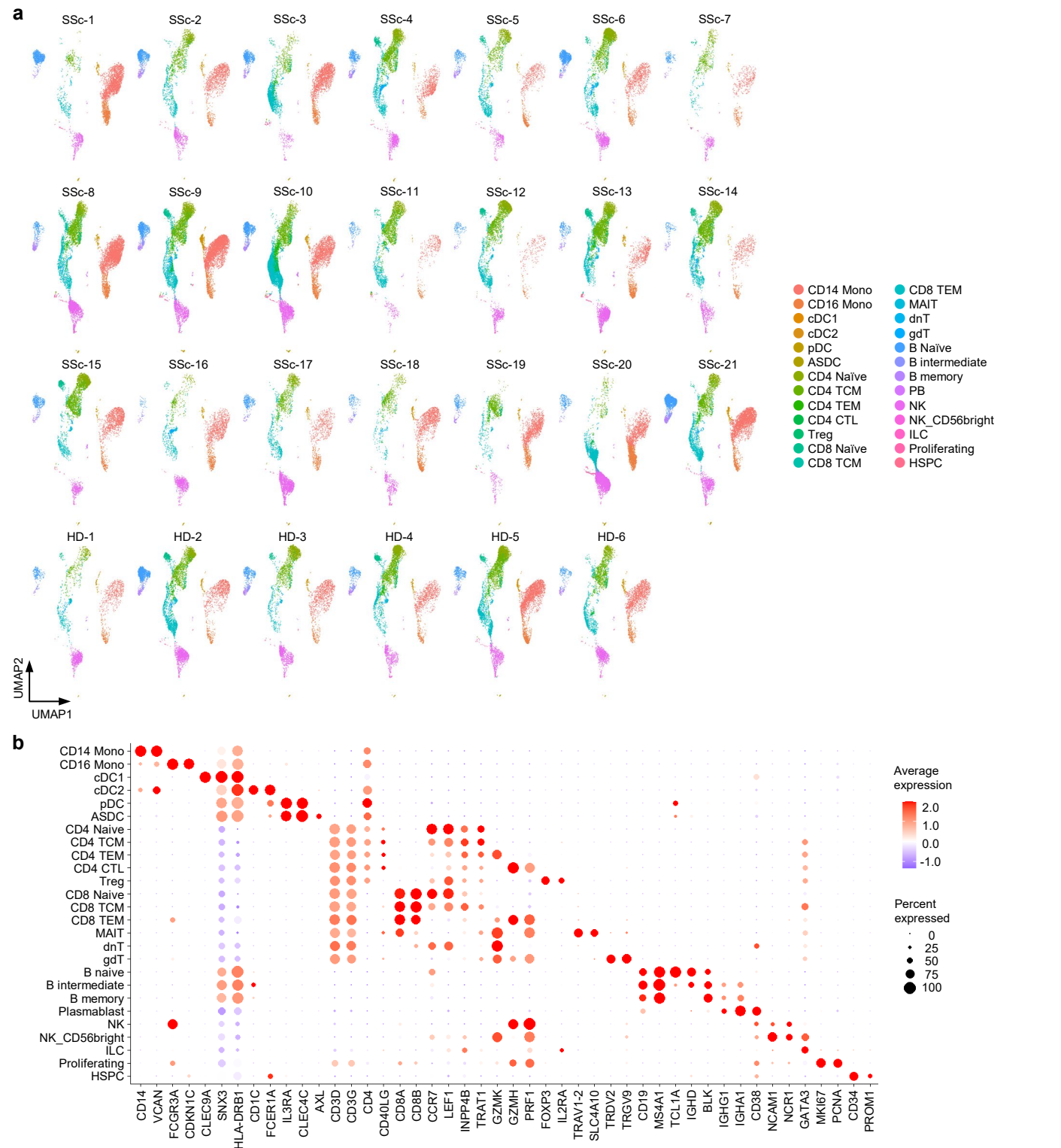
Corresponding to:

Masayuki Nishide (nishide@imed3.med.osaka-u.ac.jp), Department of Respiratory Medicine and Clinical Immunology, Graduate School of Medicine, Osaka University, Suita, Osaka, Japan.

Atsushi Kumanogoh (kumanogo@imed3.med.osaka-u.ac.jp), Department of Respiratory Medicine and Clinical Immunology, Graduate School of Medicine, Osaka University, Suita, Osaka, Japan.

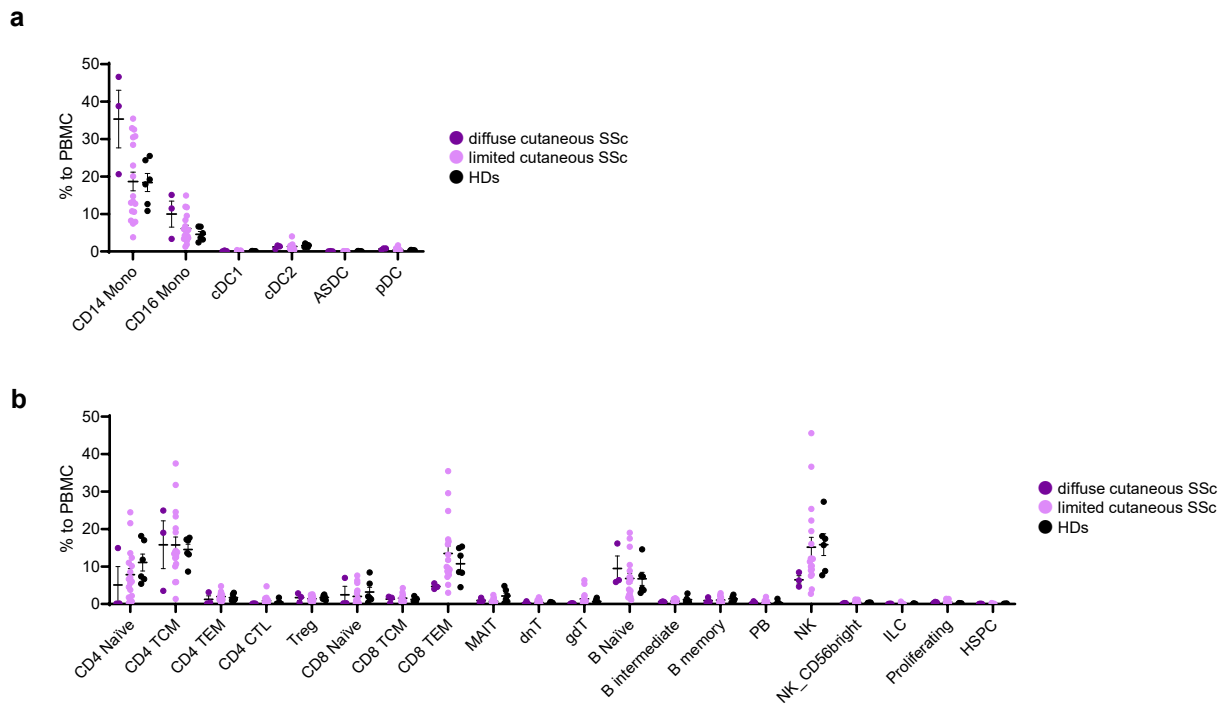
This file includes Supplementary Figures 1 – 24 and supplementary Tables 1 – 14.

Supplementary Figure 1.
UMAP plots of PBMCs derived from each SSc patients or HDs.



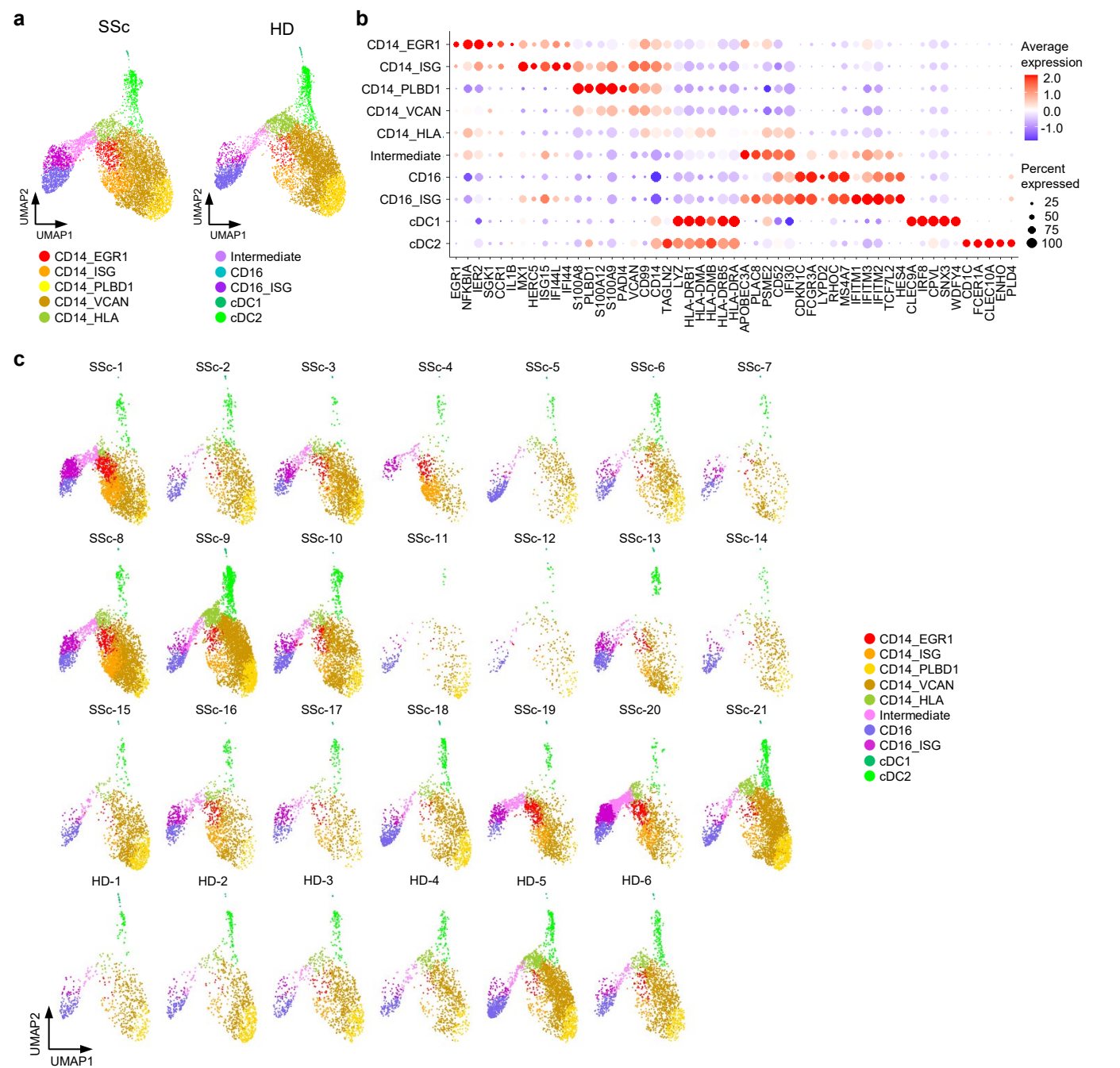
(a) UMAP plots of PBMCs in each patient with SSc or HD. Each cellular cluster was annotated with reference mapping. UMAP, uniform manifold approximation and projection; PBMC, peripheral blood mononuclear cells; SSc, systemic sclerosis; HD, healthy donor; Mono, monocytes; cDC, conventional dendritic cells; ASDC, AXL⁺ dendric cells; pDC, plasmacytoid dendritic cells; TCM, central memory T cells; TEM, effector memory T cells; CTL, cytotoxic T lymphocytes; Treg, regulatory T cells; MAIT, mucosal associated invariant T cells; dnT, double negative T cells; gdT, gamma-delta T cells; PB, plasmablasts; NK, natural killer cells; ILC, innate lymphoid cells; Proliferating, proliferating cells; HSPC, hematopoietic stem and progenitor cells. **(b)** Balloon plot showing highly expressed genes in each subpopulation shown in **(a)**.

Supplementary Figure 2.
Cellular composition of PBMCs from diffuse or limited cutaneous SSc patients or HDs.



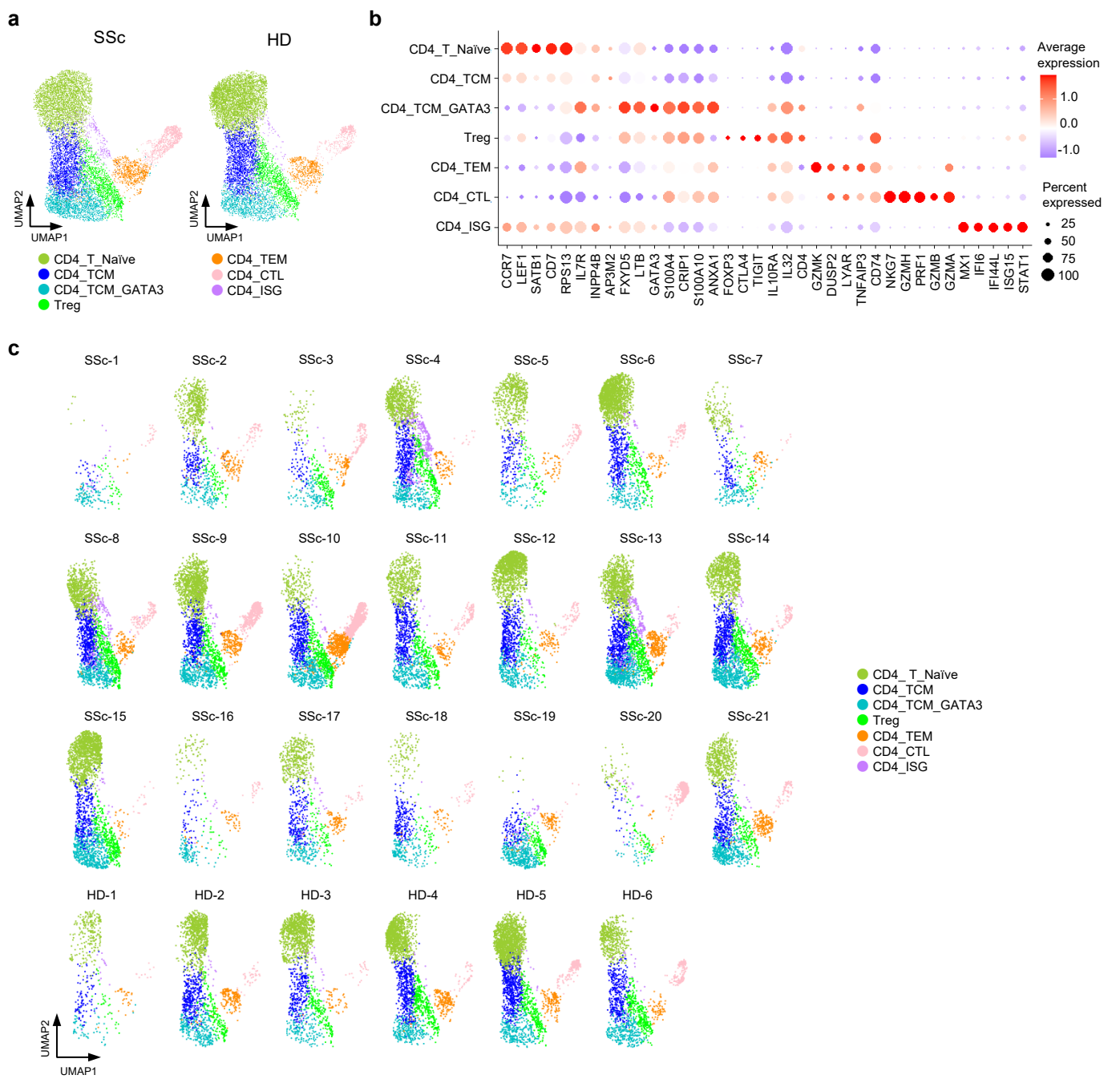
Percentages of myeloid cell populations **(a)** and lymphoid cell populations **(b)** relative to the total number of PBMCs from patients with diffuse cutaneous SSc (n=3, deep purple), limited cutaneous SSc (n=18, light purple), or HDs (n=6, black). Values represent means with standard error of the mean (SEM). Statistical analysis was performed using the Kruskal–Wallis test for each cell population; no significant differences were observed. Source data are provided as a Source Data file.

Supplementary Figure 3.
UMAP plots of Monocytes derived from each SSc patients or HDs.



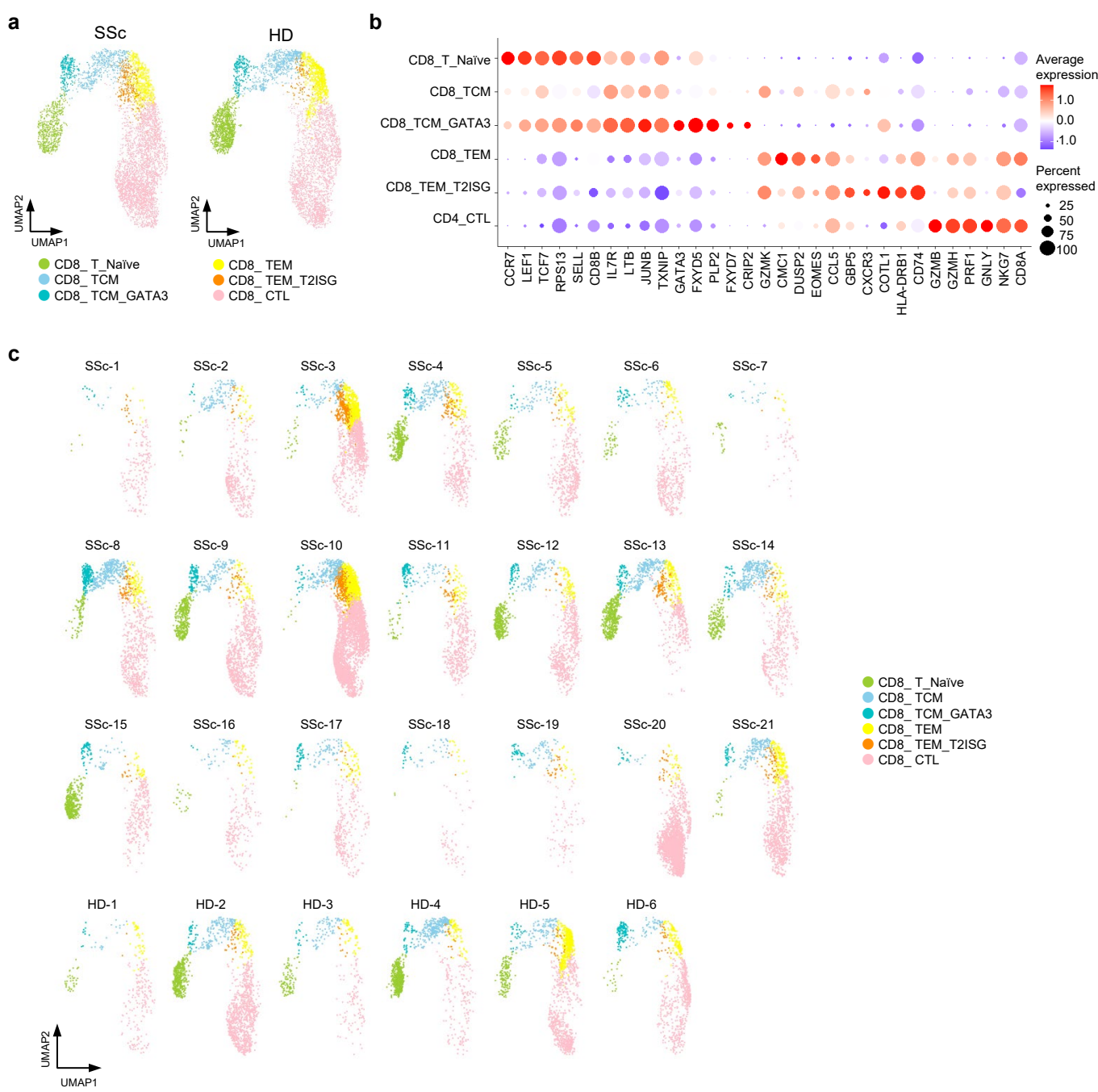
(a) UMAP plots of the monocytes in patients with SSc (SSc; n=21) and HDs (HD; n=6). Ten cellular clusters were identified; CD14⁺ monocytes with high expression of *EGR1* (CD14_EGR1), interferon signature genes (ISGs) (CD14_ISG), *PLBD1* (CD14_PLBD1), *VCAN* (CD14_VCAN), HLA (CD14_HLA), intermediate monocytes (Intermediate), CD16⁺ monocytes characterized by high expression of ISGs (CD16_ISG), other CD16⁺ monocytes (CD16), conventional type 1 dendritic cells (cDC1), and conventional type 2 dendritic cells (cDC2). Each plot shows 8,000 randomly selected cells. **(b)** Balloon plot showing highly expressed genes in each subpopulation shown in **(a)**. **(c)** UMAP plots of monocytes in each patient with SSc or HD.

Supplementary Figure 4.
UMAP plots of CD4⁺ T cells derived from each SSc patients or HDs.



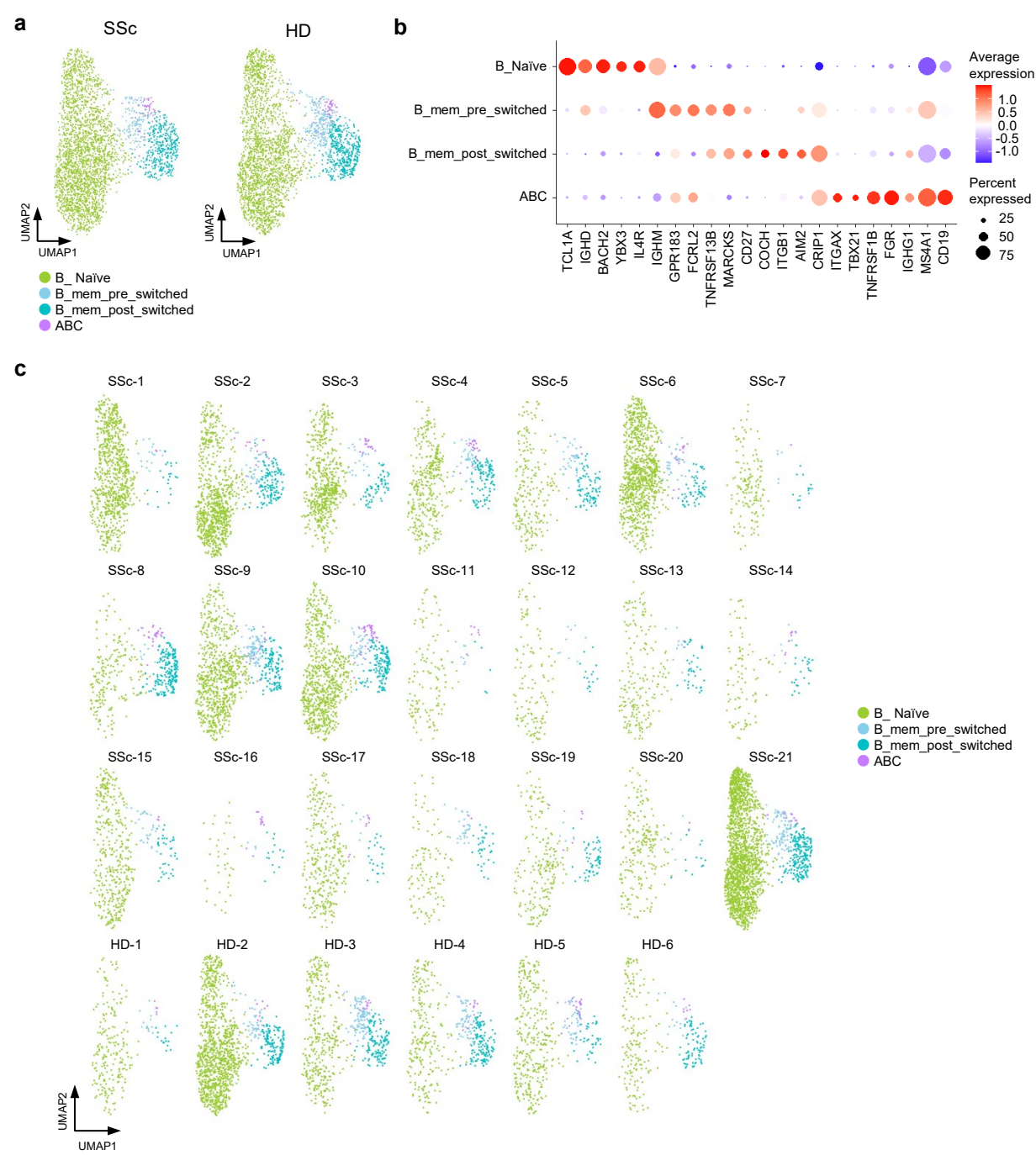
(a) UMAP plots of CD4⁺ T cells in patients with SSc (SSc; n=21) and HDs (HD; n=6). Seven cellular clusters were identified: naïve CD4⁺ T cells (CD4_Naive), central memory CD4⁺ T cells characterized by high expression of GATA3 (CD4_TCM_GATA3), other central memory CD4⁺ T cells (CD4_TCM), effector memory CD4⁺ T cells (CD4_TEM), cytotoxically active CD4⁺ T cells (CD4_CTL), and CD4⁺ T cells characterized by high expression of ISGs (CD4_ISG). Each plot shows 10,000 randomly selected cells. **(b)** Balloon plot showing highly expressed genes in each subpopulation shown in **(a)**. **(c)** UMAP plots of CD4⁺ T cells in each patient with SSc or HD.

Supplementary Figure 5.
UMAP plots of CD8⁺ T cells derived from each SSc patients or HDs.



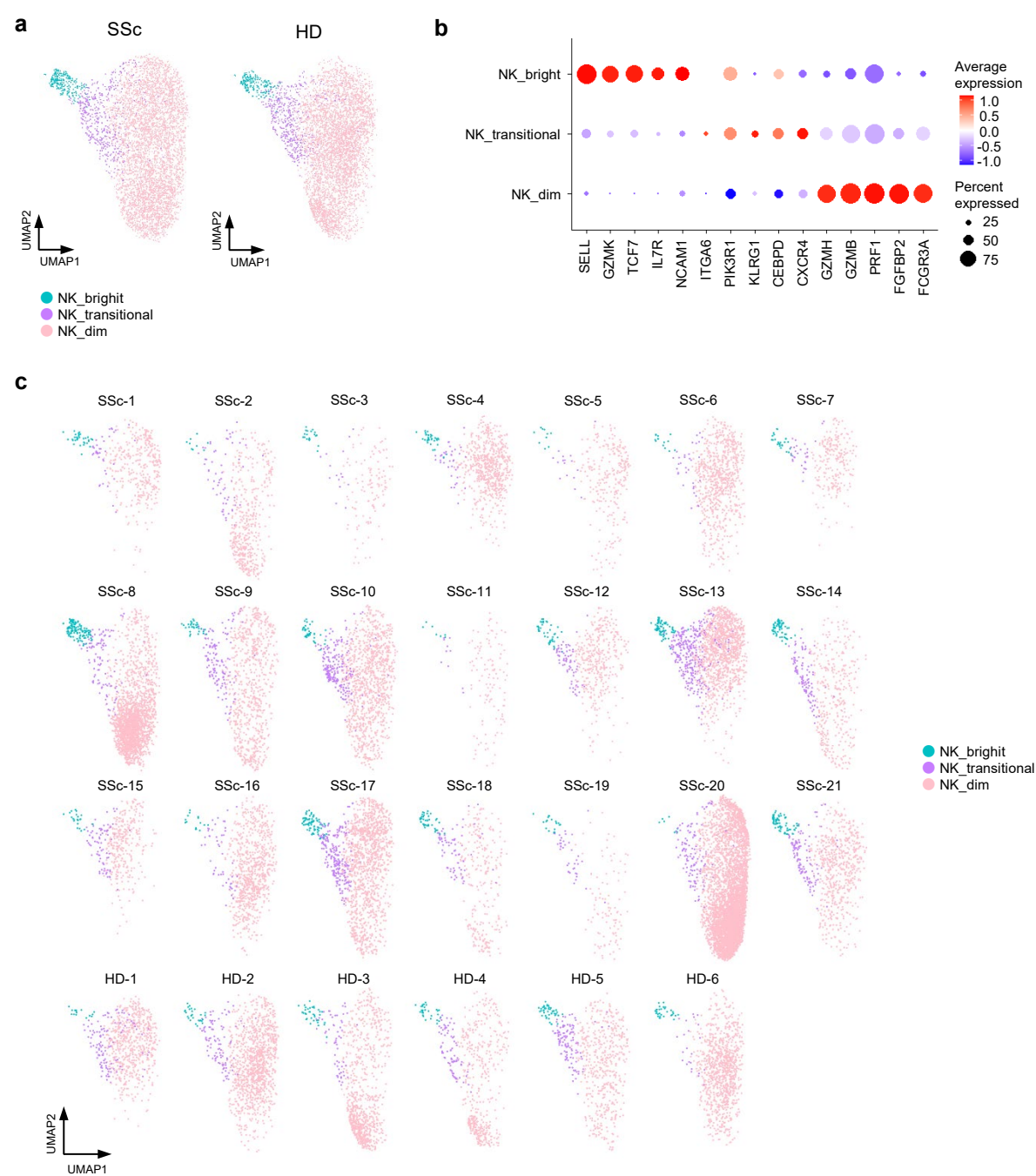
(a) UMAP plots of CD8⁺ T cells in patients with SSc (SSc; n=21) and HDs (HD; n=6). Six cellular clusters were identified: naïve CD8⁺ T cells (CD8_{T_Naive}), central memory CD8⁺ T cells characterized by high expression of GATA3 (CD8), other central memory CD8⁺ T cells (CD8), effector memory CD8⁺ T cells characterized by high expression of type 2 ISGs (CD8), other effector memory CD8⁺ T cells (CD8), and cytotoxically active CD8⁺ T cells (CD8). Each plot shows 5,000 randomly selected cells. **(b)** Balloon plot showing highly expressed genes in each subpopulation shown in **(a)**. **(c)** UMAP plots of CD8⁺ T cells in each patient with SSc or HD.

Supplementary Figure 6.
UMAP plots of B cells derived from each SSc patients or HDs.



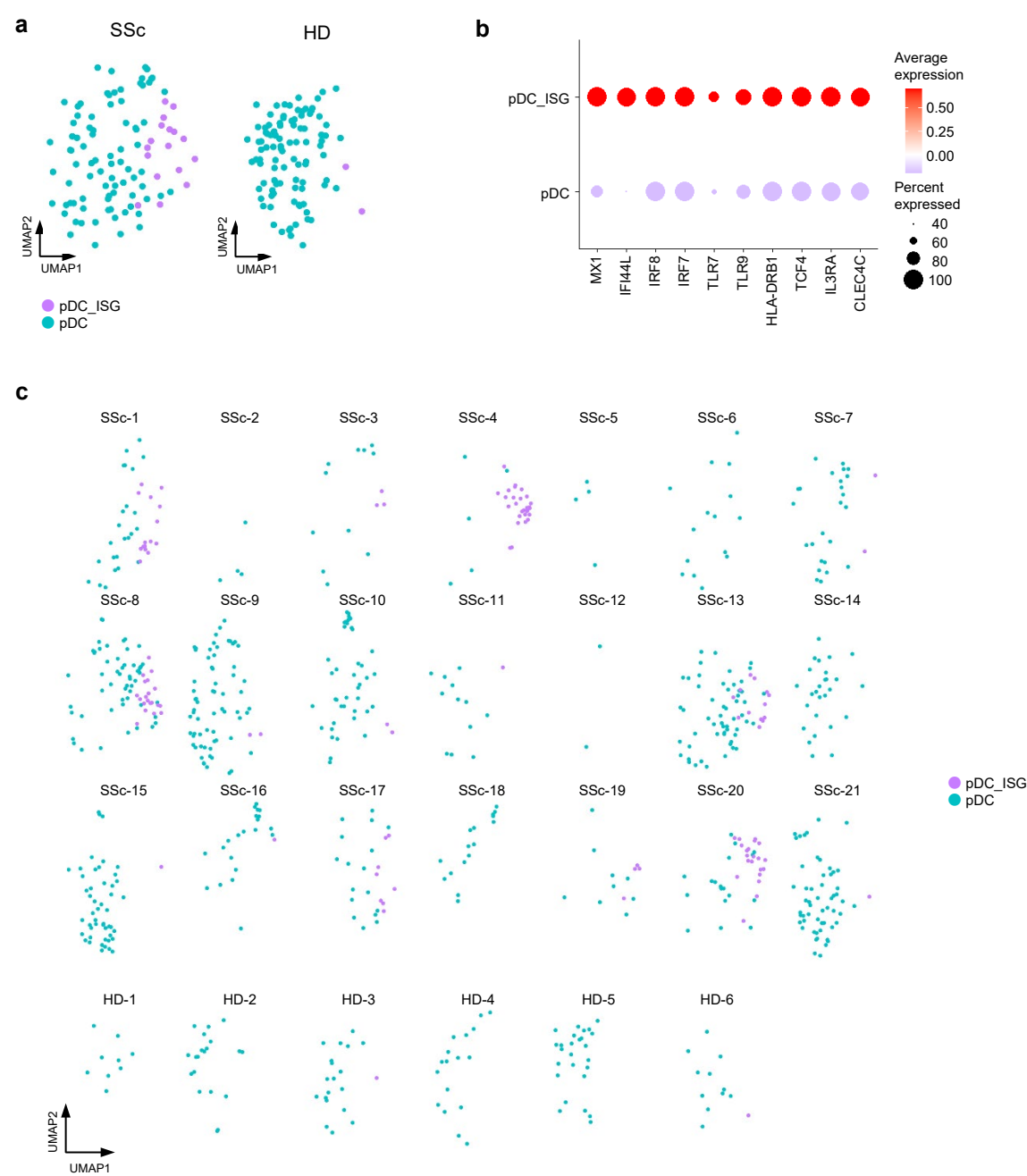
(a) UMAP plots of B cells in patients with SSc (SSc; n=21) and HDs (HD; n=6). Four cellular clusters were identified: naïve B cells (B_Naïve), pre-switched memory B cells (B_mem_pre_switched), post-switched memory B cells (B_mem_post_switched), and age-associated B cells (ABC). Each plot shows 3,000 randomly selected cells. **(b)** Balloon plot showing highly expressed genes in each subpopulation shown in **(a)**. **(c)** UMAP plots of B cells in each patient with SSc or HD.

Supplementary Figure 7.
UMAP plots of NK cells derived from each SSc patients or HDs.



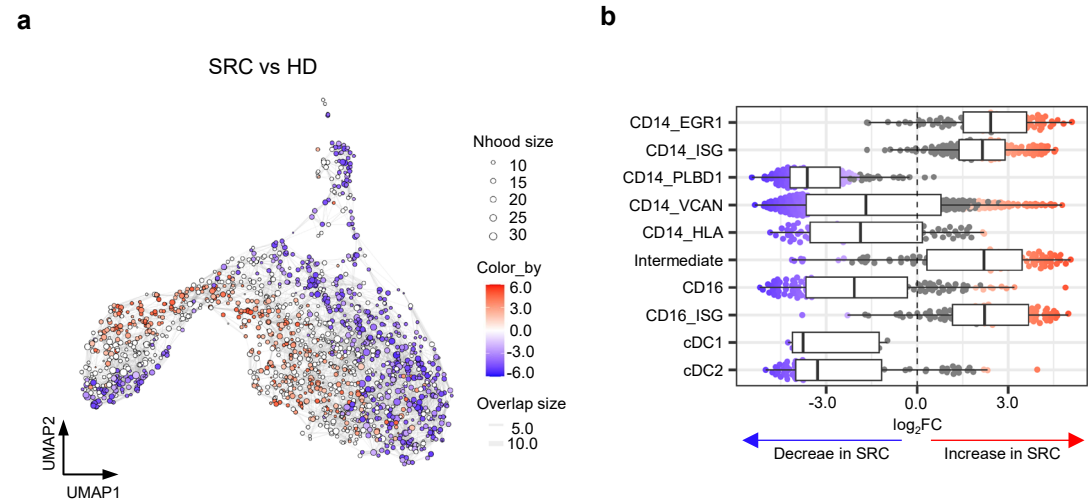
(a) UMAP plots of NK cells in patients with SSc (SSc; n=21) and HDs (HD; n=6). Three cellular clusters were identified: NK cells characterized by high expression of *NCAM1* (NK_bright), NK cells characterized by low expression of *NCAM1* and high expression of *GZMH* (NK_dim), and transitional NK cells (NK_transitional). Each plot shows 5,000 randomly selected cells. **(b)** Balloon plot showing highly expressed genes in each subpopulation shown in **(a)**. **(c)** UMAP plots of NK cells in each patient with SSc or HD.

Supplementary Figure 8.
UMAP plots of pDC derived from each SSc patients or HDs.



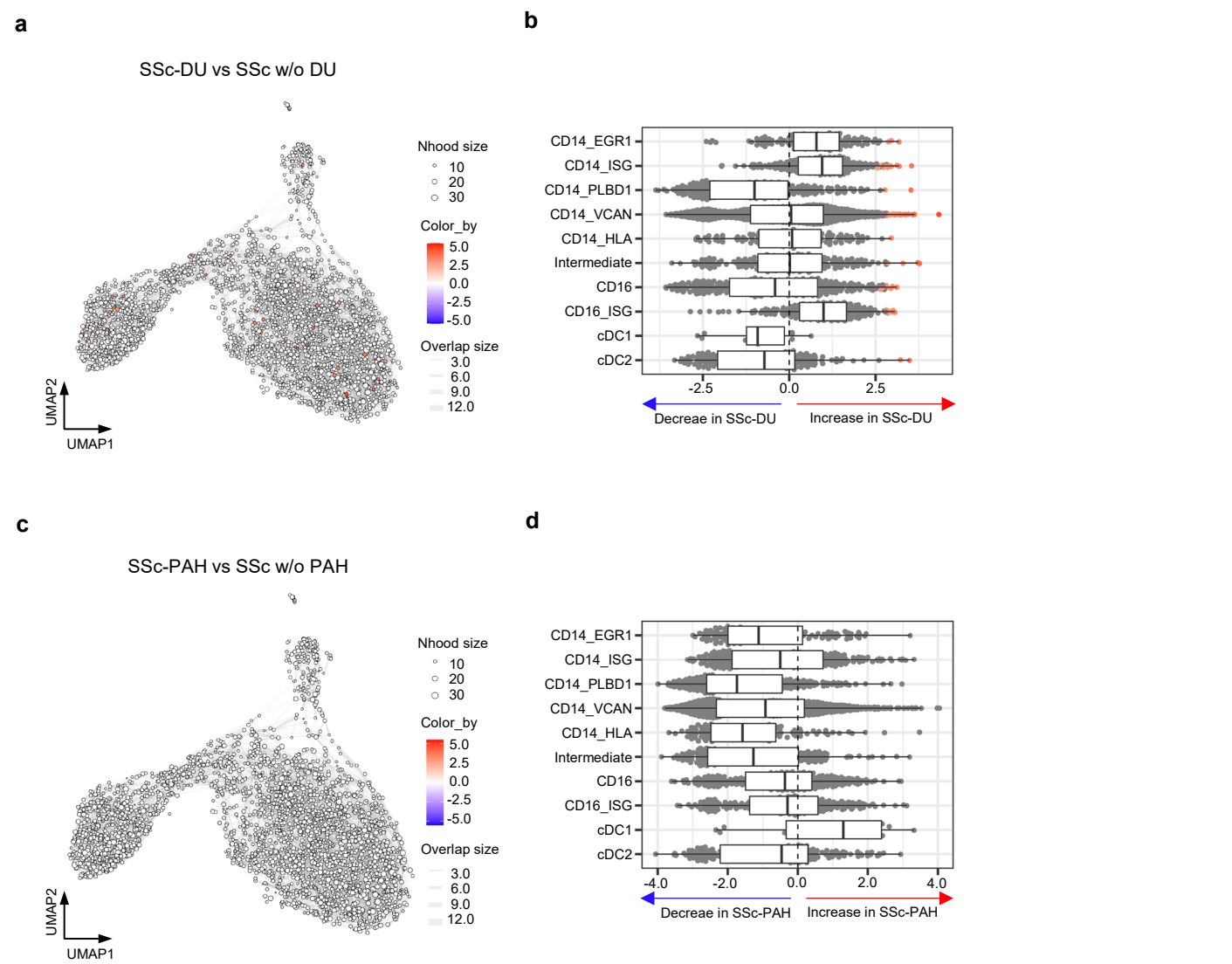
(a) UMAP plots of pDCs in patients with SSc (SSc; n=21, left) and HDs (HD; n=6, right). Two cellular clusters were identified: pDC characterized by high expression of ISGs (pDC_ISG) and other pDC (pDC). Each plot shows 100 randomly selected cells. **(b)** Balloon plot showing highly expressed genes in each subpopulation shown in **(a)**. **(c)** UMAP plots of pDCs in each patient with SSc or HD.

Supplementary Figure 9.
Differential abundance analysis of Monocytes between patients with SRC and HDs.



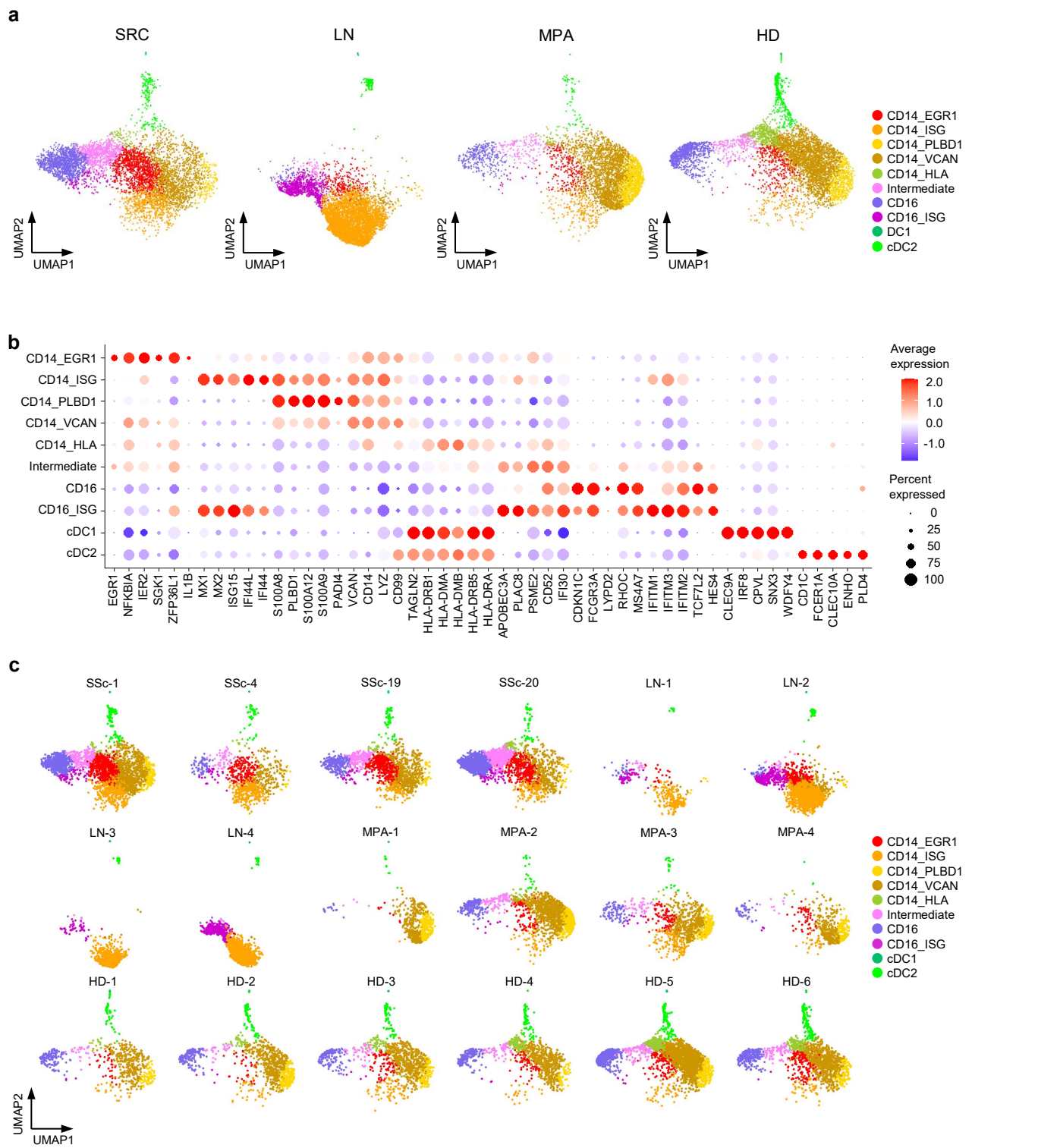
(a) Neighborhood graph of monocytes from SRC patients and HDs, generated in a similar fashion as in **Fig. 2a**. The color scale indicates the $\log_2$ -fold difference between SRC and HDs. Neighborhoods showing an increase in SRC are colored in red, while those with a decrease are in blue. **(b)** Beeswarm and box plots showing the distribution of $\log_2$ -fold differences between SRC ($n=4$) and HDs ($n=6$) in neighborhoods in different cell subsets, colored as in **(a)**. Box plots are created as in **Fig. 2b**.

Supplementary Figure 10.
Differential abundance analysis of Monocytes in SSc patients with digital ulcers or pulmonary artery hypertension.



(a) Neighborhood graph of monocytes from SSc patients, generated in a similar fashion as in **Fig. 2a**. The color scale indicates the log₂-fold difference between SSc patients with digital ulcer (SSc-DU) and those without DU (SSc w/o DU). Neighborhoods showing an increase in SSc-DU are colored in red, while those with a decrease are in blue. **(b)** Beeswarm and box plots showing the distribution of log₂-fold differences between SSc-DU (n=5) and SSc w/o DU (n=16) in neighborhoods in different cell subsets, colored as in **(a)**. Box plots are created as in **Fig. 2b**. Neighborhood graph **(c)** and Beeswarm plots **(d)** of monocytes from SSc patients with pulmonary artery hypertension (SSc-PAH, n=3) and those without PAH (SSc w/o PAH, n=18), generated in a similar fashion as in **(a)** and **(b)**, respectively. Neighborhoods showing an increase in SSc-PAH are colored in red, while those with a decrease are in blue.

Supplementary Figure 11.
UMAP plots of Monocytes derived from patients with SRC, LN, MPA, and HDs.



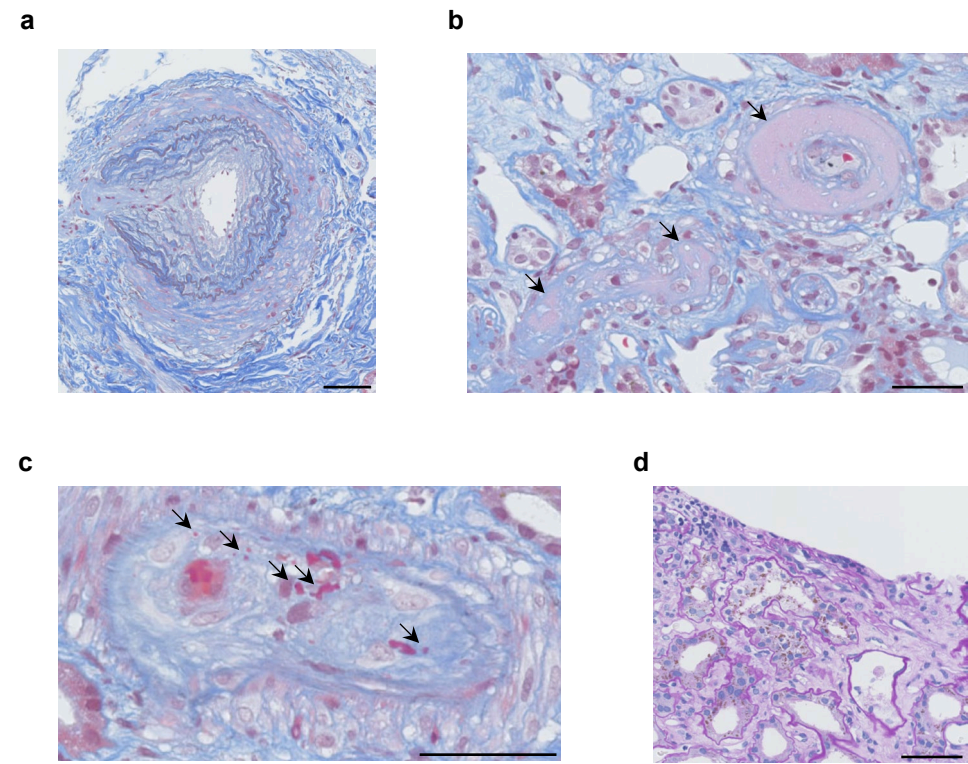
(a) UMAP plots of monocytes in SSc patients with SRC (SRC; n=4), patients with lupus nephritis (LN; n=4), patients with microscopic polyangiitis with renal involvement (MPA, n=4), and HDs (HD; n=6). Each plot shows 6,000 randomly selected cells. **(b)** Balloon plot showing highly expressed genes in each subpopulation shown in **(a)**. **(c)** UMAP plots of monocytes in each patient or HD.

Supplementary Figure 12.
Expression of selected surface antigens in monocyte subsets enriched in SSc patients with SRC.



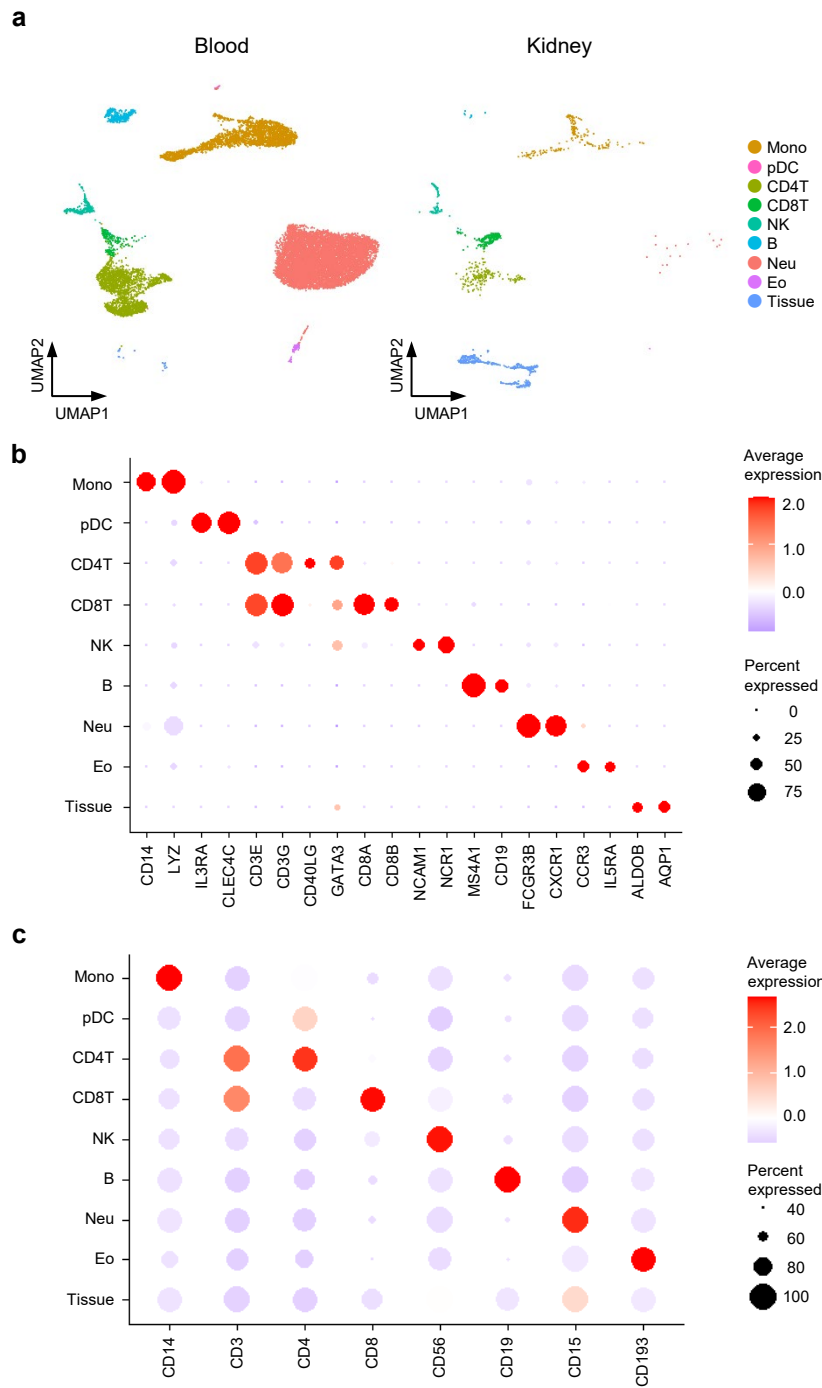
Balloon plot showing the expression levels of CD14, CD11b, CD4, CD38, and CD16 surface antigens in the CD14_EGR1, CD14_ISG, and CD16_ISG monocyte subpopulations.

Supplementary Figure 13.
Renal biopsy obtained from the SSc patient at the onset of SRC.



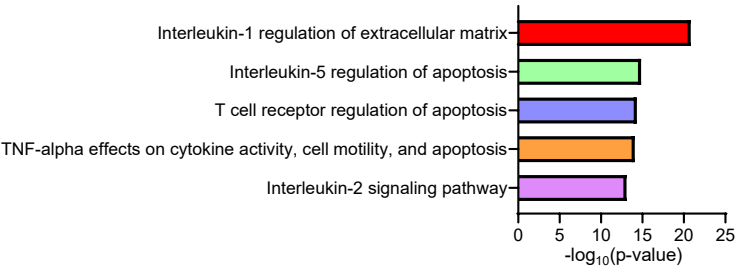
Pathological features of a kidney biopsy sample from the patient at the onset of SRC (Patient ID: SSc-19). **(a)** Intimal thickening and luminal narrowing within an artery. **(b)** Fibrinoid necrosis of arterioles (arrows). **(c)** Red blood cell fragmentations within the vessel (arrows). **(d)** Focal tubular necrosis and tubulitis. **(a)-(c)**: Masson's trichrome staining. **(d)**: Hematoxylin and eosin staining. **(a)-(d)**: Scale bar = 50 µm.

Supplementary Figure 14.
UMAP plots of renal tissue and peripheral blood cells derived from a patient at the onset of SRC.



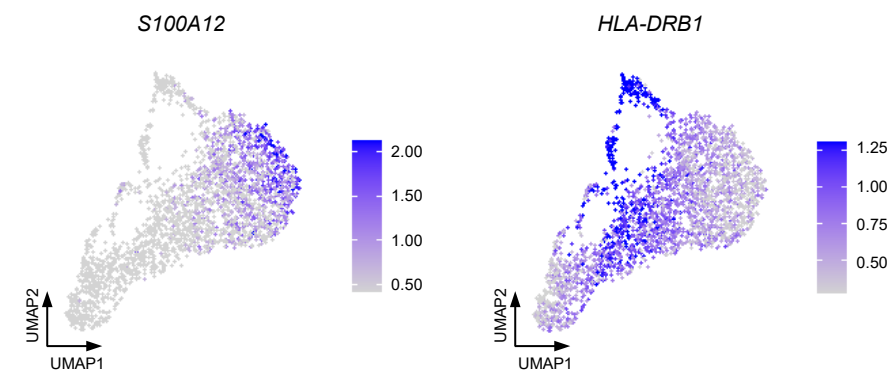
(a) UMAP plots showing Abseq data of all cells from peripheral blood (left) and renal tissue (right) derived from one patient at the onset of SRC (Patient ID: SSc-19). Mono, monocytes, macrophages, and conventional dendritic cells (cDC); pDC, plasmacytoid dendritic cells; CD4T, CD4⁺ T cells; CD8T, CD8⁺ T cells; NK, natural killer cells; B, B cells; Neu, neutrophils; Eo, eosinophils; Tissue, tissue cells. **(b)** Balloon plot showing highly expressed genes in each population shown in **(a)**. **(c)** Balloon plot showing highly expressed surface antigens in each population shown in **(a)**

Supplementary Figure 15.
Pathway analysis using differentially expressed genes of the THBS1_Mac subset.



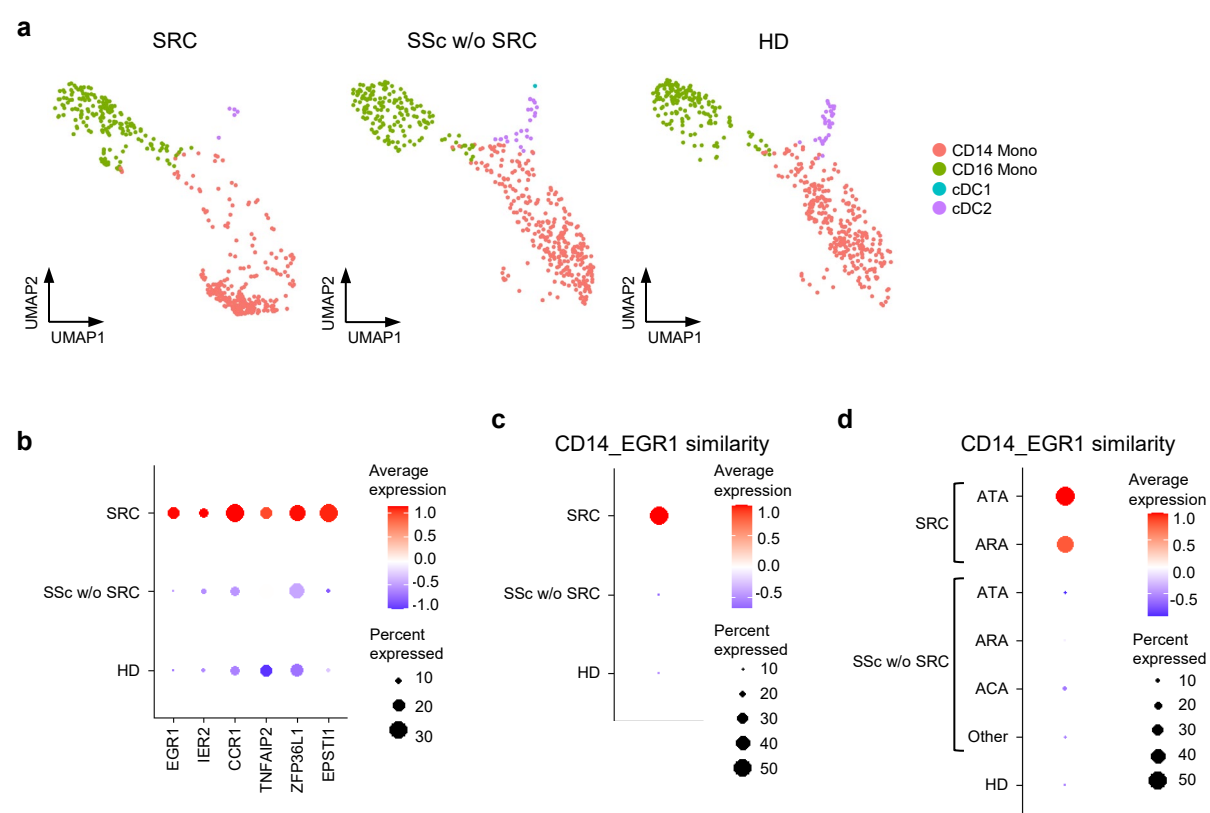
Gene set enrichment analysis of differentially expressed genes in the THBS1_Mac subset using the BioPlanet 2019. *P*-values were calculated using Fisher’s exact test, with Benjamini–Hochberg method for multiple comparison. Source data are provided as a Source Data file.

Supplementary Figure 16.
Feature plots of immature monocyte marker genes in monocytes, cDC, and macrophages derived from the patient at the onset of SRC.



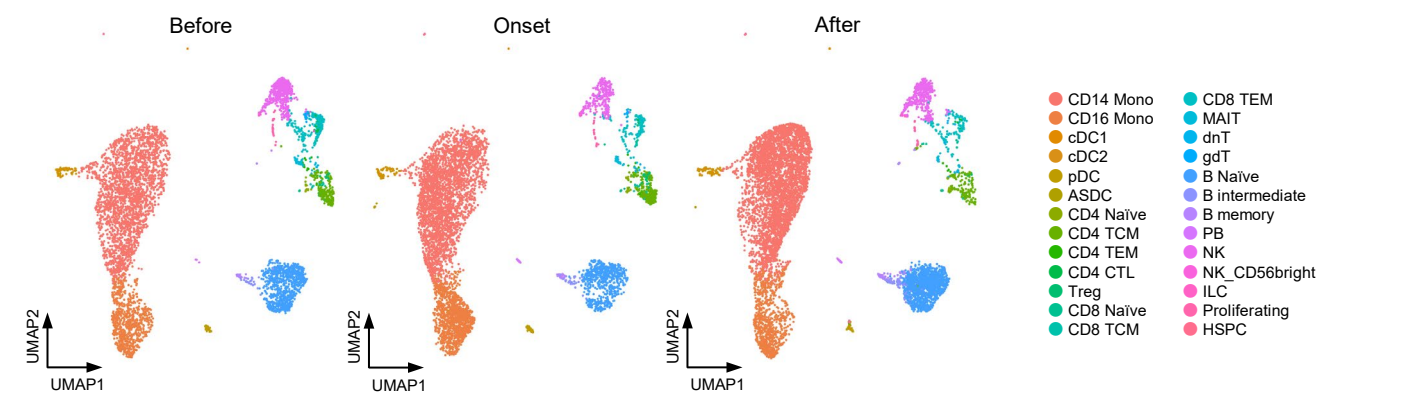
Feature plots showing the gene expression levels of *S100A12* (left), and *HLA-DRB1* (right) in monocytes, macrophages and cDCs from both peripheral blood and kidney of the patient at the onset of SRC (Patient ID: SSc-19).

Supplementary Figure 17.
Confirmation of distinct gene expression changes in monocytes from a publicly available dataset.



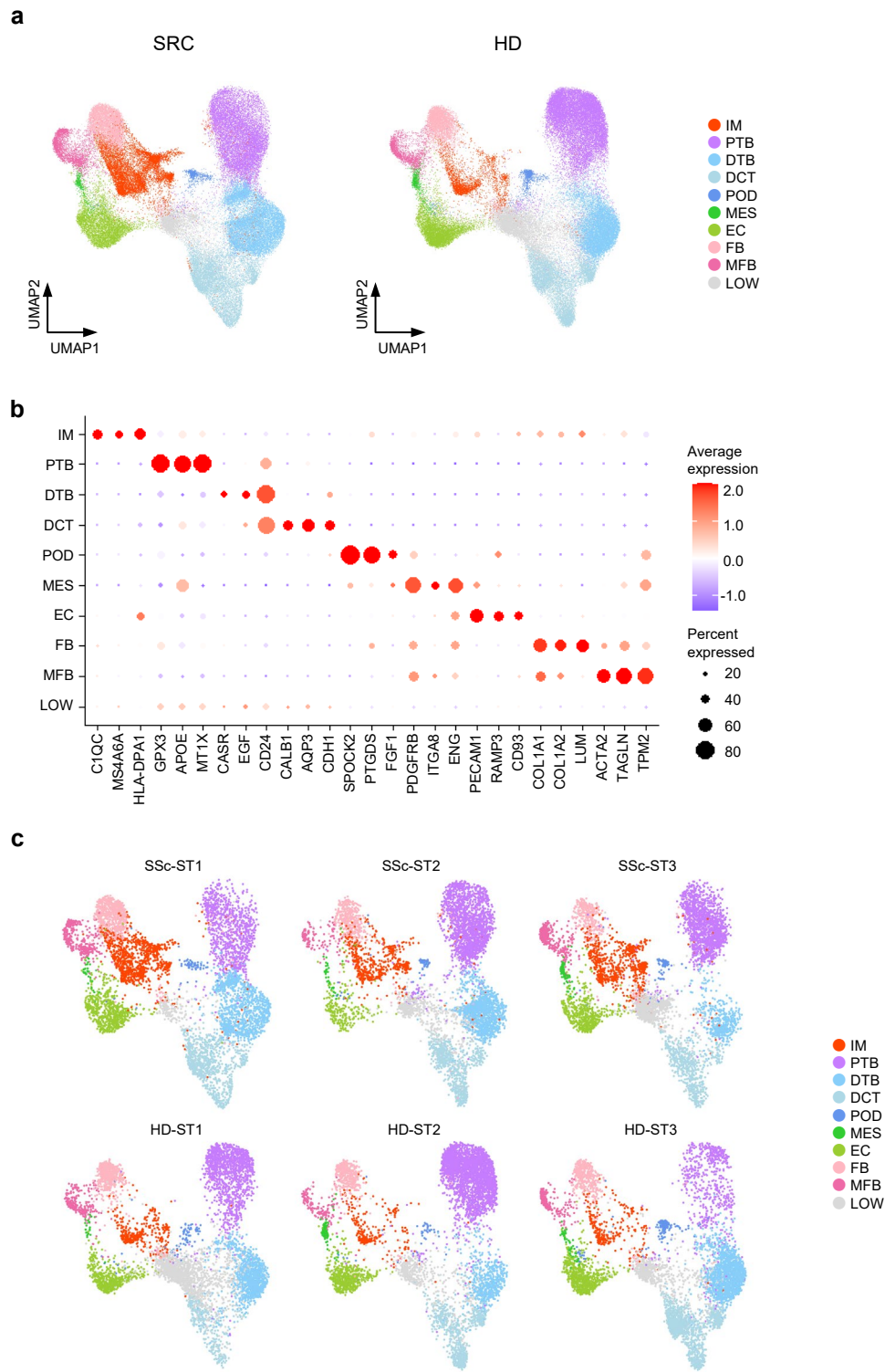
(a) UMAP plots of monocytes from SSc patients with SRC (SRC, n=3), SSc patients without SRC (SSc w/o SRC, n=28), and healthy donors (HD, n=19). The scRNA-seq data were obtained from a publicly available dataset in the gene expression omnibus under accession number GSE195452. Each cellular cluster was annotated with reference mapping. Each plot shows 700 randomly selected cells. Mono, monocytes; cDC, conventional dendritic cells. **(b)** Balloon plot showing the expression level of representative highly expressed genes of the CD14_EGR1 subset, in CD14⁺ monocytes of each disease group. **(c)** Balloon plot showing the module score in CD14⁺ monocytes of each disease group, calculated using the differentially expressed genes (fold change >0.5) of the CD14_EGR1 subset (CD14_EGR1 similarity). **(d)** Balloon plot showing CD14_EGR1 similarity in CD14⁺ monocytes, with patients separated by disease and autoantibody status. ATA, anti-topoisomerase I antibody; ARA, anti-RNA polymerase III antibody; ACA, anti-centromere antibody.

Supplementary Figure 18.
UMAP plots of PBMCs derived from a patient with SSc before the development, at the onset, and after the treatment of SRC.



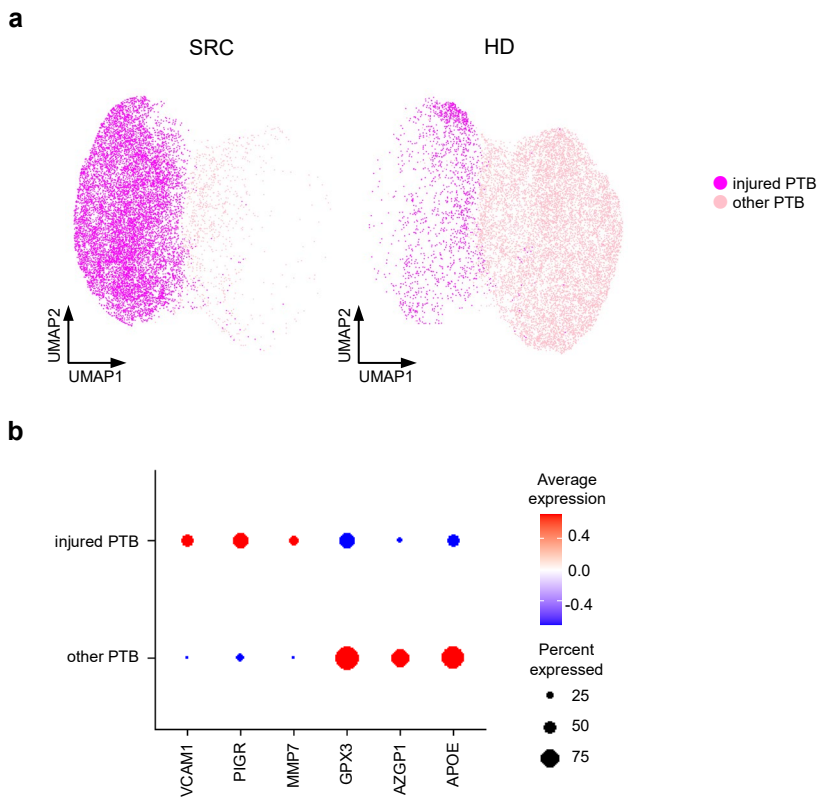
UMAP plots of PBMCs from one patient with SSc (Patient ID: SSc-1) before the development (Before), at its onset (Onset), and after the treatment (After) of SRC. Each cellular cluster was annotated with reference mapping. Mono, monocytes; cDC, conventional dendritic cells; ASDC, AXL⁺ dendritic cells; pDC, plasmacytoid dendritic cells; TCM, central memory T cells; TEM, effector memory T cells; CTL, cytotoxic T lymphocytes; Treg, regulatory T cells; MAIT, mucosal associated invariant T cells; dnT, double negative T cells; gdT, gamma-delta T cells; PB, plasmablasts; NK, natural killer cells; ILC, innate lymphoid cells; Proliferating, proliferating cells; HSPC, hematopoietic stem and progenitor cells.

Supplementary Figure 19.
UMAP plots of kidney cells analyzed through spatial transcriptomics.



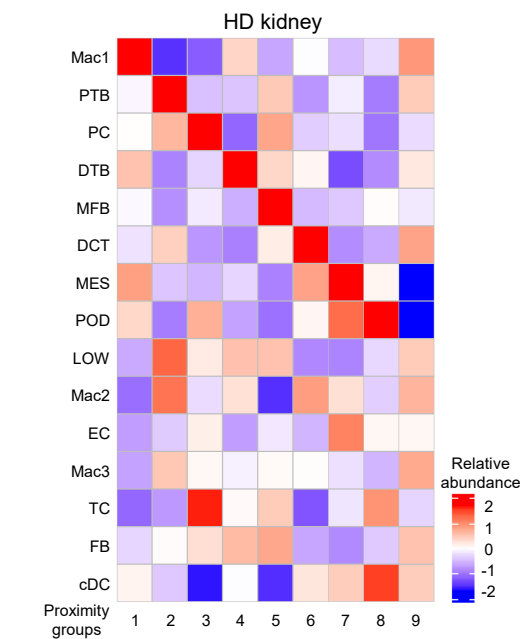
(a) UMAP plots of renal cells from patients with SRC (SRC; n=3) and HDs (HD; n=3). Ten cellular clusters were identified; IM, immune cells; PTB, proximal tubular cells; DCT, collecting duct; DTB, distal tubular cells; POD, podocytes; MES, mesangial cells; EC, endothelial cells; FB, fibroblasts; MFB, myofibroblasts; LOW, low-quality cells. Each plot shows 60,000 randomly selected cells. **(b)** Balloon plot showing highly expressed genes in each population shown in **(a)**. **(c)** UMAP plots of renal cells in each patient with SRC and HD. Each plot shows 6,000 randomly selected cells.

Supplementary Figure 20.
UMAP plots of proximal tubular cells derived from SRC patients and HDs.



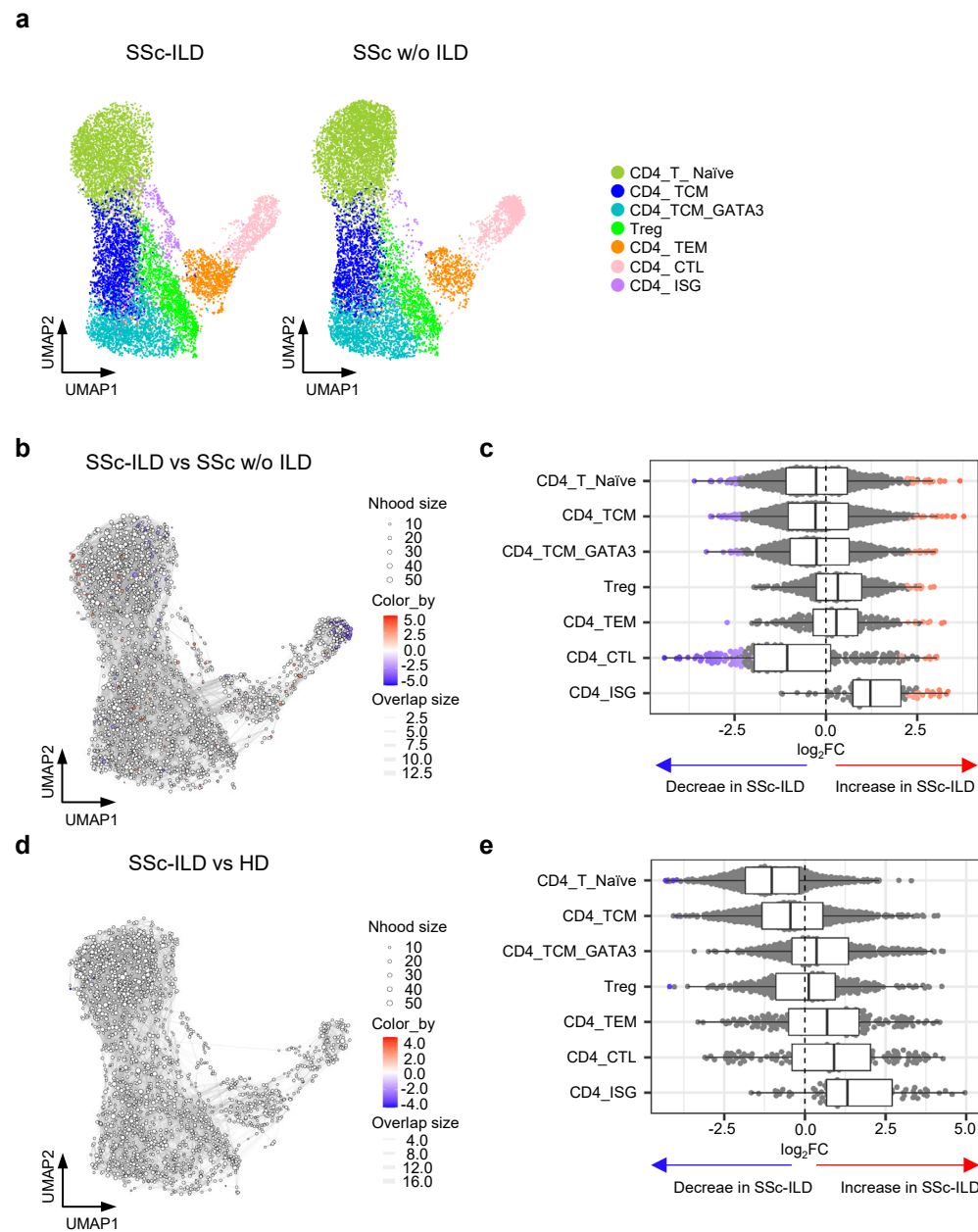
(a) UMAP plots of PTBs from SRC patients (SRC, n=3) and HDs (HD; n=3). Each plot shows 12,000 randomly selected cells. **(b)** Balloon plot showing highly expressed genes in each subpopulation shown in **(a)**.

Supplementary Figure 21.
Cellular proximity analysis on kidney tissue of HDs.



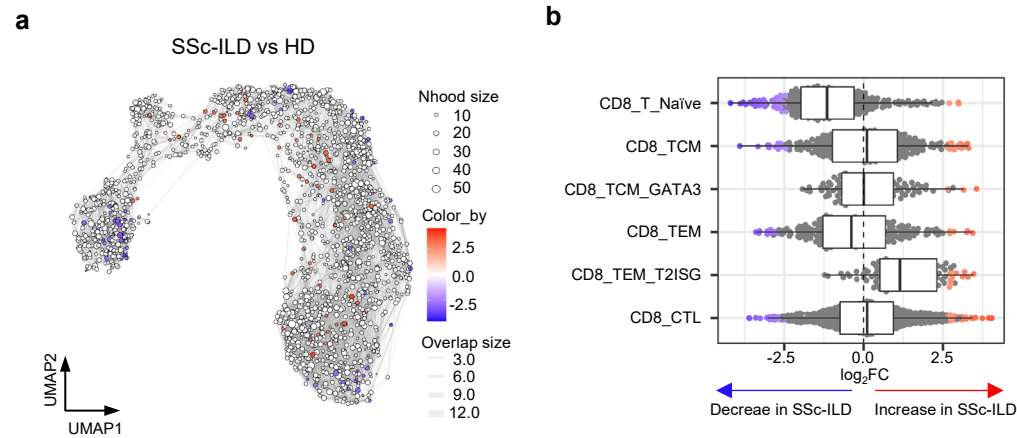
Heatmap showing the abundance of each cell subpopulation in proximity groups in the kidney of HDs. Mac1, macrophage 1; Mac2, macrophage 2; Mac3, macrophage 3; PTB, proximal tubular cells; DCT, collecting duct cells; DTB, distal tubular cells; POD, podocytes; MES, mesangial cells; EC, endothelial cells; FB, fibroblasts; MFB, myofibroblasts; LOW, low-quality cells.

Supplementary Figure 22.
Differential abundance analysis of CD4⁺ T cells derived from patients with SSc and HDs.



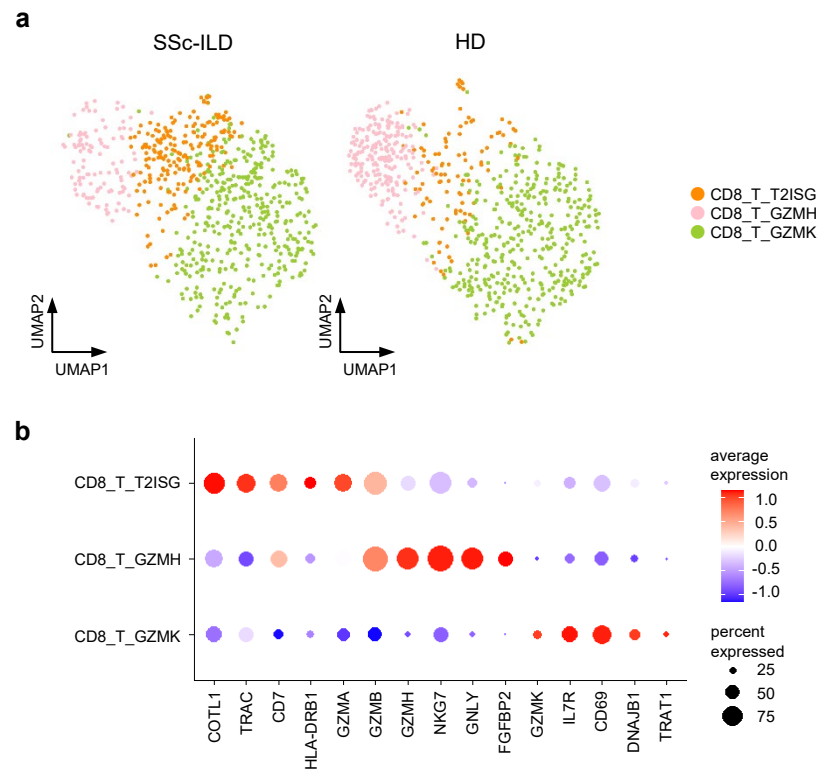
(a) UMAP plots of peripheral CD4⁺ T cells from SSc patients with interstitial lung disease (SSc-ILD; n = 12) and those without ILD (SSc w/o ILD; n = 9). Cell annotations were consistent with those described in **Supplementary Fig. 4**. Each plot shows 10,000 randomly selected cells. **(b)** Neighborhood graph of peripheral CD4⁺ T cells from SSc patients, generated in a similar fashion as in **Fig. 2a**. The color scale indicates the log₂-fold difference between SSc-ILD and SSc w/o ILD. Neighborhoods showing an increase in SSc-ILD are colored in red, while those with a decrease are in blue. **(c)** Beeswarm and box plots showing the distribution of log₂-fold differences between SSc-ILD (n=12) and SSc w/o ILD (n=9) in neighborhoods in different cell subsets, colored as in **(b)**. Box plots are created as in **Fig. 2b**. Neighborhood graph **(d)** and Beeswarm plots **(e)** of peripheral CD4⁺ T cells from SSc-ILD (n=12) and HDs (n=6), generated in a similar fashion as in **(b)** and **(c)**, respectively. Neighborhoods showing an increase in SSc-ILD are colored in red, while those with a decrease are in blue.

Supplementary Figure 23.
Differential abundance analysis of CD8⁺ T cells between patients with SSc-ILD and HDs.



(a) Neighborhood graph of peripheral CD8⁺ T cells from SSc-ILD and HDs, generated in a similar fashion as in **Fig. 2a**. The color scale indicates the log₂-fold difference between SSc-ILD and HDs. Neighborhoods showing an increase in SSc-ILD are colored in red, while those with a decrease are in blue. **(b)** Beeswarm and box plots showing the distribution of log₂-fold differences between SSc-ILD (n=12) and HDs (n=6) in neighborhoods in different cell subsets, colored as in **(a)**. Box plots are created as in **Fig. 2b**.

Supplementary Figure 24.
UMAP plots of lung CD8⁺ T cells derived from patients with advanced SSc-ILD and HDs.



(a) UMAP plots of lung CD8⁺ T cells from SSc patients with advanced ILD (SSc-ILD; n=8) and HDs (HD; n=8). Each plot shows 700 randomly selected cells. **(b)** Balloon plot showing highly expressed genes in each subpopulation shown in **(a)**.

Supplementary Table 1.
Scoring for the classification of each patient with SSc according to 2013 ACR/EULAR criteria.

Patient ID (SSc-)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Skin thickening	9	4	9	9	4	4	4	4	4	4	4	4	9	9	9	4	9	4	9	9	4
Fingertip lesions	3	0	3	0	0	0	0	3	0	0	0	0	0	0	0	3	3	0	0	0	0
Telangiectasia	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	2	0	0	0	0	0
Abnormal nailfold capillaries	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
PAH or ILD	2	0	2	2	0	2	2	2	0	2	2	0	2	2	0	2	2	0	0	0	0
Raynaud's phenomenon	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Autoantibody	3	3	3	3	3	3	3	3	3	3	3	3	3	0	3	0	3	3	3	3	3
Sum	20	10	20	17	10	12	14	15	10	12	12	10	17	14	15	14	20	10	15	15	10

Patients with a total score of ≥9 are classified as systemic sclerosis on the basis of 2013 ACR/EULAR classification criteria.

SSc, systemic sclerosis; PAH, pulmonary artery hypertension; ILD, interstitial lung disease; n/a, not assessed.

Supplementary Table 2.
Individual characteristics of systemic sclerosis patients.

Patient ID (SSc-)		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Age (years)		67	56	82	72	64	60	80	58	47	76	81	57	46	61	50	62	77	67	53	74	73
Sex		M	F	F	F	F	M	F	F	M	F	F	F	F	F	F	F	F	F	M	M	F
Duration (years)		0.7	20	0.3	7	17	3	13	7	4	14	3	14	4	6	0.7	6	2	10	5	4	32
mRSS		33	4	6	9	2	2	5	2	2	2	2	2	10	4	28	4	3	2	17	6	2
Dc or Lc		Dc	Lc	Lc	Lc	Lc	Lc	Lc	Lc	Lc	Lc	Lc	Lc	Lc	Lc	Dc	Lc	Lc	Lc	Dc	Lc	Lc
Autoantibody		ARA	ACA	ARA	ARA	ACA	ATA	ACA	ATA	ACA	ARA	ARA	ARA	ATA	ANA (Nu)	ARA	ANA (Nu)	ACA	ACA	ARA	ARA	ACA
immunosuppressant		never	never	never	never	never	never	never	never	never	never	never	never	never	never	never	never	never	never	never	never	never
Malignancy		none	none	none	none	none	none	none	none	none	none	none	none	none	none	none	none	none	none	none	none	none
Infection		none	none	none	none	none	none	none	none	none	none	none	none	none	none	none	none	none	none	none	none	none
Organ involvement	SRC	○	-	-	○	-	-	-	-	-	-	-	-	-	-	-	-	-	-	○	○	-
	ILD	○	-	○	○	-	○	○	○	-	○	○	-	○	○	-	○	○	-	-	-	-
	PAH	-	-	-	-	-	-	○	-	-	-	-	-	-	○	-	-	○	-	-	-	-
	CIPO	-	-	-	-	-	-	-	-	○	-	-	-	-	-	-	○	-	-	-	-	-

SSc, systemic sclerosis; mRSS, modified Rodnan skin score; Dc, diffuse cutaneous; Lc, limited cutaneous; ARA, anti-RNA polymerase III antibody; ACA, anti-centromere antibody; ATA, anti-topoisomerase I antibody; ANA, anti-nuclear antibody; Nu, nucleolar pattern; SRC, scleroderma renal crisis; ILD, interstitial lung disease; PAH, pulmonary artery hypertension; CIPO, chronic intestinal pseudo-obstruction.

Supplementary Table 3.
Detailed clinical information of individual systemic sclerosis patients.

Patient ID (SSc-)			1 (Bef)	1 (Ons)	1 (Aft)	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Blood count	WBC	/μL	6700	5260	6700	8170	7160	5770	7970	5040	6590	5860	5850	8070	8320	5090	8390	7120	8630	5790	8400	6020	3440	5350	5050
	Hb	g/dL	12.8	10.7	9.6	13.5	12.6	11.6	13.7	15.9	11.2	12.8	14.5	12.6	12.6	13.0	14.8	11.8	13.0	12.3	11.3	13.0	7.9	12.1	10.5
	PLT	/μL	31.0	18.7	31.8	23.1	25.6	26.5	18.9	32.8	19.0	36.9	20.7	16.6	22.0	17.5	26.3	21.1	33.3	27.0	25.1	35.1	7.8	7.5	19.2
Biochemical	BUN	mg/dL	17	21	26	n/a	14	27	n/a	16	23	n/a	15	26	15	n/a	9	31	11	14	19	13	54	43	17
	Cr	mg/dL	0.62	1.41	1.49	0.77	0.53	1.07	0.51	0.89	1.03	0.45	0.71	1.04	0.66	0.64	0.44	1.66	0.59	0.46	0.94	0.58	6.50	4.79	0.63
	eGFR	mL/min /1.73m2	98.3	39.9	37.5	60.1	81.1	39.8	90.0	68.1	39.5	107.1	94.0	39.6	64.0	72.8	114.5	25.3	83.1	102.6	44.1	77.8	8.0	10.1	65.1
	AST	IU/L	25	27	24	31	23	25	n/a	19	20	18	18	26	18	n/a	23	16	14	21	23	20	19	21	27
	ALT	IU/L	18	14	13	45	14	10	21	17	8	9	12	12	9	12	23	8	10	12	16	11	12	15	22
	Alb	mg/dL	3.4	3.3	3.4	n/a	3.9	4.3	4.1	4.3	4.4	4.1	4.1	3.6	3.5	4.3	4.2	3.8	3.8	4.2	3.9	3.8	3.8	4.3	3.5
Endocrine	BNP	pg/ml	60.1	50.4	64.2	14.9	24.6	93.7	20.6	n/a	191.2	n/a	5.7	n/a	74.7	21.8	n/a	n/a	n/a	26.5	403.6	n/a	373.2	27.0	n/a
Blood pressure	systolic	mmHg	119	146	125	131	114	118	100	108	110	n/a	118	122	n/a	n/a	117	121	101	n/a	123	n/a	123	121	100
	diastolic	mmHg	73	77	72	81	64	52	60	62	55	n/a	84	60	n/a	n/a	66	74	72	n/a	66	n/a	77	81	55

SSc, systemic sclerosis; Bef, before the onset of scleroderma renal crisis (SRC); Ons, at the onset of SRC; Aft, after the improvement of SRC; WBC, white blood cell; Hb, hemoglobin; PLT, platelet; BUN, blood urea nitrogen; Cr, creatinine; eGFR, estimated glomerular filtration rate; AST, aspartate aminotransferase; ALT, alanine aminotransferase; Alb, albumin; BNP, brain natriuretic peptide; n/a, not assessed.

Supplementary Table 4.
Clinical characteristics of lupus nephritis patients.

Patient ID		LN-1		LN-2		LN-3		LN-4	
Age		57		53		62		73	
Sex		Female		Female		Male		Female	
Immunosuppressant		never		never		never		never	
Classification criteria	Entry criterion	ANA titer	1:2560	1:640	1:640	1:640	1:80		
		Constitutional	2	0	2	2	2		
		Hematologic	0	3	4	3	3		
		Neuropsychiatric	0	0	0	0	0		
		Mucocutaneous	0	6	0	6	6		
		Serosal	5	0	0	5	5		
	Additive criteria	Musculoskeletal	0	0	0	0	0		
		Renal	10	10	10	10	10		
		Antiphospholipid	2	2	0	2	2		
		Complement	4	4	4	0	0		
		Autoantibodies	6	6	6	6	6		
		Sum	29	31	26	34	34		
Autoantibody		dsDNA, Sm		dsDNA, Sm		Sm		dsDNA	
Occult blood (Semi-quantitative)	mg/dL	0.5		0.1		0.2		0.06	
Up/Ucr	g/gCr	2.45		3.62		1.07		1.47	
Urinary cast		Granular, RBC		Granular		Granular, RBC		None	
Renal biopsy class		IV		III+V		IV		III+V	

Patients with a total score of ≥10 in additive criteria are classified as systemic lupus erythematosus on the basis of 2019 EULAR/ACR classification criteria.

LN, lupus nephritis; Up/Ucr, urine protein/urine creatinine ratio; ANA, anti-nuclear antibody; dsDNA, anti-double stranded DNA antibody; Sm, anti-Smith antibody; Granular, granular cast; RBC, red blood cell cast; Renal biopsy class, the class of lupus nephritis according to International Society of Nephrology/Renal Pathology Society 2003 classification.

Supplementary Table 5.
Clinical characteristics of microscopic polyangiitis patients.

Patient ID			MPA-1	MPA-2	MPA-3	MPA-4
Age			81	75	70	82
Sex			Male	Female	Male	Male
Immunosuppressant			never	never	never	never
Classification criteria	Nasal involvement		-	-	-	-
	MPO-ANCA positive		6	6	6	6
	Interstitial lung disease		3	-	3	3
	Pauci-immune glomerulonephritis on biopsy		n/a	3	n/a	n/a
	PR3-ANCA positive		-	-	-	-
	Blood eosinophil count		-	-	-	-
Sum			9	9	9	9
Urine	Occult Blood		2+	2+	2+	2+
	Occult Blood (Semi-Quantitative)	mg/dL	0.2	0.2	0.2	0.5
	Dysmorphic RBC		+	+	+	+
	UP/Ucr	g/gCr	0.37	n/a	n/a	0.17
Biochemical	Creatinine	mg/dL	1.21	0.62	0.98	1.26
	eGFR	mL/min/1.73 m2	44.9	70.3	58.6	42.5
	CRP	mg/dL	15.91	8.28	5.15	4.75
Autoantibody	MPO-ANCA	IU/mL	1730	76.5	1690	430
	PR3-ANCA	IU/mL	<1.0	<1.0	1.4	<1.0

Patients with a total score of ≥6 in classification criteria are classified as microscopic polyangiitis on the basis of 2022 ACR/EULAR classification criteria.

MPA, microscopic polyangiitis; MPO, Myeloperoxidase; PR3, Proteinase 3; RBC, red blood cell; Up/Ucr, urine protein/urine creatinine ratio; eGFR, estimated glomerular filtration rate; CRP, C-reactive protein; n/a, not assesed.

Supplementary Table 6.
Highly expressed genes in the CD14_EGR1 subset.

Gene Name	Fold Change	Adjusted P-value	Gene Name	Fold Change	Adjusted P-value
EGR1	1.158271	2.17E-240	OAS2	0.359836	6.21E-89
APOBEC3A	0.976742	*	PID1	0.358443	2.90E-51
IFI6	0.781818	1.82E-246	HLA-DRB1	0.355888	4.91E-146
DUSP2	0.781811	1.09E-142	CD14	0.352586	7.06E-54
IER2	0.738572	7.37E-79	PLAC8	0.349175	2.20E-37
BTG2	0.736477	9.57E-107	PSMB9	0.34179	4.89E-66
LY6E	0.736218	3.04E-278	RASGEF1B	0.341778	1.58E-60
IFI44L	0.734229	*	AOAH	0.33926	2.68E-27
ISG15	0.695093	2.82E-229	APOL6	0.337521	4.34E-68
MARCKS	0.694066	3.96E-189	KLF6	0.336397	2.04E-33
ZFP36	0.687984	4.21E-98	PLSCR1	0.330976	3.90E-62
LGALS2	0.685241	3.36E-202	IFI35	0.326648	3.08E-59
LAP3	0.653139	1.55E-166	SECTM1	0.326392	7.61E-74
ZFP36L1	0.649951	2.01E-125	FTH1	0.323322	2.82E-75
IL1B	0.649486	3.88E-108	EIF2AK2	0.322508	6.18E-78
MX1	0.644929	3.61E-215	FCGR2A	0.322086	1.77E-49
DUSP6	0.63286	5.50E-160	PLEKHO1	0.318742	1.33E-43
EPSTI1	0.611404	2.38E-207	PIM3	0.317313	2.16E-32
STAT1	0.580824	5.57E-153	FCGR1A	0.316323	5.76E-53
IFITM3	0.569403	6.00E-232	GBP5	0.315832	5.89E-51
TYMP	0.563584	1.04E-160	KLF10	0.313556	1.73E-32
GBP1	0.559666	3.25E-108	CLEC7A	0.311451	4.71E-40
CCL3	0.55723	4.54E-56	GBP2	0.309896	1.20E-46
SGK1	0.552449	7.12E-78	IFNGR2	0.304918	6.35E-41
NFKBIA	0.534898	6.53E-48	GBP4	0.300944	9.46E-60
MAFB	0.519799	3.27E-101	TMEM123	0.295089	4.58E-45
FOS	0.519454	2.37E-30	JUND	0.294136	6.33E-41
PSME2	0.498056	1.67E-130	NFKBIZ	0.293079	8.77E-13
SIGLEC1	0.493446	2.51E-277	RHOB	0.291691	1.44E-27
IFIT3	0.490553	5.72E-154	ATP2B1-AS1	0.291623	2.48E-22
RNF213	0.485568	5.18E-119	FGL2	0.291278	2.99E-37
PARP14	0.481031	1.36E-108	CAMK2D	0.287329	6.30E-77
CD83	0.476977	1.36E-68	PFKFB3	0.286775	5.43E-49
XAF1	0.476277	6.98E-127	VAMP5	0.285805	2.66E-47
SCO2	0.475432	7.11E-118	NAGK	0.283312	2.73E-41
IFIT2	0.466043	2.84E-115	SAMD9L	0.283129	1.25E-58
NAMPT	0.462738	1.14E-70	ADAR	0.280842	1.36E-48
IRF7	0.460575	2.57E-129	NPC2	0.280068	2.35E-50
JUNB	0.457997	1.96E-50	STAT2	0.279287	6.77E-46
DUSP1	0.456272	3.80E-35	PARP9	0.276651	1.42E-55
TNFAIP2	0.454408	1.87E-65	YBX3	0.273014	2.61E-41
IFI44	0.446014	4.88E-175	TNFSF13B	0.272231	1.33E-37
OAS3	0.444138	3.93E-144	BST2	0.27179	2.74E-33
CCR1	0.442989	3.49E-110	ETV6	0.269927	3.68E-30
MX2	0.429879	8.29E-93	BLVRA	0.268984	1.15E-45
HLA-DMA	0.427767	9.36E-128	IFI16	0.268236	1.49E-30
NCF1	0.427174	7.63E-60	FYB1	0.267832	8.07E-36
EGR2	0.417652	2.76E-129	DDX21	0.266457	2.41E-33
CCL3L1	0.417644	6.89E-51	OASL	0.264701	3.87E-76
NEAT1	0.415835	2.79E-64	PLAAT4	0.263787	7.50E-36
TNFSF10	0.408292	5.41E-67	MT2A	0.263221	1.54E-25
CDKN1A	0.402519	6.06E-74	DOK2	0.263217	2.56E-41
ODF3B	0.401084	5.43E-77	BACH1	0.262152	5.75E-29
CD300E	0.398247	1.27E-66	PPP1R15A	0.261136	1.11E-19
HERC5	0.393793	1.01E-128	GIMAP4	0.260141	6.43E-27
SAT1	0.392196	2.97E-77	TAP1	0.259376	1.76E-37
EGR3	0.387468	1.92E-135	KLF2	0.257686	3.72E-45
MS4A6A	0.386594	3.95E-86	TRIM22	0.257234	2.90E-41
UBE2L6	0.384559	2.93E-81	SP110	0.256426	4.73E-35
SERPING1	0.378507	3.54E-176	IGSF6	0.253578	8.31E-24
ATF5	0.368051	1.22E-91	GABARAP	0.252385	2.95E-36
IRF1	0.363032	9.29E-20	CPVL	0.252358	8.67E-42
HLA-DMB	0.361114	2.59E-76	TPM4	0.25104	3.84E-33

A list of genes highly expressed in CD14_EGR1. The *P*-values were calculated using Wilcoxon rank sum test, with the Bonferroni correction for multiple comparison. Genes that shows 0.25 < fold change were listed.

*Adjusted *P*-values were smaller than 1E-280.

Supplementary Table 7.
Highly expressed genes in the THBS1_Mac subset.

Gene Name	Fold Change	Adjusted P-value	Gene Name	Fold Change	Adjusted P-value	Gene Name	Fold Change	Adjusted P-value	Gene Name	Fold Change	Adjusted P-value
IL1B	1.580517	5.59E-42	OLR1	0.573384	2.80E-32	PNP	0.434256	4.01E-08	GTF2B	0.339835	5.59E-06
THBS1	1.443928	7.03E-52	FOSL2	0.568487	6.04E-08	RAB20	0.433299	7.21E-08	TAF13	0.338688	0.000675
DUSP2	1.279657	1.32E-55	FSIP1	0.561203	6.27E-57	PPP1R10	0.432674	9.63E-05	ZMIZ1	0.335069	0.000556
PRDM1	1.236803	8.97E-52	MAFB	0.559206	3.15E-08	TREM1	0.431822	1.16E-09	DCUN1D3	0.333713	5.39E-21
EREG	1.158141	2.86E-76	CYT1P	0.557132	8.76E-13	MARCKSL1	0.42832	1.05E-05	CLIP4	0.332697	0.00539
LDLR	1.073555	2.44E-46	NINJ1	0.557078	1.96E-14	ETV3	0.427693	7.85E-05	KBTBD8	0.331982	9.30E-19
ATF3	1.070931	2.08E-50	TIMP1	0.543202	1.10E-12	ATF5	0.423983	1.90E-05	PTGER2	0.331496	0.00579
PPIF	1.023098	2.90E-25	WARS	0.541636	1.36E-14	CCL2	0.423589	6.50E-08	PRDM8	0.330206	2.41E-24
GPR183	1.014359	9.14E-28	NFKB1	0.540687	3.48E-09	SLAMF7	0.422182	0.00185	CHRA1	0.32757	0.00556
NAMPT	0.984733	4.75E-28	TNF	0.5386	2.11E-06	PNPLA8	0.420787	2.62E-05	SKIL	0.326066	0.0269
TIPARP	0.984456	2.60E-27	MYADM	0.537668	2.87E-16	NDEL1	0.41803	0.000222	DNAJB9	0.325732	3.23E-05
G0S2	0.976618	7.01E-36	ATP2B1	0.536863	2.00E-13	RUNX3	0.415276	7.29E-07	SLC3A2	0.323104	0.00126
AC245128.3	0.975957	3.18E-25	APOBEC3A	0.536492	1.04E-07	CYCS	0.408305	1.27E-05	EIF1	0.320462	1.52E-15
CDKN1A	0.944242	3.24E-25	MALT1	0.532531	1.08E-10	AGO2	0.408121	2.87E-05	TRAF1	0.31983	5.32E-08
FOSB	0.939475	7.61E-24	STX11	0.532124	1.55E-14	RASSF5	0.404924	6.96E-11	FOSL1	0.319696	8.08E-17
SAMSN1	0.925624	3.36E-25	HCAR2	0.531487	5.53E-17	VDR	0.403877	0.000374	AVP11	0.318746	8.12E-15
TNFAIP3	0.894575	3.29E-19	BCL2A1	0.531055	4.74E-09	SYAP1	0.401832	1.15E-05	CTNNB1	0.318704	0.00201
IER3	0.884859	7.98E-14	DDX3Y	0.526316	5.49E-10	KYNU	0.39973	5.78E-05	RNMT	0.317883	0.00288
BIRC3	0.873767	4.08E-21	HIVEP1	0.525166	1.77E-08	LACC1	0.399066	1.72E-07	MIR3142HG	0.317124	1.82E-17
PDE4B	0.849936	2.21E-21	PHACTR1	0.522453	4.06E-11	GLA	0.396329	8.73E-07	SFPQ	0.314184	2.66E-07
BCL3	0.84406	1.14E-28	OTUD1	0.521699	1.61E-10	GCH1	0.395538	4.32E-06	FLT1	0.313724	1.18E-13
SOD2	0.842605	4.52E-27	CD55	0.517386	1.21E-13	PAPSS2	0.390583	0.0147	CEMP2	0.312793	0.00516
CXCL10	0.841318	2.71E-19	GBP1	0.516198	0.0375	GRASP	0.39046	1.49E-22	SLC2A6	0.312716	0.0394
SODCS3	0.839517	8.81E-27	REL	0.514873	9.94E-14	SDC4	0.386541	1.86E-32	HERPUD1	0.310861	0.00861
CXCL2	0.839083	2.58E-34	CCRL2	0.512925	2.94E-30	TNFAIP6	0.385836	5.50E-08	LPCAT1	0.310846	0.00507
INSIG1	0.830625	4.65E-16	CLK1	0.509391	4.76E-13	DDX3X	0.385658	3.76E-12	EGR3	0.310607	5.89E-11
NR4A2	0.819575	9.25E-26	TP53INP2	0.50687	8.01E-32	SLC43A2	0.384857	2.50E-05	ATP1A1	0.310123	0.000197
NR4A1	0.811603	1.41E-17	B4GALT5	0.504583	2.56E-08	HIC1	0.384795	4.12E-23	SLC39A8	0.308954	6.37E-11
LRG1	0.808774	1.71E-48	SPATA13	0.500946	2.08E-05	MAP3K8	0.382026	0.0146	EPB41L3	0.308904	0.00119
CXCL8	0.805957	9.19E-10	SLC38A2	0.495042	1.23E-09	PPP1R15B	0.380733	0.00135	SPP1	0.308287	1.43E-46
CD83	0.805793	5.02E-18	METRNL	0.494583	1.45E-10	TGIF1	0.380393	2.48E-06	PLK3	0.308015	4.19E-07
HBEGF	0.801275	2.05E-30	MAPK6	0.49437	7.40E-09	ATF4	0.379576	2.70E-08	VRK2	0.307432	0.0218
NR4A3	0.783366	3.90E-66	IRF2BP1	0.492268	3.70E-05	NLRP3	0.378678	0.0182	ZEB2.AS1	0.307089	0.0165
PTX3	0.781423	1.07E-20	GK	0.491716	7.14E-07	SRGN	0.377348	9.57E-17	ZNFX1	0.30185	0.00871
ZC3H12A	0.773529	6.85E-26	MAFF	0.488832	1.04E-20	MARCKS	0.37636	3.77E-07	SH2B3	0.300565	9.42E-07
LMNA	0.76736	7.17E-19	DDX21	0.487425	2.22E-15	GABARAPL1	0.375173	2.08E-07	HLA.DRA	0.299506	3.13E-07
PPP1R15A	0.753415	6.24E-18	RIPK2	0.486482	1.89E-05	GADD45B	0.372629	0.0422	SLC31A2	0.29862	0.000802
PLAUR	0.746652	2.36E-18	CXCL16	0.486284	9.66E-10	CHMP1B	0.371566	0.000116	LONRF3	0.297225	3.63E-06
SLC2A3	0.731162	1.52E-10	MIR22HG	0.475745	3.87E-10	TOD2	0.37156	0.000330	RAP1B	0.287849	7.86E-05
THBD	0.723934	1.22E-13	AP000944.2	0.475742	1.55E-32	GBP4	0.370807	0.0234	CRK	0.284268	0.00329
SERPINB9	0.722014	1.75E-19	PIM3	0.472939	5.41E-07	DNAJA1	0.36911	2.06E-05	LAMB3	0.282819	2.80E-51
CYP1B1	0.716447	3.29E-07	NAB1	0.472892	7.47E-08	KMO	0.368672	0.00228	MCL1	0.28266	2.03E-08
KDM6B	0.712864	6.31E-20	MN1	0.472224	5.44E-16	PTPRE	0.368041	9.15E-09	NUP98	0.282368	0.0489
CREM	0.70559	2.03E-20	ATP1B3	0.472024	3.80E-14	FTH1	0.365557	3.14E-21	RARG	0.280519	0.0453
ZNFX1	0.698768	2.62E-11	NFKBID	0.471461	1.44E-08	SIK2	0.362161	0.00174	STARD8	0.280406	6.77E-05
SERPINB2	0.69606	1.33E-14	EMP1	0.469674	2.61E-05	CSRNP1	0.360823	6.56E-06	IPMK	0.27803	0.0431
NFE2L2	0.673084	4.98E-21	WTAP	0.467285	1.24E-08	MTHFD2	0.359499	0.0144	BRD2	0.277291	3.87E-06
NFKBIA	0.670248	6.59E-15	IRF8	0.46484	0.000356	ZBTB21	0.358964	0.000153	ICOSLG	0.274141	3.25E-08
PTGS2	0.66467	2.83E-11	PFKFB3	0.463398	1.20E-06	EHD1	0.358405	3.18E-07	TRA2B	0.271126	0.00725
DDIT4	0.66313	1.47E-33	TFRC	0.46235	1.24E-05	FEM1C	0.358035	7.31E-06	SECTM1	0.269615	0.0250
ARL5B	0.662029	4.23E-14	PHLDA1	0.461287	8.70E-46	C15orf48	0.357414	1.91E-10	BTG3	0.269428	0.000142
MXD1	0.661754	1.31E-14	EZR	0.459145	1.51E-11	NFKB2	0.356979	6.12E-05	RBKS	0.2676	0.00884
ICAM1	0.660757	3.62E-15	TRMT6	0.459018	9.56E-05	ETF1	0.356807	9.32E-06	ACAT2	0.261639	0.000585
ARL4C	0.659243	1.30E-07	IRAK2	0.457512	8.22E-21	LINC00877	0.356406	0.000989	TMEM88	0.26155	1.86E-12
IL1A	0.657966	4.65E-68	ADM	0.449877	1.08E-09	SELENOK	0.355569	0.000792	TAGLN2	0.261206	0.000237
CCL4	0.645928	4.02E-30	MB21D2	0.443941	1.02E-38	MIR3945HG	0.353478	1.75E-23	GNA15	0.261136	0.0319
SRC	0.62608	8.87E-16	CHD1	0.443755	4.77E-10	ACSL1	0.352054	0.0464	RAB1A	0.260809	0.00470
AREG	0.603583	2.86E-45	AHR	0.443047	0.000814	BTG2	0.351448	6.12E-07	NFKBIB	0.260168	0.00784
RGCC	0.601026	9.57E-12	ZNFX2	0.441293	2.51E-08	CCNL1	0.350921	1.68E-05	SERTAD1	0.259573	6.96E-06
C5AR1	0.600628	2.20E-17	FCAR	0.440147	1.08E-11	OXSR1	0.350461	0.000471	CD44	0.253635	0.00698
ATP13A3	0.591687	2.14E-09	LITAF	0.440006	1.19E-09	MAFG	0.349345	0.000455	SNHG15	0.25283	0.000583
SEMA6B	0.589178	1.62E-52	USP36	0.438716	1.55E-06	ERN1	0.348092	0.000180	PHLDA2	0.251836	9.68E-31
RASGEF1B	0.583057	5.77E-11	TICAM1	0.43774	1.48E-07	TPRA1	0.34629	0.00132			
SLC7A5	0.581387	8.26E-56	RYBP	0.43708	3.25E-06	CCL4L2	0.346026	2.36E-08			

A list of genes highly expressed in THBS1_Mac. The *P*-values were calculated using Wilcoxon rank sum test, with the Bonferroni correction for multiple comparison. Genes that shows 0.25 < fold change were listed.

Supplementary Table 8.
Individual characteristics of patients with scleroderma renal crisis and healthy donors whose kidney tissue was used for spatial transcriptomic analysis.

Patient ID		SSc-ST1	SSc-ST2	SSc-ST3	HD-ST1	HD-ST2	HD-ST3
Age (years)		53	58	72	62	68	53
Sex		M	F	F	F	F	M
Duration (years)		5	0.3	1			
mRSS		17	35	40			
Dc or Lc		Dc	Dc	Dc			
Autoantibody		ARA	ATA	ARA			
immunosuppressant (at biopsy)		none	PSL, IVCY	none			
immunosuppressant (prior use)		never	PSL, IVCY	MMF			
Malignancy		none	none	none			
Infection		none	none	none			
Pathological findings in renal biopsy	intimal thickening and luminal narrowing	○	○	○			
	fibrinoid necrosis	○	○	○			
	glomerular shrinkage	○	○	○			

SSc, systemic sclerosis; HD, healthy donor; ST, spatial transcriptome; mRSS, modified Rodnan skin score; Dc, diffuse cutaneous; Lc, limited cutaneous; ARA, anti-RNA polymerase III antibody; ATA, anti-topoisomerase I antibody; MMF, mycophenolate mofetil; PSL, prednisolone; IVCY, intravenous cyclophosphamide pulse therapy. SSc-ST1 is the same patient as SSc-19 in scRNA-seq experiments (Supplementary Tables 1-3).

Supplementary Table 9.
Highly expressed genes in the Mac1 subset in the spatial transcriptomic analysis.

Gene Name	Fold Change	Adjusted P-value	Gene Name	Fold Change	Adjusted P-value	Gene Name	Fold Change	Adjusted P-value
MEG3	2.704333	*	PTEN	0.945905	2.96E-59	EGFR	0.490007	1.72E-17
CARMN	2.277462	3.89E-214	SPRY4	0.939849	7.06E-32	CD63	0.481774	5.72E-41
COL1A1	2.158605	*	ADGRF5	0.930095	5.36E-42	ESR1	0.479502	3.72E-17
COL1A2	2.105193	*	PSD3	0.92898	3.29E-45	ITGA8	0.473603	3.74E-19
NR2F2	2.076379	*	TPM2	0.91542	1.68E-80	ARID5B	0.470324	5.13E-20
COL3A1	2.039325	*	EPHA2	0.910759	1.66E-38	SMAD3	0.461907	2.49E-11
ITGA1	2.025868	4.70E-220	ANGPT1	0.888116	2.39E-27	ACTA2	0.451784	1.03E-22
PDGFRB	1.938838	1.91E-285	DST	0.875352	5.13E-28	SMAD4	0.438682	8.12E-17
COL16A1	1.897626	1.11E-163	COL5A3	0.865515	1.69E-23	DLL1	0.417255	6.61E-16
PDGFRA	1.851367	4.92E-236	TGFB2	0.86538	4.55E-88	IGF2	0.415437	3.03E-10
COL6A1	1.793651	1.64E-219	NGFR	0.860063	1.37E-37	FLT3LG	0.402453	2.32E-18
COL14A1	1.789535	1.12E-125	TNFSF15	0.852643	3.40E-28	ITGB1	0.380228	1.88E-26
COL6A3	1.739708	9.39E-189	WNT5A	0.850076	8.25E-20	SELENOP	0.378259	1.77E-44
OSMR	1.724404	3.17E-120	PLCG1	0.845699	3.47E-49	RXR8	0.37209	3.71E-25
COL6A2	1.713243	4.27E-241	THBS1	0.834587	5.84E-102	KITLG	0.369647	9.74E-10
COL5A1	1.712738	5.41E-136	MYL9	0.831456	9.68E-92	VIM	0.363543	8.79E-36
THBS2	1.700404	4.64E-122	C11orf96	0.823636	2.61E-68	VEGFB	0.363121	1.92E-24
COL27A1	1.671706	9.31E-97	LGALS3BP	0.823099	1.46E-83	HSP90B1	0.362171	9.09E-24
IL34	1.657756	5.53E-74	NEAT1	0.79608	1.17E-80	SPARCL1	0.358431	3.99E-22
TNXA.B	1.65387	4.64E-152	INHBA	0.778039	2.20E-24	RPS4Y1	0.352804	3.99E-31
CDH11	1.632467	4.92E-82	IGFBP7	0.759286	2.77E-129	RARB	0.345206	1.56E-16
G0S2	1.608399	5.23E-164	HMGCS1	0.754579	1.02E-26	IL4R	0.343908	6.88E-14
MXRA8	1.602373	5.00E-184	TPM1	0.750023	1.14E-79	VEGFA	0.338033	6.14E-13
ENG	1.570799	2.38E-199	ACACB	0.737704	3.20E-39	PTK2	0.334456	2.68E-18
LUM	1.552633	4.36E-223	IL1R1	0.727505	3.23E-26	STAT6	0.317762	4.44E-19
COL15A1	1.522043	3.10E-115	TM4SF1	0.727255	2.04E-21	FZD8	0.316596	1.02E-08
TSHZ2	1.493397	1.02E-53	NUPR1	0.708384	5.59E-61	BST2	0.31338	6.08E-35
MRC2	1.490605	1.52E-163	HSPG2	0.681715	1.09E-58	BMP4	0.309121	5.01E-14
LDB2	1.479809	2.93E-99	RXRA	0.663472	7.44E-36	CD44	0.307944	3.01E-25
COL4A2	1.474494	7.65E-159	TAGLN	0.66182	5.01E-62	TNFRSF14	0.301304	5.93E-23
COL18A1	1.458633	1.38E-152	THSD4	0.659983	3.30E-21	MAPK14	0.298802	8.79E-18
PTGDS	1.449686	2.50E-72	ETS1	0.659477	7.14E-36	ROR1	0.28879	2.96E-14
PXDN	1.449086	1.30E-89	NR1H3	0.655615	1.91E-34	TLR4	0.28306	7.46E-14
BMP5	1.430487	7.52E-60	ABL1	0.654245	8.28E-29	PSSA	0.279771	1.33E-18
COL4A1	1.427977	9.27E-167	ACVRL1	0.652484	1.67E-40	FZD1	0.279375	3.54E-12
COL12A1	1.408909	5.33E-97	TIMP1	0.649953	1.39E-54	IGFBP5	0.279337	7.79E-24
ADGRA2	1.398589	5.64E-109	ITGA9	0.620837	2.29E-41	RAMP1	0.266568	8.49E-15
LAMA4	1.397445	1.21E-76	IGF2R	0.618338	7.92E-19	ELANE	0.264012	1.08E-13
LIFR	1.377897	4.11E-72	DDR2	0.617271	4.20E-26	CALM2	0.258591	2.85E-27
HGF	1.373486	1.39E-95	NCAM1	0.611882	1.26E-13			
MMP2	1.361842	7.59E-128	CD81	0.60173	2.14E-67			
DCN	1.347683	1.72E-229	CYP1B1	0.590867	3.01E-36			
BGN	1.261271	1.60E-167	TNFRSF1A	0.584329	1.81E-49			
RARRES2	1.247356	1.03E-150	BASP1	0.581026	7.68E-53			
SNAI2	1.218505	1.23E-78	MALAT1	0.577775	6.25E-69			
CSF1	1.174652	4.05E-89	TNFRSF11B	0.574489	1.21E-13			
IGFBP3	1.174491	4.85E-65	LTBR	0.569611	1.92E-37			
VCAM1	1.166001	5.05E-62	NR3C1	0.567795	1.72E-34			
SORBS1	1.158165	9.73E-33	FAS	0.559303	2.74E-23			
MGP	1.143577	5.99E-152	HDAC4	0.55391	4.63E-27			
CXCL12	1.131781	7.85E-124	SNAI1	0.54296	5.16E-34			
IFITM1	1.12706	1.01E-142	SQSTM1	0.542185	4.26E-60			
FGF7	1.118311	2.48E-52	SREBF1	0.538148	1.38E-18			
COL5A2	1.117315	1.31E-30	RYK	0.533308	3.39E-16			
SERPINH1	1.113099	2.91E-78	STAT3	0.531528	2.13E-26			
VCAN	1.07391	3.89E-41	IFITM3	0.530289	1.92E-55			
IL6ST	1.072264	2.01E-132	BMP1	0.524252	8.32E-17			
CALD1	1.070877	2.95E-109	SPRY2	0.522339	1.10E-14			
FN1	1.051251	3.06E-50	EFNB1	0.516698	6.51E-14			
NOTCH3	1.032188	5.44E-40	NPR2	0.516636	3.94E-21			
MMP14	1.030685	9.18E-75	ADGRE5	0.516454	4.09E-34			
CACNA1C	1.006423	8.79E-40	CCDC80	0.516316	4.31E-20			
CCL21	0.996741	2.43E-48	PLAC9	0.506096	3.74E-22			
JAG1	0.950446	9.92E-58	SLC40A1	0.495322	1.57E-60			

A list of genes highly expressed in Mac1. The *P*-values were calculated using Wilcoxon rank sum test, with the Bonferroni correction for multiple comparison. Genes that shows 0.25 < fold change were listed. *Adjusted *P*-values were smaller than 1E-300.

Supplementary Table 10.
Highly expressed genes in the CD8_TEM_T2ISG subset.

Gene Name	Fold Change	Adjusted P-value	Gene Name	Fold Change	Adjusted P-value	Gene Name	Fold Change	Adjusted P-value	Gene Name	Fold Change	Adjusted P-value
CD74	1.580585	*	VIM	0.395588	0.000342	CD84	0.319389	3.63E-49	GALM	0.278428	4.92E-63
GZMK	1.555568	*	LIMS1	0.395051	9.75E-78	GPR183	0.317972	9.59E-64	FLNA	0.277711	1.26E-17
COTL1	1.402714	1.83E-236	SUB1	0.393905	1.03E-11	HIST1H1D	0.31649	3.77E-11	MT-CO3	0.277586	4.92E-09
HLA-DRA	1.245813	1.58E-240	MYL6	0.390611	6.16E-15	GBP4	0.315695	2.65E-33	LSP1	0.276216	3.19E-08
HLA-DRB1	0.928799	7.65E-134	MXD4	0.388636	6.77E-33	CHI3L2	0.314747	1.35E-38	RGS1	0.275165	9.75E-112
GAPDH	0.867229	1.69E-49	GSTK1	0.385915	5.56E-33	PIIB	0.31392	1.39E-14	WNK1	0.273691	5.52E-24
CNN2	0.815756	5.57E-86	PSME1	0.383567	1.39E-16	ATP5MC2	0.313569	0.0156	PSMD8	0.272855	7.89E-18
HLA-DRB5	0.760765	1.56E-99	H2AFV	0.381925	3.24E-11	YWHA8	0.31311	1.18E-20	ANXA6	0.272451	1.28E-13
CLDN1	0.682801	2.23E-78	LIMD2	0.376821	1.33E-16	ARHGDIB	0.312167	0.000901	LYST	0.272042	1.78E-22
CD27	0.663479	3.90E-49	WIPI1	0.373296	3.94E-34	TRAT1	0.311786	4.22E-63	HNRNPFF	0.271351	3.96E-10
GZMA	0.645231	5.15E-54	DYNLL1	0.371889	2.19E-24	CD82	0.310953	1.95E-69	MX1	0.271165	7.03E-17
ACTG1	0.641273	0.00193	UCP2	0.370589	0.00325	TAGLN2	0.309795	1.10E-17	SIRPG	0.271057	9.94E-24
HLA-DPA1	0.623706	4.18E-80	PPP1CA	0.36926	7.83E-20	LCK	0.309066	7.40E-14	PPM1G	0.270999	2.44E-17
PFN1	0.613574	4.31E-44	GMFG	0.367724	1.28E-20	ETS1	0.308634	1.06E-27	MT-CO1	0.270816	1.93E-20
TIGIT	0.598728	5.59E-53	CFL1	0.364439	0.00149	COX6A1	0.308396	6.93E-05	MRPL10	0.27081	5.02E-17
HLA-DQA1	0.589734	2.47E-75	LCP1	0.363349	1.84E-13	OAZ1	0.307233	1.09E-18	IL10RA	0.270301	2.34E-26
HLA-DQB1	0.571533	3.29E-124	CAPZB	0.361931	1.39E-15	TRAC	0.307062	1.67E-19	SPTNB1	0.270194	3.25E-26
ITM2A	0.568944	1.50E-56	ATP5F1B	0.361798	1.77E-11	CHCHD2	0.306828	1.11E-12	HLA-DQA2	0.269917	4.32E-19
GBP5	0.561658	2.32E-56	MCUB	0.360471	1.85E-39	ITGA4	0.304946	1.84E-17	CLTA	0.268845	1.33E-15
CORO1A	0.559831	3.27E-31	STK17A	0.35629	6.96E-23	SEPTIN6	0.304341	1.97E-13	FAS	0.268752	2.30E-54
CXCR3	0.552395	1.91E-110	TMSB4X	0.355882	3.82E-06	CD28	0.304145	2.83E-102	GBP2	0.268617	2.15E-12
CCL5	0.550999	9.07E-50	PSMB10	0.352079	4.95E-23	ELOVL5	0.302189	1.05E-39	MSN	0.26856	1.03E-11
ARPC1B	0.543707	2.27E-43	DENND2D	0.351994	1.48E-11	YWHA8	0.302155	9.18E-34	NDUFA13	0.268102	8.14E-11
HLA-DPB1	0.542775	2.29E-58	GBP1	0.351436	6.48E-21	PARP1	0.302082	3.27E-26	RHOG	0.267868	3.33E-19
ISG20	0.523046	1.41E-56	CD81	0.350444	5.12E-39	PSMB2	0.300378	3.54E-23	RCS1D1	0.267783	1.65E-18
LIME1	0.515039	2.52E-35	FYB1	0.346784	1.77E-19	PPP1R18	0.298504	5.30E-15	H3F3A	0.26745	0.000613
DUSP2	0.514383	2.38E-93	GIMAP4	0.346691	8.57E-15	SLFN5	0.29839	5.41E-22	ARHGAP30	0.266976	2.40E-18
SLC25A5	0.512088	4.98E-26	ALOX5AP	0.344	4.18E-22	CD2	0.298142	1.75E-13	NOP10	0.266863	2.74E-20
ACTB	0.505854	5.91E-08	PLAAT4	0.343705	7.30E-18	MT1E	0.296903	9.28E-24	GNAS	0.266593	1.45E-07
SH2D1A	0.503096	1.53E-62	ATP5F1C	0.342332	1.20E-15	FYN	0.29586	6.93E-22	CXCR6	0.266018	5.10E-94
PSME2	0.490289	3.49E-33	CD99	0.342158	7.32E-13	PSMB3	0.29445	6.29E-14	MYADM	0.264871	1.25E-15
PHACTR2	0.485428	1.34E-126	ARPC3	0.339692	4.84E-08	TERF2IP	0.294107	8.77E-25	IL2RG	0.264307	6.34E-10
STAT1	0.474959	2.69E-41	LYAR	0.33926	6.22E-25	S1PR4	0.293961	1.61E-14	ARL6IP1	0.261057	6.77E-08
HMGB2	0.473916	1.93E-40	HMGB1	0.339074	5.80E-13	NDUFB9	0.293677	2.51E-10	WDR1	0.260458	0.000493
IDH2	0.473495	1.49E-45	TXN	0.337175	2.13E-28	ACTR3	0.293598	1.04E-05	UBC	0.259537	1.08E-11
HIST1H1E	0.469711	5.29E-21	TTN	0.335936	9.09E-39	ATP5MG	0.291732	3.10E-06	SEC61B	0.259043	3.59E-11
IL32	0.467553	1.00E-34	CYTOR	0.334834	7.68E-38	ATP5F1E	0.290649	4.90E-06	SFPQ	0.258831	2.10E-12
ANXA5	0.462333	4.84E-39	CD5	0.334002	1.26E-25	CSK	0.287028	9.67E-11	ATP5MC3	0.258703	0.00374
NEAT1	0.460025	3.29E-37	CD44	0.333997	1.62E-26	TRAPP1	0.286588	3.90E-13	SRSF3	0.257632	8.61E-09
TAP1	0.457407	2.37E-36	PARK7	0.333807	1.43E-10	PSMA4	0.285426	2.29E-18	TPM4	0.257461	5.02E-06
ANXA2	0.44138	1.78E-30	HIST1H1C	0.332914	7.77E-31	H1FX	0.285374	6.77E-08	EIF4A1	0.257063	0.000212
FABP5	0.438261	6.09E-104	TNFAIP3	0.332333	1.29E-25	SEM1	0.285332	9.97E-11	PSMB1	0.256963	6.35E-10
HLA-DMA	0.436777	6.49E-80	MT2A	0.329702	0.000134	ATP5MF	0.285259	4.11E-06	SLF1	0.256433	3.04E-52
RNF213	0.422178	9.95E-39	OPTN	0.329389	5.35E-37	SLC25A3	0.28422	2.83E-08	PDCD1	0.255749	3.06E-128
PSMB9	0.421714	8.67E-29	RAC2	0.328985	4.85E-08	APOBEC3G	0.281881	4.50E-10	S100A11	0.254701	0.000563
PSMB8	0.416996	3.92E-23	S100A10	0.327131	7.27E-10	TALDO1	0.281683	2.00E-15	CDCA7	0.254491	2.26E-123
MYH9	0.416183	2.01E-35	JPT1	0.326997	4.51E-29	MCL1	0.281512	2.04E-18	IKZF3	0.25443	1.07E-17
UBE2L6	0.410697	1.25E-41	HINT1	0.326623	3.02E-20	IFI16	0.281291	8.13E-13	DNAJB1	0.254412	8.46E-21
HNRNPPLL	0.410118	8.09E-114	EML4	0.325777	5.09E-41	PBXIP1	0.279581	2.89E-21	HIGD2A	0.252955	0.000153
ISG15	0.408887	3.29E-31	COX5A	0.323156	1.73E-12	CAPZA1	0.279446	1.61E-13	PTTG1	0.252293	9.31E-33
CLIC1	0.408242	2.63E-21	EMB	0.321822	1.67E-30	SMCHD1	0.279315	4.60E-19	DEK	0.252247	2.94E-14
CRIP1	0.404028	4.55E-16	NIN	0.321157	6.89E-35	COPE	0.27876	7.16E-14	NDUFA7	0.251982	3.87E-19
AHNAK	0.402107	2.92E-44	CALM3	0.32085	1.19E-08	EPSTI1	0.278731	4.15E-43	HNRNPA2B1	0.250964	0.0183

A list of genes highly expressed in CD8_TEM_T2ISG. The *P*-values were calculated using Wilcoxon rank sum test, with the Bonferroni correction for multiple comparison. Genes that shows 0.25 < fold change were listed. *Adjusted *P*-values were smaller than 1E-240.

Supplementary Table 11.
The list of DNA-barcoded antibodies used for CITE-seq experiments conducted on the 10x chromium platform.

Antigen	Clone	Barcode sequence	Catalog number
CD3	UCHT1	CTCATTGTAAC TCCT	300479
CD4	RPA-T4	TGTTCCCGCTCAACT	300567
CD8a	RPA-T8	GCTGCGCTTTCCATT	301071
CD11b	ICRF44	GACAAGTGATCTGCA	301359
CD14	M5E2	TCTCAGACCTCCGTA	301859
CD16	3G8	AAGTTCAC TCTTGC	302065
CD19	H1B19	CTGGGCAATTACTCG	302265
CD20	2H7	TTCTGGGTCCCTAGA	302363
CD25	BC96	TTTGTCTGTACGCC	302649
CD27	O323	GCACTCCTGCATGTA	302861
CD28	CD28.2	TGAGAACGACCCTAA	302963
CD38	HIT2	TGTACCCGCTTGTGA	303543
CD45	HI30	TGCAATTACCCGGAT	304068
CD45RA	HI100	TCAATCCTTCCGCTT	304163
CD45RO	UCHL1	CTCCGAATCATGTTG	304259
CD123	6H6	CTTCACTCTGTCAGG	306045
HLA-DR	L243	AATAGCGAGCAAGTA	307663
CD117	104D2	AGACTAATAGCTGAC	313243
CD206	15-2	TCAGAACGTCTAACT	321147
FcεR1a	AER-37	CTCGTTTCCGTATCG	334641
CD161	HP-3G10	GTACGCAGTCCTTCT	339947
IgD	IA6-2	CAGTCTCCGTAGAGT	348245
CD294	BM16	TGTTTACGAGAGCCC	350137
CD127	A019D5	GTGTGTTGTCTATG	351356
CD197	G043H7	AGTTCAGTCAACCGA	353251
CD196	G034E3	GATCCCTTTGTCACT	353440
CD183	G025H7	GCGATGGTAGATTAT	353747
CD185	J252D4	AATTCAACCGTCGCC	356939
CD194	L291H4	AGCTTACCTGCACGA	359425
CD56	5.1H11	TCCTTTCCTGATAGG	362559
CD33	P67.6	TAAC TCAGGGCCTAT	366637
CD11c	S-HCL-3	TACGCCTATAACTTG	371521
CD66b	6/40c	AGCTGTAAGTTTCGG	392909
CD45R	RA3-6B2	CCTACACCTCATAAT	103273
CD138	MI15	ACTCTTTCGTTTACG	356539
CD5	UCHT2	CATTAAACGGGATGCC	300637
CD10	HI10a	CAGCCATT CATTAGG	312233
CD24	ML5	AGATTCCTTCGTGTT	311143
CD80	2D10	ACGAATCAATCTGTG	305243
IgM	MHM-88	TAGCGAGCCCGTATA	314547
IgG	M1310G05	CTGGAGCGATTAGAA	410727
CD21	Bu32	AACCTAGTAGTTCCGG	354923
PD-1	EH12.2H7	ACAGCGCCGTATTTA	329963

Supplementary Table 12.
The Sequence information in CITE-seq experiments conducted on the 10x chromium platform.

Patient ID	Estimated Number of Cells	Mean Reads per Cell	Median Genes per Cell	Number of Reads	Sequencing Saturation	Fraction Reads in Cells	Median UMI Counts per Cell	Antibody: Mean Reads per Cell	Antibody: Number of Reads	Antibody: Sequencing Saturation	Antibody: Median UMIs per Cell
SSc-1 (before)	6,447	98,811	2,879	637,034,145	78.70%	90.60%	8,651	102,490	660,751,300	86.60%	1,839
SSc-1 (onset)	7,721	62,967	2,763	486,165,870	69.30%	88.50%	8,348	70,720	546,030,267	84.40%	1,702
SSc-1 (after)	10,029	48,580	1,828	487,204,535	77.40%	85.30%	3,813	62,967	631,499,306	75.20%	1,912
SSc-2	7,312	58,675	973	429,030,330	45.50%	73.40%	1,939	68,159	498,380,129	81.30%	2,450
SSc-3	7,753	47,834	1,394	370,858,975	52.90%	85.40%	2,993	71,639	555,417,057	73.00%	2,827
SSc-4	8,225	55,816	2,299	459,087,884	74.90%	84.20%	6,078	92,655	762,086,936	89.40%	1,564
SSc-5	6,796	58,638	1,415	398,503,708	71.40%	67.40%	2,880	93,428	634,938,268	77.30%	2,887
SSc-6	7,542	56,972	2,276	429,684,598	76.20%	92.10%	6,422	86,427	651,835,708	90.10%	1,398
SSc-7	2,582	209,065	1,632	539,805,385	93.50%	73.90%	3,468	297,836	769,012,895	48.30%	4,694
SSc-8	18,052	29,067	1,496	524,720,322	66.00%	84.60%	3,253	43,724	789,312,904	77.60%	2,148
SSc-9	19,682	25,285	1,559	497,665,763	56.20%	84.00%	3,420	26,040	512,519,101	81.70%	1,286
SSc-10	19,978	26,730	1,832	534,015,279	53.30%	75.40%	4,348	36,941	737,999,126	79.60%	2,142
SSc-11	4,128	73,595	2,272	303,802,023	82.70%	86.30%	6,852	196,942	812,977,462	82.80%	2,798
SSc-12	5,779	42,532	2,059	245,790,556	72.30%	88.20%	6,478	122,033	705,231,394	85.90%	1,850
SSc-13	10,201	23,368	1,333	238,375,287	61.00%	80.20%	2,950	83,511	851,898,341	48.50%	4,743
SSc-14	6,107	40,296	2,162	246,086,249	71.10%	91.30%	6,401	128,281	783,414,586	72.90%	3,351
SSc-15	7,235	32,111	2,092	232,324,690	62.10%	91.90%	6,703	104,620	756,924,678	74.60%	3,212
SSc-16	5,261	43,010	1,833	226,275,390	58.80%	78.40%	4,309	114,538	602,586,825	89.40%	1,483
SSc-17	7,685	38,609	1,656	296,711,048	66.30%	80.40%	3,621	92,269	709,086,643	89.60%	1,359
SSc-18	6,612	29,108	1,544	192,463,101	42.60%	69.00%	3,176	107,286	709,375,928	86.90%	1,749
SSc-19	5,190	43,183	1,387	224,120,941	46.20%	38.50%	3,152	115,866	601,345,365	87.50%	2,298
SSc-20	19,657	29,127	1,742	572,544,994	71.30%	90.20%	3,540	35,390	695,667,807	87.40%	1,108
SSc-21	12,691	38,041	2,002	482,774,094	68.60%	92.60%	5,305	52,210	662,593,151	78.80%	2,166
LN-1	3,452	95,446	1,676	329,481,254	90.40%	90.70%	3,764	147,523	509,250,061	93.70%	1,512
LN-2	11,580	25,431	1,606	294,493,646	58.80%	84.10%	3,763	43,330	501,771,245	77.50%	2,653
LN-3	2,716	99,434	1,616	270,062,921	82.40%	80.20%	3,786	192,484	522,786,730	83.00%	3,973
LN-4	9,228	84,211	1,754	777,103,326	83.30%	85.00%	4,117	76,529	706,206,719	80.60%	3,538
MPA-1	4,167	75,412	1,094	314,243,177	81.30%	90.80%	4,888	141,971	591,597,028	87.60%	2,138
MPA-2	10,502	22,590	1,657	237,241,645	63.60%	94.60%	3,956	68,938	723,982,392	83.70%	3,242
MPA-3	6,540	73,821	1,604	482,786,785	67.80%	79.90%	3,840	63,910	417,969,169	86.00%	2,233
MPA-4	1,742	275,801	1,734	480,445,850	91.10%	74.70%	4,169	277,367	483,172,592	97.50%	430
HD-1	5,589	59,355	1,095	331,732,486	75.80%	44.30%	2,243	103,354	577,647,526	61.20%	3,212
HD-2	9,007	34,896	1,391	314,309,187	79.80%	93.20%	3,276	67,105	604,413,016	52.40%	4,080
HD-3	6,276	57,835	1,916	362,973,245	80.60%	92.90%	5,205	83,195	522,133,217	46.40%	4,506
HD-4	8,488	55,189	2,311	468,444,069	74.70%	90.20%	6,400	92,958	789,029,089	90.40%	1,502
HD-5	13,459	31,027	1,888	417,589,245	61.80%	85.20%	4,647	44,485	598,722,132	79.70%	1,818
HD-6	8,917	50,316	2,239	448,667,195	69.80%	85.70%	5,731	86,456	770,923,996	88.90%	1,637

UMI, Unique molecular identifiers; SSc, systemic sclerosis; LN, lupus nephritis; MPA, microscopic polyangitis; HD, healthy donor; before, before the onset of scleroderma renal crisis (SRC); onset, at the onset of SRC; after, after the improvement of SRC.

Supplementary Table 13.
The list of DNA-barcoded antibodies used for Abseq experiments conducted on the BD Rhapsody Express System.

Antigen	Clone	Oligo ID	Catalog number
CD3	UCHT1	AHS0231	571970
CD4	SK3	AHS0032	571970
CD8	SK1	AHS0228	571970
CD11b	ICRF44	AHS0184	940266
CD11c	B-Ly6	AHS0056	571970
CD14	MPHIP9	AHS0037	571970
CD15	W6D3	AHS0196	940274
CD16	3G8	AHS0053	571970
CD19	SJ25C1	AHS0030	571970
CD22	HIB22	AHS0195	940273
CD25	2A3	AHS0026	571970
CD27	M-T271	AHS0025	571970
CD28	L293	AHS0138	571970
CD45RA	HI100	AHS0009	571970
CD56	NCAM16	AHS0019	571970
CD62L	DREG-56	AHS0049	571970
CD127	HIL-7R-M21	AHS0028	571970
CD134	ACT35	AHS0013	571970
CD137	4B4-1	AHS0003	571970
CD161	HP-3G10	AHS0205	571970
CD183	1C6/CXCR3	AHS0031	571970
CD185	RF8B2	AHS0039	571970
CD186	13B 1E5	AHS0148	571970
CD193	5E8	AHS0159	940245
CD196	11A9	AHS0034	571970
CD197	G043H7	AHS0273	571970
CD272	J168-540	AHS0052	571970
CD278	DX29	AHS0012	571970
CD279	EH12.1	AHS0014	571970
CD357	V27-580	AHS0104	571970
CD366	7D3	AHS0016	571970
HLA-DR	G46-6	AHS0035	571970
IgD	IA6-2	AHS0058	571970
IdM	G20-127	AHS0198	571970
FceR1a	AER-37	AHS0129	940220

Supplementary Table 14.
The Sequence information in Abseq experiments conducted on the BD Rhapsody Express System.

Patient ID	sample	Putative Cell Count	Percent Reads from Putative Cells	Mean Reads per Cell	Median Molecules per Cell	Total Reads After Quality Filtering	Sequencing Saturation	Antibody: Mean Reads per Cell	Antibody: Median Molecules per Cell	Antibody: Total Reads After Quality Filtering	Antibody: Sequencing Saturation
SSc-19	blood	17601	80.36%	20186.62	4416	585436168	88.55%	30837.53	14092	710537561	78.23%
SSc-19	kidney	4275	82.27%	77748.38	5976	561304734	95.48%	30101.35	7200	719512681	57.98%