Supplementary materials

Table S1. List of antibodies for Western Blot and IF.

Reagent	Art.NO.	Brand
CD73	Bsm-30125M-APC	Bioss
CD90	Bsm-3010M-FITC	Bioss
CD105	Bsm-30132M-APC-Cy7	Bioss
CD34	Bsm-30097M-PE-Cy5	Bioss
CD45	Bsm-30095M-PE	Bioss
CD9	20597-1-AP	Proteintech
CD81	27855-1-AP	Proteintech
CD63	ER1905-64	HUABIO
beta Actin Rabbit mAb	R23613	Proteintech
GAPDH Monoclonal antibody	60004-1-lg	Proteintech
TGFβ1 Polyclonal antibody	IPB0036	Baijia
Smad2/3 Polyclonal antibody	IPB0670	Baijia
Phospho-Smad2/3 Rabbit pAb	IPB0231	Baijia
Smad7(Acetyl Lys70) rabbit pAb	IPB11718	Baijia
LYVE-1 Polyclonal antibody	51011-1-AP	Proteintech
Ki67	ab279653	Abcam
RIPA Lysate	P0013B	Beyotime
QuickBlock™ Western Blocking solution	P0239	Beyotime
TBST	P0239	Beyotime
Western Antibody Dilution	P0239	Beyotime
Ultra High Sensitive ECL Kit	P0018S	Beyotime
Goat Anti-Mouse IgG H&L（HRP）	511103	Zenbio
Goat Anti-Rabbit IgG H&L（HRP）	511203	Zenbio
iF488-Tyramide(tsa)	G1231	Servicebio
CY3-Tyramide(tsa)	G1223	Servicebio
Blocking with Rabbit Serum	SL034	Solarbio

Table S2. Transwell Migration and Invasion Assays

Experiment	Method
Migration assay	Cells were seeded into 6-well plates (three replicates per group) and treated as designated. After 24 hours, cells were trypsinized, counted, and resuspended in serum-free medium at a density of 7×10^4 cells per 200 µl. For each sample, 200 µl of this suspension was added to the upper chamber of a Transwell insert (8.0 µm pore size, Corning), while 700 µl of complete medium containing 10% FBS was added to the lower chamber in a 24-well plate. After 24 hours of incubation at 37°C with 5% CO_2, non-migrated cells on the upper membrane surface were removed using a PBS-moistened cotton swab. Migrated cells on the lower surface were fixed in 100% methanol for 20 minutes at room temperature, stained with 0.1% crystal violet for 1–2 hours in the dark, and rinsed gently with distilled water. The membranes were then imaged under a light microscope (10×), with three random fields per well selected for quantification. Cell numbers were counted using ImageJ software.
Invasion assay	For invasion assays, the upper chambers were pre-coated with 100 µl Matrigel (200 µg/ml, growth factor-reduced) and allowed to solidify at 37°C. Cells in the logarithmic growth phase were resuspended in serum-free RPMI-1640 or DMEM medium at 7×10^4 cells per 200 µl and seeded into the upper chamber. The lower chamber was filled with 700 µl medium containing 10% FBS as a chemoattractant. After 48 hours of incubation, non-invaded cells on the upper surface were removed, and the invaded cells on the lower membrane were fixed with methanol, stained with 1% crystal violet, and imaged under a microscope at 100× magnification in three random fields. Cell counts were analyzed using ImageJ.

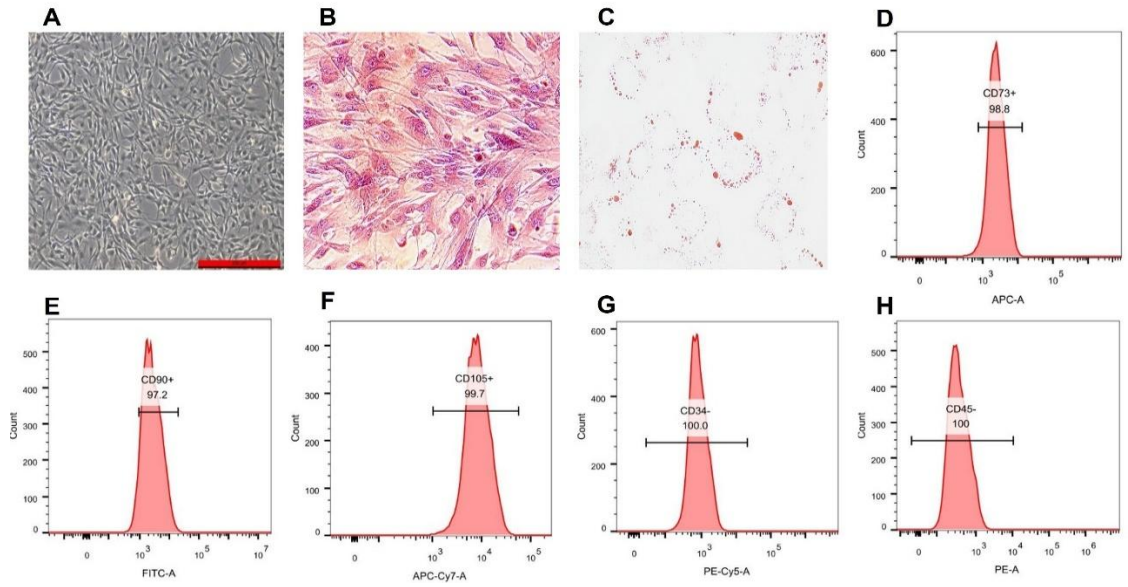


Figure S1. ADSCs isolation and identification.

A. Morphology of ADSCs under bright field. B-C. Representative image of ADSCs osteogenic differentiation. Scale bar: 200 μm. C. Representative image of ADSCs adipogenic differentiation. Scale bar: 200 μm. D-H. Identification of ADSCs by flow cytometry. Cells were positive for CD73, CD90 and CD105, but negative for CD34, CD45.

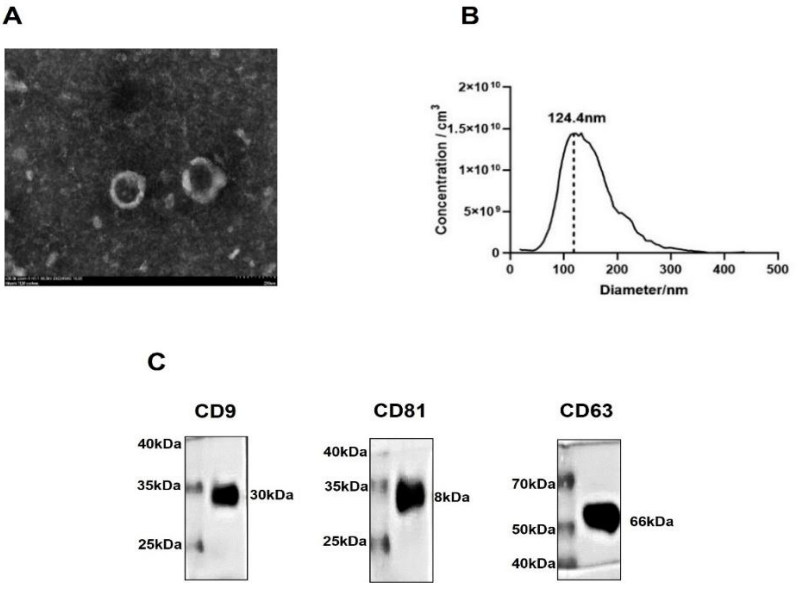


Figure S2. ADSC-Exs isolation and identification.

A. Electron micrograph analysis of whole-mount ADSC-Exs. Scale bar= 200nm. B. qNano analysis of the exosomes diameter (nm) isolated from ADSCs/VEGF-C conditioned medium. C. Western blot analysis showing exosome marker CD9, CD81 and CD63 in the exosome.

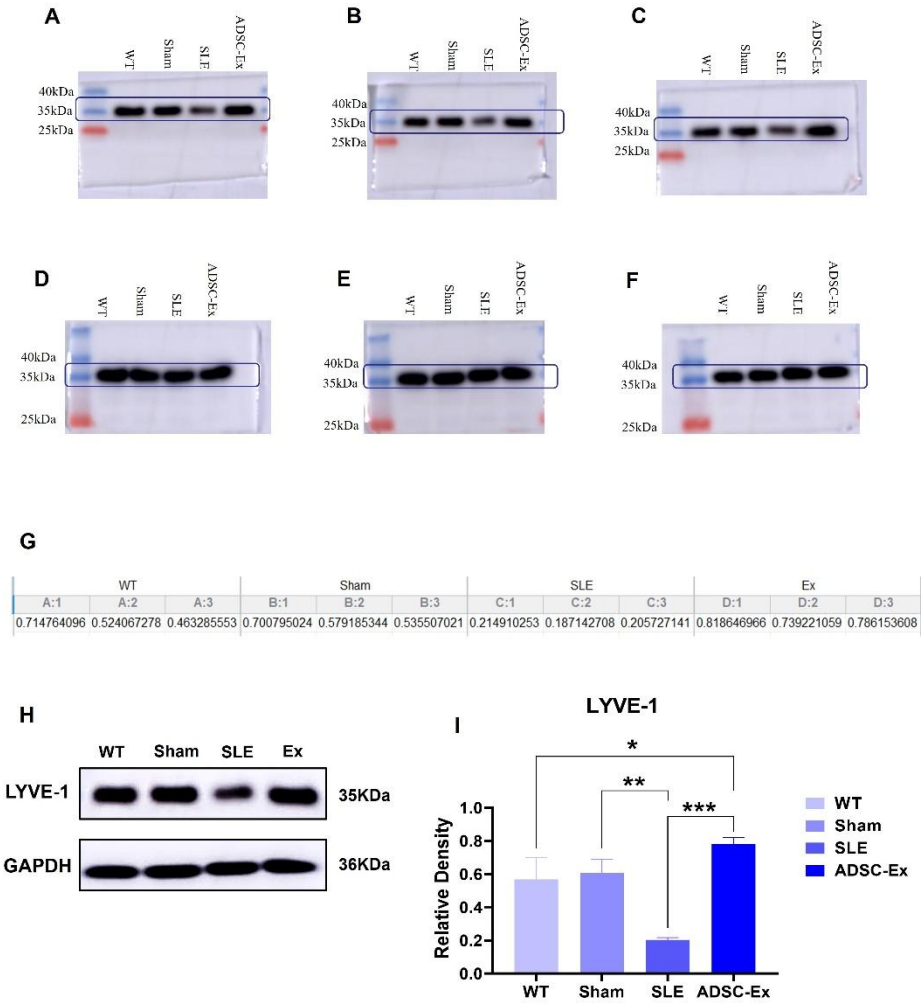


Figure S3. The full uncropped Gels and Blots image(s) of LYVE-1 and GAPDH

A-C. The full uncropped Gels and Blots image(s) of LYVE-1. D-F. The full uncropped Gels and Blots image(s) of GAPDH. G. Relative expression data of three times by image J software. H-I. Representative Western blot images and analysis of LYVE-1 expression level in edematous regions. Group WT, Sham, SLE and group ADSC-Ex were compared with one another, n=3 for each group. Ordinary one-way ANOVA and Tukey's multiple-comparisons test were applied. *P<0.05, **P 0.01, ***P<0.001

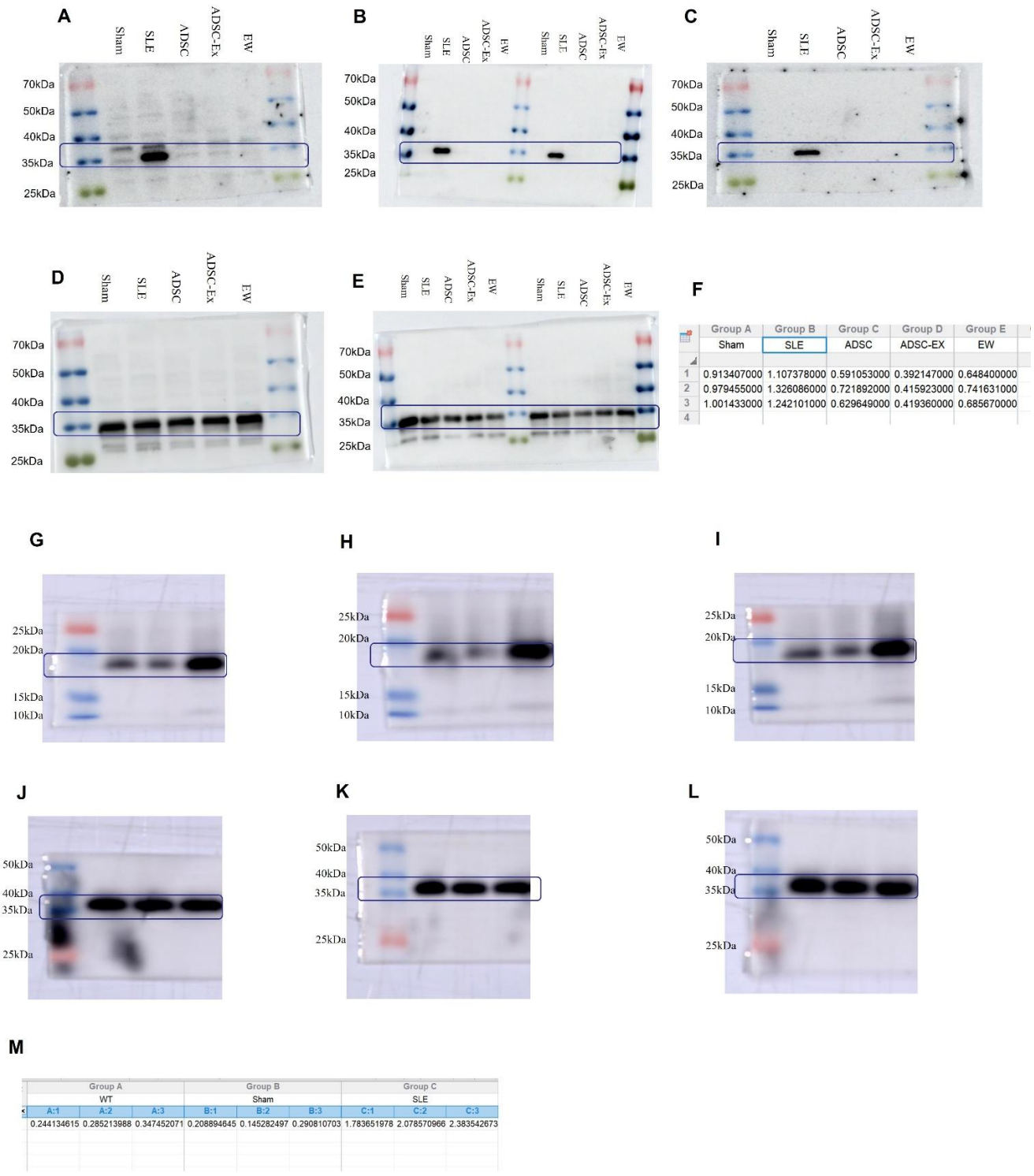
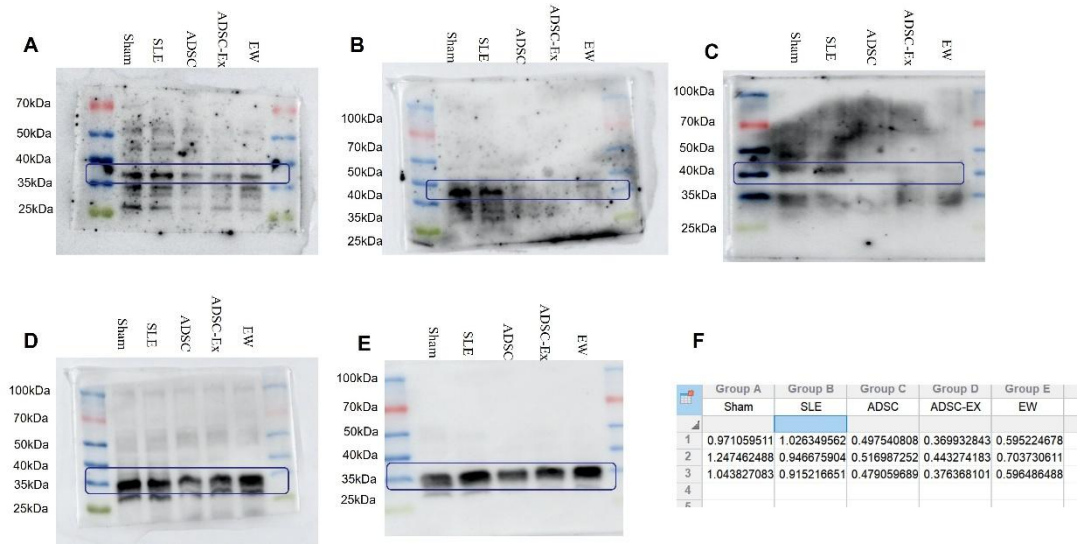


Figure S4. The full uncropped Gels and Blots image(s) of TGFβ1 and GAPDH

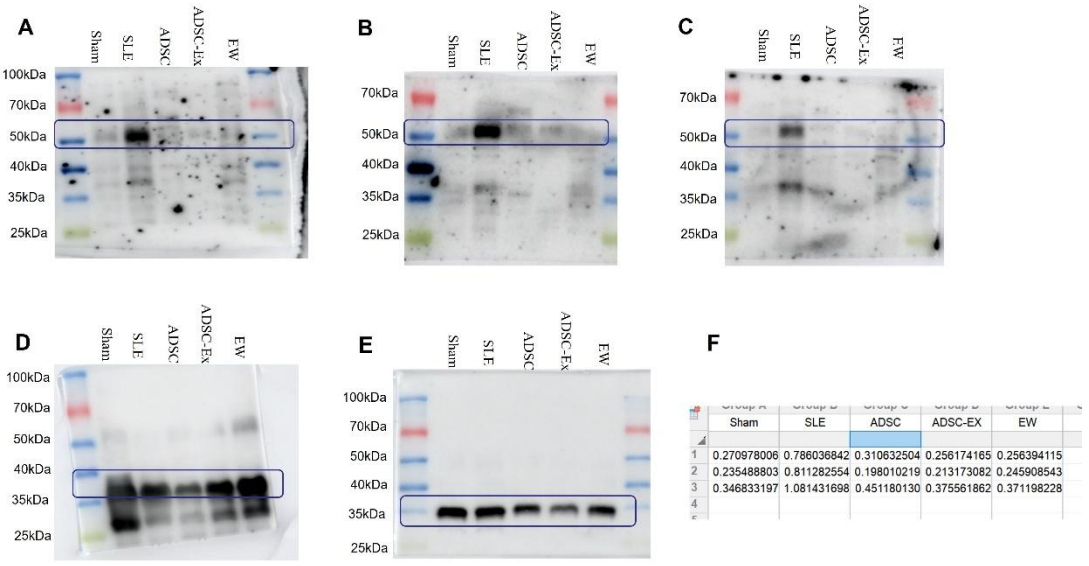
A-C. The full uncropped Gels and Blots image(s) of TGFβ1 of 5 groups(Sham/SLE/ADSC/ADSC-Ex/EW). D-E. The full uncropped Gels and Blots image(s) of GAPDH of 5groups. F. Relative expression data of three times by image J software. G-I. The full uncropped Gels and Blots image(s) of TGFβ1 of 3 groups (WT/Sham/SLE). J-L: The full uncropped Gels and Blots image(s) of GAPDH of 3 groups. M. Relative expression data of three times by image J software.



	Group A	Group B	Group C	Group D	Group E
	Sham	SLE	ADSC	ADSC-EX	EW
1	0.971059511	1.026349562	0.497540808	0.369932843	0.595224678
2	1.247462488	0.946675904	0.516987252	0.443274183	0.703730611
3	1.043827083	0.915216651	0.479059689	0.376368101	0.596486488

Figure S5. The full uncropped Gels and Blots image(s) of Smad2/3 and β-actin

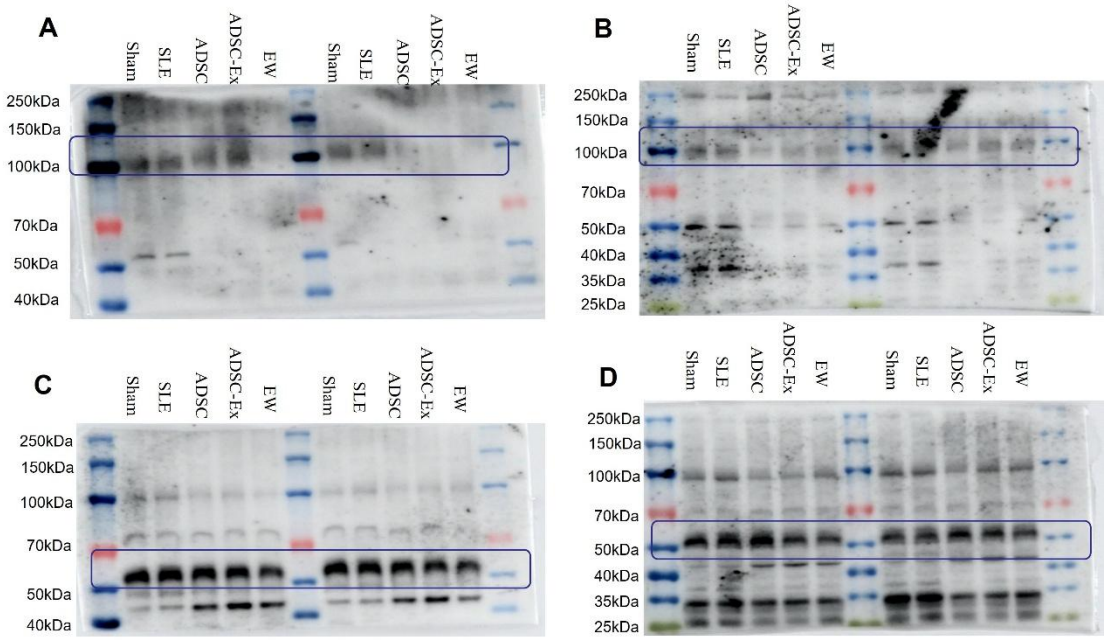
A-C. The full uncropped Gels and Blots image(s) of Smad2/3. D-E. The full uncropped Gels and Blots image(s) of β-actin. F. Relative expression data of three times by image J software.



	Sham	SLE	ADSC	ADSC-EX	EW
1	0.270978006	0.786036842	0.310632504	0.256174165	0.256394115
2	0.235488803	0.811282554	0.198010219	0.213173082	0.245908543
3	0.346833197	1.081431698	0.451180130	0.375561862	0.371198228

Figure S6. The full uncropped Gels and Blots image(s) of P-Smad2/3 and β-actin

A-C. The full uncropped Gels and Blots image(s) of P-Smad2/3. D-E. The full uncropped Gels and Blots image(s) of β-actin. F. Relative expression data of three times by image J software.

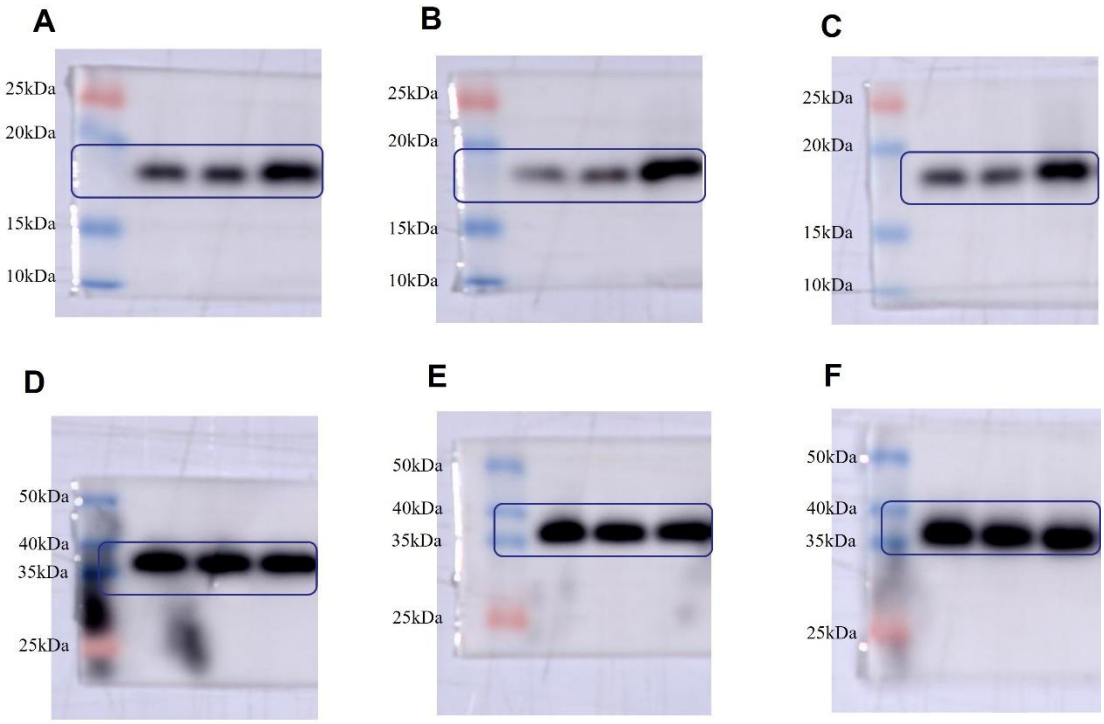


E

Group A	Group B	Group C	Group D	Group E
Sham	SLE	ADSC	ADSC-EX	EW
0.302945390	0.252964861	0.278162088	0.398921177	0.085684089
0.321382205	0.285152105	0.314805681	0.493768674	0.097799630
0.436687134	0.379103732	0.309603792	0.465435212	0.081556556

Figure S7. The full uncropped Gels and Blots image(s) of Smad7 and β-actin

A-B. The full uncropped Gels and Blots image(s) of Smad7. C-D. The full uncropped Gels and Blots image(s) of β-actin. E. Relative expression data of three times by image J software.



G

at:	Group A			Group B			Group C		
	WT			Sham			SLE		
	A:1	A:2	A:3	B:1	B:2	B:3	C:1	C:2	C:3
	0.260441155	0.166086276	0.253267344	0.322818109	0.248867139	0.249340984	0.900652401	1.289770720	1.160814258

Figure S8. The full uncropped Gels and Blots image(s) of IL4 and β-actin

A-C. The full uncropped Gels and Blots image(s) of IL4. D-F. The full uncropped Gels and Blots image(s) of GAPDH. E. Relative expression data of three times by image J software.

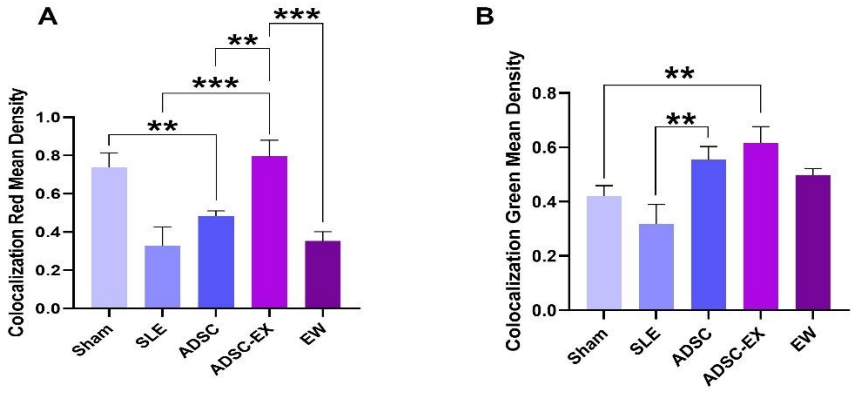


Figure S9. The Colocalization Mean Density of podoplanin and Ki67.

A. Colocalization Red Mean Density (podoplanin). B. Colocalization Green Mean Density (Ki67)