

**Supplementary table 1: Primer sequences used for real-time PCR analysis**

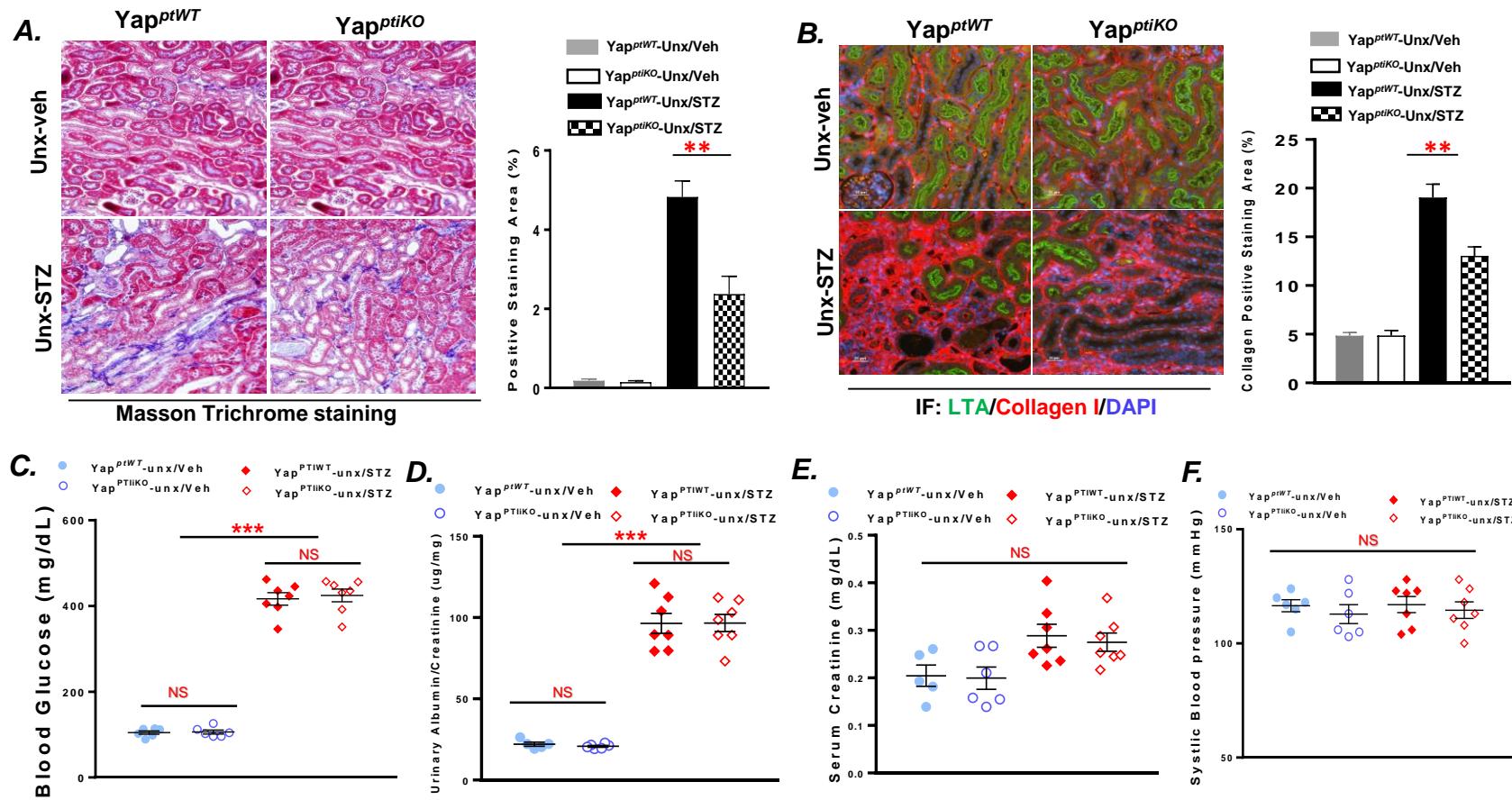
Gene ID			Sequence (5'->3')
CCN2 (CTGF)	Homo sapiens	F	TGGAAGAGAACATTAAGAAGGGC
<a href="#">NM_001901.3</a>		R	CCGTCGGTACATACTCCACA
CCL2	Homo sapiens	F	TCAAACGTAAAGCTCGCACTCT
<a href="#">NM_002982.4</a>		R	GCATTGATTGCATCTGGCTG
THBS1	Homo sapiens	F	ACCAACCGCATTCCAGAGTC
<a href="#">NM_003246.4</a>		R	ACTTGTCATCAGGCACAGGG
COL3A1	Homo sapiens	F	GCAGGGTCTCCTGGTTCAA
<a href="#">NM_000090.3</a>		R	CGGGACCCATTCGCCCTTA
TGFβ2	Homo sapiens	F	ACAAAATAGACATGCCGCC
<a href="#">NM_001135599.3</a>		R	CATCAAGGTACCCACAGAGCA
ACTB ( $\beta$ -actin)	Homo sapiens	F	TTCCCTCCTGGGCATGGAGT
<a href="#">NM_001101.5</a>		R	AATGCCAGGGTACATGGTGG
Acta 2 actin ( $\alpha$ -SMA)	Mus musculus	F	CCCAGACATCAGGGAGTAATGG
<a href="#">NM_007392.3</a>		R	TCTATCGGATACTTCAGCGTCA
1a1 (Collagen type I alpha	Mus musculus	F	AGCAGACGGGAGTTCTCCT
<a href="#">NM_007742.4</a>		R	AGCTGACTTCAGGGATGTCTTC
Actb ( $\beta$ -actin)	Mus musculus	F	GGCTGTATTCCCCTCCATCG
<a href="#">NM_007393.5</a>		R	CCAGTTGGTAACAATGCCATGT

**Supplementary table 2: Results of relative mRNA expression of 84 profiled human fibrosis associated genes in the RT<sup>2</sup> PCR Array in the hYAP1S127A-HEK cells compared with the vector transfected HEK cells**

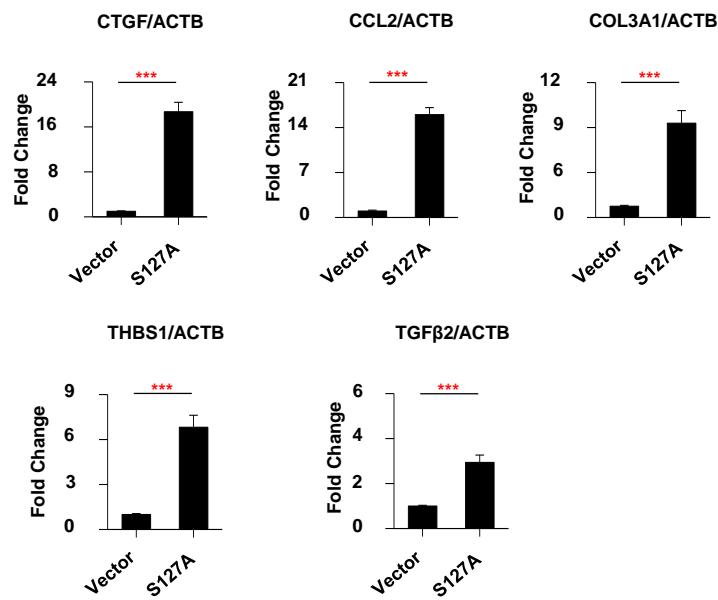
Target Genes	ΔΔ Ct Mean	ΔΔ Ct SD	ΔΔ Ct SE	p-Value
CCL2	4.97	1.002	0.578	0.0054
CTGF	3.52	0.268	0.155	0.0007
THBS1	3.45	0.242	0.140	0.0002
COL3A1	3.01	0.310	0.179	0.0155
CXCR4	2.48	0.553	0.319	0.0148
TGFB2	2.36	0.191	0.110	0.0015
ACTA2	2.03	0.880	0.508	0.0323
MMP1	1.78	1.347	0.778	0.3291
PDGFA	1.71	0.297	0.171	0.0338
CCL3	1.70	1.151	0.665	0.4982
MMP3	1.68	0.709	0.410	0.2857
SERPINA1	1.66	1.257	0.726	0.4815
EGF	1.62	0.149	0.086	0.0557
SERPINE1	1.60	0.916	0.529	0.0690
ITGA1	1.58	0.378	0.218	0.0125
PLG	1.56	1.367	0.789	0.5837
MMP8	1.48	1.225	0.707	0.0685
GREM1	1.48	0.301	0.174	0.0523
IL13RA2	1.39	1.041	0.601	0.3624
CAV1	1.35	0.565	0.326	0.0105
FASLG	1.30	1.148	0.663	0.5284
IL5	1.27	0.665	0.384	0.2495
LOX	1.24	0.134	0.078	0.0254
THBS2	1.22	0.568	0.328	0.5021
ITGAV	1.20	0.269	0.155	0.0155
COL1A2	1.20	1.456	0.841	0.5467
SMAD7	1.19	0.132	0.076	0.0681
AGT	1.17	0.745	0.430	0.3507
LTBP1	1.13	0.230	0.133	0.0429
MYC	1.11	0.316	0.182	0.0305
PDGFB	1.11	0.789	0.456	0.5565
SMAD6	1.11	0.320	0.185	0.1600
ITGB1	1.09	0.258	0.149	0.0246
TNF	1.07	0.401	0.231	0.5560
ITGB8	1.04	0.220	0.127	0.0171
IL4	1.03	0.471	0.272	0.3392
IFNG	1.03	0.522	0.301	0.4353
IL1B	1.01	0.825	0.476	0.2484
TIMP3	1.00	0.139	0.080	0.0190
IL10	0.97	0.700	0.404	0.6312
DCN	0.97	0.455	0.262	0.0247

STAT1	0.94	0.374	0.216	0.0443
MMP13	0.94	0.617	0.356	0.2124
SMAD2	0.93	0.109	0.063	0.0754
SMAD4	0.92	0.136	0.078	0.0176
INHBE	0.91	0.809	0.467	0.7632
MMP14	0.91	0.243	0.140	0.4299
SERPINH1	0.89	0.158	0.091	0.0273
TGFB1	0.88	0.224	0.130	0.0017
STAT6	0.86	0.103	0.060	0.0918
MMP9	0.81	0.208	0.120	0.2566
SMAD3	0.79	0.087	0.050	0.0258
ITGB5	0.78	0.181	0.104	0.0050
ILK	0.77	0.088	0.051	0.0043
NFKB1	0.76	0.104	0.060	0.0405
IL1A	0.75	0.352	0.203	0.1698
PLAT	0.74	1.019	0.588	0.1882
CCL11	0.68	0.497	0.287	0.7334
CEPB	0.67	0.210	0.121	0.1725
CCR2	0.65	0.077	0.044	0.6856
SP1	0.60	0.388	0.224	0.1300
VEGFA	0.60	0.495	0.286	0.5307
TGFBR2	0.60	0.220	0.127	0.0225
SNAI1	0.60	0.222	0.128	0.0663
EDN1	0.59	0.337	0.195	0.1023
TIMP4	0.53	0.223	0.129	0.1971
TIMP1	0.52	0.128	0.074	0.1764
BMP7	0.52	0.262	0.151	0.0576
TGIF1	0.51	0.150	0.087	0.1280
ITGA2	0.51	0.095	0.055	0.0784
TGFBR1	0.49	0.025	0.014	0.0751
IL13	0.44	0.270	0.156	0.1463
ENG	0.43	0.619	0.357	0.5446
PLAU	0.43	0.319	0.184	0.5301
ITGB3	0.37	0.112	0.065	0.5085
HGF	0.35	0.603	0.348	0.8361
JUN	0.25	0.350	0.202	0.4751
AKT1	0.16	0.047	0.027	0.4707
ITGA3	0.16	0.239	0.138	0.7087
BCL2	0.05	0.108	0.062	0.7265
TIMP2	0.00	0.222	0.128	0.9904
TGFB3	-0.02	0.165	0.095	0.9483
ITGB6	-0.17	0.748	0.432	0.7333
MMP2	-0.42	0.083	0.048	0.3590

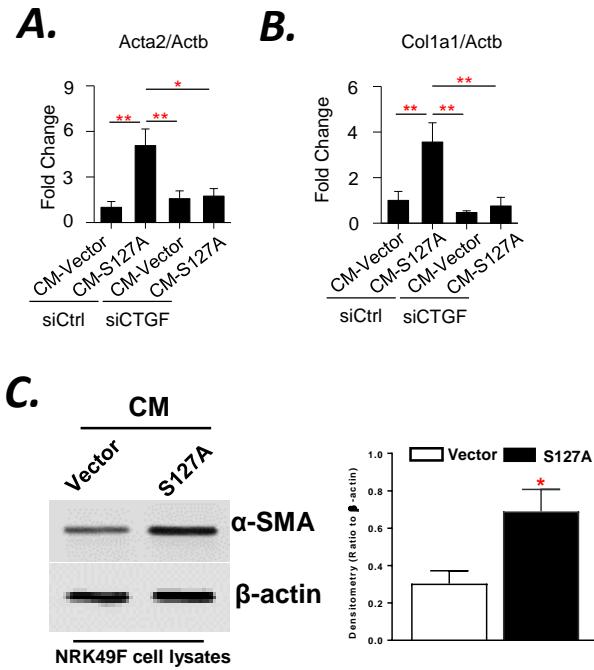
**Fig S1.**



**Fig S2.**



**Fig S3.**



**Supplementary data figure legends:**

**Supplementary table 1:** Primer sequences used for real-time PCR analysis.

**Supplementary table 2:** Results of differential expression of 84 profiled human fibrosis associated genes in the RT<sup>2</sup> PCR Array between the hYAP1<sup>S127A</sup>-HEK cells and the vector transfected HEK-293 cells.

**Supplementary Fig 1:** Kidney interstitial fibrosis in diabetic Yap<sup>ptiWT</sup> or Yap<sup>ptiKO</sup> mice was evaluated by Masson Trichrome staining (**A**) or immunofluorescence staining of collagen I (**B**); Renal proximal tubule epithelial cell YAP deletion did not affect hyperglycemia (**C**), proteinuria (**D**), serum creatinine (**E**) and systolic blood pressure (**F**). Values are mean ± SEM (the data was from at least three separate experiments). \*\*:P<0.01; \*\*\*P<0.001. NS: Non-significant difference.

**Supplementary Fig 2** Confirmation of real time PCR analysis of mRNA expression levels of genes altered in hYAP1S127A-HEK in the RT2 Profiler Human Fibrosis PCR Array: CTGF (CCN2), MCP-1 (CCL2), Thrombospondin 1 (THBS1), Collagen type III alpha I (COL3A1) and TGFβ2. \*\*\*:P<0.001.

**Supplementary Fig 3:** hYAP1<sup>S127A</sup>-HEK (S127A) or vector transfected HEK-293 cells were transfected with control or CTGF siRNA, and the conditioned medium from these cells was collected to treat the mouse fibroblasts. The relative mRNA expression of α-SMA (**A**) and collagen I (**B**) in these fibroblasts was analyzed by real-time PCR. Exposure of a well characterized rat kidney fibroblasts, NRK49F to the conditioned medium from S127A also induced α-SMA expression (**C**). CM: Conditioned medium; S127A: hYAP1<sup>S127A</sup>-HEK; Vector: vector transfected HEK-293 cells. \*:P<0.05; \*\*:P<0.01.