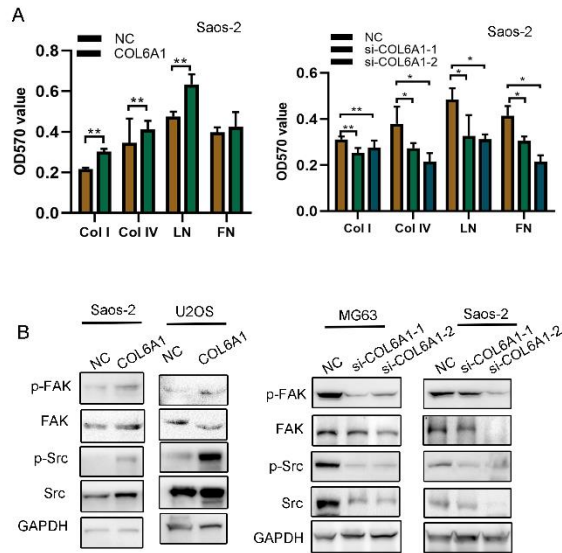
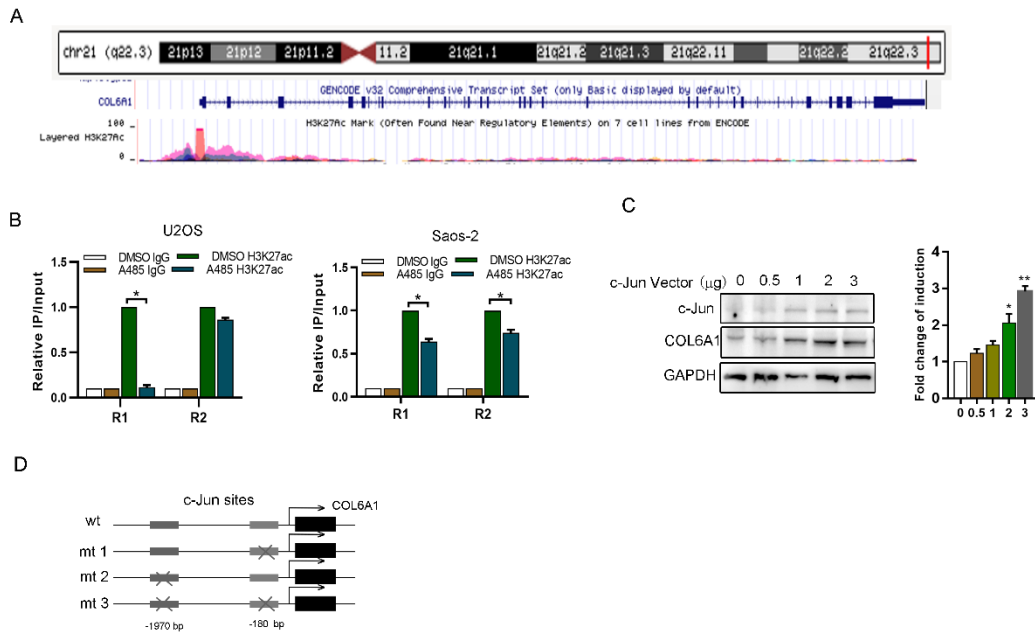


1
 2 **Figure S1. The function of COL6A1 in OS cells.** **A.** The expression of COL6A1 in OS cell lines
 3 U2OS, Saos-2 and MG63 and osteoblast cell lines hFOB1.19 was detected by qRT-PCR, western blot
 4 and Immunofluorescence. Confocal imaging showed that COL6A1 located in the cytoplasm (Scale
 5 bars: 50 μ m). **B.** The invasion ability of OS cell lines U2OS, Saos-2 and MG63 was detected by
 6 transwell assay. **C.** The transfection efficiency of COL6A1 plasmid and siRNA was confirmed by
 7 Western blot and qRT-PCR analysis. **D.** Colony formation assay was performed on control and
 8 COL6A1-overexpressing Saos-2 and U2OS cells. **E.** A cell counting and CCK8 was performed on
 9 control and COL6A1-overexpressing OS cells. **F.** Western blot was performed to detect the apoptosis
 10 on COL6A1-overexpressing and knockdown OS cell lines. **G.** Annexin V-PI assay was performed to
 11 detect the apoptosis on COL6A1-overexpressing OS cells. **H.** The effect of rhCOL6A1 on the
 12 expression of COL6A1 in OS cells detected by western blot. **I.** The effect of rhCOL6A1 on the
 13 expression of COL6A1 in OS cells detected by immunofluorescence (Scale bars: 50 μ m). **J.** The effect

14 of rhCOL6A1 on the migration of OS cells detected by transwell assay. Data represent the mean \pm SD
 15 of 3 separate determinations. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ by Student's t test.

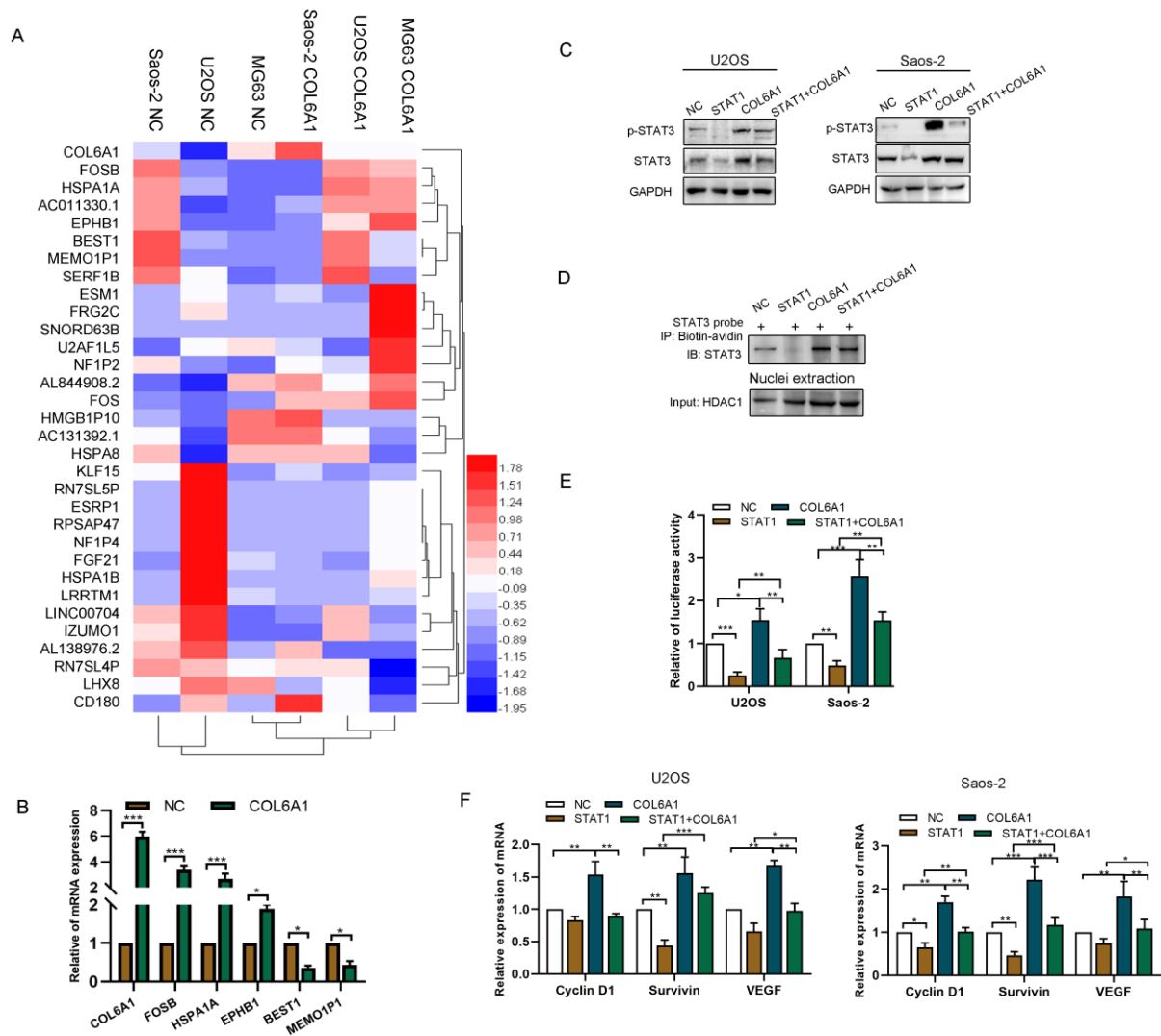


16
 17 **Figure S2. The COL6A1 effects on cell adhesion signaling pathway.** A COL6A1-overexpressing,
 18 COL6A1 knockdown or control cells were subjected to cell-matrix adhesion assay to collagen I (Col I),
 19 collagen IV (Col IV), laminin (LN), and fibronectin (FN). B. Western blotting analysis of phosphorylation
 20 of FAK and Src and total FAK and Src in COL6A1-overexpressing, COL6A1 knockdown and control
 21 cells. Data represent the mean \pm SD of 3 separate determinations. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$
 22 by Student's t test.



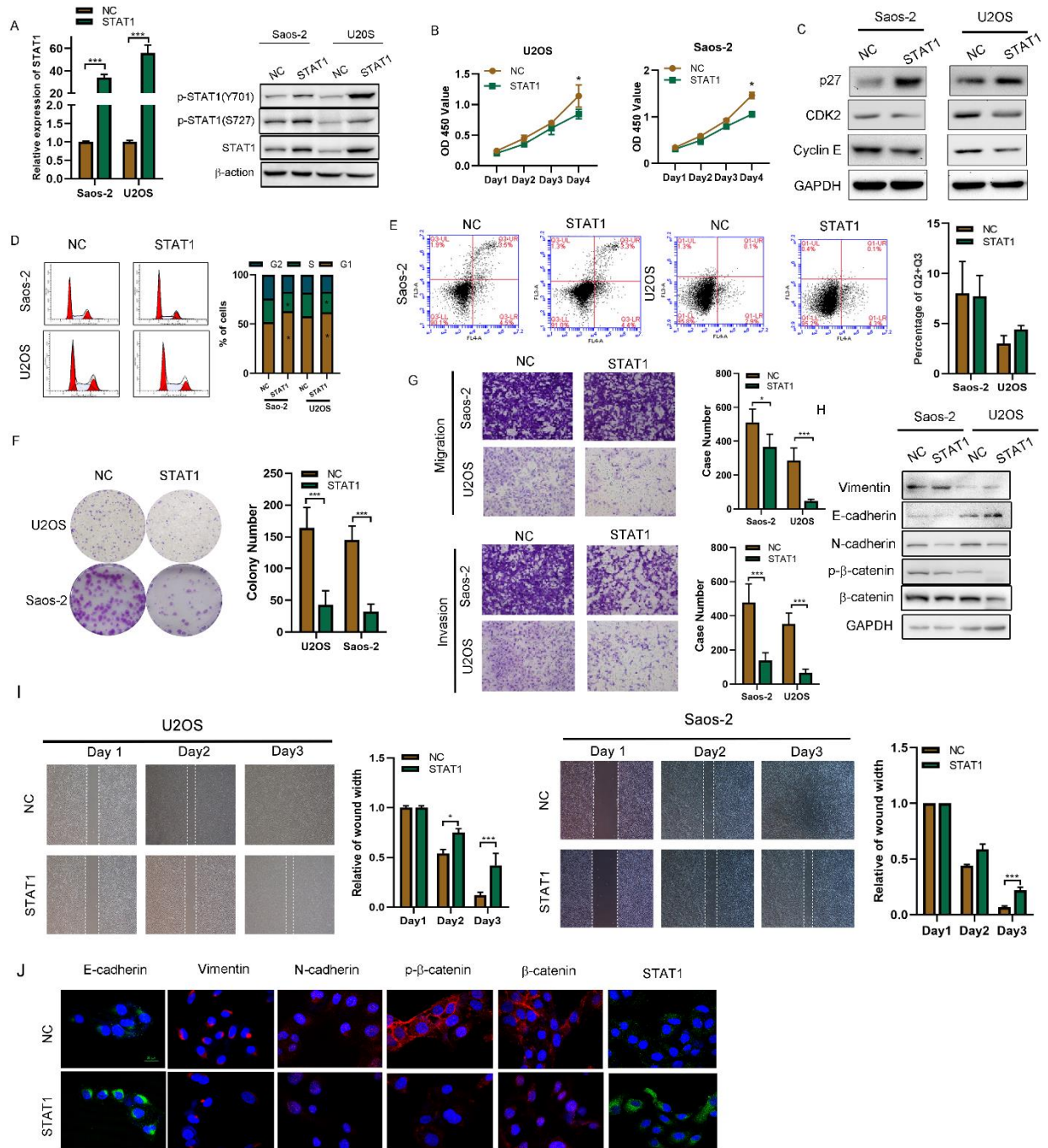
23

24 **Figure S3. H3K27 acetylation in COL6A1 promoter region.** **A.** The genome bioinformatics analysis
 25 showed that H3K27ac was enriched at the promoter of COL6A1 by using UCSC Genome
 26 Bioinformatics Site (<http://genome.ucsc.edu/>). **B.** ChIP assay demonstrated that H3K27 acetylation
 27 occurred in the promoter of COL6A1 in OS cell lines, U2OS and Saos-2, using two primers upon
 28 treatment of A485. **C.** The expression and transcription activation of COL6A1 was detected by
 29 westernblot and luciferase reporter upon transfection of c-Jun in U2OS. **D.** Schematic presentation of
 30 c-Jun binding sites in the promoter region of COL6A1. Data represent the mean \pm SD of 3 separate
 31 determinations. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ by Student's t test.



32

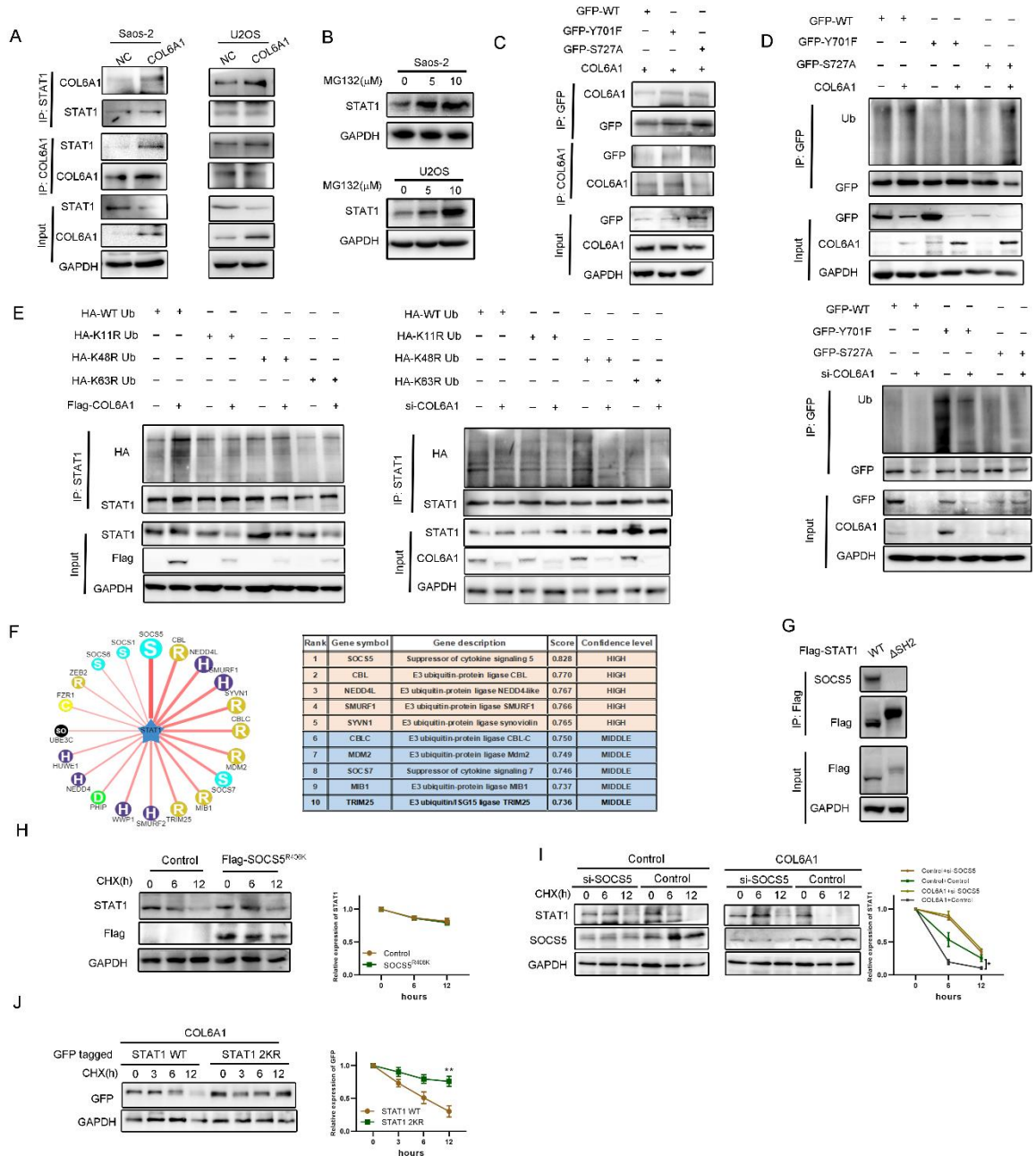
33 **Figure S4. A.** Top different expression genes in COL6A1 overexpression and control cell using three
 34 OS cell lines was shown. **B.** The mRNA expression levels of the indicated genes were determined in
 35 COL6A1 overexpression and control cell lines using qRT-PCR. **C.** The expression of p-STAT3 and
 36 STAT3 was detected in indicated transfected OS cells. **D.** Biotin pull-down assay with a STAT3 probe
 37 was used to determine its DNA binding after transfecting COL6A1. **E.** STAT3 transcription luciferase
 38 reporter constructs were transiently transfected into the indicated cells, and luciferase activity was
 39 analyzed after 48 hours. **F.** The mRNA expression of STAT3 downstream genes cyclin D1, survivin and
 40 VEGF was detected in indicated transfected OS cells by qRT-PCR. Data represent the mean \pm SD of 3
 41 separate determinations. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ by Student's t test.



42

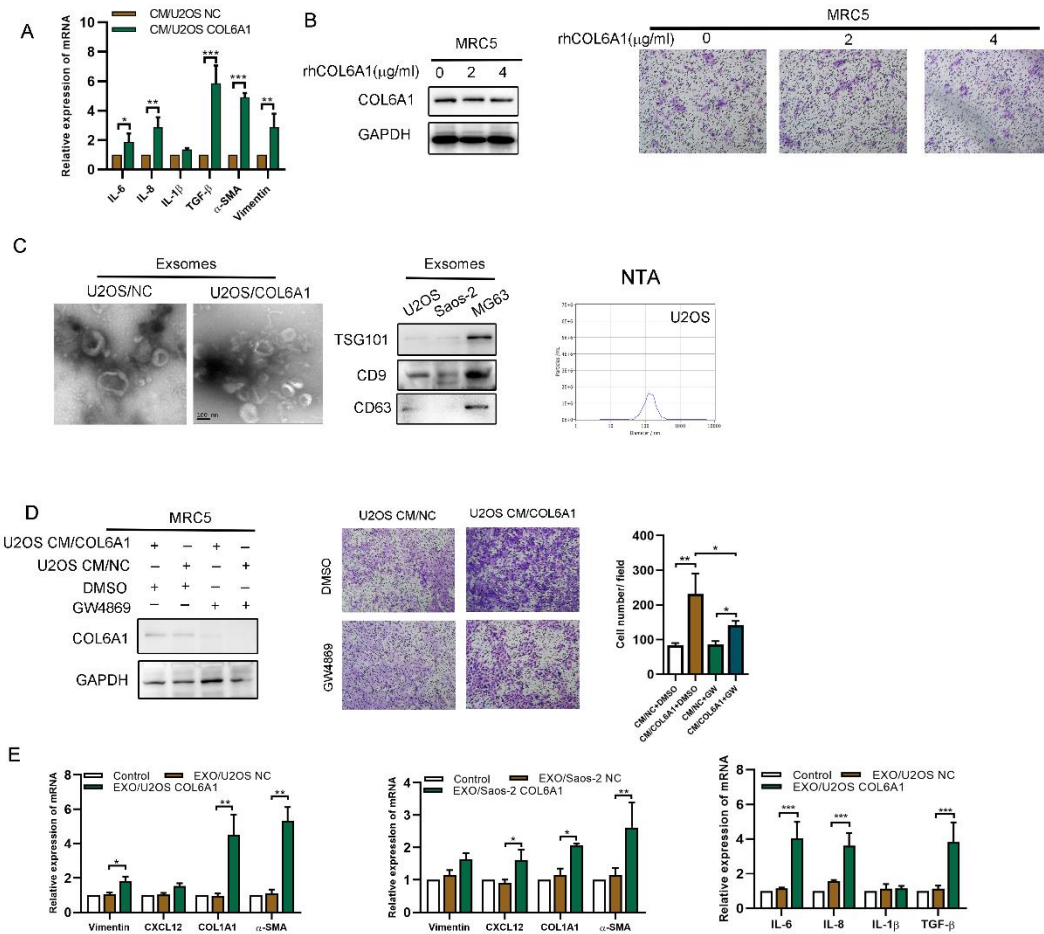
43 **Figure S5. The function of STAT1 in OS cells.** **A.** The effect of STAT1 overexpression in U2OS and
 44 Saos-2 cells was determined by qRT-PCR and western blot analysis. **B.** A Cell Counting Kit-8 assay
 45 was performed on control and STAT1 overexpression U2OS and Saos-2 cells. **C.** The expression of
 46 cell cycle biomarkers was detected in control and STAT1-overexpressing OS cells by western blot. **D.**
 47 Cell cycle was detected on control and STAT1-overexpressing OS cells using flow cytometry. **E.** Cell
 48 apoptosis was detected by Annexin V-PI stain assay. **F.** Colony formation assays were performed on
 49 control and STAT1-overexpressing OS cells. **G.** Transwell assay was performed on control and

50 STAT1-overexpressing cells to detect the invasion and migration ability. **H.** The expression of EMT
 51 biomarkers was detected in STAT1 overexpression OS cells by westernblot. **I.** Wound healing assay
 52 was performed in STAT1 overexpression or control OS cell. **J.** The expression of EMT biomarkers was
 53 detected by immunofluorescence. Data represent the mean \pm SD of 3 separate determinations (Scale
 54 bars: 50 μ m). * p < 0.05, ** p < 0.01, *** p < 0.001 by Student's t test.

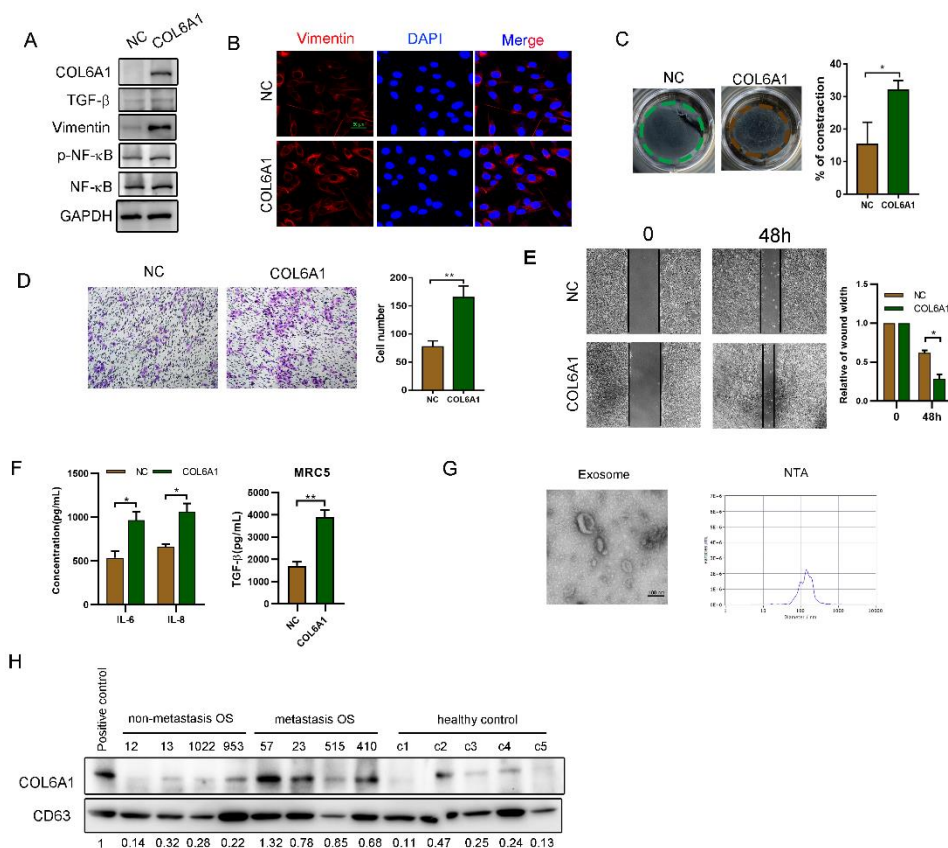


55
 56 **Figure S6. The ubiquitination of STAT1 mediated with COL6A1.** **A.** The interaction of endogenous
 57 COL6A1 and STAT1 was investigated by using co-immunoprecipitation experiments in Saos-2 and

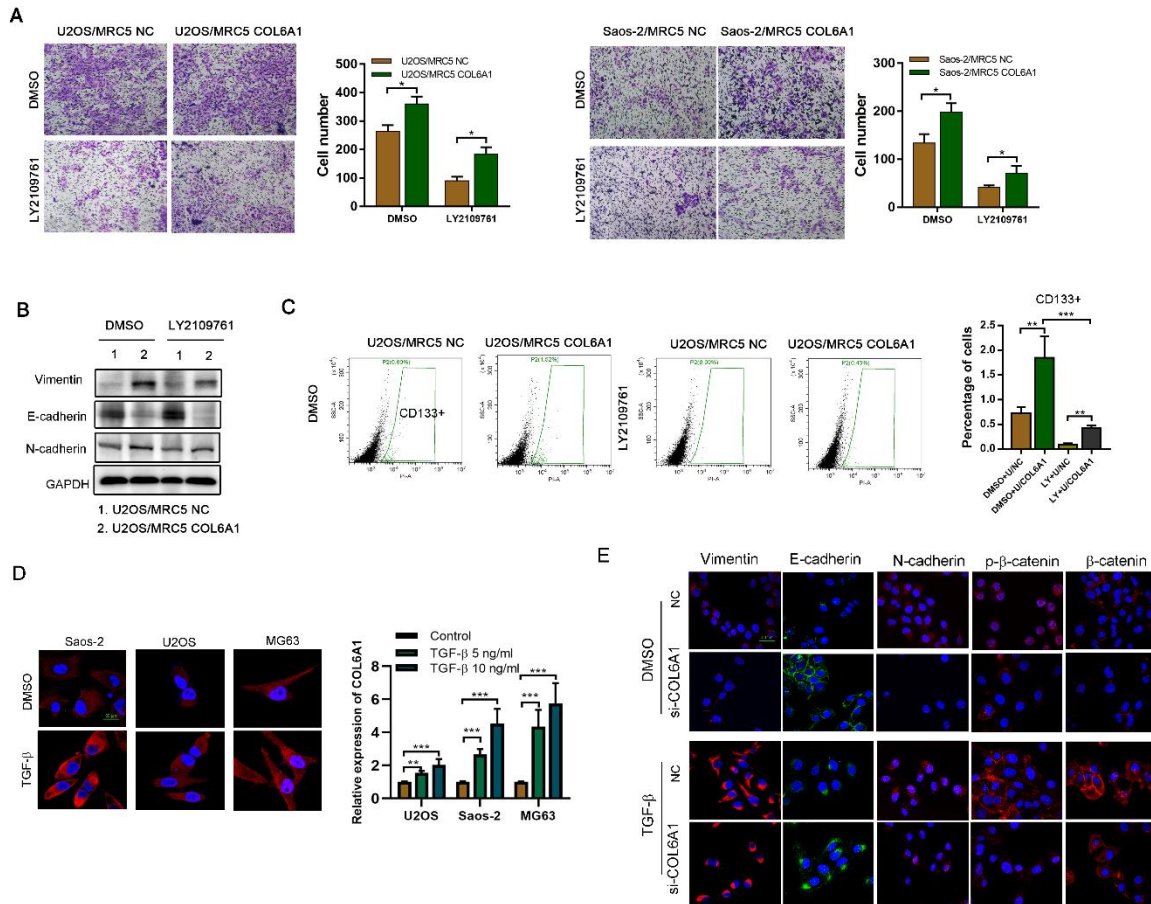
58 U2OS cells treated with or without COL6A transfection. Co-immunoprecipitation was carried out using
59 anti-STAT1, or anti-COL6A1 antibody. **B.** Saos-2 and U2OS cell lines were treated in the presence of
60 0-10 μ M MG132 for 24 h. Total cell lysates were then prepared for immunoblot detection of STAT1 and
61 β -actin. **C.** GFP-STAT1 (WT), GFP-STAT1 (Y701F), or GFP-STAT1 (S727A) were transfected into
62 Saos-2 cells. Co-immunoprecipitation was performed using GFP antibody and immunoblotting was
63 done using an anti-COL6A1 antibody. **D.** GFP-STAT1 (WT), GFP-STAT1 (Y701F), or GFP-STAT1
64 (S727A) were transfected into Saos-2 cells together with COL6A1 plasmid or siRNA. STAT1
65 ubiquitination was detected by immunoprecipitation with anti-GFP antibody and immunoblotting with
66 anti-Ub antibody. **E.** HA-WT, HA-K11R, HA-K48R and HA-K63R were transfected into Saos-2 with
67 COL6A1 or si-COL6A1 transfection. Similar results were observed in three independent experiments.
68 **F.** SOCS5 is predicted as the specific E3 ligase of STAT1 by UbiBrowser database. **G.** Flag-wide type
69 and SH2 domain deletion plasmids were transfected into U2OS. STAT1 Co-immunoprecipitation was
70 performed using Flag antibody and immunoblotting was done using an anti-SOCS5 antibody. **H.** The
71 cells expressing mutant SOCS5 were treated with cycloheximide (CHX, 200 μ g/mL). The protein levels
72 of STAT1 and Flag were analyzed by western blot. **I.** The cells with indicated treatment were treated
73 with CHX (200 μ g/mL). The protein levels of STAT1 and SOCS5 were analyzed by western blot. **J.** The
74 cells with indicated transfection were treated with CHX (200 μ g/mL). The protein levels of GFP were
75 analyzed by western blot.



76
 77 **Figure S7. The exosomal COL6A1 derived from OS cells.** **A.** Indicated gene expression of MRC5
 78 treated with CM by COL6A1-transfection OS cells or blank control were detected by qRT-PCR
 79 analysis. **B.** The expression of COL6A1 in MRC5 cells detected by westernblot after treated with
 80 different concentration of rhCOL6A1 (left panel). The migration ability of MRC5 cells was detected by
 81 transwell assay after treated with different concentration of rhCOL6A1(right panel). **C.** Exosomes
 82 released by U2OS/NC and U2OS/COL6A1 cells were detected by electron microscopy,
 83 Immunoblotting assay and Nanoparticle Tracking Analysis (NTA) (Scale bar:100 nm). **D.** COL6A1
 84 expression was detected in parental OS cells treated with exosomes derived from CM/COL6A1 and
 85 CM/NC incubated with DMSO or GW4869 (left panel). Cell migration potential was determined in
 86 MRC5 cells incubated with DMSO or GW4869, upon treatment with CM/COL6A1 and CM/NC (right
 87 panel). **E.** The mRNA expression of indicated gene was detected in MRC5 treated with the exosomes
 88 derived from OS cells. Data represent the mean \pm SD of 3 separate determinations. * $p < 0.05$, ** $p <$
 89 0.01 , *** $p < 0.001$ by Student's t test.



90
 91 **Figure S8. Function of COL6A1 in MRC5 cells.** **A.** The expression of indicated protein was detected
 92 by westernblot after COL6A1 transfection in MRC5 cells. **B.** The expression of Vimentin was detected
 93 by immunofluorescence in control and COL6A1 transfection MRC5 cells (Scale bars: 50 μ m). **C.**
 94 MRC5 cells transfected with COL6A1 or control were assessed for their ability to contract collagen.
 95 Collagen contraction was quantified by the ImageJ software. **D.** The migration ability of control and
 96 COL6A1 transfection MRC5 cells was detected by transwell assay and wound healing assay. **E.** The
 97 secretory protein level of IL-6, IL-8 and TGF- β was detected by ELISA. **F.** The rate of lung metastasis
 98 after tail-vein injection indicated treatment cells. **G.** Exosomes released by different cancer cells were
 99 detected by electron microscopy and Nanosight particle tracking analysis (Scale bar: 200 nm). **H.** The
 100 expression of COL6A1 was detected in exosomes derived from healthy people and OS patient's
 101 serum. COL6A1 transfected cell protein was used as positive control. Data represent the mean \pm SD
 102 of 3 separate determinations. Scale bars: 100 μ m. * p < 0.05, ** p < 0.01, *** p < 0.001 by
 103 Student's t test.



104
 105 **Figure S9. The activated CAF secreted TGF-β.** **A.** The migration of OS cells with indicated treatment
 106 were detected by the transwell assay. **B.** The expression of EMT biomarkers was detected by
 107 westernblot in the indicated cell treated with TGF-β inhibitor LY2109761 (50 nM). **C.** The percentage of
 108 CD133 positive cells was determined by fluorescence-activated cell sorting analysis in indicated cells
 109 treated with TGF-β inhibitor LY2109761 (50 nM). **D.** The expression of COL6A1 in OS cells treated
 110 with TGF-β was detected by immunofluorescence and qRT-PCR (Scale bars: 20 μm). **E.** Confocal
 111 microscope assay was performed to detect the expression of indicated protein expression in
 112 siCOL6A1 or control U2OS cells treated with TGF-β (Scale bars: 50 μm). Data represent the mean ±
 113 SD of 3 separate determinations. *p < 0.05, **p < 0.01, ***p < 0.001 by Student's t test.

114

Table S1. Clinical parameters of 181 OS patients

NO.	Gender	Age	Group	Size	Group	Location	Stage	Meta	Follow	Status	IHC Score	Group
1	F	9	1	0.3	1	scapula	3	1	11	1	12	1
2	M	16	1	1	1	scapula	1	1	28	1	9	1
3	M	13	1	1	1	scapula	3	1	7	1	8	1
4	M	10	1	1	1	scapula	2	1	3	1	6	2
5	F	18	1	1.5	1	scapula	2	0	16	0	4	2
6	M	11	1	1.5	1	scapula	1	0	42	0	12	1
7	M	10	1	1.7	1	scapula	3	0	19	0	12	1
8	M	20	1	2	1	scapula	3	0	24	0	6	2
9	F	16	1	2	1	humerus	2	0	0	0	6	2
10	F	16	1	2	1	humerus	3	0	1	0	4	2
11	M	10	1	2	1	calcaneus	3	1	5	1	12	1
12	F	6	1	2	1	ilium	2	1	7	1	6	2
13	F	15	1	2.5	1	ilium	2	1	19	1	12	1
14	F	12	1	1.5	1	ilium	1	1	6	1	6	2
15	M	9	1	1	1	rib	2	0	35	0	6	2
16	M	9	1	2.3	1	rib	3	0	12	0	6	2
17	F	8	1	2.6	1	ulna	1	0	16	0	8	1
18	M	8	1	2.5	1	pubis	2	0	34	0	4	2
19	M	18	1	2.6	1	pubis	1	0	4	0	3	2
20	M	14	1	2.1	1	clavicle	3	0	17	0	12	1
21	M	13	1	2.0	1	clavicle	3	0	43	0	6	2
22	F	10	1	1.5	1	NA	3	0	21	0	8	1
23	F	31	2	1.5	1	NA	3	0	4	0	12	1
24	M	50	2	9.6	1	Femur	2	1	3	1	12	1
25	F	57	2	1.6	1	Femur	3	0	19	0	12	1
26	F	46	2	1.4	1	Femur	3	0	11	0	12	1
27	F	55	2	0.9	1	Femur	1	0	1	0	0	2
28	M	81	2	1.3	1	Femur	1	0	6	0	8	1
29	M	26	2	0.8	1	Femur	1	0	17	0	8	1
30	F	35	2	0.5	1	Femur	1	0	6	0	4	2
31	M	50	2	0.6	1	Femur	1	0	3	1	12	1
32	F	46	2	2.5	1	Femur	3	0	3	1	12	1
33	F	54	2	2.5	1	Femur	3	0	9	1	8	1
34	F	52	2	1	1	Femur	2	0	35	0	4	2
35	M	45	2	1	1	Femur	1	0	1	0	8	1
36	M	42	2	1.5	1	Femur	2	0	22	0	12	1
37	F	47	2	2.2	1	Femur	3	0	40	1	12	1
38	F	36	2	2.4	1	Femur	2	0	22	1	9	1
39	F	65	2	1	1	Femur	3	0	4	0	12	1
40	M	59	2	2.3	1	Jawbone	3	0	16	0	8	1
41	M	36	2	1	1	Jawbone	3	1	7	1	12	1
42	M	44	2	1	1	Jawbone	3	1	3	1	8	1
43	F	47	2	2.4	1	Jawbone	1	0	2	0	3	2
44	M	46	2	1	1	Jawbone	3	0	36	0	6	2
45	F	43	2	2.5	1	Jawbone	1	0	50	0	8	1
46	M	28	2	1	1	Jawbone	3	0	38	0	12	1
47	M	27	2	1	1	Jawbone	1	0	21	0	12	1
48	M	25	2	1.5	1	Tibia	3	0	12	0	12	1
49	M	53	2	2.8	1	Tibia	3	0	6	0	3	2
50	M	26	2	0.5	1	Tibia	3	0	24	0	12	1
51	F	34	2	2.8	1	Tibia	2	0	2	0	8	1
52	F	58	2	1.6	1	Tibia	3	0	19	0	12	1
53	M	43	2	2.7	1	Tibia	3	0	19	0	4	2
54	F	13	1	2.5	1	Tibia	2	0	4	0	8	1
55	M	15	1	3	1	Tibia	2	0	24	0	6	2
56	M	22	1	1.4	1	Tibia	2	0	12	0	12	1
57	F	13	1	2.7	1	Tibia	3	0	3	0	8	1
58	M	13	1	1.9	1	Tibia	1	0	43	0	8	1
59	M	20	1	2.5	1	Tibia	2	0	58	0	12	1
60	F	9	1	2.5	1	Tibia	2	0	5	0	6	2

61	F	20	1	2.0	1	Tibia	2	1	2	1	9	1
62	M	13	1	3.5	2	scapula	1	1	8	1	12	1
63	F	14	1	4	2	scapula	3	0	5	0	6	2
64	M	21	1	4	2	scapula	3	0	9	0	6	2
65	M	15	1	4.5	2	scapula	2	0	23	0	4	2
66	F	18	1	4.5	2	scapula	2	0	2	0	9	1
67	M	7	1	5	2	humerus	1	0	9	0	4	2
68	F	12	1	5.5	2	humerus	3	0	8	0	12	1
69	F	16	1	6	2	humerus	1	0	2	0	6	2
70	F	8	1	6	2	humerus	3	0	19	0	8	1
71	M	11	1	6	2	humerus	3	0	15	0	8	1
72	M	8	1	6	2	humerus	1	0	9	0	2	2
73	M	9	1	6	2	calcaneus	1	0	1	0	3	2
74	F	8	1	7	2	calcaneus	1	1	2	1	8	1
75	F	12	1	7	2	calcaneus	3	1	6	1	9	1
76	M	21	1	10	2	calcaneus	2	1	21	1	8	1
77	M	13	1	10	2	ilium	3	1	6	1	0	2
78	M	11	1	10.6	2	ilium	3	1	19	1	12	1
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82	M	14	1	8	2	rib	3	0	10	0	4	2
83	M	9	1	5	2	ulna	3	0	49	0	8	1
84	F	20	1	4	2	ulna	1	0	15	0	2	2
85	F	17	1	13	2	ulna	3	0	13	0	12	1
86	F	17	1	6	2	pubis	3	0	9	0	0	2
87	F	12	1	7	2	pubis	2	0	1	0	8	1
88	M	13	1	7	2	clavicle	3	0	7	0	8	1
89	F	20	1	8	2	NA	3	0	44	0	12	1
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91	M	13	1	6	2	NA	3	0	8	0	2	2
92	M	13	1	8.5	2	Femur	3	1	6	1	4	2
93	F	21	1	6	2	Femur	3	1	16	1	12	1
94	F	15	1	12	2	Femur	3	0	18	0	6	2
95	M	15	1	6	2	Femur	2	0	8	0	2	2
96	F	31	2	6	2	Femur	3	0	2	0	3	2
97	F	34	2	10	2	Femur	3	0	4	0	8	1
98	M	47	2	4.5	2	Femur	2	0	14	0	6	2
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101	M	40	2	7	2	Femur	2	0	16	0	4	2
102	M	62	2	5	2	Femur	3	0	5	0	8	1
103	M	52	2	7	2	Femur	2	0	13	0	1	2
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111	M	31	2	6	2	Femur	1	0	18	1	6	2
112	M	49	2	4.8	2	Femur	3	0	5	1	8	1
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115	F	66	2	3.5	2	Femur	3	0	20	1	8	1
116	M	27	2	6	2	Femur	2	0	10	1	0	2
117	F	66	2	4	2	Femur	1	0	10	0	8	1
118	F	10	2	2	2	Femur	3	0	23	0	6	2
119	M	44	2	4	2	Femur	3	0	7	0	2	2
120	M	45	2	7	2	Femur	3	0	10	0	3	2

117

118

121	F	34	2	4	2	Femur	2	0	3	0	8	1
122	M	34	2	4.8	2	Femur	3	0	2	0	12	1
123	M	37	2	11	2	Femur	3	0	15	1	8	1
124	F	34	2	8	2	Femur	1	0	20	1	8	1
125	M	33	2	4.5	2	Femur	3	0	67	1	8	1
126	F	32	2	5	2	Femur	3	0	23	1	6	2
127	M	31	2	8	2	Femur	3	0	6	1	12	1
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130	M	43	2	3.5	2	Femur	2	0	3	1	12	1
131	M	38	2	5	2	Femur	3	0	7	0	2	2
132	M	30	2	4.8	2	Femur	1	0	8	0	8	1
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134	F	26	2	4.8	2	Femur	1	0	0	0	8	1
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137	M	58	2	6	2	Jawbone	1	1	2	0	12	1
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139	F	12	1	8.5	2	Jawbone	3	0	18	0	4	2
140	M	16	1	8	2	Jawbone	3	0	3	1	4	2
141	F	14	1	5	2	Jawbone	3	0	3	0	4	2
142	M	16	1	9	2	Jawbone	3	0	4	0	4	2
143	M	12	1	5	2	Jawbone	1	0	17	0	9	1
144	M	13	1	7	2	Jawbone	3	0	4	0	2	2
145	M	18	1	5	2	Jawbone	3	0	9	0	4	2
146	M	20	1	5	2	Jawbone	3	0	10	0	12	1
147	F	9	1	12	2	Jawbone	1	0	15	0	2	2
148	F	18	1	3	2	Jawbone	3	0	4	0	8	1
149	F	17	1	14	2	Jawbone	3	0	4	0	12	1
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152	M	16	1	6	2	Jawbone	3	0	21	0	2	2
153	M	16	1	8	2	Tibia	1	1	2	1	12	1
154	F	15	1	6	2	Tibia	3	1	10	1	4	2
155	M	14	1	8	2	Tibia	3	1	2	1	8	1
156	M	13	1	8	2	Tibia	2	0	17	0	4	2
157	F	13	1	7	2	Tibia	3	0	1	0	4	2
158	M	12	1	7	2	Tibia	3	0	4	0	4	2
159	F	12	1	9	2	Tibia	2	0	9	0	8	1
160	F	12	1	4.8	2	Tibia	1	0	3	0	6	2
161	M	11	1	5	2	Tibia	2	0	4	0	4	2
162	F	10	1	6	2	Tibia	2	0	10	1	12	1
163	M	9	1	4.9	2	Tibia	1	0	24	0	9	1
164	M	8	1	4.8	2	Tibia	3	0	4	0	6	2
165	F	8	1	8.5	2	Tibia	2	0	22	0	2	2
166	F	14	1	6.5	2	Tibia	2	0	7	0	1	2
167	M	13	1	5.4	2	Tibia	3	0	3	0	6	2
168	F	22	1	4.7	2	Tibia	1	0	22	0	8	1
169	F	19	1	4.5	2	Tibia	3	0	3	0	1	2
170	F	19	1	4	2	Tibia	3	0	12	0	8	1
171	F	19	1	6	2	Tibia	3	0	10	0	12	1
172	F	18	1	12	2	Tibia	3	0	4	0	2	2
173	F	14	1	9.4	2	Tibia	1	0	2	0	12	1
174	M	60	2	5	2	Tibia	1	0	4	0	8	1
175	F	43	2	8.5	2	Tibia	3	1	2	1	12	1
176	F	51	2	7	2	Tibia	2	1	18	0	4	2
177	M	33	2	5	2	Tibia	1	0	26	0	4	2
178	F	53	2	6.8	2	Tibia	3	0	1	0	4	2
179	F	29	2	7.5	2	Tibia	3	0	11	0	2	2
180	F	39	2	7	2	Tibia	3	0	4	0	4	2
181	M	26	2	7.5	2	Tibia	3	0	21	0	6	2

120 **Table S2. Sequence of primers**

COL6A1	F: 5'-TCAAGAGCCTGCAGTGGATG-3'; R: 5'-TGGACACTTCTTGTCTATGCAG-3'
GAPDH	F:5'-AGAAGGCTGGGCTCATTTG-3'; R: 5'-AGGGGCCATCCACAGTCTTC-3'
IL-1 β	F: 5'-ATGATGGCTTATTACAGTGGCAA-3'; R: 5'-GTCGGAGATTTCGTAGCTGGA-3'
IL-6	F: 5'-ACTCACCTCTTCAGAACGAATTG-3'; R: 5'-CCATCTTTGGAAGGTTTCAGGTTG-3'
IL-8	F: 5'-TTTTGCCAAGGAGTGCTAAAGA-3'; R: 5'-AACCTCTGCACCCAGTTTTTC-3'
CD133	F: 5'-GCCACCGCTCTAGATACTGC-3'; R: 5'-TGTTGTGATGGGCTTGTCAT-3'
E-cadherin	F: 5'-TGCCCAGAAAATGAAAAAGG-3'; R: 5'-GTGTATGTGGCAATGCGTTC-3'
Vimentin	F: 5'-GAGAACTTTGCCGTTGAAGC-3'; R: 5'-GCTTCCTGTAGGTGGCAATC-3'
N-cadherin	F: 5'- ACCAGCCTCCAACCTGGTAT-3'; R: 5'-TACGACGTTAGCCTCGTTC-3'
STAT1	F: 5'-CAGCTTGACTCAAATTCCTGGA-3'; R: 5'-TGAAGATTACGCTTGCTTTTCCT-3'
STAT3	F: 5'-CAGCAGCTTGACACACGGTA-3'; R: 5'-AAACACCAAAGTGGCATGTGA-3'
CXCL12	F: 5'-ATTCTCAACACTCCAACCTGTGC; R: 5'-ACTTTAGCTTCGGGTCAATGC-3'
COL1A1	F: 5'-GAGGGCCAAGACGAAGACATC-3'; R: 5'-CAGATCACGTCATCGCACAAAC-3'
COL3A1	F:5'-GGAGCTGGCTACTTCTCGC-3'; R: 5'-GGGAACATCCTCCTTCAAACAG-3'
FOSB	F: 5'-GCTGCAAGATCCCCTACGAAG-3'; R: 5'-ACGAAGAAGTGTACGAAGGGTT-3'
EPHB1	F: 5'-GGCTGCGATGGAAGAAACG-3'; R: 5'-CTGGTTGGGCTCGAAGACATT-3'
BEST1	F: 5'-CTGGGCTTCTACGTGACGC-3'; R: 5'-TTGCTCGTCCTTGCCTTCG-3'
HSPA1A	F: 5'-AGCTGGAGCAGGTGTGTAAC-3'; R: 5'-CAGCAATCTTGGAAGGCC-3'
P300	F: 5'GACCCTCAGCTTTTAGGAATCC-3'; R: 5'-TGCCGTAGCAACACAGTGTCT-3'
TGF- β	F: 5'-GGGCATGTGGCTTCTATGGT-3'; R: 5'-CCCCAAGCGCATCTCGTAG-3'
COL6A1 promoter1	F: 5'-GACACGCTGGTTTTCAGACG-3'; R: 5'-GCAGTTCAGTCCCCTGTCA-3'
COL6A1 promoter2	F: 5'-AACAAATTCAGCTCACCGGCGA-3'; R: 5'-ACCCAGGGAGAGTTCCTTGA-3'
Cyclin D1	F:5'-GGATGCTGGAGGTCTGCGA -3'; R: 5'-TAGAGGCCACGAACATGCAAG-3'
Survivin	F:5'-CAAGGAGCTGGAAGGCTGG-3'; R:5'-GTTCTTGGCTCTTTCTCTGTCC-3'
VEGF	F:5'-AAAGGAGCCTACAAGA-3'; R:5'-TTCACAAGCAGCCAAT-3'

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