

Table S1: Arithmetic mean and standard deviation of the healing area.

Table S2: Assay of quality control of the RNA

Figure S1: Quality control of mRNA expression levels of housekeeping genes.

Table S3: Up-down regulation of genes on DS-treated group (comparing to control group)

Table S1: Arithmetic mean and standard deviation of the healing area

Days after wound	Control group			Test group (DS treatment)		
	arithmetic average	Standard deviation	N	arithmetic average	Standard deviation	N
0	1045,75	85,49	4	1022,67	147,31	3
2	769,75	104,47	4	927,25	45,13	4
4	713,5	113,11	4	812,25	59,02	4
7	584,5	155,59	4	658	124,97	4
9	375	72,95	4	403,75	40,09	4
11	144,75	95,17	4	230,5	121,71	4
14	62,5	86,26	4	132	90,26	4
17	17	20,96	4	18	36	4

N = number of mice per group.

Table S2: Assay of quality control of the RNA

	Sample Name	S1	S2	S3	S10	S11	S12
Row	Internal controls	Ave Ct					
A	ACTB*	30,48	20,38	22,74	17,29	20,52	17,06
B	HPRT1*	17,02	17,49	19,46	17,04	18,31	16,88
C	RTC	21,59	35	35	20,11	21,35	22,37
D	PPC	18,38	18,34	18,23	17,3	17,96	17,87
E	GDC	35	35	35	35	35	35
F	NRT	35	31,22	35	35	35	32,78
G	PPC - H2O	19	18,63	18,14	35	35	35
H	NTC	35	35	35	35	35	35
Reverse Trasciption Control (RTC): Are RNA sample impurities affecting reverse transcription?							
CtC - CtG		2,59	16,37	16,86	-14,89	-13,65	-12,63
Cut-off 5		NO	Perhaps	Perhaps	NO	NO	NO
Positive PCR Control (PPC): Are RNA sample impurities affecting PCR?							
CtD - CtG		-0,62	-0,29	0,09	-17,7	-17,04	-17,13
Cut-off 3		NO	NO	NO	Perhaps	Perhaps	Perhaps
No Reverse Transcription (NRT) control: Is genomic DNA contamination detectable?							
CtF		35	31,22	35	35	35	32,78
Cut-off 35		NO	YES	NO	NO	NO	YES
Genomic DNA Contamination (GDC) control: Will it affect the results?							
CtE		35	35	35	35	35	35
Cut-off 35		NO	NO	NO	NO	NO	NO
No Template Control (NTC): Is the PCR system clean?							
CtH		35	35	35	35	35	35
Cut-off 34		YES	YES	YES	YES	YES	YES

CT: Cycle Threshold

S1-S3 and S10-S12: RNA samples (control and treatment groups)

*Housekeeping genes

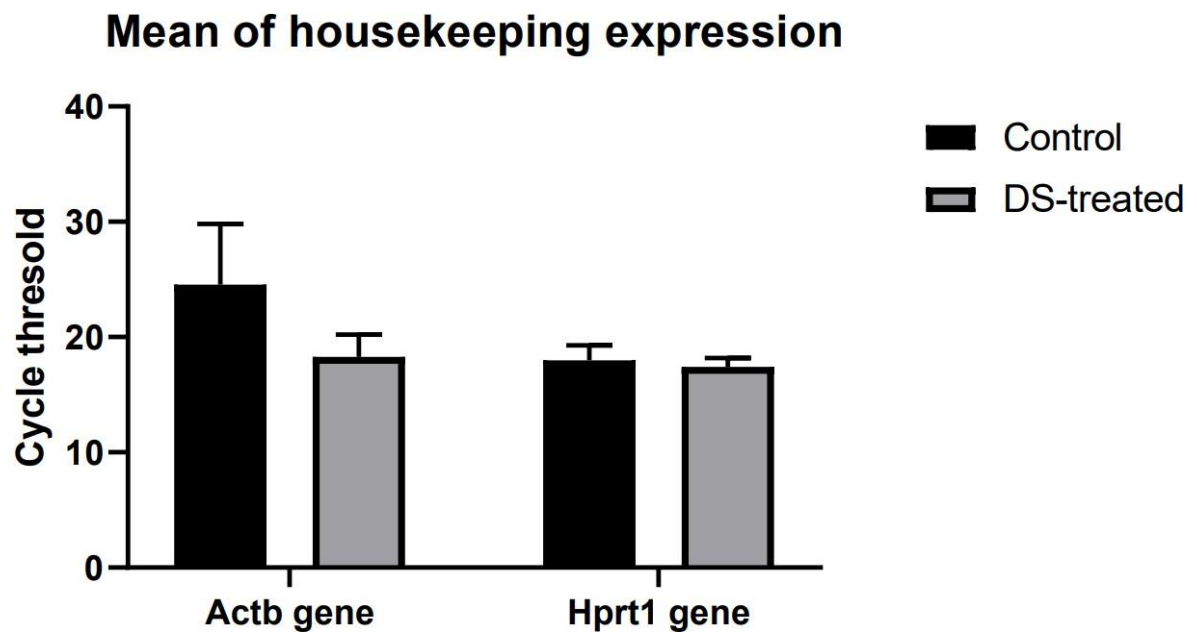


Figure S1: Quality control of mRNA expression levels of housekeeping genes. Analysis of two constitutive genes actin beta and hypoxanthine phosphoribosyltransferase 1 (Actb and Hprt1, respectively) were detected, which demonstrated stable baseline concentration of Hprt1 and non-statistical variation of the Actb gene.

Table S3: Up-down regulation of genes on DS-treated group (comparing to control group)

Gene	Fold Regulation	p-value
Acta2	1.01	0.874869
Actc1	1.01	0.874869
Angpt1	-1153.08	0.018693
Ccl12	-122120.35	0.013677
Ccl7	-1.23	0.408155
Cd40lg	17.29	0.005399
Cdh1	1.01	0.874869
Col14a1	1.81	0.047092
Col1a1	2584.00	0.007833
Col1a2	7924.23	0.001016
Col3a1	69.33	0.000039
Col4a1	5.32	0.032162
Col4a3	-1535.63	0.004485
Col5a1	1.01	0.874869
Col5a2	4.59	0.004717
Col5a3	4.26	0.013494
Csf2	8.12	0.000069

Csf3	35.89	0.001219
Ctgf	91.06	0.033101
Ctnnb1	26.58	0.009025
Ctsg	2.35	0.099407
Ctsk	4.98	0.004561
Ctsl	1.01	0.874869
Cxcl1	119119.98	0.010777
Cxcl11	42.58	0.021374
Cxcl3	-6002.21	0.015707
Cxcl5	1.01	0.874869
Egf	-49.68	0.137766
Egfr	1.64	0.022645
F13a1	1099.06	0.035764
F3	705.28	0.024809
Fga	11.57	0.035049
Fgf10	15.99	0.113947
Fgf2	229.45	0.013049
Fgf7	3393.89	0.006725
Hbegf	43.47	0.063086
Hgf	-38.26	0.000513
Ifng	148.61	0.108057
Igf1	14.74	0.026152
Il10	1.01	0.874869
Il1b	1590.64	0.015092
Il2	1.01	0.874869
Il4	-4.30	0.000508
Il6	1.01	0.874869
Il6st	91.48	0.003735
Itga1	671.88	0.016488
Itga2	115328.47	0.028990
Itga3	1.01	0.874869
Itga4	-4.19	0.001601
Itga5	-8.46	0.001387
Itga6	1.01	0.874869
Itgav	3.96	0.006900
Itgb1	1.50	0.207414
Itgb3	1.01	0.874869
Itgb5	1.01	0.874869
Itgb6	77555326.11	0.000338
Mapk1	40705559.86	0.001989
Mapk3	46299.93	0.133961
Mif	99017.04	0.172904
Mmp1a	-6507.75	0.053707
Mmp2	80.19	0.070737
Mmp7	1.43	0.231791
Mmp9	172.69	0.058591

Pdgfa	1.01	0.874869
Plat	3.16	0.023533
Plau	1.25	0.167182
Plaur	485.07	0.075561
Plg	12.60	0.014003
Pten	139.95	0.052366
Ptgs2	19154.41	0.023692
Rac1	65.14	0.207252
Rhoa	1346.86	0.041658
Serpine1	1.01	0.874869
Stat3	91114.26	0.048767
Tagln	9087104.21	0.046402
Tgfa	165.27	0.014793
Tgfb1	1.01	0.874869
Tgfbr3	1.01	0.874869
Timp1	1.01	0.874869
Tnf	1.01	0.874869
Vegfa	-3527.94	0.171114
Vtn	-3471.34	0.002632
Wisp1	1.01	0.874869
Wnt5a	-43.35	0.165277
Actb	14727976.14	0.021116
B2m	27276.85	0.128710
Gapdh	1.01	0.874869
Gusb	1.01	0.874869
Hsp90ab1	-1.26	0.284365

Bold genes: threshold of fold regulation and p-values are 2 and < 0.05, respectively.