SUPPLEMENTARY TABLES

Table S-1. Summary of mouse numbers used in each experimental group. Histology at early time points (3 days) was performed only to confirm absence or presence of inflammatory cell infiltration at later time points. For ease of visualization, outcomes performed in the "7-14 days" range are reported together. Macroscopic joint surface photography, histology, and qPCR of individual tissues was performed at 1 week for injured mice, macroscopic joint surface photography for sham was performed at 2 weeks, and qPCR of all whole joints was performed at 12 days. All Taqman single gene qPCR ($\dagger$) was performed in technical triplicates for each RNA extract.

Experimental Outcome	Genotype	Treatment(s)	Naïve	3 days	7-14 days	28 days
Macroscopic Joint Surface Photography	WT	Naïve	4	–	–	–
		Sham	–	–	2	2
		Injured	–	–	3	3
	Has1KO	Naïve or Injured	4	–	2	3
Histology	WT	Naïve	3	–	–	–
		Sham	–	–	3	3
		Injured	–	2	4	4
	Has1KO	Naïve or Injured	3	1	2	2
Taqman[†] and gene array qPCR (whole joints)	WT	Naïve	3	–	–	–
		Sham	–	–	3	3
		Injured	–	3	4	4
	Has1KO	Naïve or Injured	3	3	4	4
Taqman[†] qPCR (individual tissues)	WT	Naïve	12	–	–	–
		Sham	–	–	–	–
		Injured	0	–	12	12
	Has1KO	Naïve or Injured	12	–	12	12
	WT	Subtotals	22	5	31	31
	Has1KO		22	4	20	21
TOTAL			**156 mice**			

Table S-2. Inventoried murine Taqman® probes were used for qPCR of cDNA preparations derived from whole joint and pooled individual tissue RNA extracts.

Gene	Abbreviation	Inventory Number
Aggrecan	*Acan*	Mm00545794_m1
Collagen, type 1, alpha 1	*Col1a1*	Mm00801666_g1
Collagen, type 2, alpha 1	*Col2a1*	Mm01309565_m1
Collagen, type 3, alpha 1	*Col3a1*	Mm00802331_m1
Glyceraldehyde-3-phosphate dehydrogenase *	*Gapdh*	Mm99999915_g1
Hyaluronan synthase 1	*Has1*	Mm00468496_m1
Hyaluronan synthase 2	*Has2*	Mm00515089_m1
Hyaluronan synthase 3	*Has3*	Mm00515092_m1
Inter-alpha trypsin inhibitor, heavy chain 1	*Itih1*	Mm00434529_m1
Inter-alpha trypsin inhibitor, heavy chain 2	*Itih2*	Mm00434529_m1
Tumor necrosis factor, alpha-induced protein 6	*Tnfaip6*	Mm00493736_m1
Versican V1 isoform (formerly V0)	*Vcan V1*	AI7ZZKW
Versican V2 isoform (formerly V1)	*Vcan V2*	Mm00490173_m1

* Housekeeping gene

Table S-3. Effect of cartilage injury on mRNA abundance relative to *Gapdh* of ECM and HA network genes in isolated tissue pools from Has1$^{-/-}$ mice.

	Acan	Vcan V1	Vcan V2	Col1a1	Col2a1	Col3a1	Has2	Tnfaip6	Itih2
Naive									
Cartilage/ SC Bone	10.47	15.00	ND	3317	0.85	0.95	ND	0.40	ND
Meniscus/ Synovium	0.14	19.21	ND	611.1	ND	24.62	0.35	0.60	0.90
Patellar Tendon	0.06	6.28	0.14	2935	ND	2.35	0.31	3.95	0.76
1 week									
Cartilage/ SC Bone	5.25 (0.5)†	18.12 (1.21)	0.11 (8.56)	3301 (1.00)	2.10 (2.48)	29.38 (31.0)	0.05 (-)	1.13 (2.85)	0.16 (-)
Meniscus/ Synovium	22.35 (162)	9.57 (0.50)	4.45 (55.1)	9042 (14.8)	0.67 (-)	4014 (9790)	1.52 (4.41)	28.59 (47.5)	2.87 (3.18)
Patellar Tendon	14.05 (222)	9.49 (1.51)	9.73 (70.7)	12770 (4.35)	0.23 (-)	1455 (620)	2.92 (9.36)	39.83 (10.1)	1.10 (1.44)
4 weeks									
Cartilage/ SC Bone	7.28 (0.69)	10.15 (0.68)	0.19 (14.6)	5272 (1.59)	2.61 (3.08)	42.48 (44.9)	0.07 (-)	2.05 (5.16)	0.18 (-)
Meniscus/ Synovium	1.48 (10.7)	2.11 (0.11)	0.76 (9.4)	2287 (3.74)	0.21 (-)	1084 (1210)	0.39 (1.12)	32.78 (54.5)	2.17 (2.41)
Patellar Tendon	7.77 (123)	9.08 (1.45)	3.41 (24.8)	8021 (2.73)	2.31 (-)	1283 (547)	1.33 (4.27)	78.12 (19.8)	5.95 (7.80)

† *Numbers in parentheses are the fold change relative to Naïve. ND = not detected (Ct > 35).*

Table S-4. Transcript abundance relative to *Gapdh* of NF-κB signaling target genes in naïve WT and Has1$^{-/-}$ joints. Increases/decreases by <2(+/ ↓), 2-4 (++/ ↓ ↓), 4-8 (+++/ ↓ ↓ ↓), 8-16 (++++/ ↓ ↓ ↓ ↓), or 16+ (+++++/ ↓ ↓ ↓ ↓ ↓) fold, or no change (↔),indicated. Statistical significance between genotypes indicated for $p < 0.05$ (*).

Gene	WT	Has1-/-	Fold-Change	Gene	WT	Has1-/-	Fold-Change
Adm	1.27	2.17	+	Il1b	301.52	396.51	+
Agt	32.22	32.55	↔	Il1r2	189.56	304.87	+
Akt1	235.66	270.37	+	Il1rn	28.90	80.62	++
Aldh3a2	120.51	118.33	↔	Il2	0.70	4.08	+++
Bcl2a1a	17.72	35.41	++	Il2ra	5.80	23.19	+++
Bcl2l1	314.41	449.90	+	Il4	1.40	13.51	++++
Birc2	109.78	111.13	↔	Il6	0.93	8.76	++++ *
Birc3	183.43	226.19	+	Ins2	0.51	8.99	+++++
C3	764.61	805.84	+	Irf1	174.48	243.00	+
C4a	0.84	2.51	++	Lta	1.04	3.13	++
Ccl12	5.99	10.32	+	Ltb	82.05	95.95	+
Ccl22	1.48	5.49	++	Map2k6	25.88	53.50	++
Ccl5	86.00	120.54	+	Mitf	35.01	46.57	+
Ccnd1	84.06	138.27	+	Mmp9	3189.06	6580.82	++
Ccr5	26.15	29.93	+	Myc	146.84	444.10	++
Cd40	22.78	41.47	+	Myd88	19.78	28.89	+
Cd74	2833.46	2773.61	↔	Ncoa3	91.62	105.98	+
Cd80	15.53	22.51	+	Nfkb1	230.85	527.52	++
Cd83	100.79	108.95	+	Nfkb2	14.39	27.08	+
Cdkn1a	117.97	161.72	+	Nfkbia	474.46	1036.87	++
Cfb	102.95	171.40	+	Nqo1	65.28	127.51	+
Csf1	86.34	118.65	+	Nr4a2	12.44	27.36	++
Csf2	0.83	1.44	+	Pdgfb	63.07	78.17	+
Csf2rb	39.17	158.88	+++	Plau	33.01	49.26	+
Csf3	0.42	1.81	+++	Ptgs2	6.95	13.72	+
Cxcl1	1.06	4.87	+++	Rel	109.36	193.48	+
Cxcl10	21.07	33.87	+	Rela	148.20	176.39	+
Cxcl3	1.13	2.38	++	Relb	16.45	18.39	+
Cxcl9	26.84	18.43	↓	Sele	30.43	51.44	+
Egfr	48.39	54.67	+	Selp	13.09	214.54	+++++
Egr2	17.21	41.80	++	Snap25	0.30	3.23	++++
F3	20.58	33.86	+	Sod2	105.21	234.89	++
F8	22.04	40.18	+	Stat1	219.89	450.25	++
Fas	36.72	75.70	++	Stat3	87.32	232.47	++
Fasl	5.19	10.83	++	Stat5b	139.59	180.14	+
Gadd45b	38.48	62.68	+	Tnf	20.09	41.83	++
Icam1	49.74	58.45	+	Tnfrsf1b	86.45	139.34	+
Ifnb1	0.84	2.75	++	Tnfsf10	12.91	40.82	++
Ifng	1.83	6.13	++	Traf2	20.19	79.09	++
Il12b	1.03	1.91	+	Trp53	180.30	327.07	+
Il15	85.41	86.20	↔	Vcam1	624.77	1332.34	++
Il1a	25.36	68.02	++	Xiap	149.87	225.44	+

Table S-5. Transcript abundance relative to *Gapdh* of fibrosis associated genes in naïve WT and Has1$^{-/-}$ joints. Increases/decreases by <2(+/↓), 2-4 (++/↓↓), 4-8 (+++/↓↓↓), 8-16 (++++/↓↓↓↓), or 16+ (+++++/↓↓↓↓↓) fold, or no change (↔),indicated.

Gene	WT	Has1-/-	Fold-Change	Gene	WT	Has1-/-	Fold-Change
Acta2	116.83	250.47	++	Ltbp1	260.88	314.38	+
Bcl2	38.67	41.69	+	Mmp13	2682.85	2797.68	↔
Bmp7	11.52	9.93	↓	Mmp14	156.33	281.85	+
Cav1	236.38	252.78	+	Mmp1a	24.89	40.96	+
Ccl11	2.99	10.38	++	Mmp2	515.39	467.08	↓
Ccl3	10.74	15.09	+	Mmp3	2.39	19.49	++++
Ccr2	368.41	277.06	↓	Mmp8	2006.94	2340.96	+
Cebpb	794.67	236.62	↓↓	Myc	174.55	442.91	++
Col1a2	29633.70	22290.13	↓	Pdgfa	30.81	60.28	+
Col3a1	3473.36	4072.74	+	Plat	13.48	32.37	++
Ctgf	2506.08	2645.12	+	Plg	0.37	3.04	++++
Cxcr4	1627.25	1381.88	↓	Serpina1a	46.07	48.59	+
Dcn	8663.40	7957.97	↓	Serpine1	11.99	33.81	++
Edn1	4.87	6.49	+	Serpinh1	529.54	811.48	+
Egf	2.90	6.84	++	Smad2	104.98	193.83	+
Eng	115.12	162.05	+	Smad3	49.65	113.82	++
Grem1	32.08	22.44	↓	Smad4	184.08	374.98	++
Hgf	44.84	33.49	↓	Smad6	14.98	27.39	+
Il10	0.86	3.24	++	Smad7	36.53	59.39	+
Il13	0.49	1.44	++	Snai1	6.67	8.70	+
Il13ra2	8.77	11.17	+	Sp1	289.15	445.92	+
Il5	0.72	2.86	++	Stat6	65.75	58.11	↓
Ilk	568.15	1059.02	+	Tgfb1	443.24	1009.28	++
Inhbe	0.25	1.02	+++	Tgfb2	32.40	63.70	+
Itga1	75.42	81.47	+	Tgfb3	13.58	68.68	+++
Itga2	45.58	79.45	+	Tgfbr1	113.64	188.47	+
Itga3	4.33	7.26	+	Tgfbr2	207.87	457.03	++
Itgav	314.73	356.95	+	Tgif1	14.57	36.93	++
Itgb1	791.67	1108.95	+	Thbs1	1180.99	1945.09	+
Itgb3	377.41	703.07	+	Thbs2	172.87	347.49	++
Itgb5	143.77	227.04	+	Timp1	2.24	21.31	++++
Itgb6	8.88	9.53	+	Timp2	558.94	1291.67	++
Itgb8	4.00	12.50	++	Timp3	225.90	545.54	++
Jun	76.34	89.11	+	Timp4	34.12	88.27	++
Lox	325.68	393.80	+	Vegfa	62.32	162.22	++

Table S-6. Fold-change in expression of NF-κB signaling target genes in WT and Has1$^{-/-}$ joints at 12 and 28 d post injury. Values shown are relative to naïve levels for the respective genotype. Significance between genotypes at each post-injury time point (*) are indicated for p< 0.05.

Gene	WT 12d	WT 28d	Has1$^{-/-}$ 12d	Has1$^{-/-}$ 28d	Gene	WT 12d	WT 28d	Has1$^{-/-}$ 12d	Has1$^{-/-}$ 28d
Adm	1.61	-1.79	3.78	1.04	Il1b	-1.82	-1.31	1.01	-1.23
Agt	-2.08	-1.91	-1.25	-1.85	Il1r2	-2.95	1.03	1.54	-1.14
Akt1	-1.10	-1.41	2.00	-1.99	Il1rn	-1.91	-1.02	-1.77	1.05
Aldh3a2	-1.32	-1.51	1.30	-1.66	Il2	-6.42	-3.31	-5.20 *	-6.62
Bcl2a1a	-1.68	-1.23	-1.14	-2.19	Il2ra	-1.53	1.06	-2.10	-3.24
Bcl2l1	-2.12	-1.21	1.49	-2.34	Il4	-2.54	-1.86	-6.32	-1.40
Birc2	-1.43	-1.61	1.95	-1.66	Il6	4.73	1.77	1.40	1.13
Birc3	-1.57	-1.26	2.18	-1.61	Ins2	-7.21	-3.26	-20.69 *	-10.94
C3	-1.23	-1.61	1.47	-1.95	Irf1	-1.49	-1.14	1.09	-1.57
C4a	-4.24	-1.98	1.82	-3.19	Lta	-2.80	-1.67	-1.17	-3.04
Ccl12	2.15	2.07	4.43	1.41	Ltb	-1.86	-1.48	-1.77	-1.64
Ccl22	1.19	-2.96	-1.66	-2.10	Map2k6	-1.05	-1.43	1.02	-1.36
Ccl5	-1.62	-1.06	1.04	-1.42	Mitf	1.01	-1.33	1.65	1.12
Ccnd1	-1.06	-1.53	1.64	-1.43	Mmp9	-1.61	1.06	-1.02	-1.53
Ccr5	1.69	-1.33	1.66	1.07	Myc	-1.54	1.29	-1.20	-1.73
Cd40	-1.58	-1.16	1.42	-2.25	Myd88	-1.12	-2.19	1.04	-1.07
Cd74	-1.38	-1.23	1.07	-1.99	Ncoa3	1.04	-1.55	1.69	-2.18
Cd80	-1.05	-1.40	2.22	-1.34	Nfkb1	-1.01	-1.30	-1.21	-1.30
Cd83	-1.95	-1.23	1.95	-1.92	Nfkb2	1.10	-1.10	2.00	-1.12
Cdkn1a	1.35	-1.27	3.44	-1.35	Nfkbia	-1.37	1.06	-1.26	1.04
Cfb	1.72	-1.43	2.59	-1.83	Nqo1	-1.57	-1.01	-1.52	-1.58
Csf1	-1.16	-1.20	1.60	-1.81	Nr4a2	5.08	1.23	5.59	2.32
Csf2	-7.29	-2.44	1.36 *	-1.82	Pdgfb	1.02	-1.47	1.33	-1.39
Csf2rb	2.31	2.16	1.20	-1.47	Plau	1.54	-1.09	1.24	-1.17
Csf3	-2.16	-1.16	1.53	-4.85	Ptgs2	4.35	-1.20	3.09	2.33
Cxcl1	3.37	-1.01	2.60	1.89	Rel	-1.62	-1.29	-2.14	-1.43
Cxcl10	1.19	-1.23	1.33	-2.16	Rela	-1.08	-1.05	1.82	-1.49
Cxcl3	1.19	-2.28	2.42	1.19	Relb	1.11	-1.12	2.47	-1.13
Cxcl9	-1.20	-1.21	1.55	-2.46	Sele	-1.26	-1.06	-1.14	-1.39
Egfr	2.24	-1.27	4.04	-1.14	Selp	5.67	6.72	-2.28	-1.03
Egr2	1.36	1.17	1.69	-1.61	Snap25	-1.98	-1.82	-3.78	-6.28
F3	1.08	-1.28	2.37	-1.50	Sod2	1.02	-1.03	-1.23	1.52
F8	-2.33	-1.40	-1.29	-1.90	Stat1	-1.21	-1.01	-1.84	-1.53
Fas	-1.32	-1.12	1.25	-1.50	Stat3	1.47	-1.47	-1.43	-1.11
Fasl	-2.53	-1.20	-1.20	-1.96	Stat5b	-1.39	1.09	1.98	1.34
Gadd45b	1.31	-1.61	1.89	-1.43	Tnf	-1.46	-1.31	-2.18	-1.68
Icam1	1.00	-1.56	1.91	1.05	Tnfrsf1b	-1.11	-1.30	-1.70	-1.40
Ifnb1	-9.15	-2.90	-1.59	-4.66	Tnfsf10	1.16	-1.31	-1.97	-1.23
Ifng	-1.59	-2.63	-1.97	-3.74	Traf2	-1.12	-1.18	-2.09	-1.61
Il12b	1.02	-1.96	1.33	-3.09	Trp53	-1.23	-1.05	-1.61	-1.58
Il15	-2.03	-1.51	1.17	-1.33	Vcam1	-2.12	1.42	-2.21	-1.57
Il1a	-2.24	-1.04	-1.81	-2.01	Xiap	-1.22	-1.05	-1.29	-1.15

Table S-7. Fold-change in expression of fibrosis genes in injured WT and Has1$^{-/-}$ joints at 12 and 28 d post injury. Values shown are relative to naïve levels for the respective genotype. Significance between injured and naïve within the genotype (#) and between genotypes at each post-injury time point (*) and are indicated for p< 0.05.

Gene	WT 12d	WT 28d	Has1$^{-/-}$ 12d	Has1$^{-/-}$ 28d	Gene	WT 12d	WT 28d	Has1$^{-/-}$ 12d	Has1$^{-/-}$ 28d
Acta2	1.67	1.25	1.55	-1.12	Ltbp1	1.08	-1.52	1.23	1.02
Bcl2	-2.80	-2.43	-1.45	-1.85	Mmp13	-2.63	-1.57	-1.43	-1.34
Bmp7	-4.16	-2.28	-1.33	-1.36	Mmp14	1.68	-1.19	1.19	-1.23
Cav1	-1.57	-2.71	1.84	-1.07	Mmp1a	-9.71	-16.73	-8.49	1.18
Ccl11	1.35	1.75	-3.56	-1.36	Mmp2	2.58	1.13	5.95 #	2.21
Ccl3	-4.16	-1.48	-2.34 *	-1.70	Mmp3	43.24	18.79	11.8 #	11.6 #
Ccr2	-3.59	-1.60	-3.16	-1.21	Mmp8	-3.37	-1.48	-2.91	-1.33
Cebpb	-7.47	-1.33	2.61	1.17	Myc	-1.81	-1.23	-2.95	-2.36
Col1a2	-2.04	-1.16	2.40 *	1.36	Pdgfa	1.01	-1.28	-1.10	-1.22
Col3a1	4.49	2.24	12.3 #	4.76	Plat	2.76	-1.52	1.34	1.60
Ctgf	-2.43	-1.16	2.24 *	-1.06	Plg	-1.81	-1.26	-7.20	-5.15
Cxcr4	-3.94	-2.09	-3.22	-1.78	Serpina1a	-3.42	-2.67	-2.90	-2.66
Dcn	-1.45	-1.20	1.83	1.44	Serpine1	2.47	1.29	1.64	2.00
Edn1	-1.18	-1.62	1.77	1.19	Serpinh1	1.65	-1.12	2.03	1.09
Egf	-1.40	-1.82	-1.91	-3.49	Smad2	-1.87	-1.44	-1.58	-1.30
Eng	-1.80	-1.79	-1.58	-1.88	Smad3	1.22	-1.58	-1.37	-1.70
Grem1	-8.02	-2.56	-2.50 *	-1.95	Smad4	-1.05	-1.43	-1.77	-1.53
Hgf	-3.00	-1.32	-1.60	-1.52	Smad6	-1.16	-1.43	1.25	-1.57
Il10	-1.98	1.34	-1.46	-1.71	Smad7	-1.17	-1.45	-1.05	-2.30
Il13	-5.97	-1.58	-1.94	-2.15	Snai1	1.36	-1.26	2.36	-1.29
Il13ra2	-4.05	-1.52	-1.84	1.17	Sp1	-1.44	-1.49	-1.54	-1.68
Il5	-1.90	-1.74	-2.72	-2.18	Stat6	-1.04	-1.33	1.42	-2.35
Ilk	-2.49	-1.49	-2.99	-1.66	Tgfb1	-1.25	-1.40	-2.55	-1.76
Inhbe	-1.43	1.48	-1.27	-2.01	Tgfb2	2.09	-1.99	1.33	-1.18
Itga1	-2.86	-1.68	-1.99	-1.43	Tgfb3	7.41	1.92	2.27	1.20
Itga2	-2.75	-1.66	-3.43	-1.67	Tgfbr1	-1.04	-1.31	-1.23	-1.32
Itga3	-2.06	-1.69	-2.34	-1.27	Tgfbr2	1.65	-1.59	-1.07	-1.63
Itgav	-3.39	-1.39	-1.62	-1.46	Tgif1	1.40	-1.62	-1.92	-1.28
Itgb1	-1.20	-1.44	1.16	-1.08	Thbs1	1.28	-1.23	1.00	-1.30
Itgb3	-1.76	1.20	-1.88	-1.91	Thbs2	7.41	1.08	4.77	1.99
Itgb5	1.38	-1.39	1.07	-1.36	Timp1	1.53	1.19	-2.85	3.69
Itgb6	1.21	-2.75	1.26	-1.29	Timp2	3.05	-1.02	2.23	1.28
Itgb8	1.42	-1.47	-2.00	-1.49	Timp3	1.14	-1.30	-1.43	-1.26
Jun	1.13	-1.25	1.20	1.04	Timp4	-4.08	-2.67	-4.42	-2.77
Lox	1.24	-1.58	1.23	1.12	Vegfa	1.05	-2.04	-1.36	-1.48