

Supplementary Materials

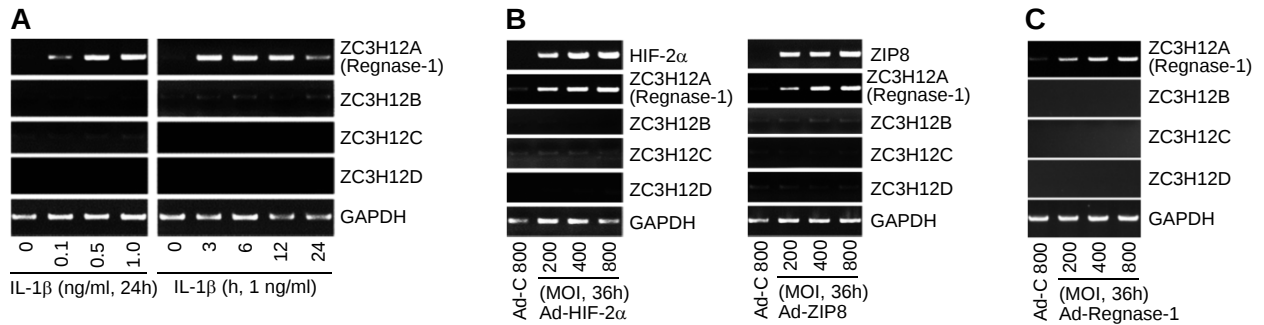
Up-regulated endonuclease Regnase-1 suppresses osteoarthritis by forming a negative feedback loop of catabolic signaling in chondrocytes

Jeong-In Yang and Jang-Soo Chun

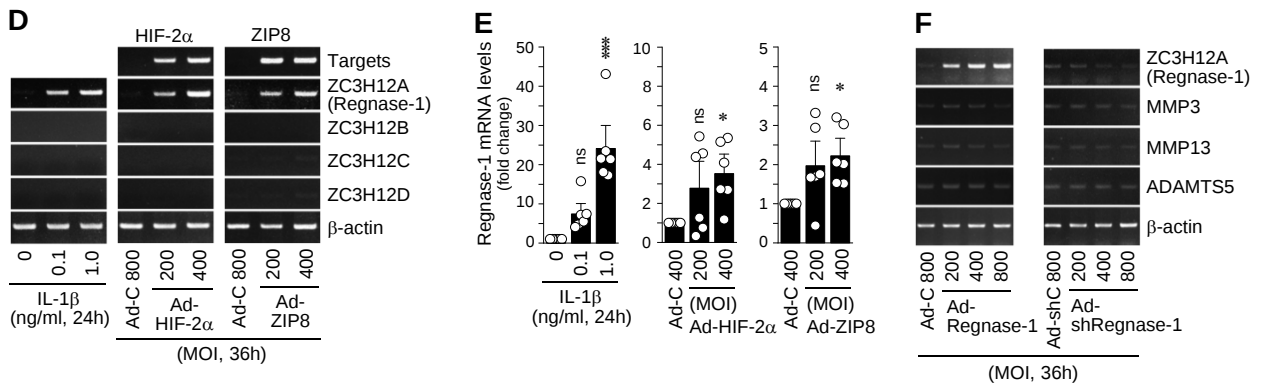
Supplementary Figure 1-5

Supplementary Table 1-6

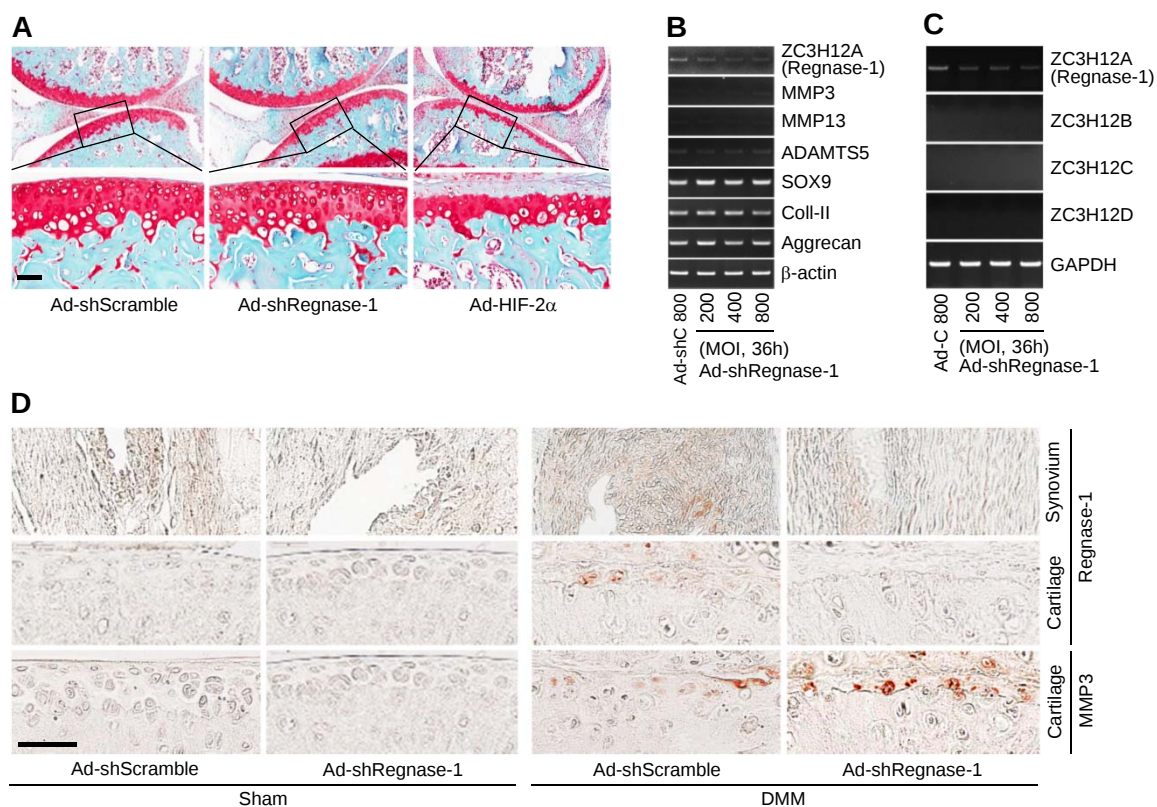
Chondrocytes



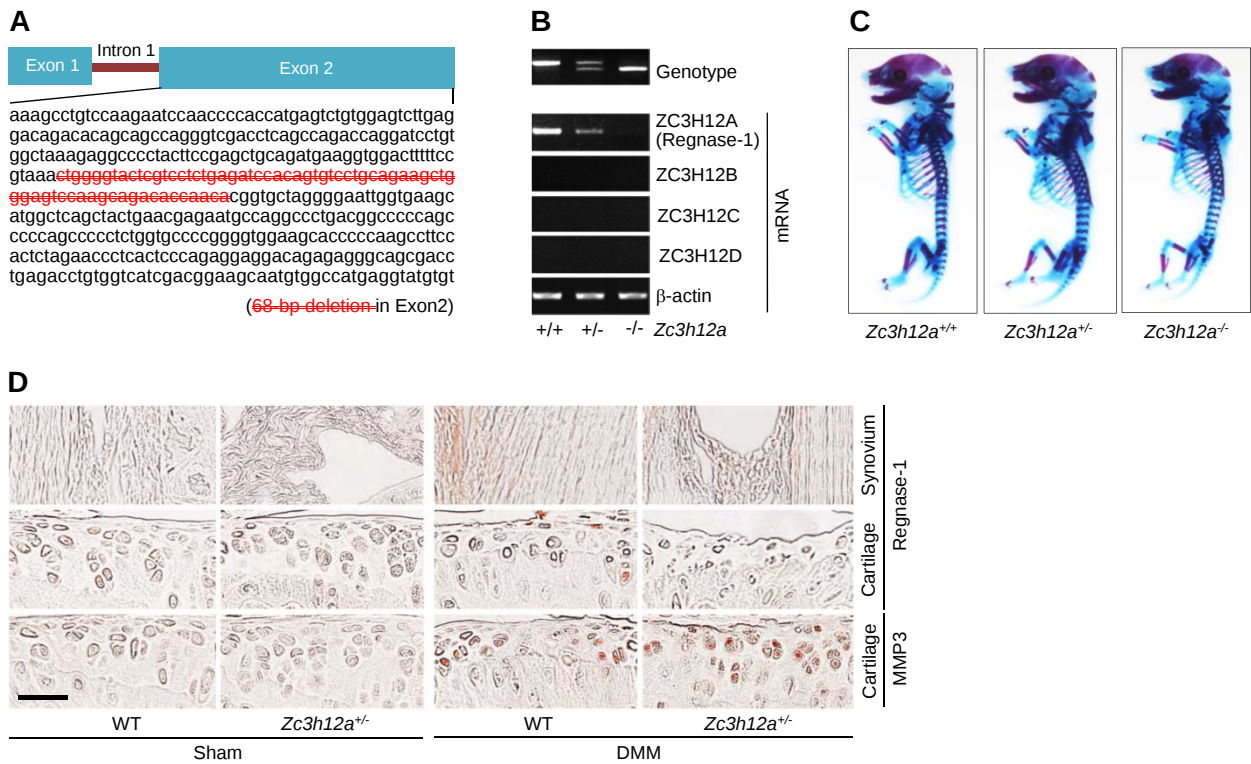
Fibroblast-like synoviocytes (FLS)



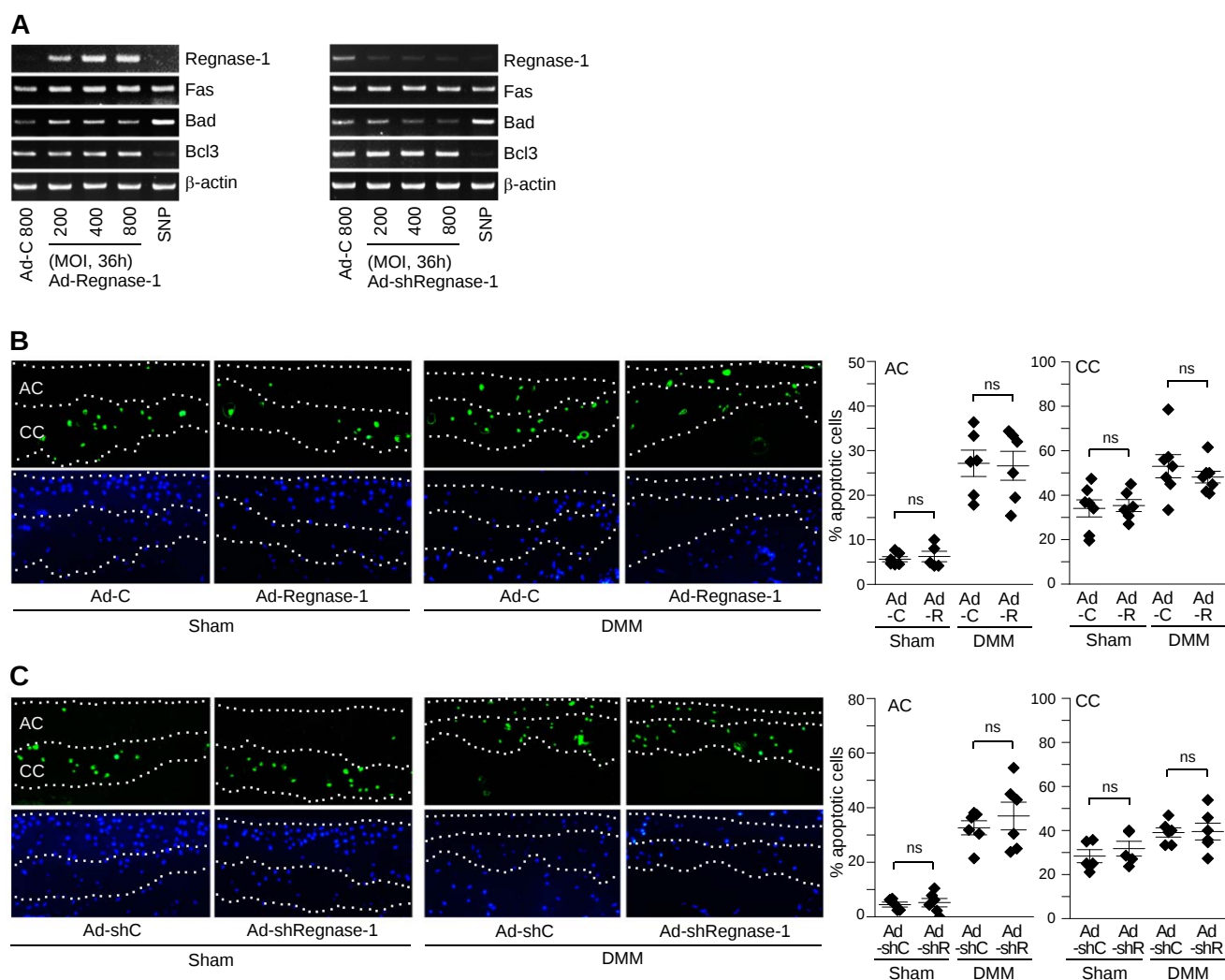
Supplementary Fig. 1. Upregulation of Regnase-1 in chondrocytes and fibroblast-like synoviocytes (FLS) treated with OA-associated catabolic factors. **A–C** RT-PCR analysis of ZC3H12 family members in chondrocytes treated with IL-1 β (**A**), infected with Ad-HIF-2 α or Ad-ZIP8 (**B**), or infected with Ad-Regnase-1 (**C**). **D** and **E** RT-PCR (**D**) and qRT-PCR (**E**) analysis of ZC3H12 family members in FLS treated with IL-1 β or infected with Ad-HIF-2 α or Ad-ZIP8. **F** RT-PCR analysis of the indicate molecules in FLS infected with Ad-Regnase-1 or Ad-shRegnase-1. Images are representative of the results obtained from five independent primary cultures of chondrocytes or FLS. Values are means $\pm$ s.e.m. and one-way ANOVA with Bonferroni's *post hoc* test. * $p < 0.05$, *** $p < 0.0005$. ns, not significant.



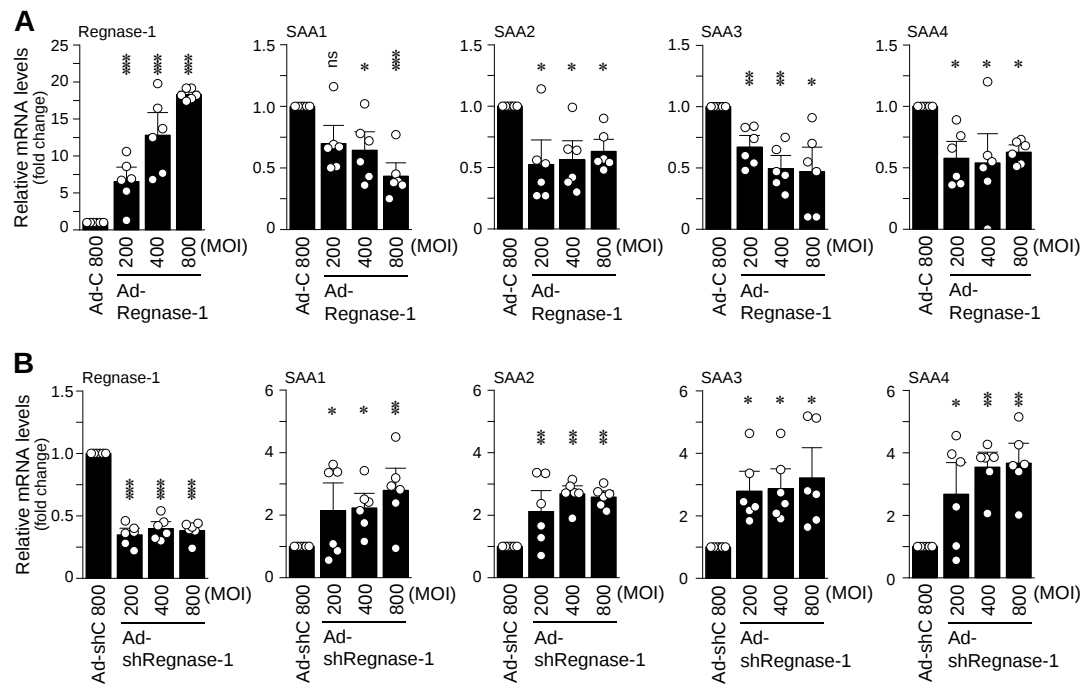
Supplementary Fig. 2. Knockdown of Regnase-1 alone in joint tissues is not sufficient to cause OA-like changes in mice. **A** Representative Safranin-O staining images of joint sections from mice IA-injected with Ad-shScramble (Ad-shC), Ad-shRegnase-1, or Ad-HIF-2 α ($n = 10$ mice per group). IA injection of Ad-HIF-2 α was used as a positive control. **B** and **C** Representative RT-PCR images ($n = 4$) of the indicated molecules in primary-culture chondrocytes infected with Ad-shControl (Ad-shC) or Ad-shRegnase-1. **D** Representative immunohistochemical staining images ($n \geq 5$ mice per group) of the indicated molecules in cartilage and synovium of sham- or DMM-operated mice injected with As-shScramble or Ad-shRegnase-1. Scale bar: 50 μ m.



Supplementary Fig. 3. Characterization of Regnase-1 knockout mice. **A** A 68-bp deletion in exon 2 of the Regnase-1 gene (*Zc3h12a*) was used to generate *Zc3h12a*^{-/-} mice. **B** Genotypes and mRNA levels of ZC3H12A family members in *Zc3h12a* homozygous (-/-) KO mice, heterozygous (+/-) mice, and their WT (+/+) littermates. **C** Skeletal staining of E18.5 embryos of *Zc3h12a* homozygous (-/-) KO mice, heterozygous (+/-) KO mice, and their WT (+/+) littermates. **D** Representative immunohistochemical staining images ($n \geq 5$ mice per group) of the indicated molecules in cartilage or synovium of sham- or DMM-operated WT mice and *Zc3h12a*^{+/-} mice. Scale bar: 50 μ m.



Supplementary Fig. 4. Regnase-1 does not modulate apoptosis of chondrocytes. **A** Representative RT-PCR images of the indicated molecules in chondrocytes infected with Ad-Regnase-1 or Ad-shRegnase-1 ($n = 3$). SNP (sodium nitroprusside) was used as a positive control. **B** and **C** Representative images of TUNEL assays (left panels) and quantitation of apoptotic chondrocytes (right panels) in cartilage sections of sham- or DMM-operated mice IA injected with Ad-Regnase-1 (**B**) or Ad-shRegnase-1 (**C**) ($n \geq 4$ mice per group). Values are means $\pm$ s.e.m. and one-way ANOVA with Bonferroni's *post hoc* test. * $p < 0.05$, ** $p < 0.005$, *** $p < 0.0005$. ns, not significant. AC, articular cartilage; CC, calcified cartilage.



Supplementary Fig. 5. Regnase-1 modulates the expression levels of SAA family members in chondrocytes. **A** and **B** qRT-PCR analysis ($n = 6$) of SAA family members (SAA1, SAA2, SAA3, and SAA4) in chondrocytes infected with 800 MOI of control adenovirus (Ad-C or Ad-shC) or the indicated MOI of Ad-Regnase-1 (**A**) and Ad-shRegnase-1 (**B**) for 36 hours. Values are means $\pm$ s.e.m. and one-way ANOVA with Bonferroni's *post hoc* test. * $p < 0.05$, ** $p < 0.005$, *** $p < 0.0005$. ns, not significant.

Supplementary Table 1. PCR primers and conditions.

Genes	Strand	Primer sequences	Size (bp)	AT (°C)	Origin
<i>Acan</i> (Aggrecan)	S AS	5'-CTGTCTTTGTACCCACACATG-3' 5'-GAAGACGACATCACCATCCAG-3'	581	58	Mouse
<i>Adamts5</i>	S AS	5'-GCCATTGTAATAACCCTGCACC-3' 5'-TCAGTCCCATCCGTAACCTTTG-3'	292	58	Mouse
<i>Actb</i> (β -actin)	S AS	5'-ATATCGCTGCGCTGGTCGTC-3' 5'-AGGATGGCGTGAGGGAGAGC-3'	517	58	Mouse
<i>Bad</i>	S AS	5'-AGGGATGGAGGAGGAGCTTA-3' 5'-TAGAGTTCCGGGATGTGGAG-3'	280	60	Mouse
<i>Bcl3</i>	S AS	5'-GTGGAGAACAACAGCCTGAACATGG-3' 5'-GCAGGAAGGCAGGTGTAGATGTTG-3'	445	60	Mouse
<i>Col2a1</i>	S AS	5'-CACACTGGTAAGTGGGGCAAGACCG-3' 5'-GGATTGTGTTGTTTCAGGGTTCGGG-3'	173	57	Mouse
<i>Epas1</i> (HIF-2 α)	S AS	5'-CGAGAAGAACGACGTGGTGTTC-3' 5'-GTGAAGGCTGGCAGGCTCC-3'	333	64	Mouse
<i>Fas</i>	S AS	5'-CTCTGGTGCTTGCTGGCTCACAGTTAAG-3' 5'-TTTCAGGTTGGCATGGTTGACAGC-3'	162	56	Mouse
<i>Mmp13</i>	S AS	5'-TGATGGACCTTCTGGTCTTCTGG-3' 5'-CATCCACATGGTTGGGAAGTTCT-3'	473	58	Mouse
<i>Mmp3</i>	S AS	5'-AGGGATGATGATGCTGGTATGG-3' 5'-CCATGTTCTCCAAGTCAAAGG-3'	434	58	Mouse
<i>Saa1</i>	S AS	5'-TCCTCCTCAAGCAGTTACTACTGCAA-3' 5'-ATGAAGGAAGCTAACTGGAAAACTC-3'	423	60	Mouse
<i>Saa2</i>	S AS	5'-TCCTCCTCAAGCAGTTACTACTGCTC-3' 5'-ATGAAGGAAGCTGGCTGGAAAGATGG-3'	420	60	Mouse
<i>Saa3</i>	S AS	5'-GCCACCATGAAGCCTTCCATTGCCATCATT-3' 5'-TCAGTATCTTTTAGGCAGGCCAGCAG-3'	375	60	Mouse
<i>Saa4</i>	S AS	5'-GAGGTCTTGCTCGTGATTCACT-3' 5'-TTTCTGGGTAGCCTGCAGGGTT-3'	373	66	Mouse
<i>Slc39a8</i> (ZIP8)	S AS	5'-GAACAATTGCCTGGATGATCACGC-3' 5'-AAGCCGGTTAACATCCCTGCATTC-3'	430	58	Mouse
<i>Sox9</i>	S AS	5'-CACTGGCAGTTACGGCATCAG-3' 5'-CATGTAAGTGAAGGTGGAGTAGAGC-3'	457	61	Mouse
<i>Zc3h12a</i>	S AS	5'-AGATGTCAGAATTATGGGGCGTGC-3' 5'-GCGTCTCATTACAGTTCTACCAGG-3'	389	64	Mouse
<i>Zc3h12b</i>	S AS	5'-GAGGGTGGTCTGCTATGATGA-3' 5'-GAAATTCTCAAGGCTCGGACC-3'	217	60	Mouse
<i>Zc3h12c</i>	S AS	5'-CTCAGGATCAAAGACCACAGG-3' 5'-AATATCCAACGTCAACAGGGG-3'	120	60	Mouse
<i>Zc3h12d</i>	S AS	5'-GGCGATCTCGGGTCTCCAAT-3' 5'-GGTTGTGCTGACTCCGAAGG-3'	212	60	Mouse

AT, annealing temperature; S, sense; AS, antisense

Supplementary Table 2. mRNA levels of RNases in chondrocytes treated with IL-1 β (1 ng/ml, 36 h) or infected with 800 MOI of Ad-HIF-2 α or Ad-ZIP8 (36 h).

Gene symbol	Definition	Fold change		
		IL-1 β	Ad-HIF-2 α	Ad-ZIP8
Endonuclease				
<i>Ago2</i>	Argonaute RISC catalytic subunit 2	1.069 $\pm$ 0.08	1.143 $\pm$ 0.13	1.033 $\pm$ 0.12
<i>Ang2</i>	Angiogenin, ribonuclease A family, member 2	1.219 $\pm$ 0.20	1.074 $\pm$ 0.43	1.280 $\pm$ 0.76
<i>Ang4</i>	Angiogenin, ribonuclease A family, member 4	0.757 $\pm$ 0.65	0.991 $\pm$ 0.63	0.876 $\pm$ 0.30
<i>Ang5</i>	Angiogenin, ribonuclease A family, member 5	0.973 $\pm$ 0.14	1.025 $\pm$ 0.31	1.121 $\pm$ 0.31
<i>Ang6</i>	Angiogenin, ribonuclease A family, member 6	1.117 $\pm$ 0.24	0.987 $\pm$ 0.26	0.919 $\pm$ 0.32
<i>Apex1</i>	Apurinic/apyrimidinic endonuclease 1	0.818 $\pm$ 0.18	0.985 $\pm$ 0.07	1.149 $\pm$ 0.06
<i>Apex2</i>	Apurinic/apyrimidinic endonuclease 2	0.898 $\pm$ 0.08	0.924 $\pm$ 0.11	0.871 $\pm$ 0.15
<i>Cpsf3</i>	Cleavage and polyadenylation specificity factor 3	0.868 $\pm$ 0.12	0.881 $\pm$ 0.10	0.903 $\pm$ 0.13
<i>Dclre1c</i>	DNA cross-link repair 1C, PSO2 homolog	1.363 $\pm$ 0.22	1.052 $\pm$ 0.23	1.160 $\pm$ 0.18
<i>Dicer1</i>	ElaC homolog 2 (E. coli)	0.600 $\pm$ 0.22	0.792 $\pm$ 0.15	0.779 $\pm$ 0.16
<i>Ear1</i>	Eosinophil-associated, ribonuclease A family, member 1	0.919 $\pm$ 0.49	1.156 $\pm$ 0.59	1.050 $\pm$ 0.65
<i>Ear10</i>	Eosinophil-associated, ribonuclease A family, member 10	0.917 $\pm$ 0.16	0.958 $\pm$ 0.32	1.091 $\pm$ 0.40
<i>Ear11</i>	Eosinophil-associated, ribonuclease A family, member 11	-	1.286 $\pm$ 0.21	1.190 $\pm$ 0.33
<i>Ear2</i>	Eosinophil-associated, ribonuclease A family, member 2	1.055 $\pm$ 0.21	1.031 $\pm$ 0.20	1.071 $\pm$ 0.22
<i>Ear4</i>	Eosinophil-associated, ribonuclease A family, member 4	-	0.950 $\pm$ 0.37	0.914 $\pm$ 0.29
<i>Ear5</i>	Eosinophil-associated, ribonuclease A family, member 5	-	0.977 $\pm$ 0.21	0.975 $\pm$ 0.36
<i>Ear7</i>	Eosinophil-associated, ribonuclease A family, member 7	-	1.125 $\pm$ 0.40	1.156 $\pm$ 0.41
<i>Elac1</i>	Zinc phosphodiesterase ELAC protein 1	1.117 $\pm$ 0.16	1.101 $\pm$ 0.15	1.002 $\pm$ 0.20
<i>Elac2</i>	Zinc phosphodiesterase ELAC protein 2	0.779 $\pm$ 0.12	0.829 $\pm$ 0.05	0.830 $\pm$ 0.07
<i>Eme1</i>	Essential meiotic endonuclease 1 homolog 1	0.853 $\pm$ 0.27	1.142 $\pm$ 0.35	1.017 $\pm$ 0.24
<i>Endod1</i>	Endonuclease domain containing 1	0.991 $\pm$ 0.11	1.068 $\pm$ 0.14	1.049 $\pm$ 0.17
<i>Endog</i>	Endonuclease G	0.769 $\pm$ 0.16	0.924 $\pm$ 0.19	0.873 $\pm$ 0.18
<i>Endou</i>	Endonuclease, polyU-specific	1.050 $\pm$ 0.21	1.097 $\pm$ 0.15	0.994 $\pm$ 0.25
<i>Endov</i>	Inosine-specific endoribonuclease	1.017 $\pm$ 0.04	0.839 $\pm$ 0.17	0.893 $\pm$ 0.17
<i>Ern2</i>	Endoplasmic reticulum (ER) to nucleus signaling 2	-	1.006 $\pm$ 0.21	1.001 $\pm$ 0.28
<i>Exo1</i>	Exonuclease 1	0.496 $\pm$ 0.26	1.687 $\pm$ 0.24	1.944 $\pm$ 0.24
<i>Exog</i>	Exo/endonuclease G	0.617 $\pm$ 0.20	0.773 $\pm$ 0.14	0.757 $\pm$ 0.17
<i>Fan1</i>	FANCD2/FANCI-associated nuclease 1	0.900 $\pm$ 0.35	0.938 $\pm$ 0.19	0.888 $\pm$ 0.26
<i>Fen1</i>	Flap structure specific endonuclease 1	0.622 $\pm$ 0.32	1.216 $\pm$ 0.16	1.163 $\pm$ 0.13
<i>Hrsp12</i>	Heat-responsive protein 12	1.250 $\pm$ 0.13	1.019 $\pm$ 0.16	1.000 $\pm$ 0.13
<i>Mre11a</i>	Meiotic recombination 11 homolog A (S. cerevisiae)	0.735 $\pm$ 0.23	0.927 $\pm$ 0.19	0.950 $\pm$ 0.12
<i>Mrpl44</i>	Mitochondrial ribosomal protein L44	1.009 $\pm$ 0.09	0.880 $\pm$ 0.13	0.975 $\pm$ 0.16
<i>Mus81</i>	MUS81 endonuclease homolog (yeast)	1.049 $\pm$ 0.16	1.013 $\pm$ 0.15	0.920 $\pm$ 0.18
<i>Pelo</i>	Pelota mRNA surveillance and ribosome rescue factor	0.906 $\pm$ 0.06	0.869 $\pm$ 0.11	0.863 $\pm$ 0.14
<i>Pld6</i>	Phospholipase D family, member 6	0.946 $\pm$ 0.18	0.971 $\pm$ 0.19	1.121 $\pm$ 0.18

<i>Rnase4</i>	Ribonuclease, RNase A family 4	-	0.907 ± 0.39	1.431 ± 0.36
<i>Rnase6</i>	Ribonuclease, RNase A family, 6	0.966 ± 0.40	1.001 ± 0.19	1.042 ± 0.13
<i>Rnaseh1</i>	Ribonuclease H1	-	0.904 ± 0.07	0.934 ± 0.08
<i>Rnase1</i>	Ribonuclease L	1.597 ± 0.31	1.337 ± 0.27	1.363 ± 0.32
<i>Rnaset2b</i>	Ribonuclease T2	0.827 ± 0.33	0.866 ± 0.17	0.886 ± 0.19
<i>Slx4</i>	SLX4 structure-specific endonuclease subunit	1.008 ± 0.08	0.957 ± 0.17	0.990 ± 0.17
<i>Tsen34</i>	tRNA splicing endonuclease 34 homolog	0.869 ± 0.18	1.138 ± 0.11	1.052 ± 0.13
<i>Tsn</i>	Translin RNase	0.894 ± 0.18	0.978 ± 0.14	1.016 ± 0.10
<i>Zc3h12a</i>	Zinc finger CCCH type containing 12A	7.781 ± 0.14	4.744 ± 0.47	3.949 ± 0.44
<i>Zc3h12b</i>	Zinc finger CCCH type containing 12B	1.323 ± 0.37	0.940 ± 0.34	1.025 ± 0.29
<i>Zc3h12c</i>	Zinc finger CCCH type containing 12C	0.948 ± 0.20	1.208 ± 0.16	1.163 ± 0.19
Exonucleases				
<i>Apex1</i>	apurinic/apyrimidinic endonuclease 1	0.818 ± 0.18	0.985 ± 0.07	1.149 ± 0.06
<i>Apex2</i>	apurinic/apyrimidinic endonuclease 2	0.898 ± 0.08	0.924 ± 0.11	0.871 ± 0.15
<i>Cnot6</i>	CCR4-NOT transcription complex, subunit 6	0.966 ± 0.24	0.968 ± 0.17	0.962 ± 0.14
<i>Cnot6l</i>	CCR4-NOT transcription complex, subunit 6-like	1.006 ± 0.12	0.975 ± 0.10	0.941 ± 0.13
<i>Cnot7</i>	CCR4-NOT transcription complex, subunit 7	1.279 ± 0.17	0.918 ± 0.07	0.892 ± 0.08
<i>Cnot8</i>	CCR4-NOT transcription complex, subunit 8	0.881 ± 0.17	0.821 ± 0.16	0.807 ± 0.13
<i>Cpsf3</i>	cleavage and polyadenylation specificity factor 3	0.868 ± 0.12	0.881 ± 0.10	0.903 ± 0.13
<i>Ddx1</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	0.798 ± 0.08	0.938 ± 0.10	0.909 ± 0.09
<i>Dis3</i>	DIS3 mitotic control homolog (S. cerevisiae)	0.578 ± 0.02	0.778 ± 0.25	0.831 ± 0.18
<i>Dis3l</i>	DIS3 mitotic control homolog (S. cerevisiae)-like	0.857 ± 0.09	0.959 ± 0.23	0.979 ± 0.32
<i>Dis3l2</i>	DIS3 mitotic control homolog (S. cerevisiae)-like 2	1.104 ± 0.17	1.076 ± 0.18	1.051 ± 0.24
<i>Dxo</i>	decapping exoribonuclease	1.042 ± 0.16	1.002 ± 0.17	0.955 ± 0.26
<i>Eri1</i>	exoribonuclease 1	0.707 ± 0.25	1.100 ± 0.15	1.128 ± 0.17
<i>Eri2</i>	exoribonuclease 2	1.043 ± 0.26	1.142 ± 0.20	1.135 ± 0.23
<i>Eri3</i>	exoribonuclease 3	0.904 ± 0.24	0.913 ± 0.28	0.900 ± 0.29
<i>Exd1</i>	exonuclease 3-5 domain containing 1	1.190 ± 0.18	1.157 ± 0.19	1.274 ± 0.27
<i>Exd2</i>	exonuclease 3-5 domain containing 2	0.939 ± 0.13	0.932 ± 0.38	0.955 ± 0.39
<i>Exosc3</i>	exosome component 3	0.932 ± 0.18	0.990 ± 0.22	0.979 ± 0.17
<i>Exosc9</i>	exosome component 9	0.862 ± 0.08	0.897 ± 0.12	0.921 ± 0.08
<i>Isq20</i>	interferon-stimulated protein	0.917 ± 0.09	1.072 ± 0.08	1.040 ± 0.10
<i>Isq20l2</i>	interferon stimulated exonuclease gene 20-like 2	0.827 ± 0.12	0.953 ± 0.04	0.990 ± 0.06
<i>Pan2</i>	PAN2 polyA specific ribonuclease subunit homolog	0.903 ± 0.08	1.030 ± 0.14	0.955 ± 0.23
<i>Parn</i>	poly(A)-specific ribonuclease (deadenylation nuclease)	0.858 ± 0.16	0.905 ± 0.11	0.992 ± 0.09
<i>Pnpt1</i>	phosphodiesterase 12	0.778 ± 0.34	0.878 ± 0.13	0.944 ± 0.11
<i>Rexo1</i>	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	0.934 ± 0.09	0.986 ± 0.19	0.925 ± 0.19
<i>Rexo2</i>	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	0.922 ± 0.13	1.066 ± 0.11	1.044 ± 0.08
<i>Rexo4</i>	REX4, RNA exonuclease 4 homolog (S. cerevisiae)	0.970 ± 0.16	0.934 ± 0.05	0.942 ± 0.09
<i>Xrn1</i>	5-3 exoribonuclease 1	1.206 ± 0.19	1.025 ± 0.22	0.994 ± 0.17
<i>Xrn2</i>	5-3 exoribonuclease 2	0.894 ± 0.09	1.047 ± 0.13	1.039 ± 0.11

Supplementary Table 3. List of down-regulated genes (< 0.6-fold) following overexpression of Regnase-1 via Ad-Regnase-1 infection in chondrocytes.

Gene symbol	Definition	Fold change				
		Ad-Regnase-1	Ad-shRegnase-1	IL-1 β	Ad-HIF-2 α	Ad-ZIP8
<i>Fgf21</i>	Fibroblast growth factor 21	0.248 $\pm$ 0.56	1.004 $\pm$ 0.48	0.128 $\pm$ 0.30	0.407 $\pm$ 0.23	0.509 $\pm$ 0.27
<i>Abi3bp</i>	ABI gene family, member 3 (NESH) binding protein	0.303 $\pm$ 0.28	1.088 $\pm$ 0.24	1.110 $\pm$ 0.25	0.690 $\pm$ 0.21	0.917 $\pm$ 0.26
<i>Mir434</i>	MicroRNA 434	0.338 $\pm$ 0.43	1.331 $\pm$ 0.75	0.242 $\pm$ 0.29	0.357 $\pm$ 0.46	0.471 $\pm$ 0.50
<i>Pycr1</i>	Pyrroline-5-carboxylate reductase 1	0.361 $\pm$ 0.28	0.857 $\pm$ 0.28	0.412 $\pm$ 0.17	0.494 $\pm$ 0.19	0.573 $\pm$ 0.19
<i>Gm12829</i>	Predicted gene 12829	0.362 $\pm$ 0.26	1.206 $\pm$ 0.51	0.411 $\pm$ 0.44	0.423 $\pm$ 0.30	0.715 $\pm$ 0.48
<i>Cnn1</i>	Calponin 1	0.381 $\pm$ 0.42	0.938 $\pm$ 0.25	0.856 $\pm$ 0.23	0.345 $\pm$ 0.31	0.415 $\pm$ 0.28
<i>Npr3</i>	Natriuretic peptide receptor 3	0.387 $\pm$ 0.22	0.951 $\pm$ 0.13	0.262 $\pm$ 0.28	0.512 $\pm$ 0.17	0.529 $\pm$ 0.35
<i>Chrdl1</i>	Chordin-like 1	0.387 $\pm$ 0.34	1.016 $\pm$ 0.36	0.549 $\pm$ 0.27	0.305 $\pm$ 0.41	0.426 $\pm$ 0.23
<i>Igfbp5</i>	Insulin-like growth factor binding protein 5	0.391 $\pm$ 0.31	0.942 $\pm$ 0.15	0.242 $\pm$ 0.32	0.913 $\pm$ 0.42	0.651 $\pm$ 0.40
<i>Mir136</i>	MicroRNA 136	0.403 $\pm$ 0.49	1.306 $\pm$ 0.78	0.203 $\pm$ 0.62	0.313 $\pm$ 0.50	0.448 $\pm$ 0.47
<i>Gm23508</i>	Predicted gene 23508	0.408 $\pm$ 0.29	1.302 $\pm$ 0.20	0.229 $\pm$ 0.26	0.338 $\pm$ 0.53	0.404 $\pm$ 0.45
<i>Rassf4</i>	Ras association (RalGDS/AF-6) domain family member 4	0.419 $\pm$ 0.24	0.954 $\pm$ 0.15	1.251 $\pm$ 0.30	1.532 $\pm$ 0.35	1.654 $\pm$ 0.34
<i>Clmn</i>	Calmin	0.420 $\pm$ 0.42	1.246 $\pm$ 0.41	0.572 $\pm$ 0.17	0.536 $\pm$ 0.26	0.581 $\pm$ 0.22
<i>Cyb5r2</i>	Cytochrome b5 reductase 2	0.421 $\pm$ 0.43	0.715 $\pm$ 0.38	0.285 $\pm$ 0.17	0.312 $\pm$ 0.32	0.456 $\pm$ 0.27
<i>Mir154</i>	MicroRNA 154	0.422 $\pm$ 0.48	1.279 $\pm$ 0.48	0.372 $\pm$ 0.32	0.275 $\pm$ 0.31	0.384 $\pm$ 0.65
<i>Gm22962</i>	Predicted gene 22962	0.424 $\pm$ 0.13	1.134 $\pm$ 0.30	0.364 $\pm$ 0.20	0.435 $\pm$ 0.28	0.46 $\pm$ 0.22
<i>Mir493</i>	MicroRNA 493	0.425 $\pm$ 0.40	1.107 $\pm$ 0.44	0.324 $\pm$ 0.56	0.331 $\pm$ 0.37	0.338 $\pm$ 0.51
<i>Mir543</i>	MicroRNA 543	0.428 $\pm$ 0.76	1.359 $\pm$ 0.44	0.543 $\pm$ 0.29	0.404 $\pm$ 0.36	0.432 $\pm$ 0.51
<i>Mir1906-1</i>	MicroRNA 1906-1	0.429 $\pm$ 0.35	1.146 $\pm$ 0.71	0.369 $\pm$ 0.52	0.338 $\pm$ 0.31	0.433 $\pm$ 0.39
<i>Mir485</i>	MicroRNA 485	0.433 $\pm$ 0.51	1.466 $\pm$ 0.21	0.385 $\pm$ 0.49	0.399 $\pm$ 0.35	0.438 $\pm$ 0.27
<i>Mir377</i>	MicroRNA 377	0.435 $\pm$ 0.38	1.138 $\pm$ 0.31	0.362 $\pm$ 0.38	0.356 $\pm$ 0.35	0.371 $\pm$ 0.44
<i>Cmtm5</i>	CKLF-like MARVEL transmembrane domain 5	0.440 $\pm$ 0.33	1.103 $\pm$ 0.33	0.221 $\pm$ 0.28	0.258 $\pm$ 0.51	0.464 $\pm$ 0.36
<i>Mir379</i>	MicroRNA 379	0.443 $\pm$ 0.33	1.188 $\pm$ 0.25	0.420 $\pm$ 0.26	0.450 $\pm$ 0.26	0.487 $\pm$ 0.27
<i>Mir1224</i>	MicroRNA 1224	0.443 $\pm$ 0.34	1.167 $\pm$ 0.36	0.398 $\pm$ 0.46	0.641 $\pm$ 0.64	0.688 $\pm$ 0.54
<i>Gm23736</i>	Predicted gene 23736	0.444 $\pm$ 0.25	1.094 $\pm$ 0.21	0.211 $\pm$ 0.41	0.351 $\pm$ 1.02	0.519 $\pm$ 1.20
<i>Fibin</i>	Fin bud initiation factor homolog	0.447 $\pm$ 0.42	1.155 $\pm$ 0.29	0.849 $\pm$ 0.05	0.564 $\pm$ 0.31	0.690 $\pm$ 0.21
<i>Lrp4</i>	Low density lipoprotein receptor-related protein 4	0.448 $\pm$ 0.40	0.985 $\pm$ 0.27	0.327 $\pm$ 0.22	0.761 $\pm$ 0.29	1.106 $\pm$ 0.25
<i>Gm6260</i>	Predicted gene 6260	0.452 $\pm$ 0.45	0.949 $\pm$ 0.40	0.222 $\pm$ 0.44	0.527 $\pm$ 0.22	0.633 $\pm$ 0.23
<i>Igdcc4</i>	Immunoglobulin superfamily, DCC subclass, member 4	0.452 $\pm$ 0.26	1.171 $\pm$ 0.29	0.663 $\pm$ 0.25	0.530 $\pm$ 0.20	0.678 $\pm$ 0.15

<i>Dmrta1</i>	Doublesex and mab-3 related TF like family A1	0.460 ± 0.28	0.883 ± 0.47	0.326 ± 0.20	0.366 ± 0.35	0.457 ± 0.32
<i>Pde7b</i>	Phosphodiesterase 7B	0.460 ± 0.33	0.720 ± 0.24	0.408 ± 0.28	0.384 ± 0.19	0.488 ± 0.15
<i>Mir337</i>	MicroRNA 337	0.469 ± 0.47	1.306 ± 0.34	0.450 ± 0.58	0.393 ± 0.36	0.374 ± 0.54
<i>Mir432</i>	MicroRNA 432	0.470 ± 0.23	1.106 ± 0.43	0.279 ± 0.28	0.430 ± 0.53	0.538 ± 0.39
<i>Gm22205</i>	Predicted gene 22205	0.475 ± 0.26	1.587 ± 0.24	0.246 ± 0.40	0.306 ± 0.28	0.349 ± 0.28
<i>Frzb</i>	Frizzled-related protein	0.477 ± 0.61	1.259 ± 0.51	0.262 ± 0.27	0.414 ± 0.29	0.557 ± 0.23
<i>Gjc3</i>	Gap junction protein, gamma 3	0.479 ± 0.65	0.838 ± 0.52	0.307 ± 0.40	0.525 ± 0.46	0.666 ± 0.60
<i>Boc</i>	Biregional cell adhesion molecule-related by Cdon	0.480 ± 0.28	1.108 ± 0.09	0.711 ± 0.15	0.495 ± 0.24	0.542 ± 0.24
<i>Slc17a9</i>	Solute carrier family 17, member 9	0.490 ± 0.26	0.985 ± 0.20	0.396 ± 0.16	0.688 ± 0.17	0.680 ± 0.22
<i>Mir667</i>	MicroRNA 667	0.490 ± 0.33	0.973 ± 0.25	0.486 ± 0.22	0.397 ± 0.66	0.413 ± 0.59
<i>Gm25854</i>	Predicted gene 25854	0.493 ± 0.34	1.312 ± 0.26	0.346 ± 0.41	0.422 ± 0.40	0.448 ± 0.34
<i>Apela</i>	Apelin receptor early endogenous ligand	0.496 ± 0.46	0.816 ± 0.51	0.435 ± 0.24	0.560 ± 0.63	0.384 ± 0.48
<i>Mir300</i>	MicroRNA 300	0.497 ± 0.27	1.285 ± 0.45	0.349 ± 0.66	0.295 ± 0.71	0.324 ± 0.59
<i>Smoc2</i>	SPARC related modular calcium binding 2	0.497 ± 0.23	1.274 ± 0.31	0.258 ± 0.31	0.321 ± 0.32	0.480 ± 0.27
<i>Mir382</i>	MicroRNA 382	0.498 ± 0.29	1.619 ± 0.29	0.363 ± 0.50	0.361 ± 0.32	0.360 ± 0.40
<i>Gm23787</i>	Predicted gene 23787	0.501 ± 0.35	1.341 ± 0.31	0.341 ± 0.34	0.474 ± 0.37	0.599 ± 0.50
<i>Ppp1r3c</i>	Protein phosphatase 1, regulatory subunit 3C	0.502 ± 0.52	1.113 ± 0.37	1.171 ± 0.21	1.221 ± 0.25	0.715 ± 0.30
<i>Mir380</i>	MicroRNA 380	0.503 ± 0.54	1.306 ± 0.40	0.329 ± 0.43	0.393 ± 0.42	0.365 ± 0.70
<i>Gm24564</i>	Predicted gene 24564	0.505 ± 0.45	1.604 ± 0.18	0.257 ± 0.18	0.280 ± 0.21	0.312 ± 0.22
<i>Cth</i>	Cystathionase (cystathionine gamma-lyase)	0.505 ± 0.44	1.024 ± 0.30	0.540 ± 0.19	0.864 ± 0.13	0.923 ± 0.11
<i>Osgin2</i>	Oxidative stress induced growth inhibitor member 2	0.506 ± 0.33	1.097 ± 0.18	0.254 ± 0.30	0.605 ± 0.31	0.698 ± 0.28
<i>Fxyd6</i>	FXYD domain-containing ion transport regulator 6	0.506 ± 0.47	1.044 ± 0.29	0.136 ± 0.39	0.382 ± 0.29	0.424 ± 0.32
<i>Acot2</i>	Acyl-CoA thioesterase 2	0.508 ± 0.35	0.841 ± 0.28	0.524 ± 0.25	0.658 ± 0.23	0.813 ± 0.20
<i>Mir3070b</i>	MicroRNA 3070b	0.509 ± 0.38	1.167 ± 0.42	0.472 ± 0.46	0.445 ± 0.27	0.458 ± 0.47
<i>Mir679</i>	MicroRNA 679	0.510 ± 0.32	1.104 ± 0.31	0.539 ± 0.28	0.483 ± 0.31	0.394 ± 0.37
<i>Sorbs2</i>	Sorbin and SH3 domain containing 2	0.510 ± 0.11	1.154 ± 0.19	0.974 ± 0.40	0.764 ± 0.23	0.720 ± 0.19
<i>Gm24679</i>	Predicted gene 24679	0.514 ± 0.56	0.607 ± 0.63	0.902 ± 0.16	0.949 ± 0.41	1.124 ± 0.38
<i>Cpa4</i>	Carboxypeptidase A4	0.514 ± 0.46	0.882 ± 0.31	1.176 ± 0.31	1.332 ± 0.37	1.209 ± 0.23
<i>Pdgfrl</i>	Platelet-derived growth factor receptor-like	0.515 ± 0.21	1.118 ± 0.21	1.129 ± 0.15	1.176 ± 0.13	1.103 ± 0.08
<i>Rab2b</i>	RAB2B, member RAS oncogene family	0.515 ± 0.09	0.943 ± 0.19	1.109 ± 0.18	0.935 ± 0.17	0.985 ± 0.16
<i>Car3</i>	Carbonic anhydrase 3	0.517 ± 0.22	0.803 ± 0.70	0.516 ± 0.48	0.384 ± 0.47	0.370 ± 0.60
<i>Meg3</i>	Maternally expressed 3	0.518 ± 0.20	1.092 ± 0.19	0.471 ± 0.17	0.445 ± 0.24	0.501 ± 0.37
<i>Mir1197</i>	MicroRNA 1197	0.522 ± 0.11	1.391 ± 0.10	0.360 ± 0.57	0.368 ± 0.33	0.381 ± 0.52

<i>Zfp185</i>	Zinc finger protein 185	0.522 ± 0.26	1.110 ± 0.18	0.608 ± 0.41	0.584 ± 0.29	0.834 ± 0.21
<i>Cthrc1</i>	Collagen triple helix repeat containing 1	0.523 ± 0.18	0.948 ± 0.29	0.420 ± 0.14	0.475 ± 0.27	0.605 ± 0.21
<i>Gm25856</i>	Predicted gene 25856	0.523 ± 0.38	1.494 ± 0.27	0.328 ± 0.50	0.324 ± 0.32	0.383 ± 0.38
<i>Mir453</i>	MicroRNA 453	0.527 ± 0.33	1.156 ± 0.24	0.362 ± 0.34	0.427 ± 0.17	0.372 ± 0.32
<i>Mir322</i>	MicroRNA 322	0.528 ± 0.30	1.228 ± 0.24	0.971 ± 0.30	0.934 ± 0.22	1.001 ± 0.20
<i>Svep1</i>	Sushi, von Willebrand factor type A	0.528 ± 0.31	1.247 ± 0.26	2.385 ± 0.16	0.807 ± 0.24	0.945 ± 0.18
<i>Cpxm2</i>	carboxypeptidase X 2 (M14 family)	0.529 ± 0.41	1.173 ± 0.20	0.961 ± 0.14	1.053 ± 0.14	1.345 ± 0.08
<i>Gm23600</i>	Predicted gene 23600	0.529 ± 0.47	1.574 ± 0.28	0.328 ± 0.21	0.341 ± 0.26	0.375 ± 0.24
<i>Dkk3</i>	Dickkopf homolog 3	0.531 ± 0.41	0.794 ± 0.29	1.861 ± 0.18	1.031 ± 0.42	1.120 ± 0.47
<i>AF357425</i>	SnoRNA AF357425	0.532 ± 0.26	1.139 ± 0.15	0.394 ± 0.23	0.473 ± 0.13	0.545 ± 0.22
<i>Nynrin</i>	NYN domain and retroviral integrase containing	0.533 ± 0.29	1.027 ± 0.30	0.692 ± 0.18	0.503 ± 0.26	0.616 ± 0.20
<i>Pck2</i>	Phosphoenolpyruvate carboxykinase 2	0.533 ± 0.30	0.954 ± 0.21	0.398 ± 0.20	0.710 ± 0.16	0.761 ± 0.11
<i>Penk</i>	Preproenkephalin	0.534 ± 0.34	1.088 ± 0.19	1.502 ± 0.17	0.930 ± 0.15	0.922 ± 0.17
<i>Lrrc61</i>	Leucine rich repeat containing 61	0.537 ± 0.21	0.676 ± 0.25	0.708 ± 0.14	0.747 ± 0.18	0.880 ± 0.15
<i>Mir376b</i>	MicroRNA 376b	0.537 ± 0.51	1.377 ± 0.41	0.646 ± 0.21	0.295 ± 0.79	0.332 ± 0.82
<i>Mir323</i>	MicroRNA 323	0.537 ± 0.35	1.054 ± 0.37	0.370 ± 0.05	0.357 ± 0.67	0.362 ± 0.52
<i>Magel2</i>	Melanoma antigen, family L, 2	0.538 ± 0.47	1.003 ± 0.50	0.231 ± 0.30	0.410 ± 0.19	0.594 ± 0.32
<i>Rian</i>	RNA imprinted and accumulated in nucleus	0.538 ± 0.37	1.309 ± 0.18	0.346 ± 0.10	0.420 ± 0.26	0.489 ± 0.33
<i>Srebfl</i>	Sterol regulatory element binding transcription factor 1	0.539 ± 0.28	1.095 ± 0.26	0.530 ± 0.20	0.835 ± 0.14	0.852 ± 0.12
<i>Snhg18</i>	Small nucleolar RNA host gene 18	0.540 ± 0.30	1.109 ± 0.17	0.910 ± 0.21	0.751 ± 0.16	0.759 ± 0.16
<i>Gm23347</i>	Predicted gene 23347	0.542 ± 0.19	1.288 ± 0.45	0.374 ± 0.67	0.422 ± 0.30	0.427 ± 0.26
<i>Aldh1l2</i>	Aldehyde dehydrogenase 1 family, member L2	0.544 ± 0.30	0.994 ± 0.09	0.432 ± 0.15	0.675 ± 0.22	0.702 ± 0.19
<i>Gm22659</i>	Predicted gene 22659	0.544 ± 0.31	0.807 ± 0.50	1.121 ± 0.55	0.886 ± 0.30	0.935 ± 0.33
<i>Col10a1</i>	Collagen, type X, alpha 1	0.545 ± 0.70	0.854 ± 0.50	0.174 ± 0.20	0.416 ± 0.34	0.399 ± 0.39
<i>AF357426</i>	SnoRNA AF357426	0.546 ± 0.24	1.173 ± 0.21	0.485 ± 0.44	0.440 ± 0.37	0.557 ± 0.55
<i>Sh3rf2</i>	SH3 domain containing ring finger 2	0.546 ± 0.14	0.935 ± 0.42	0.709 ± 0.15	0.657 ± 0.22	0.818 ± 0.14
<i>Gm24899</i>	Predicted gene 24899	0.546 ± 0.18	1.473 ± 0.23	0.331 ± 0.21	0.427 ± 0.31	0.468 ± 0.26
<i>Trp53inp2</i>	Transformation related protein 53	0.547 ± 0.16	0.704 ± 0.13	1.432 ± 0.20	1.246 ± 0.13	1.276 ± 0.16
<i>Fbxw18</i>	F-box and WD-40 domain protein 18	0.547 ± 0.27	1.165 ± 0.24	0.328 ± 0.46	0.574 ± 0.36	0.707 ± 0.44
<i>Omd</i>	Osteomodulin	0.548 ± 0.24	1.072 ± 0.23	0.353 ± 0.30	0.358 ± 0.32	0.499 ± 0.29
<i>Vmn2r5</i>	Vomer nasal 2, receptor 5	0.548 ± 0.28	0.753 ± 0.27	0.981 ± 0.41	1.014 ± 0.42	1.395 ± 0.58
<i>Clcn5</i>	Chloride channel 5	0.550 ± 0.18	0.934 ± 0.18	0.587 ± 0.09	0.648 ± 0.09	0.723 ± 0.06
<i>Rps6ka2</i>	Ribosomal protein S6 kinase, polypeptide 2	0.550 ± 0.21	0.964 ± 0.25	0.382 ± 0.19	0.441 ± 0.34	0.650 ± 0.25

<i>Slc16a14</i>	Solute carrier family 16, member 14	0.550 ± 0.59	0.762 ± 0.47	0.257 ± 0.35	0.196 ± 0.45	0.289 ± 0.32
<i>Ogn</i>	Osteoglycin	0.551 ± 0.15	1.162 ± 0.13	0.829 ± 0.11	0.466 ± 0.33	0.663 ± 0.11
<i>Gm13293</i>	Predicted gene 13293	0.551 ± 0.50	1.307 ± 0.32	2.525 ± 0.24	4.398 ± 0.24	2.987 ± 0.22
<i>Trib3</i>	Tribbles homolog 3 (Drosophila)	0.552 ± 0.34	0.969 ± 0.25	0.546 ± 0.16	0.666 ± 0.24	0.773 ± 0.19
<i>Cdkl5</i>	Cyclin-dependent kinase-like 5	0.554 ± 0.11	0.932 ± 0.13	0.704 ± 0.24	0.549 ± 0.32	0.664 ± 0.26
<i>Gm25394</i>	Predicted gene 25394	0.556 ± 0.12	0.632 ± 0.14	0.902 ± 0.22	1.002 ± 1.94	1.010 ± 1.99
<i>Ldlrad3</i>	LDL receptor class A domain containing 3	0.556 ± 0.15	1.005 ± 0.12	0.364 ± 0.12	0.517 ± 0.11	0.634 ± 0.13
<i>Aldh6a1</i>	Aldehyde dehydrogenase family 6, subfamily A1	0.558 ± 0.29	1.214 ± 0.23	1.279 ± 0.23	0.879 ± 0.22	1.037 ± 0.17
<i>AF357428</i>	SnoRNA AF357428	0.559 ± 0.37	1.092 ± 0.18	0.480 ± 0.46	0.460 ± 0.60	0.549 ± 0.42
<i>Pygo1</i>	Pygopus 1	0.562 ± 0.19	1.195 ± 0.21	0.872 ± 0.24	0.602 ± 0.24	0.783 ± 0.23
<i>Fam13c</i>	Family with sequence similarity 13, member C	0.562 ± 0.24	1.000 ± 0.09	0.795 ± 0.14	0.722 ± 0.25	0.924 ± 0.16
<i>Srpx</i>	Sushi-repeat-containing protein	0.563 ± 0.43	1.256 ± 0.29	0.451 ± 0.32	0.423 ± 0.31	0.548 ± 0.27
<i>Cybrd1</i>	Cytochrome b reductase 1	0.564 ± 0.54	1.191 ± 0.29	0.317 ± 0.26	0.386 ± 0.35	0.524 ± 0.32
<i>Creb3l1</i>	cAMP responsive element binding protein 3-like 1	0.564 ± 0.26	0.683 ± 0.25	1.315 ± 0.04	1.150 ± 0.13	1.090 ± 0.13
<i>Sec16b</i>	SEC16 homolog B (S. cerevisiae)	0.565 ± 0.26	1.019 ± 0.21	0.446 ± 0.12	0.751 ± 0.25	0.746 ± 0.29
<i>Smarca1</i>	SWI/SNF related, matrix associated, member 1	0.565 ± 0.22	1.287 ± 0.24	0.639 ± 0.18	0.583 ± 0.24	0.623 ± 0.20
<i>Smpd3</i>	Sphingomyelin phosphodiesterase 3, neutral	0.566 ± 0.57	1.587 ± 0.61	0.163 ± 0.17	0.210 ± 0.37	0.304 ± 0.36
<i>Ap3s2</i>	Adaptor-related protein complex 3, sigma 2 subunit	0.568 ± 0.22	0.822 ± 0.22	0.985 ± 0.14	0.842 ± 0.16	0.856 ± 0.20
<i>Hacd1</i>	3-hydroxyacyl-CoA dehydratase 1	0.568 ± 0.15	0.975 ± 0.10	1.197 ± 0.28	0.856 ± 0.31	0.902 ± 0.33
<i>Lctf</i>	Lactase-like	0.571 ± 0.36	1.006 ± 0.20	0.519 ± 0.24	0.811 ± 0.32	0.981 ± 0.28
<i>Arsi</i>	Arylsulfatase	0.571 ± 0.10	0.814 ± 0.32	0.479 ± 0.25	0.512 ± 0.30	0.538 ± 0.35
<i>Mir1193</i>	MicroRNA 1193	0.571 ± 0.35	1.018 ± 0.44	0.467 ± 0.31	0.443 ± 0.36	0.463 ± 0.41
<i>Cdon</i>	Cell adhesion molecule-related by oncogenes	0.573 ± 0.17	1.145 ± 0.12	1.412 ± 0.11	0.836 ± 0.12	0.846 ± 0.12
<i>Atf5</i>	Activating transcription factor 5	0.575 ± 0.19	0.892 ± 0.17	0.794 ± 0.12	0.805 ± 0.18	0.893 ± 0.21
<i>Camk4</i>	Calcium/calmodulin-dependent protein kinase IV	0.576 ± 0.25	0.863 ± 0.24	0.606 ± 0.17	0.517 ± 0.24	0.645 ± 0.19
<i>Ptgis</i>	Prostaglandin I2 synthase	0.576 ± 0.27	1.041 ± 0.28	0.641 ± 0.14	0.733 ± 0.19	0.589 ± 0.18
<i>Slc16a2</i>	Solute carrier family 16, member 2	0.578 ± 0.33	1.181 ± 0.31	2.459 ± 0.08	2.224 ± 0.12	1.987 ± 0.18
<i>Slc13a5</i>	Solute carrier family 13, member 5	0.580 ± 0.94	1.568 ± 0.83	0.468 ± 0.49	0.985 ± 0.46	1.109 ± 0.40
<i>Mir411</i>	MicroRNA 411	0.581 ± 0.28	1.443 ± 0.36	0.613 ± 0.51	0.560 ± 0.34	0.587 ± 0.40
<i>Sorbs2os</i>	Sorbin and SH3 domain containing 2, opposite strand	0.581 ± 0.09	1.284 ± 0.19	1.100 ± 0.30	0.908 ± 0.29	0.944 ± 0.22
<i>Fndc1</i>	Fibronectin type III domain containing 1	0.582 ± 0.46	0.980 ± 0.33	2.794 ± 0.20	1.693 ± 0.51	1.004 ± 0.50
<i>Mir341</i>	MicroRNA 341	0.582 ± 0.34	1.522 ± 0.41	0.496 ± 0.22	0.545 ± 0.17	0.583 ± 0.23
<i>6430411K18Rik</i>	RIKEN cDNA 6430411K18 gene	0.582 ± 0.32	1.313 ± 0.16	0.527 ± 0.24	0.458 ± 0.40	0.455 ± 0.32

<i>Gm24598</i>	Predicted gene 24598	0.582 ± 0.36	1.538 ± 0.29	0.293 ± 0.76	0.373 ± 0.37	0.436 ± 0.46
<i>Snord123</i>	Small nucleolar RNA, C/D box 123	0.584 ± 0.18	0.960 ± 0.16	0.919 ± 0.11	0.924 ± 0.85	0.955 ± 0.81
<i>Fry</i>	Furry homolog (Drosophila)	0.585 ± 0.35	1.429 ± 0.20	0.421 ± 0.64	0.564 ± 0.46	0.571 ± 0.30
<i>Dhrs3</i>	Dehydrogenase/reductase (SDR family) member 3	0.585 ± 0.36	1.077 ± 0.11	1.520 ± 0.10	0.998 ± 0.12	0.907 ± 0.16
<i>Gpc4</i>	Glypican 4	0.585 ± 0.15	1.008 ± 0.25	0.787 ± 0.13	0.596 ± 0.18	0.666 ± 0.10
<i>Phyh</i>	Phytanoyl-CoA hydroxylase	0.586 ± 0.25	1.254 ± 0.14	0.573 ± 0.20	0.993 ± 0.16	0.963 ± 0.20
<i>Scin</i>	Scinderin	0.586 ± 0.39	1.103 ± 0.35	0.347 ± 0.12	0.711 ± 0.20	0.719 ± 0.28
<i>Paqr3</i>	Progesterin and adipoQ receptor family member III	0.587 ± 0.56	1.095 ± 0.40	0.432 ± 0.18	0.557 ± 0.26	0.703 ± 0.16
<i>Gm25518</i>	Predicted gene 25518	0.587 ± 0.34	0.866 ± 0.43	1.009 ± 0.97	0.954 ± 0.59	1.277 ± 0.83
<i>Tmem161a</i>	Transmembrane protein 161A	0.587 ± 0.15	1.118 ± 0.17	0.870 ± 0.09	0.671 ± 0.13	0.799 ± 0.18
<i>Mir541</i>	MicroRNA 541	0.587 ± 0.33	1.073 ± 0.23	0.386 ± 0.42	0.490 ± 0.26	0.540 ± 0.31
<i>Dact1</i>	Dapper homolog 1, antagonist of beta-catenin (xenopus)	0.587 ± 0.36	0.908 ± 0.26	0.240 ± 0.34	0.394 ± 0.17	0.513 ± 0.23
<i>Fads1</i>	Fatty acid desaturase 1	0.589 ± 0.17	1.045 ± 0.15	0.595 ± 0.19	0.665 ± 0.13	0.771 ± 0.12
<i>Panx3</i>	Pannexin 3	0.589 ± 0.41	0.878 ± 0.38	0.591 ± 0.15	0.488 ± 0.42	0.585 ± 0.43
<i>Fcgrt</i>	Fc receptor, IgG, alpha chain transporter	0.591 ± 0.30	1.257 ± 0.27	1.667 ± 0.12	1.294 ± 0.25	1.317 ± 0.21
<i>Plcd1</i>	Phospholipase C, delta 1	0.591 ± 0.21	1.063 ± 0.17	0.759 ± 0.09	0.761 ± 0.10	0.813 ± 0.09
<i>Slc35f1</i>	Solute carrier family 35, member F1	0.592 ± 0.37	0.863 ± 0.43	0.286 ± 0.18	0.15 ± 0.23	0.203 ± 0.44
<i>AI464131</i>	Expressed sequence AI464131	0.592 ± 0.17	0.967 ± 0.13	0.855 ± 0.22	1.011 ± 0.16	1.026 ± 0.11
<i>Saa3</i>	Serum amyloid A3	0.593 ± 2.19	2.642 ± 1.59	41.471 ± 0.70	19.970 ± 0.66	19.198 ± 0.66
<i>Copz2</i>	Coatomer protein complex, subunit zeta 2	0.593 ± 0.15	1.019 ± 0.08	0.725 ± 0.13	0.719 ± 0.15	0.746 ± 0.15
<i>Sh3tc2</i>	SH3 domain and tetratricopeptide repeats 2	0.593 ± 0.34	1.049 ± 0.25	0.361 ± 0.22	0.503 ± 0.34	0.644 ± 0.24
<i>Gm5947</i>	Predicted pseudogene 5947	0.593 ± 0.25	0.738 ± 0.22	0.883 ± 0.30	0.966 ± 0.65	1.056 ± 0.57
<i>Olf1265</i>	Olfactory receptor 1265	0.594 ± 0.29	1.045 ± 0.37	0.946 ± 0.73	0.834 ± 0.39	1.097 ± 0.31
<i>Fkbp7</i>	FK506 binding protein 7	0.594 ± 0.17	1.030 ± 0.15	1.024 ± 0.22	1.001 ± 0.13	0.878 ± 0.16
<i>Mir431</i>	MicroRNA 431	0.594 ± 0.27	1.180 ± 0.17	0.542 ± 0.17	0.555 ± 0.21	0.587 ± 0.28
<i>Tubb2a</i>	Tubulin, beta 2A class IIA	0.595 ± 0.23	1.038 ± 0.21	0.351 ± 0.12	0.537 ± 0.19	0.549 ± 0.29
<i>Tbx5</i>	T-box 5	0.595 ± 0.27	0.983 ± 0.26	0.809 ± 0.12	0.805 ± 0.38	0.781 ± 0.29
<i>Col1a1</i>	Collagen, type I, alpha 1	0.595 ± 0.20	0.949 ± 0.17	0.984 ± 0.16	0.937 ± 0.31	0.961 ± 0.34
<i>Mir30e</i>	MicroRNA 30e	0.596 ± 0.54	0.626 ± 0.41	1.078 ± 0.44	1.207 ± 0.73	1.103 ± 0.91
<i>Itpkb</i>	Inositol 1,4,5-trisphosphate 3-kinase B	0.596 ± 0.31	1.140 ± 0.32	0.637 ± 0.16	0.790 ± 0.14	0.787 ± 0.15
<i>Fam213b</i>	Family with sequence similarity 213, member B	0.596 ± 0.30	1.034 ± 0.30	0.890 ± 0.07	1.385 ± 0.39	1.219 ± 0.26
<i>Rhox3f</i>	Reproductive homeobox 3F	0.596 ± 0.37	0.846 ± 0.76	0.701 ± 0.48	0.846 ± 0.97	0.855 ± 0.92
<i>Clip3</i>	CAP-GLY domain containing linker protein 3	0.597 ± 0.21	0.877 ± 0.28	1.281 ± 0.09	0.890 ± 0.16	0.865 ± 0.22

Supplementary Table 4. List of up-regulated genes (> 1.5-fold) following knock-down of Regnase-1 via Ad-shRegnase-1A infection in chondrocytes.

Gene Symbol	Definition	Fold change				
		Ad-shRegnase-1	Ad-Regnase-1	IL-1 β	Ad-HIF-2 α	Ad-ZIP8
<i>Cxcl5</i>	Chemokine (C-X-C motif) ligand 5	3.482 $\pm$ 0.99	1.709 $\pm$ 0.70	93.775 $\pm$ 0.20	41.737 $\pm$ 0.30	43.135 $\pm$ 0.39
<i>Saa3</i>	Serum amyloid A 3	2.642 $\pm$ 1.59	0.593 $\pm$ 2.19	41.471 $\pm$ 0.70	19.97 $\pm$ 0.66	19.198 $\pm$ 0.66
<i>Steap4</i>	STEAP family member 4	2.579 $\pm$ 0.87	1.143 $\pm$ 0.62	59.772 $\pm$ 0.56	21.25 $\pm$ 0.65	21.596 $\pm$ 0.65
<i>Gm25357</i>	Predicted gene, 25357	2.345 $\pm$ 1.57	1.331 $\pm$ 1.14	0.956 $\pm$ 0.57	0.525 $\pm$ 1.07	0.631 $\pm$ 1.03
<i>Mir181a-1</i>	MicroRNA 181a-1	2.195 $\pm$ 0.72	1.155 $\pm$ 0.32	2.189 $\pm$ 0.61	0.975 $\pm$ 0.81	1.207 $\pm$ 0.90
<i>Vmn1r127</i>	Vomerolateral 1 receptor 127	2.152 $\pm$ 0.30	1.606 $\pm$ 0.27	0.994 $\pm$ 0.67	1.418 $\pm$ 1.00	0.916 $\pm$ 1.09
<i>Angptl4</i>	Angiopoietin-like 4	1.993 $\pm$ 0.60	1.218 $\pm$ 0.25	6.622 $\pm$ 0.33	7.342 $\pm$ 0.65	5.672 $\pm$ 0.61
<i>Mmp3</i>	Matrix metalloproteinase 3	1.847 $\pm$ 0.71	2.374 $\pm$ 0.37	157.581 $\pm$ 0.19	116.517 $\pm$ 0.58	63.661 $\pm$ 0.68
<i>Gm23474</i>	Predicted gene 23474	1.828 $\pm$ 0.83	0.780 $\pm$ 0.50	0.429 $\pm$ 1.08	0.363 $\pm$ 1.03	0.423 $\pm$ 1.13
<i>Gm22740</i>	Predicted gene 22740	1.814 $\pm$ 0.37	0.916 $\pm$ 0.66	0.632 $\pm$ 0.43	0.847 $\pm$ 0.77	0.877 $\pm$ 0.65
<i>Gm26827</i>	Predicted gene 26827	1.767 $\pm$ 0.34	0.838 $\pm$ 0.28	0.881 $\pm$ 0.19	1.543 $\pm$ 0.17	1.406 $\pm$ 0.21
<i>Zscan4b</i>	Zinc finger and SCAN domain containing 4B	1.758 $\pm$ 0.43	1.208 $\pm$ 0.34	1.237 $\pm$ 0.50	0.890 $\pm$ 0.38	0.939 $\pm$ 0.50
<i>Mir335</i>	MicroRNA 335	1.757 $\pm$ 0.30	1.064 $\pm$ 0.34	0.608 $\pm$ 1.17	1.168 $\pm$ 0.50	0.964 $\pm$ 0.45
<i>Mir743</i>	MicroRNA 743	1.709 $\pm$ 0.42	1.595 $\pm$ 0.63	1.574 $\pm$ 0.61	1.055 $\pm$ 0.51	1.167 $\pm$ 0.54
<i>Gm4825</i>	Predicted pseudogene 4825	1.704 $\pm$ 0.50	1.213 $\pm$ 0.46	1.215 $\pm$ 0.62	0.798 $\pm$ 0.40	0.637 $\pm$ 0.28
<i>Gm26151</i>	Predicted gene 26151	1.698 $\pm$ 0.48	1.242 $\pm$ 0.32	1.568 $\pm$ 0.60	1.194 $\pm$ 0.49	0.668 $\pm$ 0.37
<i>Hp</i>	Haptoglobin	1.696 $\pm$ 0.47	1.576 $\pm$ 0.41	67.397 $\pm$ 0.30	62.303 $\pm$ 0.30	42.068 $\pm$ 0.30
<i>Gm22019</i>	Predicted gene 22019	1.690 $\pm$ 0.61	1.214 $\pm$ 0.68	1.007 $\pm$ 0.39	0.806 $\pm$ 0.85	0.760 $\pm$ 0.83
<i>Prg4</i>	Proteoglycan 4	1.678 $\pm$ 0.95	2.019 $\pm$ 0.72	7.197 $\pm$ 0.16	8.533 $\pm$ 0.48	3.577 $\pm$ 0.57
<i>Gm25724</i>	Predicted gene, 25724	1.636 $\pm$ 0.35	1.309 $\pm$ 0.28	0.934 $\pm$ 0.43	0.708 $\pm$ 0.56	0.522 $\pm$ 0.34
<i>mt-Ts2</i>	Mitochondrially encoded tRNA serine 2	1.625 $\pm$ 0.66	2.011 $\pm$ 0.79	0.825 $\pm$ 0.96	0.827 $\pm$ 0.43	0.905 $\pm$ 0.55
<i>Mir382</i>	MicroRNA 382	1.619 $\pm$ 0.29	0.498 $\pm$ 0.29	0.363 $\pm$ 0.50	0.361 $\pm$ 0.32	0.360 $\pm$ 0.40
<i>Gm24960</i>	Predicted gene 24960	1.614 $\pm$ 0.13	1.323 $\pm$ 0.51	0.796 $\pm$ 0.55	1.243 $\pm$ 0.77	1.637 $\pm$ 0.80
<i>Gm23297</i>	Predicted gene 23297	1.612 $\pm$ 0.24	1.393 $\pm$ 0.40	1.207 $\pm$ 0.14	1.003 $\pm$ 0.68	0.821 $\pm$ 0.82
<i>Mir1955</i>	MicroRNA 1955	1.611 $\pm$ 0.44	1.122 $\pm$ 0.27	1.546 $\pm$ 0.67	1.128 $\pm$ 0.25	1.108 $\pm$ 0.25
<i>Gm24564</i>	Predicted gene, 24564	1.604 $\pm$ 0.18	0.505 $\pm$ 0.45	0.257 $\pm$ 0.18	0.28 $\pm$ 0.21	0.312 $\pm$ 0.22
<i>Chil1</i>	Chitinase-like 1	1.599 $\pm$ 1.09	0.722 $\pm$ 1.61	15.791 $\pm$ 0.37	9.608 $\pm$ 0.43	8.597 $\pm$ 0.43
<i>Mir186</i>	MicroRNA 186	1.595 $\pm$ 0.55	1.511 $\pm$ 0.47	1.553 $\pm$ 0.32	0.653 $\pm$ 0.34	0.679 $\pm$ 0.76
<i>Mirlet7c-1</i>	MicroRNA let7c-1	1.594 $\pm$ 0.40	0.772 $\pm$ 0.27	1.111 $\pm$ 0.68	1.025 $\pm$ 0.47	1.058 $\pm$ 0.17
<i>Smpd3</i>	Sphingomyelin phosphodiesterase 3	1.587 $\pm$ 0.61	0.566 $\pm$ 0.57	0.163 $\pm$ 0.17	0.210 $\pm$ 0.37	0.304 $\pm$ 0.36
<i>Gm22205</i>	Predicted gene 22205	1.587 $\pm$ 0.24	0.475 $\pm$ 0.26	0.246 $\pm$ 0.40	0.306 $\pm$ 0.28	0.349 $\pm$ 0.28
<i>Vnn1</i>	Vanin 1	1.586 $\pm$ 0.49	0.994 $\pm$ 0.49	61.952 $\pm$ 0.25	13.662 $\pm$ 0.57	14.634 $\pm$ 0.56
<i>Gm22263</i>	Predicted gene 22263	1.584 $\pm$ 0.26	0.97 $\pm$ 0.24	0.902 $\pm$ 0.85	1.245 $\pm$ 0.81	0.838 $\pm$ 0.82
<i>Trbj1-7</i>	T cell receptor beta joining 1-7	1.583 $\pm$ 0.73	1.043 $\pm$ 0.67	1.144 $\pm$ 0.28	0.895 $\pm$ 0.37	0.743 $\pm$ 0.46

<i>Gm10944</i>	Predicted gene 10944	1.582 ± 0.74	1.259 ± 1.05	1.287 ± 0.68	0.738 ± 0.96	0.726 ± 1.17
<i>Gm5174</i>	Predicted gene 5174	1.580 ± 0.41	1.171 ± 0.15	1.312 ± 0.25	1.074 ± 0.32	1.103 ± 0.26
<i>Sema3d</i>	Sema domain, Ig domain, short basic domain	1.578 ± 0.34	1.018 ± 0.33	0.321 ± 0.47	0.786 ± 0.36	0.645 ± 0.28
<i>Gm23600</i>	Predicted gene 23600	1.574 ± 0.28	0.529 ± 0.47	0.328 ± 0.21	0.341 ± 0.26	0.375 ± 0.24
<i>Slc13a5</i>	Solute carrier family 13, member 5	1.568 ± 0.83	0.580 ± 0.94	0.468 ± 0.49	0.985 ± 0.46	1.109 ± 0.4
<i>Mir466e</i>	MicroRNA 466e	1.563 ± 0.47	1.111 ± 0.43	1.457 ± 0.64	1.166 ± 0.57	0.680 ± 0.60
<i>Ddx3y</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	1.563 ± 0.98	1.413 ± 0.98	0.870 ± 0.54	0.921 ± 0.31	0.869 ± 0.29
<i>Gm23199</i>	Predicted gene 23199	1.560 ± 0.36	1.207 ± 0.37	0.603 ± 0.53	0.892 ± 0.39	1.043 ± 0.13
<i>Klk1b27</i>	Kallikrein 1-related peptidase b27	1.558 ± 0.37	1.360 ± 0.54	1.086 ± 0.35	0.988 ± 0.40	1.092 ± 0.67
<i>Uty</i>	Ubiquitously transcribed tetra-tricopeptide repeat gene	1.556 ± 0.81	1.386 ± 0.81	1.393 ± 0.55	1.056 ± 0.39	0.948 ± 0.38
<i>Stfa3</i>	Stefin A3	1.551 ± 0.33	1.065 ± 0.25	0.674 ± 0.27	0.892 ± 0.54	0.978 ± 0.47
<i>Gm24599</i>	Predicted gene 24599	1.549 ± 0.42	1.111 ± 0.32	0.917 ± 0.48	1.149 ± 0.32	1.237 ± 0.46
<i>Gm24561</i>	Predicted gene 24561	1.546 ± 1.13	2.500 ± 0.61	1.184 ± 1.05	1.078 ± 0.56	1.443 ± 0.59
<i>Mir130a</i>	MicroRNA 130a	1.541 ± 0.60	0.787 ± 0.21	1.046 ± 0.49	0.638 ± 0.59	0.933 ± 0.49
<i>DQ267100</i>	SnoRNA DQ267100	1.540 ± 0.20	0.619 ± 0.26	0.343 ± 0.20	0.477 ± 0.31	0.508 ± 0.23
<i>Gm24598</i>	Predicted gene 24598	1.538 ± 0.29	0.582 ± 0.36	0.293 ± 0.76	0.373 ± 0.37	0.436 ± 0.46
<i>Oxct2a</i>	3-oxoacid CoA transferase 2A	1.537 ± 0.37	1.148 ± 0.28	0.828 ± 0.33	0.974 ± 0.54	1.157 ± 0.62
<i>Aspn</i>	Asporin	1.537 ± 0.68	1.049 ± 0.57	0.307 ± 0.51	0.261 ± 1.30	0.252 ± 1.19
<i>Phf1os</i>	Putative homeodomain transcription factor 1	1.529 ± 0.19	1.419 ± 0.13	1.121 ± 0.26	0.989 ± 0.13	0.979 ± 0.4
<i>Mir450-1</i>	MicroRNA 450-1	1.528 ± 0.47	1.133 ± 0.39	1.081 ± 0.49	1.04 ± 0.49	0.836 ± 0.33
<i>Saa2</i>	Serum amyloid A 2	1.526 ± 0.54	1.257 ± 0.39	60.528 ± 0.10	94.964 ± 0.74	55.081 ± 0.76
<i>Mterf1a</i>	Mitochondrial transcription termination factor 1a	1.524 ± 0.57	1.377 ± 0.31	1.605 ± 0.24	0.823 ± 0.32	0.992 ± 0.42
<i>Eif2s3y</i>	Eukaryotic translation initiation factor 2, subunit 3	1.524 ± 0.96	1.299 ± 0.95	0.903 ± 0.84	0.834 ± 0.26	0.919 ± 0.29
<i>Gm3715</i>	Predicted gene 3715	1.524 ± 0.51	1.263 ± 0.49	1.201 ± 0.24	1.146 ± 0.38	1.124 ± 0.57
<i>Mir341</i>	MicroRNA 341	1.522 ± 0.41	0.582 ± 0.34	0.496 ± 0.22	0.545 ± 0.17	0.583 ± 0.23
<i>Gm24475</i>	Predicted gene 24475	1.516 ± 0.68	1.230 ± 0.60	1.102 ± 0.37	1.103 ± 0.86	0.904 ± 0.86
<i>Gm5316</i>	Predicted gene 5316	1.515 ± 0.27	1.176 ± 0.40	1.041 ± 0.20	1.941 ± 0.37	1.691 ± 0.29
<i>Gm24391</i>	Predicted gene 24391	1.515 ± 0.27	1.150 ± 0.30	1.179 ± 0.17	1.095 ± 0.33	0.834 ± 0.63
<i>Traj7</i>	T cell receptor alpha joining 7	1.510 ± 0.70	1.307 ± 0.41	0.874 ± 0.53	0.806 ± 0.73	0.762 ± 0.93
<i>Snora44</i>	Small nucleolar RNA, H/ACA box 44	1.508 ± 0.25	1.095 ± 0.31	0.985 ± 0.10	1.990 ± 0.75	1.794 ± 0.87
<i>Cxcl3</i>	Chemokine (C-X-C motif) ligand 3	1.506 ± 0.97	2.377 ± 0.59	251.887 ± 0.48	80.900 ± 0.55	56.658 ± 0.71
<i>Gm16427</i>	Predicted gene 16427	1.501 ± 0.55	1.283 ± 0.55	1.288 ± 0.48	1.282 ± 0.51	1.081 ± 0.42
<i>Gm22296</i>	Predicted gene 22296	1.501 ± 0.30	1.100 ± 0.19	0.935 ± 0.13	1.114 ± 0.71	1.070 ± 0.81

Supplementary Table 5. List of up-regulated genes (> 2.0-fold) following overexpression of Regnase-1 via Ad-Regnase-1 infection in chondrocytes.

Gene symbol	Definition	Fold change				
		Ad-Regnase-1	Ad-shRegnase-1	IL-1 β	Ad-HIF-2 α	Ad-ZIP8
<i>Hspa1a</i>	Heat shock protein 1A	21.073 $\pm$ 0.39	0.830 $\pm$ 0.37	1.554 $\pm$ 0.39	2.249 $\pm$ 0.45	12.68 $\pm$ 0.58
<i>Hspa1b</i>	Heat shock protein 1B	11.706 $\pm$ 0.36	0.872 $\pm$ 0.32	2.001 $\pm$ 0.2	2.594 $\pm$ 0.46	9.391 $\pm$ 0.41
<i>Gm13238</i>	Carnitine deficiency-associated gene expressed in ventricle	7.051 $\pm$ 0.58	0.872 $\pm$ 0.22	0.822 $\pm$ 0.77	0.698 $\pm$ 0.49	0.776 $\pm$ 0.37
<i>Gpnmb</i>	Glycoprotein (transmembrane) nmb	5.007 $\pm$ 0.61	1.138 $\pm$ 0.40	1.740 $\pm$ 0.52	3.896 $\pm$ 0.96	3.736 $\pm$ 0.96
<i>Kitl</i>	Kit ligand	4.790 $\pm$ 0.40	0.653 $\pm$ 0.65	5.222 $\pm$ 0.44	2.417 $\pm$ 0.34	1.719 $\pm$ 0.41
<i>Nov</i>	Nephroblastoma overexpressed gene	4.757 $\pm$ 0.63	0.874 $\pm$ 0.39	2.053 $\pm$ 0.16	1.643 $\pm$ 0.39	1.659 $\pm$ 0.44
<i>Gm3776</i>	Predicted gene 3776	4.726 $\pm$ 0.55	1.103 $\pm$ 0.61	0.963 $\pm$ 0.25	2.255 $\pm$ 0.67	2.36 $\pm$ 0.72
<i>Zc3h12a</i>	Zinc finger CCCH type containing 12A	4.327 $\pm$ 0.14	0.870 $\pm$ 0.47	7.781 $\pm$ 0.14	4.744 $\pm$ 0.47	3.949 $\pm$ 0.44
<i>Ptpn22</i>	Protein tyrosine phosphatase, non-receptor type 22	4.302 $\pm$ 0.66	0.863 $\pm$ 0.45	1.052 $\pm$ 0.27	1.040 $\pm$ 0.25	1.087 $\pm$ 0.13
<i>Fosl1</i>	Fos-like antigen 1	4.296 $\pm$ 0.36	0.727 $\pm$ 0.07	8.040 $\pm$ 0.26	7.144 $\pm$ 0.53	3.244 $\pm$ 0.43
<i>Ly6c1</i>	Lymphocyte antigen 6 complex, locus C1	4.033 $\pm$ 0.47	1.201 $\pm$ 0.11	1.060 $\pm$ 0.28	1.343 $\pm$ 0.5	1.005 $\pm$ 0.28
<i>Serpinb2</i>	Serine (or cysteine) peptidase inhibitor, clade B, member 2	3.882 $\pm$ 0.57	1.121 $\pm$ 0.41	1.272 $\pm$ 0.18	1.526 $\pm$ 0.42	1.200 $\pm$ 0.26
<i>Ifi204</i>	Interferon activated gene 204	3.859 $\pm$ 0.28	0.827 $\pm$ 0.50	6.508 $\pm$ 0.64	8.860 $\pm$ 0.38	6.310 $\pm$ 0.49
<i>Gm20481</i>	Predicted gene 20481	3.782 $\pm$ 0.28	1.027 $\pm$ 0.20	1.101 $\pm$ 0.37	1.634 $\pm$ 0.49	3.131 $\pm$ 0.46
<i>Snora17</i>	Small nucleolar RNA, H/ACA box 17	3.508 $\pm$ 0.25	1.123 $\pm$ 0.39	0.951 $\pm$ 0.10	1.133 $\pm$ 0.51	1.057 $\pm$ 0.49
<i>Serpinb9e</i>	Serine (or cysteine) peptidase inhibitor, clade B, member 9e	3.476 $\pm$ 0.33	0.838 $\pm$ 0.28	1.303 $\pm$ 0.32	1.395 $\pm$ 0.71	1.161 $\pm$ 0.43
<i>Slitrk6</i>	SLIT and NTRK-like family, member 6	3.294 $\pm$ 0.31	0.951 $\pm$ 0.12	14.520 $\pm$ 0.16	5.640 $\pm$ 0.44	2.330 $\pm$ 0.48
<i>Tnfrsf23</i>	Tumor necrosis factor receptor superfamily, member 23	3.247 $\pm$ 0.20	0.717 $\pm$ 0.43	1.717 $\pm$ 0.13	2.319 $\pm$ 0.39	1.563 $\pm$ 0.33
<i>U90926</i>	cDNA sequence U90926	3.242 $\pm$ 0.45	0.942 $\pm$ 0.3	24.151 $\pm$ 0.32	6.695 $\pm$ 0.62	6.18 $\pm$ 0.59
<i>Gm2115</i>	Predicted gene 2115	3.220 $\pm$ 0.51	0.785 $\pm$ 0.70	4.873 $\pm$ 0.20	3.051 $\pm$ 0.41	1.932 $\pm$ 0.35
<i>Mnda</i>	Myeloid cell nuclear differentiation antigen	3.217 $\pm$ 0.18	0.953 $\pm$ 0.16	3.804 $\pm$ 0.31	5.703 $\pm$ 0.33	3.444 $\pm$ 0.50
<i>Dusp6</i>	Dual specificity phosphatase 6	3.195 $\pm$ 0.37	0.675 $\pm$ 0.42	2.666 $\pm$ 0.22	2.388 $\pm$ 0.52	2.428 $\pm$ 0.49
<i>S100a4</i>	S100 calcium binding protein A4	3.106 $\pm$ 0.59	0.834 $\pm$ 0.44	1.669 $\pm$ 0.21	2.489 $\pm$ 0.37	2.133 $\pm$ 0.47
<i>Ndst3</i>	N-deacetylase/N-sulfotransferase	3.092 $\pm$ 0.63	0.874 $\pm$ 0.31	0.948 $\pm$ 0.27	1.007 $\pm$ 0.26	1.111 $\pm$ 0.13
<i>Lrrn3</i>	Leucine rich repeat protein 3, neuronal	3.068 $\pm$ 0.61	0.675 $\pm$ 0.48	0.979 $\pm$ 0.30	1.700 $\pm$ 0.30	2.129 $\pm$ 0.25
<i>Pla2g7</i>	Phospholipase A2, group VII	3.004 $\pm$ 0.28	0.938 $\pm$ 0.67	0.570 $\pm$ 0.24	1.200 $\pm$ 0.36	0.851 $\pm$ 0.31
<i>Cd68</i>	CD68 antigen	2.944 $\pm$ 0.27	0.864 $\pm$ 0.52	2.327 $\pm$ 0.15	1.725 $\pm$ 0.55	1.782 $\pm$ 0.29

<i>Gm6634</i>	Predicted gene 6634	2.911 ± 0.48	0.917 ± 0.51	1.780 ± 0.40	1.713 ± 0.35	2.417 ± 0.33
<i>Rtp4</i>	Receptor transporter protein 4	2.905 ± 1.02	0.957 ± 0.28	1.194 ± 0.13	1.282 ± 0.24	1.292 ± 0.18
<i>Tnfrsf22</i>	Tumor necrosis factor receptor superfamily, member 22	2.888 ± 0.17	0.811 ± 0.27	1.186 ± 0.22	1.244 ± 0.32	1.478 ± 0.23
<i>Ccnd1</i>	Cyclin D1	2.860 ± 0.30	0.779 ± 0.38	0.610 ± 0.19	0.579 ± 0.25	0.816 ± 0.19
<i>Tmem74</i>	Transmembrane protein 74	2.854 ± 0.21	0.695 ± 0.22	3.009 ± 0.29	2.863 ± 0.56	1.537 ± 0.40
<i>Hmga1-rs1</i>	High mobility group AT-hook 1, related sequence 1	2.834 ± 0.17	0.729 ± 0.19	1.274 ± 0.32	1.837 ± 0.40	1.832 ± 0.36
<i>LOC102638521</i>	60S ribosomal protein L23a	2.828 ± 0.26	1.070 ± 0.45	0.717 ± 0.18	0.865 ± 0.34	0.949 ± 0.39
<i>Ly6c2</i>	Lymphocyte antigen 6 complex, locus C2	2.801 ± 0.97	0.902 ± 0.13	0.825 ± 0.28	2.441 ± 0.43	1.221 ± 0.38
<i>Sncg</i>	Synuclein, gamma	2.779 ± 0.55	0.673 ± 0.23	1.759 ± 0.33	1.876 ± 0.59	1.653 ± 0.47
<i>Hmga2-ps1</i>	High mobility group AT-hook 2, pseudogene 1	2.775 ± 0.47	1.008 ± 0.36	1.420 ± 0.30	3.505 ± 0.57	1.332 ± 0.20
<i>Slfn9</i>	Schlafen 9	2.773 ± 0.34	0.725 ± 1.04	0.503 ± 0.29	3.184 ± 0.38	3.390 ± 0.36
<i>Ptgs2</i>	Prostaglandin-endoperoxide synthase 2	2.766 ± 0.53	0.862 ± 0.49	7.772 ± 0.16	2.793 ± 0.42	2.255 ± 0.37
<i>Ank</i>	Progressive ankyloses	2.750 ± 0.23	0.921 ± 0.36	0.967 ± 0.10	1.583 ± 0.32	1.381 ± 0.20
<i>Prrg4</i>	Proline rich Gla (G-carboxyglutamic acid) 4	2.738 ± 0.33	0.796 ± 0.58	1.368 ± 0.24	1.286 ± 0.36	0.941 ± 0.21
<i>Adam8</i>	A disintegrin and metalloproteinase domain 8	2.736 ± 0.26	0.714 ± 0.52	1.250 ± 0.22	1.546 ± 0.17	1.082 ± 0.35
<i>Ddias</i>	DNA damage-induced apoptosis suppressor	2.713 ± 0.38	0.632 ± 0.08	2.248 ± 0.33	2.074 ± 0.44	1.852 ± 0.32
<i>Spp1</i>	Secreted phosphoprotein 1	2.687 ± 0.36	1.031 ± 0.34	4.198 ± 0.28	4.731 ± 0.34	3.522 ± 0.37
<i>Gm25053</i>	Predicted gene 25053	2.678 ± 0.34	0.955 ± 0.21	0.933 ± 0.19	1.080 ± 0.64	1.173 ± 0.55
<i>Cd34</i>	CD34 antigen	2.667 ± 0.49	1.057 ± 0.58	0.812 ± 0.23	1.178 ± 0.54	1.608 ± 0.55
<i>Ifi202b</i>	Interferon activated gene 202B	2.633 ± 0.24	1.078 ± 0.35	4.270 ± 0.42	7.271 ± 0.49	4.653 ± 0.57
<i>Layn</i>	Layilin	2.631 ± 0.39	0.823 ± 0.24	2.497 ± 0.20	3.835 ± 0.36	2.092 ± 0.34
<i>Eda2r</i>	Ectodysplasin A2 receptor	2.631 ± 0.39	0.734 ± 0.30	4.225 ± 0.33	1.209 ± 0.38	1.125 ± 0.21
<i>Mcpt8</i>	Mast cell protease 8	2.628 ± 0.33	1.099 ± 0.23	1.203 ± 0.12	1.246 ± 0.36	1.357 ± 0.27
<i>Ngf</i>	Nerve growth factor	2.625 ± 0.24	0.766 ± 0.37	2.202 ± 0.28	1.530 ± 0.64	1.123 ± 0.50
<i>Zfp52</i>	Zinc finger protein 52	2.611 ± 0.36	0.880 ± 0.28	2.020 ± 0.50	1.684 ± 0.51	1.329 ± 0.57
<i>Ahnak2</i>	AHNAK nucleoprotein 2	2.602 ± 0.41	1.243 ± 0.24	2.066 ± 0.70	1.675 ± 0.60	1.528 ± 0.63
<i>Glpr1</i>	GLI pathogenesis-related 1	2.600 ± 0.56	0.612 ± 0.19	4.190 ± 0.30	5.148 ± 0.55	3.606 ± 0.54
<i>Cadm1</i>	Cell adhesion molecule 1	2.597 ± 0.44	0.891 ± 0.31	0.976 ± 0.10	0.856 ± 0.13	0.821 ± 0.17
<i>Gm12603</i>	Predicted gene 12603	2.594 ± 0.64	1.195 ± 0.31	1.047 ± 0.17	0.861 ± 0.28	0.873 ± 0.28
<i>Pi15</i>	Peptidase inhibitor 15	2.580 ± 0.32	0.922 ± 0.62	1.598 ± 0.46	0.953 ± 0.38	0.961 ± 0.28

<i>Gm8074</i>	Predicted gene 8074	2.571 ± 0.35	1.139 ± 0.28	0.802 ± 0.24	1.407 ± 0.54	1.445 ± 0.50
<i>Mlkl</i>	Mixed lineage kinase domain-like	2.538 ± 0.31	0.772 ± 0.18	1.473 ± 0.34	1.719 ± 0.47	1.414 ± 0.44
<i>Cd44</i>	CD44 antigen	2.530 ± 0.42	0.649 ± 0.44	2.583 ± 0.13	2.607 ± 0.18	2.334 ± 0.23
<i>9930111J21 Rik2</i>	RIKEN cDNA 9930111J21 gene 2	2.517 ± 1.14	0.927 ± 0.29	1.020 ± 0.29	0.936 ± 0.38	1.018 ± 0.41
<i>Trgj4</i>	T cell receptor gamma joining 4	2.509 ± 0.38	0.917 ± 0.31	1.125 ± 0.27	0.989 ± 0.11	1.068 ± 0.17
<i>Ifi203</i>	Interferon activated gene 203	2.502 ± 0.27	0.958 ± 0.41	1.147 ± 0.28	1.368 ± 0.15	1.213 ± 0.18
<i>Gm24561</i>	Predicted gene 24561	2.500 ± 0.61	1.546 ± 0.30	1.184 ± 1.05	1.078 ± 0.56	1.443 ± 0.59
<i>Xdh</i>	Xanthine dehydrogenase	2.494 ± 0.43	1.408 ± 0.21	12.478 ± 0.37	14.346 ± 0.38	10.058 ± 0.55
<i>Gm1045</i>	Predicted gene 1045	2.493 ± 0.26	1.185 ± 0.30	1.209 ± 0.40	1.26 ± 0.50	1.000 ± 0.42
<i>Cdh2</i>	Cadherin 2	2.467 ± 0.32	0.769 ± 1.13	1.375 ± 0.13	1.134 ± 0.26	1.160 ± 0.24
<i>Rerg</i>	RAS-like, estrogen-regulated, growth-inhibitor	2.467 ± 0.31	0.898 ± 0.72	1.283 ± 0.31	1.700 ± 0.33	1.698 ± 0.29
<i>Nrg1</i>	Neuregulin 1	2.440 ± 0.50	0.747 ± 0.19	4.055 ± 0.30	1.244 ± 0.18	1.659 ± 0.26
<i>Abcb1b</i>	ATP-binding cassette, sub-family B, member 1B	2.438 ± 0.54	0.675 ± 0.32	1.792 ± 0.44	1.478 ± 0.37	1.339 ± 0.26
<i>Igkj1</i>	Immunoglobulin kappa joining 1	2.421 ± 0.27	0.999 ± 0.19	1.106 ± 0.25	0.996 ± 0.52	0.906 ± 0.45
<i>Ifit1</i>	Interferon-induced protein with tetratricopeptide repeats 1	2.414 ± 0.49	0.796 ± 0.54	1.094 ± 0.32	1.317 ± 0.24	1.173 ± 0.25
<i>Hmga2</i>	High mobility group AT-hook 2	2.412 ± 0.52	0.729 ± 0.58	1.022 ± 0.18	1.727 ± 0.31	1.639 ± 0.27
<i>Gm5424</i>	Argininosuccinate synthase pseudogene	2.410 ± 0.27	0.732 ± 0.29	1.723 ± 0.12	1.288 ± 0.22	1.209 ± 0.41
<i>Ppargc1a</i>	Peroxisome proliferative activated receptor, gamma	2.406 ± 0.47	0.973 ± 0.34	0.813 ± 0.27	1.098 ± 0.40	1.294 ± 0.34
<i>Stom</i>	stomatin	2.404 ± 0.30	0.798 ± 0.43	2.430 ± 0.18	3.980 ± 0.35	2.138 ± 0.36
<i>Il18rap</i>	interleukin 18 receptor accessory protein	2.400 ± 0.39	0.923 ± 0.32	2.242 ± 0.24	1.785 ± 0.42	1.446 ± 0.26
<i>Hspa4l</i>	Heat shock protein 4 like	2.388 ± 0.53	0.967 ± 0.60	2.093 ± 0.37	2.417 ± 0.34	1.937 ± 0.32
<i>Tigit</i>	T cell immunoreceptor with Ig and ITIM domains	2.385 ± 0.40	0.911 ± 0.21	0.967 ± 0.28	0.935 ± 0.31	1.080 ± 0.29
<i>Cd55</i>	CD55 molecule, decay accelerating factor	2.383 ± 0.31	0.863 ± 0.35	1.068 ± 0.44	0.570 ± 0.27	0.545 ± 0.54
<i>Slc16a10</i>	Solute carrier family 16, member 10	2.378 ± 0.40	0.977 ± 0.29	1.087 ± 0.09	1.613 ± 0.35	1.692 ± 0.31
<i>Cxcl3</i>	Chemokine (C-X-C motif) ligand 3	2.377 ± 0.59	1.506 ± 0.38	251.887 ± 0.48	80.900 ± 0.55	56.658 ± 0.71
<i>Mmp3</i>	Matrix metalloproteinase 3	2.374 ± 0.37	1.847 ± 0.09	157.581 ± 0.19	116.517 ± 0.58	63.661 ± 0.68
<i>Gbp7</i>	Guanylate binding protein 7	2.366 ± 0.81	0.887 ± 0.20	2.549 ± 0.35	2.181 ± 0.37	1.924 ± 0.38
<i>Perp</i>	PERP, TP53 apoptosis effector	2.334 ± 0.40	0.617 ± 0.97	1.493 ± 0.23	0.798 ± 0.32	0.667 ± 0.26
<i>Ranbp3l</i>	RAN binding protein 3-like	2.327 ± 0.31	1.101 ± 0.71	1.481 ± 0.13	4.460 ± 0.68	3.028 ± 0.55
<i>Cyp1b1</i>	Cytochrome P450, family 1, subfamily b, polypeptide 1	2.305 ± 0.29	1.149 ± 0.67	3.505 ± 0.27	2.026 ± 0.36	1.889 ± 0.47

<i>Errfi1</i>	ERBB receptor feedback inhibitor 1	2.303 ± 0.10	0.854 ± 0.36	3.102 ± 0.19	2.155 ± 0.26	1.512 ± 0.16
<i>Gprc5a</i>	G protein-coupled receptor, family C, group 5, member A	2.280 ± 0.29	0.710 ± 0.20	1.514 ± 0.37	1.501 ± 0.26	1.472 ± 0.32
<i>Dynap</i>	Dynactin associated protein	2.270 ± 0.59	0.948 ± 0.29	0.849 ± 0.24	0.868 ± 0.20	0.948 ± 0.16
<i>Procr</i>	Protein C receptor, endothelial	2.267 ± 0.25	0.996 ± 0.14	1.359 ± 0.15	1.394 ± 0.22	1.210 ± 0.23
<i>Rgs16</i>	Regulator of G-protein signaling 16	2.258 ± 0.25	1.047 ± 0.49	3.366 ± 0.37	1.844 ± 0.19	2.863 ± 0.29
<i>S100a7a</i>	S100 calcium binding protein A7A	2.246 ± 0.59	0.761 ± 0.29	1.001 ± 0.32	0.949 ± 0.15	0.993 ± 0.19
<i>Sat1</i>	Spermidine/spermine N1-acetyl transferase 1	2.218 ± 0.28	0.899 ± 0.16	1.401 ± 0.27	2.119 ± 0.30	1.938 ± 0.28
<i>Pdpn</i>	Podoplanin	2.214 ± 0.34	1.031 ± 0.17	1.521 ± 0.14	2.542 ± 0.28	1.835 ± 0.27
<i>Serpinb8</i>	Serine (or cysteine) peptidase inhibitor, clade B, member 8	2.205 ± 0.72	0.836 ± 0.20	0.884 ± 0.21	1.682 ± 0.16	1.573 ± 0.38
<i>Fabp4</i>	Fatty acid binding protein 4, adipocyte	2.197 ± 0.83	1.171 ± 0.44	11.881 ± 0.64	22.810 ± 0.91	6.871 ± 0.91
<i>2810474O19 Rik</i>	RIKEN cDNA 2810474O19 gene	2.197 ± 0.11	0.787 ± 0.23	0.993 ± 0.38	1.166 ± 0.17	1.218 ± 0.18
<i>Gzme</i>	Granzyme E	2.196 ± 1.32	0.830 ± 0.38	1.024 ± 0.14	1.205 ± 0.87	1.460 ± 0.82
<i>Itgb7</i>	Integrin beta 7	2.189 ± 0.19	0.963 ± 0.66	1.174 ± 0.13	1.231 ± 0.42	1.148 ± 0.15
<i>Samd5</i>	Sterile alpha motif domain containing 5	2.183 ± 0.27	0.587 ± 0.80	1.122 ± 0.16	1.149 ± 0.32	1.310 ± 0.25
<i>Dsp</i>	Desmoplakin	2.182 ± 0.63	0.646 ± 0.13	0.691 ± 0.26	1.744 ± 0.35	0.778 ± 0.24
<i>Gcnt4</i>	Glucosaminyl transferase 4, core 2	2.182 ± 0.35	0.694 ± 0.55	1.202 ± 0.44	1.781 ± 0.49	1.501 ± 0.32
<i>Angptl2</i>	Angiopoietin-like 2	2.181 ± 0.32	0.879 ± 0.2	1.163 ± 0.20	1.529 ± 0.34	0.633 ± 0.22
<i>Gm8979</i>	Very large inducible GTPase 1 pseudogene	2.177 ± 0.48	0.838 ± 0.17	0.869 ± 0.28	0.892 ± 0.22	0.992 ± 0.26
<i>Adm</i>	Adrenomedullin	2.169 ± 0.30	0.964 ± 0.6	13.538 ± 0.24	17.308 ± 0.52	4.192 ± 0.4
<i>Kcnn4</i>	Potassium intermediate/small conductance calcium-activated	2.159 ± 0.25	0.919 ± 0.36	0.927 ± 0.24	1.331 ± 0.20	1.030 ± 0.14
<i>Fam111a</i>	Family with sequence similarity 111, member A	2.158 ± 0.38	0.695 ± 0.30	0.688 ± 0.21	3.163 ± 0.35	3.350 ± 0.36
<i>Ccl5</i>	Chemokine (C-C motif) ligand 5	2.141 ± 0.43	0.913 ± 0.35	20.147 ± 0.68	20.685 ± 0.26	13.567 ± 0.35
<i>Tm4sf1</i>	Transmembrane 4 superfamily member 1	2.135 ± 0.43	0.846 ± 0.42	2.592 ± 0.14	5.148 ± 0.49	3.841 ± 0.45
<i>P2rx7</i>	Purinergic receptor P2X, ligand-gated ion channel, 7	2.130 ± 0.24	0.839 ± 0.12	1.849 ± 0.21	1.276 ± 0.28	1.402 ± 0.38
<i>Met</i>	Met proto-oncogene	2.126 ± 0.26	1.030 ± 0.49	1.105 ± 0.19	1.564 ± 0.28	1.335 ± 0.31
<i>Gm34039</i>	Predicted gene 34039	2.124 ± 0.32	0.906 ± 0.41	1.393 ± 0.17	1.171 ± 0.27	1.086 ± 0.22
<i>Ifih1</i>	Interferon induced with helicase C domain 1	2.114 ± 0.47	0.954 ± 0.46	1.637 ± 0.29	1.559 ± 0.25	1.461 ± 0.27
<i>2010300F17 Rik</i>	RIKEN cDNA 2010300F17 gene	2.111 ± 1.14	0.903 ± 0.22	0.543 ± 0.38	0.824 ± 0.41	0.872 ± 0.53
<i>Dtna</i>	Dystrobrevin alpha	2.111 ± 0.48	1.060 ± 0.21	1.718 ± 0.17	1.264 ± 0.25	1.221 ± 0.30
<i>Dock11</i>	Dedicator of cytokinesis 11	2.110 ± 0.27	0.796 ± 0.26	1.748 ± 0.51	1.823 ± 0.25	1.618 ± 0.27

<i>S1pr3</i>	Sphingosine-1-phosphate receptor 3	2.108 ± 0.23	0.973 ± 0.17	0.926 ± 0.11	0.992 ± 0.14	0.992 ± 0.11
<i>Ccnf</i>	Cyclin F	2.106 ± 0.27	0.780 ± 1.01	0.756 ± 0.14	1.594 ± 0.19	1.634 ± 0.21
<i>Rrm2</i>	Ribonucleotide reductase M2	2.104 ± 0.39	0.714 ± 0.20	0.594 ± 0.25	2.495 ± 0.33	2.678 ± 0.34
<i>Kctd12</i>	Potassium channel tetramerisation domain	2.099 ± 0.50	0.648 ± 0.19	3.137 ± 0.45	1.773 ± 0.23	1.982 ± 0.18
<i>Bmpr1b</i>	Bone morphogenetic protein receptor, type 1B	2.096 ± 0.27	1.008 ± 0.38	1.323 ± 0.29	1.581 ± 0.25	1.491 ± 0.42
<i>Sh3kbp1</i>	SH3-domain kinase binding protein 1	2.095 ± 0.15	0.771 ± 0.35	1.624 ± 0.11	1.461 ± 0.20	0.981 ± 0.13
<i>Diaph3</i>	Diaphanous related formin 3	2.079 ± 0.27	0.773 ± 0.51	0.765 ± 0.16	2.140 ± 0.33	2.171 ± 0.32
<i>Il1rl1</i>	Interleukin 1 receptor-like 1	2.077 ± 0.68	0.823 ± 0.60	2.574 ± 0.41	1.451 ± 0.42	1.706 ± 0.40
<i>Itga2</i>	Integrin alpha 2	2.074 ± 0.68	0.972 ± 0.33	0.316 ± 0.36	0.688 ± 0.14	0.623 ± 0.28
<i>Ddit4l</i>	DNA-damage-inducible transcript 4-like	2.069 ± 0.18	1.019 ± 0.10	3.449 ± 0.34	1.539 ± 0.33	1.410 ± 0.30
<i>Masp1</i>	Mannan-binding lectin serine peptidase 1	2.061 ± 0.50	0.680 ± 0.41	1.639 ± 0.26	1.277 ± 0.32	1.252 ± 0.36
<i>Il13ra1</i>	Interleukin 13 receptor, alpha 1	2.059 ± 0.36	1.237 ± 0.67	7.171 ± 0.29	14.384 ± 0.37	5.319 ± 0.35
<i>Cks2</i>	CDC28 protein kinase regulatory subunit 2	2.050 ± 0.46	0.917 ± 0.70	0.679 ± 0.47	2.040 ± 0.31	2.195 ± 0.32
<i>Gfra1</i>	Glial cell line derived neurotrophic factor	2.043 ± 0.23	0.864 ± 0.40	1.097 ± 0.12	1.754 ± 0.17	1.329 ± 0.30
<i>mt-Tf</i>	Mitochondrially encoded tRNA phenylalanine	2.033 ± 0.40	1.151 ± 0.58	2.290 ± 0.47	1.778 ± 0.15	1.314 ± 0.30
<i>Pdgfc</i>	Platelet-derived growth factor, C polypeptide	2.029 ± 0.26	0.936 ± 0.58	1.674 ± 0.16	1.658 ± 0.19	1.354 ± 0.18
<i>Prg4</i>	Proteoglycan 4	2.019 ± 0.72	1.678 ± 0.58	7.197 ± 0.16	8.533 ± 0.48	3.577 ± 0.57
<i>Ptgs1</i>	Prostaglandin-endoperoxide synthase 1	2.012 ± 0.23	0.927 ± 0.37	1.167 ± 0.23	1.986 ± 0.47	1.268 ± 0.36
<i>mt-Ts2</i>	Mitochondrially encoded tRNA serine 2	2.011 ± 0.79	1.625 ± 0.38	0.825 ± 0.96	0.827 ± 0.43	0.905 ± 0.55
<i>Hist1h3g</i>	Histone cluster 1, H3g	2.008 ± 0.63	0.930 ± 0.33	0.482 ± 0.54	1.309 ± 0.58	1.546 ± 0.51
<i>Hhip</i>	Hedgehog-interacting protein	2.006 ± 0.49	1.104 ± 0.95	0.807 ± 0.30	0.495 ± 0.42	0.539 ± 0.39
<i>Nabp1</i>	Nucleic acid binding protein 1	2.006 ± 0.34	0.760 ± 0.18	2.606 ± 0.21	1.707 ± 0.32	1.557 ± 0.38
<i>Hmox1</i>	Heme oxygenase 1	2.003 ± 0.15	1.132 ± 0.66	1.484 ± 0.11	0.908 ± 0.23	1.682 ± 0.32

Supplementary Table 6. List of down-regulated genes (< 0.7-fold) following knock-down of Regnase-1 via Ad-shRegnase-1 infection in chondrocytes.

Gene Symbol	Definition	Fold change				
		Ad-shRegnase-1	Ad-Regnase-1	IL-1 β	Ad-HIF-2 α	Ad-ZIP8
<i>Cd80</i>	CD80 antigen	0.398 $\pm$ 0.41	1.663 $\pm$ 0.39	6.498 $\pm$ 0.19	2.802 $\pm$ 0.68	2.104 $\pm$ 0.54
<i>Hist1h2bg</i>	Histone cluster 1, H2bg	0.464 $\pm$ 0.28	1.095 $\pm$ 0.23	0.744 $\pm$ 0.46	1.788 $\pm$ 0.58	1.740 $\pm$ 0.56
<i>Krt19</i>	Keratin 19	0.481 $\pm$ 0.70	1.761 $\pm$ 0.40	1.050 $\pm$ 0.41	1.633 $\pm$ 0.28	0.828 $\pm$ 0.22
<i>Gm23470</i>	Predicted gene 23470	0.500 $\pm$ 0.40	1.081 $\pm$ 0.41	1.035 $\pm$ 0.84	1.218 $\pm$ 0.33	1.154 $\pm$ 0.31
<i>Gm23119</i>	Predicted gene 23119	0.520 $\pm$ 0.96	0.803 $\pm$ 0.09	1.011 $\pm$ 0.23	1.122 $\pm$ 0.32	0.974 $\pm$ 0.32
<i>Prr11</i>	Proline rich 11	0.521 $\pm$ 0.43	1.278 $\pm$ 0.33	0.490 $\pm$ 0.14	2.254 $\pm$ 0.26	2.306 $\pm$ 0.26
<i>Tmem47</i>	Transmembrane protein 47	0.542 $\pm$ 0.26	1.259 $\pm$ 0.27	0.720 $\pm$ 0.12	0.721 $\pm$ 0.09	0.831 $\pm$ 0.16
<i>Gm24655</i>	Predicted gene 24655	0.545 $\pm$ 0.40	0.835 $\pm$ 0.43	1.605 $\pm$ 1.08	0.682 $\pm$ 0.53	0.782 $\pm$ 0.54
<i>Hist1h3e</i>	Histone cluster 1, H3e	0.547 $\pm$ 0.43	0.905 $\pm$ 0.29	0.589 $\pm$ 0.50	2.213 $\pm$ 0.61	2.474 $\pm$ 0.57
<i>Gm22303</i>	Predicted gene 22303	0.559 $\pm$ 0.29	1.005 $\pm$ 0.29	0.581 $\pm$ 0.39	0.964 $\pm$ 0.35	1.016 $\pm$ 0.32
<i>mt-Tk</i>	Mitochondrially encoded tRNA lysine	0.559 $\pm$ 0.48	0.757 $\pm$ 0.43	0.688 $\pm$ 0.65	0.938 $\pm$ 0.31	1.047 $\pm$ 0.38
<i>Traj54</i>	T cell receptor alpha joining 54	0.559 $\pm$ 0.71	0.799 $\pm$ 0.28	0.635 $\pm$ 0.44	1.164 $\pm$ 0.46	1.332 $\pm$ 0.53
<i>Emp1</i>	Epithelial membrane protein 1	0.561 $\pm$ 0.48	1.444 $\pm$ 0.29	0.711 $\pm$ 0.16	1.143 $\pm$ 0.19	0.990 $\pm$ 0.21
<i>Hibadh</i>	3-hydroxyisobutyrate dehydrogenase	0.565 $\pm$ 0.77	1.097 $\pm$ 0.78	0.504 $\pm$ 1.10	0.969 $\pm$ 0.70	1.090 $\pm$ 0.84
<i>Gm22973</i>	Predicted gene 22973	0.582 $\pm$ 0.32	0.922 $\pm$ 0.86	1.708 $\pm$ 1.30	1.075 $\pm$ 0.65	1.189 $\pm$ 0.96
<i>Lgals9</i>	Lectin, galactose binding, soluble 9	0.587 $\pm$ 0.47	1.079 $\pm$ 0.21	1.781 $\pm$ 0.29	1.151 $\pm$ 0.27	1.264 $\pm$ 0.26
<i>Samd5</i>	Sterile alpha motif domain containing 5	0.587 $\pm$ 0.17	2.183 $\pm$ 0.27	1.122 $\pm$ 0.16	1.149 $\pm$ 0.32	1.310 $\pm$ 0.25
<i>Egr1</i>	Early growth response 1	0.590 $\pm$ 0.59	1.384 $\pm$ 0.24	1.412 $\pm$ 0.31	1.696 $\pm$ 0.24	1.882 $\pm$ 0.23
<i>Gtse1</i>	G two S phase expressed protein 1	0.593 $\pm$ 0.35	1.712 $\pm$ 0.27	1.588 $\pm$ 0.35	1.908 $\pm$ 0.26	1.735 $\pm$ 0.24
<i>Gm22358</i>	Predicted gene 22358	0.595 $\pm$ 0.20	1.069 $\pm$ 0.22	0.656 $\pm$ 0.28	1.017 $\pm$ 0.26	1.077 $\pm$ 0.25
<i>Kifc1</i>	Kinesin family member C1	0.601 $\pm$ 0.69	1.211 $\pm$ 0.43	0.695 $\pm$ 0.22	1.200 $\pm$ 0.42	1.249 $\pm$ 0.39
<i>Inhba</i>	Inhibin beta-A	0.603 $\pm$ 0.41	1.688 $\pm$ 0.27	4.050 $\pm$ 0.45	2.449 $\pm$ 0.44	1.465 $\pm$ 0.38
<i>Gm24519</i>	Predicted gene 24519	0.605 $\pm$ 0.50	0.658 $\pm$ 0.46	1.406 $\pm$ 0.29	0.773 $\pm$ 0.58	0.874 $\pm$ 0.54
<i>Gm24679</i>	Predicted gene 24679	0.607 $\pm$ 0.63	0.514 $\pm$ 0.56	0.902 $\pm$ 0.16	0.949 $\pm$ 0.41	1.124 $\pm$ 0.38
<i>Tnfrsf10b</i>	Tumor necrosis factor receptor superfamily, member 10b	0.609 $\pm$ 0.23	1.342 $\pm$ 0.22	1.533 $\pm$ 0.16	1.049 $\pm$ 0.19	0.915 $\pm$ 0.19
<i>E2f8</i>	E2F transcription factor 8	0.611 $\pm$ 0.22	1.001 $\pm$ 0.12	0.157 $\pm$ 0.28	1.127 $\pm$ 0.27	1.227 $\pm$ 0.29

<i>Hist1h2ai</i>	Histone cluster 1, H2ai	0.612 ± 0.28	1.226 ± 0.19	0.823 ± 0.29	1.397 ± 0.38	1.946 ± 0.43
<i>Glpr1</i>	GLI pathogenesis-related 1	0.612 ± 0.62	2.600 ± 0.56	4.190 ± 0.30	5.148 ± 0.55	3.606 ± 0.54
<i>Tgfb1i1</i>	Transforming growth factor beta 1 induced transcript 1	0.614 ± 0.51	0.729 ± 0.22	1.000 ± 0.19	0.861 ± 0.16	0.837 ± 0.16
<i>Crip2</i>	Cysteine rich protein 2	0.616 ± 0.19	1.464 ± 0.20	1.331 ± 0.12	1.481 ± 0.17	1.403 ± 0.17
<i>Perp</i>	PERP, TP53 apoptosis effector	0.617 ± 0.36	2.334 ± 0.40	1.493 ± 0.23	0.798 ± 0.32	0.667 ± 0.26
<i>Gm2573</i>	Predicted gene 2573	0.618 ± 0.59	0.695 ± 0.14	0.875 ± 0.09	0.816 ± 0.09	0.867 ± 0.17
<i>Olfr331</i>	Olfactory receptor 331	0.620 ± 0.37	0.739 ± 0.40	1.099 ± 0.44	1.047 ± 0.47	1.170 ± 0.50
<i>Hist1h3d</i>	Histone cluster 1, H3d	0.621 ± 0.26	1.500 ± 0.21	0.827 ± 0.53	1.411 ± 0.68	1.916 ± 0.60
<i>Gm23130</i>	Predicted gene 23130	0.622 ± 0.23	0.745 ± 0.15	0.791 ± 0.32	0.985 ± 0.11	1.082 ± 0.11
<i>1700007K13Rik</i>	RIKEN cDNA 1700007K13 gene	0.622 ± 0.18	1.892 ± 0.45	3.677 ± 0.25	0.956 ± 0.34	1.126 ± 0.29
<i>Mir30e</i>	MicroRNA 30e	0.626 ± 0.41	0.596 ± 0.54	1.078 ± 0.44	1.207 ± 0.73	1.103 ± 0.91
<i>Gm23058</i>	Predicted gene 23058	0.629 ± 0.40	0.971 ± 0.37	1.124 ± 0.63	1.021 ± 0.43	1.016 ± 0.40
<i>Gm7665</i>	Predicted pseudogene 7665	0.629 ± 0.63	0.902 ± 0.40	1.265 ± 0.32	1.204 ± 0.41	0.973 ± 0.49
<i>Sfxn3</i>	Sideroflexin 3	0.630 ± 0.34	1.007 ± 0.09	1.932 ± 0.11	1.515 ± 0.16	1.388 ± 0.18
<i>Ddias</i>	DNA damage-induced apoptosis suppressor	0.632 ± 0.58	2.713 ± 0.38	2.248 ± 0.33	2.074 ± 0.44	1.852 ± 0.32
<i>Gm25394</i>	Predicted gene 25394	0.632 ± 0.14	0.556 ± 0.12	0.902 ± 0.22	1.002 ± 1.94	1.010 ± 1.99
<i>Rnu3a</i>	U3A small nuclear RNA	0.634 ± 0.17	0.681 ± 0.14	1.428 ± 0.33	1.627 ± 1.25	1.345 ± 1.28
<i>Nop56</i>	NOP56 ribonucleoprotein	0.635 ± 0.20	0.722 ± 0.21	0.768 ± 0.68	0.954 ± 0.53	0.949 ± 0.53
<i>Fhdc1</i>	FH2 domain containing 1	0.635 ± 0.41	1.791 ± 0.38	0.804 ± 0.13	0.907 ± 0.12	0.968 ± 0.16
<i>Actg1</i>	Actin, gamma, cytoplasmic 1	0.637 ± 0.33	0.864 ± 0.33	0.990 ± 0.53	0.932 ± 0.25	0.902 ± 0.19
<i>Gm13770</i>	Predicted gene 13770	0.638 ± 0.57	0.708 ± 0.09	0.889 ± 0.13	0.827 ± 0.20	0.851 ± 0.22
<i>Cxx1a</i>	CAAX box 1A	0.639 ± 0.49	0.745 ± 0.26	1.051 ± 0.21	1.073 ± 0.38	0.890 ± 0.48
<i>Itga3</i>	Integrin alpha 3	0.639 ± 0.34	1.456 ± 0.28	0.888 ± 0.13	0.810 ± 0.18	0.767 ± 0.17
<i>Slc18b1</i>	Solute carrier family 18, subfamily B, member 1	0.640 ± 0.30	0.705 ± 0.12	1.421 ± 0.19	1.044 ± 0.37	1.094 ± 0.37
<i>Olfr147</i>	Olfactory receptor 147	0.642 ± 0.37	0.718 ± 0.34	0.868 ± 0.41	0.956 ± 0.43	0.843 ± 0.37
<i>Stil</i>	Scl/Tal1 interrupting locus	0.643 ± 0.47	1.420 ± 0.24	0.537 ± 0.21	1.871 ± 0.36	1.884 ± 0.37
<i>Olfr710</i>	Olfactory receptor 710	0.643 ± 0.29	0.627 ± 0.31	1.128 ± 0.19	1.143 ± 0.28	1.186 ± 0.25
<i>Jph2</i>	Junctophilin 2	0.643 ± 0.47	0.802 ± 0.25	1.119 ± 0.28	0.496 ± 0.26	0.677 ± 0.35
<i>Wdr46</i>	WD repeat domain 46	0.644 ± 0.40	0.904 ± 0.10	0.756 ± 0.08	0.858 ± 0.23	0.949 ± 0.10

<i>Ccnb2</i>	Cyclin B2	0.645 ± 0.24	1.125 ± 0.16	0.362 ± 0.19	2.194 ± 0.24	1.969 ± 0.23
<i>Krt17</i>	Keratin 17	0.645 ± 0.99	0.963 ± 0.59	0.513 ± 0.36	0.958 ± 0.62	0.705 ± 0.78
<i>Dsp</i>	Desmoplakin	0.646 ± 0.60	2.182 ± 0.63	0.691 ± 0.26	1.744 ± 0.35	0.778 ± 0.24
<i>Kctd12</i>	Potassium channel tetramerisation domain	0.648 ± 0.60	2.099 ± 0.50	3.137 ± 0.45	1.773 ± 0.23	1.982 ± 0.18
<i>Ly6e</i>	Lymphocyte antigen 6 complex, locus E	0.648 ± 0.28	1.710 ± 0.22	1.676 ± 0.18	2.260 ± 0.40	1.860 ± 0.43
<i>Cd44</i>	CD44 antigen	0.649 ± 0.41	2.530 ± 0.42	2.583 ± 0.13	2.607 ± 0.18	2.334 ± 0.23
<i>Fam198b</i>	Family with sequence similarity 198, member B	0.649 ± 0.55	0.978 ± 0.33	0.746 ± 0.17	0.426 ± 0.21	0.516 ± 0.23
<i>G530011006 Rik</i>	RIKEN cDNA G530011O06 gene	0.649 ± 0.21	0.987 ± 0.19	1.39 ± 0.35	1.353 ± 0.55	1.372 ± 0.23
<i>Gm26443</i>	Predicted gene 26443	0.651 ± 0.50	1.123 ± 0.71	0.929 ± 0.63	0.981 ± 0.48	0.759 ± 0.53
<i>Gm20634</i>	Predicted gene 20634	0.651 ± 0.23	0.766 ± 0.14	1.147 ± 0.19	1.086 ± 0.29	1.049 ± 0.41
<i>Trav13d-4</i>	T cell receptor alpha variable 13D-4	0.651 ± 0.40	0.634 ± 0.63	0.788 ± 0.45	0.95 ± 0.34	1.001 ± 0.32
<i>Kitl</i>	Kit ligand	0.653 ± 0.39	4.790 ± 0.40	5.222 ± 0.44	2.417 ± 0.34	1.719 ± 0.41
<i>Vps33b</i>	Vacuolar protein sorting 33B	0.653 ± 0.30	0.832 ± 0.06	1.011 ± 0.13	1.048 ± 0.29	0.971 ± 0.19
<i>Rela</i>	v-rel reticuloendotheliosis viral oncogene homolog A	0.653 ± 0.28	0.958 ± 0.05	1.381 ± 0.17	1.162 ± 0.15	1.033 ± 0.15
<i>Gm23237</i>	Predicted gene 23237	0.654 ± 0.37	0.746 ± 0.40	0.897 ± 0.33	1.179 ± 1.04	1.37 ± 0.76
<i>Bax</i>	BCL2-associated X protein	0.655 ± 0.58	1.221 ± 0.14	1.633 ± 0.07	1.134 ± 0.14	1.036 ± 0.17
<i>Gm23272</i>	Predicted gene 23272	0.656 ± 0.60	0.969 ± 0.65	0.774 ± 0.38	0.946 ± 0.45	1.104 ± 0.49
<i>Sdpr</i>	Serum deprivation response	0.656 ± 0.43	1.914 ± 0.48	1.905 ± 0.24	0.712 ± 0.37	0.805 ± 0.37
<i>Elovl7</i>	ELOVL family member 7	0.657 ± 0.30	1.610 ± 0.39	1.205 ± 0.35	1.011 ± 0.20	1.027 ± 0.28
<i>Hist1h4d</i>	Histone cluster 1, H4d	0.659 ± 0.82	1.006 ± 0.53	0.624 ± 0.90	1.399 ± 1.01	1.571 ± 1.06
<i>Hist1h4i</i>	Histone cluster 1, H4i	0.660 ± 0.57	1.673 ± 0.30	1.055 ± 0.43	1.715 ± 0.55	1.948 ± 0.48
<i>Ndc80</i>	NDC80 homolog, kinetochore complex component	0.661 ± 0.42	1.326 ± 0.40	0.317 ± 0.29	2.413 ± 0.47	2.693 ± 0.45
<i>MsrB3</i>	Methionine sulfoxide reductase B3	0.662 ± 0.18	0.846 ± 0.18	0.817 ± 0.06	0.899 ± 0.16	0.835 ± 0.16
<i>Id1</i>	Inhibitor of DNA binding 1	0.663 ± 0.27	1.091 ± 0.16	0.973 ± 0.16	0.616 ± 0.19	0.914 ± 0.27
<i>Sfrp1</i>	Secreted frizzled-related protein 1	0.663 ± 0.22	1.042 ± 0.14	0.814 ± 0.29	0.909 ± 0.07	1.031 ± 0.07
<i>Pqlc3</i>	PQ loop repeat containing	0.664 ± 0.28	1.674 ± 0.27	2.827 ± 0.27	1.483 ± 0.26	1.135 ± 0.27
<i>B4galt1</i>	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase	0.664 ± 0.08	1.009 ± 0.07	1.894 ± 0.23	2.169 ± 0.16	1.788 ± 0.17
<i>Mcm5</i>	Minichromosome maintenance deficient 5, cell division cycle 4	0.665 ± 0.47	1.462 ± 0.19	0.459 ± 0.18	1.763 ± 0.25	1.772 ± 0.21
<i>Dusp1</i>	Dual specificity phosphatase 1	0.666 ± 0.42	0.977 ± 0.28	1.841 ± 0.31	0.989 ± 0.23	1.034 ± 0.31

<i>Gm22672</i>	Predicted gene 22672	0.667 ± 0.46	0.934 ± 0.29	1.269 ± 0.16	1.157 ± 0.46	1.023 ± 0.47
<i>Gm12185</i>	Predicted gene 12185	0.668 ± 0.38	0.924 ± 0.29	1.017 ± 0.39	0.981 ± 0.39	1.076 ± 0.40
<i>Angptl7</i>	Angiopoietin-like 7	0.668 ± 0.5	0.714 ± 0.36	1.333 ± 0.35	0.804 ± 0.37	0.951 ± 0.41
<i>Ar16ip1</i>	ADP-ribosylation factor-like 6 interacting protein 1	0.669 ± 0.19	1.292 ± 0.08	0.965 ± 0.12	1.451 ± 0.12	1.428 ± 0.14
<i>Gm25188</i>	Predicted gene 25188	0.669 ± 0.30	1.001 ± 0.27	0.814 ± 0.50	1.038 ± 0.25	1.012 ± 0.26
<i>Zfp365</i>	Zinc finger protein 365	0.669 ± 0.20	1.172 ± 0.13	1.422 ± 0.20	0.803 ± 0.16	0.836 ± 0.15
<i>Krtap19-9b</i>	Keratin associated protein 19-9B	0.670 ± 0.24	0.665 ± 0.30	1.074 ± 0.41	1.029 ± 0.40	1.340 ± 0.54
<i>Nes</i>	Nestin	0.671 ± 0.59	1.457 ± 0.48	0.493 ± 0.24	0.773 ± 0.41	0.861 ± 0.36
<i>9030617O03 Rik</i>	RIKEN cDNA 9030617O03 gene	0.672 ± 0.41	1.823 ± 0.26	3.105 ± 0.32	1.376 ± 0.28	1.071 ± 0.27
<i>Gm23406</i>	Predicted gene 23406	0.672 ± 0.32	1.237 ± 0.37	0.764 ± 0.49	0.917 ± 0.54	0.924 ± 0.63
<i>Gm25776</i>	Predicted gene 25776	0.673 ± 0.32	0.811 ± 0.29	0.784 ± 0.85	1.072 ± 1.69	0.937 ± 1.51
<i>Sncg</i>	Synuclein, gamma	0.673 ± 0.49	2.779 ± 0.55	1.759 ± 0.33	1.876 ± 0.59	1.653 ± 0.47
<i>Gm23513</i>	Predicted gene 23513	0.674 ± 0.28	0.719 ± 0.19	1.047 ± 0.25	0.984 ± 0.78	1.005 ± 0.67
<i>Gm15726</i>	Predicted gene 15726	0.675 ± 0.26	1.302 ± 0.47	0.985 ± 0.08	1.084 ± 0.69	1.180 ± 0.48
<i>Rab39b</i>	RAB39B, member RAS oncogene family	0.675 ± 0.17	0.630 ± 0.15	0.327 ± 0.16	0.543 ± 0.21	0.625 ± 0.33
<i>Dusp6</i>	Dual specificity phosphatase 6	0.675 ± 0.48	3.195 ± 0.37	2.666 ± 0.22	2.388 ± 0.52	2.428 ± 0.49
<i>Abcb1b</i>	ATP-binding cassette, sub-family B member 1B	0.675 ± 0.58	2.438 ± 0.54	1.792 ± 0.44	1.478 ± 0.37	1.339 ± 0.26
<i>Twist2</i>	Twist basic helix-loop-helix transcription factor 2	0.675 ± 0.36	1.298 ± 0.20	0.905 ± 0.39	1.276 ± 0.47	1.361 ± 0.48
<i>Gm25970</i>	Predicted gene 25970	0.675 ± 0.37	0.760 ± 0.35	1.136 ± 0.92	1.190 ± 1.35	1.198 ± 1.31
<i>Unc13c</i>	Unc-13 homolog	0.675 ± 0.42	1.794 ± 0.60	0.846 ± 0.28	0.882 ± 0.30	1.010 ± 0.14
<i>Olfir870</i>	Olfactory receptor 870	0.675 ± 0.42	0.676 ± 0.22	0.984 ± 0.26	0.904 ± 0.29	1.031 ± 0.18
<i>Lrrn3</i>	Leucine rich repeat protein 3, neuronal	0.675 ± 0.51	3.068 ± 0.61	0.979 ± 0.30	1.700 ± 0.30	2.129 ± 0.25
<i>Lrrc61</i>	Leucine rich repeat containing 61	0.676 ± 0.25	0.537 ± 0.21	0.708 ± 0.14	0.747 ± 0.18	0.880 ± 0.15
<i>Hist1h4f</i>	Histone cluster 1, H4f	0.677 ± 0.22	0.855 ± 0.23	0.955 ± 0.38	0.934 ± 0.29	0.983 ± 0.39
<i>9230114K14 Rik</i>	RIKEN cDNA 9230114K14 gene	0.677 ± 0.24	1.402 ± 0.31	3.265 ± 0.39	1.316 ± 0.23	1.169 ± 0.23
<i>Fam83h</i>	Family with sequence similarity 83, member H	0.678 ± 0.43	1.077 ± 0.26	1.096 ± 0.12	0.966 ± 0.13	0.891 ± 0.27
<i>H2afx</i>	H2A histone family, member X	0.678 ± 0.37	1.294 ± 0.08	0.397 ± 0.24	1.639 ± 0.11	1.597 ± 0.13
<i>Mir344e</i>	MicroRNA 344e	0.679 ± 0.49	0.697 ± 0.51	0.863 ± 0.43	0.916 ± 0.58	0.987 ± 0.57
<i>Abi2</i>	Abl-interactor 2	0.680 ± 0.04	0.910 ± 0.06	0.979 ± 0.14	0.760 ± 0.11	0.838 ± 0.04

<i>Masp1</i>	Mannan-binding lectin serine peptidase 1	0.680 ± 0.49	2.061 ± 0.50	1.639 ± 0.26	1.277 ± 0.32	1.252 ± 0.36
<i>Gm25762</i>	Predicted gene 25762	0.681 ± 0.52	0.877 ± 0.47	0.732 ± 0.59	1.026 ± 0.32	1.003 ± 0.52
<i>Gm25443</i>	Predicted gene 25443	0.681 ± 0.69	0.894 ± 0.18	0.977 ± 0.10	1.058 ± 0.27	0.989 ± 0.21
<i>Krtap1-5</i>	Keratin associated protein 1-5	0.681 ± 0.43	1.127 ± 0.17	0.770 ± 0.29	0.987 ± 0.44	1.232 ± 0.58
<i>Pparg</i>	Peroxisome proliferator activated receptor gamma	0.681 ± 0.43	1.899 ± 0.46	1.029 ± 0.21	0.656 ± 0.22	0.827 ± 0.23
<i>Osr1</i>	Odd-skipped related 1	0.682 ± 0.14	0.701 ± 0.18	1.892 ± 0.17	0.894 ± 0.44	1.021 ± 0.49
<i>Taf9b</i>	TAF9B RNA polymerase II, TBP-associated factor	0.682 ± 0.27	0.666 ± 0.28	0.490 ± 0.20	0.731 ± 0.14	0.622 ± 0.16
<i>P4ha3</i>	Procollagen-proline, 2-oxoglutarate 4-dioxygenase	0.682 ± 0.23	0.629 ± 0.15	0.317 ± 0.20	0.375 ± 0.21	0.500 ± 0.22
<i>Hist1h4n</i>	Histone cluster 1, H4n	0.683 ± 0.44	1.412 ± 0.48	1.115 ± 0.62	1.940 ± 0.66	1.891 ± 0.40
<i>Creb3l1</i>	cAMP responsive element binding protein 3-like 1	0.683 ± 0.25	0.564 ± 0.26	1.315 ± 0.04	1.150 ± 0.13	1.090 ± 0.13
<i>P3h2</i>	Prolyl 3-hydroxylase 2	0.685 ± 0.04	0.908 ± 0.10	0.490 ± 0.18	0.778 ± 0.28	0.600 ± 0.17
<i>Lce3c</i>	Late cornified envelope 3C	0.686 ± 0.82	1.097 ± 0.62	1.578 ± 0.82	1.272 ± 0.34	1.575 ± 0.22
<i>Plk1</i>	Polo-like kinase 1	0.686 ± 0.30	1.284 ± 0.20	0.355 ± 0.14	2.139 ± 0.12	2.048 ± 0.13
<i>Tagln</i>	Transgelin	0.687 ± 0.70	0.660 ± 0.38	0.641 ± 0.50	0.412 ± 0.21	0.545 ± 0.23
<i>Jun</i>	Jun proto-oncogene	0.687 ± 0.39	1.689 ± 0.19	2.359 ± 0.16	1.492 ± 0.31	1.090 ± 0.21
<i>Gm22327</i>	Predicted gene 22327	0.687 ± 0.49	0.920 ± 0.39	1.107 ± 0.85	1.410 ± 0.42	1.625 ± 0.47
<i>Ctxn1</i>	Cortexin 1	0.687 ± 0.06	1.342 ± 0.09	2.261 ± 0.26	1.324 ± 0.27	1.390 ± 0.21
<i>LOC105244345</i>	Small nuclear ribonucleoprotein Sm D1-like	0.688 ± 0.34	0.947 ± 0.26	0.677 ± 0.39	0.869 ± 0.20	0.905 ± 0.21
<i>Eif2s3x</i>	Eukaryotic translation initiation factor 2, subunit 3	0.688 ± 0.29	0.999 ± 0.16	0.937 ± 0.17	0.888 ± 0.26	0.902 ± 0.27
<i>Zwilch</i>	Zwilch kinetochore protein	0.688 ± 0.37	1.093 ± 0.17	0.434 ± 0.12	1.471 ± 0.21	1.499 ± 0.24
<i>Wdr83os</i>	WD repeat domain 83 opposite strand	0.689 ± 0.16	0.909 ± 0.08	0.920 ± 0.31	0.974 ± 0.27	1.143 ± 0.24
<i>Ifit1bl2</i>	Interferon induced protein with tetratricopeptide repeats 1B	0.689 ± 0.28	0.767 ± 0.2	0.773 ± 0.2	0.896 ± 0.32	0.937 ± 0.32
<i>Ska3</i>	Spindle and kinetochore associated complex subunit 3	0.689 ± 0.51	1.749 ± 0.32	0.431 ± 0.29	1.896 ± 0.42	1.978 ± 0.36
<i>Ifi44</i>	Interferon-induced protein 44	0.690 ± 0.19	1.986 ± 1.28	0.538 ± 0.18	0.463 ± 0.24	0.640 ± 0.26
<i>Fxyd5</i>	FXYD domain-containing ion transport regulator 5	0.691 ± 0.15	1.496 ± 0.19	1.455 ± 0.19	2.509 ± 0.38	1.541 ± 0.33
<i>Gm11487</i>	Predicted gene 11487	0.691 ± 0.56	0.690 ± 0.54	1.091 ± 0.59	1.300 ± 0.50	1.138 ± 0.40
<i>Ibsp</i>	Integrin binding sialoprotein	0.692 ± 0.26	0.739 ± 0.26	2.754 ± 0.84	1.205 ± 0.18	1.493 ± 0.25
<i>Bub1</i>	Budding uninhibited by benzimidazoles 1 homolog	0.692 ± 0.52	1.44 ± 0.29	0.369 ± 0.22	2.425 ± 0.3	2.342 ± 0.29
<i>D430020J02 Rik</i>	RIKEN cDNA D430020J02 gene	0.693 ± 0.30	1.046 ± 0.11	0.653 ± 0.12	1.250 ± 0.09	1.125 ± 0.14

<i>Gcnt4</i>	Glucosaminyl transferase 4, core 2	0.694 ± 0.36	2.182 ± 0.35	1.202 ± 0.44	1.781 ± 0.49	1.501 ± 0.32
<i>Gm17019</i>	Predicted gene 17019	0.694 ± 0.17	0.601 ± 0.30	1.058 ± 0.40	1.167 ± 0.48	1.416 ± 0.59
<i>Fam111a</i>	Family with sequence similarity 111, member A	0.695 ± 0.49	2.158 ± 0.38	0.688 ± 0.21	3.163 ± 0.35	3.350 ± 0.36
<i>Rhou</i>	Ras homolog gene family, member U	0.695 ± 0.32	1.136 ± 0.23	1.600 ± 0.22	0.993 ± 0.22	1.217 ± 0.31
<i>Shcbp1</i>	Shc SH2-domain binding protein 1	0.695 ± 0.62	1.338 ± 0.44	0.310 ± 0.12	2.813 ± 0.20	2.768 ± 0.28
<i>Cbl1</i>	Casitas B-lineage lymphoma-like 1	0.695 ± 0.19	1.045 ± 0.20	1.072 ± 0.16	0.948 ± 0.13	0.970 ± 0.09
<i>Lsm2</i>	LSM2 homolog, U6 small nuclear RNA associated	0.695 ± 0.40	1.247 ± 0.19	0.702 ± 0.31	1.038 ± 0.25	1.037 ± 0.15
<i>Tmem74</i>	Transmembrane protein 74	0.695 ± 0.13	2.854 ± 0.21	3.009 ± 0.29	2.863 ± 0.56	1.537 ± 0.40
<i>Cdc6</i>	Cell division cycle 6	0.696 ± 0.45	1.241 ± 0.23	0.637 ± 0.16	1.737 ± 0.32	1.928 ± 0.17
<i>Art2b</i>	ADP-ribosyltransferase 2b	0.697 ± 0.31	0.752 ± 0.23	1.140 ± 0.25	0.993 ± 0.52	1.054 ± 0.38
<i>Arhgap19</i>	Rho GTPase activating protein 19	0.698 ± 0.38	1.160 ± 0.27	0.690 ± 0.22	1.435 ± 0.21	1.424 ± 0.19
<i>Sorbs3</i>	Sorbin and SH3 domain containing 3	0.699 ± 0.29	0.751 ± 0.13	0.915 ± 0.07	1.002 ± 0.21	0.925 ± 0.24
<i>Hist1h2bk</i>	Histone cluster 1, H2bk	0.699 ± 0.44	1.123 ± 0.14	0.272 ± 0.53	2.002 ± 0.41	2.190 ± 0.57
<i>Gchfr</i>	GTP cyclohydrolase I feedback regulator	0.700 ± 0.16	1.447 ± 0.33	1.214 ± 0.30	1.314 ± 0.24	1.247 ± 0.25