

**Table i.** PCR Primers of genes selected for PCR validation.

Gene symbol	PCR primer	Product length
CH3L1	Forward: TGTTCCGAGGTCAGGAGGAT	108 bp
	Reverse: TGCCCATCACCAGCTTACTG	
NFAM1	Forward: CCTGAGTGTAGTGGGCACG	190 bp
	Reverse: ATCCTCATTCTCGATGCAGGC	
BARX2	Forward: TCTCCAAGGAGACCTGCGAT	136 bp
	Reverse: ATCACCGAGAGGAGCGGATA	
ATF3	Forward: GGAGTGCCTGCAGAAAGAGT	147 bp
	Reverse: CCATTCTGAGCCCGGACAAT	
WISP2	Forward: TGCCTCCTCTCAAAGGTGC	249 bp
	Reverse: GCTGTCGTCCTTGCCAAGA	
LEPR	Forward: ACAGCATCAGTGACATGTGGT	241 bp
	Reverse: AGGGTTGTCTCTGGCTTTTCG	
FAM83G	Forward: CCAAGACTGGCCCAAATGC	114 bp
	Reverse: GGCCTTTAGGTGCTTCGACT	
BMP3	Forward: CCTCATCGGAAGAGCCAGAC	207 bp
	Reverse: AGACTTTGGCATGGGGAAT	
ACE	Forward: TCTGGCAGAACTTCACGGAC	115 bp
	Reverse: TTGCTTAGCAGGGCGTTGTA	
GAS7	Forward: GGACCCTGTACCCCTTCTCC	176 bp
	Reverse: CATTCCAGGCTTCTCCAGCA	
CRLF1	Forward: ACTGCTCCAACCTCAGCTTC	133 bp
	Reverse: TATCTGGCAGGACCTCTCGC	
JUN	Forward: GAGCTGGAGCGCCTGATAAT	104 bp
	Reverse: CCCTCCTGCTCATCTGTCAC	
C3	Forward: CTGCCAGTTTCGAGGTCAT	196 bp
	Reverse: CAATCGGAATGCGCTTGAGG	
GALNT16	Forward: GCTGCCACCTCCACCTTAAT	126 bp

	Reverse: GAGGCCACTGACTGAATGCT	
C7	Forward: CTGTTCAGGTGGCATGTCCT	147 bp
	Reverse: TTCTCCCAGCGCTGACATTT	
ASPN	Forward: TTGAAGGGGTGACGGTGTTT	165 bp
	Reverse: GGCCCAGCCTTTGTAGTTCT	
PRELP	Forward: TTTGCCCAACGACCTAGTG	105 bp
	Reverse: TGGGCGGCTTCAAGTAGTTT	
EVX1	Forward: AGTACCAGCACAGCAAAGGG	150 bp
	Reverse: GGTAACGACGCATCTGGTCA	
ADAM12	Forward: ACGGTAATTCTGGGTCACTGT	232
	Reverse: CAGCGAGGTTTGGTGTGTTG	
ENST00000453554	Forward: TCTCAGTGTCGTCATCCG	121
	Reverse: AAGAAGGTGGGCTTATTGG	
NONHSAT005013.2	Forward: CTGGGTCCTGGGTGTTGTG	155
	Reverse: AGTGTAAGCGGGAGGAGGG	
MSTRG.138716.2	Forward: GGAAATGGGATGGATAGA	116
	Reverse: GGAATGACAGTAAGGGT	
MSTRG.99593.3	Forward: TGACAGCTTCAGTACAGGGC	124
	Reverse: CAGCCTTCTCCTCCTTGGTG	
ENST00000439539	Forward: TGGCCTGGCCTAACACCT	113
	Reverse: CCAAGCCCTTTCCTCCT	
ENST00000554988	Forward: CGTCATCAACCCGCTCCA	104
	Reverse: ACTCCCCTGTCCCTCACA	
NONHSAT123215.2	Forward: GAAAGTGGGAGGAAGAAC	126
	Reverse: CTGGACGACAGAGTGAGA	
MSTRG.44186.2	Forward: GGGCTGGCACACATAGAACT	137
	Reverse: GCAGTTTGTGGGAATGCTG	
NONHSAT044053.2	Forward: GCTTCCTACTTACCCTCCTT	123
	Reverse: CACTCGGTGGTCTTATTTG	
NONHSAT186094.1	Forward: TACTATCAGATGGAGGAAC	158
	Reverse: TTATTGTGACAGAAGGGT	

**Table ii.** Top 15 differential expressed mRNAs (normal vs OA).

Gene ID	Gene name	Regulation	Log <sub>2</sub> FC	p-value
ENSG00000217576	RP11-248G5.8	Up	8.164798	0.000332
ENSG00000267645	RP11-577H5.5	Up	7.344509	0.000826
ENSG00000255730	CTC-435M10.3	Up	5.791933	0.001951
ENSG00000143340	FAM163A	Up	5.728896	0.003071
ENSG00000136267	DGKB	Up	5.722004	0.004869
ENSG00000112218	GPR63	Up	5.203071	0.000999
ENSG00000137033	IL33	Up	4.970196	0.000585
ENSG00000095596	CYP26A1	Up	4.930212	0.006337
ENSG00000159167	STC1	Up	4.696848	0.0053
ENSG00000112175	BMP5	Up	4.679747	2.29E-05
ENSG00000228549	RP11-108M9.3	Up	4.67377	5.25E-05
ENSG00000248672	LY75-CD302	Up	4.593474	0.000724
ENSG00000280537	RP11-33O4.2	Up	4.413503	0.004464
ENSG00000170579	DLGAP1	Up	4.406405	3.93E-05
ENSG00000157103	SLC6A1	Up	4.361763	0.002072
ENSG00000259001	RPPH1	Down	-11.5428	0.000114
ENSG00000171564	FGB	Down	-6.34944	0.008213
ENSG00000258588	TRIM6-TRIM34	Down	-5.66762	0.001527
ENSG00000163631	ALB	Down	-5.56662	0.002397
ENSG00000260772	RP11-311C24.1	Down	-5.56335	1.61E-07
ENSG00000256837	CACNA1C-IT1	Down	-5.36579	0.008004
ENSG00000114638	UPK1B	Down	-5.25163	0.000496
ENSG00000040731	CDH10	Down	-5.17124	3.14E-06
ENSG00000258529	RP11-108O10.8	Down	-5.11656	0.008286
ENSG00000118271	TTR	Down	-5.04354	0.007127
ENSG00000273167	RP11-307N16.6	Down	-5.0401	0.001085
ENSG00000261832	RP11-435I10.4	Down	-4.8645	0.000719
ENSG00000241563	CORT	Down	-4.72312	0.009017
ENSG00000255835	RP4-559A3.7	Down	-4.57875	0.005028
ENSG00000183072	NKX2-5	Down	-4.44362	0.002477

**Table iii.** KEGG enrichment of up-regulated DEGs (normal vs OA).

Pathway ID	Description	Gene ratio	p-value	Count	Genes	Enrich factor
hsa04614	Renin-angiotensin system	2/98	6.426e-03	2	ACE AGTR2	7.08
hsa02010	ABC transporters	4/98	2.143e-03	4	ABCC9 ABCA1 ABCA6 ABCA4	5.47
hsa04610	Complement and coagulation cascades	6/98	4.703e-04	6	SERPING1 C4B VWF THBD C3 C4A	5.23
hsa04320	Dorso-ventral axis formation	2/98	1.846e-02	2	ETS1 ETV7	4.81
hsa04960	Aldosterone-regulated sodium reabsorption	3/98	1.229e-02	3	PIK3R1 PRKCB HSD11B1	4.30
hsa04270	Vascular smooth muscle contraction	8/98	4.865e-04	8	ADCY1 PTGIR CACNA1C RAMP3 MYH11 PRKCB GUCY1A3 MYLK	4.15
hsa05142	Chagas disease (American trypanosomiasis)	6/98	4.889e-03	6	ADCY1 MAPK11 PIK3R1 JUN ACE C3	3.47
hsa05211	Renal cell carcinoma	4/98	1.510e-02	4	PIK3R1 ETS1 JUN FIGF	3.44
hsa05143	African trypanosomiasis	2/98	4.467e-02	2	SELE PRKCB	3.44
hsa04640	Hematopoietic cell lineage	5/98	9.025e-03	5	KITLG CD8A KIT IL7 CD34	3.42
hsa04020	Calcium signaling pathway	10/98	7.181e-04	10	PDGFRB ADCY1 PDE1A PLN CACNA1C PHKG1 PTGER3 PRKCB MYLK ERBB4	3.40
hsa05218	Melanoma	4/98	1.598e-02	4	PDGFRB FGF7 PIK3R1 FGF13	3.39
hsa00565	Ether lipid metabolism	2/98	4.801e-02	2	PLPP3 LPCAT2	3.34
hsa05140	Leishmaniasis	4/98	1.785e-02	4	MAPK11 JUN C3 PRKCB	3.30
hsa05150	Staphylococcus aureus infection	3/98	3.218e-02	3	C4B C3 C4A	3.22
hsa04912	GnRH signaling pathway	5/98	1.707e-02	5	ADCY1 MAPK11 JUN CACNA1C PRKCB	2.98
hsa05210	Colorectal cancer	3/98	4.463e-02	3	PIK3R1 JUN DCC	2.91
hsa05219	Bladder cancer	2/98	7.075e-02	2	DAPK2 FIGF	2.86
hsa04350	TGF-beta signaling pathway	4/98	3.229e-02	4	PITX2 GDF7 ACVR1C BMP5	2.83
hsa05214	Glioma	3/98	5.181e-02	3	PDGFRB PIK3R1 PRKCB	2.78
hsa04012	ErbB signaling pathway	4/98	3.528e-02	4	PIK3R1 JUN PRKCB ERBB4	2.77
hsa04914	Progesterone-mediated oocyte maturation	4/98	3.528e-02	4	ADCY1 PDE3B MAPK11 PIK3R1	2.77
hsa04973	Carbohydrate digestion and absorption	2/98	7.935e-02	2	PIK3R1 PRKCB	2.73
hsa04540	Gap junction	4/98	4.009e-02	4	PDGFRB ADCY1 PRKCB GUCY1A3	2.67
hsa04514	Cell adhesion molecules (CAMs)	6/98	1.983e-02	6	NCAM2 CD8A HLA-E SELE NRXN2 CD34	2.65
hsa04975	Fat digestion and absorption	2/98	8.846e-02	2	PLPP3 ABCA1	2.61
hsa04720	Long-term potentiation	3/98	6.521e-02	3	ADCY1 CACNA1C PRKCB	2.58
hsa04330	Notch signaling pathway	2/98	9.319e-02	2	DTX4 JAG1	2.56
hsa04976	Bile secretion	3/98	6.811e-02	3	AQP4 ADCY1 EPHX1	2.54
hsa04666	Fc gamma R-mediated phagocytosis	4/98	4.901e-02	4	PIK3R1 PLPP3 PRKCB ARPC5	2.53
hsa04930	Type II diabetes mellitus	2/98	9.805e-02	2	PIK3R1 CACNA1C	2.51
hsa04060	Cytokine-cytokine receptor interaction	11/98	5.652e-03	11	PDGFRB NGFR KITLG IL19 CCL8 LEP KIT TNFSF13B IL7 PRL FIGF	2.50
hsa04971	Gastric acid secretion	3/98	7.726e-02	3	ADCY1 PRKCB MYLK	2.44
hsa04662	B cell receptor signaling pathway	3/98	8.045e-02	3	PIK3R1 JUN PRKCB	2.41

hsa00561	Glycerolipid metabolism	2/98	1.081e-01	2	PLPP3 DGKB	2.41
hsa04916	Melanogenesis	4/98	6.127e-02	4	KITLG ADCY1 KIT PRKCB	2.38
hsa04722	Neurotrophin signaling pathway	5/98	4.642e-02	5	NGFR NTRK3 MAPK11 PIK3R1 JUN	2.37
hsa04370	VEGF signaling pathway	3/98	8.372e-02	3	MAPK11 PIK3R1 PRKCB	2.37
hsa04620	Toll-like receptor signaling pathway	4/98	6.348e-02	4	MAPK11 PIK3R1 LBP JUN	2.36
hsa05144	Malaria	2/98	1.133e-01	2	ACKR1 SELE	2.36
hsa04150	mTOR signaling pathway	2/98	1.187e-01	2	PIK3R1 FIGF	2.31
hsa04070	Phosphatidylinositol signaling system	3/98	9.047e-02	3	PIK3R1 DGKB PRKCB	2.31
hsa04664	Fc epsilon RI signaling pathway	3/98	9.396e-02	3	MAPK11 PIK3R1 PRKCB	2.28
hsa00564	Glycerophospholipid metabolism	3/98	9.752e-02	3	PLPP3 LPCAT2 DGKB	2.26
hsa05223	Non-small cell lung cancer	2/98	1.297e-01	2	PIK3R1 PRKCB	2.23
hsa04660	T cell receptor signaling pathway	4/98	7.779e-02	4	CD8A MAPK11 PIK3R1 JUN	2.23
hsa04080	Neuroactive ligand-receptor interaction	10/98	1.776e-02	10	S1PR1 GABRE PTGER4 P2RY1 PTGIR LEP AGTR2 PTGER3 PRL PTGDR	2.21
hsa05200	Pathways in cancer	12/98	1.127e-02	12	PDGFRB DAPK2 KITLG FGF7 PIK3R1 ETS1 JUN KIT DCC PRKCB FGF13 FIGF	2.21
hsa00140	Steroid hormone biosynthesis	2/98	1.470e-01	2	HSD11B1 CYP19A1	2.11
hsa04510	Focal adhesion	7/98	4.750e-02	7	PDGFRB VWF PIK3R1 JUN PRKCB MYLK FIGF	2.11
hsa05221	Acute myeloid leukemia	2/98	1.530e-01	2	PIK3R1 KIT	2.07
hsa04970	Salivary secretion	3/98	1.328e-01	3	ADCY1 PRKCB GUCY1A3	2.03
hsa05414	Dilated cardiomyopathy	3/98	1.371e-01	3	ADCY1 PLN CACNA1C	2.00
hsa04310	Wnt signaling pathway	5/98	9.331e-02	5	SFRP2 SFRP1 DKK2 JUN PRKCB	1.99
hsa05323	Rheumatoid arthritis	3/98	1.459e-01	3	JUN TNFSF13B MMP3	1.96
hsa04630	Jak-STAT signaling pathway	5/98	1.032e-01	5	IL19 PIK3R1 LEP IL7 PRL	1.94
hsa05131	Shigellosis	2/98	1.781e-01	2	MAPK11 ARPC5	1.94
hsa04010	MAPK signaling pathway	8/98	8.796e-02	8	PDGFRB FGF7 MAPK11 RASGRF2 JUN CACNA1C PRKCB FGF13	1.80
hsa05120	Epithelial cell signaling in Helicobacter pylori infection	2/98	2.185e-01	2	MAPK11 JUN	1.77
hsa04730	Long-term depression	2/98	2.327e-01	2	PRKCB GUCY1A3	1.72
hsa05212	Pancreatic cancer	2/98	2.327e-01	2	PIK3R1 FIGF	1.72
hsa05146	Amoebiasis	3/98	2.146e-01	3	ADCY1 PIK3R1 PRKCB	1.70
hsa04810	Regulation of actin cytoskeleton	6/98	1.527e-01	6	PDGFRB FGF7 PIK3R1 FGF13 MYLK ARPC5	1.69
hsa05100	Bacterial invasion of epithelial cells	2/98	2.399e-01	2	PIK3R1 ARPC5	1.69
hsa05416	Viral myocarditis	2/98	2.472e-01	2	HLA-E MYH11	1.67
hsa04612	Antigen processing and presentation	2/98	2.925e-01	2	CD8A HLA-E	1.54
hsa04670	Leukocyte transendothelial migration	3/98	2.769e-01	3	MAPK11 PIK3R1 PRKCB	1.54
hsa00230	Purine metabolism	4/98	2.857e-01	4	ADCY1 PDE3B PDE1A GUCY1A3	1.49
hsa05410	Hypertrophic cardiomyopathy (HCM)	2/98	3.322e-01	2	CACNA1C ACE	1.45
hsa04380	Osteoclast differentiation	3/98	3.453e-01	3	MAPK11 PIK3R1 JUN	1.41
hsa05215	Prostate cancer	2/98	3.816e-01	2	PDGFRB PIK3R1	1.35
hsa05160	Hepatitis C	3/98	3.915e-01	3	MAPK11 PIK3R1 EIF2AK2	1.34

hsa04650	Natural killer cell mediated cytotoxicity	3/98	3.982e-01	3	HLA-E PIK3R1 PRKCB	1.33
hsa04910	Insulin signaling pathway	3/98	4.118e-01	3	PDE3B PIK3R1 PHKG1	1.31
hsa05322	Systemic lupus erythematosus	3/98	4.118e-01	3	C4B C3 C4A	1.31
hsa04062	Chemokine signaling pathway	4/98	4.343e-01	4	ADCY1 PIK3R1 CCL8 PRKCB	1.27
hsa04972	Pancreatic secretion	2/98	4.850e-01	2	ADCY1 PRKCB	1.19
hsa04145	Phagosome	3/98	5.390e-01	3	HLA-E COLEC12 C3	1.16

**Table iv.** Top 15 differentially expressed lncRNAs (normal vs OA).

LncRNA ID	Regulation	Type	Log <sub>2</sub> FC	p-value
ENST00000453554	Up	exonic_sense	8.576146	2.83E-06
NONHSAT005013.2	Up	exonic_sense	7.999183	1.20E-08
MSTRG.138716.2	Up	intronic_sense	7.301053	0.004792
MSTRG.99593.3	Up	intronic_sense	7.192839	0.001003
ENST00000439539	Up	exonic_antisense	7.126536	0.000296
NONHSAT170549.1	Up	exonic_sense	7.045598	0.000183
ENST00000415386	Up	exonic_sense	6.775349	0.001515
MSTRG.165172.5	Up	intronic_sense	6.727005	0.020503
ENST00000429315	Up	exonic_antisense	6.727005	0.020521
NONHSAT118916.2	Up	bidirectional	6.723426	0.001725
NONHSAT163508.1	Up	exonic_sense	6.422505	0.002738
NONHSAT092195.2	Up	exonic_sense	6.377123	0.017316
ENST00000614991	Up	exonic_antisense	6.119579	0.005753
NONHSAT005482.2	Up	exonic_sense	6.015161	9.09E-09
NONHSAT034483.2	Up	intergenic	5.956669	0.009964
ENST00000554988	Down	exonic_antisense	-11.5318	0.000657
NONHSAT123215.2	Down	intergenic	-7.29403	1.31E-06
MSTRG.44186.2	Down	intronic_sense	-6.85899	0.010778
NONHSAT044053.2	Down	bidirectional	-6.8399	0.002961
NONHSAT186094.1	Down	intergenic	-6.83028	0.005159
NONHSAT040991.2	Down	intergenic	-6.72244	0.000978
NONHSAT215766.1	Down	intergenic	-6.71797	0.00083
NONHSAT186173.1	Down	exonic_sense	-6.69692	0.005375
NONHSAT193823.1	Down	exonic_sense	-6.62357	0.000158
NONHSAT163340.1	Down	exonic_sense	-6.29626	0.000225
ENST00000470274	Down	exonic_sense	-6.2894	0.009197
ENST00000523205	Down	intergenic	-6.21582	0.00631
MSTRG.157948.2	Down	intronic_sense	-6.17621	0.039306
NONHSAT017779.2	Down	exonic_antisense	-6.15205	0.001396
ENST00000534866	Down	exonic_sense	-6.09055	0.023695

**Table v.** KEGG enrichment of target genes of up-regulated DEGs (normal vs OA).

Pathway	Description	Gene ratio	P-value	Count	Enrich factor
hsa00730	Thiamine metabolism	3/1205	1.142e-02	3	4.30
hsa00670	One carbon pool by folate	10/1205	2.029e-03	10	2.87
hsa00604	Glycosphingolipid biosynthesis - ganglio series	7/1205	1.118e-02	7	2.68
hsa00130	Ubiquinone and other terpenoid-quinone biosynthesis	5/1205	2.777e-02	5	2.61
hsa00603	Glycosphingolipid biosynthesis - globo series	6/1205	2.546e-02	6	2.46
hsa01040	Biosynthesis of unsaturated fatty acids	8/1205	4.384e-02	8	2.00
hsa04142	Lysosome	42/1205	6.629e-05	42	1.96
hsa04973	Carbohydrate digestion and absorption	15/1205	1.428e-02	15	1.91
hsa00750	Vitamin B6 metabolism	2/1205	1.783e-01	2	1.91
hsa00561	Glycerolipid metabolism	19/1205	9.748e-03	19	1.85
hsa00900	Terpenoid backbone biosynthesis	7/1205	8.460e-02	7	1.83
hsa04961	Endocrine and other factor-regulated calcium reabsorption	15/1205	2.086e-02	15	1.83
hsa01212	Fatty acid metabolism	15/1205	2.494e-02	15	1.79
hsa03440	Homologous recombination	9/1205	6.862e-02	9	1.78
hsa00310	Lysine degradation	16/1205	2.439e-02	16	1.77
hsa03060	Protein export	7/1205	1.043e-01	7	1.75
hsa04122	Sulfur relay system	3/1205	2.001e-01	3	1.72
hsa04920	Adipocytokine signaling pathway	21/1205	1.522e-02	21	1.72
hsa00072	Synthesis and degradation of ketone bodies	3/1205	2.001e-01	3	1.72
hsa01210	2-Oxocarboxylic acid metabolism	5/1205	1.614e-01	5	1.69
hsa00512	Mucin type O-Glycan biosynthesis	9/1205	9.901e-02	9	1.67



hsa04115	p53 signaling pathway	20/1205	2.468e-02	20	1.66
hsa05211	Renal cell carcinoma	19/1205	2.979e-02	19	1.65
hsa00460	Cyanoamino acid metabolism	2/1205	2.504e-01	2	1.64
hsa04931	Insulin resistance	31/1205	8.651e-03	31	1.63
hsa04918	Thyroid hormone synthesis	20/1205	3.262e-02	20	1.62
hsa04960	Aldosterone-regulated sodium reabsorption	11/1205	9.082e-02	11	1.62
hsa04911	Insulin secretion	24/1205	2.044e-02	24	1.62
hsa03020	RNA polymerase	9/1205	1.171e-01	9	1.61
hsa00511	Other glycan degradation	5/1205	1.978e-01	5	1.59
hsa04978	Mineral absorption	14/1205	7.753e-02	14	1.58
hsa04141	Protein processing in endoplasmic reticulum	46/1205	4.006e-03	46	1.56
hsa04971	Gastric acid secretion	20/1205	4.812e-02	20	1.55
hsa00520	Amino sugar and nucleotide sugar metabolism	13/1205	9.427e-02	13	1.55
hsa04664	Fc epsilon RI signaling pathway	18/1205	6.137e-02	18	1.54
hsa04260	Cardiac muscle contraction	21/1205	4.537e-02	21	1.54
hsa04150	mTOR signaling pathway	16/1205	7.861e-02	16	1.53
hsa00533	Glycosaminoglycan biosynthesis - keratan sulfate	4/1205	2.502e-01	4	1.53
hsa04213	Longevity regulating pathway - multiple species	17/1205	7.389e-02	17	1.52
hsa04261	Adrenergic signaling in cardiomyocytes	39/1205	1.251e-02	39	1.51
hsa04964	Proximal tubule bicarbonate reclamation	6/1205	2.245e-01	6	1.50
hsa04932	Non-alcoholic fatty liver disease (NAFLD)	39/1205	1.695e-02	39	1.48
hsa04611	Platelet activation	31/1205	3.748e-02	31	1.46
hsa04012	ErbB signaling pathway	22/1205	7.482e-02	22	1.45
hsa05032	Morphine addiction	23/1205	6.996e-02	23	1.45

hsa00564	Glycerophospholipid metabolism	24/1205	6.544e-02	24	1.45
hsa00340	Histidine metabolism	6/1205	2.627e-01	6	1.43
hsa00071	Fatty acid degradation	11/1205	1.811e-01	11	1.43
hsa00100	Steroid biosynthesis	5/1205	2.823e-01	5	1.43
hsa00380	Tryptophan metabolism	10/1205	1.950e-01	10	1.43
hsa04211	Longevity regulating pathway - mammal	23/1205	9.426e-02	23	1.40
hsa05210	Colorectal cancer	15/1205	1.679e-01	15	1.39
hsa04066	HIF-1 signaling pathway	25/1205	9.007e-02	25	1.39
hsa00051	Fructose and mannose metabolism	8/1205	2.583e-01	8	1.39
hsa03410	Base excision repair	8/1205	2.583e-01	8	1.39
hsa00592	alpha-Linolenic acid metabolism	6/1205	3.038e-01	6	1.38
hsa00030	Pentose phosphate pathway	7/1205	2.800e-01	7	1.38
hsa04666	Fc gamma R-mediated phagocytosis	22/1205	1.219e-01	22	1.37
hsa01200	Carbon metabolism	27/1205	9.370e-02	27	1.37
hsa04723	Retrograde endocannabinoid signaling	24/1205	1.156e-01	24	1.36
hsa05231	Choline metabolism in cancer	24/1205	1.156e-01	24	1.36
hsa04530	Tight junction	33/1205	7.359e-02	33	1.36
hsa00910	Nitrogen metabolism	4/1205	3.583e-01	4	1.35
hsa00450	Selenocompound metabolism	4/1205	3.583e-01	4	1.35
hsa04921	Oxytocin signaling pathway	37/1205	7.141e-02	37	1.34
hsa00020	Citrate cycle (TCA cycle)	7/1205	3.185e-01	7	1.34
hsa03013	RNA transport	40/1205	6.325e-02	40	1.34
hsa03040	Spliceosome	31/1205	1.069e-01	31	1.33
hsa05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	17/1205	2.114e-01	17	1.32
hsa03015	mRNA surveillance pathway	21/1205	1.706e-01	21	1.32

hsa00280	Valine, leucine and isoleucine degradation	11/1205	2.828e-01	11	1.31
hsa04210	Apoptosis	32/1205	1.160e-01	32	1.31
hsa00250	Alanine, aspartate and glutamate metabolism	8/1205	3.286e-01	8	1.31
hsa05016	Huntington,s disease	44/1205	7.497e-02	44	1.31
hsa05410	Hypertrophic cardiomyopathy (HCM)	19/1205	1.980e-01	19	1.31
hsa04930	Type II diabetes mellitus	11/1205	2.828e-01	11	1.31
hsa04710	Circadian rhythm	7/1205	3.593e-01	7	1.30
hsa00970	Aminoacyl-tRNA biosynthesis	10/1205	3.077e-01	10	1.30
hsa03050	Proteasome	10/1205	3.077e-01	10	1.30
hsa00410	beta-Alanine metabolism	7/1205	3.593e-01	7	1.30
hsa04725	Cholinergic synapse	25/1205	1.753e-01	25	1.29
hsa04966	Collecting duct acid secretion	6/1205	3.941e-01	6	1.28
hsa00565	Ether lipid metabolism	10/1205	3.402e-01	10	1.28
hsa00010	Glycolysis / Gluconeogenesis	15/1205	2.697e-01	15	1.28
hsa04925	Aldosterone synthesis and secretion	18/1205	2.518e-01	18	1.28
hsa05205	Proteoglycans in cancer	45/1205	1.039e-01	45	1.27
hsa04713	Circadian entrainment	21/1205	2.345e-01	21	1.27
hsa04913	Ovarian steroidogenesis	11/1205	3.431e-01	11	1.26
hsa04120	Ubiquitin mediated proteolysis	30/1205	1.885e-01	30	1.26
hsa05010	Alzheimer,s disease	37/1205	1.436e-01	37	1.26
hsa04152	AMPK signaling pathway	27/1205	2.169e-01	27	1.25
hsa04068	FoxO signaling pathway	29/1205	2.154e-01	29	1.24
hsa04722	Neurotrophin signaling pathway	26/1205	2.326e-01	26	1.24
hsa00650	Butanoate metabolism	6/1205	4.428e-01	6	1.23
hsa00630	Glyoxylate and dicarboxylate metabolism	6/1205	4.428e-01	6	1.23
hsa04750	Inflammatory mediator regulation of TRP channels	21/1205	2.909e-01	21	1.23

hsa04923	Regulation of lipolysis in adipocytes	12/1205	3.756e-01	12	1.23
hsa04919	Thyroid hormone signaling pathway	25/1205	2.839e-01	25	1.22
hsa04370	VEGF signaling pathway	13/1205	3.748e-01	13	1.22
hsa05414	Dilated cardiomyopathy	19/1205	3.149e-01	19	1.22
hsa04976	Bile secretion	15/1205	3.715e-01	15	1.21
hsa05221	Acute myeloid leukemia	12/1205	4.076e-01	12	1.21
hsa00531	Glycosaminoglycan degradation	4/1205	4.803e-01	4	1.21
hsa05012	Parkinson,s disease	30/1205	2.575e-01	30	1.21
hsa04024	cAMP signaling pathway	42/1205	1.984e-01	42	1.21
hsa04910	Insulin signaling pathway	29/1205	2.916e-01	29	1.20
hsa04270	Vascular smooth muscle contraction	25/1205	3.209e-01	25	1.20
hsa04912	GnRH signaling pathway	19/1205	3.607e-01	19	1.20
hsa04668	TNF signaling pathway	23/1205	3.268e-01	23	1.20
hsa05169	Epstein-Barr virus infection	42/1205	2.203e-01	42	1.20
hsa04390	Hippo signaling pathway	32/1205	2.834e-01	32	1.19
hsa03018	RNA degradation	16/1205	3.962e-01	16	1.19
hsa03460	Fanconi anemia pathway	11/1205	4.441e-01	11	1.19
hsa04510	Focal adhesion	42/1205	2.318e-01	42	1.19
hsa05120	Epithelial cell signaling in Helicobacter pylori infection	14/1205	4.330e-01	14	1.18
hsa04726	Serotonergic synapse	23/1205	3.686e-01	23	1.18
hsa04144	Endocytosis	53/1205	2.181e-01	53	1.18
hsa04130	SNARE interactions in vesicular transport	7/1205	4.937e-01	7	1.18
hsa04727	GABAergic synapse	18/1205	4.147e-01	18	1.17
hsa02010	ABC transporters	9/1205	4.889e-01	9	1.17
hsa00510	N-Glycan biosynthesis	10/1205	4.848e-01	10	1.17
hsa04010	MAPK signaling pathway	52/1205	2.410e-01	52	1.17
hsa04724	Glutamatergic synapse	23/1205	3.905e-01	23	1.17
hsa00190	Oxidative phosphorylation	27/1205	3.717e-01	27	1.16

hsa01230	Biosynthesis of amino acids	15/1205	4.585e-01	15	1.16
hsa04360	Axon guidance	35/1205	3.365e-01	35	1.16
hsa05142	Chagas disease (American trypanosomiasis)	21/1205	4.242e-01	21	1.16
hsa00240	Pyrimidine metabolism	21/1205	4.489e-01	21	1.15
hsa00220	Arginine biosynthesis	4/1205	5.451e-01	4	1.15
hsa00270	Cysteine and methionine metabolism	9/1205	5.306e-01	9	1.15
hsa00062	Fatty acid elongation	5/1205	5.473e-01	5	1.15
hsa05133	Pertussis	15/1205	4.893e-01	15	1.15
hsa04810	Regulation of actin cytoskeleton	43/1205	3.191e-01	43	1.15
hsa00052	Galactose metabolism	6/1205	5.457e-01	6	1.15
hsa04071	Sphingolipid signaling pathway	24/1205	4.301e-01	24	1.15
hsa00330	Arginine and proline metabolism	10/1205	5.241e-01	10	1.15
hsa00563	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	5/1205	5.473e-01	5	1.15
hsa00230	Purine metabolism	35/1205	3.699e-01	35	1.15
hsa04730	Long-term depression	12/1205	5.104e-01	12	1.15
hsa00920	Sulfur metabolism	2/1205	5.091e-01	2	1.15
hsa04922	Glucagon signaling pathway	20/1205	4.815e-01	20	1.14
hsa05161	Hepatitis B	29/1205	4.212e-01	29	1.14
hsa04933	AGE-RAGE signaling pathway in diabetic complications	20/1205	4.815e-01	20	1.14
hsa05014	Amyotrophic lateral sclerosis (ALS)	10/1205	5.644e-01	10	1.13
hsa04022	cGMP-PKG signaling pathway	33/1205	4.167e-01	33	1.13
hsa04550	Signaling pathways regulating pluripotency of stem cells	28/1205	4.484e-01	28	1.13
hsa05200	Pathways in cancer	78/1205	2.808e-01	78	1.13

hsa04670	Leukocyte transendothelial migration	23/1205	5.091e-01	23	1.12
hsa03420	Nucleotide excision repair	9/1205	5.734e-01	9	1.12
hsa05230	Central carbon metabolism in cancer	13/1205	5.730e-01	13	1.11
hsa01100	Metabolic pathways	240/1205	1.283e-01	240	1.11
hsa04146	Peroxisome	16/1205	5.751e-01	16	1.11
hsa04728	Dopaminergic synapse	25/1205	5.167e-01	25	1.11
hsa00601	Glycosphingolipid biosynthesis - lacto and neolacto series	5/1205	6.065e-01	5	1.10
hsa04915	Estrogen signaling pathway	19/1205	5.738e-01	19	1.10
hsa05213	Endometrial cancer	10/1205	6.056e-01	10	1.10
hsa05100	Bacterial invasion of epithelial cells	15/1205	5.860e-01	15	1.10
hsa04350	TGF-beta signaling pathway	16/1205	6.073e-01	16	1.09
hsa04721	Synaptic vesicle cycle	12/1205	6.212e-01	12	1.09
hsa04630	Jak-STAT signaling pathway	30/1205	5.642e-01	30	1.09
hsa04072	Phospholipase D signaling pathway	27/1205	5.946e-01	27	1.08
hsa04914	Progesterone-mediated oocyte maturation	18/1205	6.456e-01	18	1.08
hsa05160	Hepatitis C	25/1205	6.165e-01	25	1.08
hsa05222	Small cell lung cancer	16/1205	6.731e-01	16	1.07
hsa05145	Toxoplasmosis	22/1205	6.527e-01	22	1.07
hsa04070	Phosphatidylinositol signaling system	18/1205	7.084e-01	18	1.05
hsa04062	Chemokine signaling pathway	34/1205	7.019e-01	34	1.05
hsa00430	Taurine and hypotaurine metabolism	2/1205	6.027e-01	2	1.04
hsa04962	Vasopressin-regulated water reabsorption	8/1205	7.246e-01	8	1.04
hsa05212	Pancreatic cancer	12/1205	7.374e-01	12	1.04
hsa05162	Measles	24/1205	8.194e-01	24	1.02

hsa04610	Complement and coagulation cascades	14/1205	8.128e-01	14	1.02
hsa04621	NOD-like receptor signaling pathway	10/1205	8.196e-01	10	1.01
hsa04514	Cell adhesion molecules (CAMs)	25/1205	8.578e-01	25	1.01
hsa05203	Viral carcinogenesis	36/1205	8.800e-01	36	1.01
hsa04014	Ras signaling pathway	40/1205	8.661e-01	40	1.01

**Table vi.** Overlapping genes of DEGs and target genes of DELs.

Gene symbol	LncRNA ID	Related diseases or biological function	Up/down regulation
ABCC6	NONHSAT033428.2	Allogeneic tissue mineralization; Elastic pseudo-xanthoma	Down
ABCC9	NONHSAT102764.2	Allogeneic tissue mineralization; Elastic pseudo-xanthoma	Up
AC007192.4	NONHSAT157787.1	Unknown	Up
ACE	NONHSAT118916.2	Osteoarthritis; angiogenesis	Up
ACTC1	NONHSAT155839.1	Mesoderm differentiation; Myocardium	Down
ADAM12	NONHSAT016936.2	Osteoarthritis	Down
ADAMTS6	ENST00000504507	Bone marrow; Tumor	Down
ADCY1	NONHSAT160399.1	Hair cell function and hearing	Up
ADGRG2	NONHSAT170496.1	Tumor, cell adhesion and migration	Down
ADGRV1	NONHSAT185433.1	Tumor, cell adhesion and migration	Down
ALPK2	MSTRG.67144.1	Down-regulated by oncogenic KRAS	Down
ANK3	ENST00000470274	Two-way affective disorder	Down
APBB2	NONHSAT027475.2	Alzheimer	Up
APOL6	NONHSAT208573.1	Atherosclerosis	Up
ARL2-SNX15	ENST00000554194	Unknown	Up
ARPC5	NONHSAT186173.1	Neoplasms; Neointimal smooth muscle cells; Frontal cortex	Up
ASPN	NONHSAT221014.1	Osteoarthritis	Down
ATF3	NONHSAT009385.2	Osteoarthritis; Osteoclasts; Bone formation	Up



ATP5S	NONHSAT186 173.1	hepatic carcinoma	Up
BARX2	NONHSAT169 400.1	Cartilage formation; Tumor	Down
BCAR3	NONHSAT220 387.1	Tumor	Up
BEST1	NONHSAT108 610.2	Autosomal lesion	Up
BMP3	ENST00000554 369	Cartilage repair, bone formation	Up
BORCS7- ASMT	NONHSAT186 094.1	Schizophrenia	Up
BVES	NONHSAT170 496.1	Myocardium; Tumor	Down
C3	ENST00000554 614	Osteoarthritis	Up
C6orf223	ENST00000422 059	Unknown	Down
C7	NONHSAT040 991.2	Heterotopic ossification	Up
CACNA1C	ENST00000542 984	Myocardium	Up
CACNG8	ENST00000615 045	Myocardium	Down
CASC10	MSTRG.10632 1.4	Unknown	Up
CCDC64B	NONHSAT118 916.2	Unknown	Down
CD180	ENST00000554 614	Rheumatoid disease	Down
CD34	NONHSAT170 496.1	Rheumatoid disease	Up
CDC42EP3	NONHSAT035 511.2	Cancer-associated fibroblast	Up
CDC42SE2	NONHSAT025 082.2	Cancer-associated fibroblast	Up
CDH11	NONHSAT142 967.2	Osteosarcoma	Up
CDON	ENST00000582 823	Cardiac remodeling	Down

CHI3L1	NONHSAT179 467.1	Osteoarthritis	Up
CHN2	NONHSAT084 703.2	Axonal guidance	Up
CHRDL2	NONHSAT160 508.1	BMP antagonist; Tumor	Up
CNNM1	NONHSAT160 399.1	Stem cells; cell cycle; differentiation	Down
COL3A1	NONHSAT183 286.1	Ehlers-Danlos Syndrome	Down
COLEC12	NONHSAT044 053.2	Diabetes	Up
CTD- 2192J16.20	NONHSAT170 496.1	Unknown	Down
DAPK2	NONHSAT040 991.2	Apoptotic factor; Tumour	Up
DAW1	NONHSAT183 681.1	Freezing tolerance	Down
DGKB	NONHSAT044 053.2	Glucose metabolism	Up
DIO3	ENST00000554 735	Tumor	Up
DLGAP1	NONHSAT192 222.1	Schizophrenia	Up
DNAJC22	NONHSAT066 036.2	Unknown	Down
DRAM1	ENST00000470 274	Autophagy	Up
DSC3	NONHSAT186 094.1	Cadherin gene; Prostate	Down
DSG2	NONHSAT202 728.1	Adhesion	Down
DSP	NONHSAT015 141.2	BMP 1related	Down
DTNA	ENST00000613 388	Multiple congenital defects	Up
EIF2AK2	NONHSAT044 053.2	Inflammation; Autophagy	Up
ELL2	MSTRG.12825 2.2	Tumor	Up

ENOX1	NONHSAT166 682.1	Tumor	Down
ERBB3	ENST00000631 276	Tumor; Osteosarcoma	Down
ESPNP	ENST00000414 828	Unknown	Down
EVX1	ENST00000519 050	Joint formation	Up
FAM132B	NONHSAT034 217.2	Aplastic anemia	Down
FAM217B	NONHSAT122 067.2	Unknown	Up
FAM46C	NONHSAT152 168.1	Tumor	Up
FAM83G	NONHSAT073 110.2	type I BMP	Down
FBLIM1	NONHSAT044 053.2	osteomyelitis	Up
FBLN7	NONHSAT180 247.1	Congenital heart disease	Up
FER1L5	NONHSAT182 197.1	Mediate myoblast fusion	Up
FGD4	NONHSAT159 123.1	Tumor	Up
FGF13	NONHSAT093 248.2	Tumor	Up
FN1	NONHSAT169 400.1	Tumor	Down
FSIP2	NONHSAT070 821.2	Unknown	Up
GALNT16	NONHSAT044 053.2	TGF-beta/BMP signaling	Down
GAPDHP71	NONHSAT203 623.1	Unknown	Down
GAS7	NONHSAT034 217.2	Osteogenic differentiation	Up
GINS3	NONHSAT169 400.1	Myocardium	Down
GIPR	NONHSAT075 369.2	Neuroendocrine tumor	Down

GNS	NONHSAT016 733.2	Saint Philippe syndrome type D	Up
GPAA1P1	NONHSAT073 162.2	Unknown	Down
GUCY1A3	ENST00000569 449	Coronary heart disease; Glioma	Up
HERC6	ENST00000550 290	Seminal pouch	Up
HHIPL1	ENST00000529 392	Unknown	Down
HLA-E	NONHSAT108 552.2	Tumor	Up
HSD17B13	NONHSAT186 173.1	Unknown	Up
HYPK	NONHSAT204 114.1	Autophagy	Up
IL11	ENST00000444 184	Leukemia and lymphoma	Down
ISLR2	NONHSAT016 408.2	Unknown	Down
JUN	NONHSAT149 025.1	Osteoarthritis	Up
KCNC1	NONHSAT160 123.1	Potassium channel protein	Down
KCNJ6	MSTRG.9596.3	Hyperkinetic Movement Disorder	Down
KLHL23	NONHSAT075 369.2	Gastric cancer	Up
L3MBTL4	ENST00000623 938	Hypertension; Breast cancer	Up
LEP	NONHSAT039 419.2	Tumor	Up
LEPR	NONHSAT219 548.1	Osteoarthritis	Up
LIN7A	NONHSAT029 682.2	Cerebral cortex	Up
LPCAT2	NONHSAT017 313.2	Prostate cancer	Up
LPO	NONHSAT066 036.2	Oxidation	Down
LRRIQ1	ENST00000560 351	Unknown	Down

LYL1	NONHSAT028 689.2	Transcription factor	Up
MAGIX	NONHSAT044 053.2	Unknown	Up
MGAT4A	ENST00000560 351	Diabetes	Up
MYH11	NONHSAT047 895.2	Leukemia	Up
MYLK	NONHSAT135 075.2	Tumor	Up
MYLK4	ENST00000470 274	Tumor	Up
NFAM1	NONHSAT215 706.1	Osteoclast formation and bone resorption	Up
NTRK3	NONHSAT180 557.1	Tumor	Up
PALM	NONHSAT028 689.2	Tumor	Up
PAWR	NONHSAT123 215.2	prostate cancer; Schizophrenia	Up
PCDH11X	NONHSAT044 053.2	Alzheimer	Down
PCDH9	NONHSAT170 496.1	Gliomas	Up
PDE3B	NONHSAT123 178.2	Adipose tissue	Up
PDE4C	NONHSAT180 247.1	Gliomas	Down
PDLIM3	NONHSAT087 257.2	Heart disease	Down
PFKFB4	NONHSAT195 727.1	Tumor	Down
PHKG1	NONHSAT192 222.1	Muscle	Up
PLA2G16	NONHSAT196 540.1	Osteosarcoma	Up
PLPP3	MSTRG.5006.2	Nerve	Up
POC1B- GALNT4	ENST00000560 351	Unknown	Down
POPDC3	ENST00000369 122	Gastric cancer	Down

POU5F1B	NONHSAT040 991.2	Gastric cancer	Up
PRELP	MSTRG.48927. 2	Osteoclasts, osteoblasts, cartilage	Down
PRRG4	NONHSAT183 160.1	commissureless axon guidance gene; Tumor	Down
PTGIR	NONHSAT026 320.2	Endometrium	Up
RASGRF2	NONHSAT202 812.1	Neuron	Up
RASSF8	ENST00000631 276	Tumor	Up
RASSF9	NONHSAT170 496.1	Epidermis	Up
RNF152	NONHSAT059 613.2	Apoptosis	Down
RP11- 235E17.2	NONHSAT180 247.1	Unknown	Down
RP11- 577H5.5	NONHSAT128 168.2	Unknown	Up
SBSPON	NONHSAT155 394.1	Unknown	Down
SCUBE3	NONHSAT040 991.2	Tumor	Up
SDCBP2	NONHSAT188 349.1	Unknown	Up
SLC16A10	NONHSAT123 215.2	Unknown	Down
SLC22A3	NONHSAT115 901.2	Tumor	Up
SLC26A4	ENST00000560 351	Pendred syndrome	Up
SLC47A1	MSTRG.15794 8.2	Diabetes; organic cation transporter 3	Down
SLC7A11	ENST00000550 290	Diabetes; organic cation transporter 3	Down
SORT1	NONHSAT101 044.2	Heart disease	Down
SOX13	NONHSAT123 178.2	Diabetes	Up

STAC2	NONHSAT180 247.1	Root neuron	Up
STEAP4	NONHSAT121 869.2	Rheumatoid Arthritis	Up
STK26	MSTRG.17485 5.1	Unknown	Up
SULT1C2	NONHSAT039 419.2	Unknown	Up
SYNE3	NONHSAT105 836.2	Unknown	Up
TAGLN	NONHSAT024 386.2	Tumor	Up
TF	NONHSAT189 610.1	Control the level of free iron	Down
TMEM105	NONHSAT171 020.1	Unknown	Down
TMEM107	NONHSAT123 178.2	Unknown	Up
TPSB2	ENST00000515 466	Unknown	Up
TRIM29	MSTRG.31035. 1	Tumor	Down
UNC13C	NONHSAT123 215.2	Unknown	Up
UPK1B	NONHSAT172 567.1	Urethra	Down
USP2	ENST00000498 979	Tumor	Down
VGLL3	NONHSAT160 497.1	Transcription factor; Tumor	Up
VIT	NONHSAT070 090.2	Unknown	Up
VWA7	NONHSAT196 540.1	Unknown	Down
WDR62	NONHSAT160 399.1	Nerve	Down
WDR74	NONHSAT196 540.1	Unknown	Up
WISP2	NONHSAT188 800.1	Rheumatoid arthritic; cartilage	Up

ZDHHC14	ENST00000529 392	Tumor	Up
ZNF155	ENST00000592 946	Unknown	Up
ZNF546	NONHSAT108 739.2	Unknown	Up
ZNF548	NONHSAT039 675.2	Unknown	Up
ZNRF3	NONHSAT016 733.2	Tumor	Up



**Table vii.** KEGG enrichment of overlapping collection of up-regulated DEGs and target genes of DELs (normal vs OA).

Pathway	Description	Gene ratio	p-value	Count	genes	Enrich factor
hsa00565	Ether lipid metabolism	3/37	2.93E-04	3	ENSG00000087253 ENSG00000162407 ENSG00000176485	12.46
hsa04924	Renin secretion	4/37	8.32E-05	4	ENSG00000159640 ENSG00000164116 ENSG00000152270 ENSG00000151067	11.68
hsa04923	Regulation of lipolysis in adipocytes	3/37	6.66E-04	3	ENSG00000176485 ENSG00000164742 ENSG00000152270	10.01
hsa04270	Vascular smooth muscle contraction	6/37	1.85E-05	6	ENSG00000145949 ENSG00000160013 ENSG00000164742 ENSG00000164116 ENSG00000151067 ENSG00000065534	9.34
hsa00564	Glycerophospholipid metabolism	4/37	5.13E-04	4	ENSG00000087253 ENSG00000162407 ENSG00000176485 ENSG00000136267	7.87
hsa04611	Platelet activation	5/37	1.91E-04	5	ENSG00000145949 ENSG00000160013 ENSG00000164742 ENSG00000164116 ENSG00000065534	7.66
hsa04971	Gastric acid secretion	3/37	1.86E-03	3	ENSG00000145949 ENSG00000164742 ENSG00000065534	7.58
hsa05231	Choline metabolism in cancer	4/37	6.75E-04	4	ENSG00000162407 ENSG00000136267 ENSG00000177606 ENSG00000146477	7.4
hsa05142	Chagas disease (American trypanosomiasis)	4/37	7.70E-04	4	ENSG00000125730 ENSG00000159640 ENSG00000164742 ENSG00000177606	7.19
hsa04921	Oxytocin signaling pathway	6/37	1.03E-04	6	ENSG00000145949 ENSG00000164742 ENSG00000164116 ENSG00000151067 ENSG00000065534 ENSG00000177606	7.1
a04022	cGMP-PKG signaling pathway	6/37	1.45E-04	6	ENSG00000145949 ENSG00000164742 ENSG00000164116 ENSG00000152270 ENSG00000151067 ENSG00000065534	6.71
hsa00561	Glycerolipid metabolism	2/37	9.48E-03	2	ENSG00000162407 ENSG00000136267	6.33

hsa04912	GnRH signaling pathway	3/37	3.93E-03	3	ENSG00000164742 ENSG00000151067 ENSG00000177606	6.16
hsa04713	Circadian entrainment	3/37	4.58E-03	3	ENSG00000164742 ENSG00000164116 ENSG00000151067	5.9
hsa04720	Long-term potentiation	2/37	1.29E-02	2	ENSG00000164742 ENSG00000151067	5.66
hsa05031	Amphetamine addiction	2/37	1.34E-02	2	ENSG00000151067 ENSG00000177606	5.58
hsa04920	Adipocytokine signaling pathway	2/37	1.51E-02	2	ENSG00000174697 ENSG00000116678	5.34
hsa04918	Thyroid hormone synthesis	2/37	1.57E-02	2	ENSG00000164742 ENSG00000091137	5.26
hsa04020	Calcium signaling pathway	5/37	1.41E-03	5	ENSG00000145949 ENSG00000164742 ENSG00000151067 ENSG00000065534 ENSG00000164776	5.22
hsa05140	Leishmaniasis	2/37	1.63E-02	2	ENSG00000125730 ENSG00000177606	5.19
133	Pertussis	2/37	1.82E-02	2	ENSG00000125730 ENSG00000177606	4.98
hsa04724	Glutamatergic synapse	3/37	8.43E-03	3	ENSG00000164742 ENSG00000170579 ENSG00000151067	4.96
hsa04610	Complement and coagulation cascades	2/37	2.09E-02	2	ENSG00000125730 ENSG00000112936	4.73
hsa04925	Aldosterone synthesis and secretion	2/37	2.23E-02	2	ENSG00000164742 ENSG00000151067	4.61
hsa05410	Hypertrophic cardiomyopathy (HCM)	2/37	2.38E-02	2	ENSG00000159640 ENSG00000151067	4.5
hsa04911	Insulin secretion	2/37	2.53E-02	2	ENSG00000164742 ENSG00000151067	4.4
hsa05132	Salmonella infection	2/37	2.61E-02	2	ENSG00000162704 ENSG00000177606	4.35
hsa04727	GABAergic synapse	2/37	2.77E-02	2	ENSG00000164742 ENSG00000151067	4.25
hsa04540	Gap junction	2/37	2.77E-02	2	ENSG00000164742 ENSG00000164116	4.25
hsa04970	Salivary secretion	2/37	2.86E-02	2	ENSG00000164742 ENSG00000164116	4.2
hsa05414	Dilated cardiomyopathy	2/37	2.86E-02	2	ENSG00000164742 ENSG00000151067	4.2
hsa05032	Morphine addiction	2/37	3.03E-02	2	ENSG00000164742 ENSG00000152270	4.11
hsa04666	Fc gamma R-mediated phagocytosis	2/37	3.12E-02	2	ENSG00000162704 ENSG00000162407	4.06

hsa04072	Phospholipase D signaling pathway	3/37	1.88E-02	3	ENSG00000162407 ENSG00000164742 ENSG00000136267	3.92
hsa04914	Progesterone-mediated oocyte maturation	2/37	3.48E-02	2	ENSG00000164742 ENSG00000152270	3.89
hsa04915	Estrogen signaling pathway	2/37	3.77E-02	2	ENSG00000164742 ENSG00000177606	3.78
hsa04024	cAMP signaling pathway	4/37	1.23E-02	4	ENSG00000164742 ENSG00000152270 ENSG00000151067 ENSG00000177606	3.76
hsa04932	Non-alcoholic fatty liver disease (NAFLD)	3/37	2.25E-02	3	ENSG00000174697 ENSG00000116678 ENSG00000177606	3.71
hsa04723	Retrograde endocannabinoid signaling	2/37	3.97E-02	2	ENSG00000164742 ENSG00000151067	3.7
hsa04922	Glucagon signaling pathway	2/37	3.97E-02	2	ENSG00000152270 ENSG00000164776	3.7
hsa04810	Regulation of actin cytoskeleton	4/37	1.65E-02	4	ENSG00000162704 ENSG00000145949 ENSG00000129682 ENSG00000065534	3.49
hsa04725	Cholinergic synapse	2/37	5.05E-02	2	ENSG00000164742 ENSG00000151067	3.37
hsa00230	Purine metabolism	3/37	3.64E-02	3	ENSG00000164742 ENSG00000164116 ENSG00000152270	3.2
hsa04722	Neurotrophin signaling pathway	2/37	6.14E-02	2	ENSG00000140538 ENSG00000177606	3.11
hsa05168	Herpes simplex infection	3/37	4.34E-02	3	ENSG00000125730 ENSG00000055332 ENSG00000177606	3.03
hsa04152	AMPK signaling pathway	2/37	6.66E-02	2	ENSG00000174697 ENSG00000116678	3.01
hsa04010	MAPK signaling pathway	4/37	3.24E-02	4	ENSG00000129682 ENSG00000151067 ENSG00000113319 ENSG00000177606	2.93
hsa05322	Systemic lupus erythematosus	2/37	8.06E-02	2	ENSG00000125730 ENSG00000112936	2.79
hsa04510	Focal adhesion	3/37	5.71E-02	3	ENSG00000145949 ENSG00000065534 ENSG00000177606	2.78
hsa05203	Viral carcinogenesis	3/37	5.98E-02	3	ENSG00000125730 ENSG00000055332 ENSG00000177606	2.73
hsa04910	Insulin signaling pathway	2/37	8.81E-02	2	ENSG00000152270 ENSG00000164776	2.69

hsa04261	Adrenergic signaling in cardiomyocytes	2/37	1.02E-01	2	ENSG00000164742 ENSG00000151067	2.53
hsa04014	Ras signaling pathway	3/37	8.14E-02	3	ENSG00000176485 ENSG00000129682 ENSG00000113319	2.47
hsa04145	Phagosome	2/37	1.11E-01	2	ENSG00000125730 ENSG00000158270	2.44
hsa04630	Jak-STAT signaling pathway	2/37	1.20E-01	2	ENSG00000174697 ENSG00000116678	2.37
hsa05166	HTLV-I infection	3/37	1.18E-01	3	ENSG00000162772 ENSG00000164742 ENSG00000177606	2.17
hsa05164	Influenza A	2/37	1.51E-01	2	ENSG00000055332 ENSG00000177606	2.14
hsa04080	Neuroactive ligand-receptor interaction	3/37	1.44E-01	3	ENSG00000174697 ENSG00000160013 ENSG00000116678	2.02
hsa05200	Pathways in cancer	4/37	1.52E-01	4	ENSG00000164742 ENSG00000129682 ENSG00000035664 ENSG00000177606	1.88
hsa05169	Epstein-Barr virus infection	2/37	2.06E-01	2	ENSG00000055332 ENSG00000177606	1.86

**Table viii.** Top 15 differentially expressed circRNAs (normal vs OA).

circRNA ID	Regulation	Known circRNA	p-value	Parental gene
circRNA.43	down	Has-circ-0000205	0.021737	WDR37
circRNA.576	down	-	0.026975	ATM
circRNA.934 1	down	-	0.028434	PSD3
circRNA.428 0	down	hsa_circ_0016733	0.041776	CDC42BPA
circRNA.177 8	UP	hsa_circ_0002571	0.012132	SNHG23
circRNA.374 8	UP	hsa_circ_0000107	0.012736	ST7L
circRNA.795 6	UP	hsa_circ_0001633	0.013079	SOBP
circRNA.125 7	UP	hsa_circ_0004815	0.013892	PPHLN1
circRNA.892 5	UP	hsa_circ_0007567	0.014349	BBS9
circRNA.720 4	UP	hsa_circ_0069562	0.01675	APBB2
circRNA.481 6	UP	hsa_circ_0004994	0.018501	UQCC1
circRNA.358 2	UP	hsa_circ_0000907	0.021572	MYO9B
circRNA.347 9	UP	hsa_circ_0007528	0.022567	PIGN
circRNA.185 8	UP	hsa_circ_0031584	0.023514	ARHGAP5
circRNA.452 2	UP	-	0.024542	ZCCHC11
circRNA.791 9	UP	-	0.024762	RHOBTB3
circRNA.339 7	UP	-	0.02593	ELP2

circRNA.633 5	UP	hsa_circ_0067582	0.02724	RASA2
circRNA.490 3	UP	hsa_circ_0006458	0.029916	TCFL5
circRNA.339 6	UP	hsa_circ_0000842	0.029958	RPRD1A