Supplementary Material

Table i. Differentially expressed long non-coding RNAs

Group	Genes	logFC	FDR
Up-regulated	LINC00654	1.72	1.47E-11
	ISM1-AS1	2.61	3.52E-10
	FAM225A	2.72	2.13E-07
	LNX1-AS1	2.48	3.85E-07
	SLC8A1-AS1	3.14	4.81E-06
	MIR31HG	2.15	2.65E-05
	MAGI2-AS2	2.88	0.000114017
	CELF2-AS2	1.94	0.000114017
	LINC00839	2.57	0.000193969
	ABCC5-AS1	3.15	0.000461161
	AC091057.1	2.56	0.001449837
	PART1	1.86	0.001454048
	STAU2-AS1	2.27	0.002128781
	TMLHE-AS1	1.84	0.003343697
	LINC00536	2.87	0.00414953
	ZFHX4-AS1	2.67	0.004160348
	APCDD1L-DT	1.72	0.005121319
	LINC00710	1.56	0.01357933
	LINC01545	2.41	0.01378791
	LINC00622	2.56	0.021008114
	ZBED3-AS1	1.66	0.038730176
Down-regulated	AL360012.1	-2.74	1.81E-13
	Z93241.1	-2.73	3.40E-12
	ILF3-DT	-1.56	3.52E-10
	MATN1-AS1	-2.52	1.41E-09
	MIR210HG	-1.66	4.72E-08
	SMG7-AS1	-2.09	1.36E-07
	AFDN-DT	-2.20	2.13E-07
	PROSER2-AS1	-1.62	2.49E-07
	LINC00167	-1.82	3.19E-07
	TOB1-AS1	-2.27	1.41E-06
	LGALS8-AS1	-3.02	2.94E-06
	RNF157-AS1	-3.59	2.11E-05
	LINC00309	-3.81	2.49E-05
	LINC01558	-3.12	3.05E-05
	ALDH1L1-AS2	-2.27	7.63E-05
	AC020916.1	-2.63	0.000114017
	PRKAG2-AS1	-1.81	0.000218044
	COL4A2-AS1	-4.18	0.000378937
	TBC1D3P1-DHX40P1	-3.65	0.001017107
	LINC00313	-2.30	0.001189683
	LINC01554	-2.97	0.001778482
	ENO1-AS1	-2.41	0.002721741
	LINC00311	-1.53	0.0031138
	LINC00051	-2.59	0.01378791
	HCP5	-1.71	0.015321904
	LINC00323	-2.64	0.017775418
	SYNJ2-IT1	-1.72	0.037369971
	LINC00461	-2.17	0.039452646

FC, fold change; FDR, false discovery rate.

Table ii. Significantly enriched gene ontology terms

Category	Number	Term	Count	FDR	Genes
BP	GO:0030198	Extracellular matrix organization	24	1.08E-07	*ICAM1, ELF3, TNC, COL3A1, ELN, CCDC80, COL2A1, POSTN, ITGB2, NFKB2, SPARC, ITGA4, SOX9, COL5A2, ITGAM, COL5A1, SMOC2, COL6A3, TGFBI, COL1A2, BCL3, COL1A1, COL8A1, FN1*
BP	GO:0030574	Collagen catabolic process	11	0.0021	*ADAMTS14, COL3A1, COL6A3, COL1A2, COL2A1, COL1A1, COL8A1, ADAMTS2, MMP13, COL5A2, COL5A1*
BP	GO:0030199	Collagen fibril organization	9	0.003	*ADAMTS14, COL3A1, COL1A2, COL2A1, COL1A1, ADAMTS2, COL5A2, COL5A1, DPT*
BP	GO:003409	Response to cytokine	10	0.003	*FOS, JUN, CD274, COL3A1, JUND, RARA, NFKB2, IL6R, SPARC, JUNB*
BP	GO:0045892	Negative regulation of transcription, DNA-templated	30	0.004	*WNT5A, HMGB2, ELF3, SPI1, SOX9, PRDM16, BCL3, PER1, BCL6, RARA, BHLHE40, LOXL3, ATOH8, BCL7A, BHLHE41, BCOR, PITX1, CEBPB, CEBPD, KLF10, KLF11, CENPF, BASP1, HMGA2, DDIT3, HES1, CDKN1B, JUN, IRF1, KLF4*
BP	GO:1901653	Cellular response to peptide	6	0.004	*KLF5, KLF10, KLF11, KLF15, KLF2, KLF4*
BP	GO:0045944	Positive regulation of transcription from RNA polymerase II promoter	46	0.004	*WNT5A, HMGB2, FOSL2, ELF3, ARNT2, SPI1, NFKBIA, NFKB2, SOX9, FOS, NOD2, JUND, BCL3, PER1, ZC3H12A, KDM3A, RARA, ARNTL2, TOP2A, PITX1, SERTAD1, EGR1, KLF5, MAFF, CEBPB, CEBPD, SOX11, NR4A2, CCNL1, KLF15, FOSB, NR4A3, FZD5, HMGA2, JUNB, DDIT3, HES1, ATF3, JUN, CSRNP1, ETS2, VEGFA, IRF1, UBC, KLF2, KLF4*
BP	GO:0042493	Response to drug	22	0.007	*ICAM1, CDK1, HMGB2, PTGS2, GRIN2A, CENPF, FOSB, AQP1, PNP, JUNB, SOD2, FOS, CDKN1A, CYBB, CCND1, CDKN1B, APOD, JUN, JUND, TGIF1, SEMA3C, COL1A1*
BP	GO:0000122	Negative regulation of transcription from RNA polymerase II promoter	36	0.017	*FRK, EFNA1, SPI1, NFKB2, PRDM16, JUND, PER1, BCL6, RARA, BHLHE40, BHLHE41, NFIL3, BCOR, EGR1, ZFP36, KLF5, HIST1H1E, KLF10, SOX11, KLF11, NR4A2, FOSB, NR4A3, HMGA2, JUNB, DDIT3, HES1, CCND1, PLK3, ATF3, BTG2, ETS2, VEGFA, UBC, TGIF1, KLF4*
BP	GO:0045893	Positive regulation of transcription, DNA-templated	29	0.019	*WNT5A, HMGB2, ELF3, HOXA11, ARNT2, SPI1, RORC, SOX9, PRDM16, IL31RA, FOS, BCL3, KDM3A, RARA, ARNTL2, ATOH8, ING1, EGR1, KLF5, SOX11, PIM2, HMGA2, DDIT3, JUN, ETS2, IRF1, COL1A1, KLF2, KLF4*
BP	GO:0007155	Cell adhesion	27	0.019	*MYBPC2, CCR1, TNC, ITGB2, POSTN, SPOCK1, CDH2, ITGAM, FAP, COL6A3, TGFBI, RHOB, COL8A1, THBS2, THBS3, FN1, DPT, ICAM1, ASTL, ITGA4, COL5A1, THY1, HES1, STAB1, COL1A1, ADAM12, THEMIS2*
MF	GO:0001077	Transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	22	6.53E-05	*KLF5, EGR1, CEBPB, ELF3, CEBPD, SOX11, ARNT2, NR4A2, SPI1, NFKB2, NR4A3, FOSB, KLF15, HMGA2, SOX9, JUNB, DDIT3, FOS, JUN, IRF1, PITX1, KLF4*
MF	GO:0003700	Transcription factor activity, sequence-specific DNA binding	46	0.001	*WNT5A, HMGB2, FOSL2, ELF3, ARNT2, SCML1, SPI1, RORC, NFKB2, SOX9, ZKSCAN4, FOS, JUND, BCL3, BCL6, RARA, KDM3A, BHLHE40, ARNTL2, ATOH8, NFIL3, PITX1, ELMSAN1, RFX8, EGR1, KLF5, MAFF, L3MBTL4, CEBPB, KLF9, CEBPD, KLF10, SOX11, KLF11, FOSB, DDIT3, HES1, ATF3, JUN, CSRNP1, ETS2, IRF1, TGIF1, ST18, KLF2, KLF4*
MF	GO:0000978	RNA polymerase II core promoter proximal region sequence-specific DNA binding	25	0.001	*KLF5, RFX8, CEBPB, FOSL2, ELF3, CEBPD, ARNT2, SPI1, NFKB2, NR4A3, FOSB, JUNB, DDIT3, ZNF331, FOS, ATF3, JUN, ETS2, JUND, IRF1, TGIF1, PER1, ZNF395, BHLHE41, PITX1*
MF	GO:0005044	Scavenger receptor activity	9	0.011	*SBSPON, MARCO, HPN, MSR1, STAB1, CFI, LOXL3, SSC5D, CD163*
MF	GO:000813	Transcription factor binding	20	0.02	*KLF5, HMGB2, CEBPB, CENPF, NFKBIA, FOSB, HMGA2, JUNB, DDIT3, TRIB1, HES1, FOS, CCND1, JUN, JUND, BCL3, PER1, RARA, BCOR, ELMSAN1*
MF	GO:0043565	Sequence-specific DNA binding	28	0.034	*FOSL2, ELF3, HOXA11, RORC, PRDM16, ZKSCAN4, FOS, JUND, BCL6, RARA, NFIL3, PITX1, EGR1, KLF5, MAFF, CEBPB, SNAPC1, NR4A2, NR4A3, FOSB, DDIT3, HES1, ATF3, JUN, ETS2, CSRNP1, IRF1, KLF2*
CC	GO:0005578	Proteinaceous extracellular matrix	26	8.19E-07	*ASPN, SBSPON, WNT5A, CTHRC1, MAMDC2, ADAMTS14, ADAMTS16, ELN, SPOCK1, POSTN, SPARC, ECM1, MMP13, COL5A2, COL5A1, OGN, SMOC2, SMOC1, VEGFA, TGFBI, COL6A3, COL1A2, ADAMTS2, ADAMTS5, DPT, FN1*
CC	GO:0005581	Collagen trimer	14	9.34E-05	*CTHRC1, MSR1, COL3A1, COL2A1, C1QC, MMP13, COL5A2, COL5A1, C1QA, MARCO, C1QB, COL6A3, COL1A2, COL1A1*
CC	GO:0031012	Extracellular matrix	23	5.12E-04	*ASPN, SBSPON, TNC, COL3A1, COL2A1, POSTN, ECM1, MMP13, COL5A2, COL5A1, OGN, HTRA1, CLEC3B, COL6A3, TGFBI, COL1A2, COL1A1, COL8A1, THBS2, SSC5D, FN1, DPT, TUBB4B*

BP, biological process; CC, cellular component; FDR, false discovery rate; GO, gene ontology; MF, molecular function.

Table iii. Significantly enriched Kyoto Encyclopedia of Genes and Genomes terms

ID	Description	GeneRatio	BgRatio	p-value	p.adjust	q-value	geneID	Count
hsa04380	Osteoclast differentiation	0.073684	128/7891	< 0.001	0.000337	0.000256	695/2214/2353/2354/2355/3725/3726/3727/4791/4792/8651/9021/6688/7305	14
hsa04068	FoxO signalling pathway	0.073684	131/7891	< 0.001	0.000337	0.000256	604/664/595/901/1026/1027/1647/4616/8660/10365/10769/1263/6502/6648	14
hsa04115	p53 signalling pathway	0.052632	72/7891	< 0.001	0.000601	0.000458	595/901/983/1021/1026/54205/1647/4616/6241/83667	10
hsa04668	TNF signalling pathway	0.063158	112/7891	< 0.001	0.000627	0.000477	602/1051/2353/3383/3659/3725/3726/4792/64127/5743/9021/7133	12
hsa05222	Small cell lung cancer	0.057895	92/7891	< 0.001	0.000627	0.000477	595/1021/1026/1027/54205/2335/1647/4616/4792/5743/6502	11
hsa04974	Protein digestion and absorption	0.057895	95/7891	< 0.001	0.000627	0.000477	1277/1278/1280/1281/1289/1290/1293/2006/4311/117247/206358	11
hsa04933	AGE-RAGE signalling pathway in diabetic complications	0.057895	100/7891	< 0.001	0.000879	0.000668	595/1027/1277/1278/1281/1536/1958/2335/3383/3725/7422	11
hsa04151	PI3K-Akt signalling pathway	0.115789	354/7891	< 0.001	0.001033	0.000786	595/1021/1026/1027/1277/1278/1280/1293/54541/1942/2335/2997/3570/3676/3815/4803/118788/23533/7058/7059/3371/7422	22
hsa05202	Transcriptional misregulation in cancer	0.078947	186/7891	< 0.001	0.001033	0.000786	9915/604/1026/1027/1051/1649/1647/4616/8091/3207/3684/8013/5328/5914/6688	15
hsa05224	Breast cancer	0.068421	147/7891	< 0.001	0.001193	0.000908	595/1021/1026/2353/7855/1647/4616/3280/3725/3815/4791/399694/7474	13
hsa05166	Human T-cell leukemia virus 1 infection	0.078947	219/7891	< 0.001	0.004499	0.003423	113/701/595/1026/1958/2114/2353/3383/3689/3725/4791/4792/6513/6688/7538	15
hsa04926	Relaxin signalling pathway	0.057895	129/7891	< 0.001	0.004499	0.003423	113/1277/1278/1281/2353/3725/4322/4792/339403/399694/7422	11
hsa04510	Focal adhesion	0.073684	199/7891	< 0.001	0.004802	0.003653	595/1277/1278/1280/1293/2335/3676/3725/4633/399694/7058/7059/3371/7422	14
hsa05169	Epstein-Barr virus infection	0.073684	201/7891	< 0.001	0.004988	0.003795	695/595/1021/1026/1027/54205/1647/4616/3280/3383/3725/4791/4792/6502	14
hsa05165	Human papillomavirus infection	0.1	330/7891	< 0.001	0.005005	0.003807	595/1021/1026/1027/1277/1278/1280/1293/2335/7855/3280/3659/3676/5743/7058/7059/3371/7422/7474	19
hsa05167	Kaposi sarcoma-associated herpesvirus infection	0.068421	186/7891	0.001	0.005999	0.004563	595/1230/1021/1026/54205/2353/3383/3725/4792/23533/5743/7422/7538	13
hsa04110	Cell cycle	0.052632	124/7891	0.001	0.008089	0.006153	699/701/595/983/1021/1026/1027/1647/4616/6502	10
hsa04145	Phagosome	0.052632	152/7891	0.004	0.02676	0.020357	64581/1536/2214/3684/3689/8685/4481/7058/7059/10383	10

AGE, advanced glycation end product; RAGE, receptor for advanced glycation end products; TNF, tumour necrosis factor.

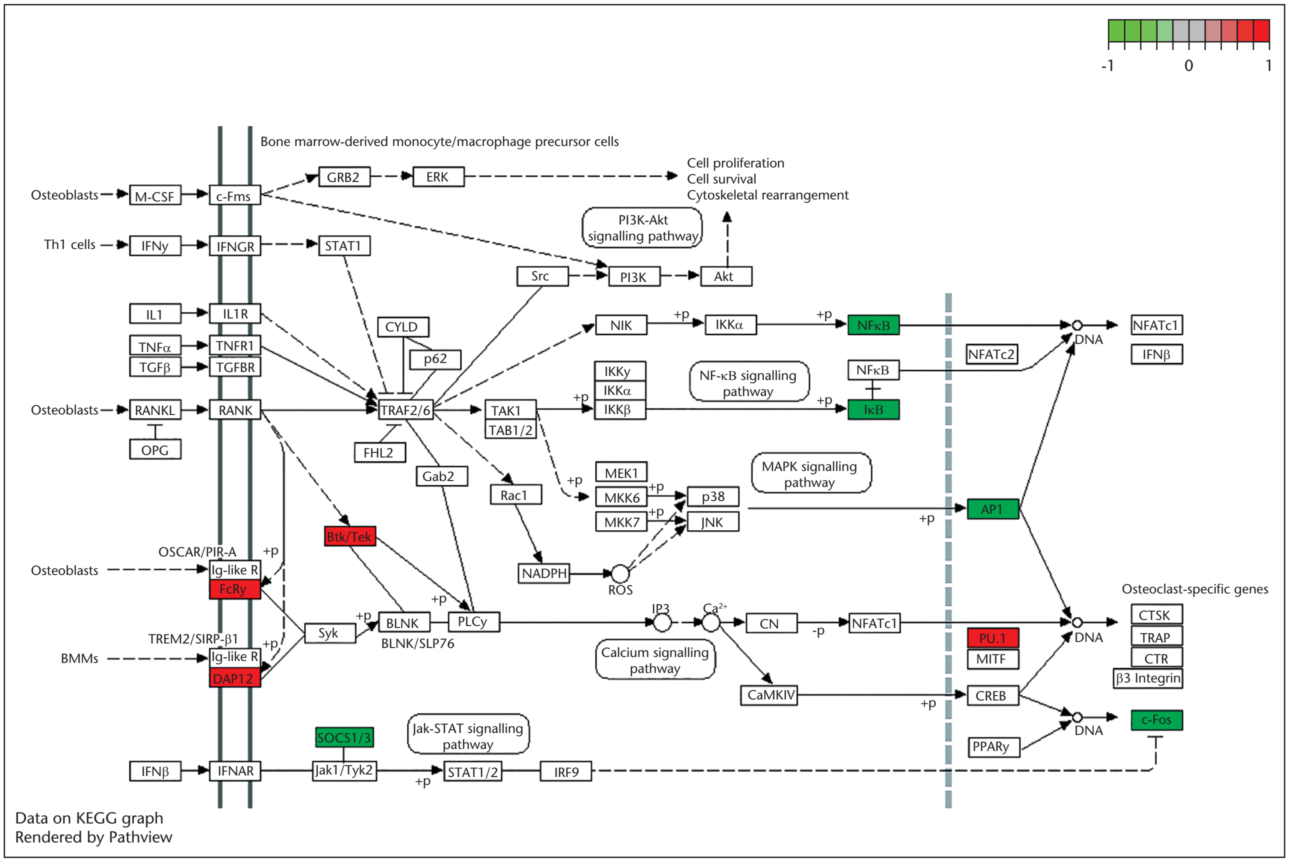

Fig. aa

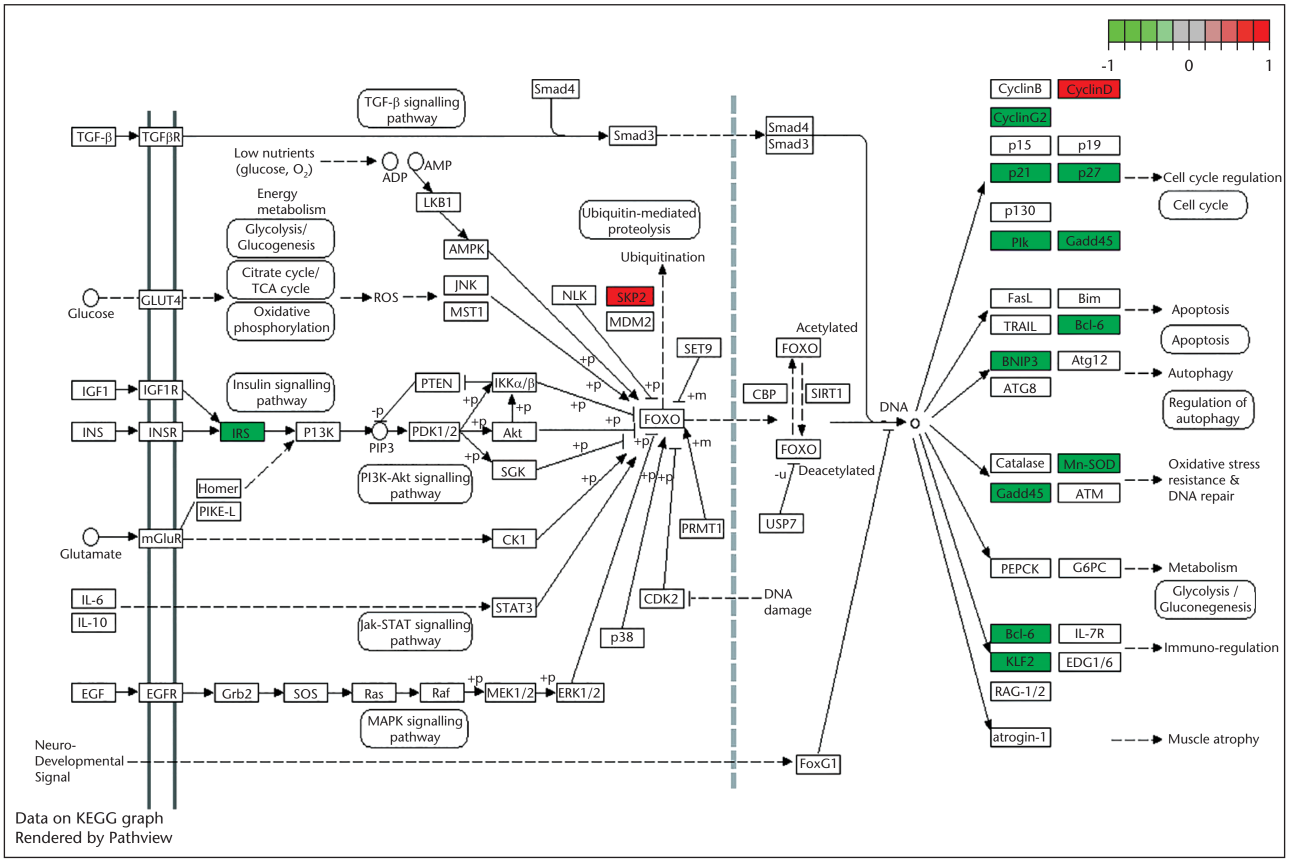

Fig. ab

(Continued)

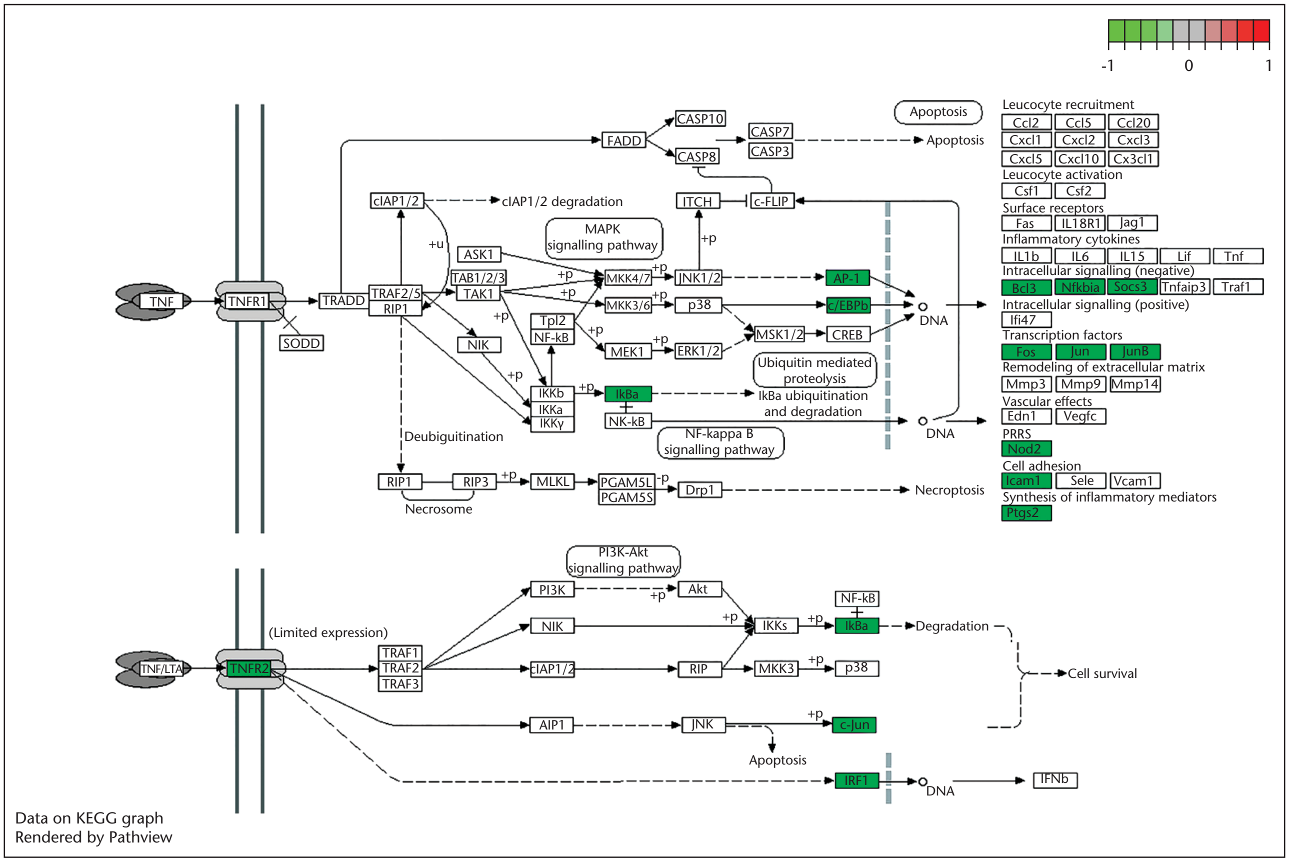

Fig. ac

Pathview analysis of the top three differentially enriched pathways in osteoarthritis (OA) tissues and normal tissues of knee articular cartilage. a) Osteoclast differentiation; b) FoxO signalling pathway; c) tumour necrosis factor (TNF) signalling pathway. Gene expression levels are indicated as significantly higher (red), unchanged (grey), or significantly lower (green). KEGG, Kyoto Encyclopedia of Genes and Genomes.

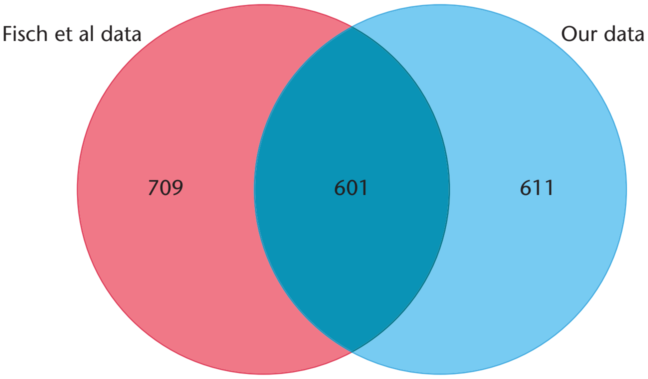

Fig. b

Venn diagram showing the overlapping messenger RNA (mRNA) between the data from Fisch et al[1] and our data.

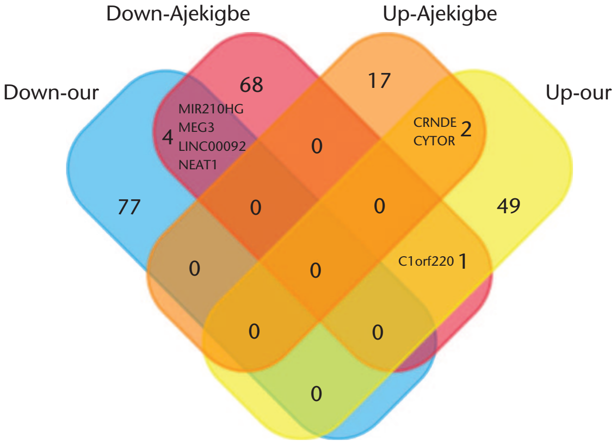

Fig. c

Venn diagram showing the overlapping long non-coding RNA (lncRNA) between the data from Ajekigbe et al[2] and our data.

References

1. **Fisch KM, Gamini R, Alvarez-Garcia O, et al.** Identification of transcription factors responsible for dysregulated networks in human osteoarthritis cartilage by global gene expression analysis. *Osteoarthritis Cartilage*. 2018;26(11):1531-1538.
2. **Ajekigbe B, Cheung K, Xu Y, et al.** Identification of long non-coding RNAs expressed in knee and hip osteoarthritic cartilage. *Osteoarthritis Cartilage*. 2019;27(4):694-702.