

Table S1 Differentially expressed gene enriched KEGG pathway

ID	Description	Count	P value	Symbols
hsa05322	Systemic lupus erythematosus	47	4.33E-12	HIST1H2AB, C7, HIST1H4K, HIST1H2AG, C5, HIST1H2AE, HLA-DMB, HLA-DMA, HIST1H2BO, HIST2H2AB, HIST1H2BM, HIST1H2BN, HIST1H2BK, HIST1H4A, HIST1H4B, HIST1H2BL, HIST1H2BI, HIST1H2BJ, H2AFZ, H2AFX, HIST3H2A, HLA-DPB1, HLA-DOA, HIST3H2BB, FCGR3B, HIST1H3J, HIST1H2BB, HIST1H2BC, HIST1H2BD, HIST1H2BE, HIST1H2BG, ACTN2, HLA-DQA2, HIST2H3D, HIST2H2BE, HIST2H2BF, HIST1H3A, SNRPB, HIST1H2AI, HIST1H2AH, HIST1H3C, HIST1H2AK, HIST1H2AM, HIST1H2AL, HIST1H3H, HIST1H3I, HLA-DRA
hsa04110	Cell cycle	41	9.46E-10	E2F3, DBF4, PKMYT1, TTK, CHEK1, CHEK2, PTTG1, CCNE2, CCNE1, CDC45, MCM7, CDKN2B, CDKN2C, BUB1, ORC5, ORC6, CCNA2, ORC1, STAG2, TFDP1, CDC7, CDK1, CDC6, RBL1, SKP2, ESPL1, CDC20, CDK6, RB1, MCM2, CDC25C, MCM4, CDC27, CDC25A, MCM6, CCNB1, MAD2L1, CCNB2, PLK1, PCNA, BUB1B
hsa05034	Alcoholism	46	2.99E-07	HIST1H2AB, HIST1H4K, HIST1H2AG, HIST1H2AE, CAMKK1, HIST1H2BO, HIST2H2AB, HIST1H2BM, HIST1H2BN, HIST1H2BK, HIST1H4A, PPP1R1B, HIST1H4B, HIST1H2BL, HIST1H2BI, HIST1H2BJ, H2AFZ, CREB3L1, H2AFX, HIST3H2A, HIST3H2BB, SHC2, HIST1H3J, HIST1H2BB, HIST1H2BC, HIST1H2BD, HIST1H2BE, MAOA, HIST1H2BG, MAOB, CREB5, HIST2H3D, HIST2H2BE, HIST2H2BF, GNG10, MAPK3, HIST1H3A, HIST1H2AI, HIST1H2AH, HIST1H3C, HIST1H2AK, HDAC9, HIST1H2AM, HIST1H2AL, HIST1H3H, HIST1H3I
hsa03030	DNA replication	14	1.33E-04	MCM2, RNASEH2A, MCM4, MCM6, RPA3, RFC5, PRIM1, DNA2, RFC3, RFC4, MCM7, POLE2, PCNA, FEN1
hsa04974	Protein digestion and absorption	24	1.54E-04	COL4A4, COL18A1, COL4A3, COL13A1, SLC16A10, COL3A1, COL15A1, MME, ATP1A1, ATP1A2, COL5A2, COL5A1, KCNN4, COL6A6, COL6A5, COL1A2, MEP1A, COL12A1, COL1A1, KCNQ1, SLC1A1, CPB2, COL11A1, DPP4
hsa04512	ECM-receptor interaction	23	3.53E-04	COL4A4, COL4A3, TNXB, TNC, COL3A1, DAG1, ITGB3, COL5A2, COL5A1, HMMR, COL6A6, LAMC3, COL6A5, ITGAV, COMP, ITGA8, COL1A2, COL1A1, THBS2, COL11A1, SPP1, THBS4, ITGA2B
hsa00512	Mucin type O-Glycan biosynthesis	12	5.21E-04	GALNT1, GALNT7, WBSCR17, GALNT5, GALNT15, GALNT18, GCNT1, GALNT12, C1GALT1, GALNT14, B4GALT5, ST6GALNAC1
hsa04514	Cell adhesion molecules (CAMs)	31	9.49E-04	CLDN7, CLDN18, OCLN, CADM1, CLDN3, CLDN5, LRRC4B, HLA-DMB, HLA-DMA, ALCAM, VCAM1, ITGAV, CD22, CNTNAP2, ESAM, HLA-DPB1, HLA-DOA, CD6, NRXN2, NRXN3, SELL, ICAM3, NFASC, NTNG1, HLA-DQA2, CD34, ITGA8, CD58, NLGN4X, VCAN, HLA-DRA
hsa03460	Fanconi anemia pathway	15	2.62E-03	BLM, EME1, BRCA2, BRIP1, RMI2, RMI1, BRCA1, RAD51, RPA3, FANCM, FANCI, FANCD2, FANCG, UBE2T, FANCB

Table S1 (continued)

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ID	Description	Count	P value	Symbols
hsa05203	Viral carcinogenesis	38	5.04E-03	HIST1H4K, CHEK1, PKM, HIST1H2BO, CCNE2, CCNE1, HIST1H2BM, HIST1H2BN, HIST1H2BK, HIST1H4A, CDKN2B, HIST1H4B, HIST1H2BL, HIST1H2BI, HIST1H2BJ, GTF2A2, CREB3L1, HIST3H2BB, CCNA2, RASA2, CDK1, HIST1H2BB, HIST1H2BC, HPN, HIST1H2BD, HIST1H2BE, HIST1H2BG, RBL1, SKP2, CREB5, CDK6, ACTN2, CDC20, RB1, HIST2H2BE, HIST2H2BF, MAPK3, HDAC9
hsa04914	Progesterone-mediated oocyte maturation	19	1.16E-02	CDK1, ADCY2, PKMYT1, MAPK10, CDC25C, CDC27, CDC25A, PGR, CCNB1, SPDYA, CCNB2, MAD2L1, ADCY9, PLK1, RPS6KA2, MAPK14, MAPK3, BUB1, CCNA2
hsa00790	Folate biosynthesis	6	1.81E-02	ALPL, DHFR, GGH, QDPR, ALPP, MOCS1
hsa05222	Small cell lung cancer	18	1.93E-02	COL4A4, COL4A3, CKS1B, E2F3, CYCS, SKP2, CDK6, RB1, BIRC2, CCNE2, CCNE1, CDKN2B, LAMC3, ITGAV, CKS2, NOS2, APAF1, ITGA2B
hsa05202	Transcriptional misregulation in cancer	30	2.17E-02	IL1R2, MMP9, ARNT2, TSPAN7, ZBTB16, MEIS1, CDKN2C, PAX8, ETV1, ETV5, RUNX2, CEBPA, HIST1H3J, IL2RB, BAIAP3, RUNX1T1, WHSC1, HMGA2, HIST2H3D, EYA1, NUPR1, NTRK1, SIX1, HIST1H3A, HIST1H3C, PBX1, IGFBP3, PLAU, HIST1H3H, HIST1H3I
hsa04115	p53 signaling pathway	15	2.25E-02	CDK1, CYCS, CHEK1, CDK6, CHEK2, GTSE1, SESN3, CCNB1, CCNE2, CCNE1, CCNB2, RRM2, APAF1, IGFBP3, TP53AIP1

Table S2 miRNA-targeted mRNA-enriched KEGG pathway

ID	Description	Count	P value	Symbols
hsa04120	Ubiquitin mediated proteolysis	8	8.3711E-05	UBE2K, NEDD4, SKP2, ELOC, UBE2D1, CUL4B, UBA6, UBE2W
hsa04514	Cell adhesion molecules (CAMs)	7	0.000734402	CD34, VCAM1, ITGA8, NRXN3, NRXN2, CNTNAP2, OCLN
hsa04151	PI3K-Akt signaling pathway	15	0.002803457	CDK6, EFNA1, FGF2, FGF14, ITGB3, PPP2R1B, PRLR, ITGA8, CREB5, PDGFD, ABL2, RASA2, PLA2G3, PARD6B, MYLK
hsa05200	Pathways in cancer	10	0.007589755	RUNX1T1, CDK6, DCC, FGF2, FGF14, MMP9, SKP2, ELOC, CYCS, HHIP
hsa04975	Fat digestion and absorption	3	0.008381767	APOB, SCARB1, PLA2G3
hsa04110	Cell cycle	5	0.008909536	CDK6, MCM4, SKP2, CDC45, STAG2
hsa00600	Sphingolipid metabolism	3	0.012193919	UGCG, B4GALT6, CERS4
hsa01212	Fatty acid metabolism	3	0.012910784	ACADSB, ELOVL6, SCD5
hsa04640	Hematopoietic cell lineage	7	0.017446042	CD34, ITGB3, MME, TFRC, SCARB1, TUBB2A, TLR6
hsa04144	Endocytosis	7	0.01762409	FOLR1, NEDD4, TFRC, WASHC4, RAB11FIP1, PARD6B, MVB12B
hsa04668	TNF signaling pathway	4	0.024768822	MMP9, VCAM1, CREB5, MLKL
hsa05230	Central carbon metabolism in cancer	3	0.028762185	LDHA, NTRK3, SLC7A5
hsa04530	Tight junction	7	0.030438944	NEDD4, PPP2R1B, RAP2C, PARD6B, OCLN, SCARB1, EIF2AK1
hsa04152	AMPK signaling pathway	4	0.035500794	PFKFB4, PPP2R1B, CREB5, SCD5
hsa00562	Inositol phosphate metabolism	3	0.036015518	SYNJ2, PLCH1, IPMK
hsa05202	Transcriptional misregulation in cancer	5	0.03751654	RUNX2, RUNX1T1, MEIS1, MMP9, PBX1

Table S3 The KEGG pathway enriched by lncRNA proximity gene function

ID	Description	Count	P value	Symbols
hsa04060	Cytokine-cytokine receptor interaction	12	0.005127277	AMHR2, CD27, LTBR, CCL3, CCL4, CCL14, CCL15, CCL16, CCL18, CCL23, TNFRSF1A, PIK3R3
hsa04068	FoxO signaling pathway	9	0.006099922	S1PR1, SMAD4, PTEN, STK4, PIK3R3, BCL2L11, NLK, ERBB3, NF1
hsa04144	Endocytosis	10	0.010893506	ERBB3, PSD, RAB5B, GBF1, CYTH1, RNF41, RAB10, ASAP1, RAB11FIP4, IQSEC3
hsa04350	TGF-beta signaling pathway	8	0.012274461	AMHR2, BMP4, BMP6, SMAD4, SP1, DLG2, LIMD1, CRB2
hsa00640	Propanoate metabolism	5	0.0151618	HADHA, ECHDC1, ACSS1, ACADL, ACSBG1
hsa04530	Tight junction	7	0.022123508	RUNX1, DLG2, MAP3K1, MYL6, PCNA, CLDN10, MYL6B
hsa04960	Aldosterone-regulated sodium reabsorption	3	0.022375956	NR3C2, SCNN1A, PIK3R3
hsa04010	MAPK signaling pathway	9	0.025073881	DUSP1, MAP3K1, NF1, NFKB2, PTPRR, STK4, TNFRSF1A, MAP3K12, NLK
hsa00230	Purine metabolism	7	0.025414164	ADSS, ENTPD1, PDE9A, PDE10A, PDE7B, NT5C1B, NT5C1B-RDH14
hsa05166	HTLV-I infection	9	0.025628812	BUB1B, LTBR, SMAD4, MAP3K1, NFKB2, PCNA, TNFRSF1A, PIK3R3, ANAPC10
hsa04512	ECM-receptor interaction	4	0.045582184	CD47, LAMA2, THBS4, AGRN

Table S4 The KEGG pathway enriched by the source gene of circRNA

ID	Description	Count	P value	Symbols
hsa00310	Lysine degradation	7	3.85E-04	ALDH2, EZH2, PLOD2, NSD2, AASS, NSD3, KMT2E
hsa04520	Adherens junction	11	6.09E-03	ERBB2, FER, PTPRM, TJP1, FARP2, PARD3, MYH10, PRKAA1, TJP2, MPP5, CGNL1
hsa03013	RNA transport	10	6.16E-03	EIF4B, KPNB1, XPO1, EIF4G3, CYFIP1, UPF2, CYFIP2, TRNT1, NUP54, SENP2
hsa04360	Axon guidance	10	7.21E-03	DPYSL2, NFATC3, PDK1, PIK3CB, PTK2, SEMA4B, SEMA3C, NTNG1, ARHGEF12, PARD3
hsa04015	Rap1 signaling pathway	11	9.30E-03	KRIT1, FGFR2, ITGAL, KITLG, PIK3CB, DOCK4, FARP2, PRKD3, APBB1IP, PARD3, SIPA1L2
hsa04810	Regulation of actin cytoskeleton	11	9.94E-03	FGFR2, ITGA1, ITGA7, ITGAL, MYH10, PIK3CB, PTK2, CYFIP1, ARHGEF12, CYFIP2, SPATA13
hsa05132	Salmonella infection	6	1.41E-02	MYH10, PKN1, TJP1, PLEKHM2, DYNC1LI1, NLRC4
hsa00600	Sphingolipid metabolism	4	2.23E-02	UGCG, DEGS1, SGPL1, SGMS1
hsa00280	Valine, leucine, and isoleucine degradation	5	2.39E-02	ACADM, ALDH2, HMGCS1, PCCA, MLYCD
hsa04141	Protein processing in endoplasmic reticulum	8	3.76E-02	CANX, NFE2L2, DNAJC3, MAN1A2, SEC63, UBQLN1, MBTPS2, UGGT2
hsa04120	Ubiquitin mediated proteolysis	7	3.84E-02	UBE2K, CUL5, CUL3, HERC2, HERC1, UBA2, BIRC6
hsa03410	Base excision repair	5	3.91E-02	OGG1, POLE2, NEIL3, DNA2, RFC1

Table S5 The expression of these key genes by data analysis in the RNA-seq results

Symbol	Gene	P value	Up or down
CircRNA	hsa_circ_0000053	0.01004889	Down
	hsa_circ_0001495	3.26E-05	Up
miRNA	hsa-miR-196b-5p	8.74E-16	Up
	hsa-miR-9-5p	7.66E-11	Up
	hsa-miR-9-3p	2.66E-09	Up
	hsa-miR-223-5p	0.000171629	Up
	hsa-miR-135a-5p	1.31E-05	Down
LncRNA	ADAMTS9-AS2	0.011928338	Down
	TEX41	5.93E-04	Up
mRNA	HOXA5	0.000349063	Down
	MEIS1	3.82E-06	Down
	SCARB1	6.24E-05	Down
	RUNX2	5.39E-10	Up

Table S6 Primer sequence of qRT-PCR reactions

Gene	Sequences (5'-3')
hsa_circ_0000053 Forward	ACACACCCAGAAGCTATGTCC
hsa_circ_0000053 Reverse	CACTGCACTATGCTTGGCAC
hsa_circ_00001495 Forward	CCTACTGGGTCGGGAAGTCA
hsa_circ_00001495 Reverse	GACTACATTCTTAGCCAGGTGCT
lncRNA ADAMTS9-AS2 Forward	GACCCTCTCCAGAAGGCAC
lncRNA ADAMTS9-AS2 Reverse	GGACAAGCGAAGGACATCC
lncRNA TEX41 Forward	TCGCCTCAGGGCATTCAITTT
lncRNA TEX41 Reverse	ATATTGGTGGGGCAACAGGG
hsa-miR-196b-5p Forward	ACTGGTCGGTGATTTAGGTAGT
hsa-miR-196b-5p Reverse	AATGAAGGCAGTGTCGTGCT
hsa-miR-196a-5p Forward	GCTGATCTGTGGCTTAGGTAGT
hsa-miR-196a-5p Reverse	CCCTCGACGAAAACCGACT
hsa-miR-223-3p Forward	CGCTCCGTGATTTTGACAAGC
hsa-miR-223-3p Reverse	TGCCGCACTTGGGGTATTTG
hsa-miR-135a-5p Forward	CGCAGTATGGCTTTTTTATTCT
hsa-miR-135a-5p Reverse	GGTCCAGTTTTTTTTTTTTTTTTCACA
hsa-miR-9 Forward	GGAAGCGAGTTGTTATCTTTGGT
hsa-miR-9 Reverse	TCGGTTATCTAGCTTTATGAAGACC
SCARB1 Forward	GATCGGACCCTCTGGCCAAC
SCARB1 Reverse	AGAACAGGCAGAGTAGTGGCA
RUNX2 Forward	CTGAGATTTGTGGGCCGGAG
RUNX2 Reverse	CTGCCTGGCTCTTCTTACTGA
HOXA5 Forward	GTTCCGTGAGCGAGCAATTC
HOXA5 Reverse	CGGGTCAGGTAACGGTTGAA
MEIS1 Forward	CACGGGACTCACCATCCTTC
MEIS1 Reverse	ACTCACACCCATTGGACCAC