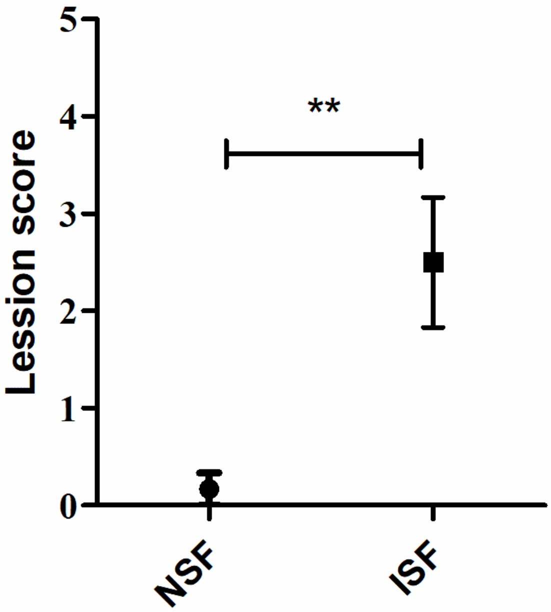
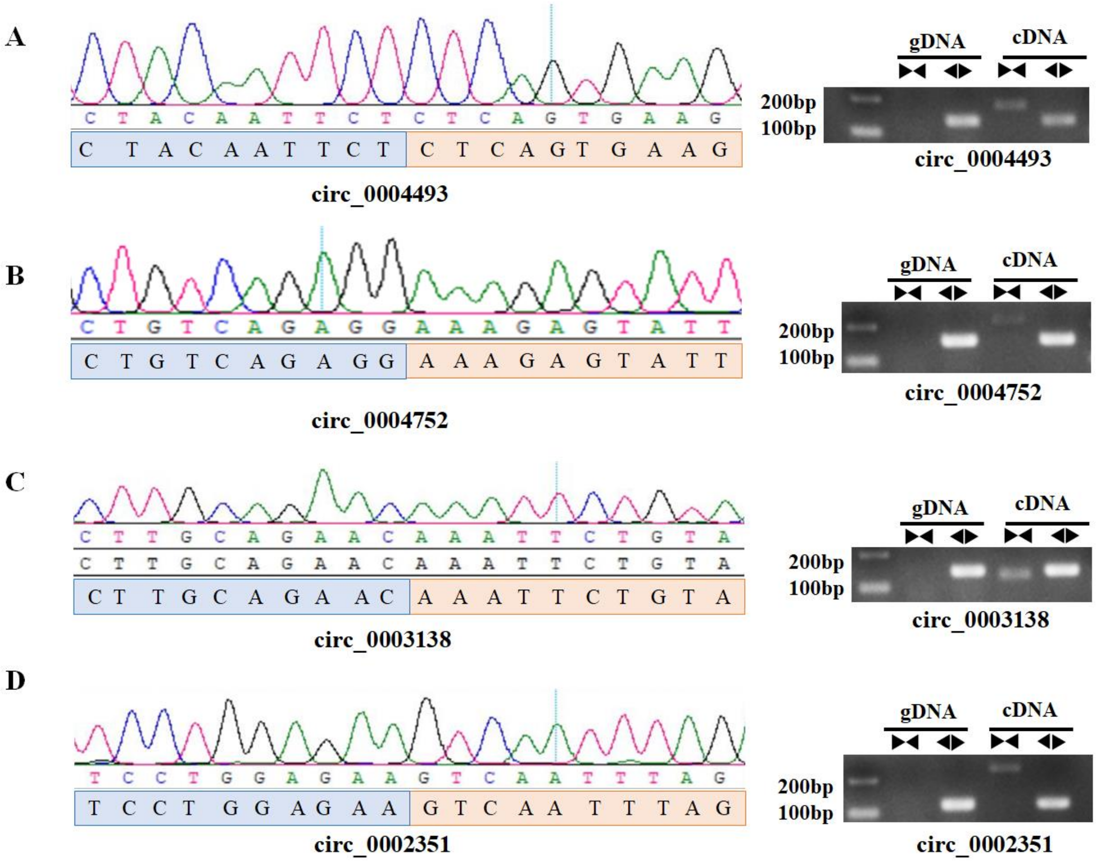
Supplementary Figures and Tables

Supplementary Figure 1



Coccidiosis causes weight loss and intestinal lesions in chickens. The lesion scores of the caeca of the *Eimeria tenella* infected chickens were significantly higher than that of the control group at the 4 days of post infection.

Supplementary Figure 2



Verification of the circular structure of the selected DEcircRNAs. (A) The junction sequence of *circ_0004493* was verified by Sanger sequence and agarose gel. (B) The junction sequence of *circ_0004752* was verified by Sanger sequence and agarose gel. (C) The junction sequence of *circ_0003138* was verified by Sanger sequence and agarose gel. (D) The junction sequence of *circ_0002351* was verified by Sanger sequence and agarose gel.

Supplementary table 1

Supplementary table 1 Primer sequence

Name		Primer sequence	Length (bp)	Temperature (℃)	Use
circ_0004493	F	CATGAAGAGAAAGCAGAACGAATAA	214	56	qPCR
	R	AGAAAATCTGTCATAAGCCCAAGTC			
circ_0004752	F	TGGTCAAAGGCGGAGAGAAGCAT	270	56	qPCR
	R	TCATTGGGGAAACCTCAGGGAGA			
circ_0003138	F	CAGCCTCTGTTTACTCTCA	150	56	qPCR
	R	GCGTTTGTACTCCTGTTTT			
circ_0002351	F	CAGTATGTGCTTCACGAGG	293	56	qPCR
	R	TTTCTGTGTTCTGGGGTCT			
circ_0004143 (circMGAT5)	F	GGAACAGGAGCAAACTCTACCA	293	56	qPCR
	R	ACCAAAAGTCACCAGAAAAAAG			
0004493-Con	F	TCCCAGTGAACCCTATCAAGG	149	56	PCR
	R	CATGCTACGTTCAGCAATGG			
0004752-Con	F	GGTCCACATCAAACGACCCA	180	56	PCR
	R	CTGTGAGGGCTGGCATTAGA			
0003138-Con	F	AGGACTCTGGATTTCGACCC	163	56	PCR
	R	GGGAGGACACCTCTCCGAA			
0002351-Con	F	GACAGCAGGCTTCACCTCTT	132	56	PCR
	R	AGGAAAGCGCCTGTTCAAAG			
0004143-Con	F	TTTTTCTGGTGACTTTTGGT	134	56	PCR
	R	TGCTTTGATGTATCTTTTGC			
ASS1	F	GGTCACCAACACCAGGAATG	120	58	qPCR
	R	ACAAAGCGGTTCTCCACAAT			
BF1	F	CACCAAGAGGAAATGGGAGG	183	58	qPCR
	R	CGGCAGGACAAGGTCAGGAT			
CCL19	F	TGCCTGCGGACGAGCGAGAA	209	58	qPCR

	R	TTGCCTTGATTTGGGACCTT			
IL18R1	F	AATGCAGTGATCTGTCTGTCA	192	58	qPCR
	R	CCAGCCTGATTGTATTGGTGC			
IRF1	F	ATAAAGCTGCTCGAACCCAC	159	58	qPCR
	R	CATGCGGAACTCCAACTCTG			
TAPBP	F	GGGCACCTACATCTGCTCCG	115	58	qPCR
	R	AGCCACCACCAGGTTCTTCG			
GBP	F	CAACAACCCAGCATCCAACT	119	58	qPCR
	R	CCTCCAGGTACTCGTCCTCA			
MMD	F	GGATCTATGGCATGGGGCTC	187	58	qPCR
	R	GCTAGAGGTCCAAGCTCACG			
F4/80	F	GCACCATCTTGCTGGAGACT	222	60	qPCR
	R	CTGGGGCCCCTGTAGATACT			
MHC-II	F	CTCGAGGTCATGATCAGCAA	277	60	qPCR
	R	TGTAAACGTCTCCCCTTTGG			
β-actin	F	ACCACAGGACTCCATACCCAAGAAAG	210	52-60	qPCR
	R	GCCGAGAGAGAAATTGTGCGTGAC			

Supplementary table 2

Supplementary table 2 the DEcircRNA-DEmiRNA-DEmRNA networks constructed in this study

Up_DEcircRNA	Down_DEmiRNA	Up_DEmRNA
novel_circ_0003805	*gga-miR-458b-5p*	*FAM49A*
novel_circ_0004143	*gga-miR-132c-5p*	*KCNB2*
novel_circ_0004143	*gga-miR-132c-5p*	*MMD*
novel_circ_0004143	*gga-miR-132c-5p*	*DERL1*
novel_circ_0004143	*gga-miR-132c-5p*	*IFNGR2*
novel_circ_0004143	*gga-miR-132c-5p*	*EPN2*
novel_circ_0004143	*gga-miR-132c-5p*	*PHC3*
novel_circ_0004143	*gga-miR-132c-5p*	*LYN*
novel_circ_0004143	*gga-miR-132c-5p*	*CCL4*
novel_circ_0004493	*gga-miR-1729-5p*	*PLA2G15*
novel_circ_0004493	*gga-miR-1729-5p*	*BCAT1*
novel_circ_0004493	*gga-miR-1729-5p*	*SPSB1*
novel_circ_0004493	*gga-miR-1729-5p*	*DENND1B*
novel_circ_0004493	*gga-miR-1729-5p*	*AFF1*
novel_circ_0004493	*gga-miR-1729-5p*	*GMFB*
novel_circ_0004433_junction_seq	*gga-miR-1798-3p*	*NLRC5*
novel_circ_0004433_junction_seq	*gga-miR-1798-3p*	*FRYL*
novel_circ_0004433_junction_seq	*gga-miR-1798-3p*	*MMD*
novel_circ_0004433_junction_seq	*gga-miR-1798-3p*	*ABHD18*
novel_circ_0004433_junction_seq	*gga-miR-1798-3p*	*C1R*
novel_circ_0004433_junction_seq	*gga-miR-1798-3p*	*IPPK*
novel_circ_0004433_junction_seq	*gga-miR-1798-3p*	*MPP7*
novel_circ_0004433_junction_seq	*gga-miR-1798-3p*	*RAB4A*
novel_circ_0004433_junction_seq	*gga-miR-1798-3p*	*PTPN2*
novel_circ_0004433_junction_seq	*gga-miR-1798-3p*	*MFSD11*
novel_circ_0004433_junction_seq	*gga-miR-1798-3p*	*BCL11B*
novel_circ_0001674	*gga-miR-1798-3p*	*NLRC5*
novel_circ_0001674	*gga-miR-1798-3p*	*FRYL*
novel_circ_0001674	*gga-miR-1798-3p*	*MMD*
novel_circ_0001674	*gga-miR-1798-3p*	*ABHD18*
novel_circ_0001674	*gga-miR-1798-3p*	*C1R*
novel_circ_0001674	*gga-miR-1798-3p*	*IPPK*
novel_circ_0001674	*gga-miR-1798-3p*	*MPP7*
novel_circ_0001674	*gga-miR-1798-3p*	*RAB4A*
novel_circ_0001674	*gga-miR-1798-3p*	*PTPN2*
novel_circ_0001674	*gga-miR-1798-3p*	*MFSD11*
novel_circ_0001674	*gga-miR-1798-3p*	*BCL11B*
novel_circ_0001674_junction_seq	*gga-miR-1798-3p*	*NLRC5*
novel_circ_0001674_junction_seq	*gga-miR-1798-3p*	*FRYL*

novel_circ_0001674_junction_seq	*gga-miR-1798-3p*	*MMD*
novel_circ_0001674_junction_seq	*gga-miR-1798-3p*	*ABHD18*
novel_circ_0001674_junction_seq	*gga-miR-1798-3p*	*C1R*
novel_circ_0001674_junction_seq	*gga-miR-1798-3p*	*IPPK*
novel_circ_0001674_junction_seq	*gga-miR-1798-3p*	*MPP7*
novel_circ_0001674_junction_seq	*gga-miR-1798-3p*	*RAB4A*
novel_circ_0001674_junction_seq	*gga-miR-1798-3p*	*PTPN2*
novel_circ_0001674_junction_seq	*gga-miR-1798-3p*	*MFSD11*
novel_circ_0001674_junction_seq	*gga-miR-1798-3p*	*BCL11B*
novel_circ_0001674	*gga-miR-214b-3p*	*ATP2B1*
novel_circ_0001674	*gga-miR-214b-3p*	*MMD*
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novel_circ_0001674	*gga-miR-214b-3p*	*B3GNT5*
novel_circ_0001674	*gga-miR-214b-3p*	*BCL11B*
novel_circ_0001674	*gga-miR-214b-3p*	*C25H1ORF43*
novel_circ_0001674	*gga-miR-214b-3p*	*EHD3*
novel_circ_0001674	*gga-miR-214b-3p*	*SGK3*
novel_circ_0001674	*gga-miR-214b-3p*	*IPO7*
novel_circ_0001674	*gga-miR-214b-3p*	*NBN*
novel_circ_0001674	*gga-miR-214b-3p*	*IPPK*
novel_circ_0001674	*gga-miR-214b-3p*	*UBASH3A*
novel_circ_0001674	*gga-miR-214b-3p*	*DTX3L*
novel_circ_0001674	*gga-miR-214b-3p*	*PCGF5*
novel_circ_0001674	*gga-miR-214b-3p*	*MCM2*
novel_circ_0001674	*gga-miR-214b-3p*	*PTPRE*
novel_circ_0001674	*gga-miR-214b-3p*	*NUDC*
novel_circ_0001674	*gga-miR-214b-3p*	*NSMF*
novel_circ_0001674	*gga-miR-214b-3p*	*ANP32E*
novel_circ_0001674	*gga-miR-214b-3p*	*44080*
novel_circ_0001674	*gga-miR-214b-3p*	*BEND3*
novel_circ_0001674	*gga-miR-214b-3p*	*ABHD17B*
novel_circ_0001674	*gga-miR-214b-3p*	*STAT1*
novel_circ_0001674	*gga-miR-214b-3p*	*ABHD18*
novel_circ_0001674	*gga-miR-214b-3p*	*HIF1A*
novel_circ_0001674	*gga-miR-214b-3p*	*MOCS1*
novel_circ_0001674	*gga-miR-214b-3p*	*KCNB2*
novel_circ_0001674	*gga-miR-214b-3p*	*PSMA1*
novel_circ_0001674	*gga-miR-214b-3p*	*DNM1L*
novel_circ_0001674	*gga-miR-214b-3p*	*EHD4*
novel_circ_0001674	*gga-miR-214b-3p*	*FAM91A1*
novel_circ_0001674	*gga-miR-214b-3p*	*KCNMA1*
novel_circ_0001674	*gga-miR-214b-3p*	*TAF4B*
novel_circ_0001674	*gga-miR-214b-3p*	*EPN2*
novel_circ_0003805	*gga-miR-30e-3p*	*DENND1B*

novel_circ_0003805	*gga-miR-30e-3p*	*PHC3*
novel_circ_0003805	*gga-miR-30e-3p*	*FAS*
novel_circ_0003805	*gga-miR-30e-3p*	*PDXK*
novel_circ_0003805	*gga-miR-30e-3p*	*ETV6*
novel_circ_0003805	*gga-miR-30e-3p*	*C1GALT1*
novel_circ_0003805	*gga-miR-30e-3p*	*RIF1*
novel_circ_0003805	*gga-miR-30e-3p*	*RFFL*
novel_circ_0003805	*gga-miR-30e-3p*	*FAM49A*
novel_circ_0004433	*gga-miR-30e-3p*	*DENND1B*
novel_circ_0004433	*gga-miR-30e-3p*	*PHC3*
novel_circ_0004433	*gga-miR-30e-3p*	*FAS*
novel_circ_0004433	*gga-miR-30e-3p*	*PDXK*
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novel_circ_0004433	*gga-miR-30e-3p*	*C1GALT1*
novel_circ_0004433	*gga-miR-30e-3p*	*RIF1*
novel_circ_0004433	*gga-miR-30e-3p*	*RFFL*
novel_circ_0004433	*gga-miR-30e-3p*	*FAM49A*
novel_circ_0003805	*gga-miR-458b-5p*	*SNX13*
novel_circ_0003805	*gga-miR-458b-5p*	*LYN*
novel_circ_0003805	*gga-miR-458b-5p*	*KCNMA1*
down_DEcircRNA	up_DEmiRNA	down_DEmRNA
novel_circ_0003969	*gga-miR-92-3p*	*RBPMS2*
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novel_circ_0003969	*gga-miR-92-3p*	*SDC2*
novel_circ_0003969	*gga-miR-92-3p*	*TOB1*
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novel_circ_0003969	*gga-miR-92-3p*	*NKX2-3*
novel_circ_0003969	*gga-miR-92-3p*	*RAB39A*
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novel_circ_0003969	*gga-miR-92-3p*	*LRRC8C*
novel_circ_0003969	*gga-miR-92-3p*	*DGKZ*
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novel_circ_0003969	*gga-miR-92-3p*	*SSBP3*
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novel_circ_0003969	*gga-miR-92-3p*	*ANO1*
novel_circ_0003969	*gga-miR-92-3p*	*DPP10*
novel_circ_0003969	*gga-miR-92-3p*	*KIAA1191*

novel_circ_0003969	*gga-miR-92-3p*	*LMO2*
novel_circ_0003969	*gga-miR-92-3p*	*GSAP*
novel_circ_0003969	*gga-miR-92-3p*	*GUCD1*
novel_circ_0003969	*gga-miR-92-3p*	*PPCS*
novel_circ_0004752	*gga-miR-92-3p*	*RBPMS2*
novel_circ_0004752	*gga-miR-92-3p*	*SCFD1*
novel_circ_0004752	*gga-miR-92-3p*	*SDC2*
novel_circ_0004752	*gga-miR-92-3p*	*TOB1*
novel_circ_0004752	*gga-miR-92-3p*	*ADAM23*
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novel_circ_0004752	*gga-miR-92-3p*	*SH3PXD2A*
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novel_circ_0004752	*gga-miR-92-3p*	*NKX2-3*
novel_circ_0004752	*gga-miR-92-3p*	*RAB39A*
novel_circ_0004752	*gga-miR-92-3p*	*TOB2*
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novel_circ_0004752	*gga-miR-92-3p*	*SRPK2*
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novel_circ_0004752	*gga-miR-92-3p*	*RRBP1*
novel_circ_0004752	*gga-miR-92-3p*	*SPHKAP*
novel_circ_0004752	*gga-miR-92-3p*	*ANO1*
novel_circ_0004752	*gga-miR-92-3p*	*DPP10*
novel_circ_0004752	*gga-miR-92-3p*	*KIAA1191*
novel_circ_0004752	*gga-miR-92-3p*	*LMO2*
novel_circ_0004752	*gga-miR-92-3p*	*GSAP*
novel_circ_0004752	*gga-miR-92-3p*	*GUCD1*
novel_circ_0004752	*gga-miR-92-3p*	*PPCS*
novel_circ_0003253	*gga-miR-223*	*ANO1*
novel_circ_0003253	*gga-miR-223*	*FAM49A*
novel_circ_0003253	*gga-miR-223*	*AGAP1*
novel_circ_0003253	*gga-miR-223*	*MAP1LC3B2*
novel_circ_0003253	*gga-miR-223*	*KIF3B*
novel_circ_0003253	*gga-miR-223*	*EZR*
novel_circ_0003253	*gga-miR-223*	*RCOR3*
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novel_circ_0003253	*gga-miR-223*	*NTRK2*
novel_circ_0003253	*gga-miR-223*	*DDX60*

novel_circ_0003253	*gga-miR-223*	*FAM49A*
novel_circ_0003253	*gga-miR-223*	*ANKRD17*
novel_circ_0003253	*gga-miR-223*	*ANO1*
novel_circ_0001305	*gga-miR-200b-3p*	*PTPN13*
novel_circ_0001305	*gga-miR-200b-3p*	*PLCL1*
novel_circ_0001305	*gga-miR-200b-3p*	*TMEM135*
novel_circ_0001305	*gga-miR-200b-3p*	*TOB1*
novel_circ_0001305	*gga-miR-200b-3p*	*EDEM3*
novel_circ_0001305	*gga-miR-200b-3p*	*CYTH3*
novel_circ_0001305	*gga-miR-200b-3p*	*ZNF652*
novel_circ_0001305	*gga-miR-200b-3p*	*RIMKLB*
novel_circ_0001305	*gga-miR-200b-3p*	*GUCD1*
novel_circ_0001305	*gga-miR-200b-3p*	*TARDBP*
novel_circ_0001305	*gga-miR-200b-3p*	*SH3PXD2A*
novel_circ_0001305	*gga-miR-200b-3p*	*TPCN1*
novel_circ_0001305	*gga-miR-200b-3p*	*SYT1*
novel_circ_0001305	*gga-miR-200b-3p*	*FAM49A*
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novel_circ_0001305	*gga-miR-200b-3p*	*SDC2*
novel_circ_0001305	*gga-miR-200b-3p*	*GLCCI1*
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novel_circ_0001305	*gga-miR-200b-3p*	*ELK3*
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novel_circ_0001305	*gga-miR-200b-3p*	*ABHD18*
novel_circ_0001305	*gga-miR-200b-3p*	*PCNP*
novel_circ_0001305	*gga-miR-200b-3p*	*TMEM263*
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novel_circ_0001305	*gga-miR-200b-3p*	*PRDM16*
novel_circ_0001305	*gga-miR-200b-3p*	*CBX4*
novel_circ_0001305	*gga-miR-200b-3p*	*PDP1*
novel_circ_0001305	*gga-miR-200b-3p*	*CNNM2*
novel_circ_0001305	*gga-miR-200b-3p*	*GSAP*
novel_circ_0001305	*gga-miR-200b-3p*	*SNX8*
novel_circ_0002663	*gga-miR-128-1-5p*	*RAP1GAP2*
novel_circ_0002663	*gga-miR-12247-5p*	*KIF3B*

Supplementary table 3

Supplementary table 3 the top 20 GO terms enriched by the DEcircRNAs

GO_accession	Description	Term_type	Over_represented_pValue
GO:0043231	intracellular membrane-bounded organelle	cellular_component	6.22E-05
GO:0043247	telomere maintenance in response to DNA damage	biological_process	6.32E-05
GO:0043227	membrane-bounded organelle	cellular_component	6.85E-05
GO:0043229	intracellular organelle	cellular_component	0.000292
GO:0043226	organelle	cellular_component	0.000325
GO:0006464	cellular protein modification process	biological_process	0.000717
GO:0036211	protein modification process	biological_process	0.000717
GO:0043412	macromolecule modification	biological_process	0.001118
GO:0005634	nucleus	cellular_component	0.001142
GO:0044260	cellular macromolecule metabolic process	biological_process	0.001193
GO:0006281	DNA repair	biological_process	0.001251
GO:0006259	DNA metabolic process	biological_process	0.00138
GO:0043170	macromolecule metabolic process	biological_process	0.001812
GO:0033326	cerebrospinal fluid secretion	biological_process	0.002862
GO:0019538	protein metabolic process	biological_process	0.002944
GO:0000266	mitochondrial fission	biological_process	0.003024
GO:0006950	response to stress	biological_process	0.003189
GO:0061512	protein localization to cilium	biological_process	0.003581
GO:0006303	double-strand break	biological_process	0.004137

	repair via nonhomologous end joining		
GO:0006289	nucleotide-excision repair	biological_process	0.004193

Supplementary table 4

Supplementary table 4 the top 20 KEGG pathways enriched by the DEcircRNAs

ID	Term	P-Value
gga03420	Nucleotide excision repair	0.005411
gga03450	Non-homologous end-joining	0.036377
gga05164	Influenza A	0.053726
gga05168	Herpes simplex infection	0.063438
gga03022	Basal transcription factors	0.102782
gga00510	N-Glycan biosynthesis	0.125592
gga04622	RIG-I-like receptor signaling pathway	0.147842
gga04350	TGF-beta signaling pathway	0.181374
gga04070	Phosphatidylinositol signaling system	0.195353
gga04912	GnRH signaling pathway	0.199961
gga04540	Gap junction	0.206826
gga04620	Toll-like receptor signaling pathway	0.213634
gga04114	Oocyte meiosis	0.224855
gga04270	Vascular smooth muscle contraction	0.251162
gga03040	Spliceosome	0.261867
gga04910	Insulin signaling pathway	0.289016
gga04530	Tight junction	0.289016
gga04120	Ubiquitin mediated proteolysis	0.30122
gga04630	Jak-STAT signaling pathway	0.303234
gga04020	Calcium signaling pathway	0.373952

Supplementary table 5

Supplementary table 5 the top 20 GO terms enriched by the DEmiRNAs

GO_accession	Description	Term_type	Over_represented_pValue
GO:0001071	nucleic acid binding transcription factor activity	molecular_function	3.47E-09
GO:0003700	transcription factor activity, sequence-specific DNA binding	molecular_function	3.47E-09
GO:0000975	regulatory region DNA binding	molecular_function	3.46E-08
GO:0001067	regulatory region nucleic acid binding	molecular_function	3.46E-08
GO:0044212	transcription regulatory region DNA binding	molecular_function	3.46E-08
GO:0006366	transcription from RNA polymerase II promoter	biological_process	3.93E-08
GO:0006357	regulation of transcription from RNA polymerase II promoter	biological_process	4.05E-08
GO:0007399	nervous system development	biological_process	2.84E-07
GO:0000976	transcription regulatory region sequence-specific DNA binding	molecular_function	4.23E-07
GO:0030182	neuron differentiation	biological_process	4.88E-07
GO:0043565	sequence-specific DNA binding	molecular_function	8.36E-07
GO:0000981	RNA polymerase II transcription factor activity, sequence-specific DNA binding	molecular_function	9.37E-07
GO:0001012	RNA polymerase II regulatory region DNA binding	molecular_function	4.80E-06
GO:0010468	regulation of gene expression	biological_process	5.76E-06
GO:0006355	regulation of transcription,	biological_process	6.27E-06

GO:1903506	DNA-templated regulation of nucleic acid-templated transcription	biological_process	8.88E-06
GO:2001141	regulation of RNA biosynthetic process	biological_process	8.88E-06
GO:0000977	RNA polymerase II regulatory region sequence-specific DNA binding	molecular_function	9.20E-06
GO:0022008	neurogenesis	biological_process	1.06E-05
GO:0006351	transcription, DNA-templated	biological_process	1.20E-05

Supplementary table 6

Supplementary table 6 the top 20 KEGG pathways enriched by the DEmiRNAs

Pathway_term	P-Value
Intestinal immune network for IgA production	0.003503
Notch signaling pathway	0.004602
Salmonella infection	0.035502
Calcium signaling pathway	0.038652
Phenylalanine metabolism	0.04175
Cell adhesion molecules (CAMs)	0.059811
Lysine degradation	0.061167
Other glycan degradation	0.078013
Influenza A	0.079057
Galactose metabolism	0.101482
Selenocompound metabolism	0.110337
TGF-beta signaling pathway	0.113496
Ribosome	0.141481
beta-Alanine metabolism	0.141632
Steroid hormone biosynthesis	0.144572
Herpes simplex infection	0.168547
Cardiac muscle contraction	0.171007
Oxidative phosphorylation	0.186108
Riboflavin metabolism	0.189984
FoxO signaling pathway	0.196324

Supplementary table 7

Supplementary table 7 the top 20 GO terms enriched by the DEmRNAs

GO_accession	Description	Term_type	Over_represented_pValue
GO:0006955	immune response	biological_process	1.03E-12
GO:0002376	immune system process	biological_process	1.05E-11
GO:0002252	immune effector process	biological_process	3.40E-09
GO:0002682	regulation of immune system process	biological_process	4.36E-09
GO:0050776	regulation of immune response	biological_process	4.58E-09
GO:0019221	cytokine-mediated signaling pathway	biological_process	3.35E-08
GO:0048584	positive regulation of response to stimulus	biological_process	6.00E-08
GO:0002684	positive regulation of immune system process	biological_process	9.45E-07
GO:0009967	positive regulation of signal transduction	biological_process	1.03E-06
GO:0010647	positive regulation of cell communication	biological_process	1.14E-06
GO:0023056	positive regulation of signaling	biological_process	1.58E-06
GO:0071345	cellular response to cytokine stimulus	biological_process	1.61E-06
GO:0070013	intracellular organelle lumen	cellular_component	1.88E-06
GO:0031974	membrane-enclosed lumen	cellular_component	1.97E-06
GO:0043233	organelle lumen	cellular_component	2.02E-06
GO:0051707	response to other organism	biological_process	2.87E-06
GO:0044428	nuclear part	cellular_component	3.37E-06
GO:0034097	response to cytokine stimulus	biological_process	3.50E-06
GO:0043231	intracellular membrane-bounded organelle	cellular_component	3.70E-06
GO:0048518	positive regulation of biological process	biological_process	4.02E-06

Supplementary table 8

Supplementary table 8 the top 20 KEGG pathways enriched by the DEmRNAs

ID	Term	P-Value
gga04630	Jak-STAT signaling pathway	0.000641
gga04060	Cytokine-cytokine receptor interaction	0.00223
gga05168	Herpes simplex infection	0.005513
gga03010	Ribosome	0.005891
gga04620	Toll-like receptor signaling pathway	0.02735
gga04144	Endocytosis	0.033923
gga00790	Folate biosynthesis	0.043411
gga03060	Protein export	0.048304
gga04142	Lysosome	0.052436
gga00770	Pantothenate and CoA biosynthesis	0.059954
gga00860	Porphyrin and chlorophyll metabolism	0.067731
gga03018	RNA degradation	0.081236
gga04672	Intestinal immune network for IgA production	0.125962
gga00250	Alanine, aspartate and glutamate metabolism	0.125962
gga04122	Sulfur relay system	0.133486
gga05164	Influenza A	0.137539
gga04115	p53 signaling pathway	0.150279
gga04150	mTOR signaling pathway	0.190862
gga01210	2-Oxocarboxylic acid metabolism	0.191506
gga00020	Citrate cycle (TCA cycle)	0.231483