

SUPPLEMENTARY TABLES

Supplementary Table 1. Sequences of RT-qPCR primers used.

Gene Name	Forward (5'-3')	Reverse (5'-3')
GAPDH	CCTGCACCACCAACTGCTTA	GGCCATCCACAGTCTTCTGAG
U6	CTCGCTTCGGCAGCACAA	AACGCTTCACGAATTTGCGT
OTUD6B-AS	GACATATCCGGGTGACGTTTT	TTGTTCCACTGTCTTCTGGCATT
has_circ_0010029	AGCTGCTGCTGACTTGAGTG	TTGCTAGTTCTGGAGGCACC
ADM2	TACACGCAGTGCTGGTACG	CTGCTCGTCCAGACATGGC
CAPN6	CAGCAGACTTTTCTGTGATCCA	GGGGACGTTTCCACACCAC
CPXM2	GTGCGCGGGAAGAAATGAC	CCTCCCTTGAGTGATGACACC
HCAR1	AATTTGGCCGTGGCTGATTTT	CCGTAAGGAACACGATGCTCC
NDUFA4L2	CCTGAGCCCCAATGACCAATA	TCTGGCCGGTCTTCTTCA
SORCS2	GTCACCACCGTCATCGACAAT	TTCGTCTGCGCTGAGGAATAG
CA9	GGATCTACCTACTGTTGAGGCT	CATAGCGCCAATGACTCTGGT
MKX	CGAACACTACCATGATGGGAAA	TTCTGATGACGATGGAGACACTA
NLGN4X	GGTTTACCGCCAATTTGGATACT	CCGTGGGCACGTAGATGTT
SULT1B1	TTTATCTGGCTCGTAATGCCAAG	CCATAGGCCACTTTTCCAGTT
HOXA3	GCAAAAAGCGACCTACTACGA	CGTCGGCGCCCAAAG
COL2A1	TGAGCCATGATTTCGCTCG	CCCTTTGGTCTCTGGTTGCC
SOX9	CTGGGAACAACCCGTCTACA	TTCTGGTTGGTCTCTCTTTCTT
MMP13	CACCTTATGCTTCTGATGACG	TCCTCGGAGACTGGTAATGG
si-HOXA3		
HOXA3-homo-1	CCAACGGGUUCGCUUAUAATT	UUAUAAGCGAACCCGUUGGTT
HOXA3-homo-2	GUGGCUAUCUGAACUCUAUTT	AUAGAGUUCAGAUAGCCACTT
HOXA3-homo-3	CCAGCCCUCUUUGGUCUAATT	UUAGACCAAAGAGGGCUGGTT

Please browse Full Text version to see the data of Supplementary Tables 2 and 3.

Supplementary Table 2. Detailed differentially expressed mRNAs between miR-10a-5p overexpression group(exp) and control group(ctrl).

Supplementary Table 3. Detailed differentially expressed lncRNAs between miR-10a-5p overexpression group(exp) and control group(ctrl).

Supplementary Table 4. Detailed differentially expressed miRNAs between miR-10a-5p overexpression group(exp) and control group(ctrl).

miRNA	Chr_Start_End_Strand	miRBaseID	logFC	foldChange	PValue	pAdj	diffState	M3	M4	NC-3	NC-4
hsa-miR-10a-5p	chr17_48579904_48579926_-	MIMAT0000253	13.23001	9607.938	1.2E-106	4.3E-104	up	404.4072	475.7128	0	0.06014
hsa-miR-100-5p	chr11_122152275_122152296_-	MIMAT0000098	1.00197	0.499319	1.19E-05	0.001587	down	1604.797	1714.644	2999.09	3574.008
hsa-miR-193b-3p	chr16_14304017_14304038_+	MIMAT0002819	1.09184	0.469164	1.32E-05	0.001587	down	361.7629	296.0147	452.3804	933.9764
hsa-miR-3619-3p	chr22_46091090_46091111_+	MIMAT0019219	8.58005	0.002613	0.000192	0.013839	down	0	0	4.471834	7.096537
hsa-miR-496	chr14_101060628_101060649_+	MIMAT0002818	8.80211	0.00224	0.00012	0.010782	down	0	0	5.438717	8.058779

Supplementary Table 5. Detailed differentially expressed circRNAs between miR-10a-5p overexpression group(exp) and control group(ctrl).

Chr_Start_E nd_Strand	circBankI D	circbas eID	spliced SeqLen gth	Gene	mouse_cons erved_circR NA	startE ndReg ion	log FC	fold Cha nge	PV alu e	pA dj	diff Sta te	M1	M2	NC -3	NC -4
chr17_81042813_81043199_+				MET RNL		exon- exon	6.4 620 89	88.1 6225	2.8 8E- 05	0.0 037 01	up	1.0 425 8	0.2 273 58	0	0
chr14_99723 807_9972417 6_-	hsa_circBC L11B_002	hsa_cir c_0033 144	369	BCL1 1B	mmu_circ_0 000414	exon- exon	6.0 104 97	64.4 6734	8.6 5E- 06	0.0 016 69	up	0.4 170 32	0.5 305 03	0	0
chr15_89656 955_8965975 2_+	hsa_circAB HD2_007	hsa_cir c_0007 099	300	ABH D2	mmu_circ_0 014410	exon- exon	6.0 028	64.1 2433	7.1 2E- 05	0.0 054 99	up	0.6 950 53	0.2 273 58	0	0
chr13_76195898_76335174_+				LMO 7		exon- exon	5.3 222 77	40.0 0966	0.0 002 88	0.0 159 07	up	0.3 475 27	0.2 273 58	0	0
chr7_262328 70_26232993 _-	hsa_circHN RNPA2B1_ 019	hsa_cir c_0001 689	123	HNR NPA2 B1		exon- exon	5.3 222 77	40.0 0966	0.0 002 88	0.0 159 07	up	0.3 475 27	0.2 273 58	0	0
chr14_35331 249_3533152 8_-	hsa_circBA Z1A_004	hsa_cir c_0006 137	279	BAZ1 A		exon- exon	4.9 202 85	30.2 7982	0.0 017 35	0.0 768 06	up	0.2 085 16	0.2 273 58	0	0
chr16_85667 519_8566773 8_+	hsa_circKI AA0182_00 1	hsa_cir c_0000 722	219	GSE1	mmu_circ_0 001730	exon- exon	4.1 109 17	17.2 7864	6.6 8E- 05	0.0 054 99	up	0.4 170 32	1.5 915 09	0	0.0 907 27
chr1_155646 338_1556493 03_-	hsa_circYY IAP1_008	hsa_cir c_0014 606	459	YY1 API		exon- exon	2.4 501 28	5.46 4644	0.0 028 27	0.0 991 92	up	0.9 730 75	0.4 547 17	0.1 604 78	0.0 907 27
chr5_647473 01_64769779 _-	hsa_circAD AMTS6_00 4	hsa_cir c_0072 688	1352	ADA MTS6	mmu_circ_0 004419	exon- exon	2.1 296 8	0.22 8508	0.0 019 68	0.0 768 06	do wn	0.1 390 11	0.3 031 45	0.8 023 89	1.0 887 2
chr1_141049 12_14109326 _+	hsa_circPR DM2_011	hsa_cir c_0010 029	4414	PRD M2		exon- exon	5.2 503 5	0.02 6272	0.0 019 9	0.0 768 06	do wn	0	0	0.1 604 78	0.3 629 07

Please browse Full Text version to see the data of Supplementary Tables 6 to 10.

Supplementary Table 6. Detailed GO analysis (biological process) of differentially expressed mRNAs.

Supplementary Table 7. Detailed GO analysis (cellular component) of differentially expressed mRNAs.

Supplementary Table 8. Detailed GO analysis(molecular function) of differentially expressed mRNAs.

Supplementary Table 9. Detailed KEGG analysis of differentially expressed mRNAs.

Supplementary Table 10. Detailed GO analysis(biological process) of ci-genes of differentially expressed lncRNAs.

Supplementary Table 11. Detailed GO analysis (cellular component) of ci-genes of differentially expressed lncRNAs.

databaseID	Description	type	geneRatio	bgRatio	pvalue	padj	qvalue	enrichScore	overlapGeneList	overlapGeneCount
GO:0030120	vesicle coat	cellular component	5/267	48/18678	0.000596	0.177015	0.177015	7.286985	PEF1/COPZ1/EPN2/SYNRG/SEC24B	5
GO:0030117	membrane coat	cellular component	6/267	86/18678	0.001459	0.177015	0.177015	4.880585	PEF1/COPZ1/EPN2/SYNRG/VPS33B/SEC24B	6
GO:0048475	coated membrane	cellular component	6/267	86/18678	0.001459	0.177015	0.177015	4.880585	PEF1/COPZ1/EPN2/SYNRG/VPS33B/SEC24B	6
GO:0031463	Cu3-RING ubiquitin ligase complex	cellular component	3/267	34/18678	0.012465	0.640758	0.640758	6.172505	ENC1/GAN/PEF1	3
GO:0005667	transcription factor complex	cellular component	9/267	270/18678	0.015966	0.640758	0.640758	2.331835	BRF1/BRF2/JUNB/SFPQ/SNF8/HAND2/SIX1/TBX2/NFYC	9
GO:0030658	transport vesicle membrane	cellular component	7/267	188/18678	0.018699	0.640758	0.640758	2.60471	PEF1/RAB1A/SCAMP1/DNM1L/SPRED2/SYNRG/SEC24B	7
GO:0030118	clathrin coat DNA	cellular component	3/267	41/18678	0.020646	0.640758	0.640758	5.118663	EPN2/SYNRG/VPS33B	3
GO:0044815	packaging complex	cellular component	5/267	113/18678	0.023175	0.640758	0.640758	3.095356	HIST2H3D/SMC4/H2BFWT/HIST1H2AI/HIST4H4	5
GO:0062023	collagen-containing extracellular matrix	cellular component	11/267	399/18678	0.02902	0.640758	0.640758	1.928586	A1BG/ADAMTS1/COL4A5/COL9A2/FGA/FMOD/SERP1NB6/LOXL1/ADAMTS9/IGFBP7/LTBP3	11
GO:0030135	coated vesicle	cellular component	8/267	261/18678	0.034503	0.640758	0.640758	2.144216	EPGN/PEF1/SCAMP1/COPZ1/EPN2/SYNRG/VPS33B/SEC24B	8
GO:0030662	coated vesicle membrane	cellular component	6/267	169/18678	0.034792	0.640758	0.640758	2.483611	EPGN/PEF1/COPZ1/EPN2/SYNRG/SEC24B	6
GO:0031012	extracellular matrix	cellular component	12/267	468/18678	0.037407	0.640758	0.640758	1.793719	A1BG/ADAMTS1/CHI3L1/COL4A5/COL9A2/FGA/FMOD/SERP1NB6/LOXL1/ADAMTS9/IGFBP7/LTBP3	12

Supplementary Table 12. Detailed GO analysis(molecular function) of ci-genes of differentially expressed lncRNAs.

databaseID	Description	type	geneRatio	bgRatio	pvalue	padj	qvalue	enrichScore	overlapGeneList	Overlap GeneCount
GO:0016651	oxidoreductase activity, acting on NAD(P)H	molecular function	6/247	96/16969	0.002787	0.375998	0.372662	4.293775	AKR1C2/AKR1C3/CBR1/TXNRD2/DHRS4/MIOX	6
GO:0004033	aldo-keto reductase (NADP) activity	molecular function	3/247	23/16969	0.004351	0.375998	0.372662	8.960922	AKR1C2/AKR1C3/MIOX	3
GO:0004722	protein serine/threonine phosphatase activity	molecular function	4/247	49/16969	0.005557	0.375998	0.372662	5.608196	CTDSP2/DUSP4/PPA2/UBLCP1	4
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	molecular function	3/247	26/16969	0.006186	0.375998	0.372662	7.92697	FKBP11/FKBP2/FKBP8	3
GO:0016859	cis-trans isomerase activity	molecular function	3/247	28/16969	0.007629	0.375998	0.372662	7.360758	FKBP11/FKBP2/FKBP8	3
GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	molecular function	6/247	120/16969	0.008242	0.375998	0.372662	3.43502	AKR1C2/AKR1C3/CBR1/DHRS4/MIOX/VKORC1L1	6
GO:0016655	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor	molecular function	4/247	57/16969	0.009467	0.375998	0.372662	4.821081	AKR1C2/AKR1C3/CBR1/DHRS4	4
GO:0097718	disordered domain specific binding	molecular function	3/247	31/16969	0.010139	0.375998	0.372662	6.648426	FKBP8/KCNA1/GAPDH GABPB1/APOA2/BCL2/HIST2H3D/PEF1/SMC4/SRGAP2C/TMCC1/HAND2/H2BFWT/HIST1H2A1/HIST4H4/NFYC/SUCLG2	3
GO:0046982	protein heterodimerization activity	molecular function	14/247	497/16969	0.014367	0.480885	0.476619	1.935223	BCL2/EIF2AK3/PPP1R3G/SYK/JAK1/VCP/MAGI2	14
GO:0019902	phosphatase binding	molecular function	7/247	177/16969	0.015129	0.480885	0.476619	2.716965	BCL2/EIF2AK3/PPP1R3G/SYK/JAK1/VCP/MAGI2	7
GO:0004715	non-membrane spanning protein tyrosine kinase activity	molecular function	3/247	37/16969	0.016446	0.487889	0.483561	5.570303	CLK1/SYK/JAK1	3
GO:0016706	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	molecular function	3/247	40/16969	0.020259	0.514465	0.509901	5.15253	ASPHD1/EGLN1/KDM4C	3
GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	molecular function	5/247	108/16969	0.02084	0.514465	0.509901	3.180574	AKR1C2/AKR1C3/CBR1/DHRS4/MIOX	5
GO:0005201	extracellular matrix structural constituent	molecular function	6/247	158/16969	0.028244	0.514465	0.509901	2.608876	CHI3L1/COL4A5/COL9A2/FGA/FMOD/IGFBP7	6
GO:0016853	isomerase activity	molecular function	5/247	122/16969	0.03299	0.514465	0.509901	2.81559	FKBP11/FKBP2/FKBP8/HPGDS/K	5

GO ID	GO Term	Category	Count	bgCount	pvalue	padj	qvalue	enrichScore	Overlap Genes	Count
GO:0070888	E-box binding	molecular function	3/247	49/16969	0.034364	0.514465	0.509901	4.206147	ATNAL1 SFPQ/HAND2/TFAP4	3
GO:0019903	protein phosphatase binding	molecular function	5/247	132/16969	0.043906	0.514465	0.509901	2.602288	BCL2/EIF2AK3/PPP1R3G/JAK1/VCP	5
GO:0015171	amino acid transmembrane transporter activity	molecular function	3/247	55/16969	0.045956	0.514465	0.509901	3.747295	SLC25A22/SLC36A1/SLC6A18	3

Supplementary Table 13. Detailed KEGG analysis of ci-genes of differentially expressed lncRNAs.

databaseID	Description	geneRatio	bgRatio	pvalue	padj	qvalue	enrichScore	overlapGeneList	overlapGeneCount
hsa04724	Glutamatergic synapse	5/102	114/7946	0.015404	0.823484	0.823484	3.416753	GNAI1/GNG11/GRM6/DLGAP1/SHANK2	5
hsa05034	Alcoholism	6/102	184/7946	0.030703	0.823484	0.823484	2.540281	GNAI1/GNG11/HIST2H3D/H2BFWT/HIST1H2AI/HIST4H4	6
hsa05202	Transcriptional misregulation in cancer	6/102	186/7946	0.032134	0.823484	0.823484	2.512966	HIST2H3D/IGFBP3/TGFB2/ID2/SIX1/ZBTB16	6
hsa04974	Protein digestion and absorption	4/102	95/7946	0.033515	0.823484	0.823484	3.280083	COL4A5/COL9A2/SLC36A1/SLC7A7	4
hsa00240	Pyrimidine metabolism	3/102	57/7946	0.036469	0.823484	0.823484	4.100103	DCTD/NT5E/NT5M	3
hsa05134	Legionellosis	3/102	57/7946	0.036469	0.823484	0.823484	4.100103	CLK1/RAB1A/VCP	3
hsa00590	Arachidonic acid metabolism	3/102	63/7946	0.046869	0.823484	0.823484	3.709617	AKR1C3/CBR1/HPGDS	3

Please browse Full Text version to see the data of Supplementary Table 14.

Supplementary Table 14. Detailed GO analysis (biological process) of parent genes of differentially expressed circRNAs.

Supplementary Table 15. Detailed GO analysis(cellular component) of parent genes of differentially expressed circRNAs.

Database ID	Description	type	geneRatio	bgRatio	pvalue	padj	qvalue	enrichScore	Overlap GeneList	Overlap GeneCount
GO:0070603	SWI/SNF superfamily-type complex	cellular component	2/9	68/18678	0.000462	0.013516	0.007114	61.03922	YY1AP1/BAZ1A	2
GO:1904949	ATPase complex	cellular component	2/9	92/18678	0.000845	0.013516	0.007114	45.11594	YY1AP1/BAZ1A	2
GO:0097524	sperm plasma membrane	cellular component	1/9	6/18678	0.002888	0.030805	0.016213	345.8889	ABHD2	1
GO:0031010	ISWI-type complex	cellular component	1/9	11/18678	0.005289	0.038433	0.020228	188.6667	BAZ1A	1
GO:0031011	Ino80 complex	cellular component	1/9	15/18678	0.007206	0.038433	0.020228	138.3556	YY1AP1	1
GO:0033202	DNA helicase complex	cellular component	1/9	15/18678	0.007206	0.038433	0.020228	138.3556	YY1AP1	1
GO:0000790	nuclear chromatin	cellular component	2/9	309/18678	0.009095	0.041578	0.021883	13.43258	YY1AP1/BAZ1A	2
GO:0097346	INO80-type complex	cellular component	1/9	22/18678	0.010553	0.042213	0.022217	94.33333	YY1AP1	1
GO:0044454	nuclear chromosome part	cellular component	2/9	469/18678	0.020151	0.071649	0.03771	8.850036	YY1AP1/BAZ1A	2
GO:0000785	chromatin	cellular component	2/9	500/18678	0.022729	0.072732	0.03828	8.301333	YY1AP1/BAZ1A	2
GO:0015030	Cajal body	cellular component	1/9	75/18678	0.035571	0.096195	0.050629	27.67111	HNRNPA2B1	1
GO:0071013	catalytic step 2 spliceosome	cellular component	1/9	82/18678	0.038833	0.096195	0.050629	25.30894	HNRNPA2B1	1
GO:0036126	sperm flagellum	cellular component	1/9	84/18678	0.039763	0.096195	0.050629	24.70635	ABHD2	1
GO:0097729	9+2 motile cilium	cellular component	1/9	89/18678	0.042085	0.096195	0.050629	23.31835	ABHD2	1
GO:0001669	acrosomal vesicle	cellular component	1/9	103/18678	0.04856	0.099885	0.052571	20.14887	ABHD2	1
GO:0016363	nuclear matrix	cellular component	1/9	106/18678	0.049942	0.099885	0.052571	19.57862	HNRNPA2B1	1

Supplementary Table 16. Detailed GO analysis (molecular function) of parent genes of differentially expressed circRNAs.

Database ID	Description	type	geneRatio	bgRatio	pvalue	padj	qvalue	enrichScore	Overlap GeneList	overlapGene Count
GO:0097157	pre-mRNA intronic binding	molecular function	1/10	6/16969	0.003531	0.047093	0.022776	282.8167	HNRNPA2B1	1
GO:0047372	acylglycerol lipase activity	molecular function	1/10	7/16969	0.004119	0.047093	0.022776	242.4143	ABHD2	1
GO:1990247	methyladenosine-containing RNA binding	molecular function	1/10	7/16969	0.004119	0.047093	0.022776	242.4143	HNRNPA2B1	1
GO:0098505	G-rich strand telomeric DNA binding	molecular function	1/10	10/16969	0.005879	0.047093	0.022776	169.69	HNRNPA2B1	1
GO:0043047	single-stranded telomeric DNA binding	molecular function	1/10	11/16969	0.006465	0.047093	0.022776	154.2636	HNRNPA2B1	1
GO:0098847	sequence-specific single stranded DNA binding	molecular function	1/10	13/16969	0.007637	0.047093	0.022776	130.5308	HNRNPA2B1	1

GO:0035 198	miRNA binding	molecular function	1/10	31/16969	0.0181 24	0.077857	0.037655	54.73871	HNRNPA2 B1	1
GO:0042 162	telomeric DNA binding DNA-binding transcription	molecular function	1/10	34/16969	0.0198 62	0.077857	0.037655	49.90882	HNRNPA2 B1	1
GO:0001 228	activator activity, RNA polymerase II-specific	molecular function	2/10	390/1696 9	0.0209 86	0.077857	0.037655	8.702051	BCL11B/P RDM2	2
GO:0061 980	regulatory RNA binding histone-lysine	molecular function	1/10	37/16969	0.0215 97	0.077857	0.037655	45.86216	HNRNPA2 B1	1
GO:0018 024	N- methyltransfe rase activity	molecular function	1/10	43/16969	0.0250 6	0.077857	0.037655	39.46279	PRDM2	1
GO:0042 054	histone methyltransfe rase activity steroid	molecular function	1/10	52/16969	0.0302 33	0.077857	0.037655	32.63269	PRDM2	1
GO:0003 707	hormone receptor activity	molecular function	1/10	54/16969	0.0313 79	0.077857	0.037655	31.42407	ABHD2	1
GO:0036 002	pre-mRNA binding protein-lysine	molecular function	1/10	54/16969	0.0313 79	0.077857	0.037655	31.42407	HNRNPA2 B1	1
GO:0016 279	N- methyltransfe rase activity	molecular function	1/10	57/16969	0.0330 96	0.077857	0.037655	29.77018	PRDM2	1
GO:0016 278	lysine N- methyltransfe rase activity	molecular function	1/10	58/16969	0.0336 68	0.077857	0.037655	29.2569	PRDM2	1
GO:0003 730	mRNA 3'- UTR binding	molecular function	1/10	67/16969	0.0388	0.084446	0.040842	25.32687	HNRNPA2 B1	1
GO:0008 276	protein methyltransfe rase activity	molecular function	1/10	80/16969	0.0461 69	0.087124	0.042137	21.21125	PRDM2	1
GO:0042 562	hormone binding	molecular function	1/10	81/16969	0.0467 34	0.087124	0.042137	20.94938	ABHD2	1
GO:0008 170	N- methyltransfe rase activity	molecular function	1/10	86/16969	0.0495 53	0.087124	0.042137	19.7314	PRDM2	1

Supplementary Table 17. Detailed KEGG analysis of parent genes of differentially expressed circRNAs.

databaseID	Description	geneRatio	bgRatio	pvalue	padj	qvalue	enrichScore	overlapGeneList	overlapGeneCount
hsa00310	Lysine degradation	1/3	61/7946	0.022857	0.039856	0.013984	43.42077	PRDM2	1
hsa04520	Adherens junction	1/3	71/7946	0.02657	0.039856	0.013984	37.30516	LMO7	1

Please browse Full Text version to see the data of Supplementary Tables 18 to 20.

Supplementary Table 18. Detailed GSEA(biological process) of differentially expressed mRNAs.

Supplementary Table 19. Detailed GSEA(KEGG) of differentially expressed mRNAs.

Supplementary Table 20. The network degree analysis of all the differentially-expressed mRNAs using CytoHubba.