

## **Supplementary tables**

**Table S3.** Information of primers and probes used in this study.

**Table S4.** The distribution of putative spliced length of exonic circRNAs.

**Table S5.** Exon numbers of identified exonic circRNAs.

**Table S6.** The circRNAs expressed higher than its host genes.

**Table S7.** The number of circRNAs produced from one gene.

**Table S12.** Information of tissue-specific RBPs.

**Table S3. Information of primers and probes used in this study**

Name	Sequence (5'-3')	Usage	Target name
F1	GCTCGTAAAATTAGACTGACTGCATTG	RT-qPCR	circLIFR
R1	ATGAGGAGCCCCCTTTTTCTGG		
F2	ATTTGTCTGCTGATTTCTCAACCTC		
R2	TAAATGTTGATAACAGCCACTGGA	divergent primer for PCR	LIFR
F3	GCATTGCACAGATGATGGATATT	convergent primer for PCR	
R3	TGTTCCAGAGGGTGCTTTC		
F4	TTCTGTTTCTGCAAGTAGTGGA	divergent primer for PCR	LIFR
R4	GTATCTTTGCCATTCAGAGTTGTG	convergent primer for PCR	
F5	CACAACTCTGAATGGCAAAGATAC		
R5	TCCACTACTTGCAGAAACAGAA		
F6	ACATCATCCCTGCCTCTACT	PCR	GAPDH
R6	CTCTCTTCCTCTTGCTCTTG		
F7	CGCTTCGGCAGCACATATAC	RT-qPCR	U6
R7	AGGGGCCATGCTAATCTTCT		
F8	AGGCCAACCGCGAGAAGATG	RT-qPCR	Actin
R8	GCCAGAGGCGTACAGGGATA		
F9	TTCAGCGATACCACAACCTCC	RT-qPCR	Vinculin
R9	AGTTAGCTGCCCTCTCATCA		
F10	ATTTTTTTTATTTTATGCAGGACTGACTG CATTGCACAGAT	Cloning	circLIFR
R10	TTGGAATTTTGAATACTTACTAATTTTACG AGCTCCATACTCTCTTTACG		
probe1	GCAATGCAGTCAGTCTAATTTTACGAGCT	FISH probe	circLIFR
probe2	GCTAATCTTCTCTGTATCGTTCCAATTTT AGTATATGTGCTGCCG	FISH probe	U6
probe3	CATGGCTTAATCTTTGAGAC	FISH probe	18S
F11	TGCTGGGACTTCCTATGTG	RT-qPCR	FN1
R11	CCTCGATTATCCTTCTTGC		
F12	CCACCAAAGTCACGCTGAAT	RT-qPCR	CDH1
R12	CCAGGAGAGGAGTTGGGAAA		
F13	CCGTTGGCATGAAGTGTATGA	RT-qPCR	CLDN1
R13	GCCAGACCTGCAAGAAGAAATA		
F14	TGTTTCCAAGCCTGACCTCA	RT-qPCR	Vimentin
R14	CGTACTCAGTGGACTCCTG		
F15	TAGTGGGTGGGATTGAGGTATG	RT-qPCR	AGR
R15	CTCCATGGCAACTCTGGATTC		
F16	ATTCAGAGGCATCGTTGGAC	RT-qPCR	COL17A 1
R16	TAAGACGAGAGGTCCTCCAC		

F17	CAAGCACAGCCAGTCCA	RT-qPCR	AXL
R17	TCCTAGCAGTACATACCACCA		
F18	CCTCAACGGCGAGATCAG	RT-qPCR	ID1
R18	ACCCACAGAGCACGTAATTC		
F19	CAGCCAACGAGCGGAAA	RT-qPCR	LGALS3
R19	CATCCTTGAGGGTTTGGGTT		
F20	CCTGAATCTCAAACCTGGAGAG	RT-qPCR	LGALS1
R20	CACAGGTTGTTGCTGTCTTTG		
F21	GAAGAGATGGAGCGTGCC	RT-qPCR	LTBP3
R21	GCACATGCCGTCCTCTC		
F22	TATGACCCAGGTGTACGAGAG	RT-qPCR	IRAK1
R22	AGTGCTGGACACGTAGGA		
F23	GCGAGTCTGAATGGAAGGATAC	RT-qPCR	C1QBP
R23	TCGGCAAGGAAATCCATTAGG		
F24	GACACTCCATCACAGTCACTAC	RT-qPCR	VTCN1
R24	ACCTTCCTTCAGCCATTGTATC		
F25	CGCAGGGTGTGCAGATT	RT-qPCR	HSPD1
R25	GCGAGTGAGGGACAGAGT		
F26	CACATCAGCACCAAGACCATAG	RT-qPCR	SERPIN E2
R26	TTCAGCGGCTCCTTCAAATC		
F27	TGCTTATTGGACCTCAGTGTG	RT-qPCR	ITGB6
R27	CTACTTGGGAGACAGGGTTTTTC		

Sequences that spanning junction site within the qPCR primers are marked in grey.

**Table S4. The distribution of putative spliced length of exonic circRNAs**

<b>Putative spliced length of circRNA</b>	<b>CircRNA number</b>	<b>Percentage (%)</b>
0~200	2,152	3.65
200~400	16,914	28.66
400~600	12,942	21.93
600~800	8,484	14.37
800~1000	5,516	9.34
1000~1200	3,646	6.18
1200~1400	2,444	4.14
1400~1600	1,736	2.94
1600~1800	1,253	2.12
1800~2000	960	1.63
>2000	2,973	5.04

**Table S5. Exon numbers of identified exonic circRNAs**

<b>Exon number of exonic circRNA</b>	<b>CircRNA number</b>	<b>Percentage (%)</b>
1	1,952	3.31
2	11,406	19.33
3	10,756	18.22
4	8,580	14.54
5	6,490	11.00
6	4,867	8.25
7	3,564	6.04
8	2,671	4.52
9	2,018	3.42
10	1,443	2.44
>10	5,273	8.93

**Table S6. The circRNAs expressed higher than its host genes**

<b>circRNA</b>	<b>Host gene</b>	<b>Average junction ratio of circRNA</b>	<b>Average FPKM expression of gene</b>
hsa_circ_0000471	N4BP2L2	0.7824974	46.558716
hsa_circ_0099634	RMST	0.9566105	83.866626
hsa_circ_0000284	HIPK3	0.6274854	33.628894
hsa_circ_0006374	ARCN1	0.9990338	16.093043
hsa_circ_0007383	ARCN1	0.9987578	16.093043
hsa_circ_0005589	ARCN1	0.9937304	16.093043
hsa_circ_0000835	MIB1	0.8985182	14.372139
hsa_circ_0007817	HUWE1	0.9958366	21.997406
hsa_circ_0006192	ZHX3	0.7328196	14.649046
hsa_circ_0003910	SUMF1	0.9457619	14.209606
hsa_circ_0005232	SLC8A1	0.7920198	15.600111
hsa_circ_0000994	SLC8A1	0.5780236	15.600111
hsa_circ_0008260	RGPD5	0.6850834	11.916058
hsa_circ_0006139	RGPD6	0.9840918	11.119681
hsa_circ_0007951	ABI2	0.7374374	16.954799
hsa_circ_0002316	OMA1	0.8840141	14.269048
hsa_circ_0008433	PDE4B	0.8253544	16.107127
hsa_circ_0006091	RGS12	0.5231434	10.879712
hsa_circ_0126176	PCDH7	0.9815851	12.986978
hsa_circ_0001451	FBXW7	0.7319191	16.447917
hsa_circ_0002210	ZNF706	0.5163743	25.501214
hsa_circ_0136839	ERICH1	0.9365828	10.706035

**Table S7. The number of circRNAs produced from one gene**

<b>CircRNA number produced from one gene</b>	<b>Gene number</b>	<b>Percentage (%)</b>
1	2,279	26.46
2	1,274	14.79
3	850	9.87
4	634	7.36
5	527	6.12
6	378	4.39
7	339	3.93
8	275	3.19
9	241	2.80
10	195	2.26
>10	1,622	18.83

**Table S12. Information of tissue-specific RBPs**

<b>RBP</b>	<b>Gene ID</b>	<b>Type</b>	<b>Tissue</b>	<b>Tissue specificity index (TSI)</b>
ADARB2	ENSG00000185736.11	Deaminase	Brain	0.953734
CELF3	ENSG00000159409.10	RNA splicing	Brain	0.991312
KHDRBS3	ENSG00000131773.9	RNA splicing	Brain	0.906729
NOVA1	ENSG00000139910.15	RNA splicing	Brain	0.903156
QKI	ENSG00000112531.12	RNA splicing	Brain	0.863486
RBFOX1	ENSG00000078328.15	RNA splicing	Brain	0.997668
RPP21	ENSG00000241370.1	Endonuclease	Esophagus	0.926018
SRSF12	ENSG00000154548.8	RNA splicing	Brain	0.899597