Table S1. Primers used for qRT-PCR

Target	Primer	Sequence
Hsa_circ_0062558	F	CTAGCTATGCCTACTTCCTGCG
	R	CCAGAGCCTTCACCTTCACA
MMP11	F	GGAGAAGACGGACCTCACCTACAG
	R	CAGTACCTGGCGAAGTCGATCATG
GPRIN1	F	CCCCTCCCCAACCTGCTTCTC
	R	AGGACACAGGCTCTGGCTTCC
NR3C2	F	GCTGGAAGAAATGATTGCATCA
	R	AACTTCTTTGACTTTCGTGCTC
SCL19A3	F	GGCCTACTACGCCTACATATAC
	R	TGACGTTGAGGTAAAAGTACGA
18S	F	GTAACCCGTTGAACCCCATT
	R	CCATCCAATCGGTAGTAGCG
GAPDH	F	CAGGAGGCATTGCTGATGAT
	R	GAAGGCTGGGGCTCATTT
Hsa-miR-661	RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACACGCGC
	F	TGCCTGGGTCTCTGGCCT
Hsa-miR-1204	RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACATAATG
	F	GCGTCGTGGCCTGGTCTC
Hsa-miR-1207	RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCCCCTC
	F	CGTGGCAGGGAGGCTGG
Hsa-miR-4736	RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCAGCCC
	F	GCGCGAGGCAGGTTATCT
Hsa-miR-4763-3p	RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCCCGCC
	F	GCAGGGGCTGGTGCTG
Hsa-miR-7150	RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTACCTC
	F	CGCGCTGGCAGGGGGA
miRNA	Universal R	AGTGCAGGGTCCGAGGTATT
U6	F	CTCGCTTCGGCAGCACA
	R	AACGCTTCACGAATTTGCGT

Table S2. Part of DE circRNAs and common DE genes as host genes in BC (fold change > ±10, $P < 0.05$)

circRNA_ID	Fold change	*P* value	Best transcript	Host gene	Fold change	*P* value
hsa_circ_0069094	103.613626	0.0024	NM_005980	S100P	68.69675	0.0021
hsa_circ_0062558	23.567239	0.0007	NM_005940	MMP11	29.80927	0.0007
hsa_circ_0074026	17.7777225	0.0065	NM_002653	PITX1	17.7219	0.0053
hsa_circ_0074027	17.1288669	0.0042	NM_002653	PITX1	17.7219	0.0053
hsa_circ_0079876	15.3805703	0.0005	NM_018685	ANLN	8.402977	0.0028
hsa_circ_0079866	14.9940773	0.0002	NM_018685	ANLN	8.402977	0.0028
hsa_circ_0001925	12.6093883	0.0005	NM_012310	KIF4A	8.248154	0.0008
hsa_circ_0079872	12.5857654	0.0003	NM_018685	ANLN	8.402977	0.0028
hsa_circ_0015977	12.3346156	0.0007	NM_014176	UBE2T	8.724626	0.0013
hsa_circ_0079878	12.2509349	0.0014	NM_018685	ANLN	8.402977	0.0028
hsa_circ_0079944	11.9347553	0.0030	NM_002192	INHBA	8.253856	0.0067
hsa_circ_0090955	11.7859099	0.0019	NM_012310	KIF4A	8.248154	0.0008
hsa_circ_0007051	11.2504408	0.0020	NM_030919	FAM83D	12.67857	0.0028
hsa_circ_0015763	10.9603632	0.0022	NM_018136	ASPM	5.985841	0.0104
hsa_circ_0012026	10.7941726	0.0143	NM_001255	CDC20	7.659971	0.0274
hsa_circ_0015765	10.0719392	0.0007	NM_018136	ASPM	5.985841	0.0104
hsa_circ_0017545	-10.540751	0.0054	NM_003739	AKR1C3	-8.21863	0.0073
hsa_circ_0066033	-10.749973	0.0003	NM_020163	SEMA3G	-8.17348	0.0012
hsa_circ_0074574	-10.789315	0.0063	NM_002084	GPX3	-12.2012	0.0193
hsa_circ_0017544	-12.174178	0.0073	NM_003739	AKR1C3	-8.21863	0.0073
hsa_circ_0017532	-13.693181	0.0160	NM_001353	AKR1C1	-13.4497	0.0118
hsa_circ_0074576	-14.143032	0.0088	NM_002084	GPX3	-12.2012	0.0193
hsa_circ_0017650	-15.71248	0.0005	NM_030569	ITIH5	-22.415	0.0011
hsa_circ_0017546	-16.153601	0.0097	NM_003739	AKR1C3	-8.21863	0.0073
hsa_circ_0017528	-16.294634	0.0138	NM_001353	AKR1C1	-13.4497	0.0118
hsa_circ_0017538	-18.242858	0.0217	NM_001353	AKR1C1	-13.4497	0.0118
hsa_circ_0017535	-19.83211	0.0158	NM_001353	AKR1C1	-13.4497	0.0118
hsa_circ_0017536	-24.758651	0.0129	NM_001353	AKR1C1	-13.4497	0.0118
hsa_circ_0017537	-26.490034	0.0143	NM_001353	AKR1C1	-13.4497	0.0118
hsa_circ_0019218	-46.176021	0.0107	NM_006744	RBP4	-52.1616	0.0039
hsa_circ_0019217	-68.617726	0.0057	NM_006744	RBP4	-52.1616	0.0039