Supplementary Materials

Supplementary Tables

Table S1. Basic traits of the seven microarray datasets from the Gene Expression Omnibus and The Cancer Genome Atlas.

Data source	Platform	Series	Sample size (T/N)
mRNA	GPL13376	GSE28425	7/4
	GPL6102	GSE36004	7/4
	GPL20148	GSE99671	18/18
	GPL20301	GSE126209	6/5
	NONE	TARGET	172/0
miRNA	GPL8227	GSE28425	7/4
miRNA	GPL15497	GSE79181	25/0
circRNA	GPL27741	GSE140256	3/3

circRNA: circular RNA; miRNA: microRNA; TARGET: Therapeutically Applicable Research To Generate Effective Treatments; T/N: Tumor/Normal

Table S2. Basic characteristics of the nine differentially expressed circRNAs

Circbase ID	Circbank ID	Position	logFC	Best Transcript.	Gene symbol
hsa_circ_0000006	hsa_circSLC35E2B_001	chr1:1601102-1666274	-5.726396	ENSG00000189339	SLC35E2B
hsa_circ_0010220	hsa_circARHGEF10L_022	chr1:17907047-18024370	4.720786	ENSG00000074964	ARHGEF10L
hsa_circ_0046264	hsa_circP4HB_004	chr17:79813017-79817263	-5.151344	ENSG00000185624	P4HB
hsa_circ_0000253	hsa_circBLNK_001	chr10:97999787-97999925	3.918484	ENSG00000095585	BLNK
hsa_circ_0078767	hsa_circFAM120B_001	chr6:170615843-170639638	-3.408189	ENSG00000112584	FAM120B
hsa_circ_0094088	hsa_circSFMBT2_016	chr10:7318853-7407477	-3.031948	ENSG00000198879	SFMBT2
hsa_circ_0096041	hsa_circFADS2_007	chr11:61615630-61616333	-3.652404	ENSG00000134824	FADS2
hsa_circ_0020378	hsa_circDOCK1_001	chr10:128594022-128926028	2.257567	ENSG00000150760	DOCK1
hsa_circ_0049271	hsa_circKEAP1_001	chr19:10610070-10610756	-2.305592	ENSG00000079999	KEAP1

Table S3. Index of concordance (C-index) and variance inflation factor (VIF) of ABCA8, CXCL12, and CAT.

RNAs	C-index	se.std(c-d)	VIF
ABCA8	0.71265378	0.07185655	1.047288
CXCL12	0.76449912	0.06377504	1.040183
CAT	0.79964851	0.04708802	1.088380
ALL	0.87170475	0.03595308	

Table S4. LASSO and cox analysis of ceRNA with coef/se(coef) < 0.01 and *P*-value of proportional hazards assumption (PH) > 0.05.

RNAs	beta	Hazard_Ratio	coef/se(coef)	Chi-sq	p-value
ABCA8	-0.44	0.65	0.01	1.12	0.29
CAT	-0.68	0.51	<0.01	2.01	0.16
CXCL12	-0.47	0.62	<0.01	0.69	0.41

Table S5. Robust rank aggregation analysis of ABCA8, CXCL12, and CAT. LogFC in the four datasets and RRA score of the three RNAs.

RNAs	GSE99671	GSE36004	GSE28425	GSE126209	Score	Regulation
ABCA8	-1.46	-2.11	-2.12	1.20	0.030856845	down
CAT	-1.42	-3.02	-3.01	-0.08	0.020256705	down
CXCL12	-1.46	-4.67	-4.67	-4.89	0.003133094	down