## Identification of circular RNAs as a promising new class of diagnostic biomarkers for human breast cancer

## SUPPLEMENTARY MATERIALS

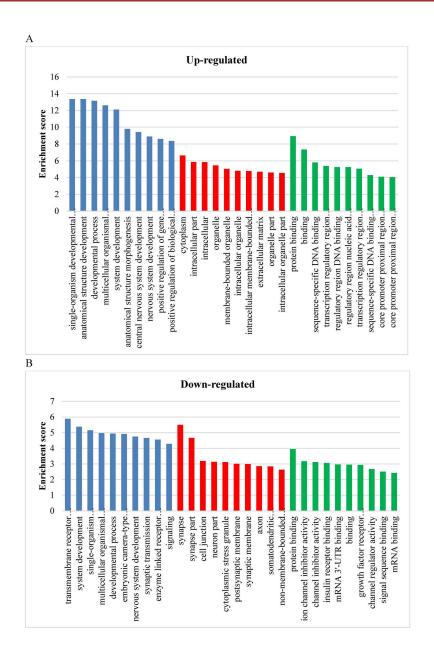
## SUPPLEMENTARY TABLES AND FIGURES

Supplementary Table	1: Detailed information about	the four patients included in	the microarray analysis
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No	Ages	Ethnic	Menopausal	TNM	ER	PR	HER2	Histological type
1	46	Chinese Han	pre-	T2N0M0	positive	positive	negative	invasive ductal carcinoma
2	62	Chinese Han	post-	T2N0M0	positive	positive	positive	invasive ductal carcinoma
3	41	Chinese Han	pre-	T2N2M0	positive	negative	negative	invasive ductal carcinoma
4	74	Chinese Han	post-	T1N0M0	negative	negative	positive	invasive ductal carcinoma

Supplementary Table 2: The circRNA levels ( $\Delta Ct$ ) and clinical factors of patients with breast cancer

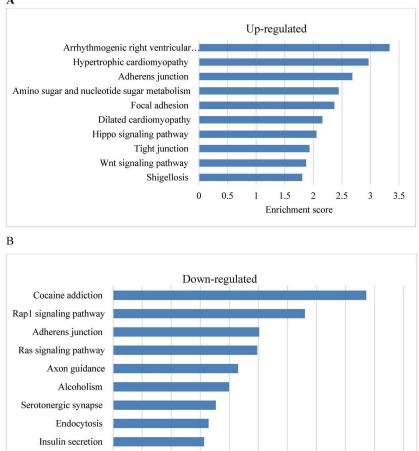
See Supplementary File 1



**Supplementary Figure 1: GO analysis of the biological functions of circRNA target genes. (A)** GO annotation corresponding to the target genes of upregulated circRNAs. **(B)** GO annotation corresponding to the target genes of downregulated circRNAs.

5

4.5



Supplementary Figure 2: KEGG pathway analysis. (A) Pathways corresponding to upregulated circRNAs. (B) Pathways corresponding to downregulated circRNAs.

1.5

2

2.5

Enrichment score

3

3.5

4

0.5

1

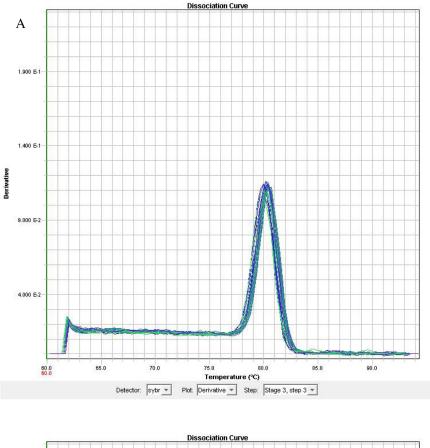
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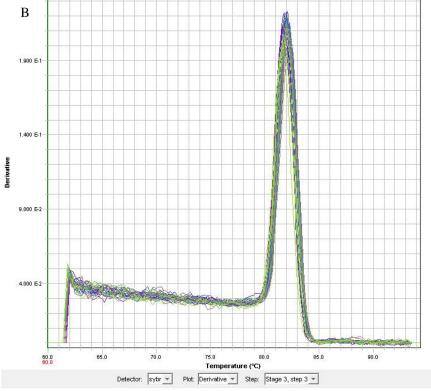


Dopaminergic synapse

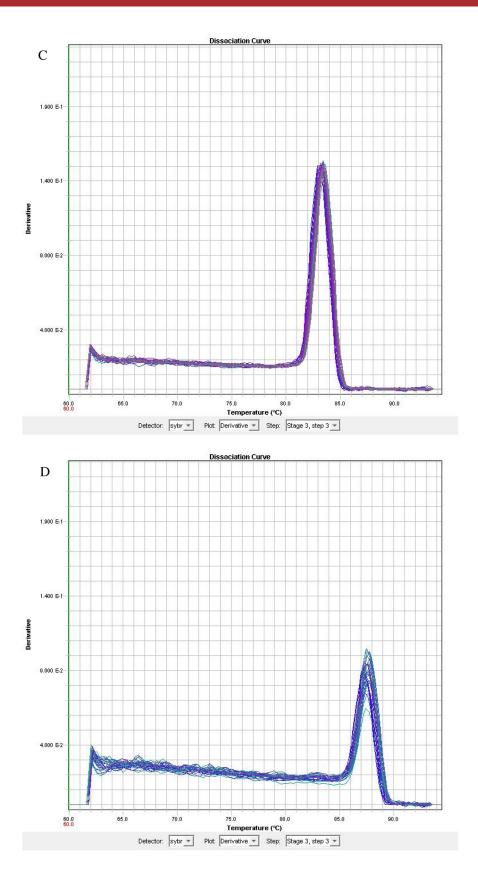
hsa-miR-339-5p and hsa_circ_103110		Dealthan
88 <u>Smer</u> 109 5'-ctTGA-CTGAAGGAGGACAGGGa-3' UTR 11 3'-gcaCUCGAGGACCUCCUGUCCCu-5' miRNA 3'pairing Seed	BacAGGGA	
hsa-miR-143-5p and hsa_circ_104689		
97 5'-agaAAAGAAACAGCTAACTGCACt-3' UTR 3'-uggUCUCuCGUCG-UGA-CGUCG-5' miRNA 3'pairing Seed	ACTGCAC Thun -	
hsa-miR-409-3p and hsa_circ_104821		
Offset   88 Gmer 109   5'-gattaTGCACTGTGCAACATcc-3' UTR IIII:IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Offset 6mer	
385 <u>Ter-m8</u> 466 5'-gctgactatgtacGCAACATTr-3' UTR 1)	Tmer-m8	
hsa-miR-153-3p and has_circ_104821		
76 5'-gcgtatgacTCTGATTATGCAC-3' UTR 3'-cuagugaaaaCACUGGAUACGUu-5' miRNA 3'patring Seed	Gmer	·
Imperfect 376 5'-aaagcCGTTGCTGACTATGTGAC-3' UTR 3'-cuaguGAAAACACUGAUACGUu-5' miRNA 3'pairing Seed	Imperfect	
hsa-miR-145-5p and has_circ_104821		
183. 5'-gcatgaagTTGCCAAGCAATCGGAC-3' UTR 111111111111111111111111111111111111	AACTGGA	
482 5'-ttcGATTTAAGAGAGCAATTGGAt-3' UTR 1: 1: 1: 1:1:1 3'-uccCUAAGGACCUU-USGACCUg-5' miRNA 3'pairing Seed	Imperfect	
hsa-miR-298 and hsa_circ_100219		
342 5'-tgcGAGGGCTGGCCACTTCTGCt-3' UTR 3'-acCCUCUUGGAGGGGACGAACGa-5' miRNA 3'-acCCUCUUGGAGGGACGAACGa-5' miRNA 3'patring Seed	CTTCTGC Innovation -	
hsa-miR-485-3p and hsa_circ_100219		
290 <u>"mer-ms 311</u> 5'-ggtaAAGAGAAATGTGTATGAC-3' UTR 1111 :111111 3'-ucucUCCUCLGGCACALACUge5' miRNA 3'pairing Seed	TGTATGA	
hsa-miR-100-3p and hsa_circ_406697		
347 - <u>Zmer-m8</u> 369 5'-tgatCCTGTAGTGACAACTTC-3' UTR 1::!! 3'-guauGGAUAUCUA-UGUUCGAAc-5' miRNA 3'pairing Seed	CAAGCTT III	! -

Supplementary Figure 3: Detailed annotation of circRNA/miRNA interactions. The 2D structure displays the MRE sequence, the target miRNA seed type (7mer-m8, 8mer, 6mer, offset 6mer, imperfect) and the pairing of target miRNA nucleotides 13-16. The precise base positions are shown in the alignments in the upper left and right corners. The "local AU" displays the 30 nucleotides upstream and downstream of the seed sequence. Black bars stand for G/C and low accessibility. Red bars stand for A/U and high accessibility of the seed. The height of the bar represents the extent of accessibility. The position column displays the most likely relative MRE position on the linearized circRNA sequence.

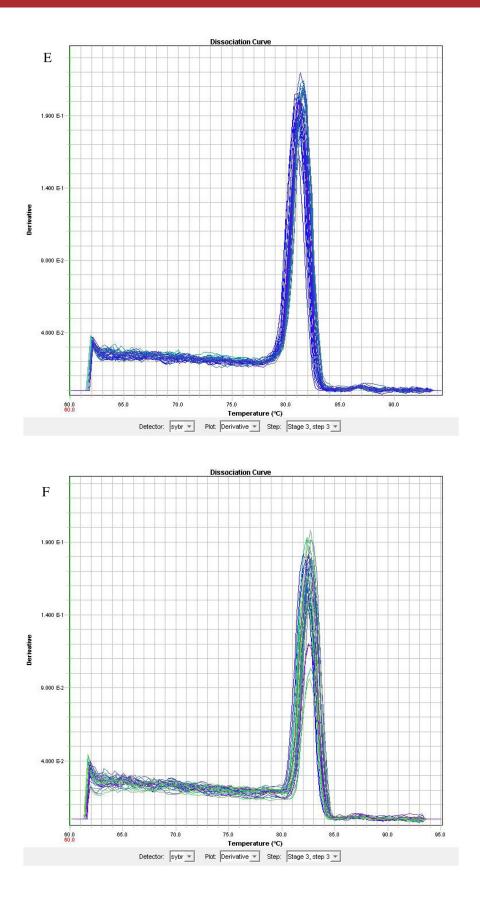




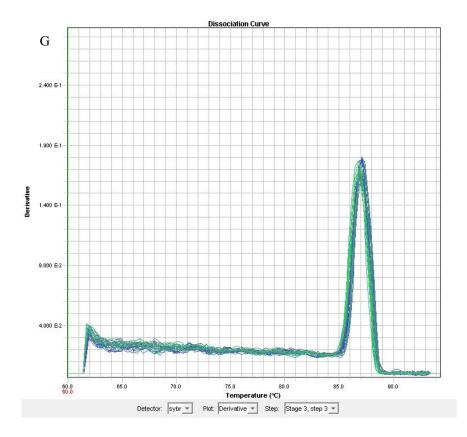
(*Continued*)



(Continued)



(*Continued*)



**Supplementary Figure 4: Melting curves of differentially expressed circRNAs. (A)** hsa\_circ\_103110; **(B)** hsa\_circ\_104689; **(C)** hsa\_circ\_104821; **(D)** hsa\_circ\_006054; **(E)** hsa\_circ\_100219; **(F)** hsa\_circ\_406697; **(G)** *GAPDH*.