Supplementary Figure

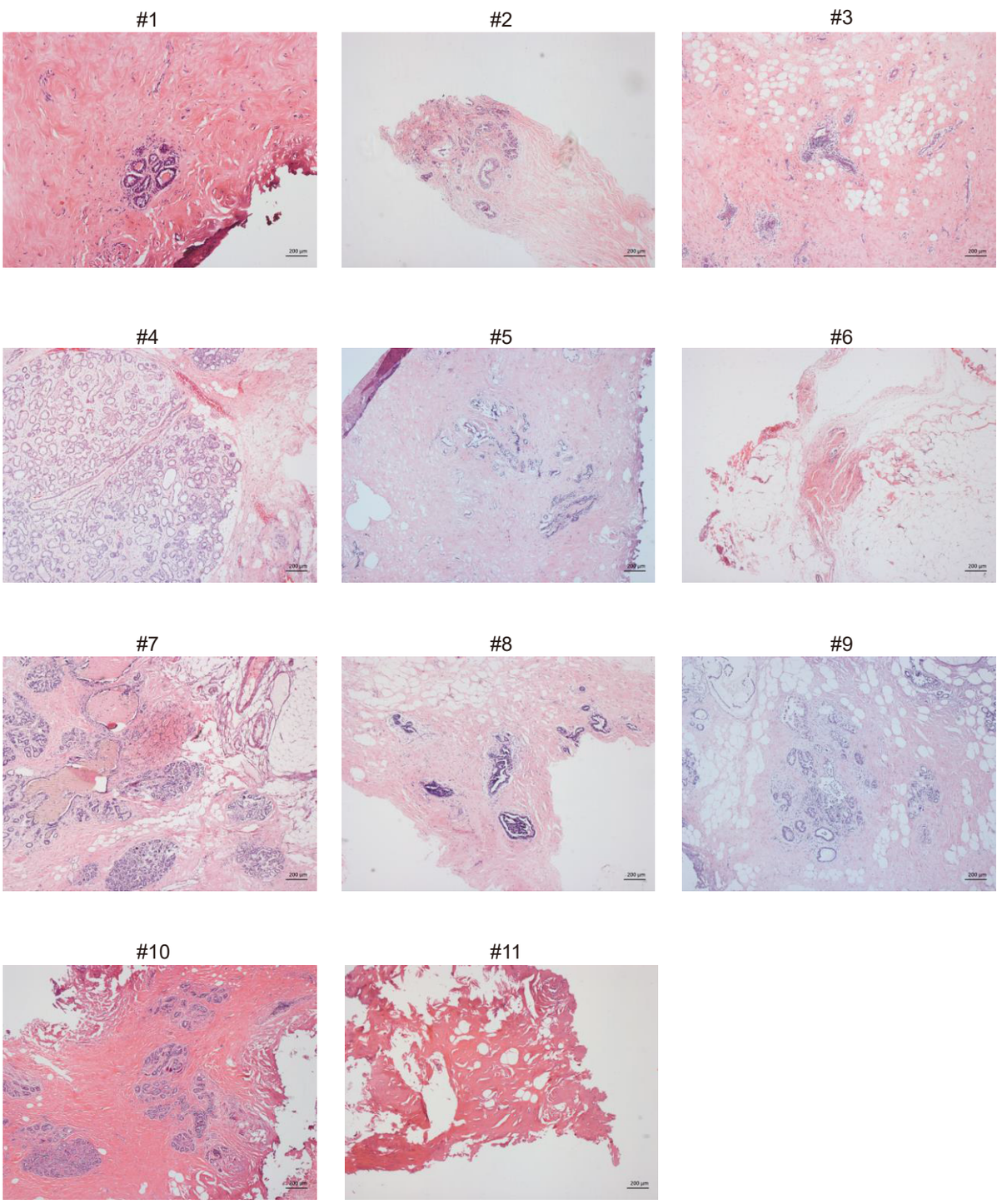


Figure S1. H & E staining of human normal mammary gland tissues (N = 11).

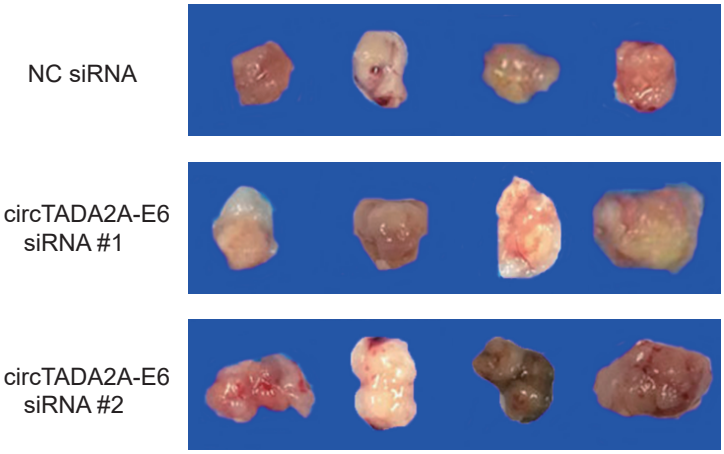


Figure S2. Images of isolated tumors.

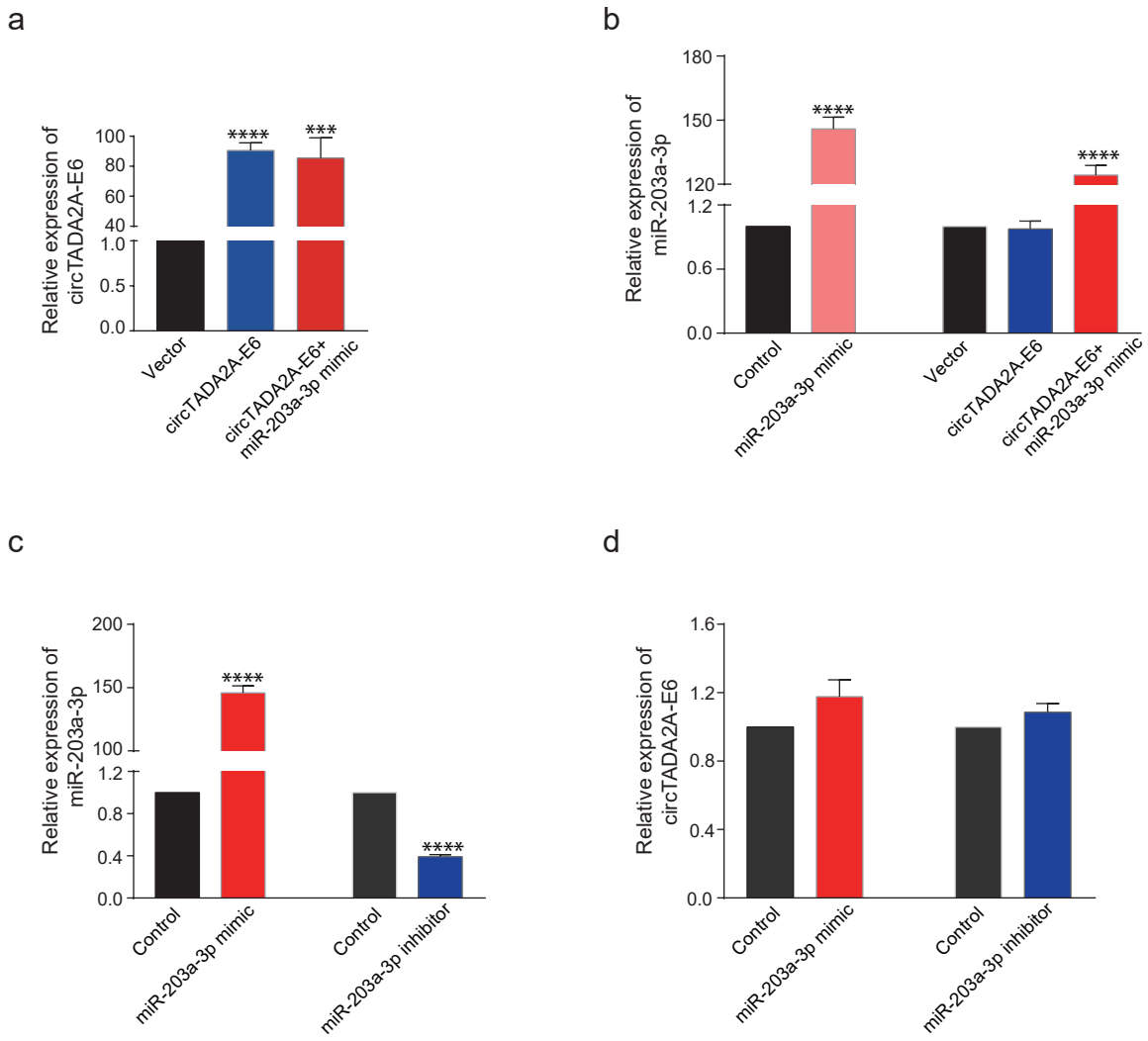


Figure S3. The relative expression of circTADA2A-E6 and miR-203a-3p.

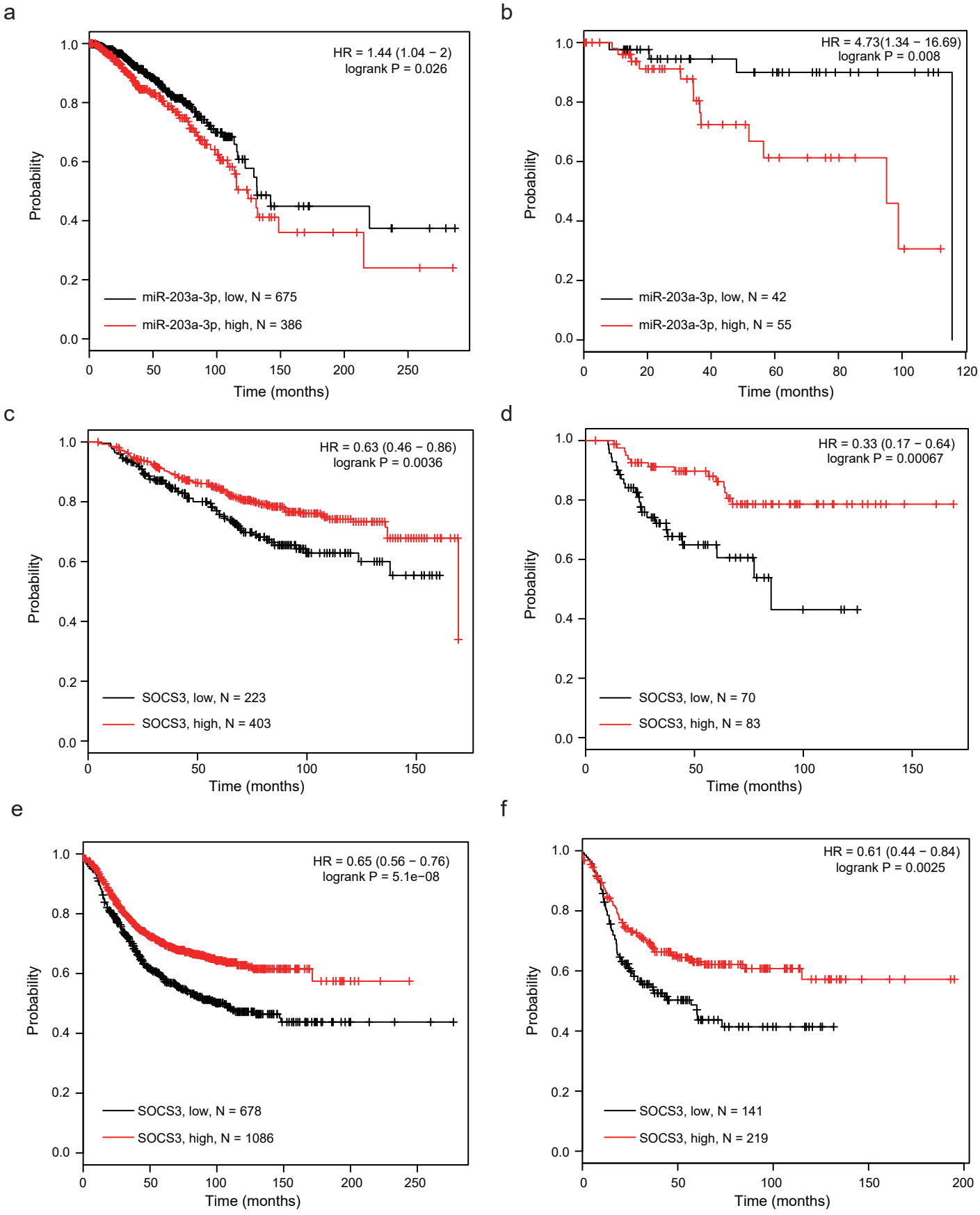
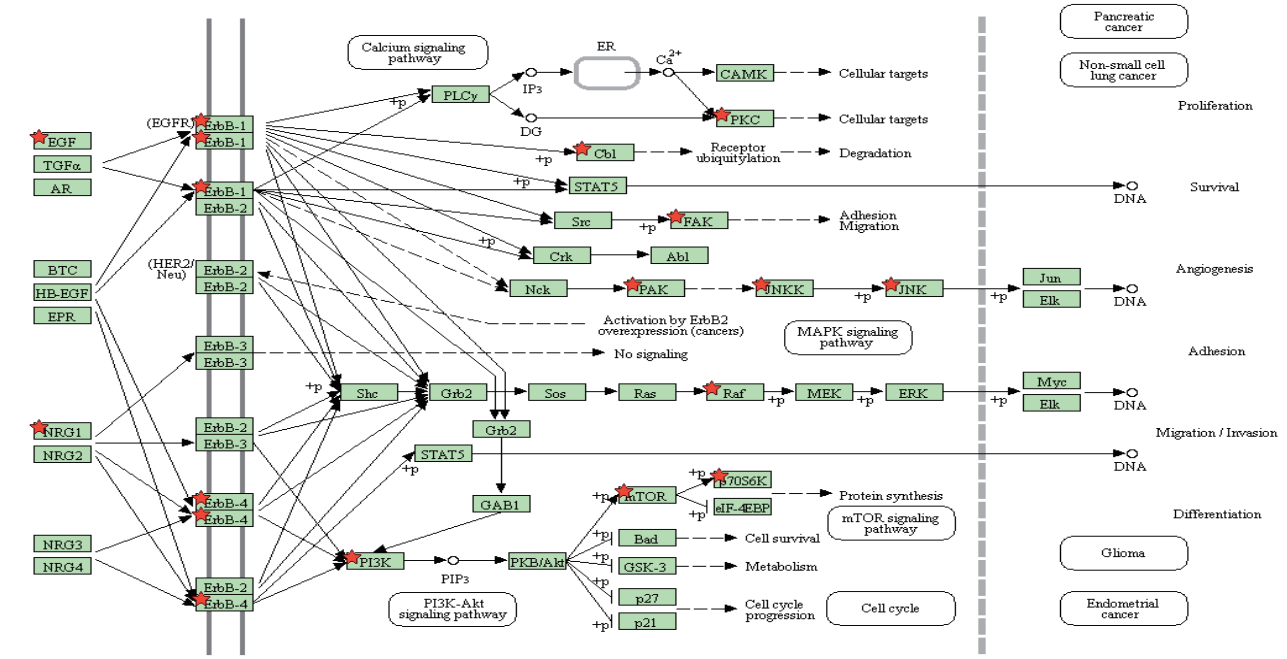


Figure S4. Kaplan–Meier survival curve analysis for the correlation between miR-203a-3p or SOCS3 expression and overall survival (OS) in all patients (a,c) or in TNBC(b,d). The correlation between SOCS3 expression and recurrence-free survival (RFS) in all patients(e) and in TNBC(f).

a



b

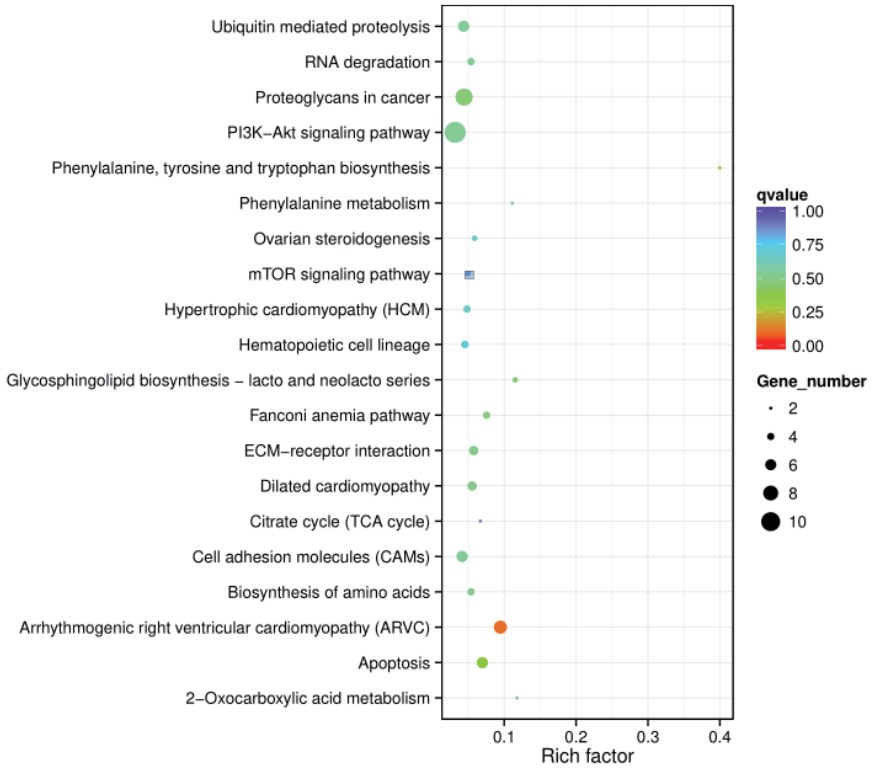


Figure S5. KEGG and GO analysis of circRNAs/miRNA/mRNA axis profiles.(a) The blinking showing the target genes could be regulated by circCDC27/miR-7 or miR-1276/mRNA axis. (b) Signaling pathway enriched by circTADA2A-E6/miR-203a-3p and miR-302c-3p/mRNA axis.

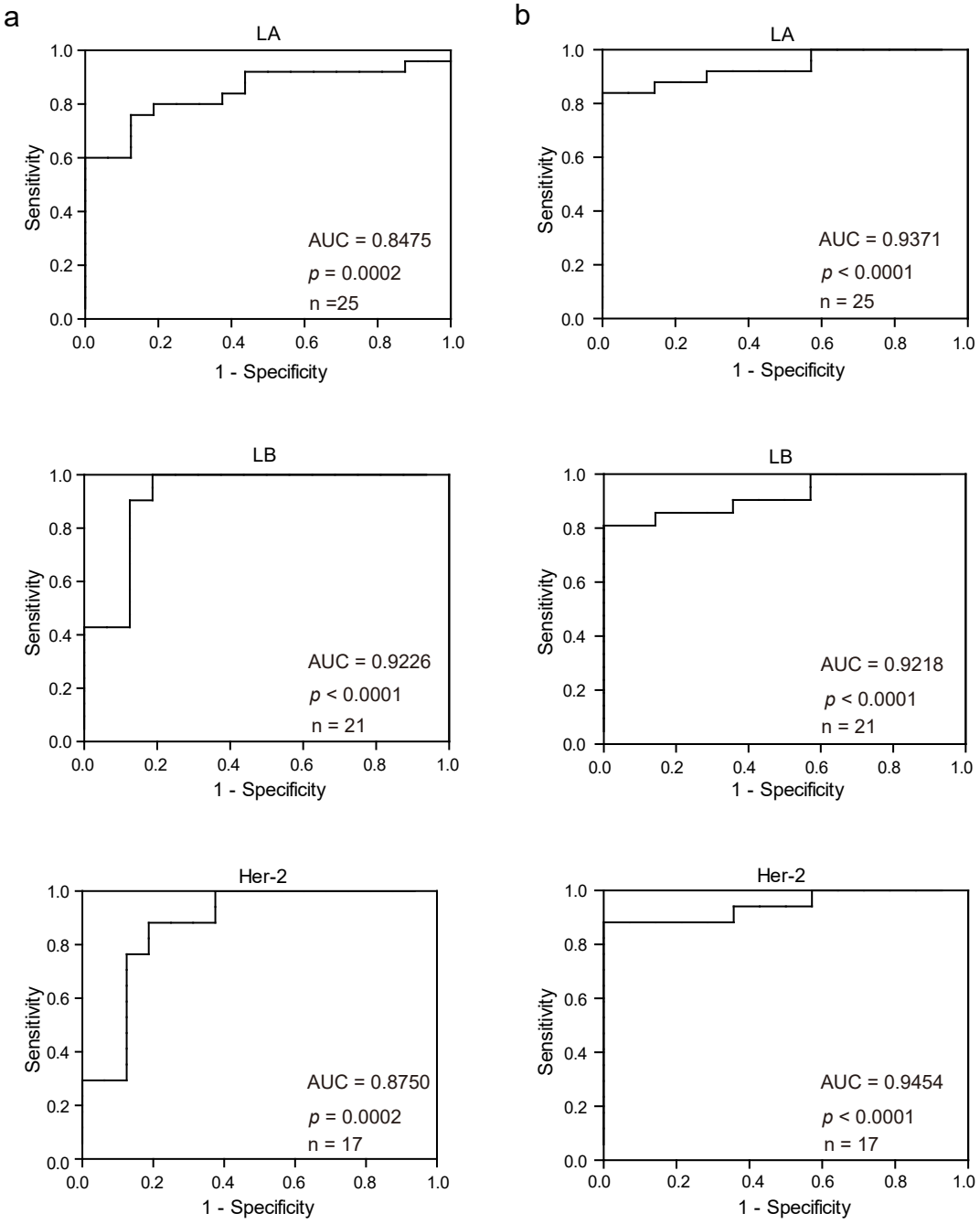


Figure S6. ROC analysis for circTADA2A-E6 (a**) and circTADA2A-E5/E6 (**b**) in LA , LB and Her-2 breast cancer subtypes.**

a

b

Figure S7. Schematic representation of the circTADA2A-E6 vectors.
(a) pLCDH-CMV-circTADA2A-EF1-copGFP-puro. (b) phRluc-circTADA2A-E6.

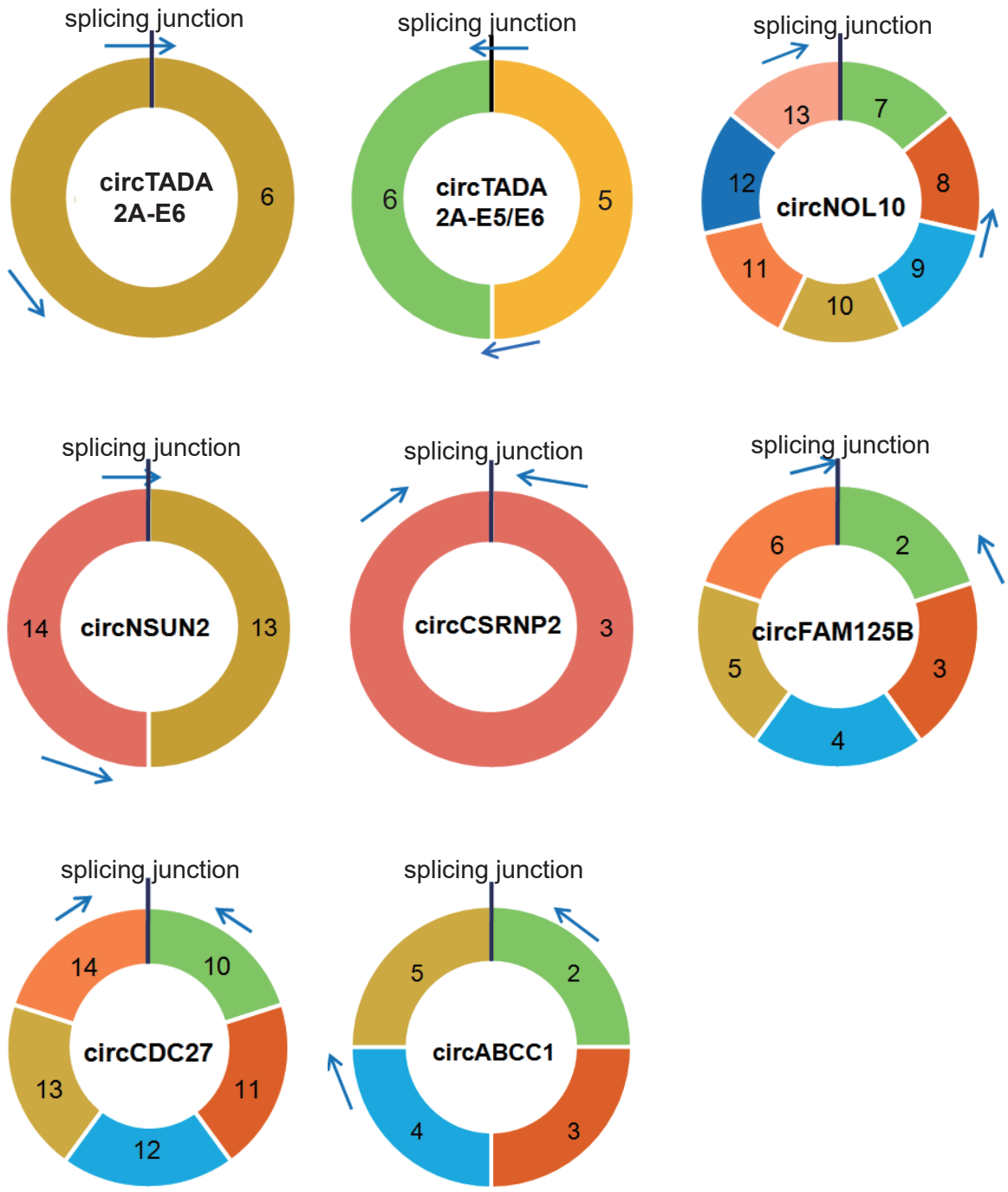
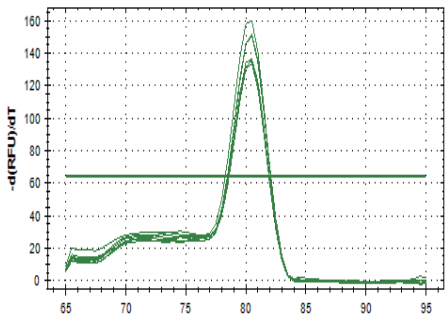
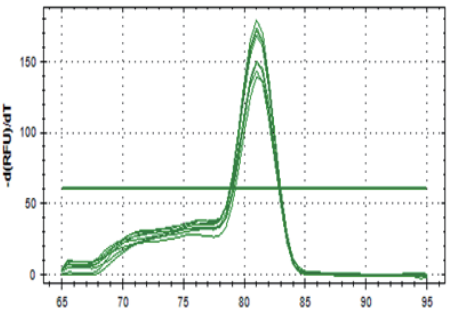


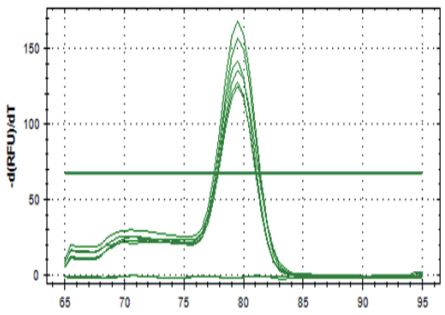
Figure S8. Schematic representation of the eight circRNAs formed by gene exon splicing. The arrows stand for divergent primers locus for qRT-PCR.



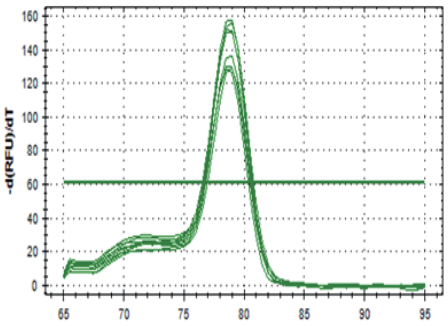
circTADA2A-E5/E6



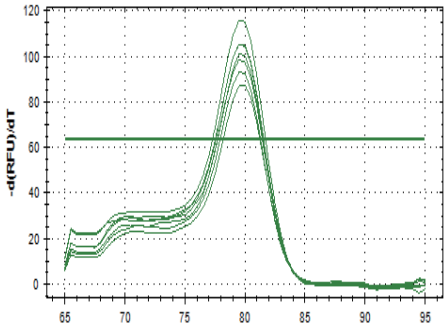
circNOL10



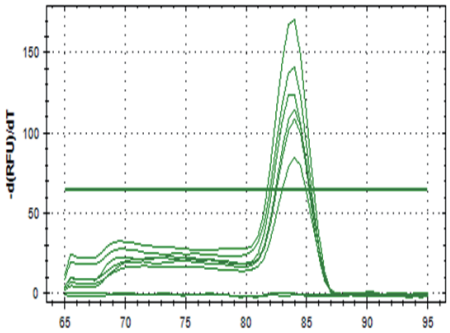
circTADA2A-E6



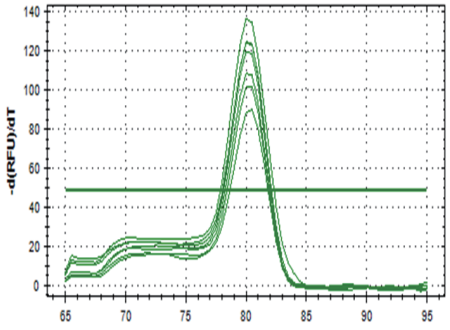
circNSUN2



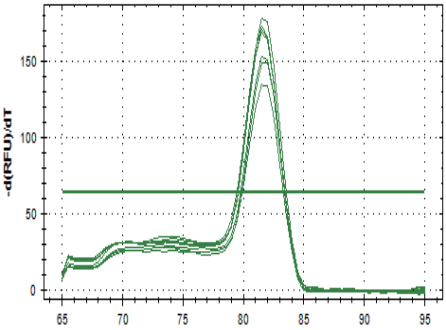
circCSRNP2



circFAM125B



circCDC27



circABCC1

Figure S9. Melting curve of qRT-PCR showing a single, distinct product of the expected size for eight individual circRNAs.

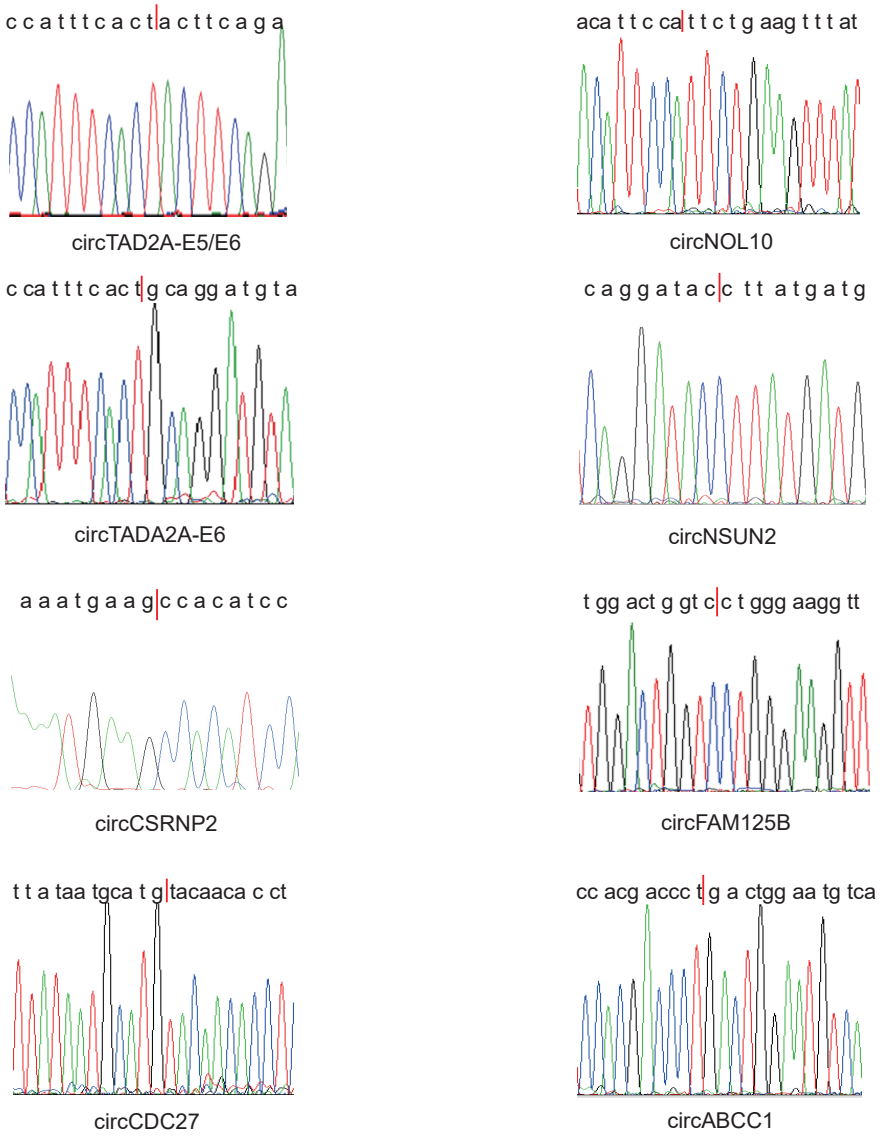


Figure S10. Sanger sequencing showing head-to-tail splicing for eight individual circRNAs. Sanger sequencing for qRT-PCR product confirmed the existing of a head-to-tail junction, the red lines indicated the backsplice junction.