



Figure S1 The expression patterns of representative differentially expressed AS (DEAS) events identified based on TCGA datasets. (A) Splicing pattern of SLK/STX2/CLSTN1/NFYA in breast cancer (BRCA) and their paired normal tissues (n=6) as detected by RT-PCR. Percent-Spliced-In (PSI) were presented under the gels. (B) Paired scatter plots depicted the RT-PCR results of SLK/STX2/CLSTN1/NFYA. Paired *t*-test was used.

Table S1 Sequences of RT-PCR primers

Name	Sequences
SLK-F	GCCTGGAACAAGAGCACACA
SLK-R	TCCCAAATTGCAGCTTCTCG
STX2-F	CCACAGACTATGTAGAACACGCT
STX2-R	TCCAAGGATCACAAGCAAAACAA
CLSTN1-F	GAGGATTACCCGCTCCATCC
CLSTN1-R	CCTCTGCCACTGTCTTCGAG
NFYA-F	GAGCAGATTGTTGTCCAGGC
NFYA-R	GGGTTGGCCAGTTGATGTGA

Table S2 Clinical characteristics of TCGA BRCA cohort

Characteristics	No. of patients (%), (n=930)
Age	
Median	61(53-68)
<60	509(54.7%)
≥60	421(45.3%)
Histology	
ILC	658(70.8%)
IDC	188(20.2%)
Others	84(9.0%)
T	
T1	245(26.3%)
T2	540(58.1%)
T3	123(13.2%)
T4	22(2.4%)
N	
N0	445(47.8%)
N1	324(34.8%)
N2	97(10.4%)
N3	64(6.9%)
Stage	
I	167(18.0%)
II	541(58.2%)
III	208(22.4%)
IV	14(1.5%)
ER	
Positive	718(77.2%)
Negative	212(22.8%)
PR	
Positive	631(67.8%)
Negative	299(32.2%)
Subtype_PAM50	
Normal	116(12.5%)
LumA	448(48.2%)
LumB	155(16.7%)
Her2	61(6.6%)
Basal	150(16.1%)
Relapsed/Progressed	
No	834(89.7%)
Yes	96(10.3%)
Death	
No	811(87.2%)
Yes	119(12.8%)