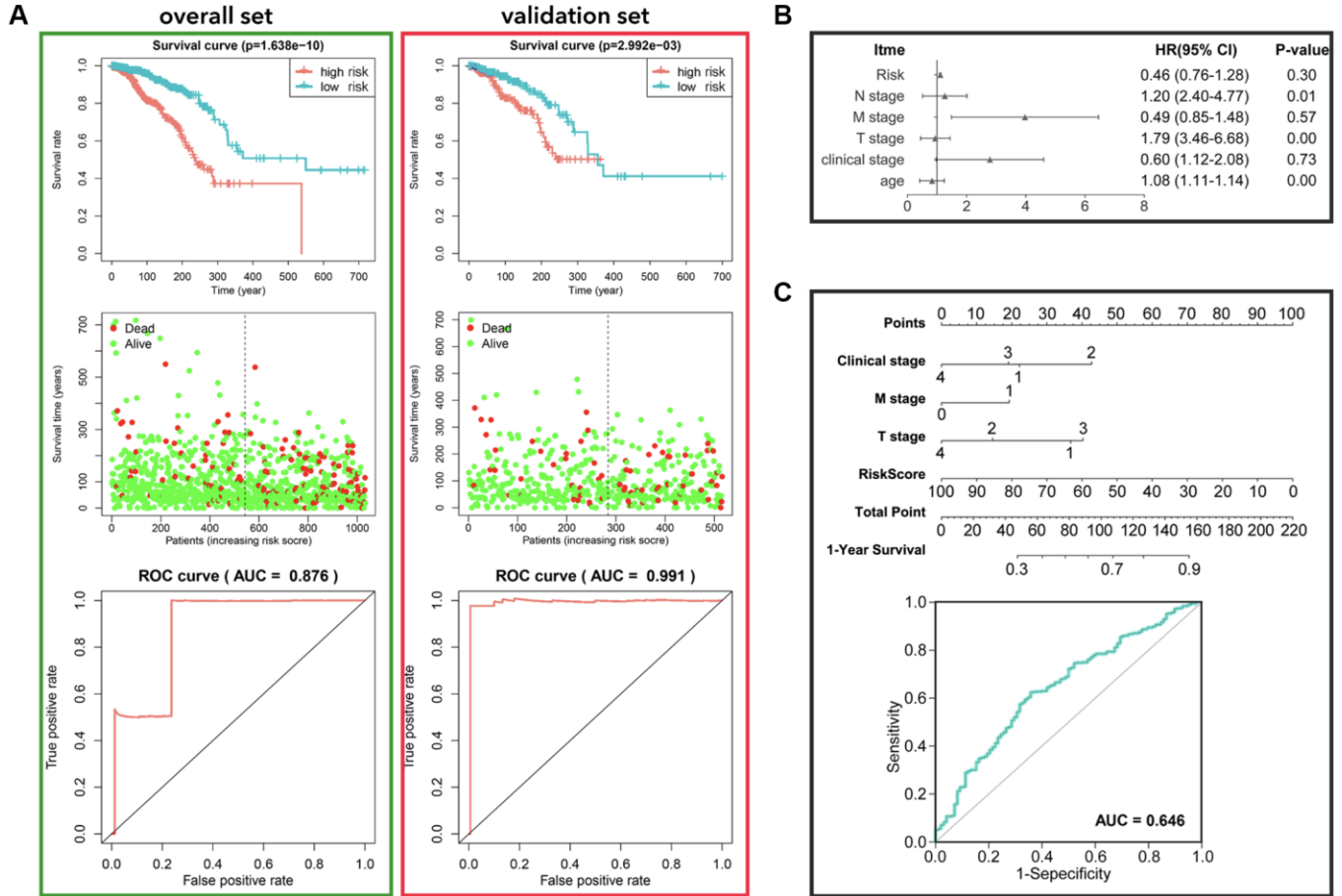
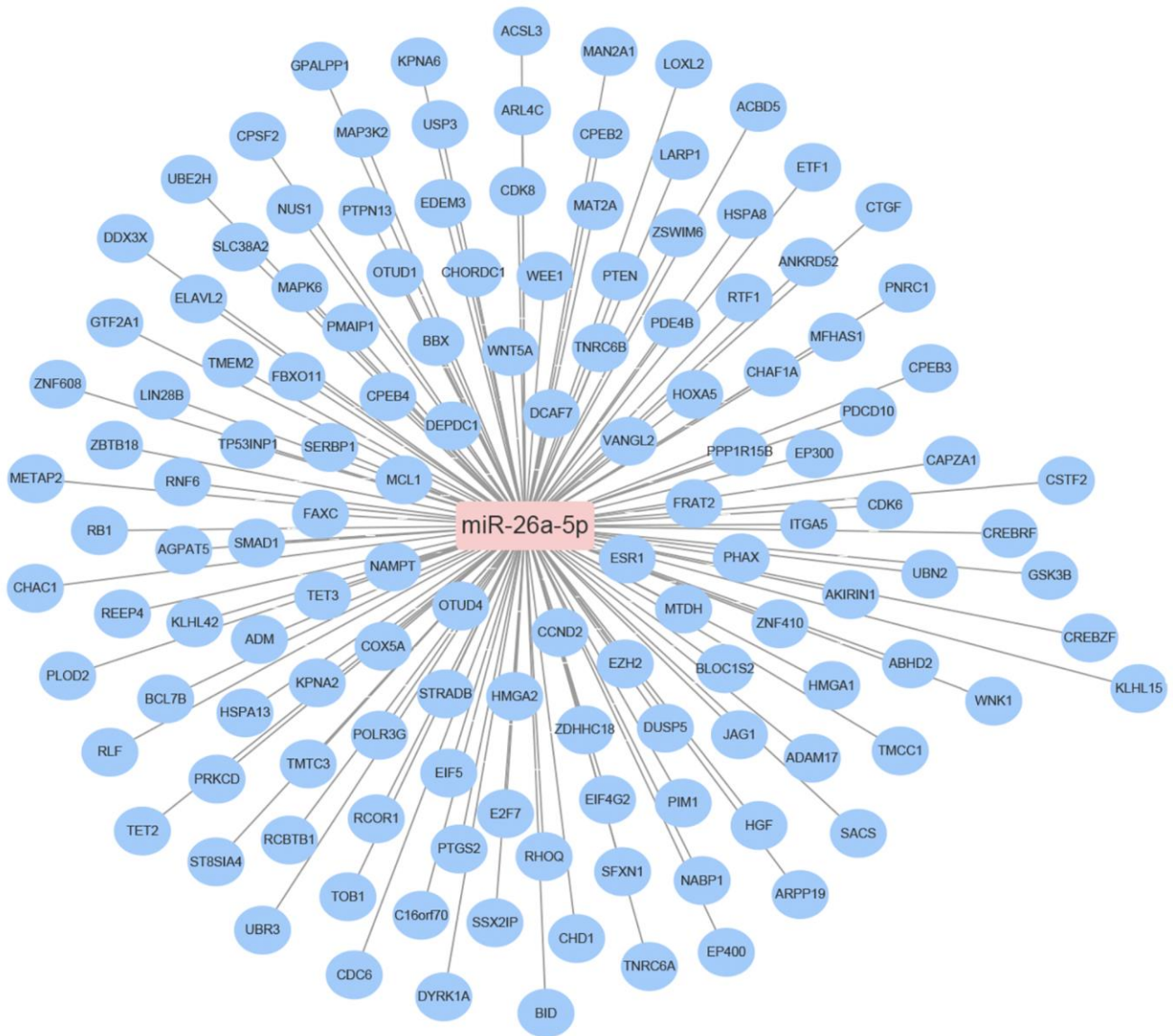


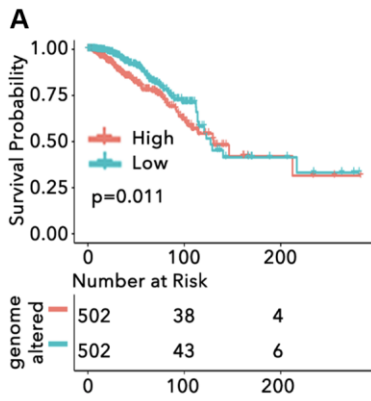
SUPPLEMENTARY FIGURES



Supplementary Figure 1. The predict model of prognosis in breast cancer. (A) Breast samples from TCGA were divided into training group and validation group. 22 identified miRNA were analyzed to establish prognosis predict model. (B) Multivariate logistics regression analysis screened the independent risk factors. (C) Establishing a nomogram by R, and the ROC value was 0.646.



Supplementary Figure 2. The targeted genes of miR-26a-5p. 133 targeted genes of miR-26a-5p were identified by miRDB, miRTarBase and TargetScan database.

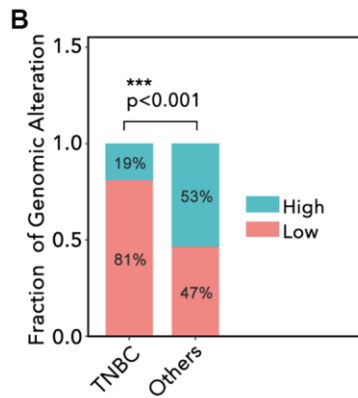


let-7b-3p		
DDR	R-value	p-value
PPP4C	-0.2334	3.40E-14
SEM1	-0.2297	8.69E-14
POLD1	-0.2247	3.05E-13
RECQL4	-0.2216	6.56E-13
RFC2	-0.2177	1.66E-12
MSH3	0.2342	2.75E-14
RAD50	0.2527	1.89E-16
POLR2A	0.2551	9.40E-17
XPA	0.2667	3.25E-18
CCNH	0.2826	2.39E-20

59 negative co-expression
36 positive co-expression

miR-26a-5p		
DDR	R-value	p-value
POLM	0.2556	8.30E-17
POLL	0.2636	8.10E-18
PARP3	0.2723	5.92E-19
NEIL1	0.3143	5.09E-25
RAD51	-0.2682	2.05E-18
MSH6	-0.2646	6.12E-18
NEIL3	-0.2603	2.10E-17
TDG	-0.2416	3.91E-15
XRCC5	-0.2384	9.12E-15
PRKDC	-0.2355	1.95E-14

69 negative co-expression
26 positive co-expression



miR-151a-5p		
DDR	R-value	p-value
PARP3	-0.3221	2.85E-26
PCNA	0.3268	4.89E-27
NEIL3	0.338	6.52E-29
PRKDC	0.3474	1.45E-30
POLR2K	0.3724	3.31E-35
RAD51	0.3769	4.42E-36
RAD54B	0.378	2.75E-36
ELOC	0.3951	8.67E-40
RAD54L	0.4104	4.53E-43
RECQL4	0.4313	7.11E-48

20 negative co-expression
85 positive co-expression

Supplementary Figure 3. The effect of genomic instability in breast cancer. (A) K–M analysis of prognosis grouped by genomic instability. (B) The genomic instability of subtypes of breast cancer. Displaying DDR-associated genes which were co-expressed with let-7b-3p, miR-151a-5p and miR-26a-5p.