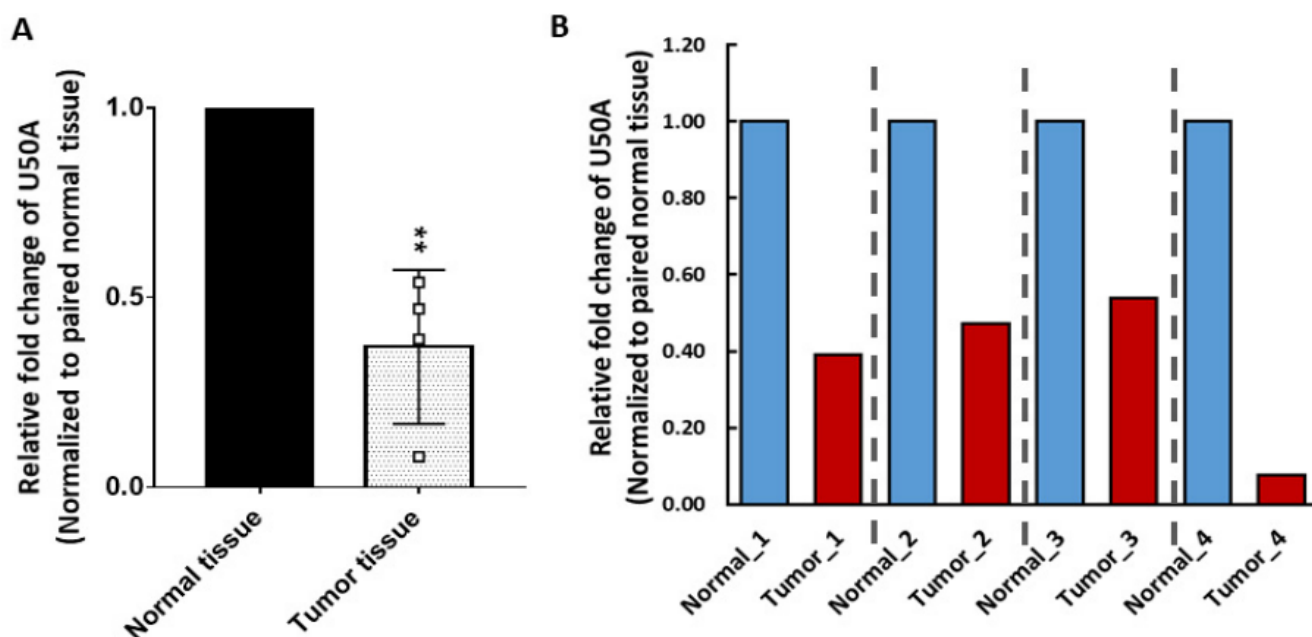
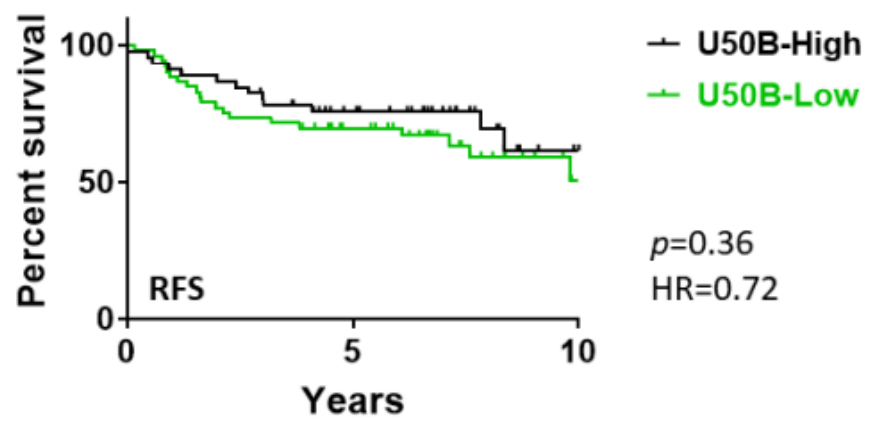
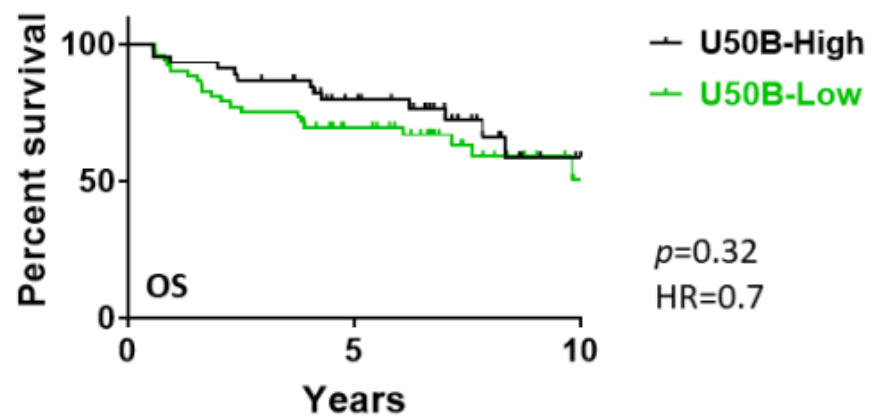
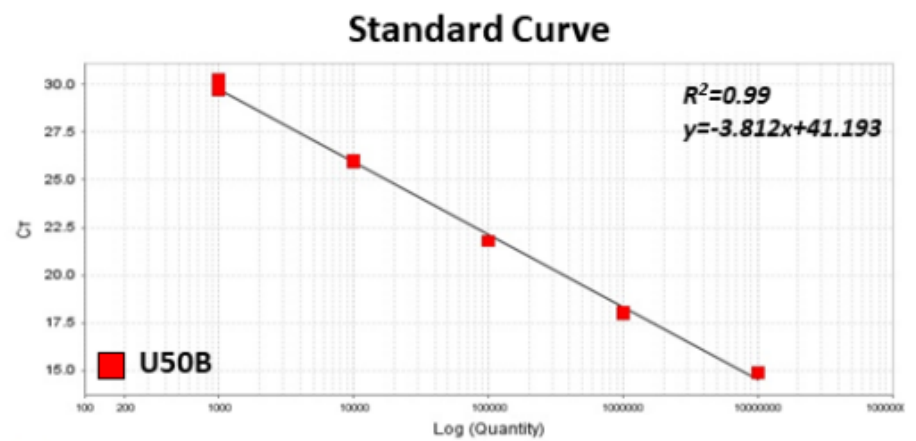


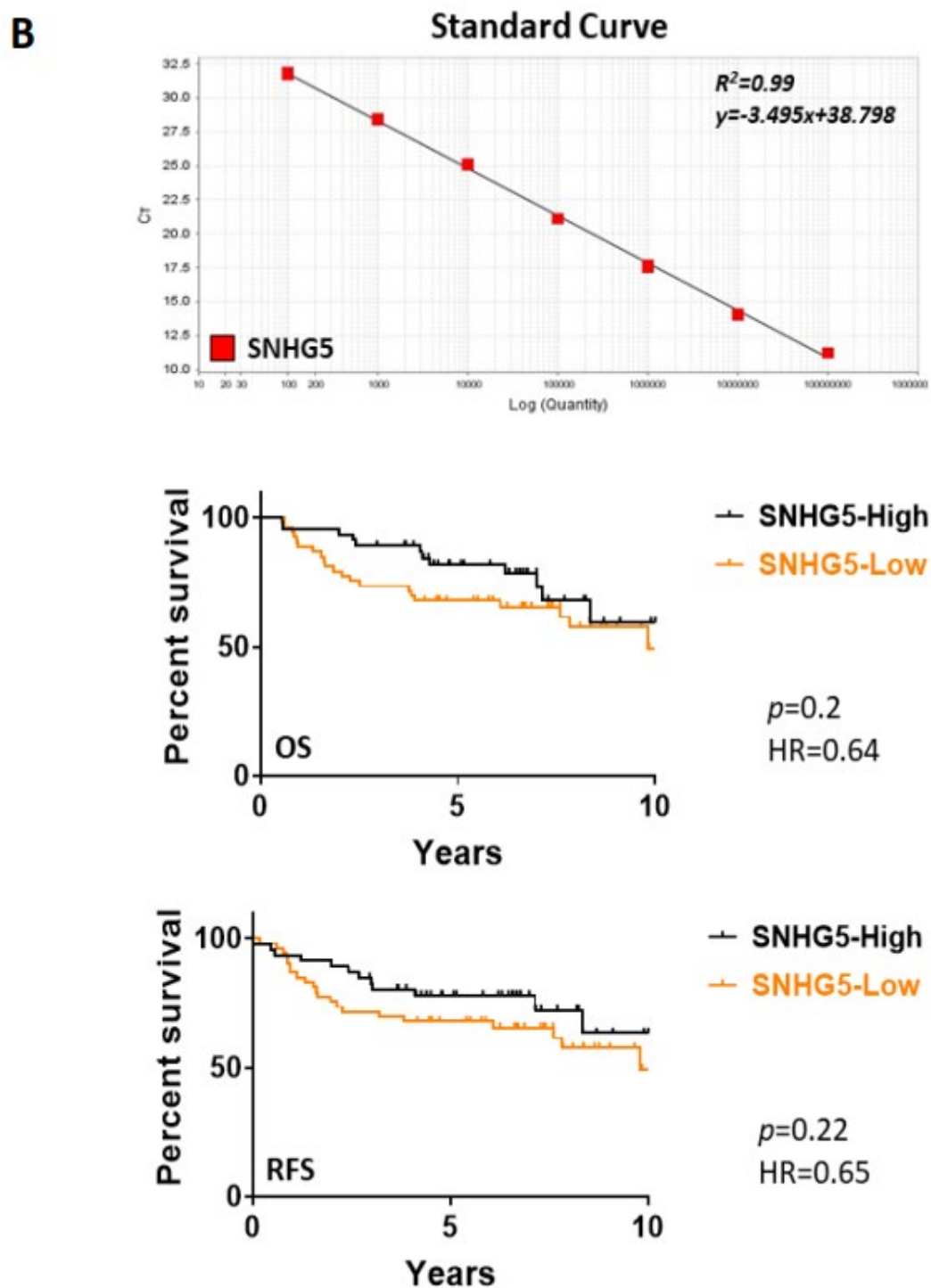
# Supplementary Materials: Expression of SnoRNA U50A Is Associated with Better Prognosis and Prolonged Mitosis in Breast Cancer

Jie-Ning Li, Ming-Yang Wang, Yi-Ting Chen, Yao-Lung Kuo and Pai-Sheng Chen

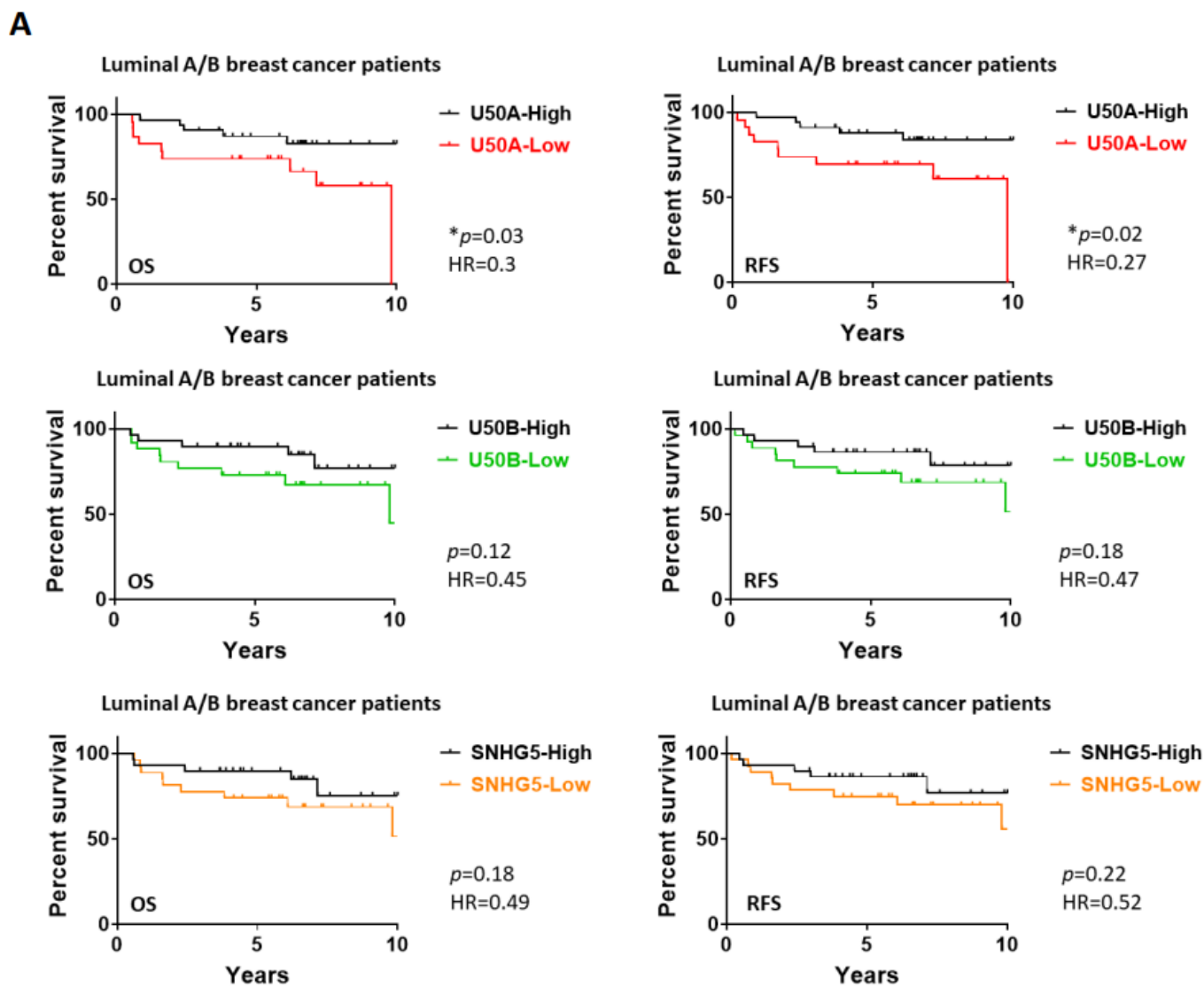


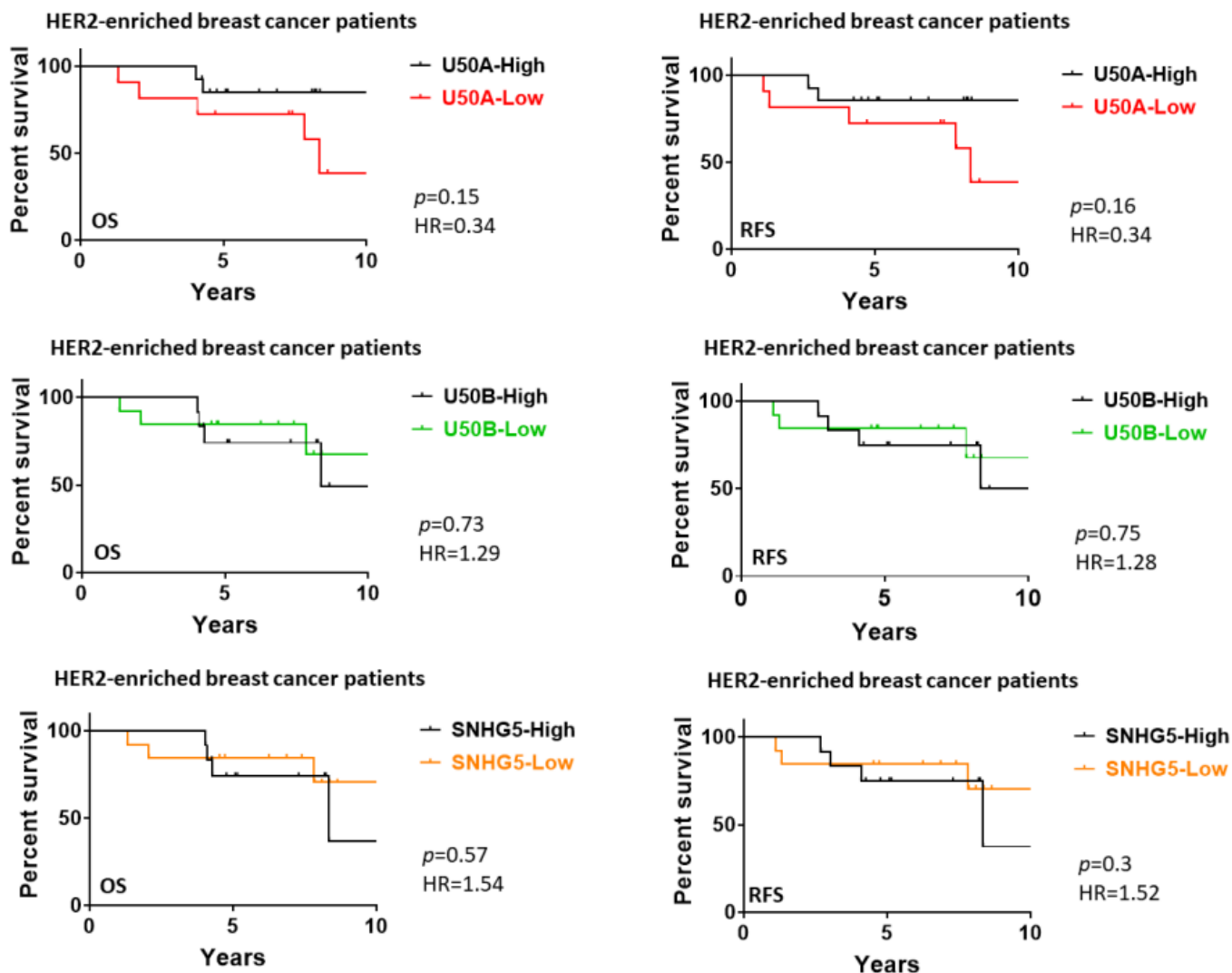
**Figure S1.** U50A expression in paired tumor and normal counterpart (Normal) tissues. U50A expression in four paired normal and tumor tissues from the same patients was analyzed by qPCR. **(A)** Relative fold changes were shown and was statistically analyzed using paired t-test (\*\*  $p < 0.01$ ). U50A expression in individual paired normal and tumor tissues were shown in **(B)**.

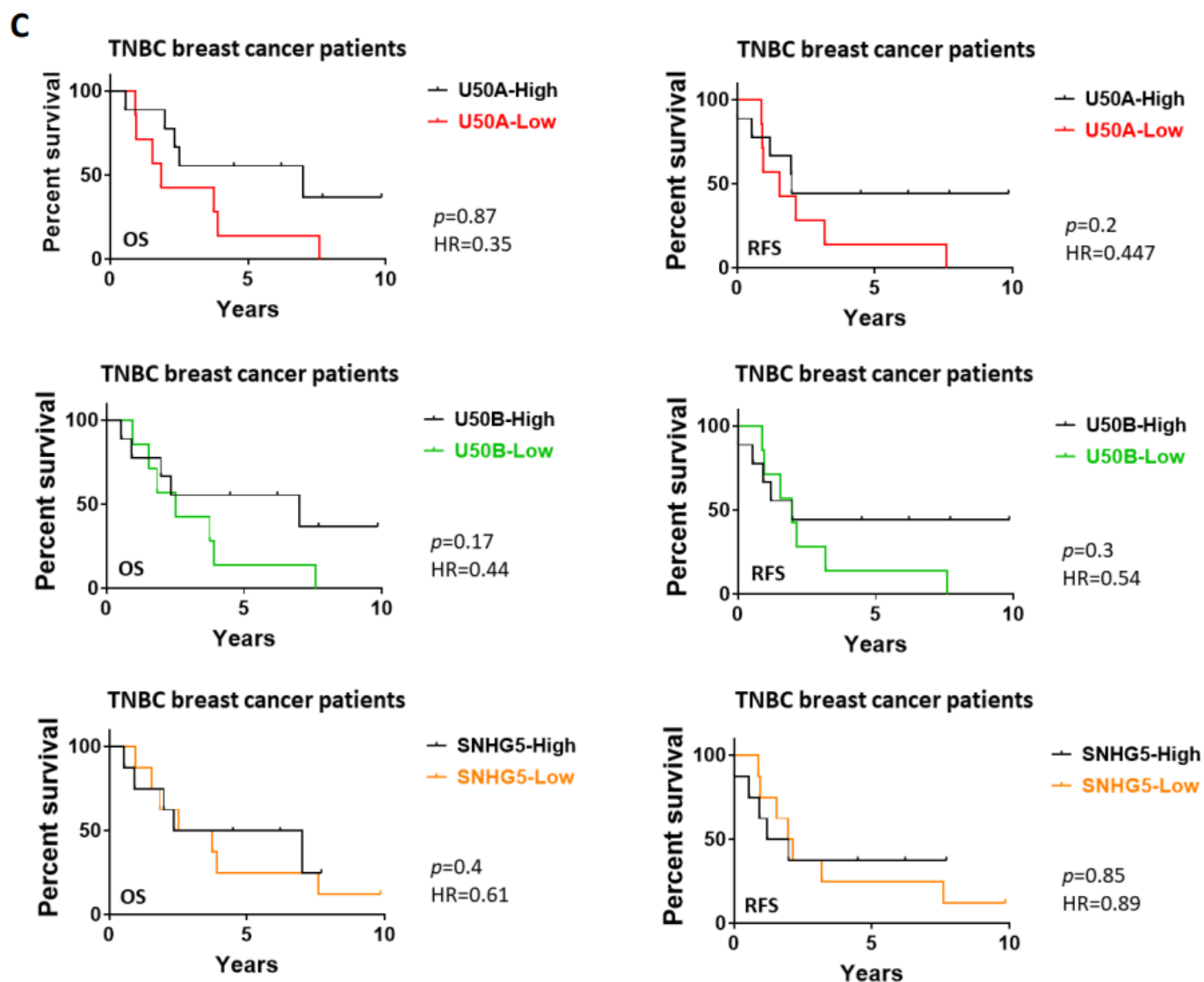
**A**



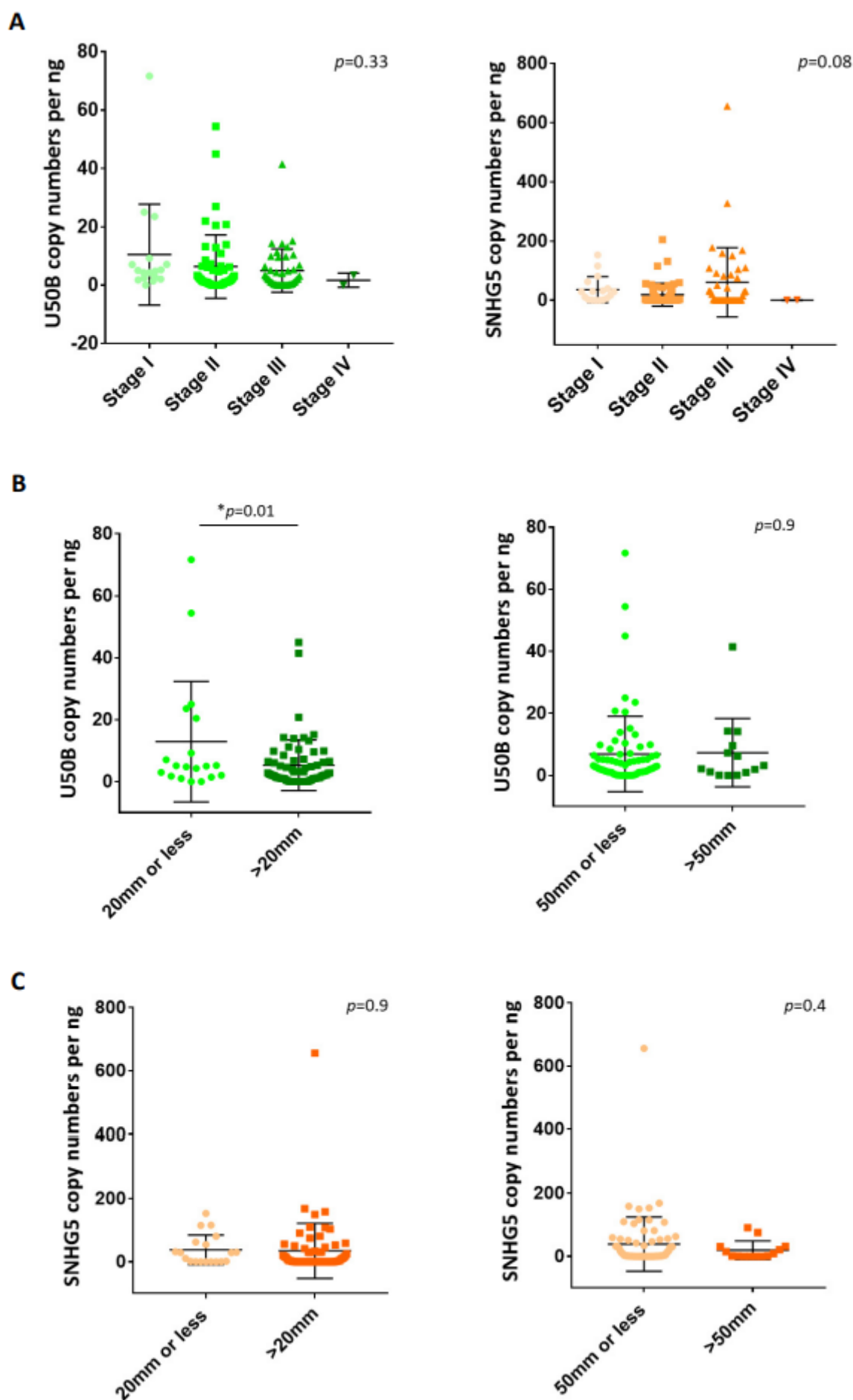
**Figure S2.** Survival analysis of U50B and SNHG5 in breast cancer patients. Absolute quantification of copy number of U50B and SNHG5. The standard curve of U50B (A) and SNHG5 (B). Ten-fold serial dilutions of plasmid templates were used. Kaplan-Meier curves for overall survival (OS) and relapse-free survival (RFS) of breast cancer patients. Median was used as the cutoff to separate U50B-high and U50B-low group or SNHG5-high and SNHG5-low group.



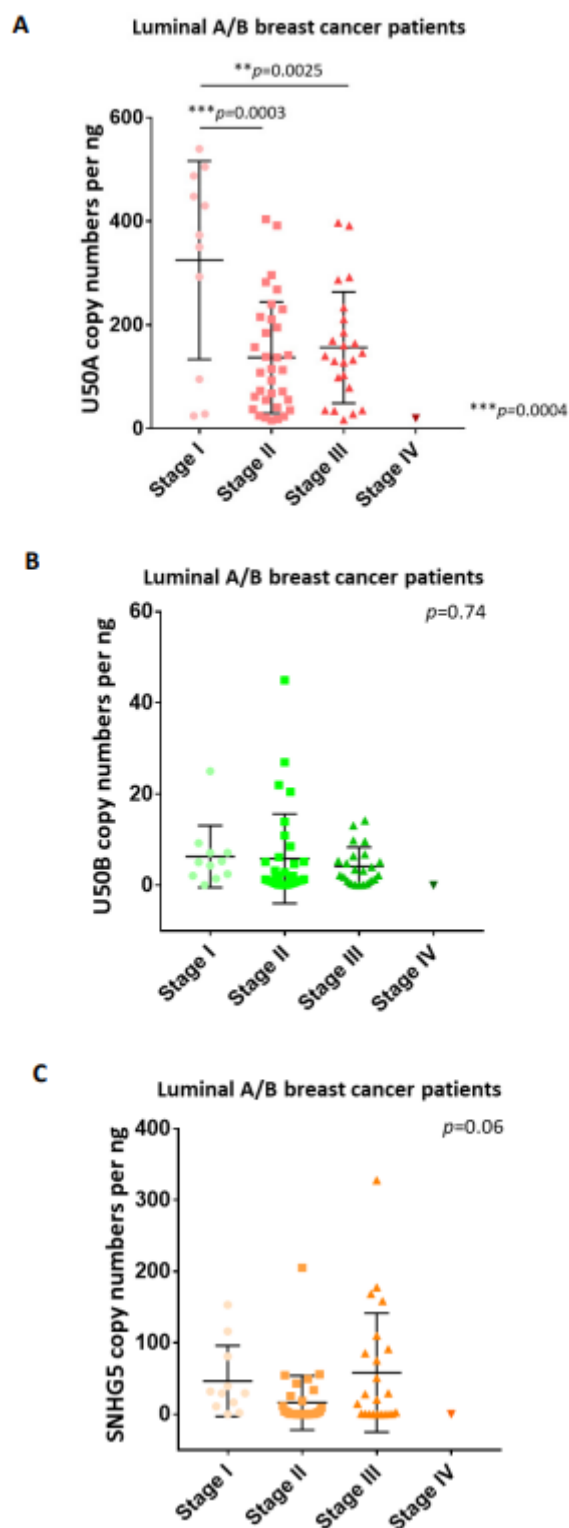
**B**



**Figure S3.** Survival analysis of U50A, U50B and SNHG5 in individual breast cancer subtypes. Overall survival and relapse-free survival, using U50A, U50B or SNHG5 as prognostic marker, in luminal A/B (A), HER2-enriched (B) and TNBC (C) breast cancer patients. \*  $p < 0.05$ .

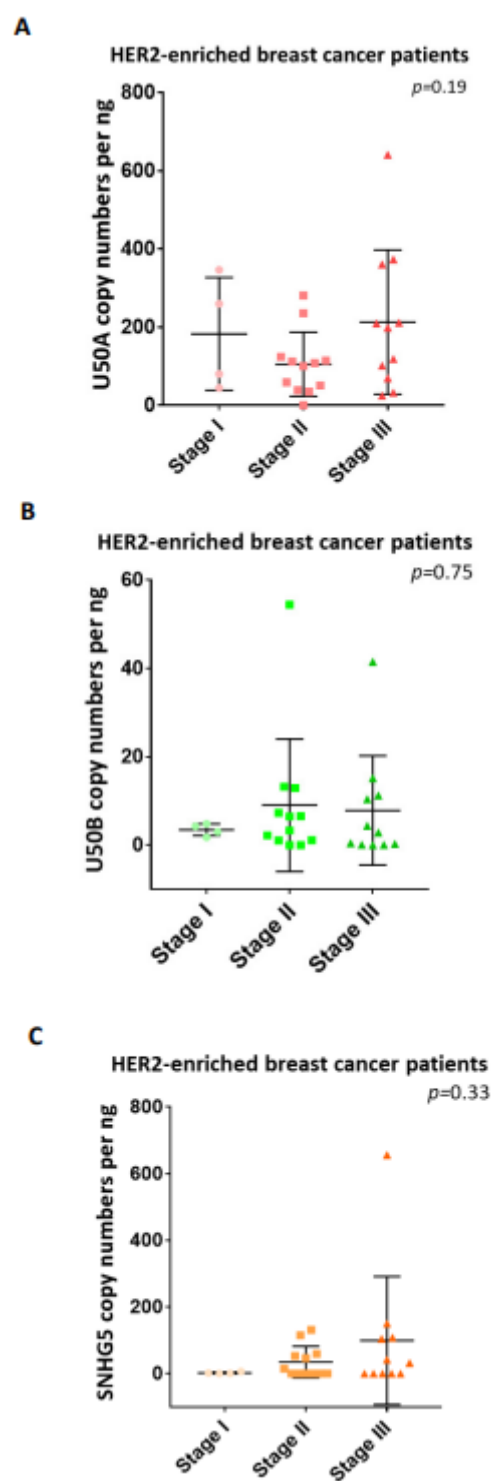


**Figure S4.** Correlation between clinical characteristic and U50B, SNHG5 in breast cancer patients. Correlation between tumor stage (A), tumor size 20 mm (B), tumor size 50 mm (C) and U50B or SNHG5 in breast cancer patients. \*  $p < 0.05$ .

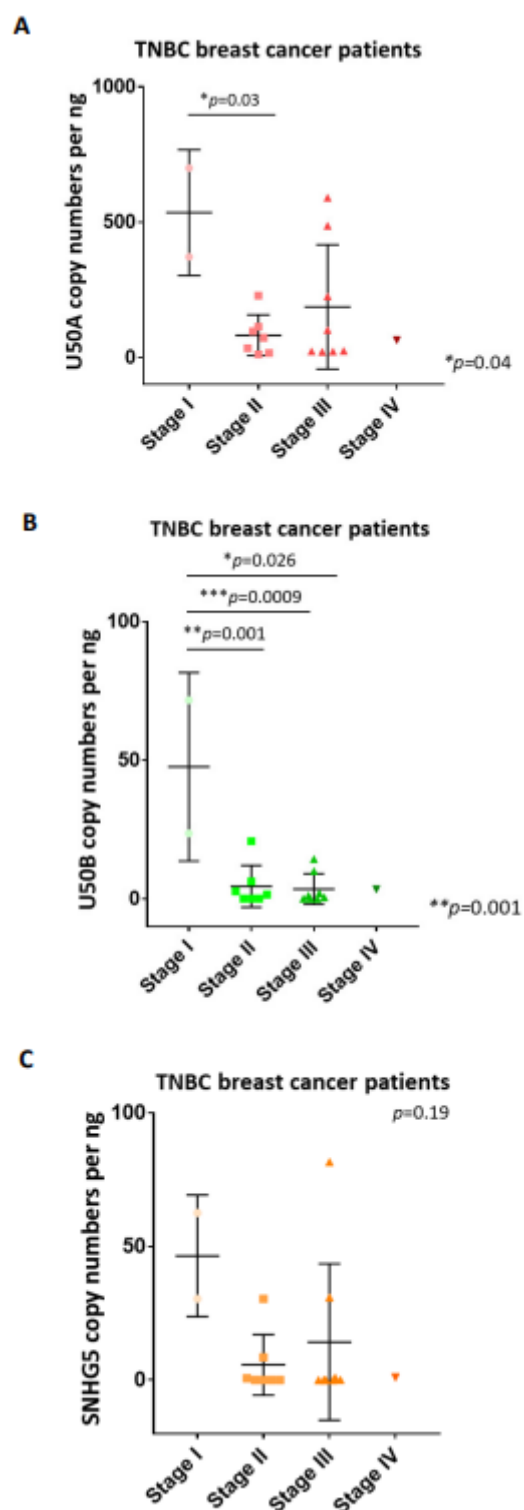


**Figure S5.** Correlation between clinical characteristic and U50A, U50B, SNHG5 in luminal A/B breast cancer patients. Correlation between tumor stage and U50A (A), U50B (B), SNHG5 (C) in luminal A/B breast cancer patients. \*\*\*  $p < 0.001$ .

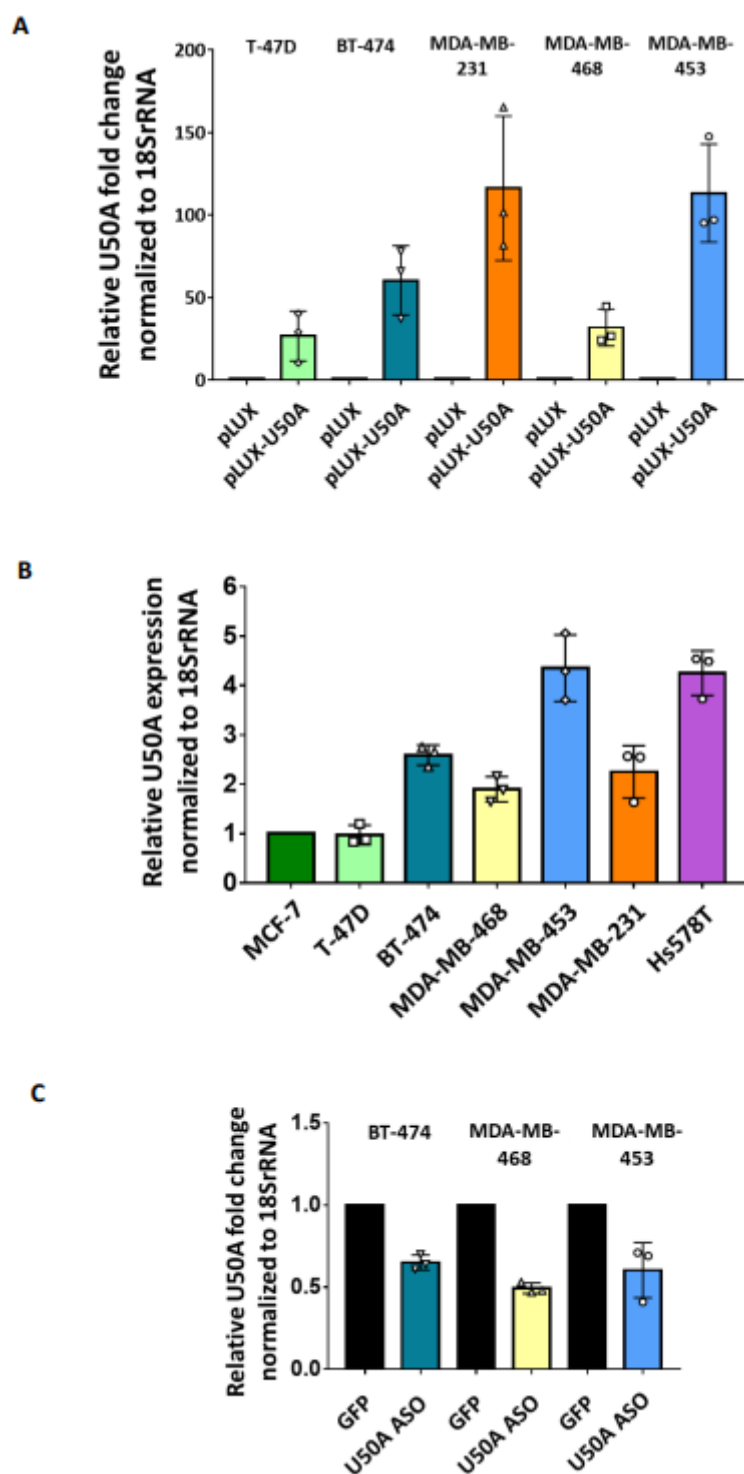




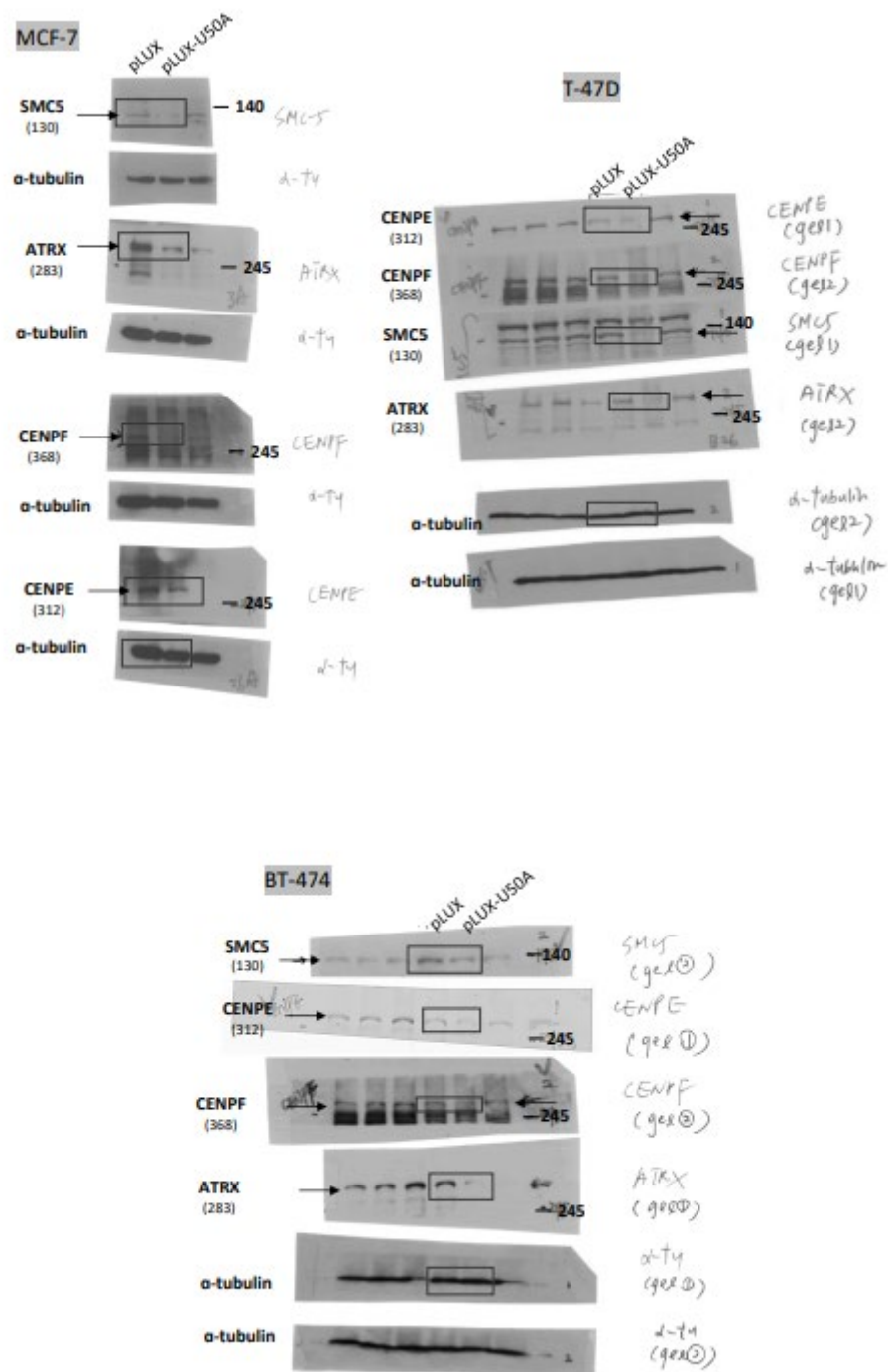
**Figure S6.** Correlation between clinical characteristic and U50A, U50B, SNHG5 in HER2-enriched breast cancer patients. Correlation between tumor stage and U50A (A), U50B (B), SNHG5 (C) in HER2-enriched breast cancer patients.



**Figure S7.** Correlation between clinical characteristic and U50A, U50B, SNHG5 in TNBC patients. Correlation between tumor stage and U50A (A), U50B (B), SNHG5 (C) in TNBC patients. \*  $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$



**Figure S8.** U50A expression in modulated groups. (A) U50A fold change in U50A-overexpressing breast cancer cell lines. (B) Relative endogenous U50A expression in several breast cancer cell lines. (C) U50A fold change in U50A-inhibiting breast cancer cell lines.



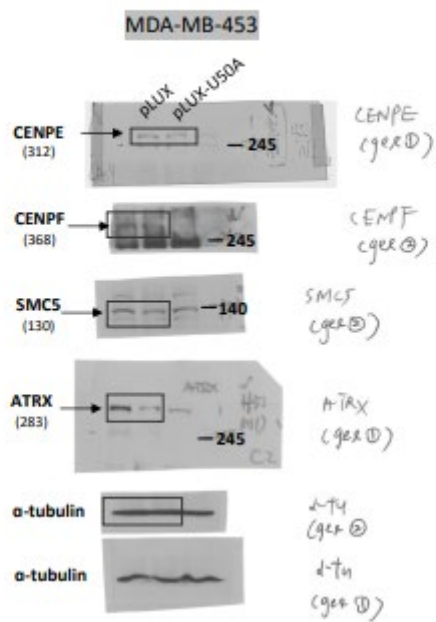
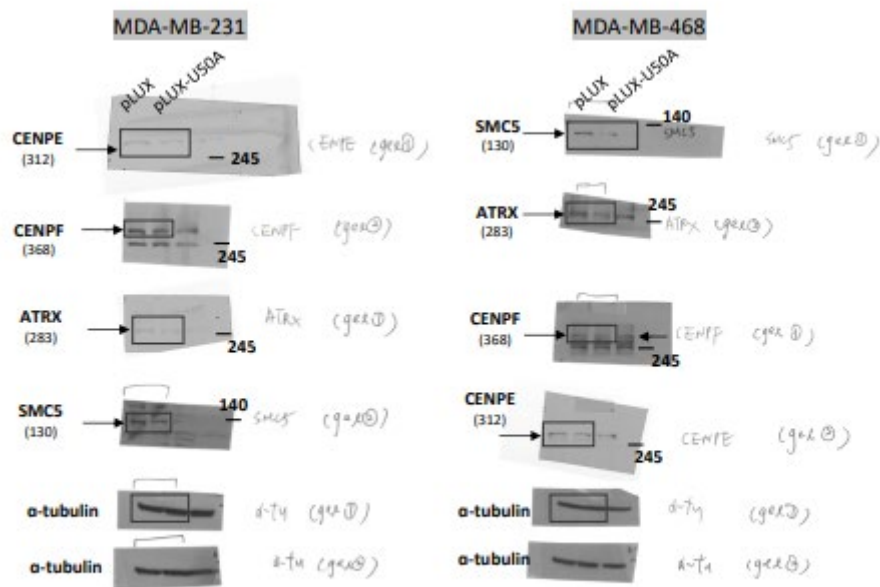
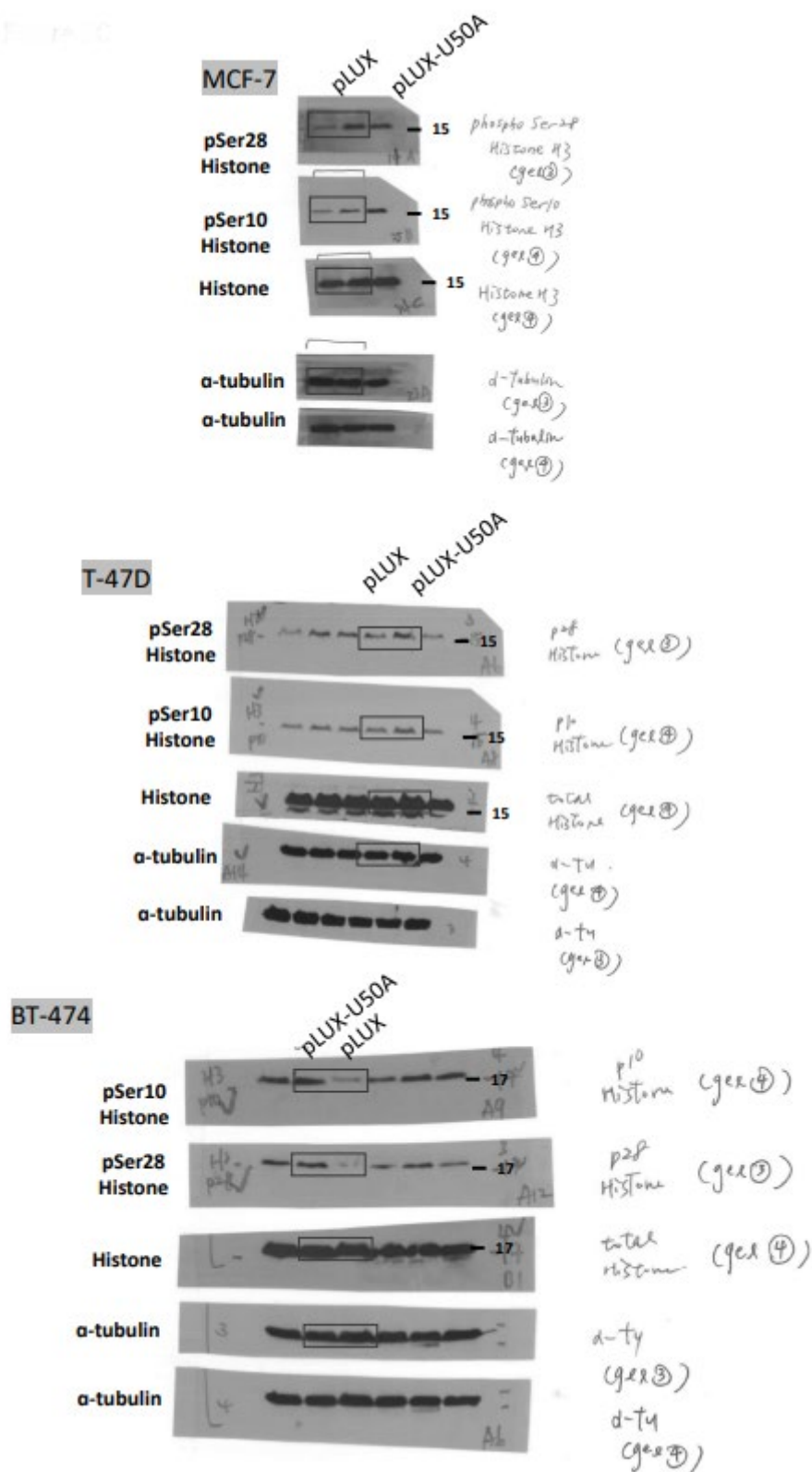
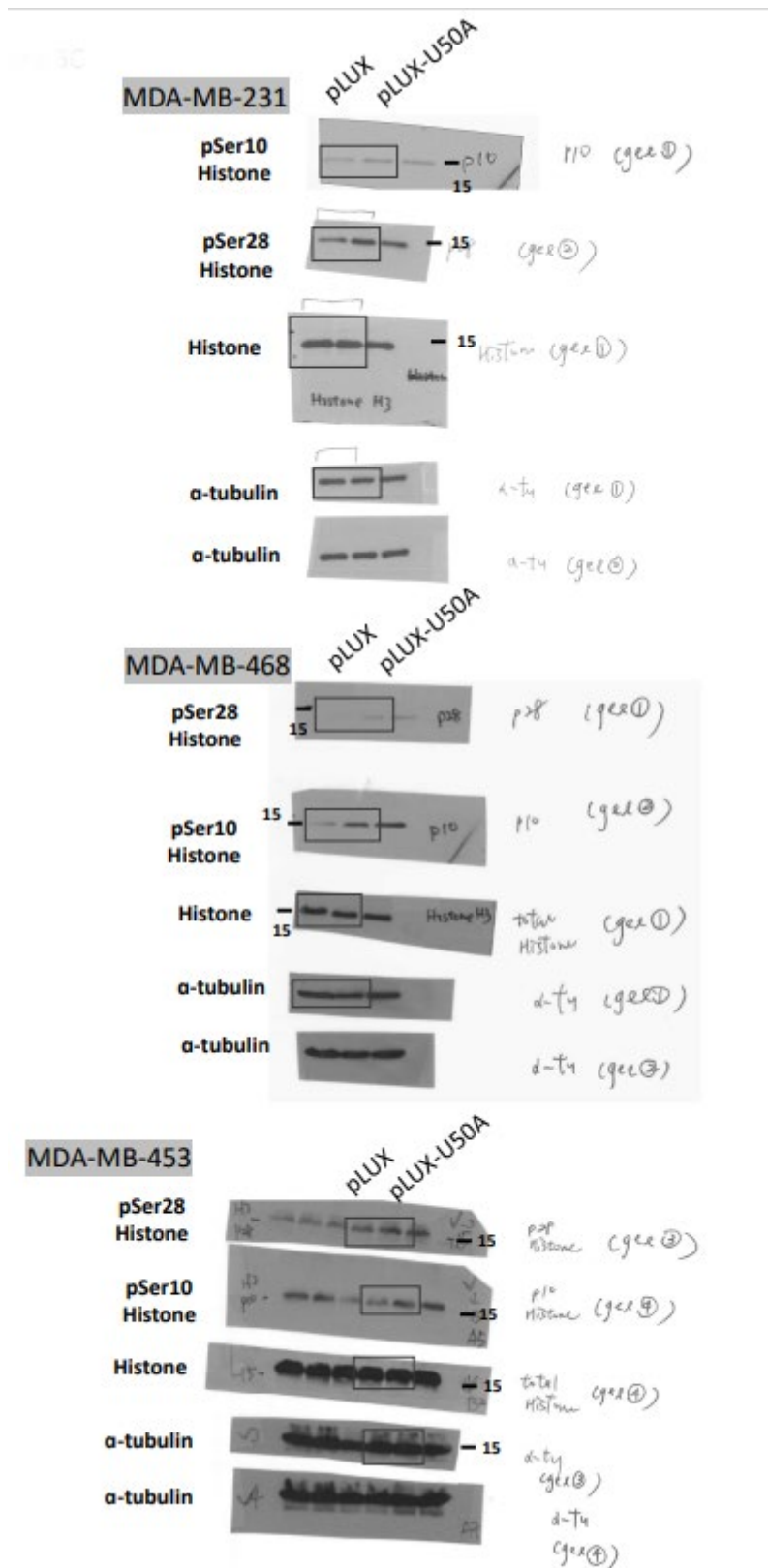
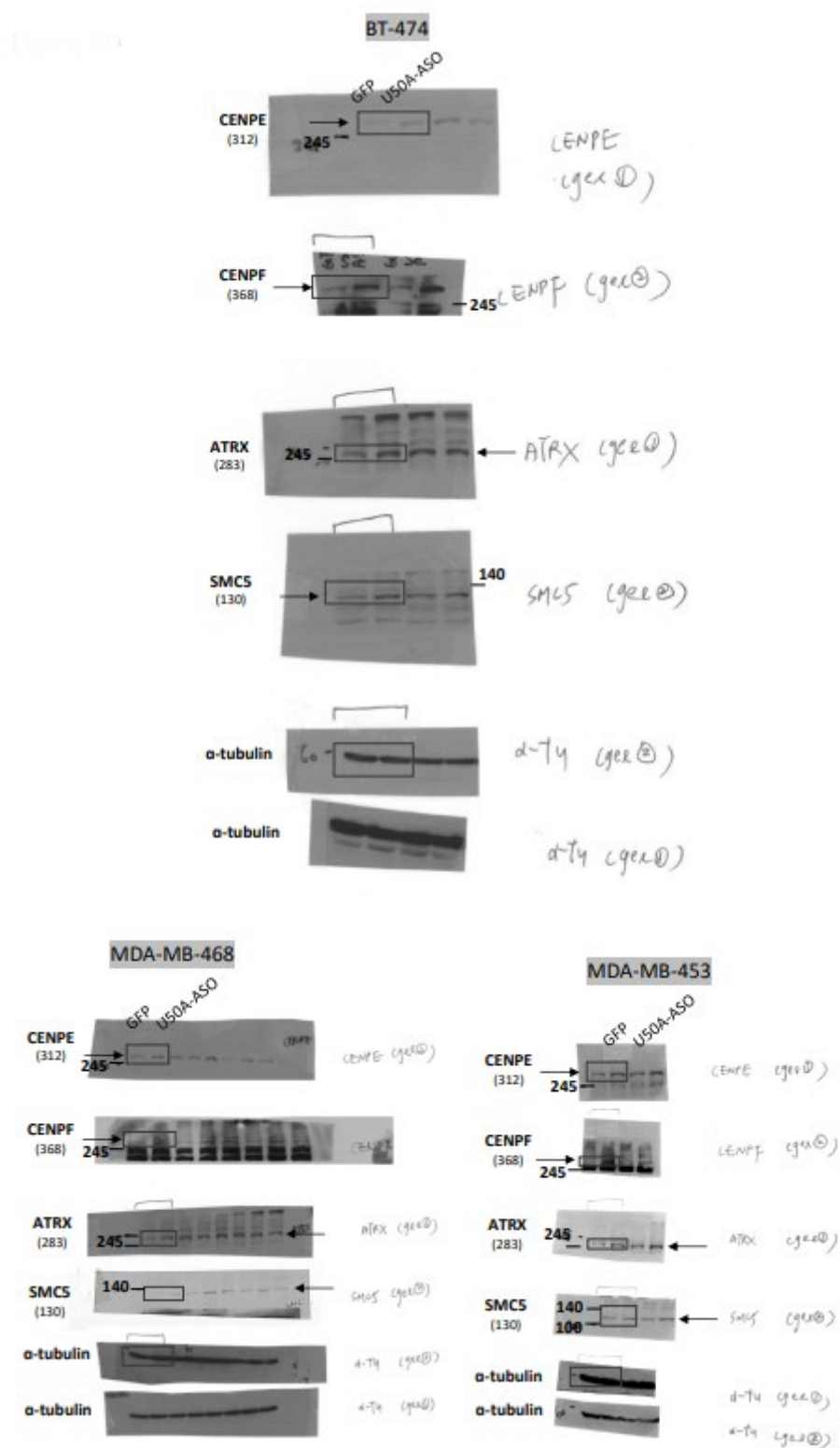


Figure 10









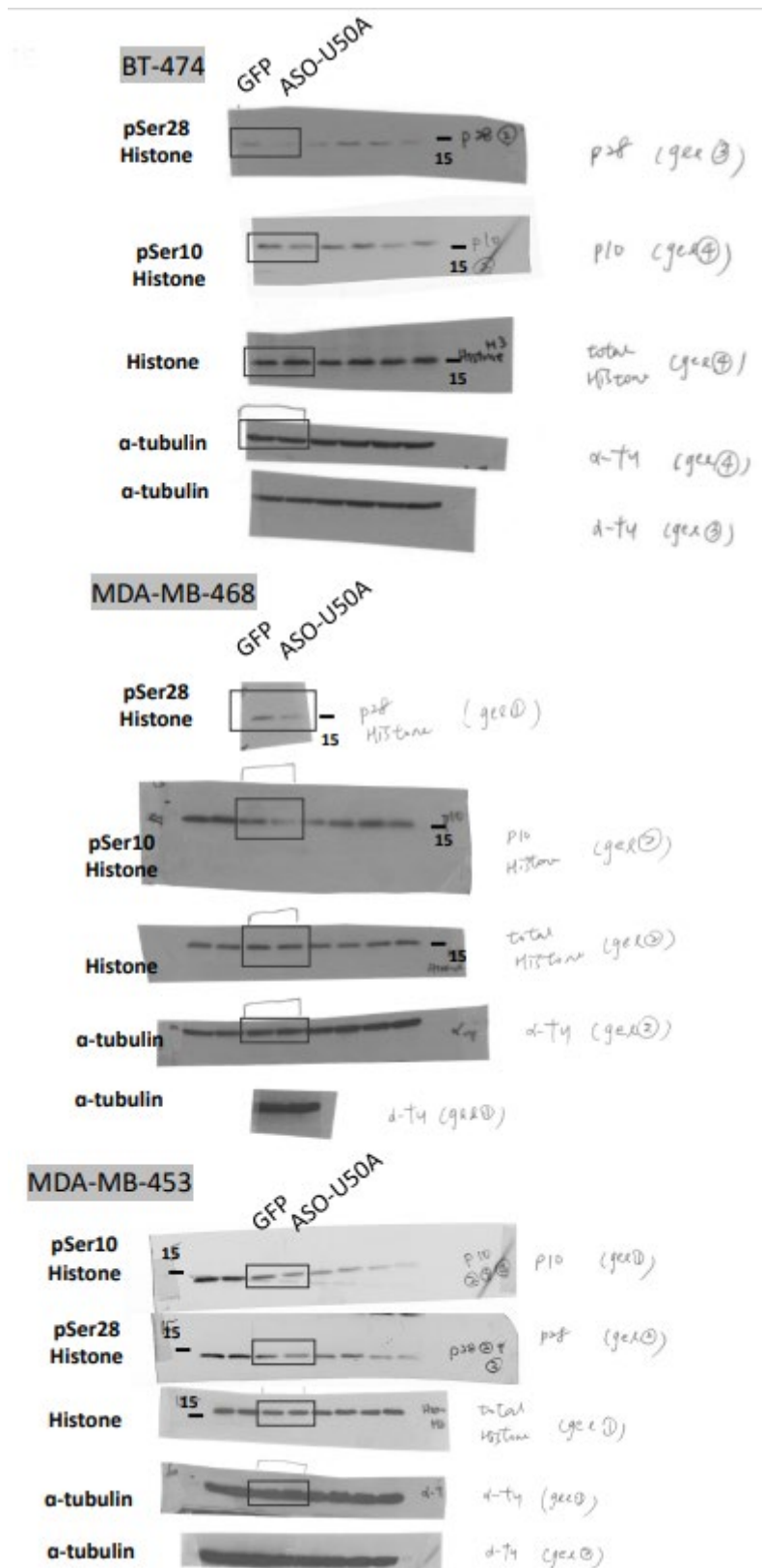


Figure S9. Uncropped WB for Figure 3B,C,D,E.

**Table S1.** Survival analysis of U50A, U50B and SNHG5 in breast cancer subtypes (number of patients).

Marker	Luminal A/B (68)				HER2-enriched (28)				Triple-negative (18)			
	OS		RFS		OS		RFS		OS		RFS	
U50A	<i>p</i>	HR	<i>p</i>	HR	<i>p</i>	HR	<i>p</i>	HR	<i>p</i>	HR	<i>p</i>	HR
	0.03 *	0.3 #	0.02 *	0.27 #	0.15	0.34 #	0.16	0.34 #	0.87	0.35#	0.2	0.45 #
U50B	OS		RFS		OS		RFS		OS		RFS	
	<i>p</i>	HR	<i>p</i>	HR	<i>p</i>	HR	<i>p</i>	HR	<i>p</i>	HR	<i>p</i>	HR
	0.12	0.45#	0.18	0.47#	0.73	1.29	0.75	1.28	0.17	0.44 #	0.3	0.54
SNHG5	OS		RFS		OS		RFS		OS		RFS	
	<i>p</i>	HR	<i>p</i>	HR	<i>p</i>	HR	<i>p</i>	HR	<i>p</i>	HR	<i>p</i>	HR
	0.18	0.49 #	0.22	0.52	0.57	1.54	0.3	1.52	0.4	0.61	0.85	0.89

Survival analysis was analyzed by Log-rank test. # Hazard ratio (HR) <0.5. \*  $p < 0.05$ . Original data from Figure S2.

**Table S2.** Correlation between copy numbers of U50A, U50B or SNHG5 with pathological stages in breast cancer subtypes.

Luminal A/B Marker	Stage (Mean $\pm$ S.D.)				
	I	II	III	IV	<i>p</i>
U50A	325 $\pm$ 191.3	137.2 $\pm$ 107.4	156.6 $\pm$ 107.3	20 $\pm$ 0	*** 0.0004
U50B	6.28 $\pm$ 6.8	5.81 $\pm$ 9.8	4.17 $\pm$ 4.15	0.01 $\pm$ 0	0.74
SNHG5	46.45 $\pm$ 49.57	16.09 $\pm$ 38.07	58.42 $\pm$ 83.23	0.01 $\pm$ 0	0.06
HER2-enriched					
Marker					
U50A	182.6 $\pm$ 144.2	104.8 $\pm$ 81.97	212.7 $\pm$ 184.6	-	0.19
U50B	3.46 $\pm$ 1.34	9.05 $\pm$ 15	7.84 $\pm$ 12.38	-	0.75
SNHG5	2.18 $\pm$ 2.81	35.08 $\pm$ 47.25	99.35 $\pm$ 192.3	-	0.33
TNBC					
Marker					
U50A	536 $\pm$ 232.1	82.33 $\pm$ 75.56	187.1 $\pm$ 231	64.4 $\pm$ 0	* 0.04
U50B	47.63 $\pm$ 34.02	4.46 $\pm$ 7.53	3.49 $\pm$ 5.48	3.4 $\pm$ 0	** 0.0012
SNHG5	46.51 $\pm$ 22.73	5.67 $\pm$ 11.35	14.23 $\pm$ 29.3	0.97 $\pm$ 0	0.19

S.D.: Standard error of the mean, \*  $p < 0.05$ , \*\*  $p < 0.01$ , \*\*\*  $p < 0.001$ . Stage according to the recommendations of the American Cancer Society, Use One-way ANOVA, Tukey's multiple comparisons test, original data from Figures S4–S6.

**Table S3.** Multivariate Analysis of breast cancer prognostic markers.

Variable	Overall survival (OS)			Relapse-free survival (RFS)		
	<i>p</i>	95% Confidence Interval	Hazard Ratio	<i>p</i>	95% Confidence Interval	Hazard Ratio
T	0.01 *	1.293–6.475	2.894	0.008 **	1.333–6.745	2.999
N	0.78	0.210–3.227	0.823	0.741	0.203–3.103	0.795
Stage	0.024 *	1.211–16.10	4.416	0.028 *	1.170–15.721	4.288
U50A	0.098	0.239–1.128	0.519	0.063	0.222–1.039	0.480

Based on Cox proportional hazards model. \*  $p < 0.05$ , \*\*  $p < 0.01$