

SUPPLEMENTARY TABLES

Supplementary Table 1. The clinicopathological characteristics of patients with breast cancer from TCGA.

Characteristic	Levels	Overall
n		1083
T stage, n (%)	T1	277 (25.6%)
	T2	629 (58.2%)
	T3	139 (12.9%)
	T4	35 (3.2%)
N stage, n (%)	N0	514 (48.3%)
	N1	358 (33.6%)
	N2	116 (10.9%)
M stage, n (%)	N3	76 (7.1%)
	M0	902 (97.8%)
	M1	20 (2.2%)
Pathologic stage, n (%)	Stage I	181 (17.1%)
	Stage II	619 (58.4%)
	Stage III	242 (22.8%)
	Stage IV	18 (1.7%)
Race, n (%)	Asian	60 (6%)
	Black or African American	181 (18.2%)
Age, n (%)	White	753 (75.8%)
	<=60	601 (55.5%)
PR status, n (%)	>60	482 (44.5%)
	Negative	342 (33.1%)
Histological type, n (%)	Indeterminate	4 (0.4%)
	Positive	688 (66.5%)
ER status, n (%)	Infiltrating Ductal Carcinoma	772 (79%)
	Infiltrating Lobular Carcinoma	205 (21%)
HER2 status, n (%)	Negative	240 (23.2%)
	Indeterminate	2 (0.2%)
PAM50, n (%)	Positive	793 (76.6%)
	Negative	558 (76.8%)
Menopause status, n (%)	Indeterminate	12 (1.7%)
	Positive	157 (21.6%)
radiation_therapy, n (%)	Normal	40 (3.7%)
	LumA	562 (51.9%)
OS event, n (%)	LumB	204 (18.8%)
	Her2	82 (7.6%)
Anatomic neoplasm subdivisions, n (%)	Basal	195 (18%)
	Pre	229 (23.6%)
radiation_therapy, n (%)	Peri	40 (4.1%)
	Post	703 (72.3%)
radiation_therapy, n (%)	Left	563 (52%)
	Right	520 (48%)
radiation_therapy, n (%)	No	434 (44%)
	Yes	553 (56%)
radiation_therapy, n (%)	Yes	553 (56%)
	Alive	931 (86%)

DSS event, n (%)	Dead	152 (14%)
	Alive	978 (92%)
PFI event, n (%)	Dead	85 (8%)
	Alive	936 (86.4%)
Age, median (IQR)	Dead	147 (13.6%)
		58 (48.5, 67)

Supplementary Table 2. Correlations between OS and mRNA expression of SORBS1 analyzed by univariate and multivariate Cox regression.

Characteristics	Total (N)	Univariate analysis		Multivariate analysis	
		Hazard ratio (95% CI)	P-value	Hazard ratio (95% CI)	P-value
T stage	1061				
T1&T2	889	Reference			
T3&T4	172	1.673 (1.152-2.429)	0.007	1.640 (0.773-3.480)	0.198
N stage	1045				
N0	507	Reference			
N1&N2&N3	538	2.145 (1.497-3.073)	<0.001	1.110 (0.545-2.264)	0.774
M stage	909				
M0	889	Reference			
M1	20	4.327 (2.508-7.465)	<0.001	3.262 (1.020-10.433)	0.046
Pathologic stage	1041				
Stage I&Stage II	785	Reference			
Stage III&Stage IV	256	2.519 (1.787-3.549)	<0.001	2.976 (1.289-6.873)	0.011
Age	1064				
<=60	588	Reference			
>60	476	2.036 (1.468-2.822)	<0.001	3.169 (1.642-6.115)	<0.001
Menopause status	955				
Pre&Peri	263	Reference			
Post	692	2.405 (1.445-4.002)	<0.001	2.119 (0.880-5.105)	0.094
ER status	1014				
Negative	237	Reference			
Positive	777	0.704 (0.487-1.017)	0.062	0.412 (0.231-0.735)	0.003
PR status	1011				
Negative	338	Reference			
Positive	673	0.762 (0.541-1.074)	0.120		
HER2 status	705				
Negative	548	Reference			
Positive	157	1.611 (0.981-2.644)	0.059	0.781 (0.405-1.508)	0.462
SORBS1	1064				
Low	531	Reference			
High	533	0.580 (0.414-0.812)	0.002	0.474 (0.271-0.829)	0.009

Supplementary Table 3. Correlations between DSS and mRNA expression of SORBS1 analyzed by univariate and multivariate Cox regression.

Characteristics	Total (N)	Univariate analysis		Multivariate analysis	
		Hazard ratio (95% CI)	P-value	Hazard ratio (95% CI)	P-value
T stage	1042				
T1&T2	877	Reference			
T3&T4	165	2.037 (1.252-3.314)	0.004	0.740 (0.373-1.469)	0.390
N stage	1027				
N0	504	Reference			
N1&N2&N3	523	3.584 (2.089-6.148)	<0.001	1.781 (0.908-3.491)	0.093
M stage	891				
M0	872	Reference			
M1	19	7.697 (4.112-14.407)	<0.001	4.950 (2.304-10.633)	<0.001
Pathologic stage	1024				
Stage I&Stage II	776	Reference			
Stage III&Stage IV	248	3.870 (2.474-6.055)	<0.001	2.793 (1.348-5.788)	0.006
Age	1045				
<=60	578	Reference			
>60	467	1.418 (0.913-2.201)	0.120		
Menopause status	945				
Pre&Peri	261	Reference			
Post	684	1.591 (0.872-2.904)	0.130		
ER status	996				
Negative	230	Reference			
Positive	766	0.523 (0.326-0.838)	0.007	0.432 (0.185-1.008)	0.052
PR status	993				
Negative	331	Reference			
Positive	662	0.529 (0.336-0.833)	0.006	0.850 (0.374-1.931)	0.697
HER2 status	695				
Negative	541	Reference			
Positive	154	1.481 (0.740-2.965)	0.267		
SORBS1	1045				
Low	521	Reference			
High	524	0.485 (0.306-0.771)	0.002	0.528 (0.304-0.917)	0.023

Supplementary Table 4. QPCR primer sequence with siRNA interference sequence information.

Gene name	Forward primer	Reverse primer
SORBS1	CTGGAGGCCACTTGTGGTTC	CCTGGGCATGTCTTGCTTATG-3
CD68	ATGAGGCTGGCTGTGCTTTT	CTAGTGGTGGCAGGACTGTG
CD206	CCAAACGCCTTCATTTGCCA	ACCTTCCTTGCACCCCTGATG
β -actin	CTCGCCTTT GCCGATCC	TTCTCCATGTCGTCCCAGTT
Si-SORBS1	GGUACAAGACUAUGUUUAAAC	UUAAACAUAGUCUUGUACCAG
Si-SORBS2	GGUACUUCAAGAAGGACAAAG	UUGUCCUUCUUGAAGUACCAA
Si-SORBS3	CAGAAGAGAUAGAUUUAAAGA	UUUAAAUCUAUCUCUUCUGGG