

Supplementary references

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Table SI. Gene mutation and putative copy-number alterations of UBQLN1 in five breast cancer studies (cBioPortal).

Study, year of publication	No. of patients	Mutation (%)	Amplification (%)	Deep deletion (%)	Total (%)	(Refs.)
METABRIC; Nature, 2012; and Nat Commun, 2016	2,173	0 (0)	8 (0.37)	0 (0)	8 (0.37)	(1-3)
TCGA Cell, 2015	817	3 (0.37)	3 (0.37%)	3 (0.37)	9 (1.1)	(4)
TCGA Firehose Legacy	1,099	2 (0.18)	6 (0.55)	3 (0.27)	11 (1)	GDAC Firehose ^a
TCGA Nature, 2012	803	1 (0.12)	3 (0.37)	1 (0.12)	5 (0.62)	
TCGA Pancancer Atlas	1,084	2 (0.18)	2 (0.18)	2 (0.18)	6 (0.54)	
Total	5,976	8 (0.13)	22 (0.37)	9 (0.15)	39 (0.7)	(6)

Source data from GDAC Firehose^a (http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/BRCA/20160128/). TCGA, The Cancer Genome Atlas; UBQLN1, ubiquilin-1.

Table SII. UBQLN1 mRNA expression level (z-scores) relative to diploid samples (microarray) in five breast cancer studies.

Study, year of publication	No. of patients	mRNA high, n (%)	mRNA low, n (%)	(Refs.)
METABRIC; Nature, 2012; and Nat Commun, 2016	1,904	75 (3.95)	42 (2.21)	(1-3)
TCGA Cell 2015	421	22 (5.23)	16 (3.80)	(4)
TCGA Firehose Legacy	529	27 (5.13)	21 (3.99)	GDAC Firehose ^a
TCGA Nature, 2012	526	25 (4.75)	20 (3.80)	(5)
TCGA Pancancer Atlas	1,082	74 (6.84)	13 (1.20)	(6)
Total	4,462	223 (5.00)	112 (2.51)	

Source data from GDAC Firehose^a (http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/BRCA/20160128/). TCGA, The Cancer Genome Atlas; UBQLN1, ubiquilin-1.

Table SIII. Association between UBQLN1 mRNA expression and clinicopathological parameters of breast cancer in TCGA database (UALCAN).

Clinicopathological features	No. of patients	UBQLN1 mRNA expression					Compared groups	P-value
		Low	Lower quartile	Median	Upper quartile	High		
TNM stage								
I	183	22.83	51.61	65.65	88.97	138.48	Stage 1 vs. stage 2	0.023 ^a
II	615	14.83	53.17	71.30	89.93	147.94	Stage 1 vs. stage 3	0.014 ^a
III	247	7.99	54.47	71.22	90.80	147.18		
IV	20	23.25	46.26	64.68	78.033	116.68		
Age, years								
20-40	97	21.49	55.57	73.82	93.94	149.63		>0.05
41-60	505	7.99	53.00	68.59	89.63	147.18		
61-80	431	14.84	52.85	71.00	88.99	143.55		
80-100	54	18.59	52.74	77.37	96.32	137.91		
Major subclasses								
Luminal	566	14.23	55.39	74.34	90.67	143.98		>0.05
HER2 positive	37	38.60	52.70	68.86	92.27	143.37		
Triple-negative	116	7.99	47.22	63.88	84.00	147.94		
Menopause status								
Pre-menopause	230	14.23	55.36	72.64	91.03	145.68		>0.05
Peri-menopause	37	7.99	52.07	61.56	93.55	143.37		
Post-menopause	700	16.05	53.62	70.58	89.43	145.79		
Nodal metastasis status								
N0	516	7.99	52.39	67.46	87.82	143.55	N0-vs-N1	0.001 ^b
N1	362	14.23	55.96	74.57	92.80	149.67	N0-vs-N2	0.001 ^b
N2	120	16.89	60.16	77.10	94.98	153.91	N1-vs-N3	0.036 ^a
N3	77	21.81	46.26	64.57	82.56	131.75	N2-vs-N3	0.006 ^a
TP53 mutation status								
Mutant	334	14.23	53.22	69.97	90.494	150.03		>0.05
Non-mutant	698	7.99	53.13	70.76	89.975	147.18		

^aP<0.05; ^bP<0.001. N0, no regional lymph node metastasis; N1, metastases in 1 to 3 axillary lymph nodes; N3, metastases in 4 to 9 axillary lymph nodes; N4, metastases in 10 or more axillary lymph nodes; UBQLN1, ubiquilin-1.

Table SIV. Evaluation of the outcome significance of UBQLN1 and clinical factors using the Cox proportional hazard model (TIMER2.0).

Factor	Coef.	HR	SE (coef.)	95% CI		z value	P-value
				Lower	Upper		
UBQLN1	0.288	1.333	0.139	1.016	1.749	2.076	0.038 ^a
Age, years	0.033	1.034	0.007	1.020	1.048	4.752	<0.001 ^b
Sex (male)	-0.546	0.579	1.010	0.080	4.195	-0.540	0.589
Race: Of African origin	0.149	1.161	0.616	0.347	3.882	0.242	0.808
Race: Caucasian	-0.175	0.839	0.595	0.262	2.692	-0.295	0.768
Stage 2	0.515	1.674	0.282	0.964	2.907	1.831	0.067
Stage 3	1.188	3.279	0.298	1.829	5.881	3.985	<0.001 ^b
Stage 4	2.651	14.171	0.378	6.758	29.716	7.018	<0.001 ^b

^aP<0.05; ^bP<0.0001. Coef, coefficient; SE, standard error; HR, hazard ratio; CI, confidence interval; UBQLN1, ubiquilin-1.