Supplementary Materials: The Ubiquilin Networking in Cancers

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Table S1. The Cancer Genome Atlas (TCGA) and non-TCGA studies for breast, lung, and ovary cancer were screened for amplification and/or deletions of *UBQLNs*. Only non-redundant studies were included in this analysis. The database stores 3116, 884, and 583 samples of breast, lung, and ovary cancer, respectively.

Cancer	Genetic Variants	
	Amplification	Deletion
Breast	8/3116 (0.26%) (UBQLN1)	0/3116 (0.0%) (UBQLN1)
	15/3116 (0.48%) (UBQLN2)	1/3116 (0.03%) (UBQLN2)
	20/3116 (0.68%) (UBQLN3)	15/3116 (0.48%) (UBQLN3)
	446/3116 (14.96%) (UBQLN4)	0/3116 (0.0% (UBQLN4)
Lung	2/2884 (0.07%) (UBQLN1)	15/2884 (0.52%) (UBQLN1)
	12/2884 (0.42%) (UBQLN2)	19/2884 (0.66%) (UBQLN2)
	2/2884 (0.07%) (UBQLN3)	12/2884 (0.42%) (UBQLN3)
	171/2884 (5.39%) (UBQLN4)	0/2884 (0.0%) (UBQLN4)
Ovary	0/583 (0.0%) (UBQLN1)	0/583 (0.0%) (UBQLN1)
	15/583 (2.57%) (UBQLN2)	3/583 (0.51%) (UBLQN2)
	2/583 (0.34%) (UBLQN3)	2/583 (0.34%) (UBQLN3)
	59/583 (10.12%) (UBQLN4)	0/583 (0.0%) (UBQLN4)

Table S2. The Cancer Genome Atlas (TCGA) and non-TCGA studies for breast were analyzed in order to identify *UBLQN*'s mutations. Allele frequency is shown as percentage (%) of variants reads out of 103 total from Whole-exome sequencing of 817 breast invasive carcinoma tumor/normal pairs. Table lists all mutations with allele frequency higher than 15%.

Gene	Mutation Type	Protein Change	Allele Frequency (%)
UBLQN1	Missense	Q539E	47
	Nonsense	Q176*	31
UBQLN2	Missense	V191G	26
	Missense	E42Q	3
UBLQN3	Missense	P108S	26
	Missense	I403L	15
UBQLN4	Missense	P108H	30
	Missense	Q422E	36
	Missense	M537T	32
	Missense	E273Q	19
	Missense	W333C	17
	Missense	S408T	16

Table S3. The Cancer Genome Atlas (TCGA) and non-TCGA studies on Lung adenocarcinoma were analyzed in order to identify *UBLQN*'s mutations. Allele frequency is shown as percentage (%) of variants reads out of 150 total from Whole-exome sequencing of 660 lung ADC and 484 lung SqCC tumor/normal pairs. Table lists all mutations with allele frequency higher than 15%.

Gene	Mutation Type	Protein Change	Allele Frequency (%)
UBLQN1	Nonsense	G499*	53
	Missense	L91W	46
	Frame_shift	T475Nfs*27	46
	Missense	N577S	41
	Missense	R274C	3
	Missense	M454V	27
	Missense	G492E	27
	Missense	M235I	17
	Missense	L149I	19
	Missense	S333L	16
UBQLN2	Missense	P440Q	68
	Missense	H90N	54
	Missense	G481V	54
	Missense	G526C	50
	Missense	P414R	47
	Missense	V505F	43
	Missense	M271I	40
	Missense	M386I	38
	Missense	G288W	30
	Missense	Q173L	23
	Missense	S444L	23
	Missense	Q170H	22
	Missense	Q174P	21
	Missense	Q327H	20
	Missense	S140C	17
	Missense	S256R	16
UBQLN3	Missense	M546I	88
	Missense	I247L	79
	Missense	A268S	71
	Missense	G312A	7
	Missense	S294L	51
	Frame shift	P382Hfs*20	54
	Missense	Q198H	50
	Missense	D321N	48
	Missense	Y258C	48
	Missense	R295S	46
	Missense	P214T	44
	Missense	L89Q	41
	Missense	E232D	37
	Missense	R53H	34
	Missense	R225L	31
	Missense	V240L	31
	Missense	A430S	31
	Missense	Q198K	30
	Missense	G431W	30
	Missense	Q636L	30
	Missense	A7S	29
	Missense	S106C	29
	Missense	P472T	29
	Missense	L566F	29

	Missense	D443Y	28
	Missense	M626G	28
	Missense	D263H	27
	Missense	M262I	25
	Missense	L511F	25
	Missense	G589V	25
	Missense	D284Y	23
	Missense	E101K	21
	Missense	S36T	18
	Missense	Q394K	16
	Missense	A516T	16
UBQLN4	Missense	P255A	36
	Missense	M261V	30
	Missense	M218I	30
	Missense	S516F	27
	Missense	V78D	18