

Supplementary Table S1: Clinico-pathological parameters for the three cohorts of breast cancer patients utilized in this study

Variables	Cohort 1	Cohort 2	Cohort 3
	Houston RPPA (n = 712)	Consecutive TMA (n = 512)	TCGA RPPA (n = 410)
Age at Diagnosis			
Median (Range)	60 (23 - 89)	65 (27 - 96)	58 (26 - 89)
Missing	136 (19.1%)	-	-
Survival Data			
Available	575 (80.8%)	439 (85.7%)	-
Missing	137 (19.2%)	73 (14.3%)	-
Tumor Size			
≤2cm	179 (25.1%)	267 (60.4%)	-
>2cm	246 (34.6%)	175 (39.6%)	-
Missing	287 (40.3%)	-	-
Tumor Grade			
I	65 (9.1%)	107 (24.2%)	-
II	149 (20.9%)	180 (40.7%)	-
III	243 (34.1%)	154 (34.8%)	-
Missing	255 (35.8%)	1 (0.2%)	-
Nodal status			
N0	283 (39.7%)	246 (55.7%)	161 (39.3%)
N1+	255 (35.8%)	148 (33.5%)	171 (41.7%)
Missing	174 (24.4%)	48 (10.9%)	78 (19.0%)
ER status*			
ER negative	262 (36.8%)	65 (14.7%)	99 (24.1%)
ER positive	429 (60.3%)	353 (79.9%)	304 (74.1%)
Missing	21 (2.9%)	24 (5.4%)	7 (1.7%)
PR status			
PR negative	367 (51.5%)	125 (28.3%)	156 (38.0%)
PR positive	333 (46.8%)	203 (45.9%)	247 (60.2%)
Missing	12 (1.7%)	114 (25.8%)	7 (1.7%)
Her2 status			
Her2 Negative	561 (78.8%)	376 (85.1%)	217 (52.9%)
Her2 Positive	140 (19.7%)	43 (9.7%)	74 (18.0%)
Missing	11 (1.5%)	23 (5.2%)	19 (29.0%)

*ER status was determined by 10% positively stained nuclei from independent histological scoring.

Supplementary Table S2: Association of PRDX1 expression with clinicopathological parameters in the RPPA cohort (cohort 1)

Variables	PRDX1 Protein Expression [#]		p-value
	Low (n=356)	High (n=356)	
Age at Diagnosis			<0.001
≤50	93 (33.5)	61 (20.5)	
>50	185 (66.5)	237 (79.5)	
Missing	78	58	
Tumor Size			0.138
≤2cm	91 (38.7)	88 (46.3)	
>2cm	144 (61.3)	102 (53.7)	
Missing	121	166	
Tumor Grade			<0.001*
I	25 (10)	40 (19.2)	
II	71 (28.5)	78 (37.5)	
III	153 (153)	90 (43.3)	
Missing	107	148	
Nodal status			0.07
N0	124 (48.4)	159 (56.4)	
N1+	132 (51.6)	123 (43.6)	
Missing	100	74	
ER status			0.05
ER negative	143 (41.7)	119 (34.2)	
ER positive	200 (58.3)	229 (65.8)	
Missing	13	8	
PR status			0.291
PR negative	190 (54.4)	177 (50.4)	
PR positive	159 (45.6)	174 (49.6)	
Missing	7	5	
Her2 status			0.001
FISH negative	262 (75.1)	299 (84.9)	
FISH positive	87 (24.9)	53 (15.1)	
Missing	7	4	

*Linear-by-linear χ^2 analysis; Others by Fisher's Exact test

[#]PRDX1 protein expression levels are stratified by the median protein expression value.

Supplementary Table S3: Association of PRDX1 expression with clinicopathological parameters in the consecutive cohort (cohort 2)

Variables	PRDX1 Protein Expression [#]		p-value
	Low (n=221)	High (n=221)	
Age at Diagnosis			0.066
≤50	42 (19.0)	27 (12.2)	
>50	179 (81.0)	194 (87.8)	
Tumor Size			0.011
≤2cm	120 (54.3)	147 (66.5)	
>2cm	101(45.7)	74 (33.5)	
Histological type			0.003*
Indeterminate	13 (5.9)	14 (6.3)	
Ductal	159 (71.9)	131 (59.3)	
Lobular	23 (10.4)	45 (20.4)	
Tubular	10 (4.5)	18 (8.1)	
Medullary	11 (5.0)	3 (1.4)	
Mucinous	5 (2.3)	10 (4.5)	
Tumor Grade			0.002*
I	40 (18.2)	67 (30.3)	
II	88 (40.0)	92 (41.6)	
III	92 (41.8)	62 (28.1)	
Missing	1	0	
Nodal status			0.755
N0	126 (63.3)	120 (61.5)	
N1+	73 (36.7)	75 (38.5)	
Missing	22	26	
ER status			0.043
ER negative	40 (19.2)	25 (11.9)	
ER positive	168 (80.8)	185 (88.1)	
Missing	13	11	
PR status			0.307
PR negative	68 (41)	57 (35.2)	
PR positive	98 (59)	105 (64.8)	
Missing	55	60	
Her2 status			0.151
0 - 2 +	183 (87.6)	193 (91.9)	
3+	26 (12.4)	17 (8.1)	
Missing	12	11	
Ki67 status			0.004
0 – 10%	60 (29.3)	90 (43.3)	
11 - 100%	145 (70.7)	118 (56.7)	
Missing	16	13	

*Linear-by-linear χ^2 analysis; Others by Fisher's Exact test

[#]PRDX1 protein expression levels are stratified by the median protein expression value.

Supplementary Table S4: Proteins that correlate with PRDX1 protein expression in the ER-positive and/or ER-negative cohort

	Protein	ER-positive (n = 304)		ER-negative (n = 99)	
		p	r	p	r
Correlate in ER-positive tumors only	ACC-pS79	0.045	0.115	0.063	-0.188
	ACC1	0.000	0.288	0.985	-0.002
	Akt-pS473	0.011	-0.146	0.254	-0.116
	Akt-pT308	0.001	-0.190	0.805	0.025
	B.Raf	0.012	0.143	0.455	-0.076
	Beclin	0.011	-0.146	0.322	0.101
	Bid	0.000	-0.233	0.295	-0.106
	Bim	0.000	0.199	0.055	0.193
	c.Met	0.000	-0.314	0.054	-0.194
	c.Met-pY1235	0.002	-0.177	0.138	0.150
	CDK1	0.027	-0.127	0.294	0.107
	Chk2	0.000	0.229	0.503	-0.068
	cIAP	0.001	0.192	0.267	0.113
	Collagen-VI	0.000	-0.232	0.136	-0.151
	COX.2	0.002	-0.174	0.355	0.094
	Cyclin-B1	0.002	0.177	0.312	0.103
	Cyclin-E1	0.000	0.264	0.087	0.173
	E.Cadherin	0.007	0.154	0.255	-0.116
	eEF2	0.000	0.237	0.264	-0.113
	EGFR	0.000	-0.240	0.410	-0.084
	EGFR-pY1068	0.011	-0.145	0.287	-0.108
	EGFR-pY1173	0.000	-0.218	0.921	-0.010
	EGFR-pY992	0.001	-0.198	0.566	-0.058
	ER-alpha	0.024	0.129	0.707	0.038
	FAK	0.011	-0.146	0.102	-0.165
	Fibronectin	0.007	-0.153	0.171	0.139
	FOXO3a	0.023	-0.130	0.648	-0.046
	GSK3.alpha.beta	0.000	0.325	0.329	-0.099
	HER3-pY1298	0.009	-0.150	0.241	-0.119
	HSP70	0.000	-0.265	0.942	-0.007
	IRS1	0.000	-0.247	0.090	-0.171
	K.Ras	0.001	-0.192	0.731	-0.035
	MAPK-pT202-Y204	0.002	-0.179	0.096	-0.168
	MIG.6	0.001	0.186	0.388	0.088
	Mre11	0.002	-0.174	0.120	0.157
	NF2	0.038	0.119	0.145	0.148
	Notch1	0.018	-0.136	0.761	-0.031
	p21	0.025	-0.129	0.111	-0.161
	p38-MAPK	0.002	0.177	0.235	0.120
	p70S6K	0.039	0.119	0.989	0.001
	PARP-cleaved	0.027	-0.127	0.152	0.145
	PDK1-pS241	0.004	0.163	0.928	-0.009
	PI3K.p110.alpha	0.000	0.334	0.638	0.048
	PKC.alpha	0.041	-0.117	0.281	-0.109
	PKC.alpha-pS657	0.016	-0.138	0.451	-0.077
	Rb	0.000	-0.222	0.671	0.043
	S6	0.000	0.248	0.215	0.126
S6-pS240-S244	0.028	0.126	0.811	-0.024	
Src-pY527	0.000	-0.206	0.621	-0.050	
STAT3-pY705	0.000	-0.202	0.401	0.085	
Stathmin	0.002	-0.179	0.239	0.119	
Syk	0.003	0.172	0.115	0.159	
VEGFR2	0.000	0.271	0.774	0.029	
X4E.BP1	0.000	0.200	0.566	0.058	
XBP1	0.000	-0.204	0.297	-0.106	
YAP	0.000	-0.202	0.722	-0.036	

Correlate in opposite direction across both cohorts	C.Raf	<i>0.004</i>	0.163	<i>0.011</i>	-0.254
	C.Raf-pS338	<i>0.005</i>	-0.162	<i>0.015</i>	0.244
	CD31	<i>0.043</i>	-0.116	<i>0.004</i>	0.288
	Chk1-pS345	<i>0.004</i>	-0.164	<i>0.011</i>	0.255
	mTOR	<i>0.000</i>	0.224	<i>0.039</i>	-0.208
	Rab25	<i>0.005</i>	-0.160	<i>0.003</i>	0.295
	SETD2	<i>0.047</i>	-0.114	<i>0.002</i>	0.306
	Snail	<i>0.005</i>	-0.161	<i>0.006</i>	0.274
Correlate in the same direction across both cohorts	A.Raf-pS299	<i>0.000</i>	0.272	<i>0.001</i>	0.320
	Bax	<i>0.003</i>	0.172	<i>0.001</i>	0.337
	Bcl.xL	<i>0.004</i>	0.165	<i>0.001</i>	0.334
	c.Jun-pS73	<i>0.000</i>	-0.315	<i>0.002</i>	-0.312
	c.Myc	<i>0.000</i>	-0.260	<i>0.001</i>	-0.315
	Caspase.7-cleavedD198	<i>0.018</i>	0.136	<i>0.000</i>	0.344
	Caveolin.1	<i>0.010</i>	-0.148	<i>0.021</i>	-0.232
	CD49b	<i>0.019</i>	0.135	<i>0.045</i>	0.202
	Claudin.7	<i>0.000</i>	0.284	<i>0.023</i>	0.228
	DJ.1	<i>0.002</i>	0.177	<i>0.003</i>	0.292
	eIF4E	<i>0.000</i>	0.214	<i>0.011</i>	0.255
	MEK1-pS217-S221	<i>0.034</i>	-0.121	<i>0.001</i>	-0.323
	Notch3	<i>0.000</i>	-0.218	<i>0.024</i>	-0.226
	Paxillin	<i>0.023</i>	-0.130	<i>0.000</i>	-0.500
	PCNA	<i>0.000</i>	0.276	<i>0.002</i>	0.305
	PTCH	<i>0.000</i>	-0.210	<i>0.001</i>	-0.343
	RBM3	<i>0.000</i>	0.215	<i>0.026</i>	0.224
	Smac	<i>0.000</i>	0.351	<i>0.003</i>	0.298
	Transglutaminase	<i>0.018</i>	0.135	<i>0.008</i>	0.266
	VASP	<i>0.000</i>	0.265	<i>0.000</i>	0.389
	XIAP	<i>0.001</i>	-0.190	<i>0.022</i>	-0.231
	XRCC1	<i>0.001</i>	0.197	<i>0.008</i>	0.265
Correlate in ER-negative tumors only	X53BP1	0.695	-0.023	<i>0.005</i>	-0.282
	Akt	0.790	0.015	<i>0.002</i>	-0.311
	AMPK-pT172	0.671	0.024	<i>0.050</i>	-0.198
	ATM	0.749	0.018	<i>0.050</i>	-0.198
	beta.Catenin	0.363	0.052	<i>0.006</i>	-0.274
	Caspase.8	0.391	0.049	<i>0.048</i>	0.199
	Chk1	0.142	-0.084	<i>0.001</i>	0.324
	eEF2K	0.817	-0.013	<i>0.015</i>	-0.243
	ERK2	0.516	0.037	<i>0.000</i>	-0.350
	GAB2	0.067	0.105	<i>0.014</i>	-0.245
	GSK3.alpha.beta-pS21-S9	0.634	-0.027	<i>0.005</i>	-0.279
	IGF.1R.beta	0.856	0.010	<i>0.011</i>	-0.255
	Ku80	0.405	0.048	<i>0.000</i>	-0.362
	LBK1	0.203	-0.073	<i>0.045</i>	0.202
	Lck	0.405	0.048	<i>0.020</i>	0.234
	MSH2	0.208	0.072	<i>0.019</i>	-0.236
	p27-pT157	0.284	-0.062	<i>0.044</i>	0.203
	p90RSK-pT359-S363	0.101	-0.094	<i>0.001</i>	-0.317
	Pea.15	0.893	0.008	<i>0.000</i>	0.345
	Rad50	0.832	-0.012	<i>0.030</i>	-0.218
	Rad51	0.685	-0.023	<i>0.010</i>	0.256
	Src-pY416	0.404	-0.048	<i>0.001</i>	0.325
	STAT5.alpha	0.379	-0.051	<i>0.002</i>	-0.310
	Tuberin	0.703	0.022	<i>0.000</i>	-0.444
	X14.3.3-epsilon	0.143	0.084	<i>0.002</i>	0.313
	X4E.BP1-pT37	0.353	-0.053	<i>0.013</i>	-0.248

Significant value ($p < 0.05$) highlighted in *italics*. Pearson's correlation values represented by r .