Figure S1. Standardization of DEG expression levels. (A-C) The standardization of DEGs in the (A) GSE21422, (B) GSE29431 datasets and (C) GSE61304 datasets. The blue and red bars represent the data before and after normalization, respectively. DEG, differentially expressed gene.
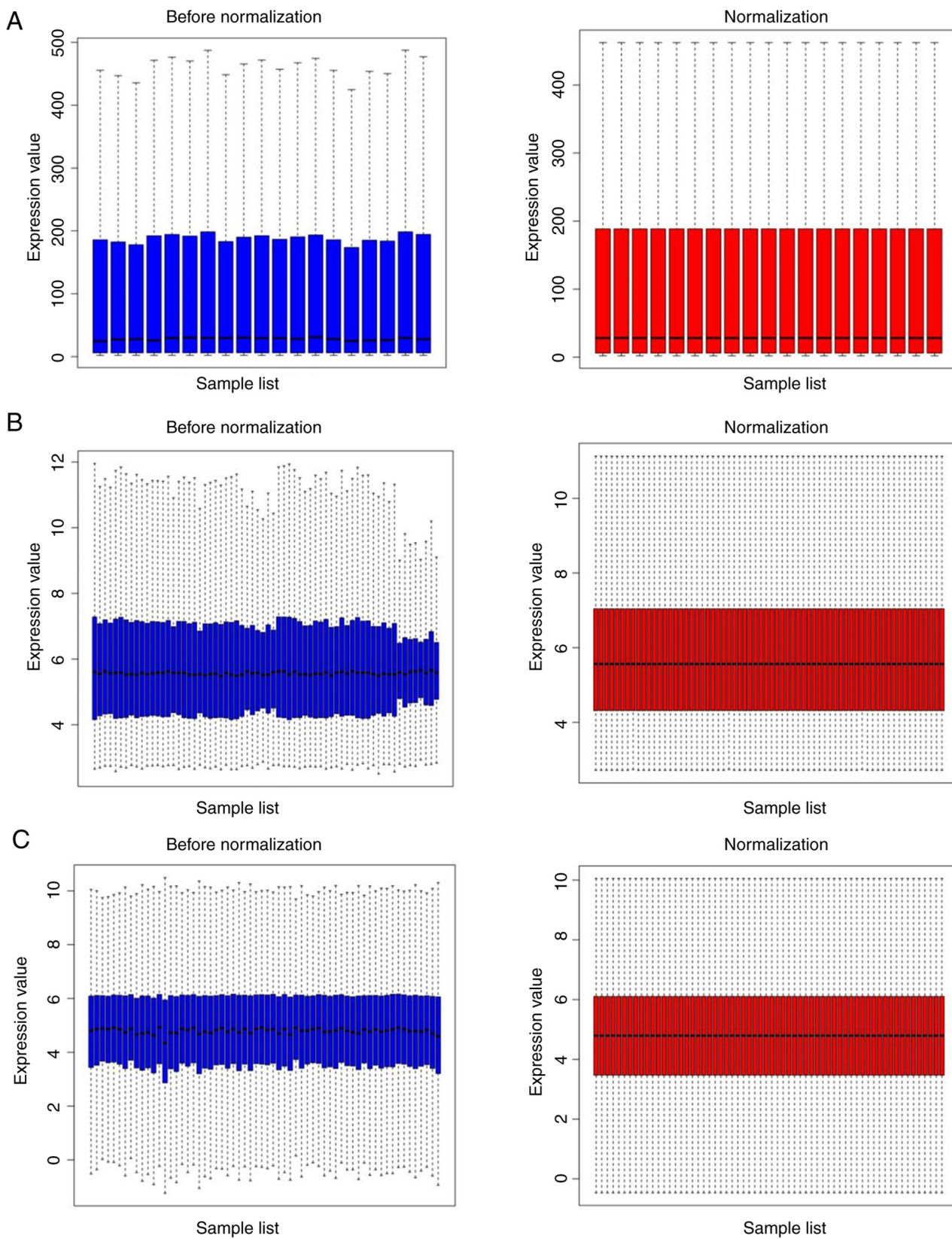
Figure S2. Volcano plots of DEGs in the three different datasets. (A-C) DEGs in the (A) GSE21422, (B) GSE29431 and (C) GSE61304 datasets. The red and green dots represent up- and downregulated DEGs, respectively. The black dots represent genes with no significant difference in expression levels. FC, fold change; DEGs, differentially expressed genes.
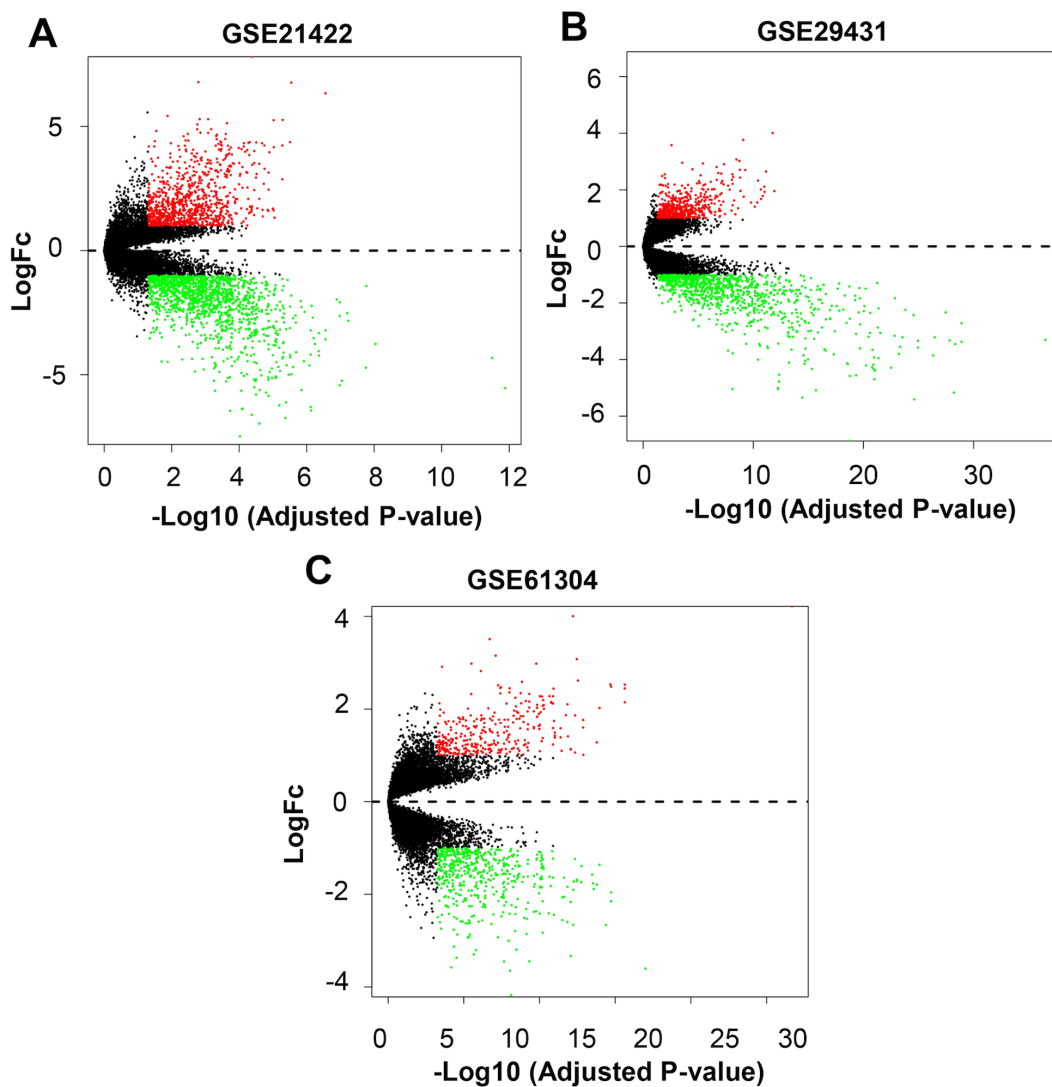
Figure S3. PPI network of module 1 (A) and module 2 (B). Circles represent genes, lines represent interactions between gene-encoded proteins and line colors represent evidence of interactions between proteins.
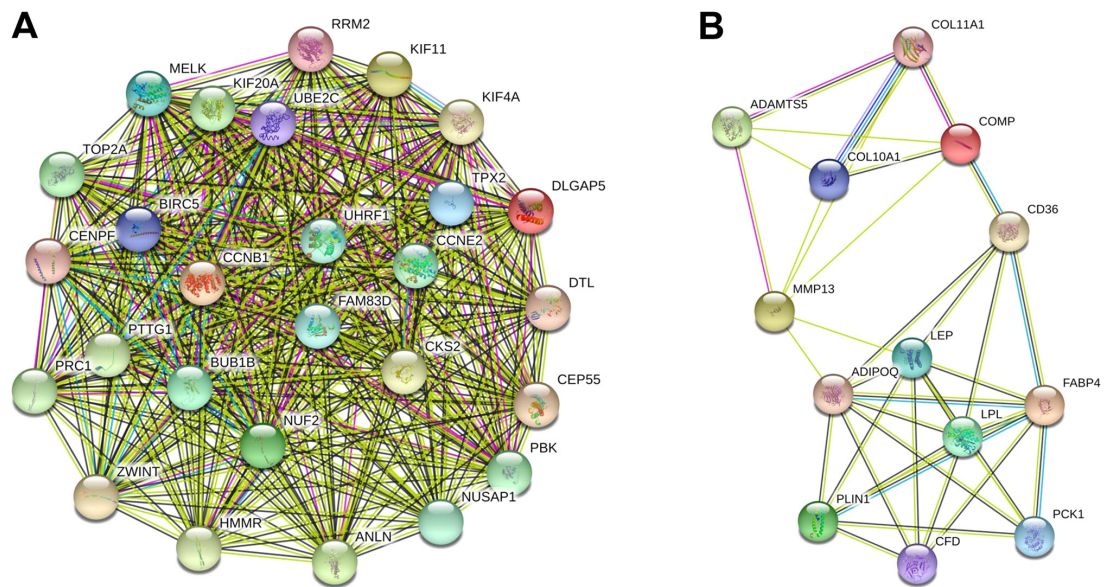
Table SI. Screening differentially expressed genes in patients with breast cancer using the Robust Rank Aggregation method.

Upregulated genes	log(FC)	P-values	Downregulated genes	log(FC)	P-values
COL10A1	4.85	1.88×10^{-11}	LEP	-5.91	1.01×10^{-10}
COL11A1	4.16	2.02×10^{-09}	PLIN1	-4.78	1.72×10^{-09}
GJB2	3.52	2.36×10^{-09}	TNMD	-4.37	2.36×10^{-09}
COMP	3.52	1.06×10^{-08}	TIMP4	-5.05	3.58×10^{-09}
RRM2	3.87	1.62×10^{-08}	C2orf40	-3.91	2.51×10^{-08}
S100P	4.29	2.03×10^{-08}	CA4	-3.74	4.64×10^{-08}
CXCL10	2.98	2.34×10^{-08}	PCK1	-4.26	6.36×10^{-08}
ADAMDEC1	3.06	5.45×10^{-08}	FABP4	-3.90	7.02×10^{-08}
MELK	2.88	7.72×10^{-08}	ADIPOQ	-3.96	7.72×10^{-08}
PTTG1	2.69	8.09×10^{-08}	TMEM132C	-3.55	8.09×10^{-08}
UBE2C	2.79	8.09×10^{-08}	GPIHBP1	-3.64	9.26×10^{-08}
FAM83D	2.83	1.19×10^{-07}	PCOLCE2	-4.66	1.01×10^{-07}
NUSAP1	2.70	1.29×10^{-07}	CHRDL1	-3.56	1.05×10^{-07}
ANLN	2.72	1.34×10^{-07}	ADH1B	-3.66	1.05×10^{-07}
UHRF1	2.91	1.45×10^{-07}	PLIN4	-4.68	1.15×10^{-07}
MMP1	3.27	1.87×10^{-07}	AQPEP	-3.44	1.29×10^{-07}
HMMR	2.46	2.77×10^{-07}	MME	-3.43	1.56×10^{-07}
TOP2A	2.74	3.22×10^{-07}	SDPR	-3.44	1.81×10^{-07}
INHBA	2.62	3.31×10^{-07}	CFD	-3.78	1.94×10^{-07}
KIF4A	2.47	3.51×10^{-07}	LPL	-4.25	3.31×10^{-07}
DLGAP5	2.43	4.36×10^{-07}	ADH1C	-3.32	3.41×10^{-07}
ZWINT	2.51	4.72×10^{-07}	MAOA	-3.76	4.14×10^{-07}
DTL	2.56	4.96×10^{-07}	FMO2	-3.05	4.36×10^{-07}
NUF2	2.47	5.22×10^{-07}	LOC101930114	-3.49	4.96×10^{-07}
PRC1	2.53	6.03×10^{-07}	ZBTB16	-3.72	5.09×10^{-07}
CEACAM6	3.39	6.47×10^{-07}	SEMA3G	-3.34	5.61×10^{-07}
CEP55	2.71	7.41×10^{-07}	SLC19A3	-3.72	5.75×10^{-07}
CKS2	2.81	8.98×10^{-07}	TGFBR3	-2.88	5.89×10^{-07}
KIF20A	2.36	8.98×10^{-07}	AOC3	-3.49	6.77×10^{-07}
MMP13	2.53	9.38×10^{-07}	CD36	-3.01	6.93×10^{-07}
KIF11	2.28	1.01×10^{-06}	SFRP1	-2.73	7.91×10^{-07}
BUB1B	2.68	1.03×10^{-06}	TUSC5	-3.93	8.08×10^{-07}
CCNB1	2.57	1.14×10^{-06}	LRRN4CL	-3.07	8.08×10^{-07}
PBK	2.62	1.23×10^{-06}	HLF	-2.80	1.16×10^{-06}
CXCL11	2.68	1.50×10^{-06}	ITIH5	-3.44	1.25×10^{-06}
TPX2	2.86	1.63×10^{-06}	GPD1	-3.59	1.3×10^{-06}
CENPF	2.08	1.72×10^{-06}	ADAMTS5	-2.65	1.52×10^{-06}
BIRC5	2.35	1.78×10^{-06}	LOC101926960	-3.35	1.55×10^{-06}
GINS1	2.26	1.86×10^{-06}	SCARA5	-3.11	1.69×10^{-06}
CCNE2	2.18	1.89×10^{-06}	LOC284825	-3.39	1.72×10^{-06}
			ATP1A2	-2.78	1.72×10^{-06}
			PGM5-AS1	-2.80	1.8×10^{-06}
			SCN4B	-2.89	1.93×10^{-06}
			HOXA5	-2.81	2.15×10^{-06}
			EBF1	-2.68	2.25×10^{-06}

Table SII. GO and Kyoto Encyclopedia of Genes and Genomes analyses of upregulated genes associated with breast cancer.

Term	Description	Count	P-value
GO:0051301	Cell division	13	1.31×10^{-11}
GO:0007067	Mitotic nuclear division	11	1.80×10^{-10}
GO:0005819	Spindle	7	2.06×10^{-7}
GO:0000281	Mitotic cytokinesis	5	5.66×10^{-7}
GO:0005876	Spindle microtubule	5	2.30×10^{-6}
GO:0008017	Microtubule binding	7	7.57×10^{-6}
GO:0030496	Midbody	6	7.80×10^{-6}
GO:0008283	Cell proliferation	8	1.86×10^{-5}
GO:0019901	Protein kinase binding	8	2.15×10^{-5}
GO:0000922	Spindle pole	5	8.48×10^{-5}
hsa04110	Cell cycle	4	2.22×10^{-3}
hsa04115	P53 signaling pathway	3	9.04×10^{-3}
hsa04512	ECM-receptor interaction	3	1.49×10^{-2}
hsa04114	Oocyte meiosis	3	2.36×10^{-2}

Count, number of enriched genes in each term; GO, Gene Ontology; hsa, homosapien.

Table SIII. GO and Kyoto Encyclopedia of Genes and Genomes analyses of downregulated genes associated in breast cancer.

Term	Description	Count	P-value
GO:0009986	Cell surface	8	1.33×10^{-4}
GO:0008201	Heparin binding	5	2.57×10^{-4}
GO:0005615	Extracellular space	11	4.12×10^{-4}
GO:0071356	Cellular response to tumor necrosis factor	4	1.54×10^{-3}
GO:0014823	Response to activity	3	3.61×10^{-3}
GO:0070543	Response to linoleic acid	2	4.16×10^{-3}
GO:0006629	Lipid metabolic process	4	4.21×10^{-3}
GO:0071320	Cellular response to camp	3	5.24×10^{-3}
GO:0005576	Extracellular region	10	5.95×10^{-3}
GO:0042632	Cholesterol homeostasis	3	7.85×10^{-3}
hsa03320	PPAR signaling pathway	6	1.36×10^{-5}
hsa00350	Tyrosine metabolism	4	1.51×10^{-5}
hsa00982	Drug metabolism-cytochrome P450	4	1.08×10^{-3}
hsa04920	Adipocytokine signaling pathway	4	1.12×10^{-3}
hsa04964	Proximal tubule bicarbonate reclamation	3	2.16×10^{-3}
hsa04152	AMPK signaling pathway	4	5.86×10^{-3}
hsa00010	Glycolysis/gluconeogenesis	3	1.74×10^{-2}

GO, Gene Ontology; hsa, homosapien.

Table SIV. Basic information of tissue samples used analyzed using immunohistochemistry.

Age, years	Pathology diagnosis	TNM stage	Clinical stage	Expression levels		
				PR	HER2	ER
75	Invasive ductal carcinoma	T3N1M0	IIIA	+++	0	+++
54	Invasive ductal carcinoma	T2N2M0	IIIA	*	*	*
38	Invasive ductal carcinoma	T2N1M0	IIB	++	0	+++
69	Invasive ductal carcinoma	T2N1M0	IIB	-	0	-
72	Invasive ductal carcinoma	T2N0M0	IIA	+++	0	+++
40	Invasive ductal carcinoma	T2N0M0	IIA	-	0	-
42	Invasive ductal carcinoma	T1N0M0	IA	+++	0	+++
61	Invasive ductal carcinoma	T4N0M0	IIIB	++	0	+++
41	Invasive ductal carcinoma	T2N0M0	IIA	+++	0	+++
64	Invasive ductal carcinoma	T2N0M0	IIA	-	0	++
46	Invasive ductal carcinoma	T3N0M0	IIB	+++	0	++
48	Invasive ductal carcinoma	T4N2M0	IIIB	+++	0	+++
50	Invasive ductal carcinoma	T2N1M0	IIB	+++	0	+++
47	Invasive ductal carcinoma	T1N0M0	IA	-	0	+
48	Invasive ductal carcinoma	T2N1M0	IIB	-	0	+
38	Invasive ductal carcinoma	T2N1M0	IIB	-	0	-
51	Invasive ductal carcinoma	T2N0M0	IIA	-	0	+++
60	Invasive ductal carcinoma	T2N0M0	IIA	*	*	*
57	Invasive ductal carcinoma	T2N1M0	IIB	*	0	*
50	Invasive ductal carcinoma	T4N2M0	IIIB	+++	3+	+++
44	Invasive ductal carcinoma	T4N0M0	IIIB	+	0	+++
32	Invasive ductal carcinoma	T3N1M0	IIIA	++	0	+
49	Invasive ductal carcinoma	T2N2M0	IIIA	-	0	+++
38	Invasive ductal carcinoma	T2N0M0	IIA	+++	0	+++
50	Invasive ductal carcinoma	T3N0M0	IIB	+++	0	+++
43	Invasive ductal carcinoma	T2N1M0	IIB	+++	0	+++
46	Invasive ductal carcinoma	T2N0M0	IIA	+	0	+++
43	Invasive ductal carcinoma	T1N1M0	IIA	-	0	++
70	Invasive ductal carcinoma	T2N0M0	IIA	-	0	+
39	Invasive ductal carcinoma	T2N1M0	IIB	+++	0	++
41	Invasive ductal carcinoma	T2N2M0	IIIA	+++	0	+++
52	Invasive ductal carcinoma	T2N1M0	IIB	+++	3+	+
60	Invasive ductal carcinoma	T1N0M0	IA	+	0	+++
45	Invasive ductal carcinoma	T1N0M0	IA	+++	0	+++
43	Invasive ductal carcinoma	T2N1M0	IIB	+	0	+++
38	Invasive ductal carcinoma	T2N0M0	IIA	+++	0	+++
38	Invasive ductal carcinoma	T2N0M0	IIA	+++	0	++
47	Invasive ductal carcinoma	T2N0M0	IIA	*	*	*
47	Invasive ductal carcinoma	T4N0M0	IIIB	+	3+	+
49	Invasive ductal carcinoma	T2N0M0	IIA	++	3+	++
46	Invasive ductal carcinoma	T2N0M0	IIA	-	3+	-
45	Invasive ductal carcinoma	T4N2M0	IIIB	+++	0	+++
54	Invasive ductal carcinoma	T2N1M0	IIB	-	0	++
30	Invasive ductal carcinoma	T2N0M0	IIA	+++	0	+
46	Invasive ductal carcinoma	T2N1M0	IIB	+++	0	+++
52	Invasive ductal carcinoma	T2N0M0	IIA	+	0	++
71	Invasive ductal carcinoma	T4N2M0	IIIB	++	0	+++
48	Invasive ductal carcinoma	T2N2M0	IIIA	+	0	++
49	Invasive ductal carcinoma	T2N0M0	IIA	-	0	+++
54	Invasive ductal carcinoma	T2N2M0	IIIA	++	0	+++
43	Invasive ductal carcinoma	T2N1M0	IIB	+++	0	+++
56	Invasive ductal carcinoma	T2N0M0	IIA	-	0	-
57	Invasive ductal carcinoma	T2N1M0	IIB	-	0	+++
52	Invasive ductal carcinoma	T1N0M0	IA	+	0	++
52	Invasive ductal carcinoma	T2N0M0	IIA	++	0	+++
37	Invasive ductal carcinoma	T2N0M0	IIA	+++	0	+
40	Invasive ductal carcinoma	T1N1M0	IIA	-	0	+

Table SIV. Continued.

Age, years	Pathology diagnosis	TNM stage	Clinical stage	PR	HER2	ER
				Expression levels		
54	Invasive ductal carcinoma	T2N1M0	IIB	-	0	++
39	Invasive ductal carcinoma	T2N2M0	IIIA	-	3+	+
50	Invasive ductal carcinoma	T2N0M0	IIA	-	*	++
60	Invasive ductal carcinoma	T2N0M0	IIA	+	0	+++
38	Invasive ductal carcinoma	T2N1M0	IIB	+++	0	+++
54	Invasive ductal carcinoma	T2N1M0	IIB	-	0	+++
46	Invasive ductal carcinoma	T2N0M0	IIA	++	0	+++
59	Invasive ductal carcinoma	T2N0M0	IIA	-	0	-
74	Invasive ductal carcinoma	T2N0M0	IIA	+++	0	+++
29	Invasive ductal carcinoma	T2N0M0	IIA	-	3+	-
52	Invasive ductal carcinoma	T3N0M0	IIB	-	0	++
43	Invasive ductal carcinoma	T2N0M0	IIA	-	3+	-
56	Invasive ductal carcinoma	T2N2M0	IIIA	+++	3+	+++
44	Invasive ductal carcinoma	T2N0M0	IIA	-	0	-
62	Invasive ductal carcinoma	T2N1M0	IIB	-	0	-
47	Invasive ductal carcinoma	T2N0M0	IIA	-	0	+++
41	Invasive ductal carcinoma	T3N1M0	IIIA	++	0	++
51	Invasive ductal carcinoma	T3N1M0	IIIA	-	3+	-
39	Invasive ductal carcinoma	T4N2M0	IIIB	-	0	-
49	Invasive ductal carcinoma	T2N2M0	IIIA	-	2+	-
52	Invasive ductal carcinoma	T1N1M0	IIA	-	0	+++
56	Invasive ductal carcinoma	T1N0M0	IA	++	0	+++
65	Invasive ductal carcinoma	T4N1M0	IIIB	+++	0	+++
38	Adjacent normal tissue	-	-	+	0	+
49	Adjacent normal tissue	-	-	*	*	*
45	Adjacent normal tissue	-	-	-	0	+
51	Adjacent normal tissue	-	-	-	0	++
40	Adjacent normal tissue	-	-	-	0	-
50	Adjacent normal tissue	-	-	*	*	*
40	Adjacent normal tissue	-	-	*	*	*
43	Adjacent normal tissue	-	-	++	0	+
35	Adjacent normal tissue	-	-	*	*	*
54	Adjacent normal tissue	-	-	*	*	*
43	Adjacent normal tissue	-	-	+	0	++
27	Breast tissue	-	-	+	0	-
50	Breast tissue	-	-	*	*	*
42	Breast tissue	-	-	*	*	*
19	Breast tissue	-	-	*	*	*
21	Breast tissue	-	-	*	*	*
41	Invasive lobular carcinoma	T4N0M0	IIIB	+	0	+
66	Invasive lobular carcinoma	T2N0M0	IIA	-	0	+++
70	Invasive lobular carcinoma	T4N0M0	IIIB	-	0	++
57	Invasive lobular carcinoma	T2N0M0	IIA	+++	0	+++
38	Invasive lobular carcinoma	T2N0M0	IIA	+++	0	+++
72	Invasive lobular carcinoma	T1N0M0	IA	-	0	+++
59	Invasive lobular carcinoma	T2N0M0	IIA	++	0	++
47	Invasive lobular carcinoma	T2N1M0	IIB	+	0	++
37	Invasive lobular carcinoma	T4N1M0	IIIB	+	0	+
51	Invasive lobular carcinoma	T2N1M0	IIB	*	*	*
35	Invasive lobular carcinoma	T3N0M0	IIB	+++	0	+++
73	Invasive lobular carcinoma	T4N0M0	IIIB	-	0	-
42	Invasive lobular carcinoma	T1N0M0	IA	++	0	+++
45	Invasive lobular carcinoma	T2N0M0	IIA	++	0	++
51	Invasive lobular carcinoma	T4N0M0	IIIB	++	0	++
48	Invasive lobular carcinoma	T2N0M0	IIA	+++	0	+++
47	Invasive lobular carcinoma	T3N0M0	IIB	++	0	++
47	Invasive lobular carcinoma	T4N0M0	IIIB	+++	0	+++

Table SIV. Continued.

Age, years	Pathology diagnosis	TNM stage	Clinical stage	Expression levels		
				PR	HER2	ER
52	Invasive lobular carcinoma	T2N1M0	IIB	-	0	-
50	Invasive lobular carcinoma	T2N0M0	IIA	+++	0	+++
68	Invasive lobular carcinoma	T2N0M0	IIA	-	0	++
53	Invasive lobular carcinoma	T4N1M0	IIIB	+	0	+++
58	Invasive lobular carcinoma	T1N0M0	IA	+	0	+++
39	Invasive lobular carcinoma	T2N0M0	IIA	++	0	++
49	Invasive lobular carcinoma	T3N2M0	IIIA	-	0	+
52	Invasive lobular carcinoma	T2N0M0	IIA	-	0	-
42	Invasive lobular carcinoma	T3N0M0	IIB	-	3+	+
70	Invasive lobular carcinoma	T2N2M0	IIIA	+	2+	+++
43	Invasive lobular carcinoma	T2N0M0	IIA	+++	0	+++
47	Lobular carcinoma in situ	T2N0M0	IIA	++	0	+++
49	Invasive lobular carcinoma	T2N0M0	IIA	-	0	-
46	Invasive lobular carcinoma	T2N0M0	IIA	-	0	++
52	Invasive lobular carcinoma	T4N0M0	IIIB	+	0	+++
58	Invasive lobular carcinoma	T2N0M0	IIA	+++	0	+++
49	Invasive lobular carcinoma	T3N1M0	IIIA	+	0	+++
39	Invasive lobular carcinoma	T2N3M0	IIIC	-	0	+
63	Invasive lobular carcinoma	T3N0M0	IIB	-	0	-
49	Invasive lobular carcinoma	T2N0M0	IIA	+	0	++
41	Invasive lobular carcinoma	T2N0M0	IIA	++	0	+
37	Invasive lobular carcinoma	T3N0M0	IIB	-	3+	-
64	Invasive lobular carcinoma	T2N0M0	IIA	++	0	+++
72	Invasive lobular carcinoma	T2N1M0	IIB	+	1+	+
31	Invasive lobular carcinoma	T2N0M0	IIA	-	1+	-
58	Invasive lobular carcinoma	T2N0M0	IIA	+++	0	+++
55	Invasive lobular carcinoma	T2N0M0	IIA	++	0	+++
53	Invasive lobular carcinoma	T2N0M0	IIA	+	0	++
50	Invasive lobular carcinoma	T1N0M0	IA	+++	0	+++
52	Invasive lobular carcinoma	T2N1M0	IIB	-	2+	-
60	Invasive lobular carcinoma	T2N0M0	IIA	+++	0	+++
40	Invasive lobular carcinoma	T2N1M0	IIB	+	0	+
40	Invasive lobular carcinoma	T2N0M0	IIA	-	0	+++
66	Invasive lobular carcinoma	T2N0M0	IIA	+++	0	+++
48	Invasive lobular carcinoma	T2N1M0	IIB	++	1+	+++
44	Invasive lobular carcinoma	T2N2M0	IIIA	-	0	+
60	Invasive lobular carcinoma	T2N1M0	IIB	-	0	+++
50	Invasive lobular carcinoma	T2N2M0	IIIA	+	0	+
57	Invasive lobular carcinoma	T2N0M0	IIA	-	3+	-
46	Invasive lobular carcinoma	T2N0M0	IIA	-	0	-
47	Invasive lobular carcinoma	T2N0M0	IIA	++	0	+++
46	Invasive lobular carcinoma	T2N0M0	IIA	*	*	*
64	Invasive lobular carcinoma	T2N0M0	IIA	-	0	+++
44	Invasive lobular carcinoma	T2N0M0	IIA	++	0	+++
54	Invasive lobular carcinoma	T2N1M0	IIB	+++	0	+++
50	Invasive lobular carcinoma	T2N1M0	IIB	-	0	-
59	Invasive lobular carcinoma	T2N0M0	IIA	*	*	*
36	Invasive lobular carcinoma	T3N1M0	IIIA	+++	0	++
47	Invasive lobular carcinoma	T4N0M0	IIIB	++	0	+++
60	Invasive lobular carcinoma	T3N0M0	IIB	-	0	+++
39	Invasive lobular carcinoma	T3N0M0	IIB	+++	0	+++
47	Invasive lobular carcinoma	T2N0M0	IIA	-	0	+++
55	Invasive lobular carcinoma	T2N2M0	IIIA	-	3+	++
45	Invasive lobular carcinoma	T2N0M0	IIA	+++	0	+++
45	Invasive lobular carcinoma	T2N1M0	IIB	+++	0	+++
54	Invasive lobular carcinoma	T2N1M0	IIB	-	0	+
48	Invasive lobular carcinoma	T3N0M0	IIB	*	*	*

Table SIV. Continued.

Age, years	Pathology diagnosis	TNM stage	Clinical stage	Expression levels		
				PR	HER2	ER
45	Invasive lobular carcinoma	T2N1M0	IIB	+	0	++
51	Invasive lobular carcinoma	T2N0M0	IIA	+++	0	+++
56	Invasive lobular carcinoma	T2N0M0	IIA	-	0	+++
65	Invasive lobular carcinoma	T2N0M0	IIA	+	0	-
35	Invasive lobular carcinoma	T1N0M0	IA	++	2+	+++
54	Adjacent normal tissue	-	-	*	*	*
48	Adjacent normal tissue	-	-	++	0	+
54	Adjacent normal tissue	-	-	*	*	*
43	Adjacent normal tissue	-	-	-	0	*
55	Adjacent normal tissue	-	-	-	0	+
42	Adjacent normal tissue	-	-	*	*	*
47	Cancer adjacent tissue	-	-	+	*	+
40	Cancer adjacent tissue	-	-	+	0	+
45	Cancer adjacent tissue	-	-	*	*	*
42	Adjacent normal tissue	-	-	+++	0	+
46	Cancer adjacent tissue	-	-	*	*	*
48	Adjacent normal tissue	-	-	+	0	-
36	Adjacent normal tissue	-	-	*	*	*
33	Adjacent normal tissue	-	-	-	0	+
36	Breast tissue	-	-	+	0	+
35	Breast tissue	-	-	+	0	*

Note: '*' means the value is missing; '+', '++' and '+++' mean weak, medium and strong expression, respectively. '3+' means HER2 is positive and '0-1+' means negative, while '2+' means the sample required FISH analysis to determine whether HER2 status was positive or negative. ER, estrogen receptor; PR, progesterone receptor; HER2, human epidermal growth factor receptor-2; TNM, Tumor-Node-Metastasis.