Figure S1. Quality control validation of MS data. (A-C) Mass error distribution of all peptides identified in the acetylome, succinylome and quantitative proteome, respectively. (D-F) Length distribution of peptides identified in the acetylome, succinylome and quantitative proteome, respectively.

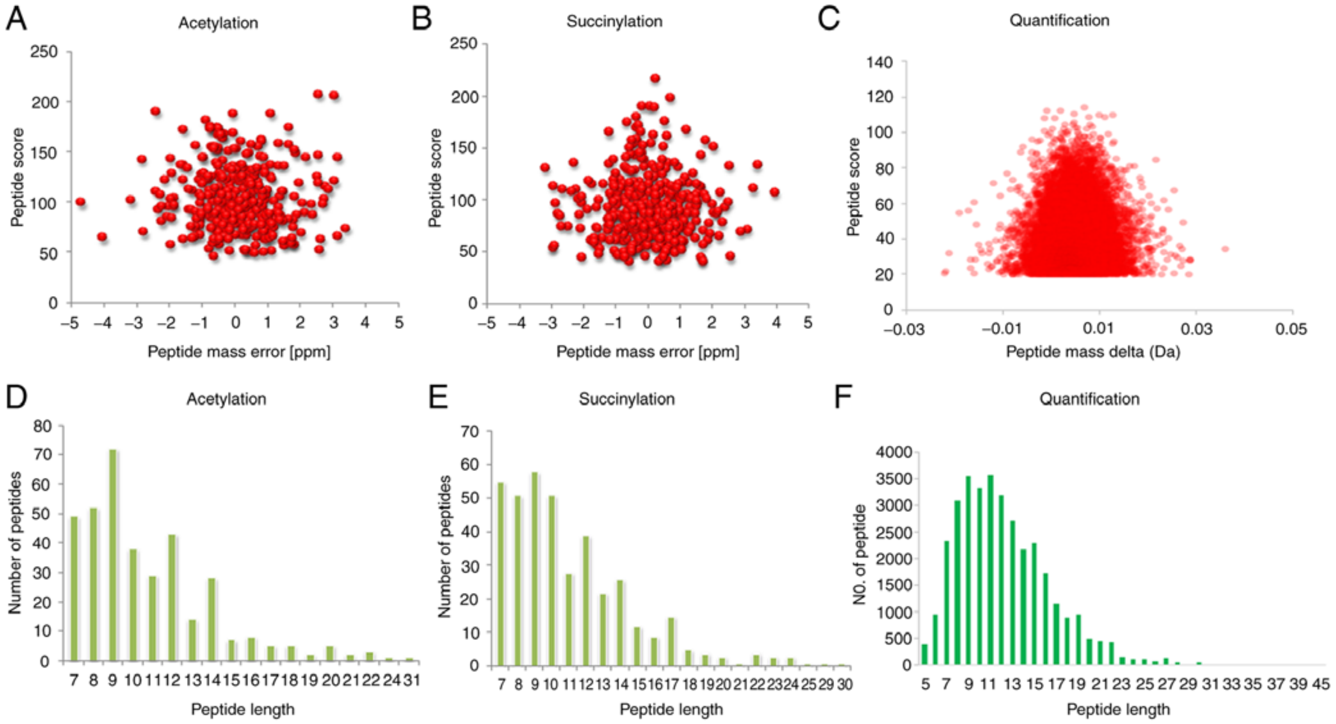

Figure S2. Comparison of modification level between breast cancer tissue and normal tissue. Comparison of acetylation level (A) and succinylation level (B) between breast cancer tissue and normal tissue. Data are medians and were analyzed using Wilcoxon Signed Rank Test. $^{**}P<0.01$.

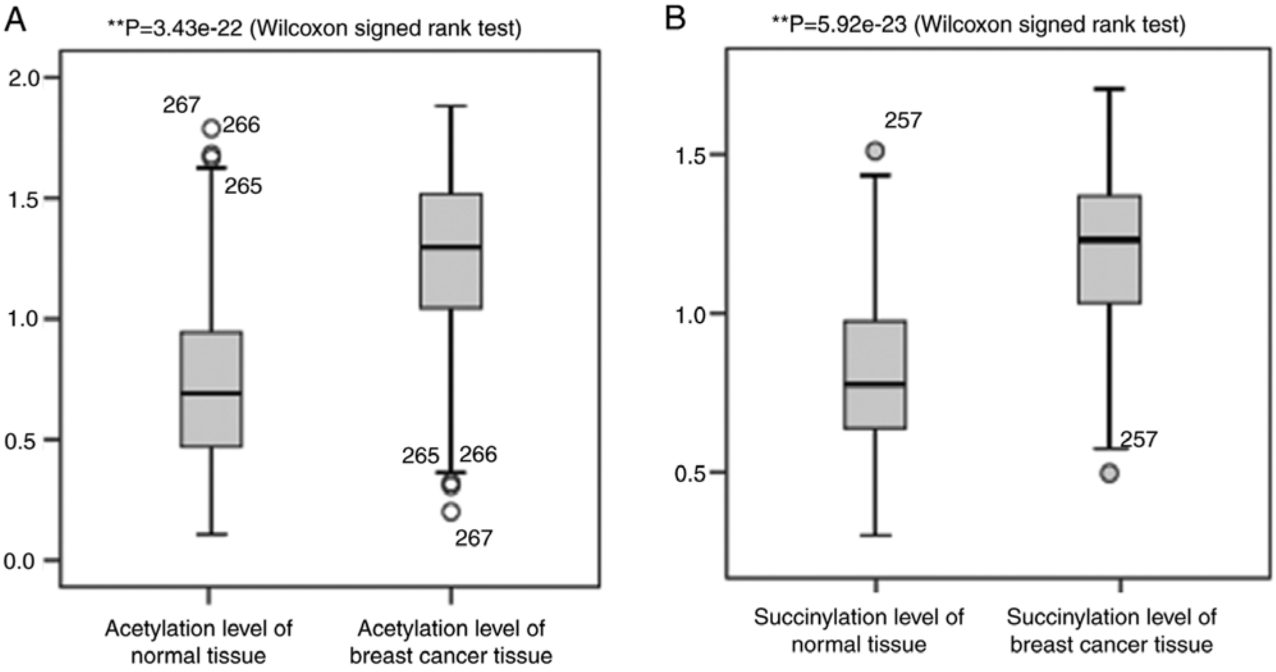

Table SI. Protein sites whose acetylation and succinylation levels were both significantly upregulated in breast cancer tissues (fold change ≥1.5 compared with normal tissues).

Protein ID	Protein name	Modification site
P54868	HMCS2	310K
Q15063	POSTN	549K
Q99715	COCA1	1601K
P51572	BAP31	72K
P07237	PDLA1	328K
Q06830	PRDX1	192K
P48735	IDHP	180K
P30101	PDIA3	417K
P0DMV9	HS71B	526K
Q01995	TAGL	21K
P06748	NPM1	27K
Q00325	MPCP	209K
P00488	F13A	69K
P02545	LMNA	260K
P08133	ANXA6	478K
P02452	CO1A1	751K

Table SII. Protein sites whose acetylation and succinylation levels were both significantly downregulated in breast cancer tissues (fold change ≥1.5 compared with normal tissues).

Protein ID	Protein name	Modification site
RET4	P02753	30K
PSG2	P07585	142K
HBA	P69905	12K
IGKC	P01834	80K
HBA	P69905	8K

Table SIII. All proteins whose expression level were significantly upregulated in breast cancer tissues (fold change ≥1.5 compared with normal tissues).

Protein ID	Protein description	Ratio (cancer vs. normal)	P-value
P29762	Cellular retinoic acid-binding protein 1 OS=*Homo sapiens* GN=CRABP1 PE=2 SV=2	4.5485	0.005237
P05787	Keratin, type II cytoskeletal 8 OS=*Homo sapiens* GN=KRT8 PE=1 SV=7	3.3785	3.49E-13
Q01105	Protein SET OS=*Homo sapiens* GN=SET PE=1 SV=3	2.846	0.000294
Q9NZJ9	Diphosphoinositol polyphosphate phosphohydrolase 2 OS=*Homo sapiens* GN=NUDT4 PE=1 SV=2	2.814	0.002214
P40121	Macrophage-capping protein OS=*Homo sapiens* GN=CAPG PE=1 SV=2	2.808	0.0001
Q8WX93	Palladin OS=*Homo sapiens* GN=PALLD PE=1 SV=3	2.7565	5.55E-06
Q9UQP3	Tenascin-N OS=*Homo sapiens* GN=TNN PE=1 SV=2	2.724	0.00859
P15924	Desmoplakin OS=*Homo sapien*s GN=DSP PE=1 SV=3	2.7135	3.49E-14
Q13153	Serine/threonine-protein kinase PAK 1 OS=*Homo sapiens* GN=PAK1 PE=1 SV=2	2.713	0.003549
P23528	Cofilin-1 OS=*Homo sapiens* GN=CFL1 PE=1 SV=3	2.702	1.4E-08
Q12874	Splicing factor 3A subunit 3 OS=*Homo sapiens* GN=SF3A3 PE=1 SV=1	2.699	0.009968
Q15063	Periostin OS=*Homo sapiens* GN=POSTN PE=1 SV=2	2.6945	1.37E-12
Q13185	Chromobox protein homolog 3 OS=*Homo sapiens* GN=CBX3 PE=1 SV=4	2.6695	0.00138
Q8TF66	Leucine-rich repeat-containing protein 15 OS=*Homo sapiens* GN=LRRC15 PE=1 SV=2	2.661	0.002947
Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=*Homo sapiens* GN=PDXDC1 PE=1 SV=2	2.635	1.09E-05
P35442	Thrombospondin-2 OS=*Homo sapiens* GN=THBS2 PE=1 SV=2	2.621	7.37E-05
P13611	Versican core protein OS=*Homo sapiens* GN=VCAN PE=1 SV=3	2.617	4.99E-06
Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3 OS=*Homo sapiens* GN=FKBP3 PE=1 SV=1	2.529	0.006514
P08727	Keratin, type I cytoskeletal 19 OS=*Homo sapiens* GN=KRT19 PE=1 SV=4	2.493	1.01E-10
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=*Homo sapiens* GN=FKBP4 PE=1 SV=3	2.465	8.29E-05
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=*Homo sapiens* GN=HNRNPA2B1 PE=1 SV=2	2.459	2.66E-07
Q05682	Caldesmon OS=*Homo sapiens* GN=CALD1 PE=1 SV=3	2.4345	2.5E-06
Q9P258	Protein RCC2 OS=*Homo sapiens* GN=RCC2 PE=1 SV=2	2.4015	0.009156
P30520	Adenylosuccinate synthetase isozyme 2 OS=*Homo sapiens* GN=ADSS PE=1 SV=3	2.391	0.003515
Q5SSJ5	Heterochromatin protein 1-binding protein 3 OS=*Homo sapiens* GN=HP1BP3 PE=1 SV=1	2.375	0.001099
P05783	Keratin, type I cytoskeletal 18 OS=*Homo sapiens* GN=KRT18 PE=1 SV=2	2.3525	1.38E-08
P21266	Glutathione S-transferase Mu 3 OS=*Homo sapiens* GN=GSTM3 PE=1 SV=3	2.348	2.27E-05
Q6EEV6	Small ubiquitin-related modifier 4 OS=*Homo sapiens* GN=SUMO4 PE=1 SV=2	2.311	0.008154
P10253	Lysosomal alpha-glucosidase OS=*Homo sapiens* GN=GAA PE=1 SV=4	2.2855	0.001327
P17844	Probable ATP-dependent RNA helicase DDX5 OS=*Homo sapiens* GN=DDX5 PE=1 SV=1	2.249	0.000284
P50454	Serpin H1 OS=*Homo sapiens* GN=SERPINH1 PE=1 SV=2	2.211	6.02E-06
P23193	Transcription elongation factor A protein 1 OS=*Homo sapiens* GN=TCEA1 PE=1 SV=2	2.203	0.004442
P39748	Flap endonuclease 1 OS=*Homo sapiens* GN=FEN1 PE=1 SV=1	2.197	0.005466
Q8TE77	Protein phosphatase Slingshot homolog 3 OS=*Homo sapiens* GN=SSH3 PE=1 SV=2	2.185	0.0028
P0CW22	40S ribosomal protein S17-like OS=*Homo sapiens* GN=RPS17L PE=1 SV=1	2.171	0.007463
Q92544	Transmembrane 9 superfamily member 4 OS=*Homo sapiens* GN=TM9SF4 PE=1 SV=2	2.17	0.003809
P10155	60 kDa SS-A/Ro ribonucleoprotein OS=*Homo sapiens* GN=TROVE2 PE=1 SV=2	2.168	0.000968
P63208	S-phase kinase-associated protein 1 OS=*Homo sapiens* GN=SKP1 PE=1 SV=2	2.165	0.000695

Table SIII. Continued.

Protein ID	Protein description	Ratio (cancer vs. normal)	P-value
Q8IV36	Protein HID1 OS=*Homo sapiens* GN=HID1 PE=1 SV=1	2.1405	0.002398
Q9Y266	Nuclear migration protein nudC OS=*Homo sapiens* GN=NUDC PE=1 SV=1	2.124	3.41E-06
P62753	40S ribosomal protein S6 OS=*Homo sapiens* GN=RPS6 PE=1 SV=1	2.113	0.004002
P15170	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=*Homo sapiens* GN=GSPT1 PE=1 SV=1	2.109	0.006605
Q13148	TAR DNA-binding protein 43 OS=*Homo sapiens* GN=TARDBP PE=1 SV=1	2.092	5.22E-05
Q9Y2X3	Nucleolar protein 58 OS=*Homo sapiens* GN=NOP58 PE=1 SV=1	2.087	0.005814
Q99715	Collagen alpha-1(XII) chain OS=*Homo sapiens* GN=COL12A1 PE=1 SV=2	2.084	1.36E-11
Q9UGI8	Testin OS=*Homo sapiens* GN=TES PE=1 SV=1	2.08	0.001602
O43390	Heterogeneous nuclear ribonucleoprotein R OS=*Homo sapiens* GN=HNRNPR PE=1 SV=1	2.069	5.72E-05
P52272	Heterogeneous nuclear ribonucleoprotein M OS=*Homo sapiens* GN=HNRNPM PE=1 SV=3	2.066	8.9E-08
P12830	Cadherin-1 OS=*Homo sapiens* GN=CDH1 PE=1 SV=3	2.0585	1.43E-05
P26373	60S ribosomal protein L13 OS=*Homo sapiens* GN=RPL13 PE=1 SV=4	2.047	0.006719
P08621	U1 small nuclear ribonucleoprotein 70 kDa OS=*Homo sapiens* GN=SNRNP70 PE=1 SV=2	2.045	0.000827
Q9UNE7	E3 ubiquitin-protein ligase CHIP OS=*Homo sapiens* GN=STUB1 PE=1 SV=2	2.043	0.000282
P22234	Multifunctional protein ADE2 OS=*Homo sapiens* GN=PAICS PE=1 SV=3	2.04	0.005675
Q15233	Non-POU domain-containing octamer-binding protein OS=*Homo sapiens* GN=NONO PE=1 SV=4	2.0385	1.4E-08
P50851	Lipopolysaccharide-responsive and beige-like anchor protein OS=*Homo sapiens* GN=LRBA PE=1 SV=4	2.0365	0.000609
Q13765	Nascent polypeptide-associated complex subunit alpha OS=*Homo sapiens* GN=NACA PE=1 SV=1	2.029	0.001067
Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase OS=*Homo sapiens* GN=NSUN2 PE=1 SV=2	2.0205	0.008385
O75223	Gamma-glutamylcyclotransferase OS=*Homo sapiens* GN=GGCT PE=1 SV=1	2.006	0.003327
P20700	Lamin-B1 OS=*Homo sapiens* GN=LMNB1 PE=1 SV=2	1.982	6.8E-05
P43487	Ran-specific GTPase-activating protein OS=*Homo sapiens* GN=RANBP1 PE=1 SV=1	1.9695	0.007456
P30050	60S ribosomal protein L12 OS=*Homo sapiens* GN=RPL12 PE=1 SV=1	1.961	0.000103
P08729	Keratin, type II cytoskeletal 7 OS=*Homo sapiens* GN=KRT7 PE=1 SV=5	1.96	3.5E-08
P49585	Choline-phosphate cytidylyltransferase A OS=*Homo sapiens* GN=PCYT1A PE=1 SV=2	1.949	0.009506
P15311	Ezrin OS=*Homo sapiens* GN=EZR PE=1 SV=4	1.937	0.000112
P19338	Nucleolin OS=*Homo sapiens* GN=NCL PE=1 SV=3	1.9285	4.89E-05
Q9NR99	Matrix-remodeling-associated protein 5 OS=*Homo sapiens* GN=MXRA5 PE=2 SV=3	1.9275	0.004449
Q8IUX7	Adipocyte enhancer-binding protein 1 OS=*Homo sapiens* GN=AEBP1 PE=1 SV=1	1.912	0.004188
Q15459	Splicing factor 3A subunit 1 OS=*Homo sapiens* GN=SF3A1 PE=1 SV=1	1.911	0.002117
P38919	Eukaryotic initiation factor 4A-III OS=*Homo sapiens* GN=EIF4A3 PE=1 SV=4	1.91	0.008213
Q9UHB6	LIM domain and actin-binding protein 1 OS=*Homo sapiens* GN=LIMA1 PE=1 SV=1	1.9085	0.001674
P47813	Eukaryotic translation initiation factor 1A, X-chromosomal OS=*Homo sapiens* GN=EIF1AX PE=1 SV=2	1.9045	0.008956
Q9NR45	Sialic acid synthase OS=*Homo sapiens* GN=NANS PE=1 SV=2	1.9025	5.07E-05
Q14103	Heterogeneous nuclear ribonucleoprotein D0 OS=*Homo sapiens* GN=HNRNPD PE=1 SV=1	1.893	0.002203
P49207	60S ribosomal protein L34 OS=*Homo sapiens* GN=RPL34 PE=1 SV=3	1.887	0.005138
Q32P51	Heterogeneous nuclear ribonucleoprotein A1-like 2 OS=*Homo sapiens* GN=HNRNPA1L2 PE=2 SV=2	1.885	0.000146
P24821	Tenascin OS=*Homo sapiens* GN=TNC PE=1 SV=3	1.874	4.26E-06

Table SIII. Continued.

Protein ID	Protein description	Ratio (cancer vs. normal)	P-value
Q96G03	Phosphoglucomutase-2 OS=*Homo sapiens* GN=PGM2 PE=1 SV=4	1.8655	0.000367
P23246	Splicing factor, proline- and glutamine-rich OS=*Homo sapiens* GN=SFPQ PE=1 SV=2	1.865	0.002261
Q8IWE2	Protein NOXP20 OS=*Homo sapiens* GN=FAM114A1 PE=1 SV=2	1.863	0.001082
P62249	40S ribosomal protein S16 OS=*Homo sapiens* GN=RPS16 PE=1 SV=2	1.858	6.55E-05
Q07955	Serine/arginine-rich splicing factor 1 OS=*Homo sapiens* GN=SRSF1 PE=1 SV=2	1.853	0.002282
Q99816	Tumor susceptibility gene 101 protein OS=*Homo sapiens* GN=TSG101 PE=1 SV=2	1.846	0.009029
Q00839	Heterogeneous nuclear ribonucleoprotein U OS=*Homo sapiens* GN=HNRNPU PE=1 SV=6	1.8445	0.000159
P13010	X-ray repair cross-complementing protein 5 OS=*Homo sapiens* GN=XRCC5 PE=1 SV=3	1.844	3.97E-06
Q9Y3I0	tRNA-splicing ligase RtcB homolog OS=*Homo sapiens* GN=RTCB PE=1 SV=1	1.844	7.55E-06
P49591	Serine--tRNA ligase, cytoplasmic OS=*Homo sapiens* GN=SARS PE=1 SV=3	1.84	0.006389
Q9H3P7	Golgi resident protein GCP60 OS=*Homo sapiens* GN=ACBD3 PE=1 SV=4	1.836	0.000973
Q8N1S5	Zinc transporter ZIP11 OS=*Homo sapiens* GN=SLC39A11 PE=2 SV=3	1.835	0.007755
Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=*Homo sapiens* GN=MCCC2 PE=1 SV=1	1.834	0.000145
Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=*Homo sapiens* GN=GFPT1 PE=1 SV=3	1.832	6.28E-05
P62241	40S ribosomal protein S8 OS=*Homo sapiens* GN=RPS8 PE=1 SV=2	1.82	0.003301
P53621	Coatomer subunit alpha OS=*Homo sapiens* GN=COPA PE=1 SV=2	1.819	3.57E-08
Q96DI7	U5 small nuclear ribonucleoprotein 40 kDa protein OS=*Homo sapiens* GN=SNRNP40 PE=1 SV=1	1.806	0.001541
P18077	60S ribosomal protein L35a OS=*Homo sapiens* GN=RPL35A PE=1 SV=2	1.797	0.007925
P49321	Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2	1.795	0.006417
P61604	10 kDa heat shock protein, mitochondrial OS=*Homo sapiens* GN=HSPE1 PE=1 SV=2	1.795	0.000664
Q15437	Protein transport protein Sec23B OS=*Homo sapiens* GN=SEC23B PE=1 SV=2	1.795	0.002945
P09874	Poly [ADP-ribose] polymerase 1 OS=*Homo sapiens* GN=PARP1 PE=1 SV=4	1.7915	0.007477
O14979	Heterogeneous nuclear ribonucleoprotein D-like OS=*Homo sapiens* GN=HNRNPDL PE=1 SV=3	1.789	0.006895
Q9UBE0	SUMO-activating enzyme subunit 1 OS=*Homo sapiens* GN=SAE1 PE=1 SV=1	1.788	0.000538
Q9NY33	Dipeptidyl peptidase 3 OS=*Homo sapiens* GN=DPP3 PE=1 SV=2	1.774	0.000323
P18031	Tyrosine-protein phosphatase non-receptor type 1 OS=*Homo sapiens* GN=PTPN1 PE=1 SV=1	1.768	0.001796
P43243	Matrin-3 OS=*Homo sapiens* GN=MATR3 PE=1 SV=2	1.765	0.001315
Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=*Homo sapiens* GN=CAND1 PE=1 SV=2	1.764	2.34E-10
Q7Z7H5	Transmembrane emp24 domain-containing protein 4 OS=*Homo sapiens* GN=TMED4 PE=1 SV=1	1.752	0.009125
O43583	Density-regulated protein OS=*Homo sapiens* GN=DENR PE=1 SV=2	1.7465	0.006164
P61081	NEDD8-conjugating enzyme Ubc12 OS=*Homo sapiens* GN=UBE2M PE=1 SV=1	1.743	0.0036
P78527	DNA-dependent protein kinase catalytic subunit OS=*Homo sapiens* GN=PRKDC PE=1 SV=3	1.733	1.09E-10
P12956	X-ray repair cross-complementing protein 6 OS=*Homo sapiens* GN=XRCC6 PE=1 SV=2	1.7255	6E-06
O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=*Homo sapiens* GN=DDAH1 PE=1 SV=3	1.721	0.000901
Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2 OS=*Homo sapiens* GN=BZW2 PE=1 SV=1	1.7205	0.00566
Q7L014	Probable ATP-dependent RNA helicase DDX46 OS=*Homo sapiens* GN=DDX46 PE=1 SV=2	1.718	0.00122
P46777	60S ribosomal protein L5 OS=*Homo sapiens* GN=RPL5 PE=1 SV=3	1.714	0.005829
Q96A35	39S ribosomal protein L24, mitochondrial OS=*Homo sapiens* GN=MRPL24 PE=1 SV=1	1.7105	0.004032

Table SIII. Continued.

Protein ID	Protein description	Ratio (cancer vs. normal)	P-value
P22307	Non-specific lipid-transfer protein OS=*Homo sapiens* GN=SCP2 PE=1 SV=2	1.71	0.005982
P14678	Small nuclear ribonucleoprotein-associated proteins B and B~ OS=*Homo sapiens* GN=SNRPB PE=1 SV=2	1.709	0.003967
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	1.708	5.46E-08
O76094	Signal recognition particle subunit SRP72 OS=*Homo sapiens* GN=SRP72 PE=1 SV=3	1.706	0.000613
P29372	DNA-3-methyladenine glycosylase OS=*Homo sapiens* GN=MPG PE=1 SV=3	1.7045	0.009488
Q9BZK7	F-box-like/WD repeat-containing protein TBL1XR1 OS=*Homo sapiens* GN=TBL1XR1 PE=1 SV=1	1.704	0.003795
Q02818	Nucleobindin-1 OS=*Homo sapiens* GN=NUCB1 PE=1 SV=4	1.695	0.000262
Q04637	Eukaryotic translation initiation factor 4 gamma 1 OS=*Homo sapiens* GN=EIF4G1 PE=1 SV=4	1.6945	0.000316
P26641	Elongation factor 1-gamma OS=*Homo sapiens* GN=EEF1G PE=1 SV=3	1.6905	0.001651
Q9NZB2	Constitutive coactivator of PPAR-gamma-like protein 1 OS=*Homo sapiens* GN=FAM120A PE=1 SV=2	1.69	2.25E-05
Q14192	Four and a half LIM domains protein 2 OS=*Homo sapiens* GN=FHL2 PE=1 SV=3	1.687	0.007932
P02786	Transferrin receptor protein 1 OS=*Homo sapiens* GN=TFRC PE=1 SV=2	1.684	0.002904
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=*Homo sapiens* GN=HNRNPC PE=1 SV=4	1.677	0.004032
P49915	GMP synthase [glutamine-hydrolyzing] OS=*Homo sapiens* GN=GMPS PE=1 SV=1	1.671	0.000175
Q00341	Vigilin OS=*Homo sapiens* GN=HDLBP PE=1 SV=2	1.665	1.07E-05
Q10471	Polypeptide N-acetylgalactosaminyltransferase 2 OS=*Homo sapiens* GN=GALNT2 PE=1 SV=1	1.665	0.008749
P27694	Replication protein A 70 kDa DNA-binding subunit OS=*Homo sapiens* GN=RPA1 PE=1 SV=2	1.664	0.005447
Q9NR12	PDZ and LIM domain protein 7 OS=*Homo sapiens* GN=PDLIM7 PE=1 SV=1	1.664	0.003813
Q13263	Transcription intermediary factor 1-beta OS=*Homo sapiens* GN=TRIM28 PE=1 SV=5	1.661	0.000231
Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=*Homo sapiens* GN=PRPF8 PE=1 SV=2	1.656	0.000792
P13637	Sodium/potassium-transporting ATPase subunit alpha-3 OS=*Homo sapiens* GN=ATP1A3 PE=1 SV=3	1.6545	0.003404
Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=*Homo sapiens* GN=HNRNPUL2 PE=1 SV=1	1.653	6.92E-08
Q99961	Endophilin-A2 OS=*Homo sapiens* GN=SH3GL1 PE=1 SV=1	1.6525	0.000942
O14976	Cyclin-G-associated kinase OS=*Homo sapiens* GN=GAK PE=1 SV=2	1.651	0.006435
P22102	Trifunctional purine biosynthetic protein adenosine-3 OS=*Homo sapiens* GN=GART PE=1 SV=1	1.646	0.001881
P61978	Heterogeneous nuclear ribonucleoprotein K OS=*Homo sapiens* GN=HNRNPK PE=1 SV=1	1.643	0.00023
O00571	ATP-dependent RNA helicase DDX3X OS=*Homo sapiens* GN=DDX3X PE=1 SV=3	1.639	0.000361
P06748	Nucleophosmin OS=*Homo sapiens* GN=NPM1 PE=1 SV=2	1.637	0.005875
Q03154	Aminoacylase-1 OS=*Homo sapiens* GN=ACY1 PE=1 SV=1	1.636	0.000373
P13639	Elongation factor 2 OS=*Homo sapiens* GN=EEF2 PE=1 SV=4	1.6355	7.16E-15
P31948	Stress-induced-phosphoprotein 1 OS=*Homo sapiens* GN=STIP1 PE=1 SV=1	1.633	3.68E-10
O15269	Serine palmitoyltransferase 1 OS=*Homo sapiens* GN=SPTLC1 PE=1 SV=1	1.632	0.008343
P22059	Oxysterol-binding protein 1 OS=*Homo sapiens* GN=OSBP PE=1 SV=1	1.6315	0.001194
P51884	Lumican OS=*Homo sapiens* GN=LUM PE=1 SV=2	1.6295	6.54E-13
P49959	Double-strand break repair protein MRE11A OS=*Homo sapiens* GN=MRE11A PE=1 SV=3	1.629	0.000368
Q9P2J5	Leucine--tRNA ligase, cytoplasmic OS=*Homo sapiens* GN=LARS PE=1 SV=2	1.629	0.003611
P07686	Beta-hexosaminidase subunit beta OS=*Homo sapiens* GN=HEXB PE=1 SV=3	1.6235	0.00036
Q92945	Far upstream element-binding protein 2 OS=*Homo sapiens* GN=KHSRP PE=1 SV=4	1.6195	0.00836

Table SIII. Continued.

Protein ID	Protein description	Ratio (cancer vs. normal)	P-value
Q92598	Heat shock protein 105 kDa OS=*Homo sapiens* GN=HSPH1 PE=1 SV=1	1.618	0.002145
O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=*Homo sapiens* GN=SNRNP200 PE=1 SV=2	1.6155	9.88E-06
Q9NZU5	LIM and cysteine-rich domains protein 1 OS=*Homo sapiens* GN=LMCD1 PE=1 SV=1	1.613	0.00555
O75821	Eukaryotic translation initiation factor 3 subunit G OS=*Homo sapiens* GN=EIF3G PE=1 SV=2	1.6125	0.003627
Q92896	Golgi apparatus protein 1 OS=*Homo sapiens* GN=GLG1 PE=1 SV=2	1.6125	8.79E-05
P37802	Transgelin-2 OS=*Homo sapiens* GN=TAGLN2 PE=1 SV=3	1.61	4.79E-05
Q07065	Cytoskeleton-associated protein 4 OS=*Homo sapiens* GN=CKAP4 PE=1 SV=2	1.6095	5.18E-06
P07108	Acyl-CoA-binding protein OS=*Homo sapiens* GN=DBI PE=1 SV=2	1.6085	0.002783
Q92878	DNA repair protein RAD50 OS=*Homo sapiens* GN=RAD50 PE=1 SV=1	1.606	1.08E-07
O94906	Pre-mRNA-processing factor 6 OS=*Homo sapiens* GN=PRPF6 PE=1 SV=1	1.6055	0.002135
O60264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=*Homo sapiens* GN=SMARCA5 PE=1 SV=1	1.601	0.000291
P18085	ADP-ribosylation factor 4 OS=*Homo sapiens* GN=ARF4 PE=1 SV=3	1.601	0.007549
Q9NZM1	Myoferlin OS=*Homo sapiens* GN=MYOF PE=1 SV=1	1.6005	1.12E-11
P55265	Double-stranded RNA-specific adenosine deaminase OS=*Homo sapiens* GN=ADAR PE=1 SV=4	1.6	0.002871
P26639	Threonine--tRNA ligase, cytoplasmic OS=*Homo sapiens* GN=TARS PE=1 SV=3	1.598	0.002426
Q15029	116 kDa U5 small nuclear ribonucleoprotein component OS=*Homo sapiens* GN=EFTUD2 PE=1 SV=1	1.596	9.65E-05
P48735	Isocitrate dehydrogenase [NADP], mitochondrial OS=*Homo sapiens* GN=IDH2 PE=1 SV=2	1.594	8.24E-07
P52566	Rho GDP-dissociation inhibitor 2 OS=*Homo sapiens* GN=ARHGDIB PE=1 SV=3	1.5915	0.005657
Q00796	Sorbitol dehydrogenase OS=*Homo sapiens* GN=SORD PE=1 SV=4	1.59	0.005068
P68032	Actin, alpha cardiac muscle 1 OS=*Homo sapiens* GN=ACTC1 PE=1 SV=1	1.588	8.76E-07
P31942	Heterogeneous nuclear ribonucleoprotein H3 OS=*Homo sapiens* GN=HNRNPH3 PE=1 SV=2	1.587	0.000225
P62805	Histone H4 OS=*Homo sapiens* GN=HIST1H4A PE=1 SV=2	1.581	1.62E-08
Q9NUU7	ATP-dependent RNA helicase DDX19A OS=*Homo sapiens* GN=DDX19A PE=1 SV=1	1.577	0.003185
Q96HC4	PDZ and LIM domain protein 5 OS=*Homo sapiens* GN=PDLIM5 PE=1 SV=5	1.5745	0.003093
P18583	Protein SON OS=*Homo sapiens* GN=SON PE=1 SV=4	1.571	0.006112
Q5VTE0	Putative elongation factor 1-alpha-like 3 OS=*Homo sapiens* GN=EEF1A1P5 PE=5 SV=1	1.571	0.000188
P30044	Peroxiredoxin-5, mitochondrial OS=*Homo sapiens* GN=PRDX5 PE=1 SV=4	1.568	0.00136
P08107	Heat shock 70 kDa protein 1A/1B OS=*Homo sapiens* GN=HSPA1A PE=1 SV=5	1.566	2.83E-06
P52306	Rap1 GTPase-GDP dissociation stimulator 1 OS=*Homo sapiens* GN=RAP1GDS1 PE=1 SV=3	1.564	0.008914
Q71UM5	40S ribosomal protein S27-like OS=*Homo sapiens* GN=RPS27L PE=1 SV=3	1.5635	0.002824
P62826	GTP-binding nuclear protein Ran OS=*Homo sapiens* GN=RAN PE=1 SV=3	1.5605	0.003168
P61247	40S ribosomal protein S3a OS=*Homo sapiens* GN=RPS3A PE=1 SV=2	1.5585	0.002946
Q15833	Syntaxin-binding protein 2 OS=*Homo sapiens* GN=STXBP2 PE=1 SV=2	1.558	0.005127
P30519	Heme oxygenase 2 OS=*Homo sapiens* GN=HMOX2 PE=1 SV=2	1.557	0.001182
Q9HB07	UPF0160 protein MYG1, mitochondrial OS=*Homo sapiens* GN=C12orf10 PE=1 SV=2	1.553	0.00384
P14866	Heterogeneous nuclear ribonucleoprotein L OS=*Homo sapiens* GN=HNRNPL PE=1 SV=2	1.5525	0.001427
Q7L2E3	Putative ATP-dependent RNA helicase DHX30 OS=*Homo sapiens* GN=DHX30 PE=1 SV=1	1.552	0.001734

Table SIII. Continued.

Protein ID	Protein description	Ratio (cancer vs. normal)	P-value
P48444	Coatomer subunit delta OS=*Homo sapiens* GN=ARCN1 PE=1 SV=1	1.5485	0.000167
P19012	Keratin, type I cytoskeletal 15 OS=*Homo sapiens* GN=KRT15 PE=1 SV=3	1.548	0.003923
Q14847	LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2	1.5415	0.008203
P40763	Signal transducer and activator of transcription 3 OS=*Homo sapiens* GN=STAT3 PE=1 SV=2	1.537	0.000895
A0AVT1	Ubiquitin-like modifier-activating enzyme 6 OS=*Homo sapiens* GN=UBA6 PE=1 SV=1	1.5345	0.000467
P04792	Heat shock protein beta-1 OS=*Homo sapiens* GN=HSPB1 PE=1 SV=2	1.534	7.78E-05
P52565	Rho GDP-dissociation inhibitor 1 OS=*Homo sapiens* GN=ARHGDIA PE=1 SV=3	1.525	0.002866
P12814	Alpha-actinin-1 OS=*Homo sapiens* GN=ACTN1 PE=1 SV=2	1.522	2.46E-10
O75937	DnaJ homolog subfamily C member 8 OS=*Homo sapiens* GN=DNAJC8 PE=1 SV=2	1.519	0.001697
P08123	Collagen alpha-2(I) chain OS=*Homo sapiens* GN=COL1A2 PE=1 SV=7	1.515	6.11E-10
Q15185	Prostaglandin E synthase 3 OS=*Homo sapiens* GN=PTGES3 PE=1 SV=1	1.5115	0.000382
Q13177	Serine/threonine-protein kinase PAK 2 OS=*Homo sapiens* GN=PAK2 PE=1 SV=3	1.5095	0.009002
Q15113	Procollagen C-endopeptidase enhancer 1 OS=*Homo sapiens* GN=PCOLCE PE=1 SV=2	1.509	0.00308
P11142	Heat shock cognate 71 kDa protein OS=*Homo sapiens* GN=HSPA8 PE=1 SV=1	1.5085	2.5E-13
Q14980	Nuclear mitotic apparatus protein 1 OS=*Homo sapiens* GN=NUMA1 PE=1 SV=2	1.5065	3.59E-05
O60763	General vesicular transport factor p115 OS=*Homo sapiens* GN=USO1 PE=1 SV=2	1.506	3.32E-05
O75083	WD repeat-containing protein 1 OS=*Homo sapiens* GN=WDR1 PE=1 SV=4	1.5025	0.001385
Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1 OS=*Homo sapiens* GN=PPIL1 PE=1 SV=1	1.502	0.001209

Table SIV. All proteins whose expression level were significantly downregulated in breast cancer tissues (fold change ≤1/1.5 compared with normal tissues).

Protein ID	Protein description	Ratio (cancer vs. normal)	P-value
Q96FV2	Secernin-2 OS=*Homo sapiens* GN=SCRN2 PE=1 SV=3	0.666	0.001084
P30041	Peroxiredoxin-6 OS=*Homo sapiens* GN=PRDX6 PE=1 SV=3	0.665	1.29E-09
Q9BX97	Plasmalemma vesicle-associated protein OS=*Homo sapiens* GN=PLVAP PE=2 SV=1	0.665	0.006584
P10643	Complement component C7 OS=*Homo sapiens* GN=C7 PE=1 SV=2	0.6645	0.001107
P51648	Fatty aldehyde dehydrogenase OS=*Homo sapiens* GN=ALDH3A2 PE=1 SV=1	0.664	0.000786
P11498	Pyruvate carboxylase, mitochondrial OS=*Homo sapiens* GN=PC PE=1 SV=2	0.663	8.92E-06
P01031	Complement C5 OS=*Homo sapiens* GN=C5 PE=1 SV=4	0.662	2.81E-07
P05556	Integrin beta-1 OS=*Homo sapiens* GN=ITGB1 PE=1 SV=2	0.6605	1.89E-06
P07099	Epoxide hydrolase 1 OS=*Homo sapiens* GN=EPHX1 PE=1 SV=1	0.6585	4.9E-06
P43652	Afamin OS=*Homo sapiens* GN=AFM PE=1 SV=1	0.658	8.22E-10
P01024	Complement C3 OS=*Homo sapiens* GN=C3 PE=1 SV=2	0.656	1.66E-52
P08294	Extracellular superoxide dismutase [Cu-Zn] OS=*Homo sapiens* GN=SOD3 PE=1 SV=2	0.653	0.000636
P02774	Vitamin D-binding protein OS=*Homo sapiens* GN=GC PE=1 SV=1	0.649	1.78E-19
O43491	Band 4.1-like protein 2 OS=*Homo sapiens* GN=EPB41L2 PE=1 SV=1	0.648	3.43E-05
P16930	Fumarylacetoacetase OS=*Homo sapiens* GN=FAH PE=1 SV=2	0.647	1.5E-08
P21399	Cytoplasmic aconitate hydratase OS=*Homo sapiens* GN=ACO1 PE=1 SV=3	0.645	6.23E-07
P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=*Homo sapiens* GN=ALDH4A1 PE=1 SV=3	0.643	1.11E-09
B9A064	Immunoglobulin lambda-like polypeptide 5 OS=*Homo sapiens* GN=IGLL5 PE=2 SV=2	0.6425	4.63E-10
Q13418	Integrin-linked protein kinase OS=*Homo sapiens* GN=ILK PE=1 SV=2	0.6425	1.9E-10
O43175	D-3-phosphoglycerate dehydrogenase OS=*Homo sapiens* GN=PHGDH PE=1 SV=4	0.642	2.11E-05
P05546	Heparin cofactor 2 OS=*Homo sapiens* GN=SERPIND1 PE=1 SV=3	0.642	6.94E-07
P01859	Ig gamma-2 chain C region OS=*Homo sapiens* GN=IGHG2 PE=1 SV=2	0.6415	1.39E-17
P08758	Annexin A5 OS=*Homo sapiens* GN=ANXA5 PE=1 SV=2	0.6405	1.57E-19
P02765	Alpha-2-HS-glycoprotein OS=*Homo sapiens* GN=AHSG PE=1 SV=1	0.6395	4.78E-06
P80748	Ig lambda chain V-III region LOI OS=*Homo sapiens* PE=1 SV=1	0.638	0.003355
Q8IWA5	Choline transporter-like protein 2 OS=*Homo sapiens* GN=SLC44A2 PE=1 SV=3	0.6375	0.000756
Q16134	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=*Homo sapiens* GN=ETFDH PE=1 SV=2	0.634	1.98E-05
Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 OS=*Homo sapiens* GN=HSDL2 PE=1 SV=1	0.633	4.73E-06
Q8IV08	Phospholipase D3 OS=*Homo sapiens* GN=PLD3 PE=1 SV=1	0.6305	0.007753
P08670	Vimentin OS=*Homo sapiens* GN=VIM PE=1 SV=4	0.6295	4.82E-30
Q15124	Phosphoglucomutase-like protein 5 OS=*Homo sapiens* GN=PGM5 PE=1 SV=2	0.629	7.02E-06
P01615	Ig kappa chain V-II region TEW OS=*Homo sapiens* PE=1 SV=1	0.628	6.91E-06
P30043	Flavin reductase (NADPH) OS=*Homo sapiens* GN=BLVRB PE=1 SV=3	0.628	0.000447
P48059	LIM and senescent cell antigen-like-containing domain protein 1 OS=*Homo sapiens* GN=LIMS1 PE=1 SV=4	0.628	0.000175
Q9P2R7	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=*Homo sapiens* GN=SUCLA2 PE=1 SV=3	0.627	0.00109
P02790	Hemopexin OS=*Homo sapiens* GN=HPX PE=1 SV=2	0.6255	4.59E-14
Q15404	Ras suppressor protein 1 OS=*Homo sapiens* GN=RSU1 PE=1 SV=3	0.624	2.99E-05
P12429	Annexin A3 OS=*Homo sapiens* GN=ANXA3 PE=1 SV=3	0.6235	3.05E-11

Table SIV. Continued.

Protein ID	Protein description	Ratio (cancer vs. normal)	P-value
P13671	Complement component C6 OS=*Homo sapiens* GN=C6 PE=1 SV=3	0.622	1.56E-07
Q12797	Aspartyl/asparaginyl beta-hydroxylase OS=*Homo sapiens* GN=ASPH PE=1 SV=3	0.621	1.5E-07
P07355	Annexin A2 OS=*Homo sapiens* GN=ANXA2 PE=1 SV=2	0.6195	4.3E-15
P04003	C4b-binding protein alpha chain OS=*Homo sapiens* GN=C4BPA PE=1 SV=2	0.619	1.4E-16
Q02952	A-kinase anchor protein 12 OS=Homo sapiens GN=AKAP12 PE=1 SV=4	0.618	1.6E-05
P01602	Ig kappa chain V-I region EU OS=*Homo sapiens* PE=1 SV=1	0.6095	0.000199
O43866	CD5 antigen-like OS=*Homo sapiens* GN=CD5L PE=1 SV=1	0.6085	1.72E-05
P60903	Protein S100-A10 OS=*Homo sapiens* GN=S100A10 PE=1 SV=2	0.608	1.87E-08
P61981	14-3-3 protein gamma OS=*Homo sapiens* GN=YWHAG PE=1 SV=2	0.6075	5.05E-10
P05452	Tetranectin OS=*Homo sapiens* GN=CLEC3B PE=1 SV=3	0.6015	0.009635
P01767	Ig heavy chain V-III region BUT OS=*Homo sapiens* PE=1 SV=1	0.6	0.000617
Q14624	Inter-alpha-trypsin inhibitor heavy chain H4 OS=*Homo sapiens* GN=ITIH4 PE=1 SV=4	0.599	1.14E-10
O15247	Chloride intracellular channel protein 2 OS=*Homo sapiens* GN=CLIC2 PE=1 SV=3	0.597	0.004253
P01764	Ig heavy chain V-III region TIL OS=*Homo sapiens* PE=1 SV=1	0.594	2.76E-05
P00488	Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4	0.593	8.16E-10
P02656	Apolipoprotein C-III OS=*Homo sapiens* GN=APOC3 PE=1 SV=1	0.593	0.005001
Q86TX2	Acyl-coenzyme A thioesterase 1 OS=*Homo sapiens* GN=ACOT1 PE=1 SV=1	0.593	0.001438
P01019	Angiotensinogen OS=*Homo sapiens* GN=AGT PE=1 SV=1	0.591	0.000114
P09972	Fructose-bisphosphate aldolase C OS=*Homo sapiens* GN=ALDOC PE=1 SV=2	0.588	0.005795
P21589	5~-nucleotidase OS=*Homo sapiens* GN=NT5E PE=1 SV=1	0.586	0.007598
P56199	Integrin alpha-1 OS=*Homo sapiens* GN=ITGA1 PE=1 SV=2	0.5855	0.001597
P01009	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	0.584	8.1E-131
P32119	Peroxiredoxin-2 OS=*Homo sapiens* GN=PRDX2 PE=1 SV=5	0.5835	3.3E-12
P27338	Amine oxidase [flavin-containing] B OS=*Homo sapiens* GN=MAOB PE=1 SV=3	0.582	9.63E-05
P02775	Platelet basic protein OS=*Homo sapiens* GN=PPBP PE=1 SV=3	0.58	0.00072
P27169	Serum paraoxonase/arylesterase 1 OS=*Homo sapiens* GN=PON1 PE=1 SV=3	0.5795	6.91E-05
P01834	Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	0.579	5.45E-35
Q13813	Spectrin alpha chain, non-erythrocytic 1 OS=*Homo sapiens* GN=SPTAN1 PE=1 SV=3	0.578	1.53E-48
P01619	Ig kappa chain V-III region WOL OS=*Homo sapiens* PE=1 SV=1	0.577	0.002903
P27144	Adenylate kinase 4, mitochondrial OS=*Homo sapiens* GN=AK4 PE=1 SV=1	0.5765	0.005733
P01876	Ig alpha-1 chain C region OS=*Homo sapiens* GN=IGHA1 PE=1 SV=2	0.575	4.78E-14
P04264	Keratin, type II cytoskeletal 1 OS=*Homo sapiens* GN=KRT1 PE=1 SV=6	0.575	8.93E-05
P04114	Apolipoprotein B-100 OS=*Homo sapiens* GN=APOB PE=1 SV=2	0.573	3.43E-39
Q9HBL0	Tensin-1 OS=*Homo sapiens* GN=TNS1 PE=1 SV=2	0.572	1.91E-07
P12277	Creatine kinase B-type OS=*Homo sapiens* GN=CKB PE=1 SV=1	0.568	4.28E-09
P02768	Serum albumin OS=*Homo sapiens* GN=ALB PE=1 SV=2	0.567	0
P00450	Ceruloplasmin OS=*Homo sapiens* GN=CP PE=1 SV=1	0.565	7.44E-18
P10301	Ras-related protein R-Ras OS=*Homo sapiens* GN=RRAS PE=1 SV=1	0.565	0.0018

Table SIV. Continued.

Protein ID	Protein description	Ratio (cancer vs. normal)	P-value
P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=*Homo sapiens* GN=ACAA2 PE=1 SV=2	0.563	5.09E-07
P35555	Fibrillin-1 OS=*Homo sapiens* GN=FBN1 PE=1 SV=3	0.56	8.91E-34
P01871	Ig mu chain C region OS=*Homo sapiens* GN=IGHM PE=1 SV=3	0.559	2.06E-05
P02794	Ferritin heavy chain OS=*Homo sapiens* GN=FTH1 PE=1 SV=2	0.5585	0.000236
P24043	Laminin subunit alpha-2 OS=*Homo sapiens* GN=LAMA2 PE=1 SV=4	0.5585	0.003258
Q9Y4G6	Talin-2 OS=*Homo sapiens* GN=TLN2 PE=1 SV=4	0.556	4.41E-20
P01715	Ig lambda chain V-IV region Bau OS=*Homo sapiens* PE=1 SV=1	0.5535	0.000713
P98160	Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4	0.5525	8.13E-32
Q01082	Spectrin beta chain, non-erythrocytic 1 OS=*Homo sapiens* GN=SPTBN1 PE=1 SV=2	0.548	2.22E-31
P00533	Epidermal growth factor receptor OS=*Homo sapiens* GN=EGFR PE=1 SV=2	0.5475	0.004924
P00352	Retinal dehydrogenase 1 OS=*Homo sapiens* GN=ALDH1A1 PE=1 SV=2	0.547	3.32E-07
Q15847	Adipogenesis regulatory factor OS=*Homo sapiens* GN=ADIRF PE=1 SV=1	0.547	0.009361
P00387	NADH-cytochrome b5 reductase 3 OS=*Homo sapiens* GN=CYB5R3 PE=1 SV=3	0.546	2.24E-14
P27105	Erythrocyte band 7 integral membrane protein OS=*Homo sapiens* GN=STOM PE=1 SV=3	0.544	3.39E-14
P01860	Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2	0.543	2.29E-07
P16219	Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=*Homo sapiens* GN=ACADS PE=1 SV=1	0.5425	8.46E-05
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	0.54	1.28E-35
P01857	Ig gamma-1 chain C region OS=*Homo sapiens* GN=IGHG1 PE=1 SV=1	0.539	3.17E-68
P54289	Voltage-dependent calcium channel subunit alpha-2/delta-1 OS=*Homo sapiens* GN=CACNA2D1 PE=1 SV=3	0.538	0.002164
P06727	Apolipoprotein A-IV OS=*Homo sapiens* GN=APOA4 PE=1 SV=3	0.535	0.000564
P02652	Apolipoprotein A-II OS=*Homo sapiens* GN=APOA2 PE=1 SV=1	0.534	5.74E-07
Q9NTX5	Ethylmalonyl-CoA decarboxylase OS=*Homo sapiens* GN=ECHDC1 PE=1 SV=2	0.5335	2.05E-05
P04275	von Willebrand factor OS=*Homo sapiens* GN=VWF PE=1 SV=4	0.531	2.95E-20
P04083	Annexin A1 OS=*Homo sapiens* GN=ANXA1 PE=1 SV=2	0.529	5.73E-18
P26447	Protein S100-A4 OS=*Homo sapiens* GN=S100A4 PE=1 SV=1	0.526	0.00022
O94911	ATP-binding cassette sub-family A member 8 OS=*Homo sapiens* GN=ABCA8 PE=1 SV=3	0.524	0.001428
O76070	Gamma-synuclein OS=*Homo sapiens* GN=SNCG PE=1 SV=2	0.518	8.58E-06
P23229	Integrin alpha-6 OS=*Homo sapiens* GN=ITGA6 PE=1 SV=5	0.518	0.000497
O95810	Serum deprivation-response protein OS=*Homo sapiens* GN=SDPR PE=1 SV=3	0.514	0.000148
Q6NY19	KN motif and ankyrin repeat domain-containing protein 3 OS=*Homo sapiens* GN=KANK3 PE=2 SV=1	0.5135	0.005888
P07942	Laminin subunit beta-1 OS=*Homo sapiens* GN=LAMB1 PE=1 SV=2	0.513	2.26E-13
P08697	Alpha-2-antiplasmin OS=*Homo sapiens* GN=SERPINF2 PE=1 SV=3	0.51	3.55E-06
P22105	Tenascin-X OS=Homo sapiens GN=TNXB PE=1 SV=3	0.508	8.7E-30
Q86VB7	Scavenger receptor cysteine-rich type 1 protein M130 OS=*Homo sapiens* GN=CD163 PE=1 SV=2	0.506	1.55E-10
Q14112	Nidogen-2 OS=*Homo sapiens* GN=NID2 PE=1 SV=3	0.504	9.4E-07
O14558	Heat shock protein beta-6 OS=*Homo sapiens* GN=HSPB6 PE=1 SV=2	0.493	0.000232
P07195	L-lactate dehydrogenase B chain OS=*Homo sapiens* GN=LDHB PE=1 SV=2	0.493	1.61E-11
O14791	Apolipoprotein L1 OS=*Homo sapiens* GN=APOL1 PE=1 SV=5	0.491	3.92E-05

Table SIV. Continued.

Protein ID	Protein description	Ratio (cancer vs. normal)	P-value
P01766	Ig heavy chain V-III region BRO OS=*Homo sapiens* PE=1 SV=1	0.49	0.001082
Q9NVD7	Alpha-parvin OS=Homo sapiens GN=PARVA PE=1 SV=1	0.49	1.64E-07
P15088	Mast cell carboxypeptidase A OS=*Homo sapiens* GN=CPA3 PE=1 SV=2	0.4855	6.16E-05
P07225	Vitamin K-dependent protein S OS=*Homo sapiens* GN=PROS1 PE=1 SV=1	0.4845	0.000876
P06703	Protein S100-A6 OS=*Homo sapiens* GN=S100A6 PE=1 SV=1	0.482	0.000436
Q6NZI2	Polymerase I and transcript release factor OS=*Homo sapiens* GN=PTRF PE=1 SV=1	0.482	1.24E-07
P08572	Collagen alpha-2(IV) chain OS=*Homo sapiens* GN=COL4A2 PE=1 SV=4	0.479	1.09E-14
Q96AC1	Fermitin family homolog 2 OS=*Homo sapiens* GN=FERMT2 PE=1 SV=1	0.477	1.09E-10
P06737	Glycogen phosphorylase, liver form OS=*Homo sapiens* GN=PYGL PE=1 SV=4	0.4765	3.3E-10
O43301	Heat shock 70 kDa protein 12A OS=*Homo sapiens* GN=HSPA12A PE=1 SV=2	0.476	1.06E-06
P07738	Bisphosphoglycerate mutase OS=*Homo sapiens* GN=BPGM PE=1 SV=2	0.476	3.02E-05
Q687X5	Metalloreductase STEAP4 OS=*Homo sapiens* GN=STEAP4 PE=1 SV=1	0.476	0.00341
Q6NUM9	All-trans-retinol 13,14-reductase OS=*Homo sapiens* GN=RETSAT PE=1 SV=2	0.476	0.000171
O00159	Unconventional myosin-Ic OS=*Homo sapiens* GN=MYO1C PE=1 SV=4	0.47	6.17E-19
Q16851	UTP--glucose-1-phosphate uridylyltransferase OS=*Homo sapiens* GN=UGP2 PE=1 SV=5	0.469	2.52E-18
Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=*Homo sapiens* GN=HADH PE=1 SV=3	0.4665	2.37E-05
P00966	Argininosuccinate synthase OS=*Homo sapiens* GN=ASS1 PE=1 SV=2	0.466	5.42E-08
Q01469	Fatty acid-binding protein, epidermal OS=*Homo sapiens* GN=FABP5 PE=1 SV=3	0.4595	6.48E-11
P11532	Dystrophin OS=*Homo sapiens* GN=DMD PE=1 SV=3	0.4575	1.89E-05
P48163	NADP-dependent malic enzyme OS=*Homo sapiens* GN=ME1 PE=1 SV=1	0.455	0.003812
P02462	Collagen alpha-1(IV) chain OS=*Homo sapiens* GN=COL4A1 PE=1 SV=3	0.454	1.74E-12
P01833	Polymeric immunoglobulin receptor OS=*Homo sapiens* GN=PIGR PE=1 SV=4	0.453	8.44E-05
P11171	Protein 4.1 OS=*Homo sapiens* GN=EPB41 PE=1 SV=4	0.45	1.7E-06
P02675	Fibrinogen beta chain OS=*Homo sapiens* GN=FGB PE=1 SV=2	0.447	1.48E-27
P62070	Ras-related protein R-Ras2 OS=*Homo sapiens* GN=RRAS2 PE=1 SV=1	0.444	0.00112
P39059	Collagen alpha-1(XV) chain OS=*Homo sapiens* GN=COL15A1 PE=1 SV=2	0.435	7.28E-06
P01705	Ig lambda chain V-II region NEI OS=*Homo sapiens* PE=1 SV=1	0.433	0.001372
P55290	Cadherin-13 OS=*Homo sapiens* GN=CDH13 PE=1 SV=1	0.432	0.007346
P14543	Nidogen-1 OS=*Homo sapiens* GN=NID1 PE=1 SV=3	0.429	1.34E-13
P02671	Fibrinogen alpha chain OS=*Homo sapiens* GN=FGA PE=1 SV=2	0.427	1.77E-37
Q9BX66	Sorbin and SH3 domain-containing protein 1 OS=*Homo sapiens* GN=SORBS1 PE=1 SV=3	0.4265	2.65E-07
P24298	Alanine aminotransferase 1 OS=*Homo sapiens* GN=GPT PE=1 SV=3	0.4235	0.000311
P00746	Complement factor D OS=*Homo sapiens* GN=CFD PE=1 SV=5	0.4195	0.000662
P42330	Aldo-keto reductase family 1 member C3 OS=*Homo sapiens* GN=AKR1C3 PE=1 SV=4	0.418	6.51E-06
O75781	Paralemmin-1 OS=*Homo sapiens* GN=PALM PE=1 SV=2	0.416	0.000497
P31323	cAMP-dependent protein kinase type II-beta regulatory subunit OS=*Homo sapiens* GN=PRKAR2B PE=1 SV=3	0.412	0.00013
Q13683	Integrin alpha-7 OS=*Homo sapiens* GN=ITGA7 PE=1 SV=3	0.411	1.82E-06
P61764	Syntaxin-binding protein 1 OS=*Homo sapiens* GN=STXBP1 PE=1 SV=1	0.409	0.002761

Table SIV. Continued.

Protein ID	Protein description	Ratio (cancer vs. normal)	P-value
Q16363	Laminin subunit alpha-4 OS=*Homo sapiens* GN=LAMA4 PE=1 SV=4	0.408	6.88E-13
P55268	Laminin subunit beta-2 OS=*Homo sapiens* GN=LAMB2 PE=1 SV=2	0.398	2.13E-28
Q5TDH0	Protein DDI1 homolog 2 OS=*Homo sapiens* GN=DDI2 PE=1 SV=1	0.3975	0.005594
P05091	Aldehyde dehydrogenase, mitochondrial OS=*Homo sapiens* GN=ALDH2 PE=1 SV=2	0.395	7.35E-06
Q03135	Caveolin-1 OS=*Homo sapiens* GN=CAV1 PE=1 SV=4	0.395	1.28E-11
P48509	CD151 antigen OS=*Homo sapiens* GN=CD151 PE=1 SV=3	0.3945	3.57E-06
P43121	Cell surface glycoprotein MUC18 OS=*Homo sapiens* GN=MCAM PE=1 SV=2	0.393	3.68E-08
P11047	Laminin subunit gamma-1 OS=*Homo sapiens* GN=LAMC1 PE=1 SV=3	0.3905	2.57E-23
P23141	Liver carboxylesterase 1 OS=*Homo sapiens* GN=CES1 PE=1 SV=2	0.389	2.9E-07
P51636	Caveolin-2 OS=*Homo sapiens* GN=CAV2 PE=1 SV=2	0.387	0.004128
P12273	Prolactin-inducible protein OS=*Homo sapiens* GN=PIP PE=1 SV=1	0.386	3.52E-31
P33121	Long-chain-fatty-acid--CoA ligase 1 OS=*Homo sapiens* GN=ACSL1 PE=1 SV=1	0.383	1.12E-16
Q92781	11-cis retinol dehydrogenase OS=*Homo sapiens* GN=RDH5 PE=1 SV=1	0.373	0.002732
P02647	Apolipoprotein A-I OS=*Homo sapiens* GN=APOA1 PE=1 SV=1	0.369	1.81E-67
P21397	Amine oxidase [flavin-containing] A OS=*Homo sapiens* GN=MAOA PE=1 SV=1	0.3655	1.62E-06
P0DOY2	Ig lambda-2 chain C regions OS=*Homo sapiens* GN=IGLC2 PE=1 SV=1	0.363	0.002176
Q9NP78	ATP-binding cassette sub-family B member 9 OS=*Homo sapiens* GN=ABCB9 PE=1 SV=1	0.361	0.006078
P63096	Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=*Homo sapiens* GN=GNAI1 PE=1 SV=2	0.357	0.000178
O76061	Stanniocalcin-2 OS=*Homo sapiens* GN=STC2 PE=1 SV=1	0.3525	0.000914
Q9NZN4	EH domain-containing protein 2 OS=*Homo sapiens* GN=EHD2 PE=1 SV=2	0.352	3.22E-21
P02679	Fibrinogen gamma chain OS=*Homo sapiens* GN=FGG PE=1 SV=3	0.347	5.36E-28
P22676	Calretinin OS=*Homo sapiens* GN=CALB2 PE=1 SV=2	0.3465	1.05E-06
Q13642	Four and a half LIM domains protein 1 OS=*Homo sapiens* GN=FHL1 PE=1 SV=4	0.342	2.72E-08
Q9BRX8	Redox-regulatory protein FAM213A OS=*Homo sapiens* GN=FAM213A PE=1 SV=3	0.34	4.48E-09
O60240	Perilipin-1 OS=*Homo sapiens* GN=PLIN1 PE=1 SV=2	0.3295	1.6E-16
Q13361	Microfibrillar-associated protein 5 OS=*Homo sapiens* GN=MFAP5 PE=1 SV=1	0.328	0.001865
P02792	Ferritin light chain OS=*Homo sapiens* GN=FTL PE=1 SV=2	0.324	0.000142
Q05469	Hormone-sensitive lipase OS=*Homo sapiens* GN=LIPE PE=1 SV=4	0.323	1.22E-10
P02730	Band 3 anion transport protein OS=*Homo sapiens* GN=SLC4A1 PE=1 SV=3	0.322	4.59E-08
P07451	Carbonic anhydrase 3 OS=*Homo sapiens* GN=CA3 PE=1 SV=3	0.319	3.35E-05
O00763	Acetyl-CoA carboxylase 2 OS=*Homo sapiens* GN=ACACB PE=1 SV=3	0.309	0.000547
P35612	Beta-adducin OS=*Homo sapiens* GN=ADD2 PE=1 SV=3	0.309	0.000879
P02549	Spectrin alpha chain, erythrocytic 1 OS=*Homo sapiens* GN=SPTA1 PE=1 SV=5	0.306	3.31E-26
P04040	Catalase OS=*Homo sapiens* GN=CAT PE=1 SV=3	0.2995	1.39E-18
O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=*Homo sapiens* GN=ALDH1L1 PE=1 SV=2	0.297	1.07E-08
Q16853	Membrane primary amine oxidase OS=*Homo sapiens* GN=AOC3 PE=1 SV=3	0.297	2.46E-20
Q6UXB8	Peptidase inhibitor 16 OS=*Homo sapiens* GN=PI16 PE=1 SV=1	0.297	0.001811
P00915	Carbonic anhydrase 1 OS=*Homo sapiens* GN=CA1 PE=1 SV=2	0.296	6.97E-23

Table SIV. Continued.

Protein ID	Protein description	Ratio (cancer vs. normal)	P-value
P21695	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=*Homo sapiens* GN=GPD1 PE=1 SV=4	0.292	1.71E-18
P00918	Carbonic anhydrase 2 OS=*Homo sapiens* GN=CA2 PE=1 SV=2	0.2845	6.86E-10
P02654	Apolipoprotein C-I OS=*Homo sapiens* GN=APOC1 PE=1 SV=1	0.283	3.76E-05
P11277	Spectrin beta chain, erythrocytic OS=*Homo sapiens* GN=SPTB PE=1 SV=5	0.276	1.8E-27
P02511	Alpha-crystallin B chain OS=*Homo sapiens* GN=CRYAB PE=1 SV=2	0.275	1.68E-08
O95969	Secretoglobin family 1D member 2 OS=*Homo sapiens* GN=SCGB1D2 PE=2 SV=1	0.27	0.004236
P16157	Ankyrin-1 OS=*Homo sapiens* GN=ANK1 PE=1 SV=3	0.263	4.28E-25
P15090	Fatty acid-binding protein, adipocyte OS=*Homo sapiens* GN=FABP4 PE=1 SV=3	0.262	7.87E-53
P16452	Erythrocyte membrane protein band 4.2 OS=*Homo sapiens* GN=EPB42 PE=1 SV=3	0.2605	8.99E-06
P16671	Platelet glycoprotein 4 OS=*Homo sapiens* GN=CD36 PE=1 SV=2	0.26	7.48E-14
A8MVG2	Putative selection and upkeep of intraepithelial T-cells protein 1 homolog OS=*Homo sapiens* GN=SKINT1 PE=5 SV=2	0.259	0.000392
Q96Q06	Perilipin-4 OS=*Homo sapiens* GN=PLIN4 PE=2 SV=2	0.253	1.13E-48
P00325	Alcohol dehydrogenase 1B OS=*Homo sapiens* GN=ADH1B PE=1 SV=2	0.2495	5.63E-55
P69891	Hemoglobin subunit gamma-1 OS=*Homo sapiens* GN=HBG1 PE=1 SV=2	0.246	1.14E-20
P02042	Hemoglobin subunit delta OS=*Homo sapiens* GN=HBD PE=1 SV=2	0.2345	5.33E-25
P69905	Hemoglobin subunit alpha OS=*Homo sapiens* GN=HBA1 PE=1 SV=2	0.206	4.43E-75
P68871	Hemoglobin subunit beta OS=*Homo sapiens* GN=HBB PE=1 SV=2	0.203	6.9E-166