

Table W1. Demographics of the Patients Included in the Proteomic Study.

	Node-Negative (<i>n</i> = 12)	Node-Positive (<i>n</i> = 12)	<i>P</i>
Age (years)	68.17 ± 11.71	62.08 ± 12.30	.670
Sex			
Male	8	6	.680
Female	4	6	
Ethnicity*			
White	7	6	.415
African-American	3	6	
Maximum diameter of the tumor (cm)	4.75 ± 1.99	5.32 ± 1.99	.464
Histologic grade			
Moderate	11	10	1.000
Poor	1	2	
Primary site			
Left colon	7	6	1.000
Right colon	3	4	
Rectum	2	2	
Primary tumor			
T2	2	1	1.000
T3	10	10	
T4	0	1	

*The ethnicity information of two patients from the node-negative group was missing.

Table W2. Proteins Identified by 2D-DIGE and MS.

Accession No.	Protein Name	MASCOT Algorithm		SEQUEST Algorithm		Peptides	Sequence Coverage (%)	MW	pI	D Score	Fold Change	FDR (%)
		MASCOT Score	CI (%)	P	Sf Score							
Upregulated in node-positive cancer												
Q01995	Transgelin	96	100			11	44	22,653	8.87	2.85	2.06	0
P40925	Cytosolic malate dehydrogenase			2.584e-08	3.587517	4	18	36,403	7.17	2.33	1.52	0
Q01995	Transgelin	127	100			11	46	22,653	8.87	2.14	1.89	7.18
Q01995	Transgelin	145	100			15	61	22,653	8.87	1.99	2.04	7.18
Downregulated in node-positive cancer												
P30837	Aldehyde dehydrogenase X, mitochondrial precursor	72	99.102			14	29	57,658	6.36	-2.65	-1.96	0
P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor	108	100			17	21	70,745	8.92	-2.13	-1.75	0
Upregulated in cancer												
P40121	Macrophage-capping protein	68	98.079			5	13	38,786	5.32	3.31	2.55	0
Q9Y427	Tropomyosin 1 α chain isoform 2			3.982e-09	2.785449	3	13.03	32,658	4.25	2.93	2.26	0
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	181	100			11	49	37,464	8.97	2.87	1.71	0
Q8IUD2	ELKS/RAB6-interacting/CAST family member 1	73	99.406			33	21	108,840	6.19	2.83	1.80	0
Q9NZL3	Zinc finger protein 224	68	98.166			25	27	84,894	9.03	2.57	1.65	0
P38919	Eukaryotic initiation factor 4A-III	120	100			16	36	47,088	6.08	2.5	1.81	0
Q15084	Protein disulfide-isomerase A6 precursor	122	100			14	32	46,512	4.95	2.39	1.68	0
P67936	Tropomyosin α -4 chain, isoform 2	115	100			12	34	32,874	4.69	2.32	1.90	0
P02792	Ferritin light chain	145	100			6	44	16,441	5.65	2.31	2.16	0
P06702	Protein S100-A9	74	99.433			7	77	13,291	5.71	2.24	2.17	0
P14618	Pyruvate kinase isozymes M1/M2	146	100			20	39	58,470	7.96	2.22	1.62	0
Q6ZWB8	cDNA FLJ14346 fis, clone BRAWH2005315, moderately similar to Neuronal-STOP protein (MAP6 protein)	75	99.55			20	32	51,297	8.88	2.22	1.61	0
Downregulated in cancer												
P10809	60 kDa heat shock protein, mitochondrial precursor (HSP60)	126	100			17	27	61,187	5.70	2.2	1.58	0
P08670	Vimentin	184	100			28	55	53,676	5.06	2.2	1.59	0
P13796	Plastin-2	113	100			18	26	70,815	5.20	2.14	1.50	0
P14618	Pyruvate kinase isozymes M1/M2	174	100			17	35	58,512	7.96	1.96	1.73	0
P29401	TKT protein	66	96.813			10	26	50,335	8.02	1.96	1.80	0
P37837	Transaldolase 1			.0001081	1.946282	4	13.35	37,516	6.00	1.94	1.47	0
O00299	Chloride intracellular channel protein 1			1.284e-08	1.903239	2	14.29	23,528	4.25	1.94	1.66	0
Q15019	Septin-2			2.973e-09	5.429678	5	17.24	46,556	6.00	1.89	1.52	0
O00299	Chloride intracellular channel protein 1			4.272e-10	1.872898	2	14.29	23,528	4.25	1.89	1.37	0
Q7Z5Z4	SHUJUN-1	105	100			7	39	17,047	4.21	1.88	1.37	0
Q7KZF4	Staphylococcal nuclease domain-containing protein 1 (p100 coactivator)	76	99.681			26	29	100,313	6.62	1.86	1.43	0
O43707	α -Actinin-4	170	100			28	33	102,661	5.27	1.84	1.44	0

Downregulated in cancer

P00915	Carbonic anhydrase I	1.535e - 11	10,67389	9	56,30	28,852	7.13	-6.54	-4.90	0
P56470	Galectin 4	7.614e - 10	3,753924	5	19,20	35,918	10,07	-5.06	-3.05	0
P05787	Keratin, type II cytoskeletal 8			27	48	55,874	5.62	-4.33	-3.41	0
P05787	Keratin, type II cytoskeletal 8			26	50	53,641	5.52	-3.99	-2.67	0
Q14376	UDP-galactose-4-epimerase	7.494e - 10	4,446128	4	18,39	38,257	6.00	-3.84	-2.36	0
P35900	Keratin, type I cytoskeletal 20			19	41	48,514	5.52	-3.68	-2.28	0
P17931	LEG3_HUMAN Galectin-3 (Galactose-specific lectin 3) (Mac-2 antigen) (IgE-binding)	2.435e - 09	1,997028	6	28,40	26,172	9.88	-3.65	-2.18	0
O95994	Anterior gradient protein 2 homolog precursor			7	42	20,024	9.03	-3.43	-2.78	0
O95994	Anterior gradient protein 2 homolog precursor			7	42	20,024	9.03	-3.36	-2.76	0
P05787	Keratin, type II cytoskeletal 8			25	46	55,787	5.62	-3.12	-2.50	0
P17931	Galectin-3			5	46	15,630	9.41	-3.08	-1.95	0
O75947	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit d isoform	5.883e - 06	0,9162297	2	8,07	18,480	4.25	-2.89	-1.84	0
P13645	Keratin, type I cytoskeletal 10			19	31	59,020	5.09	-2.84	-1.74	0
P05787	Keratin, type II cytoskeletal 8			19	35	53,641	5.52	-2.7	-1.94	0
P21796	Voltage-dependent anion-selective channel protein 1			11	43	30,818	8.63	-2.55	-1.78	0
P62826	GTP-binding nuclear protein Ran			4	21	23,307	9.02	-2.33	-1.65	0
P47985	Cytochrome <i>b-c1</i> complex subunit Rieske, mitochondrial precursor (ubiquinol-cytochrome <i>c</i> reductase iron-sulfur subunit, mitochondrial precursor)			8	30	29,959	8.55	-2.31	-1.67	0
Q99798	Aconitate hydratase, mitochondrial precursor			20	29	86,113	7.36	-2.31	-1.61	0
Q8TF65	PDZ domain protein GIPC2	1.683e - 10	1,945089	2	7,62	34,333	6.00	-2.14	-1.56	0
P52597	Heretogenous nuclear ribonucleoprotein F			8	23	45,985	5.38	-1.99	-1.50	0
P68871	Hemoglobin subunit β			8	54	15,970	7.98	-1.96	-1.64	0
P30041	Peroxioredoxin-6			12	46	25,133	6.00	-1.92	-1.55	0
P04075	Fructose-bisphosphate aldolase A			13	35	39,852	8.30	-1.89	-1.76	0
P30048	Thioredoxin-dependent peroxidase reductase, mitochondrial precursor			6	26	26,107	7.04	-1.84	-1.55	0
Q9UJ70	<i>N</i> -Acetylglucosamine kinase			11	35	37,694	5.81	-1.84	-1.51	0
A4D0V4	Capping protein (actin filament) muscle Z-line, α 2	1.175e - 06	1,73486	3	17,83	32,929	5.13	-1.81	-1.43	0
O00151	PDZ and LIM domain 1 (elfin)	5.059e - 09	1,168792	2	9,42	36,049	6.00	-1.8	-1.44	0
P32119	Peroxioredoxin-2			10	38	22,014	6.84	-1.8	-1.49	0
P00491	Purine nucleoside phosphorylase			11	43	32,325	6.45	-1.78	-1.60	0
Q9H2G3	CTCL tumor antigen sc20-7 [fragment]			25	24	73,884	5.57	-1.77	-1.59	0
P00558	Phosphoglycerate kinase 1			12	29	44,973	8.30	-1.73	-1.49	0
P50213	Isocitrate dehydrogenase [NAD] subunit α , mitochondrial precursor			9	28	40,022	6.47	-1.72	-1.40	0

Table W3. Sequences Inserted in TAGLN miRNA Plasmids.

DNA Oligos	Top Strand (5'-3')
Hmi416872 top	TGCTGATCTGAAGGCCAATGACATGCGTTTTGGCCACTGACTGACGCATGTCAGGCCTTCAGAT
Hmi416872 bottom	CCTGATCTGAAGGCCTGACATGCGTCAGTCAGTGGCCAAAACGCATGTCATTGGCCTTCAGATC
Hmi416873 top	TGCTGAACCTGATGATCTGCCGAGGTCGTTTTGGCCACTGACTGACGACCTCGGGATCATCAGTT
Hmi416873 bottom	CCTGAACCTGATGATCCCAGGTCGTCAGTCAGTGGCCAAAACGCCTCGGCAGATCATCAGTTC
Hmi416874 top	TGCTGTGCACTTCGCGGCTCATGCCAGTTTTGGCCACTGACTGACTGGCATGACGCGAAGTGCA
Hmi416874 bottom	CCTGTGCACTTCGCGTCATGCCAGTCAGTCAGTGGCCAAAACGGCATGAGCCGGAAGTGCA
Hmi416875 top	TGCTGTGTAATCCCTCTTATGCTCGTTTTGGCCACTGACTGACGAGCATAAGGGAATTCACA
Hmi416875 bottom	CCTGTGTAATCCCTTATGCTCGTCAGTCAGTGGCCAAAACGAGCATAAGGGAATTCACAC

Table W4. Primers for Real-time RT-PCR.

Gene	Forward Primer (5'-3')	Reverse Primer (5'-3')
<i>TAGLN</i>	GTCCAGACTGTTGACCTCTTT	CTGCGCTTTCATCAAACC
<i>TAGLN3</i>	ATGGGAAGGAAGGACATGGC	GCTGGCTTTCCTGTGAAACC
<i>ECAD</i>	ATACACTCTCTTCTCAGCTGTG	AAGAGCACCTTCCATGACAGAC
<i>OCCL</i>	CCTGATGAATCAAACCGAATC	AGGAGAGGTCCATTTGTAGAAGTGA
<i>CTTNB1</i>	AAATGCTTGGTTCACCAGTGGAT	CCTGCTTTTCTTCTTCTTCTT
<i>VIM</i>	TTCAGACAGGATGTGACAATGC	GGATTCCTCTTCGTGGAGTTTC
<i>FN1</i>	CGAGAGTAAACCTGAAGCTGAAGAG	GATGCAGGTACAGTCCCAGATC
<i>GAPDH</i>	ACAGCCTCAAGATCATCAGCAAT	ATGGACTGTGGTCATGAGTCCTT