

Table SI. Clinical details of the adrenocortical tumors used in the present study.													
			Tumor	Ki-67				Proteomics	RT-qPCR analysis of (a)				
Case	Sex	Age	size	index	Meta-	Follow-up ^b		screening ^a	<i>IGF2</i>	<i>miR-483-3p</i>		Western blot analysis	
no. ^c	M/ F	(years)	(cm)	(%)	stasis	Months	Outcome	Ref (41)	<i>H19</i>	<i>miR-483-5p</i>	<i>miR-675</i>	OXPPOS	NDUFC1
Adrenocortical adenomas													
ACA 1	F	38	2.5		No	231	Alive	-	Yes	Yes	Yes	-	Yes
ACA 2	F	63	6.0		No	195	Deceased	-	Yes	Yes	Yes	-	Yes
ACA 3	F	66	1.5		No	119	Alive	-	Yes	Yes	Yes	-	-
ACA 4	F	35	4.0		No	93	Alive	-	Yes	Yes	Yes	Yes	Yes
ACA 5	F	42	3.5		No	87	Alive	Yes	Yes	Yes	Yes	Yes	Yes
ACA 6	F	81	2.5		No	23	Alive	-	Yes	Yes	Yes	Yes	Yes
ACA 7	M	52	3.2		No	27	Alive	-	Yes	Yes	Yes	Yes	Yes
ACA 8	F	70	4.5		No	32	Alive	-	Yes	Yes	Yes	-	-
ACA 9	F	60	4.0		No	24	Alive	-	Yes	Yes	Yes	-	-
ACA 10	F	80	2.5		No	18	Deceased	-	Yes	Yes	Yes	-	Yes
ACA 11	F	27	4.0		No	39	Alive	-	Yes	Yes	-	Yes	Yes
ACA 12	F	75	5.0		No	12	Deceased	-	Yes	Yes	-	Yes	Yes
ACA 13	F	40	6.5		No	14	Alive	-	Yes	Yes	-	Yes	Yes
ACA 14	F	50	2.0		No	258	Alive	-	Yes	Yes	Yes	Yes	Yes
ACA 15	M	47	2.5		No	219	Alive	-	Yes	Yes	Yes	-	-
ACA 16	F	29	2.0		No	218	Alive	Yes	Yes	Yes	Yes	-	Yes
ACA 17	F	79	2.0		No	112	Deceased	-	Yes	Yes	Yes	Yes	Yes
ACA 18	F	49	2.3		No	21	Alive	-	Yes	Yes	Yes	-	-
ACA 19	F	60	1.5		No	26	Alive	-	Yes	Yes	Yes	-	-
ACA 20	F	58	1.6		No	30	Alive	-	Yes	Yes	Yes	-	-

ACA 21	M	55	1.2		No	26	Alive	-	Yes	Yes	Yes	-	-
ACA 22	M	50	1.3		No	30	Alive	-	Yes	Yes	Yes	-	-
ACA 23	F	24	2.0		No	29	Alive	-	Yes	Yes	Yes	-	-
ACA 24	F	46	4.7		No	66	Alive	-	Yes	Yes	-	-	-
ACA 25	F	34	0.9		No	111	Alive	-	Yes	Yes	-	-	-
ACA 26	M	24	1.5		No	15	Alive	-	Yes	Yes	-	-	-
ACA 27	F	16	1.5		No	140	Alive	-	Yes	Yes	-	-	-
ACA 28	F	65	4.1		No	20	Alive	-	Yes	Yes	-	-	-
ACA 29	M	42	1.2		No	18	Alive	-	Yes	Yes	-	-	-
ACA 30	F	63	5.0		No	216	Alive	-	Yes	Yes	Yes	-	Yes
ACA 31	M	63	4.0		No	215	Alive	-	Yes	Yes	Yes	Yes	Yes
ACA 32	F	42	2.5		No	89	Alive	-	Yes	Yes	Yes	-	Yes
ACA 33	F	64	4.0		No	163	Alive	Yes	Yes	Yes	Yes	-	Yes
ACA 34	F	63	4.0		No	158	Alive	Yes	Yes	Yes	Yes	-	Yes
ACA 35	M	66	4.0		No	117	Deceased	Yes	Yes	Yes	Yes	-	Yes
ACA 36	F	54	4.0		No	107	Alive	Yes	Yes	Yes	Yes	-	Yes
ACA 37	F	59	2.5		No	104	Alive	-	Yes	Yes	Yes	-	Yes
ACA 38	M	62	4.0		No	19	Alive	-	Yes	Yes	Yes	-	-
ACA 39	F	63	4.0		No	20	Alive	-	Yes	Yes	Yes	-	-
ACA 40	M	46	3.5		No	12	Alive	-	Yes	Yes	-	-	Yes
ACA 41	M	66	5.3		No	29	Alive	-	Yes	Yes	-	-	Yes
ACA 42	M	65	3.5		No	43	Alive	-	Yes	Yes	-	-	Yes
ACA 43	F	50	4.7		No	24	Alive	-	Yes	Yes	-	-	Yes
Adrenocortical carcinomas													
ACC 1	F	63	20.0	-	Yes	6	DOD	-	Yes	Yes	Yes	Yes	Yes

ACC 2	M	78	15.0	-	No	3	DOD	Yes	Yes	Yes	Yes	Yes	Yes
ACC 3	F	72	7.0	-	No	5	Deceased	Yes	Yes	Yes	Yes	-	Yes
ACC 4	M	30	10.0	-	Yes	58	DOD	Yes	Yes	Yes	Yes	-	Yes
ACC 5	M	72	11.0	-	Yes	162	DOD	-	Yes	Yes	Yes	Yes	Yes
ACC 6	F	40	18.0	-	No	188	Alive	Yes	Yes	Yes	Yes	Yes	Yes
ACC 7, 7b	F	56	9.0	-	No	9	Deceased	-	Yes	Yes	Yes	Yes	Yes
ACC 8	F	54	15.0	-	Yes	4	DOD	-	Yes	Yes	Yes	Yes	Yes
ACC 9	M	68	15.0	6	No	145	Alive	-	Yes	Yes	Yes	Yes	Yes
ACC 10	M	52	11.0	3	No	132	Alive	Yes	Yes	Yes	Yes	-	Yes
ACC 11	M	68	12.0	15	Yes	69	DOD	Yes	Yes	Yes	Yes	-	Yes
ACC 12, 12b	F	84	19.0	5	Yes	29	Deceased	Yes	Yes	Yes	Yes	Yes	Yes
ACC 13	M	64	21.0	3	Yes	91	Alive	-	Yes	Yes	Yes	Yes	Yes
ACC 14	M	67	19.0	20	No	65	Deceased	-	Yes	Yes	Yes	Yes	Yes
ACC 15	M	77	11.0	2	Yes	78	Alive	-	Yes	Yes	Yes	-	Yes
ACC 16	M	69	n.a.	10	Yes	27	DOD	-	Yes	Yes	Yes	-	-
ACC 17	F	68	10.0	70	Yes	13	DOD	-	Yes	Yes	Yes	-	-
ACC 18	F	38	21.0	15	No	53	Alive	-	Yes	Yes	Yes	-	Yes
ACC 19	F	61	14.0	25	No	51	Alive	-	Yes	Yes	Yes	-	Yes
ACC 20, 20b	M	60	9.6	6	No	48	Alive	-	Yes	Yes	Yes	-	Yes
ACC 21	F	40	9.6	3	Yes	42	Alive	-	Yes	Yes	Yes	-	-
ACC 21 Met	F	43						-	Yes	-	-	-	Yes
ACC 22, 22b	F	66	10.0	12	Yes	22	DOD	-	Yes	Yes	Yes	-	Yes
ACC 23	F	63	9.0	20	Yes	25	Alive	-	Yes	Yes	Yes	-	-
ACC 24	F	54	20.0	8	Yes	20	Alive	-	Yes	Yes	Yes	-	-
ACC 25	M	49	16.0	60	Yes	2	DOD	-	Yes	Yes	Yes	-	Yes

ACC 26	F	68	12.0	25	Yes	168	Alive	-	Yes	-	-	-	Yes
ACC 27	F	48	10.0	-	Yes	18	DOD	-	Yes	-	-	-	Yes
ACC 28	M	51	19.0	-	No	39	DOD	-	Yes	-	-	-	Yes
ACC 29	F	35	8.5	-	No	195	Alive	-	Yes	-	-	-	Yes
ACC 31	F	35	9.0	1	No	108	Alive	Yes	-	-	-	-	-

^aData for *miR-483-3p* and *miR-483-5p* were previously published for a subset of the cases (27). ^bTime between surgery and follow-up; ^cCases where a second sample from the same tumor was included are indicated as NNb; ACC 21 Met refers to metastasis from the same case. ACC, adrenocortical carcinoma; ACA, adrenocortical adenoma; F, female; M, male; DOD, dead of disease; n.a., not available.

Table SII. Proteins exhibiting an inverse correlation with *miR-483-5p*.

UniProt accession no.	Protein name	Gene symbol	Pearson's correlation	Median protein ratios ^a			Predicted targets ^b
				Adenomas (n=6)	Carcinomas (n=8)	P-value	
P49821	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	<i>NDUFV1</i>	-0.65	1.77	0.53	<0.001	No
Q13813	Spectrin alpha chain, brain	<i>SPTAN1</i>	-0.64	1.68	0.71	<0.001	No
Q01082	Spectrin beta chain, brain 1	<i>SPTBN1</i>	-0.61	1.59	0.74	<0.001	No
Q9NXW2	DnaJ homolog subfamily B member 12	<i>DNAJB12</i>	-0.56	1.57	0.86	<0.001	No
O43676	NADH dehydrogenase 1 beta subcomplex subunit 3	<i>NDUFB3</i>	-0.59	1.76	0.57	<0.001	No
O43677	NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial	<i>NDUFC1</i>	-0.62	1.89	0.7	<0.001	Yes
O95298	NADH dehydrogenase [ubiquinone] 1 subunit C2	<i>NDUFC2</i>	-0.55	1.86	0.64	<0.001	No
Q9H6X2	Anthrax toxin receptor 1	<i>ANTXR1</i>	-0.58	1.64	0.47	<0.001	No
O43505	N-acetyllactaminide beta-1,3-N-acetylglucaminyltransferase	<i>B4GAT1</i>	-0.59	1.55	0.69	0.001	No
Q96LZ7	Regulator of microtubule dynamics protein 2	<i>RMDN2</i>	-0.53	2.08	0.31	0.001	No
P07237	Protein disulfide-isomerase	<i>PDIA 3, 6</i>	-0.56	1.65	0.52	0.002	No
Q96AG4	Leucine-rich repeat-containing protein 59	<i>LRRC59</i>	-0.52	1.51	0.57	0.002	No
P07099	Epoxide hydrolase 1	<i>EPHX1</i>	-0.55	1.9	0.58	0.002	No
P51648	Fatty aldehyde dehydrogenase	<i>ALDH3A2</i>	-0.52	1.82	0.65	0.002	No
Q6PIU2	Neutral cholesterol ester hydrolase 1	<i>NCEH1</i>	-0.55	1.82	0.55	0.002	Yes
Q53TN4	Cytochrome b reductase 1	<i>CYBRD1</i>	-0.62	2.02	0.48	0.002	No
P36021	Monocarboxylate transporter 8	<i>SLC16A2</i>	-0.56	1.38	0.73	0.003	No
P17568	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	<i>NDUFB7</i>	-0.52	1.81	0.83	0.003	No
Q9NX57	Ras-related protein Rab-20	<i>RAB20</i>	-0.57	1.73	0.8	0.004	No
O95477	ATP-binding cassette sub-family A member 1	<i>ABCA1</i>	-0.58	2.08	0.37	0.005	No
Q14914	Prostaglandin reductase 1	<i>PTGR1</i>	-0.69	1.39	0.84	0.005	No

O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	<i>DDAHI</i>	-0.59	1.71	0.45	0.006	No
Q9Y6M9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	<i>NDUFB9</i>	-0.54	1.53	0.68	0.007	No
Q96LJ7	Dehydrogenase/reductase SDR family member 1	<i>DHRS1</i>	-0.63	1.96	0.43	0.007	No
C9JYW0	Proline-rich protein 24	<i>PRR24</i>	-0.54	1.89	0.23	0.008	No
P42892	Endothelin-converting enzyme 1	<i>ECE1</i>	-0.62	1.5	1	0.008	No
Q9HBL0	Tensin-1	<i>TNS1</i>	-0.65	1.46	1.03	0.009	No
P10620	Micromal glutathione S-transferase 1	<i>MGST1</i>	-0.6	1.67	0.59	0.01	No
O95816	BAG family molecular chaperone regulator 2	<i>BAG2</i>	-0.66	1.29	0.84	0.012	No
O15394	Neural cell adhesion molecule 2	<i>NCAM2</i>	-0.52	1.8	0.36	0.012	No
Q99541	Perilipin-2	<i>PLIN2</i>	-0.57	1.96	0.39	0.012	No
Q9NYU2	UDP-glucose:glycoprotein glucyltransferase 1	<i>UGGT1</i>	-0.56	1.4	0.73	0.013	Yes
Q9UN36	Protein NDRG2	<i>NDRG2</i>	-0.56	1.81	0.69	0.014	Yes
O95479	GDH/6PGL endoplasmic bifunctional protein	<i>H6PD</i>	-0.7	1.43	0.98	0.014	No
P60604	Ubiquitin-conjugating enzyme E2 G2	<i>UBE2G2</i>	-0.54	1.51	0.8	0.016	No
Q16853	Membrane primary amine oxidase	<i>AOC3</i>	-0.57	1.46	0.77	0.016	No
P00325	Alcohol dehydrogenase 1B	<i>ADH1B</i>	-0.56	1.63	0.35	0.016	No
Q99805	Transmembrane 9 superfamily member 2	<i>TM9SF2</i>	-0.61	1.47	0.98	0.022	No
O15127	Secretory carrier-associated membrane protein 2	<i>SCAMP2</i>	-0.63	1.52	0.5	0.032	No
P51148	Ras-related protein Rab-5C	<i>RAB5C</i>	-0.55	1.78	1.06	0.032	No
O60462	Neuropilin-2	<i>NRP2</i>	-0.52	1.65	1.12	0.034	No
Q9Y679	Ancient ubiquitous protein 1	<i>AUP1</i>	-0.69	1.6	0.79	0.035	No
Q0ZGT2	Nexilin	<i>NEXN</i>	-0.59	1.25	0.53	0.036	No
P14384	Carboxypeptidase M	<i>CPM</i>	-0.68	1.46	0.82	0.037	No
Q13586	Stromal interaction molecule 1	<i>STIM1</i>	-0.57	1.26	0.73	0.037	No
Q9BTV4	Transmembrane protein 43	<i>TMEM43</i>	-0.52	1.6	0.85	0.048	No
A0FGR8	Extended synaptotagmin-2	<i>ESYT2</i>	-0.54	1.79	0.82	0.050	No

O43914	TYRO protein tyrine kinase-binding protein	<i>TYROBP</i>	-0.53	1.28	0.88	0.052	No
Q99536	Synaptic vesicle membrane protein VAT-1 homolog	<i>VAT1</i>	-0.56	1.49	0.77	0.054	Yes
Q92959	Solute carrier organic anion transporter family member 2A1	<i>SLCO2A1</i>	-0.59	1.83	0.28	0.056	No
P02656	Apolipoprotein C-III	<i>APOC3</i>	-0.54	1.45	0.66	0.062	No
Q9UBI6	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12	<i>GNGI2</i>	-0.59	1.14	0.73	0.070	No
Q14203	Dynactin subunit 1	<i>DCTN1</i>	-0.59	1.27	1.05	0.076	No
Q8WWP7	GTPase IMAP family member 1	<i>GIMAP1</i>	-0.55	1.37	0.72	0.085	No
O00483	NADH dehydrogenase 1 alpha subcomplex subunit 4	<i>NDUFA4</i>	-0.52	1.66	0.63	0.088	No
O00159	Myin-Ic	<i>MYO1C</i>	-0.56	1.3	0.72	0.099	No
P42765	3-ketoacyl-CoA thiolase, mitochondrial	<i>ACAA2</i>	-0.55	1.6	0.63	0.107	No
Q9NZV5	Selenoprotein N	<i>SELENON</i>	-0.59	1.37	0.98	0.11	No
Q99715	Collagen alpha-1(XII) chain	<i>COL12A1</i>	-0.55	1.41	0.78	0.143	No
O15270	Serine palmitoyltransferase 2	<i>SPTLC2</i>	-0.6	1.52	0.78	0.146	Yes
P22897	Macrophage mannose receptor 1	<i>MRC1</i>	-0.57	1.7	0.31	0.152	No
P24557	Thromboxane-A synthase	<i>TBXAS1</i>	-0.58	1.53	0.6	0.156	No
P53985	Monocarboxylate transporter 1	<i>SLC16A1</i>	-0.58	1.68	0.89	0.159	No
Q9BZZ2	Sialoadhesin	<i>SIGLEC1</i>	-0.56	1.53	0.23	0.16	No
Q01995	Transgelin	<i>TAGLN</i>	-0.55	1.34	0.4	0.167	No
Q02952	A-kinase anchor protein 12	<i>AKAP12</i>	-0.69	1.74	0.62	0.177	No
P14550	Aldo-keto reductase family 1 member A1	<i>AKR1A1</i>	-0.52	1.4	0.89	0.200	No
Q96CW5	Gamma-tubulin complex component 3	<i>TUBGCP3</i>	-0.52	1.36	0.98	0.208	No
P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	<i>ACADVL</i>	-0.56	1.46	0.63	0.215	No
Q4KMQ2	Anoctamin-6	<i>ANO6</i>	-0.7	1.48	0.74	0.220	No
P00387	NADH-cytochrome b5 reductase 3	<i>CYB5R3</i>	-0.66	1.59	0.78	0.239	Yes
P62070	Ras-related protein R-Ras2	<i>RRAS2</i>	-0.71	1.45	0.72	0.240	No

Q86VB7	Scavenger receptor cysteine-rich type 1 protein M130	<i>CDI63</i>	-0.53	1.42	0.31	0.240	No
Q2TAA2	Isoamyl acetate-hydrolyzing esterase 1 homolog	<i>IAHI</i>	-0.58	1.04	0.85	0.245	No
P42356	Phosphatidylinositol 4-kinase alpha	<i>PI4KA</i>	-0.63	1.39	1	0.281	No
P17301	Integrin alpha-2	<i>ITGA2</i>	-0.62	1.68	0.54	0.281	No
P62736	Actin. aortic smooth muscle	<i>ACTA2</i>	-0.55	1.51	0.58	0.294	No
O15031	Plexin-B2	<i>PLXNB2</i>	-0.57	1.4	1.09	0.335	No
Q9NY15	Stabilin-1	<i>STAB1</i>	-0.54	1.44	0.53	0.343	No
Q687X5	Metalloreductase STEAP4	<i>STEAP4</i>	-0.55	1.49	0.44	0.355	No
P40939	Trifunctional enzyme subunit alpha, mitochondrial	<i>HADHA</i>	-0.57	1.36	0.83	0.393	No
Q969Q5	Ras-related protein Rab-24	<i>RAB24</i>	-0.66	1.49	0.89	0.399	No
P07355	Annexin A2	<i>ANXA2</i>	-0.59	1.06	0.81	0.402	No
P50148	Guanine nucleotide-binding protein G(q) subunit alpha	<i>GNAQ</i>	-0.65	1.41	0.85	0.405	No
P06756	Integrin alpha-V	<i>ITGAV</i>	-0.57	1.15	0.9	0.408	No
Q9Y5S1	Transient receptor potential cation channel subfamily V member 2	<i>TRPV2</i>	-0.53	1.65	0.54	0.446	Yes
P61026	Ras-related protein Rab-10	<i>RAB10</i>	-0.68	1.38	0.87	0.446	Yes
Q99969	Retinoic acid receptor responder protein 2	<i>RARRES2</i>	-0.56	1.48	0.59	0.450	No
P46940	Ras GTPase-activating-like protein IQGAP1	<i>IQGAP1</i>	-0.56	1.38	0.92	0.467	No
P04040	Catalase	<i>CAT</i>	-0.53	1.16	0.53	0.524	No
P23142	Fibulin-1	<i>FBLN1</i>	-0.64	1.32	0.48	0.648	No
Q6EMK4	Vasorin	<i>VASN</i>	-0.55	1.59	1.09	0.703	No
Q14344	Guanine nucleotide-binding protein subunit alpha-13	<i>GNAI3</i>	-0.59	1.32	0.71	0.726	No
Q15005	Signal peptidase complex subunit 2	<i>SPCS2</i>	-0.6	1.26	0.89	0.788	No
P34910	Protein EVI2B	<i>EVI2B</i>	-0.52	1.26	0.79	0.825	No
P30536	Translocator protein	<i>TSPO</i>	-0.56	0.98	0.71	0.830	No
P01766	Ig heavy chain V-III region BRO	<i>IGHV3-13</i>	-0.53	1.23	0.69	0.846	No
Q9UIQ6	Leucyl-cystinyl aminopeptidase	<i>LNPEP</i>	-0.6	1.27	0.99	0.856	No

P48960	CD97 antigen	<i>CD97</i>	-0.62	1.25	1.23	0.896	No
P61009	Signal peptidase complex subunit 3	<i>SPCS3</i>	-0.53	1.29	1.08	0.907	No
P63092	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	<i>GNAS</i>	-0.52	1.13	1	0.951	No

^aCompared to the internal standard (pool of all samples); ^bpredicted using TargetScan 7.1. Statistically significant differences between carcinomas and adenomas are indicated in bold font.

Table SIII. Proteins correlating with *IGF2* mRNA.

UniProt accession no.	Gene symbol	Protein name	Pearson's correlation	Median protein ratios ^a		
				Adenoma (n=6)	Carcinoma (n=8)	P-value
P49821	<i>NDUFV1</i>	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	-0.51	1.77	0.53	<0.001
Q9H6X2	<i>ANTXR1</i>	Anthrax toxin receptor 1	-0.52	1.64	0.47	<0.001
Q9NX57	<i>RAB20</i>	Ras-related protein Rab-20	-0.52	1.73	0.8	0.004
Q14914	<i>PTGR1</i>	Prostaglandin reductase 1	-0.58	1.39	0.84	0.005
P42892	<i>ECE1</i>	Endothelin-converting enzyme 1	-0.61	1.5	1	0.008
Q9HBL0	<i>TNSI</i>	Tensin-1	-0.57	1.46	1.03	0.009
P51784	<i>USP11</i>	Ubiquitin carboxyl-terminal hydrolase 11	0.63	0.72	1.98	0.009
P10620	<i>MGST1</i>	Microsomal glutathione S-transferase 1	-0.51	1.67	0.59	0.01
Q9NYU2	<i>UGGT1</i>	UDP-glucose:glycoprotein glucosyltransferase 1	-0.62	1.4	0.73	0.013
O95479	<i>H6PD</i>	GDH/6PGL endoplasmic bifunctional protein	-0.72	1.43	0.98	0.014
Q16853	<i>AOC3</i>	Membrane primary amine oxidase	-0.52	1.46	0.77	0.016
P09972	<i>ALDOC</i>	Fructose-bisphosphate aldolase C	0.52	0.63	1.42	0.021
Q99805	<i>TM9SF2</i>	Transmembrane 9 superfamily member 2	-0.61	1.47	0.98	0.022
P55060	<i>CSE1L</i>	Exportin-2	0.56	0.69	1.19	0.022
Q99735	<i>MGST2</i>	Microsomal glutathione S-transferase 2	-0.56	1.48	0.82	0.024
Q5TC12	<i>ATPAF1</i>	ATP synthase mitochondrial F1 complex assembly factor 1	0.66	0.63	1.29	0.024
Q9NUJ1	<i>ABHD10</i>	Abhydrolase domain-containing protein 10. mitochondrial	0.68	0.58	1.8	0.024
P11216	<i>PYGB</i>	Glycogen phosphorylase. brain form	0.65	0.67	1.6	0.028
P38646	<i>HSPA9</i>	Stress-70 protein. mitochondrial	0.85	0.52	2.03	0.030
Q9H078	<i>CLPB</i>	Caseinolytic peptidase B protein homolog	0.56	0.94	1.42	0.030
Q15437	<i>SEC23B</i>	Protein transport protein Sec23B	0.83	0.8	1.32	0.031
O15127	<i>SCAMP2</i>	Secretory carrier-associated membrane protein 2	-0.53	1.52	0.5	0.032
Q9Y679	<i>AUP1</i>	Ancient ubiquitous protein 1	-0.67	1.6	0.79	0.035
Q9Y2G8	<i>DNAJC16</i>	DnaJ homolog subfamily C member 16	-0.54	1.76	0.75	0.037
P01344	<i>IGF2</i>	Insulin-like growth factor II	0.51	0.3	1.24	0.040
Q6FI81	<i>CIAPIN1</i>	Anamorsin	0.61	0.58	1.18	0.044

Q9GZS3	<i>WDR61</i>	WD repeat-containing protein 61	0.86	0.76	1.3	0.045
Q9NSK0	<i>KLC4</i>	Kinesin light chain 4	0.69	0.83	1.27	0.049
P46379	<i>BAG6</i>	Large proline-rich protein BAG6	0.61	0.91	1.13	0.051
Q16836	<i>HADH</i>	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	0.53	0.59	2.03	0.051
Q9HAV7	<i>GRPEL1</i>	GrpE protein homolog 1, mitochondrial	0.77	0.44	1.15	0.059
P43897	<i>TSFM</i>	Elongation factor Ts, mitochondrial	0.81	0.43	1.36	0.069
Q7Z3D6	<i>C14orf159</i>	UPF0317 protein C14orf159, mitochondrial	0.69	0.82	1.66	0.070
Q9NUD5	<i>ZCCHC3</i>	Zinc finger CCHC domain-containing protein 3	0.57	0.42	1.36	0.076
P36551	<i>CPOX</i>	Coproporphyrinogen-III oxidase, mitochondrial	0.66	0.65	1.21	0.076
Q9Y2Z4	<i>YARS2</i>	Tyrosine--tRNA ligase, mitochondrial	0.76	0.51	1.35	0.081
P60468	<i>SEC61B</i>	Protein transport protein Sec61 subunit beta	-0.54	1.36	0.99	0.084
P40926	<i>MDH2</i>	Malate dehydrogenase, mitochondrial	0.54	0.79	1.77	0.086
P00505	<i>GOT2</i>	Aspartate aminotransferase, mitochondrial	0.71	0.48	1.6	0.086
Q12931	<i>TRAP1</i>	Heat shock protein 75 kDa, mitochondrial	0.63	0.7	1.07	0.088
Q9UNF1	<i>MAGED2</i>	Melanoma-associated antigen D2	0.95	0.57	1.48	0.088
Q8N183	<i>NDUFAF2</i>	Mimitin, mitochondrial	0.61	0.68	1.51	0.09
Q96I99	<i>SUCLG2</i>	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	0.59	0.78	1.8	0.091
Q15185	<i>PTGES3</i>	Prostaglandin E synthase 3	0.68	0.48	1.15	0.092
Q8TCS8	<i>PNPT1</i>	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	0.58	0.85	1.76	0.093
P80723	<i>BASPI</i>	Brain acid soluble protein 1	0.64	0.52	1.12	0.093
P16070	<i>CD44</i>	CD44 antigen	0.55	0.78	1.45	0.099
Q9UBQ0	<i>VPS29</i>	Vacuolar protein sorting-associated protein 29	0.6	0.88	1.15	0.105
P78347	<i>GTF2I</i>	General transcription factor II-I	0.81	0.8	1.11	0.106
Q15545	<i>TAF7</i>	Transcription initiation factor TFIID subunit 7	0.78	0.57	1.14	0.108
Q13283	<i>G3BP1</i>	Ras GTPase-activating protein-binding protein 1	0.86	0.8	1.22	0.108
Q9BYD2	<i>MRPL9</i>	39S ribosomal protein L9, mitochondrial	0.91	0.8	1.12	0.109
Q9BWH2	<i>FUNDC2</i>	FUN14 domain-containing protein 2	0.66	0.68	1.55	0.110
Q9NZV5	<i>SEPN1</i>	Selenoprotein N	-0.53	1.37	0.98	0.11
Q9P0B6	<i>CCDC167</i>	Coiled-coil domain-containing protein 167	0.8	0.81	1.1	0.113
Q9H3N1	<i>TMX1</i>	Thioredoxin-related transmembrane protein 1	-0.55	1.4	1.03	0.114

Q96EY8	<i>MMAB</i>	Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	0.58	0.6	1.24	0.115
P04035	<i>HMGCR</i>	3-hydroxy-3-methylglutaryl-coenzyme A reductase	0.52	0.25	0.4	0.119
P09651	<i>HNRNPA1</i>	Heterogeneous nuclear ribonucleoprotein A1	0.68	0.92	1.45	0.128
Q9H4G0	<i>EPB41L1</i>	Band 4.1-like protein 1	0.59	0.69	1.12	0.138
P49675	<i>STAR</i>	Steroidogenic acute regulatory protein, mitochondrial	0.9	0.56	1.51	0.138
Q8NFV4	<i>ABHD11</i>	Abhydrolase domain-containing protein 11	0.69	0.41	0.8	0.142
O94826	<i>TOMM70A</i>	Mitochondrial import receptor subunit TOM70	0.83	0.87	1.52	0.142
Q15555	<i>MAPRE2</i>	Microtubule-associated protein RP/EB family member 2	0.71	0.87	1.4	0.150
O00170	<i>AIP</i>	AH receptor-interacting protein	0.69	0.71	1	0.153
Q9GZT6	<i>CCDC90B</i>	Coiled-coil domain-containing protein 90B, mitochondrial	0.57	0.76	1.4	0.158
P53985	<i>SLC16A1</i>	Monocarboxylate transporter 1	-0.58	1.68	0.89	0.159
Q8WWM7	<i>ATXN2L</i>	Ataxin-2-like protein	0.53	0.82	1.25	0.159
Q6Y7W6	<i>GIGYF2</i>	PERQ amino acid-rich with GYF domain-containing protein 2	0.84	0.88	1.13	0.160
Q9Y383	<i>LUC7L2</i>	Putative RNA-binding protein Luc7-like 2	0.94	0.63	1.46	0.164
P29350	<i>PTPN6</i>	Tyrosine-protein phosphatase non-receptor type 6	0.53	0.82	0.97	0.17
P38606	<i>ATP6V1A</i>	V-type proton ATPase catalytic subunit A	0.59	0.93	1.39	0.172
P50750	<i>CDK9</i>	Cyclin-dependent kinase 9	0.52	0.86	1.31	0.174
Q13190	<i>STX5</i>	Syntaxin-5	-0.53	1.22	0.96	0.176
P53701	<i>HCCS</i>	Cytochrome c-type heme lyase	0.62	0.56	0.71	0.177
P30048	<i>PRDX3</i>	Thioredoxin-dependent peroxide reductase, mitochondrial	0.92	0.55	1.5	0.179
Q6IPR1	<i>LYRM5</i>	LYR motif-containing protein 5	0.62	0.29	0.93	0.179
Q53GQ0	<i>HSD17B12</i>	Estradiol 17-beta-dehydrogenase 12	-0.52	1.3	0.94	0.182
Q14694	<i>USP10</i>	Ubiquitin carboxyl-terminal hydrolase 10	0.81	0.88	1.33	0.183
Q96DA6	<i>DNAJC19</i>	Mitochondrial import inner membrane translocase subunit TIM14	0.57	0.78	1.4	0.187
Q9H444	<i>CHMP4B</i>	Charged multivesicular body protein 4b	0.54	0.67	1.36	0.187
Q9Y3D7	<i>PAM16</i>	Mitochondrial import inner membrane translocase subunit TIM16	0.59	0.61	1.42	0.189
Q08426	<i>EHHADH</i>	Peroxisomal bifunctional enzyme	0.57	0.7	1.43	0.192
Q5T1M5	<i>FKBP15</i>	FK506-binding protein 15	0.61	0.77	0.99	0.195
Q14498	<i>RBM39</i>	RNA-binding protein 39	0.64	1.17	1.29	0.195
Q9BX68	<i>HINT2</i>	Histidine triad nucleotide-binding protein 2, mitochondrial	0.56	0.58	0.91	0.197

P08865	<i>RPSA</i>	40S ribosomal protein SA	0.59	1.04	1.25	0.200
P51553	<i>IDH3G</i>	Isocitrate dehydrogenase [NAD] subunit gamma. mitochondrial	0.54	0.76	1.26	0.201
O94925	<i>GLS</i>	Glutaminase kidney isoform. mitochondrial	0.73	0.66	0.83	0.203
P30042	<i>C21orf33</i>	Isoform Short of ES1 protein homolog. mitochondrial	0.75	0.78	1.15	0.204
Q9BRX2	<i>PELO</i>	Protein pelota homolog	0.63	0.79	1.2	0.206
Q96CW5	<i>TUBGCP3</i>	Gamma-tubulin complex component 3	-0.53	1.36	0.98	0.208
O95166	<i>GABARAP</i>	Gamma-aminobutyric acid receptor-associated protein	0.6	0.8	1.37	0.209
Q9UGM6	<i>WARS2</i>	Tryptophan--tRNA ligase. mitochondrial	0.62	0.83	1.27	0.210
P42704	<i>LRPPRC</i>	Leucine-rich PPR motif-containing protein. mitochondrial	0.9	0.98	1.32	0.212
Q7L2J0	<i>MEPCE</i>	7SK snRNA methylphosphate capping enzyme	0.83	0.85	1.37	0.213
Q9UKM9	<i>RALY</i>	RNA-binding protein Raly	0.9	0.99	1.07	0.214
Q9H2W6	<i>MRPL46</i>	39S ribosomal protein L46. mitochondrial	0.76	0.66	1	0.216
Q8N7H5	<i>PAF1</i>	RNA polymerase II-associated factor 1 homolog	0.71	0.94	1.19	0.217
Q4KMQ2	<i>ANO6</i>	Anoctamin-6	-0.6	1.48	0.74	0.220
O75023	<i>LILRB5</i>	Leukocyte immunoglobulin-like receptor subfamily B member 5	0.75	0.28	0.39	0.221
O00330	<i>PDHX</i>	Pyruvate dehydrogenase protein X component. mitochondrial	0.52	0.88	1.34	0.222
P0CB43	<i>FAM203A/FAM20</i>	Protein FAM203B	0.9	0.87	1.06	0.227
Q13057	<i>COASY</i>	Bifunctional coenzyme A synthase	0.82	0.88	1.04	0.229
P30038	<i>ALDH4A1</i>	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	0.85	0.62	1.23	0.230
Q14197	<i>ICT1</i>	Peptidyl-tRNA hydrolase ICT1, mitochondrial	0.94	0.68	0.94	0.234
O95573	<i>ACSL3</i>	Long-chain-fatty-acid--CoA ligase 3	-0.52	1.47	0.8	0.236
Q99757	<i>TXN2</i>	Thioredoxin, mitochondrial	0.56	0.41	0.86	0.237
Q9H3Z4	<i>DNAJC5</i>	DnaJ homolog subfamily C member 5	0.51	0.88	1.39	0.238
Q96RF0	<i>SNX18</i>	Sorting nexin-18	0.97	0.86	1	0.240
P62070	<i>RRAS2</i>	Ras-related protein R-Ras2	-0.55	1.45	0.72	0.240
Q2TAY7	<i>SMU1</i>	WD40 repeat-containing protein SMU1	0.58	0.98	1.38	0.244
O75521	<i>ECI2</i>	Enoyl-CoA delta isomerase 2, mitochondrial	0.52	1.03	1.04	0.245
Q8NBN7	<i>RDH13</i>	Retinol dehydrogenase 13	0.9	0.63	0.78	0.245
Q9HCU5	<i>PREB</i>	Prolactin regulatory element-binding protein	-0.57	1.29	0.91	0.250
Q8N5N7	<i>MRPL50</i>	39S ribosomal protein L50, mitochondrial	0.8	0.64	0.9	0.252

P46100	<i>ATRX</i>	Transcriptional regulator ATRX	0.71	0.81	1.27	0.253
Q9NXV6	<i>CDKN2AIP</i>	CDKN2A-interacting protein	0.75	0.98	1.19	0.254
Q9Y5K8	<i>ATP6V1D</i>	V-type proton ATPase subunit D	0.51	0.77	1.08	0.266
Q92878	<i>RAD50</i>	DNA repair protein RAD50	0.72	0.97	1.28	0.268
Q96I45	<i>TMEM141</i>	Transmembrane protein 141	0.6	0.81	0.92	0.269
Q04446	<i>GBE1</i>	1,4-alpha-glucan-branching enzyme	0.84	0.89	1.29	0.270
Q96DV4	<i>MRPL38</i>	39S ribosomal protein L38, mitochondrial	0.94	0.87	0.97	0.274
Q9H0F6	<i>SHARPIN</i>	Sharpin	0.86	0.7	1.11	0.277
Q13576	<i>IQGAP2</i>	Ras GTPase-activating-like protein IQGAP2	0.54	0.86	1.09	0.279
Q15119	<i>PKD2</i>	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, mitochondrial	0.62	0.86	0.77	0.279
Q9UN37	<i>VPS4A</i>	Vacuolar protein sorting-associated protein 4A	0.53	0.89	1.11	0.280
P42356	<i>PI4KA</i>	Phosphatidylinositol 4-kinase alpha	-0.52	1.39	1	0.281
P17301	<i>ITGA2</i>	Integrin alpha-2	-0.51	1.68	0.54	0.281
P36543	<i>ATP6V1E1</i>	V-type proton ATPase subunit E 1	0.59	0.74	1.31	0.284
Q9P032	<i>NDUFAF4</i>	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor	0.54	0.74	0.78	0.284
Q6PI48	<i>DARS2</i>	Aspartate--tRNA ligase, mitochondrial	0.53	0.97	0.79	0.284
O75427	<i>LRCH4</i>	Leucine-rich repeat and calponin homology domain-containing protein 4	0.83	0.95	0.96	0.287
Q9Y5X3	<i>SNX5</i>	Sorting nexin-5	0.52	0.58	0.77	0.288
O95202	<i>LETM1</i>	LETM1 and EF-hand domain-containing protein 1, mitochondrial	0.61	0.85	1.19	0.293
C4AMC7	<i>WASH3P</i> <i>ATP5J2-</i>	Putative WAS protein family homolog 3	0.61	0.82	0.96	0.293
O75127	<i>PTCD1/PT</i>	Pentatricopeptide repeat-containing protein 1	0.86	0.76	1.14	0.296
Q8N8Q8	<i>COX18</i>	Mitochondrial inner membrane protein COX18	0.76	0.96	0.88	0.301
Q92900	<i>UPF1</i>	Regulator of nonsense transcripts 1	0.73	0.87	1.2	0.301
O75208	<i>COQ9</i>	Ubiquinone biosynthesis protein COQ9, mitochondrial	0.66	0.74	0.61	0.306
Q14847	<i>LASP1</i>	LIM and SH3 domain protein 1	0.8	1.06	1.12	0.309
Q02218	<i>OGDH</i>	2-oxoglutarate dehydrogenase, mitochondrial	0.59	1.07	1.24	0.313
Q14061	<i>COX17</i>	Cytochrome c oxidase copper chaperone	0.68	0.8	0.71	0.318
Q8N983	<i>MRPL43</i>	39S ribosomal protein L43, mitochondrial	0.86	0.82	1.09	0.318
Q9BX59	<i>TAPBPL</i>	Tapasin-related protein	0.65	0.99	0.88	0.318
Q6P996	<i>PDXDC1</i>	Pyridoxal-dependent decarboxylase domain-containing protein 1	0.6	0.88	1.29	0.320

O15119	<i>TBX3</i>	T-box transcription factor TBX3	0.52	0.67	1.02	0.335
P49411	<i>TUFM</i>	Elongation factor Tu, mitochondrial	0.84	0.55	0.67	0.340
Q9NUQ8	<i>ABCF3</i>	ATP-binding cassette sub-family F member 3	0.89	0.81	1.04	0.341
Q8TAE8	<i>GADD45GIP1</i>	Growth arrest and DNA damage-inducible proteins-interacting protein 1	0.83	0.89	0.96	0.350
P51151	<i>RAB9A</i>	Ras-related protein Rab-9A	0.85	1.13	1.38	0.352
O00291	<i>HIP1</i>	Huntingtin-interacting protein 1	0.77	0.88	0.96	0.354
Q9BYD1	<i>MRPL13</i>	39S ribosomal protein L13, mitochondrial	0.66	1.17	1.4	0.358
O75348	<i>ATP6V1G1</i>	V-type proton ATPase subunit G 1	0.67	0.71	0.91	0.363
Q02318	<i>CYP27A1</i>	Sterol 26-hydroxylase, mitochondrial	0.78	0.85	0.83	0.364
Q8TDB4	<i>MGARP</i>	Uncharacterized protein C4orf49	0.68	0.81	1.33	0.367
Q86XL3	<i>ANKLE2</i>	Ankyrin repeat and LEM domain-containing protein 2	0.57	1.02	1.05	0.385
Q53H12	<i>AGK</i>	Acylglycerol kinase, mitochondrial	0.77	1.03	1.27	0.388
Q9Y2S7	<i>POLDIP2</i>	Polymerase delta-interacting protein 2	0.91	0.95	0.98	0.389
Q92820	<i>GGH</i>	Gamma-glutamyl hydrolase	0.64	0.97	1.4	0.395
Q96PK6	<i>RBM14</i>	RNA-binding protein 14	0.7	0.96	1.16	0.397
Q14683	<i>SMC1A</i>	Structural maintenance of chromosomes protein 1A	0.54	0.84	1.19	0.404
P46783	<i>RPS10</i>	40S ribosomal protein S10	0.75	1.1	1.27	0.412
Q96CM8	<i>ACSF2</i>	Acyl-CoA synthetase family member 2, mitochondrial	0.91	1.09	1.34	0.413
O95793	<i>STAU1</i>	Isoform Short of Double-stranded RNA-binding protein Staufen homolog 1	0.61	0.96	0.83	0.418
P46199	<i>MTIF2</i>	Translation initiation factor IF-2, mitochondrial	0.76	0.96	1.01	0.427
Q07955	<i>SRSF1</i>	Isoform ASF-3 of Serine/arginine-rich splicing factor 1	0.6	1.01	1.14	0.437
Q96I24	<i>FUBP3</i>	Far upstream element-binding protein 3	0.86	0.92	1.23	0.437
Q96CW1	<i>AP2M1</i>	AP-2 complex subunit	0.57	1.17	1.18	0.441
Q9NP92	<i>MRPS30</i>	28S ribosomal protein S30, mitochondrial	0.69	1.18	1.17	0.443
P22626	<i>HNRNPA2B1</i>	Heterogeneous nuclear ribonucleoproteins A2/B1	0.7	1.2	1.13	0.444
P61026	<i>RAB10</i>	Ras-related protein Rab-10	-0.59	1.38	0.87	0.446
O43399	<i>TPD52L2</i>	Tumor protein D54	0.51	0.54	1.06	0.452
P51153	<i>RAB13</i>	Ras-related protein Rab-13	0.63	1.07	1.16	0.453
Q9NNW7	<i>TXNRD2</i>	Thioredoxin reductase 2, mitochondrial	0.8	0.95	0.72	0.459
Q7Z7H8	<i>MRPL10</i>	39S ribosomal protein L10, mitochondrial	0.8	1.06	0.96	0.461

Q9BQC6	<i>MRP63</i>	Ribosomal protein 63. mitochondrial	0.91	1.03	0.91	0.471
O15228	<i>GNPAT</i>	Dihydroxyacetone phosphate acyltransferase	0.58	1.17	1.33	0.471
Q9BXP5	<i>SRRT</i>	Serrate RNA effector molecule homolog	0.53	0.9	1.3	0.483
Q6P2E9	<i>EDC4</i>	Enhancer of mRNA-decapping protein 4	0.85	1.03	0.86	0.486
Q96ER9	<i>CCDC51</i>	Coiled-coil domain-containing protein 51	0.53	1.04	0.72	0.486
P14927	<i>UQCRB</i>	Cytochrome b-c1 complex subunit 7	0.66	0.9	1.31	0.488
Q7L099	<i>RUFY3</i>	Protein RUFY3	0.79	0.99	0.87	0.497
Q7L2E3	<i>DHX30</i>	Putative ATP-dependent RNA helicase DHX30	0.65	1.09	0.96	0.503
Q9H019	<i>FAM54B</i>	Protein FAM54B	0.53	1	0.93	0.515
P33897	<i>ABCD1</i>	ATP-binding cassette sub-family D member 1	0.56	1.18	1.2	0.516
P51114	<i>FXR1</i>	Fragile X mental retardation syndrome-related protein 1	0.63	1.09	0.87	0.540
P62753	<i>RPS6</i>	40S ribosomal protein S6	0.71	0.92	1.13	0.563
Q8WUD1	<i>RAB2B</i>	Ras-related protein Rab-2B	-0.63	1.21	1.03	0.563
P62314	<i>SNRPD1</i>	Small nuclear ribonucleoprotein Sm D1	0.65	1.07	1.04	0.582
Q92615	<i>LARP4B</i>	La-related protein 4B	0.54	1.11	1.04	0.593
Q9BYN8	<i>MRPS26</i>	28S ribosomal protein S26, mitochondrial	0.83	0.95	0.81	0.603
P84103	<i>SRSF3</i>	Serine/arginine-rich splicing factor 3	0.52	1.18	1.45	0.607
Q7Z2W9	<i>MRPL21</i>	39S ribosomal protein L21, mitochondrial	0.78	1.19	1.11	0.607
Q5T653	<i>MRPL2</i>	39S ribosomal protein L2, mitochondrial	0.77	1.12	1.13	0.607
Q13151	<i>HNRNPA0</i>	Heterogeneous nuclear ribonucleoprotein A0	0.7	1.13	0.79	0.614
Q14165	<i>MLEC</i>	Malectin	0.63	0.87	0.97	0.617
Q14258	<i>TRIM25</i>	E3 ubiquitin/ISG15 ligase TRIM25	0.76	1.05	0.93	0.635
Q8NFAQ8	<i>TOR1AIP2</i>	Torsin-1A-interacting protein 2	0.52	1.26	0.95	0.647
O15254	<i>ACOX3</i>	Peroxisomal acyl-coenzyme A oxidase 3	0.65	1.12	1.06	0.647
Q9BZE1	<i>MRPL37</i>	39S ribosomal protein L37, mitochondrial	0.78	1.1	0.99	0.661
O14976	<i>GAK</i>	Cyclin-G-associated kinase	0.78	1.11	1	0.665
Q9P0M9	<i>MRPL27</i>	39S ribosomal protein L27. mitochondrial	0.56	1.12	0.87	0.700
O15027	<i>SEC16A</i>	Protein transport protein Sec16A	0.65	1.33	0.89	0.703
P13473	<i>LAMP2</i>	Lysosome-associated membrane glycoprotein 2	0.56	1.1	1.42	0.707
Q9BUJ2	<i>HNRNPUL1</i>	Heterogeneous nuclear ribonucleoprotein U-like protein 1	0.59	1.14	1.12	0.731

Q9UGQ2	<i>CACFD1</i>	Calcium channel flower homolog	0.59	1.14	1.17	0.743
Q8IXB1	<i>DNAJC10</i>	DnaJ homolog subfamily C member 10	-0.56	1.12	1.22	0.77
Q9Y676	<i>MRPS18B</i>	28S ribosomal protein S18b, mitochondrial	0.58	1	1.06	0.771
Q9H3G5	<i>CPVL</i>	Probable serine carboxypeptidase CPVL	0.61	0.86	0.94	0.777
P23246	<i>SFPQ</i>	Splicing factor, proline- and glutamine-rich	0.68	1.36	1.45	0.788
P29590	<i>PML</i>	Isoform PML-14 of Protein PML	0.79	1.1	1	0.793
Q9H270	<i>VPS11</i>	Vacuolar protein sorting-associated protein 11 homolog	0.68	1.12	1.01	0.800
P22307	<i>SCP2</i>	Isoform SCP2 of Non-specific lipid-transfer protein	0.61	1.05	1.06	0.832
P15924	<i>DSP</i>	Isoform DPII of Desmoplakin	0.65	1.01	0.92	0.843
Q9UL46	<i>PSME2</i>	Proteasome activator complex subunit 2	-0.62	1.21	1.01	0.845
P17252	<i>PRKCA</i>	Protein kinase C alpha type	0.65	1.32	1.02	0.867
Q8N128	<i>FAM177A1</i>	Protein FAM177A1	-0.55	1.16	1.07	0.882
P48960	<i>CD97</i>	CD97 antigen	-0.53	1.25	1.23	0.896
Q8N5G0	<i>C4orf52</i>	Uncharacterized protein C4orf52	0.53	1.38	1.28	0.927
Q5HYI8	<i>RABL3</i>	Rab-like protein 3	0.57	1.02	0.95	0.962
P51571	<i>SSR4</i>	Translocon-associated protein subunit delta	-0.54	1.17	1.13	0.964

^aCompared to the internal standard (pool of all samples). Statistically significant differences between carcinomas and adenomas are indicated in bold font.

Table SIV. Proteins correlating with *H19* RNA.

UniProt accession no.	Gene symbol	Protein name	Pearson's correlation	Median protein ratios ^a		
				Adenoma (n=6)	Carcinoma (n=8)	P-value
O43676	<i>NDUFB3</i>	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	0.67	1.76	0.57	<0.001
P62341	<i>SELT</i>	Selenoprotein T	0.54	1.59	0.84	0.001
O95302	<i>FKBP9</i>	Peptidyl-prolyl cis-trans isomerase FKBP9	0.63	1.5	0.88	0.001
P17568	<i>NDUFB7</i>	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	0.71	1.81	0.83	0.003
Q14914	<i>PTGR1</i>	Prostaglandin reductase 1	0.66	1.39	0.84	0.005
O94760	<i>DDAH1</i>	N(G).N(G)-dimethylarginine dimethylaminohydrolase 1	0.86	1.71	0.45	0.006
O43301	<i>HSPA12A</i>	Heat shock 70 kDa protein 12A	0.59	1.75	0.66	0.007
O95292	<i>VAPB</i>	Vesicle-associated membrane protein-associated protein B/C	0.54	1.38	0.73	0.007
Q0IIM8	<i>TBC1D8B</i>	TBC1 domain family member 8B	0.56	1.29	0.75	0.008
P51784	<i>USP11</i>	Ubiquitin carboxyl-terminal hydrolase 11	-0.56	0.72	1.98	0.009
P26885	<i>FKBP2</i>	Peptidyl-prolyl cis-trans isomerase FKBP2	0.6	1.45	0.68	0.011
O95816	<i>BAG2</i>	BAG family molecular chaperone regulator 2	0.65	1.29	0.84	0.012
Q99541	<i>PLIN2</i>	Perilipin-2	0.56	1.96	0.39	0.012
O43181	<i>NDUFS4</i>	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	0.53	1.48	0.67	0.013
Q16853	<i>AOC3</i>	Membrane primary amine oxidase	0.63	1.46	0.77	0.016
P00325	<i>ADH1B</i>	Alcohol dehydrogenase 1B	0.62	1.63	0.35	0.016
Q9HBK9	<i>AS3MT</i>	Arsenite methyltransferase	0.57	1.61	0.82	0.029
Q15493	<i>RGN</i>	Regucalcin	0.74	1.34	0.75	0.030
P15121	<i>AKR1B1</i>	Aldose reductase	0.82	1.85	0.44	0.034
O60462	<i>NRP2</i>	Isoform B0 of Neuropilin-2	0.55	1.65	1.12	0.034
P14384	<i>CPM</i>	Carboxypeptidase M	0.64	1.46	0.82	0.037
Q9P2B2	<i>PTGFRN</i>	Prostaglandin F2 receptor negative regulator	0.62	1.46	0.48	0.040
P51787	<i>KCNQ1</i>	Potassium voltage-gated channel subfamily KQT member 1	0.59	2.27	0.44	0.049
Q12981	<i>BNIP1</i>	Vesicle transport protein SEC20	0.66	1.48	1.11	0.052
Q99536	<i>VAT1</i>	Synaptic vesicle membrane protein VAT-1 homolog	0.57	1.49	0.77	0.054
P07339	<i>CTSD</i>	Cathepsin D	0.51	1.41	0.7	0.066

Q9UBI6	<i>GNG12</i>	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12	0.63	1.14	0.73	0.070
P54709	<i>ATP1B3</i>	Sodium/potassium-transporting ATPase subunit beta-3	0.52	1.53	0.82	0.075
P15311	<i>EZR</i>	Ezrin	0.7	1.17	0.79	0.116
Q00765	<i>REEP5</i>	Receptor expression-enhancing protein 5	0.64	1.38	0.94	0.118
O96005	<i>CLPTM1</i>	Cleft lip and palate transmembrane protein 1	0.6	1.31	0.9	0.127
P21399	<i>ACO1</i>	Cytoplasmic aconitate hydratase ATP-	0.51	1.37	0.99	0.144
P46063	<i>RECQL</i>	dependent DNA helicase	-0.6	0.92	1.09	0.147
Q96PU8	<i>QKI</i>	Q1 Protein quaking	-0.51	1.04	1.45	0.151
Q8WTV0	<i>SCARB1</i>	Scavenger receptor class B member 1	0.76	1.35	0.82	0.155
P05023	<i>ATP1A1</i>	Isoform Short of Sodium/potassium-transporting ATPase subunit alpha-	0.59	1.26	0.93	0.167
Q99747	<i>NAPG</i>	Gamma-soluble NSF attachment protein	0.58	1.23	1.06	0.188
Q99442	<i>SEC62</i>	Translocation protein SEC62	0.55	1.3	1.05	0.206
P16930	<i>FAH</i>	Fumarylacetoacetase	0.73	1.15	0.83	0.213
P48163	<i>ME1</i>	NADP-dependent malic enzyme	0.62	1.31	0.75	0.213
P30086	<i>PEBP1</i>	Phosphatidylethanolamine-binding protein 1	0.6	1.15	0.96	0.221
Q09666	<i>AHNAK</i>	Neuroblast differentiation-associated protein AHNAK	0.79	1.2	0.79	0.221
P00167	<i>CYB5A</i>	Cytochrome b5	0.52	1.23	0.88	0.244
Q8TAT6	<i>NPLOC4</i>	Nuclear protein localization protein 4 homolog	-0.58	1.04	1.33	0.259
Q8NCA5	<i>FAM98A</i>	Protein FAM98A	-0.55	1.08	1.12	0.269
P10301	<i>RRAS</i>	Ras-related protein R-Ras	0.56	1.26	0.91	0.277
P40925	<i>MDH1</i>	Malate dehydrogenase. cytoplasmic	0.54	1.24	0.9	0.278
A6NCN2		Keratin-81-like protein	0.52	0.05	0.1	0.308
O76021	<i>RSL1D1</i>	Ribosomal L1 domain-containing protein 1	-0.52	1.01	1.11	0.318
Q9NSB4	<i>KRT82</i>	Keratin. type II cuticular Hb2 Tissue alpha-	0.52	0.05	0.08	0.320
P04066	<i>FUCA1</i>	L-fucosidase	0.56	1.25	0.98	0.367
P16083	<i>NQO2</i>	Ribosyldihydronicotinamide dehydrogenase [quinone]	0.71	1.14	0.9	0.424
P09382	<i>LGALS1</i>	Galectin-1	0.57	0.77	1.31	0.481
P29992	<i>GNA11</i>	Guanine nucleotide-binding protein subunit alpha-11	0.76	1.13	0.91	0.519
P61916	<i>NPC2</i>	Epididymal secretory protein E1	0.56	1	0.99	0.530
P46087	<i>NOP2</i>	Putative ribosomal RNA methyltransferase NOP2	-0.53	1.04	1.07	0.533

O43493	<i>TGOLN2</i>	Isoform TGN46 of Trans-Golgi network integral membrane protein 2	0.62	1.15	0.95	0.552
P54289	<i>CACNA2D1</i>	Voltage-dependent calcium channel subunit alpha-2/delta-1	0.68	1.28	0.92	0.571
P36871	<i>PGM1</i>	Phosphoglucomutase-1	0.56	1.19	1.05	0.583
P80303	<i>NUCB2</i>	Nucleobindin-2	0.58	1.36	0.86	0.61
O00186	<i>STXBP3</i>	Syntaxin-binding protein 3	0.56	1.24	0.92	0.654
Q9UKS6	<i>PACSIN3</i>	Protein kinase C and casein kinase substrate in neurons protein 3	0.69	1.29	0.86	0.674
Q12959	<i>DLG1</i>	Disks large homolog 1	0.53	0.9	0.76	0.703
O14745	<i>SLC9A3R1</i>	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	0.61	1.11	0.84	0.716
P62745	<i>RHOB</i>	Rho-related GTP-binding protein RhoB	0.57	0.94	0.96	0.814
P12955	<i>PEPD</i>	Xaa-Pro dipeptidase	0.55	1.17	1.33	0.820
Q13042	<i>CDC16</i>	Cell division cycle protein 16 homolog	-0.56	1.29	1.22	0.821
O75368	<i>SH3BGRL</i>	SH3 domain-binding glutamic acid-rich-like protein	0.65	0.96	1.03	0.883
P35241	<i>RDX</i>	Radixin	0.59	0.9	0.64	0.963
Q13449	<i>LSAMP</i>	Limbic system-associated membrane protein	0.52	1.17	0.74	0.966
Q8N335	<i>GPD1L</i>	Glycerol-3-phosphate dehydrogenase 1-like protein	0.69	0.99	0.94	0.997

^aCompared to the internal standard (pool of all samples). Statistically significant differences between carcinomas and adenomas are indicated in bold font.

Table SV. Proteins exhibiting an inverse correlation with *miR-483-3p*.

UniProt accession no.	Protein name	Gene Symbol	Pearson's correlation	Median protein ratios ^a			Predicted targets ^b
				Adenoma (n=6)	Carcinoma (n=8)	P-value	
O95479	GDH/6PGL endoplasmic bifunctional protein	<i>H6PD</i>	-0.53	1.43	0.98	0.01	No
O95816	BAG family molecular chaperone regulator 2	<i>BAG2</i>	-0.53	1.29	0.84	0.01	No
P60604	Ubiquitin-conjugating enzyme E2 G2	<i>UBE2G2</i>	-0.58	1.51	0.8	0.02	Yes
Q14203	Dynactin subunit 1	<i>DCTN1</i>	-0.54	1.27	1.05	0.08	No
Q02952	A-kinase anchor protein 12	<i>AKAP12</i>	-0.53	1.74	0.62	0.18	No
Q8NBL1	Protein O-glucosyltransferase 1	<i>POGLUT1</i>	-0.56	1.39	1.12	0.18	No
Q9NR31	GTP-binding protein SAR1a	<i>SAR1A</i>	-0.54	1.23	1.13	0.4	No

^aCompared to the internal standard (pool of all samples); ^btargets predicted using TargetScan 7.1. Statistically significant differences between carcinomas and adenomas are indicated in bold font.

Table SVI. Proteins exhibiting an inverse correlation with *miR-675*.

UniProt accession no.	Protein name	Gene symbol	Pearson correlation	Median protein ratios ^a			Predicted targets ^b
				Adenomas (n=6)	Carcinomas (n=8)	P-value	
P24043	Laminin subunit alpha-2	<i>LAMA2</i>	-0.57	1.08	1.73	0.22	No
Q9H4G4	Golgi-associated plant pathogenesis-related protein 1	<i>GLIPR2</i>	-0.57	0.96	1.25	0.27	No
P30499	HLA class I histocompatibility antigen, Cw-1 alpha chain	<i>HLA-C</i>	-0.59	0.86	1.46	0.3	No
Q9H019	Protein FAM54B/ Mitochondrial fission regulator 1-like	<i>MTFR1L</i>	-0.54	1	0.93	0.51	No
P11182	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	<i>DBT</i>	-0.56	1.19	0.77	0.57	No
Q03169	Tumor necrosis factor alpha-induced protein 2	<i>TNFAIP2</i>	-0.57	1.29	1.1	0.62	Yes
O95782	AP-2 complex subunit alpha-1	<i>AP2A1</i>	-0.58	1.22	1.21	0.67	No
P09496	Clathrin light chain A	<i>CLTA</i>	-0.6	0.98	1.11	0.81	No
P02649	Apolipoprotein E	<i>APOE</i>	-0.52	0.84	1.11	0.94	No
Q96CX2	BTB/POZ domain-containing protein KCTD12	<i>KCTD12</i>	-0.56	1.26	1.19	0.97	No
Q16698	2,4-dienoyl-CoA reductase, mitochondrial	<i>DECRI</i>	-0.63	1.27	1.04	1	No

^aCompared to the internal standard (pool of all samples); ^bPredicted using TargetScan 7.1.

Table SVII. Results from ingenuity pathway analysis of proteins correlating with *IGF2* mRNA analysis.

Top networks		
Associated network functions	Score	
RNA post-transcriptional modification, Gene expression, Molecular transport	71	
Carbohydrate metabolism, Lipid metabolism, Small molecule biochemistry	49	
Protein trafficking, Amino acid metabolism, Small molecule biochemistry	47	
Cell morphology, Infectious disease, Post-translational modification	32	
Hereditary disorder, Metabolic disease, Nucleic acid metabolism	26	

Top biological functions	P-value	No. of molecules
Molecular and cellular functions		
Energy production	1.15E-04 - 2.34E-02	11
Lipid metabolism	1.15E-04 - 4.63E-02	31
Small molecule biochemistry	1.15E-04 - 4.63E-02	44
RNA post-transcriptional modification	2.07E-04 - 5.12E-02	12
Molecular transport	2.48E-04 - 4.63E-02	46
Physiological system development and function		
Embryonic development	3.69E-03 - 4.63E-02	10
Hematological system development and function	3.69E-03 - 4.63E-02	10
Hematopoiesis	3.69E-03 - 4.63E-02	5
Lymphoid tissue structure and development	3.69E-03 - 2.34E-02	2
Organ development	3.69E-03 - 4.63E-02	9

Top canonical pathways	P-value	Ratio
Fatty acid beta-oxidation I	4.03E-04	4/45 (0.089)
Fatty acid beta-oxidation III (Unsaturated, odd number)	4.11E-04	2/5 (0.4)
Telomere extension by telomerase	6.61E-04	3/17 (0.176)
Mitochondrial dysfunction	1.15E-03	7/174 (0.04)
NRF2-mediated oxidative stress response	1.34E-03	8/192 (0.042)

Top Molecules	Expression value
Other upregulated molecules	
HSPA9	1.51
HADH	1.44
USP11	1.26
ABHD10	1.22
GOT2	1.12
SUCLG2	1.02
MDH2	0.98
PRDX3	0.95
STAR	0.95
ZCCHC3	0.94
Other downregulated molecules	
NDUFV1	-1.24
ANTXR1	-1.17
ITGA2	-1.14
MGST1	-1.08
SCAMP2	-1.02
DNAJC16	-1.01
RAB20	-0.93
AUP1	-0.81
SLC16A1	-0.79
ANO6	-0.74

Top upstream regulators	P-value
HNF4A	3.40E-07
TP53	7.93E-07
KHDRBS1	3.71E-04
MYC	3.23E-03

HOXD10

5.11E-03
