

**Supplemental Table 2.** Proteins showing differential expression in Panc1 cells by transfection of siNR4A1<sup>a</sup>.

	Accession number <sup>b</sup>	Protein	Location	Function	MW (kD)	PI	Sequence Coverage	Fold change
1	P07237	Protein disulfide-isomerase A1	ER	Chaperone	57	4.8	18	1.5
2	P11021	BiP protein (GRP78)	ER	Chaperone	72	5.0	11	3.5
3	B7Z841	Neural cell adhesion molecule 2	CM	Cell adhesion	47	5.0	10	2.5
4	Q9UKZ4	Tenascin-M1	CM	Signal transduction	30	6.0	12	2.2
5	P30101	Disulfide isomerase ER-60 (ERp60)	ER	Chaperone	54	5.6	26	2
6	Q59GC9	Syntaxin binding protein 1	CM	Unknown	47	6.1	9	1.6
7	P00558	Phosphoglycerate kinase 1 (PGK1)	C	Glycolysis (ATP synthesis)	44	8.3	26	0.6
8		HCG1775343	UN	Unknown	6	11.9	25	0.45
9	Q92851	Heat shock 10kDa protein 1	C	Apoptosis	13	9.5	30	0.4
10	A0N4V7	HCG2039797	UN	Unknown	2	9.8	38	0.55
11	P35232	Prohibitin	M	DNA synthesis	29	5.6	24	1.5
12	P23528	Cofilin-1	C	Anti-apoptosis	18	8.2	21	1.5
13	Q9H8E5	Unnamed protein product	UN	Unknown	23	11.0	10	0.47
14	Q96DC8	Enoyl-CoA hydratase domain-containing protein 3	M	Catalytic activity	24	8.3	10	0.48
15	Q06830	Peroxiredoxin-1	C	Antioxidant	22	8.3	33	0.6
16	Q9Y2B7	Unnamed protein product	UN	Unknown	22	8.9	11	0.45
17	P10809	60 kDa heat shock protein, mitochondrial	M	Chaperone	61	5.7	58	1.8
18	P60709	Actin, cytoplasmic 1	C	Structural constituent	42	5.3	28	2

	<b>Accession number<sup>b</sup></b>	<b>Protein</b>	<b>Location</b>	<b>Function</b>	<b>MW (kD)</b>	<b>PI</b>	<b>Sequence Coverage</b>	<b>Fold change</b>
19	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	N	mRNA processing	36	8.7	30	0.5
20	P45880	VDAC-2 (porin)	M	Transport	38	6.3	35	0.5
21	P45880	VDAC-2 (porin)	M	Transport	38	6.3	20	0.5
22	Q01151	CD83 antigen	CM	Signal transduction	24	7.6	4	0.5
23	Q4JM62	Envelope protein	UN		42	8.7	10	0.6
24	P14866	Heterogeneous nuclear ribonucleoprotein L	N	Ribonucleo-protein	60	6.7	15	0.54
25	P06733	Alpha-enolase isoform 1	C	Repressor	47	7.0	32	0.5
26	O95460	Matrilin-4	S	Protein binding	54	5.5	10	0.3
27	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 isoform B1	N	mRNA processing	37	9.0	17	0.45
28	P24752	Mitochondrial Acetoacetyl-CoA Thiolase	M	Acyltransferase	41	8.2	14	0.5
29	Q9NZ23	Gastric-associated differentially-expressed protein YA61P	UN	Oxidoreduc-tase activity	14	6.8	19	0.44
30	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 isoform A2	N	mRNA processing	36	8.7	13	0.5
31	Q8WVY7	Ubiquitin-like domain-containing CTD phosphatase 1	N	phosphopro-tein phosphata-se activity	37	6.3	10	2.3
32	P00367	Chain A, Structure of Human Glutamate Dehydrogenase-Apo Form	M	Oxidoreduc-tase	56	6.7	14	0.44
33	P09622	Dihydrolipoamide dehydrogenase precursor	M	Oxidoreduc-tase	54	8.2	11	0.56

	<b>Accession number<sup>b</sup></b>	<b>Protein</b>	<b>Location</b>	<b>Function</b>	<b>MW (kD)</b>	<b>PI</b>	<b>Sequence Coverage</b>	<b>Fold change</b>
34	Q65ZQ3	Heterogeneous nuclear ribonucleoprotein A3 pseudogene 1	N	Nucleic acid binding	29	8.5	9	0.4
35	Q969X6	Unnamed protein product	N	Protein binding	77	9.0	9	0.4
36	P25705	ATP synthase subunit alpha (ATP5A1)	M	ATP synthesis	59	9.2	10	0.45
37	Q9H2K8	STE20-like kinase	C	DNA repair	106	7.5	10	0.6
38	B4DNH8	Annexin A2	C	Angiogenesis	21	6.0	25	0.6

<sup>a</sup> Cells were analyzed 60 hr post-transfection with each siRNA.

<sup>b</sup> The Swiss-Prot/TrEMBL database accession number.

CM: cell membrane, ER: endoplasmic reticulum, M: mitochondria, N: nucleus, C: cytoplasm, S: secreted, UN: unknown.