

Supplementary Table 1. Differentially Expressed Cell Line-Specific Proteins and Their Relative Levels of Expression.

	Cell line 4	Cell line 1	Cell line 2	Cell line 3	Cell line 5
Identified Proteins (120)	WT	ccm1	ccm2	ccm3	mock
Putative uncharacterized protein Q3TQ13	112.80	144.09	147.85	127.45	140.37
Elongation factor EF2	105.31	129.58	157.70	142.95	116.15
MFLJ00343 protein (Fragment) Q6KAM8	111.27	80.10	80.19	59.64	100.42
Alpha-enolase ENOA	79.14	108.11	110.29	110.52	96.69
Putative uncharacterized protein Q3UBU0	114.64	87.22	64.46	52.00	101.27
Pyruvate kinase isozymes M1/M2 KPYM_MOUSE	85.43	90.44	95.65	94.76	88.10
Putative uncharacterized protein Q9DC41	112.67	86.21	64.19	64.56	107.20
Heat shock protein HSP 90-alpha HS90A	55.77	104.64	89.51	86.09	69.91
Glyceraldehyde-3-phosphate dehydrogenase D2KHZ9	72.54	73.36	93.79	84.45	78.65
Transitional endoplasmic reticulum ATPase TERA	58.80	51.88	53.26	44.56	84.34
Elongation factor 1-alpha 1 EF1A1	65.50	81.40	78.87	79.18	77.10
Clathrin, heavy polypeptide (Hc) Q5SXR6	43.79	46.46	11.70	28.55	1.86
Putative uncharacterized protein Q3TIZ0	68.75	78.61	82.39	76.96	49.56
Ahnak protein (Fragment) A0PJF4	28.12	6.73	13.44	19.86	38.20
Myosin-9 MYH9	1	34.52	0.00	161.97	1
Heat shock protein 84b Q71LX8	67.76	68.61	72.49	60.65	46.94
Tubulin beta-4 chain TBB4	51.55	71.32	66.14	77.35	53.27

	Cell line 4	Cell line 1	Cell line 2	Cell line 3	Cell line 5
L-lactate dehydrogenase A chain LDHA	57.30	64.33	66.19	64.65	40.31
Putative uncharacterized protein Q3UAA9	60.03	57.17	63.05	58.92	69.96
Myb-binding protein 1A MBB1A	32.28	20.52	25.18	11.41	3.97
Putative uncharacterized protein Q3UCD3	55.59	39.14	45.19	59.56	51.06
Protein disulfide-isomerase A3 PDIA3	47.17	38.99	20.21	4.74	70.36
Putative uncharacterized protein Q8BV87	54.68	60.94	33.74	35.38	51.31
Putative uncharacterized protein Q8CE30	26.43	13.79	22.16	15.12	28.35
Protein disulfide-isomerase PDIA1	43.11	34.20	15.79	26.89	57.60
Fructose-bisphosphate aldolase A6ZI44	20.68	15.00	48.91	37.70	19.25
Putative uncharacterized protein (Fragment) Q3U7N9	24.46	3.37	12.72	12.34	31.21
Putative uncharacterized protein Q3UXC2	24.84	33.24	35.65	36.05	31.71
Triosephosphate isomerase TPIS	26.78	44.90	38.66	40.78	31.46
Putative uncharacterized protein Q3TVD2	41.23	27.32	23.02	11.31	39.25
Putative uncharacterized protein Q3U8U8	25.49	10.34	7.24	7.76	6.73
Tln1 protein Q0V930	10.01	4.60	2.06	2.89	28.49
Protein disulfide-isomerase A4 PDIA4	26.43	7.71	1.01	0.96	27.54
60 kDa heat shock protein, mitochondrial CH60	32.47	24.36	1.05	0.00	52.67
Adenylyl cyclase-associated protein Q3TC53	35.28	30.86	32.79	25.86	38.74

	Cell line 4	Cell line 1	Cell line 2	Cell line 3	Cell line 5
Non-muscle alpha-actinin 4 Q1A602	18.11	5.50	2.12	0.00	5.58
Peroxioredoxin 1 B1AXW7	17.67	28.40	20.22	23.91	18.55
Gag-pro-pol polyprotein Q1KYL9	24.62	6.89	5.18	7.59	7.29
Phosphoglycerate kinase 1 PGK1	9.79	11.24	20.12	27.53	10.10
Putative uncharacterized protein Q3TXW2	8.29	2.22	12.39	3.58	10.05
Ubiquitin B Q6NZC5	36.03	28.96	30.71	33.17	44.37
Glucose-6-phosphate isomerase G6PI	18.14	26.17	22.14	26.65	17.44
Putative uncharacterized protein Q8BGJ5	12.76	1.06	3.20	9.71	4.47
Annexin A1 B7STB7	19.17	17.23	17.93	20.86	24.48
Putative uncharacterized protein Q564E8	24.71	28.96	30.67	21.59	19.65
Tubulin beta-5 chain TBB5	30.37	34.47	34.98	30.37	28.75
Cofilin-1 COF1	26.49	27.65	33.88	20.95	31.81
Ubiquitin-activating enzyme E1 B9EHN0	1.91	5.90	12.91	2.92	2.77
Elongation factor 1-gamma EF1G	17.01	16.08	13.54	17.94	12.16
T-complex protein 1 subunit epsilon TCPE	11.26	8.97	9.45	7.69	14.07
D-3-phosphoglycerate dehydrogenase SERA	19.08	18.54	24.29	13.23	7.99
Phosphoglycerate mutase 1 PGAM1	23.65	31.35	27.45	26.62	25.98
Putative uncharacterized protein Q3U9Y8	30.46	25.35	10.64	9.55	2.81
Putative uncharacterized protein Q3UXQ6	18.11	24.13	32.75	25.73	14.63

	Cell line 4	Cell line 1	Cell line 2	Cell line 3	Cell line 5
Ahnak protein (Fragment) A0JLR7	11.64	3.45	10.57	19.83	14.73
Ribosomal protein, large, P0 Q5FWB6	20.14	39.30	28.37	22.75	6.33
6-phosphogluconate dehydrogenase, decarboxylating 6PGD	2.03	14.94	16.73	25.70	10.15
MKIAA0002 protein (Fragment) Q6A0F1	4.22	0.00	10.37	9.22	0.00
Putative uncharacterized protein Q3TI62	15.36	25.13	24.16	22.58	15.98
Protein disulfide-isomerase A6 PDIA6	20.74	18.30	11.68	6.66	26.18
Annexin A5 ANXA5	17.17	13.71	19.07	18.07	17.04
Putative uncharacterized protein Q3U536	21.74	24.22	30.45	20.89	20.51
Putative uncharacterized protein Q3UB67	15.67	16.26	17.93	13.40	15.58
Putative uncharacterized protein Q542X7	8.32	5.65	13.79	6.70	9.15
14-3-3 protein epsilon 1433E	19.93	30.93	23.05	23.67	18.70
Peptidyl-prolyl cis-trans isomerase Q3UAJ1	23.46	16.10	27.52	20.79	22.37
Transgelin-2 TAGL2	9.92	13.80	21.02	15.08	14.88
T-complex protein 1 subunit delta Q3TII0	8.51	8.05	13.73	8.49	3.82
Putative uncharacterized protein Q3UBI6	22.49	19.54	25.34	18.90	12.97
Putative uncharacterized protein Q3U6X2	14.04	17.49	15.91	10.41	15.68
Putative uncharacterized protein Q3UCL7	5.32	7.79	25.21	22.65	4.72
40S ribosomal protein S7 RS7	24.08	19.76	26.25	18.97	22.67

	Cell line 4	Cell line 1	Cell line 2	Cell line 3	Cell line 5
Guanine nucleotide-binding protein subunit beta-2-like 1 GBLP	14.39	13.77	22.20	16.08	0.85
Down syndrome cell adhesion molecule-like protein (Fragment) Q8R4B4	24.08	19.62	23.15	21.05	17.79
Laminin receptor (Fragment) B2CY77	13.29	24.36	17.93	14.19	15.98
Putative uncharacterized protein Q3UM23	3.81	0.00	0.00	21.03	3.77
Putative uncharacterized protein Q3UMM1	14.20	22.81	31.68	17.14	16.14
Putative uncharacterized protein Q3TXS9	13.33	19.53	22.10	18.90	4.73
Putative uncharacterized protein Q3TFK4	14.08	0.00	9.45	10.05	13.12
Profilin Q8CEH8	19.27	20.44	16.92	19.83	16.89
Putative uncharacterized protein Q8C483	14.26	5.76	7.34	15.09	2.71
Identified yet undeclared protein #25315 in ProteinLynx output. FAKE_25315	0.00	5.83	5.28	5.76	10.96
Galectin-1 LEG1	16.96	14.84	12.65	20.86	17.84
Alcohol dehydrogenase 1 ADH1	8.51	3.45	9.36	5.74	8.35
Putative uncharacterized protein Q3TJ69	9.70	2.29	12.74	23.67	9.60
Importin-5 IPO5	0.84	2.31	0.00	7.36	1
Peroxisredoxin-6 PRDX6	5.00	8.37	15.75	11.24	10.40
Putative uncharacterized protein Q9D1S3	7.13	9.19	12.52	7.46	1.71
14-3-3 protein gamma 1433G	10.54	21.58	19.96	16.97	6.43
Heat shock protein 1-like protein B2CSK2	3.94	6.91	11.44	15.28	4.92

	Cell line 4	Cell line 1	Cell line 2	Cell line 3	Cell line 5
60S ribosomal protein L10 RL10	2.53	15.84	16.82	15.98	7.54
Inducible heat shock protein 70 A1E2B8	19.95	12.78	9.58	9.42	10.56
GTP-binding nuclear protein Ran RAN	8.94	8.03	12.65	15.42	6.58
Poly(rC)-binding protein 1 PCBP1	7.54	4.35	4.17	5.67	10.45
S-formylglutathione hydrolase ESTD	0.84	2.31	3.26	13.20	11.11
Malate dehydrogenase, mitochondrial MDHM	23.65	18.30	1.11	1	23.52
Nucleosome assembly protein 1-like 1 NP1L1	8.54	10.01	13.72	10.48	16.89
Enolase Q4FK59	12.79	19.96	16.08	14.29	14.52
60S ribosomal protein L6 Q3UCH0	10.41	11.24	16.82	7.46	4.67
Putative uncharacterized protein Q3U122	21.30	14.79	11.68	11.37	16.68
Eukaryotic translation initiation factor 5A-1 IF5A1	7.66	14.84	6.33	13.06	10.10
Putative uncharacterized protein Q5BLJ7	11.29	18.39	14.80	14.19	10.40
60S acidic ribosomal protein P2 RLA2	11.42	12.54	18.75	13.20	15.93
Putative uncharacterized protein Q58ET1	3.63	17.14	3.10	0.00	1
Identified yet undeclared protein #23114 in ProteinLynx output. FAKE_23114	3.50	16.10	13.76	29.38	7.44
Glutathione S-transferase Mu 1 GSTM1	6.82	15.92	7.28	12.30	6.48
Putative uncharacterized protein Q58EU6	9.07	0.00	5.26	1.86	6.48
ATP synthase subunit beta, mitochondrial ATPB	7.16	0.00	1	1	27.24

	Cell line 4	Cell line 1	Cell line 2	Cell line 3	Cell line 5
Heat shock protein 2 Q99KD7	11.51	7.94	7.34	13.30	8.79
Rps16 protein Q5CZY9	7.66	12.56	14.61	10.47	4.88
Histone H2B A2AB77	14.39	9.19	6.23	2.95	22.57
Histone H2A.x H2AX	20.99	18.37	3.14	1	20.81
Enolase Q3UJ20	11.70	12.59	5.34	9.29	11.26
Aldehyde dehydrogenase, mitochondrial ALDH2	0.00	1	1	1	17.74
MC3T3-E1 calyculin Q545I9	6.26	8.12	0.00	7.56	9.35
Putative uncharacterized protein Q9CWK0	9.60	12.72	11.55	10.57	7.44
Putative uncharacterized protein (Fragment) Q3U8X6	3.63	20.61	6.17	9.44	8.19
Protein S100-A11 S10AB	2.79	7.06	8.29	5.50	12.97
Putative uncharacterized protein Q3UKW2	1.06	2.46	0.00	1.89	12.06
Glutathione S-transferase Mu 2 GSTM2	0.00	12.54	0.00	0.90	1