

Supplementary Table 1. List of proteins quantitated in tumor tissue treated with versus without IPI-504

RefSeq			iTRAQ Ratio (Rx/NoRx)	iTRAQ Ratio (Rx/NoRx)	
Accession No.	Gene symbol	Protein name	panc253	panc410	
1	MYH9	NP_002464.1	myosin, heavy polypeptide 9, non-muscle	0.89	1.01
2	FCGBP	NP_003881.1	Fc fragment of IgG binding protein	1.23	0.94
3	ACTN4	NP_004915.2	actinin, alpha 4	0.92	0.76
4	ACTB	NP_001092.1	beta actin	1.18	1.07
5	KRT8	NP_002264.1	keratin 8	0.81	0.77
6	AHNAK	NP_001611.1	AHNAK nucleoprotein isoform 1	0.73	0.93
7	HSP90AB1	NP_031381.2	heat shock 90kDa protein 1, beta	0.99	0.93
8	HSPA5	NP_005338.1	heat shock 70kDa protein 5	1.71	1.66
9	HSPD1	NP_955472.1	chaperonin	0.95	0.97
10	KRT18	NP_000215.1	keratin 18	0.92	0.74
11	PKM2	NP_002645.3	pyruvate kinase 3 isoform 1	1.1	0.79
12	GAPDH	NP_002037.2	glyceraldehyde-3-phosphate dehydrogenase	1.73	0.79
13	ENO1	NP_001419.1	enolase 1	1.13	0.71
14	P4HB	NP_000909.2	prolyl 4-hydroxylase, beta subunit	1.09	0.88
15	PLEC1	NP_958782.1	plectin 1 isoform 6	0.95	0.9
16	AGR2	NP_006399.1	anterior gradient 2 homolog	1.27	1.02
17	HSP90B1	NP_003290.1	tumor rejection antigen (gp96) 1	1.29	1.13
18	PDIA3	NP_005304.3	protein disulfide isomerase-associated 3	1.07	0.83
19	ANXA2	NP_001002858.1	annexin A2 isoform 1	0.89	0.67
20	LGALS4	NP_006140.1	galectin 4	1.05	1.06
21	CLTC	NP_004850.1	clathrin heavy chain 1	1.1	1.26
22	HSPA8	NP_006588.1	heat shock 70kDa protein 8 isoform 1	1.82	1.59
23	TUBB	NP_821133.1	tubulin, beta polypeptide	1.06	1.52
24	KRT19	NP_002267.2	keratin 19	0.83	0.82
25	H2AFJ	NP_808760.1	H2A histone family, member J isoform 2	1.8	1.46
26	VCP	NP_009057.1	valosin-containing protein	1.21	0.93
27	VIM	NP_003371.2	vimentin	0.96	1.89
28	TUBA1C	NP_116093.1	tubulin alpha 6	0.89	1.43
29	ATP5B	NP_001677.2	ATP synthase, mitochondrial F1 complex, beta subunit	0.87	1.3
30	OLFM4	NP_006409.3	olfactomedin 4	1.13	0.31
31	EEF1A1	NP_001393.1	eukaryotic translation elongation factor 1 alpha 1	1.07	1.47
32	SPTBN1	NP_003119.2	spectrin, beta, non-erythrocytic 1 isoform 1	0.81	0.91
33	TPM3	NP_705935.1	tropomyosin 3 isoform 2	0.93	1.1
34	HNRPA2B1	NP_112533.1	heterogeneous nuclear ribonucleoprotein A2/B1 isoform B1	1.18	0.8
35	HIST2H4B	NP_001029249.1	histone cluster 2, H4b	1.21	1.2
36	PDIA4	NP_004902.1	protein disulfide isomerase-associated 4	1.31	1.16
37	ALDOA	NP_000025.1	aldolase A	1.08	1.1
38	SPTAN1	NP_003118.1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	0.88	0.97
39	MVP	NP_005106.2	major vault protein	0.9	0.95
40	EEF2	NP_001952.1	eukaryotic translation elongation factor 2	0.95	1.37
41	HNRPU	NP_004492.2	heterogeneous nuclear ribonucleoprotein U isoform b	0.99	1.13
42	DYNC1H1	NP_001367.2	dynein, cytoplasmic, heavy polypeptide 1	1.11	1.1
43	FLNB	NP_001448.2	filamin B, beta (actin binding protein 278)	0.83	1.03
44	PYGB	NP_002853.2	brain glycogen phosphorylase	1.04	0.79
45	HSPA1B	NP_005337.1	heat shock 70kDa protein 1B	2.7	1.55
46	HNRPA3	NP_919223.1	heterogeneous nuclear ribonucleoprotein A3	0.89	1.09
47	LDHA	NP_005557.1	lactate dehydrogenase A	1.25	0.64

48	PGK1	NP_000282.1	phosphoglycerate kinase 1	1.2	0.83
49	PDIA6	NP_005733.1	protein disulfide isomerase-associated 6	1.25	0.73
50	CALR	NP_004334.1	calreticulin	1.06	1.18
51	ATP5A1	NP_001001937.1	ATP synthase, mitochondrial F1 complex, alpha subunit	0.89	1.63
52	CANX	NP_001019820.1	calnexin	1.06	0.85
53	LMNA	NP_733821.1	lamin A/C isoform 1	0.84	1.03
54	CES1	NP_001020366.1	carboxylesterase 1 isoform a	1.04	1.24
55	KRT7	NP_005547.3	keratin 7	0.85	1.06
56	CPS1	NP_001866.2	carbamoyl-phosphate synthetase 1, mitochondrial	1.08	0.85
57	ANXA1	NP_000691.1	annexin I	0.96	0.77
58	HSP90AA1	NP_005339.2	heat shock protein 90kDa alpha, class A member 1 isoform 2	1	1.08
59	YWHAZ	NP_003397.1	tyrosine 3/tryptophan 5 -monooxygenase activation protei	1.02	0.86
60	CHGA	NP_001266.1	chromogranin A	1.03	0.92
61	MYL6	NP_524147.2	myosin, light chain 6, smooth muscle and non-muscle isoform 2	0.93	1.67
62	MYH14	NP_001070654.1	myosin, heavy chain 14 isoform 1	0.87	0.96
63	CKAP4	NP_006816.2	cytoskeleton-associated protein 4	0.95	1.03
64	HSPA9	NP_004125.3	heat shock 70kDa protein 9B	1.11	0.98
65	NCL	NP_005372.2	nucleolin	0.81	0.91
66	ANXA5	NP_001145.1	annexin 5	1.14	0.62
67	IDH1	NP_005887.2	isocitrate dehydrogenase 1 (NADP+), soluble	1.14	0.99
68	MDH2	NP_005909.2	mitochondrial malate dehydrogenase	1.18	0.79
69	HNRPA1	NP_112420.1	heterogeneous nuclear ribonucleoprotein A1 isoform b	0.72	0.81
70	LOC654188	XP_945701.2	PREDICTED: similar to peptidylprolyl isomerase A isoform 1	1.48	0.95
71	ACTN1	NP_001093.1	actinin, alpha 1	1.01	0.77
72	RPS13	NP_001008.1	ribosomal protein S13	1.38	1.38
73	HBA1	NP_000549.1	alpha 1 globin	0.58	0.74
74	ANXA4	NP_001144.1	annexin IV	1	0.59
75	MSN	NP_002435.1	moesin	1.1	1.23
76	FGB	NP_005132.2	fibrinogen, beta chain	0.98	0.57
78	GFPT1	NP_002047.1	glucosamine-fructose-6-phosphate aminotransferase	1.21	1.03
79	HNRPK	NP_002131.2	heterogeneous nuclear ribonucleoprotein K isoform a	1.11	0.99
80	LGALS3	NP_002297.2	galectin 3	1.9	1.5
81	HIST1H1C	NP_005310.1	histone cluster 1, H1c	0.51	0.7
82	PFN1	NP_005013.1	profilin 1	1.27	1.23
83	TPM1	NP_001018006.1	tropomyosin 1 alpha chain isoform 4	1.02	0.99
84	YWHAE	NP_006752.1	tyrosine 3/tryptophan 5 -monooxygenase activation protei	0.98	1.08
85	TLN1	NP_006280.2	talin 1	0.99	1.23
86	GANAB	NP_938148.1	alpha glucosidase II alpha subunit isoform 2	1.16	0.83
87	TMSB4X	NP_066932.1	thymosin, beta 4	1.08	0.87
87	TMSL3	NP_898870.1	thymosin-like 3	1.13	1.1
88	VDAC1	NP_003365.1	voltage-dependent anion channel 1	1.09	1.39
89	RRBP1	NP_004578.2	ribosome binding protein 1	0.87	0.98
90	S100A6	NP_055439.1	S100 calcium-binding protein A6	1.16	0.87
91	BLVRB	NP_000704.1	biliverdin reductase B (flavin reductase (NADPH))	1.36	0.75
92	GSTP1	NP_000843.1	glutathione transferase	1.37	0.81
93	HSPB1	NP_001531.1	heat shock 27kDa protein 1	1.05	1.23
94	SERPINH1	NP_001226.2	serine (or cysteine) proteinase inhibitor, clade H, member 1	0.99	1.3
95	FLNA	NP_001447.2	filamin A, alpha	0.93	1.35
96	HIST2H2BF	NP_001019770.1	histone 2, H2bf	2.97	1.12
97	RPN1	NP_002941.1	ribophorin I	1.14	1.1
98	CA2	NP_000058.1	carbonic anhydrase II	1.2	0.49
99	PRDX1	NP_002565.1	peroxiredoxin 1	1.11	1.15

100	MRCL3	NP_006462.1	myosin regulatory light chain MRCL3	0.87	1.24
101	RPL4	NP_000959.2	ribosomal protein L4	0.95	0.96
102	HYOU1	NP_006380.1	oxygen regulated protein	1.09	1.09
103	HSD17B12	NP_057226.1	steroid dehydrogenase homolog	0.81	1.16
104	IQGAP1	NP_003861.1	IQ motif containing GTPase activating protein 1	1.08	1.05
105	CCT3	NP_005989.3	chaperonin containing TCP1, subunit 3 isoform a	1.03	0.78
106	VIL1	NP_009058.1	villin 1	0.88	0.99
107	ARF3	NP_001650.1	ADP-ribosylation factor 3	1.25	1.4
108	ALDH1A1	NP_000680.2	aldehyde dehydrogenase 1A1	1.27	0.52
109	KRT17	NP_000413.1	keratin 17	0.92	1.32
110	H3F3B	NP_005315.1	H3 histone, family 3B	0.97	0.99
111	UBE1	NP_695012.1	ubiquitin-activating enzyme E1	1.01	1.18
112	WDR1	NP_059830.1	WD repeat-containing protein 1 isoform 1	1.11	1.15
113	CALM1	NP_008819.1	calmodulin 1	0.67	0.69
114	NPM1	NP_002511.1	nucleophosmin 1 isoform 1	0.83	1.05
115	LCP1	NP_002289.1	L-plastin	1.32	1.37
116	LOC643576	XP_947649.1	PREDICTED: similar to Phosphoglycerate mutase 1 isoform 1	1.63	0.92
117	UGCG1	NP_064505.1	UDP-glucose ceramide glucosyltransferase-like 1 isoform 1	1.13	0.69
118	LOC730855	XP_001130382.1	PREDICTED: similar to Mucin-5AC	1.2	0.78
119	CNDP2	NP_060705.1	CNDP dipeptidase 2 (metallopeptidase M20 family)	1	0.77
120	ERO1L	NP_055399.1	ERO1-like	1.19	1.14
121	PSME1	NP_006254.1	proteasome activator subunit 1 isoform 1	1.11	0.95
122	VCL	NP_054706.1	vinculin isoform meta-VCL	0.85	0.96
123	CCT2	NP_006422.1	chaperonin containing TCP1, subunit 2	1	1.42
124	ATP2A2	NP_733765.1	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	0.88	1.03
125	GLUD1	NP_005262.1	glutamate dehydrogenase 1	0.93	1.03
126	TST	NP_003303.2	thiosulfate sulfurtransferase	1.02	0.87
127	EIF4A1	NP_001407.1	eukaryotic translation initiation factor 4A isoform 1	0.98	1.34
128	NME1-NME2	NP_001018146.1	NME1-NME2 protein	1.08	1.12
129	RPN2	NP_002942.2	ribophorin II	0.9	1.28
130	LDHB	NP_002291.1	lactate dehydrogenase B	1.12	0.7
131	RTN4	NP_065393.1	reticulon 4 isoform A	1.26	0.54
132	GSN	NP_000168.1	gelsolin isoform a	0.91	1.16
133	CCT5	NP_036205.1	chaperonin containing TCP1, subunit 5 (epsilon)	1.08	1.09
134	PHB	NP_002625.1	prohibitin	0.9	1.47
135	RPL10A	NP_009035.3	ribosomal protein L10a	0.96	1.14
136	EEF1G	NP_001395.1	eukaryotic translation elongation factor 1 gamma	1.18	0.94
137	TPI1	NP_000356.1	triosephosphate isomerase 1	1.15	1.13
138	TMED10	NP_006818.3	transmembrane emp24 domain-containing protein 10	1.6	0.89
139	RPLP2	NP_000995.1	ribosomal protein P2	0.83	0.99
140	TUFM	NP_003312.3	Tu translation elongation factor, mitochondrial	1.05	1.11
141	GARS	NP_002038.2	glycyl-tRNA synthetase	1.26	0.9
142	H2AFV	NP_036544.1	H2A histone family, member V isoform 1	0.92	1.07
143	PPIB	NP_000933.1	peptidylprolyl isomerase B	1.53	1.1
144	MYH11	NP_001035202.1	smooth muscle myosin heavy chain 11 isoform SM2B	1.03	1.09
145	CAST	NP_001035907.1	calpastatin isoform h	0.87	0.7
146	SF3B2	NP_006833.2	splicing factor 3B subunit 2	0.99	1.01
147	RPS3	NP_000996.2	ribosomal protein S3	1.05	1.05
148	HIST1H1B	NP_005313.1	histone cluster 1, H1b	0.93	1.13
149	IDH2	NP_002159.2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	1.29	0.91
150	VIL2	NP_003370.2	villin 2	0.98	0.8
151	TAGLN2	NP_003555.1	transgelin 2	1.14	0.97

152	TUBB2C	NP_006079.1	tubulin, beta, 2	1.05	1.16
153	HNRPM	NP_005959.2	heterogeneous nuclear ribonucleoprotein M isoform a	0.96	1.15
154	ACTC1	NP_005150.1	cardiac muscle alpha actin 1 proprotein	0.76	1.74
155	HNRPC	NP_001070911.1	heterogeneous nuclear ribonucleoprotein C isoform b	0.91	1.13
156	CFL1	NP_005498.1	cofilin 1 (non-muscle)	1.25	1.01
157	COPB1	NP_057535.1	coatamer protein complex, subunit beta	1.14	1.05
158	LMNB1	NP_005564.1	lamin B1	1.09	1.27
159	PRDX5	NP_036226.1	peroxiredoxin 5 , isoform a	2.4	1.25
160	PFKP	NP_002618.1	phosphofructokinase, platelet	1	1.03
161	PRDX6	NP_004896.1	peroxiredoxin 6	1.17	0.71
162	RCN1	NP_002892.1	reticulocalbin 1	1.1	1.05
163	BCAP31	NP_005736.3	B-cell receptor-associated protein 31	0.79	1.22
164	LOC645441	XP_947749.1	PREDICTED: similar to 60S ribosomal protein L17 isoform 1	0.84	1
165	SLC25A5	NP_001143.1	solute carrier family 25, member 5	0.86	0.68
166	FASN	NP_004095.4	fatty acid synthase	0.93	0.95
167	CS	NP_004068.2	citrate synthase , isoform a	1.09	0.84
168	HADHA	NP_000173.2	mitochondrial trifunctional protein, alpha subunit	1.04	1.03
169	RPS3A	NP_000997.1	ribosomal protein S3a	0.95	1.07
170	HSPE1	NP_002148.1	heat shock 10kDa protein 1 (chaperonin 10)	1.5	0.76
171	ARPC2	NP_005722.1	actin related protein 2/3 complex subunit 2	1.16	1.05
172	ATIC	NP_004035.2	5-,4-carboxamide ribonucleotide formyltransferase	1.28	1
173	ARCN1	NP_001646.2	archain	1.1	0.93
174	KRT20	NP_061883.1	keratin 20	1.02	0.62
175	CAP1	NP_006358.1	adenylyl cyclase-associated protein	1.16	1.26
176	RPL6	NP_001019833.1	ribosomal protein L6	0.77	0.82
177	HNRPH1	NP_005511.1	heterogeneous nuclear ribonucleoprotein H1	1.05	0.91
178	DNAJB11	NP_057390.1	DnaJ (Hsp40) homolog, subfamily B, member 11	1.01	0.98
179	ATP1A1	NP_000692.2	Na ⁺ /K ⁺ -ATPase alpha 1 subunit isoform a proprotein	1.11	0.97
180	RPS2	NP_002943.2	ribosomal protein S2	0.92	1.23
181	CLIC1	NP_001279.2	chloride intracellular channel 1	1.1	0.84
182	S100A10	NP_002957.1	S100 calcium binding protein A10	0.87	0.97
183	DPYSL2	NP_001377.1	dihydropyrimidinase-like 2	1.08	1.13
184	CKB	NP_001814.2	brain creatine kinase	1.15	0.75
185	SYNCRIP	NP_006363.3	synaptotagmin binding, cytoplasmic RNA interacting protein	1.01	1
186	FBL	NP_001427.2	fibrillarin	0.83	1.66
187	CTNNA1	NP_001894.2	catenin, alpha 1	0.99	1.04
188	ACTR2	NP_005713.1	actin-related protein 2 isoform b	1.25	1.45
189	FN1	NP_997641.1	fibronectin 1 isoform 5	0.96	1.14
190	H2AFY	NP_001035248.1	H2A histone family, member Y isoform 2	0.96	1.15
191	CAPZB	NP_004921.1	F-actin capping protein beta subunit	1.05	1.41
192	EPPK1	NP_112598.1	epiplakin 1	1.08	0.89
193	LOC652826	XP_947602.1	PREDICTED: similar to 26S protease regulatory subunit 6B	1.15	1.29
194	TMPO	NP_001027454.1	thymopoietin isoform beta	0.82	1.09
195	ATP6V1B2	NP_001684.2	vacuolar H ⁺ -ATPase B2	1.25	1.33
196	STIP1	NP_006810.1	Hsp70/Hsp90-organizing protein	1.03	0.72
197	QSOX1	NP_002817.2	quiescin Q6 isoform a	0.84	1.03
198	COPA	NP_004362.1	coatamer protein complex, subunit alpha	1.21	0.98
199	EIF5A	NP_001961.1	eukaryotic translation initiation factor 5A	1.1	1.28
200	ACTR3	NP_005712.1	ARP3 actin-related protein 3 homolog	1.4	1.16
201	ALDH2	NP_000681.2	mitochondrial aldehyde dehydrogenase 2	1.09	0.98
202	COL12A1	NP_004361.3	collagen, type XII, alpha 1 long isoform	0.79	1.23
203	HMG2	NP_005508.1	high-mobility group nucleosomal binding domain 2	0.92	1.49

204	PGD	NP_002622.2	phosphogluconate dehydrogenase	1.4	1.22
205	C1QBP	NP_001203.1	complement component 1, q subcomponent binding protein	1.42	0.83
206	TKT	NP_001055.1	transketolase	0.96	0.85
207	RPS20	NP_001014.1	ribosomal protein S20	0.82	1.4
208	RAB1A	NP_004152.1	RAB1A, member RAS oncogene family	2.16	2.1
209	GSTK1	NP_057001.1	glutathione transferase kappa 1	1.09	0.55
210	NUCB1	NP_006175.2	nucleobindin 1	0.95	0.82
211	PRDX3	NP_006784.1	peroxiredoxin 3 isoform a	1.12	0.86
212	IMMT	NP_006830.1	inner membrane protein, mitochondrial	0.92	0.9
213	EPRS	NP_004437.2	glutamyl-prolyl tRNA synthetase	0.8	1.12
214	CAND1	NP_060918.2	TIP120 protein	0.71	0.93
215	PRDX2	NP_005800.3	peroxiredoxin 2 isoform a	1.05	0.84
216	DHX9	NP_001348.2	DEAH (Asp-Glu-Ala-His) box polypeptide 9	1.09	0.84
217	ETFB	NP_001014763.1	electron-transfer-flavoprotein, beta polypeptide isoform 2	0.82	0.94
218	CALU	NP_001210.1	calumenin	0.87	0.97
219	XRCC5	NP_066964.1	ATP-dependent DNA helicase II	1.24	0.89
220	DDOST	NP_005207.2	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	0.69	1.49
221	STAT1	NP_009330.1	signal transducer and activator of transcription 1 isoform alpha	1.26	1.4
222	LRPPRC	NP_573566.2	leucine-rich PPR motif-containing protein	1.44	0.9
223	ACAA2	NP_006102.1	acetyl-coenzyme A acyltransferase 2	0.75	0.95
224	TPM4	NP_003281.1	tropomyosin 4	0.99	0.9
225	UQCRC1	NP_003356.2	ubiquinol-cytochrome c reductase core protein I	1.06	1.3
226	PLS1	NP_002661.1	plastin 1	1.1	0.63
227	TALDO1	NP_006746.1	transaldolase 1	0.96	1.31
228	PHB2	NP_009204.1	prohibitin 2	0.93	1.44
229	UQCRC2	NP_003357.2	ubiquinol-cytochrome c reductase core protein II	0.89	1.13
230	AHCY	NP_000678.1	S-adenosylhomocysteine hydrolase	0.96	1.06
231	YWHAH	NP_003396.1	tyrosine 3/tryptophan 5 -monooxygenase activation protein, eta	0.9	1.1
232	GOLM1	NP_808800.1	golgi phosphoprotein 2	0.61	0.51
233	MYH10	NP_005955.1	myosin, heavy polypeptide 10, non-muscle	0.99	1.13
234	AKR1B10	NP_064695.2	aldo-keto reductase family 1, member B10	1.38	0.85
235	RPLP0	NP_000993.1	ribosomal protein P0	1.3	0.97
236	AKR1A1	NP_006057.1	aldo-keto reductase family 1, member A1	1.72	1.11
237	HDLBP	NP_005327.1	high density lipoprotein binding protein	1.13	0.88
238	CBR1	NP_001748.1	carbonyl reductase 1	1.23	1
239	KHDRBS1	NP_006550.1	KH domain containing, signal transduction associated 1	1.28	0.91
240	DLST	NP_001924.2	dihydrolipoamide S-succinyltransferase	0.67	1.21
241	RAN	NP_006316.1	ras-related nuclear protein	1.09	1.42
242	TMED9	NP_059980.2	transmembrane emp24 protein transport domain containing 9	0.6	1.5
243	RPS7	NP_001002.1	ribosomal protein S7	0.9	0.76
244	PSMD6	NP_055629.1	proteasome 26S subunit, non-ATPase, 6	0.97	1.26
245	TTN	NP_596869.3	titin isoform N2-A	0.99	0.94
246	SFPQ	NP_005057.1	splicing factor proline/glutamine rich	0.85	1.24
247	STOML2	NP_038470.1	stomatin (EPB72)-like 2	0.81	1.02
248	GPI	NP_000166.2	glucose phosphate isomerase	1.04	0.58
249	GMDS	NP_001491.1	GDP-mannose 4,6-dehydratase	1.16	1.11
250	CTSD	NP_001900.1	cathepsin D	1.42	0.75
251	RPL13	NP_000968.2	ribosomal protein L13	0.75	1.34
252	CAPNS1	NP_001003962.1	calpain, small subunit 1	1.05	0.95
253	CORO1A	NP_009005.1	coronin, actin binding protein, 1A	1.38	0.84
254	CYB5A	NP_001905.1	cytochrome b-5 isoform 2	0.87	1.27
255	GDI2	NP_001485.2	GDP dissociation inhibitor 2	1.04	0.77

256	SLC3A2	NP_002385.3	solute carrier family 3, member 2 isoform c	1	1.24
257	HNRPD	NP_001003810.1	heterogeneous nuclear ribonucleoprotein D isoform d	1.01	1.53
258	GCN1L1	NP_006827.1	GCN1 general control of amino-acid synthesis 1-like 1	1.05	1.21
259	ACO2	NP_001089.1	aconitase 2	1.05	1.14
260	AIFM1	NP_665811.1	programmed cell death 8 isoform 2	1.01	0.86
261	ANXA3	NP_005130.1	annexin A3	0.78	0.84
262	TMSB10	NP_066926.1	thymosin, beta 10	1.07	1.28
263	FH	NP_000134.2	fumarate hydratase	0.94	0.74
264	IARS2	NP_060530.3	mitochondrial isoleucine tRNA synthetase	0.82	0.97
265	HNRPR	NP_005817.1	heterogeneous nuclear ribonucleoprotein R	1.31	1.04
266	SF3B3	NP_036558.3	splicing factor 3b, subunit 3	0.9	1.19
267	UQCRCFS1	NP_005994.1	ubiquinol-cytochrome c reductase	0.89	0.88
268	TXNDC5	NP_110437.2	thioredoxin domain containing 5 isoform 1	1.05	1.02
269	RPS14	NP_001020242.1	ribosomal protein S14	1.19	0.99
270	HIST1H2AC	NP_003503.1	H2A histone family, member L	1.16	1.7
271	CCT6A	NP_001753.1	chaperonin containing TCP1, subunit 6A isoform a	0.95	1.5
272	PRKCSH	NP_001001329.1	protein kinase C substrate 80K-H isoform 2	0.9	0.96
273	CCT7	NP_006420.1	chaperonin containing TCP1, subunit 7 isoform a	0.96	0.89
274	PBEF1	NP_005737.1	visfatin	1.31	0.6
275	KRT23	NP_056330.3	keratin 23	0.81	0.66
276	BANF1	NP_003851.1	barrier to autointegration factor 1	0.94	0.89
277	COX5A	NP_004246.1	cytochrome c oxidase subunit Va	1.18	1.34
278	RPS4X	NP_000998.1	ribosomal protein S4, X-linked X isoform	1.07	1.32
279	SF3B1	NP_036565.2	splicing factor 3b, subunit 1 isoform 1	0.82	1.49
280	CAPG	NP_001738.2	gelsolin-like capping protein	1.08	1.03
281	PSMD11	NP_002806.2	proteasome 26S non-ATPase subunit 11	0.98	1.31
282	DDX5	NP_004387.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	0.83	1.92
283	RPL38	NP_001030335.1	ribosomal protein L38	2.05	1.17
284	PFKL	NP_001002021.1	liver phosphofructokinase isoform a	1.06	0.74
285	PSME2	NP_002809.2	proteasome activator subunit 2	1.07	1.14
286	XRCC6	NP_001460.1	ATP-dependent DNA helicase II, 70 kDa subunit	0.97	0.97
287	ARHGDI1B	NP_001166.3	Rho GDP dissociation inhibitor (GDI) beta	1.14	1.12
288	RPL7A	NP_000963.1	ribosomal protein L7a	1.13	1.09
289	LOC653232	XP_949197.1	PREDICTED: similar to ribosomal protein L15 isoform 4	0.86	1.21
290	TPD52	NP_001020424.1	tumor protein D52 isoform 2	1.21	1.08
291	CYCS	NP_061820.1	cytochrome c	1.35	0.88
292	RUVBL1	XP_001129908.1	PREDICTED: similar to RuvB-like 1	0.92	1.05
293	PRDX4	NP_006397.1	thioredoxin peroxidase	1.41	1.01
294	PDCD6IP	NP_037506.2	programmed cell death 6 interacting protein	0.88	1.03
295	UBE2L3	NP_003338.1	ubiquitin-conjugating enzyme E2L 3 isoform 1	1.13	0.69
296	HMGB1	NP_002119.1	high-mobility group box 1	0.97	1.08
297	RPL10	NP_006004.1	ribosomal protein L10	0.95	0.86
298	LMAN1	NP_005561.1	lectin, mannose-binding, 1	1.05	0.93
299	YWHAQ	NP_006817.1	tyrosine 3/tryptophan 5 -monooxygenase activation protein	0.96	0.85
300	EIF2S3	NP_001406.1	eukaryotic translation initiation factor 2, subunit 3 gamma	0.83	1.17
301	PPP2R1A	NP_055040.2	alpha isoform of regulatory subunit A, protein phosphatase 2	1.1	1.04
302	PSMA6	NP_002782.1	proteasome alpha 6 subunit	1.1	0.96
303	UGT1A6	NP_001063.2	UDP glycosyltransferase 1 family, polypeptide A6 isoform 1	1.06	0.95
304	S100P	NP_005971.1	S100 calcium binding protein P	0.9	0.72
305	SEC22B	NP_004883.2	SEC22 vesicle trafficking protein homolog B	0.93	1.04
306	FKBP3	NP_002004.1	FK506-binding protein 3	1.21	0.94
307	PPA2	NP_008834.3	inorganic pyrophosphatase 2 isoform 2	1.26	1.02

308	PDXDC1	NP_055842.1	hypothetical protein LOC23042	1.27	0.85
309	ILF2	NP_004506.2	interleukin enhancer binding factor 2	1.4	0.86
310	YWHAG	NP_036611.2	tyrosine 3-/tryptophan 5-monooxygenase activation proteir	0.89	0.99
311	AARS	NP_001596.2	alanyl-tRNA synthetase	1.29	0.95
312	RPS8	NP_001003.1	ribosomal protein S8	0.95	1.35
313	GNB2L1	NP_006089.1	guanine nucleotide binding protein, beta polypeptide 2-like 1	0.95	1.39
314	SET	NP_003002.1	SET translocation (myeloid leukemia-associated)	0.8	0.98
315	PTBP1	NP_002810.1	polypyrimidine tract-binding protein 1 isoform a	1.35	0.78
316	FUS	NP_004951.1	fusion (involved in t(12;16) in malignant liposarcoma) isoform a	0.96	1.07
317	RPS15A	NP_001025180.1	ribosomal protein S15a	1.19	1.05
318	YBX1	NP_004550.2	nuclease sensitive element binding protein 1	0.73	0.82
319	TUBA4A	NP_005991.1	tubulin, alpha 4a	1.09	1.29
320	MDH1	NP_005908.1	cytosolic malate dehydrogenase	1.62	0.95
321	DARS	NP_001340.2	aspartyl-tRNA synthetase	0.81	0.77
322	HADH	NP_005318.2	L-3-hydroxyacyl-Coenzyme A dehydrogenase	1.4	0.76
323	PPA1	NP_066952.1	pyrophosphatase 1	1.07	1.16
324	GSTA5	NP_714543.1	glutathione transferase A5	1.26	0.78
325	DDX3X	NP_001347.3	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3	0.9	1.25
326	UBC	XP_001132949.1	PREDICTED: similar to Ubiquitin-63E CG11624-PA, isoform A	0.82	0.78
327	RPSA	NP_002286.2	ribosomal protein SA	0.69	0.94
328	ALDH18A1	NP_002851.2	pyrroline-5-carboxylate synthetase isoform 1	1.02	0.98
329	RPS19	NP_001013.1	ribosomal protein S19	1.08	1.34
330	RPS6	NP_001001.2	ribosomal protein S6	0.89	0.99
331	HDGF	NP_004485.1	hepatoma-derived growth factor	1.06	0.94
332	G6PD	NP_000393.4	glucose-6-phosphate dehydrogenase isoform a	0.91	1.74
333	RPS11	NP_001006.1	ribosomal protein S11	1.13	1.57
334	PABPC1	NP_002559.2	poly(A) binding protein, cytoplasmic 1	0.87	1.17
335	LOC653888	XP_941344.1	PREDICTED: similar to Actin-related protein 2/3 complex	1.12	1.2
336	ATP2B1	NP_001673.2	plasma membrane calcium ATPase 1 isoform 1b	0.87	0.85
337	RAB14	NP_057406.2	GTPase Rab14	1.27	0.89
338	HNRPF	NP_004957.1	heterogeneous nuclear ribonucleoprotein F	0.97	1.36
339	GATM	NP_001473.1	L-arginine:glycine amidinotransferase	0.85	0.85
340	CSTB	NP_000091.1	cystatin B	1.23	0.82
341	PSMC6	NP_002797.2	proteasome 26S ATPase subunit 6	0.91	1
342	GALNT7	NP_059119.1	polypeptide N-acetylgalactosaminyltransferase 7	0.89	0.82
343	PSMC1	NP_002793.2	proteasome 26S ATPase subunit 1	1.03	1.24
344	PSMD2	NP_002799.3	proteasome 26S non-ATPase subunit 2	0.88	1.32
345	CTNND1	NP_001322.1	catenin (cadherin-associated protein), delta 1	1.24	1.35
346	BGN	NP_001702.1	biglycan	1.5	1.84
347	RPL5	NP_000960.2	ribosomal protein L5	0.98	1.26
348	RAB7A	NP_004628.4	RAB7, member RAS oncogene family	1.54	1.29
349	PSMD3	NP_002800.2	proteasome 26S non-ATPase subunit 3	1.46	0.87
350	CAT	NP_001743.1	catalase	1.32	0.56
351	HSD17B11	NP_057329.1	dehydrogenase/reductase (SDR family) member 8	1.12	1.06
352	C22orf28	NP_055121.1	hypothetical protein LOC51493	1.05	0.58
353	GALNT3	NP_004473.1	polypeptide N-acetylgalactosaminyltransferase 3	1.13	0.95
354	PRELP	NP_002716.1	proline arginine-rich end leucine-rich repeat protein	1.39	0.92
355	PSMA7	NP_002783.1	proteasome alpha 7 subunit	1.43	0.66
356	KIF5B	NP_004512.1	kinesin family member 5B	0.93	0.83
357	SEPT9	NP_006631.2	septin 9	0.91	0.76
358	ETFA	NP_000117.1	electron transfer flavoprotein, alpha polypeptide	1.15	1.2
360	CYB5R3	NP_000389.1	cytochrome b5 reductase isoform 1	0.52	0.98

361	SSB	NP_003133.1	autoantigen La	1.35	0.96
362	EFTUD2	NP_004238.2	U5 snRNP-specific protein, 116 kD	0.94	0.83
363	PRKDC	NP_008835.5	protein kinase, DNA-activated, catalytic polypeptide isoform 1	0.79	1.03
364	SLC9A3R1	NP_004243.1	solute carrier family 9, isoform 3 regulator 1	0.79	0.94
365	HSD17B10	NP_001032900.1	hydroxysteroid (17-beta) dehydrogenase 10 isoform 2	1.08	0.82
366	SPR	NP_003115.1	sepiapterin reductase	1.31	1.03
367	PSMD7	NP_002802.2	proteasome 26S non-ATPase subunit 7	1.46	0.99
368	MTPN	NP_665807.1	myotrophin	1.26	0.77
369	CAMK2D	NP_001212.2	calcium/calmodulin-dependent protein kinase II delta isoform 3	1.28	1.53
370	RPS9	NP_001004.2	ribosomal protein S9	0.94	1.03
371	LOC653949	XP_948961.1	PREDICTED: similar to 60S ribosomal protein L7 isoform 2	1.25	1.01
372	GSTO1	NP_004823.1	glutathione-S-transferase omega 1	0.96	0.7
373	CES2	NP_003860.2	carboxylesterase 2 isoform 1	1.42	1.23
374	PIGR	NP_002635.2	polymeric immunoglobulin receptor	1	0.26
375	SERPINB1	NP_109591.1	serine (or cysteine) proteinase inhibitor, clade B, member 1	1.2	0.82
376	ENO3	NP_001967.1	enolase 3	1.31	1.03
377	HIST1H1A	NP_005316.1	histone cluster 1, H1a	1.19	0.99
378	ANXA11	NP_001148.1	annexin A11	0.93	0.55
379	UGP2	NP_001001521.1	UDP-glucose pyrophosphorylase 2 isoform b	0.89	0.79
380	CD2AP	NP_036252.1	CD2-associated protein	1.02	0.96
381	PCK2	NP_004554.2	mitochondrial phosphoenolpyruvate carboxykinase 2 isoform 1	0.75	1.19
382	PSMC2	NP_002794.1	proteasome 26S ATPase subunit 2	4.07	1.42
383	CLU	NP_001822.2	clusterin isoform 1	0.89	0.96
384	COX5B	NP_001853.2	cytochrome c oxidase subunit Vb	0.85	1.15
385	LOC653147	XP_931301.1	PREDICTED: similar to 60S ribosomal protein L26-like 1	0.91	1.31
386	PGRMC2	NP_006311.1	progesterone receptor membrane component 2	1.06	1.17
387	DSP	NP_004406.2	desmoplakin isoform I	0.92	0.91
388	RAC1	NP_008839.2	ras-related C3 botulinum toxin substrate 1 isoform Rac1	1	1.93
389	SND1	NP_055205.2	staphylococcal nuclease domain containing 1	0.93	1.06
390	ARHGDI	NP_004300.1	Rho GDP dissociation inhibitor (GDI) alpha	1.06	1.17
391	FBP1	NP_000498.2	fructose-1,6-bisphosphatase 1	1.01	0.59
392	NPEPPS	NP_006301.2	aminopeptidase puromycin sensitive	0.95	0.66
393	RPL22	NP_000974.1	ribosomal protein L22 proprotein	1.09	1.03
394	RDH11	NP_057110.2	androgen-regulated short-chain dehydrogenase/reductase 1	0.84	0.88
395	RPS12	NP_001007.2	ribosomal protein S12	0.93	1
396	LOC441246	XP_943894.1	PREDICTED: similar to 60S ribosomal protein L35 isoform 5	0.94	1.31
397	LOC653566	XP_949583.1	PREDICTED: similar to Signal peptidase complex subunit 2	1.06	1.47
398	HSPA4	NP_002145.3	heat shock 70kDa protein 4 isoform a	0.91	0.91
399	PSMC3	NP_002795.2	proteasome 26S ATPase subunit 3	0.96	0.88
400	FAM62A	NP_056107.1	family with sequence similarity 62, member A	0.83	0.98
401	LOC283340	XP_944577.1	PREDICTED: similar to ribosomal protein L13a isoform 1	2.23	0.96
402	GPSN2	NP_612510.1	glycoprotein, synaptic 2	0.94	1.17
403	AGR3	NP_789783.1	breast cancer membrane protein 11	1.12	0.68
404	CCT8	NP_006576.2	chaperonin containing TCP1, subunit 8 (theta)	0.89	0.99
405	C14orf173	NP_071934.2	hypothetical protein LOC64423 isoform 2	1.12	0.96
406	VDP	NP_003706.1	vesicle docking protein p115	1.05	0.98
407	VAPA	NP_003565.4	vesicle-associated membrane protein-associated protein A	0.84	1.08
408	SULT1C2	NP_001047.1	sulfotransferase family, cytosolic, 1C, member 1 isoform a	1	0.88
409	DYNLL1	NP_001032584.1	dynein light chain 1	0.83	2.21
410	RPS10	NP_001005.1	ribosomal protein S10	0.83	1.39
411	UGDH	NP_003350.1	UDP-glucose dehydrogenase	2.12	1.43
412	ANXA6	NP_001146.2	annexin VI isoform 1	1.12	1.66

413	ITIH3	NP_002208.2	inter-alpha (globulin) inhibitor H3	0.79	0.95
414	PGM1	NP_002624.2	phosphoglucomutase 1	0.86	1.08
415	SPP1	NP_001035147.1	secreted phosphoprotein 1 isoform a	0.92	0.93
416	SEC24C	NP_940999.1	SEC24-related protein C	1.07	0.9
417	NARS	NP_004530.1	asparaginyl-tRNA synthetase	0.9	0.82
418	MATR3	NP_954659.1	matrin 3	0.83	0.98
419	PSMC5	NP_002796.4	proteasome 26S ATPase subunit 5	0.74	1.33
420	ARPC4	NP_005709.1	actin related protein 2/3 complex subunit 4 isoform a	0.91	1.53
421	ST13	NP_003923.2	heat shock 70kD protein binding protein	0.94	0.59
422	AKR1C3	NP_003730.4	aldo-keto reductase family 1, member C3	1.22	0.72
423	ALDH9A1	NP_000687.3	aldehyde dehydrogenase 9A1	1.67	0.98
424	SCYE1	NP_004748.2	small inducible cytokine subfamily E, member 1	1.16	1.03
425	PRPF8	NP_006436.3	U5 snRNP-specific protein	0.77	0.78
426	ANPEP	NP_001141.1	membrane alanine aminopeptidase	1.07	0.44
427	TMED4	NP_872353.2	transmembrane emp24 protein transport domain containing 4	0.96	0.97
428	RPS24	NP_001017.1	ribosomal protein S24 isoform c	1.34	1.34
429	EIF2S1	NP_004085.1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	1.02	0.74
430	LOC653972	XP_943872.1	PREDICTED: similar to chromobox homolog 3	0.88	1.25
431	MAPK1	NP_002736.3	mitogen-activated protein kinase 1	1.14	0.66
432	PRKAR2A	NP_004148.1	cAMP-dependent protein kinase, regulatory subunit alpha 2	1.06	1.01
433	RPL9	NP_001020092.1	ribosomal protein L9	1.1	1.08
434	TXNDC4	NP_055866.1	thioredoxin domain containing 4 (endoplasmic reticulum)	1.05	1.1
435	NSF	NP_006169.1	N-ethylmaleimide-sensitive factor	0.69	1.04
436	LOC402057	XP_944575.1	PREDICTED: similar to 40S ribosomal protein S17 isoform 2	0.9	0.84
437	COPG	NP_057212.1	coatamer protein complex, subunit gamma 1	0.89	0.89
438	MUC13	NP_149038.2	mucin 13, epithelial transmembrane	1.2	0.88
439	EIF3A	NP_003741.1	eukaryotic translation initiation factor 3, subunit 10 theta	1.02	1.17
440	FAM83H	NP_940890.2	hypothetical protein LOC286077	0.87	0.78
441	PSMD1	NP_002798.2	proteasome 26S non-ATPase subunit 1	1.08	0.83
442	EIF4A3	NP_055555.1	eukaryotic translation initiation factor 4A, isoform 3	0.82	1.27
443	HK1	NP_277035.1	hexokinase 1 isoform HKI-td	0.98	0.87
444	RPS16	NP_001011.1	ribosomal protein S16	0.76	1.99
445	NUCB2	NP_005004.1	nucleobindin 2	1.03	1.44
446	ARL8B	NP_060654.1	ADP-ribosylation factor-like 10C	0.98	1.25
447	HMGN4	NP_006344.1	high mobility group nucleosomal binding domain 4	1.02	1.37
448	RPS15	NP_001009.1	ribosomal protein S15	1.06	1.22
449	ATP6V1E1	NP_001687.1	vacuolar H+ ATPase E1 isoform a	1.12	0.97
450	CLCA1	NP_001276.2	chloride channel, calcium activated, family member 1	1.01	1.05
451	YWHAB	NP_003395.1	tyrosine 3-/tryptophan 5-monooxygenase activation protein	1.08	1.16
452	HADHB	NP_000174.1	mitochondrial trifunctional protein, beta subunit	1.13	0.86
453	NONO	NP_031389.3	non-POU domain containing, octamer-binding	1.08	0.94
454	HNRPL	NP_001524.2	heterogeneous nuclear ribonucleoprotein L isoform a	0.67	1.86
455	CHMP4B	NP_789782.1	chromatin modifying protein 4B	0.83	1.33
456	NDUFA9	NP_004993.1	NADH dehydrogenase 1 alpha subcomplex, 9, 39kDa	0.97	0.86
457	PARP1	NP_001609.1	poly (ADP-ribose) polymerase family, member 1	0.86	1.46
458	PCBP3	NP_065389.1	poly(rC) binding protein 3	0.86	1.05
459	NQO1	NP_001020604.1	NAD(P)H menadione oxidoreductase 1	1.12	0.61
460	TXN	NP_003320.2	thioredoxin	1.43	0.77
461	KPNB1	NP_002256.2	karyopherin beta 1	1.01	1.1
462	SEPT2	NP_006146.1	septin 2	0.86	1.15
463	PA2G4	NP_006182.2	ErbB3-binding protein 1	0.8	1.08
464	TMOD3	NP_055362.1	tropomodulin 3 (ubiquitous)	0.96	0.98

465	LOC644166	XP_947020.1	PREDICTED: similar to 40S ribosomal protein S26	1.06	1.29
466	DMBT1	NP_060049.1	deleted in malignant brain tumors 1 isoform c	1.03	0.72
467	PSMD13	NP_787128.1	proteasome 26S non-ATPase subunit 13 isoform 2	0.92	1.18
468	LOC387934	XP_942601.1	PREDICTED: similar to Fatty acid-binding protein, epidermal	2.27	0.96
469	AP2B1	NP_001025177.1	adaptor-related protein complex 2, beta 1 subunit isoform a	0.98	0.87
470	FGG	NP_068656.2	fibrinogen, gamma chain isoform gamma-B	0.97	0.63
471	SF1	NP_004621.2	splicing factor 1 isoform 1	0.7	1.42
472	IGF2BP3	NP_006538.2	insulin-like growth factor 2 mRNA binding protein 3	0.8	0.91
473	FAM49B	NP_057707.3	hypothetical protein LOC51571	0.98	0.99
474	LMAN2	NP_006807.1	lectin, mannose-binding 2	1.14	1.22
475	SNRNP	NP_937859.1	small nuclear ribonucleoprotein polypeptide B/B' isoform B'	1	1.02
476	TWF1	NP_002813.2	twinfilin 1	1.13	1.09
477	EPHX1	NP_000111.1	epoxide hydrolase 1, microsomal (xenobiotic)	0.92	0.95
478	COX4I1	NP_001852.1	cytochrome c oxidase subunit IV isoform 1	0.69	0.79
479	CCT4	NP_006421.2	chaperonin containing TCP1, subunit 4 (delta)	1.41	1.18
480	RBMX	NP_002130.2	RNA binding motif protein, X-linked	0.68	1.66
481	NNT	NP_036475.3	nicotinamide nucleotide transhydrogenase	0.78	0.9
482	SELENBP1	NP_003935.2	selenium binding protein 1	0.96	0.81
483	TPM1	NP_001018008.1	tropomyosin 1 alpha chain isoform 6	1	1.18
484	EFHD2	NP_077305.2	EF hand domain family, member D2	0.79	0.78
485	SF3A1	NP_005868.1	splicing factor 3a, subunit 1, 120kDa isoform 1	0.69	1.02
486	RBM14	NP_006319.1	RNA binding motif protein 14	0.75	1.11
487	TM9SF2	NP_004791.1	transmembrane 9 superfamily member 2	0.82	1.3
488	DDX21	NP_004719.2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	0.82	1.06
489	LGMN	NP_001008530.1	legumain	1.01	0.74
490	EEF1D	NP_115754.2	eukaryotic translation elongation factor 1 delta isoform 1	1.04	1.4
491	SFRS3	NP_003008.1	splicing factor, arginine/serine-rich 3	0.84	1
492	EIF3C	NP_001032897.1	eukaryotic translation initiation factor 3, subunit 8, 110kDa	0.94	1.32
493	RHOA	NP_001655.1	ras homolog gene family, member A	1.14	1.39
494	CLINT1	NP_055481.1	epsin 4	0.99	0.95
495	NAP1L4	NP_005960.1	nucleosome assembly protein 1-like 4	1.3	1.18
496	RPS27	NP_001021.1	ribosomal protein S27	0.84	0.84
497	LOC646195	XP_945678.1	PREDICTED: similar to 40S ribosomal protein S28 isoform 2	1.21	1.17
498	LASP1	NP_006139.1	LIM and SH3 protein 1	1.04	1.28
499	C19orf21	NP_775752.1	hypothetical protein LOC126353	0.71	1.33
500	ADH5	NP_000662.3	class III alcohol dehydrogenase 5 chi subunit	0.95	1.28
501	HNRPAB	NP_004490.2	heterogeneous nuclear ribonucleoprotein AB isoform b	1.36	1.28
502	CDC37	NP_008996.1	cell division cycle 37 protein	1.12	0.91
503	SCP2	NP_002970.2	sterol carrier protein 2 isoform 1 proprotein	0.89	0.88
504	RPL23	NP_000969.1	ribosomal protein L23	0.78	1.57
505	B2M	NP_004039.1	beta-2-microglobulin	0.7	0.99
506	DKFZP564	NP_056274.3	hypothetical protein LOC25923	0.82	1.22
507	SSBP1	NP_003134.1	single-stranded DNA binding protein 1	0.83	0.69
508	SEL1L	NP_005056.3	sel-1 suppressor of lin-12-like	0.84	1.93
509	RAP1GDS1	NP_066982.2	RAP1, GTP-GDP dissociation stimulator 1	1.21	1.32
510	DNAJA1	NP_001530.1	DnaJ (Hsp40) homolog, subfamily A, member 1	1.05	1.9
511	C8orf55	NP_057731.1	mesenchymal stem cell protein DSCD75	1.35	1
512	C20orf3	NP_065392.1	chromosome 20 open reading frame 3	0.99	0.83
513	ATP6V1A	NP_001681.2	ATPase, H ⁺ transporting, lysosomal 70kD, V1 subunit A	1.21	1.52
514	SLC2A1	NP_006507.1	solute carrier family 2	0.72	1.15
515	LTB4DH	NP_036344.1	NADP-dependent leukotriene B4 12-hydroxydehydrogenase	0.87	0.78
516	EIF6	NP_002203.1	integrin beta 4 binding protein isoform a	1.07	0.85

517	DHRS7	NP_057113.1	dehydrogenase/reductase (SDR family) member 7	0.92	1.01
518	TMEM4	NP_055070.1	transmembrane protein 4	1.01	1.01
519	PARK7	NP_009193.2	DJ-1 protein	1	0.51
520	PSMB4	NP_002787.2	proteasome beta 4 subunit	1.18	0.55
521	SAR1A	NP_064535.1	SAR1a gene homolog 1	0.96	1.23
522	LOC285053	XP_950562.1	PREDICTED: similar to ribosomal protein L18a isoform 6	1.06	1.63
523	TXNL1	NP_004777.1	thioredoxin-like 1	0.75	0.9
524	RBP1	NP_002890.1	retinol binding protein 1, cellular	0.92	1.12
525	MYO1E	NP_004989.2	myosin IE	0.82	0.89
526	SMC3	NP_005436.1	structural maintenance of chromosomes 3	0.9	1.25
527	DNM2	NP_001005362.1	dynammin 2 isoform 4	0.87	0.96
528	DDX1	NP_004930.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	0.98	0.97
529	WARS	NP_776049.1	tryptophanyl-tRNA synthetase isoform a	1.13	1.27
530	CDH17	NP_004054.2	cadherin 17	0.88	1.09
531	ARF5	NP_001653.1	ADP-ribosylation factor 5	1.37	0.99
532	ILF3	NP_004507.2	interleukin enhancer binding factor 3 isoform b	0.97	1
533	ARF4	XP_001132763.1	PREDICTED: similar to ADP-ribosylation factor 4	1.1	1.33
534	PAK2	NP_002568.2	p21-activated kinase 2	1.1	0.97
535	SH3BGR13	NP_112576.1	SH3 domain binding glutamic acid-rich protein like 3	0.91	1.41
536	LOC440567	XP_951370.1	PREDICTED: similar to Ubiquinol-cytochrome c reductase	1.02	0.61
537	CLTA	NP_009027.1	clathrin, light polypeptide A isoform b	0.87	1.21
538	SNRPD2	NP_004588.1	small nuclear ribonucleoprotein polypeptide D2	1.04	0.98
539	HSD17B2	NP_002144.1	hydroxysteroid (17-beta) dehydrogenase 2	1.3	0.75
540	RARS	NP_002878.2	arginyl-tRNA synthetase	1.56	0.98
541	NT5C	NP_055410.1	5',3'-nucleotidase, cytosolic	1.07	0.97
542	GNAS	NP_536350.2	GNAS complex locus isoform c	0.86	0.75
543	ATP6V0A1	NP_005168.2	ATPase, H+ transporting, lysosomal V0 subunit a isoform 1	0.97	0.83
544	ECHS1	NP_004083.2	mitochondrial short-chain enoyl-coenzyme A hydratase 1	1.09	0.82
545	CYP51A1	NP_000777.1	cytochrome P450, family 51	0.72	1.19
546	FARSA	NP_004452.1	phenylalanyl-tRNA synthetase, alpha subunit	0.9	0.89
547	PSMB1	NP_002784.1	proteasome beta 1 subunit	1.06	0.7
548	FLJ45422	NP_001004349.1	hypothetical protein LOC441140	0.68	0.7
549	SNRPD1	NP_008869.1	small nuclear ribonucleoprotein D1 polypeptide 16kDa	1.45	1.22
550	ARHGAP1	NP_004299.1	Rho GTPase activating protein 1	0.9	1.15
551	SEPT6	NP_665801.1	septin 6 isoform D	0.92	0.99
552	GLS	NP_055720.2	glutaminase C	0.77	0.68
553	HK2	NP_000180.2	hexokinase 2	0.7	1.41
554	RALY	NP_031393.2	RNA binding protein short isoform	0.85	1.05
555	MRPL12	NP_002940.2	mitochondrial ribosomal protein L12	1.33	0.52
556	ATP5H	NP_006347.1	ATP synthase, H+ transporting, mitochondrial F0 complex	0.88	0.91
557	SOD2	NP_001019637.1	manganese superoxide dismutase isoform B	1.52	1.19
558	P4HA1	NP_001017962.1	prolyl 4-hydroxylase, alpha I subunit isoform 2	1.02	1.31
559	ARPC3	NP_005710.1	actin related protein 2/3 complex subunit 3	1.91	0.97
560	CIB1	NP_006375.1	calcium and integrin binding 1 (calmyrin)	0.92	0.33
561	PSMA1	NP_002777.1	proteasome alpha 1 subunit isoform 2	0.86	0.78
562	MTHFD1	NP_005947.2	methylenetetrahydrofolate dehydrogenase 1	0.96	0.81
563	RPL12	NP_000967.1	ribosomal protein L12	0.98	1.17
564	TPD52L2	NP_955394.1	tumor protein D52-like 2 isoform c	0.93	1.37
565	FER1L3	NP_038479.1	myoferlin isoform a	1.05	1.47
566	ATP5J	NP_001003703.1	ATP synthase, H+ transporting, mitochondrial F0 complex	1.07	0.55
567	SPTLC2	NP_004854.1	serine palmitoyltransferase, long chain base subunit 2	0.81	1.12
568	RPL8	NP_000964.1	ribosomal protein L8	0.75	1.28

569	MUC1	NP_001018016.1	mucin 1 isoform 2	1.83	0.73
570	MAOA	NP_000231.1	monoamine oxidase A	1.22	0.96
571	FKBP4	NP_002005.1	FK506-binding protein 4	1.03	1.38
572	DPP3	NP_569710.2	dipeptidyl peptidase III	1.64	1.52
573	CAPN5	NP_004046.2	calpain 5	0.87	1.49
574	FLJ20035	NP_060101.2	hypothetical protein LOC55601	1.03	1.51
575	TCP1	NP_110379.2	T-complex protein 1 isoform a	1.01	1.11
576	HMGA1	NP_665911.1	high mobility group AT-hook 1 isoform a	0.82	0.97
577	LUC7L2	NP_057103.2	LUC7-like 2	0.73	0.86
578	MAT2A	NP_005902.1	methionine adenosyltransferase II, alpha	1.1	1.08
579	PABPN1	NP_004634.1	poly(A) binding protein, nuclear 1	0.93	0.91
580	PTPN6	NP_536858.1	protein tyrosine phosphatase, non-receptor type 6 isoform 2	1.27	1.71
581	NDUFS1	NP_004997.4	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa	0.93	0.66
582	MYH13	NP_003793.2	myosin, heavy polypeptide 13, skeletal muscle	0.87	0.88
583	IMPDH2	NP_000875.2	inosine monophosphate dehydrogenase 2	1.09	1.08
584	PMPCB	NP_004270.2	mitochondrial processing peptidase beta subunit	1.33	0.85
585	SFRS1	NP_008855.1	splicing factor, arginine/serine-rich 1 isoform 1	0.72	1.41
586	DSG2	NP_001934.2	desmoglein 2	1.32	1.11
587	DDX39	NP_005795.2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	0.84	1.37
588	ZYX	NP_001010972.1	zyxin	0.86	0.95
589	CMPK	NP_057392.1	cytidylate kinase	1.17	1.03
590	HIST2H3PS2	NP_001020474.1	histone H2, H3-like	1.1	1.68
591	MIA3	XP_948966.1	PREDICTED: similar to melanoma inhibitory activity 3	1.05	1.19
592	AP3B1	NP_003655.3	adaptor-related protein complex 3, beta 1 subunit	1.01	1.17
593	HMGCS2	NP_005509.1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	1.13	0.63
594	KLK15	NP_612631.1	kallikrein-related peptidase 15 isoform 3	5.84	0.42
595	COX6C	NP_004365.1	cytochrome c oxidase subunit VIc proprotein	1.12	1.05
596	PSMD12	NP_002807.1	proteasome 26S non-ATPase subunit 12	1.22	1.39
597	PSMA2	NP_002778.1	proteasome alpha 2 subunit	1.15	0.71
598	RER1	NP_008964.3	RER1 retention in endoplasmic reticulum 1	1.12	1.06
599	GRPEL1	NP_079472.1	GrpE-like 1, mitochondrial	1.14	1.28
600	GCS1	NP_006293.1	mannosyl-oligosaccharide glucosidase	0.98	1.28
601	LOC649821	XP_950889.1	PREDICTED: similar to 60S ribosomal protein L14 isoform 2	1.04	1.56
602	ERP29	NP_006808.1	endoplasmic reticulum protein 29 isoform 1	1.55	0.96
603	LOC652071	XP_946489.1	PREDICTED: similar to 60S ribosomal protein L23a	0.69	1.57
604	ABCB11	NP_003733.2	ATP-binding cassette, sub-family B (MDR/TAP), member 11	0.85	1.14
605	LGALS3BP	NP_005558.1	galectin 3 binding protein	0.99	1.23
606	LOC728378	XP_001130062.1	PREDICTED: similar to Prostate, testis expressed protein	1.05	1.2
607	GORASP2	NP_056345.3	golgi reassembly stacking protein 2	0.84	1.46
608	COTL1	NP_066972.1	coactosin-like 1	1.07	1.91
609	COPB2	NP_004757.1	coatamer protein complex, subunit beta 2 (beta prime)	0.9	0.96
610	TFG	NP_001007566.1	TRK-fused	1.06	0.62
611	LETM1	NP_036450.1	leucine zipper-EF-hand containing transmembrane protein 1	1.04	0.95
612	COL6A3	NP_004360.2	alpha 3 type VI collagen isoform 1	1.05	0.92
613	TM9SF3	NP_064508.2	transmembrane 9 superfamily member 3	0.71	0.75
614	RANBP1	NP_002873.1	RAN binding protein 1	1.12	0.9
615	DNM1L	NP_036193.1	dynamitin 1-like protein isoform 2	1.2	1.19
616	SGPL1	NP_003892.2	sphingosine-1-phosphate lyase 1	0.85	2.3
617	CORO1B	NP_001018080.1	coronin, actin binding protein, 1B	1.07	0.9
618	TRAP1	NP_057376.1	TNF receptor-associated protein 1	1.13	0.98
619	PRPF19	NP_055317.1	PRP19/PSO4 pre-mRNA processing factor 19 homolog	1.04	1.23
621	CPNE3	NP_003900.1	copine III	0.81	1.29

622	SDHA	NP_004159.1	succinate dehydrogenase complex, subunit A, flavoprotein	0.8	0.86
623	HMGB2	NP_002120.1	high-mobility group box 2	1.05	1.14
624	GOLIM4	NP_055313.1	golgi phosphoprotein 4	0.78	0.95
625	LRRC59	NP_060979.2	leucine rich repeat containing 59	0.98	1.02
626	C14orf166	NP_057123.1	homeobox prox 1	1.15	1.16
627	ITPR3	NP_002215.1	inositol 1,4,5-triphosphate receptor, type 3	0.63	1.34
628	OPLAH	NP_060040.1	5-oxoprolinase (ATP-hydrolysing)	0.57	0.8
629	DDAH2	NP_039268.1	dimethylarginine dimethylaminohydrolase 2	1.03	0.82
630	IARS	NP_002152.2	isoleucine-tRNA synthetase	1.12	0.84
631	LOC728168	XP_001126742.1	PREDICTED: hypothetical protein	0.66	0.85
632	SLC7A5	NP_003477.4	solute carrier family 7, member 5	0.38	0.88
633	CRYAB	NP_001876.1	crystallin, alpha B	0.83	1.89
634	RPL11	NP_000966.2	ribosomal protein L11	1.16	1.27
635	STARD10	NP_006636.2	START domain containing 10	0.94	1.01
636	PDS5A	NP_056015.1	SCC-112 protein	0.46	0.77
637	PGAM5	NP_612642.1	Bcl-XL-binding protein v68	0.8	0.88
638	CADPS2	NP_060424.8	Ca2+-dependent activator protein for secretion 2 isoform a	1.03	1.37
639	FUBP1	NP_003893.2	far upstream element-binding protein	1.1	1.28
640	BZW1	XP_001126385.1	PREDICTED: similar to basic leucine zipper and W2 domains 1	3.19	0.83
641	USP7	NP_003461.1	ubiquitin specific protease 7 (herpes virus-associated)	1.27	0.93
642	H2AFX	NP_002096.1	H2A histone family, member X	1.34	1.19
643	DCHS1	NP_003728.1	dachsous 1	1.11	1.19
644	EEA1	NP_003557.2	early endosome antigen 1, 162kD	0.98	0.53
645	SIM2	NP_005060.1	single-minded homolog 2 long isoform	1.05	1.38
646	TPR	NP_003283.2	nuclear pore complex-associated protein TPR	0.96	1
647	VPS35	NP_060676.2	vacuolar protein sorting 35	1.36	1.72
648	ACSL1	NP_001986.2	acyl-CoA synthetase long-chain family member 1	0.78	1.28
649	PSMA3	NP_002779.1	proteasome alpha 3 subunit isoform 1	1.11	0.85
650	CAPRIN1	NP_976240.1	membrane component chromosome 11 surface marker	1.23	0.85
651	IDE	NP_004960.1	insulysin	0.87	1.01
652	DLAT	NP_001922.2	dihydrolipoamide S-acetyltransferase	1.37	1.25
653	FARSB	NP_005678.3	phenylalanyl-tRNA synthetase, beta subunit	0.65	1.07
654	UQCRB	NP_006285.1	ubiquinol-cytochrome c reductase binding protein	0.83	1.11
655	GNAI2	NP_002061.1	guanine nucleotide binding proteir	0.95	2.29
656	DKFZp686	NP_001017992.1	hypothetical protein LOC345651	1.35	0.6
657	S100A11	NP_005611.1	S100 calcium binding protein A11	1.15	1.11
658	NUMA1	NP_006176.2	nuclear mitotic apparatus protein 1	0.79	0.86
660	CSNK2A1	NP_001886.1	casein kinase II alpha 1 subunit isoform a	1.21	0.92
661	DDX17	NP_006377.2	DEAD box polypeptide 17 isoform p82	1.21	0.76
662	DNAH2	NP_065928.2	dynein heavy chain domain 3	0.96	0.88
663	HNRPH2	NP_062543.1	heterogeneous nuclear ribonucleoprotein H2	0.9	1.26
664	STXBP2	NP_008880.1	syntaxin binding protein 2	0.64	1.38
665	GNL3	NP_996562.1	guanine nucleotide binding protein-like 3 isoform 2	0.78	1.04
666	SDF4	NP_057260.2	calcium binding protein Cab45	0.86	0.82
667	LOC647153	XP_946879.1	PREDICTED: similar to voltage-dependent anion channel 2	0.72	1.07
668	HIST1H1E	NP_005312.1	histone cluster 1, H1e	0.98	1.03
669	MLL	NP_005924.2	myeloid/lymphoid or mixed-lineage leukemia	1	1.18
671	PDIA5	NP_006801.1	protein disulfide isomerase-associated 5	1.24	0.92
672	RPL18	NP_000970.1	ribosomal protein L18	1.19	0.81
673	FEN1	NP_004102.1	flap structure-specific endonuclease 1	0.82	0.97
674	VPS26A	NP_004887.2	vacuolar protein sorting 26 A isoform 1	0.69	0.88
675	LSM14A	NP_056393.1	LSM14 homolog A	0.85	0.9

676	IGF2R	NP_000867.2	insulin-like growth factor 2 receptor	0.98	0.81
677	SFRS7	NP_001026854.1	splicing factor, arginine/serine-rich 7	1.04	0.8
678	TARDBP	NP_031401.1	TAR DNA binding protein	1.32	1.58
679	CHP	NP_009167.1	calcium binding protein P22	1.12	0.76
680	CENPE	NP_001804.2	centromere protein E	0.95	0.97
681	RAB11A	NP_004654.1	Ras-related protein Rab-11A	0.98	1.52
683	REEP6	NP_612402.1	polyposis locus protein 1-like 1	0.7	0.83
684	ABCA4	NP_000341.2	ATP-binding cassette, sub-family A member 4	0.36	0.94
685	HLA-B	NP_005505.2	major histocompatibility complex, class I, B	0.71	0.71
686	CDC42	NP_001034891.1	cell division cycle 42 isoform 1	1.13	1.11
687	RAB2A	NP_002856.1	RAB2, member RAS oncogene family	2.63	1.26
688	SMC1A	NP_006297.2	structural maintenance of chromosomes 1A	0.84	1.09
689	ASCC3L1	NP_054733.2	activating signal cointegrator 1 complex subunit 3-like 1	1.44	1.91
690	ASL	NP_001020115.1	argininosuccinate lyase isoform 2	0.95	1.08
691	PSMB3	NP_002786.2	proteasome beta 3 subunit	1.25	1.01
692	VAT1	NP_006364.2	vesicle amine transport protein 1	1.17	1.09
693	SNX27	NP_112180.4	sorting nexin family member 27	1.11	0.94
694	CTSB	NP_001899.1	cathepsin B	1.05	1.19
695	SHMT2	NP_005403.2	serine hydroxymethyltransferase 2 (mitochondrial)	1.23	0.85
696	RPS6KA3	NP_004577.1	ribosomal protein S6 kinase, 90kDa, polypeptide 3	1.26	1
697	FLNC	NP_001449.3	gamma filamin	0.82	0.78
698	TOP1	NP_003277.1	DNA topoisomerase I	0.77	1.03
699	LACTB2	NP_057111.1	lactamase, beta 2	0.94	0.97
700	ECH1	NP_001389.2	peroxisomal enoyl-coenzyme A hydratase-like protein	0.8	0.28
701	CAD	NP_004332.2	carbamoylphosphate synthetase 2	0.9	0.93
702	DHX15	NP_001349.2	DEAH (Asp-Glu-Ala-His) box polypeptide 15	1.03	1.32
703	LIMA1	NP_057441.1	epithelial protein lost in neoplasm beta	0.78	0.89
704	RBM42	NP_077297.2	hypothetical protein LOC79171	1.22	0.94
705	HP1BP3	NP_057371.2	HP1-BP74	0.87	0.76
706	SORD	NP_003095.1	sorbitol dehydrogenase	0.9	0.66
707	NSFL1C	NP_057227.2	p47 protein isoform a	1.01	1.17
708	OSBP	NP_002547.1	oxysterol binding protein	1.12	0.93
709	EPS8	NP_004438.3	epidermal growth factor receptor pathway substrate 8	0.58	0.72
710	ACAT1	NP_000010.1	acetyl-Coenzyme A acetyltransferase 1	0.91	0.92
711	LOC645619	XP_933725.1	PREDICTED: similar to Adenylate kinase isoenzyme 4	0.9	1.85
712	CALD1	NP_004333.1	caldesmon 1 isoform 2	0.9	1.18
713	MYO18A	NP_976063.1	myosin 18A isoform b	0.69	1.18
714	C7orf20	NP_057033.2	hypothetical protein LOC51608	1.27	0.79
715	VBP1	NP_003363.1	von Hippel-Lindau binding protein 1	0.48	1.24
716	H1FO	NP_005309.1	H1 histone family, member 0	1.28	1.56
717	CEP290	NP_079390.3	centrosomal protein 290kDa	0.79	1.04
718	KTN1	NP_891556.1	kinectin 1 isoform a	0.97	1.05
719	UNC84B	NP_056189.1	unc-84 homolog B	0.66	0.99
720	SEC23A	NP_006355.2	SEC23-related protein A	0.92	0.99
721	LPP	NP_005569.1	LIM domain containing preferred translocation partner	0.87	0.56
722	TM9SF4	NP_055557.1	transmembrane 9 superfamily protein member 4	0.93	0.85
723	ATP5D	NP_001001975.1	ATP synthase, H+ transporting, mitochondrial F1 complex	0.73	1.2
724	PDCD10	NP_665859.1	programmed cell death 10	1.06	0.7
725	LOC150739	XP_092267.4	PREDICTED: similar to Keratin, type II cytoskeletal 8	1.01	1.17
726	ABCF2	NP_009120.1	ATP-binding cassette, sub-family F, member 2 isoform a	1.61	1.51
727	CAPN2	NP_001739.1	calpain 2, large subunit	1.17	0.87
728	LOC646817	XP_942225.1	PREDICTED: similar to Protein SET	0.88	0.49

729	CSDA	NP_003642.2	cold shock domain protein A	1.07	0.74
730	ARF6	NP_001654.1	ADP-ribosylation factor 6	1.32	0.95
731	TJP2	NP_004808.2	tight junction protein 2 (zona occludens 2) isoform 1	1.04	0.76
732	FLOT1	NP_005794.1	flotillin 1	0.85	0.78
733	FLOT2	NP_004466.2	flotillin 2	0.66	0.84
734	SLC16A1	NP_003042.3	solute carrier family 16, member 1	0.76	0.96
736	NDUFAB1	NP_004994.1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex	0.74	1.02
737	RAB1B	NP_112243.1	RAB1B, member RAS oncogene family	1.34	1.41
738	EHD1	NP_006786.2	EH-domain containing 1	0.75	1.34
739	MYO15A	NP_057323.3	myosin XV	1.08	0.76
740	SEC31A	NP_055748.2	SEC31 homolog A isoform 1	0.96	0.92
741	CP	NP_000087.1	ceruloplasmin	1.38	0.48
742	CTNNB1	NP_001895.1	catenin (cadherin-associated protein), beta 1, 88kDa	1.02	0.91
743	KRT6B	NP_005546.2	keratin 6B	1.39	0.59
744	ANKRD28	NP_056014.2	ankyrin repeat domain 28	0.77	1.7
745	THOC4	NP_005773.2	THO complex 4	0.9	1.07
746	DBN1	NP_004386.2	drebrin 1 isoform a	0.63	0.85
747	ACADS	NP_000008.1	acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain	0.98	0.83
748	PAFAH1B3	NP_002564.1	platelet-activating factor acetylhydrolase, isoform II	0.87	0.95
749	MRPL28	NP_006419.2	mitochondrial ribosomal protein L28	1.03	0.76
750	FAM135A	NP_065870.2	hypothetical protein LOC57579	1.03	1.34
751	STX7	NP_003560.1	syntaxin 7	0.97	1.14
752	DNAJA2	NP_005871.1	DnaJ subfamily A member 2	1.04	1.28
753	N-PAC	NP_115958.2	cytokine-like nuclear factor n-pac	0.99	0.79
754	KARS	NP_005539.1	lysyl-tRNA synthetase	0.76	0.86
755	SCFD2	NP_689753.2	sec1 family domain containing 2	0.79	0.99
756	ITLN2	NP_543154.1	intelectin 2	1.03	1.75
757	AADACL1	NP_065843.3	arylacetamide deacetylase-like 1	0.8	0.74
758	MARS	NP_004981.2	methionine-tRNA synthetase	0.95	0.95
759	UNQ501	NP_940938.1	hypothetical protein LOC374882	0.84	0.93
760	CCDC109A	NP_612366.1	coiled-coil domain containing 109A	0.95	1.11
761	USP14	NP_001032411.1	ubiquitin specific protease 14 isoform b	1.04	1.38
762	COPS8	NP_006701.1	COP9 signalosome subunit 8 isoform 1	4.84	4.5
763	COPE	NP_009194.2	epsilon subunit of coatomer protein complex isoform a	0.93	0.69
764	CPT2	NP_000089.1	carnitine palmitoyltransferase II	1.3	0.86
765	TCIRG1	NP_006010.2	T-cell, immune regulator 1 isoform a	0.62	1.17
766	TIMM44	NP_006342.2	translocase of inner mitochondrial membrane 44	1.44	0.73
767	TSG101	NP_006283.1	tumor susceptibility gene 101	1.32	0.98
768	ENY2	NP_064574.1	enhancer of yellow 2 homolog	1.07	1.34
769	SMARCC1	NP_003065.2	SWI/SNF-related matrix-associated regulator	0.63	0.12
770	POSTN	NP_006466.1	periostin, osteoblast specific factor	0.88	1.56
771	SNAP23	NP_570710.1	synaptosomal-associated protein 23 isoform SNAP23B	0.73	1.94
772	ZC3H11A	NP_055642.3	zinc finger CCCH-type containing 11A	1.16	0.86
773	GALE	NP_000394.2	UDP-galactose-4-epimerase	2.23	0.93
774	SSR4	NP_006271.1	signal sequence receptor, delta	0.99	0.81
775	ANXA10	NP_009124.2	annexin A10	0.87	0.78
777	RPL36	NP_378669.1	ribosomal protein L36	1.2	1
778	BAT2D1	NP_055987.2	HBxAg transactivated protein 2	0.94	1
779	ABI1	NP_001012770.1	abl-interactor 1 isoform d	0.88	1.33
780	SLC25A13	NP_055066.1	solute carrier family 25, member 13 (citrin)	0.73	1.04
781	KIAA0090	NP_055862.1	hypothetical protein LOC23065	1.02	1.22
782	EML4	NP_061936.2	echinoderm microtubule associated protein like 4	0.6	1.58

783	ACSL3	NP_976251.1	acyl-CoA synthetase long-chain family member 3	0.6	0.82
785	FLJ25076	XP_059689.4	PREDICTED: similar to CG4502-PA, isoform A	0.57	2.82
786	PRMT1	NP_001527.2	HMT1 hnRNP methyltransferase-like 2 isoform 1	1.42	1.56
787	HMGCS1	NP_002121.3	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	1.48	0.4
788	DYNC1I2	NP_001369.1	dynein, cytoplasmic, intermediate polypeptide 2	0.76	0.56
789	ZC3H15	NP_060941.2	erythropoietin 4 immediate early response	0.93	1.21
790	SLC1A1	NP_004161.4	solute carrier family 1, member 1	1.72	0.73
791	NACA	NP_005585.1	nascent-polypeptide-associated complex alpha polypeptide	0.76	0.97
792	EIF3G	NP_003746.2	eukaryotic translation initiation factor 3, subunit 4 delta	2.33	1.78
793	RPL19	NP_000972.1	ribosomal protein L19	0.63	1.29
794	OSTF1	NP_036515.3	osteoclast stimulating factor 1	1.52	1.13
795	VNN1	NP_004657.1	vanin 1	0.84	0.43
796	PAFAH1B2	NP_002563.1	platelet-activating factor acetylhydrolase, isoform II	0.69	1.46
797	LYAR	NP_060286.1	hypothetical protein FLJ20425	0.73	1.27
798	EIF3J	NP_003749.2	eukaryotic translation initiation factor 3, subunit 1 alpha	1.09	1.17
799	KRT71	NP_258259.1	keratin 6 irs	2.26	1.1
800	SEC63	NP_009145.1	SEC63-like protein	2.3	1.27
802	TPP2	NP_003282.1	tripeptidyl peptidase II	1.04	1.01
803	RRAGD	NP_067067.1	Ras-related GTP binding D	1.06	1.18
804	LOH11CR2A	NP_055437.2	BCSC-1 isoform 1	0.39	0.6
805	C20orf116	NP_076424.1	hypothetical protein LOC65992	0.75	1.52
806	IPO9	NP_060555.2	importin 9	0.53	1.71
807	EHD2	NP_055416.2	EH-domain containing 2	0.84	1.78
808	DECR1	NP_001350.1	2,4-dienoyl CoA reductase 1	0.72	0.6
809	QARS	NP_005042.1	glutaminyl-tRNA synthetase	0.99	0.93
810	CMAS	NP_061156.1	cytidine 5'-monophosphate N-acetylneuraminic acid synthetase	0.96	3.83
811	ARHGEF16	NP_055263.1	Rho guanine exchange factor 16	0.74	0.82
812	DNAJC5	NP_079495.1	DnaJ (Hsp40) homolog, subfamily C, member 5	1.19	0.33
813	SEPT7	NP_001011553.1	cell division cycle 10 isoform 2	1.07	0.97
814	SKP1A	NP_733779.1	S-phase kinase-associated protein 1A isoform b	1.12	0.82
815	LOC645691	XP_941883.1	PREDICTED: similar to nuclear ribonucleoprotein A1	0.97	1.6
817	NME1	NP_000260.1	non-metastatic cells 1, protein expressed in isoform b	0.95	0.85
818	SLC25A6	NP_001627.1	solute carrier family 25, member A6	0.83	0.6
819	SFN	NP_006133.1	stratifin	1.12	0.63
820	ANXA13	NP_001003954.1	annexin A13 isoform b	0.69	0.41
821	NAP1L1	NP_004528.1	nucleosome assembly protein 1-like 1	0.98	1.13
822	SFRS9	NP_003760.1	splicing factor, arginine/serine-rich 9	0.98	1.47
824	PPIL1	NP_057143.1	peptidylprolyl isomerase-like 1	0.81	1.06
825	TGFB1	NP_000349.1	transforming growth factor, beta-induced, 68kDa	1	1.11
826	XPNPEP1	NP_065116.2	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	0.99	0.5
827	POLR2A	NP_000928.1	DNA directed RNA polymerase II polypeptide A	0.91	0.97
828	DKC1	NP_001354.1	dyskerin	0.96	0.97
829	ZMPSTE24	NP_005848.2	zinc metalloproteinase STE24	0.81	0.72
830	MTCH2	NP_055157.1	mitochondrial carrier homolog 2	2.57	1.26
831	PRPF3	NP_004689.1	PRP3 pre-mRNA processing factor 3 homolog	1.28	0.99
832	SFRS2	NP_003007.2	splicing factor, arginine/serine-rich 2	1.26	0.78
833	STT3B	NP_849193.1	source of immunodominant MHC-associated peptides	1.77	0.91
835	DCPS	NP_054745.1	mRNA decapping enzyme	1.04	1.07
836	FDPS	NP_001995.1	farnesyl diphosphate synthase	0.49	0.73
837	AQP1	NP_932766.1	aquaporin 1	1.2	0.8
838	ASNS	NP_899199.1	asparagine synthetase	1.16	1.31
839	HINT2	NP_115982.1	PKCI-1-related HIT protein	1.16	0.93

840	MARCKS	NP_002347.4	myristoylated alanine-rich protein kinase C substrate	0.59	0.46
841	HAGH	NP_005317.2	hydroxyacyl glutathione hydrolase isoform 1	0.8	0.7
842	VAMP2	NP_055047.1	vesicle-associated membrane protein 2 (synaptobrevin 2)	0.73	0.95
843	TIMM50	NP_001001563.1	translocase of inner mitochondrial membrane 50 homolog	1.3	0.89
844	C20orf77	NP_067038.1	hypothetical protein LOC58490	1.83	0.83
845	TMED2	NP_006806.1	coated vesicle membrane protein	0.93	1.02
846	NEDD8	NP_006147.1	neural cell expressed, developmentally down-regulated 8	0.8	0.69
847	PAPSS1	NP_005434.4	3'-phosphoadenosine 5'-phosphosulfate synthase 1	0.97	1.15
848	SH3BGRL	NP_003013.1	SH3 domain binding glutamic acid-rich protein like	0.85	0.84
849	ABCD3	NP_002849.1	ATP-binding cassette, sub-family D, member 3	0.95	0.73
850	BID	NP_932070.1	BH3 interacting domain death agonist isoform 1	1.56	1.1
852	TMEM111	NP_060917.1	hypothetical protein LOC55831	1.46	1.14
853	PSMB8	NP_683720.2	proteasome beta 8 subunit isoform E2 proprotein	1.43	1.01
854	RP2	NP_008846.1	XRP2 protein	0.77	1.91
855	MAP2K1	NP_002746.1	mitogen-activated protein kinase kinase 1	1.01	1.65
856	IMPA1	NP_005527.1	inositol(myo)-1(or 4)-monophosphatase 1	1.12	0.7
857	GOT1	NP_002070.1	aspartate aminotransferase 1	1.12	0.91
858	DTYMK	NP_036277.2	deoxythymidylate kinase (thymidylate kinase)	1.59	2.27
859	HSD17B13	NP_835236.1	hydroxysteroid (17-beta) dehydrogenase 13	1.41	1.24
860	ABHD11	NP_683711.1	abhydrolase domain containing 11 isoform 2	1.17	1.16
861	TIPRL	NP_690866.1	TIP41, TOR signalling pathway regulator-like isoform 1	0.79	1.37
863	PFDN2	NP_036526.2	prefoldin subunit 2	0.82	1.75
864	VPS29	NP_057310.1	vacuolar protein sorting 29 isoform 1	2.09	0.96
865	COPZ1	NP_057141.1	coatamer protein complex, subunit zeta 1	1.08	0.79
866	SEC11A	NP_055115.1	SEC11-like 1	0.88	1.99
867	MESDC2	NP_055969.1	mesoderm development candidate 2	1.4	1.55
868	APRT	NP_001025189.1	adenine phosphoribosyltransferase isoform b	0.9	1.11
869	GRHPR	NP_036335.1	glyoxylate reductase/hydroxypyruvate reductase	1.11	0.8
870	SPCS1	NP_054760.2	signal peptidase complex subunit 1 homolog	1.01	1.13
871	BRCC3	NP_001018065.1	BRCA1/BRCA2-containing complex, subunit 3 isoform 2	1.15	0.91
872	SSR3	NP_009038.1	signal sequence receptor gamma subunit	1.17	1.4
873	ARL6IP5	NP_006398.1	ADP-ribosylation-like factor 6 interacting protein 5	1.15	1.05
874	PSMD14	NP_005796.1	26S proteasome-associated pad1 homolog	0.94	1.09
875	GMFB	NP_004115.1	glia maturation factor, beta	0.94	0.92
876	SERPINB5	NP_002630.1	serine (or cysteine) proteinase inhibitor, clade B, member 5	1.55	0.64
877	MGST2	NP_002404.1	microsomal glutathione S-transferase 2	0.87	1.31
878	TP53I11	NP_006025.2	p53-induced protein	0.66	1.13
879	FAM84B	NP_777571.1	breast cancer membrane protein 101	0.64	0.69
880	PSMD9	NP_002804.2	proteasome 26S non-ATPase subunit 9	1.13	0.85
881	DBI	NP_001073332.1	diazepam binding inhibitor isoform 2	0.88	0.66
882	PTPLAD1	NP_057479.2	butyrate-induced transcript 1	1.25	0.7
883	BPNT1	NP_006076.4	3'(2'), 5'-bisphosphate nucleotidase 1	1.27	0.94
884	COQ5	NP_115690.3	coenzyme Q5 homolog, methyltransferase	1.05	0.77
885	FLJ10292	NP_060518.1	mago-nashi homolog 2	0.79	0.94
886	LOC644820	XP_944971.1	PREDICTED: similar to eukaryotic translation elongation factor 1	1.24	0.72
887	HMOX2	NP_002125.3	heme oxygenase (decyclizing) 2	1.13	0.81
888	PTRH2	NP_057161.1	Bcl-2 inhibitor of transcription isoform b	1.82	2.47
889	TRIM25	NP_005073.2	tripartite motif-containing 25	0.92	1.33
890	NDUFB4	NP_004538.2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4	1.03	0.79
891	GNG12	NP_061329.3	G-protein gamma-12 subunit	1.11	0.84
892	TBCA	NP_004598.1	tubulin-specific chaperone a	1.28	0.69
893	SYNGR2	NP_004701.1	synaptogyrin 2	0.88	0.98

894	TACSTD1	NP_002345.1	tumor-associated calcium signal transducer 1	2.94	0.55
895	C19orf10	NP_061980.1	chromosome 19 open reading frame 10	1.01	0.64
896	RCN3	NP_065701.2	reticulocalbin 3, EF-hand calcium binding domain	1.86	1.82
897	VAMP8	NP_003752.2	vesicle-associated membrane protein 8	1.09	1.42
898	REG4	NP_114433.1	regenerating islet-derived family, member 4	1.87	1
899	MAP2K1IP1	NP_068805.1	mitogen-activated protein kinase kinase 1 interacting protein 1	1.23	1.32
900	SHANK3	NP_001073889.1	proline-rich synapse-associated protein 2	0.8	1.17
901	PCLO	XP_940803.2	PREDICTED: similar to Protein piccolo (Aczonin) isoform 7	1.1	0.64
902	RPL31	NP_000984.1	ribosomal protein L31	1.09	1.93
903	C14orf78	XP_001132404.1	PREDICTED: similar to AHNAK nucleoprotein isoform 1	0.72	1.23
904	CLTB	NP_009028.1	clathrin, light polypeptide isoform b	0.78	1.02
905	DNASE2	NP_001366.1	deoxyribonuclease II, lysosomal	1.66	2
906	FAM46C	NP_060179.2	hypothetical protein LOC54855	0.83	0.63
907	CRYZ	NP_001880.2	crystallin, zeta	1.27	0.92
908	PINK1	NP_115785.1	PTEN induced putative kinase 1	1.07	1.11
909	ARFGEF2	NP_006411.1	ADP-ribosylation factor guanine nucleotide-exchange factor 2	1.28	0.46
910	NOP5	NP_057018.1	nucleolar protein NOP5/NOP58	0.91	1.05
911	MYO1C	NP_001074419.1	myosin IC isoform b	1.07	0.64
912	HSD17B4	NP_000405.1	hydroxysteroid (17-beta) dehydrogenase 4	1.08	1.39
913	C9orf93	NP_775821.2	hypothetical protein LOC203238	0.92	1.02
914	RPL21	XP_940793.1	PREDICTED: similar to 60S ribosomal protein L21	0.8	1.02
915	SRC	NP_005408.1	proto-oncogene tyrosine-protein kinase SRC	1.07	1.17
916	SPTB	NP_001020029.1	spectrin beta isoform a	0.86	1.08
917	PCNT	NP_006022.3	pericentrin (kendrin)	0.82	1.08
918	D2HGDH	NP_689996.4	D-2-hydroxyglutarate dehydrogenase	1.16	1.06
919	PCNA	NP_002583.1	proliferating cell nuclear antigen	0.82	0.73
920	CPT1A	NP_001867.2	carnitine palmitoyltransferase 1A isoform 1	0.46	0.56
921	HEXB	NP_000512.1	hexosaminidase B	2.02	0.89
922	LETM2	NP_653253.1	leucine zipper-EF-hand containing transmembrane protein 2	0.77	1.15
923	NCBP1	NP_002477.1	nuclear cap binding protein subunit 1, 80kDa	0.85	0.67
924	LZIC	NP_115744.2	leucine zipper and CTNNBIP1 domain containing	0.98	0.8
926	C20orf7	NP_077025.2	hypothetical protein LOC79133 isoform 1	0.78	1.29
927	TMED5	NP_057124.2	transmembrane emp24 protein transport domain containing 5	0.95	2.81
928	MAPRE1	NP_036457.1	microtubule-associated protein, RP/EB family, member 1	0.73	1.2
930	TXNDC1	NP_110382.2	thioredoxin domain containing	0.75	0.94
931	APC2	NP_005874.1	adenomatosis polyposis coli 2	0.97	1.34
932	SBDS	NP_057122.2	Shwachman-Bodian-Diamond syndrome protein	1.22	0.85
933	GOLGB1	NP_004478.1	golgi autoantigen, golgin subfamily b, macrogolgin	0.58	1.1
934	COL24A1	NP_690850.2	collagen, type XXIV, alpha 1	1.42	0.75
935	COL16A1	NP_001847.3	alpha 1 type XVI collagen	0.94	0.83
936	ATPIF1	NP_057395.1	ATPase inhibitory factor 1 isoform 1	1.12	0.86
937	SPTBN4	NP_066022.2	spectrin, beta, non-erythrocytic 4 isoform sigma1	0.74	1.25
938	DNAJC8	NP_055095.2	DnaJ (Hsp40) homolog, subfamily C, member 8	1.11	0.96
939	GDI1	NP_001484.1	GDP dissociation inhibitor 1	0.7	0.52
940	SARM1	NP_055892.1	sterile alpha and TIR motif containing 1	0.46	1.05
941	SRP68	NP_055045.2	signal recognition particle 68kDa	0.97	0.88
942	DCBLD2	NP_563615.3	discoidin, CUB and LCCL domain containing 2	1.45	0.55
943	SYNE2	NP_878918.2	spectrin repeat containing, nuclear envelope 2 isoform 5	0.91	1.06
944	SNX6	NP_689419.2	sorting nexin 6 isoform b	1.02	1.76
945	SUMO2	NP_001005849.1	SMT3 suppressor of mif two 3 homolog 2 isoform b	1.05	1.26
946	HIST3H2BB	NP_778225.1	histone H2B	2.13	1.49
947	KRBA1	NP_115923.2	KIAA1862 protein	1.14	0.56

949	PSMD5	NP_005038.1	proteasome 26S non-ATPase subunit 5	1.21	0.9
950	TLOC1	NP_003253.1	translocation protein 1	0.72	1.18
952	MAGI1	NP_001028229.1	membrane associated guanylate kinase	1.01	0.67
953	MRPL44	NP_075066.1	mitochondrial ribosomal protein L44	1.26	1.36
955	CGN	NP_065821.1	cingulin	0.78	0.82
956	RBBP8	NP_002885.1	retinoblastoma binding protein 8 isoform a	0.9	1.2
957	LOC731947	XP_001131366.1	PREDICTED: hypothetical protein	0.88	0.82
958	DNAH5	NP_001360.1	dynein, axonemal, heavy polypeptide 5	0.74	0.67
959	NAV1	NP_065176.2	neuron navigator 1	1.28	0.73
960	CDC42BPB	NP_006026.3	CDC42-binding protein kinase beta	1.2	1.04
961	SYNE1	NP_892006.1	nesprin 1 longest	1.01	0.88
962	HNRPA0	NP_006796.1	heterogeneous nuclear ribonucleoprotein A0	1.91	0.54
963	ATP2C1	NP_001001487.1	calcium-transporting ATPase 2C1 isoform 1b	0.45	0.56
964	DLD	NP_000099.2	dihydrolipoamide dehydrogenase	0.88	0.95
966	FAM3C	NP_001035109.1	family with sequence similarity 3, member C	0.73	0.9
967	EIF3E	NP_001559.1	eukaryotic translation initiation factor 3, subunit 6 48kDa	1.11	1.12
968	ATP5E	NP_008817.1	ATP synthase, H+ transporting, mitochondrial F1 complex	1.05	0.94
969	PCGF2	NP_009075.1	ring finger protein 110	0.48	1.28
970	EWSR1	NP_005234.1	Ewing sarcoma breakpoint region 1 isoform EWS	1.21	1
972	LOC401206	XP_942473.1	PREDICTED: similar to 40S ribosomal protein S25	1.19	1.65
973	PANK2	NP_705902.2	pantothenate kinase 2 isoform 1	1.1	1.17
974	RPL27	NP_000979.1	ribosomal protein L27	1.22	1.23
975	TPM2	NP_998839.1	tropomyosin 2 (beta) isoform 2	0.98	1.35
978	CCDC67	NP_857596.2	coiled-coil domain containing 67	0.83	1.39
979	FLJ20273	NP_061900.1	hypothetical protein LOC54502	1.12	1.74
980	SUPT5H	NP_003160.2	suppressor of Ty 5 homolog	1.22	0.82
981	ABCC11	NP_660187.1	ATP-binding cassette, sub-family C, member 11 isoform b	0.96	1
982	LOC729297	XP_001129875.1	PREDICTED: similar to vitamin A-deficient protein 1	0.46	0.92
983	LOC728317	XP_001127165.1	PREDICTED: similar to melanoma associated antigen	1.01	0.89
984	PCNXL3	XP_950319.2	PREDICTED: similar to pecanex-like 3 isoform 5	1.1	0.67
985	LOC731074	XP_001128332.1	PREDICTED: hypothetical protein	1.01	1.26
986	TAGLN3	NP_001008274.1	transgelin 3	0.69	2.08
987	HIST2H2AA3	NP_003507.1	H2A histone family, member O	0.91	1.31
988	KRT85	NP_002274.1	keratin 85	1	1.16
989	EIF4G1	NP_937884.1	eukaryotic translation initiation factor 4 gamma, 1 isoform 1	0.83	0.99
990	KIAA1641	NP_079466.2	hypothetical protein LOC57730	0.89	1.17
991	PGRMC1	NP_006658.1	progesterone receptor membrane component 1	1.22	1.72
992	AHDC1	NP_001025053.1	AT hook, DNA binding motif, containing 1	0.38	1.57
993	LRIG2	NP_055628.1	leucine-rich repeats and immunoglobulin-like domains 2	0.84	0.94
994	MUC19	XP_497341.3	PREDICTED: similar to mucin 19	0.91	1.24
995	C1orf77	NP_056422.2	hypothetical protein LOC26097	1.24	1.1
996	CYP26C1	NP_899230.2	cytochrome P450, family 26, subfamily C, polypeptide 1	1.49	1.65
997	IDH3A	NP_005521.1	isocitrate dehydrogenase 3 (NAD+) alpha	1.36	0.91
998	CHD5	NP_056372.1	chromodomain helicase DNA binding protein 5	1.01	1
999	PTF1A	NP_835455.1	pancreas specific transcription factor, 1a	0.94	0.9
1000	LOC389816	XP_944413.1	PREDICTED: similar to slit CG8355-PC, isoform C	0.87	0.87
1001	COL5A1	NP_000084.3	alpha 1 type V collagen	0.82	1.02
1002	OPA1	NP_570850.1	optic atrophy 1 isoform 8	1.17	1.3
1003	PSMD10	NP_736606.1	proteasome 26S non-ATPase subunit 10 isoform 2	0.91	0.95
1004	PDZRN3	NP_055824.1	PDZ domain containing RING finger 3	0.84	1.2
1005	ADSS	NP_001117.2	adenylosuccinate synthase	0.56	0.95
1008	PFKM	NP_000280.1	phosphofructokinase, muscle	1.01	0.94

1009	C14orf159	NP_079228.3	hypothetical protein LOC80017	0.44	1.09
1010	VTN	NP_000629.3	vitronectin	0.63	1.78
1011	ACADVL	NP_000009.1	acyl-Coenzyme A dehydrogenase, very long chain isoform 1	0.78	1.12
1012	S100A16	NP_525127.1	S100 calcium binding protein A16	0.91	1.09
1013	CEP152	NP_055800.2	centrosomal protein 152kDa	1.08	0.93
1014	ATP5O	NP_001688.1	mitochondrial ATP synthase, O subunit	0.92	1.1
1015	CACYBP	NP_055227.1	calcyclin binding protein isoform 1	0.73	1.34
1016	HIST1H4G	NP_003538.1	H4 histone family, member L	0.65	0.65
1017	BAHCC1	XP_001134463.1	PREDICTED: similar to BAH domain	1.37	0.84
1018	EXOC5	NP_006535.1	SEC10 protein	0.76	1.12
1019	BRI3BP	NP_542193.3	BRI3-binding protein	0.85	0.9
1020	SMC4	NP_005487.3	SMC4 structural maintenance of chromosomes 4	0.97	1.64
1021	KIAA1429	NP_056311.2	hypothetical protein LOC25962 isoform 1	1.11	0.51
1022	DACT1	NP_057735.2	dapper 1 isoform 1	0.85	0.97
1024	USP5	NP_003472.1	Ubiquitin isopeptidase T	0.87	0.88
1025	PPT1	NP_000301.1	palmitoyl-protein thioesterase 1	1.27	0.69
1026	JMJD4	NP_075383.1	jumonji domain containing 4	0.59	1.01
1027	PXN	NP_002850.1	paxillin	2.04	0.68
1028	POFUT1	NP_056167.1	protein O-fucosyltransferase 1 isoform 1	1.18	0.98
1029	MGA	NP_001074010.1	MAX dimerization protein 5	0.88	0.87
1030	EIF4ENIF1	NP_062817.1	eukaryotic translation initiation factor 4E nuclear import factor 1	1.09	0.75
1031	C4orf15	NP_078787.2	hypothetical protein LOC79441	1.09	1.34
1032	GSPT2	NP_060564.2	peptide chain release factor 3	0.89	1.08
1033	MEGF6	NP_001400.3	EGF-like-domain, multiple 3	0.98	1.24
1034	TANC2	XP_947427.1	PREDICTED: similar to TPR domain	0.84	0.91
1035	LOC139249	XP_001125784.1	PREDICTED: similar to Protein FAM47A	1.02	1.95
1036	DST	NP_001714.1	dystonin isoform 1e	0.86	1.32
1037	DAG1	NP_004384.1	dystroglycan 1	0.97	0.79