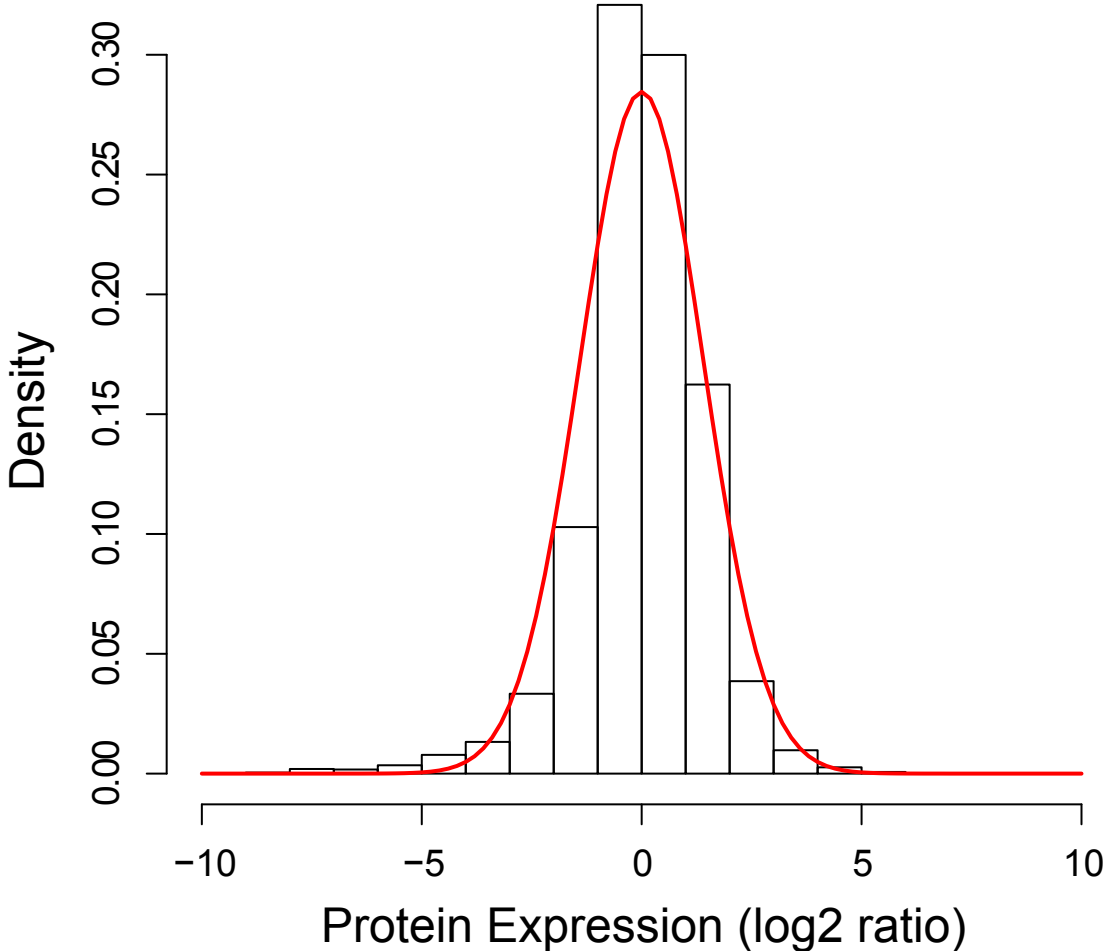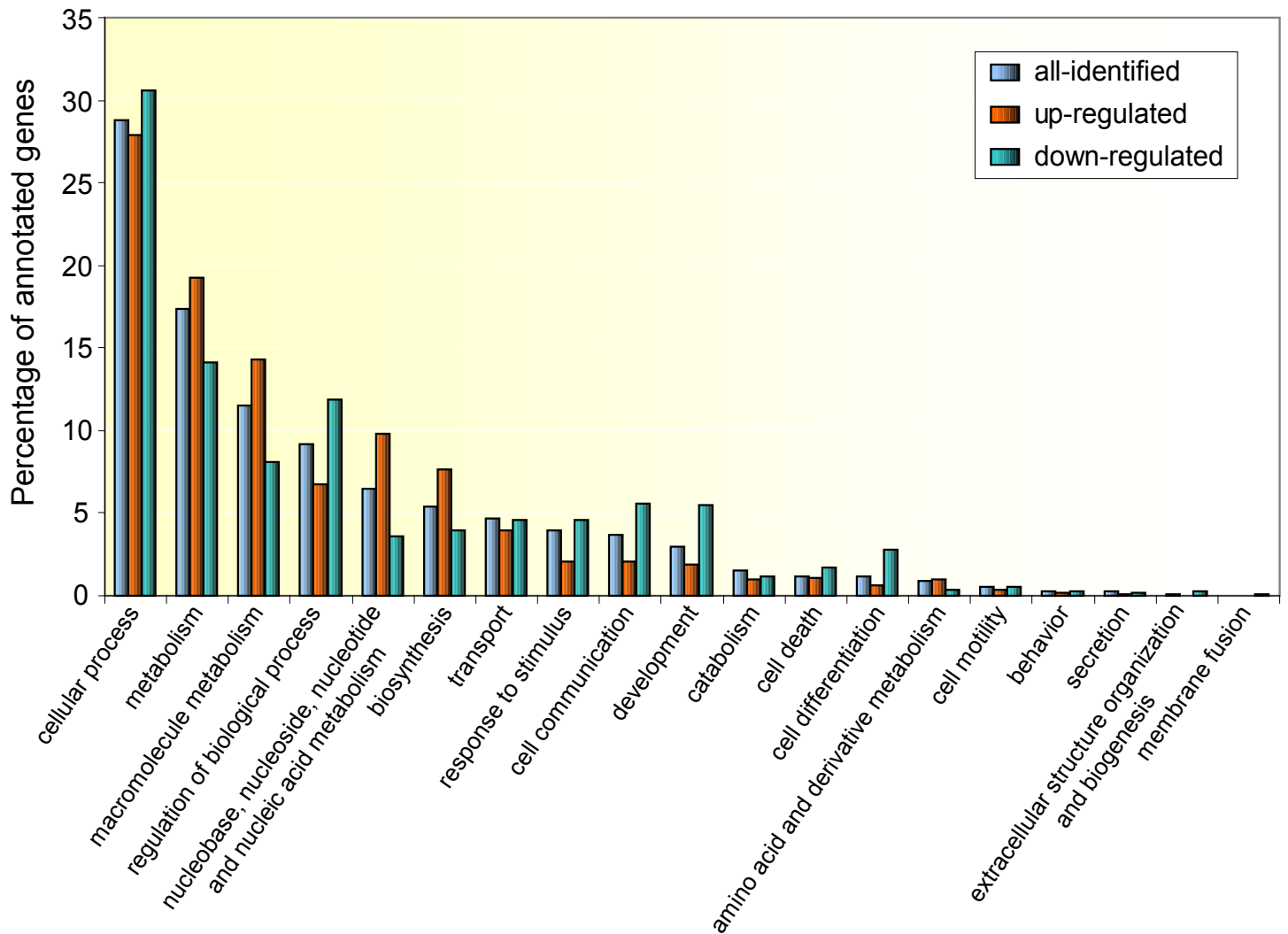Supplemental Fig 1.

Supplemental Fig 1. The protein expression ratios (log2 transformed) between 4+ tumor and 1- tumor are in a normal distribution.

Supplemental Fig 2.

Supplemental Fig 2. GO functional categories of the identified proteins in low and high-risk neuroblastoma. GO functional categories of all ICAT identified proteins as well as different expressed proteins in 4+ and 1- tumors are represented by GOSlim terms, which are a subset of GO and provide a higher level of annotation than the standard GO. Cellular process, metabolism, biosynthesis, regulation of biological processes are high in both up- and down-regulated protein groups. The processes involved in development, cell differentiation, cell death, and cell communication are relatively high in down-regulated protein group.

Supplemental Table 1. Additional Neuroblastoma Turmor Sample Information

	AgeAtDiagnosis	Stage	MYCN_Status	Survival	Source	TestingType
NB110	0.11 yrs	1	not amp	Alive	DZNSG	ICAT
NB108	5.56 yrs	1	not amp	Alive	DZNSG	Western Blot
NB109	0 yrs	1	not amp	Alive	DZNSG	Western Blot
NB111	3.74 yrs	1	not amp	Alive	DZNSG	Western Blot
NB112	0.5 yrs	1	not amp	Alive	DZNSG	Western Blot
NB113	11.22 yrs	1	not amp	Alive	DZNSG	Western Blot
NB103	1.56 yrs	4	amp	Dead	DZNSG	ICAT
NB535	1.04 yrs	4	amp	Dead	CHTN	Western Blot
NB545	3.36 yrs	4	amp	Dead	CHTN	Western Blot
NB547	1.54 yrs	4	amp	Dead	CHTN	Western Blot
NB561	0.55 yrs	4	amp	Dead	CHTN	Western Blot
NB581	1.58 yrs	4	amp	Dead	CHTN	Western Blot

Note: DZNSG: German Cancer Research Center, CHTN: Cooperative Human Tissue Network

Supplemental Table 2: GSEA analysis of protein expression changes in neuroblastoma

	NAME	SIZE	ES	NES	NOM p-val	FDR q-val
Up-regulated in 4+ tumor	MYC_TARGETS	17	0.77	2.10	0.000	0.000
	RIBOSOMAL_PROTEINS	30	0.67	2.06	0.000	0.001
	HSA03010_RIBOSOME	24	0.70	2.04	0.000	0.001
	ADIP_DIFF_CLUSTER4	15	0.71	1.87	0.000	0.009
	ELECTRON_TRANSPORT_CHAIN	22	0.65	1.85	0.001	0.009
	HUMAN_MITODB_6_2002	77	0.52	1.87	0.000	0.010
	HDACI_COLON_BUT12HRS_DN	20	0.64	1.82	0.000	0.013
	HDACI_COLON_BUT_DN	45	0.54	1.78	0.000	0.021
	HDACI_COLON_BUT48HRS_DN	19	0.63	1.78	0.001	0.021
	HSA00190_OXIDATIVE_PHOSPHORYLATION	22	0.61	1.75	0.000	0.024
	MRNA_SPLICING	16	0.65	1.76	0.005	0.025
	MANALO_HYPOXIA_DN	26	0.58	1.71	0.001	0.041
	HDACI_COLON_BUT16HRS_DN	21	0.59	1.69	0.005	0.044
	POD1_KO_UP	75	0.47	1.69	0.001	0.046
	PRMT5_KD_UP	48	0.50	1.67	0.002	0.048
	MOOTHA_VOXPHOS	15	0.64	1.68	0.008	0.048
	UVB_NHEK2_UP	20	0.60	1.67	0.005	0.050
	STEMCELL_EMBRYONIC_UP	264	0.41	1.66	0.000	0.052
	MITOCHONDRIA	81	0.45	1.65	0.002	0.057
	STEMCELL_NEURAL_UP	388	0.40	1.63	0.000	0.064
	VHL_NORMAL_UP	76	0.45	1.62	0.001	0.067
	BHATTACHARYA_ESC_UP	18	0.59	1.61	0.010	0.073
	BRCA_PROGNOSIS_NEG	17	0.59	1.60	0.015	0.082
	HSA04110_CELL_CYCLE	18	0.57	1.58	0.021	0.091
	MRNA_PROCESSING_REACTOME	33	0.49	1.57	0.017	0.094
Down-regulated in 4+ tumor	HSA04514_CELL_ADHESION_MOLECULES	18	-0.71	-2.30	0.000	0.001
	HSA04360_AXON_GUIDANCE	24	-0.65	-2.33	0.000	0.003
	BRENTANI_CELL_ADHESION	20	-0.64	-2.18	0.000	0.004
	CELL_ADHESION_MOLECULE_ACTIVITY	25	-0.55	-2.05	0.000	0.012
	CELL_ADHESION	29	-0.50	-1.97	0.000	0.020
	HSA04610_COMPLEMENT_AND_COAGULATION_CASCADES	38	-0.48	-1.95	0.006	0.020
	AGEING_BRAIN_UP	34	-0.48	-1.89	0.000	0.023
	CALCIUM_REGULATION_IN_CARDIAC_CELLS	22	-0.54	-1.90	0.000	0.024
	SMOOTH_MUSCLE_CONTRACTION	20	-0.50	-1.76	0.009	0.055
	AGEING_KIDNEY_UP	51	-0.39	-1.72	0.007	0.064
	HSC_MATURE_ADULT	38	-0.41	-1.69	0.017	0.072

Supplemental Table 3. GSEA details for the leading edge subset of proteins in up-regulated gene set STEMCELL_NEURAL_UP

GENE SYMBOL	GENE_TITLE	RANK IN GENE LIST	RANK METRIC SCORE	RUNNING ES	CORE ENRICHMENT
ARFRP1	ADP-ribosylation factor related protein 1	4	3.65	0.01	Yes
SSRP1	structure specific recognition protein 1	5	3.54	0.02	Yes
MCM2	MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae)	11	3.30	0.02	Yes
TRIO	triple functional domain (PTPRF interacting)	20	3.16	0.02	Yes
FBL	fibrillarin	21	3.09	0.03	Yes
RPS28	ribosomal protein S28	22	3.06	0.04	Yes
HSPD1	heat shock 60kDa protein 1 (chaperonin)	23	3.04	0.04	Yes
HMGB2	high-mobility group box 2	25	2.99	0.05	Yes
MCM5	MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	27	2.91	0.06	Yes
DTYMK	deoxythymidylate kinase (thymidylate kinase)	30	2.86	0.06	Yes
DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	33	2.75	0.07	Yes
NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa	34	2.75	0.08	Yes
PRPS2	phosphoribosyl pyrophosphate synthetase 2	35	2.67	0.08	Yes
SMC4	structural maintenance of chromosomes 4	36	2.64	0.09	Yes
TBC1D15	TBC1 domain family, member 15	43	2.54	0.09	Yes
WDHD1	WD repeat and HMG-box DNA binding protein 1	48	2.48	0.09	Yes
PPA2	pyrophosphatase (inorganic) 2	49	2.45	0.10	Yes
DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	51	2.43	0.11	Yes
SART1	squamous cell carcinoma antigen recognised by T cells	53	2.41	0.11	Yes
RPL10A	ribosomal protein L10a	55	2.38	0.12	Yes
PSMA7	proteasome (prosome, macropain) subunit, alpha type, 7	57	2.36	0.12	Yes
HMGB1	high-mobility group box 1	63	2.30	0.12	Yes
NOLA2	nucleolar protein family A, member 2 (H/ACA small nucleolar RNPs)	67	2.28	0.13	Yes
TMPO	thymopoietin	69	2.26	0.13	Yes
LRRC59	leucine rich repeat containing 59	70	2.25	0.14	Yes
RAD21	RAD21 homolog (S. pombe)	74	2.20	0.14	Yes
HSPA14	heat shock 70kDa protein 14	75	2.20	0.15	Yes
SCARB2	scavenger receptor class B, member 2	77	2.19	0.15	Yes
GNPNAT1	glucosamine-phosphate N-acetyltransferase 1	79	2.18	0.15	Yes
RRM1	ribonucleotide reductase M1 polypeptide	81	2.16	0.16	Yes
PB1	-	85	2.13	0.16	Yes
PKM2	pyruvate kinase, muscle	86	2.12	0.17	Yes
NUP93	nucleoporin 93kDa	88	2.11	0.17	Yes
UHRF1	ubiquitin-like, containing PHD and RING finger domains, 1	89	2.11	0.18	Yes
PPIB	peptidylprolyl isomerase B (cyclophilin B)	90	2.10	0.18	Yes
MTCH2	mitochondrial carrier homolog 2 (C. elegans)	94	2.06	0.19	Yes
CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	102	2.04	0.18	Yes
APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	109	2.01	0.18	Yes
CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)	111	2.00	0.19	Yes
NMD3	NMD3 homolog (S. cerevisiae)	114	1.98	0.19	Yes
CNN3	calponin 3, acidic	116	1.97	0.20	Yes
PPA1	pyrophosphatase (inorganic) 1	130	1.86	0.19	Yes
CNBP	CCHC-type zinc finger, nucleic acid binding protein	131	1.86	0.19	Yes
NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	133	1.85	0.20	Yes
GRWD1	glutamate-rich WD repeat containing 1	147	1.80	0.19	Yes
DEK	DEK oncogene (DNA binding)	148	1.78	0.20	Yes
MCM4	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	149	1.78	0.20	Yes
ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	152	1.76	0.20	Yes
JAM3	junctional adhesion molecule 3	156	1.75	0.20	Yes
NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa	160	1.73	0.21	Yes
GLUD1	glutamate dehydrogenase 1	162	1.73	0.21	Yes
CACYBP	calcyclin binding protein	163	1.72	0.21	Yes
TSFM	Ts translation elongation factor, mitochondrial	172	1.68	0.21	Yes
DECR1	2,4-dienoyl CoA reductase 1, mitochondrial	179	1.65	0.21	Yes
RSL1D1	ribosomal L1 domain containing 1	192	1.60	0.20	Yes
ACTL6A	actin-like 6A	194	1.59	0.21	Yes
FHL1	four and a half LIM domains 1	195	1.59	0.21	Yes
OXCT1	3-oxoacid CoA transferase 1	206	1.55	0.20	Yes
DOCK7	dedicator of cytokinesis 7	208	1.54	0.21	Yes
DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	210	1.54	0.21	Yes
ASNS	asparagine synthetase	211	1.53	0.22	Yes
SFRS1	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	214	1.52	0.22	Yes
WDR5	WD repeat domain 5	216	1.52	0.22	Yes
RBBP4	retinoblastoma binding protein 4	220	1.51	0.22	Yes
H2AFY	H2A histone family, member Y	222	1.50	0.22	Yes
RRM2	ribonucleotide reductase M2 polypeptide	226	1.47	0.23	Yes
PABPC1	poly(A) binding protein, cytoplasmic 1	229	1.46	0.23	Yes
SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	231	1.46	0.23	Yes
AKAP12	A kinase (PRKA) anchor protein (gravin) 12	232	1.46	0.23	Yes
TCEA1	transcription elongation factor A (SII), 1	236	1.45	0.24	Yes
NIT2	nitrilase family, member 2	239	1.44	0.24	Yes
AQR	aquarius homolog (mouse)	241	1.43	0.24	Yes
KARS	lysyl-tRNA synthetase	242	1.43	0.24	Yes
EFTUD2	elongation factor Tu GTP binding domain containing 2	244	1.42	0.25	Yes
EFTUD1	elongation factor Tu GTP binding domain containing 1	246	1.42	0.25	Yes
SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	248	1.42	0.25	Yes
LAMA5	laminin, alpha 5	259	1.38	0.25	Yes
SFRS7	splicing factor, arginine/serine-rich 7, 35kDa	261	1.37	0.25	Yes
TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	263	1.36	0.25	Yes
GNPDA1	glucosamine-6-phosphate deaminase 1	266	1.35	0.25	Yes
GTPBP4	GTP binding protein 4	272	1.35	0.25	Yes
XRCC1	X-ray repair complementing defective repair in Chinese hamster cells 1	273	1.34	0.26	Yes
TXN	thioredoxin	278	1.34	0.26	Yes
PGK1	phosphoglycerate kinase 1	279	1.33	0.26	Yes
TM9SF2	transmembrane 9 superfamily member 2	281	1.32	0.26	Yes
LAP3	leucine aminopeptidase 3	283	1.32	0.26	Yes
BAG2	BCL2-associated athanogene 2	286	1.31	0.27	Yes
VDAC3	voltage-dependent anion channel 3	289	1.31	0.27	Yes
NKRF	NF-kappaB repressing factor	291	1.30	0.27	Yes
FUBP1	far upstream element (FUSE) binding protein 1	303	1.28	0.26	Yes
PHF5A	PHD finger protein 5A	307	1.27	0.26	Yes
RBM39	RNA binding motif protein 39	310	1.27	0.26	Yes
TUFM	Tu translation elongation factor, mitochondrial	311	1.26	0.27	Yes
PSMB1	proteasome (prosome, macropain) subunit, beta type, 1	313	1.26	0.27	Yes
EXOSC7	exosome component 7	314	1.25	0.27	Yes
EEF2	eukaryotic translation elongation factor 2	317	1.25	0.27	Yes

Gene	Description				
RANBP5	RAN binding protein 5	318	1.25	0.28	Yes
PDIA3	protein disulfide isomerase family A, member 3	320	1.24	0.28	Yes
RECQL	RecQ protein-like (DNA helicase Q1-like)	322	1.23	0.28	Yes
NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase	323	1.22	0.29	Yes
NASP	nuclear autoantigenic sperm protein (histone-binding)	330	1.21	0.28	Yes
ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	331	1.21	0.29	Yes
NOP5/NOP58	-	332	1.21	0.29	Yes
TNPO1	transportin 1	333	1.21	0.29	Yes
VBP1	von Hippel-Lindau binding protein 1	334	1.21	0.30	Yes
PSMA6	proteasome (prosome, macropain) subunit, alpha type, 6	337	1.20	0.30	Yes
SRPRB	signal recognition particle receptor, B subunit	338	1.20	0.30	Yes
MAT2A	methionine adenosyltransferase II, alpha	339	1.20	0.30	Yes
SRP19	signal recognition particle 19kDa	340	1.20	0.31	Yes
ANP32A	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	348	1.18	0.30	Yes
DC2	-	352	1.18	0.30	Yes
SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	354	1.17	0.31	Yes
EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	364	1.15	0.30	Yes
PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	366	1.15	0.30	Yes
PTN	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	367	1.15	0.31	Yes
NONO	non-POU domain containing, octamer-binding	370	1.14	0.31	Yes
SAFB	scaffold attachment factor B	372	1.13	0.31	Yes
TKT	transketolase (Wernicke-Korsakoff syndrome)	373	1.13	0.31	Yes
P4HB	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptid	377	1.12	0.31	Yes
PPP5C	protein phosphatase 5, catalytic subunit	378	1.12	0.31	Yes
SDHA	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	383	1.12	0.31	Yes
PPP4R2	protein phosphatase 4, regulatory subunit 2	384	1.12	0.32	Yes
HNRPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	385	1.12	0.32	Yes
STT3A	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	387	1.11	0.32	Yes
EIF3S9	eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa	389	1.11	0.32	Yes
CRYZ	crystallin, zeta (quinone reductase)	390	1.11	0.33	Yes
XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 7(	393	1.10	0.33	Yes
EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	397	1.09	0.33	Yes
ETFA	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	402	1.08	0.33	Yes
PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	403	1.08	0.33	Yes
MTX2	metaxin 2	405	1.07	0.33	Yes
GABPA	GA binding protein transcription factor, alpha subunit 60kDa	411	1.06	0.33	Yes
SR140	-	420	1.05	0.32	Yes
PA2G4	proliferation-associated 2G4, 38kDa	425	1.04	0.32	Yes
HNRPM	heterogeneous nuclear ribonucleoprotein M	431	1.03	0.32	Yes
CPSF2	cleavage and polyadenylation specific factor 2, 100kDa	432	1.03	0.32	Yes
RANBP1	RAN binding protein 1	433	1.03	0.33	Yes
IMPDH2	IMP (inosine monophosphate) dehydrogenase 2	435	1.02	0.33	Yes
HINT1	histidine triad nucleotide binding protein 1	438	1.02	0.33	Yes
AP1G1	adaptor-related protein complex 1, gamma 1 subunit	442	1.00	0.33	Yes
AHCY	S-adenosylhomocysteine hydrolase	443	1.00	0.33	Yes
PRPS1	phosphoribosyl pyrophosphate synthetase 1	444	1.00	0.33	Yes
HTATSF1	HIV-1 Tat specific factor 1	445	1.00	0.34	Yes
MCM7	MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	447	0.99	0.34	Yes
TARDBP	TAR DNA binding protein	448	0.99	0.34	Yes
TM9SF3	transmembrane 9 superfamily member 3	449	0.99	0.34	Yes
CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	451	0.98	0.35	Yes
SF3B1	splicing factor 3b, subunit 1, 155kDa	453	0.98	0.35	Yes
TCERG1	transcription elongation regulator 1	455	0.97	0.35	Yes
SHMT1	serine hydroxymethyltransferase 1 (soluble)	461	0.96	0.35	Yes
HNRPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	464	0.96	0.35	Yes
LRPPRC	leucine-rich PPR-motif containing	466	0.96	0.35	Yes
VPS29	vacuolar protein sorting 29 (yeast)	467	0.96	0.35	Yes
CHORDC1	cysteine and histidine-rich domain (CHORD)-containing 1	469	0.96	0.35	Yes
CYC1	cytochrome c-1	471	0.95	0.35	Yes
DLD	dihydrolipoamide dehydrogenase	475	0.94	0.35	Yes
NUDT5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	478	0.94	0.36	Yes
UBE1C	ubiquitin-activating enzyme E1C (UBA3 homolog, yeast)	480	0.94	0.36	Yes
ARIH2	ariadne homolog 2 (Drosophila)	482	0.93	0.36	Yes
SAE1	-	483	0.93	0.36	Yes
DLAT	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex	486	0.92	0.36	Yes
MRPL3	mitochondrial ribosomal protein L3	488	0.92	0.36	Yes
XPO1	exportin 1 (CRM1 homolog, yeast)	491	0.91	0.36	Yes
RHOA	ras homolog gene family, member A	492	0.90	0.37	Yes
CRKL	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	493	0.90	0.37	Yes
PPID	peptidylprolyl isomerase D (cyclophilin D)	494	0.90	0.37	Yes
SEC24B	SEC24 related gene family, member B (S. cerevisiae)	495	0.90	0.37	Yes
CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	501	0.89	0.37	Yes
COPB2	coatomer protein complex, subunit beta 2 (beta prime)	502	0.89	0.37	Yes
CCT5	chaperonin containing TCP1, subunit 5 (epsilon)	504	0.89	0.37	Yes
PDCD6IP	programmed cell death 6 interacting protein	507	0.88	0.37	Yes
IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha	508	0.88	0.38	Yes
SEC31A	SEC31 homolog A (S. cerevisiae)	509	0.87	0.38	Yes
ERH	enhancer of rudimentary homolog (Drosophila)	514	0.87	0.38	Yes
CUL4A	cullin 4A	515	0.87	0.38	Yes
SUGT1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	519	0.86	0.38	Yes
PGLS	6-phosphogluconolactonase	520	0.86	0.38	Yes
XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-bre	521	0.86	0.38	Yes
EIF3S8	eukaryotic translation initiation factor 3, subunit 8, 110kDa	523	0.86	0.39	Yes
HNRPK	heterogeneous nuclear ribonucleoprotein K	526	0.85	0.39	Yes
CSNK2B	casein kinase 2, beta polypeptide	530	0.84	0.38	Yes
PSPC1	paraspeckle component 1	532	0.84	0.39	Yes
IARS	isoleucine-tRNA synthetase	534	0.83	0.39	Yes
NUP35	nucleoporin 35kDa	536	0.83	0.39	Yes
SMAD2	SMAD, mothers against DPP homolog 2 (Drosophila)	537	0.82	0.39	Yes
RNASEH2A	ribonuclease H2, subunit A	549	0.81	0.38	Yes
CCT8	chaperonin containing TCP1, subunit 8 (theta)	552	0.80	0.38	Yes
MRPS18A	mitochondrial ribosomal protein S18A	554	0.80	0.38	Yes
STK24	serine/threonine kinase 24 (STE20 homolog, yeast)	555	0.80	0.39	Yes
KPNB1	karyopherin (importin) beta 1	556	0.79	0.39	Yes
RUVBL2	RuvB-like 2 (E. coli)	557	0.79	0.39	Yes
EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	560	0.79	0.39	Yes
EIF3S6IP	eukaryotic translation initiation factor 3, subunit 6 interacting protein	562	0.79	0.39	Yes
RAN	RAN, member RAS oncogene family	563	0.79	0.39	Yes
HSPA4	heat shock 70kDa protein 4	564	0.78	0.40	Yes

Supplemental Table 4: GO analysis of differential expressed proteins in 4+ and 1- neuroblastoma tumor

	Term	Count	PValue	FDR
Up-regulated in 4+ tumor	GO:0006396~RNA processing	52	1.67E-20	3.20E-19
	GO:0022613~ribonucleoprotein complex biogenesis and assembly	31	1.05E-15	1.91E-14
	GO:0044237~cellular metabolic process	271	2.98E-15	5.74E-14
	GO:0006397~mRNA processing	34	3.72E-15	7.01E-14
	GO:0008152~metabolic process	289	1.12E-14	2.14E-13
	GO:0006412~translation	52	1.46E-14	2.78E-13
	GO:0044249~cellular biosynthetic process	73	2.98E-14	5.69E-13
	GO:0016071~mRNA metabolic process	35	1.10E-13	2.10E-12
	GO:0008380~RNA splicing	30	1.57E-13	3.00E-12
	GO:0010467~gene expression	150	8.01E-13	1.53E-11
	GO:0044238~primary metabolic process	264	1.65E-12	3.15E-11
	GO:0043170~macromolecule metabolic process	237	1.06E-11	2.02E-10
	GO:0042254~ribosome biogenesis and assembly	18	4.28E-11	8.19E-10
	GO:0009059~macromolecule biosynthetic process	57	6.32E-11	1.21E-09
	GO:0009058~biosynthetic process	79	6.92E-11	1.32E-09
	GO:0016043~cellular component organization and biogenesis	116	1.03E-10	1.97E-09
	GO:0000398~nuclear mRNA splicing, via spliceosome	13	1.04E-07	1.99E-06
	GO:0000377~RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	13	1.04E-07	1.99E-06
	GO:0000375~RNA splicing, via transesterification reactions	13	1.04E-07	1.99E-06
	GO:0006996~organelle organization and biogenesis	59	1.56E-07	2.98E-06
	GO:0006364~rRNA processing	12	2.98E-07	5.71E-06
	GO:0016072~rRNA metabolic process	12	4.84E-07	9.25E-06
	GO:0006259~DNA metabolic process	46	6.06E-07	1.16E-05
	GO:0006457~protein folding	23	8.36E-07	1.60E-05
	GO:0009987~cellular process	341	1.34E-06	2.57E-05
	GO:0006139~nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	137	3.55E-06	6.79E-05
	GO:0044260~cellular macromolecule metabolic process	122	6.65E-06	1.27E-04
	GO:0006913~nucleocytoplasmic transport	15	8.44E-06	1.61E-04
	GO:0044267~cellular protein metabolic process	120	9.12E-06	1.74E-04
	GO:0051169~nuclear transport	15	9.91E-06	1.90E-04
	GO:0006144~purine base metabolic process	5	1.06E-05	2.03E-04
	GO:0006096~glycolysis	10	1.53E-05	2.92E-04
	GO:0006268~DNA unwinding during replication	6	1.87E-05	3.57E-04
	GO:0006605~protein targeting	18	2.11E-05	4.03E-04
	GO:0022618~protein-RNA complex assembly	13	2.13E-05	4.08E-04
	GO:0006260~DNA replication	19	3.33E-05	6.36E-04
	GO:0019538~protein metabolic process	123	3.40E-05	6.49E-04
	GO:0032392~DNA geometric change	6	3.70E-05	7.08E-04
	GO:0032508~DNA duplex unwinding	6	3.70E-05	7.08E-04
	GO:0006007~glucose catabolic process	10	5.19E-05	9.93E-04
	GO:0009113~purine base biosynthetic process	4	5.32E-05	0.001
	GO:0006414~translational elongation	7	5.33E-05	0.001
	GO:0000245~spliceosome assembly	7	7.93E-05	0.002
	GO:0065003~macromolecular complex assembly	30	8.13E-05	0.002
	GO:0042775~organelle ATP synthesis coupled electron transport	9	8.51E-05	0.002
	GO:0006120~mitochondrial electron transport, NADH to ubiquinone	8	1.16E-04	0.002
	GO:0006886~intracellular protein transport	24	1.17E-04	0.002
	GO:0022607~cellular component assembly	31	1.22E-04	0.002
	GO:0015931~nucleobase, nucleoside, nucleotide and nucleic acid transport	11	1.38E-04	0.003
	GO:0019320~hexose catabolic process	10	1.59E-04	0.003
	GO:0046365~monosaccharide catabolic process	10	1.75E-04	0.003
	GO:0042773~ATP synthesis coupled electron transport	9	1.88E-04	0.004
	GO:0046164~alcohol catabolic process	10	2.09E-04	0.004
	GO:0051276~chromosome organization and biogenesis	23	2.10E-04	0.004
	GO:0016070~RNA metabolic process	101	2.30E-04	0.004
	GO:0006323~DNA packaging	20	2.69E-04	0.005
	GO:0044271~nitrogen compound biosynthetic process	11	2.80E-04	0.005
	GO:0044275~cellular carbohydrate catabolic process	11	3.02E-04	0.006
	GO:0008652~amino acid biosynthetic process	8	3.17E-04	0.006
	GO:0043284~biopolymer biosynthetic process	8	4.42E-04	0.008
	GO:0009112~nucleobase metabolic process	5	4.65E-04	0.009
	GO:0046907~intracellular transport	33	4.85E-04	0.009
	GO:0016052~carbohydrate catabolic process	11	4.96E-04	0.009
	GO:0006325~establishment and/or maintenance of chromatin architecture	19	5.95E-04	0.011
	GO:0009309~amine biosynthetic process	9	8.15E-04	0.015
	GO:0009161~ribonucleoside monophosphate metabolic process	5	9.35E-04	0.018
	GO:0009156~ribonucleoside monophosphate biosynthetic process	5	9.35E-04	0.018
	GO:0046112~nucleobase biosynthetic process	4	0.001	0.019
	GO:0006839~mitochondrial transport	7	0.001	0.020
	GO:0045333~cellular respiration	7	0.001	0.020
	GO:0050658~RNA transport	9	0.001	0.021
	GO:0050657~nucleic acid transport	9	0.001	0.021
	GO:0051236~establishment of RNA localization	9	0.001	0.021
	GO:0009124~nucleoside monophosphate biosynthetic process	5	0.001	0.022
	GO:0009123~nucleoside monophosphate metabolic process	5	0.001	0.022
	GO:0017038~protein import	10	0.001	0.024
	GO:0006403~RNA localization	9	0.001	0.024
	GO:0006119~oxidative phosphorylation	10	0.002	0.033
	GO:0051641~cellular localization	37	0.002	0.036

	GO:0033036~macromolecule localization	35	0.002	0.036
	GO:0006006~glucose metabolic process	10	0.002	0.039
	GO:0051649~establishment of cellular localization	36	0.002	0.041
	GO:0007049~cell cycle	36	0.003	0.052
	GO:0051028~mRNA transport	8	0.003	0.052
	GO:0009060~aerobic respiration	6	0.003	0.052
	GO:0043623~cellular protein complex assembly	7	0.003	0.056
	GO:0016568~chromatin modification	13	0.003	0.061
	GO:0045184~establishment of protein localization	31	0.004	0.068
	GO:0046483~heterocycle metabolic process	8	0.004	0.073
	GO:0009168~purine ribonucleoside monophosphate biosynthetic process	4	0.004	0.075
	GO:0009167~purine ribonucleoside monophosphate metabolic process	4	0.004	0.075
	GO:0009127~purine nucleoside monophosphate biosynthetic process	4	0.004	0.075
	GO:0009126~purine nucleoside monophosphate metabolic process	4	0.004	0.075
	GO:0006376~mRNA splice site selection	4	0.004	0.075
	GO:0008104~protein localization	32	0.005	0.085
	GO:0006606~protein import into nucleus	8	0.005	0.087
	GO:0065002~intracellular protein transport across a membrane	7	0.005	0.089
	GO:0006261~DNA-dependent DNA replication	9	0.005	0.089
	GO:0006281~DNA repair	15	0.005	0.092
	GO:0006974~response to DNA damage stimulus	17	0.005	0.092
	GO:0043283~biopolymer metabolic process	153	0.005	0.093
	GO:0015031~protein transport	29	0.005	0.095
	GO:0051170~nuclear import	8	0.005	0.099
	GO:0000389~nuclear mRNA 3'-splice site recognition	3	0.005	0.099
Down-regulated in 4+ tumor	GO:0007155~cell adhesion	23	2.58E-07	4.94E-06
	GO:0022610~biological adhesion	23	2.58E-07	4.94E-06
	GO:0048731~system development	34	2.91E-06	5.57E-05
	GO:0048856~anatomical structure development	38	4.77E-06	9.12E-05
	GO:0031175~neurite development	10	8.90E-06	1.70E-04
	GO:0000902~cell morphogenesis	16	1.31E-05	2.50E-04
	GO:0032989~cellular structure morphogenesis	16	1.31E-05	2.50E-04
	GO:0007275~multicellular organismal development	39	1.41E-05	2.71E-04
	GO:0032990~cell part morphogenesis	11	2.21E-05	4.23E-04
	GO:0030030~cell projection organization and biogenesis	11	2.21E-05	4.23E-04
	GO:0048858~cell projection morphogenesis	11	2.21E-05	4.23E-04
	GO:0048812~neurite morphogenesis	9	2.66E-05	5.09E-04
	GO:0048667~neuron morphogenesis during differentiation	9	2.66E-05	5.09E-04
	GO:0048666~neuron development	10	2.83E-05	5.40E-04
	GO:0000904~cellular morphogenesis during differentiation	9	4.46E-05	8.53E-04
	GO:0032502~developmental process	47	4.57E-05	8.73E-04
	GO:0048699~generation of neurons	11	1.26E-04	0.002
	GO:0007409~axonogenesis	8	1.40E-04	0.003
	GO:0051258~protein polymerization	6	1.98E-04	0.004
	GO:0030182~neuron differentiation	10	2.06E-04	0.004
	GO:0022008~neurogenesis	11	2.34E-04	0.004
	GO:0050793~regulation of developmental process	10	2.67E-04	0.005
	GO:0009653~anatomical structure morphogenesis	22	3.07E-04	0.006
	GO:0048468~cell development	23	4.21E-04	0.008
	GO:0050767~regulation of neurogenesis	5	4.41E-04	0.008
	GO:0007399~nervous system development	17	5.87E-04	0.011
	GO:0042060~wound healing	7	6.48E-04	0.012
	GO:0032501~multicellular organismal process	48	7.20E-04	0.014
	GO:0009611~response to wounding	12	7.87E-04	0.015
	GO:0007010~cytoskeleton organization and biogenesis	13	0.001	0.023
	GO:0006066~alcohol metabolic process	10	0.001	0.024
	GO:0007596~blood coagulation	6	0.001	0.024
	GO:0050817~coagulation	6	0.001	0.026
	GO:0030154~cell differentiation	28	0.002	0.029
	GO:0048869~cellular developmental process	28	0.002	0.029
	GO:0007599~hemostasis	6	0.002	0.030
	GO:0006869~lipid transport	6	0.002	0.031
	GO:0044275~cellular carbohydrate catabolic process	6	0.002	0.038
	GO:0050770~regulation of axonogenesis	4	0.002	0.041
	GO:0044262~cellular carbohydrate metabolic process	10	0.002	0.042
	GO:0019318~hexose metabolic process	7	0.002	0.043
	GO:0005996~monosaccharide metabolic process	7	0.003	0.050
	GO:0016052~carbohydrate catabolic process	6	0.003	0.050
	GO:0051094~positive regulation of developmental process	5	0.003	0.052
	GO:0006007~glucose catabolic process	5	0.003	0.052
	GO:0050878~regulation of body fluid levels	6	0.003	0.062
	GO:0048513~organ development	21	0.003	0.065
	GO:0048518~positive regulation of biological process	19	0.004	0.067
	GO:0019320~hexose catabolic process	5	0.005	0.086
	GO:0046365~monosaccharide catabolic process	5	0.005	0.089
	GO:0065008~regulation of biological quality	16	0.005	0.096
	GO:0046164~alcohol catabolic process	5	0.005	0.097
	GO:0016043~cellular component organization and biogenesis	35	0.005	0.099

Supplemental Table 5: GO analysis of differential expressed genes with correlated mRNA and protein expression

	Term	Count	PValue	FDR
Up-regulated in 4+ tumor	GO:0006396~RNA processing	33	1.58E-16	2.11E-15
	GO:0022613~ribonucleoprotein complex biogenesis and assembly	23	1.77E-15	3.40E-14
	GO:0044237~cellular metabolic process	146	7.38E-15	1.42E-13
	GO:0008152~metabolic process	154	1.61E-14	3.08E-13
	GO:0044238~primary metabolic process	142	1.55E-12	2.96E-11
	GO:0042254~ribosome biogenesis and assembly	15	2.31E-12	4.43E-11
	GO:0043170~macromolecule metabolic process	129	1.04E-11	2.00E-10
	GO:0044249~cellular biosynthetic process	43	1.74E-11	3.33E-10
	GO:0006412~translation	31	3.61E-11	6.91E-10
	GO:0010467~gene expression	83	8.48E-11	1.62E-09
	GO:0009058~biosynthetic process	48	2.83E-10	5.42E-09
	GO:0006364~rRNA processing	11	2.99E-09	5.72E-08
	GO:0009059~macromolecule biosynthetic process	34	4.41E-09	8.44E-08
	GO:0016072~rRNA metabolic process	11	4.75E-09	9.09E-08
	GO:0008380~RNA splicing	17	8.90E-09	1.70E-07
	GO:0006397~mRNA processing	18	9.26E-09	1.77E-07
	GO:0016071~mRNA metabolic process	19	2.11E-08	4.04E-07
	GO:0006139~nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	77	1.56E-06	2.98E-05
	GO:0006260~DNA replication	14	7.06E-06	1.35E-04
	GO:0009987~cellular process	170	1.05E-05	2.01E-04
	GO:0044260~cellular macromolecule metabolic process	67	1.48E-05	2.83E-04
	GO:0000398~nuclear mRNA splicing, via spliceosome	8	1.78E-05	3.40E-04
	GO:0000377~RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	8	1.78E-05	3.40E-04
	GO:0000375~RNA splicing, via transesterification reactions	8	1.78E-05	3.40E-04
	GO:0044267~cellular protein metabolic process	66	1.82E-05	3.49E-04
	GO:0006259~DNA metabolic process	26	1.99E-05	3.80E-04
	GO:0006268~DNA unwinding during replication	5	2.15E-05	4.12E-04
	GO:0032392~DNA geometric change	5	3.69E-05	7.05E-04
	GO:0032508~DNA duplex unwinding	5	3.69E-05	7.05E-04
	GO:0006144~purine base metabolic process	4	5.18E-05	9.90E-04
	GO:0019538~protein metabolic process	67	6.28E-05	0.001
	GO:0006096~glycolysis	7	7.99E-05	0.002
	GO:0006996~organelle organization and biogenesis	30	1.12E-04	0.002
	GO:0016070~RNA metabolic process	57	1.15E-04	0.002
	GO:0006007~glucose catabolic process	7	1.85E-04	0.004
	GO:0016043~cellular component organization and biogenesis	52	2.08E-04	0.004
	GO:0006261~DNA-dependent DNA replication	8	2.91E-04	0.006
	GO:0019320~hexose catabolic process	7	4.02E-04	0.008
	GO:0022618~protein-RNA complex assembly	8	4.02E-04	0.008
	GO:0046365~monosaccharide catabolic process	7	4.28E-04	0.008
	GO:0046164~alcohol catabolic process	7	4.86E-04	0.009
	GO:0022607~cellular component assembly	18	6.39E-04	0.012
	GO:0009112~nucleobase metabolic process	4	7.67E-04	0.015
	GO:0009113~purine base biosynthetic process	3	7.89E-04	0.015
	GO:0065003~macromolecular complex assembly	17	8.17E-04	0.016
	GO:0006520~amino acid metabolic process	12	8.95E-04	0.017
	GO:0009161~ribonucleoside monophosphate metabolic process	4	0.001	0.024
	GO:0009156~ribonucleoside monophosphate biosynthetic process	4	0.001	0.024
	GO:0006913~nucleocytoplasmic transport	8	0.001	0.026
	GO:0006457~protein folding	11	0.001	0.027
	GO:0051169~nuclear transport	8	0.002	0.028
	GO:0009124~nucleoside monophosphate biosynthetic process	4	0.002	0.028
	GO:0009123~nucleoside monophosphate metabolic process	4	0.002	0.028
	GO:0044275~cellular carbohydrate catabolic process	7	0.002	0.033
	GO:0009064~glutamine family amino acid metabolic process	5	0.002	0.034
	GO:0043283~biopolymer metabolic process	82	0.002	0.040
	GO:0016052~carbohydrate catabolic process	7	0.002	0.045
	GO:0006006~glucose metabolic process	7	0.003	0.047
	GO:0044265~cellular macromolecule catabolic process	12	0.003	0.051
	GO:0006399~tRNA metabolic process	7	0.003	0.058
	GO:0007049~cell cycle	21	0.004	0.067
	GO:0008652~amino acid biosynthetic process	5	0.004	0.069
	GO:0006281~DNA repair	10	0.004	0.074
	GO:0006519~amino acid and derivative metabolic process	12	0.004	0.082
	GO:0006284~base-excision repair	4	0.004	0.082
	GO:0046112~nucleobase biosynthetic process	3	0.005	0.084
	GO:0006974~response to DNA damage stimulus	11	0.005	0.084
	GO:0006270~DNA replication initiation	4	0.005	0.099
Down-regulated in 4+ tumor	GO:0048856~anatomical structure development	20	1.38E-07	2.64E-06
	GO:0007275~multicellular organismal development	20	5.57E-07	1.07E-05
	GO:0032502~developmental process	23	9.05E-07	1.73E-05
	GO:0048812~neurite morphogenesis	7	1.49E-06	2.85E-05
	GO:0048667~neuron morphogenesis during differentiation	7	1.49E-06	2.85E-05
	GO:0032990~cell part morphogenesis	8	1.51E-06	2.89E-05
	GO:0030030~cell projection organization and biogenesis	8	1.51E-06	2.89E-05

Supplemental Table 6: mRNA and protein expression data measured by Affymetrix and ICAT

Symbol	GeneID	Log$_2$ ratio (4+ / 1-)	
		mRNA expression	Protein expression
A1BG	1	0.410	0.149
A2M	2	-0.884	-0.918
AAMP	14	-0.244	0.161
AARS	16	-0.063	0.494
ABCE1	6059	1.784	1.760
ABHD12	26090	-0.204	1.188
ABR	29	-0.744	-2.051
ACAD8	27034	0.058	-1.884
ACADVL	37	-1.142	-0.475
ACAN	176	0.066	-0.660
ACAT1	38	-0.077	1.582
ACAT2	39	0.439	0.371
ACIN1	22985	0.084	0.213
ACLY	47	-0.608	-0.664
ACO2	50	-0.071	-0.151
ACOT7	11332	-0.467	-0.357
ACP2	53	-0.533	0.066
ACSL1	2180	1.342	1.601
ACSL4	2182	-0.133	0.644
ACTB	60	-0.071	0.087
ACTL6A	86	2.070	1.590
ACTL6B	51412	-0.863	0.103
ACTN1	87	0.363	1.118
ACTN4	81	0.034	0.874
ACTR1B	10120	-0.589	-0.079
ACTR2	10097	-0.493	0.164
ACTR3	10096	0.196	0.217
ADAR	103	-0.187	0.842
ADD1	118	-0.428	-0.652
ADD2	119	0.221	-0.264
ADFP	123	0.612	0.023
ADH5	128	0.818	0.601
ADK	132	0.437	0.354
ADNP	23394	0.224	0.184
ADO	84890	0.534	1.034
ADRM1	11047	-0.132	0.283
ADSS	159	0.511	-0.420
AFG3L2	10939	0.349	1.458
AFM	173	0.150	-1.670
AGRN	375790	-2.562	0.760
AGTPBP1	23287	-0.030	-1.143
AHCY	191	2.158	1.001
AHCYL1	10768	0.345	-0.091
AIP	9049	0.650	0.724
AKAP1	8165	0.873	1.871
AKAP12	9590	-0.053	1.459
AKAP9	10142	0.471	0.034
AKR1A1	10327	0.306	-0.502
AKR1B1	231	0.366	0.438
AKR7A2	8574	-0.296	-0.321
AKT2	208	0.045	-0.933
ALAD	210	-0.640	-0.201
ALB	213	-0.701	-0.699
ALCAM	214	-2.008	-2.047
ALDH1L2	160428	1.058	0.207
ALDH2	217	-0.044	-0.027
ALDH4A1	8659	-0.337	-0.855
ALDH5A1	7915	0.461	0.208
ALDH9A1	223	0.242	-0.126
ALDOA	226	0.974	1.283
ALK	238	1.950	1.462
AMBP	259	-0.056	-1.151
AMPD2	271	0.059	0.727
ANK1	286	-1.028	-0.842
ANK2	287	0.247	-0.214
ANKFY1	51479	-0.816	-0.634

ANKHD1	54882	0.325	1.023
ANKRD17	26057	0.386	0.665
ANKRD28	23243	0.599	-0.406
ANP32A	8125	1.169	1.183
ANP32E	81611	1.401	1.212
ANXA2	302	-1.480	-2.816
ANXA4	307	-0.152	3.271
ANXA7	310	-0.173	-0.698
AOF2	23028	-0.126	1.231
AP1B1	162	-0.154	0.128
AP1G1	164	-0.002	1.001
AP2A1	160	-0.358	-0.434
AP2A2	161	-0.293	-0.151
AP2B1	163	0.213	-0.863
AP2M1	1173	-0.194	-0.176
AP3D1	8943	-0.143	0.463
AP3M1	26985	-0.020	0.370
AP3M2	10947	0.066	-0.163
APEH	327	0.109	-0.448
APEX1	328	1.447	2.012
APLP1	333	-0.749	1.123
APOA1BP	128240	0.431	0.593
APOB	338	-0.165	0.077
APOE	348	-0.997	-1.502
APOM	55937	0.280	-0.699
APP	351	0.056	2.283
AQR	9716	0.407	1.428
ARCN1	372	0.372	0.422
ARFGEF1	10565	-0.071	-0.534
ARFRP1	10139	-0.572	3.653
ARHGAP29	9411	2.045	-0.361
ARHGEF2	9181	0.112	-0.502
ARHGEF7	8874	-0.043	0.009
ARIH1	25820	0.491	0.108
ARIH2	10425	0.189	0.930
ARL3	403	-0.221	-0.176
ARMET	7873	0.805	1.683
ARPC1A	10552	0.744	0.283
ARPC1B	10095	0.127	0.332
ARPC2	10109	-0.319	0.178
ARPC5	10092	-0.217	-0.851
ARRB1	408	-0.354	-0.151
ARRB2	409	-0.314	-0.273
ARS2	51593	-0.079	0.296
ASCC3L1	23020	-0.236	1.760
ASL	435	-0.583	-0.438
ASMTL	8623	0.210	0.933
ASNA1	439	0.202	0.118
ASNS	440	0.888	1.533
ASRGL1	80150	0.505	0.679
ASS1	445	0.718	2.581
ATF7IP	55729	-0.044	1.567
ATG7	10533	0.154	0.169
ATIC	471	1.550	1.282
ATP1A1	476	-0.218	-0.188
ATP1A3	478	-1.537	-0.528
ATP1B1	481	0.062	-0.377
ATP2A2	488	-0.538	1.071
ATP2B4	493	-1.038	-2.829
ATP2C1	27032	0.318	-1.303
ATP5C1	509	0.646	0.273
ATP5O	539	0.995	0.115
ATP6V1C1	528	-0.578	-1.209
ATP8A1	10396	-0.449	-1.582
ATP9A	10079	-0.220	-0.475
ATPAF2	91647	-0.182	1.077
ATRN	8455	-0.057	-0.756
ATXN10	25814	0.067	0.077
AZGP1	563	-0.018	-0.151
BAG1	573	0.201	1.190
BAG2	9532	0.150	1.310

BAG5	9529	0.725	0.453
BAT1	7919	0.174	0.665
BAZ1B	9031	0.133	3.766
BCKDHB	594	-0.103	0.283
BGN	633	-1.589	-1.319
BIRC6	57448	0.289	0.045
BLMH	642	-0.465	0.208
BOLA2	552900	0.716	0.927
BOP1	23246	0.701	2.298
BPGM	669	0.187	-1.455
BPNT1	10380	0.027	0.623
BRUNOL4	56853	-1.613	-1.046
BRWD1	54014	0.308	0.502
BRWD2	55717	-0.346	-1.769
BTAF1	9044	0.294	1.070
BTD	686	-0.018	0.183
BUB3	9184	0.795	0.426
BUD31	8896	0.807	0.095
C11orf68	83638	0.210	0.892
C14orf166	51637	1.212	0.663
C14orf4	64207	-0.794	0.301
C17orf49	124944	-0.028	0.236
C1orf128	57095	-0.657	-1.516
C1orf163	65260	0.088	2.860
C1orf27	54953	0.306	0.886
C1R	715	-0.288	-0.711
C1S	716	-0.146	-0.759
C2	717	-0.477	-0.448
C20orf27	54976	0.535	0.874
C20orf3	57136	0.085	0.169
C21orf33	8209	0.128	0.413
C2orf3	6936	0.611	2.188
C3orf10	55845	0.702	0.541
C4orf27	54969	1.439	1.510
C5	727	0.219	-0.293
C6orf115	58527	0.830	0.034
C7orf50	84310	0.102	2.141
C8B	732	0.385	0.789
C8orf55	51337	0.107	0.586
C8orf82	414919	0.524	-1.461
C9orf125	84302	0.163	0.971
C9orf142	286257	0.135	1.087
CA3	761	-1.130	2.510
CACNA2D1	781	-0.060	0.189
CACYBP	27101	0.878	1.724
CAD	790	-0.227	0.984
CADM1	23705	-0.818	-2.767
CADM2	253559	-0.148	-0.521
CADM4	199731	-0.466	0.231
CADPS	8618	-1.203	-1.201
CALR	811	0.135	1.050
CAND1	55832	0.315	0.571
CAND2	23066	-0.120	-1.442
CANX	821	0.335	1.012
CAP1	10487	-0.997	-0.981
CAPN1	823	-0.181	-0.370
CAPN2	824	0.198	-0.151
CAPNS1	826	-0.396	-0.079
CAPZA2	830	0.074	0.135
CAPZB	832	-0.660	-0.227
CAST	831	-0.001	-0.852
CAT	847	0.787	-0.502
CBR3	874	0.386	-0.079
CBS	875	0.503	2.336
CBX5	23468	0.377	2.037
CCT2	10576	0.749	0.808
CCT3	7203	0.745	0.502
CCT4	10575	0.698	0.462
CCT5	22948	0.739	0.889
CCT7	10574	0.910	0.533
CCT8	10694	-0.069	0.799

CD14	929	-0.114	0.611
CD36	948	-0.546	0.488
CD44	960	-1.774	-1.705
CD55	1604	0.297	0.217
CD59	966	-0.323	-0.163
CD93	22918	-1.361	-0.933
CDC37	11140	-0.048	-0.420
CDC42	998	-0.036	0.283
CDC42EP4	23580	-1.201	-1.042
CDH2	1000	0.111	0.463
CENPB	1059	0.051	0.310
CEP170	9859	0.196	1.063
CFH	3075	-0.295	-0.079
CFHR2	3080	-0.475	0.066
CFI	3426	-0.314	0.371
CFL1	1072	0.207	0.506
CHCHD6	84303	0.807	1.073
CHD4	1108	0.169	1.611
CHGA	1113	0.161	1.128
CHGB	1114	-0.912	-2.209
CHN1	1123	0.397	0.291
CHORDC1	26973	0.280	0.956
CISD1	55847	0.279	1.720
CISD2	493856	1.025	1.867
CKAP5	9793	0.832	2.034
CKB	1152	0.660	1.807
CKMT2	1160	-0.347	2.001
CLASP2	23122	-0.126	-0.201
CLEC3B	7123	-0.231	-0.005
CLIC1	1192	-0.205	-0.266
CLIC2	1193	0.500	4.435
CLIC4	25932	0.081	0.023
CLSTN1	22883	-1.509	0.327
CLTB	1212	-0.298	-0.091
CLTC	1213	-0.183	0.502
CLU	1191	-1.436	-1.073
CNBP	7555	1.732	1.855
CNN2	1265	-0.159	-0.249
CNN3	1266	1.668	1.970
CNNM2	54805	-0.279	-0.253
CNOT1	23019	0.258	1.061
CNP	1267	-0.111	-0.280
CNPY3	10695	0.179	1.217
CNTN1	1272	-1.662	-1.877
COIL	8161	1.216	0.611
COL1A1	1277	-4.024	-0.842
COL3A1	1281	-3.578	-0.067
COL4A1	1282	-1.937	-0.810
COL4A2	1284	-1.619	-1.561
COL6A1	1291	-0.831	-0.279
COMMD5	28991	0.302	0.098
COMP	1311	-0.941	0.814
COPA	1314	-0.260	0.425
COPB1	1315	0.812	-0.109
COPB2	9276	0.543	0.892
COPG	22820	0.146	0.498
COPG2	26958	1.241	-0.116
COPS4	51138	-0.148	0.295
COPS6	10980	0.063	0.487
CORO1A	11151	-0.286	0.012
CORO1C	23603	0.351	0.747
COX17	10063	0.705	1.861
COX6B1	1340	0.984	0.405
CP	1356	0.368	0.510
CPNE3	8895	0.098	0.236
CPSF2	53981	0.173	1.029
CPSF3	51692	1.234	1.608
CRABP2	1382	0.358	2.409
CRBN	51185	0.623	0.034
CRELD1	78987	0.057	0.291
CRIP2	1397	-2.402	-2.233

CRKL	1399	0.368	0.904
CRMP1	1400	-0.296	-0.363
CRYZ	1429	1.285	1.112
CSDE1	7812	0.264	0.128
CSE1L	1434	1.048	0.610
CSNK2B	1460	0.677	0.839
CSRP1	1465	0.631	-2.292
CSTF2	1478	0.407	0.536
CSTF3	1479	0.573	0.892
CTBP1	1487	0.129	0.479
CTCF	10664	0.678	-0.228
CTNNA2	1496	-0.895	-0.502
CTNNB1	1499	0.746	0.264
CTNND1	1500	-0.095	0.517
CTPS	1503	0.117	0.740
CTSC	1075	-0.699	-0.290
CTSD	1509	-0.433	0.061
CTTN	2017	0.439	-0.580
CUL2	8453	0.447	-0.079
CUL4A	8451	0.401	0.867
CUL5	8065	0.779	0.542
CXADR	1525	0.063	0.077
CXXC1	30827	-0.082	0.609
CYB5R1	51706	-0.245	-0.628
CYC1	1537	0.678	0.950
CYTH1	9267	-0.387	-0.201
DARS	1615	1.008	0.087
DAZAP1	26528	1.029	0.630
DBH	1621	-0.380	0.686
DBN1	1627	-0.276	-0.253
DBNL	28988	-0.449	-0.280
DC2	58505	1.581	1.178
DCLK1	9201	-0.277	1.872
DCTN1	1639	-0.725	-0.351
DCX	1641	0.920	1.413
DCXR	51181	0.961	0.950
DDA1	79016	0.246	0.818
DDAH1	23576	-0.364	-0.810
DDAH2	23564	-0.646	-0.114
DDB1	1642	0.272	0.909
DDI2	84301	-0.069	-0.727
DDOST	1650	-0.237	0.849
DDT	1652	0.409	-0.114
DDX1	1653	0.472	0.454
DDX17	10521	-0.021	1.183
DDX18	8886	0.871	2.431
DDX19B	11269	0.438	0.700
DDX21	9188	1.271	2.752
DDX23	9416	0.446	2.193
DDX27	55661	0.143	2.215
DDX39	10212	1.413	1.829
DDX3X	1654	0.364	1.537
DDX41	51428	0.097	0.713
DDX5	1655	0.229	1.446
DDX6	1656	0.631	1.154
DECR1	1666	0.824	1.655
DEFA1	1667	-1.644	0.296
DEK	7913	1.013	1.781
DEPDC5	9681	-0.206	-0.767
DERA	51071	-1.107	0.192
DFFA	1676	-0.339	-0.733
DHX15	1665	1.062	0.852
DHX9	1660	0.509	1.283
DIAPH1	1729	-0.236	0.354
DIS3	22894	1.135	1.273
DIS3L2	129563	0.459	-0.055
DKC1	1736	1.696	1.586
DLAT	1737	0.758	0.921
DLD	1738	0.101	0.945
DLK1	8788	4.520	-0.794
DMXL2	23312	0.199	-0.377

DNAJA2	10294	0.690	0.319
DNAJA3	9093	0.578	0.479
DNAJB1	3337	2.311	-0.240
DNAJC12	56521	0.529	-0.568
DNAJC6	9829	-0.578	-0.693
DNPEP	23549	0.111	0.108
DOCK7	85440	0.364	1.544
DPYSL2	1808	-0.450	-0.266
DPYSL3	1809	-1.095	-1.821
DPYSL4	10570	-0.315	-0.688
DPYSL5	56896	-0.617	-0.488
DRAP1	10589	0.631	0.555
DST	667	-0.432	0.405
DSTN	11034	0.253	-0.530
DTYMK	1841	1.132	2.859
DUS3L	56931	0.149	1.354
DUT	1854	1.230	3.306
DYNC1H1	1778	-0.359	0.630
DYNC1LI2	1783	-0.111	0.431
DYNLL1	8655	-0.189	-0.033
ECH1	1891	-0.026	0.864
ECM1	1893	-0.439	-0.096
EDC4	23644	0.077	0.217
EEF1A1	1915	0.253	1.388
EEF1A2	1917	-0.229	0.737
EEF1B2	1933	1.552	1.203
EEF1D	1936	1.132	0.786
EEF1G	1937	-0.352	1.354
EEF2	1938	0.427	1.246
EFEMP1	2202	-0.036	-0.745
EFEMP2	30008	-0.367	-1.488
EFTUD1	79631	1.040	1.422
EFTUD2	9343	0.064	1.423
EGF	1950	-0.513	0.258
EHMT2	10919	0.101	1.405
EIF2B3	8891	-0.068	0.422
EIF2B5	8893	0.310	0.397
EIF2C1	26523	-0.386	0.035
EIF2S1	1965	0.951	1.154
EIF2S3	1968	0.830	1.087
EIF3A	8661	0.411	0.653
EIF3B	8662	0.755	1.113
EIF3C	8663	1.426	0.855
EIF3EIP	51386	0.376	0.786
EIF3G	8666	0.962	0.601
EIF3I	8668	0.125	0.915
EIF3K	27335	0.605	0.799
EIF4A1	1973	0.643	0.103
EIF4G1	1981	-0.112	0.641
EIF4H	7458	0.602	1.221
EIF5A	1984	0.436	0.518
EIF5B	9669	0.583	0.686
EIF6	3692	-0.418	0.556
ELAC2	60528	0.083	0.740
ELAVL2	1993	0.122	-0.139
ELAVL3	1995	0.004	1.840
EML2	24139	-0.449	1.217
EML4	27436	0.009	0.541
ENAH	55740	0.305	1.128
ENO2	2026	-0.686	0.397
ENPP2	5168	-0.310	0.727
EPB41	2035	-0.029	-0.664
EPB41L1	2036	-1.975	0.430
EPB41L3	23136	-2.893	-2.797
EPB42	2038	-0.189	-1.000
EPHA5	2044	-0.457	-2.664
EPHB3	2049	-0.836	-1.233
EPHX2	2053	-0.377	-0.159
EPM2AIP1	9852	0.567	0.526
EPRS	2058	0.657	0.413
ERAP1	51752	-0.429	-0.873

ERH	2079	0.545	0.867
ERO1L	30001	0.169	0.198
ESD	2098	0.818	0.485
ETFA	2108	1.690	1.077
ETFB	2109	-0.263	1.296
EXDL2	55218	0.122	0.754
EXOC1	55763	0.518	1.082
EXOC8	149371	0.686	1.717
EXOSC2	23404	0.870	1.560
EXOSC7	23016	0.812	1.255
EXOSC8	11340	0.756	1.341
EXOSC9	5393	1.133	1.707
F11	2160	-0.668	0.874
F12	2161	1.185	-0.214
F13B	2165	0.104	-1.406
F9	2158	-0.669	0.178
FABP5	2171	0.179	0.283
FAM164A	51101	-0.315	0.012
FAM44A	259282	0.495	0.734
FAM62A	23344	-0.766	-0.801
FAM91A1	157769	-0.068	1.830
FARP1	10160	0.082	-0.201
FARSA	2193	0.710	1.341
FARSB	10056	0.711	1.962
FASN	2194	-0.027	1.498
FBL	2091	2.246	3.086
FBLN1	2192	1.203	1.367
FBN1	2200	-0.002	-0.767
FBXO30	84085	-0.329	-1.217
FBXO7	25793	0.132	-0.699
FDPS	2224	0.108	0.035
FECH	2235	0.070	-0.293
FERMT2	10979	0.540	-3.510
FETUB	26998	-0.296	-0.502
FGA	2243	-0.009	-2.244
FGB	2244	0.080	-2.189
FGFBP2	83888	0.697	-0.214
FGG	2266	0.071	-2.225
FHL1	2273	-0.073	1.590
FHOD1	29109	-0.188	-0.314
FKBP1A	2280	0.095	0.319
FKBP4	2288	0.799	2.014
FKBP5	2289	0.282	0.699
FKBP8	23770	-0.147	-0.121
FLAD1	80308	0.051	-0.715
FLII	2314	-1.055	-0.472
FLNA	2316	0.159	0.713
FLNB	2317	-0.099	2.564
FLNC	2318	0.820	3.240
FLOT1	10211	-0.350	-0.652
FN1	2335	-2.900	1.686
FN3KRP	79672	0.544	0.615
FNTA	2339	0.888	0.962
FREQ	23413	0.102	0.740
FSCN1	6624	-0.011	0.077
FTH1	2495	0.003	-2.354
FTO	79068	-0.092	1.035
FUBP1	8880	0.297	1.278
FXYD6	53826	-0.070	0.336
G6PD	2539	0.277	-0.474
GAA	2548	-0.868	-0.151
GABPA	2551	0.364	1.061
GALK1	2584	0.005	-1.185
GAPDH	2597	0.789	1.169
GARNL4	23108	-0.561	0.178
GART	2618	0.511	1.219
GATM	2628	-0.017	-0.432
GCLC	2729	0.262	-0.406
GCLM	2730	0.460	-0.652
GCN1L1	10985	-0.157	0.945
GDI1	2664	-0.074	0.479

GDI2	2665	0.897	-0.010
GEMIN5	25929	0.789	1.662
GFPT1	2673	-0.212	-0.780
GFRA2	2675	0.627	3.777
GFRA3	2676	-2.280	-2.212
GGCT	79017	0.977	0.630
GIT1	28964	-0.533	0.077
GLA	2717	0.150	-0.528
GLCCI1	113263	0.770	1.164
GLG1	2734	-0.731	0.354
GLIPR2	152007	0.700	0.752
GLO1	2739	0.784	0.001
GLUD1	2746	0.345	1.730
GLUL	2752	0.079	0.593
GMPPB	29925	0.476	-0.409
GMPR	2766	0.313	-0.756
GMPS	8833	2.720	1.418
GNA11	2767	-0.226	-0.553
GNAI1	2770	-0.530	-1.887
GNAI3	2773	0.768	-0.604
GNAO1	2775	-1.203	-0.640
GNAQ	2776	-0.125	-0.076
GNAS	2778	-0.079	-0.377
GNAZ	2781	-0.796	-0.737
GNB1	2782	-0.937	-1.185
GNB2	2783	-0.104	-0.652
GNB2L1	10399	0.581	0.953
GNE	10020	0.847	0.169
GNG2	54331	-0.422	-1.933
GNG4	2786	0.920	0.190
GNL1	2794	-0.258	0.319
GNPDA1	10007	0.456	1.354
GNPNAT1	64841	1.847	2.177
GORASP2	26003	0.611	-0.222
GOT2	2806	0.772	2.280
GPD2	2820	0.157	-0.188
GPHN	10243	0.946	0.376
GPI	2821	0.067	0.861
GPKOW	27238	0.296	-2.049
GPS1	2873	0.016	0.203
GRB2	2885	-0.012	0.990
GRHPR	9380	0.747	0.149
GRN	2896	-0.882	-0.984
GRWD1	83743	0.595	1.796
GSN	2934	-0.404	-0.293
GSR	2936	0.264	0.483
GSS	2937	0.223	0.045
GSTM1	2944	-0.022	-0.033
GSTM2	2946	0.129	-0.377
GSTM3	2947	0.162	0.304
GSTO1	9446	1.429	-0.616
GSTP1	2950	0.496	0.454
GTF2I	2969	-0.249	1.118
GTF3C1	2975	0.042	-0.800
GTF3C3	9330	1.179	-2.410
GTPBP4	23560	0.970	1.347
H2AFY	9555	0.236	1.500
H2AFY2	55506	0.498	0.644
HABP2	3026	-0.241	0.045
HADHA	3030	0.292	0.322
HAGH	3029	-0.014	-0.293
HARS2	23438	-0.177	-0.434
HAT1	8520	1.014	0.615
HBB	3043	0.042	0.962
HBE1	3046	-0.272	-2.028
HBG1	3047	-2.348	-3.303
HBS1L	10767	0.273	0.273
HBZ	3050	0.139	-2.996
HCFC1	3054	0.231	0.968
HDGF	3068	0.584	0.665
HDHD1A	8226	-0.230	-1.241

HEATR2	54919	0.804	2.504
HECA	51696	-0.228	-0.688
HGF	3082	1.891	1.301
HIBCH	26275	0.120	-0.434
HINT1	3094	1.027	1.020
HINT3	135114	-0.975	-0.306
HK1	3098	-0.591	-0.176
HK2	3099	2.271	2.616
HLA-A	3105	-1.248	-2.389
HLA-DRB1	3123	-1.548	-2.140
HLTF	6596	1.040	1.754
HMGB1	3146	0.701	2.296
HMGB2	3148	1.577	2.990
HMGCL	3155	0.058	-1.233
HNRNPA1	3178	0.385	0.683
HNRNPA2B1	3181	0.384	1.116
HNRNPA3	220988	0.417	0.430
HNRNPC	3183	0.870	1.341
HNRNPD	3184	0.934	0.644
HNRNPF	3185	0.347	3.503
HNRNPH1	3187	0.110	0.962
HNRNPK	3190	0.474	0.849
HNRNPL	3191	0.743	1.541
HNRNPM	4670	0.216	1.034
HNRNPR	10236	-0.488	0.556
HNRNPU	3192	0.399	1.198
HNRPDL	9987	0.375	0.623
HP	3240	0.043	1.123
HPRT1	3251	0.832	0.861
HRG	3273	-0.405	1.301
HSD17B10	3028	0.421	1.123
HSP90AA1	3320	0.461	1.203
HSP90AB1	3326	0.418	1.092
HSP90B1	7184	0.700	-2.116
HSPA14	51182	0.432	2.203
HSPA1B	3304	1.298	0.108
HSPA4	3308	1.062	0.776
HSPA4L	22824	0.446	0.669
HSPA8	3312	0.574	0.696
HSPA9	3313	0.671	1.669
HSPC152	51504	1.424	1.626
HSPD1	3329	1.176	3.045
HSPH1	10808	1.018	1.526
HTATSF1	27336	0.484	0.998
HUWE1	10075	-0.049	0.974
HYOU1	10525	-0.146	1.341
IAH1	285148	0.712	0.571
IARS	3376	1.183	0.830
ICA1	3382	0.735	-0.033
ICAM1	3383	-0.092	0.637
IDE	3416	0.124	0.118
IDH1	3417	-0.258	-0.201
IDH2	3418	0.498	1.113
IDH3A	3419	0.568	0.880
IFI30	10437	-0.137	0.812
IFIT5	24138	0.049	2.496
IGF2	3481	1.166	0.568
IGF2BP3	10643	0.352	0.149
IGF2R	3482	0.004	0.319
IGFBP2	3485	2.155	0.336
IGFBP7	3490	-2.150	0.923
IGFBPL1	347252	1.409	2.042
IGHA1	3493	-0.333	1.349
IGHG1	3500	0.376	-0.356
IGJ	3512	0.005	0.045
IGL@	3535	-0.016	0.759
IGSF3	3321	-0.080	-0.240
ILF3	3609	0.781	1.158
ILKAP	80895	-0.092	0.564
IMPDH2	3615	0.704	1.025
IPO4	79711	0.653	1.418

IPO5	3843	1.149	1.246
IPO9	55705	0.041	0.273
IREB2	3658	0.487	-1.434
IRGQ	126298	0.088	0.593
ITFG1	81533	-0.183	0.198
ITGA2B	3674	-0.052	-0.091
ITGB1	3688	0.217	-0.789
ITGB2	3689	-0.983	-1.734
ITGB3	3690	-0.557	-0.335
ITIH2	3698	-0.204	-1.139
ITPA	3704	-0.055	0.362
ITPR1	3708	0.703	1.984
IVD	3712	0.065	0.139
JAM3	83700	0.464	1.754
JTV1	7965	1.120	0.726
KALRN	8997	0.085	0.727
KARS	3735	1.315	1.426
KBTBD6	89890	0.069	0.379
KHSRP	8570	0.031	0.734
KIAA0152	9761	-0.340	0.319
KIAA0329	9895	-0.491	-1.958
KIAA1576	57687	-0.837	-1.576
KIAA1967	57805	0.015	0.626
KIDINS220	57498	-0.195	-0.377
KIF21A	55605	0.588	0.808
KIF5B	3799	0.196	-0.102
KIF5C	3800	-0.547	0.227
KIFC1	3833	1.348	-1.093
KLC1	3831	-0.241	0.066
KLHL15	80311	0.335	-0.593
KPNA1	3836	0.200	-0.372
KPNA4	3840	0.765	-0.448
KPNB1	3837	0.644	0.793
KRT10	3858	0.250	-1.225
KSR1	8844	-0.356	-0.586
L1CAM	3897	-0.877	-1.241
LACTB2	51110	0.888	0.713
LAMA5	3911	0.054	1.382
LAMB1	3912	0.404	-0.022
LAMC1	3915	-0.013	-0.227
LAMP1	3916	-0.832	0.533
LANCL1	10314	0.090	0.128
LANCL2	55915	-0.064	-0.240
LAP3	51056	1.333	1.319
LASP1	3927	-0.226	-1.099
LCP1	3936	-0.575	-1.336
LDHB	3945	1.157	-0.365
LGALS1	3956	-0.203	-0.392
LGALS3BP	3959	-0.281	2.438
LIG3	3980	0.498	-0.381
LIMCH1	22998	1.534	0.586
LIN7C	55327	0.274	-0.139
LMAN2L	81562	-0.042	0.188
LONP1	9361	0.866	0.830
LPA	4018	-0.738	-1.100
LPCAT1	79888	-0.179	0.533
LRP1	4035	-0.415	0.837
LRPPRC	10128	1.158	0.962
LRRC40	55631	-0.013	-0.638
LRRC47	57470	-0.540	-0.377
LRRC59	55379	0.823	2.246
LSM4	25804	1.313	0.608
LTA4H	4048	0.953	0.001
LTBP1	4052	-0.481	0.707
LTBP2	4053	-0.659	0.586
LUC7L2	51631	0.230	1.747
LUM	4060	-0.477	-0.789
MAD1L1	8379	-0.096	-0.342
MAP1B	4131	-0.135	0.824
MAP2	4133	-0.295	-1.249
MAP2K4	6416	-0.555	-1.362

MAPK1	5594	-0.388	0.098
MAPK8	5599	0.014	0.418
MAPK8IP3	23162	-0.267	0.405
MAPRE1	22919	0.424	0.091
MAPT	4137	-1.566	-1.126
MAR5	54708	0.358	0.870
MARCKSL1	65108	-0.460	0.740
MASP1	5648	-0.187	-0.652
MASP2	10747	-0.753	-1.363
MAT2A	4144	-0.108	1.200
MAT2B	27430	0.336	1.305
MATR3	9782	0.351	1.026
MCAM	4162	-0.594	-0.502
MCCC2	64087	-0.057	1.406
MCM2	4171	2.279	3.298
MCM3	4172	1.531	-1.201
MCM4	4173	1.173	1.780
MCM5	4174	1.581	2.914
MCM6	4175	1.943	3.398
MCM7	4176	1.030	0.990
MCTS1	28985	1.897	1.354
MDH1	4190	0.495	0.397
MDH2	4191	0.566	2.064
MDK	4192	1.241	2.916
MDN1	23195	0.698	2.009
ME2	4200	0.710	1.045
MED12	9968	0.396	-0.010
MED20	9477	-0.215	1.319
MED8	112950	-0.440	-1.204
MEMO1	51072	0.263	0.789
MEPCE	56257	0.255	-0.044
METAP1	23173	1.026	2.332
METAP2	10988	0.971	0.159
MFN2	9927	-0.955	-1.391
MGC3207	84245	0.124	-0.524
MIF	4282	0.566	1.039
MLLT4	4301	-0.681	1.287
MMP2	4313	0.139	0.773
MPO	4353	-0.795	1.409
MPP1	4354	0.125	-0.882
MPST	4357	1.366	0.831
MRPL3	11222	1.590	0.915
MRPS18A	55168	0.314	0.799
MRPS9	64965	1.229	0.413
MRTO4	51154	0.449	1.804
MSH6	2956	0.911	-1.026
MST1	4485	-0.294	-0.335
MTA1	9112	-0.120	1.270
MTAP	4507	0.352	1.392
MTCH2	23788	0.423	2.065
MTHFD1	4522	0.550	0.277
MTMR9	66036	-0.484	0.861
MTPN	136319	1.854	0.269
MTX2	10651	0.316	1.074
MTX3	345778	0.923	1.571
MXRA5	25878	-0.031	3.269
MYH10	4628	0.198	1.487
MYH9	4627	-0.707	0.135
NA	57671	-1.044	1.314
NA	196515	-0.384	0.494
NAMPT	10135	0.842	1.438
NAPA	8775	-0.067	0.149
NARS	4677	0.597	1.799
NASP	4678	0.205	1.212
NAV1	89796	-0.206	0.310
NCAM1	4684	-0.369	-0.363
NCAN	1463	3.244	2.134
NCBP1	4686	0.234	0.768
NCL	4691	0.528	1.799
NDRG1	10397	0.026	-0.079
NDUFA10	4705	-0.308	1.024

NDUFA4	4697	0.569	0.034
NDUFA8	4702	1.189	2.264
NDUFAB1	4706	1.367	2.747
NDUFB10	4716	0.737	-0.450
NDUFB7	4713	0.119	2.159
NDUFS1	4719	0.082	1.222
NDUFS5	4725	0.340	3.165
NDUFS6	4726	0.424	1.732
NDUFV1	4723	0.360	1.734
NEK7	140609	-0.058	-1.151
NEK9	91754	0.233	1.061
NELL2	4753	0.109	2.908
NFASC	23114	-0.509	-1.249
NFXL1	152518	2.333	0.898
NHP2L1	4809	0.364	1.945
NIF3L1	60491	1.140	0.843
NIPSNAP1	8508	-0.008	-0.021
NISCH	11188	-0.316	0.255
NIT1	4817	-0.276	-0.847
NIT2	56954	1.342	1.438
NKRF	55922	0.310	1.305
NLN	57486	0.113	-0.080
NMD3	51068	0.498	1.976
NNT	23530	0.503	0.715
NOL5A	10528	-0.556	2.064
NOLA2	55651	0.666	2.280
NONO	4841	0.816	1.136
NOP5/NOP58	51602	1.121	1.208
NP	4860	0.946	-0.188
NPC2	10577	0.316	-0.873
NPEPPS	9520	-0.573	-0.420
NPM1	4869	1.897	1.846
NPTN	27020	0.021	-1.628
NRCAM	4897	-1.487	-1.634
NRD1	4898	-0.185	0.169
NRP1	8829	-1.127	-2.806
NSD1	64324	-0.036	2.754
NSUN2	54888	0.295	0.704
NTRK1	4914	-5.049	-2.413
NUBP1	4682	0.247	-0.221
NUDCD1	84955	1.347	0.805
NUDT15	55270	1.654	0.900
NUDT5	11164	1.737	0.939
NUMA1	4926	-0.622	1.973
NUP153	9972	0.322	1.397
NUP155	9631	0.922	0.812
NUP160	23279	0.305	1.278
NUP205	23165	1.267	1.243
NUP35	129401	1.219	0.830
NUP43	348995	0.654	1.252
NUP93	9688	0.353	2.110
NUTF2	10204	0.358	-0.176
OGDH	4967	-0.316	0.169
OLA1	29789	0.160	0.399
OSBPL11	114885	0.439	2.560
OSBPL1A	114876	0.453	0.886
OSBPL9	114883	-0.252	-1.080
OTUB1	55611	0.025	0.362
OXA1L	5018	0.364	1.805
OXCT1	5019	-0.019	1.550
P4HB	5034	0.531	1.123
PA2G4	5036	0.947	1.045
PABPC1	26986	0.870	1.463
PABPN1	8106	-0.049	0.345
PAF1	54623	0.699	-0.067
PAFAH1B1	5048	-0.265	0.217
PAICS	10606	1.340	2.380
PAIP1	10605	0.716	1.098
PALLD	23022	0.107	-0.044
PANK2	80025	0.846	-0.893
PARK7	11315	0.227	-0.151

PATZ1	23598	0.193	0.240
PBRM1	55193	0.170	2.128
PCBP1	5093	0.496	0.849
PCBP2	5094	0.180	0.623
PCBP3	54039	-0.843	0.422
PCCB	5096	1.214	0.590
PCIF1	63935	-0.008	-1.258
PCMT1	5110	-0.046	-0.073
PCNA	5111	2.060	3.534
PCOLCE	5118	1.207	3.248
PCYT2	5833	-0.060	-1.560
PDCD6IP	10015	0.536	0.882
PDCL3	79031	0.702	0.098
PDHA1	5160	0.985	1.077
PDIA3	2923	-0.466	1.236
PDLIM4	8572	1.214	1.405
PDS5A	23244	0.487	1.869
PDXDC1	23042	-0.315	0.713
PDXK	8566	0.025	-0.363
PDXP	57026	-0.178	0.608
PEBP1	5037	0.352	0.786
PECAM1	5175	-0.562	-3.256
PEPD	5184	-0.235	0.066
PEX11B	8799	-0.241	0.707
PF4V1	5197	-0.103	0.529
PFAS	5198	0.981	0.979
PFDN5	5204	0.304	1.081
PFKL	5211	-0.772	-0.434
PFKM	5213	0.624	1.069
PFKP	5214	0.545	0.163
PFN1	5216	0.134	0.623
PFN2	5217	0.393	0.740
PGAM1	5223	-0.012	0.034
PGD	5226	-0.415	-1.010
PGK1	5230	1.689	1.327
PGK2	5232	-0.369	-2.546
PGLS	25796	-0.016	0.861
PGLYRP2	114770	0.011	-0.888
PGM1	5236	0.863	-6.278
PGM3	5238	0.685	-0.981
PGRMC1	10857	0.564	1.895
PHB	5245	1.015	2.069
PHF5A	84844	1.351	1.273
PHF6	84295	0.615	1.558
PHGDH	26227	3.401	1.818
PHIP	55023	0.302	-0.201
PHYHIPL	84457	0.039	-0.079
PI16	221476	-0.221	-2.095
PIN1	5300	0.352	0.057
PIP5K1C	23396	-0.718	-0.528
PITPNA	5306	-0.416	0.217
PITPNB	23760	0.177	0.510
PITPNC1	26207	0.825	1.156
PKM2	5315	0.641	2.117
PLAA	9373	0.775	0.370
PLEC1	5339	-0.940	-0.502
PLS1	5357	0.446	0.156
PLXNB2	23654	-0.446	-2.767
PLXNC1	10154	-0.766	-0.461
PM20D2	135293	0.728	-2.573
PML	5371	0.133	-0.027
POLD1	5424	0.429	0.651
POR	5447	-0.457	-1.520
POSTN	10631	-0.461	1.754
PPA1	5464	1.461	1.861
PPA2	27068	1.554	2.452
PPAT	5471	2.322	2.802
PPCDC	60490	-0.019	0.264
PPIA	5478	0.582	0.950
PPIB	5479	1.113	2.103
PPID	5481	0.947	0.904

PPM1A	5494	0.830	-0.711
PPM1E	22843	0.658	0.939
PPM1G	5496	0.022	0.510
PPME1	51400	-0.098	-0.079
PPP1CA	5499	0.015	0.541
PPP1CB	5500	0.017	0.098
PPP2CA	5515	-0.110	0.327
PPP2R1A	5518	-0.061	0.159
PPP2R5B	5526	-0.635	0.502
PPP2R5C	5527	0.326	0.354
PPP2R5D	5528	-0.255	-1.217
PPP2R5E	5529	0.557	1.159
PPP4R2	151987	0.693	1.118
PPP5C	5536	0.094	1.123
PPP6C	5537	0.702	0.818
PPT1	5538	-0.342	-0.649
PPWD1	23398	0.495	0.573
PRDX2	7001	0.398	-0.126
PRDX4	10549	2.805	3.493
PRDX5	25824	0.417	0.945
PRDX6	9588	0.962	-1.291
PREP	5550	0.729	0.703
PREPL	9581	-0.152	-1.209
PRKAR2A	5576	-0.062	-0.823
PRKAR2B	5577	-0.399	-1.482
PRKCA	5578	0.416	-0.151
PRKCB	5579	-1.604	-2.770
PRKCE	5581	-1.291	-1.468
PRKCI	5584	0.303	-0.126
PRKCSH	5589	0.153	1.287
PRKDC	5591	0.708	1.050
PRMT1	3276	1.055	1.564
PRMT5	10419	1.134	0.707
PRNPIP	79033	-0.598	-0.370
PROS1	5627	0.099	0.405
PRPF3	9129	1.342	1.855
PRPF4B	8899	0.844	1.154
PRPH	5630	-1.550	-2.810
PRPS1	5631	1.111	0.998
PRPS2	5634	1.370	2.672
PRR6	201161	0.763	1.123
PRSS12	8492	1.779	1.574
PSAP	5660	-1.215	-0.163
PSAT1	29968	1.012	0.549
PSMA1	5682	0.845	0.719
PSMA5	5686	0.160	0.369
PSMA6	5687	1.287	1.203
PSMA7	5688	0.680	2.364
PSMB1	5689	0.654	1.259
PSMB3	5691	0.269	0.113
PSMC3	5702	0.425	-1.204
PSMC4	5704	0.162	0.023
PSMC5	5705	0.297	0.181
PSMD1	5707	0.098	0.586
PSMD11	5717	-0.445	0.077
PSMD12	5718	0.955	0.219
PSMD2	5708	0.273	0.446
PSMD4	5710	0.304	-0.079
PSMD6	9861	0.213	0.371
PSMD9	5715	0.013	0.034
PSME1	5720	0.141	-0.176
PSME4	23198	0.548	-0.489
PSPC1	55269	0.365	0.837
PSPH	5723	-0.270	0.345
PTBP1	5725	1.598	3.036
PTGES3	10728	-0.073	0.720
PTK7	5754	0.217	0.984
PTN	5764	-0.290	1.149
PTPN1	5770	0.018	0.422
PTPN11	5781	0.047	1.614
PTPN23	25930	-0.314	0.219

PUF60	22827	0.203	1.193
PURB	5814	0.132	0.118
PVRL1	5818	-0.063	-0.981
PYCR1	5831	0.624	1.909
PYGB	5834	-0.400	-1.475
PZP	5858	0.043	0.193
QARS	5859	0.013	-0.321
QDPR	5860	-0.086	-0.335
QSOX1	5768	-0.040	2.523
RAB10	10890	-0.086	-0.044
RAB14	51552	0.105	-0.240
RAB18	22931	-0.145	0.454
RAB21	23011	-0.055	0.354
RAB22A	57403	0.053	0.760
RAB2B	84932	0.052	0.601
RAB3GAP1	22930	0.048	0.310
RAB7A	7879	-0.005	1.169
RABGAP1	23637	-0.160	0.487
RABGGTA	5875	0.185	-0.114
RABL4	11020	-0.367	-0.092
RAC1	5879	0.278	0.461
RAD21	5885	0.372	2.205
RAN	5901	0.959	0.786
RANBP1	5902	0.642	1.026
RANBP2	5903	0.232	1.169
RANBP9	10048	0.208	0.178
RANGAP1	5905	-0.557	-0.079
RAP1B	5908	-0.034	-0.406
RAP1GDS1	5910	0.377	0.082
RARS	5917	0.068	-1.963
RASA1	5921	0.130	0.076
RBBP4	5928	0.547	1.506
RBM17	84991	0.492	1.434
RBM39	9584	0.439	1.266
RBM4	5936	0.742	0.805
RBM42	79171	0.029	1.217
RBP1	5947	-1.333	1.413
RCC1	1104	1.098	2.087
RCC2	55920	0.016	1.585
RDH13	112724	0.100	0.541
RECQL	5965	0.769	1.226
RELA	5970	0.349	0.550
RFTN1	23180	-0.607	-1.317
RG9MTD1	54931	1.043	1.349
RHOA	387	0.620	0.904
RHOB	388	-0.753	-1.136
RING1	6015	-0.289	0.264
RNASE1	6035	1.003	2.212
RNASE4	6038	-0.129	1.718
RNASEH2A	10535	1.886	0.805
RNASET2	8635	0.007	0.463
RNF114	55905	0.993	0.747
RNH1	6050	-0.631	-0.293
RNPEP	6051	0.382	0.255
ROCK2	9475	0.498	-0.930
ROD1	9991	-0.746	-0.981
RPA1	6117	0.319	0.077
RPIA	22934	0.826	-0.126
RPL10	6134	0.335	1.545
RPL10A	4736	0.680	2.384
RPL11	6135	0.328	1.762
RPL12	6136	1.008	1.469
RPL14	9045	1.001	2.111
RPL17	6139	0.669	0.549
RPL18A	6142	0.938	2.061
RPL23	9349	0.103	1.947
RPL27A	6157	0.698	1.050
RPL3	6122	0.526	1.770
RPL30	6156	0.426	2.284
RPL32	6161	0.766	2.103
RPL34	6164	0.528	2.020

RPL4	6124	0.696	0.967
RPL5	6125	0.180	1.183
RPL7A	6130	0.956	1.637
RPL9	6133	0.437	1.103
RPLP0	6175	0.614	2.061
RPN1	6184	0.221	1.047
RPS11	6205	0.813	0.518
RPS16	6217	0.716	0.623
RPS17	6218	0.962	1.626
RPS2	6187	0.734	1.747
RPS21	6227	1.181	1.349
RPS27L	51065	1.896	1.154
RPS28	6234	0.145	3.062
RPS3	6188	0.966	1.532
RPS3A	6189	0.549	1.627
RPS4X	6191	0.531	1.700
RPS4Y1	6192	4.531	3.262
RPS5	6193	1.017	1.665
RPS6	6194	0.840	1.178
RPS8	6202	0.354	2.026
RPSA	3921	0.911	1.250
RRM1	6240	1.773	2.156
RRM2	6241	3.085	1.471
RRP1	8568	-0.074	0.020
RRP1B	23076	0.581	0.960
RSF1	51773	0.347	0.487
RSL1D1	26156	1.353	1.603
RTN4	57142	-0.149	0.818
RUVBL1	8607	1.334	0.679
RUVBL2	10856	1.221	0.793
SAE1	10055	0.679	0.930
SAFB	6294	0.425	1.128
SAFB2	9667	0.430	0.549
SAMHD1	25939	0.012	0.001
SAMM50	25813	0.838	0.397
SAPS2	9701	-0.853	-0.240
SARM1	23098	-0.644	-0.528
SARS	6301	0.769	1.471
SART1	9092	0.685	2.409
SART3	9733	0.180	0.620
SBF1	6305	-0.660	-1.151
SBF2	81846	0.167	0.593
SCARB2	950	0.166	2.191
SCFD1	23256	0.523	0.178
SCLY	51540	-0.223	-0.446
SCRN1	9805	-1.008	-0.761
SDCCAG10	10283	0.413	1.188
SDHA	6389	0.303	1.118
SDHB	6390	-0.404	0.371
SEC13	6396	0.417	0.895
SEC23IP	11196	-0.218	0.273
SEC24A	10802	0.560	0.283
SEC24B	10427	1.341	0.904
SEC24C	9632	-0.342	0.166
SEC31A	22872	0.674	0.874
SEC63	11231	-0.487	-0.119
SEL1L	6400	0.174	-0.067
SELENBP1	8991	0.076	-0.832
SELL	6402	-0.065	-1.014
SEMA4C	54910	-0.190	-1.273
SEMA4D	10507	-0.291	-4.206
SEMA7A	8482	-0.058	0.354
SEP15	9403	0.969	0.502
SEP2	4735	0.352	2.543
SEP5	5413	-0.912	0.630
SEP7	989	0.096	1.623
SERPINA1	5265	-0.734	0.198
SERPINF1	5176	2.758	1.670
SERPINF2	5345	0.116	-0.676
SERPING1	710	0.221	-0.010
SF1	7536	0.228	1.113

SF3A1	10291	0.090	1.310
SF3A2	8175	0.276	1.183
SF3B1	23451	-0.116	0.979
SFPQ	6421	0.016	1.174
SFRS1	6426	0.824	1.522
SFRS7	6432	0.397	1.371
SGSH	6448	-0.481	-0.863
SGTA	6449	0.479	0.734
SH2D3C	10044	-0.162	0.139
SHMT1	6470	0.069	0.963
SKP1	6500	0.186	0.118
SLC25A12	8604	-0.154	1.220
SLC25A24	29957	-0.069	1.140
SLC25A4	291	-0.075	1.560
SLC25A5	292	1.772	1.462
SLC44A2	57153	-0.725	1.003
SLIT2	9353	0.015	1.111
SMAD2	4087	0.409	0.824
SMAD4	4089	0.281	0.963
SMARCA1	6594	0.082	0.799
SMARCC2	6601	-0.474	0.737
SMC1A	8243	-0.329	1.670
SMC3	9126	0.195	-0.261
SMC4	10051	2.940	2.639
SNRPB	6628	1.538	2.015
SNRPD2	6633	1.824	1.820
SNRPD3	6634	0.848	0.064
SNX6	58533	0.756	0.236
SOD1	6647	0.389	0.159
SON	6651	0.169	1.274
SORD	6652	1.212	0.760
SORL1	6653	-0.780	-0.406
SORT1	6272	-0.001	1.288
SPARC	6678	-3.876	1.648
SPCS2	9789	0.457	0.899
SPIN1	10927	0.242	1.502
SPTA1	6708	-0.143	-0.767
SPTAN1	6709	-0.420	1.747
SPTB	6710	-0.203	-0.883
SPTBN1	6711	-0.284	-0.281
SPTBN2	6712	-0.541	-0.593
SPTLC2	9517	0.201	-1.764
SR140	23350	1.435	1.050
SRC	6714	-0.218	0.192
SRGAP3	9901	-0.613	-0.556
SRI	6717	0.362	0.537
SRM	6723	0.122	1.426
SRP19	6728	0.601	1.198
SRP68	6730	0.577	0.630
SRP72	6731	0.791	0.734
SRP9	6726	0.469	1.327
SRPRB	58477	0.615	1.203
SRR	63826	-0.020	-0.920
SSB	6741	0.794	0.675
SSRP1	6749	0.939	3.541
SSU72	29101	-0.201	-0.050
ST13	6767	0.706	0.454
STAG2	10735	1.522	0.661
STAM	8027	0.139	-0.328
STIP1	10963	0.619	0.164
STK10	6793	0.133	-1.879
STK24	8428	0.114	0.796
STK39	27347	0.246	0.128
STOM	2040	-0.341	-0.010
STON2	85439	0.074	0.734
STRAP	11171	0.150	0.454
STRN4	29888	-0.301	-0.579
STT3A	3703	1.134	1.113
STT3B	201595	0.239	-2.887
STX12	23673	-1.135	-1.722
STXBP1	6812	-0.434	-0.488

SUCLA2	8803	0.371	0.188
SUCLG1	8802	0.099	0.255
SUGT1	10910	0.573	0.861
SUPT16H	11198	0.406	1.921
SUPT6H	6830	-0.754	0.413
SYNCRIP	10492	1.155	1.418
SYNE2	23224	0.058	1.310
SYP	6855	-0.345	-0.280
TAGLN2	8407	-0.537	-1.560
TALDO1	6888	0.622	0.255
TANC2	26115	0.051	0.574
TAOK2	9344	-0.047	0.159
TARDBP	23435	0.302	0.990
TATDN1	83940	1.131	1.522
TBC1D1	23216	0.078	0.181
TBC1D13	54662	-0.103	1.796
TBC1D15	64786	0.525	2.541
TBC1D24	57465	-0.190	0.164
TBC1D5	9779	0.736	1.651
TBCB	1155	-0.046	0.292
TBCC	6903	0.011	0.217
TCEA1	6917	0.049	1.450
TCEB1	6921	0.805	0.494
TCEB2	6923	0.450	0.533
TCERG1	10915	0.259	0.973
TCP1	6950	0.830	0.471
TDRKH	11022	-0.050	-0.314
TES	26136	1.459	1.635
TF	7018	-0.848	-0.044
TFAP2B	7021	-0.285	1.358
TFRC	7037	2.362	2.560
TGFB1I1	7041	0.627	-1.190
TGFBI	7045	-0.286	0.586
TGM2	7052	-0.280	-1.441
TH	7054	-0.741	-0.293
THBS1	7057	-0.570	0.529
THBS2	7058	0.509	0.962
THBS4	7060	0.557	1.098
THOC2	57187	1.134	1.296
THOC6	79228	0.966	1.962
THOP1	7064	1.001	1.164
THSD7A	221981	-0.782	-0.441
THUMPD1	55623	0.936	1.260
THY1	7070	-0.450	-0.528
TIMM9	26520	1.903	3.169
TIMP2	7077	-0.015	0.615
TKT	7086	1.484	1.128
TLE1	7088	0.176	0.602
TLE3	7090	0.404	3.264
TLN1	7094	-0.178	-0.114
TLN2	83660	-1.760	-1.573
TM9SF2	9375	-0.004	1.323
TM9SF3	56889	0.262	0.990
TMED9	54732	-0.585	0.127
TMEM132A	54972	-0.655	0.630
TMEM31	203562	0.074	-1.498
TMPO	7112	0.641	2.262
TNC	3371	-0.685	-1.461
TNKS1BP1	85456	-0.049	1.271
TNPO1	3842	0.658	1.208
TNPO3	23534	0.138	0.556
TOMM70A	9868	0.928	1.362
TOP1	7150	0.334	1.821
TP53BP1	7158	0.247	-0.335
TPI1	7167	0.788	0.909
TPM2	7169	-0.907	1.045
TPP2	7174	0.999	0.430
TPPP	11076	-1.316	-0.067
TPPP3	51673	-1.693	-3.217
TRAP1	10131	1.831	2.309
TRAPPC10	7109	-0.324	0.142

TRAPPC4	51399	-0.079	-1.069
TRIAP1	51499	1.688	2.038
TRIM28	10155	0.744	0.727
TRIO	7204	-0.019	3.165
TRIP12	9320	0.496	1.283
TRMT1	55621	1.037	1.659
TROVE2	6738	0.443	-1.818
TSFM	10102	0.476	1.683
TSPAN18	90139	0.656	0.413
TSTA3	7264	-0.031	-3.106
TTLL12	23170	0.772	0.765
TUBA1A	7846	-0.246	-0.873
TUBA3C	7278	-0.287	-1.100
TUBA4A	7277	-0.991	-0.488
TUBB	203068	-0.145	-1.343
TUBG1	7283	-0.141	1.187
TUFM	7284	0.272	1.260
TXN	7295	1.777	1.336
TXNDC1	81542	0.939	-0.551
TXNDC17	84817	0.388	-0.962
TXNDC4	23071	0.059	0.714
TXNDC5	81567	0.458	1.374
TXNRD2	10587	-0.421	0.601
TYMP	1890	-0.566	-1.000
U2AF2	11338	0.468	0.345
UBA1	7317	-0.203	0.310
UBA2	10054	0.429	1.422
UBA3	9039	0.261	0.936
UBE2F	140739	0.174	0.397
UBE2K	3093	0.299	0.763
UBE2L3	7332	0.182	0.465
UBE2M	9040	0.403	1.181
UBE2O	63893	0.055	0.246
UBE2Z	65264	-0.228	0.547
UBE3A	7337	0.457	0.243
UBQLN4	56893	-0.198	-0.215
UBR1	197131	0.234	-0.178
UBR4	23352	-0.498	0.056
UBR5	51366	0.301	1.082
UBR7	55148	1.357	-0.607
UBTF	7343	-0.371	1.149
UCHL1	7345	-0.208	0.001
UFC1	51506	0.371	-0.810
UGCGL1	56886	-0.131	0.288
UHRF1	29128	2.361	2.107
UIMC1	51720	0.029	1.451
UNC5C	8633	0.197	0.663
UNK	85451	-0.066	0.767
UQCRC1	7384	0.583	1.514
UQCRH	7388	0.348	1.484
UROD	7389	-0.601	-1.427
USO1	8615	0.938	0.149
USP14	9097	0.171	-0.110
USP15	9958	-0.019	-0.293
USP24	23358	-0.089	0.292
USP47	55031	0.464	0.454
USP7	7874	0.517	0.971
USP9X	8239	0.114	-0.091
VARS	7407	0.242	0.430
VAT1	10493	-1.297	-1.475
VBP1	7411	1.389	1.208
VCAM1	7412	-1.796	-0.604
VCAN	1462	2.446	2.338
VCL	7414	-0.406	-0.503
VCP	7415	0.053	0.034
VDAC1	7416	0.899	2.207
VDAC2	7417	0.860	0.364
VDAC3	7419	0.538	1.305
VEZF1	7716	0.587	0.720
VLDLR	7436	1.353	0.554
VPRBP	9730	-0.044	0.044

VPS13C	54832	-0.847	0.354
VPS28	51160	-0.664	0.502
VPS29	51699	-0.090	0.962
VPS35	55737	0.411	-0.789
VSNL1	7447	1.404	2.405
VTA1	51534	0.436	0.405
VTN	7448	-0.507	-0.377
VWF	7450	-0.250	-0.722
WARS	7453	-0.370	0.310
WASF1	8936	0.560	0.665
WDFY1	57590	-0.026	0.273
WDHD1	11169	0.598	2.484
WDR1	9948	0.145	0.188
WDR22	8816	0.082	0.281
WDR46	9277	0.573	0.330
WDR47	22911	-0.114	-0.085
WDR5	11091	0.506	1.522
WDR68	10238	0.107	1.604
WDR76	79968	0.732	-0.242
WDR77	79084	0.287	0.651
WDR82	80335	0.261	1.050
WDR92	116143	-0.199	3.685
WNK1	65125	-0.297	-0.903
WRNIP1	56897	0.224	0.637
XAB2	56949	0.578	0.132
XPO1	7514	0.266	0.909
XPO7	23039	-0.055	-0.061
XRCC1	7515	0.605	1.342
XRCC5	7520	0.648	0.861
XRCC6	2547	-0.276	1.098
YARS	8565	-0.180	-3.434
YWHAE	7531	-0.150	0.767
YWHAG	7532	-0.188	0.454
YWHAH	7533	-0.368	-0.214
YWHAQ	10971	-0.073	0.118
YWHAZ	7534	-0.183	0.127
ZC3HAV1	56829	-0.323	1.058
ZC3HAV1L	92092	0.153	0.893
ZCCHC3	85364	0.375	0.720
ZFHX3	463	-0.193	2.045
ZFR	51663	0.291	1.055
ZFYVE20	64145	0.172	0.340
ZFYVE9	9372	-0.424	-0.055
ZMIZ1	57178	-0.534	0.340
ZNF10	7556	0.059	-1.539
ZNF280C	55609	1.750	1.521
ZNF292	23036	0.442	0.947
ZNF295	49854	1.235	-0.490
ZNF428	126299	-0.617	0.016
ZNF462	58499	0.253	0.226
ZNF512	84450	0.041	1.020
ZRANB2	9406	0.361	0.045
ZYX	7791	-0.309	-0.448