

Table S1. Proteins significantly altered in neuroblastoma cells transfected with GIT2 siRNA.

Protein Uniprot IDs are displayed that demonstrated a significant (>2 SD from mean) expression alteration (siRNA_{GIT2}/con) measured using a cross-over medium/heavy SILAC doublet experiment. An average normalized ratio of protein expression from siRNA GIT2 versus control (from the SILAC doublet label-swap) was log₂ transformed for data visualization (N ratio). The simple expression ratio of the specific protein after siRNA GIT2 treatment compared control cells is also indicated.

Protein Description	Uniprot ID	average log(N-ratio)	siRNA GIT2/con
Nucleolar and coiled-body phosphoprotein 1	Q14978-2	0.65	1.57
Putative uncharacterized protein CGI-59	C9JXK6	0.44	1.36
Neutral alpha-glucosidase AB	Q14697-1	0.43	1.34
Histone H3	Q5TEC6	0.40	1.32
LDLR chaperone MESD	Q14696	0.33	1.26
Phosducin-like protein 3	Q9H2J4	0.27	1.21
Peroxiredoxin-4	Q13162	0.26	1.20
Protein FAM3C	Q92520	0.26	1.20
Sulfotransferase 1A1	P50225	0.24	1.18
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit	P21912	0.24	1.18
Tubulin-tyrosine ligase-like protein 12	Q14166	0.24	1.18
Aspartate aminotransferase, mitochondrial;Transaminase A	P00505	0.22	1.17
DERP12 (Dermal papilla derived protein 12)	Q8TE01	0.21	1.15
Thymosin beta-4-like protein 3	Q0P5N8	0.21	1.15
Activator of 90 kDa heat shock protein ATPase homolog 1	O95433	0.21	1.15
ATPase family AAA domain-containing protein 3A	Q9NVI7-1	0.21	1.15
Density-regulated protein	C9JW58	0.20	1.15
Enhancer of mRNA-decapping protein 3	Q96F86	0.20	1.15
Oxidoreductin-1-L-alpha	Q96HE7	0.20	1.15
Bisphosphate 3'-nucleotidase 1	O95861-2	0.20	1.15
Coiled-coil domain-containing protein 124	Q96CT7	0.20	1.15
Leucine aminopeptidase 3	P28838-1	0.19	1.14
Microtubule-associated protein 1B	P46821	0.19	1.14
Prefoldin subunit 4	Q9NQP4	0.19	1.14
Mitochondrial ATP-dependent protease Lon	P36776	0.19	1.14
60S ribosomal protein L14	P50914	0.19	1.14
Membrane-organizing extension spike protein	P26038	0.18	1.13
Histone H3.1	P68431	0.17	1.12
PHD finger-like domain-containing protein 5A	Q7RTV0	0.18	1.13

Signal recognition particle 14 kDa protein	P37108	0.18	1.13
NAD(P) transhydrogenase, mitochondria	Q13423	0.18	1.13
Creatine kinase U-type, mitochondrial	P12532-2	0.18	1.13
14-3-3 protein gamma	P61981	0.17	1.13
Laminin subunit gamma-1	P11047	0.17	1.13
Histone H4	P62805	0.17	1.13
Eukaryotic translation initiation factor 3 subunit F	B3KSH1	0.17	1.13
TRAF6-regulated IKK activator 1 beta Uev1A	Q13404-4	-0.17	0.89
Protein tyrosine phosphatase-like protein PTPLAD1	Q9P035	-0.17	0.89
ADP-ribosylation factor 1	P84077	-0.17	0.89
PEST proteolytic signal-containing nuclear protein	Q8WW12-1	-0.18	0.89
High-mobility group box 1 variant	P09429	-0.18	0.88
60S ribosomal protein L13a	P40429	-0.18	0.88
Chromatin-modifying protein 2a	O43633	-0.18	0.88
Phosphofructokinase 1	Q01813	-0.18	0.88
70 kDa peroxisomal membrane protein	B4DL07	-0.19	0.88
High-mobility group nucleosome binding domain 1	P05114	-0.20	0.87
33 kDa VAMP-associated protein	A6NDZ0	-0.20	0.87
Core histone macro-H2A.1	O75367-1	-0.20	0.87
Histone H2A type 1-B/E	P04908	-0.20	0.87
Adenylyl cyclase-associated protein	B4DNA3	-0.21	0.86
Spinocerebellar ataxia type 10 protein	Q9UBB4	-0.21	0.86
ATP synthase subunit delta, mitochondrial	P30049	-0.21	0.86
Synaptobrevin-3	Q15836	-0.21	0.86
Histone H2A type 1	P0C0S8	-0.22	0.86
Mitochondrial import inner membrane translocase subunit TIM44	O43615	-0.22	0.86
Guanine nucleotide binding protein (G protein), gamma 12	Q9UBI6	-0.22	0.86
Nuclear pore complex protein Nup50	Q9UKX7	-0.23	0.86
Mediator of DNA damage checkpoint protein 1	Q14676-1	-0.23	0.85
Nuclear ubiquitous casein/cyclin-dependent kinases substrate	Q9H1E3-1	-0.23	0.85
Fanconi anemia group I protein	Q9NVI1-3	-0.23	0.85
DnaJ homolog subfamily C member 8	O75937	-0.24	0.85
Histone H2A type 2-B	Q8IUE6	-0.25	0.84
Neuron-specific enolase	P09104	-0.25	0.84
Heterochromatin protein 1 homolog alpha	P45973	-0.26	0.84
26S proteasome non-ATPase regulatory subunit 7	P51665	-0.28	0.82
14-3-3 protein eta	Q04917	-0.30	0.81
Ras-related protein Rab-5B	P61020	-0.32	0.80
Splicing factor, arginine/serine-rich 15	C9J1W7	-0.32	0.80
Peptidyl-prolyl cis-trans isomerase FKBP8	Q14318-2	-0.42	0.75

Table S2. GO term analysis of GIT2 siRNA-modulated proteins. Gene Ontology (GO) term enrichment analysis was performed using standard GO-term biological process algorithms with WebGestalt (version 2). GO term IDs, number of observed enriched proteins (Observed) and enrichment probability ($p < 0.05$) value (p value) is indicated for each significantly-enriched GO term.

GO term description	GO term ID	Observed	<i>p</i> value
cellular response to stress	GO:0033554	8	0.0296
protein-DNA complex assembly	GO:0065004	5	0.0055
chromatin assembly	GO:0031497	4	0.0138
nucleosome assembly	GO:0006334	4	0.0119
purine ribonucleoside triphosphate catabolic process	GO:0009207	2	0.0303
glucose catabolic process	GO:0006007	3	0.0307
glycolysis	GO:0006096	3	0.0256
acetyl-CoA catabolic process	GO:0046356	2	0.0367
ATP catabolic process	GO:0006200	2	0.0256
I-kappaB kinase/NF-kappaB cascade	GO:0007249	4	0.0367

Table S3. Proteins significantly altered in cells transfected with Flag-GIT2 cDNA. Protein Uniprot IDs are displayed that demonstrated a significant (>2 SD from mean) expression alteration (F-GIT2/con) measured using a cross-over medium/heavy SILAC doublet experiment. An average normalized ratio of protein expression from siRNA GIT2 versus control (from the SILAC doublet label-swap) was log₂ transformed for data visualization (N-ratio). The simple expression ratio of the specific protein after siRNA GIT2 treatment compared control cells is also indicated.

Protein Description	Uniprot ID	Average log(N-ratio)	F-GIT2/con
Isoform 2 of C-terminal-binding protein 2	P56545-2	1.64	3.11
Dermal papilla derived protein 12	Q8TE01	1.35	2.56
Gastric-associated differentially-expressed protein YA61P	Q9NZ23	1.14	2.20
G2/mitotic-specific cyclin-B1	P14635	0.75	1.68
Isoform Long of Antigen KI-67	P46013-1	0.71	1.63
Aspartate aminotransferase, mitochondrial	P00505	0.42	1.34
Histone H3	Q5TEC6	0.35	1.27
Isoform 1 of Proteasome subunit alpha type-3	P25788-1	0.33	1.26
Kinesin family member 2C	Q99661-1	0.33	1.26
Eukaryotic translation initiation factor 3 subunit H	B3KS98	0.32	1.25
Histone H3.1	P68431	0.32	1.25
Histone H4	P62805	0.31	1.24
Transmembrane protein 165	Q9HC07	0.29	1.22
zinc finger protein 207 isoform c	Q59G94	0.29	1.22
Squalene synthetase	P37268	0.28	1.21
Ubiquitin-conjugating enzyme E2 S	Q16763	0.28	1.21
DNA topoisomerase 1	P11387	0.28	1.21
Isoform 2 of Transcription elongation factor SPT5	O00267-1	0.27	1.21
FUS interacting protein (Serine/arginine-rich) 1	O75494-1	0.27	1.21
Isoform 1 of Minor histocompatibility antigen H13	Q8TCT9-1	0.27	1.20
Non-histone chromosomal protein HMG-17	P05204	0.27	1.20
Eukaryotic translation initiation factor 1	P41567	0.27	1.20
Protein tyrosine phosphatase-like protein PTPLAD1	Q9P035	0.26	1.20
Msx2-interacting protein	Q96T58	0.26	1.20
Isoform 1 of Replication factor C subunit 1	P35251-1	0.25	1.19
Asparagine synthetase [glutamine-hydrolyzing]	P08243	0.25	1.19
Isoform 4 of 4F2 cell-surface antigen heavy chain	P08195-4	0.25	1.19
Isoform 1 of Golgin subfamily A member 3	Q08378-1	0.24	1.18
Non-histone chromosomal protein HMG-14	A6NEL0	0.23	1.18

Isoform 2 of Kinesin-like protein KIF23	A8MTR8	0.23	1.17
Isoform 2 of RNA-binding protein 10	P98175-1	0.23	1.17
Isoform 2 of Putative ribosomal RNA methyltransferase NOP2	A8MQ38	0.23	1.17
Transcription factor A, mitochondrial	Q00059	0.22	1.17
Isoform 1 of Erlin-2	O94905-1	0.22	1.16
Isoform 1 of Nucleolar RNA helicase 2	Q9NR30-1	0.21	1.15
39S ribosomal protein L10, mitochondrial	A6NGJ4	0.20	1.15
mRNA turnover protein 4 homolog	Q9UKD2	0.20	1.15
Isoform 1 of Surfeit locus protein 4	O15260-1	0.19	1.14
Isoform 1 of H/ACA ribonucleoprotein complex subunit 1	Q9NY12-1	0.18	1.14
Isoform 1 of Tryptophanyl-tRNA synthetase	P23381-1	0.18	1.14
Isoform 1 of Far upstream element-binding protein 1	B4DT31	0.18	1.13
Isoform 2 of UPF0488 protein C8orf33	Q9H7E9-2	0.18	1.13
Uncharacterized protein C7orf50	Q9BRJ6	0.18	1.13
Dolichyl-diphosphooligosaccharide-protein glycosyltransferase	P46977	0.18	1.13
Palmitoyl-protein thioesterase 1	Q5T0S6	0.18	1.13
Isoform 5 of AP-3 complex subunit delta-1	O14617-5	-0.17	0.89
Prolyl endopeptidase	P48147	-0.17	0.89
Serpin B6	B2RBA8	-0.17	0.89
Isoform 1 of Kinectin	Q86UP2-1	-0.18	0.89
Acetyl-CoA acetyltransferase, cytosolic	Q9BWD1	-0.18	0.88
Isoform Long of Glucose-6-phosphate 1-dehydrogenase	P11413-2	-0.18	0.88
Golgin B1	B2ZZ91	-0.19	0.88
Isocitrate dehydrogenase [NADP] cytoplasmic	O75874	-0.19	0.88
Condensin complex subunit 3	Q9BPX3	-0.19	0.88
Long-chain-fatty-acid-CoA ligase 3	O95573	-0.19	0.88
26S proteasome non-ATPase regulatory subunit 12	O00232	-0.21	0.86
Importin-9	Q96P70	-0.22	0.86
Brix domain-containing protein 2	Q8TDN6	-0.24	0.85
Tubulin-specific chaperone E	B7Z3P1	-0.27	0.83
WW domain-binding protein 11	Q9Y2W2	-0.34	0.79
Nucleolar protein 56	O00567	-0.52	0.70
Membrane-associated progesterone receptor component 2	O15173	-0.56	0.68
Casein kinase 2, beta polypeptide	Q5SRQ6	-0.64	0.64
UPF0727 protein C6orf115	Q9P1F3	-1.13	0.46
Isoform 1 of Titin	Q8WZ42-8	-1.19	0.44

Table S4. GO term analysis of Flag-GIT2-modulated proteins. Gene Ontology (GO) term enrichment analysis was performed using standard GO-term biological process algorithms with WebGestalt (version 2). GO term IDs, number of observed enriched proteins (Observed) and enrichment probability ($p < 0.05$) value (p value) is indicated for each significantly-enriched GO term.

GO term description	GO term ID	Observed	p value
cell cycle	GO:0007049	9	0.0052
ribonucleoprotein complex biogenesis	GO:0022613	5	0.0045
RNA processing	GO:0006396	5	0.0454
nuclear division	GO:0000280	4	0.0199
ncRNA processing	GO:0034470	3	0.0477
chromosome condensation	GO:0030261	2	0.0304
DNA-dependent DNA replication	GO:0006261	2	0.0491
proteasomal protein catabolic process	GO:0010498	3	0.0176
regulation of ubiquitin-protein ligase activity	GO:0051438	3	0.0096
aspartate family amino acid biosynthetic process	GO:0009067	2	0.0095

Table S5. Functional Network Analysis of total siRNA/FLAG-GIT2 modulated proteins.

Functional networks of the GIT2-regulated proteins were created using Ingenuity Pathway Analysis (IPA). Focus molecules represent the proteins that meet the applied statistical cutoffs ($p < 0.05$) and map to the Global Molecular Network sets from IPA.

Network Number	Functions	Network Score	Focus Molecules
1	<i>Cellular Assembly and Organization</i>	66	ABCD3
	<i>Cellular Function and Maintenance</i>		ASNS
	<i>DNA Replication, Recombination, and Repair</i>		BRIX1
			CBX5
			CCNB1
			FANCI
			FDFT1
			FKBP8
			H2AFY
			HIST1H2AB/HIST1H2AE
			HIST1H2AG (includes others)
			HIST1H3A (includes others)
			HIST1H4A (includes others)
			HMGN1
			HMGN2
			MKI67
			NOLC1
			NOP2
			NOP56
			PRDX4
			PTPLAD1
			RPL14
			SRP14 (includes EG:20813)
			TMSB10/TMSB4X
			TOP1
			UBE2V1
2	<i>Cellular Assembly and Organization</i>	57	ARF1
	<i>Cellular Function and Maintenance</i>		CAP1
	<i>Cellular Compromise</i>		CSNK2B
			EDC3 (includes EG:315708)
			EIF3F
			EIF3H
			HMGB1
			KIF23

			KIF2C
			LOC100505793/SRSF10
			LONP1
			MAP1B
			MSN
			PFDN4
			PSMA3
			PSMD7
			PSMD12
			RFC1
			SLC3A2
			TBCE
			TTN (includes EG:22138)
			VAPA
			WBP11
			YWHAG
			YWHAH
			ZNF207
3	<i>Cancer</i>	29	AHSA1
	<i>Cell Cycle</i>		ATXN10
	<i>Hair and Skin Development and Function</i>		C6orf115
			DENR
			ENO2
			HM13
			MESDC2
			PCNP
			PFKP
			RAB5B
			RBM10
			SDHB
			SULT1A1
			SUPT5H
			TTLL12
4	<i>Cell Cycle</i>	20	ATAD3A/ATAD3B
	<i>Reproductive System Development and Function</i>		ATP5D
	<i>Gene Expression</i>		FAM3C
			GANAB
			HIST2H2AB
			IPO9
			MDC1
			NNT
			PHF5A
			SPEN
			UBE2S

			VAMP3
5	<i>Cell Signaling</i>	17	BPNT1
	<i>Molecular Transport</i>		CHMP2A
	<i>Vitamin and Mineral Metabolism</i>		CKMT1A/CKMT1B
			EIF1
			GNG12
			GOLGA3
			LAMC1
			LAP3
			PGRMC2
			TIMM44
6	<i>Cell Cycle</i>	15	CCDC124
	<i>Skeletal and Muscular System Development and Function</i>		CTBP2
	<i>Organ Morphology</i>		DNAJC8
			ERO1L
			GOT2
			PDCL3
			PFKL
			SCAF4
			TMEM165

Table S6. IPA Canonical Signaling Pathway analysis of total combined siRNA/FLAG-GIT2 modulated proteins. Canonical signaling pathway analysis was performed upon the total complement of GIT2 ‘constellation’ proteins significantly affected by either GIT2 expression potentiation or reduction. For significant population of a specific canonical signaling pathway, at least two inclusive proteins were required, with an enrichment probability of <0.05.

Canonical Signaling Pathways	-log(p-value)	Ratio	Proteins
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	2.68E+00	6.12E-02	YWHAG,YWHAH,CCNB1
ATM Signaling	2.36E+00	5.08E-02	MDC1,CBX5,CCNB1
EIF2 Signaling	2.32E+00	2.44E-02	EIF3H,EIF3F,EIF1,RPL14,RPL13A
Protein Ubiquitination Pathway	2.43E+00	2.23E-02	PSMA3,PSMD7,DNAJC8,PSMD12,UBE2V1,UBE2S
IGF-1 Signaling	1.72E+00	2.83E-02	YWHAG,YWHAH,CSNK2B
Myc Mediated Apoptosis Signaling	1.34E+00	3.28E-02	YWHAG,YWHAH
Role of BRCA1 in DNA Damage Response	1.33E+00	3.08E-02	MDC1,RFC1
ERK5 Signaling	1.30E+00	3.12E-02	YWHAG,YWHAH
Mitotic Roles of Polo-Like Kinase	1.30E+00	3.08E-02	KIF23,CCNB1
Hypoxia Signaling in the Cardiovascular System	1.28E+00	3.08E-02	UBE2V1,UBE2S
Huntington's Disease Signaling	1.44E+00	1.69E-02	SDHB,VAMP3,UBE2S,GNG12
Actin Cytoskeleton Signaling	1.44E+00	1.66E-02	TMSB10/TMSB4X,TTN,GNG12,MSN
Regulation of eIF4 and p70S6K Signaling	1.26E+00	1.70E-02	EIF3H,EIF3F,EIF1