








Mascot Score

-  < 100
-  100-300
-  300-500
-  500-700
-  700-900
-  > 900

Function

-  Transporter
-  Phosphatase
-  Peptidase
-  Kinase
-  Enzyme
-  Transcription Regulator
-  Other

Legend

- Ap Adaptor protein
- Hist Histones
- Psm Proteasome
- Rbm RNA binding motif
- Rp Ribosomal protein

Figure S1

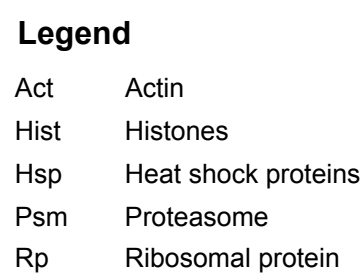
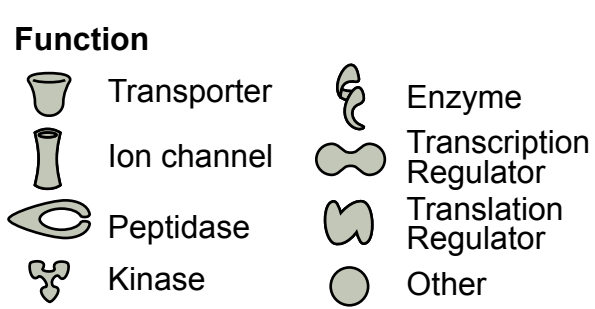
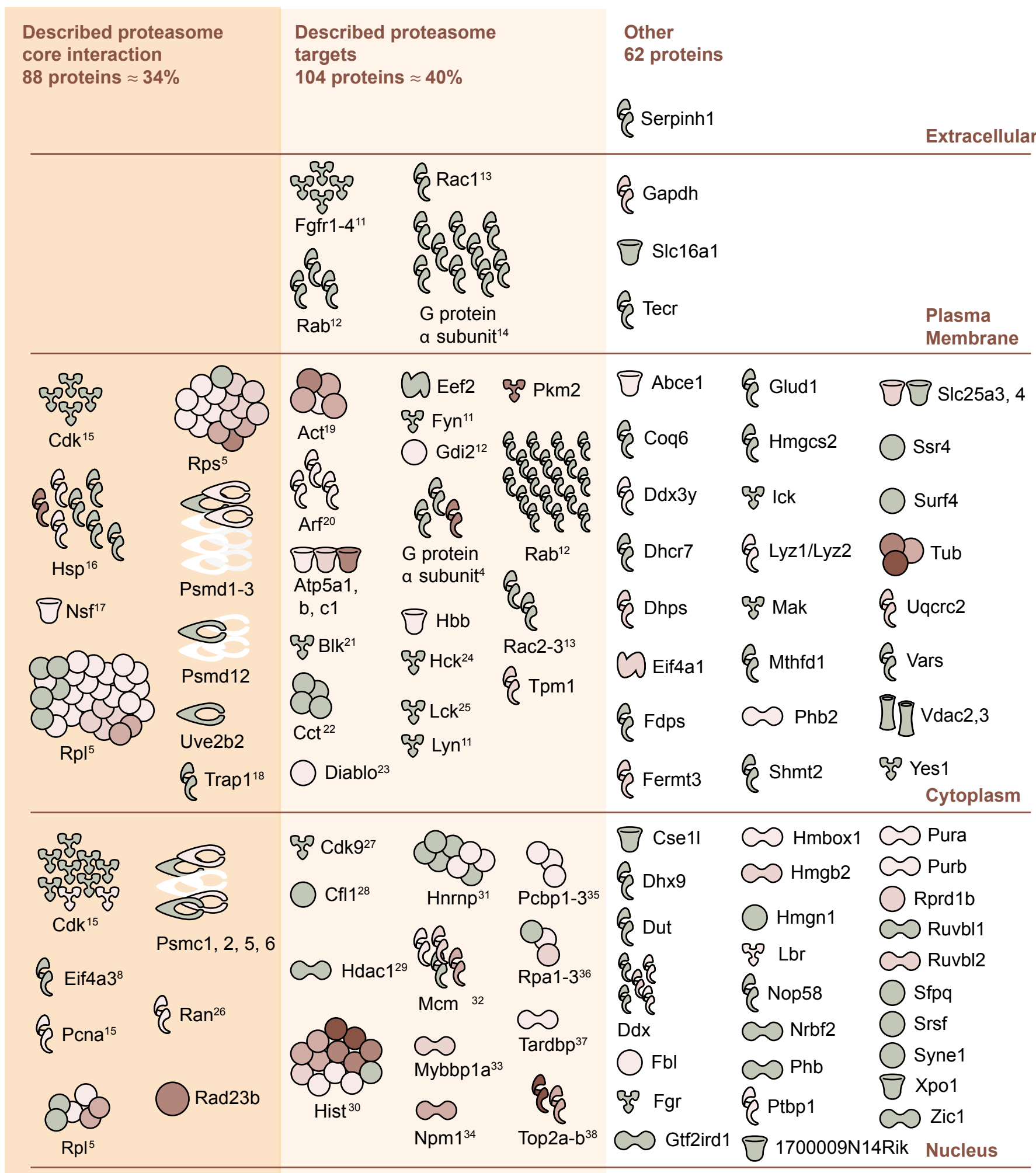


Figure S2

SUPPLEMENTARY FIGURE LEGENDS

FIG S1: Scheme of the Rad23b interactome in embryonic stem cells

Depiction of the Rad23b interactome identified in two independent ES clones expressing Rad23b-YFP-FLAG. Refer to Table S1 for detailed GO Terms and Mascot Scores; Table S2 for Ingenuity Pathways; and Table S3 for supporting literature used for classification of Rad23b interacting partners. Proteins depicted in white are part of the indicated complexes but were not picked up as significant in the Rad23b interactome.

FIG. S2: Scheme of the Rad23b interactome in erythroid cells

Depiction of the Rad23b interactome identified in I/11 and fetal liver derived erythroid cells. Refer to Table S4 for detailed GO Terms and Mascot Scores; Table S5 for Ingenuity Pathways; and Table S3 for supporting literature used for classification of Rad23b interacting partners. Proteins depicted in white are part of the indicated complexes but were not picked up as significant in the Rad23b interactome.

Symbol	Entrez Gene Name	F11 score	B11 Score	GO biological process
Actn4	actinin, alpha 4	95	132	GO:0001666 response to hypoxia
Psmc4	proteasome 26S subunit, ATPase, 4	682	776	GO:0001824 blastocyst development
Xpc	xeroderma pigmentosum, complementation group C	307	125	GO:0006281 DNA repair
Rad23a	RAD23 homolog A (<i>S. cerevisiae</i>)	64	101	GO:0006289 nucleotide-excision repair
Setx	senataxin	3339	1817	GO:0006302 double-strand break repair
Hist1h1d	histone cluster 1, H1d	218	158	GO:0006334 nucleosome assembly
Hist1h1e	histone cluster 1, H1e	218	158	GO:0006355 regulation of transcription, DNA-dependent
Ybx1	Y box binding protein 1	255	253	GO:0006364 rRNA processing
Eif4a3	eukaryotic translation initiation factor 4A3	223	174	GO:0006396 RNA processing
Ssb	Sjogren syndrome antigen B (autoantigen La)	92	89	
Pabpc4	poly(A) binding protein, cytoplasmic 4 (inducible form)	408	246	
Rpl10a	ribosomal protein L10A	184	170	
Rpl11	ribosomal protein L11	60	51	
Rpl12	ribosomal protein L12	262	242	
Rpl13	ribosomal protein L13	195	210	
Rpl13a	ribosomal protein L13a	148	93	
Rpl19	ribosomal protein L19	142	137	
Rpl23	ribosomal protein L23	75	81	
Rpl27	ribosomal protein L27	60	50	
Rpl27a	ribosomal protein L27a	81	83	
Rpl3	ribosomal protein L3	210	78	
Rpl4	ribosomal protein L4	180	162	GO:0006412 translation
Rpl6	ribosomal protein L6	279	172	
Rpl7	ribosomal protein L7	155	175	
Rpl8	ribosomal protein L8	64	58	
Rps11	ribosomal protein S11	127	53	
Rps16	ribosomal protein S16	130	85	
Rps23	ribosomal protein S23	60	51	
Rps26	ribosomal protein S26	147	76	
Rps27	ribosomal protein S27	121	80	
Rps27l	ribosomal protein S27-like	121	80	
Rps6	ribosomal protein S6	389	147	
Scyl2	SCY1-like 2 (<i>S. cerevisiae</i>)	242	97	GO:0006468 protein amino acid phosphorylation
Ddi2	DNA-damage inducible 1 homolog 2 (<i>S. cerevisiae</i>)	183	168	GO:0006508 proteolysis
Psm8	proteasome 26S subunit, non-ATPase, 8	280	390	
Psm1	proteasome subunit, alpha type, 1	367	476	
Psm4	proteasome subunit, alpha type, 4	315	297	GO:0006511 ubiquitin-dependent protein catabolic process
Psm5	proteasome subunit, alpha type, 5	130	318	
Psm7	proteasome subunit, alpha type, 7	713	679	
Ywhag	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	312	226	GO:0006605 protein targeting
G3bp2	GTPase activating protein (SH3 domain) binding protein 2	52	48	GO:0006810 transport
Ap2a2	adaptor-related protein complex 2, alpha 2 subunit	165	257	GO:0006886 intracellular protein transport
Ap2m1	adaptor-related protein complex 2, mu 1 subunit	59	55	
Clint1	clathrin interactor 1	406	336	GO:0006897 endocytosis
Elmo2	engulfment and cell motility 2	315	130	GO:0006909 phagocytosis
Bag3	BCL2-associated athanogene 3	70	171	GO:0006916 anti-apoptosis
Sun2	Sad1 and UNC84 domain containing 2	745	519	GO:0006998 Nuclear envelope organisation
Akap8	A kinase (PRKA) anchor protein 8	130	118	GO:0007076 mitotic chromosome condensation
Psm13	proteasome 26S subunit, non-ATPase, 13	559	666	GO:0007127 meiosis I
Dock4	dedicator of cytokinesis 4	665	210	GO:0007165 signal transduction
Spnb2	spectrin, beta, non-erythrocytic 1	851	921	GO:0007184 SMAD protein nuclear translocation
Myo5a	myosin VA (heavy chain 12, myosin)	3022	1881	GO:0007268 synaptic transmission
Ap2b1	adaptor-related protein complex 2, beta 1 subunit	146	110	GO:0007269 neurotransmitter secretion

Actg1	actin, gamma 1	754	769	GO:0007409	axonogenesis
Mtap1b	microtubule-associated protein 1B	1737	1018	GO:0007416	synapse assembly
Rps9	ribosomal protein S9	67	170	GO:0008284	positive regulation of cell proliferation
Wdr77	WD repeat domain 77	213	217	GO:0008285	negative regulation of cell proliferation
Srsf7	serine/arginine-rich splicing factor 7	158	139	GO:0008380	RNA splicing
Prpsap1	phosphoribosyl pyrophosphate synthetase-associated protein 1	196	102	GO:0009165	nucleotide biosynthetic process
Morc3	MORC family CW-type zinc finger 3	1584	578	GO:0009791	post-embryonic development
Psmb2	proteasome subunit, beta type, 2	321	325	GO:0014070	response to organic cyclic substance
Myo5b	myosin VB	942	622	GO:0015031	protein transport
Fbxo34	F-box protein 34	140	147		
Clta	clathrin, light chain A	148	112	GO:0016192	vesicle-mediated transport
Rai14	retinoic acid induced 14	117	164		
Pkp2	plakophilin 2	210	86	GO:0016337	cell-cell adhesion
Bclaf1	BCL2-associated transcription factor 1	85	65	GO:0016481	negative regulation of transcription
Psmc5	proteasome 26S subunit, ATPase, 5	895	1000		
Hist1h1c	histone cluster 1, H1c	218	158	GO:0016584	nucleosome positioning
Eif2ak3	eukaryotic translation initiation factor 2-alpha kinase 3	346	280	GO:0017148	negative regulation of translation
Fxr1	fragile X mental retardation, autosomal homolog 1	342	410		
Rps3a	ribosomal protein S3A	144	148	GO:0030154	cell differentiation
Psmb3	proteasome subunit, beta type, 3	172	283	GO:0030163	protein catabolic process
Psmc1	proteasome 26S subunit, ATPase, 1	585	600		
Psmc2	proteasome 26S subunit, ATPase, 2	809	1019		
Psmc3	proteasome 26S subunit, ATPase, 3	836	797		
Psmc6	proteasome 26S subunit, ATPase, 6	490	606		
Peg10	paternally expressed 10	95	87	GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway
Psmb5	proteasome subunit, beta type, 5	640	576	GO:0031145	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process
Psmd11	proteasome 26S subunit, non-ATPase, 11	795	1068		
Psmd12	proteasome 26S subunit, non-ATPase, 12	825	863		
Psmd4	proteasome 26S subunit, non-ATPase, 4	617	445		
Psmd6	proteasome 26S subunit, non-ATPase, 6	675	957		
Psmd1	proteasome 26S subunit, non-ATPase, 1	687	1061	GO:0042176	regulation of protein catabolic process
Psmd2	proteasome 26S subunit, non-ATPase, 2	1128	1186		
Psmd3	proteasome 26S subunit, non-ATPase, 3	1329	1333		
Rpl7a	ribosomal protein L7A	315	268	GO:0042254	ribosome biogenesis
Rplp0	ribosomal protein, large, P0	371	456		
Rpl14	ribosomal protein L14	126	126	GO:0042273	ribosomal large subunit biogenesis
Rad23b	RAD23 homolog B (S. cerevisiae)	1194	1322	GO:0043161	proteasomal ubiquitin-dependent protein catabolic process
Hist4h4	histone cluster 4, H4	145	59	GO:0045653	negative regulation of megakaryocyte differentiation
Rbm14	RNA binding motif protein 14	130	188	GO:0045944	positive regulation of transcription from RNA polymerase II promoter
Dck	deoxycytidine kinase	145	59	GO:0046092	deoxycytidine metabolic process
Alpl	alkaline phosphatase, liver/bone/kidney	402	98	GO:0046677	response to antibiotic
Flii	flightless I homolog (Drosophila)	1135	469	GO:0051014	actin filament severing
Jup	junction plakoglobin	84	181	GO:0051291	protein heterooligomerization
Psma3	proteasome subunit, alpha type, 3	216	215	GO:0051603	proteolysis involved in cellular protein catabolic process
Psma6	proteasome subunit, alpha type, 6	484	627		
Psmb1	proteasome subunit, beta type, 1	231	463		
Psmb4	proteasome subunit, beta type, 4	62	256		
Psmb6	proteasome subunit, beta type, 6	178	187		
Sfrs1	serine/arginine-rich splicing factor 1	389	387	GO:0060048	cardiac muscle contraction

Psm14	proteasome 26S subunit, non-ATPase, 14	311	492	GO:0061136	regulation of proteasomal protein catabolic process
Alb	albumin	511	386	GO:0070541	response to platinum ion
Vcp	valosin-containing protein	143	79	GO:0070842	aggresome assembly
Ankrd28	ankyrin repeat domain 28	202	99		
Cttn	cortactin	95	104		
Dbn1	drebrin 1	137	72		
Efhd2	EF-hand domain family, member D2	324	170		
Fxr2	fragile X mental retardation, autosomal homolog 2	80	110		
Mrip	myosin phosphatase Rho interacting protein	75	88		
Myadm	myeloid-associated differentiation marker	109	113		
Otud4	OTU domain containing 4	408	365		
Rbm10	RNA binding motif protein 10	294	160		
Serpinb3d	serpin peptidase inhibitor, clade B (ovalbumin), member 3	118	107		

Table S1: GO Term Classification

GO Term search (www.ensembl.org/biomart) of Rad23b interacting proteins in ES cells. The Mascot Score from each ES cell clone (B11, F11) is indicated. Corresponds to Figure S1.

Ingenuity Canonical Pathways	-log(p-value)	Ratio	Molecules
Protein Ubiquitination Pathway	25.2	0.1020	Psmb3, Psma3, Psma7, Psmb6, Psmc5, Psmc6, Psmc14, Psmc2, Psmb4, Psma6, Psmb5, Psmc4, Psmc13, Psmc4, Psmc6, Psmc3, Psma1, Psmc8, Psmc11, Psmc1, Psmb2, Psmc2, Psmc12, Psma5, Psmc1, Psma4, Psmc1, Psmc4, Psmc3
Purine Metabolism	4.23	0.0228	Psmc1, Dck, Psmc6, Prpsap1, Vcp, Psmc4, Psmc6, Psmc2, Psmc3, Psmc5
GABA Receptor Signaling	3.51	0.0714	Ap2b1, Ap2m1, Myo5b, Ap2a2
Virus Entry via Endocytic Pathways	3.40	0.0500	Ap2b1, Ap2m1, Clta, Actg1, Ap2a2
Clathrin-mediated Endocytosis Signaling	3.08	0.0351	Ap2b1, Ap2m1, Clta, Actg1, Ap2a2, Ctnn
CTLA4 Signaling in Cytotoxic T Lymphocytes	2.37	0.0396	Ap2b1, Ap2m1, Clta, Ap2a2
Granzyme A Signaling	2.12	0.1000	Hist1h1c, Hist1h1e
Nucleotide Excision Repair Pathway	1.61	0.0571	Xpc, Rad23b
Germ Cell-Sertoli Cell Junction Signaling	1.61	0.0238	Jup, Actn4, Clint1, Actg1
Antigen Presentation Pathway	1.50	0.0465	Psmb5, Psmb6
Agrin Interactions at Neuromuscular Junction	1.09	0.0290	Actg1, Ctnn
Caveolar-mediated Endocytosis Signaling	1.03	0.0235	Alb, Actg1
Taurine and Hypotaurine Metabolism	1.00	0.0213	Myo5b
Endoplasmic Reticulum Stress Pathway	0.93	0.0556	Eif2ak3
EIF2 Signaling	0.91	0.0192	Rps6, Eif2ak3
VEGF Signaling	0.89	0.0196	Actn4, Actg1
NRF2-mediated Oxidative Stress Response	0.88	0.0156	Vcp, Eif2ak3, Actg1
Lipid Antigen Presentation by CD1	0.88	0.0435	Ap2a2
Fcy Receptor-mediated Phagocytosis in Macrophages and Monocytes	0.87	0.0196	Myo5a, Actg1
Folate Biosynthesis	0.85	0.0125	Alpl
Leukocyte Extravasation Signaling	0.84	0.0151	Actn4, Actg1, Ctnn
Protein Kinase A Signaling	0.79	0.0123	Hist1h1c, Ywhag, Hist1h1e, Akap8
Antiproliferative Role of TOB in T Cell Signaling	0.78	0.0385	Pabpc4
p70S6K Signaling	0.68	0.0150	Ywhag, Rps6
Cellular Effects of Sildenafil (Viagra)	0.64	0.0132	Pabpc4, Actg1
Pentose Phosphate Pathway	0.63	0.0112	Prpsap1
Glutamate Metabolism	0.63	0.0128	Myo5b
Mechanisms of Viral Exit from Host Cells	0.61	0.0222	Actg1
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	0.58	0.0204	Ywhag
Alanine and Aspartate Metabolism	0.58	0.0114	Myo5b
MSP-RON Signaling Pathway	0.56	0.0196	Actg1
β -alanine Metabolism	0.51	0.0102	Myo5b
Myc Mediated Apoptosis Signaling	0.45	0.0156	Ywhag
Butanoate Metabolism	0.45	0.0076	Myo5b
ILK Signaling	0.44	0.0105	Actn4, Actg1
ERK5 Signaling	0.43	0.0145	Ywhag
Macropinocytosis Signaling	0.42	0.0132	Actn4
Integrin Signaling	0.41	0.0098	Actn4, Actg1
VDR/RXR Activation	0.38	0.0123	Psmc5
Acute Myeloid Leukemia Signaling	0.37	0.0118	Jup
Actin Cytoskeleton Signaling	0.36	0.0084	Actn4, Actg1
FAK Signaling	0.33	0.0096	Actg1
Neuregulin Signaling	0.33	0.0095	Rps6
Crosstalk between Dendritic Cells and Natural Killer Cells	0.32	0.0102	Actg1
IGF-1 Signaling	0.32	0.0100	Ywhag
RhoA Signaling	0.28	0.0091	Actg1
Regulation of eIF4 and p70S6K Signaling	0.28	0.0074	Rps6
Type I Diabetes Mellitus Signaling	0.27	0.0083	Myo5b
14-3-3-mediated Signaling	0.25	0.0081	Ywhag
Hereditary Breast Cancer Signaling	0.25	0.0076	Xpc
PI3K/AKT Signaling	0.24	0.0070	Ywhag
Cardiac β -adrenergic Signaling	0.23	0.0066	Akap8

Table S2: Ingenuity Pathway Analysis.

Canonical Pathways represented by Rad23b interacting partners common to ES clones B11 and F11, as calculated by Ingenuity Pathway Analysis. Corresponds to Figure S1.

Nr.	Gene Symbol	Relation to proteasome	Reference
1	CltA	Core interaction	"The ubiquitin-proteasome system and endocytosis". Strous <i>et al</i> , J Cell Sci. 1999 May;112 (Pt 10):1417-23. Review.
2	Jup	Target	"Differential interaction of plakoglobin and beta-catenin with the ubiquitin-proteasome system". Sadot <i>et al</i> , Oncogene. 2000 Apr 13;19(16):1992-2001.
3	Spnb2	Target	"Spectrin ubiquitination and oxidative stress: potential roles in blood and neurological disorders". Sangerman <i>et al</i> , Cell Mol Biol Lett. 2001;6(3):607-36. Review.
4	Fbxo34	Core	"Systematic analysis and nomenclature of mammalian F-box proteins". Jin <i>et al</i> , Genes Dev. 2004 Nov 1;18(21):2573-80.
5	Rp	Core	"Ubiquitin and ubiquitin-like proteins in the nucleolus: multitasking tools for a ribosome factory". Shcherbik <i>et al</i> , Genes Cancer. 2010 Jul 1;1(7):681-689.
6	Otud4	Core	"Genome-wide loss-of-function analysis of deubiquitylating enzymes for zebrafish development". Tse <i>et al</i> , BMC Genomics. 2009 Dec 30;10:637.
7	Bag3	Target	"Transcriptional upregulation of BAG3 upon proteasome inhibition". Wang <i>et al</i> , Biochem Biophys Res Commun. 2008 Jan 11;365(2):381-5.
8	Eif4a3	Core	"A novel function of Drosophila eIF4A as a negative regulator of Dpp/BMP signalling that mediates SMAD degradation". Li <i>et al</i> , Nat Cell Biol. 2006 Dec;8(12):1407-14.
9	G3bp2	Core	"Ras-GAP SH3 domain binding protein (G3BP) is a modulator of USP10, a novel human ubiquitin specific protease". Soncini <i>et al</i> , Oncogene. 2001 Jun 28;20(29):3869-79.
10	Ybx1	Target	"RBBP6 interacts with multifunctional protein YB-1 through its RING finger domain, leading to ubiquitination and proteasomal degradation of YB-1". Chibi <i>et al</i> , J Mol Biol. 2008 Dec 26;384(4):908-16.
11	Fgfr, Fyn, Lyn	Target	"Cbl-mediated degradation of Lyn and Fyn induced by constitutive fibroblast growth factor receptor-2 activation supports osteoblast differentiation". Kaabeche <i>et al</i> , J Biol Chem. 2004 Aug 27;279(35):36259-67.
12	Rab and Gdi2	Target	"The ubiquitin-proteasome system regulates membrane fusion of yeast vacuoles". Kleijnen <i>et al</i> , EMBO J. 2007 Jan 24;26(2):275-87.
13	Rac1	Target	"Proteasome-mediated degradation of Rac1-GTP during epithelial cell scattering". Lynch <i>et al</i> , Mol Biol Cell. 2006 May;17(5):2236-42.
14	G protein	Target	"Gettin' down with ubiquitin: turning off cell-surface receptors, transporters and channels". Hicke L., Trends Cell Biol. 1999 Mar;9(3):107-12. Review.
15	Cdk and PcnA	Core	"Interaction with cyclin-dependent kinases and PCNA modulates proteasome-dependent degradation of p21". Cayrol <i>et al</i> , Oncogene. 1998 Nov 12;17(19):2437-44.
16	Hsp	Core	"HSP27 and HSP70: potentially oncogenic apoptosis inhibitors". Garrido <i>et al</i> , Cell Cycle. 2003 Nov-Dec;2(6):579-84. Review.
17	Nsf	Core	"Golgi reassembly after mitosis: the AAA family meets the ubiquitin family". Meyer HH, Biochim Biophys Acta. 2005 Jul 10;1744(3):481-92. Review.
18	Trap1	Core	"TRAP1 and the proteasome regulatory particle TBP7/Rpt3 interact in the endoplasmic reticulum and control cellular ubiquitination of specific mitochondrial proteins". Amoroso <i>et al</i> , Cell Death Differ. 2012 Apr;19(4):592-604.
19	Act	Target	"Novel interactions between actin and the proteasome revealed by complex haploinsufficiency". Haarer <i>et al</i> , PLoS Genet. 2011 Sep;7(9):e1002288.
20	Arf	Target	"The promiscuity of ARF interactions with the proteasome". Pollice <i>et al</i> , FEBS Lett. 2008 Oct 15;582(23-24):3257-62.
21	Blk	Target	"Regulation of the Src family tyrosine kinase Blk through E6AP-mediated ubiquitination". Oda <i>et al</i> , Proc Natl Acad Sci U S A. 1999 Aug 17;96(17):9557-62.
22	Cct	Target	"Proteasome-dependent degradation of cytosolic chaperonin CCT". Yokota <i>et al</i> , Biochem Biophys Res Commun. 2000 Dec 20;279(2):712-7.
23	Diablo	Target	"Proteasome-mediated degradation of Smac during apoptosis: XIAP promotes Smac ubiquitination in vitro". MacFarlane <i>et al</i> , J Biol Chem. 2002 Sep 27;277(39):36611-6.

24	Hck	Target	"Membrane-anchored Cbl suppresses Hck protein-tyrosine kinase mediated cellular transformation". Howlett <i>et al</i> , <i>Oncogene</i> . 2002 Mar 7;21(11):1707-16.
25	Lck	Target	"Regulation of the Src family kinase Lck by Hsp90 and ubiquitination". Giannini <i>et al</i> , <i>Mol Cell Biol</i> . 2004 Jul;24(13):5667-76.
26	Ran	Core	"The cyclophilin-like domain mediates the association of Ran-binding protein 2 with subunits of the 19 S regulatory complex of the proteasome". Ferreira <i>et al</i> , <i>J Biol Chem</i> . 1998 Sep 18;273(38):24676-82.
27	Cdk9	Target	"Interaction between cyclin T1 and SCF(SKP2) targets CDK9 for ubiquitination and degradation by the proteasome". Kiernan <i>et al</i> , <i>Mol Cell Biol</i> . 2001 Dec;21(23):7956-70.
28	Cfl1	Target	"Tyrosine phosphorylation of cofilin at Y68 by v-Src leads to its degradation through ubiquitin-proteasome pathway". Yoo <i>et al</i> , <i>Oncogene</i> . 2010 Jan 14;29(2):263-72.
29	Hdac1	Target	"Rapid induction of histone hyperacetylation and cellular differentiation in human breast tumor cell lines following degradation of histone deacetylase-1". Zhou <i>et al</i> , <i>J Biol Chem</i> . 2000 Nov 10;275(45):35256-63.
30	Hist	Target	"Ubiquitin proteasome system (UPS): what can chromatin do for you?" O'Connell <i>et al</i> , <i>Curr Opin Cell Biol</i> . 2007 Apr;19(2):206-14. Epub 2007 Feb 20. Review.
31	Hnrnp	Target	"hnRNP K: an HDM2 target and transcriptional coactivator of p53 in response to DNA damage". Moumen <i>et al</i> , <i>Cell</i> . 2005 Dec 16;123(6):1065-78.
32	Mcm	Target	"The ubiquitin-proteasome system is a key component of the SUMO-2/3 cycle". Schimmel <i>et al</i> , <i>Mol Cell Proteomics</i> . 2008 Nov;7(11):2107-22.
33	Mybbp1a	Target	"Quantitative proteomics identifies the Myb-binding protein p160 as a novel target of the von Hippel-Lindau tumor suppressor". Lai <i>et al</i> , <i>PLoS One</i> . 2011 Feb 28;6(2):e16975.
34	Npm1	Target	"Recruitment of phosphorylated NPM1 to sites of DNA damage through RNF8-dependent ubiquitin conjugates". Koike <i>et al</i> , <i>Cancer Res</i> . 2010 Sep 1;70(17):6746-56.
35	Pcbp	Target	"Activation of the HIF prolyl hydroxylase by the iron chaperones PCBP1 and PCBP2". Nandal <i>et al</i> , <i>Cell Metab</i> . 2011 Nov 2;14(5):647-57.
36	Rpa	Target	"Cell cycle- and proteasome-dependent formation of etoposide-induced replication protein A (RPA) or Mre11/Rad50/Nbs1 (MRN) complex repair foci". Robison <i>et al</i> , <i>Cell Cycle</i> . 2007 Oct 1;6(19):2399-407.
37	Tardbp	Target	"Degradation of TDP-43 and its pathogenic form by autophagy and the ubiquitin-proteasome system". Wang <i>et al</i> , <i>Neurosci Lett</i> . 2010 Jan 18;469(1):112-6.
38	Top	Target	"26 S proteasome-mediated degradation of topoisomerase II cleavable complexes". Mao <i>et al</i> , <i>J Biol Chem</i> . 2001 Nov 2;276(44):40652-8.

Table S3: Literature Support

Literature supporting relationships to the proteasome not found in Ingenuity Pathway Analysis or Ensembl GO term classification. Corresponds to Figures S1 and S2.

Symbol	Entrez Gene Name	Score	GO biological process
Rpl24	ribosomal protein L24	134	GO:0000027 ribosomal large subunit assembly
Rps14	ribosomal protein S14	279	GO:0000028 ribosomal small subunit assembly
Rps6	ribosomal protein S6	369	
Npm1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	627	GO:0000055 ribosomal large subunit export from nucleus
Cdk6	cyclin-dependent kinase 6	46	GO:0000080 G1 phase of mitotic cell cycle
Cdk4	cyclin-dependent kinase 4	46	GO:0000082 G1/S transition of mitotic cell cycle
Cdk14	cyclin-dependent kinase 14	46	GO:0000086 G2/M transition of mitotic cell cycle
Fgfr2	fibroblast growth factor receptor 2	46	
Fgfr3	fibroblast growth factor receptor 3	46	
Hdac1	histone deacetylase 1	70	GO:0000122 negative regulation of transcription from RNA polymerase II promoter
Pcna	proliferating cell nuclear antigen	125	
Phb	prohibitin	88	
Xpo1	exportin 1 (CRM1 homolog, yeast)	41	
Eif4a3	eukaryotic translation initiation factor 4A3	71	GO:0000184 nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
Tuba1b	tubulin, alpha 1b	660	GO:0000226 microtubule cytoskeleton organization
Ddx39b	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B	64	GO:0000245 spliceosome assembly
Cdk13	cyclin-dependent kinase 13	46	
Hnrmpm	heterogeneous nuclear ribonucleoprotein M	128	GO:0000380 alternative nuclear mRNA splicing, via spliceosome
Sfpq	splicing factor proline/glutamine-rich	65	
Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	112	GO:0000381 regulation of alternative nuclear mRNA splicing, via spliceosome
Srsf1	serine/arginine-rich splicing factor 1	62	GO:0000395 nuclear mRNA 5'-splice site recognition
			GO:0000462 maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
Rps24	ribosomal protein S24	109	
Psm12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	50	GO:0000502 proteasome complex
Top2a	topoisomerase (DNA) II alpha 170kDa	1280	GO:0000712 resolution of meiotic recombination intermediates
Top2b	topoisomerase (DNA) II beta 180kDa	583	
Rad23b	RAD23 homolog B (S. cerevisiae)	827	GO:0000715 nucleotide-excision repair, DNA damage recognition
Hmgn1	high mobility group nucleosomal binding domain 1	70	GO:0000720 pyrimidine dimer repair by nucleotide-excision repair
Hspa1a	heat shock 70kDa protein 1A	86	GO:0000723 telomere maintenance
H2afx	H2A histone family, member X	947	GO:0000724 double-strand break repair via homologous recombination
Rpa1	replication protein A1, 70kDa	309	
Hspa1l	heat shock 70kDa protein 1-like	86	
Hspa2	heat shock 70kDa protein 2	86	GO:0000902 cell morphogenesis
Hspa8	heat shock 70kDa protein 8	86	
Cfl1	cofilin 1 (non-muscle)	92	
Rab35	RAB35, member RAS oncogene family	72	GO:0000910 cytokinesis
Gnas	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	44	GO:0001501 skeletal system development
Zic1	Zic family member 1	44	
Atp5b	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	411	
Fgfr1	fibroblast growth factor receptor 1	46	GO:0001525 angiogenesis
Gna13	guanine nucleotide binding protein (G protein), alpha 13	44	
Dhcr7	7-dehydrocholesterol reductase	66	GO:0001568 blood vessel development
Gnat1	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 1	44	
Gnat2	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 2	44	GO:0001580 detection of chemical stimulus involved in sensory perception of bitter taste
Gnat3	guanine nucleotide binding protein, alpha transducing 3	71	
Vdac3	voltage-dependent anion channel 3	46	GO:0001662 behavioral fear response
Hsp90b1	heat shock protein 90kDa beta (Grp94), member 1	155	GO:0001666 response to hypoxia
Pkm2	pyruvate kinase, muscle	752	
Gna12	guanine nucleotide binding protein (G protein) alpha 12	44	GO:0001701 in utero embryonic development
Tpm1	tropomyosin 1 (alpha)	381	
Fgfr4	fibroblast growth factor receptor 4	46	GO:0001759 organ induction
Cdk5	cyclin-dependent kinase 5	46	GO:0001764 neuron migration
Fyn	FYN oncogene related to SRC, FGR, YES	46	

Lyn	v-src-1 Yamaguchi sarcoma viral related oncogene homolog	46	GO:0001782	B cell homeostasis
Hmgcs2	3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial)	95	GO:0001822	kidney development
Hsp90ab1	heat shock protein 90kDa alpha (cytosolic), class B member 1	738	GO:0001890	placenta development
Gnb2l1	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	861	GO:0001934	positive regulation of protein phosphorylation
Atp5a1	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	728	GO:0001937	negative regulation of endothelial cell proliferation
Hmgb2	high mobility group box 2	321	GO:0001938	positive regulation of endothelial cell proliferation
Gnai2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	44	GO:0001973	adenosine receptor signaling pathway
Gnal	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type	44	GO:0001975	response to amphetamine
Rac1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	68	GO:0002093	auditory receptor cell morphogenesis
Rab3a	RAB3A, member RAS oncogene family	72	GO:0003016	respiratory system process
Ddx21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	354		
Ddx3x	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	245		
Ddx3y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	245	GO:0005634	nucleus
Hnrnp2	heterogeneous nuclear ribonucleoprotein H2 (H')	67		
Pcbp3	poly(rC) binding protein 3	196		
Abce1	ATP-binding cassette, sub-family E (OABP), member 1	180	GO:0005737	cytoplasm
Eef2	eukaryotic translation elongation factor 2	56		
Gapdh	glyceraldehyde-3-phosphate dehydrogenase	434	GO:0006006	glucose metabolic process
1700009N14Rik	RIKEN cDNA 1700009N14 gene	66		
Gnai1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	44		
Gnai3	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	44		
Gnao1	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	44		
Rab10	RAB10, member RAS oncogene family	72		
Rab12	RAB12, member RAS oncogene family	72		
Rab14	RAB14, member RAS oncogene family	72		
Rab15	RAB15, member RAS oncogene family	72		
Rab1b	RAB1B, member RAS oncogene family	72		
Rab30	RAB30, member RAS oncogene family	72		
Rab33b	RAB33B, member RAS oncogene family	87		
Rab37	RAB37, member RAS oncogene family	72		
Rab3b	RAB3B, member RAS oncogene family	72	GO:0006184	GTP catabolic process
Rab3c	RAB3C, member RAS oncogene family	72		
Rab3d	RAB3D, member RAS oncogene family	72		
Rab43	RAB43, member RAS oncogene family	72		
Rab4a	RAB4A, member RAS oncogene family	72		
Rab4b	RAB4B, member RAS oncogene family	72		
Rab6b	RAB6B, member RAS oncogene family	72		
Rab8a	RAB8A, member RAS oncogene family	72		
Rab8b	RAB8B, member RAS oncogene family	72		
Rac2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	68		
Rac3	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)	68		
Ran	RAN, member RAS oncogene family	167		
Tuba4a	tubulin, alpha 4a	733		
Mcm2	minichromosome maintenance complex component 2	49		
Mcm4	minichromosome maintenance complex component 4	249	GO:0006260	DNA replication
Mcm6	minichromosome maintenance complex component 6	524		
Mcm7	minichromosome maintenance complex component 7	398		

Rpa3	replication protein A3, 14kDa	50		
Ruvbl2	RuvB-like 2 (E. coli)	456		
Pura	purine-rich element binding protein A	104	GO:0006268	DNA unwinding involved in replication
Purb	purine-rich element binding protein B	236		
Cdk2	cyclin-dependent kinase 2	118		
Psmc1	proteasome (prosome, macropain) 26S subunit, ATPase, 1	234		
Psmc5	proteasome (prosome, macropain) 26S subunit, ATPase, 5	84	GO:0006281	DNA repair
Psmc6	proteasome (prosome, macropain) 26S subunit, ATPase, 6	71		
Ruvbl1	RuvB-like 1 (E. coli)	88		
Cdk9	cyclin-dependent kinase 9	46	GO:0006282	regulation of DNA repair
H2afy	H2A histone family, member Y	314		
Hist1h1a	histone cluster 1, H1a	524		
Hist1h1b	histone cluster 1, H1b	722		
Hist1h1c	histone cluster 1, H1c	92		
Hist1h1d	histone cluster 1, H1d	793	GO:0006334	nucleosome assembly
Hist1h1e	histone cluster 1, H1e	687		
Hist1h2bb	histone cluster 1, H2bb	918		
Hist1h2bl	histone cluster 1, H2bl	752		
Hist2h2ac	histone cluster 2, H2ac	229		
Mybbp1a	MYB binding protein (P160) 1a	305	GO:0006351	transcription, DNA-dependent
Gtf2ird1	GTF2I repeat domain containing 1	59		
Hmbox1	homeobox containing 1	149	GO:0006355	regulation of transcription, DNA-dependent
Nrbf2	nuclear receptor binding factor 2	76		
Tardbp	TAR DNA binding protein	146		
Fbl	fibrillarlin	218		
Rpl5	ribosomal protein L5	239	GO:0006364	rRNA processing
Rps16	ribosomal protein S16	332		
Rps7	ribosomal protein S7	207		
Cdk12	cyclin-dependent kinase 12	46		
Hnrnpa2b1	heterogeneous nuclear ribonucleoprotein A2/B1	93		
Hnrnpa3	heterogeneous nuclear ribonucleoprotein A3	135		
Hnrnpc	heterogeneous nuclear ribonucleoprotein C (C1/C2)	98		
Hnrmpf	heterogeneous nuclear ribonucleoprotein F	51	GO:0006397	mRNA processing
Hnrmp1	heterogeneous nuclear ribonucleoprotein H1 (H)	67		
Hnrmpu	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	182		
Pcbp1	poly(rC) binding protein 1	252		
Ptbp1	polypyrimidine tract binding protein 1	101		
Rpl10	ribosomal protein L10	341		
Rpl10a	ribosomal protein L10A	195		
Rpl10l	ribosomal protein L10-like	221		
Rpl11	ribosomal protein L11	182		
Rpl12	ribosomal protein L12	84		
Rpl13a	ribosomal protein L13a	328		
Rpl15	ribosomal protein L15	207		
Rpl17	ribosomal protein L17	271		
Rpl18	ribosomal protein L18	288		
Rpl18a	ribosomal protein L18a	385		
Rpl19	ribosomal protein L19	236	GO:0006412	translation
Rpl22	ribosomal protein L22	600		
Rpl23	ribosomal protein L23	295		
Rpl26	ribosomal protein L26	253		
Rpl27	ribosomal protein L27	141		
Rpl27a	ribosomal protein L27a	131		
Rpl28	ribosomal protein L28	201		
Rpl29	ribosomal protein L29	123		
Rpl3	ribosomal protein L3	575		
Rpl30	ribosomal protein L30	122		
Rpl31	ribosomal protein L31	95		
Rpl32	ribosomal protein L32	121		

Rpl34	ribosomal protein L34	184	
Rpl35a	ribosomal protein L35a	121	
Rpl36	ribosomal protein L36	43	
Rpl36a	ribosomal protein L36a	61	
Rpl37a	ribosomal protein L37a	40	
Rpl4	ribosomal protein L4	698	
Rpl6	ribosomal protein L6	244	
Rpl7	ribosomal protein L7	377	
Rpl9	ribosomal protein L9	94	
Rps11	ribosomal protein S11	357	
Rps13	ribosomal protein S13	89	
Rps15a	ribosomal protein S15a	171	
Rps2	ribosomal protein S2	380	
Rps20	ribosomal protein S20	125	
Rps23	ribosomal protein S23	151	
Rps26	ribosomal protein S26	79	
Rps27	ribosomal protein S27	224	
Rps3	ribosomal protein S3	719	
Rps3a	ribosomal protein S3A	378	
Rps4x	ribosomal protein S4, X-linked	559	
Rps8	ribosomal protein S8	470	
Rps9	ribosomal protein S9	628	
Rplp0	ribosomal protein, large, P0	112	GO:0006414 translational elongation
Vars	valyl-tRNA synthetase	62	GO:0006418 tRNA aminoacylation for protein translation
Cct3	chaperonin containing TCP1, subunit 3 (gamma)	48	
Cct4	chaperonin containing TCP1, subunit 4 (delta)	90	
Cct6a	chaperonin containing TCP1, subunit 6A (zeta 1)	45	GO:0006457 protein folding
Cct6b	chaperonin containing TCP1, subunit 6B (zeta 2)	45	
Hsp90aa1	heat shock protein 90kDa alpha (cytosolic), class A member 1	111	
Trap1	TNF receptor-associated protein 1	127	
Cdk1	cyclin-dependent kinase 1	118	GO:0006461 protein complex assembly
Blk	B lymphoid tyrosine kinase	46	
Cdk15	cyclin-dependent kinase 15	46	
Cdk16	cyclin-dependent kinase 16	43	
Cdk17	cyclin-dependent kinase 17	46	
Cdk18	cyclin-dependent kinase 18	46	
Cdk20	cyclin-dependent kinase 20	46	
Fgr	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	46	GO:0006468 protein phosphorylation
Hck	hemopoietic cell kinase	46	
Ick	intestinal cell (MAK-like) kinase	46	
Lck	lymphocyte-specific protein tyrosine kinase	46	
Mak	male germ cell-associated kinase	46	
Yes1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	46	
Uqcrc2	ubiquinol-cytochrome c reductase core protein II	282	GO:0006508 proteolysis
Psmc2	proteasome (prosome, macropain) 26S subunit, ATPase, 2	146	GO:0006511 ubiquitin-dependent protein catabolic process
Glud1	glutamate dehydrogenase 1	43	GO:0006520 cellular amino acid metabolic process
Shmt2	serine hydroxymethyltransferase 2 (mitochondrial)	85	GO:0006544 glycine metabolic process
Mthfd1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	96	GO:0006548 histidine catabolic process
Nop58	NOP58 ribonucleoprotein homolog (yeast)	51	GO:0006608 snRNP protein import into nucleus
Tecr	trans-2,3-enoyl-CoA reductase	58	GO:0006629 lipid metabolic process
Fdps	farnesyl diphosphate synthase	91	GO:0006695 cholesterol biosynthetic process
Coq6	coenzyme Q6 homolog, monooxygenase (S. cerevisiae)	59	GO:0006744 ubiquinone biosynthetic process
Slc25a3	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	78	GO:0006810 transport

Atp5c1	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1	264	GO:0006811	ion transport
Nsf	N-ethylmaleimide-sensitive factor	173	GO:0006813	potassium ion transport
Vdac2	voltage-dependent anion channel 2	92	GO:0006820	anion transport
Arf1	ADP-ribosylation factor 1	111	GO:0006878	cellular copper ion homeostasis
Arf2	ADP-ribosylation factor 2	111		
Arf3	ADP-ribosylation factor 3	111	GO:0006886	intracellular protein transport
Cse1l	CSE1 chromosome segregation 1-like (yeast)	71		
Actc1	actin, alpha, cardiac muscle 1	505	GO:0006915	apoptotic process
Diablo	diablo, IAP-binding mitochondrial protein	107	GO:0006917	induction of apoptosis
Serpinh1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	51	GO:0006950	response to stress
Surf4	surfeit 4	44	GO:0007030	Golgi organization
Fermt3	fermitin family member 3	477	GO:0007155	cell adhesion
Gdi2	GDP dissociation inhibitor 2	228		
Rab26	RAB26, member RAS oncogene family	72	GO:0007264	small GTPase mediated signal transduction
Actb	actin, beta	508	GO:0007409	axonogenesis
Actbl2	actin, beta-like 2	294		
Rprd1b	regulation of nuclear pre-mRNA domain containing 1B	456	GO:0008150	biological_process
Ssr4	signal sequence receptor, delta	53		
Dhps	deoxyhypusine synthase	335	GO:0008612	peptidyl-lysine modification to hypusine
Acta1	actin, alpha 1, skeletal muscle	803	GO:0009612	response to mechanical stimulus
Pcbp2	poly(rC) binding protein 2	196	GO:0009615	response to virus
Rpa2	replication protein A2, 32kDa	251	GO:0010569	regulation of double-strand break repair via homologous recombination
Ube2v2	ubiquitin-conjugating enzyme E2 variant 2	65	GO:0010976	positive regulation of neuron projection development
Slc16a1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	96	GO:0015711	organic anion transport
Slc25a4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	399	GO:0015866	ADP transport
Lyz1	lysozyme 2	110	GO:0016998	cell wall macromolecule catabolic process
Eif4a1	eukaryotic translation initiation factor 4A1	454	GO:0031100	organ regeneration
Phb2	prohibitin 2	242	GO:0033147	negative regulation of intracellular estrogen receptor signaling pathway
Dhx9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	67	GO:0034605	cellular response to heat
Syne1	spectrin repeat containing, nuclear envelope 1	46	GO:0040023	establishment of nucleus localization
Psm1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	189		
Psm2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	171	GO:0042176	regulation of protein catabolic process
Psm3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	80		
Rpl7a	ribosomal protein L7a	572	GO:0042254	ribosome biogenesis
Actg1	actin, gamma 1	508	GO:0045214	sarcomere organization
Dut	deoxyuridine triphosphatase	51	GO:0046080	dUTP metabolic process
Lbr	lamin B receptor	144	GO:0055114	oxidation-reduction process

Table S4: GO Term Classification

GO Term search (www.ensembl.org/biomart) of Rad23b interacting proteins in erythroid (I/11, fetal liver E13.5dpc) cells. Corresponds to Figure S2.

Ingenuity Canonical Pathways	-log(p-value)	Ratio	Molecules
EIF2 Signaling	43.10	0.23	RPL24,RPL11,RPL22,RPL27A,RPL31,RPS8,RPS6,RPL26,RPS23,RPL37A,RPS11,RPL7,RPS7,RPS27,RPL6,RPS3A,RPL36A/RPL36AP8,RPL18A,RPS9,RPS16,RPL19,RPS3,RPL18,RPL4,RPL7A,RPL3,RPL34,RPL17,RPS2,RPL27,RPL12,RPL30,RPL23,RPLP0,RPL15,RPS4X,RPL5,RPL10 (includes others),RPS26,RPL28,RPL35A,EIF4A3,EIF4A1,RPL32,RPS15A,RPL13A,RPS14
Cell Cycle Control of Chromosomal Replication	13.00	0.36	MCM6,RPA3,MCM2,CDK5,CDK4,CDK6,RPA1,MCM4,CDK2,MCM7,RPA2
Regulation of eIF4 and p70S6K Signaling	9.83	0.10	RPS2,RPS6,RPS8,RPS23,RPS11,RPS7,RPS4X,RPS27,RPS3A,RPS26,EIF4A3,RPS16,EIF4A1,RPS9,RPS15A,RPS3,RPS14
mTOR Signaling	9.01	0.09	RPS2,RAC1,RPS6,RPS8,RPS23,RPS11,RPS7,RPS27,RPS4X,RPS3A,RPS26,EIF4A3,RPS16,RPS9,EIF4A1,RPS15A,RPS3,RPS14
RhoGDI Signaling	8.78	0.09	CFL1,ACTB,GNA12,GNB2L1,GDI2,GNAI1,RAC1,ACTG1,GNAI2,GNAI3,GNAT1,GNAT2,GNAO1,GNA13,ACTC1,ACTA1,GNAL
Fcy Receptor-mediated Phagocytosis in Macrophages and Monocytes	7.71	0.12	FYN,RAC2,YES1,ACTB,HCK,RAC1,LYN,ACTC1,RAC3,ACTG1,FGR,ACTA1
Ephrin Receptor Signaling	7.14	0.08	FYN,RAC2,CFL1,GNA12,GNB2L1,GNAI1,RAC1,RAC3,GNAI2,GNAI3,GNAT1,GNAT2,GNAO1,GNA13,GNAL
Inositol Phosphate Metabolism	7.03	0.07	GNAT3,CDK18,GNAI1,CDK6,CDK1,GNAI2,GNAI3,GNAT1,CDK5,GNAT2,CDK4,GNAO1,MAK,CDK2
Granzyme A Signaling	6.53	0.30	HIST1H1C,HIST1H1E,HIST1H1A,HIST1H1D,HIST1H1B,HMGB2
Role of NFAT in Regulation of the Immune Response	6.36	0.07	FYN,GNA12,GNB2L1,GNAI1,GNAI2,GNAI3,LCK,GNAT1,GNAT2,GNAO1,LYN,XPO1,GNA13,GNAL
Signaling by Rho Family GTPases	6.23	0.06	CFL1,ACTB,GNA12,GNB2L1,GNAI1,RAC1,ACTG1,GNAI2,GNAI3,GNAT1,GNAT2,GNAO1,GNA13,ACTC1,ACTA1,GNAL
Role of Tissue Factor in Cancer	6.01	0.10	BLK,FYN,LCK,YES1,CFL1,GNA12,HCK,RAC1,LYN,GNA13,FGR
G Beta Gamma Signaling	5.99	0.09	GNAI2,GNAI3,GNAT1,GNAT2,GNA12,GNAO1,GNB2L1,GNAI1,GNA13,GNAL
Androgen Signaling	5.93	0.08	GNAI2,GNAI3,GNAT1,GNAT2,GNA12,GNAO1,GNB2L1,GNAI1,GNA13,GNAL
IL-1 Signaling	5.86	0.09	GNAI2,GNAI3,GNAT1,GNAT2,GNA12,GNAO1,GNB2L1,GNAI1,GNA13,GNAL
Protein Ubiquitination Pathway	5.61	0.06	HSPA1A/HSPA1B,UBE2V2,PSMD3,HSPA2,PSMC5,HSPA8,HSP90B1,PSMC1,HSP90AB1,HSPA1L,PSMC6,PSMD2,PSMD12,HSP90AA1,PSMD1,PSMC2
CXCR4 Signaling	5.37	0.07	GNAI2,GNAI3,GNAT1,GNAT2,GNA12,GNAO1,GNB2L1,GNAI1,RAC1,LYN,GNA13,GNAL
Axonal Guidance Signaling	4.98	0.04	FYN,RAC2,CFL1,GNA12,GNB2L1,GNAI1,RAC1,TUBA4A,TUBB,TUBA1B,RAC3,GNAI2,GNAI3,GNAT1,CDK5,GNAT2,GNAO1,GNA13,GNAL
Molecular Mechanisms of Cancer	4.66	0.05	FYN,RAC2,GNA12,GNAI1,RAC1,CDK6,RAC3,GNAI2,GNAI3,GNAT1,GNAT2,CDK4,GNAO1,GNA13,DIABLO,GNAL,CDK2
Synaptic Long Term Depression	4.58	0.07	GNAI2,GNAI3,GNAT1,GNAT2,GNA12,GNAO1,GNAI1,LYN,GNA13,GNAL
Reelin Signaling in Neurons	4.53	0.10	BLK,FYN,LCK,YES1,CDK5,HCK,LYN,FGR
Germ Cell-Sertoli Cell Junction Signaling	4.51	0.07	RAC2,ACTB,RAC1,TUBA4A,TUBB,ACTC1,RAC3,ACTG1,TUBA1B,RAB8B,ACTA1
Relaxin Signaling	4.38	0.06	GNAI2,GNAI3,GNAT1,GNAT2,GNA12,GNAO1,GNB2L1,GNAI1,GNA13,GNAL
Gap Junction Signaling	4.38	0.06	GNAI2,GNAI3,ACTB,GNAI1,TUBA4A,TUBB,ACTC1,ACTG1,TUBA1B,ACTA1,GNAL
Breast Cancer Regulation by Stathmin1	4.35	0.06	GNAI2,GNAI3,GNB2L1,GNAI1,RAC1,TUBA4A,GNA13,TUBB,TUBA1B,CDK1,GNAL,CDK2
Virus Entry via Endocytic Pathways	4.12	0.08	FYN,RAC2,ACTB,RAC1,ACTC1,RAC3,ACTG1,ACTA1
Agrin Interactions at Neuromuscular Junction	4.07	0.10	RAC2,ACTB,RAC1,ACTC1,RAC3,ACTG1,ACTA1
Integrin Signaling	3.56	0.05	FYN,RAC2,ARF1,ARF3,ACTB,RAC1,Arf2,ACTC1,RAC3,ACTG1,ACTA1
Regulation of Actin-based Motility by Rho	3.50	0.08	RAC2,CFL1,ACTB,RAC1,ACTC1,RAC3,ACTA1
Cell Cycle: G1/S Checkpoint Regulation	3.49	0.09	RPL11,RPL5,CDK4,HDAC1,CDK6,CDK2
CREB Signaling in Neurons	3.48	0.05	GNAI2,GNAI3,GNAT1,GNAT2,GNA12,GNAO1,GNB2L1,GNAI1,GNA13,GNAL
Mechanisms of Viral Exit from Host Cells	3.44	0.11	ACTB,XPO1,ACTC1,ACTG1,ACTA1
Thrombin Signaling	3.12	0.05	GNAI2,GNAI3,GNAT1,GNAT2,GNA12,GNAO1,GNB2L1,GNAI1,GNA13,GNAL
Nicotinate and Nicotinamide Metabolism	3.06	0.05	CDK18,CDK5,CDK4,CDK6,MAK,CDK1,CDK2
Purine Metabolism	3.04	0.03	PKM2,NSF,ATP5C1,PSMC1,ATP5B,PSMC6,ATP5A1,HSP90AA1,PSMC2,ACTC1,PSMC5,GNAL
eNOS Signaling	3.03	0.05	HSPA8,HSP90B1,HSPA1L,HSP90AB1,HSPA1A/HSPA1B,HSP90AA1,HSPA2,GNAL
Endothelin-1 Signaling	2.97	0.05	GNAI2,GNAI3,GNAT1,GNAT2,GNA12,GNAO1,GNAI1,GNA13,GNAL
Protein Kinase A Signaling	2.96	0.04	HIST3H3,HIST1H1C,HIST1H1E,GNB2L1,HIST1H1A,GNAI1,H3F3C,GNAI2,GNAI3,HIST1H1D,GNA13,HIST1H1B,GNAL
PTEN Signaling	2.84	0.06	FGFR3,RAC2,FGFR4,FGFR1,RAC1,FGFR2,RAC3
IL-8 Signaling	2.82	0.05	GNAI2,GNAI3,RAC2,GNA12,GNB2L1,GNAI1,RAC1,GNA13,RAC3
Role of CHK Proteins in Cell Cycle Checkpoint Control	2.79	0.11	PCNA,RPA1,CDK1,CDK2

RhoA Signaling	2.77	0.06	CFL1,GNA12,ACTB,GNA13,ACTC1,ACTG1,ACTA1
RAN Signaling	2.75	0.13	CSE1L,RAN,XPO1
Sphingosine-1-phosphate Signaling	2.75	0.06	GNAI2,GNAI3,GNA12,GNAI1,RAC1,GNA13,GNAL
Sertoli Cell-Sertoli Cell Junction Signaling	2.74	0.05	ACTB,RAC1,TUBA4A,TUBB,ACTC1,ACTG1,TUBA1B,RAB8B,ACTA1
Actin Cytoskeleton Signaling	2.70	0.04	RAC2,CFL1,GNA12,ACTB,RAC1,GNA13,ACTC1,RAC3,ACTG1,ACTA1
Nucleotide Excision Repair Pathway	2.70	0.11	RPA3,RPA1,RAD23B,RPA2
Hereditary Breast Cancer Signaling	2.69	0.06	NPM1,H2AFX,CDK4,HDAC1,CDK6,RPA1,CDK1
FAK Signaling	2.64	0.06	FYN,ACTB,RAC1,ACTC1,ACTG1,ACTA1
Cardiac Hypertrophy Signaling	2.61	0.04	GNAI2,GNAI3,GNAT1,GNAT2,GNA12,GNAO1,GNB2L1,GNAI1,GNA13,GNAL
Leukocyte Extravasation Signaling	2.55	0.05	GNAI2,GNAI3,RAC2,ACTB,GNAI1,RAC1,ACTC1,ACTG1,ACTA1
SAPK/JNK Signaling	2.47	0.06	RAC2,LCK,GNA12,RAC1,GNA13,RAC3
Paxillin Signaling	2.32	0.05	ARF1,ACTB,RAC1,ACTC1,ACTG1,ACTA1
Aryl Hydrocarbon Receptor Signaling	2.26	0.04	HSP90B1,HSP90AB1,CDK4,CDK6,HSP90AA1,CDK2,MCM7
MSP-RON Signaling Pathway	2.26	0.08	ACTB,ACTC1,ACTG1,ACTA1
Caveolar-mediated Endocytosis Signaling	2.24	0.06	FYN,ACTB,ACTC1,ACTG1,ACTA1
Huntington's Disease Signaling	2.18	0.04	HSPA8,NSF,ATP5B,HSPA1L,CDK5,HSPA1A/HSPA1B,GNB2L1,HDAC1,HSPA2
Cyclins and Cell Cycle Regulation	2.14	0.06	CDK4,HDAC1,CDK6,CDK1,CDK2
Clathrin-mediated Endocytosis Signaling	2.10	0.04	HSPA8,RAB4A,ACTB,RAC1,ACTC1,ACTG1,ACTA1,RAB4B
Semaphorin Signaling in Neurons	2.07	0.08	FYN,CDK5,CFL1,RAC1
CCR3 Signaling in Eosinophils	2.07	0.05	GNAI2,GNAI3,CFL1,GNB2L1,GNAI1,RAC1
FGF Signaling	2.01	0.06	FGFR3,FGFR4,FGFR1,RAC1,FGFR2
Aldosterone Signaling in Epithelial Cells	1.97	0.04	HSPA8,HSP90B1,HSPA1L,HSP90AB1,HSPA1A/HSPA1B,HSP90AA1,HSPA2
α -Adrenergic Signaling	1.95	0.05	GNAI2,GNAI3,GNB2L1,GNAI1,GNAL
Neuregulin Signaling	1.93	0.05	HSP90B1,CDK5,HSP90AB1,HSP90AA1,RPS6
p70S6K Signaling	1.91	0.05	GNAI2,GNAI3,EEF2,GNAI1,LYN,RPS6
Mitotic Roles of Polo-Like Kinase	1.81	0.06	HSP90B1,HSP90AB1,HSP90AA1,CDK1
Hypoxia Signaling in the Cardiovascular System	1.76	0.06	HSP90B1,HSP90AB1,HSP90AA1,UBE2V2
Natural Killer Cell Signaling	1.68	0.05	FYN,RAC2,LCK,RAC1,RAC3
Fc Epsilon RI Signaling	1.66	0.05	FYN,RAC2,RAC1,LYN,RAC3
CCR5 Signaling in Macrophages	1.66	0.04	GNAI2,GNAI3,GNB2L1,GNAI1
Chemokine Signaling	1.66	0.05	GNAI2,GNAI3,CFL1,GNAI1
Mismatch Repair in Eukaryotes	1.61	0.08	PCNA,RPA1
Melatonin Signaling	1.60	0.05	GNAI2,GNAI3,GNAO1,GNAI1
fMLP Signaling in Neutrophils	1.58	0.04	GNAI2,GNAI3,GNB2L1,GNAI1,RAC1
Phospholipase C Signaling	1.56	0.03	FYN,LCK,GNB2L1,HDAC1,RAC1,LYN,GNA13,GNAL
Corticotropin Releasing Hormone Signaling	1.54	0.04	GNAI2,GNAI3,GNAO1,GNAI1,GNAL
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	1.52	0.06	TOP2B,TOP2A,CDK1
PKC θ Signaling in T Lymphocytes	1.48	0.04	FYN,RAC2,LCK,RAC1,RAC3
Tight Junction Signaling	1.47	0.04	CDK4,ACTB,RAC1,ACTC1,ACTG1,ACTA1
Prostate Cancer Signaling	1.43	0.04	HSP90B1,HSP90AB1,HSP90AA1,CDK2
One Carbon Pool by Folate	1.42	0.06	MTHFD1,SHMT2
P2Y Purigenic Receptor Signaling Pathway	1.40	0.04	GNAI2,GNAI3,GNB2L1,GNAI1,GNAL
GNRH Signaling	1.36	0.03	GNAI2,GNAI3,GNAI1,RAC1,GNAL
Biosynthesis of Steroids	1.35	0.02	FDPS,DHCR7
NF- κ B Signaling	1.34	0.03	FGFR3,LCK,FGFR4,FGFR1,HDAC1,FGFR2
VEGF Signaling	1.34	0.04	ACTB,ACTC1,ACTG1,ACTA1
Crosstalk between Dendritic Cells and Natural Killer Cells	1.31	0.04	ACTB,ACTC1,ACTG1,ACTA1
Glucocorticoid Receptor Signaling	1.30	0.03	HSPA8,HSP90B1,HSPA1L,HSP90AB1,HSPA1A/HSPA1B,RAC1,HSP90AA1,HSPA2
p53 Signaling	1.25	0.04	PCNA,CDK4,HDAC1,CDK2
ATM Signaling	1.24	0.05	H2AFX,CDK1,CDK2
Cellular Effects of Sildenafil (Viagra)	1.23	0.03	ACTB,ACTC1,ACTG1,ACTA1,GNAL
D-glutamine and D-glutamate Metabolism	1.22	0.04	GLUD1

Role of NFAT in Cardiac Hypertrophy	1.19	0.03	GNAI2,GNAI3,GNB2L1,HDAC1,GNAI1,GNAL
Induction of Apoptosis by HIV1	1.18	0.05	SLC25A4,SLC25A3,DIABLO
ERK/MAPK Signaling	1.18	0.03	HIST3H3,FYN,RAC2,RAC1,RAC3,H3F3C
Telomerase Signaling	1.17	0.04	HSP90B1,HSP90AB1,HDAC1,HSP90AA1
GM-CSF Signaling	1.15	0.04	GNB2L1,HCK,LYN
Role of PI3K/AKT Signaling in the Pathogenesis of Influenza	1.10	0.04	GNAI2,GNAI3,GNAI1
G Protein Signaling Mediated by Tubby	1.04	0.05	LCK,GNB2L1
Small Cell Lung Cancer Signaling	1.01	0.03	CDK4,CDK6,CDK2
Cell Cycle Regulation by BTG Family Proteins	0.99	0.06	CDK4,CDK2
Dopamine-DARPP32 Feedback in cAMP Signaling	0.95	0.03	GNAI2,GNAI3,CDK5,GNAI1,GNAL
Nitric Oxide Signaling in the Cardiovascular System	0.91	0.03	HSP90B1,HSP90AB1,HSP90AA1
Estrogen Receptor Signaling	0.87	0.03	HIST3H3,DDX5,PHB2,H3F3C
Human Embryonic Stem Cell Pluripotency	0.86	0.03	FGFR3,FGFR4,FGFR1,FGFR2
PI3K Signaling in B Lymphocytes	0.84	0.03	BLK,FYN,RAC1,LYN
Mitochondrial Dysfunction	0.82	0.02	ATP5C1,ATP5B,ATP5A1,UQCRC2
Valine, Leucine and Isoleucine Biosynthesis	0.80	0.02	VAR5
ILK Signaling	0.80	0.03	CFL1,ACTB,ACTC1,ACTG1,ACTA1
Synthesis and Degradation of Ketone Bodies	0.77	0.05	HMGCS2
Chronic Myeloid Leukemia Signaling	0.76	0.03	CDK4,HDAC1,CDK6
Oxidative Phosphorylation	0.74	0.03	ATP5C1,ATP5B,ATP5A1,UQCRC2
PPAR Signaling	0.74	0.03	HSP90B1,HSP90AB1,HSP90AA1
T Cell Receptor Signaling	0.72	0.03	FYN,LCK,RAC1
DNA Double-Strand Break Repair by Homologous Recombination	0.71	0.06	RPA1
Phototransduction Pathway	0.70	0.03	GNAT1,GNAT2
Glioblastoma Multiforme Signaling	0.69	0.02	CDK4,RAC1,CDK6,CDK2
Telomere Extension by Telomerase	0.68	0.06	HNRNPA2B1
Actin Nucleation by ARP-WASP Complex	0.67	0.03	GNA12,RAC1
Pancreatic Adenocarcinoma Signaling	0.65	0.03	CDK4,RAC1,CDK2
Cyanoamino Acid Metabolism	0.63	0.02	SHMT2
Methane Metabolism	0.63	0.01	SHMT2
Folate Biosynthesis	0.63	0.01	RUVBL2
IL-15 Signaling	0.61	0.03	LCK,RAC3
Calcium-induced T Lymphocyte Apoptosis	0.60	0.03	LCK,HDAC1
ERK5 Signaling	0.60	0.03	GNA12,GNA13
Non-Small Cell Lung Cancer Signaling	0.58	0.03	CDK4,CDK6
CD28 Signaling in T Helper Cells	0.57	0.02	FYN,LCK,RAC1
DNA Methylation and Transcriptional Repression Signaling	0.57	0.04	HDAC1
PPAR α /RXR α Activation	0.57	0.02	HSP90B1,HSP90AB1,HSP90AA1,GNAL
RAR Activation	0.56	0.02	RPL7A,RAC1,PSMC5,GNAL
14-3-3-mediated Signaling	0.56	0.02	TUBA4A,TUBB,TUBA1B
PI3K/AKT Signaling	0.56	0.02	HSP90B1,HSP90AB1,HSP90AA1
Glyoxylate and Dicarboxylate Metabolism	0.55	0.01	MTHFD1
Calcium Signaling	0.55	0.02	TPM1 (includes EG:22003),HDAC1,ACTC1,ACTA1
NRF2-mediated Oxidative Stress Response	0.52	0.02	ACTB,ACTC1,ACTG1,ACTA1
Role of Lipids/Lipid Rafts in the Pathogenesis of Influenza	0.51	0.04	FDPS
Antiproliferative Role of TOB in T Cell Signaling	0.48	0.04	CDK2

Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes	0.46	0.02	FYN,RAC1
Sonic Hedgehog Signaling	0.44	0.03	CDK1
B Cell Receptor Signaling	0.41	0.02	RAC2,RAC1,LYN
CDK5 Signaling	0.41	0.02	CDK5,GNAL
Glycolysis/Gluconeogenesis	0.41	0.02	PKM2,Gapdh (includes others)
Urea Cycle and Metabolism of Amino Groups	0.41	0.01	GLUD1
Bladder Cancer Signaling	0.40	0.02	FGFR3,CDK4
PAK Signaling	0.40	0.02	CFL1,RAC1
Apoptosis Signaling	0.40	0.02	DIABLO,CDK1
Aminoacyl-tRNA Biosynthesis	0.40	0.01	VARS
Inhibition of Angiogenesis by TSP1	0.39	0.03	FYN
CTLA4 Signaling in Cytotoxic T Lymphocytes	0.38	0.02	FYN,LCK
cAMP-mediated signaling	0.38	0.02	GNAI2,GNAO1,GNAI1,GNAL
Nitrogen Metabolism	0.37	0.01	GLUD1
Glioma Signaling	0.36	0.02	CDK4,CDK6
Glutamate Metabolism	0.35	0.01	GLUD1
Systemic Lupus Erythematosus Signaling	0.35	0.02	LCK,HNRNPA2B1,LYN,HNRNPC
Amyotrophic Lateral Sclerosis Signaling	0.34	0.02	RAC1,SSR4
HGF Signaling	0.34	0.02	RAC1,CDK2
Cholecystokinin/Gastrin-mediated Signaling	0.33	0.02	GNA12,GNA13
FcγRIIB Signaling in B Lymphocytes	0.33	0.02	LYN
Rac Signaling	0.32	0.02	CFL1,RAC1
Melanoma Signaling	0.32	0.02	CDK4
Wnt/β-catenin Signaling	0.32	0.02	GNAO1,HDAC1,RUVBL2
iCOS-iCOSL Signaling in T Helper Cells	0.31	0.02	LCK,RAC1
p38 MAPK Signaling	0.31	0.02	HIST3H3,H3F3C
Role of Oct4 in Mammalian Embryonic Stem Cell Pluripotency	0.30	0.02	PHB
Renin-Angiotensin Signaling	0.30	0.02	RAC1,GNAL
GABA Receptor Signaling	0.28	0.02	NSF
Gα12/13 Signaling	0.26	0.02	GNA12,GNA13
Amyloid Processing	0.26	0.02	CDK5
Primary Immunodeficiency Signaling	0.25	0.02	LCK
IL-2 Signaling	0.25	0.02	LCK
Lymphotoxin β Receptor Signaling	0.24	0.02	DIABLO
Nur77 Signaling in T Lymphocytes	0.24	0.02	HDAC1
Death Receptor Signaling	0.22	0.02	DIABLO
Butanoate Metabolism	0.22	0.01	HMGCS2
Role of BRCA1 in DNA Damage Response	0.22	0.02	RPA1
Lysine Degradation	0.22	0.01	SHMT2
Antiproliferative Role of Somatostatin Receptor 2	0.20	0.01	GNB2L1

Table S5: Ingenuity Pathway Analysis

Canonical Pathways represented by Rad23b interacting partners common to I11 and fetal liver E13.5dpc cells as calculated by Ingenuity Pathway Analysis. Corresponds to Figure S2.