Supplementary Table S4: ***Involvement of 49 HYPK-interacting partners in various Molecular Functions, Biological Processes and Pathways***

Supplementary Table S4A: Enrichment of 47 Molecular Functions (MF) with 49 HYPK-interacting proteins

GO terms (MF)	**Annotations**	**Genes**	**S**	**TS**	**Hyp**	**Hyp_c**	**Genes**
GO:0005515	protein binding (MF)	29 genes	29(45)	6618(29095)	2.67E-09	2.35E-07	ARCN1,TPI1,CHD3,RELA,HSF1,ATP6V0A4,RBPMS,TP53,TH1L,HSP90AB1,HTT,MDFI,PSME3,QKI,HSPA8,GLUD1,RHOXF2,MLF1,VIM,CDH11,LBR,LENG8,SRRT,MLF2,CEP290,EEF1A1,CALR,IKBIP,HSPB1
GO:0004352	glutamate dehydrogenase activity (MF)	2 genes	2(45)	2(29095)	2.34E-06	5.15E-05	GLUD2,GLUD1
GO:0004353	glutamate dehydrogenase [NAD(P)+] activity (MF)	2 genes	2(45)	2(29095)	2.34E-06	5.15E-05	GLUD2,GLUD1
GO:0070728	leucine binding (MF)	2 genes	2(45)	2(29095)	2.34E-06	5.15E-05	GLUD2,GLUD1
GO:0051082	unfolded protein binding (MF)	4 genes	4(45)	111(29095)	2.65E-05	0.0004663	DNAJC2,HSP90AB1,HSPA8,CALR
GO:0003677	DNA binding (MF)	10 genes	10(45)	1454(29095)	6.04E-05	0.0008863	ZNF462,CHD3,RELA,TP53,DNAJC2,MLF1,LBR,ZNF516,ZNF100,CALR
GO:0043531	ADP binding (MF)	2 genes	2(45)	19(29095)	0.0003933	0.0049448	GLUD2,GLUD1
GO:0019901	protein kinase binding (MF)	3 genes	3(45)	112(29095)	0.0007004	0.0077044	PGAM1,RELA,VIM
GO:0051087	chaperone binding (MF)	2 genes	2(45)	29(29095)	0.0009248	0.009042	TP53,CALR
GO:0004807	triose-phosphate isomerase activity (MF)	1 gene	1(45)	1(29095)	0.0015467	0.0104697	TPI1
GO:0050809	diazepam binding (MF)	1 gene	1(45)	1(29095)	0.0015467	0.0104697	HTT
GO:0051011	microtubule minus-end binding (MF)	1 gene	1(45)	1(29095)	0.0015467	0.0104697	CEP290
GO:0051183	vitamin transporter activity (MF)	1 gene	1(45)	1(29095)	0.0015467	0.0104697	GC
GO:0042802	identical protein binding (MF)	4 genes	4(45)	336(29095)	0.0017925	0.0112669	RELA,PSME3,GLUD1,HSPB1
GO:0050613	delta14-sterol reductase activity (MF)	1 gene	1(45)	2(29095)	0.003091	0.0181337	LBR
GO:0010843	promoter binding (MF)	2 genes	2(45)	77(29095)	0.0063581	0.0223803	RELA,TP53
GO:0016563	transcription activator activity (MF)	3 genes	3(45)	221(29095)	0.0048505	0.0224653	RELA,TP53,CEP290
GO:00	DNA strand	1 gene	1(45)	4(29095)	0.006	0.0226329	TP53

00739	annealing activity (MF)				1726		
GO:0004082	bisphosphoglycerate mutase activity (MF)	1 gene	1(45)	4(29095)	0.0061726	0.0226329	PGAM1
GO:0004083	2,3-bisphospho-D-glycerate 2-phosphohydrolase activity (MF)	1 gene	1(45)	4(29095)	0.0061726	0.0226329	PGAM1
GO:0004619	phosphoglycerate mutase activity (MF)	1 gene	1(45)	4(29095)	0.0061726	0.0226329	PGAM1
GO:0001849	complement component C1q binding (MF)	1 gene	1(45)	3(29095)	0.004633	0.02265	CALR
GO:0030911	TPR domain binding (MF)	1 gene	1(45)	3(29095)	0.004633	0.02265	HSP90AB1
GO:0070215	MDM2 binding (MF)	1 gene	1(45)	3(29095)	0.004633	0.02265	PSME3
GO:0005524	ATP binding (MF)	7 genes	7(45)	1467(29095)	0.0069006	0.0233558	CHD3,TP53,HSP90AB1,HSPA8,GLUD1,KIF20B,HSPA14
GO:0005499	vitamin D binding (MF)	1 gene	1(45)	5(29095)	0.0077099	0.0233957	GC
GO:0008538	proteasome activator activity (MF)	1 gene	1(45)	5(29095)	0.0077099	0.0233957	PSME3
GO:0030235	nitric-oxide synthase regulator activity (MF)	1 gene	1(45)	5(29095)	0.0077099	0.0233957	HSP90AB1
GO:0047485	protein N-terminus binding (MF)	2 genes	2(45)	73(29095)	0.0057329	0.0252248	RELA,TP53
GO:0005521	lamin binding (MF)	1 gene	1(45)	6(29095)	0.0092449	0.0254236	LBR
GO:0070087	chromo shadow domain binding (MF)	1 gene	1(45)	6(29095)	0.0092449	0.0254236	LBR
GO:0000166	nucleotide binding (MF)	8 genes	8(45)	1928(29095)	0.0087422	0.0256438	CHD3,RBPMS,HSP90AB1,HSPA8,GLUD1,KIF20B,HSPA14,EEF1A1
GO:0008553	hydrogen-exporting ATPase activity, phosphorylative mechanism (MF)	1 gene	1(45)	7(29095)	0.0107776	0.0287403	ATP6V0A4
GO:0016853	isomerase activity (MF)	2 genes	2(45)	106(29095)	0.0117546	0.0304237	PGAM1,TPI1
GO:0033613	transcription activator binding (MF)	1 gene	1(45)	8(29095)	0.012308	0.0309457	RELA
GO:0008143	poly(A) RNA binding (MF)	1 gene	1(45)	9(29095)	0.013836	0.0338213	RBPMS
GO:0042623	ATPase activity, coupled (MF)	1 gene	1(45)	10(29095)	0.0153617	0.0355745	HSPA8

GO:0070403	NAD binding (MF)	1 gene	1(45)	10(29095)	0.0153617	0.0355745	GLUD1
GO:0005525	GTP binding (MF)	3 genes	3(45)	365(29095)	0.0188377	0.0404321	GLUD2,GLUD1,EEF1A1
GO:0005246	calcium channel regulator activity (MF)	1 gene	1(45)	12(29095)	0.0184063	0.0404938	HTT
GO:0070491	transcription repressor binding (MF)	1 gene	1(45)	12(29095)	0.0184063	0.0404938	RELA
GO:0003682	chromatin binding (MF)	2 genes	2(45)	139(29095)	0.0196177	0.0411037	CHD3,TP53
GO:0051117	ATPase binding (MF)	1 gene	1(45)	14(29095)	0.0214416	0.0438805	ATP6V0A4
GO:0008134	transcription factor binding (MF)	2 genes	2(45)	153(29095)	0.0234629	0.0448855	RELA,TP53
GO:0042301	phosphate binding (MF)	1 gene	1(45)	15(29095)	0.0229558	0.0448914	RELA
GO:0051059	NF-kappaB binding (MF)	1 gene	1(45)	15(29095)	0.0229558	0.0448914	RELA

Supplementary Table S4B: Enrichment of 135 Biological Processes (BP) with 49 HYPK-interacting partners

Annotations	**Items**	**Genes**	**S**	**TS**	**Hyp**	**Hyp_c**	**Genes**
glutamate deamidation (BP)	GO:0019459	2 genes	2(45)	2(29095)	2.34E-06	0.0006	GLUD2,GLUD1
glutamate biosynthetic process (BP)	GO:0006537	2 genes	2(45)	5(29095)	2.33E-05	0.0019	GLUD2,GLUD1
cell cycle arrest (BP)	GO:0007050	4 genes	4(45)	106(29095)	2.21E-05	0.0027	TP53,MLF1,KIF20B,CALR
negative regulation of DNA binding (BP)	GO:0043392	2 genes	2(45)	9(29095)	8.36E-05	0.0034	ZNF462,MDFI
regulation of mitochondrial membrane permeability (BP)	GO:0046902	2 genes	2(45)	10(29095)	0.000104	0.0037	TP53,HTT
response to unfolded protein (BP)	GO:0006986	3 genes	3(45)	50(29095)	6.44E-05	0.0039	HSP90AB1,HSPA8,HSPB1
protein folding (BP)	GO:0006457	4 genes	4(45)	149(29095)	8.36E-05	0.0041	DNAJC2,HSP90AB1,HSPA8,CALR
embryonic development (BP)	GO:0009790	3 genes	3(45)	69(29095)	0.000169	0.0052	TPI1,HTT,MDFI
gastrulation (BP)	GO:0007369	2 genes	2(45)	15(29095)	0.000242	0.0059	TP53,HTT
response to X-ray (BP)	GO:0010165	2 genes	2(45)	15(29095)	0.000242	0.0059	TP53,IKBIP
cell aging (BP)	GO:0007569	2 genes	2(45)	27(29095)	0.000801	0.0164	TP53,HTT
regulation of apoptosis (BP)	GO:0042981	3 genes	3(45)	114(29095)	0.000737	0.0164	TP53,PSME3,CALR
citrulline metabolic process (BP)	GO:0000052	1 gene	1(45)	1(29095)	0.001547	0.0172	HTT
peptide antigen assembly with MHC class I protein complex (BP)	GO:0002502	1 gene	1(45)	1(29095)	0.001547	0.0172	CALR
positive regulation of Schwann cell differentiation (BP)	GO:0014040	1 gene	1(45)	1(29095)	0.001547	0.0172	RELA
lactate biosynthetic process from pyruvate (BP)	GO:0019244	1 gene	1(45)	1(29095)	0.001547	0.0172	HTT
olfactory lobe development (BP)	GO:0021988	1 gene	1(45)	1(29095)	0.001547	0.0172	HTT
neural plate formation (BP)	GO:0021990	1 gene	1(45)	1(29095)	0.001547	0.0172	HTT
regulation of pentose-phosphate shunt (BP)	GO:0043456	1 gene	1(45)	1(29095)	0.001547	0.0172	PGAM1
pronephros development (BP)	GO:0048793	1 gene	1(45)	1(29095)	0.001547	0.0172	CEP290
vitamin transport (BP)	GO:0051180	1 gene	1(45)	1(29095)	0.001547	0.0172	GC
cellular amino acid metabolic process (BP)	GO:0006520	2 genes	2(45)	40(29095)	0.001758	0.0187	GLUD2,GLUD1
regulation of cell cycle (BP)	GO:0051726	2 genes	2(45)	42(29095)	0.001936	0.0198	TP53,HSPA8
T cell proliferation during immune response (BP)	GO:0002309	1 gene	1(45)	2(29095)	0.003091	0.0205	TP53
glutamate catabolic process (BP)	GO:0006538	1 gene	1(45)	2(29095)	0.003091	0.0205	GLUD1

glyceraldehyde-3-phosphate metabolic process (BP)	GO:0019682	1 gene	1(45)	2(29095)	0.003091	0.0205	TPI1
negative regulation of steroid hormone receptor signaling pathway (BP)	GO:0033144	1 gene	1(45)	2(29095)	0.003091	0.0205	CALR
response to cobalamin (BP)	GO:0033590	1 gene	1(45)	2(29095)	0.003091	0.0205	RELA
long-chain fatty acid biosynthetic process (BP)	GO:0042759	1 gene	1(45)	2(29095)	0.003091	0.0205	QKI
intermediate filament-based process (BP)	GO:0045103	1 gene	1(45)	2(29095)	0.003091	0.0205	VIM
negative regulation of helicase activity (BP)	GO:0051097	1 gene	1(45)	2(29095)	0.003091	0.0205	TP53
regulation of interferon-gamma-mediated signaling pathway (BP)	GO:0060334	1 gene	1(45)	2(29095)	0.003091	0.0205	HSP90AB1
regulation of type I interferon-mediated signaling pathway (BP)	GO:0060338	1 gene	1(45)	2(29095)	0.003091	0.0205	HSP90AB1
interspecies interaction between organisms (BP)	GO:0044419	4 genes	4(45)	300(29095)	0.001183	0.0223	RELA,TP53,HSPA8,VIM
response to heat (BP)	GO:0009408	2 genes	2(45)	46(29095)	0.002318	0.0227	HSF1,HSPB1
cellular membrane organization (BP)	GO:0016044	2 genes	2(45)	58(29095)	0.003659	0.0236	ARCN1,HSPA8
anti-apoptosis (BP)	GO:0006916	3 genes	3(45)	182(29095)	0.002817	0.0256	RELA,HTT,HSPB1
ossification (BP)	GO:0001503	2 genes	2(45)	50(29095)	0.002733	0.0258	ATP6V0A4,CDH11
myeloid progenitor cell differentiation (BP)	GO:0002318	1 gene	1(45)	3(29095)	0.004633	0.0264	MLF1
response to tumor cell (BP)	GO:0002347	1 gene	1(45)	3(29095)	0.004633	0.0264	TP53
quinolinate biosynthetic process (BP)	GO:0019805	1 gene	1(45)	3(29095)	0.004633	0.0264	HTT
otic vesicle formation (BP)	GO:0030916	1 gene	1(45)	3(29095)	0.004633	0.0264	CEP290
sequestering of calcium ion (BP)	GO:0051208	1 gene	1(45)	3(29095)	0.004633	0.0264	CALR
negative regulation of transcription from RNA polymerase II promoter (BP)	GO:0000122	3 genes	3(45)	221(29095)	0.00485	0.027	TP53,MDFI,CALR
response to lipopolysaccharide (BP)	GO:0032496	2 genes	2(45)	76(29095)	0.006199	0.0281	RELA,HSF1
regulation of glycolysis (BP)	GO:0006110	1 gene	1(45)	4(29095)	0.006173	0.0285	PGAM1
embryonic development ending in birth or egg hatching (BP)	GO:0009792	1 gene	1(45)	4(29095)	0.006173	0.0285	TP53
dorsal/ventral axis specification (BP)	GO:0009950	1 gene	1(45)	4(29095)	0.006173	0.0285	MDFI
negative regulation of proteasomal ubiquitin-dependent protein catabolic process (BP)	GO:0032435	1 gene	1(45)	4(29095)	0.006173	0.0285	HSP90AB1
cellular response to glucose starvation (BP)	GO:0042149	1 gene	1(45)	4(29095)	0.006173	0.0285	TP53
L-glutamate import (BP)	GO:0051	1 gene	1(45)	4(29095)	0.006173	0.0285	HTT

	938						
nucleotide-binding oligomerization domain containing 2 signaling pathway (BP)	GO:0070431	1 gene	1(45)	4(29095)	0.006173	0.0285	RELA
M phase of mitotic cell cycle (BP)	GO:0000087	1 gene	1(45)	6(29095)	0.009245	0.0298	KIF20B
pentose-phosphate shunt (BP)	GO:0006098	1 gene	1(45)	6(29095)	0.009245	0.0298	TPI1
negative regulation of neuroblast proliferation (BP)	GO:0007406	1 gene	1(45)	6(29095)	0.009245	0.0298	TP53
striatum development (BP)	GO:0021756	1 gene	1(45)	6(29095)	0.009245	0.0298	HTT
DNA damage response, signal transduction by p53 class mediator (BP)	GO:0030330	1 gene	1(45)	6(29095)	0.009245	0.0298	TP53
G1/S DNA damage checkpoint (BP)	GO:0031571	1 gene	1(45)	6(29095)	0.009245	0.0298	TP53
vitamin D metabolic process (BP)	GO:0042359	1 gene	1(45)	6(29095)	0.009245	0.0298	GC
glucocorticoid receptor signaling pathway (BP)	GO:0042921	1 gene	1(45)	6(29095)	0.009245	0.0298	CALR
negative regulation of fibroblast proliferation (BP)	GO:0048147	1 gene	1(45)	6(29095)	0.009245	0.0298	TP53
negative regulation of retinoic acid receptor signaling pathway (BP)	GO:0048387	1 gene	1(45)	6(29095)	0.009245	0.0298	CALR
embryonic process involved in female pregnancy (BP)	GO:0060136	1 gene	1(45)	6(29095)	0.009245	0.0298	HSF1
B cell lineage commitment (BP)	GO:0002326	1 gene	1(45)	5(29095)	0.00771	0.03	TP53
T cell lineage commitment (BP)	GO:0002360	1 gene	1(45)	5(29095)	0.00771	0.03	TP53
axon cargo transport (BP)	GO:0008088	1 gene	1(45)	5(29095)	0.00771	0.03	HTT
protein maturation by protein folding (BP)	GO:0022417	1 gene	1(45)	5(29095)	0.00771	0.03	CALR
primary microRNA processing (BP)	GO:0031053	1 gene	1(45)	5(29095)	0.00771	0.03	SRRT
cellular response to UV (BP)	GO:0034644	1 gene	1(45)	5(29095)	0.00771	0.03	TP53
regulation of meiosis (BP)	GO:0040020	1 gene	1(45)	5(29095)	0.00771	0.03	CALR
paraxial mesoderm formation (BP)	GO:0048341	1 gene	1(45)	5(29095)	0.00771	0.03	HTT
iron ion homeostasis (BP)	GO:0055072	1 gene	1(45)	5(29095)	0.00771	0.03	HTT
regulation of transcription, DNA-dependent (BP)	GO:0006355	6 genes	6(45)	1063(29095)	0.005656	0.0308	CHD3,HSF1,TP53,RHOXF2,ZNF100,CALR
negative regulation of cell growth (BP)	GO:0030308	2 genes	2(45)	88(29095)	0.008229	0.031	TP53,DNAJC2
spermatogenesis (BP)	GO:0007283	3 genes	3(45)	267(29095)	0.008161	0.0312	HSF1,HTT,QKI
defense response (BP)	GO:0006952	2 genes	2(45)	74(29095)	0.005886	0.0314	HSF1,MLF2
G2 phase of mitotic cell	GO:0000	1 gene	1(45)	7(29095)	0.010778	0.0314	DNAJC2

cycle (BP)	085						
dopamine receptor signaling pathway (BP)	GO:0007212	1 gene	1(45)	7(29095)	0.010778	0.0314	HTT
response to salt stress (BP)	GO:0009651	1 gene	1(45)	7(29095)	0.010778	0.0314	TP53
cytoplasmic sequestering of transcription factor (BP)	GO:0042994	1 gene	1(45)	7(29095)	0.010778	0.0314	MDFI
positive regulation of interleukin-12 biosynthetic process (BP)	GO:0045084	1 gene	1(45)	7(29095)	0.010778	0.0314	RELA
positive regulation of SMAD protein nuclear translocation (BP)	GO:0060391	1 gene	1(45)	7(29095)	0.010778	0.0314	RBPMS
positive regulation of transcription from RNA polymerase II promoter (BP)	GO:0045944	3 genes	3(45)	291(29095)	0.010308	0.0328	ZNF462,RELA,TP53
cellular component movement (BP)	GO:0006928	2 genes	2(45)	101(29095)	0.010719	0.0337	VIM,HSPB1
determination of adult lifespan (BP)	GO:0008340	1 gene	1(45)	8(29095)	0.012308	0.0343	HTT
activation of caspase activity by cytochrome c (BP)	GO:0008635	1 gene	1(45)	8(29095)	0.012308	0.0343	TP53
response to UV-B (BP)	GO:0010224	1 gene	1(45)	8(29095)	0.012308	0.0343	RELA
positive regulation of chondrocyte differentiation (BP)	GO:0032332	1 gene	1(45)	8(29095)	0.012308	0.0343	RELA
urea cycle (BP)	GO:0000050	1 gene	1(45)	9(29095)	0.013836	0.0346	HTT
glutamate metabolic process (BP)	GO:0006536	1 gene	1(45)	9(29095)	0.013836	0.0346	GLUD2
DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator (BP)	GO:0006978	1 gene	1(45)	9(29095)	0.013836	0.0346	TP53
ER overload response (BP)	GO:0006983	1 gene	1(45)	9(29095)	0.013836	0.0346	TP53
ATP hydrolysis coupled proton transport (BP)	GO:0015991	1 gene	1(45)	9(29095)	0.013836	0.0346	ATP6V0A4
negative regulation of protein catabolic process (BP)	GO:0042177	1 gene	1(45)	9(29095)	0.013836	0.0346	RELA
muscle cell differentiation (BP)	GO:0042692	1 gene	1(45)	9(29095)	0.013836	0.0346	QKI
response to arsenic (BP)	GO:0046685	1 gene	1(45)	9(29095)	0.013836	0.0346	SRRT
vesicle transport along microtubule (BP)	GO:0047496	1 gene	1(45)	9(29095)	0.013836	0.0346	HTT
chaperone mediated protein folding requiring cofactor (BP)	GO:0051085	1 gene	1(45)	9(29095)	0.013836	0.0346	HSPA8
organ morphogenesis (BP)	GO:0009887	2 genes	2(45)	120(29095)	0.014877	0.0368	RELA,HTT
regulation of Wnt receptor signaling pathway (BP)	GO:0030111	1gene	1(45)	10(29095)	0.015362	0.0369	MDFI
COPI coating of Golgi vesicle (BP)	GO:0048205	1 gene	1(45)	10(29095)	0.015362	0.0369	ARCN1

regulation of mitochondrial membrane potential (BP)	GO:0051881	1 gene	1(45)	10(29095)	0.015362	0.0369	HTT
endoplasmic reticulum organization (BP)	GO:0007029	1 gene	1(45)	11(29095)	0.016885	0.039	HTT
membrane protein intracellular domain proteolysis (BP)	GO:0031293	1 gene	1(45)	11(29095)	0.016885	0.039	RELA
negative regulation of tumor necrosis factor production (BP)	GO:0032720	1 gene	1(45)	11(29095)	0.016885	0.039	HSF1
protein tetramerization (BP)	GO:0051262	1 gene	1(45)	11(29095)	0.016885	0.039	TP53
regulation of mitosis (BP)	GO:0007088	1 gene	1(45)	12(29095)	0.018406	0.0406	KIF20B
rRNA transcription (BP)	GO:0009303	1 gene	1(45)	12(29095)	0.018406	0.0406	TP53
hormone metabolic process (BP)	GO:0042445	1 gene	1(45)	12(29095)	0.018406	0.0406	HTT
eye photoreceptor cell development (BP)	GO:0042462	1 gene	1(45)	12(29095)	0.018406	0.0406	CEP290
respiratory burst (BP)	GO:0045730	1 gene	1(45)	12(29095)	0.018406	0.0406	PGAM1
hair follicle development (BP)	GO:0001942	1 gene	1(45)	13(29095)	0.019925	0.0424	RELA
associative learning (BP)	GO:0008306	1 gene	1(45)	13(29095)	0.019925	0.0424	HTT
cortical actin cytoskeleton organization (BP)	GO:0030866	1 gene	1(45)	13(29095)	0.019925	0.0424	CALR
positive regulation of phagocytosis (BP)	GO:0050766	1 gene	1(45)	13(29095)	0.019925	0.0424	CALR
senescence (BP)	GO:0010149	1 gene	1(45)	14(29095)	0.021442	0.0431	CALR
hindbrain development (BP)	GO:0030902	1(gene	1(45)	14(29095)	0.021442	0.0431	CEP290
T cell differentiation in the thymus (BP)	GO:0033077	1 gene	1(45)	14(29095)	0.021442	0.0431	TP53
DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis (BP)	GO:0042771	1 gene	1(45)	14(29095)	0.021442	0.0431	TP53
response to morphine (BP)	GO:0043278	1 gene	1(45)	14(29095)	0.021442	0.0431	RELA
positive regulation of cell cycle (BP)	GO:0045787	1 gene	1(45)	14(29095)	0.021442	0.0431	CALR
chromosome organization (BP)	GO:0051276	1 gene	1(45)	14(29095)	0.021442	0.0431	TP53
protein export from nucleus (BP)	GO:0006611	1 gene	1(45)	15(29095)	0.022956	0.045	CALR
induction of apoptosis by intracellular signals (BP)	GO:0008629	1 gene	1(45)	15(29095)	0.022956	0.045	TP53
response to amino acid stimulus (BP)	GO:0043200	1 gene	1(45)	15(29095)	0.022956	0.045	RELA
response to inorganic substance (BP)	GO:0010035	1 gene	1(45)	16(29095)	0.024468	0.0465	RELA
positive regulation of pathway-restricted SMAD protein phosphorylation	GO:0010862	1 gene	1(45)	16(29095)	0.024468	0.0465	RBPMS

(BP)							
social behavior (BP)	GO:0035176	1 gene	1(45)	16(29095)	0.024468	0.0465	HTT
negative regulation of insulin receptor signaling pathway (BP)	GO:0046627	1 gene	1(45)	16(29095)	0.024468	0.0465	RELA
negative regulation of DNA replication (BP)	GO:0008156	1 gene	1(45)	17(29095)	0.025977	0.0482	TP53
negative regulation of translation (BP)	GO:0017148	1 gene	1(45)	17(29095)	0.025977	0.0482	CALR
positive regulation of neuron apoptosis (BP)	GO:0043525	1 gene	1(45)	17(29095)	0.025977	0.0482	TP53
protein import into nucleus, translocation (BP)	GO:0000060	1 gene	1(45)	18(29095)	0.027485	0.0499	TP53
regulation of pH (BP)	GO:0006885	1 gene	1(45)	18(29095)	0.027485	0.0499	ATP6V0A4
negative regulation of gene-specific transcription (BP)	GO:0032582	1 gene	1(45)	18(29095)	0.027485	0.0499	RELA

Supplementary Table S4C: Enrichment of KEGG pathway with HYPK-interacting proteins

Annotations	**Total number of proteins out of 29095 proteins**	**HYPK-Interacting Proteins out of 45 protein identified**	**Corrected hypergeometric p Value**
(KEGG) 00471:D-Glutamine and D-glutamate metabolism	4	GLUD1, GLUD2	0.000329159
(KEGG) 04612:Antigen processing and presentation	81	HSP90AB1, CALR, HSPA8, PSME3	0.000357836
(KEGG) 05215:Prostate cancer	89	RELA, HSP90AB1, TP53	0.00560475
(KEGG) 00910: Nitrogen metabolism	23	GLUD1, GLUD2	0.00681114
(KEGG) 04010: MAPK signaling pathway	265	RELA, HSPB1, TP53, HSPA8	0.00702551
(KEGG) 00250:Alanine, aspartate and glutamate metabolism	31	GLUD1, GLUD2	0.00828026
(KEGG) 00330:Arginine and proline metabolism	53	GLUD1, GLUD2	0.0205831
(KEGG) 04621: NOD-like receptor signaling pathway	61	RELA, HSP90AB1	0.0210941
(KEGG) 00010:Glycolysis / Gluconeogenesis	59	PGAM1, TPI1	0.0222313
(KEGG) 05120:Epithelial cell signaling in Helicobacter pylori infection	68	RELA, ATP6V0A4	0.0234708
(KEGG) 05220:Chronic myeloid leukemia	75	RELA, TP53	0.0236635
(KEGG) 05212:Pancreatic cancer	72	RELA, TP53	0.0238474
(KEGG) 04210:Apoptosis	87	RELA, TP53	0.0270246
(KEGG) 05222:Small cell lung cancer	84	RELA, TP53	0.0271993
(KEGG) 05200:Pathways in cancer	325	RELA, HSP90AB1, TP53	0.0434377
(KEGG) 04722:Neurotrophin signaling pathway	124	RELA, TP53	0.0464941

Supplementary Table S4D: Enrichment of specific 16 pathways in the Reactome database with 49 HYPK-interacting proteins

False discovery rate	**Un-adjusted probability of seeing N or more genes in this Event by chance**	**Number of genes in your query which map to this Event**	**Total number of genes involved in this Event**	**Identifier of this Event**	**Name of this Event**	**Submitted identifiers mapping to this Event**
-	1.64E-06	3	6	REACT_25267	Association of AUF1 with Translation and Heat Shock Proteins	HSPB1, HSPA8, HSPA1A
-	9.72E-06	3	10	REACT_25315	Ubiquitination of AUF1 (hnRNP D0)	HSPB1, HSPA8, HSPA1A
-	8.89E-05	4	54	REACT_25325	Destabilization of mRNA by AUF1 (hnRNP D0)	HSPB1, HSPA8, PSME3, HSPA1A
-	0.000542031	4	86	REACT_24994	Regulation of mRNA Stability by Proteins that Bind AU-rich Elements	HSPB1, HSPA8, PSME3, HSPA1A
-	0.001669908	4	116	REACT_20605	Metabolism of mRNA	HSPB1, HSPA8, PSME3, HSPA1A
-	0.002062672	3	57	REACT_723	Glucose metabolism	CALM1, PGAM1, TPI1
-	0.00359101	4	143	REACT_21257	Metabolism of RNA	HSPB1, HSPA8, PSME3, HSPA1A
-	0.004352608	2	22	REACT_1383	Glycolysis	PGAM1, TPI1
-	0.008546792	2	31	REACT_1520	Gluconeogenesis	PGAM1, TPI1
-	0.015009709	3	116	REACT_474	Metabolism of carbohydrates	CALM1, PGAM1, TPI1
-	0.022179905	2	51	REACT_20549	Autodegradation of the E3 ubiquitin ligase COP1	PSME3, TP53
-	0.022179905	2	51	REACT_17044	Muscle contraction	CALM1, VIM
-	0.023003856	2	52	REACT_309	Stabilization of p53	PSME3, TP53
-	0.025551	2	55	REACT_1625	p53-Dependent G1 DNA Damage Response	PSME3, TP53
-	0.025551	2	55	REACT_85	p53-Dependent G1/S DNA damage checkpoint	PSME3, TP53
-	0.028208563	2	58	REACT_2254	G1/S DNA Damage Checkpoints	PSME3, TP53