

## Supplemental Data

### Supplementary Materials and Methods

#### Reagents and antibodies

Human Recombinant (rec-) FGF-2 and all inhibitors were from CalBiochem; rec-S6K2, Protein-G and -A magnetic beads and Lipofectamine RNAiMAX from Invitrogen; rec-hnRNPA1 from Novus Biological; RNAeasy, Plasmid preparation kits, Attractene, TNPO1 and TNPO2 qPCR quantitect primers from Qiagen; radiolabelled  $^{32}\text{P}$ - $\gamma$  ATP and  $^{32}\text{P}$  orthophosphate from Perkin Elmer; Quickchange site-directed mutagenesis kit and RNase inhibitor from Promega. All other reagents were from Sigma Aldrich. Mouse monoclonal antibodies: FLAG (M2),  $\beta$ -actin,  $\alpha$ -tubulin, SUMO1 (GMP1), Nxf1, ALY were from Sigma Aldrich; Rabbit polyclonals for BclXL, PDCD4, SUMO1, pERK, UBC9 from Cell Signalling Technologies. Rabbit polyclonal antibody for 14-3-3 $\epsilon$ ,  $\theta$  and  $\sigma$  and mouse monoclonals for hnRNPA1 and S6K1 from Santa Cruz. All siRNAs were from Dharmacon.

#### RNA immunoprecipitation (RNA-IP) qPCR primers

Primers used for qPCR were as follow:

BCL-XL-F: TGCGTGGAAGCGTAGACAAGGA

BCL-XL-R: AAGGCTCTAGGTGGTCATTCAGGT;

XIAP-F: CCGTGCGGTGCTTTAGTTGT;

XIAP-R: TTCCTCGGGTATATGGTGTCTGAT;

cIAP1-F: GCCTGATGCTGGATAACTGG;

cIAP1-R: GGCGACAGAAAAGTCAATGG;

GAPDH-F: AATCCCATCACCATCTTCCA;

GAPDH-R: TGGACTCCACGACGTACTCA.

#### Synthetic RNA preparation T7 primers

T7 forward and reverse primers for BCL-XL and XIAP were: BCL-XL-F, TAATACGACTCACTATAGGGCGACAGTAGGAGGCGGAGAGC; BCL-XL-R, TTTTATAATAGAGATGGGCTC;

XIAP-F, TAATACGACTCACTATAGGGCGAAATTAGAATGTTTCTTAGCGGTC; XIAP-R,  
CTTCTCTTGAAAATAGGAC.

### **Immunohistochemistry**

Tissue microarray (TMA) samples from Lung Cancer patients (n=204) or Breast Cancer patients (n=194) were stained for S6K2, hnRNPA1 and BCL-XL as described earlier (1). A semi quantitative immunohistochemical score (IHS) was used as previously described (2), assessing both the percentage of positive cells and the intensity of staining. For the intensity, a score of 0 to 3, corresponding to negative, weak, moderate and strong positivity, was recorded. The range of possible scores was thus 0 to 300. Two observers blinded to all the clinical data scored all cases and results were 99% consistent. In the 1% of discrepant results a further review was performed by both observers to achieve agreement. Lung tissue samples were further subdivided into Groups 1-4 for increasing S6K2 staining intensity scores, with Group 1 corresponding to negative staining for S6K2 (n=80); Group 2 for intensity of 1-50 (n=60); Group 3 for intensity of 51-70 (n=30) and Group 4 for intensity higher than 70 (n=34). Breast tissue samples were also subdivided into Groups 1-4 for increasing S6K2 staining scores, with Group 1 for intensity 0-80 (n=45); Group 2 for intensity of 81-150 (n=44); Group 3 for intensity of 150-200 (n=38) and Group 4 for intensity of 201-300 (n=66). Average score for BCL-XL and cytoplasmic hnRNPA1 staining intensities for the corresponding groups were calculated and correlation coefficients obtained for S6K2 vs BclXL and S6K2 vs cyto-hnRNPA1 scores. p-values were calculated using ANOVA.

### **Supplemental References**

1. Lara R, Mauri FA, Taylor H, Derua R, Shia A, Gray C, Nicols A, Shiner RJ, Schofield E, Bates PA, Waelkens E, Dallman M, Lamb J, Zicha D, Downward J, Seckl MJ, Pardo OE (2011) An siRNA screen identifies RSK1 as a key modulator of lung cancer metastasis. *Oncogene*

2. Herberger B, Puhalla H, Lehnert M, Wrba F, Novak S, Brandstetter A, Gruenberger B, Gruenberger T, Pirker R, Filipits M (2007) Activated mammalian target of rapamycin is an adverse prognostic factor in patients with biliary tract adenocarcinoma. *Clin Cancer Res* **13**: 4795-4799

## Supplementary Table and Figure Legends

### Supplementary Tables

**Table S1:** Quantitative phosphoproteomics analysis of H510 SCLC cells treated with or without FGF-

2. Trypsin digests of protein extracts from H510 cells treated with or without FGF-2 were differentially dimethyl-labelled using heavy and light versions of formaldehyde, respectively. Equal amounts of peptides from both conditions were mixed, the phospho-enriched fraction analysed by LC-MS/MS and the light to heavy ratio (L/H) calculated. The experiment was performed three times so as to obtain standard errors (Std. Err.) on the ratio. The gene identifier (ID), sequence of the detected peptide and nature of the modification are indicated. The grayed boxes indicate peptides specifically modified downstream of FGF-2, rather than SCF (Suppl. Fig 3), signalling. (n); position of the modified aa, p; phosphorylation, o; oxidation.

**Table S2:** List of proteins co-purified in the S6K2-TAP. Tandem affinity purification was performed in HEK293 cells, treated with or without FGF-2, using S6K2 as bait. Tryptic digests were analysed by LC-MS/MS and peptide count for the identified proteins (ID) performed. The difference (Diff) between the peptide count in the absence and the presence of FGF-2 is indicated (<0; decrease, >0; increase, 0; no change following treatment with FGF-2).

**Table S3:** Quantitative phosphoproteomics analysis of H510 SCLC cells treated with or without SCF. Trypsin digests of protein extracts from H510 cells treated with or without SCF were dimethyl-labelled using heavy and light versions of formaldehyde, respectively. Equal amounts of peptides

from both conditions were mixed, the phospho-enriched fraction analysed by LC-MS/MS and the light to heavy ratio (L/H) calculated. The experiment was performed three times so as to obtain standard errors (Std. Err.) on the ratio. The gene identifier (ID), sequence of the detected peptide and the nature of the modification are indicated. The grayed boxes indicate peptides specifically modified downstream of SCF, rather than FGF-2 (Suppl. Fig 1), signaling. (n); position of the modified aa, p; phosphorylation, o; oxidation.

**Table S4:** List of proteins co-purified in the hnRNPA1-TAP. Tandem affinity purification was performed in HEK293 cells, treated with or without FGF-2, using hnRNPA1 as bait. Tryptic digests were analysed by LC-MS/MS and peptide count for the identified proteins (ID) performed. The difference (Diff) between the peptide count in the absence and the presence of FGF-2 is indicated (<0; decrease, >0; increase, 0; no change following treatment with FGF-2).

#### Supplementary Figures

**Figure S1:** Overlap between phosphoproteomics and TAP-Tag hits. (A) Venn diagram showing the overlap in proteins identified between the phosphoproteomic analysis  $\pm$  FGF-2 (Suppl. Fig 1) and the S6K2 TAP-Tag (see Suppl. Fig 2). The IDs of the 9 overlapping identified proteins are listed. (B) Venn diagram showing the overlap in proteins identified by TAP to interact with S6K2 and hnRNPA1 (Suppl. Fig 2 and 4). The IDs of the 74 overlapping identified proteins are listed. (C) Gene Ontology (GO) analysis for these 74 proteins listed in (B) shows an enrichment in GO terms associated with translation-related and RNA processing activities.

**Figure S2:** Cytoplasmic depletion of hnRNPA1 is independent of protein degradation. (A) HEK293 cells were treated with FGF2 for indicated time and subjected to subcellular fractionation. Nuclear and cytoplasmic fractions were separated on SDS-PAGE and probed for the indicated proteins. Detection of Lamin and Tubulin were used to assess the purity of both fractions. HEK293 cells were treated for 1 h with 10 $\mu$ M MG132 (B) or 3  $\mu$ M Chloroquine (C), concentrations previously shown to inhibit proteosomal degradation and autophagy in our cell system, respectively. The cells were then

stimulated with FGF2 for the indicated time. The cytoplasmic fraction was analysed by SDS-PAGE/Western blotting for the indicated proteins.

**Figure S3:** FGF2-mediated phosphorylation of hnRNPA1 regulates its interaction with 14-3-3 $\sigma$  and 14-3-3 $\theta$  leading to hnRNPA1 K183 sumoylation and cytoplasmic depletion. (A) HEK293 cells expressing FLAG-tagged wild type (WT) or phospho-mutant (S4AS6A) hnRNPA1 were stimulated with FGF2 and subjected to immunoprecipitation with 14-3-3 antibodies. Immunoprecipitates were analysed by SDS-PAGE/Western blotting for the indicated proteins. (B) HEK293 cells expressing FLAG-tagged WT or sumoylation mutant (K3R, K8R or K183R) hnRNPA1 were stimulated with FGF2 for the indicated time and the cytoplasmic fraction analysed by SDS-PAGE/Western blotting for the indicated proteins. (C) Multiple sequence alignment for hnRNPA1 sequences from various species. The position of the conserved K183 residue is indicated with an asterisk.

**Figure S4:** FGF2-dependent modulation of hnRNPA1 in H510 cells. (A) H510 cells were treated  $\pm$  FGF2 and the cytoplasmic fraction analysed by SDS-PAGE/Western blotting (WB) for the indicated proteins. (B and C) H510 cells were stimulated  $\pm$  FGF2 and the whole cell lysate (B) or the cytoplasmic fraction (C) subjected to immunoprecipitation with hnRNPA1 or 14-3-3 antibodies, respectively. Immunoprecipitates and whole cell lysates were analysed by SDS-PAGE/WB for the indicated proteins. (D) H510 cells were stimulated  $\pm$  FGF2 for 30 min and the cytoplasmic fraction subjected to RNA-immunoprecipitation with an hnRNPA1 antibody. hnRNPA1-bound mRNAs were analysed by qPCR.

**Figure S5:** Schematic of the hnRNPA1 peptide array. 14 amino acid-long overlapping peptides covering the entire sequence of the hnRNPA1 protein were synthesised and covalently coupled to nitrocellulose membranes in 5 rows each containing 30 peptides (Top panel). In the last row, an S6 peptide was spotted in separate 4 positions. The sequence for each peptide and its relative position and molecular weight are indicated in the bottom panel.

**Figure S6:** Immunohistochemical staining for S6K2, hnRNPA1 and BCL-XL of tissue micro-array samples from lung (A) and breast cancer (B) patients. Sample images for S6K2, BCL-XL and hnRNPA1 staining for a representative patient from each S6K2 score group (upper panel) and the corresponding staining scores (lower panel). Staining for our proteins of interest was revealed using an HRP-conjugated secondary antibody (brown colour). Blue colour; haematoxylin staining. Magnification; x200.

**Figure S7:** Controls for RNA-IP. (A, C and E): Indicated cells stimulated with or without FGF2 were subjected to immunoprecipitation with hnRNPA1 or FLAG antibodies prior to isolation of the bound BclXL and XIAP mRNA. Half of the immunoprecipitates were used for RNA-IP (presented in Figure 5A-5C) and the rest subjected to SDS-PAGE/ Western blotting for the indicated proteins. (B, D and F): Levels of BCLXL and XIAP input mRNA normalized to unstimulated control for the RNA-IP depicted in Figs 5A-C.

Table S1

IDs	z	Sequence	L/H	Std.Err.	Modifications
ABCF1	3	LSVPTSDEEEVPAKP	0.4625	0.1436 (5) p (ST)	
ALDOA	3	GILAAESTGSIKR	0.1519	0.4551 (11) p (ST)	
ALG3	2	SGSAAQAEGLCK	0.7455	0.1439 (1) p (ST)	
ALG3	2	SGSAAQAEGLCK	0.7455	0.1439 (3) p (ST)	
APOOL	2	LGSSSEIEVPAK	1.019	0.05508 (3) p (ST)	
BCLAF1	2	IDISPSTLR	0.8161	0.02426 (4) p (ST)	
BCLAF1	2	RIDISPSTLR	0.7131	0.1141 (5) p (ST)	
BCLAF1	3	DLFDYSPPLHK	0.7851	0.03953 (6) p (ST)	
BCLAF1	3	AEGEPQEEESPLKSK	1.1	0.07141 (9) p (ST)	
BCLAF1	3	LKDLFDYSPPLHK	0.8223	0.02818 (8) p (ST)	
BCLAF1	4	LKDLFDYSPPLHK	0.7988	0.03209 (8) p (ST)	
BCLAF1	3	KAEGEPQEEESPLKSK	0.9994	0.05002 (10) p (ST)	
CANX	4	QKSDAEEDGGTVSQEEEDRKPK	1.2	0.03619 (3) p (ST)	
CANX	5	QKSDAEEDGGTVSQEEEDRKPK	1.011	0.07812 (3) p (ST)	
CANX	4	QKSDAEEDGGTVSQEEEDRKPK	1.2	0.03619 (1) p (ST)	
CANX	5	QKSDAEEDGGTVSQEEEDRKPK	1.083	0.04862 (13) p (ST)	
CANX	4	QKSDAEEDGGTVSQEEEDRKPK	1.066	0.03205 (3/11) p (ST)	
CANX	2	TVIEQSWGSPK	1.119	0.05165 (10) p (ST)	
HSPD1	3	GVMLAVDAVIAELKK	0.6389	0.2678 (3) o (M)	
HSPD1	3	ALMLQGVDLLADAVAVTMGPK	0.8979	0.03396 (18) o (M)	
HSPD1	3	ALMLQGVDLLADAVAVTMGPK	0.5012	0.3136 (3/18) o (M)	
CLDN11	3	FYYTAGSSSPTHAK	1.033	0.05342 (9) p (ST)	
CSTF3	4	RPNEDSDEEEKGAVVPPVHDIYR	0.2414	0.1873 (6) p (ST)	
CTNND1	3	GSLASLDSLRK	0.7902	0.1392 (8) p (ST)	
DKC1	3	AGLESAGPEGGSDSTTKK	0.9111	0.226 (14) p (ST)	
DLGAP4	3	ANSWQLVETPEKR	0.8508	0.1097 (9) p (ST)	
DNAJC5	3	SLSTSGESLYHVLGLDK	1.335	0.02063 (3) p (ST)	
DNAJC5	4	SLSTSGESLYHVLGLDKNATSDDIKK	1.357	0.01787 (3) p (ST)	
EEF1D	3	ATAPQTQHVSPMR	0.5439	0.02671 (10) p (ST)	
ELAVL1	3	NVALLSQLYHSPARR	0.6549	0.1455 (11) p (ST)	
FAM134A	2	QALDSEEEEEVAAK	0.6561	0.1166 (5) p (ST)	
FAM54B	2	NASVPNLR	0.5272	0.0653 (3) p (ST)	
FAM54B	2	ASSFADMMGILK	0.572	999 (3) p (ST)	
FARP1	2	LGAPENSIGSTLER	0.5955	0.04611 (11) p (ST)	
G3BP1	3	SSSPAPADIAQTVOEDLR	0.4949	0.03259 (1) p (ST)	
GFPT1	2	VDSTTCLFPVEEK	0.5651	0.0314 (3) p (ST)	
GSK3A	2	GEPNVSYICSR	0.4842	0.04359 (7) p (Y)	
HIST1H3E	4	FQSSAVMALQEACEAYLVGLFEDTNLCIAHAK	0.7377	0.02861 (7) o (M)	
HIST2H3C	4	FQSSAVMALQEACEAYLVGLFEDTNLCIAHAK	0.7973	0.04751 (7) o (M)	
HIST2H3C	5	FQSSAVMALQEACEAYLVGLFEDTNLCIAHAK	0.7564	0.08265 (7/16) o (M)/p (Y)	
HIST1H4A	2	RISGLIYEETR	0.7364	0.09754 (3) p (ST)	
HDGF	3	AGDLDLDSPKRPK	0.5801	0.06798 (8) p (ST)	
HDGF	4	RAGDLDLDSPKRPK	0.5483	0.03258 (9) p (ST)	
HMG1	3	KLKEKEEIGISQESSEEEQ	0.9305	0.0564 (1) p (ST)	
HMG1	4	KQPPVSPGTALVGSQKEPSEVPTPK	0.7742	0.02671 (14) p (ST)	
HNRNPH1	3	HTGPNSPDTANDGFVR	0.5924	0.135 (6) p (ST)	
HNRNPUL2	2	SGDETGPSSEVPDGK	1.15	0.07674 (1) p (ST)	
HNRNPA1	4	SESPKEPEQLR	1.071	0.02814 (4) p (ST)	
HNRNPA1	4	SESPKEPEQLR	0.4271	0.0245 (4/6) p (ST)	
HNRNPA3	2	SSGSPYGGGYSGGGSGGYGSR	0.8771	0.01947 (4) p (ST)	
HNRNPD	3	FGEVVDCTLKLDPITGR	0.8577	0.03011 (8) p (ST)	
HNRNPK	4	IPTLEEGQLQPSPTATSQLPESDAVECLNYQHYK	0.6288	0.03428 (15) p (ST)	
HNRNPK	4	IPTLEEGQLQPSPTATSQLPESDAVECLNYQHYK	0.6288	0.03428 (13) p (ST)	
HNRNPU	4	AKSPQPPVEEEDHFDVTVCLDTYNCDLHFK	0.9357	0.02836 (3) p (ST)	
HSP90AB1	3	EDVGSDEEDDSGKDK	0.4445	0.07292 (6) p (ST)	
HSP90AB1	3	EDVGSDEEDDSGKDKK	0.5584	0.1461 (6) p (ST)	
HUWE1	2	ESGTASDDFENLR	0.08135	1.567 (6) p (ST)	
IRF2B2	3	RKPSPEPEGEVGP	0.5616	0.1568 (4) p (ST)	
EIF2B1	2	QGSFVAAGAPAK	0.6052	0.116 (3) p (ST)	
EIF5B	3	NKPGPNIESGNEDDASFK	0.4128	0.07754 (9) p (ST)	
ITPR3	2	VASFSPGSSSR	1.165	0.2199 (3) p (ST)	
PRKAR1A	3	TDSREDEISPPPNPVVK	0.4926	0.01924 (9) p (ST)	
PRKACA	3	TWTLCGTPEYLAPEILSK	0.8217	0.08344 (3) p (ST)	
PRKACA	3	GRTWTLCGTPEYLAPEILSK	0.4866	0.6972 (5) p (ST)	
KHDRBS1	3	SGSMDPSGAHPSVR	0.5612	0.09778 (3) p (ST)	
KLC2	2	ASSLNFLNK	0.4724	0.06266 (3) p (ST)	
KRI1	3	AFVEDSEDEGAGEGGSSLLQK	0.8696	0.06729 (6) p (ST)	
SSB	4	FASDDEHDEHDENGATGPVKR	0.5605	0.05901 (3) p (ST)	
TMPO	2	SSTPLPTISSAENTR	1.35	0.02838 (3) p (ST)	
TMPO	4	GPPDFSSDEEREPTVVLGSGAAAGR	1.056	0.02981 (7) p (ST)	
TMPO	2	SSTPLPTISSAENTR	1.35	0.02838 (3) p (ST)	
TMPO	4	GPPDFSSDEEREPTVVLGSGAAAGR	1.056	0.02981 (7) p (ST)	
LMNB2	3	LKLSPPSSSR	1.09	0.3453 (4) p (ST)	
MAP1B	2	SDISPLTPR	0.338	0.3653 (7) p (ST)	
MAP1B	2	GAESPFEK	4.78	4.808 (4) p (ST)	
MAP1B	2	SPLSPSPSPLEK	0.5654	0.1312 (10) p (ST)	
MAP1B	3	EVPSKEEPSVYKAEVAEK	1.425	0.04416 (9) p (ST)	
MAP1B	3	TATCHSSSPPIDAASAEPYGFR	0.5801	0.01544 (9) p (ST)	
MAP1B	3	TATCHSSSPPIDAASAEPYGFR	0.5801	0.01544 (7) p (ST)	
MAP1B	4	KLGDVSPQTIDVQFGSKFEDTK	0.6369	0.06581 (8) p (ST)	
MAP1B	4	VLSPLRSPPLIGSESAYESFLSADDKASGR	0.4015	0.08954 (7) p (ST)	
MAP1B	4	TELSPSFINPNLEWFASEEPTESEKPLTQSGGAPPPPGGK	0.5911	0.03628 (6) p (ST)	
MATR3	3	SYSPDGKESPSDKK	1.089	0.03185 (3) p (ST)	
MATR3	4	RDSFDDRGPSLNPVLDYDHGSR	0.6921	0.01329 (3) p (ST)	
BTA1F1	4	KEskeETSIDVAGKPNEVT	1.218	0.07594 (3) p (ST)	
NDRG1	2	TASGSSVTSLDGTR	0.4198	0.02482 (3) p (ST)	
NIPBL	2	ATISLLGGGSPK	0.8254	0.05915 (10) p (ST)	
NOLC1	3	AESSNSSSSSDSSEEEKAAATPK	0.6278	0.06473 (4) p (ST)	
NOLC1	3	AASSSSSSSSSDSSEEEKAAATPK	0.9343	0.06137 (6) p (ST)	
NOLC1	4	KASSSDSDSSEEEVQGP	1.079	0.04882 (5) p (ST)	
NOLC1	3	AASSSSSSSSSDSSEEEKAAATPK	0.9343	0.06137 (4) p (ST)	
NOLC1	4	AASSSDSDSSEEEVQGP	0.07866	0.1973 (3/4/6) p (ST)	
NOLC1	4	KASSSDSDSSEEEVQGP	0.2931	0.1632 (3/4/5) p (ST)	
NOLC1	3	AAESSSDSDSDSSEDEAPSKPAGTTK	0.9249	0.1385 (11) p (ST)	
NOLC1	4	AAESSSDSDSDSSEDEAPSKPAGTTK	0.9953	999 (11) p (ST)	
NOLC1	4	ASESSSSSESSDDDEEDQKKQPVQK	0.988	0.02918 (10) p (ST)	
NOLC1	4	QQPVESSESDSDSSEEEKKPPTK	1.326	0.04023 (18) p (ST)	
NOLC1	4	QQPVESSESDSDSSEEEKKPPTK	1.326	0.04023 (17) p (ST)	
NPM1	4	CGSGPVHISGHLVAVEEDAEEDEEEEDVK	0.9123	0.05169 (22) p (ST)	
NUMA1	3	KNSLSSLEEEVSLNR	0.9792	0.3131 (6) p (ST)	
NUP35	2	TLGTPTQPGSTPR	0.8788	0.0806 (4) p (ST)	
NUP35	3	CALSSPSLAFTPIIK	0.9135	0.1916 (5) p (ST)	
NUP35	3	ASTSDYQVISDRQTPK	1.093	0.0591 (10) p (ST)	
PDHA1	3	YHGHMSDPGVSYR	13.18	0.9528 (5) p (ST)	
P4K2A	2	SSSESYTQSFQSR	0.8066	0.05918 (3) p (ST)	
PDCD4	2	SGLTVTPSPK	0.4667	0.05456 (8) p (ST)	
P4HB	4	FLESGGQDGAAGDDDDLEDLEAAEEDPMEEDDDQK	0.563	0.06642 (27) o (M)	
PELP1	3	GSPDGSLOTGKPSAPK	1.065	0.07926 (2) p (ST)	
PELP1	3	AGSNEDPILASGTPPTTIPPDFTFGGR	0.8934	0.03656 (14) p (ST)	
PGK1	3	ALESPEPFLAILGGA	0.521	0.05108 (6) p (ST)	
PGM2L1	3	AVAGVMITASHNR	0.4828	0.3025 (10) p (ST)	
PGRMC1	3	GQDQPAASGSDSDDEPPPLPR	1.011	0.06943 (10) p (ST)	
PGRMC1	3	EGEETTVYSDEEEPDESAR	1.135	0.01816 (9) p (ST)	
PGRMC1	3	IVRGDQPAASGSDSDDEPPPLPR	0.8744	0.0497 (13) p (ST)	
PGRMC1	4	IVRGDQPAASGSDSDDEPPPLPR	0.7179	0.03222 (13) p (ST)	
PGRMC1	4	EGEETTVYSDEEEPDESARK	0.9342	0.04012 (9) p (ST)	
PGRMC2	3	LLKPGEEPSEYDEEDTK	5.28	0.8286 (12) p (ST)	
PGRMC2	4	LLKPGEEPSEYDEEDTKDHNKQD	1.221	0.01793 (12) p (ST)	
PGRMC2	5	LLKPGEEPSEYDEEDTKDHNKQD	1.167	0.01493 (9) p (ST)	
PHF2	3	ESASPTIPNLDLEAHTK	0.6593	0.09732 (2) p (ST)	
PHF2	3	ESASPTIPNLDLEAHTK	0.6593	0.09732 (6) p (ST)	
NUP210	2	DLAVPAALTPR	0.8498	0.01846 (9) p (ST)	
PRRC2A	2	LIPGLSPVAR	0.6095	0.04117 (7) p (ST)	
PRKRA	2	EDSGTFSLGK	0.9999	0.04069 (3) p (ST)	
PRKRA	3	AEAPPLEREDSGTFLGK	0.4907	0.233 (11) p (ST)	
PSIP1	2	QSNASSDVEVEEK	1.184	0.1879 (6) p (ST)	
PSIP1	4	TGVTSTSDSEEEGDDQEGEKKR	0.6219	0.1233 (7) p (ST)	
PUM2	2	QASPTTEVVER	0.5308	0.1163 (3) p (ST)	
RBM15	3	DRTPPLLYR	0.7448	0.01463 (3) p (ST)	
RBM15	2	SLSPGGGAALGYR	0.7706	0.02223 (3) p (ST)	
EBAG9	3	KLSDQDILPTTVDYSSVPK	0.8441	0.02869 (3) p (ST)	
RCC1	3	RRSPPADAFK	0.8511	0.01599 (3) p (ST)	
RPL12	2	IGPLGLSPK	0.9054	0.03457 (7) p (ST)	
RPRD1B	4	TFQQIEEEDDDYPGSYPQDPSAGPLTEELIK	0.4893	0.05211 (18) p (ST)	
RPS3	2	DEILPTPISEOK	1.348	0.07858 (14) p (ST)	
RPS3	4	KPLPDHVSIVEPKDEILPTPISEOK	0.4817	0.151 (20) p (ST)	
SLC35B2	2	AVPVESPQVKV	0.9639	0.06393 (6) p (ST)	
SLC35B2	2	KAVPVESPQVKV	0.9507	0.07677 (7) p (ST)	
SLC35C2	2	GLGSPDLELLLR	0.3777	0.2572 (4) p (ST)	
SMAP	3	SASPDDDLGSSNWEEAADLGNEER	0.5969	0.9709 (3) p (ST)	
SNIP1	3	QERLSPEVAPPARH	0.6188	0.02212 (6) p (ST)	
SNIP1	3	RPDHSGSGSPPTSEPAR	43.25	1.397 (8) p (ST)	
SRF	3	ALIQTLQNSPDSPRSDPTTDQR	0.6832	0.04908 (12) p (ST)	
SRRM1	2	RYSPSPPPK	0.957	0.2308 (3) p (ST)	
SRRM1	3	HRSPPATPPPK	1.938	0.382 (4) p (ST)	
SRRM1	3	HRSPPATPPPK	0.5813	0.05095 (4/8) p (ST)	
SRRM1	3	EKTELPPEPSVK	0.7632	0.02191 (3) p (ST)	
SRRM1	3	KVELSESEEDKGGK	0.6744	0.1236 (5) p (ST)	
SRRM1	3	KETESAEADNLDDLEK	0.5255	0.04038 (5) p (ST)	
SRRM2	2	GFSASPMK	0.6948	0.1041 (6) p (ST)	
SRRM2	2	SSSPVTLEASR	0.7555	0.06322 (3) p (ST)	
SRRM2	2	SCFESSPDPELK	0.5878	0.1016 (6) p (ST)	
SRRM2	3	SSTPQCESYFGVSSQLK	0.7358	0.1477 (3) p (ST)	
SRRM2	4	GRGPSPEGSSSTESSPEHPK	0.7115	0.1034 (15) p (ST)	
SRM2	4	RGEADAPFSEPGTTSTQRPSSPETATK	0.7413	0.0383 (21) p (ST)	
SRRT	3	TQLWASEPGTTPPLTSLPSQNPILK	0.6944	0.03041 (10) p (ST)	
SRSF11	3	DYDEEEQGYDSEKEK	0.4614	0.1508 (11) p (ST)	
SRSF9	3	GSPHYFSPFRPY	0.8182	0.02475 (2) p (ST)	
SSFA2	2	SQSLPTTLSPVR	0.6505	0.09345 (3) p (ST)	
SSRP1	2	EFVSSDESSSGENK	0.9139	0.09501 (9) p (ST)	
STMN1	2	ASGOAFELLSPR	0.3397	0.1112 (11) p (ST)	
STT3B	3	ENPPVEDSSDEDDKR	1.069	0.07752 (8) p (ST)	
STT3B	3	ENPPVEDSSDEDDKR	1.478	0.1932 (8/9) p (ST)	
TCOF1	3	TSQVGAASAPAKESPR	0.6248	0.05401 (14) p (ST)	
TCOF1	3	LGAGEGGEASVSPEKTSTTSK	0.846	0.06791 (12) p (ST)	
SUB1	3	ELVSSSSSGSDSSEVDKK	0.9933	0.0778 (12) p (ST)	
TERF2IP	2	YLLGDAPVSPSSQK	0.4253	0.07066 (9) p (ST)	
TMX1	3	KVEEEQEADEEDVSEEEAEK	0.4386	0.04346 (14) p (ST)	
TP53BP1	2	STPFIVPSSPTEQGR	0.4648	0.03843 (9) p (ST)	
SPAG1	3	KQSLGELIGLTNAK	0.5493	0.05823 (3) p (ST)	
SPAG1	4	KQSLGELIGLTNAKVPADTEVVCAPPTAYIDFAR	0.2037	0.08737 (10) p (ST)	
THRAP3	2	ASAVSELSR	0.83	0.01135 (8) p (ST)	
THRAP3	2	IDISPSTFR	0.8023	0.04372 (4) p (ST)	
THRAP3	2	IDISPSTFR	0.9014	0.02172 (5) p (ST)	
THRAP3	3	ERSPALKSPLQSVVVR	0.6833	0.01584 (3) p (ST)	
UBE2J1	3	RLSTSPDVIQGHQPR	0.8016	0.1246 (3) p (ST)	
VDAC1	3	LTDFSFSFNTGKK	0.924	0.04589 (8) p (ST)	
VDAC2	3	LTFTDTTFSNTGKK	0.4555	0.1694 (8) p (ST)	
KIAA1429	2	SFLSESPSPGR	1.026	0.08994 (8) p (ST)	
ZNF828	2	GGSPDLWK	0.9038	0.0415 (3) p (ST)	

Table S2

IDs	Name	Diff
AOA5E5	Putative uncharacterized protein	-1
ACPP	Acid phosphatase 1 isoform c variant	-1
ACTA1	Actin, alpha 1, skeletal muscle	-1
ACTG1	Actin, cytoplasmic 2	-1
AIFM1	Apoptosis-inducing factor, mitochondrion-associated, 1	1
ALB	Albumine	1
ALG1	Chitobiosyldiphosphodolichol beta-mannosyltransferase	-1
ANKMY2	Ankyrin repeat and MYND domain containing 2	0
ANXA2	Annexin A2	-2
ATP1A1	Sodium/potassium-transporting ATPase subunit alpha-1	-4
ATPSA1	ATP synthase subunit alpha, mitochondrial	1
BAG2	BAG family molecular chaperone regulator 2	1
BRAF	v-raf murine sarcoma viral oncogene homolog B1	4
C22orf28	Putative uncharacterized protein HSPC117	-2
CAD	Carbamoyl-phos Sase 2, Asp transcarbamylase, and dihydroorotase	0
CAPRIN1	Caprin-1	0
CAPZA1	F-actin-capping protein subunit alpha-1	-1
CCDC124	Coiled-coil domain-containing protein 124	0
CCT2	T-complex protein 1 subunit beta	-3
CCT3	T-complex protein 1 subunit gamma	-3
CCT4	T-complex protein 1, delta subunit	1
CCT5	T-complex protein 1 subunit epsilon	-3
CCT6A	Chaperonin subunit 6A	-1
CCT7	T-complex protein 1 subunit eta	0
CCT8	T-complex protein 1 subunit theta	2
CDC37	Hsp90 co-chaperone Cdc37	1
CDC45	Cell division cycle 45 homolog	-3
CFL1	Cofilin-1	-2
CLNS1A	Methylosome subunit pICln	0
DDB1	DNA damage-binding protein 1	3
DDX1	ATD-dpt RNA helicase DEAD box polypep 1	0
DDX17	ATD-dpt RNA helicase DEAD box polypep 17	1
DDX3X	ATD-dpt RNA helicase DEAD box polypep 3X	2
DDX5	ATD-dpt RNA helicase DEAD box polypep 5	-2
DDX6	ATD-dpt RNA helicase DEAD box polypep 6	1
DHX9	ATD-dpt RNA helicase DEAD box polypep 9	2
DNAJA2	DnaJ (Hsp40) homolog, subfamily A, member 2	1
DNAJB1	DnaJ homolog subfamily B member 1	-1
DNAJC7	DnaJ homolog subfamily C member 7	3
DNJA1	DnaJ homolog subfamily A member 1	1
DNJA2	DnaJ homolog subfamily A member 2	1
EEF1A1	Elongation factor 1-alpha 1	-3
EEF1G	Elongation factor 1-gamma	-1
EIF2S2	Eukaryotic translation initiation factor 2, subu 2 beta	-2
EIF3B	Eukaryotic translation initiation factor 3, subunit 9 eta	1
EWSR1	RNA-binding protein Ewing sarcoma breakpoint region 1	-1
FAM60A	Transitional endoplasmic reticulum ATPase	-1
FKBP5	FK506-binding protein 5	8
FKBP8	FK506-binding protein 8	1
FUS	Fused in sarcoma	1
G3BP1	Ras GTPase-activating protein-binding protein 1	1
GDF5	Growth differentiation factor 5	0
GTF2I	General transcription factor II-I	3
HAT1	Histone acetyltransferase 1	1
hCG2043616	leucine-rich repeat-containing protein 15 isoform	-1
HLA-A	HLA class I alpha chain	0
→ HNRNPA1	Heterogeneous nuclear ribonucleoproteins A1	4
HNRNPA2B1	Heterogeneous nuclear ribonucleoproteins A2/B1	0
HNRNPK	Heterogeneous nuclear ribonucleoprotein K	-1
HNRNPM	Heterogeneous nuclear ribonucleoprotein M	0
HNRNPU	Heterogeneous nuclear ribonucleoprotein U	2
HSP90AA1	Heat shock protein HSP 90-alpha	5
HSP90AB1	Heat shock protein 90kDa alpha class B member 1	6
HSPA14	Heat shock 70kDa protein 14	1
HSPA1A	Heat shock 70 kDa protein 1	4
HSPA4L	Heat shock 70 kDa protein 4-like protein	0
HSPA5	78 kDa glucose-regulated protein	3
HSPA6	Heat shock 70 kDa protein 6	0
HSPA8	Heat shock cognate 71 kDa protein	-4
HSPA9	Stress-70 protein, mitochondrial	3
HSPD1	60 kDa heat shock protein, mitochondrial	1
HSPH1	Heat shock protein 105 kDa	-2
IGF2BP1	Insulin-like growth factor 2 mRNA-binding protein 1	-1
IPO5	Importin 5	0
IPO7	Importin-7	-1
IQGAP1	IQ motif containing GTPase activating protein 1	-2
KIF2A	Kinesin-like protein KIF2A	0
KIF5B	Kinesin-1 heavy chain	1
KRT1	Keratin, type II cytoskeletal 1	-4
KRT10	Keratin, type I cytoskeletal 10	-1
KRT13	Keratin, type I cytoskeletal 13	2
KRT14	Keratin, type I cytoskeletal 14	-5
KRT16	Keratin, type I cytoskeletal 16	-3
KRT2	Keratin, type II cytoskeletal 2 epidermal	0
KRT5	Keratin, type II cytoskeletal 5	-6
KRT6A	Keratin, type II cytoskeletal 6A	-2
KRT9	Keratin, type I cytoskeletal 9	0
LRPPRC	Leucine-rich PPR motif-containing protein, mitochondrial	2
LTV1	LTV1 homolog	-1
LV302	Ig lambda chain V-III region LOI	0
LYZ	Lysozyme C	1
MAGED1	Melanoma-associated antigen D1	-1
MAGED2	Melanoma-associated antigen D2	2
MCM3	Cervical cancer proto-oncogene 5	-3
MRPS22	28S ribosomal protein S22, mitochondrial	-1
MSH6	G/T mismatch-binding protein	0
MYO1C	Myosin-1c	1
NCL	Nucleolin	3
NME3	Non-metastatic cells 3, protein expressed in	-1
NONO	Non-POU domain-containing octamer-binding protein	-3
NPM1	Nucleolar phosphoprotein B23	1
NUDC	Nuclear distribution gene C homolog	-1
PCBP1	Poly(rC)-binding protein 1	-2
PCMT1	Protein-L-isoaspartate O-methyltransferase	1
PCNA	Proliferating cell nuclear antigen	2
PDCD4	Programmed cell death protein 4	2
PHGDH	Phosphoglycerate dehydrogenase	0
POLDIP3	DNA-directed polymerase , delta interacting protein 3	-1
PPM1G	Protein phosphatase 1G	-3
PPP2CA	S/T-protein phosphatase 2A catal subu alpha isoform	-1
PPP2R1A	S/T-protein phosphatase 2A reg subu A alpha	-2
PPP2R2A	S/T-protein phosphatase 2A reg subu B alpha	2
PPP6R1	Ser/thr-protein phosphatase 6 regulatory subu 1	1
PPP6R3	Ser/thr-protein phosphatase 6 regulatory subu 3	-3
PPYR1	pancreatic polypeptide receptor 1	0
PRDX1	Peroxisredoxin 1	3
PRMT1	Protein arginine N-methyltransferase 1	0
PRSS3	Trypsin-3	1
PSMC1	26S protease regulatory subunit 4	1
PSMC2	Proteasome (Prosome, macropain) 26S subunit, ATPase, 2	-4
PSMC3	26S protease regulatory subunit 6A	-1
PSMD3	proteasome 26S subu, non-ATPase, 3	-1
PSPC1	Paraspeckle component 1	-2
PTGES3	Prostaglandin E synthase 3	0
Q59GD0	Polo-like kinase variant	0
RBBP7	Retinoblastoma binding protein 7	-1
RPL13	60S ribosomal protein L13	1
RPL14	60S ribosomal protein L14	0
RPL17	60S ribosomal protein L17	-1
RPL19	60S ribosomal protein L19	1
RPL22L1	Ribosomal protein L22-like protein	1
RPL23A	60S ribosomal protein L23a	2
RPL24	Ribosomal protein L24	1
RPL26	60S ribosomal protein L26	1
RPL8	60S ribosomal protein L8	2
RPN1	Ribophorin I	-1
RPS14	Ribosomal protein S14	1
RPS17	40S ribosomal protein S17	-2
RPS18	40S ribosomal protein S18	-4
RPS19	40S ribosomal protein S19	-1
RPS2	40S ribosomal protein S2	-1
RPS25	40S ribosomal protein S25	-1
RPS3	Ribosomal protein S3	-4
RPS3A	40S ribosomal protein S3a	-2
RPS4X	40S ribosomal protein S4, X isoform	-1
RPS5	40S ribosomal protein S5	1
RPS6	40S ribosomal protein S6	0
RPS7	Ribosomal protein S7	2
RPS8	40S ribosomal protein S8	1
RUVBL1	RuvB-like 1	0
RUVBL2	RuvB-like 2	2
SERBP1	Plasminogen activator inhibitor 1 RNA-binding protein	1
SFPQ	Splicing factor, proline- and glutamine-rich	6
SHROOM3	Shroom family member 3	1
SLC25A5	ADP/ATP translocase 2	1
SLC3A2	4F2 cell-surface antigen heavy chain	-1
SNRPB	Small nuclear ribonucleoprotein polypeptide B"	-1
SSR1	Translocon-associated protein subu alpha	-1
STUB1	STIP1 homology and U-box containing protein 1	1
SUGT1	Suppressor of G2 allele of SKP1 homolog	-1
TAF15	RNA polymerase II, TBP-associated factor	-3
TCP1	T-complex protein 1 subunit alpha	0
TFAM	Mitochondrial transcription factor A	1
TIMM50	Mitochondrial import inner membrane translocase subu 50	0
TUBA1B	Tubulin alpha-1B chain	-1
TUBA1C	Tubulin alpha-1C chain	-1
TUBB	Tubulin beta chain	-1
TUBB2C	Tubulin beta-2C chain	0
TUBB3	Tubulin beta-3 chain	0
TUBB6	Tubulin beta-6 chain	-1
TUFM	Elongation factor Tu, mitochondrial	0
UBIQ	Ubiquitin	0
USP7	Ubiquitin carboxyl-terminal hydrolase 7	2
USP9X	Ubiquitin specific peptidase 9, X-linked	2
WBSR22	Williams Beuren syndrome chromosome region 22	-1
WRNIP1	Werner helicase interacting protein 1	2
XRCC5	X-ray repair complementing defective in Chinese hamster cells 5	0
YBX1	Nuclease-sensitive element-binding protein 1	1
YTHDF2	YTH domain family protein 2	-2
YWHAH	14-3-3 protein eta	1
YWHAQ	Tyr 3-/Trp 5-monooxygenase activation prot, theta polypep	-1



Table S3

ID	Z	Sequence	L/H	Std. Err.	Modifications
AP00L	2	LGSSSEIEVPAK	0.9716	0.07473 (4) p (ST)	
AP00L	2	LGSSSEIEVPAK	0.9716	0.07473 (3) p (ST)	
BCIAF1	2	IDISPSTLR	0.9337	0.02592 (4) p (ST)	
BCIAF1	3	IDISPSTLRK	0.9943	0.05885 (4) p (ST)	
BCIAF1	2	RIDISPSTLR	1.026	0.02483 (5) p (ST)	
BCIAF1	3	DLFDYSPPLHK	0.847	0.03403 (6) p (ST)	
BCIAF1	2	KAEGEPQEE SPLK	0.9641	0.0352 (10) p (ST)	
BCIAF1	3	LKDLFDYSPPLHK	0.9087	0.03193 (8) p (ST)	
BCIAF1	3	KAEGEPQEE SPLKSK	0.9401	0.03384 (10) p (ST)	
CANX	4	OKSDAEEDGGTVSQEEEDRKPK	1.017	0.03517 (3) p (ST)	
CANX	4	OKSDAEEDGGTVSQEEEDRKPK	0.9109	0.01956 (3/13) p (ST)	
CERS2	4	LVEDERSDREETESSEGEAAAGGGAK	0.7982	0.04767 (7) p (ST)	
CERS2	4	LVEDERSDREETESSEGEAAAGGGAK	0.7982	0.04767 (12) p (ST)	
CERS4	3	SDVEESDSSEAAAAQELQLK	0.732	0.05889 (8) p (ST)	
CIR1	3	NLTANDPSQEVYVASEGEEDPEVEFLK	0.8518	0.03777 (14) p (ST)	
COBRA1	3	KPSPAQAAETPALELPLSPVPAPAPL	0.9109	0.01961 (3) p (ST)	
CTAGE5	2	AFLSPPTLLEGLPR	0.8464	0.04096 (4) p (ST)	
CTNND1	3	GSLSLDSLRLK	0.7647	0.1562 (8) p (ST)	
DXH9	5	SEEVPAFGVASPPPLTDTPTTANAEGDLPTTMGGPLPPLHALK	0.8341	0.08473 (11) p (ST)	
DKC1	2	AGLESQAEPQDQSDDTTK	0.8505	0.04068 (14) p (ST)	
DNAJC5	3	SLSTSGESLYHVLGDK	1.146	0.02592 (1) p (ST)	
DNAJC5	3	SLSTSGESLYHVLGDK	1.12	0.01924 (3) p (ST)	
DNAJC5	4	SLSTSGESLYHVLGDKNATSDDIKK	0.9176	0.007932 (3) p (ST)	
DSG2	3	VVPSPFLVDQGGSLVGR	0.9982	0.06179 (13) p (ST)	
DSP	3	SSFSFSDTLEESSPIAIFDTENLEK	0.865	0.04258 (2) p (ST)	
DSP	3	SSFSFSDTLEESSPIAIFDTENLEK	0.865	0.04258 (7) p (ST)	
DTD1	2	SASSGAEGDVSSEREP	0.7591	0.06806 (4) p (ST)	
EBAG9	3	KLSGDQITPTTVDYSSVVK	0.8605	0.03228 (3) p (ST)	
EEF1D	3	ATAPQTOHVSPMR	0.6694	0.02365 (10) p (ST)	
EIF2B1	2	QGSPPVAAGAPAK	0.9968	0.0263 (3) p (ST)	
EIF3G	4	GIPLATGDTSPPEPLTLPALPPPK	0.9113	0.05062 (10) p (ST)	
EIF5B	3	NKPGPNIESGNEEDDASF	0.8088	0.04501 (9) p (ST)	
FAM54B	2	NASVPNLR	0.8438	0.05184 (3) p (ST)	
FAM54B	2	ASSFADMMGILK	0.593	0.1001 (3) p (ST)	
FARP1	2	LGAPENSGLTLER	0.9069	0.03999 (11) p (ST)	
FOXK1	3	EGSPIPHDFGSK	0.9948	0.04704 (3) p (ST)	
G3BP1	2	SSSPAPADIAQTQEDLR	0.9217	0.08376 (3) p (ST)	
GFP1T	2	VDTTCLFPVEEK	1	0.02452 (3) p (ST)	
GORASP2	3	VGDSTPVSEKPVSAAVDANASESP	0.8271	0.03414 (23) p (ST)	
GSK3B	2	GEPNVSYICSR	0.9331	0.04698 (7) p (Y)	
HDGF	3	AGDILLEDSPKRPK	0.8422	0.06093 (8) p (ST)	
HDGF	4	RAGDILLEDSPKRPK	0.723	0.04047 (9) p (ST)	
HMG1A	3	KLKEEEEEEGSQSESEEEQ	0.7618	0.05164 (14) p (ST)	
HMG1A	4	KOPPYSPGATLVSQKEPSEVPTPK	0.9048	0.02954 (14) p (ST)	
HNRNPA3	2	SSGSPYGGGYGSGGGSGGYGSR	0.9461	0.03465 (4) p (ST)	
HNRNPK	5	IPTLEEGQLPSPATSLQLPLESDAVECLNYQHYK	0.7945	0.01811 (17) p (ST)	
HNRNPK	4	IPTLEEGQLPSPATSLQLPLESDAVECLNYQHYK	0.8176	0.0176 (13) p (ST)	
HNRNPK	5	KIIPITLEEGQLPSPATSLQLPLESDAVECLNYQHYK	0.7708	0.05395 (19) p (ST)	
HNRNPU	5	AKSPQPPVEEEDHFDDTVVCLDTYNCDLHFK	0.7828	0.01885 (3) p (ST)	
HNRNPU	5	AKSPQPPVEEEDHFDDTVVCLDTYNCDLHFK	0.7828	0.01885 (18) p (ST)	
HNRNPUL2	2	SGDETGPSEVPQDK	0.9683	0.07622 (1) p (ST)	
HSP90AA1	3	ESEDKPEIEDVGSDEEEEEK	0.7535	0.0578 (13) p (ST)	
HSP90AB1	3	IEDVGSDEEDDSGDKDK	2.306	0.08044 (6) p (ST)	
HSP90AB1	3	IEDVGSDEEDDSGDKDK	1.627	0.05836 (6) p (ST)	
HSPD1	2	TVIEQSWGSPK	0.9687	0.03856 (10) p (ST)	
HSPD1	3	ALMLQGVDLLADAVAVTMGPK	0.7533	0.06721 (3/18) o (M)	
KHDRBS1	5	ASPATQPPLLPSPATGPDATVGGPAPTLLPPSATASVK	0.9461	0.04577 (2) p (ST)	
KIAA1429	2	SFLSEPPSPGR	1.122	0.1307 (8) p (ST)	
KIF1A	3	SDSLLDHQWELEK	0.9571	0.05673 (3) p (ST)	
KRI1	3	AFVEDSEDEDGAGEGGSSLLQK	0.8568	0.06957 (6) p (ST)	
MAP1B	2	SDISPLTPR	0.5232	0.1389 (7) p (ST)	
MAP1B	3	EVPSKEEPSPVKAIEVAEK	1.175	0.04861 (9) p (ST)	
MAP1B	4	KLGDVSPTOIDVQFGSFKEDTK	0.6615	0.05714 (6) p (ST)	
MAP1B	4	VLSPILRSPPLIGSESAYESFLSADDKASGR	0.7465	0.01736 (7) p (ST)	
MAP1B	4	VLSPILRSPPLIGSESAYESFLSADDKASGR	0.6473	0.04706 (3/7) p (ST)	
MAP1B	4	TELSPSFINPNPLEWFASEEPTESEKPLTQSGGAPPPPGGK	0.7965	0.01479 (4) p (ST)	
MAP1B	4	TELSPSFINPNPLEWFASEEPTESEKPLTQSGGAPPPPGGK	0.7963	0.01477 (6) p (ST)	
MAP1B	5	TELSPSFINPNPLEWFASEEPTESEKPLTQSGGAPPPPGGK	0.7743	0.02306 (6) p (ST)	
MAP4	3	VGSLDNVGHLPAGGAVK	0.8019	0.09142 (3) p (ST)	
MATR3	4	RDSFDDRGSLNPLVDYDHGSR	0.7213	0.01179 (3) p (ST)	
MYEF2	3	AEVPGATGGDSPHLQPAEPPGEP	1.201	0.02592 (11) p (ST)	
MYH9	3	KGAGDGSDEEDVGKADGAIAKPAE	0.7672	0.05487 (7) p (ST)	
NACA	4	VQGEAVSNIQENTQPTVQEESEEEVDETGEVEK	0.9373	0.02581 (22) p (ST)	
NDRG1	2	TASGSSVTSLDGTR	0.7639	0.02355 (3) p (ST)	
NIPBL	2	AITSLGSGGSPK	0.7237	0.07841 (10) p (ST)	
NOL9	4	LAADFADALEFADEEKESPVFEFTGHK	0.7263	0.09405 (17) p (ST)	
NOLC1	3	AESSNSSSSDDSSSEEEEEKLK	1.061	0.05673 (7) p (ST)	
NOLC1	3	AESSNSSSSDDSSSEEEEEKLK	1.061	0.05673 (6) p (ST)	

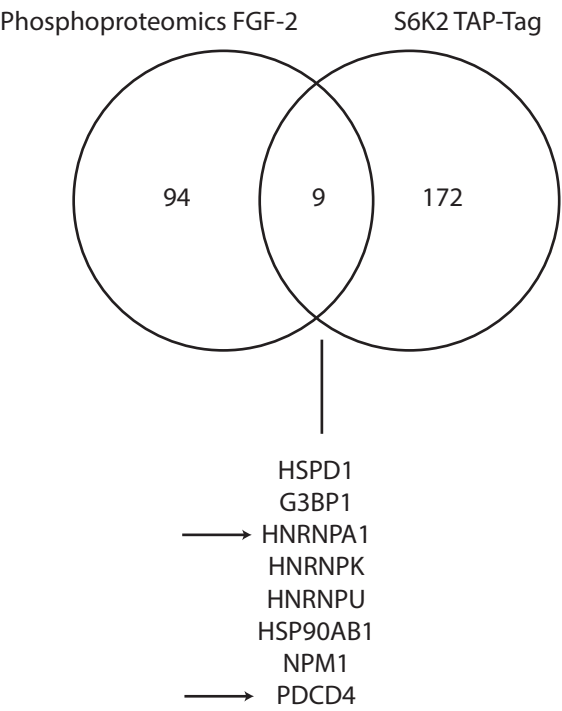
NOLC1	4	SSDSDDSSSEDEPPKNQKPK	0.9715	0.01445 (4) p (ST)
NOLC1	4	SSDSDDSSSEDEPPKNQKPK	0.9735	0.01417 (9) p (ST)
NOLC1	3	AASSSSSSSSSSSSDDSEEEKAAATPK	0.7654	0.04805 (7) p (ST)
NOLC1	4	KASSSDSEDSSEEEEEVOGPPAKK	0.7794	0.05618 (3) p (ST)
NOLC1	4	AASSSSSSSSSSSSDDSEEEKAAATPK	0.7654	0.04805 (3) p (ST)
NOLC1	4	KASSSDSEDSSEEEEEVOGPPAKK	0.7794	0.05618 (5) p (ST)
NOLC1	4	ASESSSSSEESSDDDDDEEDQKKOPVOK	0.9112	0.01664 (6) p (ST)
NOLC1	4	ASESSSSSEESSDDDDDEEDQKKOPVOK	0.9112	0.01664 (10) p (ST)
NOLC1	4	QQPVESSEDSDESDDSSSEEEKKPPTK	0.8908	0.02328 (16) p (ST)
NOLC1	4	QQPVESSEDSDESDDSSSEEEKKPPTK	0.8908	0.02328 (17) p (ST)
NOP58	4	HIKEEPLSEEEECTSTAIA SPEK	1.331	0.1888 (8) p (ST)
NOP58	4	HIKEEPLSEEEECTSTAIA SPEK	0.7663	0.09106 (8) p (ST)
NPM1	4	CGSGPVHISQHLVAVEEDAEEDEEEEDVK	1.101	0.02527 (22) p (ST)
NUMA1	3	KNLSLISLEEEVSILNR	0.8451	0.07158 (3) p (ST)
NUP35	2	TLGTITQPGSTPR	1.081	0.05633 (4) p (ST)
P4HB	4	FLESGGGDGAAGDDDDLEEEAEEDMEEDDDQK	3.394	0.04367 (27) o (M)
PGK1	3	ALESERPFLAILGGAK	0.8497	0.01295 (4) p (ST)
PGRMC1	3	GDOQPAASGDSDDDDEPPPLPR	0.7589	0.05616 (10) p (ST)
PGRMC1	3	EGEETPVYSDEEEKPDESAR	1.266	0.0312 (9) p (ST)
PGRMC1	4	IVRGDQPAASGDSDDDDEPPPLPR	0.7134	0.02287 (10) p (ST)
PGRMC1	4	EGEETPVYSDEEEKPDESARK	0.8134	0.04398 (9) p (ST)
PNISR	4	QRSPIALPVKEPPQIDAVK	0.8566	0.03866 (3) p (ST)
PRKACA	3	TWTLCGTPEYLAPEILSK	0.9055	0.02777 (3) p (ST)
PRKACA	3	GRTWTLCGTPEYLAPEILSK	0.7148	0.02782 (5) p (ST)
PRKAR1A	3	TDSEDEISPPPPMPVVVK	0.9503	0.01107 (9) p (ST)
PRPF4B	3	LCDFGSASHVADNDITPYLVSR	1.158	0.03175 (18) p (Y)
PSIP1	2	QSNASSDVEVEEK	1.026	0.1402 (6) p (ST)
RBM15	2	SLSPGGGAALGYR	0.9154	0.02346 (3) p (ST)
RBM39	2	YRSPYSGP	0.9017	0.06593 (3) p (ST)
RBM39	3	YRSPYSGP	0.000027	0.153 (3) p (ST)
RBMX2	2	EVQAEQPSSSSPR	0.9258	0.04553 (10) p (ST)
RBMX2	2	EVQAEQPSSSSPR	0.9258	0.04553 (11) p (ST)
RCC1	3	RRSPPADAIK	0.8344	0.01407 (3) p (ST)
RPL12	2	IGPLGLSPK	0.8161	0.034 (7) p (ST)
RPLP0	5	AFLADPFAVAAAPVAAATAAPAAAAAPAKVEAKEESEDEDMGFLFD	0.6218	0.08874 (41) p (ST)
RPLP2	3	VYVASYLLAALGNGSSPSAK	1.002	0.02125 (15) p (ST)
RPLP2	2	KEESEESDDMGFLFD	0.765	0.02764 (11) o (M)
RPRD1B	4	TFQQIEEEDDDYPGSYSPQDPSAGPLLTELIK	0.7185	0.04067 (18) p (ST)
RPRD1B	5	TFQQIEEEDDDYPGSYSPQDPSAGPLLTELIK	0.8116	0.02616 (18) p (ST)
RPS3	2	DEILPTPISEIQ	1.258	0.03964 (7) p (ST)
SCAF4	5	EIIQPLDMAAGTSNAAAPVAENVNNEGSPPPPVK	0.8588	0.04688 (30) p (ST)
SLC35B2	2	AVPVESPQVK	1.054	0.07057 (6) p (ST)
SLC35C2	2	GLGSSPDLELLLR	0.8965	0.02242 (4) p (ST)
SMARCA5	4	GGPEGVAAQAVASASAGPADAEMEEFDDASPGKQK	0.7985	0.1748 (32) p (ST)
SNIP1	3	QERLSPEVAPPAHR	0.8666	0.01985 (5) p (ST)
SPAG1	3	KQSLGELIGTLNAAK	0.8809	0.03595 (3) p (ST)
SPAG1	4	KQSLGELIGTLNAAKVPADTEVVCAPPTAYIDFAR	0.5266	0.05803 (10) p (ST)
SRRM1	3	HRPSPPATPPPK	0.7073	0.06718 (4) p (ST)
SRRM1	3	HRPSPPATPPPK	0.7098	0.1964 (4/8) p (ST)
SRRM1	3	EKTPPELPEPSVK	0.8477	0.01698 (3) p (ST)
SRRM2	3	SSTPPGESYFGVSSSLQLK	0.9402	0.04744 (3) p (ST)
SRRM2	4	RGEADAPFSEP GTTS TORPSSPETATK	0.9994	0.03512 (20) p (ST)
SRRM2	4	RGEADAPFSEP GTTS TORPSSPETATK	0.9994	0.03512 (21) p (ST)
SRR1	4	TQLWASEPGTTPPLTSLPSQNPILK	0.9309	0.05332 (10) p (ST)
SRR1	3	TQLWASEPGTTPPLTSLPSQNPILK	1.002	0.02693 (10) p (ST)
SRSF9	3	GSPHYFSPFRPY	0.9695	0.01236 (2) p (ST)
STT3B	3	ENPPVEDSSDEDDKR	1.109	0.05264 (8) p (ST)
STT3B	3	ENPPVEDSSDEDDKR	1.109	0.05264 (9) p (ST)
SUB1	3	ELVSSSSSGSDSDSEVDKK	0.8291	0.05701 (12) p (ST)
SUB1	3	ELVSSSSSGSDSDSEVDKK	0.8291	0.05701 (10) p (ST)
SUB1	3	SKELVSSSSSGSDSDSEVDKK	0.5331	0.09591 (14) p (ST)
TCEA1	3	KKKEPAITSQNSPEAR	0.7926	0.02504 (11) p (ST)
TCOF1	3	TSQVGAASAPAKESPR	0.7965	0.0557 (14) p (ST)
TCOF1	3	LGAGEGGEASVSPEKTSITTSK	0.8489	0.1059 (12) p (ST)
TERF2IP	2	YLLGDAPVSPSSQK	0.3456	0.07801 (9) p (ST)
THRAP3	2	ASAVSELSPR	0.9358	0.01925 (8) p (ST)
THRAP3	2	IDISPSTFR	0.9216	0.01826 (4) p (ST)
THRAP3	2	RIDISPSTFR	1.046	0.01121 (5) p (ST)
THRAP3	3	IDISPSTFRK	0.9703	0.0301 (4) p (ST)
THRAP3	3	ERSPALKSPQSVVVR	0.8625	0.02384 (3) p (ST)
TMPO	2	SSTPLPTISSAENTR	1.548	0.03367 (3) p (ST)
TMPO	5	NRPPLPAGTNSKGPPDFSSDEEREPTVLGSGAAAAAGR	0.6283	0.0464 (19) p (ST)
TMX1	3	KVEEEQEADEEDVSEEEAESK	1.056	0.04561 (14) p (ST)
TP53BP1	2	STPFIVPSSPTEQGR	0.7914	0.03368 (9) p (ST)
UBE21	3	RLSTSPDVQGHQPR	0.9708	0.08069 (3) p (ST)
UBE21	3	RLSTSPDVQGHQPR	0.9857	0.07487 (5) p (ST)
WRAP53	3	VFPPEPTESGDEEELGLPLLSTR	0.9362	0.01495 (8) p (ST)
ZRANB2	3	EVEDKESEGEDEDEDLSK	1.887	0.05523 (7) p (ST)

## Table S4

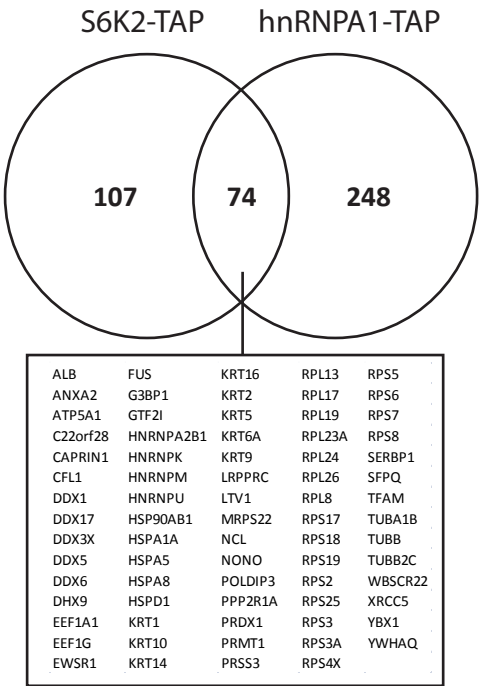
IDs	Name	Diff					
A2ML1	Alpha-2-macroglobulin-like 1	3	IGF2BP2	Insulin-like growth factor 2 mRNA binding protein 2	0	PTCD3	Pentatricopeptide repeat domain 3
ACTB	Actin, beta	2	IGH@ prot	IGH@ protein	4	Q2I377	Small proline rich protein
ADA	Adenosine deaminase	1	IGK@ prot	IGK@ protein	6	Q5K634	SCCA2/SCCA1 fusion protein isoform 1
AKAP8	A kinase (PRKA) anchor protein 8	3	IGL@	IGL@	2	RAB5A	RAB5A, member RAS oncogene family
AKR1B10	Aldo-keto reductase family 1, member B10	-3	IL36G	Interleukin 36, gamma	-2	RALY	RNA binding protein, autoantigenic
ALB	Albumin	15	ILF2	interleukin enhancer binding factor 2	-2	RBM14	RNA binding motif protein 14
ALDOA	Aldolase A, fructose-bisphosphate	-2	ILF3	Interleukin enhancer binding factor 3	3	RBM45	RNA binding motif protein 45
ANGEL2	Angel homolog 2	0	IVL	Involucrin	0	RBM6	RNA binding motif protein 6
ANXA1	Annexin A1	-3	JUP	Junction plakoglobin	8	RBMX	Heterogeneous nuclear ribonucleoprotein G
ANXA2	Annexin A2	1	KHSRP	KH-type splicing regulatory protein	2	RNMT	RNA (guanine-7-) methyltransferase
ARF3	ADP-ribosylation factor 3	0	KIAA1967	KIAA1967	-2	RPL10	Ribosomal protein L10
ARG1	Arginase, liver	-4	KPRP	Keratinoocyte proline-rich protein	-1	RPL11	Ribosomal protein L11
ASPRV1	Aspartic peptidase, retroviral-like 1	1	KRT1	Keratin 1	-1	RPL13	Ribosomal protein L13
ATP5A1	ATP ̳ase, H+ transporting, mito F1 complex, alpha 1	3	KRT10	Keratin 10	-1	RPL15	Ribosomal protein L15
ATP5B	ATP ̳ase, mitochon F1 complex, beta polypep	1	KRT14	Keratin 14	5	RPL17	Ribosomal protein L17
B2RS55	Ser-Thr kinase receptor-associated protein	-8	KRT15	Keratin 15	2	RPL19	Ribosomal protein L19
B2NR6	Zinc finger RNA binding protein	1	KRT16	Keratin 16	0	RPL23	Ribosomal protein L23
C14orf166	Chromosome 14 open reading frame 166	-3	KRT17	Keratin 17	3	RPL23A	Ribosomal protein L23a
C1orf68	Chromosome 1 open reading frame 68	2	KRT2	Keratin 2	8	RPL24	Ribosomal protein L24
C22orf28	Chromosome 22 open reading frame 28	-2	KRT33A	Keratin 33A	3	RPL26	Ribosomal protein L26
C3	Complement component 3	4	KRT34	Keratin 34	-2	RPL27A	Ribosomal protein L27a
CALML3	Calmodulin-like 3	-2	KRT5	Keratin 5	-3	RPL3	Ribosomal protein L3
CALML5	Calmodulin-like 5	-1	KRT6A	Keratin 6A	0	RPL31	Ribosomal protein L31
CANX	Calnexin	0	KRT6B	keratin 6B	-1	RPL4	Ribosomal protein L4
CAPRN1	Cell cycle associated protein 1	5	KRT6B	Keratin 6B	0	RPL6	Ribosomal protein L6
CKDN2A1F	CKDN2A interacting protein	-1	KRT6C	Keratin 6C	4	RPL7	Ribosomal protein L7
CLF1	Cofilin 1	-3	KRT6C	Keratin 6C	-2	RPL7A	Ribosomal protein L7a
CKMT1A	Creatine kinase, mitochondrial 1A	1	KRT78	Keratin 78	1	RPL8	Ribosomal protein L8
CLTC	Clathrin, heavy chain (Hc)	0	KRT79	Keratin 79	7	RPLP0	Ribosomal protein, large, P0
CSDA	Cold shock domain protein A	-1	KRT80	Keratin 80	-2	RPS10	ribosomal protein S10
CTSD	Cathepsin D	6	KRT83	keratin 83	13	RPS11	Ribosomal protein S11
DAP3	Death associated protein 3	0	KRT9	Keratin 9	4	RPS13	ribosomal protein S13
DCD	Dermcidin	1	KV303	Ig kappa chain V-III region NG9	2	RPS15A	Ribosomal protein S15a
DDX1	DEAD box polypeptide 1	1	LAMP1	Lysosomal-associated membrane protein 1	2	RPS16	Ribosomal protein S16
DDX17	DEAD box polypeptide 17	2	LARP1	La ribonucleoprotein domain family, member 1	-1	RPS17	Ribosomal protein S17
DDX28	DEAD box polypeptide 28	0	LARP3	Autoantigen La	0	RPS18	Ribosomal protein S18
DDX3X	DEAH box polypeptide 3, X-linked	0	LARP7	La ribonucleoprotein domain family, member 7	1	RPS19	Ribosomal protein S19
DDX5	DEAH box polypeptide 5	0	LCN2	Lipocalin 2	3	RPS2	Ribosomal protein S2
DDX6	DEAD box polypeptide 6	-3	LDHA	Lactate dehydrogenase A	1	RPS20	Ribosomal protein S20
DHX15	DEAH box polypeptide 15	6	LGALS7	Lectin, galactoside-binding, soluble, 7	1	RPS25	Ribosomal protein S25
DHX30	DEAH box polypeptide 30	-1	LMNA	lamin A/C	1	RPS28	Ribosomal protein S28
DHX36	DEAH box polypeptide 36	2	LRPPRC	Leucine-rich PPR-motif containing	-4	RPS3	Ribosomal protein S3
DHX9	DEAH box polypeptide 9	1	LTV1	LTV1 homolog	1	RPS3A	Ribosomal protein S3A
DIMT1L	DIM1 dimethyladenosine transferase 1-like	2	MARK2	MAP/microtubule affinity-regulating kinase 2	1	RPS4X	Ribosomal protein S4, X-linked
DJNC10	DnaJ (Hsp40) homolog, subfamily C, member 10	2	MATR3	Matrin 3	2	RPS5	Ribosomal protein S5
DSG1	Desmoglein 1	3	MOV10	Mov10, Moloney leukemia virus 10, homolog	4	RPS6	Ribosomal protein S6
DSP	Desmoplakin	2	MRP1	Mitochondrial ribosomal protein L1	0	RPS6KA1	Ribosomal protein S6 kinase, 90kDa, polypeptide 1
EEF1A1	Eukaryotic translation elongation factor 1 alpha 1	5	MRPL11	Mitochondrial ribosomal protein L11	1	RPS7	Ribosomal protein S7
EEF1G	Eukaryotic translation elongation factor 1 gamma	0	MRPL15	Mitochondrial ribosomal protein L15	-1	RPS8	Ribosomal protein S8
EEF2	Eukaryotic translation elongation factor 2	1	MRPL18	Mitochondrial ribosomal protein L18	0	RPS9	Ribosomal protein S9
EIF2B1	Eukaryotic translation initiation factor 2B, subu 1 alpha	-5	MRPL19	Mitochondrial ribosomal protein L19	-2	RPSA	Ribosomal protein SA
EIF283	eukaryotic translation initiation factor 2B, subu 3 gamma	1	MRP122	Mitochondrial ribosomal protein L22	0	S100A11	S100 calcium binding protein A11
EIF3H	Eukaryotic translation initiation factor 3, subu H	0	MRP124	Mitochondrial ribosomal protein L24	-1	S100A14	S100 calcium binding protein A14
EIF4A2	Eukaryotic translation initiation factor 4A2	0	MRPL3	Mitochondrial ribosomal protein L3	1	S100A16	S100 calcium binding protein A16
EIF4A3	Eukaryotic translation initiation factor 4A3	1	MRPL37	Mitochondrial ribosomal protein L37	-3	S100A2	S100 calcium binding protein A2
ELAVL1	ELAV-like 1 (Hu antigen R)	2	MRPL38	Mitochondrial ribosomal protein L38	0	S100A7	S100 calcium binding protein A7
ENO1	Enolase 1	-5	MRPL39	Mitochondrial ribosomal protein L39	-1	S100A8	S100 calcium binding protein A8
EPPK1	Epiplakin 1	-6	MRPL43	Mitochondrial ribosomal protein L43	2	S100A9	S100 calcium binding protein A9
EWSR1	Ewing sarcoma breakpoint region 1	0	MRPL44	Mitochondrial ribosomal protein L44	-1	SAE1	SUMO1 activating enzyme subunit 1
FAM120A	Family with sequence similarity 120A	7	MRPL45	Mitochondrial ribosomal protein L45	-1	SERPBP1	SERPINE1 mRNA binding protein 1
FAM120C	Family with sequence similarity 120C	-1	MRPL46	Mitochondrial ribosomal protein L46	-1	SERPINB3	Serpin peptidase inhibitor, clade B, member 3
FAM35A	Family with sequence similarity 35, member A	-1	MRPL48	Mitochondrial ribosomal protein L48	1	SERPINB5	Serpin peptidase inhibitor, clade B, member 5
FAM98B	Family with sequence similarity 98, member B	2	MRPS15	Mitochondrial ribosomal protein S15	0	SF3B2	Splicing factor 3b, subunit 2
FLG	Filaggrin	-5	MRPS18B	Mitochondrial ribosomal protein S18B	-1	SFN	14-3-3 protein sigma
FLG2	Filaggrin family member 2	2	MRPS2	Mitochondrial ribosomal protein S2	0	SFPQ	Splicing factor proline/ glutamine-rich
FLNA	Filamin A, alpha	-3	MRPS22	Mitochondrial ribosomal protein S22	-7	SKIV2L2	superkiller viralidic activity 2-like 2
FUS	Fused in sarcoma	-3	MRPS23	Mitochondrial ribosomal protein S23	-1	SLC25A10	39S ribosomal protein L12, mitochondrial carrier
G3BP1	GTPase activating protein binding protein 1	-1	MRPS27	mitochondrial ribosomal protein S27	-4	SDN1	Staphylococcal nuclease/tudor domain containing 1
G3BP2	GTPase activating protein binding prot 2	1	MRPS28	Mitochondrial ribosomal protein S28	0	SPRR2D	Small proline-rich protein 2D
GADD45G	Growth arrest/DNA-damage-inducible, ̳ interar prot 1	1	MRP30	Mitochondrial ribosomal protein S30	0	SRSF1	Serine/arginine-rich splicing factor 1
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	0	MRP531	Mitochondrial ribosomal protein S31	-2	SRSF10	Serine/arginine-rich splicing factor 10
GDE1	Glycerophosphodiester phosphodiesterase 1	-1	MRP535	Mitochondrial ribosomal protein S35	-1	SRSF3	Serine/arginine-rich splicing factor 3
GM2A	GM2 ganglioside activator	0	MRPS5	Mitochondrial ribosomal protein S5	-2	SRSF6	Serine/arginine-rich splicing factor 6
GNB2L1	G prot, beta polypeptide 2-like 1	5	MRP57	Mitochondrial ribosomal protein S7	-1	SRSF9	Serine/arginine-rich splicing factor 9
GSN	Gelsolin	3	MRPS9	Mitochondrial ribosomal protein S9	-1	STAU1	Staufen, RNA binding protein, homolog 1
GSTP1	Glutathione S-transferase pi 1	-5	MX1	myxovirus resist 1, interferon-inducible protein p78	-4	SYNCRIP	Heterogeneous nuclear ribonucleoprotein Q
GTF2I	General transcription factor II-I	4	MYH9	Myosin, heavy chain 9, non-muscle	5	TAGLN2	Transgelin 2
H1FX	H1 histone family, member X	-1	MYL12A	Myosin, light chain 12A, regulatory, non-sarcomeric	-2	TARDBP	TAR DNA-binding prot
H3F3A	H3 histone, family 3A	0	NAMPT	Pre-B-cell colony enhancing factor 1	-1	TF	Transferrin
HAL	Histidine ammonia-lyase	-2	NCCRP1	Non-specific cytotoxic cell receptor prot 1 homolog	-2	TFAM	Transcription factor A, mitochondrial
HIST1H1E	Histone cluster 1, H1e	-2	NCL	Nucleolin	2	TGM1	Transglutaminase 1
HIST1H2A	Histone cluster 1, H2ab	-1	NGRN	Neugrin, neurite outgrowth associated	2	TGM3	Transglutaminase 3
HNRNPA0	Heterogeneous nuclear ribonucleoprotein A0	0	NONO	Non-POU domain containing, octamer-binding	-4	THOC4	THO complex 4
HNRNPA2	Heterogeneous nuclear ribonucleoprotein A2/B1	2	UNUS5	NOP2/Sun domain family, member 5	2	TP11	Triosephosphate isomerase 1
HNRNPA3	Heterogeneous nuclear ribonucleoprotein A3	-1	NXF1	Nuclear RNA export factor 1	2	TRIM29	Tripartite motif containing 29
HNRNPA8	Heterogeneous nuclear ribonucleoprotein A/B	-2	PAHB	Prolyl 4-hydroxylase, beta polypeptide	-7	TRUB2	TruB pseudouridine (psi) synthase homolog 2
HNRNPC	Heterogeneous nuclear ribonucleoprotein C (C1/C2)	5	PABCP1	Poly(A) binding protein, cytoplasmic 1	-2	TUBA1B	Tubulin, alpha 1b
HNRNPD	Heterogeneous nuclear ribonucleoprotein D	1	PCBP2	Poly(rC) binding protein 2	-4	TUBA4A	Tubulin, alpha 4a
HNRNPF	Heterogeneous nuclear ribonucleoprotein F	-1	PFN1	Profilin 1	-1	TUBB	Tubulin, beta
HNRNPH1	Heterogeneous nuclear ribonucleoprotein H1 (H)	0	PGK1	Phosphoglycerate kinase 1	-5	TUBB2C	Tubulin, beta 2C
HNRNPH2	Heterogeneous nuclear ribonucleoprotein H2 (H')	0	PHB2	Prohibitin 2	2	TUBB4	Tubulin, beta 4
HNRNPH3	Heterogeneous nuclear ribonucleoprotein H3	0	PICALM	Phosphatidylinositol binding clathrin assembly protein	-4	TYMP	Thymidine phosphorylase
HNRNPK	Heterogeneous nuclear ribonucleoprotein K	1	PKM2	Pyruvate kinase, muscle	-3	UBA2	Ubiquitin-like modifier activating enzyme 2
HNRNPL	Heterogeneous nuclear ribonucleoprotein L	7	PKP1	Plakophilin 1	1	UPF1	UPF1 regulator of nonsense transcripts homolog
HNRNPM	Heterogeneous nuclear ribonucleoprotein M	5	PLOD1	Procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	2	VCP	Valosin containing protein
HNRNPR	Heterogeneous nuclear ribonucleoprotein R	3	PLOD1	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	-1	WSCR22	Williams Beuren syndrome chromosome region 22
HNRNPU	Heterogeneous nuclear ribonucleoprotein U	-3	PN01	Partner of NOB1 homolog	-2	WDR6	WD repeat domain 6
HNRNPUL	Heterogeneous nuclear ribonucleoprotein U-like 1	-1	PNP	Purine nucleoside phosphorylase	-1	WIBG	Within bgcn homolog
HNRNPUL	Heterogeneous nuclear ribonucleoprotein U-like 2	3	POF1B	Premature ovarian failure, 1B	-1	XRCC5	X-ray repair complex defective in Chinese hamster cells 5
HNRNPD	Heterogeneous nuclear ribonucleoprotein D-like	1	POLDIP3	DNA polymerase, delta interacting prot 3	1	XRCC6	X-ray repair complex defective in Chinese hamster cells 6
HNRNPD	Heterogeneous nuclear ribonucleoprotein D-like	1	PIPIA	Peptidylprolyl isomerase A	-2	XRND2	5'-3' exoribonuclease 2
HNRNPD	Heterogeneous nuclear ribonucleoprotein D-like	1	PPL	Periplakin	-2	YBX1	Y box binding protein 1
HSP90AB1	Heat shock protein 90kDa alpha, class B member 1	-6	PPP2R1A	Prot phosphatase 2, regulatory subunit A, alpha	-1	YTHDC2	YTH domain containing 2
HSPA1A	Heat shock 70kDa protein 1A	-3	PRDX1	Peroxiredoxin 1	3	YWHAE	14-3-3 epsilon
HSPA5	Heat shock 70kDa protein 5	-3	PRMT1	Protein arginine methyltransferase 1	-1	YWHAQ	Tyr 3-/Trp 5-monoxygenase activation prot, theta
HSPB1	Heat shock 70kDa protein 8 isoform 1	-3	PRPF19	PRP19/PSO4 pre-mRNA processing factor 19 homolog	1	YWHAZ	Tyr 3-/Trp 5-monoxygenase activation prot, zeta polypep
HSPD1	Heat shock 60kDa protein 1	-5	PRPF31	PRP31 pre-mRNA processing factor 31 homolog	0	ZC3H4V1	Zinc finger CCHC-type, antiviral 1
ICT1	Immature colon carcinoma transcript 1	1	PRSS3	Protease, serine, 3	0	ZNF326	Zinc finger protein 326
		0	PTBP1	Polypyrimidine tract binding protein 1	0		

Figure S1

A



B



C

GO annotation	Q-value	Genes in network	Genes in genome
<b>Translation-related</b>			
Translational elongation	2.30E-69	41	97
Ribosome	9.23E-59	40	150
Cytosolic ribosome	4.11E-67	39	88
Translational termination	4.11E-67	39	88
Structural constituent of ribosome	3.78E-43	29	97
Small ribosomal subunit	4.37E-33	21	55
Cytosolic small ribosomal subunit	5.26E-36	20	35
Cytosolic large ribosomal subunit	1.85E-29	19	51
Large ribosomal subunit	4.29E-27	19	65
Ribonucleoprotein complex biogenesis	3.11E-11	13	135
Cellular component biogenesis at cellular level	5.82E-11	13	142
Ribosome biogenesis	7.22E-14	12	63
Ribosomal small subunit biogenesis	4.15E-10	7	17
Regulation of translation	3.69E-03	6	106
Translational initiation	4.99E-03	5	66
Ribosomal large subunit biogenesis	6.36E-05	4	11
Cytoplasmic stress granule	5.37E-04	4	18
ATP-dependent RNA helicase activity	2.99E-02	3	20
<b>RNA processing</b>			
ncRNA processing	2.20E-11	12	100
ncRNA metabolic process	1.86E-08	12	177
RNA splicing	9.13E-07	12	250
rRNA processing	3.20E-13	11	51
rRNA metabolic process	9.45E-13	11	56
Posttranscriptional regulation of gene expression	1.79E-06	11	210
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	1.13E-05	10	196
Nuclear mRNA splicing, via spliceosome	1.13E-05	10	196
RNA splicing, via transesterification reactions	1.46E-05	10	202
mRNA processing	1.22E-04	10	256
RNA helicase activity	2.27E-08	7	28
Spliceosomal complex	4.25E-03	6	109
mRNA binding	5.98E-03	5	69
Catalytic step 2 spliceosome	1.19E-02	5	80
Nuclear body	7.21E-02	5	123
RNA-dependent ATPase activity	1.02E-03	4	21
Regulation of mRNA stability	1.71E-03	4	24
Regulation of RNA stability	1.99E-03	4	25
Ribonucleoprotein granule	2.28E-02	4	49
Alternative nuclear mRNA splicing, via spliceosome	1.88E-02	3	17
RNA stabilization	1.88E-02	3	17
Heterogeneous nuclear ribonucleoprotein complex	1.88E-02	3	17
mRNA stabilization	1.88E-02	3	17
<b>Protein complex</b>			
Cellular protein complex disassembly	3.91E-61	39	118
Protein complex disassembly	1.32E-60	39	122
Cellular macromolecular complex disassembly	2.63E-58	39	138
Macromolecular complex disassembly	8.69E-58	39	142
Cellular component disassembly at cellular level	3.28E-50	39	214
Cellular component disassembly	5.59E-50	39	217
Signalosome	8.78E-02	3	29
<b>Others</b>			
Cytosolic part	7.35E-61	40	134
Viral infectious cycle	5.37E-52	40	215
Viral reproductive process	2.86E-50	40	236
Endocrine pancreas development	3.28E-61	39	117
Pancreas development	1.69E-60	39	123
Endocrine system development	1.75E-57	39	145
Viral transcription	1.75E-57	39	145
Viral genome expression	1.75E-57	39	145
ATPase activity	1.06E-04	9	191
Intermediate filament	3.99E-07	7	41
Structural constituent of cytoskeleton	9.03E-06	7	64
Intermediate filament cytoskeleton	1.88E-05	7	72
Epidermis development	1.34E-03	7	137
Helicase activity	7.40E-06	7	62
ATPase activity, coupled	1.82E-02	6	145
Protein folding	4.59E-02	5	111
Response to unfolded protein	1.30E-02	4	41
Purine NTP-dependent helicase activity	1.38E-02	4	42
ATP-dependent helicase activity	1.38E-02	4	42
Response to topologically incorrect protein	1.88E-02	4	46
Cytoskeleton-dependent intracellular transport	9.59E-02	3	30
MHC class I protein binding	5.71E-03	3	11
Telomeric DNA binding	1.19E-02	3	14
MHC protein binding	2.58E-02	3	19
Chaperone binding	7.21E-02	3	27

**Figure S2**

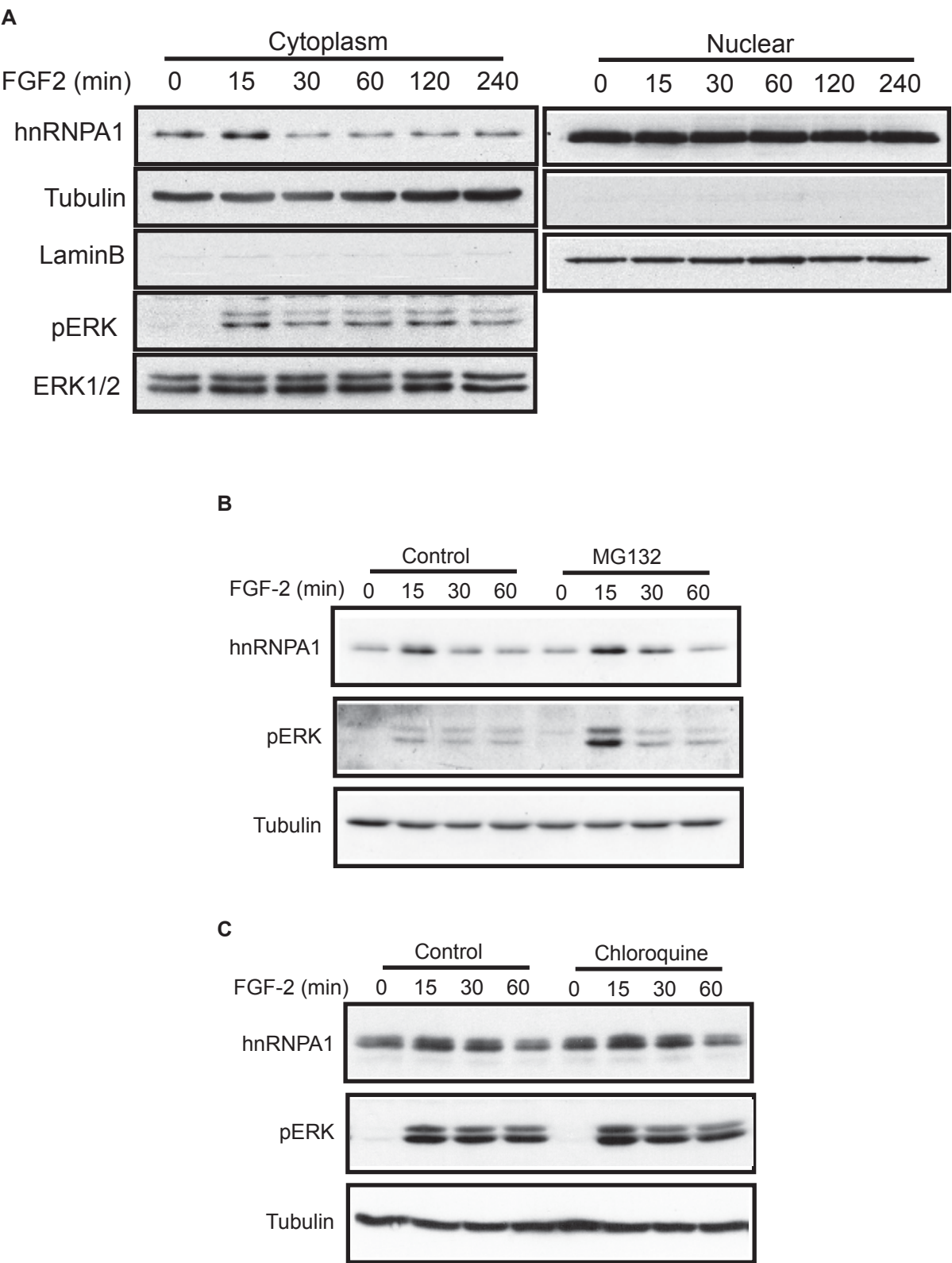


Figure S3

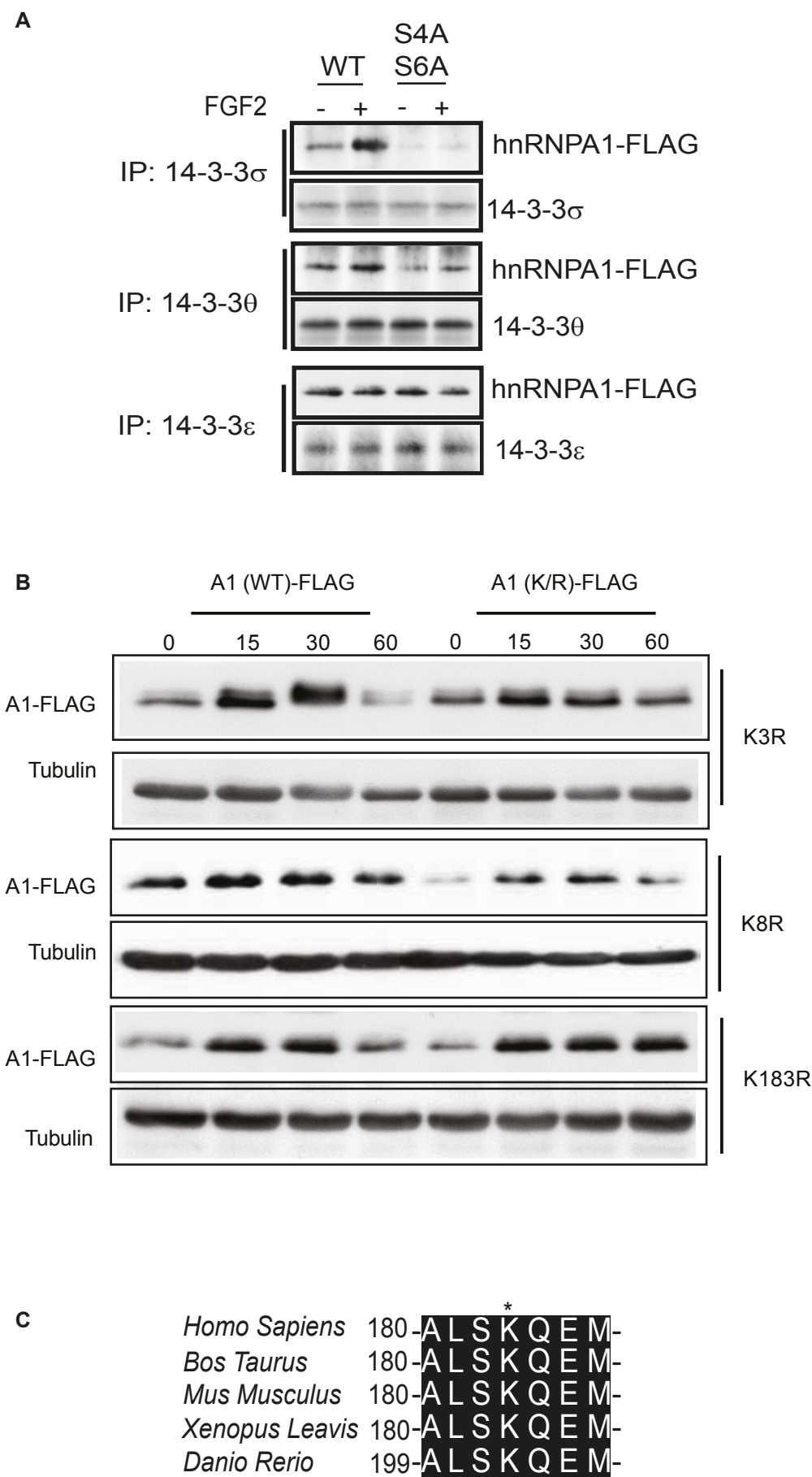


Figure S4

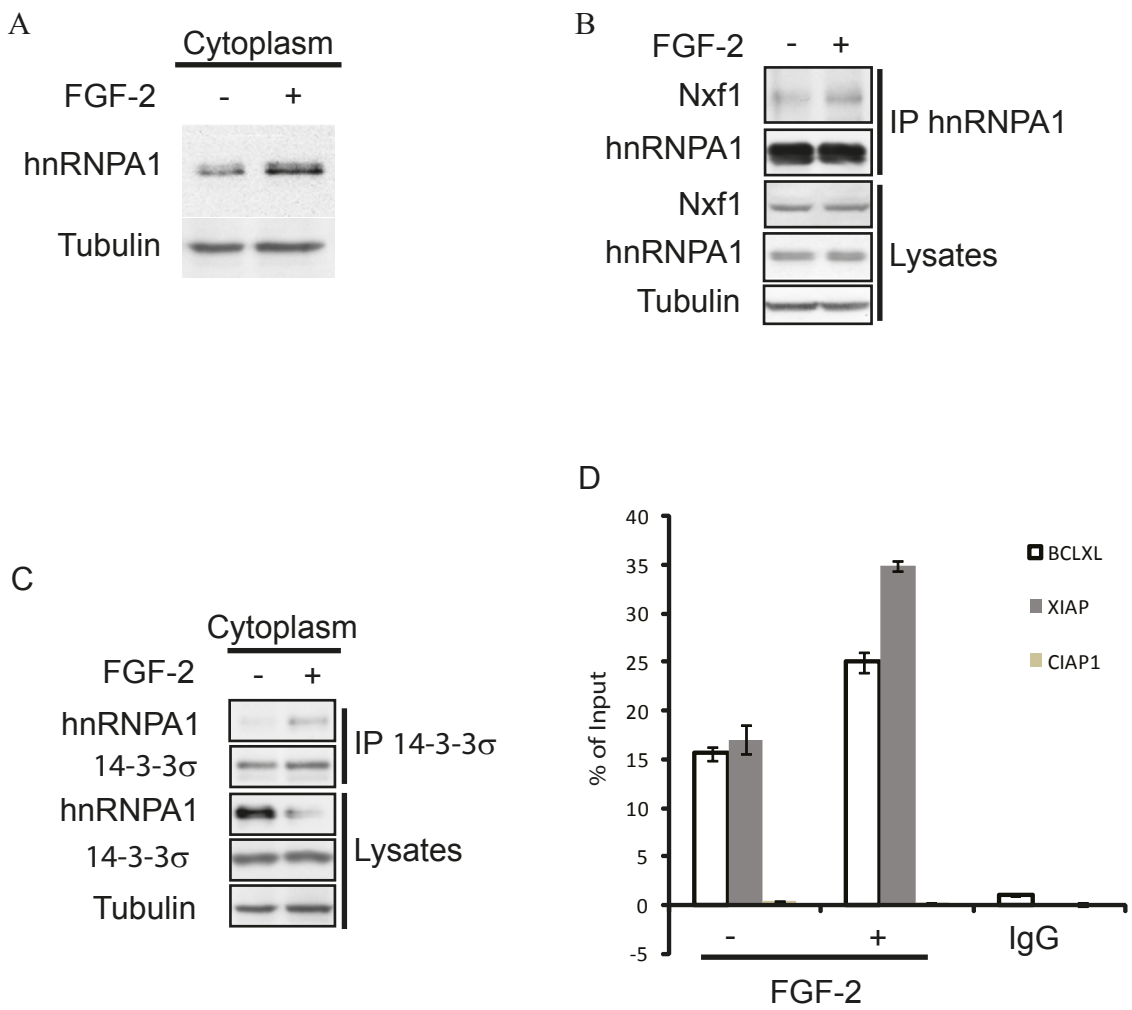




Figure S5

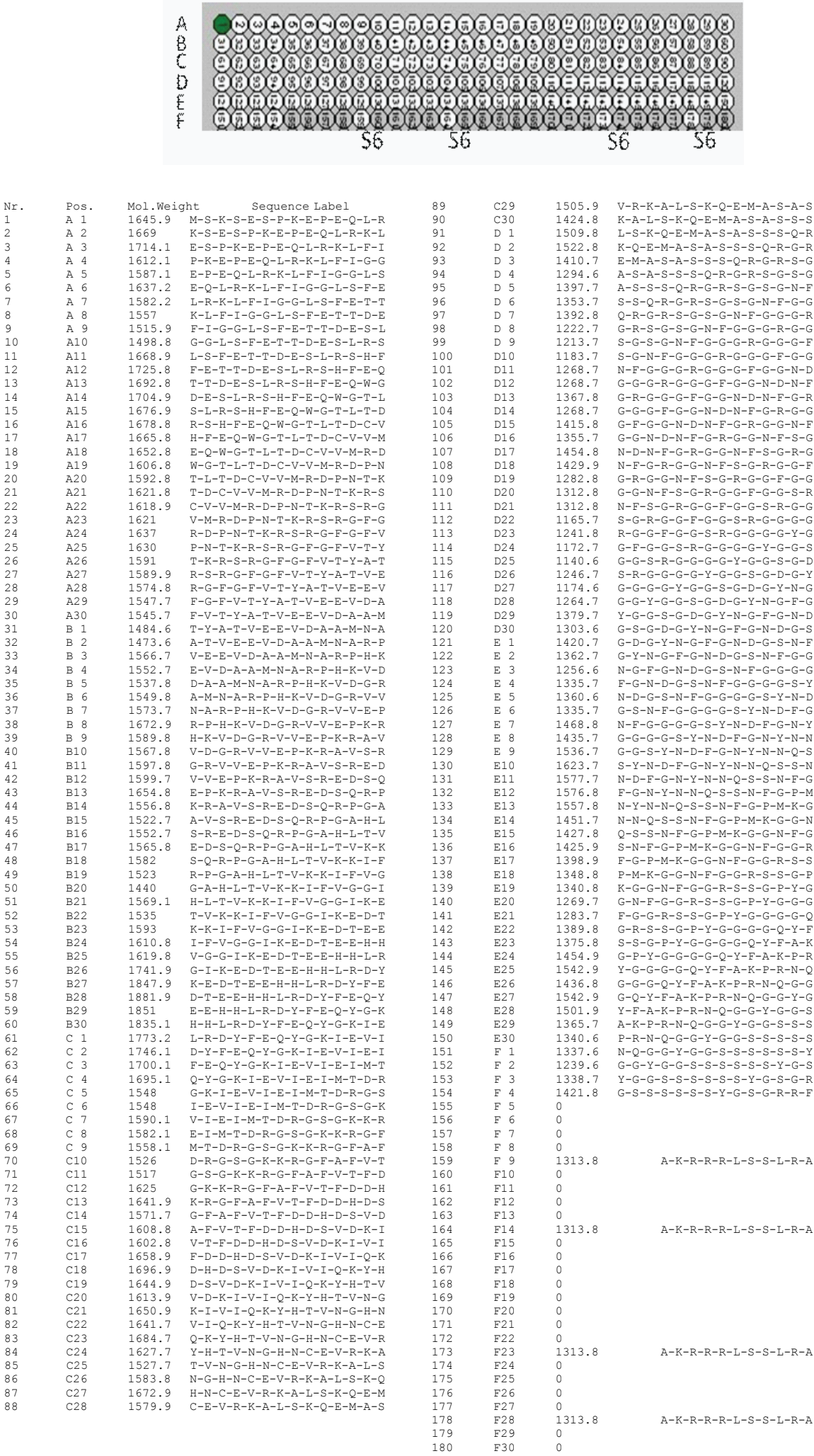
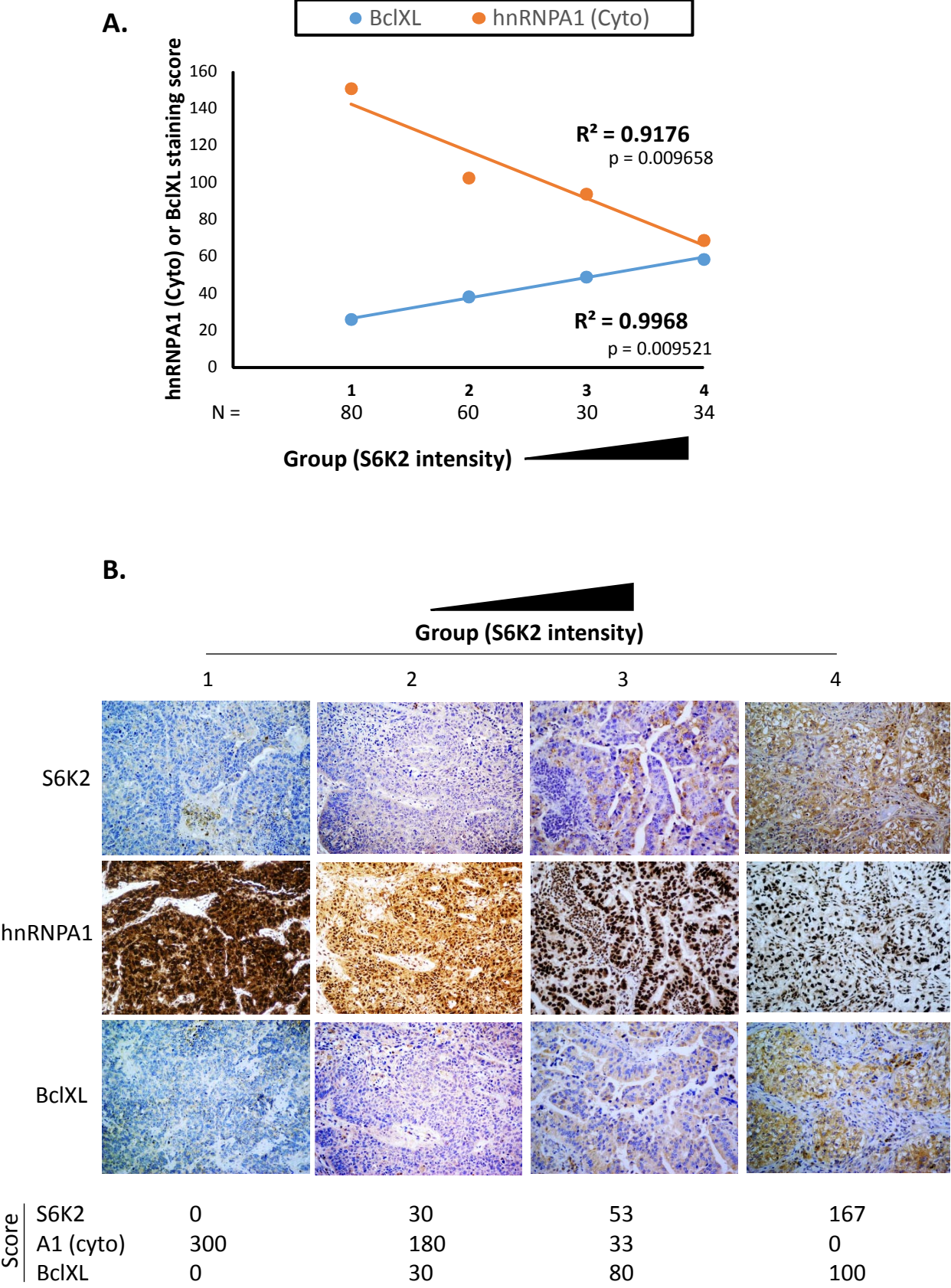


Figure S6





**Figure S7**

