

Figure legends for Supplemental data

Supplemental Figure 1. FUBP1 function in prostate cancer. **A**, Correlation between FUBP1 expression and disease progression in multiple cancers in the TCGA database. DFS, disease progression-free survival. **B**, Correlation of FUBP1 levels with biochemical recurrence in Chinese Prostate Cancer Genome and Epigenome Atlas (CPGEA). Log-rank test. **C**, Multivariate analysis of predictive factors for DFS of prostate cancer in the CPGEA dataset. HR, hazard ratios; 95% CI, 95% confidence interval. Cox proportional hazards regression. **D** and **E**, Expression of FUBP1 in prostatic tumor tissues and adjacent normal tissues. 2-tailed, unpaired student's t test. **F**, Enriched pathways based on altered gene expression in FUBP1 knocked-down LNCaP cells. **G**, Genes showing alternative splicing after FUBP1 knockdown in LNCaP cells. 2-tailed, unpaired student's t test. **H**, Enriched pathways based on alternative spliced genes regulated by FUBP1 in LNCaP cells. **I** and **J**, Effect of SLC7A11 and PDK1 on cell growth in prostate cancer cells. Scr, scrambled control shRNA. One-way ANOVA with Dunnett's multiple-comparison test. **K**, FUBP1 knockdown efficiency in RWPE1. **L**, Effect of FUBP1 on cell growth in various cell lines. * $P < 0.05$; ** $P < 0.01$.

Supplemental Figure 2. FUBP1 methylation in HEK 293T cells. **A**, Potential FUBP1 methylation sites detected by mass spectrometry. **B** and **C**, Methylation status of FUBP1 and related mutants in HEK 293T cells. AdOx, adenosine dialdehyde; sDMA, symmetric dimethylarginine antibodies; FUBP1^{3K}, FUBP1 mutant with arginine-to-lysine mutated at R359/361/363. **D**, Dot-blot experiments to detect the specificity of meFUBP1, a site-specific antibody for methylated FUBP1 at R359/R361/R363. A

synthesized peptide (FUBP1 353-367 amino acids) with R359/R361/R363 methylation was used for dot-blot assay. **E**, Peptide competition assay to validate the specificity of meFUBP1. Synthesized methylated or unmethylated FUBP1 peptides were used for the competition. **F** and **G**, Specificity of meFUBP1 to detect intracellular FUBP1 methylation.

Supplemental Figure 3. Enrichment of His-FUBP1 and Flag-PRMT5 for in vitro assay.

A, Purification of His-FUBP1. **B**, Enrichment of PRMT5 and its mutants from HEK 293T cells.

Supplemental Figure 4. Effect of various demethylases on FUBP1 methylation in

LNCaP cells. Mixed siRNAs targeting different demethylases were transiently expressed in LNCaP cells, and endogenous FUBP1 methylation was detected. Scr, scrambled control siRNA.

Supplemental Figure 5. Generation of genetic FUBP1^{3K} knock-in mice. A, Schema for

FUBP1^{3K} knock-in. **B**, Validation of FUBP1^{3K} knock-in mice. **C**, Representative H&E staining in *Fubp1*^{WT} and *Fubp1*^{3K} mice with different genetic backgrounds at age 25 weeks. Scale bars, 100 μ m (upper) and 50 μ m (lower), respectively. **D**, Expression of Slc7a11 and Pdk1 in different tissues of TRAMP⁺ mice. Scale bars, 50 μ m.

Supplemental Figure 6. BRD4 regulates PRMT5-mediated FUBP1 methylation in VCaP

cells. A, FUBP1 methylation after I-BET151 treatment in VCaP cells. I-BET151, a BRD4 inhibitor. **B**, Effect of I-BET151 on gene expression in VCaP cells. I-BET151, 2 μ M. **C**, Enrichment of BRD4 on different gene promoters after I-BET151 treatment. **D** and **E**, Effect of BRD4 on FUBP1 methylation and its function in prostate cancer cell lines. **F**,

BRD4 enrichment on different gene promoters in VCaP cells. ** $P < 0.01$. n.s., not significant. One-way ANOVA with Dunnett's (T3) multiple-comparison test.

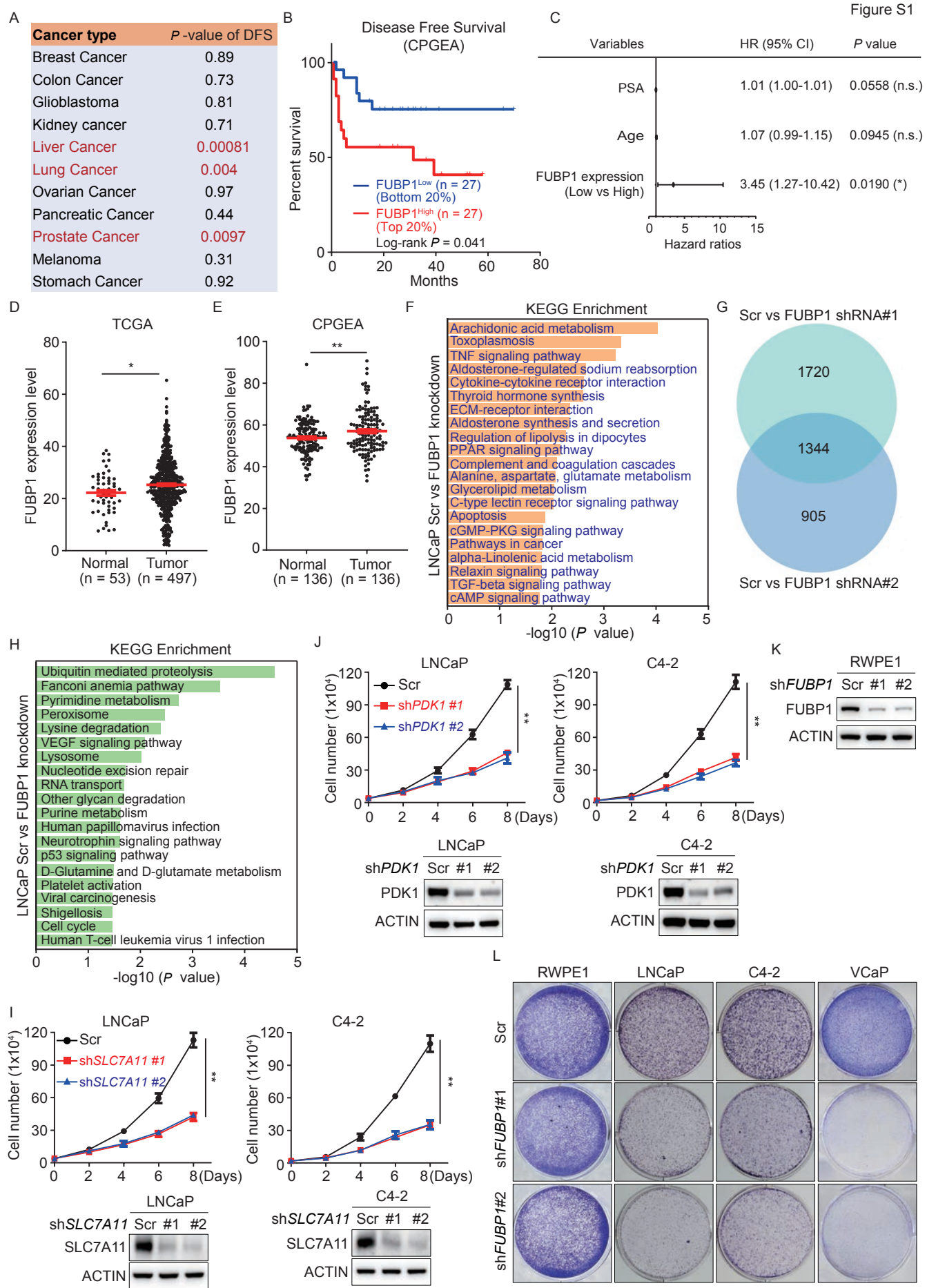
Supplemental Figure 7. Tissue microarray IHC results for meFUBP1 specificity. **A** and **B**, Specificity of meFUBP1 for IHC. LNCaP cell lysates (**A**) and LAPC4-derived xenograft (**B**) were used. Scale bar, 200 μm (upper) and 50 μm (lower), respectively. **C**, representative results of staining scores for different antibodies. Scale bar, 200 μm (left) and 100 μm (right) for each group, respectively.

Supplemental Figure 8. Schema for the FUBP1 truncations. N, N terminal; KH, K-homology motif; C, C terminal; NLS, nuclear localization sequence.

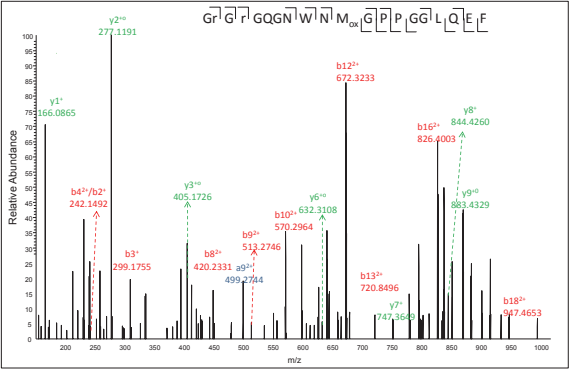
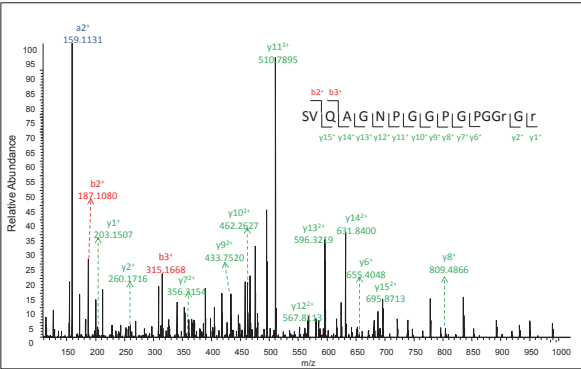
Supplemental Figure 9. Characterization of nanocomplexes. **A**, Synthetic route for branched poly (β -amino ester) (BPAE). BPAE was synthesized from diacrylate-containing monomer (**A2**), trimethylolpropane triacrylate (**B3**), and 4-amino-1-butanol (**C2**) at a molar ratio of 2:1:3.2. **B**, Size of BPAE/peptide NCs (BPAE/peptide = 2/1, w/w). **C**, Effect of PUBLISH and FUBP1 inhibitor on cell growth. FUBP1-IN-1, an FUBP1 inhibitor. One-way ANOVA with Turkey multiple-comparison test. **D** and **E**, Size and zeta potential of HA/BPAE/peptide NCs at various HA/BPAE weight ratios ($n = 3$). **F**, Mean fluorescence intensity (MFI) of LNCaP cells as determined by flow cytometry following 8-hour incubation with HA/BPAE/FITC-peptide NCs (10 μg FITC-peptide/mL) at various HA/BPAE weight ratios ($n = 3$). Results are shown as mean $\pm$ SD. ** $P < 0.01$. n.s., not significant.

Supplemental Table 1. IP-MS results for FUBP1 interacting proteins.

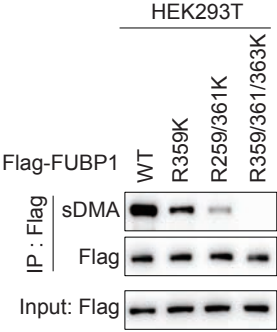
Supplemental Table 2. Sequence information for primers, siRNAs, and shRNAs.



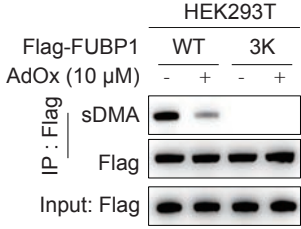
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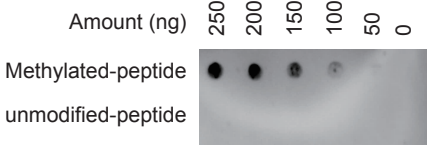
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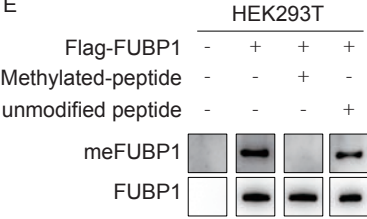
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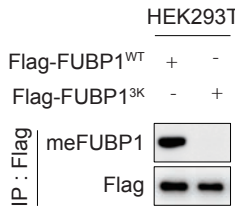
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E



F



G

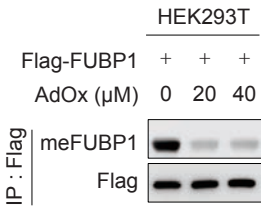


Figure S3

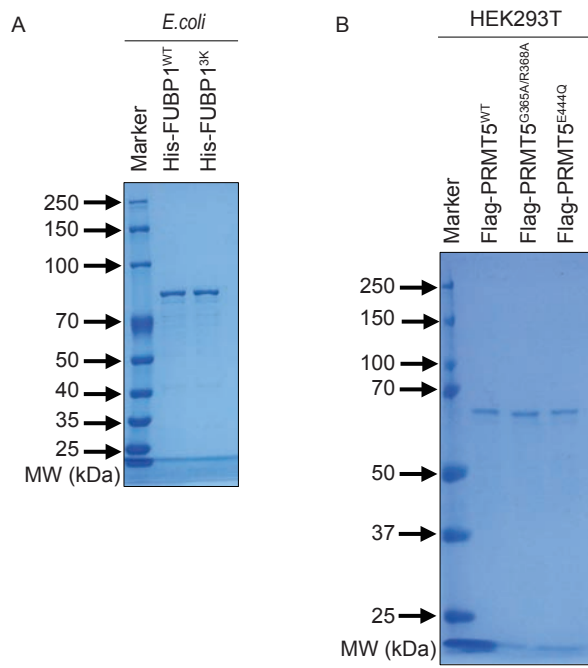
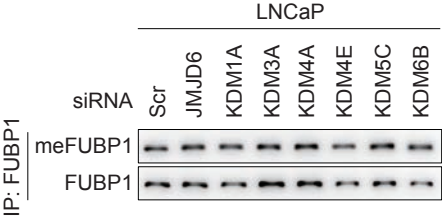
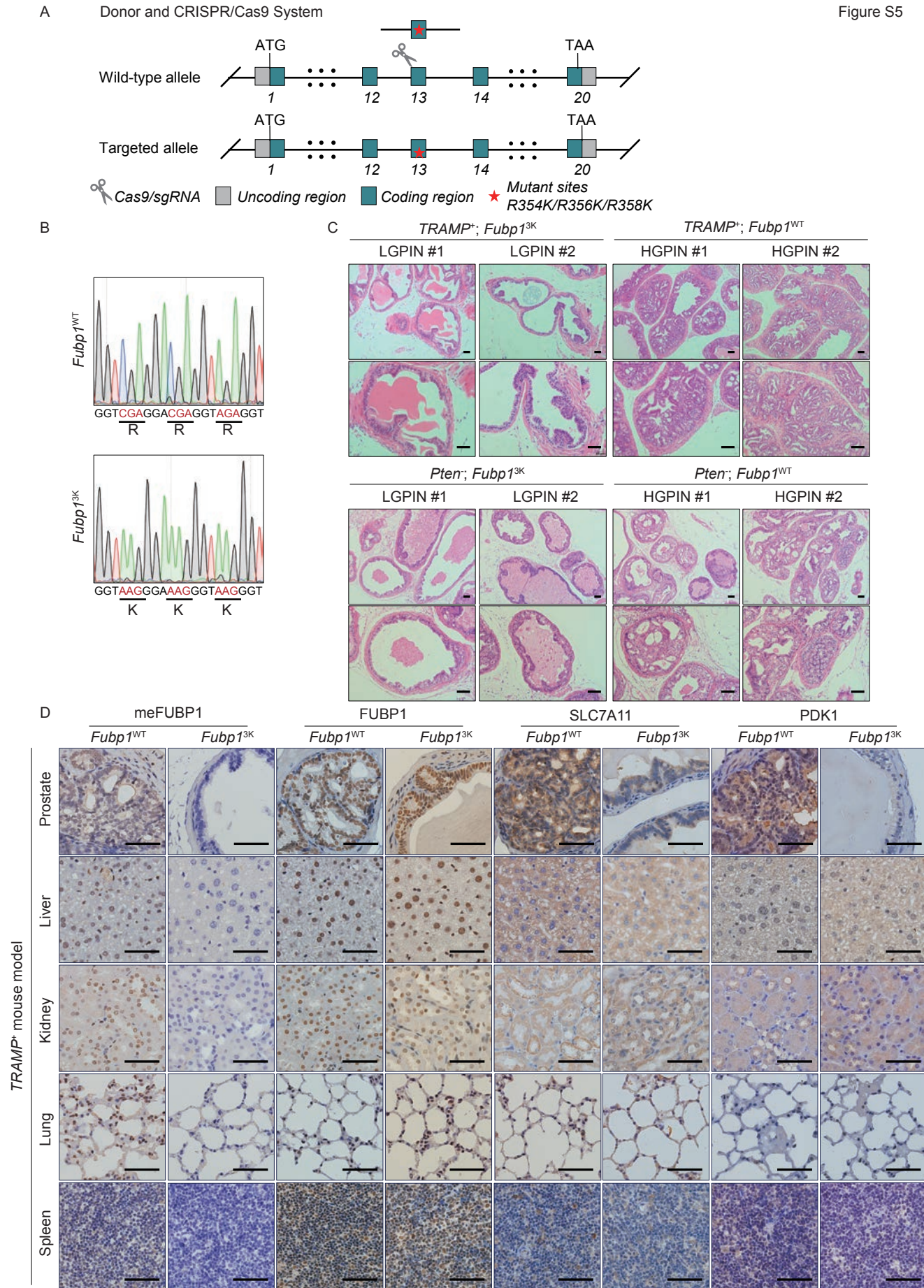
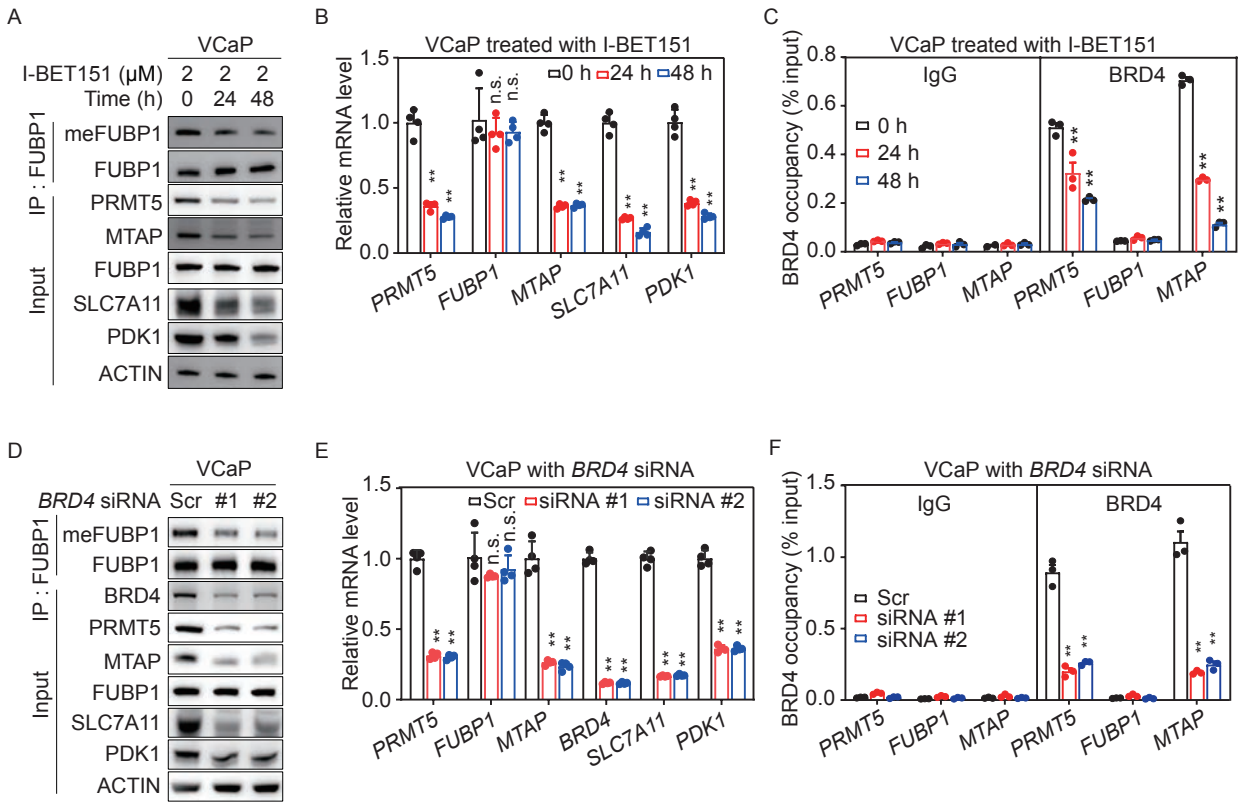


Figure S4







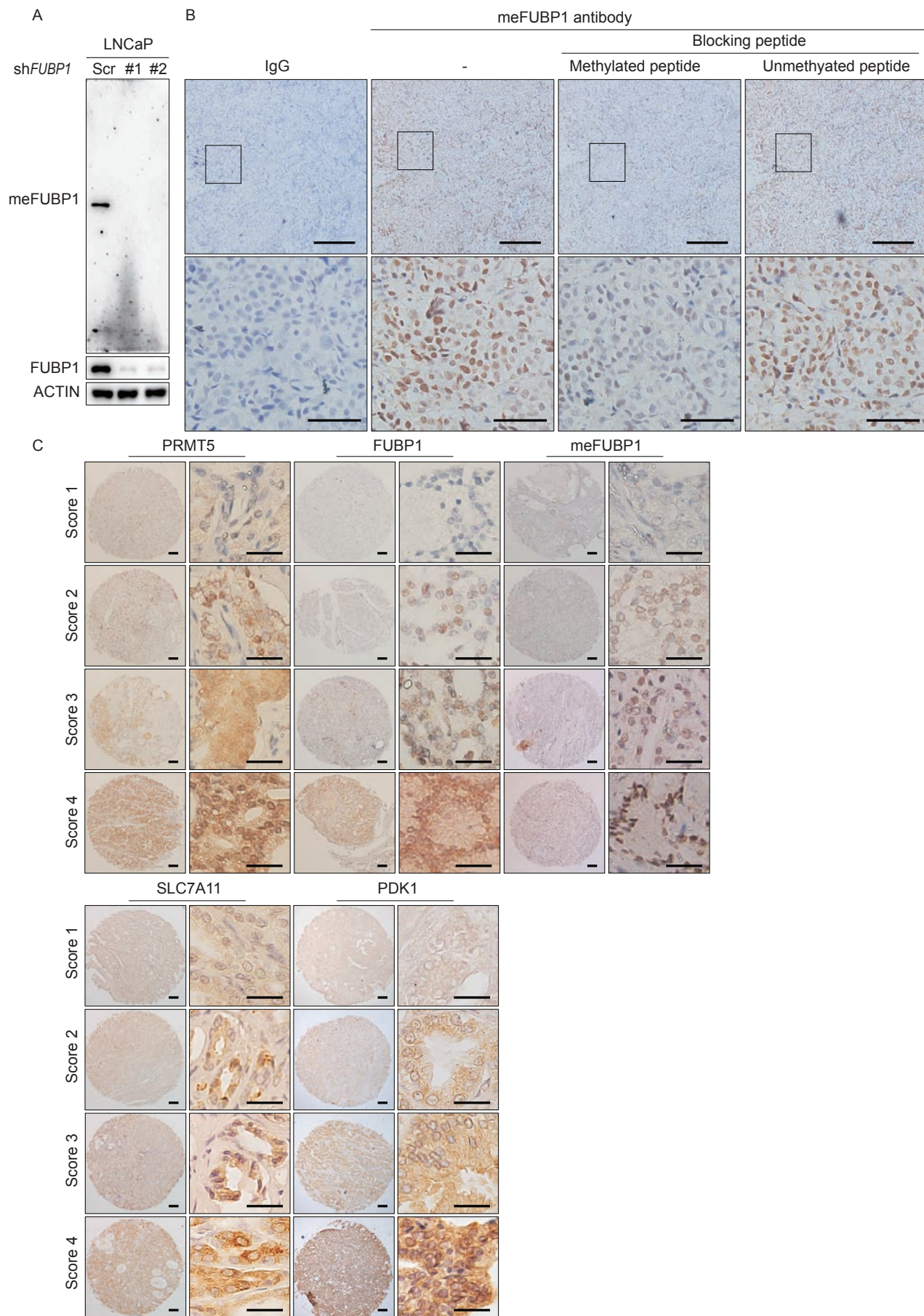
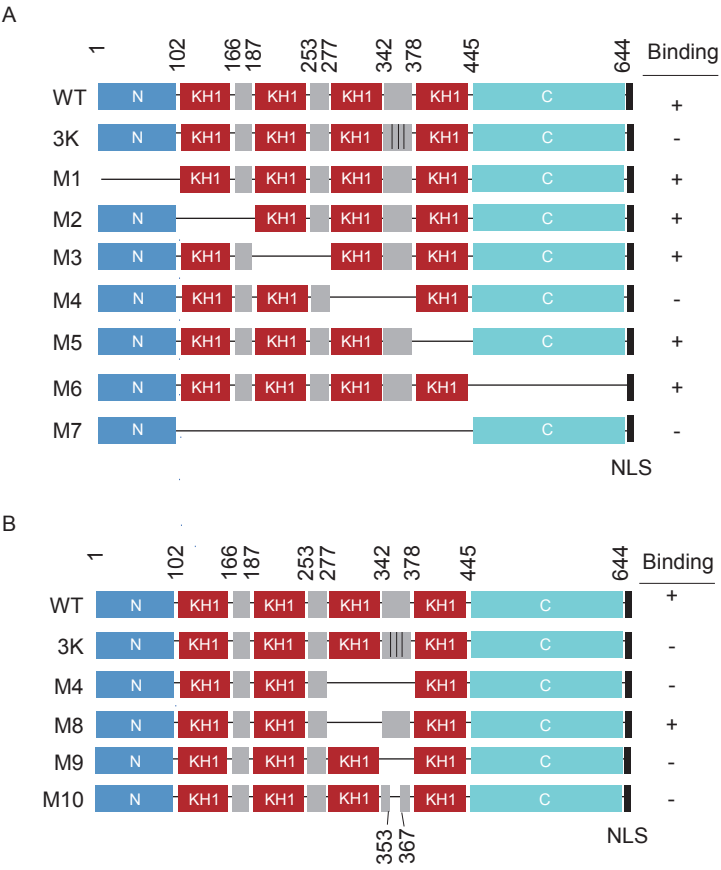
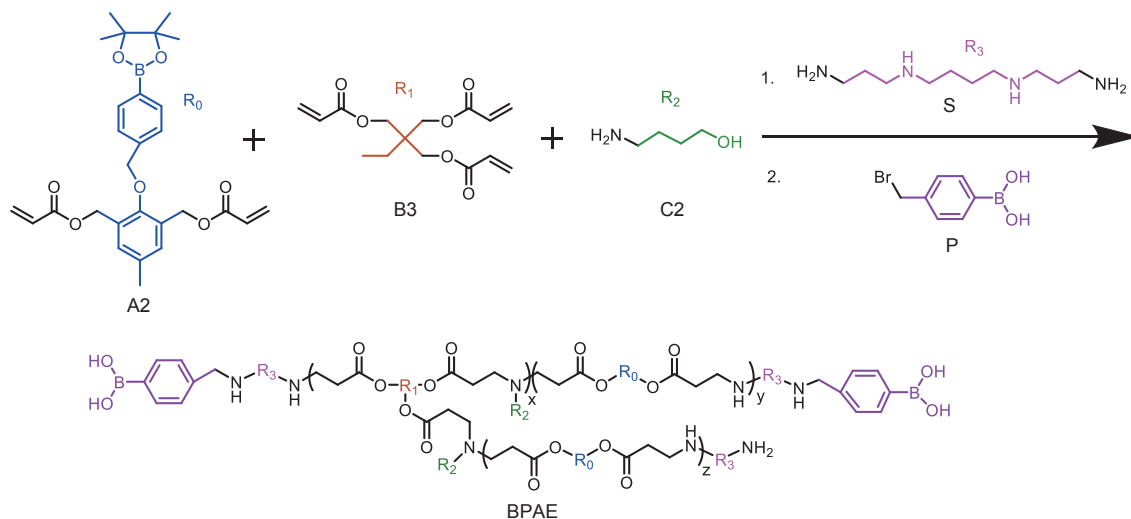


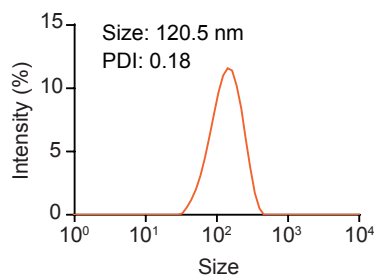
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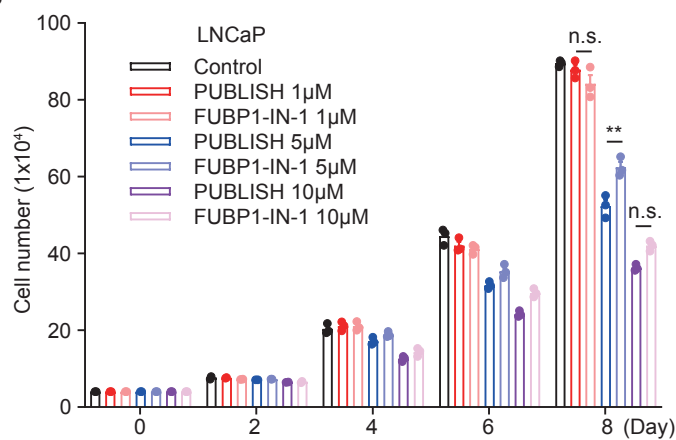
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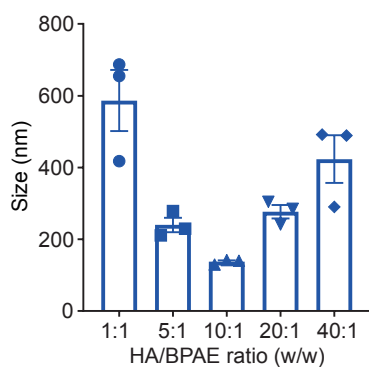
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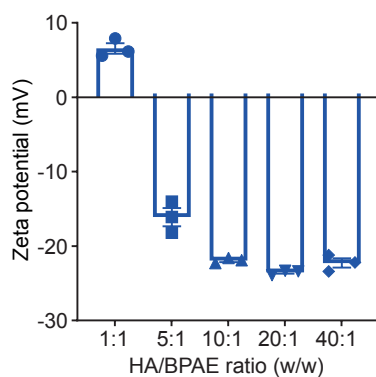
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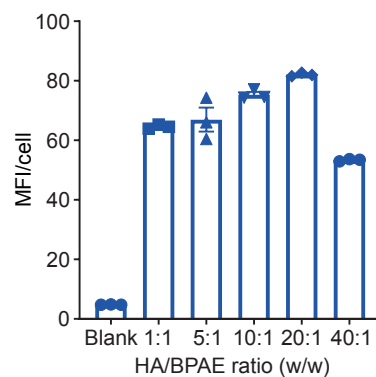
D



E



F



Supplemental Table 1. IP-MS results for FUBP1 interacting proteins.

Accession		-10lgP	#Unique	Description
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Q6PKG0	LARP1_HUMAN	329.24	68	La-related protein 1 OS=Homo sapiens OX=9606 GN=LARP1 PE=1 SV=2
Q92900	RENT1_HUMAN	327.66	56	Regulator of nonsense transcripts 1 OS=Homo sapiens OX=9606 GN=UPF1 PE=1 SV=2
P11940	PABP1_HUMAN	323.2	49	Polyadenylate-binding protein 1 OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=2
Q08211	DHX9_HUMAN	322.04	59	ATP-dependent RNA helicase A OS=Homo sapiens OX=9606 GN=DHX9 PE=1 SV=4
P52732	KIF11_HUMAN	320.21	67	Kinesin-like protein KIF11 OS=Homo sapiens OX=9606 GN=KIF11 PE=1 SV=2
Q13310	PABP4_HUMAN	314.84	32	Polyadenylate-binding protein 4 OS=Homo sapiens OX=9606 GN=PABPC4 PE=1 SV=1
P21333	FLNA_HUMAN	301.81	37	Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=4
Q9HCE1	MOV10_HUMAN	296.09	51	Helicase MOV-10 OS=Homo sapiens OX=9606 GN=MOV10 PE=1 SV=2
P09651	ROA1_HUMAN	296.05	14	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens OX=9606 GN=HNRNPA1 PE=1 SV=5
P22626	ROA2_HUMAN	295.12	33	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens OX=9606 GN=HNRNPA2B1 PE=1 SV=2
Q12906	ILF3_HUMAN	290.74	39	Interleukin enhancer-binding factor 3 OS=Homo sapiens OX=9606 GN=ILF3 PE=1 SV=3
Q00839	HNRPU_HUMAN	290.59	58	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=6
O60506	HNRPQ_HUMAN	284.29	24	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens OX=9606 GN=SYNCRIP PE=1 SV=2
O14744	ANM5_HUMAN	283.29	39	Protein arginine N-methyltransferase 5 OS=Homo sapiens OX=9606 GN=PRMT5 PE=1 SV=4
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PODMV9	HS71B_HUMAN	279.35	15	Heat shock 70 kDa protein 1B OS=Homo sapiens OX=9606 GN=HSPA1B PE=1 SV=1
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P51991	ROA3_HUMAN	275.12	26	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens OX=9606 GN=HNRNPA3 PE=1 SV=2
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P19338	NUCL_HUMAN	264.97	25	Nucleolin OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=3
P11021	BIP_HUMAN	263.25	23	Endoplasmic reticulum chaperone BiP OS=Homo sapiens OX=9606 GN=HSPA5 PE=1 SV=2

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Q10570	CPSF1_HUMAN	218.04	21	Cleavage and polyadenylation specificity factor subunit 1 OS=Homo sapiens OX=9606 GN=CPSF1 PE=1 SV=2
P26368	U2AF2_HUMAN	217.83	15	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens OX=9606 GN=U2AF2 PE=1 SV=4
P35527	K1C9_HUMAN	216.9	14	Keratin type I cytoskeletal 9 OS=Homo sapiens OX=9606 GN=KRT9 PE=1 SV=3
P15880	RS2_HUMAN	215.33	20	40S ribosomal protein S2 OS=Homo sapiens OX=9606 GN=RPS2 PE=1 SV=2
O15523	DDX3Y_HUMAN	214.2	1	ATP-dependent RNA helicase DDX3Y OS=Homo sapiens OX=9606 GN=DDX3Y PE=1 SV=2
P52597	HNRPF_HUMAN	213.93	14	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens OX=9606 GN=HNRNPF PE=1 SV=3
P55795	HNRH2_HUMAN	213.84	7	Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens OX=9606 GN=HNRNPH2 PE=1 SV=1
Q96I51	RCC1L_HUMAN	213.66	16	RCC1-like G exchanging factor-like protein OS=Homo sapiens OX=9606 GN=RCC1L PE=1 SV=2
Q9Y2Z4	SYYM_HUMAN	213.13	17	Tyrosine--tRNA ligase mitochondrial OS=Homo sapiens OX=9606 GN=YARS2 PE=1 SV=2
P31942	HNRH3_HUMAN	212.59	13	Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens OX=9606 GN=HNRNPH3 PE=1 SV=2
P23284	PPIB_HUMAN	212.52	17	Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens OX=9606 GN=PPIB PE=1 SV=2
Q9BQE3	TBA1C_HUMAN	212.5	1	Tubulin alpha-1C chain OS=Homo sapiens OX=9606 GN=TUBA1C PE=1 SV=1
P35908	K22E_HUMAN	211.48	8	Keratin type II cytoskeletal 2 epidermal OS=Homo sapiens OX=9606 GN=KRT2 PE=1 SV=2

P38919	IF4A3_HUMAN	209.34	14	Eukaryotic initiation factor 4A-III OS=Homo sapiens OX=9606 GN=EIF4A3 PE=1 SV=4
Q9NXV2	KCTD5_HUMAN	208.43	10	BTB/POZ domain-containing protein KCTD5 OS=Homo sapiens OX=9606 GN=KCTD5 PE=1 SV=1
P07910	HNRPC_HUMAN	207.84	19	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=4
Q96SI9	STRBP_HUMAN	207.48	15	Spermatid perinuclear RNA-binding protein OS=Homo sapiens OX=9606 GN=STRBP PE=1 SV=1
Q7Z417	NUFP2_HUMAN	207.39	13	Nuclear fragile X mental retardation-interacting protein 2 OS=Homo sapiens OX=9606 GN=NUFIP2 PE=1 SV=1
Q8WWM7	ATX2L_HUMAN	207.1	18	Ataxin-2-like protein OS=Homo sapiens OX=9606 GN=ATXN2L PE=1 SV=2
Q9BXP5	SRRT_HUMAN	206.46	25	Serrate RNA effector molecule homolog OS=Homo sapiens OX=9606 GN=SRRT PE=1 SV=1
Q13151	ROA0_HUMAN	205.82	10	Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens OX=9606 GN=HNRNPA0 PE=1 SV=1
Q15029	U5S1_HUMAN	202.92	14	116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens OX=9606 GN=EFTUD2 PE=1 SV=1
P39023	RL3_HUMAN	202.77	16	60S ribosomal protein L3 OS=Homo sapiens OX=9606 GN=RPL3 PE=1 SV=2
Q14498	RBM39_HUMAN	201.68	14	RNA-binding protein 39 OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=2
Q96I24	FUBP3_HUMAN	201.23	6	Far upstream element-binding protein 3 OS=Homo sapiens OX=9606 GN=FUBP3 PE=1 SV=2
Q9UN86	G3BP2_HUMAN	199.4	12	Ras GTPase-activating protein-binding protein 2 OS=Homo sapiens OX=9606 GN=G3BP2 PE=1 SV=2
Q9Y2W1	TR150_HUMAN	199.17	12	Thyroid hormone receptor-associated protein 3 OS=Homo sapiens OX=9606 GN=THRAP3 PE=1 SV=2
P62241	RS8_HUMAN	198.74	11	40S ribosomal protein S8 OS=Homo sapiens OX=9606 GN=RPS8 PE=1 SV=2
Q96EP5	DAZP1_HUMAN	198.68	10	DAZ-associated protein 1 OS=Homo sapiens OX=9606 GN=DAZAP1 PE=1 SV=1
Q14681	KCTD2_HUMAN	198.16	6	BTB/POZ domain-containing protein KCTD2 OS=Homo sapiens OX=9606 GN=KCTD2 PE=1 SV=3
P63244	RACK1_HUMAN	196.01	10	Receptor of activated protein C kinase 1 OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=3
Q9NYK5	RM39_HUMAN	195.91	15	39S ribosomal protein L39 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL39 PE=1 SV=3
Q14152	EIF3A_HUMAN	195.53	17	Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens OX=9606 GN=EIF3A PE=1 SV=1
P62081	RS7_HUMAN	195.38	12	40S ribosomal protein S7 OS=Homo sapiens OX=9606 GN=RPS7 PE=1 SV=1
Q9H9J2	RM44_HUMAN	195.24	9	39S ribosomal protein L44 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL44 PE=1 SV=1
Q7Z2W4	ZCCHV_HUMAN	195.18	9	Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens OX=9606 GN=ZC3HAV1 PE=1 SV=3
P08708	RS17_HUMAN	194.84	11	40S ribosomal protein S17 OS=Homo sapiens OX=9606 GN=RPS17 PE=1 SV=2
Q96E29	MTEF3_HUMAN	193.1	14	Transcription termination factor 3 mitochondrial OS=Homo sapiens OX=9606 GN=MTERF3 PE=1 SV=2
Q9P015	RM15_HUMAN	192.01	13	39S ribosomal protein L15 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL15 PE=1 SV=1
P68133	ACTS_HUMAN	191.7	1	Actin alpha skeletal muscle OS=Homo sapiens OX=9606 GN=ACTA1 PE=1 SV=1
P68032	ACTC_HUMAN	191.7	1	Actin alpha cardiac muscle 1 OS=Homo sapiens OX=9606 GN=ACTC1 PE=1 SV=1
Q99700	ATX2_HUMAN	190.96	10	Ataxin-2 OS=Homo sapiens OX=9606 GN=ATXN2 PE=1 SV=2
P08621	RU17_HUMAN	190.32	13	U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens OX=9606 GN=SNRNP70 PE=1 SV=2
P17066	HSP76_HUMAN	190.31	0	Heat shock 70 kDa protein 6 OS=Homo sapiens OX=9606 GN=HSPA6 PE=1 SV=2
Q9NUL3	STAU2_HUMAN	190.29	12	Double-stranded RNA-binding protein Staufen homolog 2 OS=Homo sapiens OX=9606 GN=STAU2 PE=1 SV=2
P52292	IMA1_HUMAN	189.85	9	Importin subunit alpha-1 OS=Homo sapiens OX=9606 GN=KPNA2 PE=1 SV=1
O95793	STAU1_HUMAN	189.83	12	Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens OX=9606 GN=STAU1 PE=1 SV=2
P05455	LA_HUMAN	189	14	Lupus La protein OS=Homo sapiens OX=9606 GN=SSB PE=1 SV=2

P62263	RS14_HUMAN	188.9	10	40S ribosomal protein S14 OS=Homo sapiens OX=9606 GN=RPS14 PE=1 SV=3
P39019	RS19_HUMAN	188.52	12	40S ribosomal protein S19 OS=Homo sapiens OX=9606 GN=RPS19 PE=1 SV=2
P62753	RS6_HUMAN	188.5	11	40S ribosomal protein S6 OS=Homo sapiens OX=9606 GN=RPS6 PE=1 SV=1
P08865	RSSA_HUMAN	188.42	8	40S ribosomal protein SA OS=Homo sapiens OX=9606 GN=RPSA PE=1 SV=4
P62995	TRA2B_HUMAN	187.21	9	Transformer-2 protein homolog beta OS=Homo sapiens OX=9606 GN=TRA2B PE=1 SV=1
P36578	RL4_HUMAN	187.03	15	60S ribosomal protein L4 OS=Homo sapiens OX=9606 GN=RPL4 PE=1 SV=5
P82650	RT22_HUMAN	186.85	13	28S ribosomal protein S22 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS22 PE=1 SV=1
P05388	RLA0_HUMAN	186.73	8	60S acidic ribosomal protein P0 OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1
O95232	LC7L3_HUMAN	186.67	10	Luc7-like protein 3 OS=Homo sapiens OX=9606 GN=LUC7L3 PE=1 SV=2
Q13435	SF3B2_HUMAN	186.16	15	Splicing factor 3B subunit 2 OS=Homo sapiens OX=9606 GN=SF3B2 PE=1 SV=2
Q6UN15	FIP1_HUMAN	185.73	9	Pre-mRNA 3'-end-processing factor FIP1 OS=Homo sapiens OX=9606 GN=FIP1L1 PE=1 SV=1
P49406	RM19_HUMAN	185.12	14	39S ribosomal protein L19 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL19 PE=1 SV=2
Q13509	TBB3_HUMAN	184.4	0	Tubulin beta-3 chain OS=Homo sapiens OX=9606 GN=TUBB3 PE=1 SV=2
Q12926	ELAV2_HUMAN	184.18	6	ELAV-like protein 2 OS=Homo sapiens OX=9606 GN=ELAVL2 PE=1 SV=2
Q9UKV3	ACINU_HUMAN	184.17	9	Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens OX=9606 GN=ACIN1 PE=1 SV=2
P25398	RS12_HUMAN	183.9	11	40S ribosomal protein S12 OS=Homo sapiens OX=9606 GN=RPS12 PE=1 SV=3
Q99613	EIF3C_HUMAN	180.86	13	Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens OX=9606 GN=EIF3C PE=1 SV=1
Q92945	FUBP2_HUMAN	179.45	4	Far upstream element-binding protein 2 OS=Homo sapiens OX=9606 GN=KHSRP PE=1 SV=4
Q13283	G3BP1_HUMAN	179.35	9	Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens OX=9606 GN=G3BP1 PE=1 SV=1
Q99729	ROAA_HUMAN	179.14	9	Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens OX=9606 GN=HNRNPAB PE=1 SV=2
Q9COJ8	WDR33_HUMAN	178.99	15	pre-mRNA 3' end processing protein WDR33 OS=Homo sapiens OX=9606 GN=WDR33 PE=1 SV=2
Q9Y262	EIF3L_HUMAN	178.75	10	Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens OX=9606 GN=EIF3L PE=1 SV=1
Q9P2I0	CPSF2_HUMAN	177.93	10	Cleavage and polyadenylation specificity factor subunit 2 OS=Homo sapiens OX=9606 GN=CPSF2 PE=1 SV=2
Q9BYD1	RM13_HUMAN	176.96	11	39S ribosomal protein L13 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL13 PE=1 SV=1
P46782	RS5_HUMAN	176.78	12	40S ribosomal protein S5 OS=Homo sapiens OX=9606 GN=RPS5 PE=1 SV=4
P62280	RS11_HUMAN	176.2	12	40S ribosomal protein S11 OS=Homo sapiens OX=9606 GN=RPS11 PE=1 SV=3
P09001	RM03_HUMAN	175.82	13	39S ribosomal protein L3 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL3 PE=1 SV=1
Q86U42	PABP2_HUMAN	175.69	11	Polyadenylate-binding protein 2 OS=Homo sapiens OX=9606 GN=PABPN1 PE=1 SV=3
Q13405	RM49_HUMAN	175.68	9	39S ribosomal protein L49 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL49 PE=1 SV=1
Q15366	PCBP2_HUMAN	175.44	5	Poly(rC)-binding protein 2 OS=Homo sapiens OX=9606 GN=PCBP2 PE=1 SV=1
P22090	RS4Y1_HUMAN	174.86	0	40S ribosomal protein S4 Y isoform 1 OS=Homo sapiens OX=9606 GN=RPS4Y1 PE=1 SV=2
Q9BYD3	RM04_HUMAN	174.81	10	39S ribosomal protein L4 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL4 PE=1 SV=1
Q00577	PURA_HUMAN	174.71	8	Transcriptional activator protein Pur-alpha OS=Homo sapiens OX=9606 GN=PURA PE=1 SV=2
Q9NPE2	NGRN_HUMAN	174.6	10	Neugrin OS=Homo sapiens OX=9606 GN=NGRN PE=1 SV=2
P84098	RL19_HUMAN	174.43	9	60S ribosomal protein L19 OS=Homo sapiens OX=9606 GN=RPL19 PE=1 SV=1

Q5BKZ1	ZN326_HUMAN	173.8	12	DBIRD complex subunit ZNF326 OS=Homo sapiens OX=9606 GN=ZNF326 PE=1 SV=2
PODN76	U2AF5_HUMAN	173.32	9	Splicing factor U2AF 35 kDa subunit-like protein OS=Homo sapiens OX=9606 GN=U2AF1L5 PE=1 SV=1
Q01081	U2AF1_HUMAN	173.32	9	Splicing factor U2AF 35 kDa subunit OS=Homo sapiens OX=9606 GN=U2AF1 PE=1 SV=3
P29558	RBMS1_HUMAN	172.52	8	RNA-binding motif single-stranded-interacting protein 1 OS=Homo sapiens OX=9606 GN=RBMS1 PE=1 SV=3
P84103	SRSF3_HUMAN	172.38	9	Serine/arginine-rich splicing factor 3 OS=Homo sapiens OX=9606 GN=SRSF3 PE=1 SV=1
P27635	RL10_HUMAN	172.32	13	60S ribosomal protein L10 OS=Homo sapiens OX=9606 GN=RPL10 PE=1 SV=4
O15371	EIF3D_HUMAN	171.1	7	Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens OX=9606 GN=EIF3D PE=1 SV=1
Q9Y6Y0	NS1BP_HUMAN	170.99	11	Influenza virus NS1A-binding protein OS=Homo sapiens OX=9606 GN=IVNS1ABP PE=1 SV=3
Q16629	SRSF7_HUMAN	170.73	10	Serine/arginine-rich splicing factor 7 OS=Homo sapiens OX=9606 GN=SRSF7 PE=1 SV=1
O15234	CASC3_HUMAN	169.95	10	Protein CASC3 OS=Homo sapiens OX=9606 GN=CASC3 PE=1 SV=2
Q9NXV6	CARF_HUMAN	169.73	6	CDKN2A-interacting protein OS=Homo sapiens OX=9606 GN=CDKN2AIP PE=1 SV=3
P42704	LPPRC_HUMAN	169.66	10	Leucine-rich PPR motif-containing protein mitochondrial OS=Homo sapiens OX=9606 GN=LRPPRC PE=1 SV=3
P46783	RS10_HUMAN	169.58	9	40S ribosomal protein S10 OS=Homo sapiens OX=9606 GN=RPS10 PE=1 SV=1
Q14444	CAPR1_HUMAN	168.67	9	Caprin-1 OS=Homo sapiens OX=9606 GN=CAPRIN1 PE=1 SV=2
Q14151	SAFB2_HUMAN	168.6	3	Scaffold attachment factor B2 OS=Homo sapiens OX=9606 GN=SAFB2 PE=1 SV=1
P46781	RS9_HUMAN	168.12	16	40S ribosomal protein S9 OS=Homo sapiens OX=9606 GN=RPS9 PE=1 SV=3
Q07955	SRSF1_HUMAN	167.78	9	Serine/arginine-rich splicing factor 1 OS=Homo sapiens OX=9606 GN=SRSF1 PE=1 SV=2
P26196	DDX6_HUMAN	167.24	7	Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens OX=9606 GN=DDX6 PE=1 SV=2
Q9Y383	LC7L2_HUMAN	167.05	7	Putative RNA-binding protein Luc7-like 2 OS=Homo sapiens OX=9606 GN=LUC7L2 PE=1 SV=2
P30050	RL12_HUMAN	166.95	6	60S ribosomal protein L12 OS=Homo sapiens OX=9606 GN=RPL12 PE=1 SV=1
P02533	K1C14_HUMAN	166.74	7	Keratin type I cytoskeletal 14 OS=Homo sapiens OX=9606 GN=KRT14 PE=1 SV=4
O60832	DKC1_HUMAN	166.5	8	H/ACA ribonucleoprotein complex subunit DKC1 OS=Homo sapiens OX=9606 GN=DKC1 PE=1 SV=3
P05387	RLA2_HUMAN	166.43	6	60S acidic ribosomal protein P2 OS=Homo sapiens OX=9606 GN=RPLP2 PE=1 SV=1
Q7Z2W9	RM21_HUMAN	165.91	9	39S ribosomal protein L21 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL21 PE=1 SV=2
Q15424	SAFB1_HUMAN	165.24	4	Scaffold attachment factor B1 OS=Homo sapiens OX=9606 GN=SAFB PE=1 SV=4
Q86V81	THOC4_HUMAN	164.15	9	THO complex subunit 4 OS=Homo sapiens OX=9606 GN=ALYREF PE=1 SV=3
Q8TD47	RS4Y2_HUMAN	164.06	0	40S ribosomal protein S4 Y isoform 2 OS=Homo sapiens OX=9606 GN=RPS4Y2 PE=2 SV=3
P62277	RS13_HUMAN	164.03	13	40S ribosomal protein S13 OS=Homo sapiens OX=9606 GN=RPS13 PE=1 SV=2
Q8WYQ5	DGCR8_HUMAN	164	13	Microprocessor complex subunit DGCR8 OS=Homo sapiens OX=9606 GN=DGCR8 PE=1 SV=1
Q99459	CDC5L_HUMAN	163.68	9	Cell division cycle 5-like protein OS=Homo sapiens OX=9606 GN=CDC5L PE=1 SV=2
P62249	RS16_HUMAN	163.52	9	40S ribosomal protein S16 OS=Homo sapiens OX=9606 GN=RPS16 PE=1 SV=2
P62829	RL23_HUMAN	163.4	7	60S ribosomal protein L23 OS=Homo sapiens OX=9606 GN=RPL23 PE=1 SV=1
Q8N5N7	RM50_HUMAN	162.46	7	39S ribosomal protein L50 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL50 PE=1 SV=2
Q02878	RL6_HUMAN	162.4	8	60S ribosomal protein L6 OS=Homo sapiens OX=9606 GN=RPL6 PE=1 SV=3
Q9BRS2	RIOK1_HUMAN	162.21	8	Serine/threonine-protein kinase RIO1 OS=Homo sapiens OX=9606 GN=RIOK1 PE=1 SV=2

Q92552	RT27_HUMAN	161.55	8	28S ribosomal protein S27 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS27 PE=1 SV=3
Q53F19	NCBP3_HUMAN	161.4	7	Nuclear cap-binding protein subunit 3 OS=Homo sapiens OX=9606 GN=NCBP3 PE=1 SV=2
P62750	RL23A_HUMAN	161.18	11	60S ribosomal protein L23a OS=Homo sapiens OX=9606 GN=RPL23A PE=1 SV=1
Q96CM3	RUSD4_HUMAN	160.63	12	Mitochondrial RNA pseudouridine synthase RPUSD4 OS=Homo sapiens OX=9606 GN=RPUSD4 PE=1 SV=1
P19474	RO52_HUMAN	160.34	13	E3 ubiquitin-protein ligase TRIM21 OS=Homo sapiens OX=9606 GN=TRIM21 PE=1 SV=1
Q13595	TRA2A_HUMAN	160.22	7	Transformer-2 protein homolog alpha OS=Homo sapiens OX=9606 GN=TRA2A PE=1 SV=1
P62266	RS23_HUMAN	160.11	9	40S ribosomal protein S23 OS=Homo sapiens OX=9606 GN=RPS23 PE=1 SV=3
P18621	RL17_HUMAN	159.84	11	60S ribosomal protein L17 OS=Homo sapiens OX=9606 GN=RPL17 PE=1 SV=3
Q13242	SRSF9_HUMAN	159.38	8	Serine/arginine-rich splicing factor 9 OS=Homo sapiens OX=9606 GN=SRSF9 PE=1 SV=1
P51398	RT29_HUMAN	158.8	10	28S ribosomal protein S29 mitochondrial OS=Homo sapiens OX=9606 GN=DAP3 PE=1 SV=1
Q5VTE0	EF1A3_HUMAN	158.57	10	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens OX=9606 GN=EEF1A1P5 PE=5 SV=1
P68104	EF1A1_HUMAN	158.57	10	Elongation factor 1-alpha 1 OS=Homo sapiens OX=9606 GN=EEF1A1 PE=1 SV=1
Q9UMS4	PRP19_HUMAN	158.37	10	Pre-mRNA-processing factor 19 OS=Homo sapiens OX=9606 GN=PRPF19 PE=1 SV=1
P46777	RL5_HUMAN	158.03	8	60S ribosomal protein L5 OS=Homo sapiens OX=9606 GN=RPL5 PE=1 SV=3
P61254	RL26_HUMAN	157.94	3	60S ribosomal protein L26 OS=Homo sapiens OX=9606 GN=RPL26 PE=1 SV=1
Q9Y2H1	ST38L_HUMAN	157.85	7	Serine/threonine-protein kinase 38-like OS=Homo sapiens OX=9606 GN=STK38L PE=1 SV=3
P35268	RL22_HUMAN	157.46	6	60S ribosomal protein L22 OS=Homo sapiens OX=9606 GN=RPL22 PE=1 SV=2
Q9BYC9	RM20_HUMAN	156.82	7	39S ribosomal protein L20 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL20 PE=1 SV=1
O95900	TRUB2_HUMAN	156.64	12	Mitochondrial mRNA pseudouridine synthase TRUB2 OS=Homo sapiens OX=9606 GN=TRUB2 PE=1 SV=1
Q9NRX2	RM17_HUMAN	156.58	10	39S ribosomal protein L17 mitochondrial OS=Homo sapiens OX=9606 GN=MRPL17 PE=1 SV=1
Q659C4	LAR1B_HUMAN	156.55	3	La-related protein 1B OS=Homo sapiens OX=9606 GN=LARP1B PE=1 SV=2
P62269	RS18_HUMAN	156.33	11	40S ribosomal protein S18 OS=Homo sapiens OX=9606 GN=RPS18 PE=1 SV=3
Q6P087	RUSD3_HUMAN	156.02	11	Mitochondrial mRNA pseudouridine synthase RPUSD3 OS=Homo sapiens OX=9606 GN=RPUSD3 PE=1 SV=3
Q05519	SRS11_HUMAN	155.38	7	Serine/arginine-rich splicing factor 11 OS=Homo sapiens OX=9606 GN=SRSF11 PE=1 SV=1
P55884	EIF3B_HUMAN	155.02	8	Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens OX=9606 GN=EIF3B PE=1 SV=3
Q9UKV8	AGO2_HUMAN	155	5	Protein argonaute-2 OS=Homo sapiens OX=9606 GN=AGO2 PE=1 SV=3
Q9UN81	LORF1_HUMAN	154.09	9	LINE-1 retrotransposable element ORF1 protein OS=Homo sapiens OX=9606 GN=L1RE1 PE=1 SV=1
Q9BQG0	MBB1A_HUMAN	153.14	7	Myb-binding protein 1A OS=Homo sapiens OX=9606 GN=MYBBP1A PE=1 SV=2
P54105	ICLN_HUMAN	152.64	6	Methylosome subunit pICln OS=Homo sapiens OX=9606 GN=CLNS1A PE=1 SV=1
P48634	PRC2A_HUMAN	152.25	8	Protein PRRC2A OS=Homo sapiens OX=9606 GN=PRRC2A PE=1 SV=3
Q9UKM9	RALY_HUMAN	151.61	9	RNA-binding protein Raly OS=Homo sapiens OX=9606 GN=RALY PE=1 SV=1
Q96DH6	MSI2H_HUMAN	150.88	3	RNA-binding protein Musashi homolog 2 OS=Homo sapiens OX=9606 GN=MSI2 PE=1 SV=1
P82933	RT09_HUMAN	150.78	6	28S ribosomal protein S9 mitochondrial OS=Homo sapiens OX=9606 GN=MRPS9 PE=1 SV=2
O75152	ZC11A_HUMAN	150.51	9	Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens OX=9606 GN=ZC3H11A PE=1 SV=3
P26373	RL13_HUMAN	150.25	9	60S ribosomal protein L13 OS=Homo sapiens OX=9606 GN=RPL13 PE=1 SV=4

Q9Y676	RT18B_HUMAN	149.8	7	28S ribosomal protein S18b mitochondrial OS=Homo sapiens OX=9606 GN=MRPS18B PE=1 SV=1
P05141	ADT2_HUMAN	149.5	3	ADP/ATP translocase 2 OS=Homo sapiens OX=9606 GN=SLC25A5 PE=1 SV=7
O95639	CPSF4_HUMAN	149.4	5	Cleavage and polyadenylation specificity factor subunit 4 OS=Homo sapiens OX=9606 GN=CPSF4 PE=1 SV=1
P16403	H12_HUMAN	148.67	7	Histone H1.2 OS=Homo sapiens OX=9606 GN=HIST1H1C PE=1 SV=2
P10412	H14_HUMAN	148.67	7	Histone H1.4 OS=Homo sapiens OX=9606 GN=HIST1H1E PE=1 SV=2
P16402	H13_HUMAN	148.67	7	Histone H1.3 OS=Homo sapiens OX=9606 GN=HIST1H1D PE=1 SV=2

Supplemental Table 2. Sequence information for primers, siRNAs, and shRNAs.

Primer name	Species	Direction	Sequence (5'-3')	Application
shFUBP1 #1	Human	Forward	CCGGCGACTTGATGAAGATCTTAATCTCGAGATTAAGATCTTCATCAAGTCGTTTTTG	shRNA cloning
		Reverse	AATTCAAAAACGACTTGATGAAGATCTTAATCTCGAGATTAAGATCTTCATCAAGTCG	shRNA cloning
shFUBP1 #2	Human	Forward	CCGGGATTACAGGAGACCCATATAACTCGAGTTATATGGGTCTCCTGTAATC TTTTGT	shRNA cloning
		Reverse	AATTCAAAAAGATTACAGGAGACCCATATAACTCGAGTTATATGGGTCTCCTGTAATC	shRNA cloning
shSLC7A11 #1	Human	Forward	CCGGATAATAAAGAGATAATACGCTCGAGCGTATTATCTCTTTATTATTTTTTG	shRNA cloning
		Reverse	AATTCAAAAAATAATAAAGAGATAATACGCTCGAGCGTATTATCTCTTTATTAT	shRNA cloning
shSLC7A11 #2	Human	Forward	CCGGATATATGTGTAATGACCTCCTCGAGGAGGTCATTACACATATATTTTTTG	shRNA cloning
		Reverse	AATTCAAAAAATATATGTGTAATGACCTCCTCGAGGAGGTCATTACACATATAT	shRNA cloning
shPDK1 #1	Human	Forward	CCGGCGGATCAGAAACCGACACAATCTCGAGATTGTGTCGGTTTCTGATCCGTTTTTG	shRNA cloning
		Reverse	AATTCAAAAACGACTTGATGAAGATCTTAATCTCGAGATTGTGTCGGTTTCTGATCCG	shRNA cloning
shPDK1 #2	Human	Forward	CCGGGCTCTGTCAACAGACTCAATACTCGAGTATTGAGTCTGTTGACAGAGCTTTTTG	shRNA cloning
		Reverse	AATTCAAAAAGATTACAGGAGACCCATATAACTCGAGTATTGAGTCTGTTGACAGAGC	shRNA cloning
PRMT5-SgRNA #1	Human	Forward	GGTACCCTTGGTGGCACCAG	SgRNA cloning
		Reverse	CTGGTGCCACCAAGGGTACC	SgRNA cloning
PRMT5-SgRNA #2	Human	Forward	GGTGATGGCCAGTGTGGATG	SgRNA cloning
		Reverse	CATCCACACTGGCCATCACC	SgRNA cloning
PRMT5-siRNA #1	Human	Forward	GGACCUGAGAGAUGAUUAUA	Gene knockdown
		Reverse	UAUAUCAUCUCUCAGGUCC	Gene knockdown
PRMT5-siRNA #2	Human	Forward	CCAGAAGAGGAGAAGGAUA	Gene knockdown
		Reverse	UAUCCUUCUCCUCUUCUGG	Gene knockdown
BRD4-siRNA #1	Human	Forward	GGACUAGAAACUCCCAAA	Gene knockdown
		Reverse	UUUGGGAAGUUUCUAGUCC	Gene knockdown
BRD4-siRNA #2	Human	Forward	CACGGUACCAACACAACU	Gene knockdown
		Reverse	AGUUGUGUUUGGUACCGUG	Gene knockdown
PRMT9-siRNA #1	Human	Forward	GGUAUCCAUUUGCCAACAA	Gene knockdown
		Reverse	UUGUUGGCAAUGGAUACC	Gene knockdown
PRMT9-siRNA #2	Human	Forward	GCUUAACAACAUCCCAUUAU	Gene knockdown
		Reverse	AUAUGGGAUGUUGUUAAGC	Gene knockdown
MTAP-siRNA #1	Human	Forward	GGAAGAGGGCUGUACACAU	Gene knockdown

		Reverse	AUGUGUACAGCCCUCUCC	Gene knockdown
MTAP-siRNA #2	Human	Forward	GGAGUGUGCCAUUUCCAA	Gene knockdown
		Reverse	UUGGAUAUUGGCACACUCC	Gene knockdown
JMJD6-siRNA #1	Human	Forward	GGGAGACCAAAGUUAUCAA	Gene knockdown
		Reverse	UUGAUAACUUUGGUCUCCC	Gene knockdown
JMJD6-siRNA #2	Human	Forward	CUGGCCACCUGAAUUCAAA	Gene knockdown
		Reverse	UUUGAAUUCAGGUGGCCAG	Gene knockdown
KDM1A-siRNA #1	Human	Forward	CCACGAGUCAAAACCUUUAU	Gene knockdown
		Reverse	AUAAAGGUUGACUCGUGG	Gene knockdown
KDM1A-siRNA #2	Human	Forward	GCCACCCAGAGAUUUACU	Gene knockdown
		Reverse	AGUAAUAUCUCUGGGUGGC	Gene knockdown
KDM3A-siRNA #1	Human	Forward	CCUUGUGACAUGUGGUAAU	Gene knockdown
		Reverse	AUUACCACAUGUCACAAGG	Gene knockdown
KDM3A-siRNA #2	Human	Forward	GCGGGUAGAAGGCUUCUUA	Gene knockdown
		Reverse	UAAGAAGCCUUCUACCCGC	Gene knockdown
KDM4A-siRNA #1	Human	Forward	GCCUCUUUACUCAGUACAA	Gene knockdown
		Reverse	UUGUACUGAGUAAAGAGGC	Gene knockdown
KDM4A-siRNA #2	Human	Forward	GCCGUCAGCCUUUAAGCAA	Gene knockdown
		Reverse	UUGCUUAAAGGCUGACGGC	Gene knockdown
KDM4E-siRNA #1	Human	Forward	CCUGGAUCCGCAUUCCAA	Gene knockdown
		Reverse	UUUGGAAUGCGGAUCCAGG	Gene knockdown
KDM4E-siRNA #2	Human	Forward	GGUCGUGGUCAUGGUUGUU	Gene knockdown
		Reverse	AACAACCAUGACCACGACC	Gene knockdown
KDM5C-siRNA #1	Human	Forward	GCAGAGAAAUCGGGCAUUU	Gene knockdown
		Reverse	AAAUGCCCGAUUUCUCUGC	Gene knockdown
KDM5C-siRNA #2	Human	Forward	CCUUUAAAGCUGACUACUU	Gene knockdown
		Reverse	AAGUAGUCAGCUUUAAGG	Gene knockdown
KDM6B-siRNA #1	Human	Forward	GUGACAAGGAGACCUUUAU	Gene knockdown
		Reverse	AUAAAGGUCUCCUUGUCAC	Gene knockdown
KDM6B-siRNA #2	Human	Forward	GAGACCUCGUGUGGAUUAA	Gene knockdown
		Reverse	UUAAUCCACACGAGGUCUC	Gene knockdown
ACTIN	Human	Forward	GGTGATGGCCAGTGTGGATG	qPCR

		Reverse	GGTGATGGCCAGTGTGGATG	qPCR
FUBP1	Human	Forward	CCTGGAACTCCAATGGGACC	qPCR
		Reverse	GCGTAATAAGCAGCCCAAGC	qPCR
PRMT5	Human	Forward	TATGTGGTACGGCTGCACA	qPCR
		Reverse	TGGCTGAAGGTGAAACAGG	qPCR
MTAP	Human	Forward	ACCACCGCCGTGAAGATTG	qPCR
		Reverse	GCATCAGATGGCTTGCCAA	qPCR
BRD4	Human	Forward	GAGCTACCCACAGAAGAAACC	qPCR
		Reverse	GAGTCGATGCTTGAGTTGTGTT	qPCR
PK1	Human	Forward	CTGTGATACGGATCAGAAACCG	qPCR
		Reverse	TCCACCAAACAATAAAGAGTGCT	qPCR
SLC7A11	Human	Forward	TCTCCAAAGGAGGTTACCTGC	qPCR
		Reverse	AGACTCCCCTCAGTAAAGTGAC	qPCR
FUBP1	Human	Forward	GCCTGAGGCCATTTTGAGAAA	ChIP-qPCR
		Reverse	CCATTCACCGTCACACCTCT	ChIP-qPCR
PRMT5	Human	Forward	AGCGCGAGGAGAAAGATG	ChIP-qPCR
		Reverse	CTATTTCGGGGACGCAATTC	ChIP-qPCR
MTAP	Human	Forward	GGGAGTTGTGCAAGGTCTCA	ChIP-qPCR
		Reverse	CCCAAGACTCAGGGATGACG	ChIP-qPCR