

Supplemental Figures.

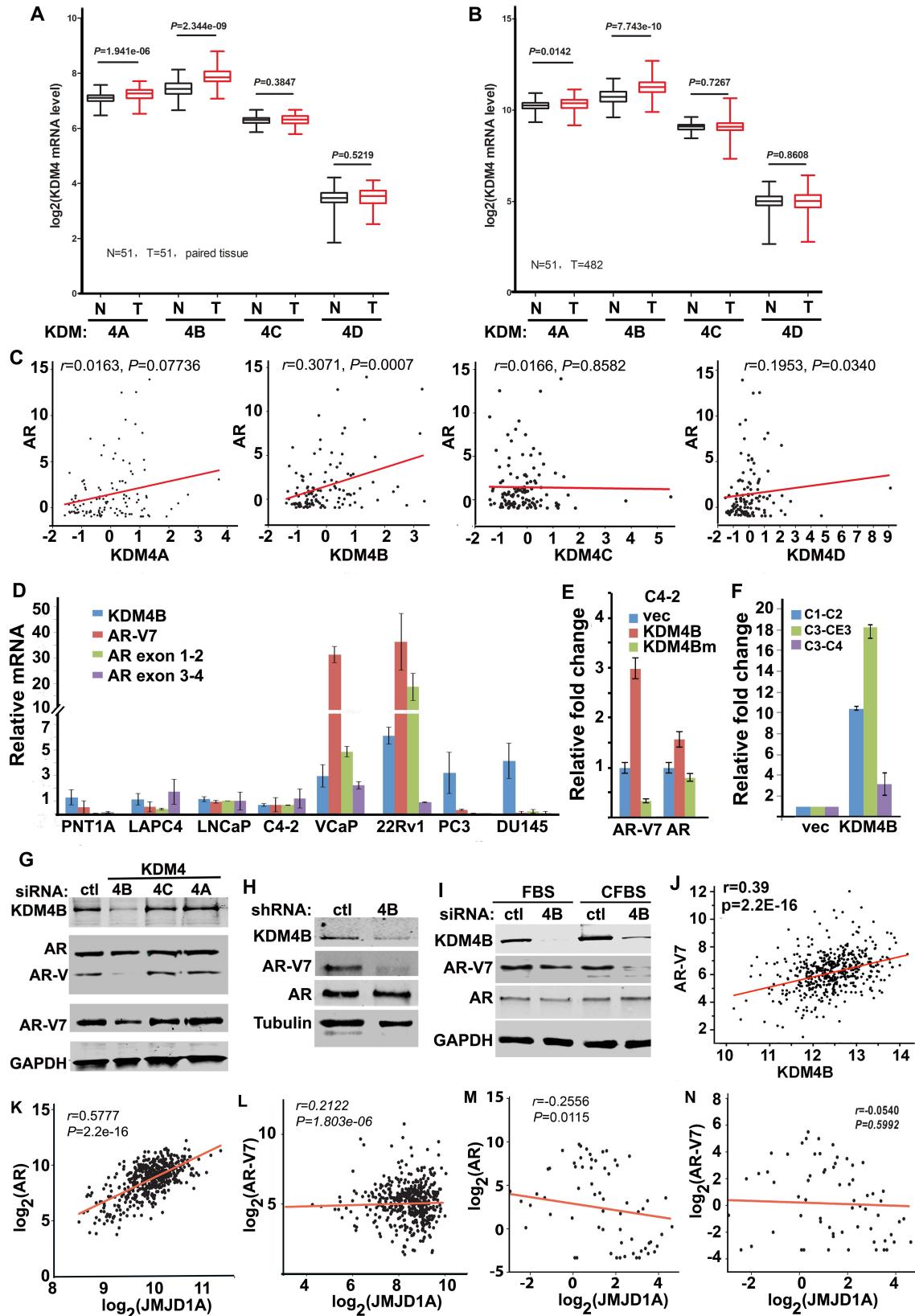


Figure S1. KDM4B promotes AR-V7 expression. (A-B) T-tests of mRNAs of KDM4 isoforms (4A-D) between prostate tumor (T) and nearby normal tissues (N) (A) and between normal tissues and all

tumors (B). Data were taken from TGCA. (C) Spearman's correlation between z-scores of AR and KDM4 isoforms. Data is from the SU2C dataset in cBioPortal. (D) Relative mRNA of KDM4B, AR-V7, and AR in various PCa cell lines. mRNAs were normalized against internal GAPDH and expressed relative to the expression of KDM4B in PNT1A cells (n=3, mean ± SD). (E) Relative fold change of AR-V7 and AR in C4-2 cells transfected with vector, KDM4B or KDM4Bm. mRNAs were normalized against internal GAPDH and expressed relative to vector-transfected cells (n=3, mean ± SD). (F) Relative mRNA of AR-V7 and AR in LNCaP cells transfected with vec or KDM4B (n=3, mean ± SD). AR-V7 was measured using the primers in exon 3 and CE3. AR mRNA was measured using primers in exons 3 and 4, and primers from exons 1 and 2. The overall AR transcription as measured by primers from C1 and C2, which give rise to AR-V7 and AR via splicing, is significantly increased in LNCaP cells transfected with KDM4B as well. Values are normalized to internal Calnexin and expressed relative to that in vector transfected cell (n=3, mean ± SD). (G) Western blot of proteins indicated from 22Rv1 cells transfected with ctl or siRNA against KDM4A, 4B, and 4C. Anti-AR NTD antibody (N20, rabbit polyclonal, Santa Cruz, no longer in production) was used for detecting AR and AR-Vs. (H) Western blot of AR-V7 and AR in 22Rv1 cells transduced with control (ctl) or KDM4B (4B) shRNA. (I) West blot of protein indicated from 22Rv1 cells transfected with ctl or KDM4B siRNA cultured under FBS or CFBS condition. (J) Spearman's correlation between KDM4B and AR from TCGA dataset. (K, L) Spearman's correlation between JMJD1A and AR (K), JMJD1A and AR-V7 (L) from TCGA dataset. (M, N) Spearman's correlation between JMJD1A and AR (M), between JMJD1A and AR-V7 (N) from the SU2C dataset.

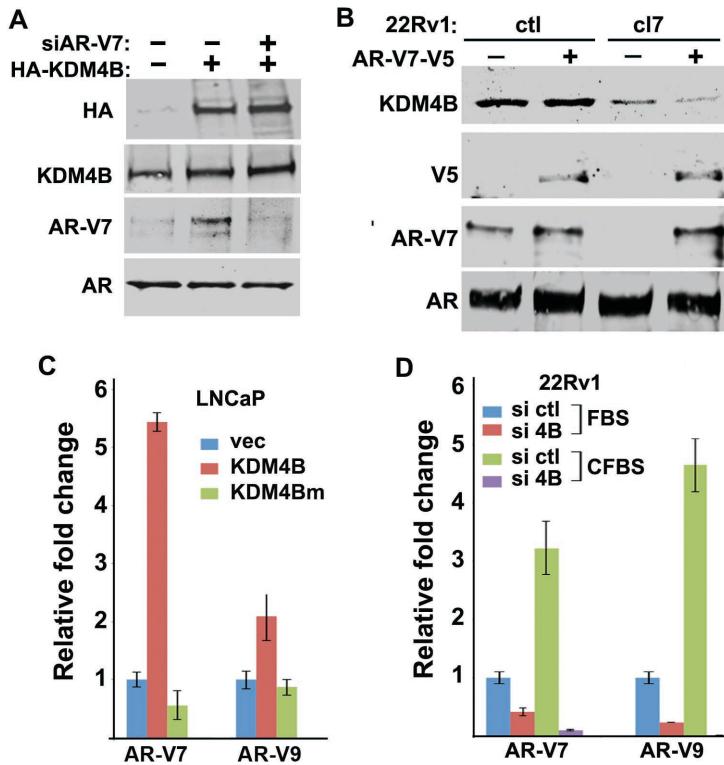


Figure S2. (A) Western blot of indicated proteins in LNCaP cells transfected with KDM4B, control or AR-V7 specific siRNA. (B) Western blot of indicated proteins in 22Rv1-ctl and KDM4B KD 22Rv1-cl7 cells transduced without or with C-terminal V5 tagged-AR-V7. (C, D) Relative mRNA of AR-V7 and AR-V9 in LNCaP cells transfected with vector, KDM4B or KDM4Bm (C) and in 22Rv1 cells transfected with control or KDM4B siRNA (D). Values are normalized against internal GAPDH and expressed relative to vector-transfected (C) or control siRNA transfected (D) cells (n=4, mean ± SEM).

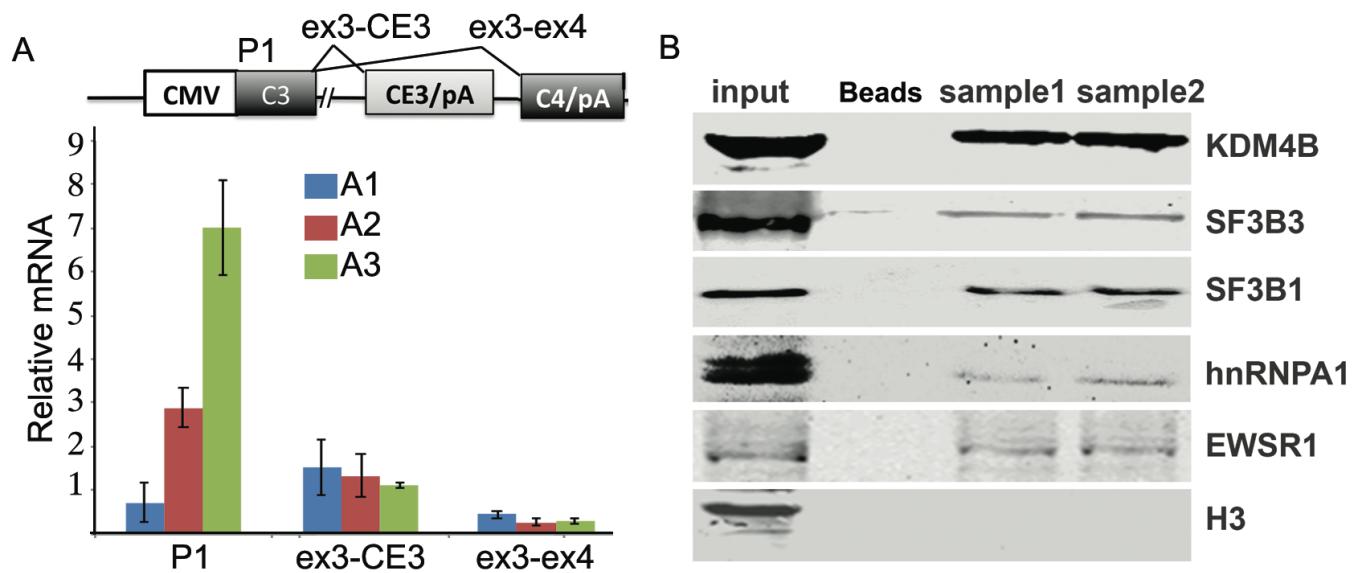


Figure S3. (A) Relative transcripts of minigenes A1, A2, and A3 in KEK294T cells. Equal amounts of minigenes were transfected into HEK293T cells with β -galactosidase. Cellular RNAs were extracted 48 hrs post-transfection and converted to cDNA. Relative mRNAs were measured with primers indicated and normalized to co-transfected β -galactosidase. (B) Western blot of proteins in biotin pulled-down complexes from 22Rv1 cells. A Biotin-labeled RNA probe containing 4BRBS (sample 1 and sample 2) was mixed with 22Rv1 cell lysates. After 4 h incubation, RNA-bound proteins were pulled down with streptavidin-beads, washed, separated on SDS-PAGE, and probed with antibodies against proteins indicated.

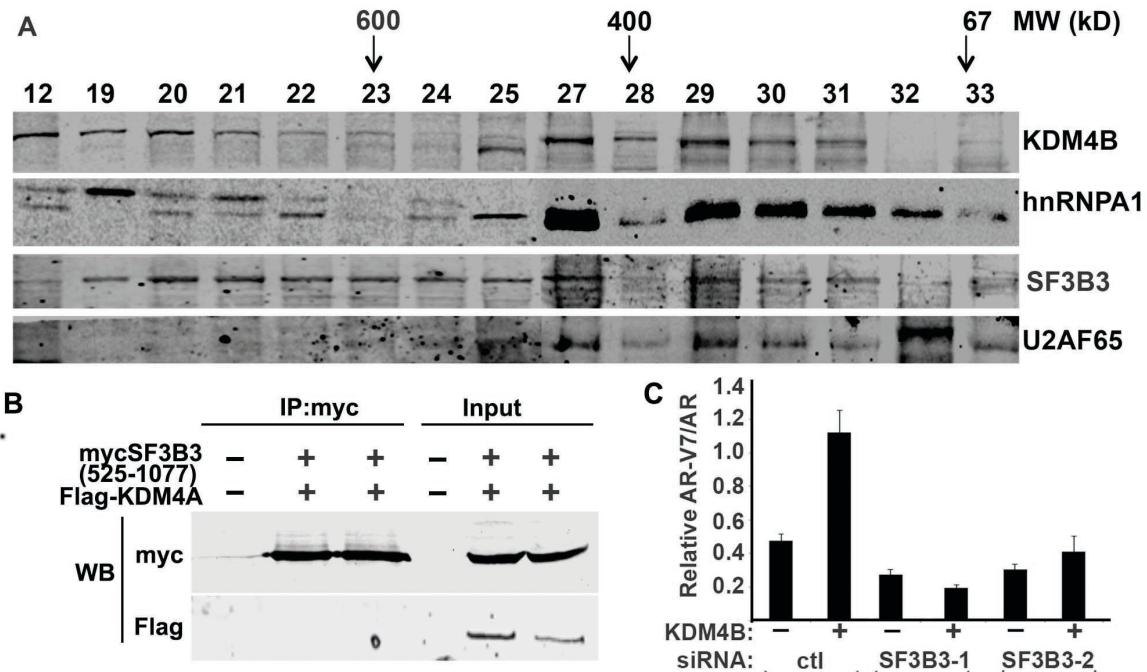


Figure S4. KDM4B is associated with the spliceosome. (A) 22Rv1 cell lysates were subjected to FPLC with a Sepharose 6 gel filtration column. Fractions were collected and subjected to Western blot analysis. The arrows mark molecular weights. Fraction numbers are marked. KDM4B co-elutes with the core components of the spliceosome SF3B3 and U2AF65. (B) 293T cells were transfected with mycSF3B3 (525-1077) and Flag-KDM4A. (C) Cell lysates were immunoprecipitated with anti-myc antibody and western blotted with anti-Flag. 293T cells were transfected with control (ctl) and SF3B3 specific siRNAs. 72 h post-transfection, cells were transfected AR-V7 minigene A1 along with or without KDM4B as indicated. Cells were harvested 48 h later and RNAs were extracted for qRT-PCR for quantification of relative AR-V7 and AR (n=3 ± SD).

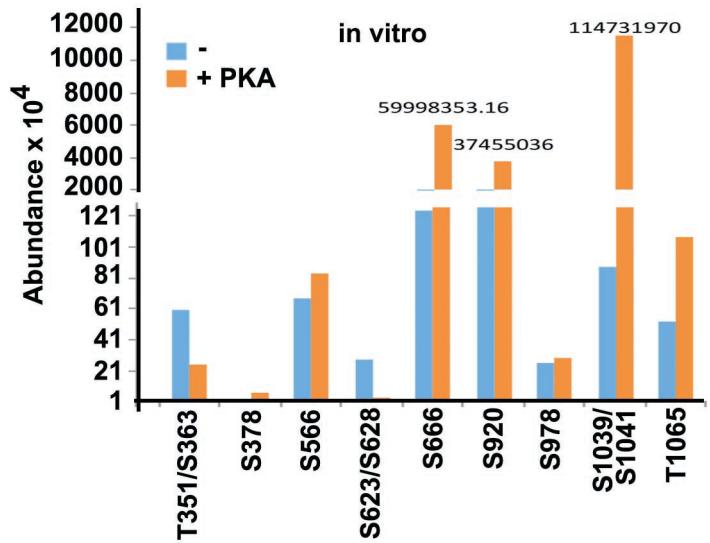


Figure S5. KDM4B is phosphorylated by PKA. Recombinant KDM4B proteins phosphorylated without or with PKA were subjected to phosphorylation analysis by MASS spectrometry.

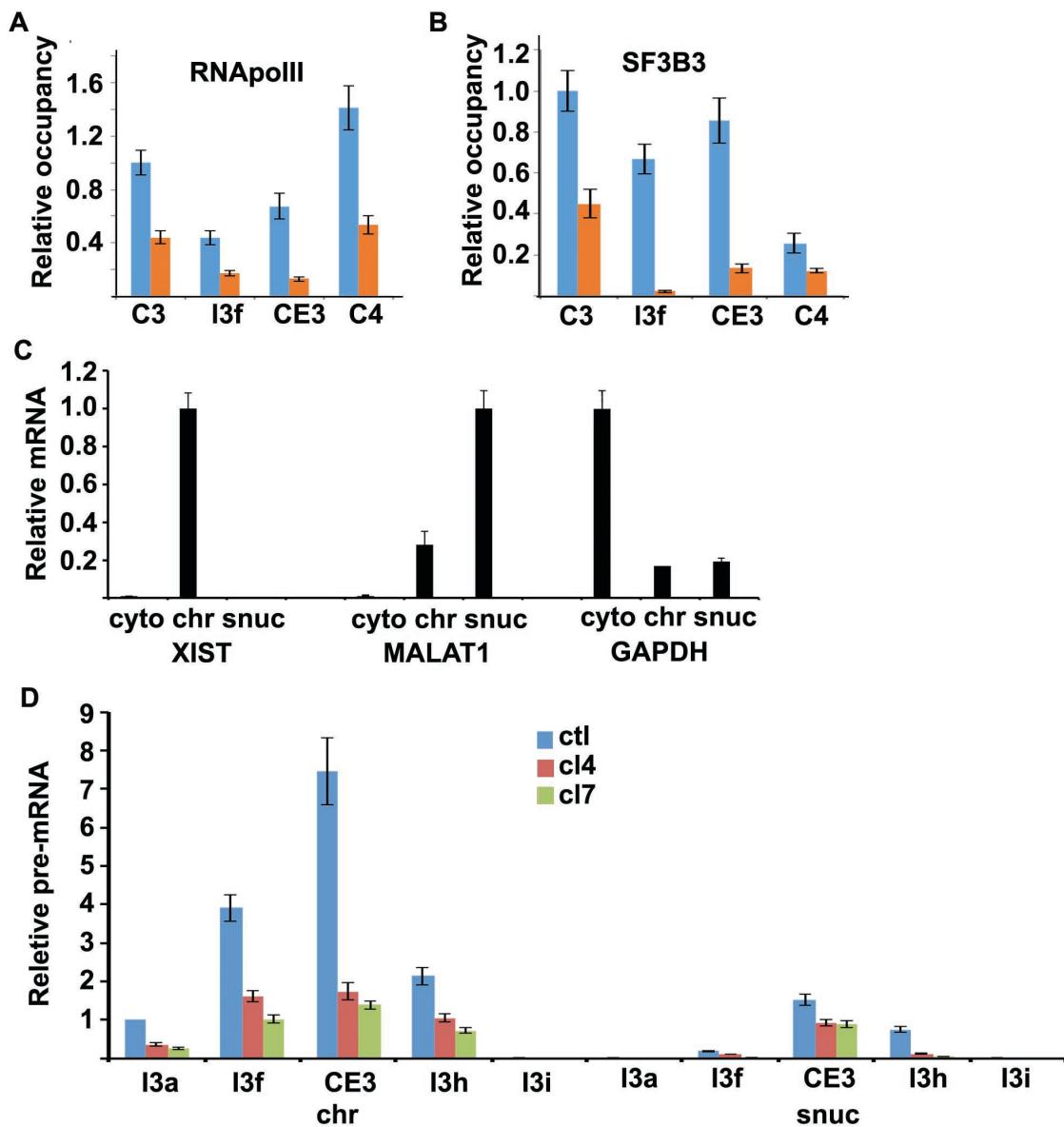


Figure S6. KDM4B binds chromatins near the CE3 region. (A-B) Relative chromatin occupancy of (A) RNApolII and (B) SF3B3 in 22Rv1-ctl and 22Rv1-cl4 cells. KDM4B KD downregulated chromatin binding of RNApolII and SF3B3 in the CE3 region. (C) Relative expression of XIST, MALAT1, and GAPDH in chromatin, soluble nuclear, and cytosol fraction of 22Rv1 cells assayed by qRT-PCR. (D) Relative pre-mRNA near CE3 of AR in chromatin and soluble nuclear fractions of control and KDM4B KD 22Rv1 cells. The PCR primer pairs used are pictured below the graph. n=3, mean \pm SD.

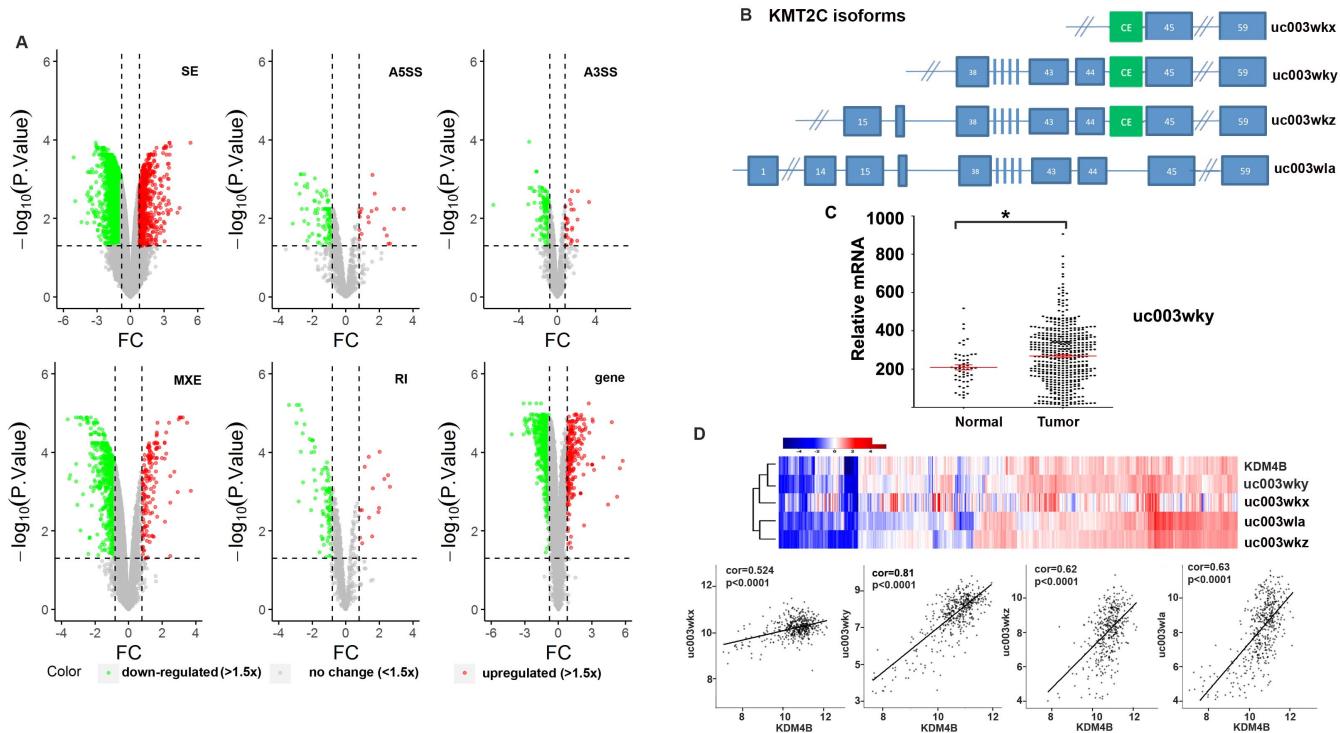


Figure S7. KDM4B targets global alternative splicing. (A) Volcano plot of differential alternative splicing events and genes between LNCaP-ctl and LNCaP-4B cells. (B) Schematics of 4 KDMT2C isoforms identified from UCSD-genome-wide browser. Isoforms uc003wkx, uc003wky, and uc003wkz contain an alternatively spliced cryptic exon ce whereas isoform uc003wla does not. (C) Relative mRNA levels of uc003wky in normal (n=50) vs tumor tissues (n=500) in TCGA database. *, $p < 0.05$. (D) Spearman's correlation analysis of levels of KDM4B vs KMT2C isoforms. The KDM4B level had strong positive correlation with KMT2C isoforms.

Table S1. Proteins identified in immunoprecipitates of LNCaP-4B cells. Stable LNCaP cells with overexpressed Flag-KDM4B/JMJD2B (LNCaP-4B) were lysed. Cell lysates were immunoprecipitated with anti-Flag antibody or control IgG, washed, eluted with 3xFlag peptide, and subjected to SDS-PAGE and mass spectrometry.

Table S2. Proteins identified in immunoprecipitates of LNCaP-4B cells. LNCaP-4B cell lysates were immunoprecipitated with anti-Flag antibody, treated with RNase, washed, and eluted with 3xFlag peptide, and subjected to SDS-PAGE and mass spectrometry.

Table S3. qRT-PCR primers used in this paper.

Table S1

Flag vs IgG

Protein (UniP)	Gene Symbol	Description	Length (AA)	mw (Da)	Indistinguishable	PSMs	Peptide Seqs	% Coverage	Modifications	SPECTRAL COUNTS		SPECTRAL INDEX (MIC SIN)		RATIO
										Flag-JMJD2B	control	Flag-JMJD2B	control	
B0QY89	EIF3L	B0QY89_HUMAN	607	61118.80	Q9Y262;Q9Y	19	11	24.20	Gln->pyro-Gl	11.96	5.98	2.34E-06	6.74E-07	2.00
P0CG05	IGLC2	LAC2_HUMAN	106	11248.50	P0CG06;	3	3	41.50		2.00	1.00	1.06E-06	4.54E-07	2.00
H7C3T4	PRDX4	H7C3T4_HUMAN	161	30592.80	Q13162;	11	6	35.40	Gln->pyro-Gl	5.00	2.50	3.65E-06	5.98E-06	2.00
E7EPB3	RPL14	E7EPB3_HUMAN	124	23471.10	P50914;	3	2	19.40		2.00	1.00	2.40E-06	8.03E-07	2.00
F8VVA6	RPL18	F8VVA6_HUMAN	130	21675.10	F8VWC5;G3V	6	2	20.00		4.00	2.00	2.66E-06	1.42E-06	2.00
P62857	RPS28	RS28_HUMAN	69	7854.21		3	2	30.40		2.00	1.00	2.87E-06	1.63E-06	2.00
P49411	TUFM	EFTU_HUMAN	452	49636.20		6	4	12.20	Gln->pyro-Gl	4.00	2.00	1.24E-06	2.36E-07	2.00
P16989	YBX3	YBOX3_HUMAN	372	38602.80	P16989-2;P1	3	2	8.30		1.98	0.99	6.14E-07	9.25E-08	2.00
P23528	CFL1	COF1_HUMAN	166	18526.70		6	3	22.30	Acetyl (Prote)	3.95	1.97	4.17E-06	8.79E-07	2.01
P68363	TUBA1B	TBA1B_HUMAN	451	50245.70		16	16	45.70	Carbamidom	9.66	4.80	1.19E-05	3.42E-06	2.01
P55884	EIF3B	EIF3B_HUMAN	814	99219.20	P55884-2;	14	8	11.90	Acetyl (Prote)	8.99	4.00	1.22E-06	2.54E-07	2.25
E7ES8A	PRPF31	E7ES8A_HUMAN	450	40861.70	Q8WVW3;Q8	13	8	29.70	Carbamidom	8.91	3.96	5.18E-06	7.16E-07	2.25
P62277	RPS13	RS13_HUMAN	151	17247.70		13	6	30.50		8.97	3.98	8.73E-06	2.00E-06	2.25
P68104	EEF1A1	EEF1A1_HUMAN	462	50279.20	Q5VTE0;	76	17	33.80	Gln->pyro-Gl	53.87	21.96	6.97E-05	9.24E-06	2.45
P07437	TUBB	TBBS_HUMAN	444	47862.10	Q5JP53;	22	22	61.30	Carbamidom	15.81	5.93	1.77E-05	4.49E-06	2.67
P04080	CSTB	CYTB_HUMAN	98	11150.60		11	4	55.10		8.00	3.00	1.23E-05	2.27E-06	2.67
Q15365	PCBP1	PCBP1_HUMAN	356	37564.00		12	7	28.10	Carbamidom	8.00	3.00	2.54E-06	5.15E-07	2.67
P68371	TUBB4B	TB8B_HUMAN	445	49925.10		15	21	54.80	Carbamidom	10.85	3.96	8.59E-06	1.10E-06	2.74
Q14152	EIF3A	EIF3A_HUMAN	1382	166883.00		27	16	15.40	Oxidation (M)	20.00	7.00	1.53E-06	4.61E-07	2.86
Q13347	EIF3I	EIF3I_HUMAN	325	36568.70		4	3	18.20		3.00	1.00	1.64E-06	2.77E-07	3.00
P62805	HIST1H4H	H4_HUMAN	103	11378.40		4	2	17.50		3.00	1.00	2.49E-06	4.55E-07	3.00
P55795	HNRNPH2	HNRN2_HUMAN	449	49358.40		8	10	29.20	Acetyl (Prote)	6.00	2.00	1.58E-06	2.89E-07	3.00
E9PH29	PRDX3	E9PH29_HUMAN	238	27747.20	P30048;	4	3	15.50		3.00	1.00	6.44E-06	2.90E-07	3.00
P36578	RPL4	RL4_HUMAN	427	47793.50		4	4	10.80		3.00	1.00	5.32E-07	7.79E-08	3.00
P05141	SLC25A5	ADT2_HUMAN	298	32903.20		5	4	13.40	Acetyl (Prote)	3.00	1.00	2.31E-06	2.88E-07	3.00
A8MWD9	SNRPGP15	RUXGL_HUMAN	76	7114.68	F5H013;P623	4	2	20.30		3.00	1.00	1.18E-05	2.67E-07	3.00
Q13247	SRSF6	SRSF6_HUMAN	344	38485.70	Q13247-3;	4	2	5.40		3.00	1.00	1.50E-06	2.45E-07	3.00
O60506	SYNCRIP	HNRPQ_HUMAN	623	58843.40	O60506-2;O6	4	3	6.30		2.97	0.99	5.12E-07	5.65E-08	3.00
P00390	GSR	GSHR_HUMAN	522	53137.50	P00390-2;P0	4	3	10.60		2.99	0.99	3.54E-07	1.28E-08	3.02
P38646	HSPA9	GRP75_HUMAN	679	73823.90		78	33	55.40	Carbamidom	59.00	19.00	3.64E-05	4.22E-06	3.11
P98175	RBM10	RBM10_HUMAN	930	103640.00	P98175-2;	18	11	15.30		13.00	4.00	1.54E-06	2.52E-07	3.25
P08238	HSP90AB1	HSP90B_HUMAN	724	83428.20		15	8	11.20		10.90	2.97	1.29E-06	1.83E-07	3.67
E9PKG1	PRMT1	E9PKG1_HUMAN	325	40612.10	H7C21;Q998	24	12	37.20	Carbamidom	18.88	4.96	6.79E-06	8.10E-07	3.81
B3KSH1	EIF3F	B3KSH1_HUMAN	372	37630.20	O00303;	10	5	17.40		7.92	1.98	2.86E-06	4.69E-07	4.00
P08107	HSPA1B	HSP71_HUMAN	641	70189.10		16	13	24.20		12.91	2.98	2.88E-06	2.29E-07	4.33
P25705	ATP5A1	ATPA_HUMAN	553	54603.80	P25705-2;	11	7	16.50		8.90	1.98	1.73E-06	1.34E-07	4.49
Q92804	TAF15	RBPS6_HUMAN	592	61683.30	Q92804-2;	11	7	18.20	Carbamidom	8.91	1.98	2.23E-06	4.93E-08	4.50
P11142	HSPA8	HSP7C_HUMAN	646	71034.30		47	27	44.70	Carbamidom	37.95	7.80	1.15E-05	8.82E-07	4.87
P60709	ACTB	ACTB_HUMAN	375	41817.80	J3KTA4;P178	72	18	61.60	Acetyl (Prote)	57.86	11.62	1.85E-04	4.29E-06	4.98
B4DLW8	DDX5	B4DLW8_HUMAN	535	69284.80	J3KTA4;P178	8	6	12.30	Oxidation (M)	5.00	1.00	1.02E-06	1.90E-07	5.00
P49327	FASN	FAS_HUMAN	2511	273993.00		32	22	10.50	Acetyl (Prote)	27.00	5.00	1.45E-06	6.71E-08	5.40
P46821	MAP1B	MAP1B_HUMAN	2468	271206.00		47	33	20.90	Acetyl (Prote)	39.92	6.99	2.27E-06	1.45E-07	5.71
B4E2Q4	EIF3M	B4E2Q4_HUMAN	242	42583.90	Q7L2H7;	7	4	16.50		5.98	1.00	1.34E-06	6.64E-08	5.98
Q15393	SF3B3	SF3B3_HUMAN	1217	15852.00		7	6	5.90		5.99	1.00	4.38E-07	4.01E-08	5.99
Q92499	DDX1	DDX1_HUMAN	740	82595.90		7	4	6.50		6.00	1.00	6.54E-07	3.38E-08	6.00
Q92734	TFG	TFG_HUMAN	400	43102.00	Q92734-2;	71	16	49.00	Acetyl (Prote)	60.64	9.92	6.47E-05	4.68E-06	6.11
P52907	CAPZA1	CAZA1_HUMAN	286	32974.40		8	5	29.00	Acetyl (Prote)	7.00	1.00	3.15E-06	1.42E-07	7.00
P04792	HSPB1	HSPB1_HUMAN	205	22822.50		8	4	25.90	Gln->pyro-Gl	7.00	1.00	5.98E-06	1.68E-07	7.00
P22626	HNRNPA2B1	ROA2_HUMAN	353	37496.80		34	17	53.50	Oxidation (M)	30.00	4.00	2.74E-05	1.17E-06	7.50
H7BY58	PCMT1	H7BY58_HUMAN	286	24717.60	J3KP72;P220	35	11	59.50	Carbamidom	30.98	4.00	4.36E-05	1.84E-06	7.75
P11021	HSP5	GRP78_HUMAN	654	72468.50		45	31	52.00	Oxidation (M)	39.00	5.00	8.06E-06	6.41E-07	7.80
E9PHS0	LANCL1	E9PHS0_HUMAN	196	45361.60	O43813;	14	7	38.80	Carbamidom	13.00	1.00	2.12E-05	2.34E-07	13.00
P35637	FUS	FUS_HUMAN	526	53466.80	P53637-2;	29	10	19.40	Ammonia-los	28.00	1.00	2.28E-05	4.34E-08	28.00
P24752	ACAT1	THIL_HUMAN	427	45296.70		3	3	8.70		3.00		1.05E-06		
Q562R1	ACTBL2	ACTBL_HUMAN	376	42084.00		1	6	17.60	Oxidation (M)	1.00		1.20E-05		
H7C550	ACTL6A	H7C550_HUMAN	161	43316.40	O96019;O96	2	2	17.40		2.00		7.42E-07		
Q5TA58	AGO1	Q5TA58_HUMAN	782	97404.30	Q9UL18;	1	2	3.20		1.00		8.91E-08		
Q9UKV8	AGO2	AGO2_HUMAN	859	93794.30	Q9UKV8-2;	4	4	5.80		4.00		4.99E-07		
Q9HG97	AGO3	AGO3_HUMAN	860	71345.50	Q9HG97-2;	1	2	4.00		0.99		8.58E-08		
P54886	ALDH18A1	P5CS_HUMAN	795	87268.60	P54886-2;	3	3	4.90		3.00		2.66E-07		
B3VOL1	ARL6IP4	B3VOL1_HUMAN	226	36279.20	F5GYV5;FW8	3	3	19.00		2.97		1.31E-06		
HOYH81	ATP5B	HOYH81_HUMAN	362	56668.70	P06576;	2	2	9.10		1.98		4.51E-07		
Q9Y224	C14orf166	CN166_HUMAN	244	28122.80		3	3	16.40		3.00		1.72E-06		
B1AK87	CAPZB1	B1AK87_HUMAN	260	30681.40	B1AK88;P477	4	3	14.60		3.98		1.79E-06		
Q00610	CLTC	CLH1_HUMAN	1675	188257.00	Q00610-2;	16	13	10.40		15.98		1.01E-06		
P62633	CNBP	CNBP_HUMAN	177	19713.70	P62633-2;P6	3	2	13.50	Carbamidom	2.97		4.74E-06		
C9JH19	CTSD	C9JH19_HUMAN	299	44631.70	CONT_CTD	3	3	19.10	Gln->pyro-Gl	2.00		7.84E-07		
Q00571	DDX3X	DDX3X_HUMAN	662	71491.00	O00571-2;	7	7	14.10	Oxidation (M)	6.98		1.35E-06		
O43143	DHX15	DHX15_HUMAN	795	91109.30		2	2	3.10		2.00		1.49E-07		
Q8XB1	DNAJC10	DJC10_HUMAN	793	91255.40		2	2	2.80		2.00		1.44E-07		
Q13011	ECH1	ECH1_HUMAN	328	35883.40		3	3	12.50		2.99		6.78E-07		
E9PI39	EEF1D	E9PI39_HUMAN	204	28612.40	E9PIZ1;E9PK0	2	2	17.50		2.00		7.54E-07		
B4DTG2	EEF1G	B4DTG2_HUMAN	487	50213.20	P26641;	3	2	5.30		3.00		5.25E-07		
B4DVY1	EIF3D	B4DVY1_HUMAN	499	64094.50	O15371;	3	2	4.80		2.97		5.39E-07		
F8VP89	EIF4B	F8VP89_HUMAN	275	31274.00		1	4	12.70		1.00		8.42E-07		
BOQYK0	EWSR1	BOQYK0_HUMAN	618	62631.10	Q01844;Q01	14	7	15.00	Carbamidom	13.86				

B4DHY1	HNRNPH3	B4DHY1_HU	238	15439.10	P31942;P31942	3	3	22.30		3.00	1.84E-06	jmjdb2 only
MOR019	HNRNPM	MOR019_HU	353	73770.50	P52272;P52272	1	2	5.90		1.00	1.37E-07	jmjdb2 only
Q99714	HSD17B10	HCD2_HUMA	261	26978.20		6	4	24.10	Oxidation (M)	5.97	3.42E-06	jmjdb2 only
P10809	HSPD1	CH60_HUMA	573	61178.50		17	13	30.00	Carbamidom	16.93	4.00E-06	jmjdb2 only
P01857	IGHG1	IGHG1_HUM	330	36173.20		8	3	9.70	Oxidation (M)	6.00	2.29E-05	jmjdb2 only
P01834	IGKC	IGKC_HUMA	106	11619.70		1	2	30.20		1.00	5.24E-06	jmjdb2 only
F5GX28	KDM4B	F5GX28_HU	1130	126326.00		45	26	25.30	Carbamidom	44.67	9.39E-06	jmjdb2 only
Q92945	KHSRP	FUBP2_HUM	711	73268.10		4	4	6.00		4.00	5.49E-07	jmjdb2 only
M0QZF9	KLK3	MOQZF9_HU	172	25153.70	M0R1F0;M0R1F0	4	3	20.30		2.98	2.47E-06	jmjdb2 only
P05787	KRT8	K2C8_HUMA	483	56717.50	P05787-2;	2	10	13.50		2.00	2.46E-07	jmjdb2 only
Q08380	LGALS3BP	LG3BP_HUM	585	65451.40		4	4	7.50		3.99	5.01E-07	jmjdb2 only
B7Z8V7	NADK2	B7Z8V7_HU	301	31768.20	Q4G0N4;Q4G0N4	3	2	9.30		2.00	3.11E-07	jmjdb2 only
J3KPD9	NME1-NME2	J3KPD9_HUN	197	32692.90	P22392;P22392	4	3	24.90		3.97	3.34E-06	jmjdb2 only
C9JYS8	NONO	C9JYS8_HUM	248	43946.20	Q15233;Q15233	2	2	9.30		1.98	8.26E-07	jmjdb2 only
E9PAL9	NT5DC2	E9PAL9_HUN	557	57311.00	Q9H857;Q9H857	2	2	4.30		2.00	3.15E-07	jmjdb2 only
H3BMW1	NUBP2	H3BMW1_HU	139	28878.90	H3BNF0;H3BNF0	1	2	45.70		1.00	6.91E-07	jmjdb2 only
Q53EL6	PDCD4	PDCD4_HUM	469	50670.60	Q53EL6-2;	2	3	10.30		2.00	5.61E-07	jmjdb2 only
O75340	PDCD6	PDCD6_HUM	191	21908.80		11	5	21.50	Oxidation (M)	10.97	1.12E-05	jmjdb2 only
Q9UVB8	PEF1	PEF1_HUMA	284	30433.30		4	3	12.00	Oxidation (M)	4.00	3.90E-06	jmjdb2 only
O43175	PHGDH	SERA_HUMA	533	53195.50	Q55ZU1;	4	4	9.60		4.00	6.48E-07	jmjdb2 only
Q9GP4	PITHD1	PITH1_HUM	211	24159.80	Q9GP4-2;	3	2	9.50		3.00	1.43E-06	jmjdb2 only
B4E0V0	PNPO	B4E0V0_HU	166	30040.80	B4E152;B4E152	2	2	10.20		1.99	1.39E-06	jmjdb2 only
P22694	PRKACB	KAPCB_HUM	351	41459.30	P22694-2;P22694-2	4	3	8.90		3.96	1.29E-06	jmjdb2 only
K7EM13	PRKAR1A	K7EM13_HU	153	43063.00	K7EPB2;K7EPB2	2	2	19.00		2.00	7.52E-07	jmjdb2 only
B5MDF5	RAN	B5MDF5_HU	233	24461.70	HOYFC6;J3KC	2	2	21.40		1.98	1.08E-06	jmjdb2 only
Q96PK6	RBM14	RBM14_HUN	669	69647.00		4	3	4.90		4.00	5.34E-07	jmjdb2 only
H0Y6E7	RBMX	HOY6E7_HUN	292	42224.30	H3BR27;H3B	2	2	34.60		1.98	4.30E-07	jmjdb2 only
D6RAN4	RPL9	D6RAN4_HU	182	21903.80	HOY9V9;P329	3	2	13.20		1.98	8.14E-07	jmjdb2 only
F8VWS0	RPLP0	F8VWS0_HU	281	27490.40	F8VZS0;P053	2	2	11.00		1.98	7.35E-07	jmjdb2 only
Q9Y3I0	RTCB	RTCB_HUMA	505	55318.90		7	7	16.00		7.00	1.88E-06	jmjdb2 only
A6PVW9	SELENBP1	A6PVW9_HU	514	45428.30	Q13228;Q13228	3	3	8.10		2.97	3.93E-07	jmjdb2 only
E9PJ04	SF3B2	E9PJ04_HUM	354	100417.00	E9PTJ3;HOYC	3	3	15.40		2.97	6.07E-07	jmjdb2 only
P23246	SFPQ	SFPQ_HUMA	707	72415.90	P23246-2;	2	2	4.20		2.00	2.25E-07	jmjdb2 only
B4DLV4	SHMT2	B4DLV4_HU	408	53565.50	G3V2Y4;G3V	2	2	11.60		2.00	4.78E-07	jmjdb2 only
F8VX8	SMARCC2	F8VX8_HU	1245	127188.00	Q8TAQ2;Q8T	4	4	3.50	Gln->pyro-G	4.00	1.97E-07	jmjdb2 only
P08621	SNRNP70	RU17_HUMA	437	19814.00	P08621-2;P08621-2	8	5	34.30		8.00	2.14E-06	jmjdb2 only
M0R268	SNRPA	M0R268_HU	256	31331.20	P09012;	10	7	36.70	Acetyl (Prote	9.00	4.62E-06	jmjdb2 only
J3KTL2	SRSF1	J3KTL2_HUM	253	22500.00	Q07955;Q07955	5	4	21.40	Carbamidom	4.95	1.69E-06	jmjdb2 only
HOYKU1	TMOD3	HOYKU1_HU	187	39660.40	HOYN8;Q9N	4	4	28.90	Gln->pyro-G	4.00	1.74E-06	jmjdb2 only
Q13263	TRIM28	TIF1B_HUMA	835	79639.60	Q13263-2;	3	2	6.10	Acetyl (Prote	2.98	3.05E-07	jmjdb2 only
A8MUB1	TUBA4A	A8MUB1_HU	433	50018.40	P68366;	5	15	45.30	Carbamidom	3.97	3.38E-06	jmjdb2 only
Q9NQH7	XPNPEP3	XPP3_HUMA	507	54780.60	Q9NQH7-4;	14	8	16.50		13.84	4.78E-06	jmjdb2 only

Table S2
KDM4B RNAse vs noRNase

Protein (UniProt)	Gene Symbol	Description	Length (AA)	mw (Da)	Indistinguishable	PSMs	Peptide Seq	% Coverage	Modifications	SPECTRAL COUNTS		SPECTRAL INDEX (MIC sin)		RATIO
										2BNRNASE	2BWTHRNASE	2BNRNASE	2BWTHRNASE	
O14744	PRMT5	ANM5_HUM	637	72817.60		70	25	43.50	Acetyl (Prote)	59.15	3.39E-05	2BNRNASE Only		
P46821	MAP1B	MAP1B_HUN	2468	271206.00		31	29	17.70	Acetyl (Prote)	30.90	1.64E-06	2BNRNASE Only		
Q9BQA1	WDR77	MEP50_HUM	342	36791.10		20	11	41.50	Carbamidom	17.96	1.78E-05	2BNRNASE Only		
E7EVX8	PRPF31	E7EVX8_HUN	493	55565.50	Q8WWYV3;	14	11	32.00	Gln->pyro-Gl	10.86	3.00E-06	2BNRNASE Only		
E7EX17	EIF4B	E7EX17_HUN	616	69290.40	P23588;	14	17	29.10		8.92	3.16E-06	2BNRNASE Only		
Q9Y2Z1	THRAFS	TR150_HUM	955	108871.00		12	9	8.90	Oxidation (M)	11.00	2.92E-06	2BNRNASE Only		
B5ME19	EIF3CL	EIFCL_HUMA	914	105548.00	H3BRV0;C99	10	10	10.20	Carbamidom	8.00	1.18E-06	2BNRNASE Only		
P98175	RBMI0	RBMI0_HUN	930	103640.00	P98175-2;	10	9	13.60	Oxidation (M)	8.00	1.19E-06	2BNRNASE Only		
Q99714	HSD17B14	HCD2_HUMA	261	26039.60	Q99714-2;	9	4	32.50		9.00	2.11E-06	2BNRNASE Only		
B4DLW8	DDX5	B4DLW8_HU	535	69284.80	J3KTA4;P178	9	14	28.40	Carbamidom	6.49	1.90E-06	2BNRNASE Only		
Q9UH65	LIMA1	LIMA1_HUM	759	85387.50	Q9UH64-4;	9	9	13.70		7.92	1.34E-06	2BNRNASE Only		
P04792	HSPB1	HSPB1_HUM	205	22822.50		9	7	50.20	Gln->pyro-Gl	7.00	5.91E-06	2BNRNASE Only		
P09012	SNRPA	SNRPA_HUM	282	31331.20		9	7	33.30	Acetyl (Prote)	4.95	3.79E-06	2BNRNASE Only		
Q15208	STK38	STK38_HUM	465	54281.40		8	8	15.90		7.00	2.82E-06	2BNRNASE Only		
B3KV1R	SNRPA	B3KV1R_HU	244	24652.10	J3QLE5;P146	8	5	26.00	Oxidation (M)	7.00	6.42E-06	2BNRNASE Only		
EPHS10	LANC1	EPHS10_HU	196	45361.60	P04813;	8	7	48.00	Carbamidom	6.00	3.13E-06	2BNRNASE Only		
P08621	SNRNP70	RU17_HUM	437	50713.40	P08621-2;	8	8	16.10		6.96	2.47E-06	2BNRNASE Only		
P13639	EEF2	EEF2_HUMAN	858	95529.10		8	8	11.00	Ammonia-los	7.00	7.00E-07	2BNRNASE Only		
P62316	SNRNP2	SM2D_HUM	118	13536.20		8	5	46.60	Acetyl (Prote)	4.96	7.59E-06	2BNRNASE Only		
Q01085	TIAL1	TIAL_HUMA	375	43529.10	Q01085-2;	7	6	20.50	Gln->pyro-Gl	6.86	2.80E-06	2BNRNASE Only		
Q14247	CTTN	SRC8_HUMA	550	61710.60		7	7	12.70	Carbamidom	6.94	1.40E-06	2BNRNASE Only		
Q6UB35	MTTDEH1	C1TM_HUMA	978	106012.00		7	6	9.40		6.99	2.73E-07	2BNRNASE Only		
E9PK09	BCLA1F	E9PK09_HUM	726	100424.00	E9PK1;E9PK	7	6	7.90	Oxidation (M)	2.99	4.12E-07	2BNRNASE Only		
OG6506	SYNCRIP	HNRQO_HUN	623	58843.40	P06505-2;O	7	6	12.90		3.97	1.12E-06	2BNRNASE Only		
Q13885	TUB282	TUB282_HUM	445	50407.00	Q9BVVA1;	7	21	53.70	Carbamidom	2.50	4.55E-07	2BNRNASE Only		
P57273	KIF11	KIF11_HUMA	1056	119391.00		6	7	7.50		6.00	8.71E-07	2BNRNASE Only		
Q90855	DSC1	DSC1_HUMA	894	94010.20	Q08554-2;	6	5	8.00	Carbamidom	4.00	1.19E-06	2BNRNASE Only		
E9PM16	C1NS1A	E9PM16_HU	167	26252.90	J3K3B;P541	6	4	34.10		4.98	1.60E-06	2BNRNASE Only		
Q14008	CKAP5	CKAP5_HUM	2032	226708.00	Q14008-2;Q	5	4	2.70		4.00	9.21E-08	2BNRNASE Only		
Q9Y2H1	STK38L	STK38L_HUMA	464	54045.50		5	7	18.10	Carbamidom	2.98	7.55E-07	2BNRNASE Only		
Q3EL6	PDCD4	PDCD4_HUM	469	50670.60	Q53E6-2;	5	5	4	12.70	5.00	6.97E-07	2BNRNASE Only		
Q29245	KHSPR	FUBP2_HUM	711	73268.10		5	6	10.80		2.98	4.31E-07	2BNRNASE Only		
E9P139	EEF1D	E9P139_HUM	204	71544.20	E9PK1;E9PK	5	3	36.90		4.00	2.09E-06	2BNRNASE Only		
J3KT12	SRSF1	DSC1_HUMA	253	22500.50	Q07955;Q07	5	5	32.30	Carbamidom	5.00	2.74E-06	2BNRNASE Only		
P26599	PTBP1	PTBP1_HUM	531	59758.00	P26599-2;P2	5	4	12.10		3.96	5.65E-07	2BNRNASE Only		
P47756	CAP2B	CAP2B_HUM	277	30681.40	P47756-2;	5	4	16.50	Acetyl (Prote)	2.95	1.43E-06	2BNRNASE Only		
P62424	RPL7A	RPL7A_HUMA	266	21585.40	P078U3;	5	4	21.50		3.00	1.24E-06	2BNRNASE Only		
B4D1P7	SNRPD3	B4D1P7_HUN	120	13943.30	P62318;	4	2	15.80	Oxidation (M)	2.00	6.40E-06	2BNRNASE Only		
K7E602	DAZAP1	K7E602_HU	225	40611.90	P096EP5;Q96	4	3	18.70	Acetyl (Prote)	2.00	6.14E-07	2BNRNASE Only		
P11717	IGF2R	MPLR_HUMA	2491	274937.00		4	4	2.00	Carbamidom	3.00	6.53E-08	2BNRNASE Only		
Q13247	SRSF6	SRSF6_HUM	344	38485.70	J3K247-3;	4	4	11.00	Gln->pyro-Gl	2.98	1.53E-06	2BNRNASE Only		
AGPVW9	SELENBP1	AGPVW9_HU	514	45458.10	P13228;Q13	4	4	13.50		4.00	7.80E-07	2BNRNASE Only		
Q8WU73	PRUNE2	PRUNE2_HUM	3088	33760.70	Q8WU73-2;Q	4	3	1.40	Gln->pyro-Gl	3.00	6.36E-08	2BNRNASE Only		
Q9UKV8	AGO2	AGO2_HUM	859	93794.30	Q9UKV8-2;	4	4	5.10		3.00	2.43E-07	2BNRNASE Only		
P67936	TPM4	TPM4_HUM	248	28575.60		4	2	7.30		0.99	9.74E-08	2BNRNASE Only		
D6RAF8	HNRNP	D6RAF8_HU	221	32904.10	J14103;Q14	4	6	29.90	Carbamidom	0.99	1.50E-06	2BNRNASE Only		
J3KS22	DCXR	J3KS22_HUM	224	25968.60	J3QS36;Q724	4	3	14.70		3.00	1.28E-06	2BNRNASE Only		
O75533	SFB1	SFB1_HUMA	1304	146116.00		4	3	3.30		4.00	2.24E-07	2BNRNASE Only		
P03090	GSPR	GSHR_HUMA	522	47363.30	P00990-2;P0	4	4	12.50	Carbamidom	3.99	1.56E-06	2BNRNASE Only		
P10644	PRKAR1A	PRKAR1A_HUMA	381	43063.00		4	4	4.90		3.00	2.00E-07	2BNRNASE Only		
Z23246	SFPQ	SFPQ_HUMA	707	76299.70		4	4	6.40		3.00	4.95E-07	2BNRNASE Only		
P25285	CFL1	CFL1_HUMA	166	18526.70		4	5	39.20	Acetyl (Prote)	2.95	3.41E-06	2BNRNASE Only		
P26641	EEF1G	EEF1G_HUMA	437	50213.20		4	3	8.50	Acetyl (Prote)	2.00	1.87E-07	2BNRNASE Only		
Q9JAB2	SRSF7	S9JAB2_HUM	235	26050.30	J16629;Q16	3	3	31.80		3.00	1.47E-06	2BNRNASE Only		
I3L380	C1QBQ	I3L380_HUM	178	31417.40	J3L37;Q07	3	3	33.90	Carbamidom	3.00	5.08E-07	2BNRNASE Only		
P62805	HIST1H4H	H4_HUMAN	103	11378.00		3	3	29.10		3.00	6.37E-06	2BNRNASE Only		
Q35Y84	SERPINB1	Q35Y84_HU	425	46355.10	P096P63;	3	4	9.00	Oxidation (M)	2.00	8.69E-07	2BNRNASE Only		
Q9UBV8	PEF1	PEF1_HUMA	284	30433.60		3	2	8.00	Oxidation (M)	2.00	1.61E-07	2BNRNASE Only		
Q9YJQ9	RPL22L1	C9YJQ9_HUN	121	14633.60	H0Y8C2;Q6P	3	2	15.70		1.00	3.60E-06	2BNRNASE Only		
Q9J469	FABP5	FABP5_HUM	135	15190.60		3	2	13.30	Acetyl (Prote)	1.00	1.14E-06	2BNRNASE Only		
Q15437	SEC23B	SEC23B_HUM	767	86639.60		3	4	7.30	Acetyl (Prote)	1.00	1.07E-07	2BNRNASE Only		
HOYD4D	DLAT	HOYD4D_HU	479	69133.20	P10515;	3	3	9.60	Carbamidom	1.98	2.21E-07	2BNRNASE Only		
O75340	PDCD6	PDCD6_HUM	191	21704.70	P175340-2;	3	3	18.00		3.00	3.94E-06	2BNRNASE Only		
P21333	FLNA	FLNA_HUMA	2647	277152.00	P21333-2;Q5	3	3	1.80		3.00	4.47E-08	2BNRNASE Only		
P22694	PRKACB	PRKACB_HUM	351	41459.30	P22694-2;P2	3	3	8.90		2.97	5.88E-07	2BNRNASE Only		
P38919	EIF4A3	EIF4A3_HUMA	411	46940.20		3	3	8.50		2.92	8.35E-07	2BNRNASE Only		
P39656	DDOST	Q5T48_HUM	456	50895.00		3	3	7.20		2.99	4.13E-07	2BNRNASE Only		
P60866	RPS20	RPS20_HUMA	119	16031.50	P60866-2;	3	3	22.70		2.97	7.92E-06	2BNRNASE Only		
P61158	ACTR8	ARP3_HUMA	418	47440.30		3	3	12.90	Carbamidom	0.99	7.08E-08	2BNRNASE Only		
P62304	SNRPE	RUXE_HUMA	92	10814.70		2	2	25.00	Oxidation (M)	2.00	2.01E-06	2BNRNASE Only		
O76031	CLPX	CLPX_HUMA	633	69360.80		2	2	4.10		2.00	3.00E-07	2BNRNASE Only		
Q94919	ENDD1	ENDD1_HUM	500	55125.40		2	2	4.80		2.00	2.57E-07	2BNRNASE Only		
P05077	PURA	PURA_HUMA	322	34979.40		2	2	15.20		2.00	5.44E-07	2BNRNASE Only		
Q14011	CIRBP	CIRBP_HUM	172	18672.80		2	2	18.60		2.00	2.00E-07	2BNRNASE Only		
P4DT31	FUDP1	FUDT31_HUM	665	68742.10	P09PE5;Q96	2	2	4.80		1.98	2.52E-07	2BNRNASE Only		
P4DU0	PYCR1	PYCR1_HUM	346	33409.60	J3QK74;P323	2	2	9.90		1.98	8.32E-07	2BNRNASE Only		
P60762	S100A9	S100A9_HUM	114	13251.50		2	2	17.50		1.00	2.61E-06	2BNRNASE Only		
CTNBB1	D4GU4	D4GU4_HU	774	38576.40	P35222;	2	2	2.80	Carbamidom	1.50	9.45E-08	2BNRNASE Only		
B4DE47	C7TB	B4DE47_HUM	529	59744.60	P4DQH4;P50	2	2	5.30		0.99	4.04E-08	2BNRNASE Only		
Q9J2L7	NONO	C9J2L7_HUM	207	43946.20	P09V58;Q152	2	2	8.20		1.98	7.45E-07			

P46781	RP59	RS9_HUMAN	194	22631.60		21	10	47.90	7.99	10.98	1.22E-05	5.85E-06
B4E2W0	HADHB	B4E2W0_HU	452	51387.60	P55084;	9	6	12.20	Oxidation (M	4.94	2.96	1.85E-06
P14923	JUP	PLAK_HUMA	745	81908.90		46	21	37.40	Carbamidom	16.46	23.86	3.72E-06
F5GX28	KDM4A	F5GX28_HU	1130	122143.00	Q94953;	75	30	30.30	Acetyl (Prote	38.94	29.95	5.83E-06
P05141	SLC25A5	ADT2_HUMA	298	32903.20		13	11	34.90	Acetyl (Prote	6.00	7.00	6.26E-06
P61247	RP53A	RS3A_HUMA	264	29997.80		30	14	48.10	Carbamidom	11.59	11.66	5.53E-06
P25705	ATP5A1	ATPA_HUMA	553	59875.70		28	15	31.60	Oxidation (M	10.80	12.71	4.09E-06
P08107	HSPA1B; HSP	HSP71_HUM	641	70189.10		41	26	50.40	Carbamidom	16.81	17.86	4.15E-06
Q92804	TAF15	RBP56_HUM	592	61683.10	Q92804-2;	18	9	28.40	Gln->pyro-G	8.91	5.94	6.46E-06
Q928E1	MRLP37	RM37_HUM	423	56051.96	SAR369;	3	2	7.30		1.00	1.00	9.46E-08
P81605	DCD	DCD_HUMA	110	12442.50	P81605-2;	14	5	40.90		5.00	7.00	1.07E-05
B4DT58	DPF2	B4DT58_HU	207	44235.20	J3KMAZB_Q92	5	3	15.90	Acetyl (Prote	1.00	1.00	1.87E-07
O95831	AIFM1	AIFM1_HUM	613	66433.70	Q95831-3;	3	3	5.70		0.99	0.99	5.43E-08
Q13263	TRIM28	TIF1B_HUMA	835	79639.60	J013263-2;	5	4	9.40	Acetyl (Prote	1.98	1.98	2.22E-07
J3KRK5	RPL17	J3KRK5_HUM	174	26409.80	J3Q0T2;J3Q5	3	3	25.40		1.98	0.99	2.42E-06
P55884	EIF3B	EIF3B_HUMA	814	99219.20	P55884-2;	34	19	27.50	Acetyl (Prote	12.99	16.00	2.13E-06
BOQYKO	EWRS1	EWRS1_HU	618	62631.10	Q01844;Q01	38	8	16.20	Carbamidom	12.87	13.86	5.97E-06
Q92922	SMARCC1	SMRC1_HUN	1105	123114.00		7	5	6.60	Acetyl (Prote	2.00	1.00	2.55E-08
G5E975	SMARCB1	GSE975_HU	394	43238.60	Q12824;Q12	11	7	18.90		2.97	4.95	1.10E-06
P32119	PRDX2	PRDX2_HUM	198	21932.30		14	6	31.80	Gln->pyro-G	5.49	3.49	4.00E-06
Q8N1NA	KRT78	K2C78_HUM	520	56974.60		15	14	23.70	Carbamidom	7.98	5.97	1.67E-06
O96019	ACTL6A	ACLA6_HUMA	429	43136.10	Q96019-2;	6	4	16.50	Gln->pyro-G	2.00	1.00	3.38E-07
O14497	ARID1A	AR1A_HUM	2285	206349.00	J014497-2;O	7	7	4.00	Acetyl (Prote	2.98	1.99	6.88E-08
A43390	HNRNPB	HNRNPB_HUM	633	60590.50	J043390-2;54	2	4	7.70		0.99	0.99	4.95E-08
HOY457	RBMX	HOY667_HU	292	42224.30	H3BR27;H3B	2	2	34.60	Carbamidom	8.87	4.93	7.98E-06
Q13347	EIF3G	EIF3G_HUMA	325	36563.70		18	11	47.20	Carbamidom	11.00	5.00	6.88E-06
HOY449	YBX1	HOY449_HU	374	35929.70	P67809;	3	3	18.20		2.00	1.00	1.77E-06
BDV988	ELAVL1	BDV988_HU	353	39061.70		5	4	11.90	Carbamidom	3.98	1.00	4.04E-07
Q15393	SF3B1	SF3B3_HUM	1217	135852.00		15	12	22.70		7.00	4.99	6.89E-07
Q00796	SORD	DHSO_HUM	357	38389.90		11	7	23.50	Acetyl (Prote	4.99	3.99	2.64E-06
O43143	DHX15	DHX15_HUM	795	91109.30		14	9	11.70	Carbamidom	6.00	7.00	3.21E-06
P07437	TUBB	TBB5_HUMA	444	49765.00		21	24	62.40	Carbamidom	10.89	6.93	3.24E-06
B4DSU6	HNRNPC	B4DSU6_HU	147	27876.50	B4DY08;G3V	9	3	30.60	Oxidation (M	4.98	3.97	9.26E-06
P68363	TUBA1B	TUBA1B_HU	451	50245.70		14	14	40.40	Acetyl (Prote	7.80	4.84	5.86E-06
Q9Y3IO	RTCB	RTCB_HUMA	505	55318.90		15	8	20.80	Gln->pyro-G	7.00	3.00	2.82E-06
B4DGGM3	SMARCE1	B4DGGM3_HU	393	34441.00	J3QK57;K7E	3	2	15.80		2.00	1.00	2.40E-07
Q08211	DHK9	DHK9_HUMA	1270	141247.00		23	18	15.80	Carbamidom	13.00	5.94	1.38E-05
J3QR48	PNKP1	J3QR48_HU	149	97360.20	Q14974;	4	2	18.10		3.95	2.98	2.01E-07
F5H365	SEC23A	F5H365_HU	736	86321.40	J015436;	10	5	8.70	Acetyl (Prote	3.96	1.98	2.39E-07
P23396	RS3A	RS3A_HUMA	243	26743.50		37	15	67.90	Carbamidom	15.62	14.63	1.64E-05
HOY2W2	ATAD3A	HOY2W2_HU	572	58056.10	Q9NV17;Q9N	7	7	13.80		1.98	1.00	3.30E-06
MOR0FO	RP55	MOR0FO_HU	200	22916.10	J04782;	12	5	34.50	Acetyl (Prote	5.95	1.98	1.14E-06
B4DKM5	VDA2C	B4DKM5_HU	255	30465.10	J04580;P458	2	2	7.10		1.00	1.00	6.12E-07
H7BY58	PCMT1	H7BY58_HU	286	24717.60	J3KP72;P220	28	11	57.70	Carbamidom	13.86	9.90	9.86E-06
P62081	RP57	R57_HUMAN	194	22167.30		8	4	29.40		5.00	2.00	2.26E-06
H3BLZ8	DDX17	H3BLZ8_HUM	731	72691.20	Q92841;Q92	12	13	23.70	Carbamidom	7.43	3.96	1.28E-06
E9PH29	PRDX3	E9PH29_HU	238	27747.20	P30048;	8	4	18.50		4.00	3.00	2.50E-06
Q24995	DDX1_HUMA	740	46915.20	J015371;	6	5	15.70	Carbamidom	9.00	4.00	1.30E-06	
P54886	ALDH18A1	P5CS_HUMA	795	87268.60	P54886-2;	7	6	8.10		5.00	1.00	1.02E-06
P23526	AHCY	SAHH_HUMA	432	44737.70	J23526-2;	3	2	5.20		2.00	1.00	6.04E-07
P67079	ACTB	ACTB_HUMA	375	41817.80		116	24	64.80	Acetyl (Prote	67.21	29.17	8.73E-05
P12523	CNMT1B; CTKCRU	CNMT1B_HUMA	417	47115.30		13	7	18.50	Carbamidom	4.94	4.91	2.11E-06
Q8IX81	DNAA10	DIC10_HUM	793	91255.40		10	8	11.50	Carbamidom	7.96	1.99	7.65E-07
K7E1B1	EFTUD2	K7E1B1_HUM	962	105587.00	Q15029;Q15	4	4	5.30		2.00	1.00	1.57E-07
Q9Y22A	C14orf166	C166_HUM	244	28122.80		5	4	27.00		4.00	1.00	2.35E-08
ETERC4	SSB	ETERC4_HUM	184	46916.20	E9PGX9;P054	3	2	23.30		2.00	1.00	8.91E-07
Q12906	ILF3	ILF3_HUMAN	894	96000.50	J12906-2;Q	10	8	15.20		6.00	2.00	8.76E-07
P62258	YWHAE	YWHAE_HUM	255	29275.20		4	3	10.20		0.98	0.99	1.19E-07
P08238	HSP90AB1	HSP90B_HUM	724	83428.20		14	16	22.50	Oxidation (M	6.99	2.99	1.49E-06
P46783	RP510	RP510_HUMA	165	18012.90		6	5	33.00		4.00	2.00	1.89E-07
P24752	ACAT1	ACIL_HUMA	427	45296.70		13	10	31.90	Carbamidom	6.99	4.00	4.35E-07
P68371	TUBB4B	TBB4B_HUM	445	49925.10		12	24	58.00	Carbamidom	3.54	2.04	2.05E-06
P04843	RPN1	RPN1_HUMA	607	68706.90		4	3	6.30		3.00	1.00	3.24E-06
MOOK55	HNRNPL	MOOK55_HU	530	50654.60	J01866;P148	9	6	14.90	Carbamidom	5.98	2.00	1.26E-06
Q92506	HSD17B8	HDB8_HUMA	261	27028.80		3	3	15.30		2.00	1.00	9.88E-07
P51532	SMARCA4	SMCA4_HUN	1647	188517.00	J05152-2;P5	5	7	4.80		2.99	0.99	1.54E-07
13L3P7	RP515A	13L3P7_HUM	100	14866.00	P62244;	4	3	26.00	Oxidation (M	2.97	0.99	1.68E-08
ABMUI81	TUB4A4	ABMUI81_HU	433	50018.40	P68366;	10	13	37.40	Carbamidom	5.97	1.99	1.59E-07
DGRAN4	RP1	DGRAN4_HU	182	21903.80	J02969;	4	3	23.60		2.97	0.99	2.47E-06
Q05639	EEF1A2	EEF1A2_HUM	463	50564.40		16	11	25.50	Gln->pyro-G	4.50	1.50	5.70E-06
P55795	HNRNPH2	HNRNPH2_HUM	449	49358.40		12	10	31.60	Carbamidom	9.00	2.00	1.97E-06
P07237	P4HB	P4HB1_HUM	508	57224.80		17	12	26.00	Oxidation (M	11.81	2.97	3.02E-06
J3QLR8	MRPS23	J3QLR8_HUN	152	21811.30	Q9Y3D9;	3	3	19.70		2.00	1.00	1.12E-07
Q15365	PCBP1	PCBP1_HUM	356	37564.00		16	11	44.10	Acetyl (Prote	10.92	1.97	4.08E-06
A8MXP9	MATR3	A8MXP9_HU	895	94816.90	P43243;	6	3	5.90		3.96	0.99	2.00E-07
Q13151	HNRNPA0	ROAO_HUM	305	30911.80		8	6	25.90		6.00	2.00	3.28E-06
P52597	HNRNPF	HNRNPF_HUM	415	45750.90		12	8	23.10	Acetyl (Prote	9.00	2.00	2.54E-06
P42704	LPRP2	LPRP2_HUM	1394	158219.00		3	3	2.80	Carbamidom	2.00	1.00	1.38E-07
P61978	HNRNPK	HNRNPK_HUM	463	48658.20	P61978-2;P6	31	16	44.30	Carbamidom	22.77	6.93	9.84E-06
P68104	EEF1A1	EEF1A1_HUM	462	50279.20	J05VTE0;	46	18	47.80	Carbamidom	23.50	6.50	1.96E-05
K7ERF1	EIF3K	K7ERF1_HUN	192	25097.50	J09UBQ5;	5	3	20.30	Oxidation (M	2.97	0.99	1.16E-06
P49327	FASN	FAS_HUMAN	2511	273993.00		51	40	19.90	Acetyl (Prote	36.00	5.00	2.05E-06
P30041	PRDX6	PRDX6_HUM	224	25073.20		4	2	13.40		3.00	1.00	1.33E-06
P46777	RP55	RL5_HUMAN	297	34412.70		6	6	22.20	Carbamidom	4.00	1.00	1.80E-06
P55072	VCP	TERA_HUMA	806	89499.90		9	10	14.40	Acetyl (Prote	4.99	1.00	9.92E-07
E9PKG1	PRMT1	E9PKG1_HU	325	40612.10	J07C21;Q998	21	14	42.80	Carbamidom	15.89	2.96	4.98E-06
Q00610	CLTC	CLH1_HUMA	1675	188257.00	J00610-2;	15	12	9.40	Carbamidom	12.00	1.00	5.51E-07
P51659	HSD17B4	DH84_HUM	736	79852.40		9	9	18.50		6.94	0.99	1.25E-06
P52907	CAP2A1	CAZ1_HUMA	286	32974.40		9	6	24.50	Acetyl (Prote	6.00	1.00	2.79E-0

Table S3

RIP and Chip q-PCR primer

C3 F	AACAGAAGTACCTGTGCGCC
C3 R	CCAGAGTCATCCCTGCTTC
I3a F	AGGGATGACTCTGGGAGGTAA
I3a R	CTATGAAAGGGTCAGCCTGTG
I3b F	CACAGGCTGACCCTTCATA
I3b R	ACCTTCTGTTGGCTCCTGAT
I3c F	GCACCATGCTAGGCATTAGA
I3c R	AAAGGCAAGGCCATTACAC
I3d F	TCCCTCTCCTCTGATGC
I3d R	GGGAGCAGGAAACAGACAAT
CE1 F	AACTAGGAATGTGGCCTTGG
CE1 R	CAATTCCAGTTCTATGATGGGA
I3e F	CCTCCATTGGGTTTACCC
I3e R	CAAGCCAATTGCCTGGTCAAACCA
CE2 F	GGTGATGCAAGTGGGAAGTC
CE2 R	GCTGAGTCACAAGTTGCACA
CE5 F	CGTTGTTAAGAAGTAGAACTAA
CE5 R	AACAGATGAGCTGAAGGCTCT
I3f F	GCAGAAAATTGGACTGGCA
I3f R	CCATGCCTCATTTCCACCC
I3g F	TGAAACTGAAAGAGACTGATGACT
I3g R	GCCTAACAGCTCACTAATCAAAG
CE3 F	ACCTCCCCAACTTACATGCT
CE3 R	CAGGGTCTGGTCATTTGAGA
I3h F	GGGCTACTCTTGTGATTGCTG
I3h R	GTCCTCACAAACATCCCTGTG
I3i F	CTTCTCCAAGCCAGACTCA
I3i R	CATGTGTGTTCCCTGGCTT
I3j F	AGGCTAAGTCTGCCAAAG
I3j R	GGAGTCAGGATGCCTCATT
I3k F	TAGGCAGAGAACGCCAGAACAA
I3k R	CCCTGTGACCACAGTGGCCC
I3l F	TGAACACTCCTGGTGCTT
I3l R	ATGAGGATTCACCAAGGCA
C4 F	CACTGAGGAGACAACCCAGA
C4 R	CACTACACCTGGCTCAATGG
I4a F	GGAAAGAACATGAGGTTGGG
I4a R	GAAATTGAGACCCAGAACAGGG

siRNA oligo

KDM4B_siRNA1	CUCUUCACGCAGUACAAUA [dT][dT]
kDM4B_siRNA2	CAAAUACGUGGCCUACAU[dT][dT]
AR-V7_siRNA1	GUAGUUGUGAGUAUCAUGA [dT] [dT]

AR-V7_siRNA2 GAGGCUUAGGAGCUUAGGU [dT][dT]

RNA oligo

AR-A1	CAAUGAACUGAAAGAGACUGAUGACUCUCCUGAGGGUGG (Btn)
AR-A2	CUCAUCCCCAGUCUGAGUAUAUAGCUUAUAGUAUUUAGG (Btn)
AR-A2	CUCAUCCCCAGUCUGAGUAUAUAGCUUAUAGUAUUUAGG
AR-A2 mut	CUCAUCCCCAGUCUGAGGCCUAUAGCUUAUAGAAUUUAGC
AR-A2-1	CUCAUCCCCAGUCUGAGUAUA
AR-A2-2	UAAUGCUCUUAUAGUAUUUAGC
AR-A2-3	GUCUGAGUAUAUAGCUUAU

RIP and ChIP q-PCR primer

C3 F	AACAGAACGTACCTGTGCC
C3 R	CCAGAGTCATCCCTGCTTC
I3a F	AGGGATGACTCTGGGAGGTAA
I3a R	CTATGAAAGGGTCAGCCTGTG
I3b F	CACAGGCTGACCCTTCATA
I3b R	ACCTTCTGTTGGCTCCTGAT
I3c F	GCACCATGCTAGGCATTAGA
I3c R	AAAGGCAAGGCCATTACAC
I3d F	TCCCTCTCCTCTGATGC
I3d R	GGGAGCAGGAAACAGACAAT
CE1 F	AACTAGGAATGTGGCCTTGG
CE1 R	CAATTCCAGTTCTATGATGGGA
I3e F	CCTCCATTGGGTTTAC
I3e R	CAAGCCAATTGCCTGGTCTAACCA
CE2 F	GGTGATGCAAGTGGGAAGTC
CE2 R	GCTGAGTCACAAGTTGCACA
CE5 F	CGTTGTTAAGAAGTAGAACTAA