Supporting Information for

“Targeted Profiling of Epitranscriptomic Reader, Writer and Eraser Proteins Regulated by Histone Methylation H3K36me3”

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Supplementary Experimental Section

Neocarzinostatin (NCS) treatment

HEK293T and the isogenic *SETD2*$^{-/-}$ cells were treated with 100 ng/ml NCS and the cells were harvested at different time points for preparing for the whole-cell lysate, chromatin fraction and histone fraction. The NCS-induced alterations in H3K36me3 in core histones, METTL3 and YTHDC1 in the chromatin fractions from HEK293T cells and the isogenic cells depleted of SETD2 were conducted in three and five biological replicates, respectively. Each biological replicate was performed on a separate day.

Extraction of core histones

Nuclear pellet was extracted with Nuclear and Cytoplasmic Extraction Reagents (Thermo Scientific) following the manufacturer's recommended protocol. Nuclear pellet was incubated with chilled 0.4 N hydrochloric acid and vortexed at 4°C for 4 h. After centrifugation at 13,000 rpm for 30 min, the supernatant was transferred to a pre-chilled 1.5 mL tube. Half volume of 100% trichloroacetic acid was added dropwise to the supernatant. The mixture was incubated at 4°C for 30 min and then centrifuged at 13,000 rpm for 30 min. Histone pellet was washed with chilled acetone before concentration quantification by Bradford assay.

Western blot

The same amount of total protein lysate from each sample was denatured by heating in Laemmli loading buffer (Bio-Rad) at 95°C for 10 min and then resolved using a 10% or 15% SDS-PAGE gel. The proteins were subsequently transferred from to a nitrocellulose membrane at 100 V for 1 h at 4°C. After blocking with 5% non-fat dry milk in PBS-T (PBS with 0.05% Tween 20) for 1 h, the membrane was incubated at 4°C overnight with the following antibodies: METTL14 (Proteintech, 26158-1-AP, 1:1000), METTL3 (Proteintech, 15073-1-AP, 1:1000), YTHDC1 (Proteintech, 67911-1-Ig, 1:2000), GAPDH (Santa Cruz, sc-32233, 1:2,000), SNRNP70 (Abclonal, A6065, 1:1000), H3K36me3 (Cell Signaling Technology, 9763s, 1:1000) and histone H3 (Proteintech, 17168-1-AP, 1:5000). The membranes were thoroughly washed with PBS-T three times followed by secondary antibody incubation with HRP-fused donkey anti-rabbit secondary antibody (Sigma, A0545, 1:2500) or anti-mouse secondary antibody (Santa Cruz, m-IgGκ BP-HRP, 1:2500). After thorough washing for three times, the protein signal was developed by using Amersham ECL™ Western Blot Detecting Reagent (GE Healthcare) with LI-COR Odyssey FC imaging system. Quantification of Western blot was carried out using Image Studio Lite Version 5.2.

Real-time quantitative PCR (RT-qPCR)

Total RNA was extracted with Total RNA kit I (Omega). cDNA was generated from 2 µg of total RNA using M-MLV reverse transcriptase (Promega). RT-qPCR was performed with Luna qPCR master mixture (New England Biolabs) on CFX96 RT-qPCR detection system (Bio-Rad). The primer sequences used for qPCR are listed below:

METTL3 Forward: 5' - CAA GGC TTC AAC CAG GGT CT - 3'

METTL3 Reverse: 5' - GGT TTC CAA GGG TGA TCC AGT - 3'

GAPDH Forward: 5' - GTT CGT CAT GGG TGT GAA CC - 3'

GAPDH Reverse: 5' - CAT GGA CTG TGG TCA TGA GT - 3'

Protein-protein interaction network analysis

The protein-protein interaction (PPI) network of up- and down-regulated RWE proteins in *SETD2*$^{-/-}$ cell was constructed using STRING (https://string-db.org)[1]. Cytoscape software 3.9.1[2] was used to visualize the PPI network. Cytoscape plug-in cytoHubba was used to recognize the top 10 hub proteins with the Maximal Clique Centrality (MCC) method[3]. Visualization of the PPI network with enrichment annotations was further processed in Cytoscape 3.9.1. Kaplan-Meier survival analysis was performed with the OncoLnc webtool[4] based on TCGA data (https://www.cancer.gov/tcga).

References:

1. Szklarczyk, D.; Gable, A. L.; Lyon, D.; Junge, A.; Wyder, S.; Huerta-Cepas, J.; Simonovic, M.; Doncheva, N. T.; Morris, J. H.; Bork, P.; Jensen, L. J.; Mering, Christian v., STRING v11: protein–protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Res.* **2019,** *47*, D607-D613.
2. Shannon, P.; Markiel, A.; Ozier, O.; Baliga, N. S.; Wang, J. T.; Ramage, D.; Amin, N.; Schwikowski, B.; Ideker, T., Cytoscape: a software environment for integrated models of biomolecular interaction networks. *Genome Res.* **2003,** *13*, 2498-504.
3. Chin, C.-H.; Chen, S.-H.; Wu, H.-H.; Ho, C.-W.; Ko, M.-T.; Lin, C.-Y., cytoHubba: identifying hub objects and sub-networks from complex interactome. *BMC Syst. Biol.* **2014,** *8*, S11.
4. Anaya, J., OncoLnc: linking TCGA survival data to mRNAs, miRNAs, and lncRNAs. *PeerJ Comput. Sci.* **2016,** *2*, e67.

Figure S1. Western blot valiation of chromatin fractionation. GAPDH, SNRNP70 (small nuclear ribonucleoprotein 70), and histone H3 were used as markers for the cytoplasm, nucleoplasm, and chromatin fractions, respectively.

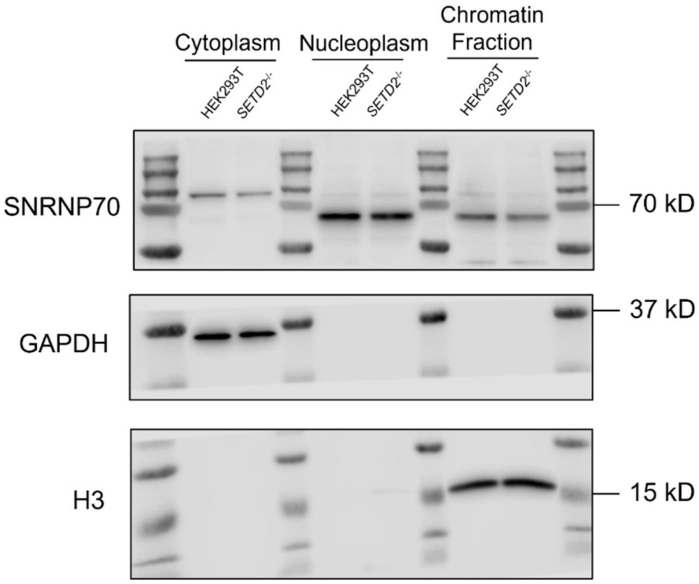

Figure S2. Comparison of the LC-PRM quantification results for RWE proteins in the chromatin fractions of *SETD2*$^{-/-}$ (n = 3) and *KAT5*$^{-/-}$ (n = 3) cells relative to parental HEK293T cells (n = 3). (a) A Venn diagram illustrating the numbers of RWE proteins quantified in the chromatin fractions of *SETD2*$^{-/-}$ (n = 3) and *KAT5*$^{-/-}$ (n = 3) cells and in the PRM library. (b) A Venn diagram depicting the numbers of up- and down-regulated RWE proteins in the chromatin fractions of *SETD2*$^{-/-}$ and *KAT5*$^{-/-}$ cells. Proteins with expression fold changes being greater than 1.5 and lower than 0.67 were considered up- and down-regulated, respectively.

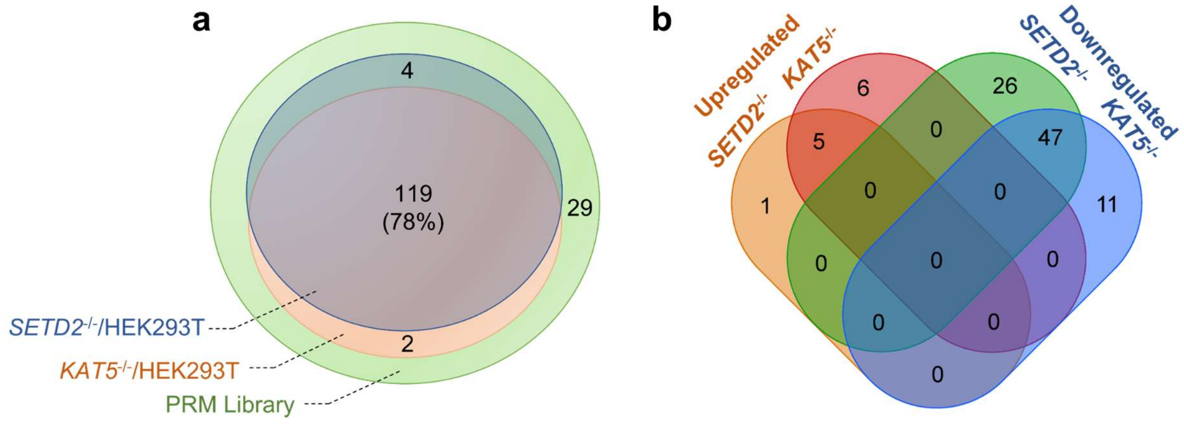

Figure S3. Bar charts showing the overall expression levels of RWE proteins down-regulated in the chromatin fraction. (a&d) RWE proteins down-regulated in chromatin fractions but up-regulated in the whole-cell lysates of *SETD2*$^{-/-}$ (a) and *KAT5*$^{-/-}$ (d) cells. (b&e) RWE proteins down-regulated in the chromatin fractions but unchanged in the whole-cell lysates of *SETD2*$^{-/-}$ (b) and *KAT5*$^{-/-}$ (e) cells. (c&f) RWE proteins down-regulated in both the chromatin fraction and whole-cell lysate of *SETD2*$^{-/-}$ (c) and *KAT5*$^{-/-}$ (f) cells. The quantification results displayed in (a-f) represent the mean and S.D. of results obtained from three independent biological replicates conducted on 3 separate days.

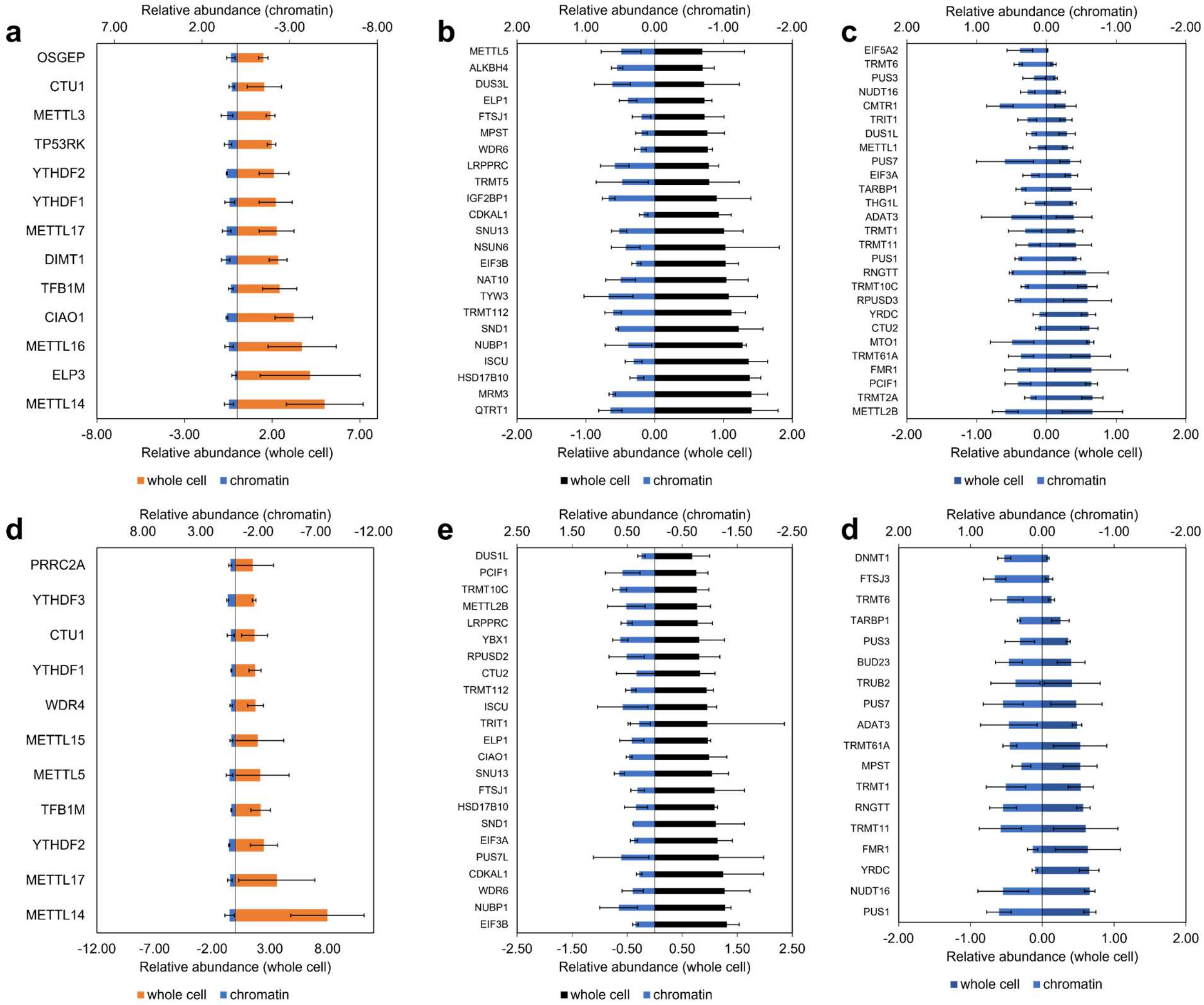

Figure S4. Extracted-ion chromatograms of tryptic peptides from METTL3, METTL14, and YTHDC1, and their corresponding SIL peptides. (a-c) Extracted-ion chromatograms of tryptic peptides LEIDEIAAPR (from METTL14, a), NPEAALSPTFR (from METTL3, b), GVWSTLPVNEK (from YTHDC1, c) and their corresponding SIL peptides showing the elevated overall expressions of METTL3 and METTL14, diminished overall expression of YTHDC1, attenuated chromatin occupancy of METTL3 and METTL14, and no change in chromatin occupancy of YTHDC1 in *SETD2*$^{-/-}$ and *KAT5*$^{-/-}$ cells relative to the parental HEK293T cells.

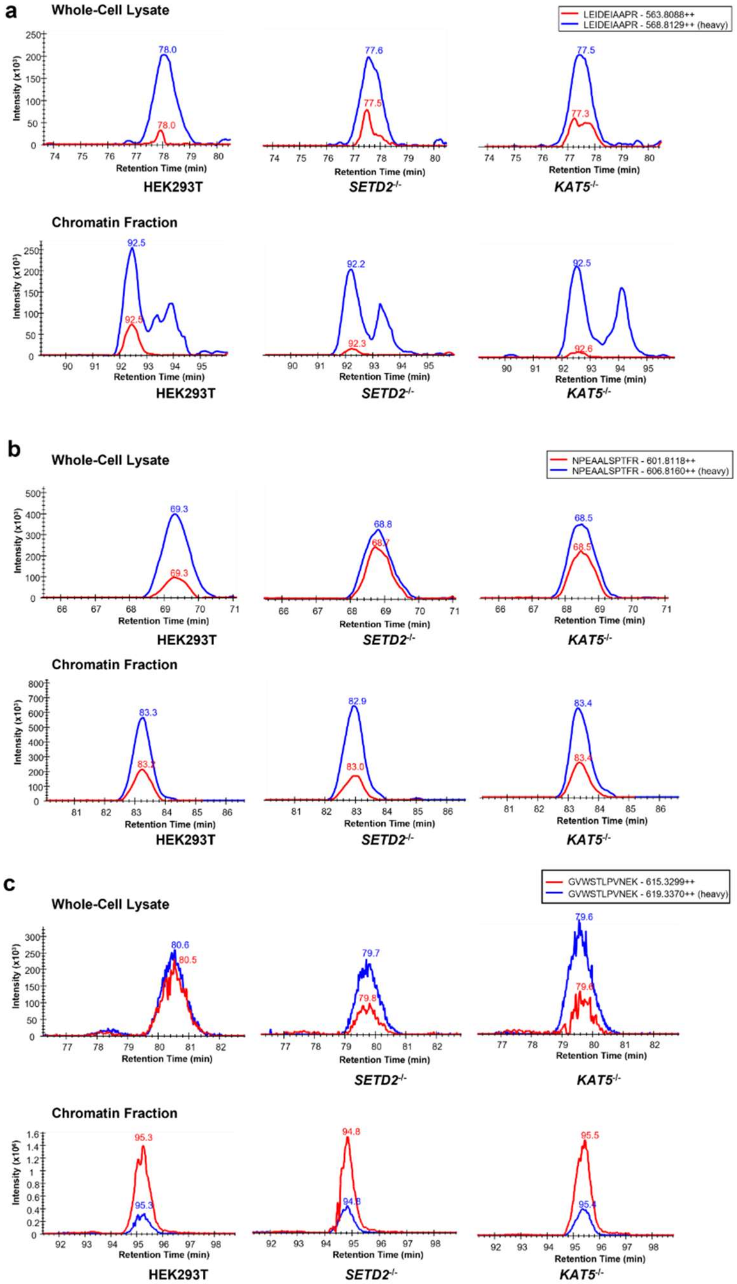

Figure S5. Western blot and RT-qPCR results for monitoring the expression levels of METTL3 protein and mRNA in HEK293T and the isogenic *SETD2*$^{-/-}$ cells. (a&b) Western blot image and quantification results of METTL3 protein in the chromatin fractions of HEK293T and the isogenic *SETD2*$^{-/-}$ cells (n = 3). Histone H3 was employed as a loading control, and GAPDH was monitored to indicate the lack of contamination of cytoplasmic proteins in the chromatin fraction. (c) RT-qPCR showing the mRNA expression levels of *METTL3* in HEK293T and the isogenic *SETD2*$^{-/-}$ cells.

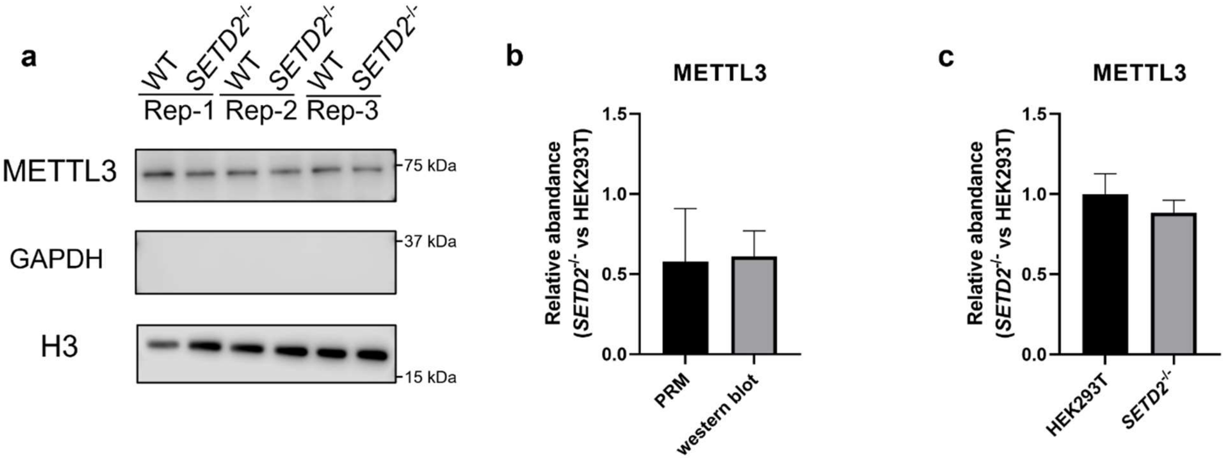

Figure S6. Western blot results showing the NCS-induced changes in H3K36me3 levels. Western blot results of H3K36me3 in the core histones extracted from HEK293T and the isogenic *SETD2*$^{-/-}$ cells during the time course of treatment with 100 ng/mL NCS. Histone H3 was employed as a loading control. The western blot results were obtained from three independent biological replicates on three different days.

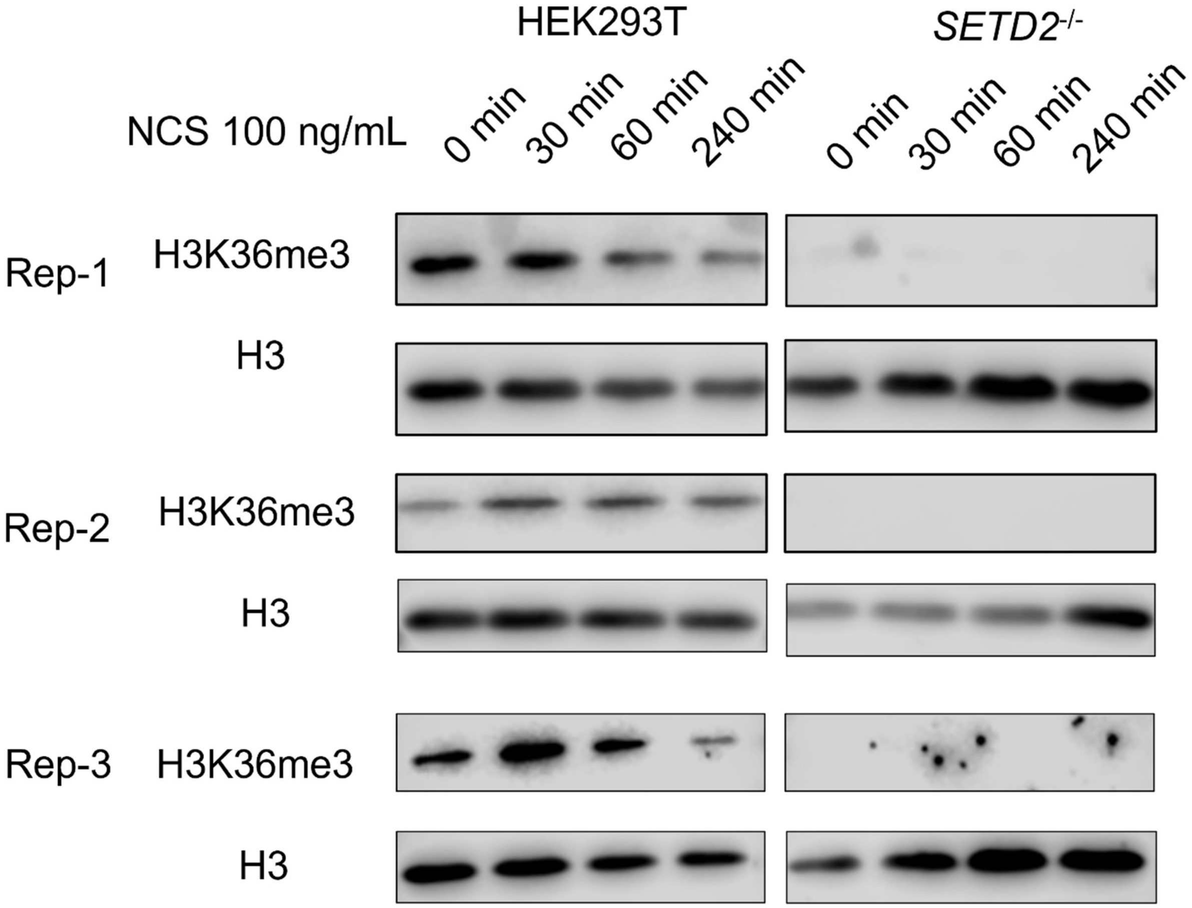

Figure S7. Western blot results of NCS-induced alterations in the chromatin occupancy of METTL3 and YTHDC1. Western blot results of METTL3 and YTHDC1 proteins in the chromatin fractions of HEK293T and the isogenic *SETD2*$^{-/-}$ cells at different time points following treatment with 100 mg/mL NCS. Histone H3 was employed as a loading control, and GAPDH was monitored to indicate the lack of contamination of cytoplasmic proteins in the chromatin fraction. The Western blot results were obtained from five independent biological replicates on different days.

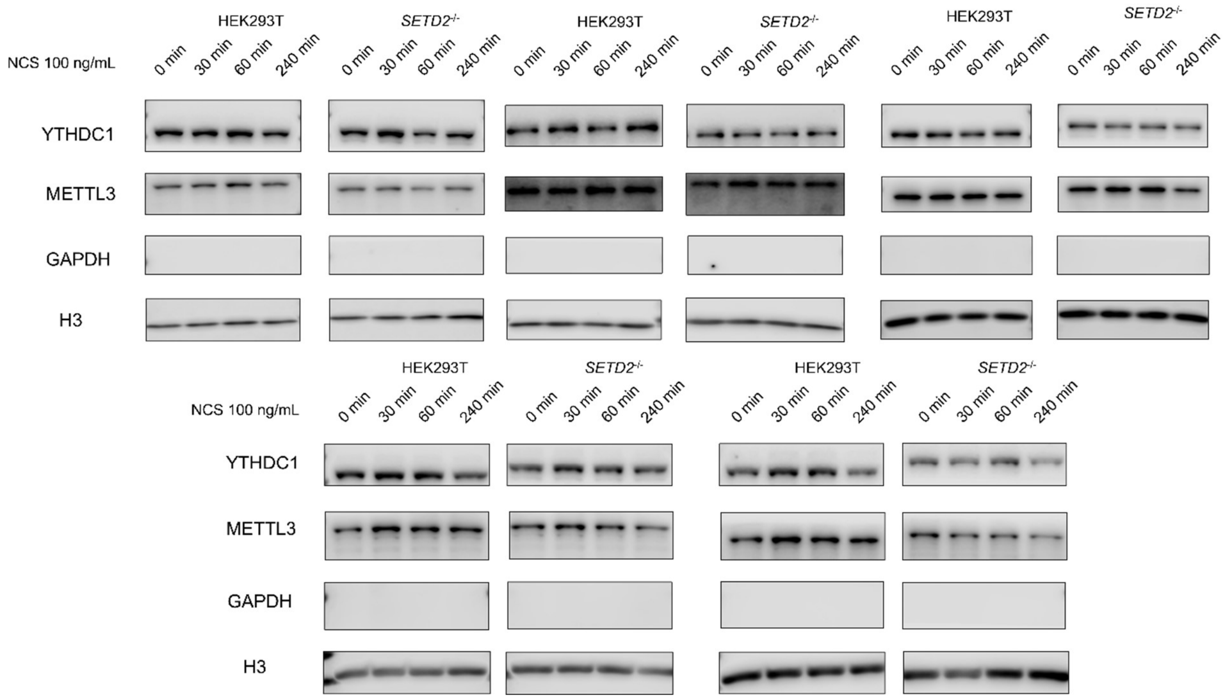

Figure S8. Western blot results for assessing the overall expression levels of METTL3 and YTHDC1 at different time points following NCS treatment. (a) Western blot results of METTL3 and YTHDC1 proteins in the whole-cell lysates of HEK293T and the isogenic *SETD2*$^{–/–}$ cells at different time points after treatment with 100 ng/mL NCS. GAPDH was employed as a loading control. (b) Western blot quantification results showing the NCS-induced changes in the levels of METTL3 and YTHDC1 proteins in the whole-cell lysates of HEK293T and the isogenic *SETD2*$^{–/–}$ cells. The quantification results displayed in (b) represent the mean and S.D. of results obtained from three independent biological replicates conducted on separate days.

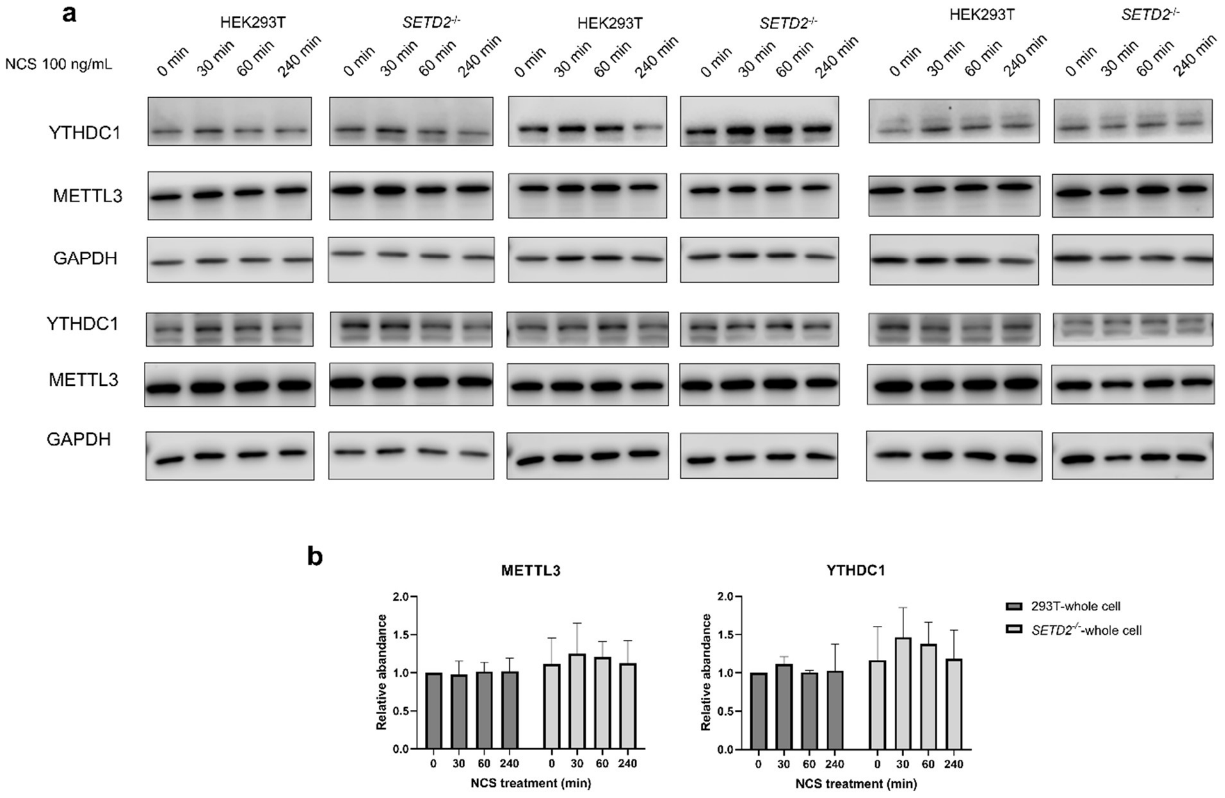

Figure S9. Protein-protein interaction (PPI) network analysis of up- and down-regulated epitranscriptomic RWE proteins in *SETD2*$^{-/-}$ cells. (a&c) PPI network of the up- (a) and down-regulated (c) epitranscriptomic RWE proteins in *SETD2*$^{-/-}$ cells relative to parental HEK293T cells using the STRING database. (b&d) Top 6 (b) and 10 (d) hub proteins in the PPI networks of up- and down-regulated RWE proteins identified by Cytoscape plugin cytoHubba with the Maximal Clique Centrality (MCC) methods, respectively. A color scale ranging from red to yellow represents the importance of hub proteins from the most important to less important.

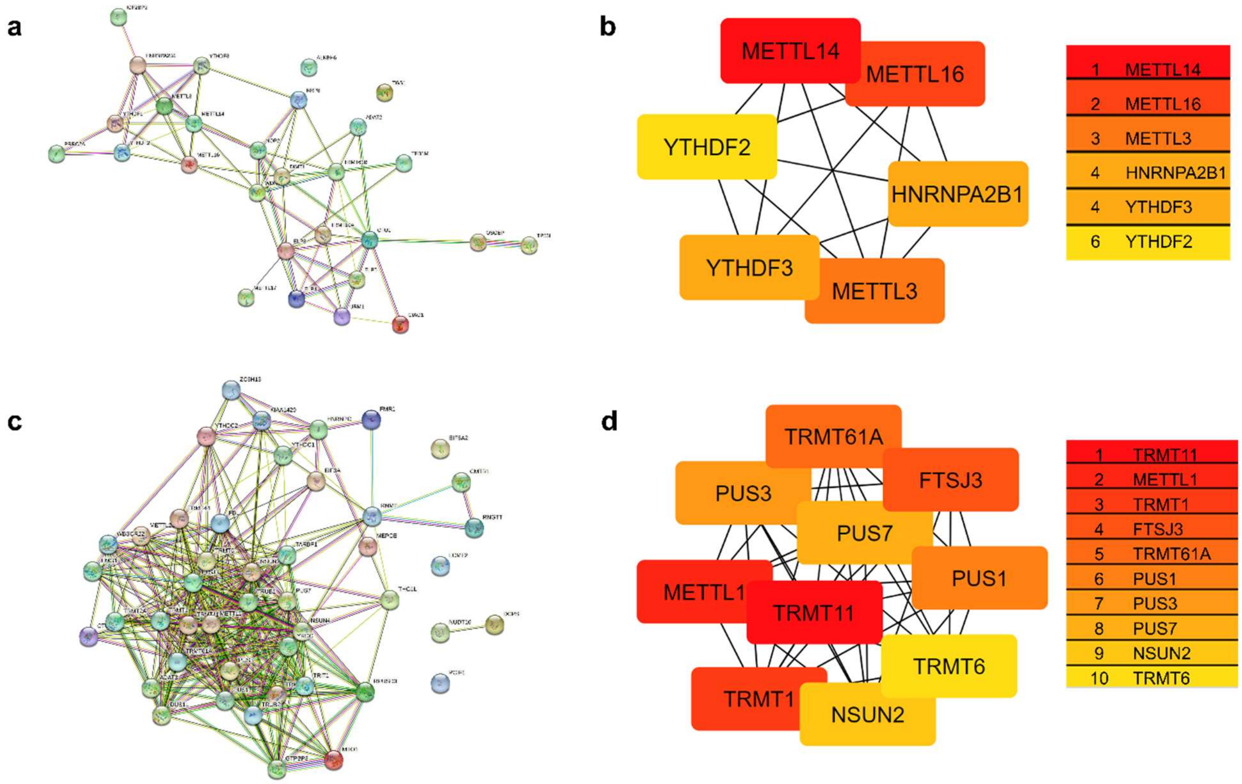

Figure S10. LC-PRM quantification and Kaplan-Meier survival analysis of METTL14 and TRMT11. (a) Extracted-ion chromatograms (EICs) of tryptic peptides LEIDEIAAPR (from METTL14) and its corresponding SIL peptide. (b) Kaplan-Meier survival analysis for KIRC in TCGA showing that higher METTL14 expression is associated with better prognosis in KIRC. (c) EICs of tryptic peptides IDALEFLPFEGK (from TRMT11) and its corresponding surrogate standard peptide (VLLATLSIPITPER*, where R* designates [$^{13}C_6$,$^{15}N_4$]-arginine). (d) Kaplan-Meier survival analysis for KIRC in TCGA showing lower TRMT11 expression is associated with better prognosis in KIRC.

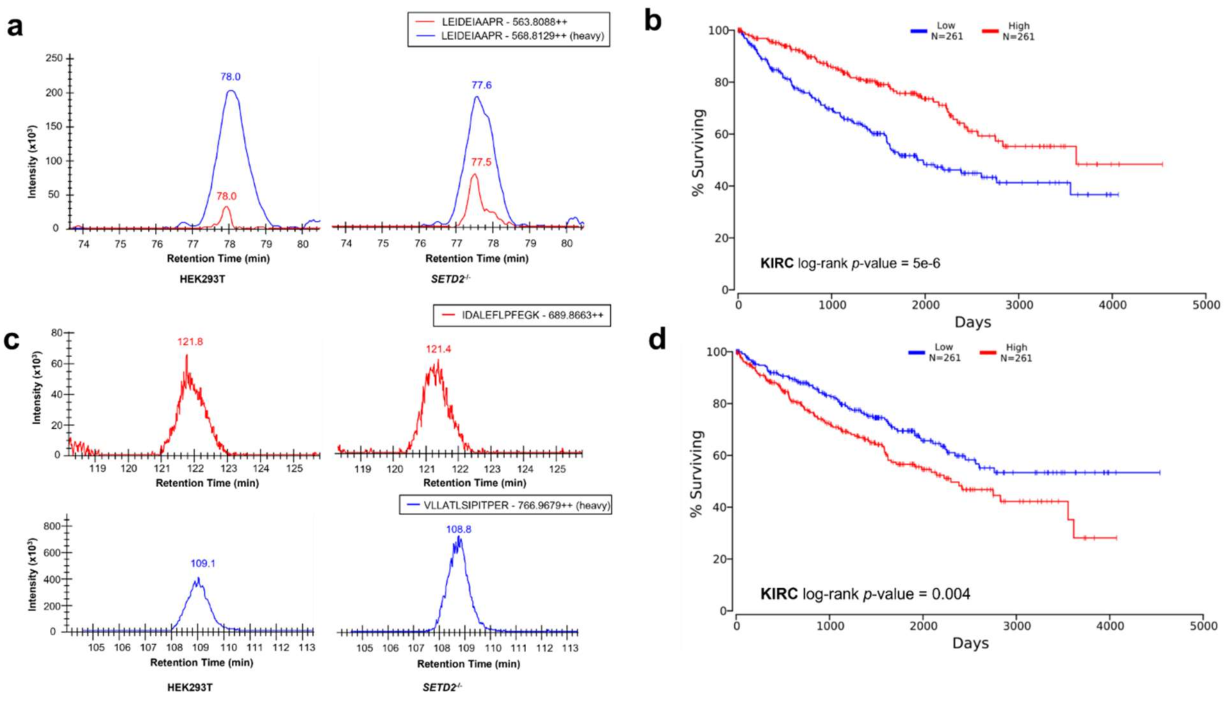

Table S1a. A comparison of the LC-PRM quantification results of RWE proteins in chromatin fraction and whole-cell lysate of *SETD2*$^{-/-}$ cells (n = 3) relative parental HEK293T cells (n=3).

	SETD2_KO/HEK293T						one samples t test	SETD2_KO/HEK293T						one samples t test
	chromatin-ratio-1	chromatin-ratio-2	chromatin-ratio-3	Ave.	S.D.	R.S.D.	*p*-value	wholec-cell-1	wholec-cell-2	wholec-cell-3	Ave.	S.D.	R.S.D.	*p*-value
ADAR	0.61	0.69	0.99	0.76	0.20	26%	0.179	0.98	0.84	0.65	0.83	0.16	20%	0.208
ADAT1	1.91	5.14	5.58	4.21	2.01	48%	0.109							
ADAT3	1.00	0.24	0.27	0.50	0.43	85%	0.182	0.44	0.12	0.62	0.39	0.26	65%	0.055
BUD23	0.46	0.80	0.94	0.73	0.25	34%	0.199	0.20	0.09	0.20	0.16	0.07	40%	0.002
CDK5RAP1	0.41	0.95	0.51	0.62	0.28	46%	0.149							
CDKAL1	0.15	0.11	0.23	0.16	0.06	38%	0.002	1.13	0.89	0.77	0.93	0.18	19%	0.585
CMTR1	0.89	0.54	0.58	0.67	0.19	29%	0.095	0.31	0.11	0.40	0.27	0.15	56%	0.014
APOBEC3G	1.06	1.05	1.44	1.19	0.22	19%	0.282							
CMTR2	0.10	0.15	0.24	0.16	0.07	46%	0.003							
CTU1	0.48	0.21	0.24	0.31	0.15	48%	0.015	2.63	1.33	0.70	1.55	0.98	63%	0.434
CTU2	0.16	0.11	0.09	0.12	0.03	29%	0.001	0.72	0.65	0.48	0.62	0.12	20%	0.032
DCP2	0.64	0.35	0.15	0.38	0.24	64%	0.048							
DIMT1	0.87	0.71	0.38	0.65	0.25	38%	0.136	2.56	2.70	1.76	2.34	0.51	22%	0.045
DUS1L	0.29	0.22	0.15	0.22	0.07	33%	0.003	0.23	0.43	0.23	0.30	0.12	39%	0.009
DUS3L	0.32	0.69	0.83	0.62	0.26	43%	0.126	1.28	0.26	0.61	0.72	0.52	72%	0.444
EIF5A2	0.59	0.29	0.26	0.38	0.18	48%	0.028	0.02	0.02	0.02	0.02	0.00	15%	0.000
ELP1	0.51	0.41	0.25	0.39	0.13	34%	0.015	0.77	0.60	0.80	0.72	0.11	15%	0.050
ELP3	0.32	0.08	0.04	0.15	0.15	101%	0.010	4.42	6.88	1.18	4.16	2.86	69%	0.195
EMG1	0.88	0.78	0.98	0.88	0.10	11%	0.168	0.76	0.60	0.59	0.65	0.09	14%	0.022
FBL	0.87	1.20	1.72	1.26	0.43	34%	0.403	0.82	0.29	0.54	0.55	0.26	48%	0.097
FTSJ1	0.34	0.12	0.11	0.19	0.13	70%	0.009	1.03	0.48	0.67	0.73	0.28	39%	0.235
HSD17B10	0.37	0.17	0.23	0.26	0.10	39%	0.006	1.40	1.53	1.21	1.38	0.16	11%	0.053
LCMT2	1.39	0.63	0.42	0.81	0.51	63%	0.585	0.76	0.18	0.89	0.61	0.38	62%	0.214
MEPCE	1.02	0.97	0.60	0.87	0.23	27%	0.420	1.03	0.46	0.34	0.61	0.37	60%	0.209

MRM1	1.12	1.28	1.95	1.45	0.44	30%	0.218							
MRM2	1.58	0.25	0.69	0.84	0.68	80%	0.725	0.96	0.56	0.72	0.75	0.20	27%	0.166
MRM3	0.64	0.56	0.65	0.62	0.05	8%	0.005	1.67	1.22	1.32	1.41	0.24	17%	0.097
MTO1	0.83	0.23	0.41	0.49	0.31	63%	0.105	0.68	0.58	0.62	0.63	0.05	8%	0.006
NAT10	0.72	0.47	0.29	0.50	0.22	44%	0.056	1.16	1.28	0.69	1.04	0.31	30%	0.840
NFS1	0.99	0.53	0.67	0.73	0.23	32%	0.182	1.49	0.49	1.06	1.01	0.50	50%	0.964
NOP2	1.45	2.32	2.77	2.18	0.67	31%	0.093	1.85	1.90	2.48	2.08	0.35	17%	0.034
NUDT16	0.38	0.17	0.26	0.27	0.10	38%	0.007	0.27	0.15	0.20	0.21	0.06	30%	0.002
PCIF1	0.62	0.33	0.28	0.41	0.18	45%	0.031	0.71	0.55	0.68	0.65	0.09	13%	0.019
QTRT1	0.82	0.48	0.64	0.64	0.17	26%	0.069	1.77	1.00	1.46	1.41	0.38	27%	0.207
RNGTT	0.53	0.50	0.48	0.51	0.03	5%	0.001	0.79	0.21	0.72	0.57	0.32	55%	0.143
RNMT	1.11	0.50	0.78	0.80	0.30	38%	0.364	0.45	0.53	0.49	0.49	0.04	8%	0.002
RPUSD3	0.36	0.51	0.49	0.46	0.09	19%	0.008	0.97	0.30	0.50	0.59	0.34	58%	0.173
RPUSD4	0.81	0.92	0.73	0.82	0.10	12%	0.085							
TARBP1	0.35	0.44	0.30	0.36	0.07	19%	0.004	0.68	0.13	0.27	0.36	0.28	79%	0.060
TFB1M	0.30	0.52	0.26	0.36	0.14	39%	0.015	2.77	3.19	1.33	2.43	0.98	40%	0.127
TGS1	0.31	0.62	1.12	0.68	0.41	60%	0.311	4.80	0.00	2.02	3.41	1.97	58%	0.000
THG1L	0.31	0.15	0.03	0.16	0.14	86%	0.009	0.35	0.00	0.41	0.38	0.04	11%	0.000
THUMPD1	1.71	0.16	0.82	0.90	0.78	86%	0.841	1.28	1.00	1.29	1.19	0.17	14%	0.188
TRIT1	0.13	0.41	0.28	0.27	0.14	50%	0.012	0.23	0.38	0.23	0.28	0.09	31%	0.005
TRMT1	0.58	0.23	0.12	0.31	0.24	78%	0.038	0.43	0.30	0.51	0.41	0.11	26%	0.011
TRMT10C	0.30	0.37	0.27	0.31	0.05	16%	0.002	0.52	0.75	0.49	0.59	0.14	24%	0.037
TRMT11	0.20	0.13	0.46	0.26	0.17	66%	0.018	0.40	0.21	0.66	0.42	0.23	53%	0.047
TRMT112	0.47	0.65	0.69	0.61	0.12	20%	0.029	1.11	1.32	0.91	1.11	0.20	18%	0.436
TRMT2A	0.32	0.19	0.18	0.23	0.08	34%	0.004	0.54	0.83	0.61	0.66	0.15	23%	0.059
TRMT5	0.91	0.27	0.23	0.47	0.38	80%	0.137	1.13	0.30	0.94	0.79	0.44	55%	0.497
TRUB2	0.75	0.91	1.20	0.95	0.23	24%	0.756	0.73	0.11	0.47	0.44	0.31	71%	0.090
TYW3	1.07	0.38	0.56	0.67	0.36	53%	0.250	1.56	0.82	0.86	1.08	0.42	39%	0.777
WDR4	1.57	0.56	0.40	0.84	0.63	75%	0.709	2.83	1.54	1.53	1.97	0.75	38%	0.154

YBX1	0.81	0.94	0.50	0.75	0.22	30%	0.192	0.89	0.48	1.25	0.87	0.39	44%	0.628
RBMX	0.95	1.27	1.46	1.23	0.26	21%	0.264	1.48	0.59	1.04	1.03	0.44	43%	0.906
ELAVL1	0.82	1.09	0.93	0.95	0.13	14%	0.556	1.18	0.94	1.08	1.07	0.12	11%	0.429
SND1	0.53	0.56	0.56	0.55	0.02	3%	0.001	1.63	1.05	0.99	1.22	0.35	29%	0.390
FMR1	0.60	0.41	0.24	0.42	0.18	43%	0.030	0.61	0.14	1.18	0.64	0.52	81%	0.360
LRPPRC	0.55	0.80	0.39	0.58	0.21	36%	0.073	0.73	0.95	0.67	0.78	0.15	19%	0.126
PUS7L	1.23	0.39	1.11	0.91	0.46	50%	0.770	1.23	0.63	0.61	0.83	0.35	43%	0.482
ALKBH2	0.23	0.06	0.09	0.13	0.09	72%	0.004							
ALKBH3	1.05	0.40	0.26	0.57	0.42	74%	0.222							
ALKBH4	0.64	0.50	0.49	0.55	0.08	15%	0.011	0.68	0.54	0.88	0.70	0.17	25%	0.093
ALKBH5	1.18	1.00	1.11	1.10	0.10	9%	0.217	1.18	0.97	0.88	1.01	0.16	15%	0.905
FTO	0.62		0.76	0.69	0.10	15%		0.90	0.94	0.77	0.87	0.09	11%	0.138
YTHDF1	0.72	0.40	0.17	0.43	0.28	65%	0.071	2.96	1.14	2.50	2.20	0.95	43%	0.159
YTHDF2	0.63	0.58	0.58	0.60	0.03	5%	0.002	2.85	1.17	2.27	2.10	0.85	41%	0.155
YTHDF3	1.02	0.74	0.76	0.84	0.16	19%	0.221	2.10	1.28	1.44	1.61	0.43	27%	0.137
YTHDC1	1.16	0.67	1.11	0.98	0.27	28%	0.913	0.35	0.29	0.34	0.33	0.03	9%	0.001
YTHDC2	1.97	3.26	2.30	2.51	0.67	27%	0.060	0.21	0.16	0.13	0.17	0.04	26%	0.001
METTL3	0.95	0.39	0.38	0.58	0.33	57%	0.154	2.17	1.91	1.65	1.91	0.26	14%	0.027
METTL14	0.72	0.19	0.47	0.46	0.26	57%	0.070	3.21	4.33	7.43	4.99	2.19	44%	0.087
METTL1	0.25	0.10	0.03	0.13	0.11	87%	0.005	0.37	0.32	0.22	0.31	0.07	25%	0.004
METTL16	0.72	0.44	0.24	0.47	0.24	52%	0.062	2.96	5.91	2.23	3.70	1.95	53%	0.138
METTL2B	0.79	0.43	0.54	0.59	0.19	31%	0.062	1.01	0.18	0.79	0.66	0.43	65%	0.307
NSUN2	1.18	0.87	0.92	0.99	0.17	17%	0.933	0.58	0.07	0.41	0.35	0.26	74%	0.050
NSUN5	0.89	0.82	1.04	0.92	0.11	12%	0.338	1.35	0.30	1.16	0.93	0.56	60%	0.859
NSUN6	0.66	0.25	0.36	0.42	0.21	50%	0.041	1.93	0.60	0.54	1.03	0.79	77%	0.961
DNMT1	0.71	0.60	0.71	0.67	0.07	10%	0.013							
TRMT61A	0.18	0.55	0.36	0.36	0.18	50%	0.027	0.68	0.90	0.33	0.63	0.29	45%	0.159
TRMT61B	0.47	1.44	0.48	0.80	0.56	70%	0.592	2.98	0.00	1.65	1.54	1.49	97%	0.593
TRMT6	0.34	0.46	0.41	0.40	0.06	14%	0.003	0.09	0.07	0.14	0.10	0.04	36%	0.001

PUS7	1.06	0.43	0.29	0.59	0.41	69%	0.228	0.40	0.45	0.17	0.34	0.15	44%	0.017
IGF2BP1	0.73	0.56	0.71	0.67	0.09	14%	0.025	1.42	0.43	0.86	0.90	0.49	55%	0.766
IGF2BP2	1.34	0.64	1.08	1.02	0.36	35%	0.935	1.13	0.55	1.00	0.90	0.30	34%	0.609
IGF2BP3	0.95	0.93	1.00	0.96	0.04	4%	0.225	1.77	1.31	1.60	1.56	0.23	15%	0.053
WTAP	1.48	0.80	0.83	1.04	0.39	37%	0.883	0.83	0.57	1.04	0.81	0.23	29%	0.295
VIRMA	1.12	0.54	0.40	0.69	0.38	55%	0.294	0.66	0.76	0.42	0.61	0.17	28%	0.062
RBM15B	1.28	0.98	2.10	1.46	0.58	40%	0.307	1.39	0.85	0.95	1.07	0.29	27%	0.732
RBM15	1.35	0.48	0.65	0.83	0.46	56%	0.585	0.96	0.71	0.36	0.68	0.30	44%	0.204
ZC3H13	3.99	1.39	2.50	2.62	1.30	50%	0.164	0.06	0.18	0.12	0.12	0.06	47%	0.001
EIF3A	0.17	0.35	0.14	0.22	0.12	53%	0.007	0.37	0.44	0.26	0.36	0.09	26%	0.007
EIF3B	0.19	0.32	0.29	0.27	0.07	25%	0.003	1.04	1.21	0.84	1.03	0.19	18%	0.797
HNRNPA2B1	1.21	1.22	1.26	1.23	0.03	2%	0.005	1.43	1.15	1.97	1.52	0.41	27%	0.162
HNRNPC	1.06	0.91	0.91	0.96	0.09	9%	0.511	0.14	0.17	0.12	0.14	0.03	20%	0.000
PUS1	0.42	0.35	0.44	0.40	0.05	11%	0.002	0.50	0.38	0.43	0.44	0.06	13%	0.004
TRUB1	0.99	0.60	0.45	0.68	0.28	41%	0.182	0.35	0.22	0.12	0.23	0.11	48%	0.007
DKC1	0.95	1.00	0.93	0.96	0.04	4%	0.212	0.98	0.49	0.87	0.78	0.26	33%	0.269
NSUN4	0.91	0.79	0.94	0.88	0.08	9%	0.127	0.71	0.45	0.77	0.64	0.17	27%	0.068
TRDMT1	0.23	0.64	0.63	0.50	0.23	47%	0.065							
ALYREF	1.80	0.92	1.82	1.51	0.51	34%	0.226	1.17	0.83	1.28	1.09	0.24	22%	0.560
METTL8	2.31	1.00	0.62	1.31	0.89	68%	0.609							
PUS3	0.36	0.09	0.08	0.18	0.16	91%	0.013	0.12	0.12	0.16	0.13	0.02	18%	0.000
ZCCHC4	1.84	1.70	0.82	1.45	0.55	38%	0.290							
CBLL1	1.64	0.77	0.91	1.11	0.47	42%	0.730	1.84	0.43	0.89	1.05	0.72	68%	0.912
CIAO1	0.62	0.61	0.54	0.59	0.04	8%	0.004	2.80	4.45	2.44	3.23	1.07	33%	0.069
DIS3L2	0.51	1.06	0.46	0.68	0.33	49%	0.236	1.97	1.21	0.82	1.33	0.58	43%	0.424
FTSJ3	1.14	0.95	0.78	0.96	0.18	19%	0.714	0.03	0.06	0.03	0.04	0.02	52%	0.000
ISCU	0.43	0.29	0.19	0.30	0.12	40%	0.010	1.58	1.05	1.47	1.37	0.28	20%	0.151
LAGE3	0.79	0.25	0.26	0.43	0.31	71%	0.085							
METTL15	0.19	0.20	0.44	0.28	0.14	52%	0.013							

METTL17	0.87	0.38	0.53	0.59	0.25	42%	0.105	1.36	2.07	3.32	2.25	0.99	44%	0.160
METTL5	0.82	0.30	0.34	0.49	0.29	59%	0.092	1.24	0.03	0.81	0.69	0.61	88%	0.477
MPST	0.28	0.12	0.17	0.19	0.09	45%	0.004	0.90	0.91	0.48	0.77	0.25	32%	0.242
SNU13	0.65	0.46	0.45	0.52	0.11	21%	0.017	0.78	1.32	0.93	1.01	0.28	28%	0.961
NUBP1	0.77	0.20	0.18	0.38	0.34	88%	0.087	1.25	1.34	1.24	1.28	0.05	4%	0.012
OSGEP	0.63	0.20	0.22	0.35	0.24	69%	0.044	1.60	1.71	1.19	1.50	0.27	18%	0.087
PRRC2A	1.17	1.14	0.42	0.91	0.43	47%	0.750	3.93	6.33	4.89	5.05	1.21	24%	0.028
TP53RK	0.74	0.34	0.43	0.50	0.21	42%	0.056	1.69	2.11	2.11	1.97	0.24	12%	0.020
TPRKB	0.15	0.32	0.37	0.28	0.12	42%	0.009							
TUT7	3.65	1.56	4.23	3.15	1.40	45%	0.118							
WDR6	0.26	0.25	0.11	0.21	0.09	41%	0.004	0.85	0.71	0.76	0.77	0.07	9%	0.029
YRDC	0.20	0.04	0.05	0.10	0.09	96%	0.003	0.68	0.64	0.49	0.60	0.10	17%	0.022

Table S1b. A comparison of the LC-PRM quantification results of RWE proteins in chromatin fraction and whole-cell lysate of *KAT5*$^{-/-}$ cells (n = 3) relative parental HEK293T cells (n=3).

	KAT5_KO/HEK293T						one samples t test	KAT5_KO/HEK293T						one samples t test
	chromatin-ratio-1	chromatin-ratio-2	chromatin-ratio-3	Ave.	S.D.	R.S.D.	*p*-value	wholec-cell-1	wholec-cell-2	wholec-cell-3	Ave.	S.D.	R.S.D.	*p*-value
ADAR	0.95	0.74	1.08	0.93	0.17	18%	0.535	1.95	0.84	1.51	1.43	0.56	39%	0.312
ADAT1	1.82	4.08	2.37	2.76	1.18	43%	0.123							
ADAT3	0.90	0.38	0.12	0.47	0.40	85%	0.145	0.56	0.43	0.46	0.48	0.07	14%	0.006
BUD23	0.30	0.44	0.66	0.46	0.19	40%	0.038	0.63	0.29	0.30	0.40	0.19	48%	0.033
CDK5RAP1	0.78	2.17	0.47	1.14	0.91	79%	0.812	4.20	1.46	0.66	2.11	1.86	88%	0.411
CDKAL1	0.32	0.30	0.23	0.28	0.05	18%	0.002	2.09	0.86	0.78	1.24	0.73	59%	0.623
CMTR1	1.29	0.50	0.63	0.81	0.42	52%	0.514	0.66	0.30	0.66	0.54	0.21	38%	0.061
APOBEC3G	0.92	0.78	0.94	0.88	0.09	10%	0.137							
CMTR2	0.08	0.12	0.26	0.16	0.09	59%	0.004							
CTU1	0.31	0.71	0.12	0.38	0.30	79%	0.071	2.55	2.10	0.38	1.68	1.14	68%	0.412
CTU2	0.75	0.18	0.07	0.33	0.36	109%	0.085	0.70	1.14	0.64	0.82	0.27	33%	0.379
DCP2	0.37	0.49	0.18	0.34	0.15	45%	0.018							
DIMT1	1.22	0.94	0.30	0.82	0.47	58%	0.583	1.69	2.23	1.90	1.94	0.27	14%	0.027
DUS1L	0.29	0.28	0.16	0.24	0.07	28%	0.003	0.70	0.99	0.36	0.68	0.31	46%	0.223
DUS3L	1.34	1.10	1.14	1.19	0.13	10%	0.117	1.64	0.69	0.44	0.93	0.63	68%	0.856
EIF5A2	1.14	0.62	0.39	0.72	0.39	54%	0.333	0.10	0.56	0.08	0.25	0.27	110%	0.041
ELP1	0.65	0.38	0.22	0.42	0.22	52%	0.043	0.98	0.91	1.01	0.97	0.05	5%	0.401
ELP3	1.04	0.81	0.58	0.81	0.23	28%	0.283	4.15	9.12	1.39	4.89	3.92	80%	0.228
EMG1	0.68	0.73	0.73	0.71	0.03	4%	0.003	0.73	0.83	0.50	0.69	0.17	25%	0.086
FBL	0.49	0.67	1.50	0.89	0.54	61%	0.747	1.19	0.46	0.57	0.74	0.39	53%	0.368
FTSJ1	0.45	0.26	0.23	0.31	0.12	39%	0.010	1.71	0.74	0.81	1.09	0.54	50%	0.808
HSD17B10	0.58	0.26	0.17	0.34	0.21	62%	0.032	1.07	1.15	1.05	1.09	0.05	5%	0.099
MEPCE	1.18	0.66	0.77	0.87	0.28	32%	0.505	1.43	2.24	0.52	1.39	0.86	62%	0.511
MRM1	0.26	0.71	0.32	0.43	0.24	57%	0.055							

MRM2	2.87	1.16	0.53	1.52	1.21	80%	0.533	1.52	1.48	0.61	1.20	0.51	42%	0.563
MRM3	1.25	1.36	0.97	1.19	0.20	17%	0.238	1.57	1.13	1.07	1.26	0.27	21%	0.240
MTO1	1.21	0.65	0.23	0.70	0.49	71%	0.399	1.17	1.26	0.77	1.07	0.26	24%	0.696
NAT10	0.72	0.54	0.89	0.72	0.17	24%	0.105	1.16	1.76	0.71	1.21	0.53	44%	0.561
NFS1	1.12	0.98	0.60	0.90	0.27	30%	0.582	1.33	0.54	0.64	0.84	0.43	51%	0.578
NOP2	1.91	2.83	6.58	3.77	2.48	66%	0.192	1.25	1.32	1.96	1.51	0.39	26%	0.151
NUDT16	0.95	0.39	0.30	0.55	0.35	65%	0.157	0.58	0.68	0.72	0.66	0.07	11%	0.015
PCIF1	0.95	0.44	0.37	0.58	0.32	54%	0.150	0.55	0.98	0.73	0.75	0.21	28%	0.185
QTRT1	1.89	0.78	0.56	1.07	0.71	66%	0.872	1.75	1.07	1.33	1.38	0.34	25%	0.191
RNGTT	0.76	0.42	0.46	0.55	0.19	35%	0.053	0.47	0.59	0.65	0.57	0.09	16%	0.015
RNMT	1.25	0.61	0.35	0.74	0.46	63%	0.431	0.69	0.76	0.79	0.75	0.05	7%	0.014
RPUSD2	0.73	0.65	0.14	0.51	0.32	63%	0.119	1.15	0.87	0.41	0.81	0.37	46%	0.474
RPUSD3	0.80	0.98	1.00	0.93	0.11	12%	0.364	1.46	1.32	0.49	1.09	0.52	48%	0.803
RPUSD4	0.20	0.25	0.39	0.28	0.10	36%	0.006							
TARBP1	0.33	0.30	0.35	0.33	0.02	8%	0.000	0.37	0.27	0.12	0.25	0.12	49%	0.009
TFB1M	0.39	0.34	0.30	0.34	0.04	12%	0.001	2.62	2.74	1.24	2.20	0.84	38%	0.131
TGS1	2.05	4.21	1.65	2.64	1.38	52%	0.176							
TRIT1	0.19	0.52	0.14	0.28	0.20	72%	0.026	2.57	0.16	0.14	0.96	1.40	146%	0.963
TRMT1	0.67	0.66	0.19	0.51	0.27	54%	0.090	0.74	0.47	0.40	0.54	0.18	33%	0.045
TRMT10C	0.76	0.64	0.51	0.64	0.12	19%	0.036	0.69	1.01	0.59	0.76	0.22	29%	0.207
TRMT11	0.47	0.37	0.92	0.58	0.30	51%	0.135	1.07	0.17	0.58	0.60	0.45	74%	0.266
TRMT112	0.35	0.42	0.54	0.44	0.09	22%	0.009	0.81	0.96	1.06	0.94	0.12	13%	0.514
TRMT5	2.35	0.71	0.45	1.17	1.03	88%	0.802	2.19	0.43	0.59	1.07	0.98	91%	0.913
TRUB2	0.05	0.34	0.73	0.37	0.34	91%	0.087	0.86	0.17	0.21	0.41	0.39	94%	0.121
TYW3	1.24	0.75	0.63	0.87	0.32	37%	0.561	1.88	1.19	0.93	1.33	0.49	37%	0.358
WDR4	0.35	0.27	0.45	0.36	0.09	26%	0.007	2.52	1.52	1.23	1.76	0.68	38%	0.192
YBX1	0.51	0.59	0.78	0.62	0.14	22%	0.042	0.77	0.37	1.29	0.81	0.46	57%	0.546
RBMX	1.19	0.96	1.45	1.20	0.24	20%	0.289	2.30	0.90	0.79	1.33	0.84	63%	0.567
ELAVL1	0.98	0.93	1.02	0.98	0.04	4%	0.422	1.37	1.25	1.47	1.36	0.11	8%	0.029

SND1	0.40	0.39	0.40	0.40	0.00	0%	0.000	1.61	1.15	0.57	1.11	0.52	47%	0.750
FMR1	0.20	0.15	0.06	0.13	0.07	54%	0.002	0.86	0.12	0.93	0.64	0.45	71%	0.297
LRPPRC	0.44	0.63	0.47	0.51	0.10	20%	0.015	0.68	1.08	0.59	0.78	0.26	34%	0.292
PUS7L	1.19	0.33	0.31	0.61	0.50	83%	0.310	2.09	0.86	0.55	1.17	0.81	70%	0.757
ALKBH2	0.33	0.15	0.17	0.21	0.10	48%	0.006							
ALKBH3	1.69	0.72	0.51	0.97	0.63	65%	0.950							
ALKBH4	0.96	0.59	0.47	0.68	0.26	38%	0.159	0.67	1.12	0.80	0.86	0.23	27%	0.406
ALKBH5	1.93	1.01	1.90	1.61	0.52	32%	0.178	1.81	1.41	1.36	1.53	0.25	16%	0.067
FTO	0.71	2.31	1.46	1.49	0.80	53%	0.396	1.00	1.47	0.68	1.05	0.40	38%	0.845
YTHDF1	0.29	0.38	0.33	0.33	0.04	12%	0.001	2.28	1.26	1.58	1.71	0.52	31%	0.143
YTHDF2	0.56	0.58	0.48	0.54	0.05	10%	0.005	3.70	1.36	2.40	2.49	1.17	47%	0.159
YTHDF3	0.69	0.71	0.56	0.66	0.08	12%	0.018	1.81	1.64	1.49	1.65	0.16	10%	0.020
YTHDC1	1.80	0.68	1.29	1.26	0.56	45%	0.512	0.26	0.66	0.43	0.45	0.20	44%	0.042
YTHDC2	3.00	2.07	1.86	2.31	0.60	26%	0.064	0.62	1.12	0.31	0.68	0.41	60%	0.314
METTL3	1.28	0.61	0.47	0.79	0.43	55%	0.482	2.06	2.39	1.71	2.06	0.34	17%	0.033
METTL14	0.96	0.20	0.31	0.49	0.41	84%	0.163	4.32	9.79	9.86	7.99	3.18	40%	0.062
METTL1	2.16	0.78	0.28	1.07	0.97	91%	0.909	0.37	0.54	0.23	0.38	0.16	42%	0.021
METTL16	1.53	0.82	0.41	0.92	0.57	62%	0.831	2.31	4.44	2.02	2.92	1.32	45%	0.128
METTL2B	0.53	0.85	0.17	0.52	0.34	66%	0.135	1.05	0.68	0.59	0.77	0.24	31%	0.244
NSUN2	0.59	0.91	0.58	0.69	0.19	28%	0.109	1.10	0.24	0.25	0.53	0.49	93%	0.239
NSUN5	0.76	0.88	0.77	0.80	0.07	8%	0.036	0.93	0.68	0.90	0.83	0.13	16%	0.167
NSUN6	1.02	0.70	0.32	0.68	0.35	52%	0.255	3.75	1.57	0.79	2.04	1.53	75%	0.361
DNMT1	0.63	0.51	0.45	0.53	0.09	17%	0.012	0.08	0.06	0.09	0.08	0.02	21%	0.000
TRMT61A	0.36	0.56	0.44	0.45	0.10	22%	0.011	0.46	0.93	0.19	0.53	0.37	71%	0.158
TRMT61B	2.98	2.47	4.14	3.20	0.86	27%	0.047	4.21	0.26	0.70	1.73	2.17	126%	0.621
TRMT6	0.36	0.75	0.36	0.49	0.22	46%	0.059	0.16	0.08	0.14	0.13	0.04	33%	0.001
PUS7	0.79	0.60	0.25	0.55	0.28	51%	0.105	0.33	0.88	0.20	0.47	0.36	76%	0.125
IGF2BP1	0.67	1.02	0.83	0.84	0.17	21%	0.253	3.33	0.71	0.98	1.67	1.44	86%	0.504
IGF2BP2	0.50	0.63	1.22	0.78	0.38	49%	0.428	1.93	0.62	1.05	1.20	0.67	56%	0.660

IGF2BP3	1.06	1.20	0.90	1.05	0.15	14%	0.585	2.71	1.61	1.42	1.91	0.70	37%	0.152
WTAP	1.79	0.93	1.11	1.28	0.45	36%	0.401	0.87	0.84	0.75	0.82	0.06	8%	0.037
VIRMA	1.11	0.61	0.51	0.74	0.32	43%	0.297	0.52	1.76	0.69	0.99	0.67	68%	0.983
RBM15B	2.04	1.29	2.47	1.93	0.60	31%	0.114	1.70	1.09	1.04	1.28	0.37	29%	0.321
RBM15	1.41	0.88	0.97	1.08	0.28	26%	0.658	1.73	4.56	1.37	2.55	1.75	68%	0.264
ZC3H13	3.39	1.43	3.59	2.81	1.19	42%	0.120	0.21	0.64	1.04	0.63	0.41	66%	0.263
EIF3A	0.43	0.40	0.30	0.38	0.07	17%	0.004	1.41	1.15	0.87	1.14	0.27	23%	0.448
EIF3B	0.39	0.29	0.37	0.35	0.05	15%	0.002	1.24	1.56	1.13	1.31	0.22	17%	0.139
HNRNPA2B1	1.12	1.02	1.10	1.08	0.05	5%	0.116	1.66	0.96	2.24	1.62	0.64	40%	0.236
HNRNPC	1.02	1.56	1.01	1.20	0.32	26%	0.391	0.42	0.67	0.46	0.51	0.14	27%	0.026
PUS1	0.67	0.73	0.41	0.60	0.17	28%	0.057	0.76	0.62	0.61	0.66	0.08	13%	0.020
TRUB1	1.01	0.73	0.53	0.76	0.24	32%	0.219	0.02	0.15	0.00	0.06	0.08	135%	0.002
DKC1	0.88	0.53	0.79	0.73	0.18	24%	0.122	0.43	0.38	0.35	0.39	0.04	10%	0.001
NSUN4	0.88	0.84	0.76	0.83	0.06	8%	0.042	0.71	0.68	0.77	0.72	0.05	6%	0.009
TRDMT1	0.72	0.71	0.99	0.80	0.16	20%	0.165							
ALYREF	0.83	0.69	0.95	0.82	0.13	16%	0.143	1.54	1.04	1.61	1.40	0.31	22%	0.156
METTL8	2.23	1.64	0.66	1.51	0.79	53%	0.382	0.25	0.00	0.53	0.26	0.27	102%	0.041
PUS3	0.52	0.31	0.11	0.31	0.21	66%	0.029	0.37	0.38	0.33	0.36	0.03	8%	0.001
ZCCHC4	1.11	0.96	0.63	0.90	0.25	27%	0.547							
CBLL1	1.25	0.68	0.87	0.93	0.29	31%	0.724	0.70	0.19	0.06	0.31	0.34	107%	0.072
CIAO1	0.43	0.45	0.53	0.47	0.05	12%	0.003	0.73	1.35	0.88	0.99	0.32	33%	0.955
DIS3L2	1.38	0.53	0.28	0.73	0.58	79%	0.506	1.54	2.77	0.99	1.77	0.91	51%	0.281
FTSJ3	0.61	0.54	0.84	0.66	0.16	23%	0.064	0.09	0.15	0.05	0.10	0.05	51%	0.001
ISCU	1.10	0.42	0.22	0.58	0.46	79%	0.255	1.09	0.77	1.01	0.96	0.17	18%	0.696
LAGE3	1.59	0.76	0.35	0.90	0.63	70%	0.813							
METTL15	0.46	0.24	0.31	0.34	0.12	35%	0.010	4.54	0.64	0.70	1.96	2.24	114%	0.536
METTL17	0.68	0.38	0.33	0.46	0.19	41%	0.039	1.97	1.46	7.39	3.60	3.29	91%	0.304
METTL5	0.81	0.31	0.37	0.50	0.27	54%	0.085	4.91	1.54	0.00	2.15	2.51	117%	0.511
MPST	0.44	0.23	0.21	0.29	0.13	45%	0.011	0.46	0.79	0.34	0.53	0.23	44%	0.073

SNU13	0.75	0.58	0.60	0.64	0.09	14%	0.021	0.70	1.26	1.16	1.04	0.30	29%	0.834
NUBP1	1.03	0.59	0.35	0.65	0.34	53%	0.224	1.17	1.31	1.37	1.28	0.11	8%	0.044
OSGEP	1.27	0.68	0.37	0.77	0.45	59%	0.479	0.78	1.38	1.07	1.08	0.30	28%	0.695
PRRC2A	0.28	0.43	0.55	0.42	0.13	32%	0.017	3.50	0.03	1.07	1.53	1.78	116%	0.656
TFB2M	1.07	0.81	0.96	0.95	0.13	14%	0.549							
TP53RK	1.18	0.63	0.23	0.68	0.48	70%	0.367	0.93	1.34	1.96	1.41	0.52	37%	0.305
TPRKB	0.06	0.39	0.41	0.29	0.20	68%	0.024							
TUT7	4.07	2.69	3.22	3.32	0.70	21%	0.029							
WDR6	0.61	0.36	0.23	0.40	0.20	49%	0.034	1.01	1.80	1.01	1.27	0.46	36%	0.412
YRDC	0.11	0.14	0.06	0.10	0.04	38%	0.001	0.61	0.81	0.54	0.65	0.14	21%	0.048

Table S1c. LC-PRM quantification results of tryptic peptides from RWE proteins in whole-cell lysate of *SETD2*$^{-/-}$ cells (n = 3) relative to parental HEK293T cells (n = 3).

Peptide	standard type	Protein Symbol	Protein Gene	SETD2_KO/HEK293T -1	SETD2_KO/HEK293T -2	SETD2_KO/HEK293T -3
YLNTNPVGGLLEYAR	surrogate standard	ADAR	ADAR ADAR1 DSRAD G1P1 IFI4	0.98	0.84	0.65
IPLVVYGCQNER	surrogate standard	ADAT2	ADAT2 DEADC1	2.46	2.71	1.43
AVGAVVVDPASDR	surrogate standard	ADAT3	ADAT3 TAD3	0.44	0.15	0.63
VFYGAPSPDGALGTR	surrogate standard	ADAT3	ADAT3 TAD3	0.05	0.07	0.18
GVLEEQCR	surrogate standard	ADAT3	ADAT3 TAD3	0.84	0.13	1.06
AVLQLYPENSEQLELITTQATK	surrogate standard	BUD23	WBSCR22 MERM1 HUSSY-03 PP3381	0.37	0.19	0.45
AGFSGGMVVDYPNSAK	surrogate standard	BUD23	WBSCR22 MERM1 HUSSY-03 PP3381	0.12	0.05	0.09
ESVFTNER	surrogate standard	BUD23	WBSCR22 MERM1 HUSSY-03 PP3381	0.12	0.02	0.06
VVEVVEETIK	surrogate standard	CDKAL1	CDKAL1	0.89	0.67	0.97
GNLASYPIDELVDR	surrogate standard	CDKAL1	CDKAL1	0.67	0.38	0.46
DIGTNLPTLLWK	surrogate standard	CDKAL1	CDKAL1	1.84	1.63	0.90
GFGMTLK	surrogate standard	CMTR1	CMTR1 FTSJD2 KIAA0082 MTR1	0.19	0.07	0.11
NTDSDVNLVVPLEVIK	surrogate standard	CMTR1	CMTR1 FTSJD2 KIAA0082 MTR1	0.74	0.24	1.09
SQIYTWDGR	surrogate standard	CMTR1	CMTR1 FTSJD2 KIAA0082 MTR1	0.02	0.00	0.02
DSTVLAHVLR	surrogate standard	CTU1	CTU1 ATPBD3 NCS6	3.77	1.38	0.51
GGGLGSPGEGGALPR	surrogate standard	CTU1	CTU1 ATPBD3 NCS6	1.48	1.27	0.89
EELLQTLR	surrogate standard	CTU2	CTU2	0.93	0.80	0.75
LQTQFPSTVSTVYR	surrogate standard	CTU2	CTU2	0.51	0.49	0.21
NILHQGQEAILQR	surrogate standard	DCPS	DCPS DCS1 HINT5 HSPC015	0.89	0.44	0.43
NPLIINSIIDK	surrogate standard	DIMT1	DIMT1 DIMT1L HUSSY-05	2.56	2.70	1.76
LQGFEFWSR	surrogate standard	DUS1L	DUS1L	0.15	0.21	0.18

LSVPVTCK	surrogate standard	DUS1L	DUS1L	0.31	0.65	0.27
YLETKPADLGPR	surrogate standard	DUS3L	DUS3L	1.37	0.22	0.68
GTQPPSIR	surrogate standard	DUS3L	DUS3L	2.11	0.32	0.63
TCGPLTDEDVVR	surrogate standard	DUS3L	DUS3L	0.36	0.24	0.52
NGFVVLK	surrogate standard	EIF5A2	EIF5A2	0.02	0.02	0.02
NEVSLVAEGFLPEDGSGR	surrogate standard	ELP1	IKBKAP ELP1 IKAP	1.08	0.33	0.86
VLVTVFR	surrogate standard	ELP1	IKBKAP ELP1 IKAP	0.11	0.23	0.09
DQLVGLGR	surrogate standard	ELP1	IKBKAP ELP1 IKAP	1.13	1.23	1.45
YDPFLQTR	surrogate standard	ELP3	ELP3	4.04	5.11	1.54
LYPTLVIR	surrogate standard	ELP3	ELP3	4.81	8.65	0.83
VEPCSLTPGYTK	surrogate standard	ELP4	ELP4 C11orf19 PAXNEB	4.40	2.48	2.08
TYELLNCDK	surrogate standard	EMG1	EMG1 C2F	0.88	0.47	1.00
VGTSFSIPVVSDVR	surrogate standard	EMG1	EMG1 C2F	0.78	0.67	0.44
VSVEYTEK	surrogate standard	EMG1	EMG1 C2F	0.60	0.64	0.35
NVMVEPHR	surrogate standard	FBL	FBL FIB1 FLRN	1.10	0.02	0.28
NLVPGESVYGEK	surrogate standard	FBL	FBL FIB1 FLRN	0.53	0.56	0.80
AVDLCAAPGSWSQVLSQK	surrogate standard	FTSJ1	FTSJ1 JM23	0.87	0.41	0.47
SYPLDLEGGSEYK	surrogate standard	FTSJ1	FTSJ1 JM23	1.19	0.55	0.86
DLALAAEALR	surrogate standard	GTPBP3	GTPBP3 MTGP1	0.57	0.32	0.66
GLVAVITGGASGLGLATAER	surrogate standard	HSD17B10	HSD17B10 ERAB HADH2 MRPP2 SCHAD XH98G2	0.72	0.62	0.73
DVQTALALAK	surrogate standard	HSD17B10	HSD17B10 ERAB HADH2 MRPP2 SCHAD XH98G2	2.41	2.69	2.12
VCNFLASQVPFPSR	surrogate standard	HSD17B10	HSD17B10 ERAB HADH2 MRPP2 SCHAD XH98G2	1.09	1.27	0.79
IPVEGEVPEAR	surrogate standard	LCMT2	LCMT2 KIAA0547 TYW4	0.76	0.18	0.89
NSCNVGGGGGGFK	surrogate standard	MEPCE	MEPCE BCDIN3	0.08	0.00	0.00

FQYGNYCK	surrogate standard	MEPCE	MEPCE BCDIN3	2.88	1.34	0.97
SCFPASLTASR	surrogate standard	MEPCE	MEPCE BCDIN3	0.13	0.05	0.06
LASALLAEQEPQPER	surrogate standard	MOCS3	MOCS3 UBA4	0.95	0.54	0.99
ILEVLPGR	surrogate standard	MRM2	FTSJ2 FJH1 MRM2	0.96	0.56	0.72
APSTWEESGLR	surrogate standard	MRM3	RNMTL1 MRM3 HC90	1.67	1.22	1.32
LGFVVGR	surrogate standard	MTO1	MTO1 CGI-02	0.02	0.03	0.00
LIPEASISTSR	surrogate standard	MTO1	MTO1 CGI-02	1.34	1.14	1.23
SLFVVVGDR	surrogate standard	NAT10	NAT10 ALP KIAA1709	0.01	0.03	0.10
LDYLGVSYGLTPR	surrogate standard	NAT10	NAT10 ALP KIAA1709	1.89	2.12	1.31
AGPNASIISLK	surrogate standard	NAT10	NAT10 ALP KIAA1709	1.56	1.70	0.65
SLEAEGFQVTYLPVQK	surrogate standard	NFS1	NFS1 NIFS HUSSY-08	1.63	1.00	1.22
VEALQSGGGQER	surrogate standard	NFS1	NFS1 NIFS HUSSY-08	2.04	0.03	1.03
AIGTDEDLAHSSIR	surrogate standard	NFS1	NFS1 NIFS HUSSY-08	0.80	0.44	0.94
IQDIVGILR	surrogate standard	NOP2	NOP2 NOL1 NSUN1	2.22	2.99	2.54
DLAQALINR	surrogate standard	NOP2	NOP2 NOL1 NSUN1	1.54	2.47	1.91
GADSELSTVPSVTK	surrogate standard	NOP2	NOP2 NOL1 NSUN1	1.70	0.97	2.15
GTDTQTPAVLSPSK	surrogate standard	NOP2	NOP2 NOL1 NSUN1	1.96	1.16	3.33
LGFPGGFVDTQDR	surrogate standard	NUDT16	NUDT16	0.27	0.15	0.20
LQELSAAYR	surrogate standard	PCIF1	PCIF1	0.71	0.55	0.68
GITTEQLDALGCR	surrogate standard	QTRT1	QTRT1 TGT TGUT	1.67	1.10	1.37
SPYDGNETLLSPEK	surrogate standard	QTRT1	QTRT1 TGT TGUT	1.87	0.90	1.55
YDSQVAEENR	surrogate standard	RNGTT	RNGTT CAP1A	0.84	0.00	0.83
FNSQPVGDCDFNVR	surrogate standard	RNGTT	RNGTT CAP1A	0.74	0.41	0.60
SVLIGEFLEK	surrogate standard	RNMT	RNMT KIAA0398	0.29	0.28	0.38

TFLEFYEEK	surrogate standard	RNMT	RNMT KIAA0398	0.27	0.13	0.40
LPLGTLSK	surrogate standard	RNMT	RNMT KIAA0398	0.79	1.18	0.70
AQPLAYYEAAVR	surrogate standard	RPUSD2	RPUSD2 C15orf19	0.83	0.74	0.76
GKPCETVFQR	surrogate standard	RPUSD2	RPUSD2 C15orf19	2.85	0.72	0.67
LSYNGQSSVVR	surrogate standard	RPUSD2	RPUSD2 C15orf19	0.15	0.04	0.01
VGTVLGQR	surrogate standard	RPUSD3	RPUSD3	0.53	0.23	0.07
DTPVELLAPLPPYFSR	surrogate standard	RPUSD3	RPUSD3	1.41	0.37	0.94
GSGGAGALPEAAR	surrogate standard	TARBP1	TARBP1 TRM3 TRP185	0.68	0.13	0.27
DGPFVYGR	surrogate standard	TFB1M	TFB1M CGI-75	2.77	3.19	1.33
YGGIPNFSHR	surrogate standard	TGS1	TGS1 HCA137 NCOA6IP PIMT	4.80		2.02
DYFEDQPLLYPPGFDGR	surrogate standard	THG1L	THG1L ICF45	0.31	0.02	0.62
VVVYPSNQTLK	surrogate standard	THG1L	THG1L ICF45	0.39	0.35	0.21
ELAGIVCTLNSENK	surrogate standard	THUMPD1	THUMPD1	1.69	1.03	1.59
AVCCLSVVK	surrogate standard	THUMPD1	THUMPD1	0.87	0.96	1.00
STLALQLGQR	surrogate standard	TRIT1	TRIT1 IPT MOD5	0.23	0.38	0.23
IAFPSANEVFYNPVQEFNR	surrogate standard	TRMT1	TRMT1	0.62	0.40	0.77
DLTCAVITEFAR	surrogate standard	TRMT1	TRMT1	0.64	0.48	0.73
FALEVPGLR	surrogate standard	TRMT1	TRMT1	0.04	0.01	0.02
DVVHSTLR	surrogate standard	TRMT10A	TRMT10A RG9MTD2	4.09	2.36	1.77
IPAVTYPK	surrogate standard	TRMT10C	TRMT10C MRPP1 RG9MTD1	1.02	1.89	0.76
EVPEHITEEELK	surrogate standard	TRMT10C	TRMT10C MRPP1 RG9MTD1	0.45	0.28	0.61
LLLTSTEK	surrogate standard	TRMT10C	TRMT10C MRPP1 RG9MTD1	0.09	0.08	0.10
IDALEFLPFEGK	surrogate standard	TRMT11	TRMT11 C6orf75 MDS024	0.40	0.21	0.66
ICPVEFNPNFVAR	surrogate standard	TRMT112	TRMT112 AD-001 HSPC152 HSPC170	1.52	2.08	1.01

GPVEGYEENEEFLR	surrogate standard	TRMT112	TRMT112 AD-001 HSPC152 HSPC170	0.71	0.55	0.81
ILCPLDPK	surrogate standard	TRMT13	TRMT13 CCDC76	1.13	0.27	0.86
AEDLVPTLVSR	surrogate standard	TRMT2A	TRMT2A HTF9C	0.54	0.83	0.61
WSAALPCAEAR	surrogate standard	TRMT44	TRMT44 C4orf23 METTL19	0.51	0.63	0.65
AVLPEGQDVTSGFSR	surrogate standard	TRMT5	TRMT5 KIAA1393 TRM5	0.97	0.57	0.85
DANPAEDVR	surrogate standard	TRMT5	TRMT5 KIAA1393 TRM5	1.30	0.03	1.04
DGFFTLDSALLR	surrogate standard	TRUB2	TRUB2	0.80	0.12	0.65
AATPQVAAELEK	surrogate standard	TRUB2	TRUB2	0.67	0.10	0.29
DQFFTTSSCAGR	surrogate standard	TYW3	TYW3 C1orf171	1.56	0.82	0.86
CTALTFIASEEK	surrogate standard	WDR4	WDR4	4.41	2.09	1.87
ISVVPTQPGLLLSSSGDGTLR	surrogate standard	WDR4	WDR4	1.24	0.99	1.19
GAEAANVTGPGGVPVQGSK	surrogate standard	YBX1	YBX1 NSEP1 YB1	1.29	1.30	1.69
NEGSESAPEGQAQQR	surrogate standard	YBX1	YBX1 NSEP1 YB1	0.97	0.02	0.90
AADPPAENSSAPEAEQGGAE	surrogate standard	YBX1	YBX1 NSEP1 YB1	0.41	0.11	1.17
ALEAVFGK	surrogate standard	RBMX	RBMX HNRPG RBMXP1	1.06	1.37	1.50
SAPSGPVR	surrogate standard	RBMX	RBMX HNRPG RBMXP1	0.27	0.00	0.01
SDLYSSGR	surrogate standard	RBMX	RBMX HNRPG RBMXP1	3.09	0.39	1.60
SLFSSIGEVESAK	surrogate standard	ELAVL1	HuR	1.42	1.10	1.02
DVEDMFSR	surrogate standard	ELAVL1	HuR	1.32	0.95	1.37
VLVDQTTGLSR	surrogate standard	ELAVL1	HuR	0.81	0.77	0.85
YTIENPR	surrogate standard	SND1	SND1 TDRD11	1.93	2.37	1.25
EVLPSTR	surrogate standard	SND1	SND1 TDRD11	2.43	0.23	1.50
LGTLSPAFSTR	surrogate standard	SND1	SND1 TDRD11	0.52	0.55	0.22
DINESDEVEVYSR	surrogate standard	FMR1	FMR1	0.72	0.08	1.44

SFLEFAEDVIQVPR	surrogate standard	FMR1	FMR1	0.50	0.20	0.93
IPENIYR	surrogate standard	LRPPRC	LRPPRC LRP130	1.46	1.88	1.26
LQWFCDR	surrogate standard	LRPPRC	LRPPRC LRP130	0.01	0.02	0.08
LDLQNLSLEDGR	surrogate standard	PUS7L	PUS7L	1.62	1.00	1.17
FGNLVETK	surrogate standard	PUS7L	PUS7L	1.44	0.54	0.59
LNIPGCYR	surrogate standard	PUS7L	PUS7L	0.64	0.36	0.07
AEAGILNYYR	isotopic standard	ALKBH1	ALKBH1 ABH ABH1 ALKBH	0.95	1.47	0.69
LLNHAVPR	surrogate standard	ALKBH1	ALKBH1 ABH ABH1 ALKBH	1.60	1.43	1.24
ELSAEFGPGGR	isotopic standard	ALKBH4	ALKBH4 ABH4	0.68	0.54	0.88
VSEPVLSLPVR	isotopic standard	ALKBH5	ALKBH5 ABH5 OFOXD1	1.18	0.97	0.88
VPALEPFR	isotopic standard	ALKBH6	ALKBH6 ABH6	2.56	4.47	2.44
ILIGNPGCTYK	surrogate standard	FTO	FTO KIAA1752	1.03	1.46	1.04
EGLPVEQR	surrogate standard	FTO	FTO KIAA1752	0.77	0.43	0.49
SGPVMGGGLPPPPIK	surrogate standard	YTHDF1	YTHDF1	4.35	1.88	3.01
SPVDYGTSAGVWSQDK	isotopic standard	YTHDF1	YTHDF1	1.57	0.39	1.99
DGLNDDDFEPYLSPQAR	isotopic standard	YTHDF2	YTHDF2 HGRG8	1.48	0.68	2.34
LGSTEVASNVPK	surrogate standard	YTHDF2	YTHDF2 HGRG8	1.77	2.43	1.99
DVPNSQLR	surrogate standard	YTHDF2	YTHDF2 HGRG8	5.31	0.41	2.49
AITDGQAGFGNDTLSK	isotopic standard	YTHDF3	YTHDF3	1.72	0.84	1.45
VPGISSIEQGMTGLK	isotopic standard	YTHDF3	YTHDF3	3.26	1.96	2.14
GNVGIGGSAVPPPPIK	isotopic standard	YTHDF3	YTHDF3	1.32	1.04	0.74
GVWSTLPVNEK	isotopic standard	YTHDC1	YTHDC1 KIAA1966 YT521	0.35	0.29	0.34
LSQSLGLVSK	surrogate standard	YTHDC2	YTHDC2	0.12	0.08	0.05
VVLIVGETGSGK	isotopic standard	YTHDC2	YTHDC2	0.30	0.25	0.20
NPEAALSPTFR	isotopic standard	METTL3	METTL3 MTA70	2.69	2.64	1.73
YLDVSILGK	surrogate standard	METTL3	METTL3 MTA70	0.99	1.72	1.00

VDEIIWVK	surrogate standard	METTL3	METTL3 MTA70	2.83	1.36	2.21
LEIDEIAAPR	isotopic standard	METTL14	METTL14 KIAA1627	3.21	4.33	7.43
VSDYVQDR	surrogate standard	METTL1	METTL1 C12orf1	0.79	0.21	0.40
AAPAGGFQNIACLR	isotopic standard	METTL1	METTL1 C12orf1	0.03	0.11	0.05
NFPAIFR	surrogate standard	METTL1	METTL1 C12orf1	0.29	0.65	0.22
LPGVAGQYLFK	surrogate standard	METTL16	METTL16 METT10D	2.96	5.91	2.23
TQTPPVEENVTQK	isotopic standard	METTL2B	METTL2B	1.01	0.18	0.79
GAEQLAEGGR	surrogate standard	NSUN2	NSUN2 SAKI TRM4	1.11	0.08	0.76
ILLTQENPFFR	surrogate standard	NSUN2	NSUN2 SAKI TRM4	0.05	0.06	0.06
QLEEPGAGTPSPVR	surrogate standard	NSUN5	NSUN5 NSUN5A WBSCR20 WBSCR20A	1.49	0.41	1.47
DALQQNPGAFR	surrogate standard	NSUN5	NSUN5 NSUN5A WBSCR20 WBSCR20A	1.21	0.18	0.84
EVASYQPLQR	isotopic standard	NSUN6	NSUN6 NOPD1	1.03	0.65	0.68
GAGLSCEQLK	surrogate standard	NSUN6	NSUN6 NOPD1	2.83	0.55	0.41
FCSFSPCIEQVQR	surrogate standard	TRMT61A	TRMT61A	0.85	0.91	0.61
TCQALAAR	isotopic standard	TRMT61A	TRMT61A	0.47	0.09	0.10
HSVDLIGR	surrogate standard	TRMT61A	TRMT61A	0.71	1.69	0.27
INTDVQLDSQEK	surrogate standard	TRMT61B	TRMT61B	2.98	0.00	1.65
AATACFGFPK	isotopic standard	TRMT6	TRMT6 KIAA1153 TRM6 CGI-09	0.08	0.05	0.07
SFLSGLYEFPLNK	surrogate standard	TRMT6	TRMT6 KIAA1153 TRM6 CGI-09	0.10	0.10	0.22
SLFPGLETK	surrogate standard	PUS7	PUS7 KIAA1897	0.08	0.08	0.04
FGTTAVPTYQVGR	isotopic standard	PUS7	PUS7 KIAA1897	0.72	0.82	0.30
QGSPVAAGAPAK	surrogate standard	IGF2BP1	IGF2BP1 CRDBP VICKZ1 ZBP1	2.75	0.16	0.87
ITISSLQDLTLYNPER	isotopic standard	IGF2BP1	IGF2BP1 CRDBP VICKZ1 ZBP1	0.77	0.61	1.00
TVNELQNLTAAEVVVPR	surrogate standard	IGF2BP1	IGF2BP1 CRDBP VICKZ1 ZBP1	0.72	0.52	0.71
LYIGNLSPAVTADDLR	isotopic standard	IGF2BP2	IGF2BP2 IMP2 VICKZ2	0.64	0.51	0.92
TVNELQNLTSAEVIVPR	surrogate standard	IGF2BP2	IGF2BP2 IMP2 VICKZ2	1.62	0.60	1.09

FTEEIPLK	surrogate standard	IGF2BP3	IGF2BP3 IMP3 KOC1 VICKZ3	2.30	1.72	2.12
ITISPLQELTLYNPER	isotopic standard	IGF2BP3	IGF2BP3 IMP3 KOC1 VICKZ3	1.25	0.90	1.08
QYEAYVQALEGK	surrogate standard	WTAP	WTAP KIAA0105	0.79	0.37	1.40
YTDLNSNDVTGLR	surrogate standard	WTAP	WTAP KIAA0105	1.07	0.91	1.33
QVQQPSVAQLR	isotopic standard	WTAP	WTAP KIAA0105	0.62	0.43	0.38
GLSYLQLK	surrogate standard	VIRMA	KIAA1429 MSTP054	0.66	0.76	0.42
NLDADLVR	isotopic standard	RBM15B	RBM15B OTT3	1.39	0.85	0.95
LQQLALGR	isotopic standard	RBM15	RBM15 OTT OTT1	0.96	0.71	0.36
LAGSELFAK	surrogate standard	ZC3H13	ZC3H13 KIAA0853	0.06	0.18	0.12
FCLQYTR	surrogate standard	EIF3A	EIF3A EIF3S10 KIAA0139	0.16	0.19	0.06
VLLATLSIPITPER	isotopic standard	EIF3A	EIF3A EIF3S10 KIAA0139	0.58	0.69	0.46
GTQGVVTNFEIFR	isotopic standard	EIF3B	EIF3B EIF3S9	1.04	1.21	0.84
LFIGGLSFETTEESLR	surrogate standard	HNRNPA2B1	HNRNPA2B1 HNRPA2B1	0.67	0.45	1.74
IDTIEIITDR	isotopic standard	HNRNPA2B1	HNRNPA2B1 HNRPA2B1	2.32	1.76	2.60
TLETVPLER	surrogate standard	HNRNPA2B1	HNRNPA2B1 HNRPA2B1	1.31	1.26	1.55
GFAFVQYVNER	isotopic standard	HNRNPC	HNRNPC HNRPC	0.14	0.17	0.12
TIEDDLVSALVR	isotopic standard	PUS1	PUS1 PP8985	0.34	0.19	0.49
LSAETLQQVNR	surrogate standard	PUS1	PUS1 PP8985	0.56	0.56	0.35
GYAPESVLER	surrogate standard	PUS1	PUS1 PP8985	0.59	0.39	0.45
AAAAVVAAAAR	isotopic standard	TRUB1	TRUB1 PUS4	0.01	0.05	0.01
GVLVVGIGSGTK	surrogate standard	TRUB1	TRUB1 PUS4	0.68	0.39	0.24
EVVAEVVK	isotopic standard	DKC1	DKC1 NOLA4	0.78	0.43	1.11
LHNAIEGGTQLSR	surrogate standard	DKC1	DKC1 NOLA4	1.17	0.55	0.62
NLAANDLSPSR	surrogate standard	NSUN4	NSUN4	1.07	0.64	0.81
WGELEGDTYDR	surrogate standard	NSUN4	NSUN4	0.27	0.07	0.60
VLVDVPCTTDR	isotopic standard	NSUN4	NSUN4	0.79	0.63	0.90

SLGTADVHFER	surrogate standard	ALYREF	THOC4	0.98	0.68	0.72
QYNGVPLDGR	surrogate standard	ALYREF	THOC4	1.41	1.16	1.16
QQLSAEELDAQLDAYNAR	isotopic standard	ALYREF	THOC4	1.12	0.65	1.97
ILAWAPVEPSFSAR	surrogate standard	PUS3	PUS3 FKSG32	0.12	0.12	0.16
DLQAHINHR	surrogate standard	CBLL1	CBLL1 HAKAI RNF188	1.84	0.43	0.89
DSLVLLGR	surrogate standard	CIAO1	CIAO1 WDR39	2.80	4.45	2.44
GTLIQGVLR	surrogate standard	DIS3L2	DIS3L2 FAM6A	0.47	0.44	0.11
DYANTLFICR	surrogate standard	DIS3L2	DIS3L2 FAM6A	3.46	1.98	1.53
EGFDSDINNR	surrogate standard	ELP5	ELP5 C17orf81 DERP6 HSPC002 MSTP071	2.92	0.09	1.58
LACDFLAR	surrogate standard	FTSJ3	FTSJ3 SB92	0.02	0.10	0.02
AANPVDFLSK	surrogate standard	FTSJ3	FTSJ3 SB92	0.03	0.02	0.04
NVGTGLVGAPACGDVMK	surrogate standard	ISCU	ISCU NIFUN	2.51	1.17	1.69
TFGCGSAIASSSLATEWVK	surrogate standard	ISCU	ISCU NIFUN	0.76	0.56	0.70
TVEEALTIK	surrogate standard	ISCU	ISCU NIFUN	1.47	1.42	2.00
LDGGFAAVSR	surrogate standard	METTL17	METTL17 METT11D1	1.36	2.07	3.32
YDLPASYK	surrogate standard	METTL5	METTL5 DC3 HSPC133	1.24	0.03	0.81
QNLPLSSGK	surrogate standard	MPST	MPST TST2	0.51	0.49	0.31
SQPAPAEFR	surrogate standard	MPST	MPST TST2	1.29	1.33	0.65
LLDLVQQSCNYK	surrogate standard	SNU13	NHP2L1	0.87	1.17	1.05
NVPYVFVR	surrogate standard	SNU13	NHP2L1	1.00	2.44	1.37
QQIQSIQQSIER	surrogate standard	SNU13	NHP2L1	0.46	0.34	0.38
VPLDPLIGK	surrogate standard	NUBP1	NUBP1 NBP NBP1	1.57	2.09	1.62
GQSFFIDAPDSPATLAYR	surrogate standard	NUBP1	NUBP1 NBP NBP1	0.94	0.59	0.86
TYVTPPGTGFLPGDTAR	surrogate standard	OSGEP	OSGEP GCPL1	0.95	0.57	0.62

LVELPYTVK	surrogate standard	OSGEP	OSGEP GCPL1	1.72	2.39	1.63
TPLSDSGVTQR	surrogate standard	OSGEP	OSGEP GCPL1	2.12	2.16	1.32
GPDELEGPDSK	surrogate standard	PRRC2A	PRRC2A BAT2 G2	0.28	0.07	1.02
SFSGLNSR	surrogate standard	PRRC2A	PRRC2A BAT2 G2	7.57	12.59	8.76
YLNEQLYSGPSSAAQR	surrogate standard	RRP8	RRP8 KIAA0409 NML hucep-1	2.31	0.38	2.70
GVDLYVLEK	surrogate standard	TP53RK	TP53RK C20orf64 PRPK	1.69	2.11	2.11
VTLPGQEEPWDIR	surrogate standard	URM1	URM1 C9orf74	1.41	1.01	2.16
GLLATASEDR	surrogate standard	WDR6	WDR6	0.85	0.71	0.76
LGSTVVDLSVPGK	surrogate standard	YRDC	YRDC DRIP3 IRIP	0.68	0.64	0.49

Table S1d. LC-PRM quantification results of RWE proteins in whole-cell lysate of *SETD2*$^{-/-}$ cells (n = 3) relative to parental HEK293T cells (n = 3).

Protein Symbol	SETD2/HEK293T-1	s.d.	SETD2/HEK293T-2	s.d.	SETD2/HEK293T-3	s.d.	Ave.	S.D.	R.S.D.	*p*-value (one samples t test)
ADAR	0.98		0.84		0.65		0.83	0.16	20%	0.208
ADAT2	2.46		2.71		1.43		2.20	0.68	31%	0.092
ADAT3	0.44	0.40	0.12	0.04	0.62	0.44	0.39	0.26	65%	0.055
BUD23	0.20	0.15	0.09	0.09	0.20	0.22	0.16	0.07	40%	0.002
CDKAL1	1.13	0.62	0.89	0.66	0.77	0.28	0.93	0.18	19%	0.585
CMTR1	0.31	0.38	0.11	0.12	0.40	0.59	0.27	0.15	56%	0.014
CTU1	2.63	1.62	1.33	0.08	0.70	0.27	1.55	0.98	63%	0.434
CTU2	0.72	0.30	0.65	0.22	0.48	0.38	0.62	0.12	20%	0.032
DCPS	0.89		0.44		0.43		0.59	0.26	45%	0.111
DIMT1	2.56		2.70		1.76		2.34	0.51	22%	0.045
DUS1L	0.23	0.11	0.43	0.31	0.23	0.06	0.30	0.12	39%	0.009
DUS3L	1.28	0.88	0.26	0.05	0.61	0.08	0.72	0.52	72%	0.444
EIF5A2	0.02		0.02		0.02		0.02	0.00	15%	0.000
ELP1	0.77	0.58	0.60	0.55	0.80	0.68	0.72	0.11	15%	0.050
ELP3	4.42	0.54	6.88	2.50	1.18	0.50	4.16	2.86	69%	0.195
ELP4	4.40		2.48		2.08		2.99	1.24	41%	0.109
EMG1	0.76	0.14	0.60	0.11	0.59	0.35	0.65	0.09	14%	0.022
FBL	0.82	0.40	0.29	0.38	0.54	0.36	0.55	0.26	48%	0.097
FTSJ1	1.03	0.23	0.48	0.10	0.67	0.28	0.73	0.28	39%	0.235
GTPBP3	0.57		0.32		0.66		0.52	0.18	34%	0.042
HSD17B10	1.40	0.89	1.53	1.06	1.21	0.79	1.38	0.16	11%	0.053
LCMT2	0.76		0.18		0.89		0.61	0.38	62%	0.214
MEPCE	1.03	1.60	0.46	0.76	0.34	0.54	0.61	0.37	60%	0.209
MOCS3	0.95		0.54		0.99		0.83	0.25	30%	0.357
MRM2	0.96		0.56		0.72		0.75	0.20	27%	0.166

MRM3	1.67		1.22		1.32		1.41	0.24	17%	0.097
MTO1	0.68	0.94	0.58	0.78	0.62	0.87	0.63	0.05	8%	0.006
NAT10	1.16	1.01	1.28	1.11	0.69	0.61	1.04	0.31	30%	0.840
NFS1	1.49	0.63	0.49	0.49	1.06	0.14	1.01	0.50	50%	0.964
NOP2	1.85	0.30	1.90	0.99	2.48	0.62	2.08	0.35	17%	0.034
NUDT16	0.27		0.15		0.20		0.21	0.06	30%	0.002
PCIF1	0.71		0.55		0.68		0.65	0.09	13%	0.019
QTRT1	1.77	0.14	1.00	0.14	1.46	0.13	1.41	0.38	27%	0.207
RNGTT	0.79	0.07	0.21	0.29	0.72	0.17	0.57	0.32	55%	0.143
RNMT	0.45	0.30	0.53	0.56	0.49	0.18	0.49	0.04	8%	0.002
RPUSD2	1.28	1.40	0.50	0.39	0.48	0.41	0.75	0.45	60%	0.444
RPUSD3	0.97	0.62	0.30	0.10	0.50	0.62	0.59	0.34	58%	0.173
TARBP1	0.68		0.13		0.27		0.36	0.28	79%	0.060
TFB1M	2.77		3.19		1.33		2.43	0.98	40%	0.127
TGS1	4.80				2.02		3.41	1.97	58%	
THG1L	0.35	0.06		0.23	0.41	0.29	0.38	0.04	11%	
THUMPD1	1.28	0.58	1.00	0.05	1.29	0.41	1.19	0.17	14%	0.188
TRIT1	0.23		0.38		0.23		0.28	0.09	31%	0.005
TRMT1	0.43	0.34	0.30	0.25	0.51	0.42	0.41	0.11	26%	0.011
TRMT10A	4.09		2.36		1.77		2.74	1.20	44%	0.130
TRMT10C	0.52	0.47	0.75	0.99	0.49	0.35	0.59	0.14	24%	0.037
TRMT11	0.40		0.21		0.66		0.42	0.23	53%	0.047
TRMT112	1.11	0.58	1.32	1.08	0.91	0.14	1.11	0.20	18%	0.436
TRMT13	1.13		0.27		0.86		0.75	0.44	58%	0.432
TRMT2A	0.54		0.83		0.61		0.66	0.15	23%	0.059
TRMT44	0.51		0.63		0.65		0.59	0.08	13%	0.011
TRMT5	1.13	0.23	0.30	0.38	0.94	0.13	0.79	0.44	55%	0.497
TRUB2	0.73	0.10	0.11	0.02	0.47	0.25	0.44	0.31	71%	0.090
TYW3	1.56		0.82		0.86		1.08	0.42	39%	0.777

WDR4	2.83	2.24	1.54	0.78	1.53	0.48	1.97	0.75	38%	0.154
YBX1	0.89	0.44	0.48	0.71	1.25	0.40	0.87	0.39	44%	0.628
RBMX	1.48	1.45	0.59	0.70	1.04	0.89	1.03	0.44	43%	0.906
ELAVL1	1.18	0.32	0.94	0.16	1.08	0.27	1.07	0.12	11%	0.429
SND1	1.63	0.99	1.05	1.15	0.99	0.68	1.22	0.35	29%	0.390
FMR1	0.61	0.16	0.14	0.09	1.18	0.36	0.64	0.52	81%	0.360
LRPPRC	0.73	1.03	0.95	1.31	0.67	0.83	0.78	0.15	19%	0.126
PUS7L	1.23	0.52	0.63	0.33	0.61	0.55	0.83	0.35	43%	0.482
ALKBH1	1.27	0.46	1.45	0.02	0.97	0.39	1.23	0.25	20%	0.247
ALKBH4	0.68		0.54		0.88		0.70	0.17	25%	0.093
ALKBH5	1.18		0.97		0.88		1.01	0.16	15%	0.905
ALKBH6	2.56		4.47		2.44		3.16	1.14	36%	0.081
FTO	0.90	0.19	0.94	0.73	0.77	0.39	0.87	0.09	11%	0.138
YTHDF1	2.96	1.96	1.14	1.05	2.50	0.72	2.20	0.95	43%	0.159
YTHDF2	2.85	2.13	1.17	1.10	2.27	0.26	2.10	0.85	41%	0.155
YTHDF3	2.10	1.02	1.28	0.60	1.44	0.70	1.61	0.43	27%	0.137
YTHDC1	0.35		0.29		0.34		0.33	0.03	9%	0.001
YTHDC2	0.21	0.13	0.16	0.12	0.13	0.11	0.17	0.04	26%	0.001
METTL3	2.17	1.03	1.91	0.66	1.65	0.61	1.91	0.26	14%	0.027
METTL14	3.21		4.33		7.43		4.99	2.19	44%	0.087
METTL1	0.37	0.39	0.32	0.29	0.22	0.17	0.31	0.07	25%	0.004
METTL16	2.96		5.91		2.23		3.70	1.95	53%	0.138
METTL2B	1.01		0.18		0.79		0.66	0.43	65%	0.307
NSUN2	0.58	0.75	0.07	0.01	0.41	0.50	0.35	0.26	74%	0.050
NSUN5	1.35	0.20	0.30	0.16	1.16	0.44	0.93	0.56	60%	0.859
NSUN6	1.93	1.27	0.60	0.07	0.54	0.19	1.03	0.79	77%	0.961
TRMT61A	0.68	0.19	0.90	0.80	0.33	0.26	0.63	0.29	45%	0.159
TRMT61B	2.98		0.00		1.65		1.54	1.49	97%	0.593
TRMT6	0.09	0.02	0.07	0.04	0.14	0.10	0.10	0.04	36%	0.001

PUS7	0.40	0.45	0.45	0.53	0.17	0.19	0.34	0.15	44%	0.017
IGF2BP1	1.42	1.16	0.43	0.24	0.86	0.14	0.90	0.49	55%	0.766
IGF2BP2	1.13	0.70	0.55	0.07	1.00	0.12	0.90	0.30	34%	0.609
IGF2BP3	1.77	0.74	1.31	0.58	1.60	0.74	1.56	0.23	15%	0.053
WTAP	0.83	0.23	0.57	0.30	1.04	0.57	0.81	0.23	29%	0.295
VIRMA	0.66		0.76		0.42		0.61	0.17	28%	0.062
RBM15B	1.39		0.85		0.95		1.07	0.29	27%	0.732
RBM15	0.96		0.71		0.36		0.68	0.30	44%	0.204
ZC3H13	0.06		0.18		0.12		0.12	0.06	47%	0.001
EIF3A	0.37	0.30	0.44	0.36	0.26	0.28	0.36	0.09	26%	0.007
EIF3B	1.04		1.21		0.84		1.03	0.19	18%	0.797
HNRNPA2B1	1.43	0.83	1.15	0.66	1.97	0.56	1.52	0.41	27%	0.162
HNRNPC	0.14		0.17		0.12		0.14	0.03	20%	0.000
PUS1	0.50	0.13	0.38	0.18	0.43	0.07	0.44	0.06	13%	0.004
TRUB1	0.35	0.48	0.22	0.24	0.12	0.16	0.23	0.11	48%	0.007
DKC1	0.98	0.28	0.49	0.09	0.87	0.35	0.78	0.26	33%	0.269
NSUN4	0.71	0.40	0.45	0.33	0.77	0.15	0.64	0.17	27%	0.068
ALYREF	1.17	0.22	0.83	0.29	1.28	0.64	1.09	0.24	22%	0.560
PUS3	0.12		0.12		0.16		0.13	0.02	18%	0.000
CBLL1	1.84		0.43		0.89		1.05	0.72	68%	0.912
CIAO1	2.80		4.45		2.44		3.23	1.07	33%	0.069
DIS3L2	1.97	2.11	1.21	1.09	0.82	1.00	1.33	0.58	43%	0.424
ELP5	2.92		0.09		1.58		1.53	1.42	93%	0.584
FTSJ3	0.03	0.01	0.06	0.06	0.03	0.01	0.04	0.02	52%	0.000
ISCU	1.58	0.88	1.05	0.44	1.47	0.68	1.37	0.28	20%	0.151
METTL17	1.36		2.07		3.32		2.25	0.99	44%	0.160
METTL5	1.24		0.03		0.81		0.69	0.61	88%	0.477
MPST	0.90	0.55	0.91	0.60	0.48	0.24	0.77	0.25	32%	0.242
SNU13	0.78	0.28	1.32	1.06	0.93	0.51	1.01	0.28	28%	0.961

NUBP1	1.25	0.44	1.34	1.06	1.24	0.54	1.28	0.05	4%	0.012
OSGEP	1.60	0.59	1.71	0.99	1.19	0.52	1.50	0.27	18%	0.087
PRRC2A	3.93	5.15	6.33	8.85	4.89	5.47	5.05	1.21	24%	0.028
RRP8	2.31		0.38		2.70		1.80	1.24	69%	0.383
TP53RK	1.69		2.11		2.11		1.97	0.24	12%	0.020
URM1	1.41		1.01		2.16		1.53	0.58	38%	0.257
WDR6	0.85		0.71		0.76		0.77	0.07	9%	0.029
YRDC	0.68		0.64		0.49		0.60	0.10	17%	0.022

Table S1e. LC-PRM quantification results of tryptic peptides from RWE proteins in whole-cell lysate of $KAT5^{-/-}$ cells (n = 3) relative to parental HEK293T cells (n = 3).

Peptide	standard type	Protein Symbol	Protein Gene	KAT5_KO/HEK293T -1	KAT5_KO/HEK293T -2	KAT5_KO/HEK293T -3
YLNTNPVGGLLEYAR	surrogate standard	ADAR	ADAR ADAR1 DSRAD G1P1 IFI4	1.88	0.92	0.79
VLIGENEK	surrogate standard	ADAR	ADAR ADAR1 DSRAD G1P1 IFI4	0.73	0.47	0.72
DGSAFEDGLR	surrogate standard	ADAR	ADAR ADAR1 DSRAD G1P1 IFI4	3.23	1.13	3.02
IPLVVYGCQNER	surrogate standard	ADAT2	ADAT2 DEADC1	2.06	2.60	1.45
AVGAVVVDPASDR	surrogate standard	ADAT3	ADAT3 TAD3	0.73	0.55	0.43
VFYGAPSPDGALGTR	surrogate standard	ADAT3	ADAT3 TAD3	0.26	0.32	0.22
GVLEEQCR	surrogate standard	ADAT3	ADAT3 TAD3	0.68	0.42	0.73
AVLQLYPENSEQLELITTQATK	surrogate standard	BUD23	WBSCR22 MERM1 HUSSY-03 PP3381	1.21	0.23	0.57
AGFSGGMVVDYPNSAK	surrogate standard	BUD23	WBSCR22 MERM1 HUSSY-03 PP3381	0.39	0.31	0.20
ESVFTNER	surrogate standard	BUD23	WBSCR22 MERM1 HUSSY-03 PP3381	0.28	0.31	0.11
VIFPDAEMEDVNNPGLR	surrogate standard	CDK5RAP1	CDK5RAP1 C20orf34 CGI-05 HSPC167	2.15	0.62	1.16
ITSASSQTLR	surrogate standard	CDK5RAP1	CDK5RAP1 C20orf34 CGI-05 HSPC167	6.26	2.31	0.15
VVEVVEETIK	surrogate standard	CDKAL1	CDKAL1	2.51	1.18	0.92
GNLASYPIDELVDR	surrogate standard	CDKAL1	CDKAL1	1.57	0.49	0.73
DIGTNLPTLLWK	surrogate standard	CDKAL1	CDKAL1	2.18	0.91	0.69
GFGMTLK	surrogate standard	CMTR1	CMTR1 FTSJD2 KIAA0082 MTR1	0.20	0.33	0.34
NTDSDVNLVVPLEVIK	surrogate standard	CMTR1	CMTR1 FTSJD2 KIAA0082 MTR1	1.69	0.37	1.61
SQIYTWDGR	surrogate standard	CMTR1	CMTR1 FTSJD2 KIAA0082 MTR1	0.08	0.20	0.03
DSTVLAHVLR	surrogate standard	CTU1	CTU1 ATPBD3 NCS6	3.99	2.44	0.13
GGGLGSPGEGGALPR	surrogate standard	CTU1	CTU1 ATPBD3 NCS6	1.10	1.76	0.64
EELLQTLR	surrogate standard	CTU2	CTU2	1.02	1.11	1.01

LQTQFPSTVSTVYR	surrogate standard	CTU2	CTU2	0.38	1.16	0.27
NILHQGQEAILQR	surrogate standard	DCPS	DCPS DCS1 HINT5 HSPC015	0.45	0.48	0.13
NPLIINSIIDK	surrogate standard	DIMT1	DIMT1 DIMT1L HUSSY-05	1.69	2.23	1.90
LQGFEFWSR	surrogate standard	DUS1L	DUS1L	0.84	0.54	0.41
LSVPVTCK	surrogate standard	DUS1L	DUS1L	0.56	1.43	0.31
YLETKPADLGPR	surrogate standard	DUS3L	DUS3L	1.89	0.72	0.21
GTQPPSIR	surrogate standard	DUS3L	DUS3L	2.20	0.75	0.28
TCGPLTDEDVVR	surrogate standard	DUS3L	DUS3L	0.82	0.60	0.84
NGFVVLK	surrogate standard	EIF5A2	EIF5A2	0.10	0.56	0.08
NEVSLVAEGFLPEDGSGR	surrogate standard	ELP1	IKBKAP ELP1 IKAP	1.92	0.46	1.51
VLVTVFR	surrogate standard	ELP1	IKBKAP ELP1 IKAP	0.09	0.31	0.10
DQLVGLGR	surrogate standard	ELP1	IKBKAP ELP1 IKAP	0.94	1.96	1.42
YDPFLQTR	surrogate standard	ELP3	ELP3	4.42	6.01	1.62
LYPTLVIR	surrogate standard	ELP3	ELP3	3.89	12.23	1.16
VEPCSLTPGYTK	surrogate standard	ELP4	ELP4 C11orf19 PAXNEB	2.72	2.76	1.55
TYELLNCDK	surrogate standard	EMG1	EMG1 C2F	1.05	0.74	0.64
VGTSFSIPVVSDVR	surrogate standard	EMG1	EMG1 C2F	0.68	0.83	0.49
VSVEYTEK	surrogate standard	EMG1	EMG1 C2F	0.45	0.93	0.37
NVMVEPHR	surrogate standard	FBL	FBL FIB1 FLRN	1.66	0.30	0.16
NLVPGESVYGEK	surrogate standard	FBL	FBL FIB1 FLRN	0.72	0.61	0.98
AVDLCAAPGSWSQVLSQK	surrogate standard	FTSJ1	FTSJ1 JM23	2.03	0.69	0.64
SYPLDLEGGSEYK	surrogate standard	FTSJ1	FTSJ1 JM23	1.40	0.78	0.98
DLALAAEALR	surrogate standard	GTPBP3	GTPBP3 MTGP1	0.78	0.59	0.80
GLVAVITGGASGLGLATAER	surrogate standard	HSD17B10	HSD17B10 ERAB HADH2 MRPP2 SCHAD XH98G2	0.91	0.32	0.62

DVQTALALAK	surrogate standard	HSD17B10	HSD17B10 ERAB HADH2 MRPP2 SCHAD XH98G2	1.69	1.92	1.65
VCNFLASQVPFPSR	surrogate standard	HSD17B10	HSD17B10 ERAB HADH2 MRPP2 SCHAD XH98G2	0.61	1.21	0.87
IPVEGEVPEAR	surrogate standard	LCMT2	LCMT2 KIAA0547 TYW4	1.53	0.69	1.11
NSCNVGGGGGGFK	surrogate standard	MEPCE	MEPCE BCDIN3	0.38	0.10	0.00
FQYGNYCK	surrogate standard	MEPCE	MEPCE BCDIN3	3.87	6.58	1.54
SCFPASLTASR	surrogate standard	MEPCE	MEPCE BCDIN3	0.03	0.04	0.01
LASALLAEQEPQPER	surrogate standard	MOCS3	MOCS3 UBA4	1.01	0.64	1.02
ILEVLPGR	surrogate standard	MRM2	FTSJ2 FJH1 MRM2	1.52	1.48	0.61
APSTWEESGLR	surrogate standard	MRM3	RNMTL1 MRM3 HC90	1.57	1.13	1.07
LGFVVGR	surrogate standard	MTO1	MTO1 CGI-02	0.35	0.73	0.41
LIPEASISTSR	surrogate standard	MTO1	MTO1 CGI-02	2.00	1.78	1.14
LDYLGVSYGLTPR	surrogate standard	NAT10	NAT10 ALP KIAA1709	1.00	1.16	0.85
AGPNASIISLK	surrogate standard	NAT10	NAT10 ALP KIAA1709	1.33	2.36	0.56
SLEAEGFQVTYLPVQK	surrogate standard	NFS1	NFS1 NIFS HUSSY-08	1.01	0.58	0.97
VEALQSGGGQER	surrogate standard	NFS1	NFS1 NIFS HUSSY-08	1.92	0.11	0.25
AIGTDEDLAHSSIR	surrogate standard	NFS1	NFS1 NIFS HUSSY-08	1.06	0.93	0.70
IQDIVGILR	surrogate standard	NOP2	NOP2 NOL1 NSUN1	1.48	1.85	2.61
DLAQALINR	surrogate standard	NOP2	NOP2 NOL1 NSUN1	0.70	1.49	1.92
GADSELSTVPSVTK	surrogate standard	NOP2	NOP2 NOL1 NSUN1	1.35	0.84	1.69
GTDTQTPAVLSPSK	surrogate standard	NOP2	NOP2 NOL1 NSUN1	1.49	1.09	1.62
LGFPGGFVDTQDR	surrogate standard	NUDT16	NUDT16	0.58	0.68	0.72
LQELSAAYR	surrogate standard	PCIF1	PCIF1	0.55	0.98	0.73
GITTEQLDALGCR	surrogate standard	QTRT1	QTRT1 TGT TGUT	1.75	1.32	1.24
SPYDGNETLLSPEK	surrogate standard	QTRT1	QTRT1 TGT TGUT	1.75	0.83	1.42

FNSQPVGDCDFNVR	surrogate standard	RNGTT	RNGTT CAP1A	0.47	0.59	0.65
SVLIGEFLEK	surrogate standard	RNMT	RNMT KIAA0398	0.85	0.78	0.93
TFLEFYEEK	surrogate standard	RNMT	RNMT KIAA0398	0.44	0.33	0.74
LPLGTLSK	surrogate standard	RNMT	RNMT KIAA0398	0.79	1.18	0.71
AQPLAYYEAAVR	surrogate standard	RPUSD2	RPUSD2 C15orf19	0.61	0.89	0.90
GKPCETVFQR	surrogate standard	RPUSD2	RPUSD2 C15orf19	2.74	1.54	0.31
LSYNGQSSVVR	surrogate standard	RPUSD2	RPUSD2 C15orf19	0.11	0.17	0.02
VGTVLGQR	surrogate standard	RPUSD3	RPUSD3	0.38	2.38	0.03
DTPVELLAPLPPYFSR	surrogate standard	RPUSD3	RPUSD3	2.53	0.25	0.94
GSGGAGALPEAAR	surrogate standard	TARBP1	TARBP1 TRM3 TRP185	0.37	0.27	0.12
DGPFVYGR	surrogate standard	TFB1M	TFB1M CGI-75	2.62	2.74	1.24
DYFEDQPLLYPPGFDGR	surrogate standard	THG1L	THG1L ICF45	0.75	0.00	0.32
VVVYPSNQTLK	surrogate standard	THG1L	THG1L ICF45	0.18	1.08	0.17
ELAGIVCTLNSENK	surrogate standard	THUMPD1	THUMPD1	0.92	0.79	1.29
AVCCLSVVK	surrogate standard	THUMPD1	THUMPD1	0.82	1.29	0.92
STLALQLGQR	surrogate standard	TRIT1	TRIT1 IPT MOD5	2.57	0.16	0.14
IAFPSANEVFYNPVQEFNR	surrogate standard	TRMT1	TRMT1	0.39	0.22	0.13
DLTCAVITEFAR	surrogate standard	TRMT1	TRMT1	1.60	0.38	0.84
FALEVPGLR	surrogate standard	TRMT1	TRMT1	0.22	0.79	0.24
DVVHSTLR	surrogate standard	TRMT10A	TRMT10A RG9MTD2	2.75	2.08	0.77
IPAVTYPK	surrogate standard	TRMT10C	TRMT10C MRPP1 RG9MTD1	0.98	2.10	0.74
EVPEHITEEELK	surrogate standard	TRMT10C	TRMT10C MRPP1 RG9MTD1	0.85	0.53	0.88
LLLTSTEK	surrogate standard	TRMT10C	TRMT10C MRPP1 RG9MTD1	0.23	0.42	0.15
IDALEFLPFEGK	surrogate standard	TRMT11	TRMT11 C6orf75 MDS024	1.07	0.17	0.58

ICPVEFNPNFVAR	surrogate standard	TRMT112	TRMT112 AD-001 HSPC152 HSPC170	1.07	1.54	1.13
GPVEGYEENEEFLR	surrogate standard	TRMT112	TRMT112 AD-001 HSPC152 HSPC170	0.55	0.39	0.98
ILCPLDPK	surrogate standard	TRMT13	TRMT13 CCDC76	2.42	3.52	0.81
HTVYEDQLAK	surrogate standard	TRMT13	TRMT13 CCDC76	2.83	0.38	0.15
AEDLVPTLVSR	surrogate standard	TRMT2A	TRMT2A HTF9C	0.42	0.91	0.95
AVLPEGQDVTSGFSR	surrogate standard	TRMT5	TRMT5 KIAA1393 TRM5	1.02	0.81	0.73
DANPAEDVR	surrogate standard	TRMT5	TRMT5 KIAA1393 TRM5	3.36	0.04	0.46
DGFFTLDSALLR	surrogate standard	TRUB2	TRUB2	1.01	0.07	0.24
AATPQVAAELEK	surrogate standard	TRUB2	TRUB2	0.72	0.27	0.19
DQFFTTSSCAGR	surrogate standard	TYW3	TYW3 C1orf171	1.88	1.19	0.93
CTALTFIASEEK	surrogate standard	WDR4	WDR4	2.41	1.44	1.36
ISVVPTQPGLLLSSSGDGTLR	surrogate standard	WDR4	WDR4	2.63	1.61	1.10
GAEAANVTGPGGVPVQGSK	surrogate standard	YBX1	YBX1 NSEP1 YB1	0.87	0.89	1.55
NEGSESAPEGQAQQR	surrogate standard	YBX1	YBX1 NSEP1 YB1	1.21	0.06	0.60
AADPPAENSSAPEAEQGGAE	surrogate standard	YBX1	YBX1 NSEP1 YB1	0.22	0.17	1.71
ALEAVFGK	surrogate standard	RBMX	RBMX HNRPG RBMXP1	1.48	1.57	1.71
SAPSGPVR	surrogate standard	RBMX	RBMX HNRPG RBMXP1	2.37	0.58	0.02
SDLYSSGR	surrogate standard	RBMX	RBMX HNRPG RBMXP1	3.05	0.56	0.64
SLFSSIGEVESAK	surrogate standard	ELAVL1	HuR	1.58	1.43	1.68
DVEDMFSR	surrogate standard	ELAVL1	HuR	1.32	0.70	1.65
VLVDQTTGLSR	surrogate standard	ELAVL1	HuR	1.22	1.63	1.08
YTIENPR	surrogate standard	SND1	SND1 TDRD11	1.23	1.18	0.87
EVLPSTR	surrogate standard	SND1	SND1 TDRD11	3.04	0.44	0.44
LGTLSPAFSTR	surrogate standard	SND1	SND1 TDRD11	0.56	1.83	0.39

DINESDEVEVYSR	surrogate standard	FMR1	FMR1	0.63	0.11	1.06
SFLEFAEDVIQVPR	surrogate standard	FMR1	FMR1	1.10	0.13	0.80
IPENIYR	surrogate standard	LRPPRC	LRPPRC LRP130	1.28	1.98	1.13
LQWFCDR	surrogate standard	LRPPRC	LRPPRC LRP130	0.08	0.19	0.04
LDLQNLSLEDGR	surrogate standard	PUS7L	PUS7L	1.13	1.06	1.05
FGNLVETK	surrogate standard	PUS7L	PUS7L	3.23	1.48	0.53
LNIPGCYR	surrogate standard	PUS7L	PUS7L	1.91	0.04	0.07
AEAGILNYYR	isotopic standard	ALKBH1	ALKBH1 ABH ABH1 ALKBH	0.99	1.38	0.92
SLLVLTGAAR	surrogate standard	ALKBH4	ALKBH4 ABH4	0.74	1.65	0.78
ELSAEFGPGGR	isotopic standard	ALKBH4	ALKBH4 ABH4	0.60	0.58	0.81
LFSQDECAK	surrogate standard	ALKBH5	ALKBH5 ABH5 OFOXD1	1.86	0.68	1.13
VSEPVLSLPVR	isotopic standard	ALKBH5	ALKBH5 ABH5 OFOXD1	1.77	2.14	1.58
VPALEPFR	isotopic standard	ALKBH6	ALKBH6 ABH6	2.02	3.48	1.97
ILIGNPGCTYK	surrogate standard	FTO	FTO KIAA1752	1.27	1.85	0.86
EGLPVEQR	surrogate standard	FTO	FTO KIAA1752	0.73	1.10	0.50
SGPVMGGGLPPPPIK	surrogate standard	YTHDF1	YTHDF1	3.32	1.98	1.79
SPVDYGTSAGVWSQDK	isotopic standard	YTHDF1	YTHDF1	1.25	0.54	1.37
DGLNDDDFEPYLSPQAR	isotopic standard	YTHDF2	YTHDF2 HGRG8	2.52	0.72	3.07
LGSTEVASNVPK	surrogate standard	YTHDF2	YTHDF2 HGRG8	1.28	2.51	3.26
DVPNSQLR	surrogate standard	YTHDF2	YTHDF2 HGRG8	7.30	0.85	0.88
AITDGQAGFGNDTLSK	isotopic standard	YTHDF3	YTHDF3	1.59	1.31	1.77
VPGISSIEQGMTGLK	isotopic standard	YTHDF3	YTHDF3	2.63	1.86	1.85
GNVGIGGSAVPPPPIK	isotopic standard	YTHDF3	YTHDF3	1.22	1.75	0.86
GVWSTLPVNEK	isotopic standard	YTHDC1	YTHDC1 KIAA1966 YT521	0.26	0.66	0.43
LSQSLGLVSK	surrogate standard	YTHDC2	YTHDC2	0.42	1.37	0.29
VVLIVGETGSGK	isotopic standard	YTHDC2	YTHDC2	0.82	0.88	0.33

NPEAALSPTFR	isotopic standard	METTL3	METTL3 MTA70	2.24	2.88	1.56
YLDVSILGK	surrogate standard	METTL3	METTL3 MTA70	1.60	1.90	1.19
VDEIIWVK	surrogate standard	METTL3	METTL3 MTA70	2.34	2.40	2.39
LEIDEIAAPR	isotopic standard	METTL14	METTL14 KIAA1627	4.32	9.79	9.86
VSDYVQDR	surrogate standard	METTL1	METTL1 C12orf1	0.67	0.41	0.31
AAPAGGFQNIACLR	isotopic standard	METTL1	METTL1 C12orf1	0.07	0.20	0.07
NFPAIFR	surrogate standard	METTL1	METTL1 C12orf1	0.37	1.01	0.30
LPGVAGQYLFK	surrogate standard	METTL16	METTL16 METT10D	2.31	4.44	2.02
TQTPPVEENVTQK	isotopic standard	METTL2B	METTL2B	1.05	0.68	0.59
QNPLYDTER	isotopic standard	METTL6	METTL6	0.60	0.21	0.04
GAEQLAEGGR	surrogate standard	NSUN2	NSUN2 SAKI TRM4	1.99	0.19	0.31
ILLTQENPFFR	surrogate standard	NSUN2	NSUN2 SAKI TRM4	0.21	0.29	0.19
QLEEPGAGTPSPVR	surrogate standard	NSUN5	NSUN5 NSUN5A WBSCR20 WBSCR20A	1.68	0.76	1.11
DALQQNPGAFR	surrogate standard	NSUN5	NSUN5 NSUN5A WBSCR20 WBSCR20A	0.18	0.60	0.68
EVASYQPLQR	isotopic standard	NSUN6	NSUN6 NOPD1	1.60	1.41	1.09
GAGLSCEQLK	surrogate standard	NSUN6	NSUN6 NOPD1	5.90	1.73	0.49
FFLLENVR	isotopic standard	DNMT1	DNMT1 AIM CXXC9 DNMT	0.08	0.06	0.09
FCSFSPCIEQVQR	surrogate standard	TRMT61A	TRMT61A	0.44	0.72	0.24
TCQALAAR	isotopic standard	TRMT61A	TRMT61A	0.59	1.11	0.08
HSVDLIGR	surrogate standard	TRMT61A	TRMT61A	0.36	0.95	0.26
INTDVQLDSQEK	surrogate standard	TRMT61B	TRMT61B	4.21	0.26	0.70
AATACFGFPK	isotopic standard	TRMT6	TRMT6 KIAA1153 TRM6 CGI-09	0.03	0.03	0.01
SFLSGLYEFPLNK	surrogate standard	TRMT6	TRMT6 KIAA1153 TRM6 CGI-09	0.29	0.13	0.28
SLFPGLETK	surrogate standard	PUS7	PUS7 KIAA1897	0.13	0.50	0.11
FGTTAVPTYQVGR	isotopic standard	PUS7	PUS7 KIAA1897	0.54	1.26	0.30
QGSPVAAGAPAK	surrogate standard	IGF2BP1	IGF2BP1 CRDBP VICKZ1 ZBP1	5.25	0.71	0.42

ITISSLQDLTLYNPER	isotopic standard	IGF2BP1	IGF2BP1 CRDBP VICKZ1 ZBP1	3.45	0.66	1.19
TVNELQNLTAAEVVVPR	surrogate standard	IGF2BP1	IGF2BP1 CRDBP VICKZ1 ZBP1	1.29	0.75	1.34
LYIGNLSPAVTADDLR	isotopic standard	IGF2BP2	IGF2BP2 IMP2 VICKZ2	1.19	0.75	1.20
TVNELQNLTSAEVIVPR	surrogate standard	IGF2BP2	IGF2BP2 IMP2 VICKZ2	2.68	0.48	0.90
FTEEIPLK	surrogate standard	IGF2BP3	IGF2BP3 IMP3 KOC1 VICKZ3	2.68	2.57	1.74
ITISPLQELTLYNPER	isotopic standard	IGF2BP3	IGF2BP3 IMP3 KOC1 VICKZ3	2.75	0.65	1.10
QYEAYVQALEGK	surrogate standard	WTAP	WTAP KIAA0105	0.85	0.63	0.76
YTDLNSNDVTGLR	surrogate standard	WTAP	WTAP KIAA0105	1.13	0.66	1.11
QVQQPSVAQLR	isotopic standard	WTAP	WTAP KIAA0105	0.62	1.24	0.36
GLSYLQLK	surrogate standard	VIRMA	KIAA1429 MSTP054	0.52	1.76	0.69
NLDADLVR	isotopic standard	RBM15B	RBM15B OTT3	1.70	1.09	1.04
LQQLALGR	isotopic standard	RBM15	RBM15 OTT OTT1	0.89	1.36	0.38
VGAGAGAAPFR	surrogate standard	RBM15	RBM15 OTT OTT1	2.57	7.76	2.36
LAGSELFAK	surrogate standard	ZC3H13	ZC3H13 KIAA0853	0.21	0.64	1.04
VLLATLSIPITPER	isotopic standard	EIF3A	EIF3A EIF3S10 KIAA0139	1.41	1.15	0.87
GTQGVVTNFEIFR	isotopic standard	EIF3B	EIF3B EIF3S9	1.24	1.56	1.13
LFIGGLSFETTEESLR	surrogate standard	HNRNPA2B1	HNRNPA2B1 HNRPA2B1	1.63	0.28	2.41
IDTIEIITDR	isotopic standard	HNRNPA2B1	HNRNPA2B1 HNRPA2B1	2.20	1.34	3.01
TLETVPLER	surrogate standard	HNRNPA2B1	HNRNPA2B1 HNRPA2B1	1.15	1.26	1.30
GFAFVQYVNER	isotopic standard	HNRNPC	HNRNPC HNRPC	0.42	0.67	0.46
TIEDDLVSALVR	isotopic standard	PUS1	PUS1 PP8985	0.97	0.18	0.58
LSAETLQQVNR	surrogate standard	PUS1	PUS1 PP8985	0.58	0.96	0.46
GYAPESVLER	surrogate standard	PUS1	PUS1 PP8985	0.73	0.71	0.78
AAAAVVAAAAR	isotopic standard	TRUB1	TRUB1 PUS4	0.02	0.15	0.00
IMLPGVLR	surrogate standard	DKC1	DKC1 NOLA4	0.01	0.01	0.00
EVVAEVVK	isotopic standard	DKC1	DKC1 NOLA4	0.66	0.46	0.83

LHNAIEGGTQLSR	surrogate standard	DKC1	DKC1 NOLA4	0.63	0.66	0.23
NLAANDLSPSR	surrogate standard	NSUN4	NSUN4	0.74	1.17	0.68
WGELEGDTYDR	surrogate standard	NSUN4	NSUN4	0.39	0.09	0.62
VLVDVPCTTDR	isotopic standard	NSUN4	NSUN4	1.02	0.78	1.02
SLGTADVHFER	surrogate standard	ALYREF	THOC4	1.32	0.88	0.74
QYNGVPLDGR	surrogate standard	ALYREF	THOC4	1.08	1.64	1.43
QQLSAEELDAQLDAYNAR	isotopic standard	ALYREF	THOC4	2.21	0.61	2.67
TESDFSNLDSEK	surrogate standard	METTL8	METTL8	0.25	0.00	0.53
ILAWAPVEPSFSAR	surrogate standard	PUS3	PUS3 FKSG32	0.37	0.38	0.33
MCPGCSDPVQR	surrogate standard	CBLL1	CBLL1 HAKAI RNF188	0.20	0.07	0.00
DLQAHINHR	surrogate standard	CBLL1	CBLL1 HAKAI RNF188	1.19	0.30	0.12
DSLVLLGR	surrogate standard	CIAO1	CIAO1 WDR39	1.45	2.42	1.76
SVLSEGHQR	surrogate standard	CIAO1	CIAO1 WDR39	0.01	0.29	0.00
GTLIQGVLR	surrogate standard	DIS3L2	DIS3L2 FAM6A	0.62	3.16	0.49
DYANTLFICR	surrogate standard	DIS3L2	DIS3L2 FAM6A	2.47	2.38	1.49
EGFDSDINNR	surrogate standard	ELP5	ELP5 C17orf81 DERP6 HSPC002 MSTP071	6.00	1.74	1.03
LACDFLAR	surrogate standard	FTSJ3	FTSJ3 SB92	0.18	0.21	0.06
TSVTDFLR	surrogate standard	FTSJ3	FTSJ3 SB92	0.00	0.01	0.00
AANPVDFLSK	surrogate standard	FTSJ3	FTSJ3 SB92	0.08	0.23	0.10
NVGTGLVGAPACGDVMK	surrogate standard	ISCU	ISCU NIFUN	1.07	0.65	0.91
TFGCGSAIASSSLATEWVK	surrogate standard	ISCU	ISCU NIFUN	1.25	0.72	0.54
TVEEALTIK	surrogate standard	ISCU	ISCU NIFUN	0.96	0.93	1.57
IASAIVQAR	surrogate standard	METTL15	METTL15 METT5D1	4.54	0.64	0.70
LDGGFAAVSR	surrogate standard	METTL17	METTL17 METT11D1	1.97	1.46	7.39
YDLPASYK	surrogate standard	METTL5	METTL5 DC3 HSPC133	4.91	1.54	0.00

QNLPLSSGK	surrogate standard	MPST	MPST TST2	0.27	0.62	0.22
SQPAPAEFR	surrogate standard	MPST	MPST TST2	0.65	0.96	0.46
LLDLVQQSCNYK	surrogate standard	SNU13	NHP2L1	0.77	1.07	1.14
NVPYVFVR	surrogate standard	SNU13	NHP2L1	0.66	2.05	1.57
QQIQSIQQSIER	surrogate standard	SNU13	NHP2L1	0.66	0.66	0.79
VPLDPLIGK	surrogate standard	NUBP1	NUBP1 NBP NBP1	1.08	1.84	1.50
GQSFFIDAPDSPATLAYR	surrogate standard	NUBP1	NUBP1 NBP NBP1	1.25	0.77	1.25
TYVTPPGTGFLPGDTAR	surrogate standard	OSGEP	OSGEP GCPL1	0.45	0.74	0.69
LVELPYTVK	surrogate standard	OSGEP	OSGEP GCPL1	0.83	1.93	1.61
TPLSDSGVTQR	surrogate standard	OSGEP	OSGEP GCPL1	1.07	1.47	0.91
GPDELEGPDSK	surrogate standard	PRRC2A	PRRC2A BAT2 G2	3.50	0.03	1.07
YLNEQLYSGPSSAAQR	surrogate standard	RRP8	RRP8 KIAA0409 NML hucep-1	0.48	0.03	0.08
GVDLYVLEK	surrogate standard	TP53RK	TP53RK C20orf64 PRPK	0.93	1.34	1.96
VTLPGQEEPWDIR	surrogate standard	URM1	URM1 C9orf74	1.16	0.72	2.62
GLLATASEDR	surrogate standard	WDR6	WDR6	1.01	1.80	1.01
LGSTVVDLSVPGK	surrogate standard	YRDC	YRDC DRIP3 IRIP	0.61	0.81	0.54

Table S1f. LC-PRM quantification results of RWE proteins in whole-cell lysate of *KAT5*$^{-/-}$ cells (n = 3) relative to parental HEK293T cells (n = 3).

Protein Symbol	KAT5_KO/HEK293T-1	s.d.	KAT5_KO/HEK293T-2	s.d.	KAT5_KO/HEK293T-3	s.d.	Ave.	S.D.	R.S.D.	*p*-value (one samples t test)
ADAR	1.95	1.25	0.84	0.34	1.51	1.31	1.43	0.56	39%	0.312
ADAT2	2.06		2.60		1.45		2.03	0.58	28%	0.090
ADAT3	0.56	0.26	0.43	0.11	0.46	0.25	0.48	0.07	14%	0.006
BUD23	0.63	0.51	0.29	0.05	0.30	0.24	0.40	0.19	48%	0.033
CDK5RAP1	4.20	2.91	1.46	1.20	0.66	0.71	2.11	1.86	88%	0.411
CDKAL1	2.09	0.48	0.86	0.35	0.78	0.12	1.24	0.73	59%	0.623
CMTR1	0.66	0.90	0.30	0.09	0.66	0.84	0.54	0.21	38%	0.061
CTU1	2.55	2.04	2.10	0.48	0.38	0.37	1.68	1.14	68%	0.412
CTU2	0.70	0.45	1.14	0.04	0.64	0.53	0.82	0.27	33%	0.379
DCPS	0.45		0.48		0.13		0.35	0.20	56%	0.030
DIMT1	1.69		2.23		1.90		1.94	0.27	14%	0.027
DUS1L	0.70	0.20	0.99	0.63	0.36	0.07	0.68	0.31	46%	0.223
DUS3L	1.64	0.72	0.69	0.08	0.44	0.35	0.93	0.63	68%	0.856
EIF5A2	0.10		0.56		0.08		0.25	0.27	110%	0.041
ELP1	0.98	0.92	0.91	0.91	1.01	0.79	0.97	0.05	5%	0.401
ELP3	4.15	0.38	9.12	4.40	1.39	0.32	4.89	3.92	80%	0.228
ELP4	2.72		2.76		1.55		2.34	0.69	29%	0.077
EMG1	0.73	0.30	0.83	0.10	0.50	0.13	0.69	0.17	25%	0.086
FBL	1.19	0.67	0.46	0.22	0.57	0.58	0.74	0.39	53%	0.368
FTSJ1	1.71	0.45	0.74	0.06	0.81	0.24	1.09	0.54	50%	0.808
GTPBP3	0.78		0.59		0.80		0.73	0.12	16%	0.055
HSD17B10	1.07	0.56	1.15	0.80	1.05	0.54	1.09	0.05	5%	0.099
LCMT2	1.53		0.69		1.11		1.11	0.42	38%	0.691
MEPCE	1.43	2.13	2.24	3.76	0.52	0.88	1.39	0.86	62%	0.511
MOCS3	1.01		0.64		1.02		0.89	0.22	25%	0.469

MRM2	1.52		1.48		0.61		1.20	0.51	42%	0.563
MRM3	1.57		1.13		1.07		1.26	0.27	21%	0.240
MTO1	1.17	1.17	1.26	0.74	0.77	0.51	1.07	0.26	24%	0.696
NAT10	1.16	0.23	1.76	0.85	0.71	0.20	1.21	0.53	44%	0.561
NFS1	1.33	0.51	0.54	0.41	0.64	0.36	0.84	0.43	51%	0.578
NOP2	1.25	0.37	1.32	0.45	1.96	0.45	1.51	0.39	26%	0.151
NUDT16	0.58		0.68		0.72		0.66	0.07	11%	0.015
PCIF1	0.55		0.98		0.73		0.75	0.21	28%	0.185
QTRT1	1.75	0.00	1.07	0.35	1.33	0.13	1.38	0.34	25%	0.191
RNGTT	0.47		0.59		0.65		0.57	0.09	16%	0.015
RNMT	0.69	0.22	0.76	0.43	0.79	0.12	0.75	0.05	7%	0.014
RPUSD2	1.15	1.40	0.87	0.69	0.41	0.45	0.81	0.37	46%	0.474
RPUSD3	1.46	1.52	1.32	1.51	0.49	0.64	1.09	0.52	48%	0.803
TARBP1	0.37		0.27		0.12		0.25	0.12	49%	0.009
TFB1M	2.62		2.74		1.24		2.20	0.84	38%	0.131
THG1L	0.46	0.40	0.54	0.76	0.24	0.11	0.42	0.15	37%	0.022
THUMPD1	0.87	0.07	1.04	0.35	1.11	0.26	1.01	0.12	12%	0.939
TRIT1	2.57		0.16		0.14		0.96	1.40	146%	0.963
TRMT1	0.74	0.75	0.47	0.30	0.40	0.38	0.54	0.18	33%	0.045
TRMT10A	2.75		2.08		0.77		1.87	1.01	54%	0.276
TRMT10C	0.69	0.40	1.01	0.94	0.59	0.39	0.76	0.22	29%	0.207
TRMT11	1.07		0.17		0.58		0.60	0.45	74%	0.266
TRMT112	0.81	0.37	0.96	0.81	1.06	0.11	0.94	0.12	13%	0.514
TRMT13	2.63	0.29	1.95	2.22	0.48	0.46	1.69	1.10	65%	0.393
TRMT2A	0.42		0.91		0.95		0.76	0.30	39%	0.292
TRMT5	2.19	1.66	0.43	0.54	0.59	0.19	1.07	0.98	91%	0.913
TRUB2	0.86	0.21	0.17	0.14	0.21	0.04	0.41	0.39	94%	0.121
TYW3	1.88		1.19		0.93		1.33	0.49	37%	0.358
WDR4	2.52	0.16	1.52	0.11	1.23	0.19	1.76	0.68	38%	0.192

YBX1	0.77	0.50	0.37	0.45	1.29	0.60	0.81	0.46	57%	0.546
RBMX	2.30	0.79	0.90	0.58	0.79	0.86	1.33	0.84	63%	0.567
ELAVL1	1.37	0.19	1.25	0.49	1.47	0.34	1.36	0.11	8%	0.029
SND1	1.61	1.28	1.15	0.69	0.57	0.26	1.11	0.52	47%	0.750
FMR1	0.86	0.33	0.12	0.02	0.93	0.19	0.64	0.45	71%	0.297
LRPPRC	0.68	0.84	1.08	1.26	0.59	0.77	0.78	0.26	34%	0.292
PUS7L	2.09	1.06	0.86	0.74	0.55	0.49	1.17	0.81	70%	0.757
ALKBH1	0.99		1.38		0.92		1.09	0.25	23%	0.576
ALKBH4	0.67	0.10	1.12	0.75	0.80	0.02	0.86	0.23	27%	0.406
ALKBH5	1.81	0.07	1.41	1.04	1.36	0.32	1.53	0.25	16%	0.067
ALKBH6	2.02		3.48		1.97		2.49	0.86	34%	0.095
FTO	1.00	0.38	1.47	0.53	0.68	0.26	1.05	0.40	38%	0.845
YTHDF1	2.28	1.47	1.26	1.02	1.58	0.30	1.71	0.52	31%	0.143
YTHDF2	3.70	3.18	1.36	1.00	2.40	1.32	2.49	1.17	47%	0.159
YTHDF3	1.81	0.73	1.64	0.29	1.49	0.55	1.65	0.16	10%	0.020
YTHDC1	0.26		0.66		0.43		0.45	0.20	44%	0.042
YTHDC2	0.62	0.28	1.12	0.35	0.31	0.03	0.68	0.41	60%	0.314
METTL3	2.06	0.40	2.39	0.49	1.71	0.61	2.06	0.34	17%	0.033
METTL14	4.32		9.79		9.86		7.99	3.18	40%	0.062
METTL1	0.37	0.30	0.54	0.42	0.23	0.14	0.38	0.16	42%	0.021
METTL16	2.31		4.44		2.02		2.92	1.32	45%	0.128
METTL2B	1.05		0.68		0.59		0.77	0.24	31%	0.244
METTL6	0.60		0.21		0.04		0.28	0.29	102%	0.049
NSUN2	1.10	1.26	0.24	0.07	0.25	0.09	0.53	0.49	93%	0.239
NSUN5	0.93	1.06	0.68	0.11	0.90	0.30	0.83	0.13	16%	0.167
NSUN6	3.75	3.04	1.57	0.22	0.79	0.43	2.04	1.53	75%	0.361
DNMT1	0.08		0.06		0.09		0.08	0.02	21%	0.000
TRMT61A	0.46	0.12	0.93	0.19	0.19	0.10	0.53	0.37	71%	0.158
TRMT61B	4.21		0.26		0.70		1.73	2.17	126%	0.621

TRMT6	0.16	0.19	0.08	0.07	0.14	0.19	0.13	0.04	33%	0.001
PUS7	0.33	0.29	0.88	0.54	0.20	0.13	0.47	0.36	76%	0.125
IGF2BP1	3.33	1.98	0.71	0.04	0.98	0.50	1.67	1.44	86%	0.504
IGF2BP2	1.93	1.05	0.62	0.19	1.05	0.21	1.20	0.67	56%	0.660
IGF2BP3	2.71	0.05	1.61	1.35	1.42	0.45	1.91	0.70	37%	0.152
WTAP	0.87	0.25	0.84	0.34	0.75	0.37	0.82	0.06	8%	0.037
VIRMA	0.52		1.76		0.69		0.99	0.67	68%	0.983
RBM15B	1.70		1.09		1.04		1.28	0.37	29%	0.321
RBM15	1.73	1.19	4.56	4.53	1.37	1.40	2.55	1.75	68%	0.264
ZC3H13	0.21		0.64		1.04		0.63	0.41	66%	0.263
EIF3A	1.41		1.15		0.87		1.14	0.27	23%	0.448
EIF3B	1.24		1.56		1.13		1.31	0.22	17%	0.139
HNRNPA2B1	1.66	0.53	0.96	0.59	2.24	0.87	1.62	0.64	40%	0.236
HNRNPC	0.42		0.67		0.46		0.51	0.14	27%	0.026
PUS1	0.76	0.20	0.62	0.40	0.61	0.17	0.66	0.08	13%	0.020
TRUB1	0.02		0.15		0.00		0.06	0.08	135%	0.002
DKC1	0.43	0.37	0.38	0.33	0.35	0.43	0.39	0.04	10%	0.001
NSUN4	0.71	0.32	0.68	0.55	0.77	0.22	0.72	0.05	6%	0.009
ALYREF	1.54	0.59	1.04	0.53	1.61	0.98	1.40	0.31	22%	0.156
METTL8	0.25		0.00		0.53		0.26	0.27	102%	0.041
PUS3	0.37		0.38		0.33		0.36	0.03	8%	0.001
CBLL1	0.70	0.70	0.19	0.17	0.06	0.09	0.31	0.34	107%	0.072
CIAO1	0.73	1.02	1.35	1.51	0.88	1.24	0.99	0.32	33%	0.955
DIS3L2	1.54	1.31	2.77	0.55	0.99	0.71	1.77	0.91	51%	0.281
ELP5	6.00		1.74		1.03		2.92	2.69	92%	0.341
FTSJ3	0.09	0.09	0.15	0.12	0.05	0.05	0.10	0.05	51%	0.001
ISCU	1.09	0.15	0.77	0.15	1.01	0.52	0.96	0.17	18%	0.696
METTL15	4.54		0.64		0.70		1.96	2.24	114%	0.536
METTL17	1.97		1.46		7.39		3.60	3.29	91%	0.304

METTL5	4.91		1.54		0.00		2.15	2.51	117%	0.511
MPST	0.46	0.27	0.79	0.24	0.34	0.17	0.53	0.23	44%	0.073
SNU13	0.70	0.07	1.26	0.71	1.16	0.39	1.04	0.30	29%	0.834
NUBP1	1.17	0.12	1.31	0.76	1.37	0.18	1.28	0.11	8%	0.044
OSGEP	0.78	0.31	1.38	0.60	1.07	0.48	1.08	0.30	28%	0.695
PRRC2A	3.50		0.03		1.07		1.53	1.78	116%	0.656
RRP8	0.48		0.03		0.08		0.20	0.25	125%	0.030
TP53RK	0.93		1.34		1.96		1.41	0.52	37%	0.305
URM1	1.16		0.72		2.62		1.50	0.99	66%	0.473
WDR6	1.01		1.80		1.01		1.27	0.46	36%	0.412
YRDC	0.61		0.81		0.54		0.65	0.14	21%	0.048

Table S1g. LC-PRM quantification results of tryptic peptides from RWE proteins in chromatin fraction of *SETD2*$^{-/-}$ cells (n = 3) relative to parental HEK293T cells (n = 3).

Peptide	standard type	Protein Symbol	Protein Gene	SETD2_KO/HEK293T-chromatin-ratio-1	SETD2_KO/HEK293T-chromatin-ratio-2	SETD2_KO/HEK293T-chromatin-ratio-3
YLNTNPVGGLLEYAR	surrogate standard	ADAR	ADAR ADAR1 DSRAD G1P1 IFI4	0.19	0.38	0.47
VLIGENEK	surrogate standard	ADAR	ADAR ADAR1 DSRAD G1P1 IFI4	0.92	0.82	1.34
DGSAFEDGLR	surrogate standard	ADAR	ADAR ADAR1 DSRAD G1P1 IFI4	0.72	0.86	1.17
GFGVQELK	surrogate standard	ADAT1	ADAT1	1.91	5.14	5.58
AVGAVVVDPASDR	surrogate standard	ADAT3	ADAT3 TAD3	1.00	0.24	0.27
AVLQLYPENSEQLELITTQATK	surrogate standard	BUD23	WBSCR22 MERM1 HUSSY-03 PP3381	0.17	0.90	1.11
AGFSGGMVVDYPNSAK	surrogate standard	BUD23	WBSCR22 MERM1 HUSSY-03 PP3381	0.57	0.82	0.70
ESVFTNER	surrogate standard	BUD23	WBSCR22 MERM1 HUSSY-03 PP3381	0.64	0.68	0.99
VIFPDAEMEDVNNPGLR	surrogate standard	CDK5RAP1	CDK5RAP1 C20orf34 CGI-05 HSPC167	0.09	1.31	0.35
ITSASSQTLR	surrogate standard	CDK5RAP1	CDK5RAP1 C20orf34 CGI-05 HSPC167	0.74	0.58	0.68
GNLASYPIDELVDR	surrogate standard	CDKAL1	CDKAL1	0.25	0.15	0.42
DIGTNLPTLLWK	surrogate standard	CDKAL1	CDKAL1	0.04	0.06	0.03
GFGMTLK	surrogate standard	CMTR1	CMTR1 FTSJD2 KIAA0082 MTR1	1.16	0.80	0.36
NTDSDVNLVVPLEVIK	surrogate standard	CMTR1	CMTR1 FTSJD2 KIAA0082 MTR1	0.25	0.23	0.53
SQIYTWDGR	surrogate standard	CMTR1	CMTR1 FTSJD2 KIAA0082 MTR1	1.25	0.59	0.84
DMATFLAEDPK	surrogate standard	APOBEC3G	APOBEC3G MDS019	1.06	1.05	1.44
TLNEAIEK	surrogate standard	CMTR2	CMTR2 AFT FTSJD1	0.10	0.15	0.24
GGGLGSPGEGGALPR	surrogate standard	CTU1	CTU1 ATPBD3 NCS6	0.48	0.21	0.24
EELLQTLR	surrogate standard	CTU2	CTU2	0.00	0.12	0.11
LQTQFPSTVSTVYR	surrogate standard	CTU2	CTU2	0.32	0.10	0.07
LYIIPGIPK	surrogate standard	DCP2	DCP2 NUDT20	0.64	0.35	0.15

NPLIINSIIDK	surrogate standard	DIMT1	DIMT1 DIMT1L HUSSY-05	0.87	0.74	0.48
LQVLVGDVLK	surrogate standard	DIMT1	DIMT1 DIMT1L HUSSY-05	0.86	0.68	0.28
LQGFEFWSR	surrogate standard	DUS1L	DUS1L	0.22	0.13	0.05
LSVPVTCK	surrogate standard	DUS1L	DUS1L	0.36	0.30	0.25
YLETKPADLGPR	surrogate standard	DUS3L	DUS3L	0.33	0.52	0.91
TCGPLTDEDVVR	surrogate standard	DUS3L	DUS3L	0.32	0.86	0.75
NGFVVLK	surrogate standard	EIF5A2	EIF5A2	0.82	0.34	0.28
YEDICPSTHNMDVPNIK	surrogate standard	EIF5A2	EIF5A2	0.36	0.25	0.24
VLVTVFR	surrogate standard	ELP1	IKBKAP ELP1 IKAP	0.51	0.41	0.25
LYPTLVIR	surrogate standard	ELP3	ELP3	0.32	0.08	0.04
TYELLNCDK	surrogate standard	EMG1	EMG1 C2F	0.72	0.95	1.32
VGTSFSIPVVSDVR	surrogate standard	EMG1	EMG1 C2F	1.48	0.83	0.86
VSVEYTEK	surrogate standard	EMG1	EMG1 C2F	0.44	0.55	0.75
NVMVEPHR	surrogate standard	FBL	FBL FIB1 FLRN	0.58	0.53	1.35
NLVPGESVYGEK	surrogate standard	FBL	FBL FIB1 FLRN	1.15	1.88	2.09
EFQLFQGVTR	surrogate standard	FTSJ1	FTSJ1 JM23	0.15	0.02	0.03
AVDLCAAPGSWSQVLSQK	surrogate standard	FTSJ1	FTSJ1 JM23	0.38	0.15	0.10
SYPLDLEGGSEYK	surrogate standard	FTSJ1	FTSJ1 JM23	0.50	0.19	0.19
GLVAVITGGASGLGLATAER	surrogate standard	HSD17B10	HSD17B10 ERAB HADH2 MRPP2 SCHAD XH98G2	0.19	0.23	0.21
DVQTALALAK	surrogate standard	HSD17B10	HSD17B10 ERAB HADH2 MRPP2 SCHAD XH98G2	0.53	0.10	0.40
VCNFLASQVPFPSR	surrogate standard	HSD17B10	HSD17B10 ERAB HADH2 MRPP2 SCHAD XH98G2	0.40	0.19	0.09
AFLEQIGAPQAALR	surrogate standard	LCMT2	LCMT2 KIAA0547 TYW4	1.39	0.63	0.42
NSCNVGGGGGGFK	surrogate standard	MEPCE	MEPCE BCDIN3	0.76	0.70	0.57
FQYGNYCK	surrogate standard	MEPCE	MEPCE BCDIN3	1.01	0.78	0.48

SCFPASLTASR	surrogate standard	MEPCE	MEPCE BCDIN3	1.31	1.44	0.75
LLLDDLVPTSR	surrogate standard	MRM1	MRM1	1.52	0.96	2.08
NSCPLTPVVSK	surrogate standard	MRM1	MRM1	0.73	1.59	1.82
ILEVLPGR	surrogate standard	MRM2	FTSJ2 FJH1 MRM2	1.58	0.25	0.69
APSTWEESGLR	surrogate standard	MRM3	RNMTL1 MRM3 HC90	0.82	0.73	0.83
DPGNLGTILR	surrogate standard	MRM3	RNMTL1 MRM3 HC90	0.45	0.40	0.48
LGFVVGR	surrogate standard	MTO1	MTO1 CGI-02	0.53	0.28	0.22
LIPEASISTSR	surrogate standard	MTO1	MTO1 CGI-02	1.14	0.17	0.61
SLFVVVGDR	surrogate standard	NAT10	NAT10 ALP KIAA1709	0.51	0.28	0.22
LDYLGVSYGLTPR	surrogate standard	NAT10	NAT10 ALP KIAA1709	0.84	0.31	0.15
AGPNASIISLK	surrogate standard	NAT10	NAT10 ALP KIAA1709	0.81	0.83	0.51
SLEAEGFQVTYLPVQK	surrogate standard	NFS1	NFS1 NIFS HUSSY-08	1.17	0.41	0.57
AIGTDEDLAHSSIR	surrogate standard	NFS1	NFS1 NIFS HUSSY-08	0.81	0.66	0.77
IQDIVGILR	surrogate standard	NOP2	NOP2 NOL1 NSUN1	1.77	1.90	1.47
DLAQALINR	surrogate standard	NOP2	NOP2 NOL1 NSUN1	1.59	1.85	1.67
LGVTNTIISHYDGR	surrogate standard	NOP2	NOP2 NOL1 NSUN1	0.99	3.67	2.25
GADSELSTVPSVTK	surrogate standard	NOP2	NOP2 NOL1 NSUN1	1.28	2.05	3.10
GTDTQTPAVLSPSK	surrogate standard	NOP2	NOP2 NOL1 NSUN1	1.64	2.13	5.35
LGFPGGFVDTQDR	surrogate standard	NUDT16	NUDT16	0.38	0.20	0.18
EELGEAAAAFR	surrogate standard	NUDT16	NUDT16	0.37	0.14	0.34
EIMNDIPIR	surrogate standard	PCIF1	PCIF1	0.22	0.19	0.22
LVYCYPVR	surrogate standard	PCIF1	PCIF1	0.70	0.38	0.17
LQELSAAYR	surrogate standard	PCIF1	PCIF1	0.94	0.42	0.45
GITTEQLDALGCR	surrogate standard	QTRT1	QTRT1 TGT TGUT	0.82	0.48	0.64

YDSQVAEENR	surrogate standard	RNGTT	RNGTT CAP1A	0.45	0.35	0.32
FNSQPVGDCDFNVR	surrogate standard	RNGTT	RNGTT CAP1A	0.62	0.65	0.64
SVLIGEFLEK	surrogate standard	RNMT	RNMT KIAA0398	1.05	0.51	0.69
TFLEFYEEK	surrogate standard	RNMT	RNMT KIAA0398	1.40	0.45	0.99
LPLGTLSK	surrogate standard	RNMT	RNMT KIAA0398	0.86	0.54	0.66
VGTVLGQR	surrogate standard	RPUSD3	RPUSD3	0.48	0.51	0.61
DTPVELLAPLPPYFSR	surrogate standard	RPUSD3	RPUSD3	0.13	0.24	0.27
TLQCLGLR	surrogate standard	RPUSD3	RPUSD3	0.46	0.79	0.60
MTLSPSYR	surrogate standard	RPUSD4	RPUSD4	0.81	0.92	0.73
GSGGAGALPEAAR	surrogate standard	TARBP1	TARBP1 TRM3 TRP185	0.61	0.62	0.64
LLPVLVQCGGAALR	surrogate standard	TARBP1	TARBP1 TRM3 TRP185	0.37	0.43	0.20
IFLDPLLDVLMK	surrogate standard	TARBP1	TARBP1 TRM3 TRP185	0.08	0.27	0.07
LPPLPTIR	surrogate standard	TFB1M	TFB1M CGI-75	0.43	0.47	0.24
DGPFVYGR	surrogate standard	TFB1M	TFB1M CGI-75	0.18	0.57	0.29
VIAIDIDPVK	surrogate standard	TGS1	TGS1 HCA137 NCOA6IP PIMT	0.31	0.62	1.12
VVVYPSNQTLK	surrogate standard	THG1L	THG1L ICF45	0.31	0.15	0.03
ELAGIVCTLNSENK	surrogate standard	THUMPD1	THUMPD1	1.71	0.16	0.82
STLALQLGQR	surrogate standard	TRIT1	TRIT1 IPT MOD5	0.13	0.41	0.28
DLTCAVITEFAR	surrogate standard	TRMT1	TRMT1	0.06	0.11	0.05
FALEVPGLR	surrogate standard	TRMT1	TRMT1	1.09	0.35	0.19
IPAVTYPK	surrogate standard	TRMT10C	TRMT10C MRPP1 RG9MTD1	0.29	0.31	0.23
LLLTSTEK	surrogate standard	TRMT10C	TRMT10C MRPP1 RG9MTD1	0.30	0.43	0.31
IDALEFLPFEGK	surrogate standard	TRMT11	TRMT11 C6orf75 MDS024	0.20	0.13	0.46
GPVEGYEENEEFLR	surrogate standard	TRMT112	TRMT112 AD-001 HSPC152 HSPC170	0.47	0.65	0.69

DDLFTSEIFK	surrogate standard	TRMT2A	TRMT2A HTF9C	0.12	0.02	0.03
AFQEFIR	surrogate standard	TRMT2A	TRMT2A HTF9C	0.53	0.37	0.34
AVLPEGQDVTSGFSR	surrogate standard	TRMT5	TRMT5 KIAA1393 TRM5	0.91	0.27	0.23
ILAVIQGSHQK	surrogate standard	TRUB2	TRUB2	0.34	1.01	0.99
DGFFTLDSALLR	surrogate standard	TRUB2	TRUB2	0.82	0.34	0.17
AATPQVAAELEK	surrogate standard	TRUB2	TRUB2	1.08	1.39	2.43
DQFFTTSSCAGR	surrogate standard	TYW3	TYW3 C1orf171	1.07	0.38	0.56
ISVVPTQPGLLLSSSGDGTLR	surrogate standard	WDR4	WDR4	1.57	0.56	0.40
GAEAANVTGPGGVPVQGSK	surrogate standard	YBX1	YBX1 NSEP1 YB1	0.91	0.94	0.59
NEGSESAPEGQAQQR	surrogate standard	YBX1	YBX1 NSEP1 YB1	0.55	0.22	0.28
AADPPAENSSAPEAEQGGAE	surrogate standard	YBX1	YBX1 NSEP1 YB1	0.98	1.64	0.64
ALEAVFGK	surrogate standard	RBMX	RBMX HNRPG RBMXP1	0.71	1.47	1.65
SAPSGPVR	surrogate standard	RBMX	RBMX HNRPG RBMXP1	1.02	1.12	1.34
SDLYSSGR	surrogate standard	RBMX	RBMX HNRPG RBMXP1	1.14	1.20	1.40
SLFSSIGEVESAK	surrogate standard	ELAVL1	HuR	0.84	1.07	0.81
DVEDMFSR	surrogate standard	ELAVL1	HuR	0.80	1.07	0.92
VLVDQTTGLSR	surrogate standard	ELAVL1	HuR	0.83	1.12	1.07
YTIENPR	surrogate standard	SND1	SND1 TDRD11	0.59	0.45	0.56
EVLPSTR	surrogate standard	SND1	SND1 TDRD11	0.43	0.45	0.57
LGTLSPAFSTR	surrogate standard	SND1	SND1 TDRD11	0.57	0.77	0.55
DINESDEVEVYSR	surrogate standard	FMR1	FMR1	0.79	0.49	0.32
SFLEFAEDVIQVPR	surrogate standard	FMR1	FMR1	0.41	0.34	0.16
IPENIYR	surrogate standard	LRPPRC	LRPPRC LRP130	0.61	0.61	0.43
LQWFCDR	surrogate standard	LRPPRC	LRPPRC LRP130	0.49	0.99	0.35

LDLQNLSLEDGR	surrogate standard	PUS7L	PUS7L	1.23	0.39	1.11
AEGLDCSYTVLFGK	surrogate standard	ALKBH2	ALKBH2 ABH2	0.28	0.11	0.15
EVEYFTGALAR	isotopic standard	ALKBH2	ALKBH2 ABH2	0.18	0.00	0.03
SQAIAQPATTAK	surrogate standard	ALKBH3	ALKBH3 ABH3 DEPC1	0.62	0.28	0.28
VCLYPGFVDVK	surrogate standard	ALKBH3	ALKBH3 ABH3 DEPC1	0.49	0.38	0.18
EDITYQQPR	isotopic standard	ALKBH3	ALKBH3 ABH3 DEPC1	2.06	0.52	0.33
TEGFCGLPSFSR	surrogate standard	ALKBH4	ALKBH4 ABH4	0.24	0.14	0.12
SLLVLTGAAR	surrogate standard	ALKBH4	ALKBH4 ABH4	0.87	0.71	0.67
ELSAEFGPGGR	isotopic standard	ALKBH4	ALKBH4 ABH4	0.82	0.66	0.69
LFSQDECAK	surrogate standard	ALKBH5	ALKBH5 ABH5 OFOXD1	1.24	0.72	0.92
GLYNEHTVDR	surrogate standard	ALKBH5	ALKBH5 ABH5 OFOXD1	1.24	0.53	0.56
VSEPVLSLPVR	isotopic standard	ALKBH5	ALKBH5 ABH5 OFOXD1	1.07	1.74	1.85
ILIGNPGCTYK	surrogate standard	FTO	FTO KIAA1752	0.62	3.28	0.76
SGPVMGGGLPPPPIK	surrogate standard	YTHDF1	YTHDF1	1.00	0.73	0.29
SPVDYGTSAGVWSQDK	isotopic standard	YTHDF1	YTHDF1	0.44	0.06	0.04
DGLNDDDFEPYLSPQAR	isotopic standard	YTHDF2	YTHDF2 HGRG8	0.38	0.46	0.37
LGSTEVASNVPK	surrogate standard	YTHDF2	YTHDF2 HGRG8	1.03	0.89	0.82
DVPNSQLR	surrogate standard	YTHDF2	YTHDF2 HGRG8	0.49	0.40	0.54
AITDGQAGFGNDTLSK	isotopic standard	YTHDF3	YTHDF3	1.25	1.02	1.08
VPGISSIEQGMTGLK	isotopic standard	YTHDF3	YTHDF3	0.90	0.43	0.46
GNVGIGGSAVPPPPIK	isotopic standard	YTHDF3	YTHDF3	0.92	0.77	0.73
SNNHENVSLAK	surrogate standard	YTHDC1	YTHDC1 KIAA1966 YT521	1.04	0.71	1.38
GVWSTLPVNEK	isotopic standard	YTHDC1	YTHDC1 KIAA1966 YT521	1.28	0.63	0.83
LSQSLGLVSK	surrogate standard	YTHDC2	YTHDC2	1.33	1.10	1.12

VVLIVGETGSGK	isotopic standard	YTHDC2	YTHDC2	0.89	3.57	0.43
LAAIAVAER	surrogate standard	YTHDC2	YTHDC2	3.70	5.10	5.34
NPEAALSPTFR	isotopic standard	METTL3	METTL3 MTA70	1.04	0.58	0.58
YLDVSILGK	surrogate standard	METTL3	METTL3 MTA70	0.86	0.21	0.17
LEIDEIAAPR	isotopic standard	METTL14	METTL14 KIAA1627	0.72	0.19	0.47
VSDYVQDR	surrogate standard	METTL1	METTL1 C12orf1	0.25	0.10	0.03
VTYTEFCQGR	surrogate standard	METTL16	METTL16 METT10D	0.85	0.44	0.32
LPGVAGQYLFK	surrogate standard	METTL16	METTL16 METT10D	0.60	0.43	0.17
TQTPPVEENVTQK	isotopic standard	METTL2B	METTL2B	0.79	0.43	0.54
GAEQLAEGGR	surrogate standard	NSUN2	NSUN2 SAKI TRM4	0.95	0.90	1.09
FYALDPSFPR	isotopic standard	NSUN2	NSUN2 SAKI TRM4	1.42	0.84	0.75
QLEEPGAGTPSPVR	surrogate standard	NSUN5	NSUN5 NSUN5A WBSCR20 WBSCR20A	0.80	0.90	1.16
DALQQNPGAFR	surrogate standard	NSUN5	NSUN5 NSUN5A WBSCR20 WBSCR20A	0.97	0.74	0.93
NLLLDELQK	surrogate standard	NSUN6	NSUN6 NOPD1	1.22	0.40	0.64
QNALLLGLNSIR	surrogate standard	NSUN6	NSUN6 NOPD1	0.01	0.03	0.04
EVASYQPLQR	isotopic standard	NSUN6	NSUN6 NOPD1	0.47	0.26	0.29
GAGLSCEQLK	surrogate standard	NSUN6	NSUN6 NOPD1	0.92	0.32	0.45
FFLLENVR	isotopic standard	DNMT1	DNMT1 AIM CXXC9 DNMT	0.44	0.50	0.44
SQGFPDTYR	surrogate standard	DNMT1	DNMT1 AIM CXXC9 DNMT	0.98	0.69	0.98
FCSFSPCIEQVQR	surrogate standard	TRMT61A	TRMT61A	0.26	0.49	0.45
TCQALAAR	isotopic standard	TRMT61A	TRMT61A	0.23	0.79	0.48
HSVDLIGR	surrogate standard	TRMT61A	TRMT61A	0.06	0.37	0.14
DISGATEDIK	isotopic standard	TRMT61B	TRMT61B	0.47	1.44	0.48
AATACFGFPK	isotopic standard	TRMT6	TRMT6 KIAA1153 TRM6 CGI-09	0.38	0.30	0.36

SFLSGLYEFPLNK	surrogate standard	TRMT6	TRMT6 KIAA1153 TRM6 CGI-09	0.13	0.37	0.11
NYQVLPDR	surrogate standard	TRMT6	TRMT6 KIAA1153 TRM6 CGI-09	0.52	0.71	0.76
SLFPGLETK	surrogate standard	PUS7	PUS7 KIAA1897	1.25	0.47	0.34
FGTTAVPTYQVGR	isotopic standard	PUS7	PUS7 KIAA1897	0.87	0.38	0.25
QGSPVAAGAPAK	surrogate standard	IGF2BP1	IGF2BP1 CRDBP VICKZ1 ZBP1	0.79	0.74	0.79
ITISSLQDLTLYNPER	isotopic standard	IGF2BP1	IGF2BP1 CRDBP VICKZ1 ZBP1	0.11	0.15	0.33
TVNELQNLTAAEVVVPR	surrogate standard	IGF2BP1	IGF2BP1 CRDBP VICKZ1 ZBP1	1.30	0.81	1.01
LYIGNLSPAVTADDLR	isotopic standard	IGF2BP2	IGF2BP2 IMP2 VICKZ2	0.48	0.51	0.62
TVNELQNLTSAEVIVPR	surrogate standard	IGF2BP2	IGF2BP2 IMP2 VICKZ2	2.21	0.77	1.53
FTEEIPLK	surrogate standard	IGF2BP3	IGF2BP3 IMP3 KOC1 VICKZ3	1.03	1.22	1.11
ITISPLQELTLYNPER	isotopic standard	IGF2BP3	IGF2BP3 IMP3 KOC1 VICKZ3	0.15	0.29	0.45
IAPAEAPDAK	surrogate standard	IGF2BP3	IGF2BP3 IMP3 KOC1 VICKZ3	1.67	1.29	1.45
QYEAYVQALEGK	surrogate standard	WTAP	WTAP KIAA0105	1.78	0.66	0.67
YTDLNSNDVTGLR	surrogate standard	WTAP	WTAP KIAA0105	0.95	0.97	1.01
QVQQPSVAQLR	isotopic standard	WTAP	WTAP KIAA0105	1.72	0.76	0.81
FPCVVYINEVR	isotopic standard	VIRMA	KIAA1429 MSTP054	1.00	0.50	0.43
GLSYLQLK	surrogate standard	VIRMA	KIAA1429 MSTP054	1.24	0.59	0.37
NLDADLVR	isotopic standard	RBM15B	RBM15B OTT3	1.24	1.06	2.78
QAAGVISLPVGGSK	surrogate standard	RBM15B	RBM15B OTT3	1.33	0.90	1.43
SLSPGGAALGYR	surrogate standard	RBM15	RBM15 OTT OTT1	1.34	0.52	0.49
LQQLALGR	isotopic standard	RBM15	RBM15 OTT OTT1	1.37	0.45	0.80
LISDSVER	isotopic standard	ZC3H13	ZC3H13 KIAA0853	6.08	1.75	3.72
LAGSELFAK	surrogate standard	ZC3H13	ZC3H13 KIAA0853	1.90	1.02	1.28
FCLQYTR	surrogate standard	EIF3A	EIF3A EIF3S10 KIAA0139	0.23	0.43	0.22

VLLATLSIPITPER	isotopic standard	EIF3A	EIF3A EIF3S10 KIAA0139	0.28	0.52	0.18
LTSLVPFVDAFQLER	surrogate standard	EIF3A	EIF3A EIF3S10 KIAA0139	0.01	0.11	0.01
TSIFWNDVK	surrogate standard	EIF3B	EIF3B EIF3S9	0.11	0.04	0.08
GTQGVVTNFEIFR	isotopic standard	EIF3B	EIF3B EIF3S9	0.21	0.30	0.26
FAVLHGEAPR	surrogate standard	EIF3B	EIF3B EIF3S9	0.27	0.63	0.52
LFIGGLSFETTEESLR	surrogate standard	HNRNPA 2B1	HNRNPA2B1 HNRPA2B1	0.83	1.72	1.05
EESGKPGAHVTVK	surrogate standard	HNRNPA 2B1	HNRNPA2B1 HNRPA2B1	0.99	1.08	0.90
IDTIEIITDR	isotopic standard	HNRNPA 2B1	HNRNPA2B1 HNRPA2B1	1.65	0.58	1.13
TLETVPLER	surrogate standard	HNRNPA 2B1	HNRNPA2B1 HNRPA2B1	1.36	1.51	1.97
GFAFVQYVNER	isotopic standard	HNRNPC	HNRNPC HNRPC	0.62	0.74	0.75
MIAGQVLDINLAAEPK	surrogate standard	HNRNPC	HNRNPC HNRPC	1.68	0.89	0.97
VPPPPPIAR	surrogate standard	HNRNPC	HNRNPC HNRPC	0.89	1.09	1.01
TIEDDLVSALVR	isotopic standard	PUS1	PUS1 PP8985	0.27	0.33	0.57
LSAETLQQVNR	surrogate standard	PUS1	PUS1 PP8985	0.57	0.40	0.45
GYAPESVLER	surrogate standard	PUS1	PUS1 PP8985	0.41	0.33	0.30
AAAAVVAAAAR	isotopic standard	TRUB1	TRUB1 PUS4	0.99	0.54	0.51
GPTSAELLNR	surrogate standard	TRUB1	TRUB1 PUS4	1.27	0.60	0.47
GVLVVGIGSGTK	surrogate standard	TRUB1	TRUB1 PUS4	0.69	0.66	0.36
IMLPGVLR	surrogate standard	DKC1	DKC1 NOLA4	0.65	0.73	0.36
EVVAEVVK	isotopic standard	DKC1	DKC1 NOLA4	1.04	1.50	1.20
LHNAIEGGTQLSR	surrogate standard	DKC1	DKC1 NOLA4	1.16	0.78	1.23
NLAANDLSPSR	surrogate standard	NSUN4	NSUN4	0.97	0.64	0.89
VLVDVPCTTDR	isotopic standard	NSUN4	NSUN4	0.86	0.93	0.99
YAMDVENK	isotopic standard	TRDMT1	TRDMT1 DNMT2	0.23	0.64	0.63

SLGTADVHFER	surrogate standard	ALYREF	THOC4	1.81	0.98	1.53
QQLSAEELDAQLDAYNAR	isotopic standard	ALYREF	THOC4	1.79	0.86	2.11
GPMETGLFPGSNATFR	surrogate standard	METTL8	METTL8	2.31	1.00	0.62
ILAWAPVEPSFSAR	surrogate standard	PUS3	PUS3 FKSG32	0.36	0.09	0.08
VLCVGTPR	surrogate standard	ZCCHC4	ZCCHC4	1.84	1.70	0.82
MCPGCSDPVQR	surrogate standard	CBLL1	CBLL1 HAKAI RNF188	0.90	0.91	0.75
DLQAHINHR	surrogate standard	CBLL1	CBLL1 HAKAI RNF188	2.38	0.63	1.07
SVLSEGHQR	surrogate standard	CIAO1	CIAO1 WDR39	0.62	0.61	0.54
GTLIQGVLR	surrogate standard	DIS3L2	DIS3L2 FAM6A	0.50	0.26	0.08
YALFSPSDHR	surrogate standard	DIS3L2	DIS3L2 FAM6A	0.53	1.86	0.84
LACDFLAR	surrogate standard	FTSJ3	FTSJ3 SB92	0.09	0.08	0.05
TSVTDFLR	surrogate standard	FTSJ3	FTSJ3 SB92	1.56	1.24	1.15
AANPVDFLSK	surrogate standard	FTSJ3	FTSJ3 SB92	1.77	1.53	1.13
NVGTGLVGAPACGDVMK	surrogate standard	ISCU	ISCU NIFUN	0.77	0.45	0.28
TFGCGSAIASSSLATEWVK	surrogate standard	ISCU	ISCU NIFUN	0.11	0.19	0.03
TVEEALTIK	surrogate standard	ISCU	ISCU NIFUN	0.42	0.24	0.26
GGVDTAAAPAGGAPPAHAPGPGR	surrogate standard	LAGE3	LAGE3 DXS9879E ESO3 ITBA2	0.79	0.25	0.26
IASAIVQAR	surrogate standard	METTL15	METTL15 METT5D1	0.31	0.26	0.33
VLSPQDQDVQDNPR	surrogate standard	METTL15	METTL15 METT5D1	0.07	0.14	0.56
FLENPDLSQTEEK	surrogate standard	METTL17	METTL17 METT11D1	1.36	0.72	0.93
LDGGFAAVSR	surrogate standard	METTL17	METTL17 METT11D1	0.37	0.04	0.12
TAVYSLHK	surrogate standard	METTL5	METTL5 DC3 HSPC133	0.82	0.30	0.34
QNLPLSSGK	surrogate standard	MPST	MPST TST2	0.04	0.00	0.00
SQPAPAEFR	surrogate standard	MPST	MPST TST2	0.53	0.24	0.34

LLDLVQQSCNYK	surrogate standard	SNU13	NHP2L1	0.73	0.47	0.51
NVPYVFVR	surrogate standard	SNU13	NHP2L1	0.47	0.40	0.26
QQIQSIQQSIER	surrogate standard	SNU13	NHP2L1	0.73	0.50	0.58
VPLDPLIGK	surrogate standard	NUBP1	NUBP1 NBP NBP1	1.41	0.37	0.30
GQSFFIDAPDSPATLAYR	surrogate standard	NUBP1	NUBP1 NBP NBP1	0.14	0.03	0.06
TYVTPPGTGFLPGDTAR	surrogate standard	OSGEP	OSGEP GCPL1	0.46	0.22	0.17
TPLSDSGVTQR	surrogate standard	OSGEP	OSGEP GCPL1	0.80	0.19	0.27
SFSGLNSR	surrogate standard	PRRC2A	PRRC2A BAT2 G2	0.98	0.57	0.44
ATPSTYSGVFR	surrogate standard	PRRC2A	PRRC2A BAT2 G2	1.36	1.71	0.40
TPQGLSNLAK	surrogate standard	TP53RK	TP53RK C20orf64 PRPK	1.33	0.40	0.41
GVDLYVLEK	surrogate standard	TP53RK	TP53RK C20orf64 PRPK	0.16	0.28	0.45
LSSQEESIGTLLDAIICR	surrogate standard	TPRKB	TPRKB CGI-121 My019	0.15	0.32	0.37
IQLEPLPPLTPK	surrogate standard	TUT7	ZCCHC6 HS2 KIAA1711 TUT7	3.65	1.56	4.23
GLLATASEDR	surrogate standard	WDR6	WDR6	0.26	0.25	0.11
AGWTEALR	surrogate standard	YRDC	YRDC DRIP3 IRIP	0.39	0.07	0.08
DLNPFTPLVGIR	surrogate standard	YRDC	YRDC DRIP3 IRIP	0.02	0.01	0.01

Table S1h. LC-PRM quantification results of RWE proteins in chromatin fraction of *SETD2*$^{-/-}$ cells (n = 3) relative to parental HEK293T cells (n = 3).

Protein Symbol	SETD2_KO/HEK293T-chromatin-ratio-1	s.d.	SETD2_KO/HEK293T-chromatin-ratio-2	s.d.	SETD2_KO/HEK293T-chromatin-ratio-3	s.d.	Ave.	S.D.	R.S.D.	*p*-value (one samples t test)
ADAR	0.61	0.38	0.69	0.27	0.99	0.46	0.76	0.20	26%	0.179
ADAT1	1.91		5.14		5.58		4.21	2.01	48%	0.109
ADAT3	1.00		0.24		0.27		0.50	0.43	85%	0.182
BUD23	0.46	0.26	0.80	0.11	0.94	0.21	0.73	0.25	34%	0.199
CDK5RAP1	0.41	0.46	0.95	0.52	0.51	0.24	0.62	0.28	46%	0.149
CDKAL1	0.15	0.15	0.11	0.07	0.23	0.27	0.16	0.06	38%	0.002
CMTR1	0.89	0.55	0.54	0.29	0.58	0.24	0.67	0.19	29%	0.095
APOBEC3G	1.06		1.05		1.44		1.19	0.22	19%	0.282
CMTR2	0.10		0.15		0.24		0.16	0.07	46%	0.003
CTU1	0.48		0.21		0.24		0.31	0.15	48%	0.015
CTU2	0.16	0.22	0.11	0.02	0.09	0.03	0.12	0.03	29%	0.001
DCP2	0.64		0.35		0.15		0.38	0.24	64%	0.048
DIMT1	0.87	0.01	0.71	0.04	0.38	0.14	0.65	0.25	38%	0.136
DUS1L	0.29	0.10	0.22	0.12	0.15	0.14	0.22	0.07	33%	0.003
DUS3L	0.32	0.00	0.69	0.24	0.83	0.12	0.62	0.26	43%	0.126
EIF5A2	0.59	0.33	0.29	0.07	0.26	0.03	0.38	0.18	48%	0.028
ELP1	0.51		0.41		0.25		0.39	0.13	34%	0.015
ELP3	0.32		0.08		0.04		0.15	0.15	101%	0.010
EMG1	0.88	0.54	0.78	0.21	0.98	0.30	0.88	0.10	11%	0.168
FBL	0.87	0.40	1.20	0.95	1.72	0.52	1.26	0.43	34%	0.403
FTSJ1	0.34	0.18	0.12	0.09	0.11	0.08	0.19	0.13	70%	0.009
HSD17B10	0.37	0.17	0.17	0.07	0.23	0.15	0.26	0.10	39%	0.006
LCMT2	1.39		0.63		0.42		0.81	0.51	63%	0.585
MEPCE	1.02	0.28	0.97	0.41	0.60	0.14	0.87	0.23	27%	0.420
MRM1	1.12	0.56	1.28	0.45	1.95	0.18	1.45	0.44	30%	0.218

MRM2	1.58		0.25		0.69		0.84	0.68	80%	0.725
MRM3	0.64	0.26	0.56	0.23	0.65	0.25	0.62	0.05	8%	0.005
MTO1	0.83	0.43	0.23	0.08	0.41	0.28	0.49	0.31	63%	0.105
NAT10	0.72	0.18	0.47	0.31	0.29	0.19	0.50	0.22	44%	0.056
NFS1	0.99	0.26	0.53	0.17	0.67	0.14	0.73	0.23	32%	0.182
NOP2	1.45	0.32	2.32	0.76	2.77	1.58	2.18	0.67	31%	0.093
NUDT16	0.38	0.00	0.17	0.04	0.26	0.11	0.27	0.10	38%	0.007
PCIF1	0.62	0.37	0.33	0.13	0.28	0.15	0.41	0.18	45%	0.031
QTRT1	0.82		0.48		0.64		0.64	0.17	26%	0.069
RNGTT	0.53	0.12	0.50	0.21	0.48	0.23	0.51	0.03	5%	0.001
RNMT	1.11	0.27	0.50	0.04	0.78	0.18	0.80	0.30	38%	0.364
RPUSD3	0.36	0.20	0.51	0.28	0.49	0.19	0.46	0.09	19%	0.008
RPUSD4	0.81		0.92		0.73		0.82	0.10	12%	0.085
TARBP1	0.35	0.27	0.44	0.18	0.30	0.30	0.36	0.07	19%	0.004
TFB1M	0.30	0.18	0.52	0.07	0.26	0.03	0.36	0.14	39%	0.015
TGS1	0.31		0.62		1.12		0.68	0.41	60%	0.311
THG1L	0.31		0.15		0.03		0.16	0.14	86%	0.009
THUMPD1	1.71		0.16		0.82		0.90	0.78	86%	0.841
TRIT1	0.13		0.41		0.28		0.27	0.14	50%	0.012
TRMT1	0.58	0.72	0.23	0.17	0.12	0.10	0.31	0.24	78%	0.038
TRMT10C	0.30	0.01	0.37	0.08	0.27	0.06	0.31	0.05	16%	0.002
TRMT11	0.20		0.13		0.46		0.26	0.17	66%	0.018
TRMT112	0.47		0.65		0.69		0.61	0.12	20%	0.029
TRMT2A	0.32	0.29	0.19	0.25	0.18	0.22	0.23	0.08	34%	0.004
TRMT5	0.91		0.27		0.23		0.47	0.38	80%	0.137
TRUB2	0.75	0.37	0.91	0.53	1.20	1.14	0.95	0.23	24%	0.756
TYW3	1.07		0.38		0.56		0.67	0.36	53%	0.250
WDR4	1.57		0.56		0.40		0.84	0.63	75%	0.709
YBX1	0.81	0.23	0.94	0.71	0.50	0.20	0.75	0.22	30%	0.192

RBMX	0.95	0.22	1.27	0.18	1.46	0.16	1.23	0.26	21%	0.264
ELAVL1	0.82	0.02	1.09	0.03	0.93	0.13	0.95	0.13	14%	0.556
SND1	0.53	0.08	0.56	0.18	0.56	0.01	0.55	0.02	3%	0.001
FMR1	0.60	0.27	0.41	0.10	0.24	0.12	0.42	0.18	43%	0.030
LRPPRC	0.55	0.08	0.80	0.27	0.39	0.05	0.58	0.21	36%	0.073
PUS7L	1.23		0.39		1.11		0.91	0.46	50%	0.770
ALKBH2	0.23	0.07	0.06	0.08	0.09	0.08	0.13	0.09	72%	0.004
ALKBH3	1.05	0.87	0.40	0.12	0.26	0.08	0.57	0.42	74%	0.222
ALKBH4	0.64	0.35	0.50	0.32	0.49	0.32	0.55	0.08	15%	0.011
ALKBH5	1.18	0.10	1.00	0.65	1.11	0.67	1.10	0.10	9%	0.217
FTO	0.62				0.76		0.69	0.10	15%	
YTHDF1	0.72	0.39	0.40	0.47	0.17	0.18	0.43	0.28	65%	0.07
YTHDF2	0.63	0.34	0.58	0.27	0.58	0.22	0.60	0.03	5%	0.00
YTHDF3	1.02	0.20	0.74	0.30	0.76	0.31	0.84	0.16	19%	0.22
YTHDC1	1.16	0.17	0.67	0.06	1.11	0.39	0.98	0.27	28%	0.91
YTHDC2	1.97	1.51	3.26	2.02	2.30	2.66	2.51	0.67	27%	0.06
METTL3	0.95	0.13	0.39	0.26	0.38	0.29	0.58	0.33	57%	0.15
METTL14	0.72		0.19		0.47		0.46	0.26	57%	0.07
METTL1	0.25		0.10		0.03		0.13	0.11	87%	0.01
METTL16	0.72	0.18	0.44	0.01	0.24	0.10	0.47	0.24	52%	0.06
METTL2B	0.79		0.43		0.54		0.59	0.19	31%	0.06
NSUN2	1.18	0.33	0.87	0.04	0.92	0.24	0.99	0.17	17%	0.93
NSUN5	0.89	0.12	0.82	0.11	1.04	0.17	0.92	0.11	12%	0.34
NSUN6	0.66	0.53	0.25	0.16	0.36	0.26	0.42	0.21	50%	0.04
DNMT1	0.71	0.38	0.60	0.14	0.71	0.39	0.67	0.07	10%	0.01
TRMT61A	0.18	0.11	0.55	0.22	0.36	0.19	0.36	0.18	50%	0.03
TRMT61B	0.47		1.44		0.48		0.80	0.56	70%	0.59
TRMT6	0.34	0.20	0.46	0.22	0.41	0.33	0.40	0.06	14%	0.00
PUS7	1.06	0.27	0.43	0.07	0.29	0.06	0.59	0.41	69%	0.23

IGF2BP1	0.73	0.60	0.56	0.36	0.71	0.35	0.67	0.09	14%	0.03
IGF2BP2	1.34	1.22	0.64	0.19	1.08	0.64	1.02	0.36	35%	0.93
IGF2BP3	0.95	0.77	0.93	0.56	1.00	0.51	0.96	0.04	4%	0.23
WTAP	1.48	0.46	0.80	0.15	0.83	0.17	1.04	0.39	37%	0.88
VIRMA	1.12	0.17	0.54	0.06	0.40	0.04	0.69	0.38	55%	0.29
RBM15B	1.28	0.06	0.98	0.12	2.10	0.96	1.46	0.58	40%	0.31
RBM15	1.35	0.03	0.48	0.05	0.65	0.22	0.83	0.46	56%	0.59
ZC3H13	3.99	2.96	1.39	0.51	2.50	1.73	2.62	1.30	50%	0.16
EIF3A	0.17	0.14	0.35	0.22	0.14	0.11	0.22	0.12	53%	0.01
EIF3B	0.19	0.08	0.32	0.29	0.29	0.22	0.27	0.07	25%	0.00
HNRNPA2B1	1.21	0.37	1.22	0.51	1.26	0.48	1.23	0.03	2%	0.00
HNRNPC	1.06	0.55	0.91	0.18	0.91	0.14	0.96	0.09	9%	0.51
PUS1	0.42	0.15	0.35	0.04	0.44	0.13	0.40	0.05	11%	0.00
TRUB1	0.99	0.29	0.60	0.06	0.45	0.08	0.68	0.28	41%	0.18
DKC1	0.95	0.27	1.00	0.43	0.93	0.50	0.96	0.04	4%	0.21
NSUN4	0.91	0.08	0.79	0.20	0.94	0.07	0.88	0.08	9%	0.13
TRDMT1	0.23		0.64		0.63		0.50	0.23	47%	0.07
ALYREF	1.80	0.01	0.92	0.09	1.82	0.41	1.51	0.51	34%	0.23
METTL8	2.31		1.00		0.62		1.31	0.89	68%	0.61
PUS3	0.36		0.09		0.08		0.18	0.16	91%	0.01
ZCCHC4	1.84		1.70		0.82		1.45	0.55	38%	0.29
CBLL1	1.64	1.05	0.77	0.20	0.91	0.23	1.11	0.47	42%	0.73
CIAO1	0.62		0.61		0.54		0.59	0.04	8%	0.00
DIS3L2	0.51	0.02	1.06	1.13	0.46	0.54	0.68	0.33	49%	0.24
FTSJ3	1.14	0.91	0.95	0.77	0.78	0.63	0.96	0.18	19%	0.71
ISCU	0.43	0.33	0.29	0.14	0.19	0.14	0.30	0.12	40%	0.01
LAGE3	0.79		0.25		0.26		0.43	0.31	71%	0.08
METTL15	0.19	0.17	0.20	0.09	0.44	0.16	0.28	0.14	52%	0.01
METTL17	0.87	0.70	0.38	0.48	0.53	0.57	0.59	0.25	42%	0.10

METTL5	0.82		0.30		0.34		0.49	0.29	59%	0.09
MPST	0.28	0.34	0.12	0.17	0.17	0.24	0.19	0.09	45%	0.00
SNU13	0.65	0.15	0.46	0.05	0.45	0.17	0.52	0.11	21%	0.02
NUBP1	0.77	0.90	0.20	0.24	0.18	0.17	0.38	0.34	88%	0.09
OSGEP	0.63	0.24	0.20	0.02	0.22	0.07	0.35	0.24	69%	0.04
PRRC2A	1.17	0.27	1.14	0.81	0.42	0.03	0.91	0.43	47%	0.75
TP53RK	0.74	0.83	0.34	0.09	0.43	0.03	0.50	0.21	42%	0.06
TPRKB	0.15		0.32		0.37		0.28	0.12	42%	0.01
TUT7	3.65		1.56		4.23		3.15	1.40	45%	0.12
WDR6	0.26		0.25		0.11		0.21	0.09	41%	0.00
YRDC	0.20	0.26	0.04	0.04	0.05	0.05	0.10	0.09	96%	0.00

Table S1i. LC-PRM quantification results of tryptic peptides from RWE proteins in chromatin fraction of *KAT5*$^{-/-}$ cells (n = 3) relative to parental HEK293T cells (n = 3).

Peptide	standard type	Protein Symbol	Protein Gene	KAT5_KO/HEK293T-chromatin-ratio-1	KAT5_KO/HEK293T-chromatin-ratio-2	KAT5_KO/HEK293T-chromatin-ratio-3
YLNTNPVGGLLEYAR	surrogate standard	ADAR	ADAR ADAR1 DSRAD G1P1 IFI4	0.33	0.64	0.87
VLIGENEK	surrogate standard	ADAR	ADAR ADAR1 DSRAD G1P1 IFI4	1.37	0.78	1.44
DGSAFEDGLR	surrogate standard	ADAR	ADAR ADAR1 DSRAD G1P1 IFI4	1.16	0.81	0.94
GFGVQELK	surrogate standard	ADAT1	ADAT1	1.82	4.08	2.37
AVGAVVVDPASDR	surrogate standard	ADAT3	ADAT3 TAD3	0.90	0.38	0.12
AVLQLYPENSEQLELITTQATK	surrogate standard	BUD23	WBSCR22 MERM1 HUSSY-03 PP3381	0.16	0.36	0.72
AGFSGGMVVDYPNSAK	surrogate standard	BUD23	WBSCR22 MERM1 HUSSY-03 PP3381	0.33	0.49	0.53
ESVFTNER	surrogate standard	BUD23	WBSCR22 MERM1 HUSSY-03 PP3381	0.40	0.46	0.74
VIFPDAEMEDVNNPGLR	surrogate standard	CDK5RAP1	CDK5RAP1 C20orf34 CGI-05 HSPC167	0.33	3.57	0.12
ITSASSQTLR	surrogate standard	CDK5RAP1	CDK5RAP1 C20orf34 CGI-05 HSPC167	1.23	0.77	0.82
GNLASYPIDELVDR	surrogate standard	CDKAL1	CDKAL1	0.58	0.46	0.39
DIGTNLPTLLWK	surrogate standard	CDKAL1	CDKAL1	0.06	0.14	0.06
GFGMTLK	surrogate standard	CMTR1	CMTR1 FTSJD2 KIAA0082 MTR1	1.83	0.62	0.51
NTDSDVNLVVPLEVIK	surrogate standard	CMTR1	CMTR1 FTSJD2 KIAA0082 MTR1	0.57	0.31	0.46
SQIYTWDGR	surrogate standard	CMTR1	CMTR1 FTSJD2 KIAA0082 MTR1	1.48	0.57	0.93
DMATFLAEDPK	surrogate standard	APOBEC3G	APOBEC3G MDS019	0.92	0.78	0.94
TLNEAIEK	surrogate standard	CMTR2	CMTR2 AFT FTSJD1	0.08	0.12	0.26
GGGLGSPGEGGALPR	surrogate standard	CTU1	CTU1 ATPBD3 NCS6	0.31	0.71	0.12
EELLQTLR	surrogate standard	CTU2	CTU2	0.80	0.13	0.06
LQTQFPSTVSTVYR	surrogate standard	CTU2	CTU2	0.69	0.23	0.09
LYIIPGIPK	surrogate standard	DCP2	DCP2 NUDT20	0.37	0.49	0.18

NPLIINSIIDK	surrogate standard	DIMT1	DIMT1 DIMT1L HUSSY-05	0.67	1.12	0.38
LQVLVGDVLK	surrogate standard	DIMT1	DIMT1 DIMT1L HUSSY-05	1.78	0.77	0.22
LQGFEFWSR	surrogate standard	DUS1L	DUS1L	0.25	0.27	0.10
LSVPVTCK	surrogate standard	DUS1L	DUS1L	0.33	0.28	0.23
YLETKPADLGPR	surrogate standard	DUS3L	DUS3L	0.83	1.72	1.42
GTQPPSIR	surrogate standard	DUS3L	DUS3L	1.67	0.29	0.91
TCGPLTDEDVVR	surrogate standard	DUS3L	DUS3L	1.50	1.30	1.09
NGFVVLK	surrogate standard	EIF5A2	EIF5A2	1.51	0.82	0.43
YEDICPSTHNMDVPNIK	surrogate standard	EIF5A2	EIF5A2	0.78	0.42	0.34
VLVTVFR	surrogate standard	ELP1	IKBKAP ELP1 IKAP	0.65	0.38	0.22
YDPFLQTR	surrogate standard	ELP3	ELP3		1.31	1.09
LYPTLVIR	surrogate standard	ELP3	ELP3	1.04	0.31	0.07
TYELLNCDK	surrogate standard	EMG1	EMG1 C2F	0.66	0.70	0.88
VGTSFSIPVVSDVR	surrogate standard	EMG1	EMG1 C2F	1.01	1.15	0.68
VSVEYTEK	surrogate standard	EMG1	EMG1 C2F	0.36	0.32	0.61
NVMVEPHR	surrogate standard	FBL	FBL FIB1 FLRN	0.32	0.20	1.69
NLVPGESVYGEK	surrogate standard	FBL	FBL FIB1 FLRN	0.65	1.15	1.30
EFQLFQGVTR	surrogate standard	FTSJ1	FTSJ1 JM23	0.16	0.05	0.07
AVDLCAAPGSWSQVLSQK	surrogate standard	FTSJ1	FTSJ1 JM23	0.54	0.41	0.17
SYPLDLEGGSEYK	surrogate standard	FTSJ1	FTSJ1 JM23	0.66	0.32	0.44
GLVAVITGGASGLGLATAER	surrogate standard	HSD17B10	HSD17B10 ERAB HADH2 MRPP2 SCHAD XH98G2	0.14	0.36	0.22
DVQTALALAK	surrogate standard	HSD17B10	HSD17B10 ERAB HADH2 MRPP2 SCHAD XH98G2	1.17	0.18	0.16
VCNFLASQVPFPSR	surrogate standard	HSD17B10	HSD17B10 ERAB HADH2 MRPP2 SCHAD XH98G2	0.42	0.25	0.14
NSCNVGGGGGGFK	surrogate standard	MEPCE	MEPCE BCDIN3	0.99	0.56	0.70

FQYGNYCK	surrogate standard	MEPCE	MEPCE BCDIN3	1.02	0.35	0.63
SCFPASLTASR	surrogate standard	MEPCE	MEPCE BCDIN3	1.55	1.07	0.99
LLLDDLVPTSR	surrogate standard	MRM1	MRM1	0.31	0.83	0.24
NSCPLTPVVSK	surrogate standard	MRM1	MRM1	0.20	0.58	0.40
ILEVLPGR	surrogate standard	MRM2	FTSJ2 FJH1 MRM2	2.87	1.16	0.53
APSTWEESGLR	surrogate standard	MRM3	RNMTL1 MRM3 HC90	1.36	1.77	1.13
DPGNLGTILR	surrogate standard	MRM3	RNMTL1 MRM3 HC90	1.14	0.94	0.81
LGFVVGR	surrogate standard	MTO1	MTO1 CGI-02	0.98	0.44	0.21
LIPEASISTSR	surrogate standard	MTO1	MTO1 CGI-02	1.45	0.87	0.25
SLFVVVGDR	surrogate standard	NAT10	NAT10 ALP KIAA1709	0.53	0.33	0.73
LDYLGVSYGLTPR	surrogate standard	NAT10	NAT10 ALP KIAA1709	0.77	0.41	0.57
AGPNASIISLK	surrogate standard	NAT10	NAT10 ALP KIAA1709	0.85	0.88	1.36
SLEAEGFQVTYLPVQK	surrogate standard	NFS1	NFS1 NIFS HUSSY-08	1.21	1.05	0.61
AIGTDEDLAHSSIR	surrogate standard	NFS1	NFS1 NIFS HUSSY-08	1.02	0.91	0.60
IQDIVGILR	surrogate standard	NOP2	NOP2 NOL1 NSUN1	2.72	2.67	4.99
DLAQALINR	surrogate standard	NOP2	NOP2 NOL1 NSUN1	1.43	2.21	3.35
LGVTNTIISHYDGR	surrogate standard	NOP2	NOP2 NOL1 NSUN1	1.36	3.05	9.49
GADSELSTVPSVTK	surrogate standard	NOP2	NOP2 NOL1 NSUN1	1.24	2.49	5.30
GTDTQTPAVLSPSK	surrogate standard	NOP2	NOP2 NOL1 NSUN1	2.78	3.75	9.79
LGFPGGFVDTQDR	surrogate standard	NUDT16	NUDT16	1.14	0.59	0.31
EELGEAAAAFR	surrogate standard	NUDT16	NUDT16	0.76	0.19	0.29
EIMNDIPIR	surrogate standard	PCIF1	PCIF1	0.80	0.25	0.30
LVYCYPVR	surrogate standard	PCIF1	PCIF1	0.92	0.52	0.30
LQELSAAYR	surrogate standard	PCIF1	PCIF1	1.12	0.53	0.50

GITTEQLDALGCR	surrogate standard	QTRT1	QTRT1 TGT TGUT	1.89	0.78	0.56
YDSQVAEENR	surrogate standard	RNGTT	RNGTT CAP1A	0.78	0.31	0.35
FNSQPVGDCDFNVR	surrogate standard	RNGTT	RNGTT CAP1A	0.75	0.52	0.56
SVLIGEFLEK	surrogate standard	RNMT	RNMT KIAA0398	1.04	0.49	0.31
TFLEFYEEK	surrogate standard	RNMT	RNMT KIAA0398	1.07	0.67	0.44
LPLGTLSK	surrogate standard	RNMT	RNMT KIAA0398	1.65	0.67	0.30
AQPLAYYEAAVR	surrogate standard	RPUSD2	RPUSD2 C15orf19	0.73	0.65	0.14
VGTVLGQR	surrogate standard	RPUSD3	RPUSD3	1.06	1.22	1.22
DTPVELLAPLPPYFSR	surrogate standard	RPUSD3	RPUSD3	0.25	0.67	0.77
TLQCLGLR	surrogate standard	RPUSD3	RPUSD3	1.10	1.05	1.01
MTLSPSYR	surrogate standard	RPUSD4	RPUSD4	0.20	0.25	0.39
GSGGAGALPEAAR	surrogate standard	TARBP1	TARBP1 TRM3 TRP185	0.56	0.59	0.66
LLPVLVQCGGAALR	surrogate standard	TARBP1	TARBP1 TRM3 TRP185	0.34	0.26	0.29
IFLDPLLDVLMK	surrogate standard	TARBP1	TARBP1 TRM3 TRP185	0.08	0.05	0.10
LPPLPTIR	surrogate standard	TFB1M	TFB1M CGI-75	0.56	0.35	0.33
DGPFVYGR	surrogate standard	TFB1M	TFB1M CGI-75	0.21	0.34	0.27
YGGIPNFSHR	surrogate standard	TGS1	TGS1 HCA137 NCOA6IP PIMT	1.41	7.95	2.58
VIAIDIDPVK	surrogate standard	TGS1	TGS1 HCA137 NCOA6IP PIMT	2.68	0.48	0.73
STLALQLGQR	surrogate standard	TRIT1	TRIT1 IPT MOD5	0.19	0.52	0.14
DLTCAVITEFAR	surrogate standard	TRMT1	TRMT1	0.10	0.17	0.06
FALEVPGLR	surrogate standard	TRMT1	TRMT1	1.24	1.15	0.32
IPAVTYPK	surrogate standard	TRMT10C	TRMT10C MRPP1 RG9MTD1	0.49	0.59	0.48
EVPEHITEEELK	surrogate standard	TRMT10C	TRMT10C MRPP1 RG9MTD1	1.43	0.77	0.75
LLLTSTEK	surrogate standard	TRMT10C	TRMT10C MRPP1 RG9MTD1	0.35	0.56	0.32

IDALEFLPFEGK	surrogate standard	TRMT11	TRMT11 C6orf75 MDS024	0.47	0.37	0.92
GPVEGYEENEEFLR	surrogate standard	TRMT112	TRMT112 AD-001 HSPC152 HSPC170	0.35	0.42	0.54
AVLPEGQDVTSGFSR	surrogate standard	TRMT5	TRMT5 KIAA1393 TRM5	2.35	0.71	0.45
ILAVIQGSHQK	surrogate standard	TRUB2	TRUB2	0.01	0.14	0.06
DGFFTLDSALLR	surrogate standard	TRUB2	TRUB2	0.01	0.09	1.88
AATPQVAAELEK	surrogate standard	TRUB2	TRUB2	0.12	0.80	0.25
DQFFTTSSCAGR	surrogate standard	TYW3	TYW3 C1orf171	1.24	0.75	0.63
ISVVPTQPGLLLSSSGDGTLR	surrogate standard	WDR4	WDR4	0.35	0.27	0.45
GAEAANVTGPGGVPVQGSK	surrogate standard	YBX1	YBX1 NSEP1 YB1	0.54	0.71	0.71
NEGSESAPEGQAQQR	surrogate standard	YBX1	YBX1 NSEP1 YB1	0.32	0.13	0.73
AADPPAENSSAPEAEQGGAE	surrogate standard	YBX1	YBX1 NSEP1 YB1	0.66	0.93	0.88
ALEAVFGK	surrogate standard	RBMX	RBMX HNRPG RBMXP1	0.90	1.07	1.60
SAPSGPVR	surrogate standard	RBMX	RBMX HNRPG RBMXP1	1.46	0.84	1.50
SDLYSSGR	surrogate standard	RBMX	RBMX HNRPG RBMXP1	1.21	0.98	1.25
SLFSSIGEVESAK	surrogate standard	ELAVL1	HuR	1.22	1.19	0.89
DVEDMFSR	surrogate standard	ELAVL1	HuR	0.71	0.63	1.04
VLVDQTTGLSR	surrogate standard	ELAVL1	HuR	1.00	0.98	1.12
YTIENPR	surrogate standard	SND1	SND1 TDRD11	0.38	0.36	0.39
EVLPSTR	surrogate standard	SND1	SND1 TDRD11	0.33	0.31	0.34
LGTLSPAFSTR	surrogate standard	SND1	SND1 TDRD11	0.47	0.52	0.45
DINESDEVEVYSR	surrogate standard	FMR1	FMR1	0.23	0.16	0.03
SFLEFAEDVIQVPR	surrogate standard	FMR1	FMR1	0.16	0.14	0.08
IPENIYR	surrogate standard	LRPPRC	LRPPRC LRP130	0.71	0.56	0.43
LQWFCDR	surrogate standard	LRPPRC	LRPPRC LRP130	0.16	0.70	0.51

LDLQNLSLEDGR	surrogate standard	PUS7L	PUS7L	1.19	0.82	0.53
FGNLVETK	surrogate standard	PUS7L	PUS7L	1.95	0.02	0.20
LNIPGCYR	surrogate standard	PUS7L	PUS7L	0.43	0.15	0.19
AEGLDCSYTVLFGK	surrogate standard	ALKBH2	ALKBH2 ABH2	0.54	0.40	0.14
AEADEIFQELEK	surrogate standard	ALKBH2	ALKBH2 ABH2	0.00	0.02	0.25
EVEYFTGALAR	isotopic standard	ALKBH2	ALKBH2 ABH2	0.46	0.02	0.11
SQAIAQPATTAK	surrogate standard	ALKBH3	ALKBH3 ABH3 DEPC1	0.80	0.64	0.49
VCLYPGFVDVK	surrogate standard	ALKBH3	ALKBH3 ABH3 DEPC1	1.38	0.96	0.81
EDITYQQPR	isotopic standard	ALKBH3	ALKBH3 ABH3 DEPC1	2.90	0.56	0.23
TEGFCGLPSFSR	surrogate standard	ALKBH4	ALKBH4 ABH4	1.17	0.20	0.22
SLLVLTGAAR	surrogate standard	ALKBH4	ALKBH4 ABH4	0.83	0.73	0.81
ELSAEFGPGGR	isotopic standard	ALKBH4	ALKBH4 ABH4	0.88	0.84	0.39
LFSQDECAK	surrogate standard	ALKBH5	ALKBH5 ABH5 OFOXD1	1.77	0.81	1.33
GLYNEHTVDR	surrogate standard	ALKBH5	ALKBH5 ABH5 OFOXD1	1.97	0.66	2.00
VSEPVLSLPVR	isotopic standard	ALKBH5	ALKBH5 ABH5 OFOXD1	2.04	1.57	2.36
ILIGNPGCTYK	surrogate standard	FTO	FTO KIAA1752	0.71	2.31	1.46
SGPVMGGGLPPPPIK	surrogate standard	YTHDF1	YTHDF1	0.59	0.74	0.53
SPVDYGTSAGVWSQDK	isotopic standard	YTHDF1	YTHDF1	0.00	0.02	0.13
DGLNDDDFEPYLSPQAR	isotopic standard	YTHDF2	YTHDF2 HGRG8	0.34	0.41	0.36
LGSTEVASNVPK	surrogate standard	YTHDF2	YTHDF2 HGRG8	0.82	0.83	0.63
DVPNSQLR	surrogate standard	YTHDF2	YTHDF2 HGRG8	0.51	0.50	0.45
AITDGQAGFGNDTLSK	isotopic standard	YTHDF3	YTHDF3	0.86	0.88	0.68
VPGISSIEQGMTGLK	isotopic standard	YTHDF3	YTHDF3	0.57	0.49	0.44
GNVGIGGSAVPPPPIK	isotopic standard	YTHDF3	YTHDF3	0.65	0.76	0.57

SNNHENVSLAK	surrogate standard	YTHDC1	YTHDC1 KIAA1966 YT521	2.39	0.60	1.61
GVWSTLPVNEK	isotopic standard	YTHDC1	YTHDC1 KIAA1966 YT521	1.21	0.76	0.97
LSQSLGLVSK	surrogate standard	YTHDC2	YTHDC2	1.17	1.17	0.84
VVLIVGETGSGK	isotopic standard	YTHDC2	YTHDC2	1.00	0.90	0.62
LAAIAVAER	surrogate standard	YTHDC2	YTHDC2	6.82	4.15	4.11
NPEAALSPTFR	isotopic standard	METTL3	METTL3 MTA70	1.31	0.95	0.70
YLDVSILGK	surrogate standard	METTL3	METTL3 MTA70	1.24	0.27	0.24
LEIDEIAAPR	isotopic standard	METTL14	METTL14 KIAA1627	0.96	0.20	0.31
NFPAIFR	surrogate standard	METTL1	METTL1 C12orf1	2.16	0.78	0.28
VTYTEFCQGR	surrogate standard	METTL16	METTL16 METT10D	1.55	0.87	0.42
LPGVAGQYLFK	surrogate standard	METTL16	METTL16 METT10D	1.52	0.77	0.40
TQTPPVEENVTQK	isotopic standard	METTL2B	METTL2B	0.30	0.47	0.17
VQNLVDR	surrogate standard	METTL2B	METTL2B	0.76	1.24	0.17
GAEQLAEGGR	surrogate standard	NSUN2	NSUN2 SAKI TRM4	0.84	1.05	0.76
FYALDPSFPR	isotopic standard	NSUN2	NSUN2 SAKI TRM4	0.77	1.20	0.72
ILLTQENPFFR	surrogate standard	NSUN2	NSUN2 SAKI TRM4	0.15	0.49	0.26
VLVYELLLGK	surrogate standard	NSUN5	NSUN5 NSUN5A WBSCR20 WBSCR20A	0.17	0.51	0.37
QLEEPGAGTPSPVR	surrogate standard	NSUN5	NSUN5 NSUN5A WBSCR20 WBSCR20A	1.16	1.08	1.19
DALQQNPGAFR	surrogate standard	NSUN5	NSUN5 NSUN5A WBSCR20 WBSCR20A	0.95	1.05	0.75
NLLLDELQK	surrogate standard	NSUN6	NSUN6 NOPD1	1.78	1.60	0.42
QNALLLGLNSIR	surrogate standard	NSUN6	NSUN6 NOPD1	0.07	0.06	0.10
EVASYQPLQR	isotopic standard	NSUN6	NSUN6 NOPD1	0.71	0.43	0.35
GAGLSCEQLK	surrogate standard	NSUN6	NSUN6 NOPD1	1.52	0.71	0.40
FFLLENVR	isotopic standard	DNMT1	DNMT1 AIM CXXC9 DNMT	0.54	0.38	0.33

SQGFPDTYR	surrogate standard	DNMT1	DNMT1 AIM CXXC9 DNMT	0.71	0.65	0.57
FCSFSPCIEQVQR	surrogate standard	TRMT61A	TRMT61A	0.32	0.54	0.47
TCQALAAR	isotopic standard	TRMT61A	TRMT61A	0.29	0.73	0.42
HSVDLIGR	surrogate standard	TRMT61A	TRMT61A	0.47	0.40	0.43
DISGATEDIK	isotopic standard	TRMT61B	TRMT61B	2.98	2.47	4.14
AATACFGFPK	isotopic standard	TRMT6	TRMT6 KIAA1153 TRM6 CGI-09	0.43	0.51	0.28
SFLSGLYEFPLNK	surrogate standard	TRMT6	TRMT6 KIAA1153 TRM6 CGI-09	0.09	0.42	0.26
NYQVLPDR	surrogate standard	TRMT6	TRMT6 KIAA1153 TRM6 CGI-09	0.57	1.32	0.56
SLFPGLETK	surrogate standard	PUS7	PUS7 KIAA1897	1.00	0.76	0.29
FGTTAVPTYQVGR	isotopic standard	PUS7	PUS7 KIAA1897	0.59	0.43	0.20
QGSPVAAGAPAK	surrogate standard	IGF2BP1	IGF2BP1 CRDBP VICKZ1 ZBP1	0.94	0.89	0.75
ITISSLQDLTLYNPER	isotopic standard	IGF2BP1	IGF2BP1 CRDBP VICKZ1 ZBP1	0.14	0.23	1.17
TVNELQNLTAAEVVVPR	surrogate standard	IGF2BP1	IGF2BP1 CRDBP VICKZ1 ZBP1	0.93	1.94	0.56
LYIGNLSPAVTADDLR	isotopic standard	IGF2BP2	IGF2BP2 IMP2 VICKZ2	0.30	0.41	0.53
TVNELQNLTSAEVIVPR	surrogate standard	IGF2BP2	IGF2BP2 IMP2 VICKZ2	0.69	0.85	1.90
FTEEIPLK	surrogate standard	IGF2BP3	IGF2BP3 IMP3 KOC1 VICKZ3	0.83	1.52	0.82
ITISPLQELTLYNPER	isotopic standard	IGF2BP3	IGF2BP3 IMP3 KOC1 VICKZ3	0.13	0.43	0.51
IAPAEAPDAK	surrogate standard	IGF2BP3	IGF2BP3 IMP3 KOC1 VICKZ3	2.22	1.65	1.38
QYEAYVQALEGK	surrogate standard	WTAP	WTAP KIAA0105	2.46	0.83	0.98
YTDLNSNDVTGLR	surrogate standard	WTAP	WTAP KIAA0105	1.28	0.90	1.26
QVQQPSVAQLR	isotopic standard	WTAP	WTAP KIAA0105	1.64	1.06	1.10
FPCVVYINEVR	isotopic standard	VIRMA	KIAA1429 MSTP054	1.10	0.56	0.57
GLSYLQLK	surrogate standard	VIRMA	KIAA1429 MSTP054	1.11	0.67	0.46
NLDADLVR	isotopic standard	RBM15B	RBM15B OTT3	2.22	1.23	3.21

QAAGVISLPVGGSK	surrogate standard	RBM15B	RBM15B OTT3	1.87	1.35	1.72
SLSPGGAALGYR	surrogate standard	RBM15	RBM15 OTT OTT1	1.70	0.87	0.65
LQQLALGR	isotopic standard	RBM15	RBM15 OTT OTT1	1.12	0.88	1.29
LISDSVER	isotopic standard	ZC3H13	ZC3H13 KIAA0853	5.20	1.74	5.65
LAGSELFAK	surrogate standard	ZC3H13	ZC3H13 KIAA0853	1.59	1.13	1.54
FCLQYTR	surrogate standard	EIF3A	EIF3A EIF3S10 KIAA0139	0.43	0.29	0.25
VLLATLSIPITPER	isotopic standard	EIF3A	EIF3A EIF3S10 KIAA0139	0.43	0.51	0.35
TSIFWNDVK	surrogate standard	EIF3B	EIF3B EIF3S9	0.27	0.06	0.20
GTQGVVTNFEIFR	isotopic standard	EIF3B	EIF3B EIF3S9	0.28	0.38	0.36
FAVLHGEAPR	surrogate standard	EIF3B	EIF3B EIF3S9	0.63	0.43	0.53
LFIGGLSFETTEESLR	surrogate standard	HNRNPA2B1	HNRNPA2B1 HNRPA2B1	0.58	1.49	1.07
EESGKPGAHVTVK	surrogate standard	HNRNPA2B1	HNRNPA2B1 HNRPA2B1	0.88	0.79	1.30
IDTIEIITDR	isotopic standard	HNRNPA2B1	HNRNPA2B1 HNRPA2B1	1.44	0.49	0.94
TLETVPLER	surrogate standard	HNRNPA2B1	HNRNPA2B1 HNRPA2B1	1.59	1.32	1.08
GFAFVQYVNER	isotopic standard	HNRNPC	HNRNPC HNRPC	0.74	0.74	0.97
MIAGQVLDINLAAEPK	surrogate standard	HNRNPC	HNRNPC HNRPC	1.38	2.79	1.18
VPPPPPIAR	surrogate standard	HNRNPC	HNRNPC HNRPC	0.94	1.15	0.88
TIEDDLVSALVR	isotopic standard	PUS1	PUS1 PP8985	0.29	0.83	0.53
LSAETLQQVNR	surrogate standard	PUS1	PUS1 PP8985	1.06	0.85	0.39
GYAPESVLER	surrogate standard	PUS1	PUS1 PP8985	0.66	0.51	0.30
AAAAVVAAAAR	isotopic standard	TRUB1	TRUB1 PUS4	1.04	0.74	0.68
GPTSAELLNR	surrogate standard	TRUB1	TRUB1 PUS4	0.98	0.69	0.41
GVLVVGIGSGTK	surrogate standard	TRUB1	TRUB1 PUS4	1.00	0.75	0.51
IMLPGVLR	surrogate standard	DKC1	DKC1 NOLA4	0.98	0.42	0.37

EVVAEVVK	isotopic standard	DKC1	DKC1 NOLA4	0.80	0.61	1.12
LHNAIEGGTQLSR	surrogate standard	DKC1	DKC1 NOLA4	0.84	0.57	0.87
NLAANDLSPSR	surrogate standard	NSUN4	NSUN4	1.22	1.10	0.84
WGELEGDTYDR	surrogate standard	NSUN4	NSUN4	0.20	0.23	0.40
VLVDVPCTTDR	isotopic standard	NSUN4	NSUN4	1.21	1.20	1.03
YAMDVENK	isotopic standard	TRDMT1	TRDMT1 DNMT2	0.72	0.71	0.99
SLGTADVHFER	surrogate standard	ALYREF	THOC4	1.30	1.06	0.97
QYNGVPLDGR	surrogate standard	ALYREF	THOC4	0.42	0.22	0.36
QQLSAEELDAQLDAYNAR	isotopic standard	ALYREF	THOC4	0.77	0.78	1.52
GPMETGLFPGSNATFR	surrogate standard	METTL8	METTL8	2.23	1.64	0.66
ILAWAPVEPSFSAR	surrogate standard	PUS3	PUS3 FKSG32	0.52	0.31	0.11
VLCVGTPR	surrogate standard	ZCCHC4	ZCCHC4	2.09	1.17	0.90
IILPTEEGYR	surrogate standard	ZCCHC4	ZCCHC4	0.12	0.75	0.35
MCPGCSDPVQR	surrogate standard	CBLL1	CBLL1 HAKAI RNF188	0.77	0.71	1.00
DLQAHINHR	surrogate standard	CBLL1	CBLL1 HAKAI RNF188	1.73	0.65	0.73
SVLSEGHQR	surrogate standard	CIAO1	CIAO1 WDR39	0.43	0.45	0.53
GTLIQGVLR	surrogate standard	DIS3L2	DIS3L2 FAM6A	1.38	0.53	0.28
LACDFLAR	surrogate standard	FTSJ3	FTSJ3 SB92	0.09	0.07	0.05
TSVTDFLR	surrogate standard	FTSJ3	FTSJ3 SB92	1.21	0.96	1.20
AANPVDFLSK	surrogate standard	FTSJ3	FTSJ3 SB92	0.52	0.59	1.26
NVGTGLVGAPACGDVMK	surrogate standard	ISCU	ISCU NIFUN	1.69	0.70	0.48
TFGCGSAIASSSLATEWVK	surrogate standard	ISCU	ISCU NIFUN	0.50	0.07	0.08
TVEEALTIK	surrogate standard	ISCU	ISCU NIFUN	1.11	0.49	0.11
GGVDTAAAPAGGAPPAHAPGPGR	surrogate standard	LAGE3	LAGE3 DXS9879E ESO3 ITBA2	1.59	0.76	0.35

IASAIVQAR	surrogate standard	METTL15	METTL15 METT5D1	0.46	0.32	0.34
VLSPQDQDVQDNPR	surrogate standard	METTL15	METTL15 METT5D1	0.47	0.15	0.28
FLENPDLSQTEEK	surrogate standard	METTL17	METTL17 METT11D1	1.26	0.72	0.54
LDGGFAAVSR	surrogate standard	METTL17	METTL17 METT11D1	0.10	0.05	0.12
TAVYSLHK	surrogate standard	METTL5	METTL5 DC3 HSPC133	0.85	0.51	0.53
SVDIEVDLIR	surrogate standard	METTL5	METTL5 DC3 HSPC133	0.77	0.11	0.22
QNLPLSSGK	surrogate standard	MPST	MPST TST2	0.12	0.08	0.00
SQPAPAEFR	surrogate standard	MPST	MPST TST2	0.76	0.38	0.41
LLDLVQQSCNYK	surrogate standard	SNU13	NHP2L1	0.92	0.51	0.70
NVPYVFVR	surrogate standard	SNU13	NHP2L1	0.34	0.45	0.41
QQIQSIQQSIER	surrogate standard	SNU13	NHP2L1	0.98	0.78	0.70
VPLDPLIGK	surrogate standard	NUBP1	NUBP1 NBP NBP1	1.78	0.97	0.41
GQSFFIDAPDSPATLAYR	surrogate standard	NUBP1	NUBP1 NBP NBP1	0.28	0.20	0.28
TYVTPPGTGFLPGDTAR	surrogate standard	OSGEP	OSGEP GCPL1	0.76	0.93	0.58
LVELPYTVK	surrogate standard	OSGEP	OSGEP GCPL1	1.95	0.52	0.07
TPLSDSGVTQR	surrogate standard	OSGEP	OSGEP GCPL1	1.10	0.59	0.46
SFSGLNSR	surrogate standard	PRRC2A	PRRC2A BAT2 G2	0.44	0.41	0.49
ATPSTYSGVFR	surrogate standard	PRRC2A	PRRC2A BAT2 G2	0.12	0.44	0.61
SLTPLDAR	surrogate standard	TFB2M	TFB2M NS5ATP5	1.07	0.81	0.96
TPQGLSNLAK	surrogate standard	TP53RK	TP53RK C20orf64 PRPK	1.74	0.92	0.33
GVDLYVLEK	surrogate standard	TP53RK	TP53RK C20orf64 PRPK	0.63	0.34	0.13
LSSQEESIGTLLDAIICR	surrogate standard	TPRKB	TPRKB CGI-121 My019	0.06	0.39	0.41
IQLEPLPPLTPK	surrogate standard	TUT7	ZCCHC6 HS2 KIAA1711 TUT7	4.07	2.69	3.22
GLLATASEDR	surrogate standard	WDR6	WDR6	0.61	0.36	0.23

AGWTEALR	surrogate standard	YRDC	YRDC DRIP3 IRIP	0.22	0.25	0.10
DLNPFTPLVGIR	surrogate standard	YRDC	YRDC DRIP3 IRIP	0.01	0.03	0.02

Table S1j. LC-PRM quantification results of RWE proteins in chromatin fraction of *KAT5*$^{-/-}$ cells (n = 3) relative to parental HEK293T cells (n = 3).

Protein Symbol	KAT5_KO/HEK293T-chromatin-ratio-1	s.d.	KAT5_KO/HEK293T-chromatin-ratio-2	s.d.	KAT5_KO/HEK293T-chromatin-ratio-3	s.d.	Ave.	S.D.	R.S.D.	*p*-value (one samples t test)
ADAR	0.95	0.55	0.74	0.09	1.08	0.31	0.93	0.17	18%	0.535
ADAT1	1.82		4.08		2.37		2.76	1.18	43%	0.123
ADAT3	0.90		0.38		0.12		0.47	0.40	85%	0.145
BUD23	0.30	0.12	0.44	0.07	0.66	0.11	0.46	0.19	40%	0.038
CDK5RAP1	0.78	0.64	2.17	1.98	0.47	0.49	1.14	0.91	79%	0.812
CDKAL1	0.32	0.37	0.30	0.22	0.23	0.23	0.28	0.05	18%	0.002
CMTR1	1.29	0.65	0.50	0.17	0.63	0.25	0.81	0.42	52%	0.514
APOBEC3G	0.92		0.78		0.94		0.88	0.09	10%	0.137
CMTR2	0.08		0.12		0.26		0.16	0.09	59%	0.004
CTU1	0.31		0.71		0.12		0.38	0.30	79%	0.071
CTU2	0.75	0.08	0.18	0.07	0.07	0.02	0.33	0.36	109%	0.085
DCP2	0.37		0.49		0.18		0.34	0.15	45%	0.018
DIMT1	1.22	0.79	0.94	0.25	0.30	0.11	0.82	0.47	58%	0.583
DUS1L	0.29	0.06	0.28	0.01	0.16	0.09	0.24	0.07	28%	0.003
DUS3L	1.34	0.45	1.10	0.73	1.14	0.26	1.19	0.13	10%	0.117
EIF5A2	1.14	0.51	0.62	0.28	0.39	0.07	0.72	0.39	54%	0.333
ELP1	0.65		0.38		0.22		0.42	0.22	52%	0.043
ELP3	1.04	0.73	0.81	0.70	0.58	0.72	0.81	0.23	28%	0.283
EMG1	0.68	0.33	0.73	0.42	0.73	0.14	0.71	0.03	4%	0.003
FBL	0.49	0.23	0.67	0.67	1.50	0.27	0.89	0.54	61%	0.747
FTSJ1	0.45	0.26	0.26	0.18	0.23	0.19	0.31	0.12	39%	0.010
HSD17B10	0.58	0.53	0.26	0.09	0.17	0.04	0.34	0.21	62%	0.032
MEPCE	1.18	0.31	0.66	0.37	0.77	0.19	0.87	0.28	32%	0.505
MRM1	0.26	0.08	0.71	0.17	0.32	0.11	0.43	0.24	57%	0.055
MRM2	2.87		1.16		0.53		1.52	1.21	80%	0.533

MRM3	1.25	0.15	1.36	0.59	0.97	0.23	1.19	0.20	17%	0.238
MTO1	1.21	0.33	0.65	0.30	0.23	0.03	0.70	0.49	71%	0.399
NAT10	0.72	0.17	0.54	0.30	0.89	0.42	0.72	0.17	24%	0.105
NFS1	1.12	0.13	0.98	0.10	0.60	0.01	0.90	0.27	30%	0.582
NOP2	1.91	0.77	2.83	0.60	6.58	2.89	3.77	2.48	66%	0.192
NUDT16	0.95	0.27	0.39	0.28	0.30	0.02	0.55	0.35	65%	0.157
PCIF1	0.95	0.17	0.44	0.16	0.37	0.11	0.58	0.32	54%	0.150
QTRT1	1.89		0.78		0.56		1.07	0.71	66%	0.872
RNGTT	0.76	0.02	0.42	0.15	0.46	0.15	0.55	0.19	35%	0.053
RNMT	1.25	0.34	0.61	0.10	0.35	0.08	0.74	0.46	63%	0.431
RPUSD2	0.73		0.65		0.14		0.51	0.32	63%	0.119
RPUSD3	0.80	0.48	0.98	0.28	1.00	0.23	0.93	0.11	12%	0.364
RPUSD4	0.20		0.25		0.39		0.28	0.10	36%	0.006
TARBP1	0.33	0.24	0.30	0.27	0.35	0.29	0.33	0.02	8%	0.000
TFB1M	0.39	0.25	0.34	0.01	0.30	0.04	0.34	0.04	12%	0.001
TGS1	2.05	0.90	4.21	5.28	1.65	1.31	2.64	1.38	52%	0.176
TRIT1	0.19		0.52		0.14		0.28	0.20	72%	0.026
TRMT1	0.67	0.81	0.66	0.69	0.19	0.19	0.51	0.27	54%	0.090
TRMT10C	0.76	0.59	0.64	0.12	0.51	0.22	0.64	0.12	19%	0.036
TRMT11	0.47		0.37		0.92		0.58	0.30	51%	0.135
TRMT112	0.35		0.42		0.54		0.44	0.09	22%	0.009
TRMT5	2.35		0.71		0.45		1.17	1.03	88%	0.802
TRUB2	0.05	0.06	0.34	0.40	0.73	1.00	0.37	0.34	91%	0.087
TYW3	1.24		0.75		0.63		0.87	0.32	37%	0.561
WDR4	0.35		0.27		0.45		0.36	0.09	26%	0.007
YBX1	0.51	0.17	0.59	0.42	0.78	0.09	0.62	0.14	22%	0.042
RBMX	1.19	0.28	0.96	0.12	1.45	0.18	1.20	0.24	20%	0.289
ELAVL1	0.98	0.25	0.93	0.28	1.02	0.12	0.98	0.04	4%	0.422
SND1	0.40	0.07	0.39	0.11	0.40	0.05	0.40	0.00	0%	0.000

FMR1	0.20	0.05	0.15	0.01	0.06	0.03	0.13	0.07	54%	0.002
LRPPRC	0.44	0.39	0.63	0.10	0.47	0.06	0.51	0.10	20%	0.015
PUS7L	1.19	0.76	0.33	0.43	0.31	0.19	0.61	0.50	83%	0.310
ALKBH2	0.33	0.29	0.15	0.22	0.17	0.07	0.21	0.10	48%	0.006
ALKBH3	1.69	1.08	0.72	0.21	0.51	0.29	0.97	0.63	65%	0.950
ALKBH4	0.96	0.18	0.59	0.34	0.47	0.30	0.68	0.26	38%	0.159
ALKBH5	1.93	0.14	1.01	0.49	1.90	0.52	1.61	0.52	32%	0.178
FTO	0.71		2.31		1.46		1.49	0.80	53%	0.396
YTHDF1	0.29	0.42	0.38	0.51	0.33	0.29	0.33	0.04	12%	0.001
YTHDF2	0.56	0.24	0.58	0.22	0.48	0.14	0.54	0.05	10%	0.005
YTHDF3	0.69	0.15	0.71	0.20	0.56	0.12	0.66	0.08	12%	0.018
YTHDC1	1.80	0.84	0.68	0.11	1.29	0.45	1.26	0.56	45%	0.512
YTHDC2	3.00	3.31	2.07	1.80	1.86	1.96	2.31	0.60	26%	0.064
METTL3	1.28	0.05	0.61	0.49	0.47	0.32	0.79	0.43	55%	0.482
METTL14	0.96		0.20		0.31		0.49	0.41	84%	0.163
METTL1	2.16		0.78		0.28		1.07	0.97	91%	0.909
METTL16	1.53	0.02	0.82	0.07	0.41	0.01	0.92	0.57	62%	0.831
METTL2B	0.53	0.33	0.85	0.55	0.17	0.00	0.52	0.34	66%	0.135
NSUN2	0.59	0.38	0.91	0.37	0.58	0.28	0.69	0.19	28%	0.109
NSUN5	0.76	0.52	0.88	0.32	0.77	0.41	0.80	0.07	8%	0.036
NSUN6	1.02	0.78	0.70	0.66	0.32	0.15	0.68	0.35	52%	0.255
DNMT1	0.63	0.12	0.51	0.19	0.45	0.17	0.53	0.09	17%	0.012
TRMT61A	0.36	0.10	0.56	0.17	0.44	0.02	0.45	0.10	22%	0.011
TRMT61B	2.98		2.47		4.14		3.20	0.86	27%	0.047
TRMT6	0.36	0.24	0.75	0.50	0.36	0.17	0.49	0.22	46%	0.059
PUS7	0.79	0.29	0.60	0.23	0.25	0.06	0.55	0.28	51%	0.105
IGF2BP1	0.67	0.46	1.02	0.86	0.83	0.31	0.84	0.17	21%	0.253
IGF2BP2	0.50	0.27	0.63	0.31	1.22	0.97	0.78	0.38	49%	0.428
IGF2BP3	1.06	1.07	1.20	0.67	0.90	0.44	1.05	0.15	14%	0.585

WTAP	1.79	0.60	0.93	0.12	1.11	0.14	1.28	0.45	36%	0.401
VIRMA	1.11	0.01	0.61	0.07	0.51	0.08	0.74	0.32	43%	0.297
RBM15B	2.04	0.25	1.29	0.09	2.47	1.05	1.93	0.60	31%	0.114
RBM15	1.41	0.41	0.88	0.01	0.97	0.45	1.08	0.28	26%	0.658
ZC3H13	3.39	2.56	1.43	0.43	3.59	2.91	2.81	1.19	42%	0.120
EIF3A	0.43	0.00	0.40	0.16	0.30	0.07	0.38	0.07	17%	0.004
EIF3B	0.39	0.20	0.29	0.20	0.37	0.17	0.35	0.05	15%	0.002
HNRNPA2B1	1.12	0.48	1.02	0.46	1.10	0.15	1.08	0.05	5%	0.116
HNRNPC	1.02	0.33	1.56	1.08	1.01	0.15	1.20	0.32	26%	0.391
PUS1	0.67	0.39	0.73	0.19	0.41	0.12	0.60	0.17	28%	0.057
TRUB1	1.01	0.03	0.73	0.03	0.53	0.14	0.76	0.24	32%	0.219
DKC1	0.88	0.09	0.53	0.10	0.79	0.38	0.73	0.18	24%	0.122
NSUN4	0.88	0.59	0.84	0.54	0.76	0.32	0.83	0.06	8%	0.042
TRDMT1	0.72		0.71		0.99		0.80	0.16	20%	0.165
ALYREF	0.83	0.44	0.69	0.43	0.95	0.58	0.82	0.13	16%	0.143
METTL8	2.23		1.64		0.66		1.51	0.79	53%	0.382
PUS3	0.52		0.31		0.11		0.31	0.21	66%	0.029
ZCCHC4	1.11	1.39	0.96	0.30	0.63	0.39	0.90	0.25	27%	0.547
CBLL1	1.25	0.68	0.68	0.05	0.87	0.19	0.93	0.29	31%	0.724
CIAO1	0.43		0.45		0.53		0.47	0.05	12%	0.003
DIS3L2	1.38		0.53		0.28		0.73	0.58	79%	0.506
FTSJ3	0.61	0.56	0.54	0.45	0.84	0.68	0.66	0.16	23%	0.064
ISCU	1.10	0.60	0.42	0.32	0.22	0.22	0.58	0.46	79%	0.255
LAGE3	1.59		0.76		0.35		0.90	0.63	70%	0.813
METTL15	0.46	0.00	0.24	0.12	0.31	0.04	0.34	0.12	35%	0.010
METTL17	0.68	0.82	0.38	0.47	0.33	0.30	0.46	0.19	41%	0.039
METTL5	0.81	0.06	0.31	0.28	0.37	0.22	0.50	0.27	54%	0.085
MPST	0.44	0.45	0.23	0.21	0.21	0.29	0.29	0.13	45%	0.011
SNU13	0.75	0.36	0.58	0.17	0.60	0.17	0.64	0.09	14%	0.021

NUBP1	1.03	1.06	0.59	0.54	0.35	0.09	0.65	0.34	53%	0.224
OSGEP	1.27	0.61	0.68	0.22	0.37	0.27	0.77	0.45	59%	0.479
PRRC2A	0.28	0.22	0.43	0.02	0.55	0.09	0.42	0.13	32%	0.017
TFB2M	1.07		0.81		0.96		0.95	0.13	14%	0.549
TP53RK	1.18	0.78	0.63	0.41	0.23	0.14	0.68	0.48	70%	0.367
TPRKB	0.06		0.39		0.41		0.29	0.20	68%	0.024
TUT7	4.07		2.69		3.22		3.32	0.70	21%	0.029
WDR6	0.61		0.36		0.23		0.40	0.20	49%	0.034
YRDC	0.11	0.15	0.14	0.15	0.06	0.05	0.10	0.04	38%	0.001