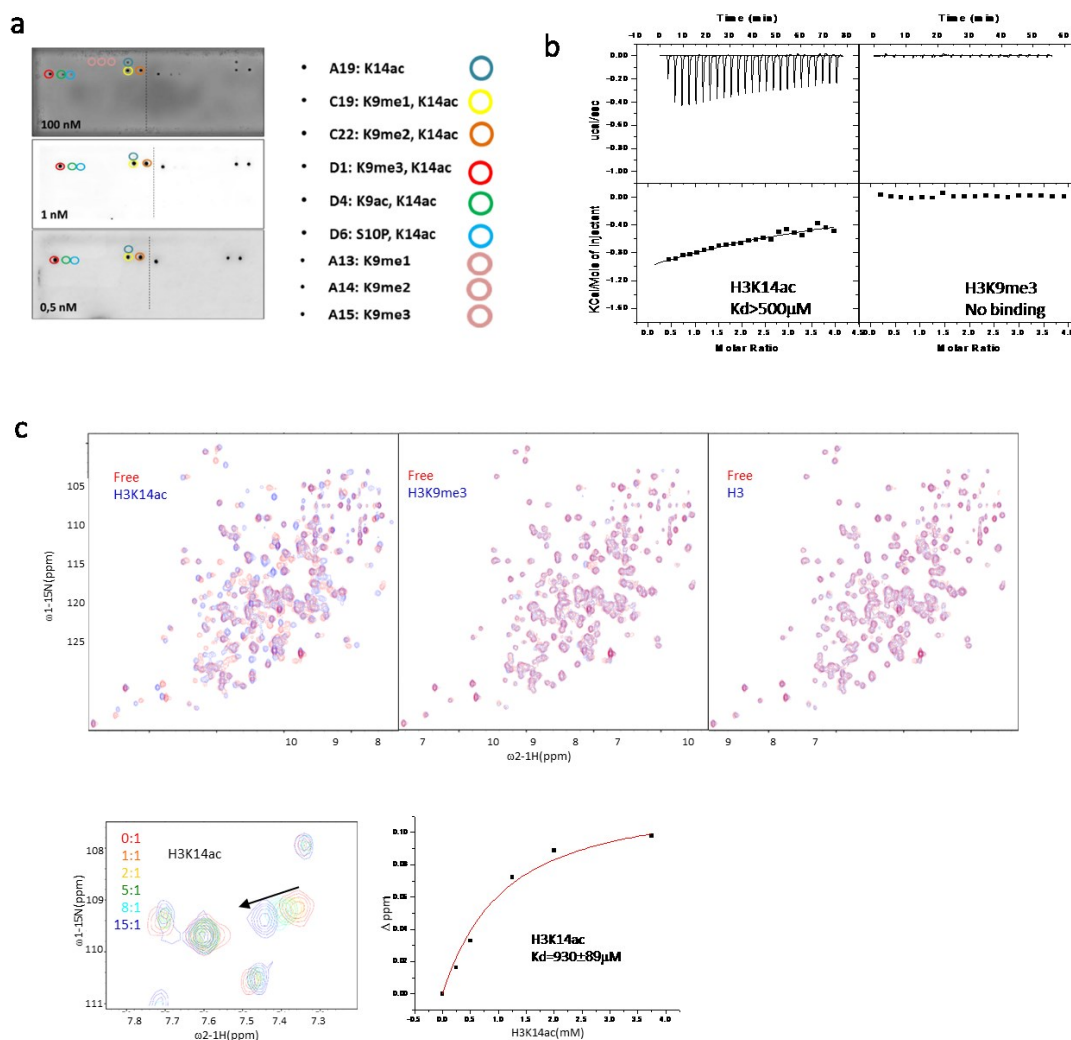
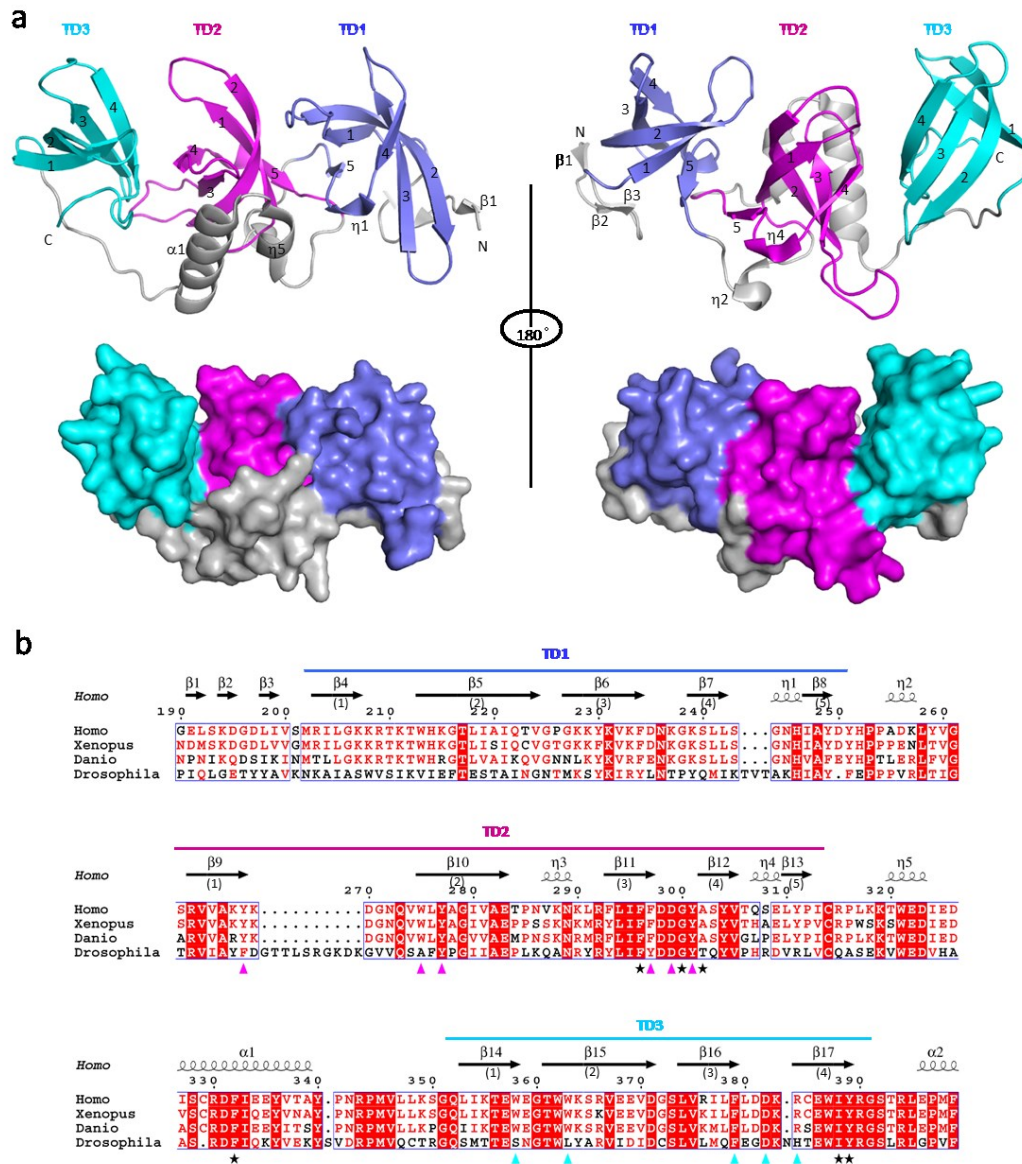


Supplementary figures

Supplementary Figure 1: Peptide binding of 3TD. (a) Titration of 3TD binding to peptide arrays. Note the specific binding to H3K9me1/2/3-K14ac double modified peptides. Binding to monomodified H3K14ac was observed only at the highest 3TD concentration (100 nM). (b) ITC analysis of 3TD binding to single modified H3 tail peptides. Data are summarized in Fig. 2b. (c) NMR chemical shift perturbation experiments carried out to detect potentially weak binding of 3TD to H3K14ac, H3K9me3 and unmodified H3. Weak binding of H3K14ac could be detected and the binding constant determined, but no detectable binding of H3K9me3 and unmodified H3 was observed. Panel a relates to Fig. 1, panels b and c to Fig. 2.

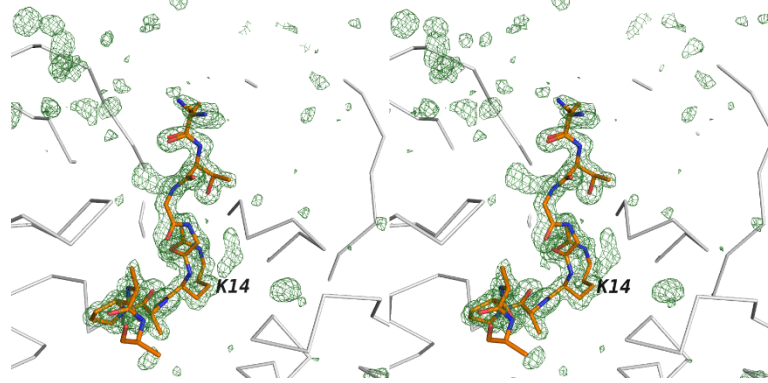


Supplementary Figure 2: Structural analysis of 3TD. (a) Overall arrangement of the individual Tudor domains in 3TD (apostructure: 3DLM). (b) Sequence alignment of 3TD regions in different species. Stars indicate residues interacting with K14ac, triangles indicate residues forming the aromatic cage in TD2 and TD3. (c) View of the incomplete aromatic pocket in TD1. This figure relates to Figs. 1a, 3 and 4.

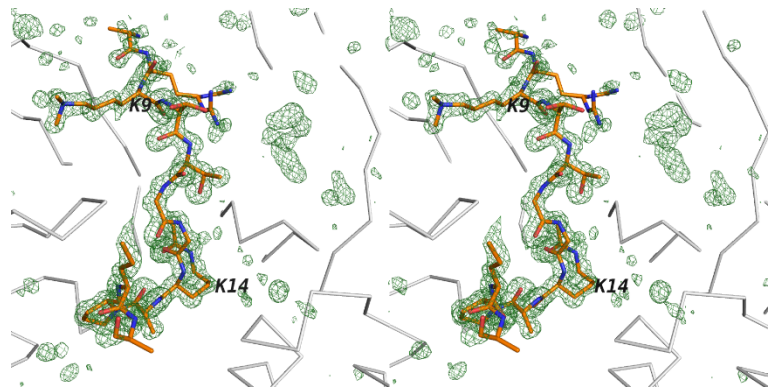


Supplementary Figure 3: Details of the structures of 3TD and W358A interacting with histone peptides. mFo-DFc omit maps for the peptide ligands were calculated with PHENIX and are displayed as a green mesh at level “3”. This figure relates to Fig. 3 and 4.

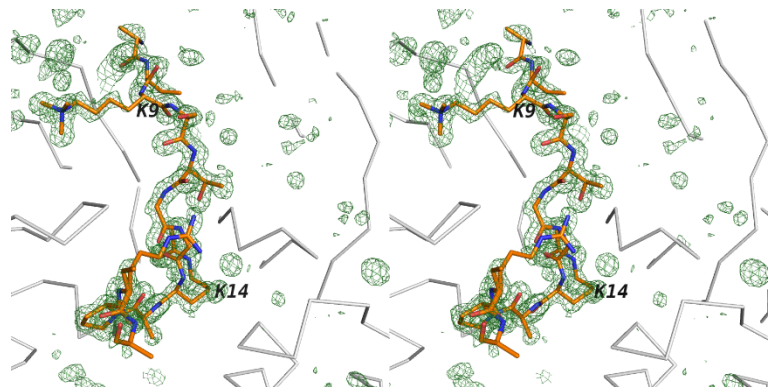
3TD-H3K9me0K14ac



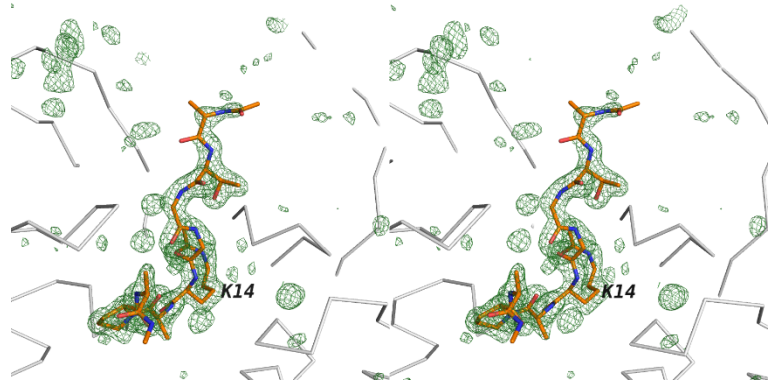
3TD-H3K9me2K14ac



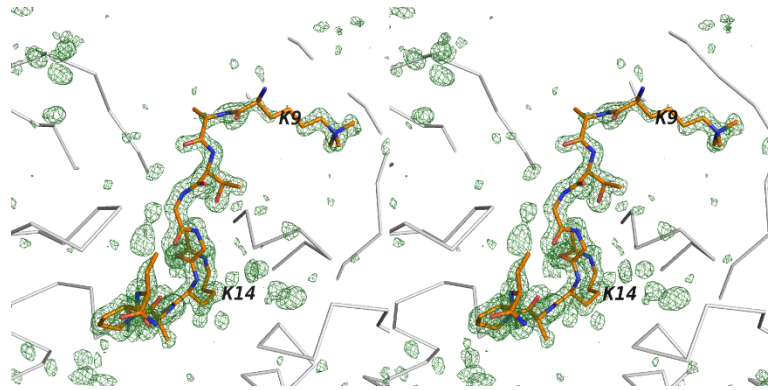
3TD-H3K9me3K14ac



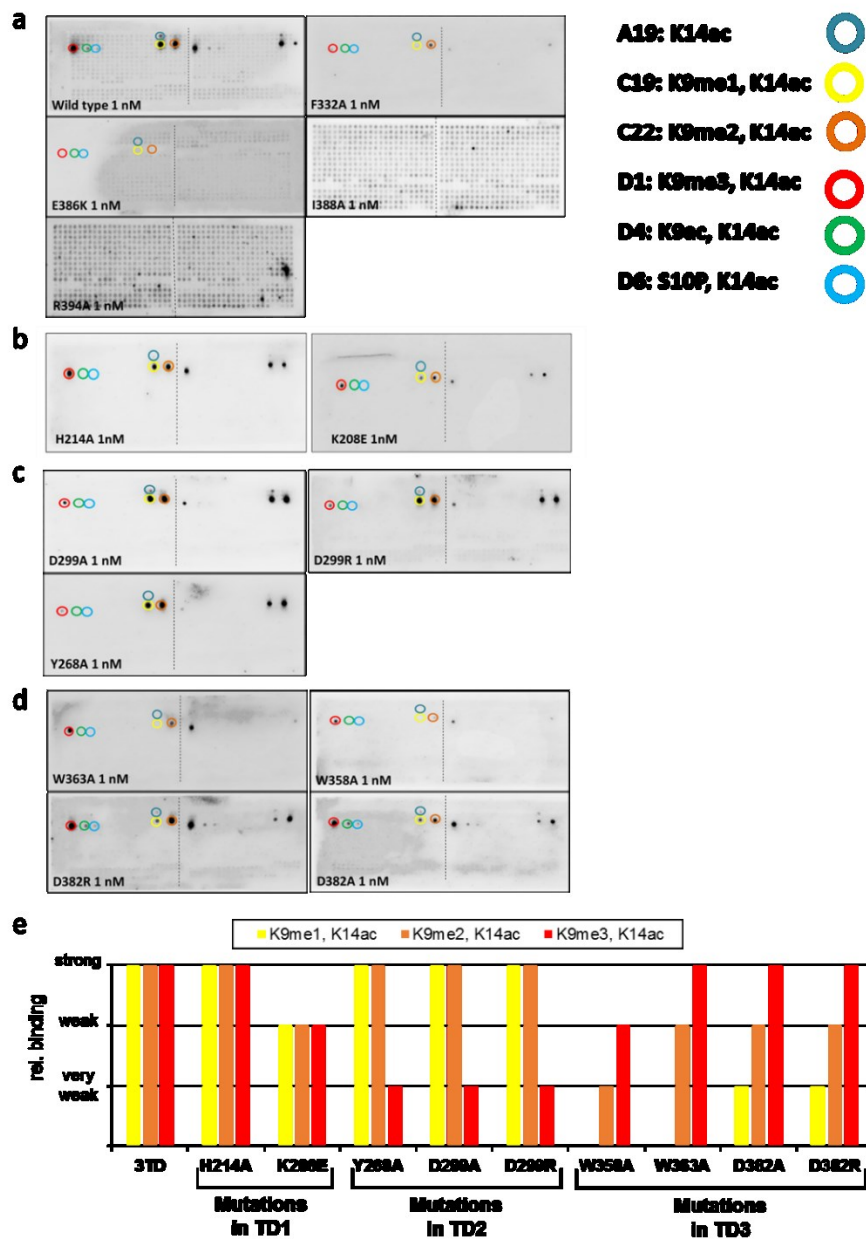
3TD(W358A)-
H3K9me2K14ac



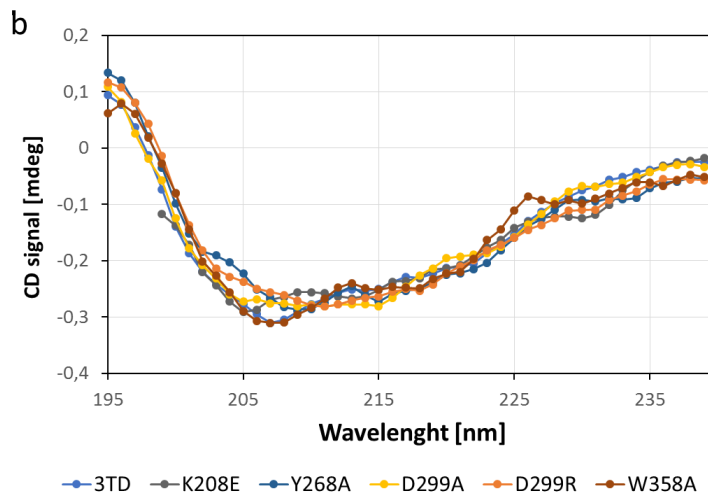
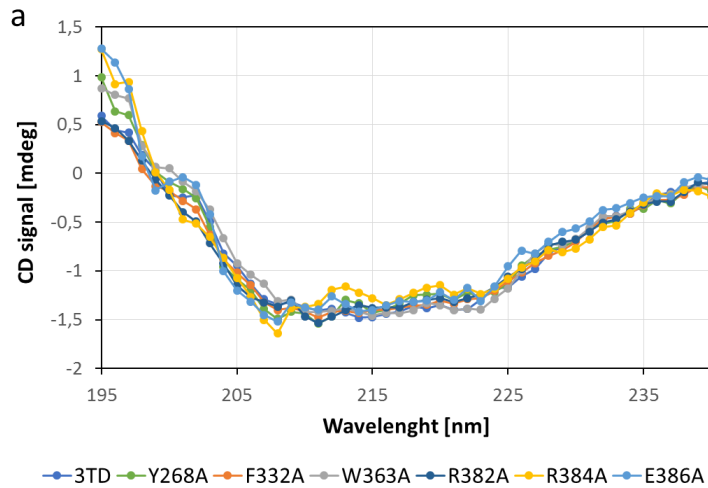
3TD(W358A)-
H3K9me3K14ac



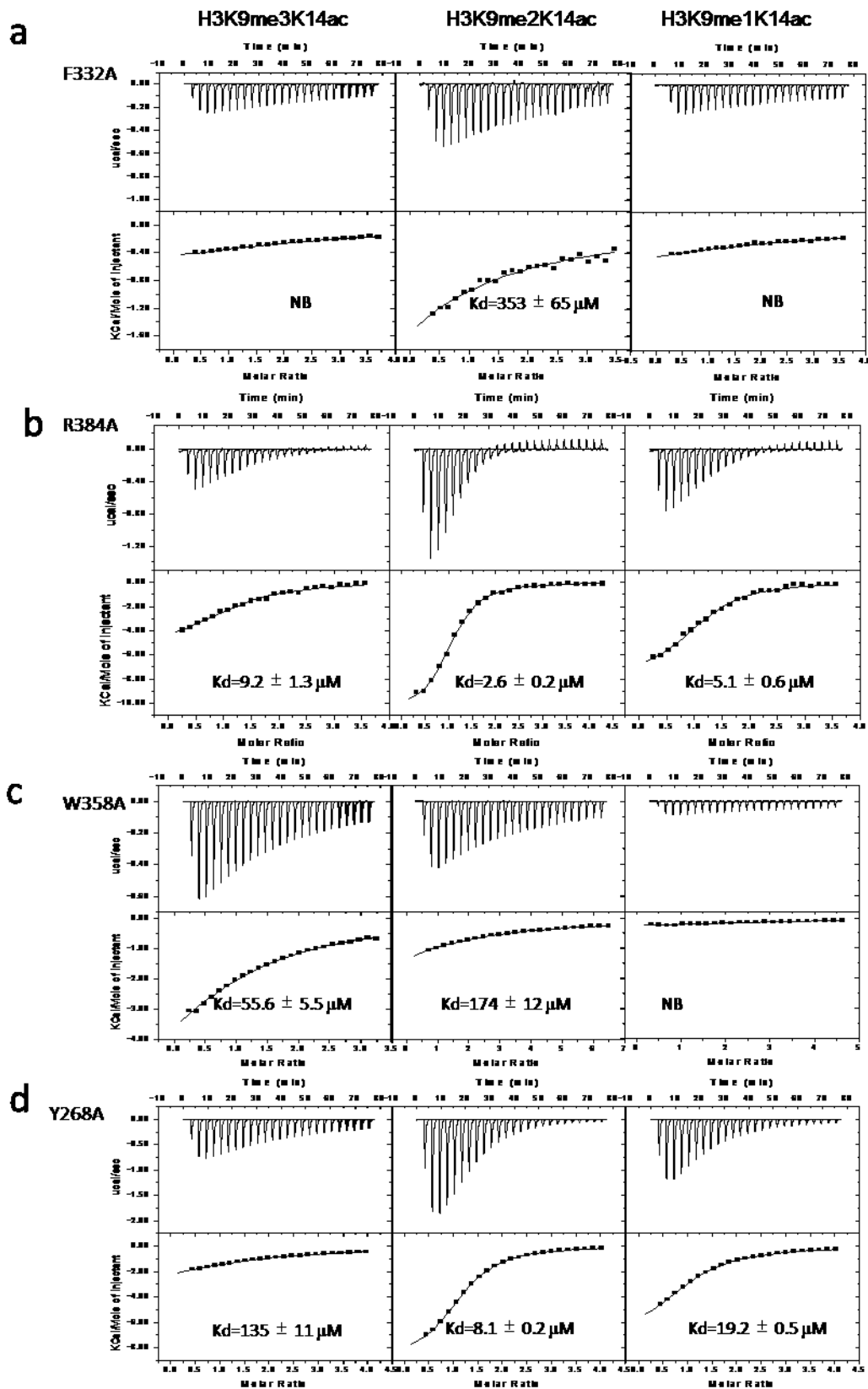
Supplementary Figure 4: Modified histone peptide array binding experiments with 3TD and 3TD mutants. (a) Mutations at the acetyl binding pocket. (b) Mutations in the TD1 domain. (c) Mutations at the methyllysine binding pockets in TD2. (d) Mutations at the methyllysine binding pockets in TD3. (e) Summary of the results of mutations in TD1, TD2 and TD3 illustrating the complementary effects of mutations in TD2 and TD3 on the specificity of binding to K9 methylated peptides. Data for Y268A and W358A are shown in Fig. 1 and were included for comparison. Correct folding of purified proteins was verified by CD spectroscopy (Supplementary Fig. 5). This figure relates to Fig. 1. Full annotations of all spots in the peptide arrays are given in Supplementary Table 2.



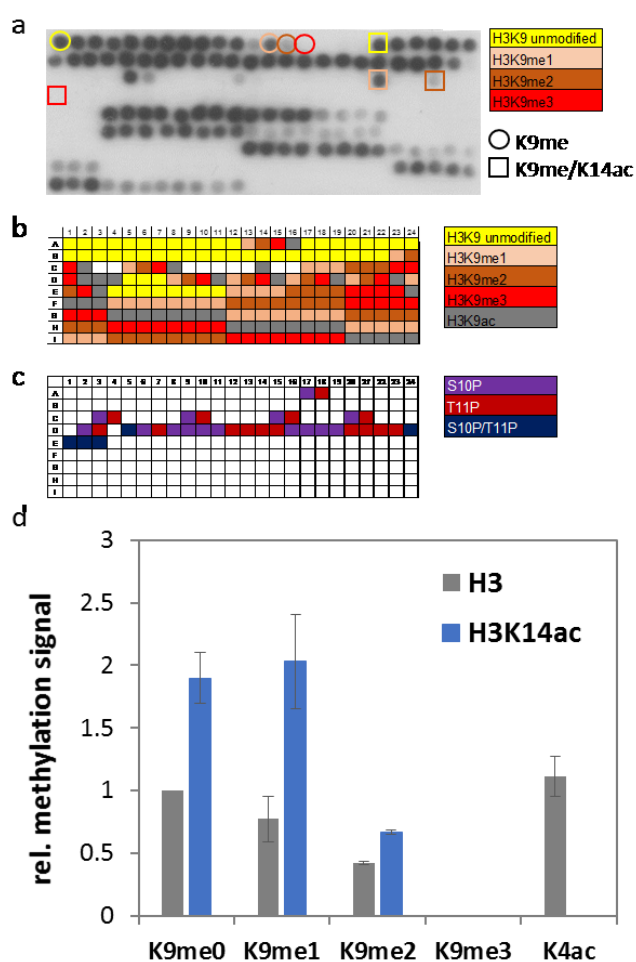
Supplementary Figure 5: Circular dichroism spectra of 3TD and representative 3TD mutants. Proteins were purified as GST fusions and the CD spectra determined at protein concentrations of 10 μ M (panel **a**) and 2 μ M (panel **b**). All CD spectra were superimposable within the level of noise indicating a similar folding of wildtype 3TD and all mutant proteins. This figure relates to Figs. 1 and 2 and Supplementary Figs. 4 and 6.



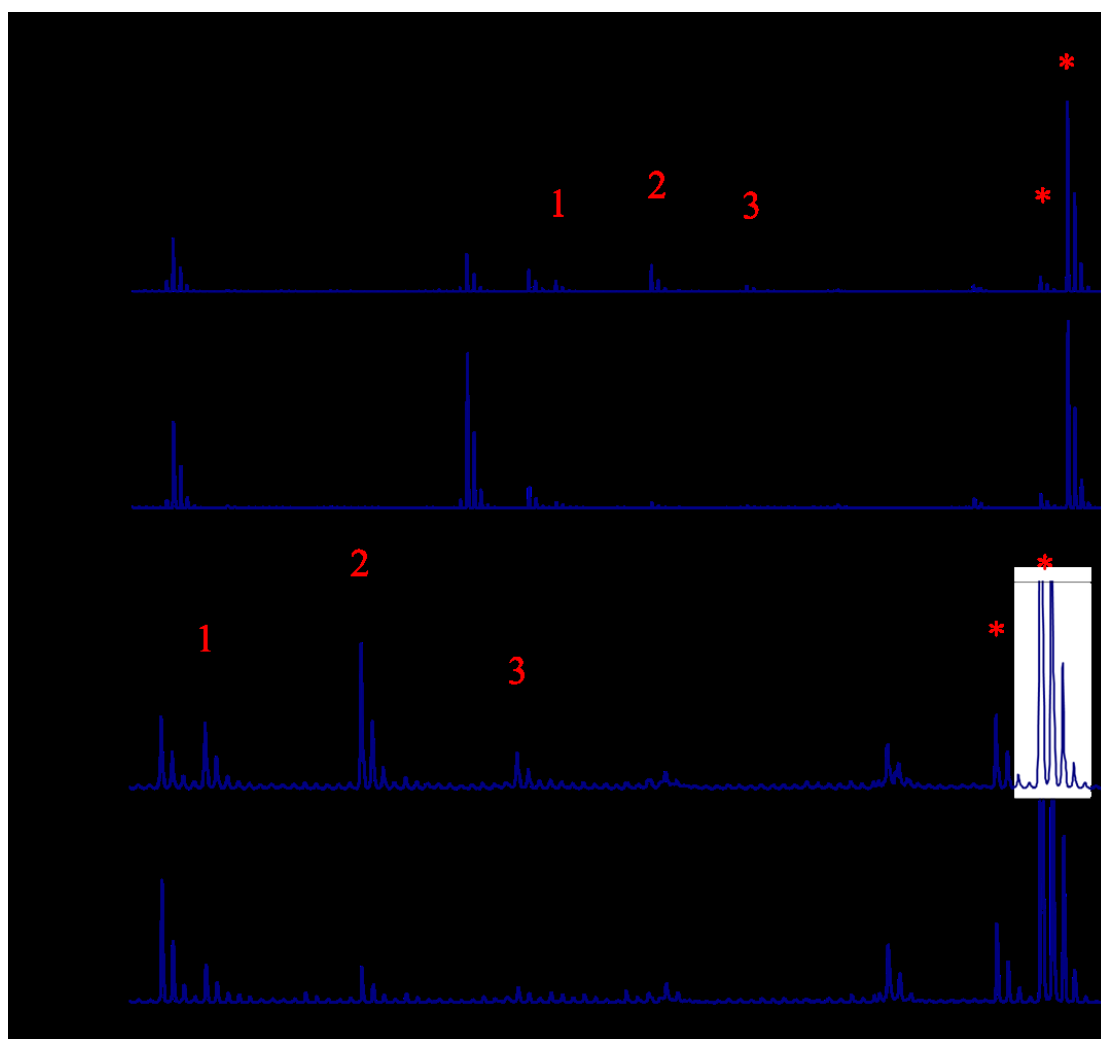
Supplementary Figure 6: ITC peptide binding experiment with 3TD mutants. Data are summarized in Fig. 2b. This figure relates to Fig. 2.

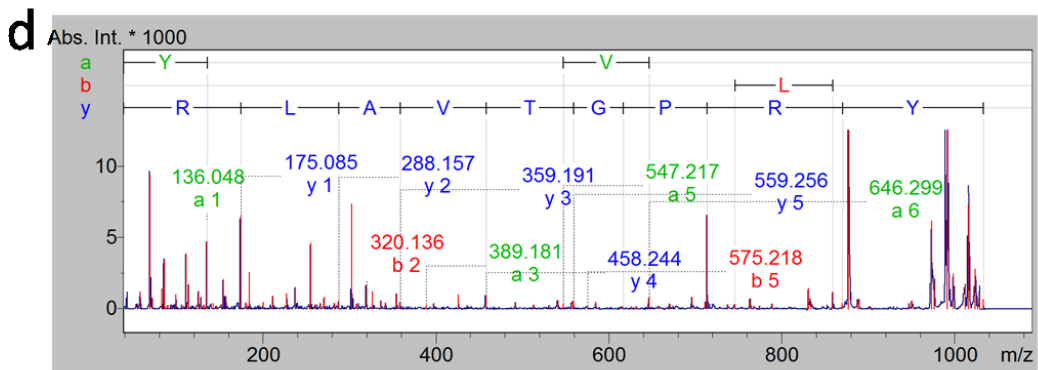
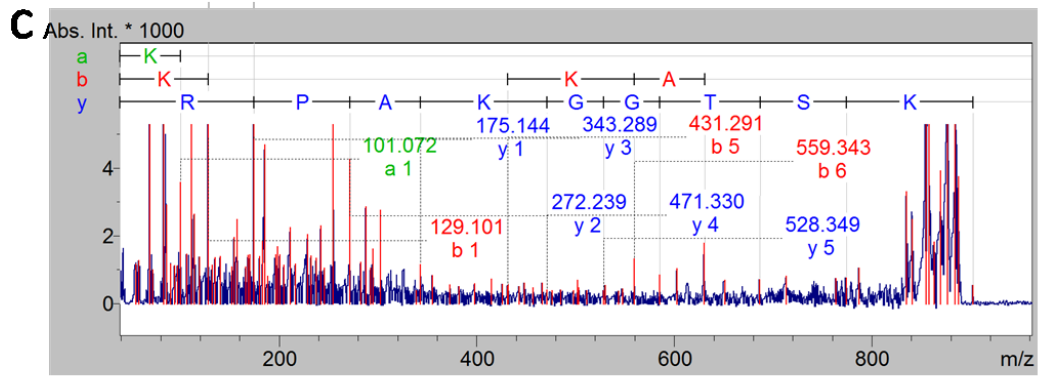


Supplementary Figure 7: Methylation of modified histone peptide arrays by recombinant SETDB1. The arrays containing covalently bound histone peptides in various modified forms were incubated with SETDB1 (190-1291) purified from Sf9 cells in the presence of radioactively labeled AdoMet and the transfer of radioactivity to the peptide spots was detected by autoradiography. The arrays contain two copies of 384 individual Histone tail peptides in different methylation states, including 219 H3 1-19 peptides, methylation of which was analyzed here. (a) Example image of the methylated arrays. (b) Annotation of the spots carrying K9 unmodified, K9me1, K9me2, K9me3, and K9ac peptides. (c) Annotation of the spots carrying S10ph, T11ph and S10ph/T11ph peptides, showing that S10ph and T11ph inhibit SETDB1. (d) Quantitative analysis of the methylation of K9me0, K9me1 and K9me2 spots with or without K14ac based on 4 experiments (two biological repeats each with two technical repeats, error bars indicate the SD). Peptides containing H3K9me3 and H3K9ac are not methylated. Acetylation of K4 (spot A9) did not influence K9 methylation. The array does not contain a peptide carrying K4 and K14 acetylation. The full annotations of all spots are given in Supplementary Table 2. This figure relates to Fig. 8b.



Supplementary Figure 8: MALDI MS analysis of the 3TD mononucleosomal pull-down. (a) Example of mass spectra shown in the range of 895-1035 Da. The peaks of the H3 (9-17) K9me1/2/3-K14ac peptides are annotated as 1, 2, and 3 in the pull-down image, the unrelated, unmodified H3 peptides used for internal normalization of input and pull-down are highlighted by asterisks. The analysis shows a strong enrichment of the K9me1/2/3-K14ac peptides in the 3TD pull-down as compared to the input. (b) Same as in panel a, but shown at enhanced x- and y-axis scale. (c) MS/MS analysis confirming the identity of the 901.521 Da peptide to be unmodified H3 (9-17). Fragment ions of the a, b, and y series are indicated in green, red and blue. (d) MS/MS analysis confirming the identity of the 1032.595 Da peptide to be unmodified H3 (41-49). (e) Compilation of all peptides identified in this study. The MS/MS analysis confirming the identity of the H3 (9-17) K9me2-K14ac peptide is shown in Fig. 5e. Peaks corresponding to the monomethylated (915.537 Da), dimethylated (929.552 Da) and trimethylated or acetylated (943.568/943.532 Da) peptides were not detected, neither in input nor pull-down. This figure relates to Fig. 5d and 5e.

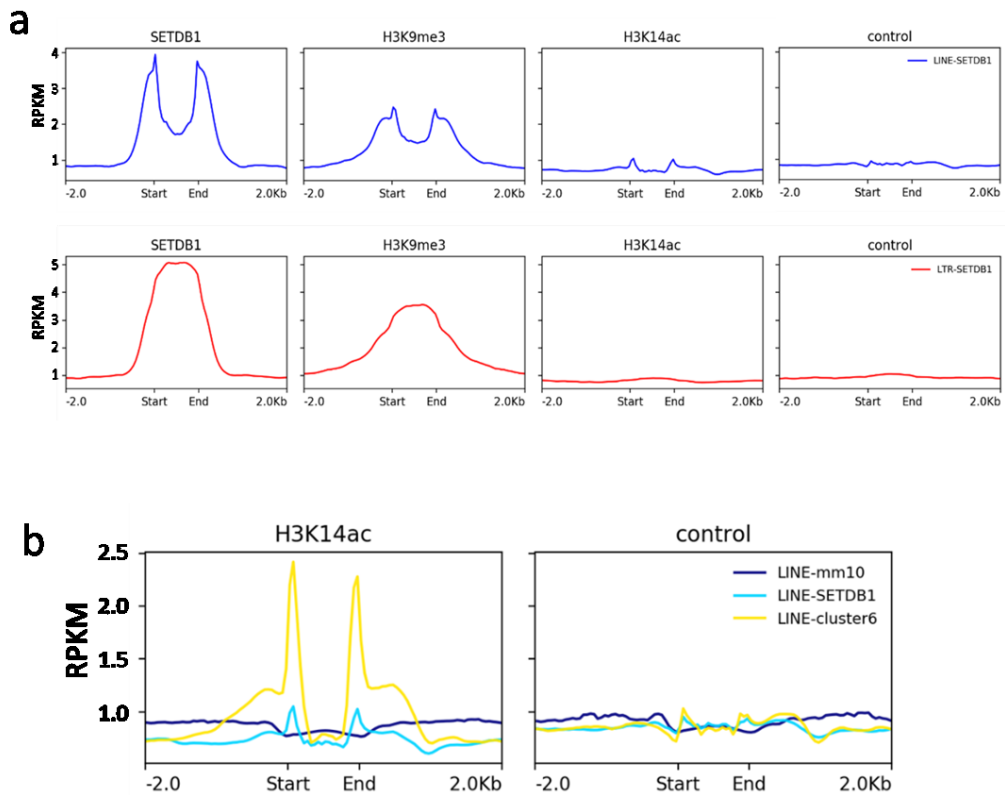




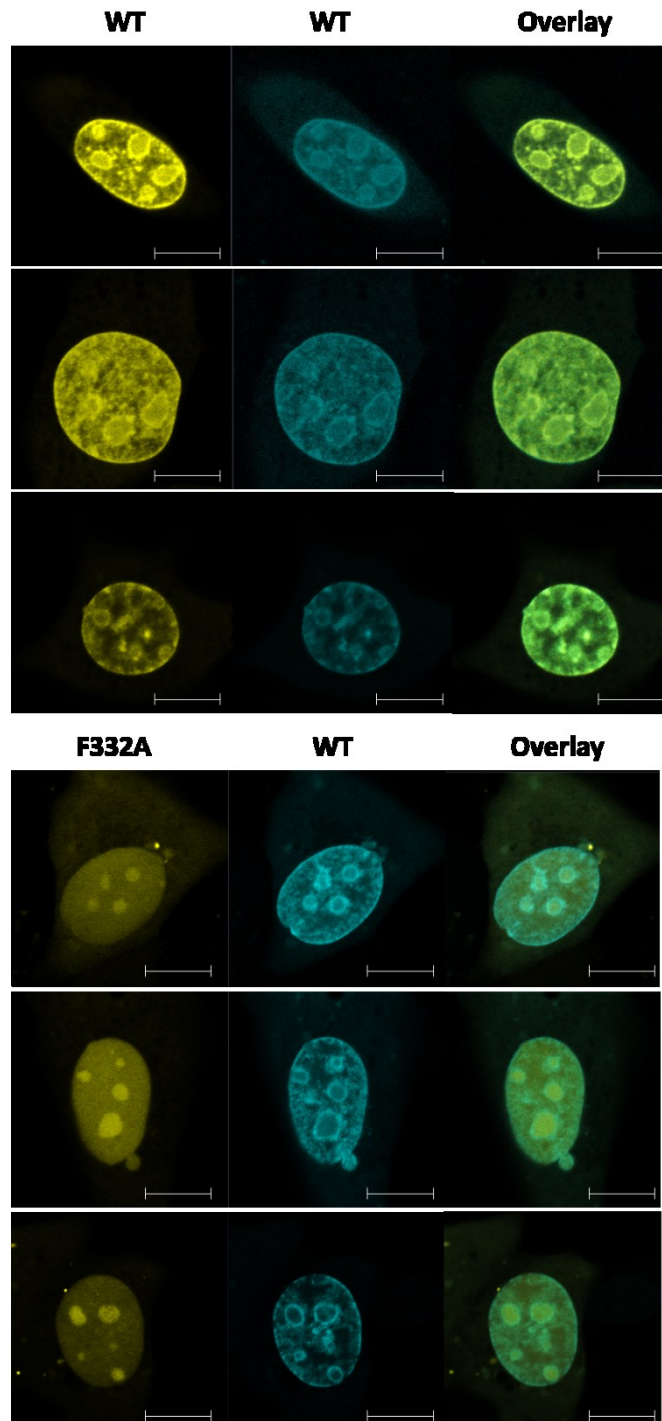
e

<i>Obs. mass [Da]</i>	<i>Peptide</i>	<i>Sequence</i>	<i>Theo. mass (MH⁺) [Da]</i>
901.509	H3(9-17)	KSTGGKAPR	901.521
957.548	H3(9-17)K9me1/K14ac	KSTGGKAPR	957.548
971.565	H3(9-17)K9me2/K14ac	KSTGGKAPR	971.563
985.573	H3(9-17)K9me3/K14ac	KSTGGKAPR	958.579
1028.612	H3(65-72)	LPFQRLVR	1028.636
1032.592	H3(41-49)	YRPGTVALR	1032.595

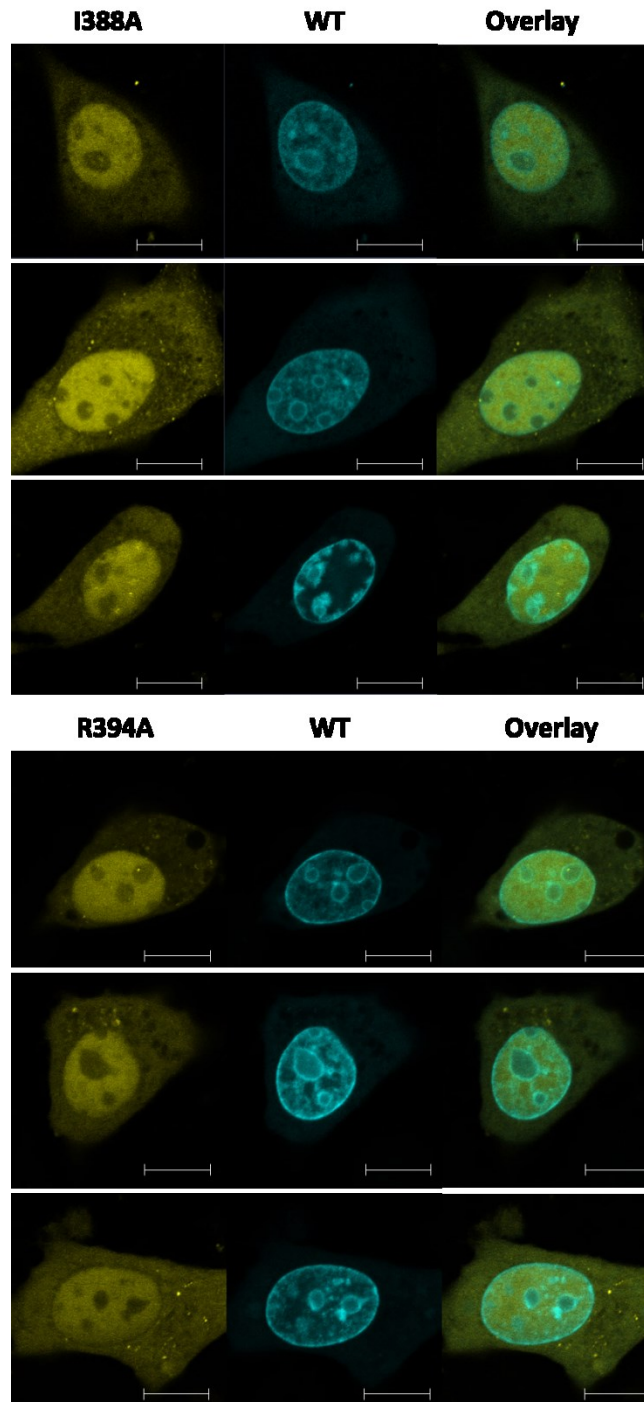
Supplementary Figure 9: Additional meta-profiles of SETDB1, H3K9me3, H3K14ac and control read density over LINE and LTR repeats. (a) Meta-profiles of SETDB1, H3K9me3, H3K14ac, and control read density on SETDB1 overlapping LINE (LINE-SETDB1, blue) and LTR elements (LTR-SETDB1, red). (b) Meta-profiles of H3K14ac and control density on all LINE elements (LINE-mm10, blue), SETDB1 overlapping LINEs (LINE-SETDB1, cyan) and LINEs from cluster 6 (LINE-cluster6, yellow). This figure relates to Fig. 6.



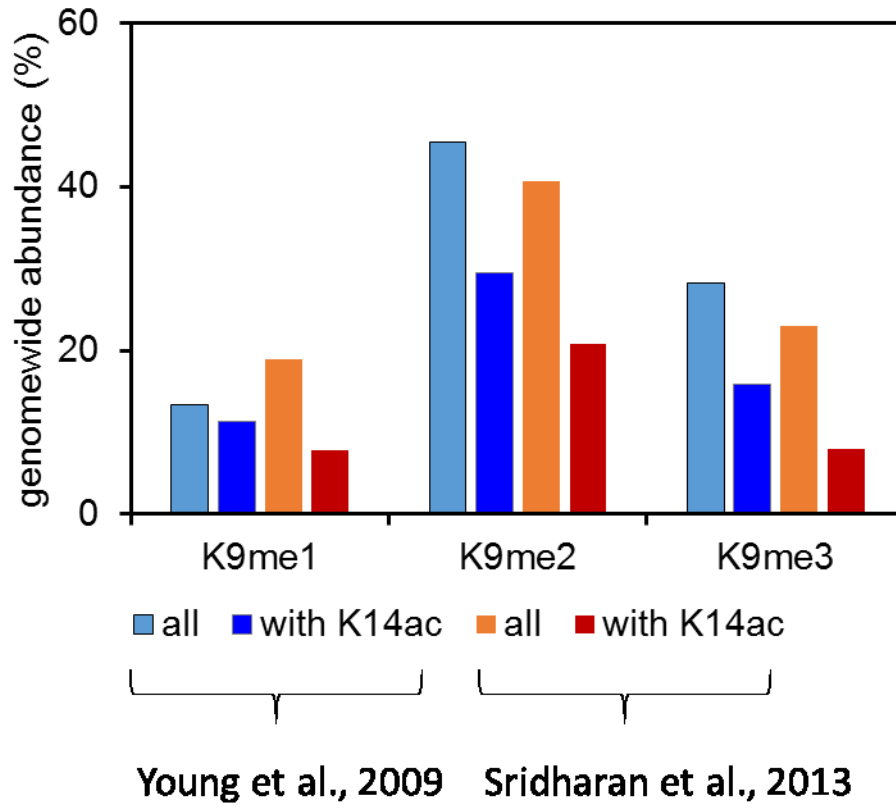
Supplementary Figure 10: Additional examples of the localization of wildtype and F332A mutant 3TD in mouse cells. 3TD and F332A were co-expressed as fusion constructs with mCerulean (shown in cyan) or mVenus (shown in yellow) in mouse NIH3T3 cells. While the wt/wt controls show a perfect overlay of the two fluorescence signals, all cells expression wt/F332A combinations showed clear differences between the localization of both fluorophores. Scale bar: 10 μ m. Statistics for this experiment are provided in Fig. 7b. This figure relates to Fig. 7.



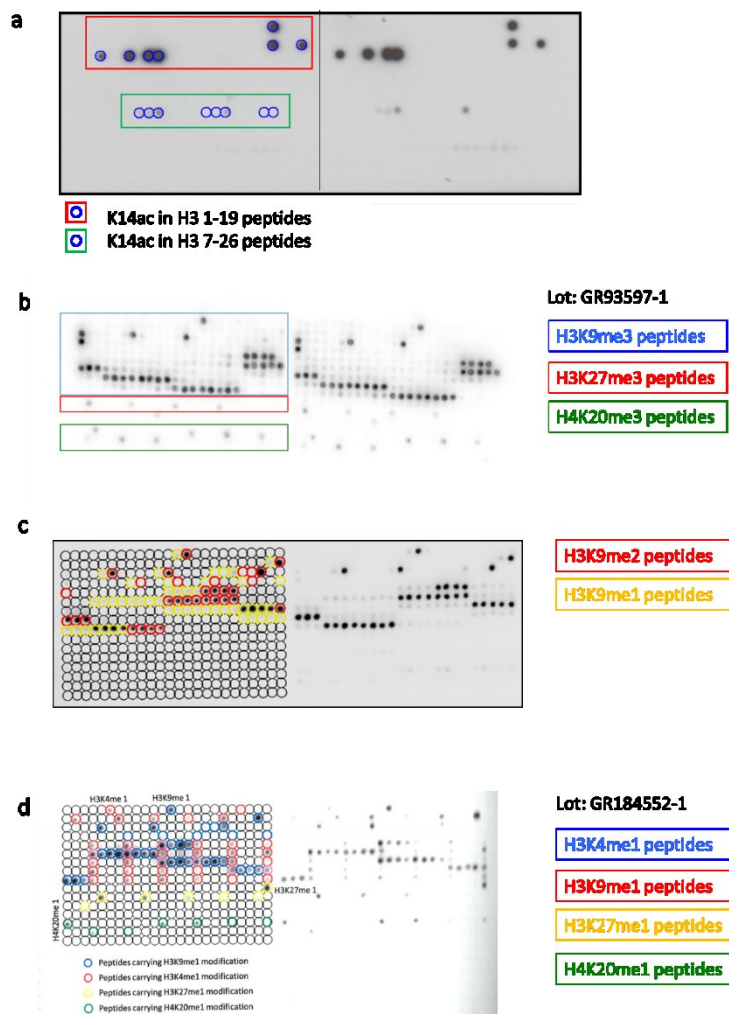
Supplementary Figure 11: Additional examples of the localization of wildtype and I388A and R394A mutants in mouse cells. 3TD and mutants were co-expressed as fusion constructs with mCerulean (3TD wildtype, shown in cyan) or mVenus (mutants, shown in yellow) in mouse NIH3T3 cells. All cells expression wt/mutant combinations showed clear differences between the localization of both fluorophores. Scale bar: 10 μ m. Statistics for this experiment are provided in Fig. 7b. This figure relates to Fig. 7.



Supplementary Figure 12: Results of published MS/MS studies of histones isolated from different human cells. These data document the co-occurrence of H3K14ac with H3K9 methylation^{1,2}.



Supplementary Figure 13: Antibody validation by specificity analysis using modified histone peptide array binding. The modified histone tail peptide arrays³ contains two copies of 384 individual Histone tail peptides in different methylation states. Annotations of all spots are provided in Supplementary Table 2. (a) Specificity analysis of the Millipore MABE351 H3K14ac antibody. The positions of H3K14ac peptides are indicated. The antibody is highly specific for H3K14ac. (b) Specificity analysis of the Abcam ab8898 H3K9me3 antibody. The positions of different trimethylated peptide spots are indicated. The antibody is highly specific for H3K9me3. (c) Specificity analysis of the Abcam ab1220 H3K9me2 antibody. The positions of different H3K9 methylated peptide spots are indicated. The antibody is highly specific for H3K9me3. (d) Specificity analysis of the Abcam ab8896 H3K9me1 antibody. The positions of different monomethylated peptide spots are indicated. The antibody shows good specificity for H3K9me1. The validation of the anti-H3K4me3 (Abcam ab8580) antibody used in this study is provided in⁴. This figure relates to Fig. 5.



Supplementary Figure 14: Uncropped pictures of the gel images shown in Fig. 5.

Fig. 5a

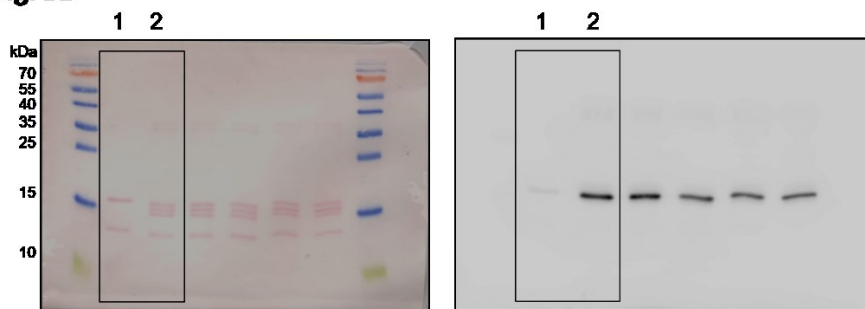


Fig. 5b

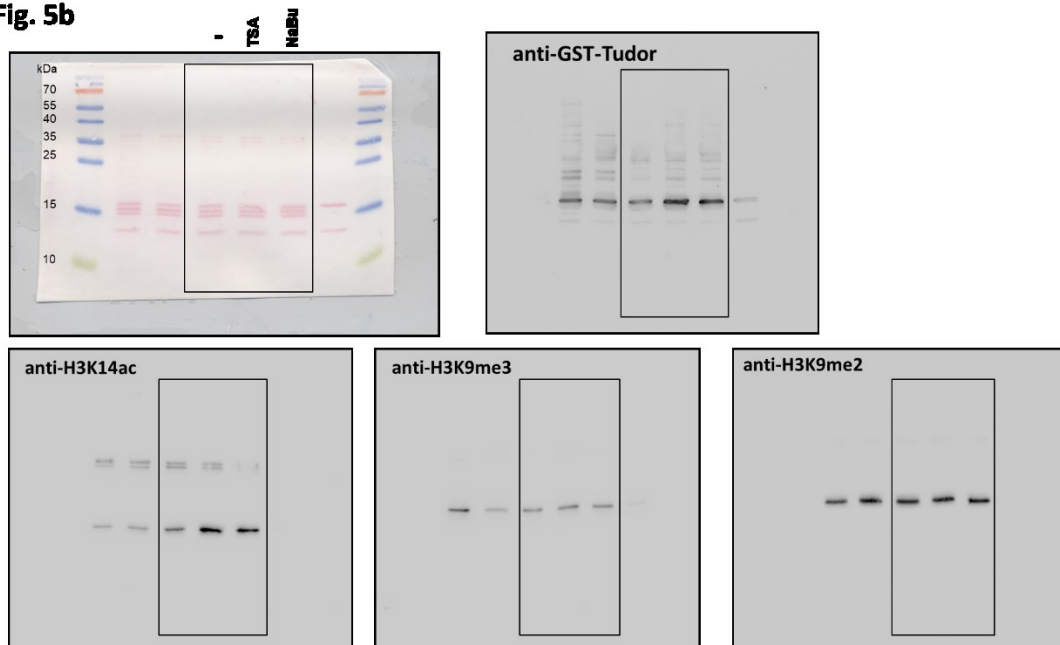
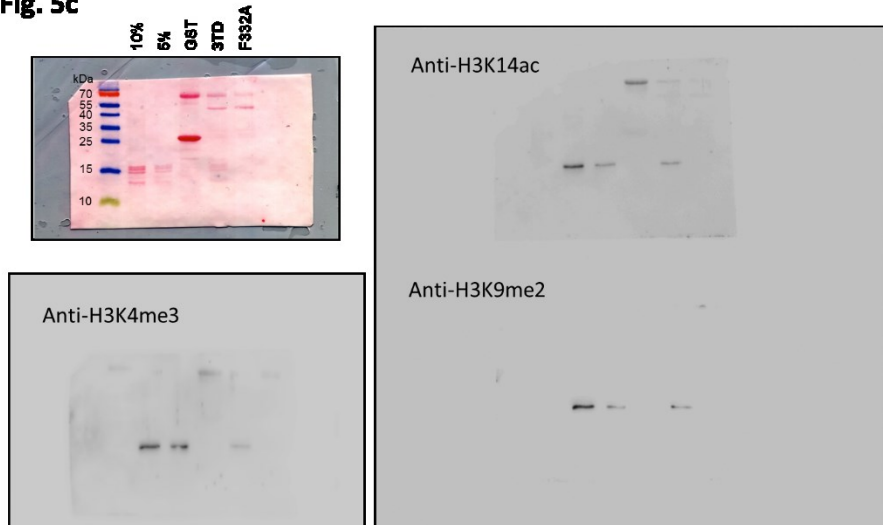


Fig. 5c



Supplementary Notes

Supplementary Note 1: Crystal structure determination. Diffraction data were collected at APS beam line 19-ID (Structural Biology Center), reduced with XDS⁵ and merged with AIMLESS⁶, unless otherwise noted. Crystals were kept under cryogenic conditions (100K) during diffraction experiments. Synchrotron sources were tuned to wavelengths between 0.96 and 0.98 Å. For 3TD in complex with K9me3/K14ac, the structure was solved by molecular replacement with SETDB1 coordinates from PDB entry 3DLM (Amaya et al., 2008) and the program PHASER⁷. For 3TD in complex with K9me2/K14ac, preliminary SETDB1 coordinates from the K9me3/K14ac complex were used as a starting model. Difference electron density in the TD2 aromatic cage of this model vaguely resembles a HEPES molecule. For the 3TD in complex with K9me0K14ac, diffraction data were collected at APS beam line 23-ID-B (GM/CA). Preliminary SETDB1 coordinates from the K9me3/K14ac complex were used as a starting model. PHENIX.REFINE⁸ was used for automated water peak picking. For the 3TD-W358A in complex with K9me2/K14ac, diffraction data were collected on a copper rotating anode source. Preliminary SETDB1 coordinates from the wildtype K9me2/K14ac complex were used as a starting model. For early refinement steps, diffraction data were reduced with HKL-3000⁹. PHENIX.REFINE was used for automated water peak picking. For the 3TD-W358A in complex with K9me3/K14ac, the structure was solved by molecular replacement with PHASER, using rotating anode data of an additional crystal and atomic coordinates from the wildtype K9me2/K14ac complex. The model was transformed with COOT¹⁰ and CCP4¹¹ program PDBSET (Evans, 1992) to align it with the other complex models presented here, and further refined against synchrotron data. Models were interactively rebuilt with COOT, refined with REFMAC¹² and validated with PHENIX.MOLPROBITY¹³. In the current models, SETDB1 residue S201 remains an outlier from MOLPROBITY Ramachandran plot contours. Anisotropic displacement parameters were analyzed on the PARVATI¹⁴ server. Deposition in the PDB and publication of the models were prepared with PDB_EXTRACT¹⁵, CCP4 and PHENIX¹⁶ and IOTBX¹⁷.

Supplementary Note 2: Statistics related to Fig. 6b. The significance of the overlap of H3K14ac peaks with the intersection of SETDB1 and H3K9me3 peaks shown in Fig. 6b was determined by randomization of the H3K14ac peak regions in the mouse genome (mm10) keeping the number and sizes of the regions constant with the Galaxy ShuffleBed tool. Next, the number of shuffled regions overlapping with the intersection of SETDB1 and H3K9me3 peaks was determined, which represents the expected by-chance overlap. 10 shuffling runs were conducted resulting in 860-940 overlap regions (906.6 ± 24.4). The small standard deviation of the number of overlapping regions in the different shuffled datasets indicates that 10 shuffle rounds are sufficient to draw conclusions. The final p-value for the experimentally observed number of H3K14ac peaks overlapping with the intersection of SETDB1 and H3K9me3 (2231) was determined for a normal distribution using Fishers exact test and found to be highly significant ($p \approx 0$).

H3K14ac shuffle #	Number of H3K14ac shuffled regions overlapping with SETDB1-H3K9me3 intersection
1	897
2	936
3	891
4	929
5	922
6	915
7	886
8	863
9	892
10	935
average	906.6
stdev	24.4
Observed number of overlapping regions	2231
p-value calculated on normal distribution (Fisher's exact test)	0.00E+00

Supplementary Note 3: Statistics related to Fig. 6d. The analysis for enrichment of the different repeat types in the different clusters by EpiExplorer (Fig. 6d) included repetitions with randomized datasets prepared by EpiExplorer. Based on 10 random repetitions, the average repeat content of each cluster was determined together with the standard error, which represents the statistically expected repeat content of each set of cluster regions. The small standard deviations of the average repeat contents of the randomized samples indicate that the number of randomizations was sufficient to draw conclusions. The p-values for enrichment of the different repeat types in the different clusters were calculated using the average and standard errors from the randomized samples based on a normal distribution by Fisher's exact test.

Repeat content in clusters 1-8

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Any repeat	83.3	98.7	99.2	90.9	97.4	97.7	93.0	94.3
LINE	17.5	23.3	23.6	40.9	17.0	88.1	48.5	37.6
SINE	27.2	8.7	8.8	14.6	10.6	9.0	12.4	14.0
Simple repeats	53.5	7.0	5.5	10.0	6.3	6.4	10.7	14.0
LTR	25.4	95.8	95.9	47.3	91.1	17.5	46.2	58.6

Repeat content in randomized data sets

	Average (%)	StDev
Any repeat	86.8	4.8
LINE	39.5	5.2
SINE	38.4	7.4
Simple repeats	28.8	6.3
LTR	29.0	5.9

p-values for enrichment

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Any repeat	7.7E-01	6.8E-03	5.1E-03	2.0E-01	1.4E-02	1.2E-02	9.9E-02	6.0E-02
LINE	1.0E+00	1.0E+00	1.0E+00	4.0E-01	1.0E+00	0.0E+00	4.1E-02	6.5E-01
SINE	9.4E-01	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
Simple repeats	4.6E-05	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00	9.9E-01
LTR	7.3E-01	0.0E+00	0.0E+00	8.8E-04	0.0E+00	9.7E-01	1.6E-03	2.2E-07

The enrichment of LTRs in clusters 2, 3 and 5 as well as LINEs in cluster 6 (fields shaded in orange) are highly significant.

Supplementary Tables

Supplementary Table 1: Data collection and refinement statistics. Values in parentheses refer to the highest-resolution shell.

	3TD- H3K9me2/K14ac	3TD- H3K9me3/K14ac	3TD- H3K9me0/K14ac	3TD(W358A)- H3K9me2/K14ac	3TD(W358A)- H3K9me3/K14ac
PDB accession	6BHD	6BHE	6BHG	6BHH	6BHI
Data collection					
Space group	P2 ₁	P2 ₁	P2 ₁	P2 ₁	P2 ₁
Cell dimensions					
<i>a</i> , <i>b</i> , <i>c</i> (Å)	37.26,72.45,52.51	37.05,71.37,52.05	37.71,72.36,52.50	37.80,71.80,52.54	37.85,71.72,52.69
α , β , γ (°)	90.00,104.84,90.00	90.00,104.23,90.00	90.00,104.75,90.00	90.00,104.42,90.00	90.00,104.48,90.00
Resolution (Å)	41.57-1.25(1.27-1.25)	41.20-1.33(1.35-1.33)	41.56-1.40(1.42-1.40)	36.61-1.82(1.86-1.82)	41.57-1.40(1.42-1.40)
<i>R</i> _{merge}	0.050(1.018)	0.049(1.153)	0.035(0.826)	0.121(1.179)	0.065(0.942)
<i>I</i> / σ <i>I</i>	15.1(1.3)	15.3(1.2)	19.9(1.4)	7.9(1.1)	12.5(1.5)
Completeness (%)	99.8(99.8)	99.8(99.9)	99.3(93.1)	99.8(99.9)	99.7(100.0)
Redundancy	3.7(3.6)	3.7(3.6)	3.7(2.8)	3.6(3.6)	3.6(3.7)
Refinement					
Resolution (Å)	41.57-1.25	35.69-1.35	41.56-1.45	36.61-1.85	41.57-1.40
No. reflections	70524/3722	54617/2872	45714/2428	22045/1197	50707/2671
<i>R</i> _{work} / <i>R</i> _{free}	0.147/0.183	0.135/0.172	0.133/0.176	0.193/0.237	0.148/0.187
No. atoms	2174	2078	2069	2010	2116
Protein	1843	1806	1747	1699	1793
Peptide	92	87	59	54	63
Water	203	149	223	221	225
Other	36	36	40	36	35
<i>B</i> -factors	16.9	20.7	22.1	24.8	18.9
Protein	15.7	19.4	20.4	23.5	17.5
Peptide	17.4	20.9	21.9	24.1	19.4
Water	26.5	31.5	33.5	32.5	28.4
Other	25.5	37.5	36.1	38.0	28.1
R.m.s. deviations					
Bond lengths (Å)	0.019	0.017	0.016	0.013	0.017
Bond angles (°)	1.9	1.8	1.7	1.4	1.8

Supplementary Table 2: Full annotation of the peptides present on the modified histone peptide array. Active Motif, MODified™ Histone Peptide Array, Catalog Nos. 13001 & 13005^{3,18}.

Pos.	Peptide sequence	Name	Mod1	Mod2	Mod 3	Mod 4	N-terminus
A 1	A R T K Q T A R K S T G G K A P R K Q	H3 1-19	unmod				free
A 2	A Rme2s T K Q T A R K S T G G K A P R K Q	H3 1-19	R2me2s				free
A 3	A Rme2a T K Q T A R K S T G G K A P R K Q	H3 1-19	R2me2a				free
A 4	A Cit T K Q T A R K S T G G K A P R K Q	H3 1-19	R2Citr				free
A 5	A R pT K Q T A R K S T G G K A P R K Q	H3 1-19	T3P				free
A 6	A R T Kme1 Q T A R K S T G G K A P R K Q	H3 1-19	K4me1				free
A 7	A R T Kme2 Q T A R K S T G G K A P R K Q	H3 1-19	K4me2				free
A 8	A R T Kme3 Q T A R K S T G G K A P R K Q	H3 1-19	K4me3				free
A 9	A R T Kac Q T A R K S T G G K A P R K Q	H3 1-19	K4ac				free
A10	A R T K Q T A Rme2s K S T G G K A P R K Q	H3 1-19	R8me2s				free
A11	A R T K Q T A Rme2a K S T G G K A P R K Q	H3 1-19	R8me2a				free
A12	A R T K Q T A Cit K S T G G K A P R K Q	H3 1-19	R8Citr				free
A13	A R T K Q T A R Kme1 S T G G K A P R K Q	H3 1-19	K9me1				free
A14	A R T K Q T A R Kme2 S T G G K A P R K Q	H3 1-19	K9me2				free
A15	A R T K Q T A R Kme3 S T G G K A P R K Q	H3 1-19	K9me3				free
A16	A R T K Q T A R Kac S T G G K A P R K Q	H3 1-19	K9ac				free
A17	A R T K Q T A R K pS T G G K A P R K Q	H3 1-19	S10P				free
A18	A R T K Q T A R K S pT G G K A P R K Q	H3 1-19	T11P				free
A19	A R T K Q T A R K S T G G Kac A P R K Q	H3 1-19	K14ac				free

A20	A Rme2s pT K Q T A R K S T G G K A P R K Q	H3 1-19	R2me2s	T3P			free
A21	A Rme2s T Kme1 Q T A R K S T G G K A P R K Q	H3 1-19	R2me2s	K4me1			free
A22	A Rme2s T Kme2 Q T A R K S T G G K A P R K Q	H3 1-19	R2me2s	K4me2			free
A23	A Rme2s T Kme3 Q T A R K S T G G K A P R K Q	H3 1-19	R2me2s	K4me3			free
A24	A Rme2s T Kac Q T A R K S T G G K A P R K Q	H3 1-19	R2me2s	K4ac			free
B 1	A Rme2a pT K Q T A R K S T G G K A P R K Q	H3 1-19	R2me2a	T3P			free
B 2	A Rme2a T Kme1 Q T A R K S T G G K A P R K Q	H3 1-19	R2me2a	K4me1			free
B 3	A Rme2a T Kme2 Q T A R K S T G G K A P R K Q	H3 1-19	R2me2a	K4me2			free
B 4	A Rme2a T Kme3 Q T A R K S T G G K A P R K Q	H3 1-19	R2me2a	K4me3			free
B 5	A Rme2a T Kac Q T A R K S T G G K A P R K Q	H3 1-19	R2me2a	K4ac			free
B 6	A Cit pT K Q T A R K S T G G K A P R K Q	H3 1-19	R2Citr	T3P			free
B 7	A Cit T Kme1 Q T A R K S T G G K A P R K Q	H3 1-19	R2Citr	K4me1			free
B 8	A Cit T Kme2 Q T A R K S T G G K A P R K Q	H3 1-19	R2Citr	K4me2			free
B 9	A Cit T Kme3 Q T A R K S T G G K A P R K Q	H3 1-19	R2Citr	K4me3			free
B10	A Cit T Kac Q T A R K S T G G K A P R K Q	H3 1-19	R2Citr	K4ac			free
B11	A R pT Kme1 Q T A R K S T G G K A P R K Q	H3 1-19	T3P	K4me1			free
B12	A R pT Kme2 Q T A R K S T G G K A P R K Q	H3 1-19	T3P	K4me2			free
B13	A R pT Kme3 Q T A R K S T G G K A P R K Q	H3 1-19	T3P	K4me3			free
B14	A R pT Kac Q T A R K S T G G K A P R K Q	H3 1-19	T3P	K4ac			free
B15	A Rme2s pT Kme1 Q T A R K S T G G K A P R K Q	H3 1-19	R2me2s	T3P	K4me 1		free
B16	A Rme2s pT Kme2 Q T A R K S T G G K A P R K Q	H3 1-19	R2me2s	T3P	K4me 2		free
B17	A Rme2s pT Kme3 Q T A R K S T G G K A P R K Q	H3 1-19	R2me2s	T3P	K4me 3		free

B18	A Rme2s pT Kac Q T A R K S T G G K A P R K Q	H3 1-19	R2me2s	T3P	K4ac		free
B19	A Rme2a pT Kme1 Q T A R K S T G G K A P R K Q	H3 1-19	R2me2a	T3P	K4me 1		free
B20	A Rme2a pT Kme2 Q T A R K S T G G K A P R K Q	H3 1-19	R2me2a	T3P	K4me 2		free
B21	A Rme2a pT Kme3 Q T A R K S T G G K A P R K Q	H3 1-19	R2me2a	T3P	K4me 3		free
B22	A Rme2a pT Kac Q T A R K S T G G K A P R K Q	H3 1-19	R2me2a	T3P	K4ac		free
B23	A R T K Q T A Rme2a Kme1 S T G G K A P R K Q	H3 1-19	R8me2s	K9me1			free
B24	A R T K Q T A Rme2a Kme2 S T G G K A P R K Q	H3 1-19	R8me2s	K9me2			free
C 1	A R T K Q T A Rme2a Kme3 S T G G K A P R K Q	H3 1-19	R8me2s	K9me3			free
C 2	A R T K Q T A Rme2a Kac S T G G K A P R K Q	H3 1-19	R8me2s	K9ac			free
C 3	A R T K Q T A Rme2a K pS T G G K A P R K Q	H3 1-19	R8me2s	S10P			free
C 4	A R T K Q T A Rme2a K S pT G G K A P R K Q	H3 1-19	R8me2s	T11P			free
C 5	A R T K Q T A Rme2a Kme1 S T G G K A P R K Q	H3 1-19	R8me2a	K9me1			free
C 6	A R T K Q T A Rme2a Kme2 S T G G K A P R K Q	H3 1-19	R8me2a	K9me2			free
C 7	A R T K Q T A Rme2a Kme3 S T G G K A P R K Q	H3 1-19	R8me2a	K9me3			free
C 8	A R T K Q T A Rme2a Kac S T G G K A P R K Q	H3 1-19	R8me2a	K9ac			free
C 9	A R T K Q T A Rme2a K pS T G G K A P R K Q	H3 1-19	R8me2a	S10P			free
C10	A R T K Q T A Rme2a K S pT G G K A P R K Q	H3 1-19	R8me2a	T11P			free
C11	A R T K Q T A Cit Kme1 S T G G K A P R K Q	H3 1-19	R8Citr	K9me1			free
C12	A R T K Q T A Cit Kme2 S T G G K A P R K Q	H3 1-19	R8Citr	K9me2			free
C13	A R T K Q T A Cit Kme3 S T G G K A P R K Q	H3 1-19	R8Citr	K9me3			free
C14	A R T K Q T A Cit Kac S T G G K A P R K Q	H3 1-19	R8Citr	K9ac			free
C15	A R T K Q T A Cit K pS T G G K A P R K Q	H3 1-19	R8Citr	S10P			free

C16	A R T K Q T A Cit K S pT G G K A P R K Q	H3 1-19	R8Citr	T11P			free
C17	A R T K Q T A R Kme1 pS T G G K A P R K Q	H3 1-19	K9me1	S10P			free
C18	A R T K Q T A R Kme1 S pT G G K A P R K Q	H3 1-19	K9me1	T11P			free
C19	A R T K Q T A R Kme1 S T G G Kac A P R K Q	H3 1-19	K9me1	K14ac			free
C20	A R T K Q T A R Kme2 pS T G G K A P R K Q	H3 1-19	K9me2	S10P			free
C21	A R T K Q T A R Kme2 S pT G G K A P R K Q	H3 1-19	K9me2	T11P			free
C22	A R T K Q T A R Kme2 S T G G Kac A P R K Q	H3 1-19	K9me2	K14ac			free
C23	A R T K Q T A R Kme3 pS T G G K A P R K Q	H3 1-19	K9me3	S10P			free
C24	A R T K Q T A R Kme3 S pT G G K A P R K Q	H3 1-19	K9me3	T11P			free
D 1	A R T K Q T A R Kme3 S T G G Kac A P R K Q	H3 1-19	K9me3	K14ac			free
D 2	A R T K Q T A R Kac pS T G G K A P R K Q	H3 1-19	K9ac	S10P			free
D 3	A R T K Q T A R Kac S pT G G K A P R K Q	H3 1-19	K9ac	T11P			free
D 4	A R T K Q T A R Kac S T G G Kac A P R K Q	H3 1-19	K9ac	K14ac			free
D 5	A R T K Q T A R K pS pT G G K A P R K Q	H3 1-19	S10P	T11P			free
D 6	A R T K Q T A R K pS T G G Kac A P R K Q	H3 1-19	S10P	K14ac			free
D 7	A R T K Q T A R K S pT G G Kac A P R K Q	H3 1-19	T11P	K14ac			free
D 8	A R T K Q T A Rme2s Kme1 pS T G G K A P R K Q	H3 1-19	R8me2s	K9me1	S10P		free
D 9	A R T K Q T A Rme2s Kme2 pS T G G K A P R K Q	H3 1-19	R8me2s	K9me2	S10P		free
D10	A R T K Q T A Rme2s Kme3 pS T G G K A P R K Q	H3 1-19	R8me2s	K9me3	S10P		free
D11	A R T K Q T A Rme2s Kac pS T G G K A P R K Q	H3 1-19	R8me2s	K9ac	S10P		free
D12	A R T K Q T A Rme2s Kme1 S pT G G K A P R K Q	H3 1-19	R8me2s	K9me1	T11P		free
D13	A R T K Q T A Rme2s Kme2 S pT G G K A P R K Q	H3 1-19	R8me2s	K9me2	T11P		free

D14	A R T K Q T A Rme2s Kme3 S pT G G K A P R K Q	H3 1-19	R8me2s	K9me3	T11P		free
D15	A R T K Q T A Rme2s Kac S pT G G K A P R K Q	H3 1-19	R8me2s	K9ac	T11P		free
D16	A R T K Q T A Rme2a Kme1 pS T G G K A P R K Q	H3 1-19	R8me2a	K9me1	S10P		free
D17	A R T K Q T A Rme2a Kme2 pS T G G K A P R K Q	H3 1-19	R8me2a	K9me2	S10P		free
D18	A R T K Q T A Rme2a Kme3 pS T G G K A P R K Q	H3 1-19	R8me2a	K9me3	S10P		free
D19	A R T K Q T A Rme2a Kac pS T G G K A P R K Q	H3 1-19	R8me2a	K9ac	S10P		free
D20	A R T K Q T A Rme2a Kme1 S pT G G K A P R K Q	H3 1-19	R8me2a	K9me1	T11P		free
D21	A R T K Q T A Rme2a Kme2 S pT G G K A P R K Q	H3 1-19	R8me2a	K9me2	T11P		free
D22	A R T K Q T A Rme2a Kme3 S pT G G K A P R K Q	H3 1-19	R8me2a	K9me3	T11P		free
D23	A R T K Q T A Rme2a Kac S pT G G K A P R K Q	H3 1-19	R8me2a	K9ac	T11P		free
D24	A R T K Q T A Rme2a Kme1 pS pT G G K A P R K Q	H3 1-19	R8me2a	K9me1	S10P	T11P	free
E 1	A R T K Q T A Rme2a Kme2 pS pT G G K A P R K Q	H3 1-19	R8me2a	K9me2	S10P	T11P	free
E 2	A R T K Q T A Rme2a Kme3 pS pT G G K A P R K Q	H3 1-19	R8me2a	K9me3	S10P	T11P	free
E 3	A R T K Q T A Rme2a Kac pS pT G G K A P R K Q	H3 1-19	R8me2a	K9ac	S10P	T11P	free
E 4	A Rme2s T Kme1 Q T A Rme2s K S T G G K A P R K Q	H3 1-19	R2me2s	K4me1	R8me 2s		free
E 5	A Rme2s T Kme2 Q T A Rme2s K S T G G K A P R K Q	H3 1-19	R2me2s	K4me2	R8me 2s		free
E 6	A Rme2s T Kme3 Q T A Rme2s K S T G G K A P R K Q	H3 1-19	R2me2s	K4me3	R8me 2s		free
E 7	A Rme2s T Kac Q T A Rme2s K S T G G K A P R K Q	H3 1-19	R2me2s	K4ac	R8me 2s		free
E 8	A Rme2a T Kme1 Q T A Rme2a K S T G G K A P R K Q	H3 1-19	R2me2a	K4me1	R8me 2a		free
E 9	A Rme2a T Kme2 Q T A Rme2a K S T G G K A P R K Q	H3 1-19	R2me2a	K4me2	R8me 2a		free
E10	A Rme2a T Kme3 Q T A Rme2a K S T G G K A P R K Q	H3 1-19	R2me2a	K4me3	R8me 2a		free
E11	A Rme2a T Kac Q T A Rme2a K S T G G K A P R K Q	H3 1-19	R2me2a	K4ac	R8me 2a		free

E12	A Rme2s T Kme1 Q T A R Kme1 S T G G K A P R K Q	H3 1-19	R2me2s	K4me1	K9me 1		free
E13	A Rme2s T Kme2 Q T A R Kme1 S T G G K A P R K Q	H3 1-19	R2me2s	K4me2	K9me 1		free
E14	A Rme2s T Kme3 Q T A R Kme1 S T G G K A P R K Q	H3 1-19	R2me2s	K4me3	K9me 1		free
E15	A Rme2s T Kac Q T A R Kme1 S T G G K A P R K Q	H3 1-19	R2me2s	K4ac	K9me 1		free
E16	A Rme2a T Kme1 Q T A R Kme2 S T G G K A P R K Q	H3 1-19	R2me2a	K4me1	K9me 2		free
E17	A Rme2a T Kme2 Q T A R Kme2 S T G G K A P R K Q	H3 1-19	R2me2a	K4me2	K9me 2		free
E18	A Rme2a T Kme3 Q T A R Kme2 S T G G K A P R K Q	H3 1-19	R2me2a	K4me3	K9me 2		free
E19	A Rme2a T Kac Q T A R Kme2 S T G G K A P R K Q	H3 1-19	R2me2a	K4ac	K9me 2		free
E20	A Rme2s T Kme1 Q T A R Kme3 S T G G K A P R K Q	H3 1-19	R2me2s	K4me1	K9me 3		free
E21	A Rme2s T Kme2 Q T A R Kme3 S T G G K A P R K Q	H3 1-19	R2me2s	K4me2	K9me 3		free
E22	A Rme2s T Kme3 Q T A R Kme3 S T G G K A P R K Q	H3 1-19	R2me2s	K4me3	K9me 3		free
E23	A Rme2s T Kac Q T A R Kme3 S T G G K A P R K Q	H3 1-19	R2me2s	K4ac	K9me 3		free
E24	A Rme2a T Kme1 Q T A R Kac S T G G K A P R K Q	H3 1-19	R2me2a	K4me1	K9ac		free
F 1	A Rme2a T Kme2 Q T A R Kac S T G G K A P R K Q	H3 1-19	R2me2a	K4me2	K9ac		free
F 2	A Rme2a T Kme3 Q T A R Kac S T G G K A P R K Q	H3 1-19	R2me2a	K4me3	K9ac		free
F 3	A Rme2a T Kac Q T A R Kac S T G G K A P R K Q	H3 1-19	R2me2a	K4ac	K9ac		free
F 4	A R T Kme1 Q T A Rme2s Kme1 S T G G K A P R K Q	H3 1-19	K4me1	R8me2 s	K9me 1		free
F 5	A R T Kme2 Q T A Rme2s Kme1 S T G G K A P R K Q	H3 1-19	K4me2	R8me2 s	K9me 1		free
F 6	A R T Kme3 Q T A Rme2s Kme1 S T G G K A P R K Q	H3 1-19	K4me3	R8me2 s	K9me 1		free
F 7	A R T Kac Q T A Rme2s Kme1 S T G G K A P R K Q	H3 1-19	K4ac	R8me2 s	K9me 1		free
F 8	A R T Kme1 Q T A Rme2a Kme1 S T G G K A P R K Q	H3 1-19	K4me1	R8me2 a	K9me 1		free
F 9	A R T Kme2 Q T A Rme2a Kme1 S T G G K A P R K Q	H3 1-19	K4me2	R8me2 a	K9me 1		free

F10	A R T Kme3 Q T A Rme2a Kme1 S T G G K A P R K Q	H3 1-19	K4me3	R8me2 a	K9me 1		free
F11	A R T Kac Q T A Rme2a Kme1 S T G G K A P R K Q	H3 1-19	K4ac	R8me2 a	K9me 1		free
F12	A R T Kme1 Q T A Rme2s Kme2 S T G G K A P R K Q	H3 1-19	K4me1	R8me2 s	K9me 2		free
F13	A R T Kme2 Q T A Rme2s Kme2 S T G G K A P R K Q	H3 1-19	K4me2	R8me2 s	K9me 2		free
F14	A R T Kme3 Q T A Rme2s Kme2 S T G G K A P R K Q	H3 1-19	K4me3	R8me2 s	K9me 2		free
F15	A R T Kac Q T A Rme2s Kme2 S T G G K A P R K Q	H3 1-19	K4ac	R8me2 s	K9me 2		free
F16	A R T Kme1 Q T A Rme2a Kme2 S T G G K A P R K Q	H3 1-19	K4me1	R8me2 a	K9me 2		free
F17	A R T Kme2 Q T A Rme2a Kme2 S T G G K A P R K Q	H3 1-19	K4me2	R8me2 a	K9me 2		free
F18	A R T Kme3 Q T A Rme2a Kme2 S T G G K A P R K Q	H3 1-19	K4me3	R8me2 a	K9me 2		free
F19	A R T Kac Q T A Rme2a Kme2 S T G G K A P R K Q	H3 1-19	K4ac	R8me2 a	K9me 2		free
F20	A R T Kme1 Q T A Rme2s Kme3 S T G G K A P R K Q	H3 1-19	K4me1	R8me2 s	K9me 3		free
F21	A R T Kme2 Q T A Rme2s Kme3 S T G G K A P R K Q	H3 1-19	K4me2	R8me2 s	K9me 3		free
F22	A R T Kme3 Q T A Rme2s Kme3 S T G G K A P R K Q	H3 1-19	K4me3	R8me2 s	K9me 3		free
F23	A R T Kac Q T A Rme2s Kme3 S T G G K A P R K Q	H3 1-19	K4ac	R8me2 s	K9me 3		free
F24	A R T Kme1 Q T A Rme2a Kme3 S T G G K A P R K Q	H3 1-19	K4me1	R8me2 a	K9me 3		free
G 1	A R T Kme2 Q T A Rme2a Kme3 S T G G K A P R K Q	H3 1-19	K4me2	R8me2 a	K9me 3		free
G 2	A R T Kme3 Q T A Rme2a Kme3 S T G G K A P R K Q	H3 1-19	K4me3	R8me2 a	K9me 3		free
G 3	A R T Kac Q T A Rme2a Kme3 S T G G K A P R K Q	H3 1-19	K4ac	R8me2 a	K9me 3		free
G 4	A R T Kme1 Q T A Rme2s Kac S T G G K A P R K Q	H3 1-19	K4me1	R8me2 s	K9ac		free
G 5	A R T Kme2 Q T A Rme2s Kac S T G G K A P R K Q	H3 1-19	K4me2	R8me2 s	K9ac		free
G 6	A R T Kme3 Q T A Rme2s Kac S T G G K A P R K Q	H3 1-19	K4me3	R8me2 s	K9ac		free
G 7	A R T Kac Q T A Rme2s Kac S T G K A P R K Q	H3 1-19	K4ac	R8me2 s	K9ac		free

G 8	A R T Kme1 Q T A Rme2a Kac S T G G K A P R K Q	H3 1-19	K4me1	R8me2 a	K9ac		free
G 9	A R T Kme2 Q T A Rme2a Kac S T G G K A P R K Q	H3 1-19	K4me2	R8me2 a	K9ac		free
G10	A R T Kme3 Q T A Rme2a Kac S T G G K A P R K Q	H3 1-19	K4me3	R8me2 a	K9ac		free
G11	A R T Kac Q T A Rme2a Kac S T G G K A P R K Q	H3 1-19	K4ac	R8me2 a	K9ac		free
G12	A Rme2s T Kme1 Q T A Rme2s Kme1 S T G G K A P R K Q	H3 1-19	R2me2s	K4me1	R8me 2s	K9me1	free
G13	A Rme2s T Kme2 Q T A Rme2s Kme1 S T G G K A P R K Q	H3 1-19	R2me2s	K4me2	R8me 2s	K9me1	free
G14	A Rme2s T Kme3 Q T A Rme2s Kme1 S T G G K A P R K Q	H3 1-19	R2me2s	K4me3	R8me 2s	K9me1	free
G15	A Rme2s T Kac Q T A Rme2s Kme1 S T G G K A P R K Q	H3 1-19	R2me2s	K4ac	R8me 2s	K9me1	free
G16	A Rme2a T Kme1 Q T A Rme2s Kme1 S T G G K A P R K Q	H3 1-19	R2me2a	K4me1	R8me 2s	K9me1	free
G17	A Rme2a T Kme2 Q T A Rme2s Kme1 S T G G K A P R K Q	H3 1-19	R2me2a	K4me2	R8me 2s	K9me1	free
G18	A Rme2a T Kme3 Q T A Rme2s Kme1 S T G G K A P R K Q	H3 1-19	R2me2a	K4me3	R8me 2s	K9me1	free
G19	A Rme2a T Kac Q T A Rme2s Kme1 S T G G K A P R K Q	H3 1-19	R2me2a	K4ac	R8me 2s	K9me1	free
G20	A Rme2s T Kme1 Q T A Rme2s Kme2 S T G G K A P R K Q	H3 1-19	R2me2s	K4me1	R8me 2s	K9me2	free
G21	A Rme2s T Kme2 Q T A Rme2s Kme2 S T G G K A P R K Q	H3 1-19	R2me2s	K4me2	R8me 2s	K9me2	free
G22	A Rme2s T Kme3 Q T A Rme2s Kme2 S T G G K A P R K Q	H3 1-19	R2me2s	K4me3	R8me 2s	K9me2	free
G23	A Rme2s T Kac Q T A Rme2s Kme2 S T G G K A P R K Q	H3 1-19	R2me2s	K4ac	R8me 2s	K9me2	free
G24	A Rme2a T Kme1 Q T A Rme2s Kme2 S T G G K A P R K Q	H3 1-19	R2me2a	K4me1	R8me 2s	K9me2	free
H 1	A Rme2a T Kme2 Q T A Rme2s Kme2 S T G G K A P R K Q	H3 1-19	R2me2a	K4me2	R8me 2s	K9me2	free
H 2	A Rme2a T Kme3 Q T A Rme2s Kme2 S T G G K A P R K Q	H3 1-19	R2me2a	K4me3	R8me 2s	K9me2	free
H 3	A Rme2a T Kac Q T A Rme2s Kme2 S T G G K A P R K Q	H3 1-19	R2me2a	K4ac	R8me 2s	K9me2	free
H 4	A Rme2s T Kme1 Q T A Rme2s Kme3 S T G G K A P R K Q	H3 1-19	R2me2s	K4me1	R8me 2s	K9me3	free
H 5	A Rme2s T Kme2 Q T A Rme2s Kme3 S T G G K A P R K Q	H3 1-19	R2me2s	K4me2	R8me 2s	K9me3	free

H 6	A Rme2s T Kme3 Q T A Rme2s Kme3 S T G G K A P R K Q	H3 1-19	R2me2s	K4me3	R8me 2s	K9me3	free
H 7	A Rme2s T Kac Q T A Rme2s Kme3 S T G G K A P R K Q	H3 1-19	R2me2s	K4ac	R8me 2s	K9me3	free
H 8	A Rme2a T Kme1 Q T A Rme2s Kme3 S T G G K A P R K Q	H3 1-19	R2me2a	K4me1	R8me 2s	K9me3	free
H 9	A Rme2a T Kme2 Q T A Rme2s Kme3 S T G G K A P R K Q	H3 1-19	R2me2a	K4me2	R8me 2s	K9me3	free
H10	A Rme2a T Kme3 Q T A Rme2s Kme3 S T G G K A P R K Q	H3 1-19	R2me2a	K4me3	R8me 2s	K9me3	free
H11	A Rme2a T Kac Q T A Rme2s Kme3 S T G G K A P R K Q	H3 1-19	R2me2a	K4ac	R8me 2s	K9me3	free
H12	A Rme2s T Kme1 Q T A Rme2s Kac S T G G K A P R K Q	H3 1-19	R2me2s	K4me1	R8me 2s	K9ac	free
H13	A Rme2s T Kme2 Q T A Rme2s Kac S T G G K A P R K Q	H3 1-19	R2me2s	K4me2	R8me 2s	K9ac	free
H14	A Rme2s T Kme3 Q T A Rme2s Kac S T G G K A P R K Q	H3 1-19	R2me2s	K4me3	R8me 2s	K9ac	free
H15	A Rme2s T Kac Q T A Rme2s Kac S T G G K A P R K Q	H3 1-19	R2me2s	K4ac	R8me 2s	K9ac	free
H16	A Rme2a T Kme1 Q T A Rme2s Kac S T G G K A P R K Q	H3 1-19	R2me2a	K4me1	R8me 2s	K9ac	free
H17	A Rme2a T Kme2 Q T A Rme2s Kac S T G G K A P R K Q	H3 1-19	R2me2a	K4me2	R8me 2s	K9ac	free
H18	A Rme2a T Kme3 Q T A Rme2s Kac S T G G K A P R K Q	H3 1-19	R2me2a	K4me3	R8me 2s	K9ac	free
H19	A Rme2a T Kac Q T A Rme2s Kac S T G G K A P R K Q	H3 1-19	R2me2a	K4ac	R8me 2s	K9ac	free
H20	A Rme2s T Kme1 Q T A Rme2a Kme1 S T G G K A P R K Q	H3 1-19	R2me2s	K4me1	R8me 2a	K9me1	free
H21	A Rme2s T Kme2 Q T A Rme2a Kme1 S T G G K A P R K Q	H3 1-19	R2me2s	K4me2	R8me 2a	K9me1	free
H22	A Rme2s T Kme3 Q T A Rme2a Kme1 S T G G K A P R K Q	H3 1-19	R2me2s	K4me3	R8me 2a	K9me1	free
H23	A Rme2s T Kac Q T A Rme2a Kme1 S T G G K A P R K Q	H3 1-19	R2me2s	K4ac	R8me 2a	K9me1	free
H24	A Rme2a T Kme1 Q T A Rme2a Kme1 S T G G K A P R K Q	H3 1-19	R2me2a	K4me1	R8me 2a	K9me1	free
I 1	A Rme2a T Kme2 Q T A Rme2a Kme1 S T G G K A P R K Q	H3 1-19	R2me2a	K4me2	R8me 2a	K9me1	free
I 2	A Rme2a T Kme3 Q T A Rme2a Kme1 S T G G K A P R K Q	H3 1-19	R2me2a	K4me3	R8me 2a	K9me1	free
I 3	A Rme2a T Kac Q T A Rme2a Kme1 S T G G K A P R K Q	H3 1-19	R2me2a	K4ac	R8me 2a	K9me1	free

I 4	A Rme2s T Kme1 Q T A Rme2a Kme2 S T G G K A P R K Q	H3 1-19	R2me2s	K4me1	R8me 2a	K9me2	free
I 5	A Rme2s T Kme2 Q T A Rme2a Kme2 S T G G K A P R K Q	H3 1-19	R2me2s	K4me2	R8me 2a	K9me2	free
I 6	A Rme2s T Kme3 Q T A Rme2a Kme2 S T G G K A P R K Q	H3 1-19	R2me2s	K4me3	R8me 2a	K9me2	free
I 7	A Rme2s T Kac Q T A Rme2a Kme2 S T G G K A P R K Q	H3 1-19	R2me2s	K4ac	R8me 2a	K9me2	free
I 8	A Rme2a T Kme1 Q T A Rme2a Kme2 S T G G K A P R K Q	H3 1-19	R2me2a	K4me1	R8me 2a	K9me2	free
I 9	A Rme2a T Kme2 Q T A Rme2a Kme2 S T G G K A P R K Q	H3 1-19	R2me2a	K4me2	R8me 2a	K9me2	free
I10	A Rme2a T Kme3 Q T A Rme2a Kme2 S T G G K A P R K Q	H3 1-19	R2me2a	K4me3	R8me 2a	K9me2	free
I11	A Rme2a T Kac Q T A Rme2a Kme2 S T G G K A P R K Q	H3 1-19	R2me2a	K4ac	R8me 2a	K9me2	free
I12	A Rme2s T Kme1 Q T A Rme2a Kme3 S T G G K A P R K Q	H3 1-19	R2me2s	K4me1	R8me 2a	K9me3	free
I13	A Rme2s T Kme2 Q T A Rme2a Kme3 S T G G K A P R K Q	H3 1-19	R2me2s	K4me2	R8me 2a	K9me3	free
I14	A Rme2s T Kme3 Q T A Rme2a Kme3 S T G G K A P R K Q	H3 1-19	R2me2s	K4me3	R8me 2a	K9me3	free
I15	A Rme2s T Kac Q T A Rme2a Kme3 S T G G K A P R K Q	H3 1-19	R2me2s	K4ac	R8me 2a	K9me3	free
I16	A Rme2a T Kme1 Q T A Rme2a Kme3 S T G G K A P R K Q	H3 1-19	R2me2a	K4me1	R8me 2a	K9me3	free
I17	A Rme2a T Kme2 Q T A Rme2a Kme3 S T G G K A P R K Q	H3 1-19	R2me2a	K4me2	R8me 2a	K9me3	free
I18	A Rme2a T Kme3 Q T A Rme2a Kme3 S T G G K A P R K Q	H3 1-19	R2me2a	K4me3	R8me 2a	K9me3	free
I19	A Rme2a T Kac Q T A Rme2a Kme3 S T G G K A P R K Q	H3 1-19	R2me2a	K4ac	R8me 2a	K9me3	free
I20	A Rme2s T Kme1 Q T A Rme2a Kac S T G G K A P R K Q	H3 1-19	R2me2s	K4me1	R8me 2a	K9ac	free
I21	A Rme2s T Kme2 Q T A Rme2a Kac S T G G K A P R K Q	H3 1-19	R2me2s	K4me2	R8me 2a	K9ac	free
I22	A Rme2s T Kme3 Q T A Rme2a Kac S T G G K A P R K Q	H3 1-19	R2me2s	K4me3	R8me 2a	K9ac	free
I23	A Rme2s T Kac Q T A Rme2a Kac S T G G K A P R K Q	H3 1-19	R2me2s	K4ac	R8me 2a	K9ac	free
I24	A Rme2a T Kme1 Q T A Rme2a Kac S T G G K A P R K Q	H3 1-19	R2me2a	K4me1	R8me 2a	K9ac	free
J 1	A Rme2a T Kme2 Q T A Rme2a Kac S T G G K A P R K Q	H3 1-19	R2me2a	K4me2	R8me 2a	K9ac	free

J 2	A Rme2a T Kme3 Q T A Rme2a Kac S T G G K A P R K Q	H3 1-19	R2me2a	K4me3	R8me 2a	K9ac	free
J 3	A Rme2a T Kac Q T A Rme2a Kac S T G G K A P R K Q	H3 1-19	R2me2a	K4ac	R8me 2a	K9ac	free
J 4	A R K S T G G K A P R K Q L A T K A A R	H3 7-26	unmod				acetylated
J 5	A R K S T G G Kac A P R K Q L A T K A A R	H3 7-26	K14ac				acetylated
J 6	A R K pS T G G Kac A P R K Q L A T K A A R	H3 7-26	K14ac	S10P			acetylated
J 7	A R K S pT G G Kac A P R K Q L A T K A A R	H3 7-26	K14ac	T11P			acetylated
J 8	A R K S T G G K A P Rme2s K Q L A T K A A R	H3 7-26	R17me2 s				acetylated
J 9	A R K S T G G K A P Rme2a K Q L A T K A A R	H3 7-26	R17me2 a				acetylated
J10	A R K S T G G K A P Cit K Q L A T K A A R	H3 7-26	R17Cit r				acetylated
J11	A R K S T G G K A P R Kac Q L A T K A A R	H3 7-26	K18ac				acetylated
J12	A R K S T G G Kac A P Rme2s K Q L A T K A A R	H3 7-26	K14ac	R17me 2s			acetylated
J13	A R K S T G G Kac A P Rme2a K Q L A T K A A R	H3 7-26	K14ac	R17me 2a			acetylated
J14	A R K S T G G Kac A P R Kac Q L A T K A A R	H3 7-26	K14ac	K18ac			acetylated
J15	A R K S T G G K A P Rme2s Kac Q L A T K A A R	H3 7-26	R17me2 s	K18ac			acetylated
J16	A R K S T G G K A P Rme2a Kac Q L A T K A A R	H3 7-26	R17me2 a	K18ac			acetylated
J17	A R K S T G G K A P Cit Kac Q L A T K A A R	H3 7-26	R17Cit r	K18ac			acetylated
J18	A R K S T G G Kac A P Rme2s Kac Q L A T K A A R	H3 7-26	K14ac	R17me 2s	K18a c		acetylated
J19	A R K S T G G Kac A P Rme2a Kac Q L A T K A A R	H3 7-26	K14ac	R17me 2a	K18a c		acetylated
J20	P R K Q L A T K A A R K S A P A T G G	H3 16-35	unmod				acetylated
J21	P R K Q L A T K A A Rme2s K S A P A T G G	H3 16-35	R26me2 s				acetylated
J22	P R K Q L A T K A A Rme2a K S A P A T G G	H3 16-35	R26me2 a				acetylated
J23	P R K Q L A T K A A Cit K S A P A T G G	H3 16-35	R26Cit r				acetylated

J24	P R K Q L A T K A A R Kme1 S A P A T G G	H3 16-35	K27me1				acetylated
K 1	P R K Q L A T K A A R Kme2 S A P A T G G	H3 16-35	K27me2				acetylated
K 2	P R K Q L A T K A A R Kme3 S A P A T G G	H3 16-35	K27me3				acetylated
K 3	P R K Q L A T K A A R Kac S A P A T G G	H3 16-35	K27ac				acetylated
K 4	P R K Q L A T K A A R K pS A P A T G G	H3 16-35	S28P				acetylated
K 5	P R K Q L A T K A A Rme2s Kme1 S A P A T G G	H3 16-35	R26me2 s	K27me 1			acetylated
K 6	P R K Q L A T K A A Rme2s Kme2 S A P A T G G	H3 16-35	R26me2 s	K27me 2			acetylated
K 7	P R K Q L A T K A A Rme2s Kme3 S A P A T G G	H3 16-35	R26me2 s	K27me 3			acetylated
K 8	P R K Q L A T K A A Rme2s Kac S A P A T G G	H3 16-35	R26me2 s	K27ac			acetylated
K 9	P R K Q L A T K A A Rme2s K pS A P A T G G	H3 16-35	R26me2 s	S28P			acetylated
K10	P R K Q L A T K A A Rme2a Kme1 S A P A T G G	H3 16-35	R26me2 a	K27me 1			acetylated
K11	P R K Q L A T K A A Rme2a Kme2 S A P A T G G	H3 16-35	R26me2 a	K27me 2			acetylated
K12	P R K Q L A T K A A Rme2a Kme3 S A P A T G G	H3 16-35	R26me2 a	K27me 3			acetylated
K13	P R K Q L A T K A A Rme2a Kac S A P A T G G	H3 16-35	R26me2 a	K27ac			acetylated
K14	P R K Q L A T K A A Rme2a K pS A P A T G G	H3 16-35	R26me2 a	S28P			acetylated
K15	P R K Q L A T K A A Cit Kme1 S A P A T G G	H3 16-35	R26Cit r	K27me 1			acetylated
K16	P R K Q L A T K A A Cit Kme2 S A P A T G G	H3 16-35	R26Cit r	K27me 2			acetylated
K17	P R K Q L A T K A A Cit Kme3 S A P A T G G	H3 16-35	R26Cit r	K27me 3			acetylated
K18	P R K Q L A T K A A Cit K pS A P A T G G	H3 16-35	R26Cit r	S28P			acetylated
K19	P R K Q L A T K A A R Kme1 pS A P A T G G	H3 16-35	K27me1	S28P			acetylated
K20	P R K Q L A T K A A R Kme2 pS A P A T G G	H3 16-35	K27me2	S28P			acetylated
K21	P R K Q L A T K A A R Kme3 pS A P A T G G	H3 16-35	K27me3	S28P			acetylated

K22	P R K Q L A T K A A R Kac pS A P A T G G	H3 16-35	K27ac	S28P			acetylated
K23	P R K Q L A T K A A Rme2s Kme1 pS A P A T G G	H3 16-35	R26me2 s	K27me 1	S28P		acetylated
K24	P R K Q L A T K A A Rme2s Kme2 pS A P A T G G	H3 16-35	R26me2 s	K27me 2	S28P		acetylated
L 1	P R K Q L A T K A A Rme2s Kme3 pS A P A T G G	H3 16-35	R26me2 s	K27me 3	S28P		acetylated
L 2	P R K Q L A T K A A Rme2s Kac pS A P A T G G	H3 16-35	R26me2 s	K27ac	S28P		acetylated
L 3	P R K Q L A T K A A Rme2a Kme1 pS A P A T G G	H3 16-35	R26me2 a	K27me 1	S28P		acetylated
L 4	P R K Q L A T K A A Rme2a Kme2 pS A P A T G G	H3 16-35	R26me2 a	K27me 2	S28P		acetylated
L 5	P R K Q L A T K A A Rme2a Kme3 pS A P A T G G	H3 16-35	R26me2 a	K27me 3	S28P		acetylated
L 6	P R K Q L A T K A A Rme2a Kac pS A P A T G G	H3 16-35	R26me2 a	K27ac	S28P		acetylated
L 7	R K S A P A T G G V K K P H R Y R P G	H3 26-45	unmod				acetylated
L 8	R K S A P A T G G V Kme1 K P H R Y R P G	H3 26-45	K36me1				acetylated
L 9	R K S A P A T G G V Kme2 K P H R Y R P G	H3 26-45	K36me2				acetylated
L10	R K S A P A T G G V Kme3 K P H R Y R P G	H3 26-45	K36me3				acetylated
L11	R K S A P A T G G V Kac K P H R Y R P G	H3 26-45	K36ac				acetylated
L12	S G R G K G G K G L G K G G A K R H R	H4 1-19	unmod				free
L13	pS G R G K G G K G L G K G G A K R H R	H4 1-19	S1P				free
L14	S G Rme2s G K G G K G L G K G G A K R H R	H4 1-19	R3me2s				free
L15	S G Rme2a G K G G K G L G K G G A K R H R	H4 1-19	R3me2a				free
L16	S G R G Kac G G K G L G K G G A K R H R	H4 1-19	K5ac				free
L17	S G R G K G G Kac G L G K G G A K R H R	H4 1-19	K8ac				free
L18	S G R G K G G K G L G Kac G G A K R H R	H4 1-19	K12ac				free
L19	S G R G K G G K G L G K G G A Kac R H R	H4 1-19	K16ac				free

L20	pS G Rme2s G K G G K G L G K G G A K R H R	H4 1-19	S1P	R3me2 s			free
L21	pS G Rme2a G K G G K G L G K G G A K R H R	H4 1-19	S1P	R3me2 a			free
L22	pS G R G Kac G G K G L G K G G A K R H R	H4 1-19	S1P	K5ac			free
L23	S G Rme2s G Kac G G K G L G K G G A K R H R	H4 1-19	R3me2s	K5ac			free
L24	S G Rme2s G K G G Kac G L G K G G A K R H R	H4 1-19	R3me2s	K8ac			free
M 1	S G Rme2a G Kac G G K G L G K G G A K R H R	H4 1-19	R3me2a	K5ac			free
M 2	S G Rme2a G K G G Kac G L G K G G A K R H R	H4 1-19	R3me2a	K8ac			free
M 3	S G R G Kac G G Kac G L G K G G A K R H R	H4 1-19	K5ac	K8ac			free
M 4	S G R G K G G Kac G L G Kac G G A K R H R	H4 1-19	K8ac	K12ac			free
M 5	S G R G K G G Kac G L G K G G A Kac R H R	H4 1-19	K8ac	K16ac			free
M 6	S G R G K G G K G L G Kac G G A Kac R H R	H4 1-19	K12ac	K16ac			free
M 7	pS G Rme2s G Kac G G K G L G K G G A K R H R	H4 1-19	S1P	R3me2 s	K5ac		free
M 8	pS G Rme2a G Kac G G K G L G K G G A K R H R	H4 1-19	S1P	R3me2 a	K5ac		free
M 9	S G Rme2s G Kac G G Kac G L G K G G A K R H R	H4 1-19	R3me2s	K5ac	K8ac		free
M10	S G Rme2a G Kac G G Kac G L G K G G A K R H R	H4 1-19	R3me2a	K5ac	K8ac		free
M11	S G R G Kac G G Kac G L G Kac G G A K R H R	H4 1-19	K5ac	K8ac	K12a c		free
M12	S G R G K G G Kac G L G Kac G G A Kac R H R	H4 1-19	K8ac	K12ac	K16a c		free
M13	pS G Rme2s G Kac G G Kac G L G K G G A K R H R	H4 1-19	S1P	R3me2 s	K5ac	K8ac	free
M14	pS G Rme2a G Kac G G Kac G L G K G G A K R H R	H4 1-19	S1P	R3me2 a	K5ac	K8ac	free
M15	S G Rme2s G Kac G G Kac G L G Kac G G A K R H R	H4 1-19	R3me2s	K5ac	K8ac	K12ac	free
M16	S G Rme2a G Kac G G Kac G L G Kac G G A K R H R	H4 1-19	R3me2a	K5ac	K8ac	K12ac	free
M17	S G R G Kac G G Kac G L G Kac G G A Kac R H R	H4 1-19	K5ac	K8ac	K12a c	K16ac	free

M18	G K G G A K R H R K V L R D N I Q G I T	H4 11-30	unmod				acetylated
M19	G Kac G G A K R H R K V L R D N I Q G I T	H4 11-30	K12ac				acetylated
M20	G K G G A Kac R H R K V L R D N I Q G I T	H4 11-30	K16ac				acetylated
M21	G K G G A K Rme2s H R K V L R D N I Q G I T	H4 11-30	R17me2 s				acetylated
M22	G K G G A K Rme2a H R K V L R D N I Q G I T	H4 11-30	R17me2 a				acetylated
M23	G K G G A K R H Rme2s K V L R D N I Q G I T	H4 11-30	R19me2 s				acetylated
M24	G K G G A K R H Rme2a K V L R D N I Q G I T	H4 11-30	R19me2 a				acetylated
N 1	G K G G A K R H R Kme1 V L R D N I Q G I T	H4 11-30	K20me1				acetylated
N 2	G K G G A K R H R Kme2 V L R D N I Q G I T	H4 11-30	K20me2				acetylated
N 3	G K G G A K R H R Kme3 V L R D N I Q G I T	H4 11-30	K20me3				acetylated
N 4	G K G G A K R H R Kac V L R D N I Q G I T	H4 11-30	K20ac				acetylated
N 5	G K G G A K R H R K V L Rme2a D N I Q G I T	H4 11-30	R24me2 a				acetylated
N 6	G K G G A K R H R K V L Rme2s D N I Q G I T	H4 11-30	R24me2 s				acetylated
N 7	G Kac G G A Kac R H R K V L R D N I Q G I T	H4 11-30	K12ac	K16ac			acetylated
N 8	G K G G A Kac Rme2s H R K V L R D N I Q G I T	H4 11-30	K16ac	R17me 2s			acetylated
N 9	G K G G A Kac Rme2a H R K V L R D N I Q G I T	H4 11-30	K16ac	R17me 2a			acetylated
N10	G K G G A Kac R H Rme2s K V L R D N I Q G I T	H4 11-30	K16ac	R19me 2s			acetylated
N11	G K G G A Kac R H Rme2a K V L R D N I Q G I T	H4 11-30	K16ac	R19me 2a			acetylated
N12	G K G G A Kac R H R Kme1 V L R D N I Q G I T	H4 11-30	K16ac	K20me 1			acetylated
N13	G K G G A Kac R H R Kme2 V L R D N I Q G I T	H4 11-30	K16ac	K20me 2			acetylated
N14	G K G G A Kac R H R Kme3 V L R D N I Q G I T	H4 11-30	K16ac	K20me 3			acetylated
N15	G K G G A Kac R H R Kac V L R D N I Q G I T	H4 11-30	K16ac	K20ac			acetylated

N16	G Kac G G A Kac R H R Kme1 V L R D N I Q G I T	H4 11-30	K12ac	K16ac	K20m e1		acetylated
N17	G Kac G G A Kac R H R Kme2 V L R D N I Q G I T	H4 11-30	K12ac	K16ac	K20m e2		acetylated
N18	G Kac G G A Kac R H R Kme3 V L R D N I Q G I T	H4 11-30	K12ac	K16ac	K20m e3		acetylated
N19	G Kac G G A Kac R H R Kac V L R D N I Q G I T	H4 11-30	K12ac	K16ac	K20a c		acetylated
N20	G K G G A K R H Rme2a Kme1 V L R D N I Q G I T	H4 11-30	R19me2 a	K20me 1			acetylated
N21	G K G G A K R H Rme2a Kme2 V L R D N I Q G I T	H4 11-30	R19me2 a	K20me 2			acetylated
N22	G K G G A K R H Rme2a Kme3 V L R D N I Q G I T	H4 11-30	R19me2 a	K20me 3			acetylated
N23	G K G G A K R H Rme2a Kac V L R D N I Q G I T	H4 11-30	R19me2 a	K20ac			acetylated
N24	G K G G A K R H Rme2s Kme1 V L R D N I Q G I T	H4 11-30	R19me2 s	K20me 1			acetylated
O 1	G K G G A K R H Rme2s Kme2 V L R D N I Q G I T	H4 11-30	R19me2 s	K20me 2			acetylated
O 2	G K G G A K R H Rme2s Kme3 V L R D N I Q G I T	H4 11-30	R19me2 s	K20me 3			acetylated
O 3	G K G G A K R H Rme2s Kac V L R D N I Q G I T	H4 11-30	R19me2 s	K20ac			acetylated
O 4	G K G G A K R H R Kme1 V L Rme2a D N I Q G I T	H4 11-30	R24me2 a	K20me 1			acetylated
O 5	G K G G A K R H R Kme2 V L Rme2a D N I Q G I T	H4 11-30	R24me2 a	K20me 2			acetylated
O 6	G K G G A K R H R Kme3 V L Rme2a D N I Q G I T	H4 11-30	R24me2 a	K20me 3			acetylated
O 7	G K G G A K R H R Kac V L Rme2a D N I Q G I T	H4 11-30	R24me2 a	K20ac			acetylated
O 8	G K G G A K R H R Kme1 V L Rme2s D N I Q G I T	H4 11-30	R24me2 s	K20me 1			acetylated
O 9	G K G G A K R H R Kme2 V L Rme2s D N I Q G I T	H4 11-30	R24me2 s	K20me 2			acetylated
O10	G K G G A K R H R Kme3 V L Rme2s D N I Q G I T	H4 11-30	R24me2 s	K20me 3			acetylated
O11	G K G G A K R H R Kac V L Rme2s D N I Q G I T	H4 11-30	R24me2 s	K20ac			acetylated
O12	S G R G K Q G G K A R A K A K S R S S	H2a 1-19	unmod				free
O13	pS G R G K Q G G K A R A K A K S R S S	H2a 1-19	S1P				free

O14	S G R G Kac Q G G K A R A K A K S R S S	H2a 1-19	K5ac					free
O15	S G R G K Q G G Kac A R A K A K S R S S	H2a 1-19	K9ac					free
O16	S G R G K Q G G K A R A Kac A K S R S S	H2a 1-19	K13ac					free
O17	pS G R G Kac Q G G K A R A K A K S R S S	H2a 1-19	S1P	K5ac				free
O18	pS G R G K Q G G Kac A R A K A K S R S S	H2a 1-19	S1P	K9ac				free
O19	pS G R G K Q G G K A R A Kac A K S R S S	H2a 1-19	S1P	K13ac				free
O20	S G R G Kac Q G G Kac A R A K A K S R S S	H2a 1-19	K5ac	K9ac				free
O21	S G R G Kac Q G G K A R A Kac A K S R S S	H2a 1-19	K5ac	K13ac				free
O22	S G R G K Q G G Kac A R A Kac A K S R S S	H2a 1-19	K9ac	K13ac				free
O23	pS G R G Kac Q G G Kac A R A K A K S R S S	H2a 1-19	S1P	K5ac	K9ac			free
O24	pS G R G Kac Q G G K A R A Kac A K S R S S	H2a 1-19	S1P	K5ac	K13a c			free
P 1	pS G R G K Q G G Kac A R A Kac A K S R S S	H2a 1-19	S1P	K9ac	K13a c			free
P 2	S G R G Kac Q G G Kac A R A Kac A K S R S S	H2a 1-19	K5ac	K9ac	K13a c			free
P 3	pS G R G Kac Q G G Kac A R A Kac A K S R S S	H2a 1-19	S1P	K5ac	K9ac	K13ac		free
P 4	P D P A K S A P A P K K G S K K A V T	H2B 1-19	unmod					free
P 5	P D P A Kac S A P A P K K G S K K A V T	H2B 1-19	K5ac					free
P 6	P D P A K S A P A P K Kac G S K K A V T	H2B 1-19	K12ac					free
P 7	P D P A K S A P A P K K G pS K K A V T	H2B 1-19	S14P					free
P 8	P D P A K S A P A P K K G S Kac K A V T	H2B 1-19	K15ac					free
P 9	P D P A Kac S A P A P K Kac G S K K A V T	H2B 1-19	K5ac	K12ac				free
P10	P D P A Kac S A P A P K K G pS K K A V T	H2B 1-19	K5ac	S14P				free
P11	P D P A Kac S A P A P K K G S Kac K A V T	H2B 1-19	K5ac	K15ac				free

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