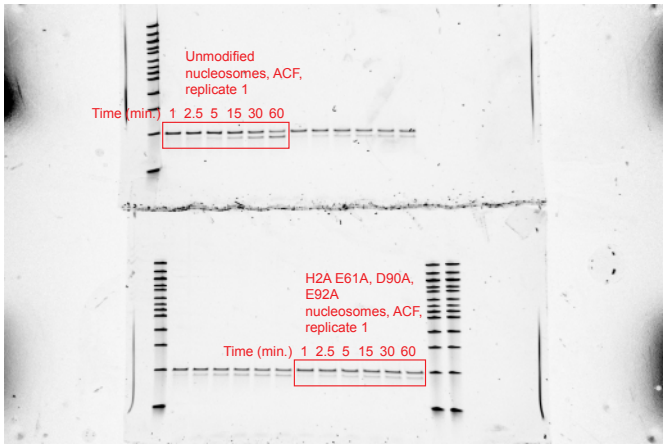
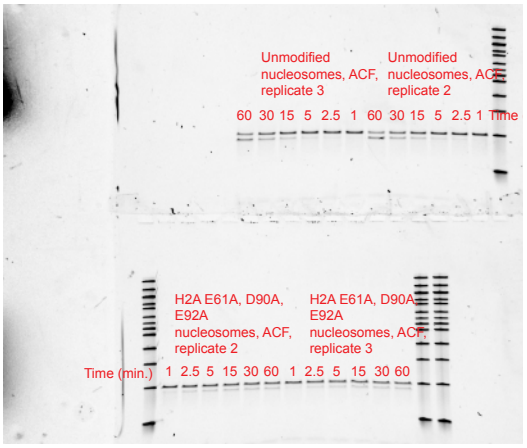
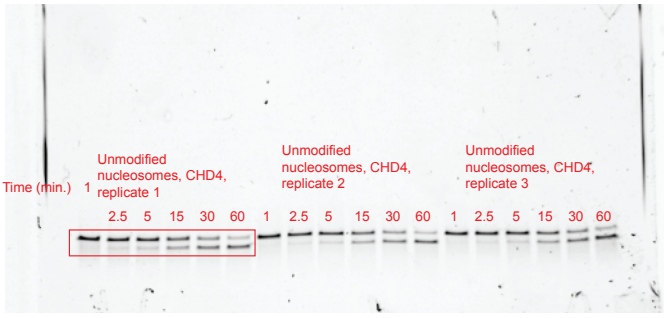
SUPPLEMENTARY INFORMATION

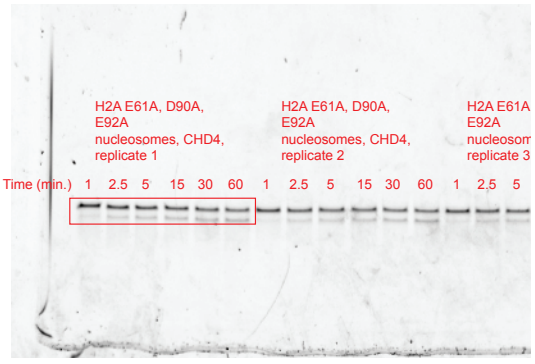
doi:10.1038/nature23671

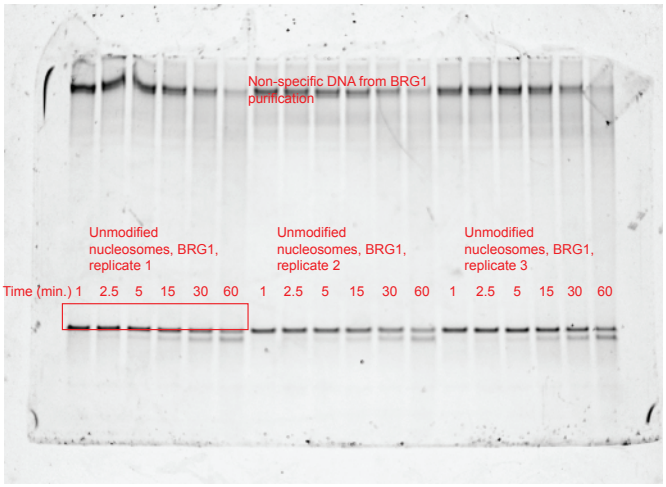
Figure 4b

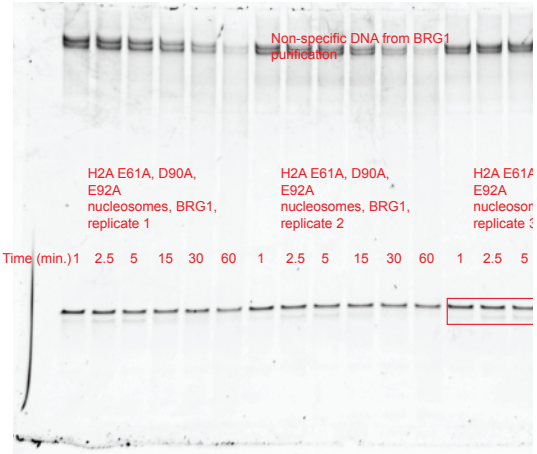




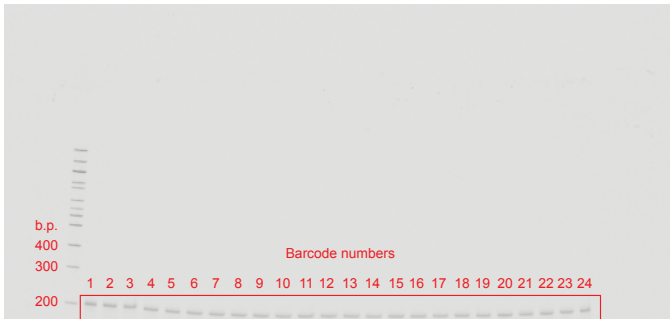


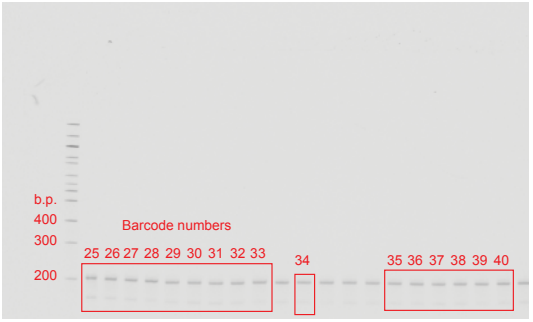


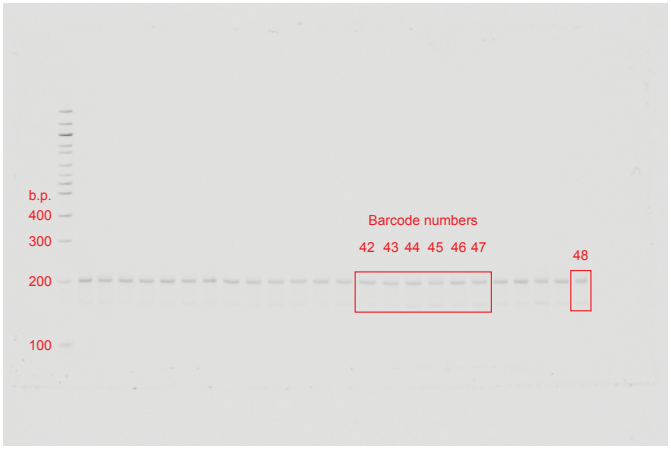


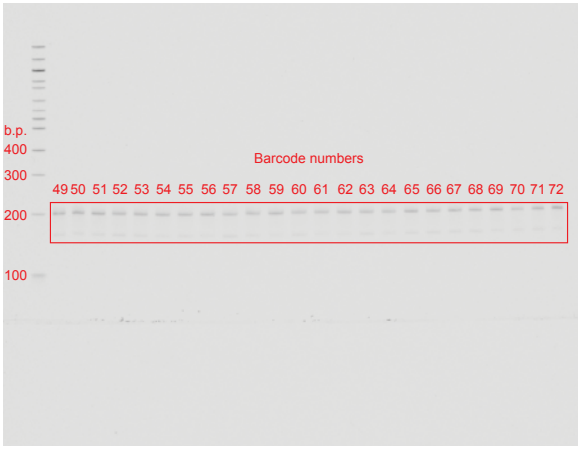


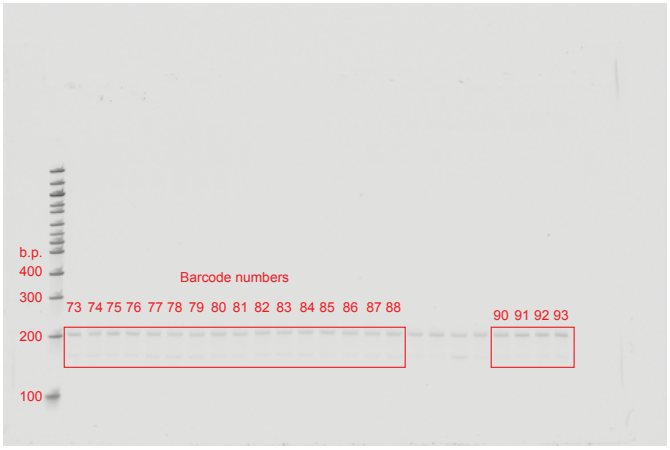
Extended Data Figure 1a

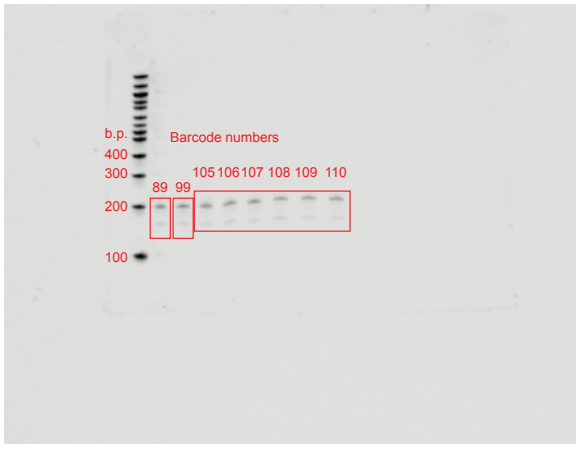


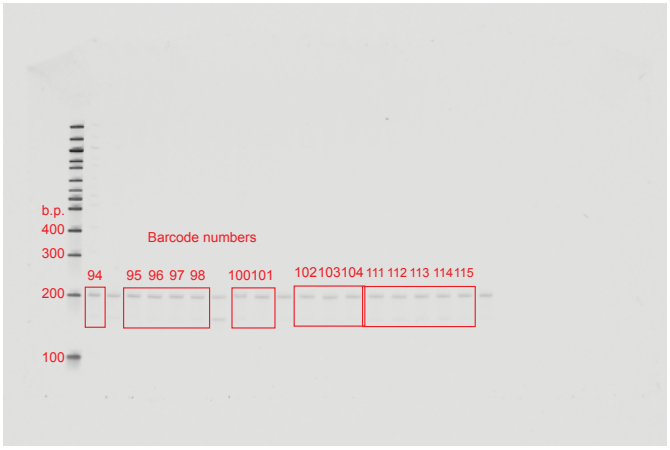




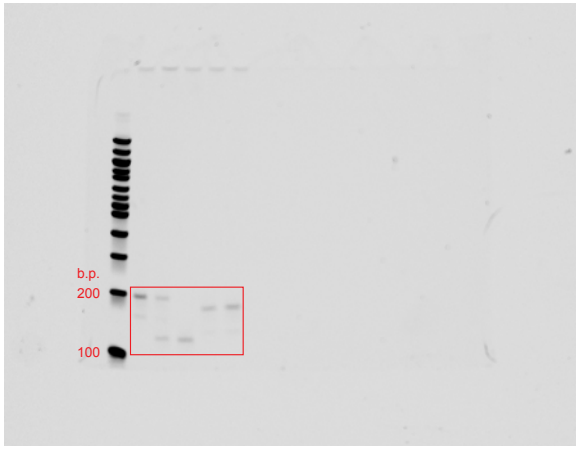




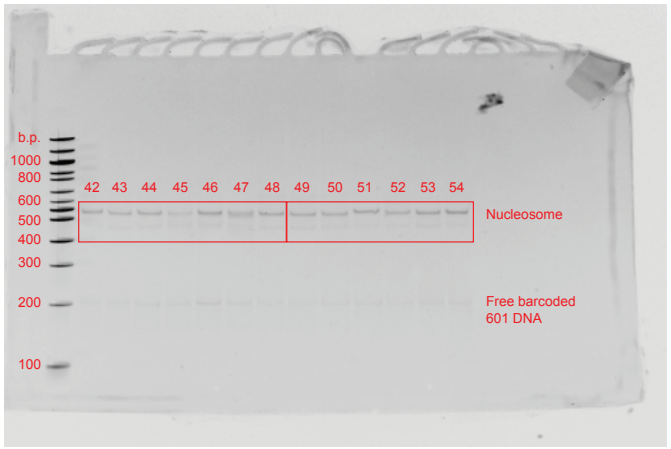


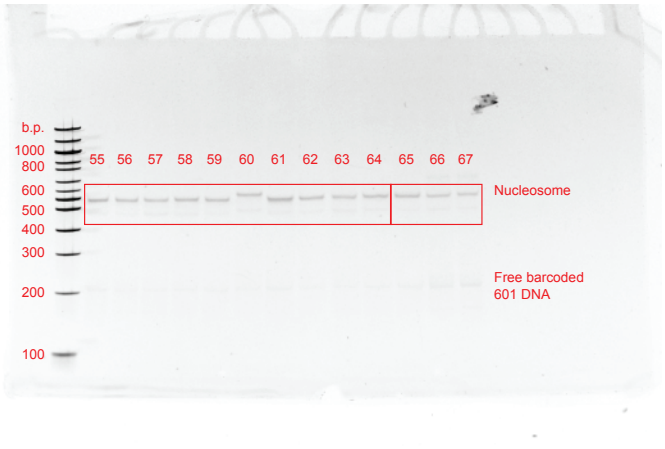


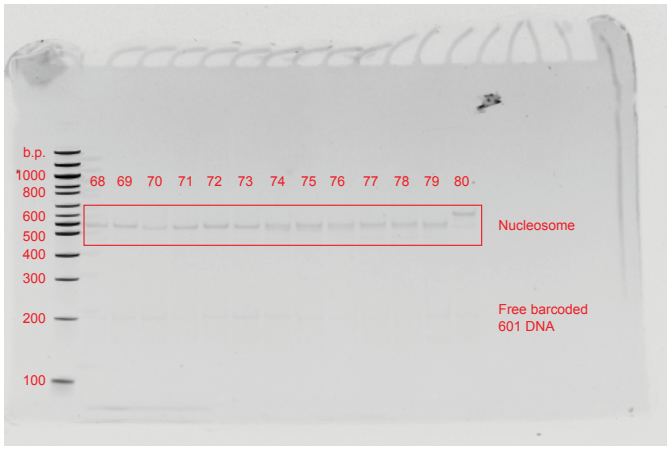
Extended Data Figure 1b

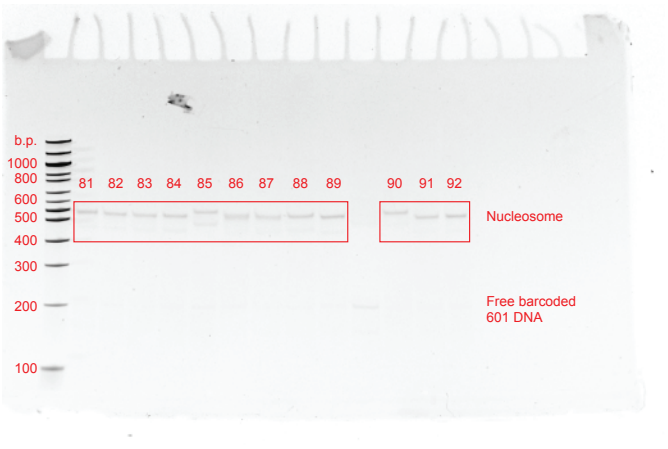


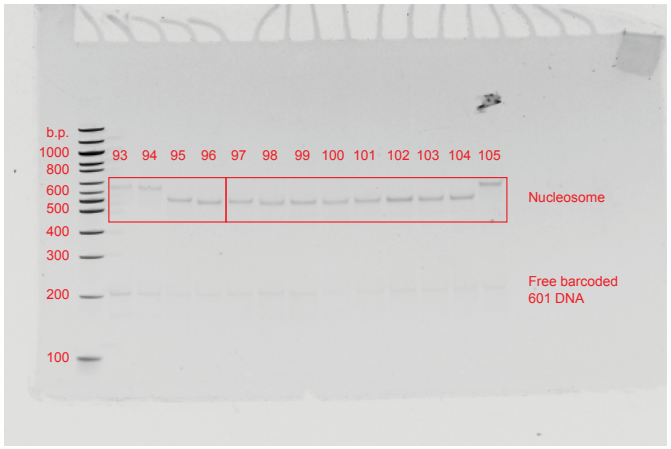
Extended Data Figure 2a

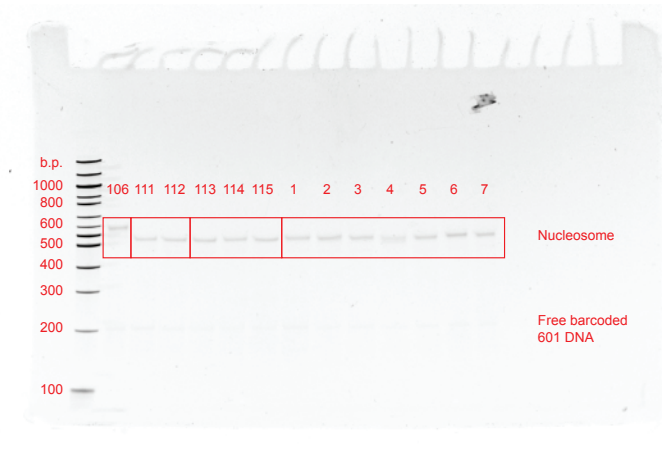


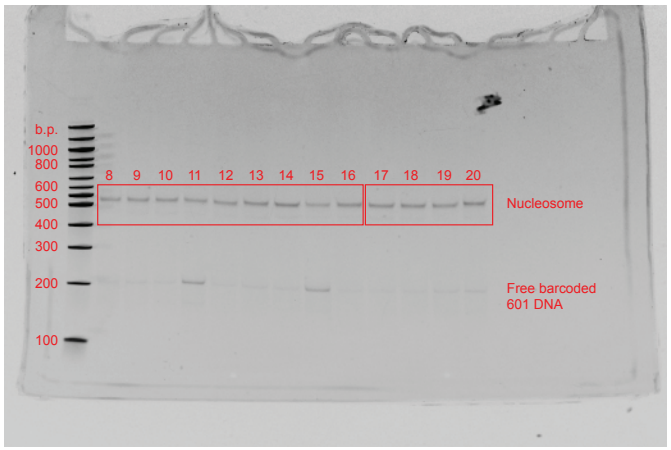


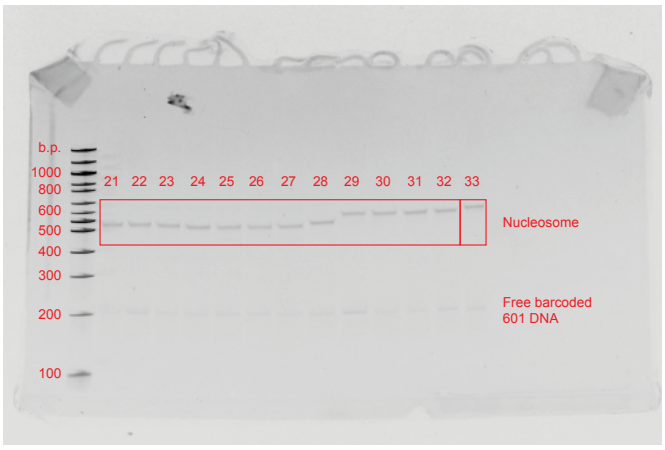


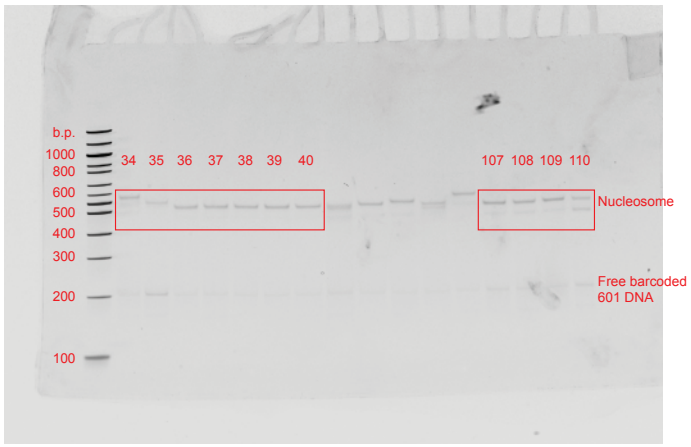




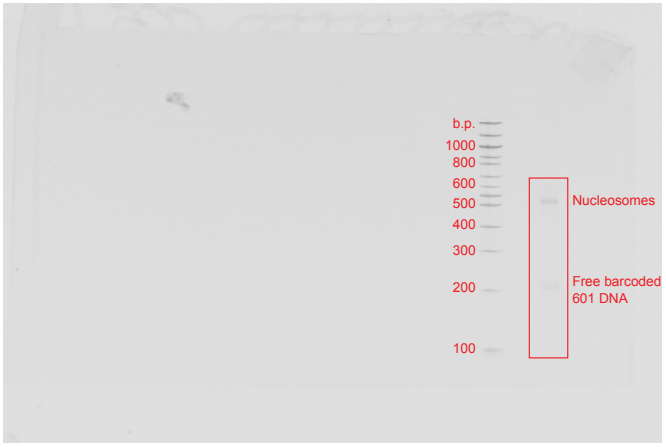




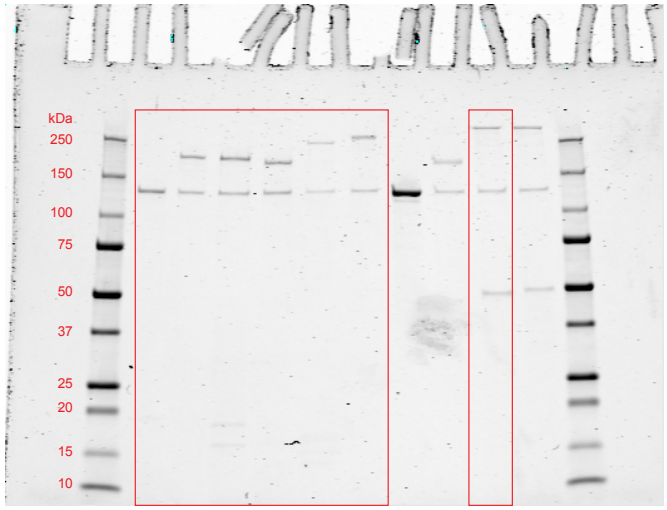




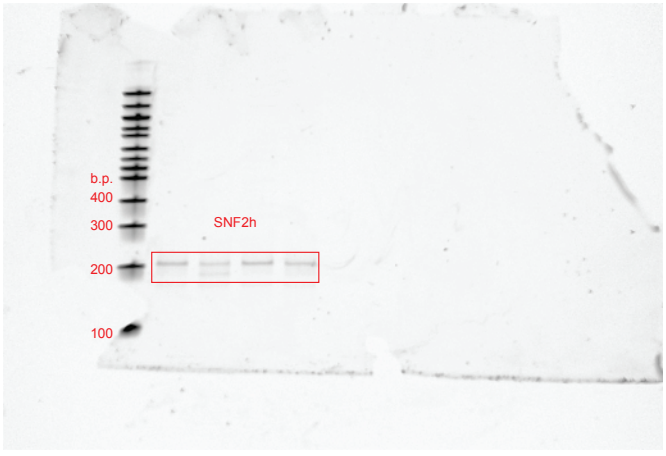
Extended Data Figure 2b

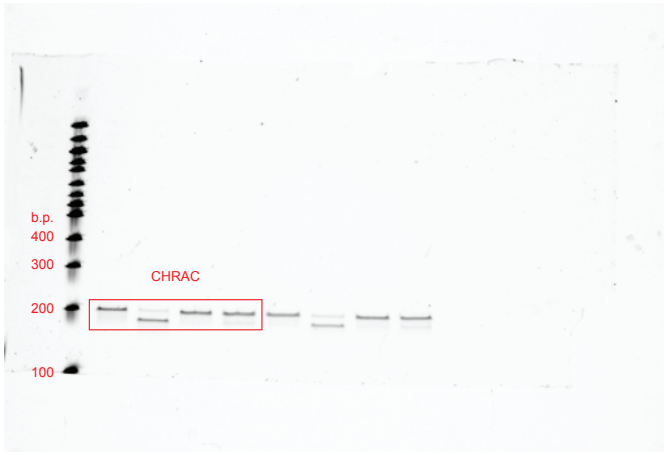


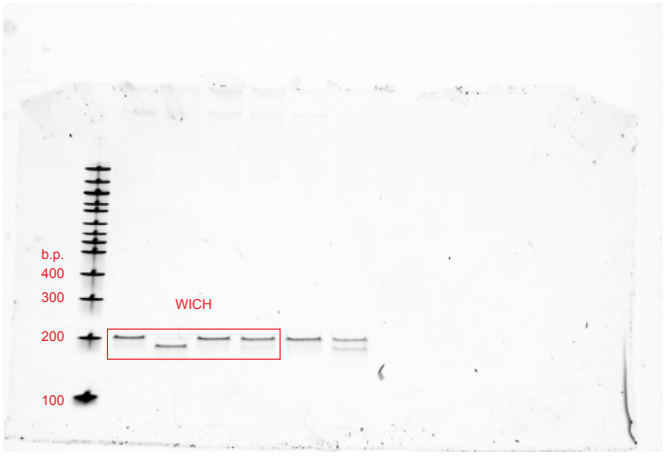
Extended Data Figure 3a

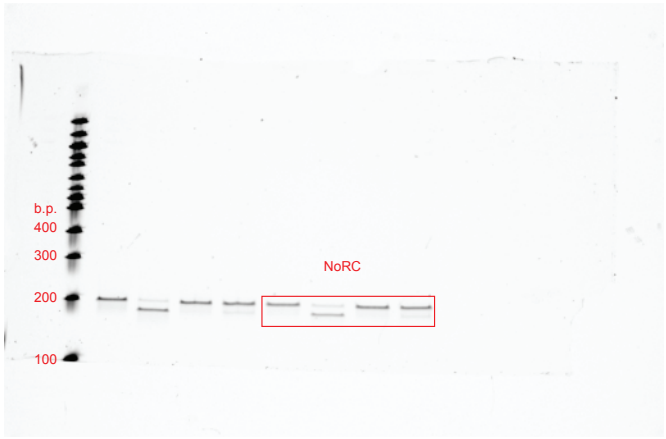


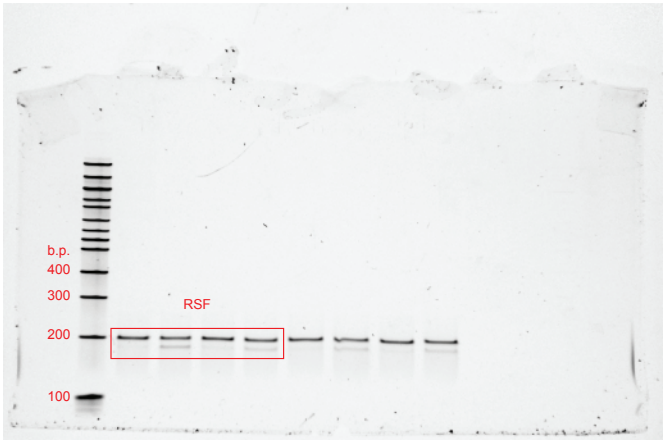
Extended Data Figure 3b

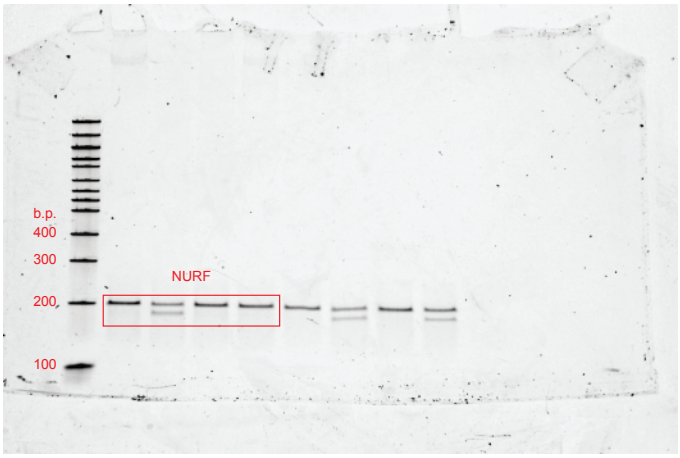




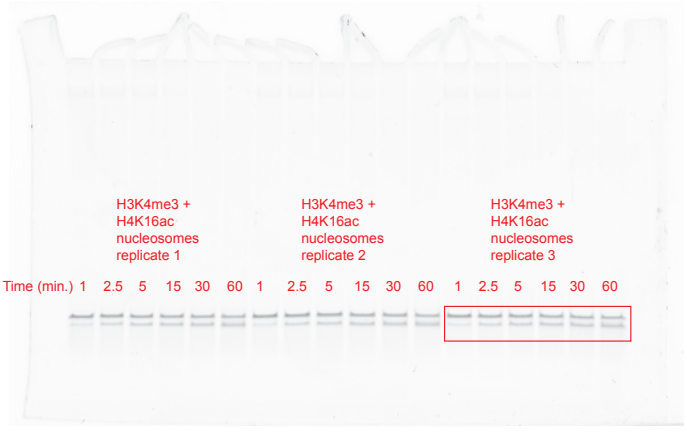




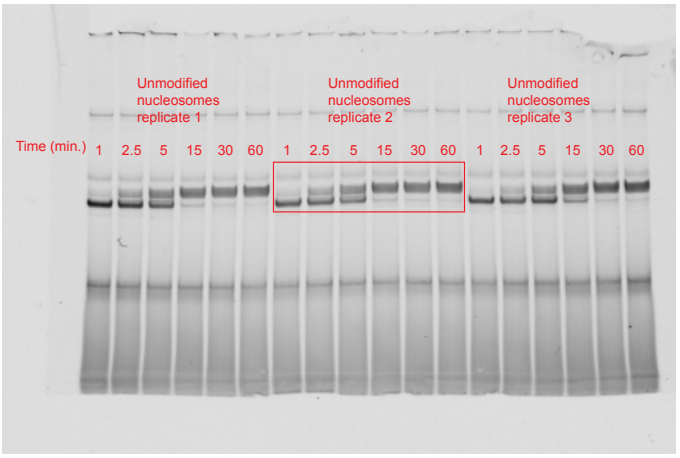


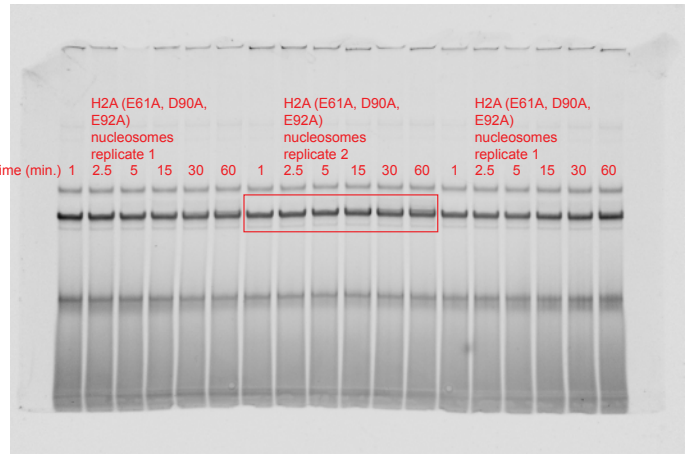


Extended Data Figure 8a

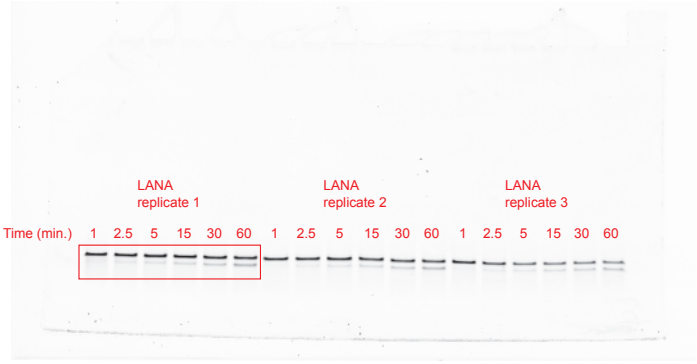


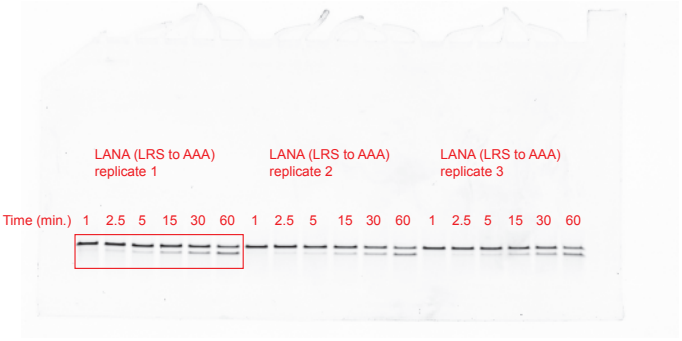
Extended Data Figure 8b





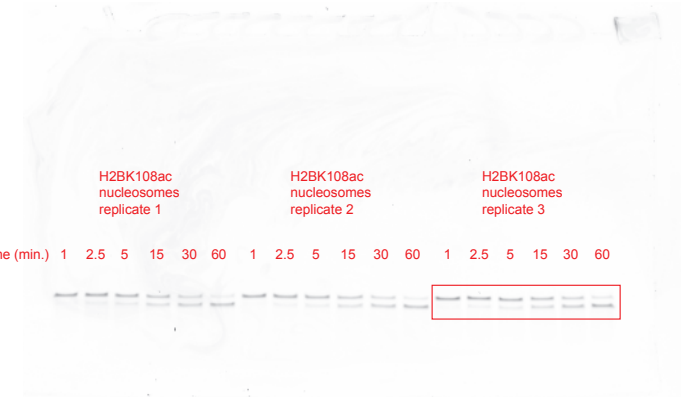
Extended Data Figure 8c

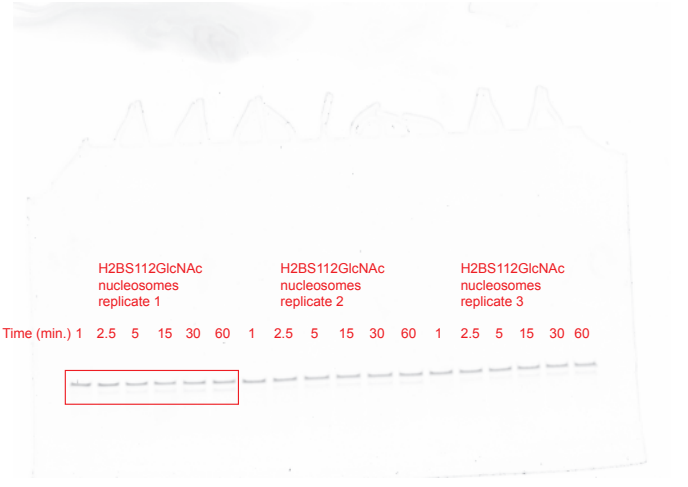




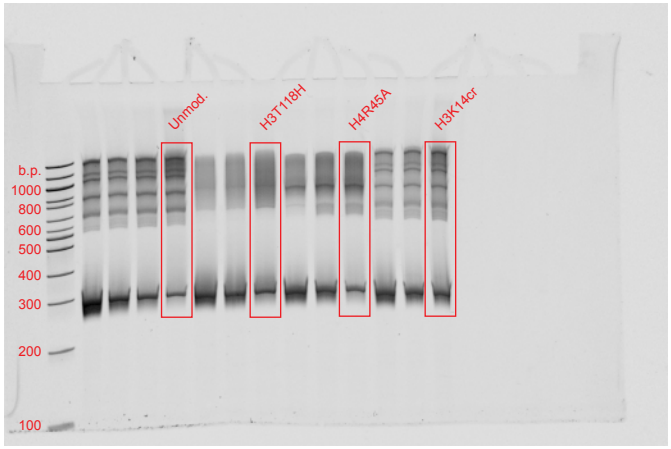
Extended Data Figure 8d

Data for unmodified nucleosomes were calculated from the same gels as in Figure 4b.

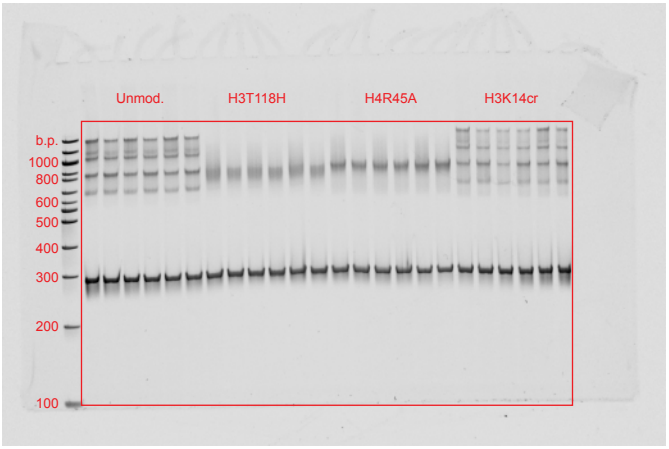




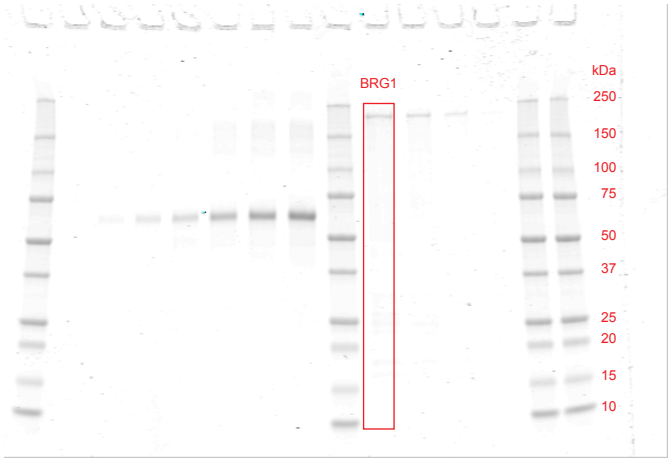
Supplementary Figure 3a

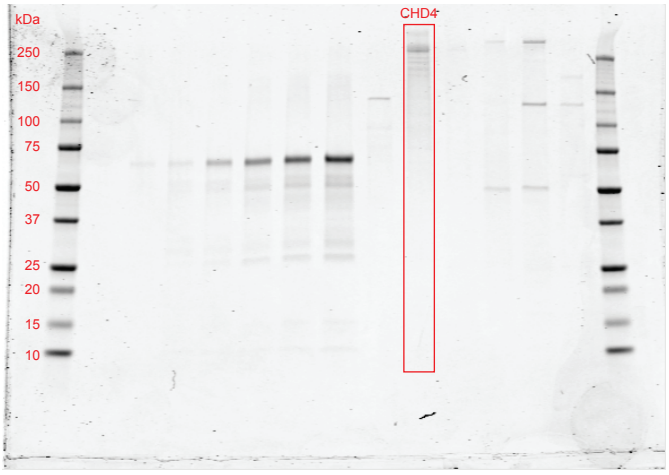


Supplementary Data Figure 3b

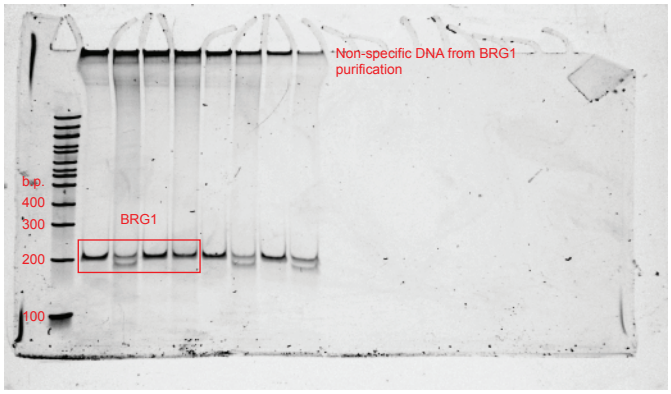


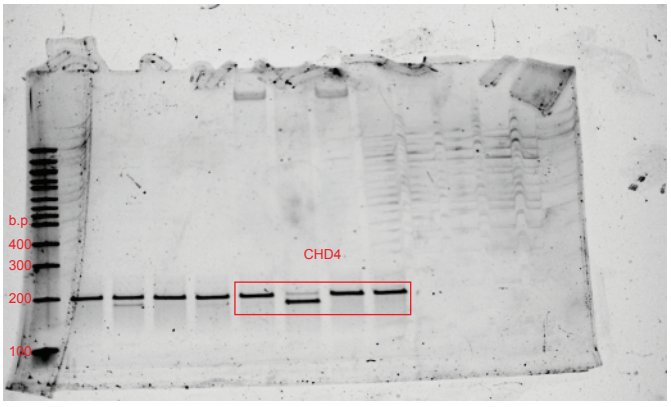
Supplementary Figure 5a





Supplementary Figure 5b

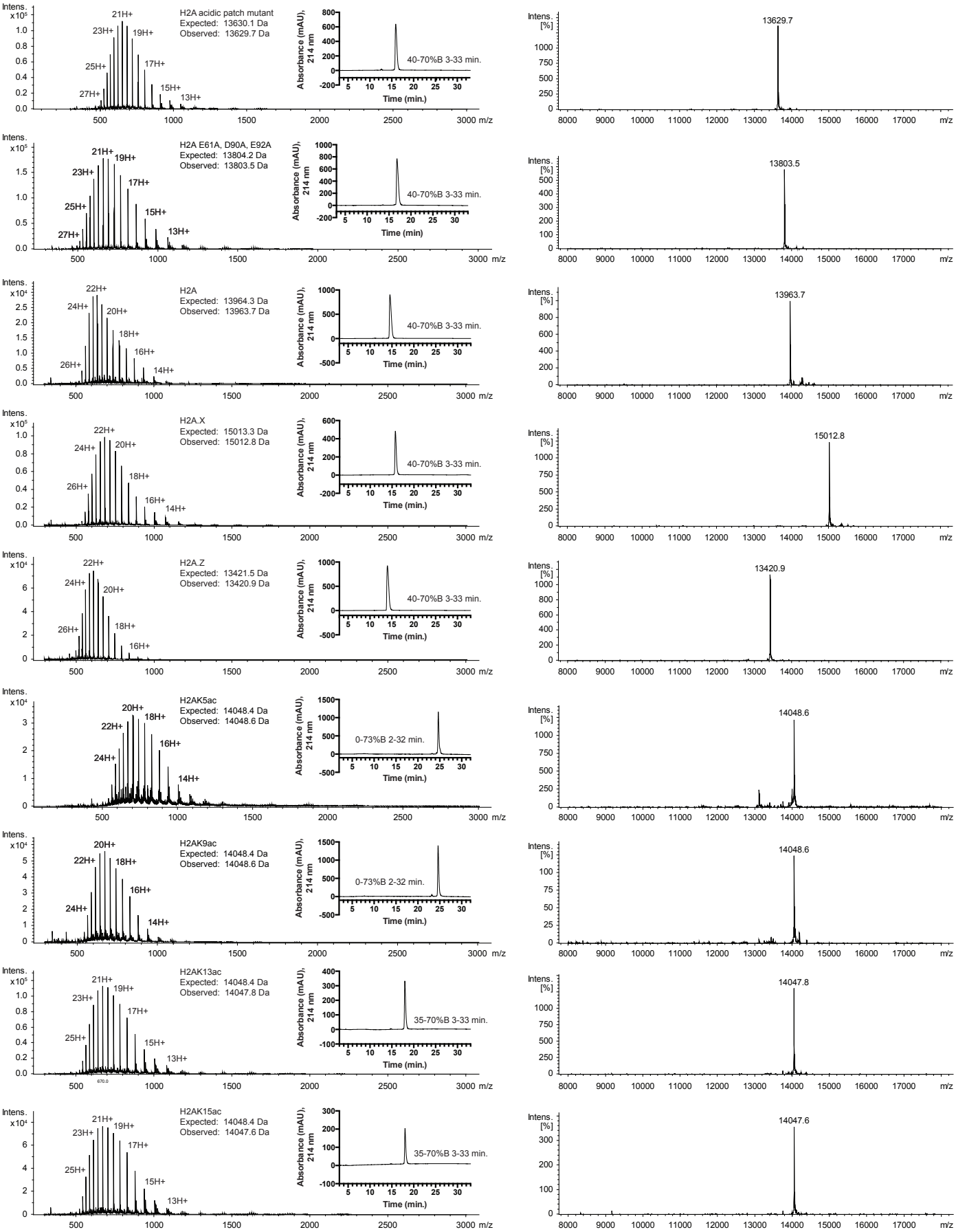


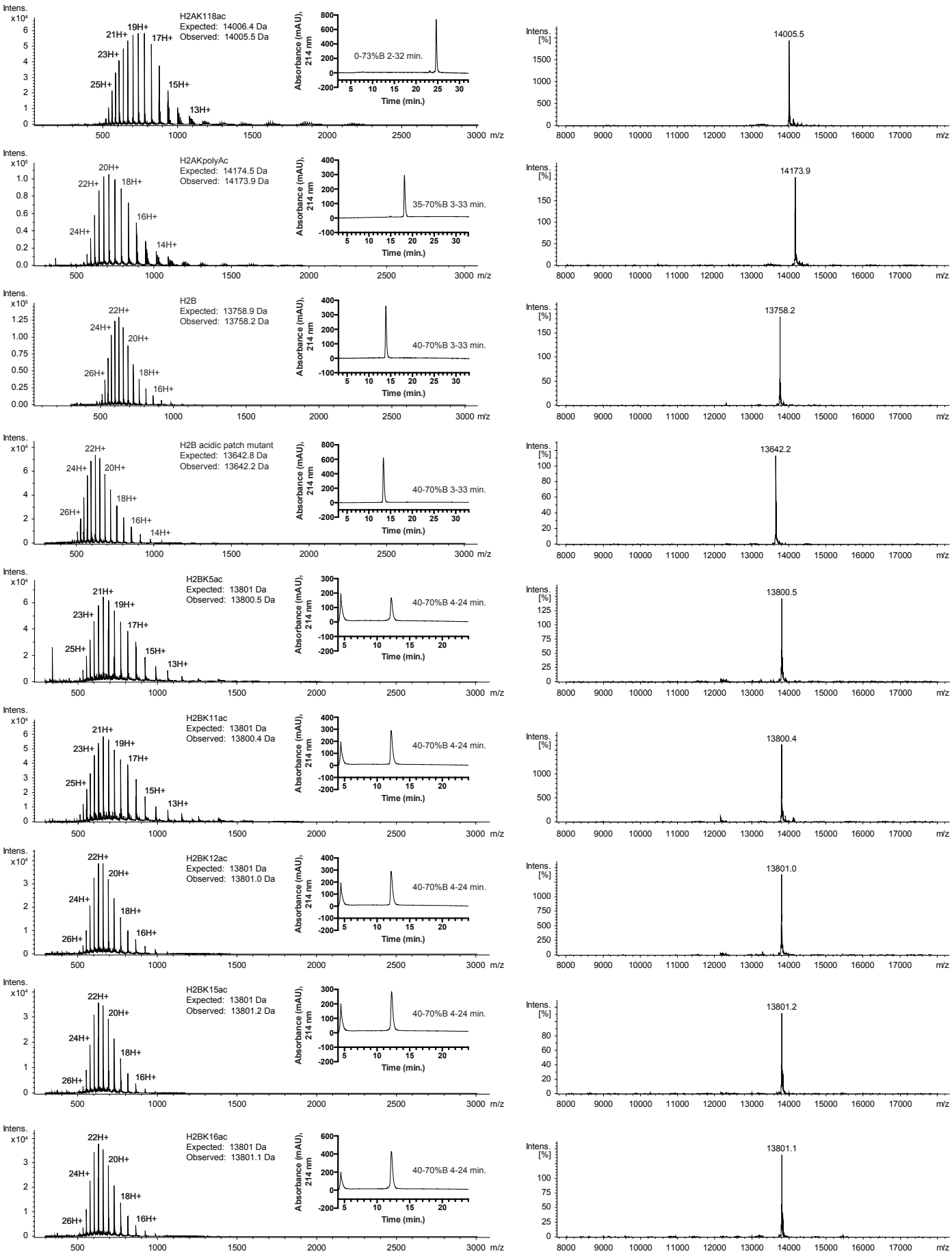


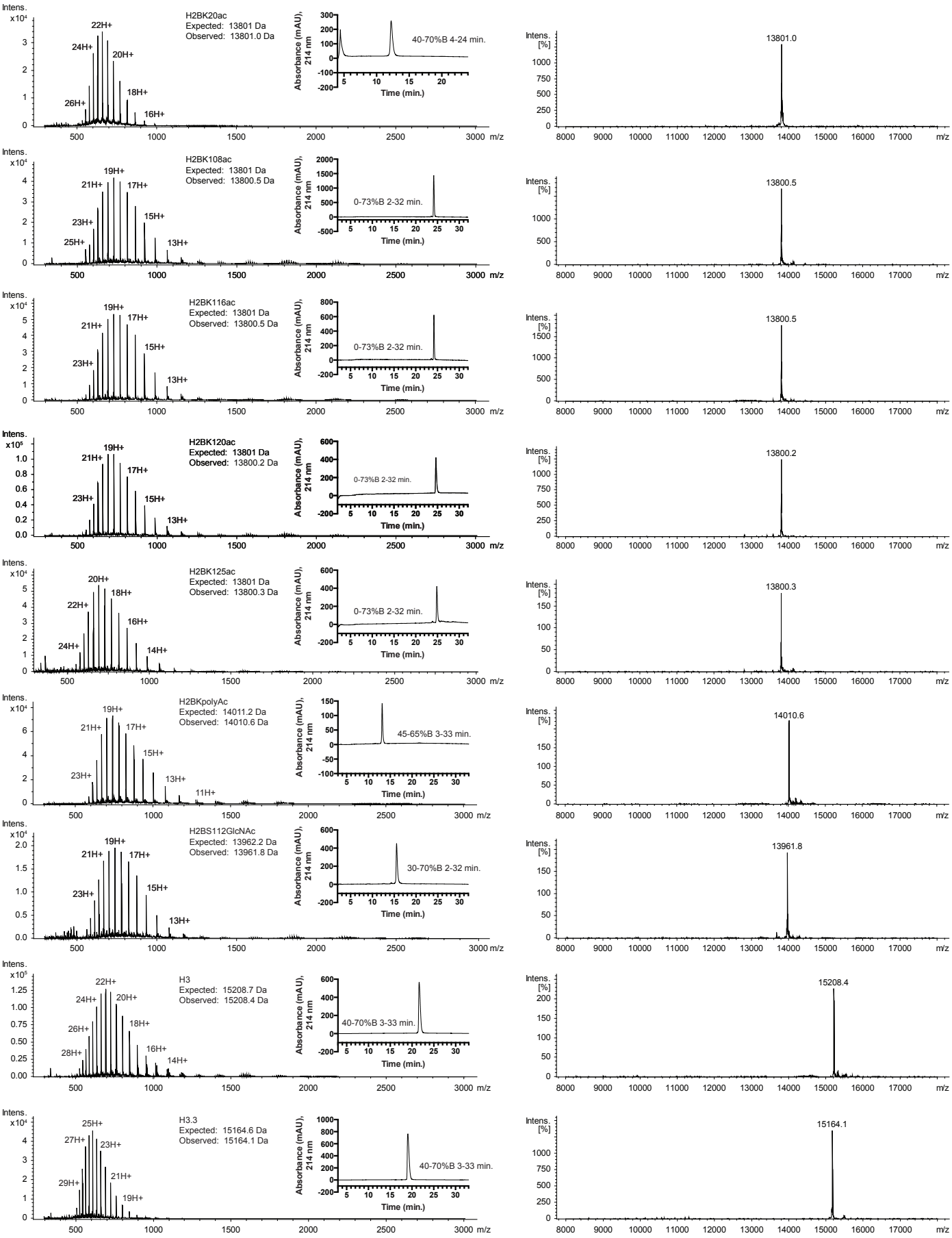
Supplementary Figure 6b

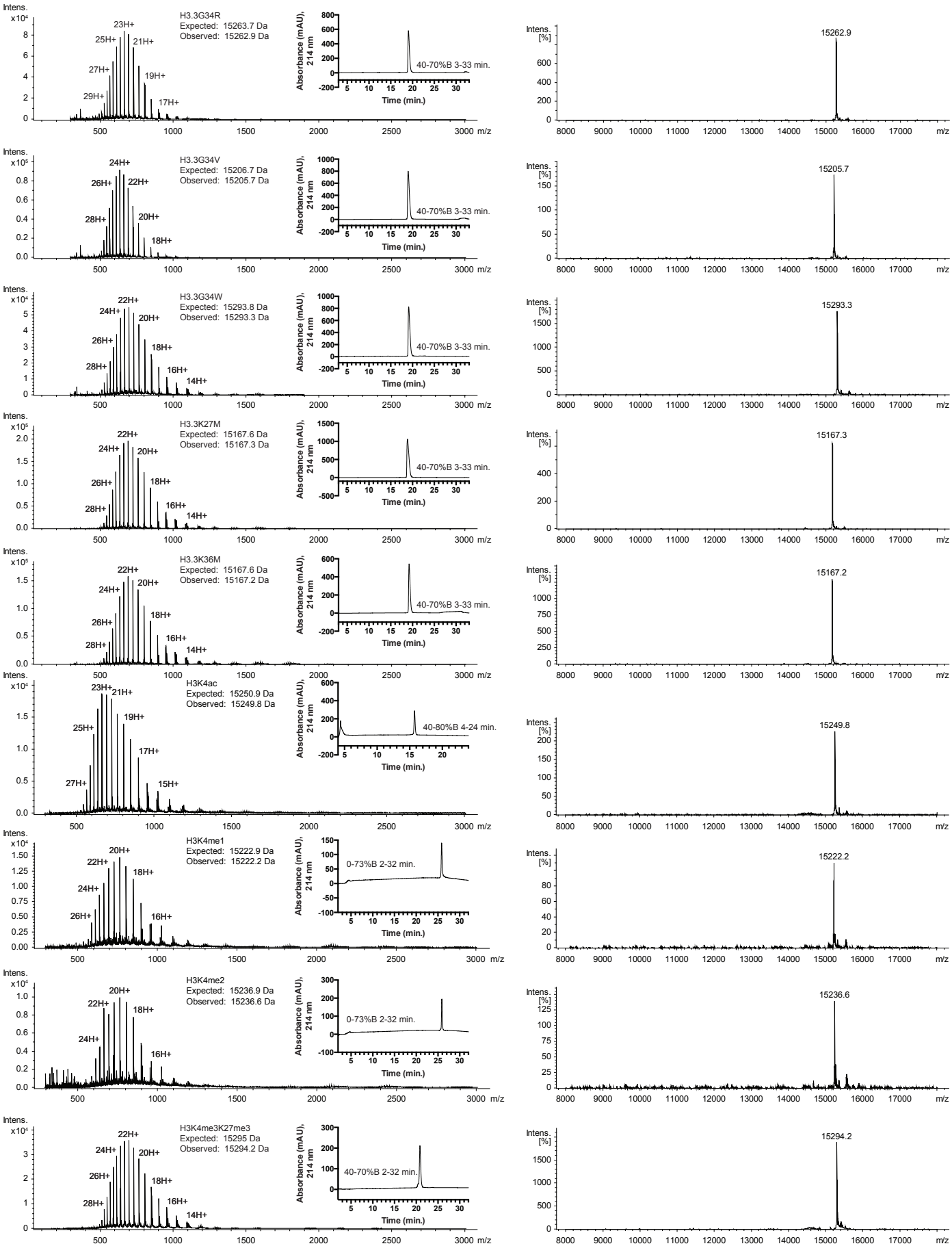
See section of this figure corresponding to 'Extended Data Figure 2a' for uncropped gels of nucleosomes in Supplementary Figure 6b

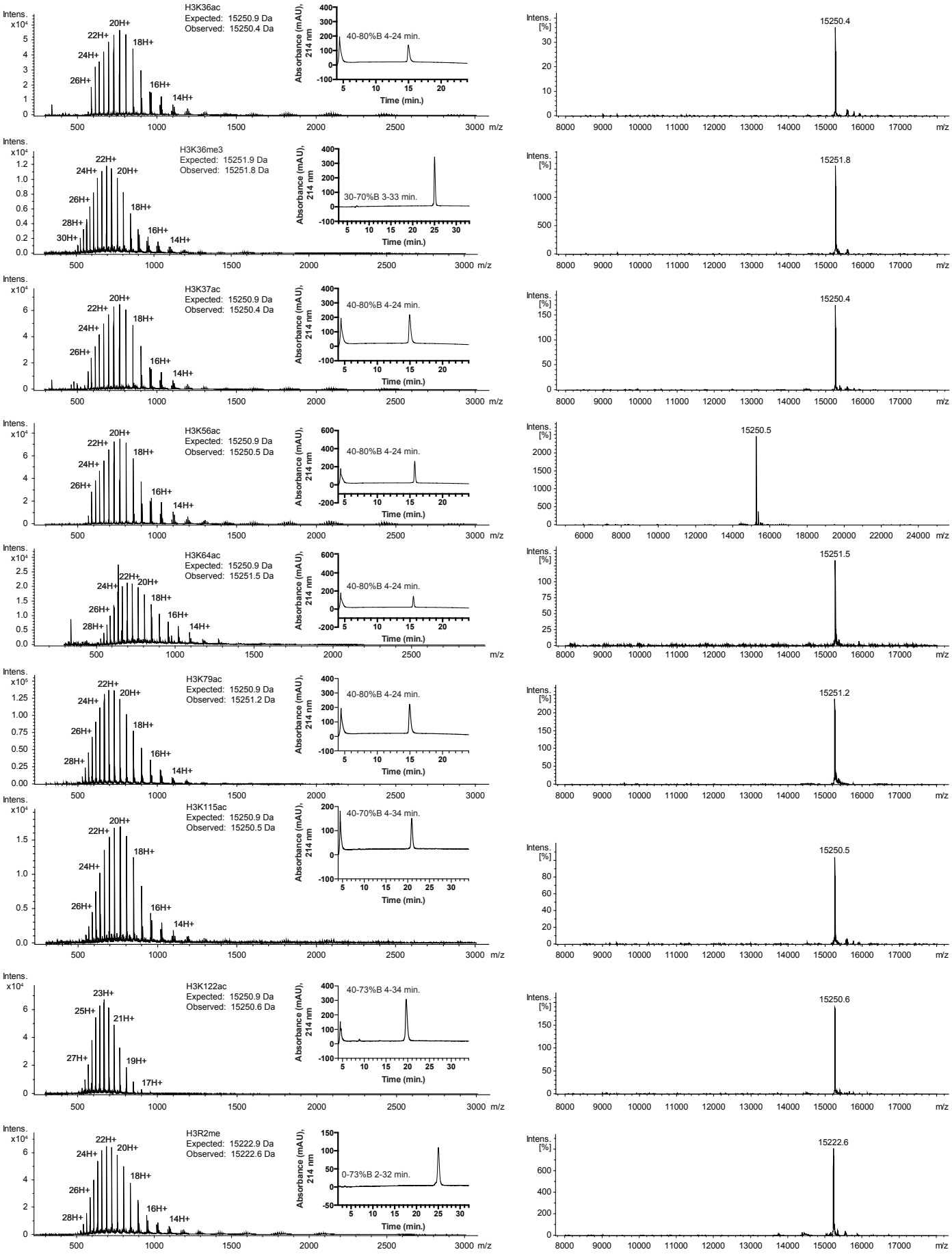
Supplementary Figure 1 | Gel Source Data. Gel source data from relevant experiments performed in this study are labeled according to their corresponding figure. Pertinent information for interpretation is noted in red, and cropped areas consistent with how they were displayed in figures are approximately enclosed in red boxes.

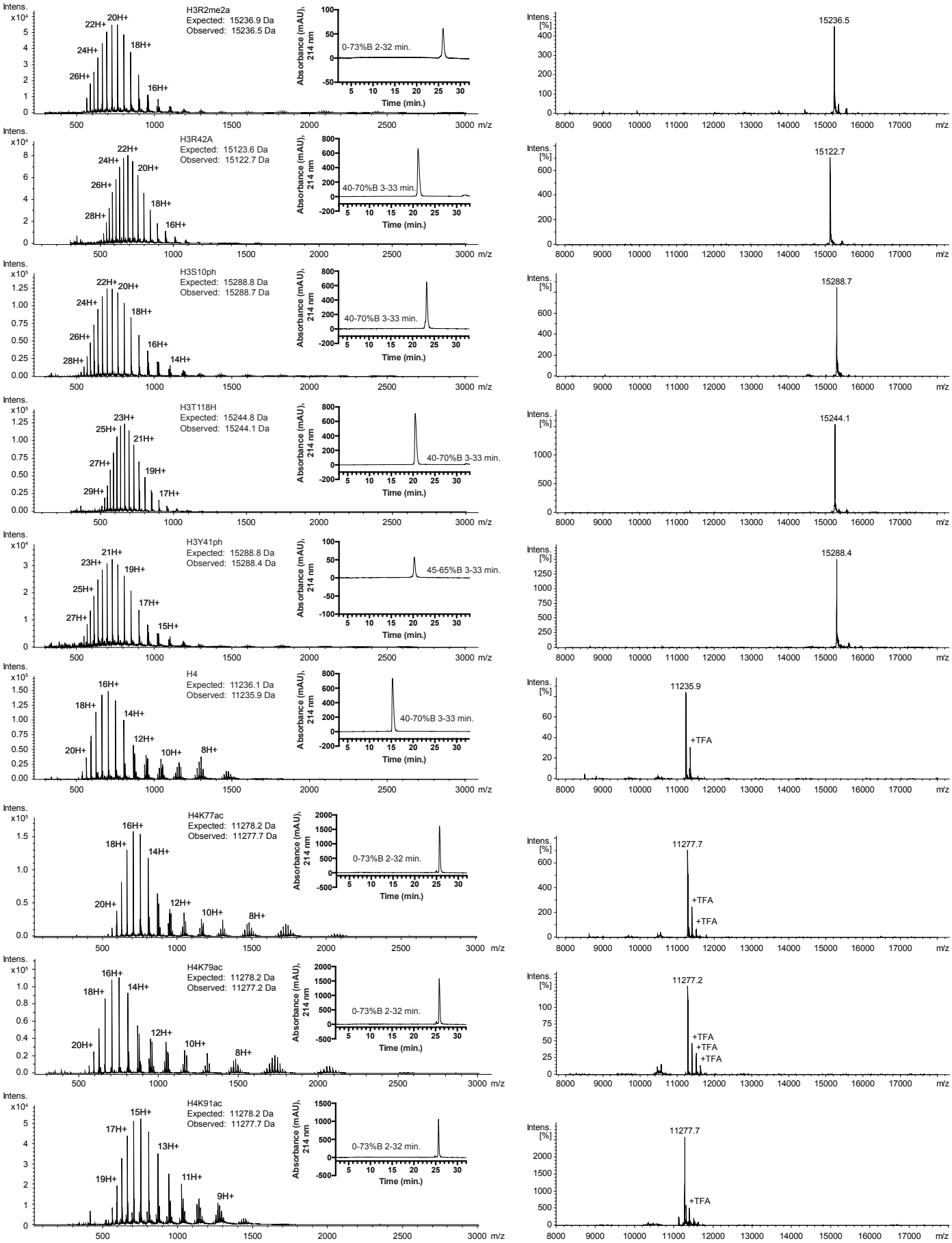

H2A acidic patch mutant
Expected: 13630.1 Da
Observed: 13629.7 Da
40-70%B 3-33 min.
13629.7
H2A E61A, D90A, E92A
Expected: 13804.2 Da
Observed: 13803.5 Da
40-70%B 3-33 min.
13803.5
H2A
Expected: 13964.3 Da
Observed: 13963.7 Da
40-70%B 3-33 min.
13963.7
H2A.X
Expected: 15013.3 Da
Observed: 15012.8 Da
40-70%B 3-33 min.
15012.8
H2A.Z
Expected: 13421.5 Da
Observed: 13420.9 Da
40-70%B 3-33 min.
13420.9
H2AK5ac
Expected: 14048.4 Da
Observed: 14048.6 Da
0-73%B 2-32 min.
14048.6
H2AK9ac
Expected: 14048.4 Da
Observed: 14048.6 Da
0-73%B 2-32 min.
14048.6
H2AK13ac
Expected: 14048.4 Da
Observed: 14047.8 Da
35-70%B 3-33 min.
14047.8
H2AK15ac
Expected: 14048.4 Da
Observed: 14047.6 Da
35-70%B 3-33 min.
14047.6
Intens.
Absorbance (mAU), 214 nm
Time (min.)
m/z

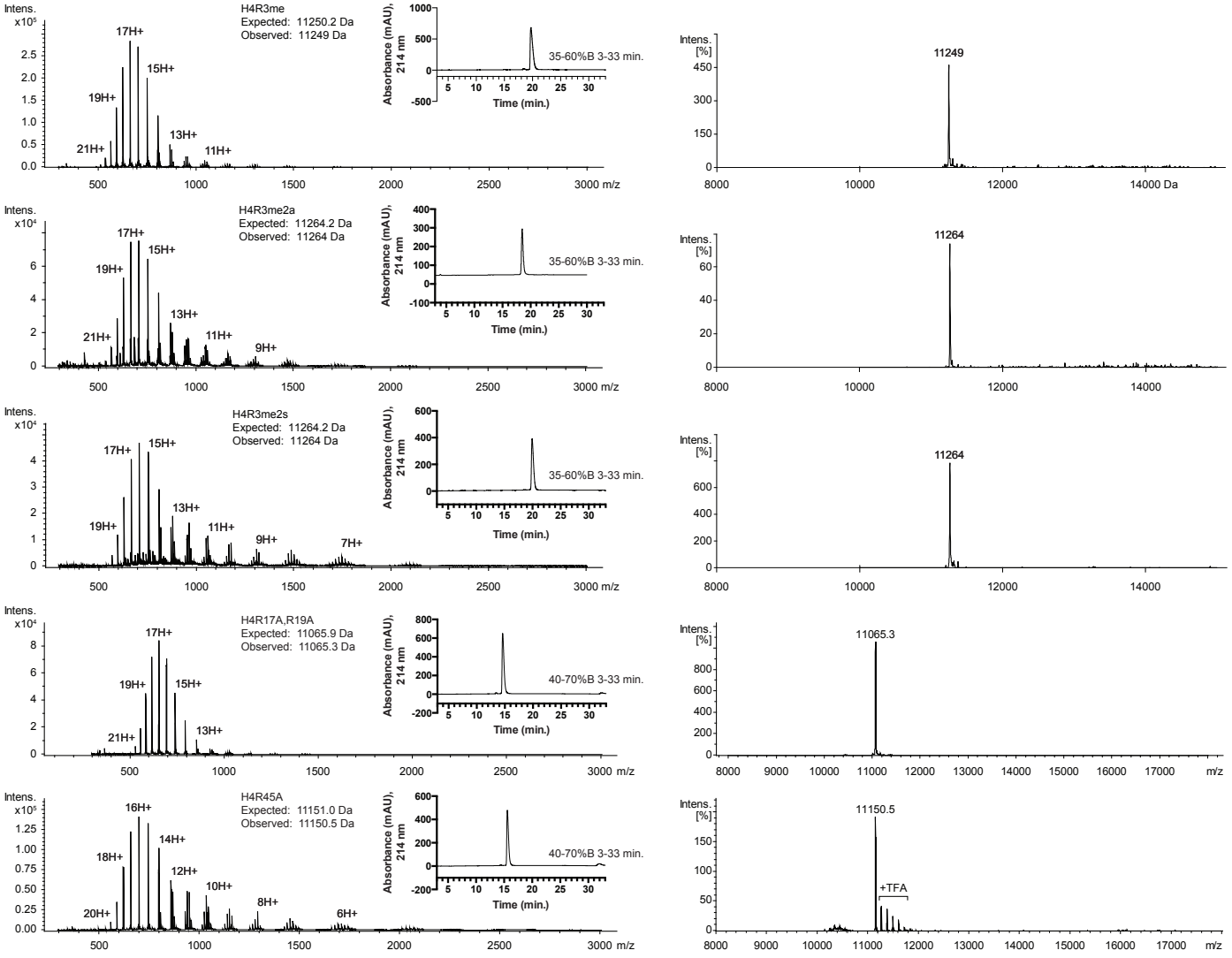

H2AK118ac
Expected: 14006.4 Da
Observed: 14005.5 Da
0-73%B 2-32 min.
14005.5
H2AKpolyAc
Expected: 14174.5 Da
Observed: 14173.9 Da
35-70%B 3-33 min.
14173.9
H2B
Expected: 13758.9 Da
Observed: 13758.2 Da
40-70%B 3-33 min.
13758.2
H2B acidic patch mutant
Expected: 13642.8 Da
Observed: 13642.2 Da
40-70%B 3-33 min.
13642.2
H2BK5ac
Expected: 13801 Da
Observed: 13800.5 Da
40-70%B 4-24 min.
13800.5
H2BK11ac
Expected: 13801 Da
Observed: 13800.4 Da
40-70%B 4-24 min.
13800.4
H2BK12ac
Expected: 13801 Da
Observed: 13801.0 Da
40-70%B 4-24 min.
13801.0
H2BK15ac
Expected: 13801 Da
Observed: 13801.2 Da
40-70%B 4-24 min.
13801.2
H2BK16ac
Expected: 13801 Da
Observed: 13801.1 Da
40-70%B 4-24 min.
13801.1
Intens.
Absorbance (mAU), 214 nm
Time (min.)
m/z


H2BK20ac
Expected: 13801 Da
Observed: 13801.0 Da
40-70%B 4-24 min.
13801.0
H2BK108ac
Expected: 13801 Da
Observed: 13800.5 Da
0-73%B 2-32 min.
13800.5
H2BK116ac
Expected: 13801 Da
Observed: 13800.5 Da
0-73%B 2-32 min.
13800.5
H2BK120ac
Expected: 13801 Da
Observed: 13800.2 Da
0-73%B 2-32 min.
13800.2
H2BK125ac
Expected: 13801 Da
Observed: 13800.3 Da
0-73%B 2-32 min.
13800.3
H2BKpolyAc
Expected: 14011.2 Da
Observed: 14010.6 Da
45-65%B 3-33 min.
14010.6
H2BS112GlcNAc
Expected: 13962.2 Da
Observed: 13961.8 Da
30-70%B 2-32 min.
13961.8
H3
Expected: 15208.7 Da
Observed: 15208.4 Da
40-70%B 3-33 min.
15208.4
H3.3
Expected: 15164.6 Da
Observed: 15164.1 Da
40-70%B 3-33 min.
15164.1
Intens.
Absorbance (mAU), 214 nm
Time (min.)
m/z

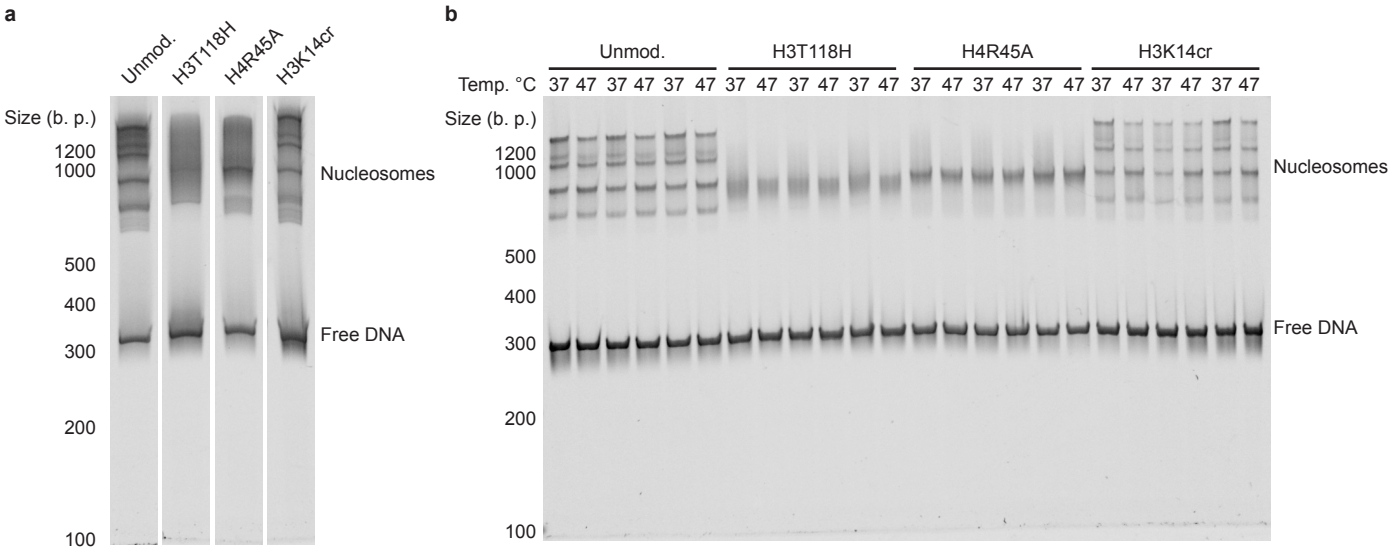

H3.3G34R
Expected: 15263.7 Da
Observed: 15262.9 Da
40-70%B 3-33 min.
15262.9
H3.3G34V
Expected: 15206.7 Da
Observed: 15205.7 Da
40-70%B 3-33 min.
15205.7
H3.3G34W
Expected: 15293.8 Da
Observed: 15293.3 Da
40-70%B 3-33 min.
15293.3
H3.3K27M
Expected: 15167.6 Da
Observed: 15167.3 Da
40-70%B 3-33 min.
15167.3
H3.3K36M
Expected: 15167.6 Da
Observed: 15167.2 Da
40-70%B 3-33 min.
15167.2
H3K4ac
Expected: 15250.9 Da
Observed: 15249.8 Da
40-80%B 4-24 min.
15249.8
H3K4me1
Expected: 15222.9 Da
Observed: 15222.2 Da
0-73%B 2-32 min.
15222.2
H3K4me2
Expected: 15236.9 Da
Observed: 15236.6 Da
0-73%B 2-32 min.
15236.6
H3K4me3K27me3
Expected: 15295 Da
Observed: 15294.2 Da
40-70%B 2-32 min.
15294.2
Intens.
Absorbance (mAU), 214 nm
Time (min.)
m/z


H3K36ac
Expected: 15250.9 Da
Observed: 15250.4 Da
40-80%B 4-24 min.
15250.4
H3K36me3
Expected: 15251.9 Da
Observed: 15251.8 Da
30-70%B 3-33 min.
15251.8
H3K37ac
Expected: 15250.9 Da
Observed: 15250.4 Da
40-80%B 4-24 min.
15250.4
H3K56ac
Expected: 15250.9 Da
Observed: 15250.5 Da
40-80%B 4-24 min.
15250.5
H3K64ac
Expected: 15250.9 Da
Observed: 15251.5 Da
40-80%B 4-24 min.
15251.5
H3K79ac
Expected: 15250.9 Da
Observed: 15251.2 Da
40-80%B 4-24 min.
15251.2
H3K115ac
Expected: 15250.9 Da
Observed: 15250.5 Da
40-70%B 4-34 min.
15250.5
H3K122ac
Expected: 15250.9 Da
Observed: 15250.6 Da
40-73%B 4-34 min.
15250.6
H3R2me
Expected: 15222.9 Da
Observed: 15222.6 Da
0-73%B 2-32 min.
15222.6
Intens.
Absorbance (mAU), 214 nm
Time (min.)
m/z

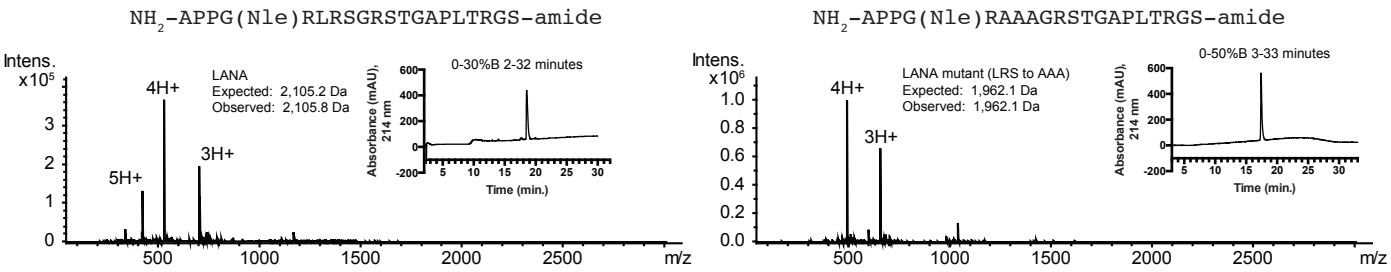

H3R2me2a
Expected: 15236.9 Da
Observed: 15236.5 Da
0-73%B 2-32 min.
15236.5
H3R42A
Expected: 15123.6 Da
Observed: 15122.7 Da
40-70%B 3-33 min.
15122.7
H3S10ph
Expected: 15288.8 Da
Observed: 15288.7 Da
40-70%B 3-33 min.
15288.7
H3T118H
Expected: 15244.8 Da
Observed: 15244.1 Da
40-70%B 3-33 min.
15244.1
H3Y41ph
Expected: 15288.8 Da
Observed: 15288.4 Da
45-65%B 3-33 min.
15288.4
H4
Expected: 11236.1 Da
Observed: 11235.9 Da
40-70%B 3-33 min.
11235.9
+TFA
H4K77ac
Expected: 11278.2 Da
Observed: 11277.7 Da
0-73%B 2-32 min.
11277.7
+TFA
+TFA
H4K79ac
Expected: 11278.2 Da
Observed: 11277.2 Da
0-73%B 2-32 min.
11277.2
+TFA
+TFA
+TFA
H4K91ac
Expected: 11278.2 Da
Observed: 11277.7 Da
0-73%B 2-32 min.
11277.7
+TFA
Intens.
Absorbance (mAU), 214 nm
Time (min.)
m/z



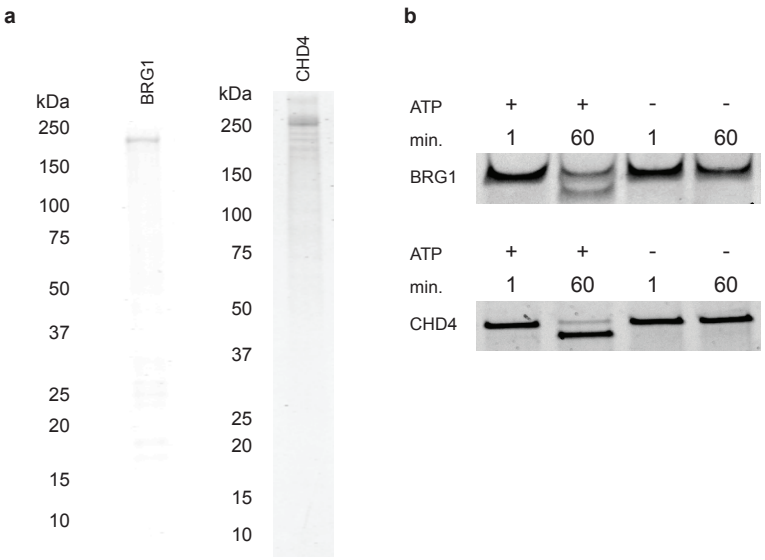
Supplementary Figure 2 | Characterization of Histones by RP-HPLC/E-SI-MS. (Left) Analytical C-18 RP-HPLC chromatograms (insets; gradients used are individually noted) and corresponding ESI-MS spectra of indicated histones prepared in this study. Corresponding deconvoluted spectra are shown on the right. Lysine acetylation: Kac; lysine mono, di, and trimethylation: Kme, Kme2 and Kme3, respectively; arginine mono, asymmetric and symmetric demethylation: Rme, Rme2a and Rme2s, respectively; serine and tyrosine phosphorylation: Sph and Yph, respectively; serine modified with N-acetylglucosamine: SGlcNAc. TFA = trifluoroacetic acid adduct.



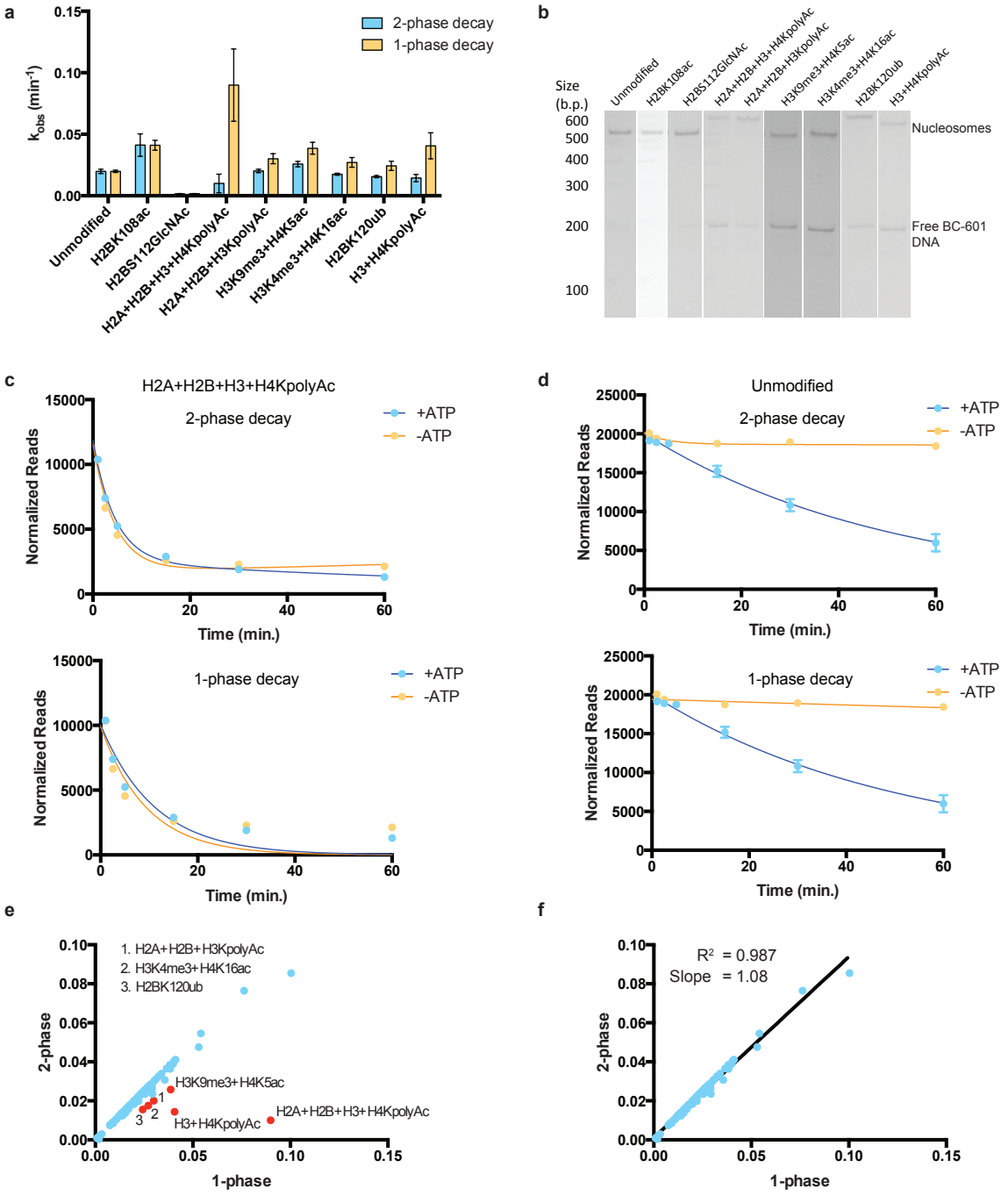
Supplementary Figure 3 | Nucleosome Thermal Mobility Shift Experiments. **a**, Nucleosomes analyzed directly after assembly by salt gradient dialysis. **b**, Nucleosomes from **a** re-analyzed after incubation for 1 hour at either 37 °C or 47 °C. Mobile nucleosomes will shift and coalesce in to the most thermodynamically favorable position along the DNA fragment used in assembly. Experimental replicates are displayed (n = 3). Unmod. = unmodified. All histones are unmodified unless otherwise specified. For gel source data, see Supplementary Fig. 1.



Supplementary Figure 4 | Characterization of LANA Peptides. Analytical C-18 RP-HPLC chromatograms (insets; gradients used are individually noted) and corresponding ESI-MS spectra of indicated peptides are shown.



Supplementary Figure 5 | Characterization of Recombinant BRG1 and CHD4 Chromatin Remodelers. a, Purified remodelers were run on a 4-20% Mini-PROTEAN® TGX™ gel (Bio-Rad) and run for 35 min at 180 V. Proteins were stained with Coomassie. Expected molecular weights: BRG1: 185 kDa, CHD4: 218 kDa. **b**, BRG1 and CHD4 remodelers display ATP-dependent nucleosome remodeling activity as detected by a restriction enzyme accessibility assay. For gel source data, see Supplementary Fig. 1.



Supplementary Figure 6 | Assessment of Modeling Nucleosome Library Remodeling as a 1- vs. 2-phase Exponential Decay. a, Rates calculated for ACF remodeling against select nucleosome library members by fitting to a 1-phase or 2-phase exponential decay equation. **b**, Gel images are the same as in Extended Data Fig. 2a. **c** and **d**, Curves used to calculate rates as in **a** for a H2A+H2B+H3+H4KpolyAc modified nucleosome (**c**) and an unmodified nucleosome (**d**) (nucleosomes 93 and 42 in Supplementary Table 1, respectively). **e**, Mean rate values (k_{obs} min^{-1}) calculated for ACF remodeling against all nucleosome library members fit to either a 1-phase or 2-phase exponential decay equation. Nucleosomes remodeled at a faster rate when fit to a 1-phase vs. a 2-phase exponential decay equation are highlighted in red and labeled. **f**, Same as in **e**, but without highlighted nucleosomes. For **a**, **c**, and **d** data are represented as the mean of experimental replicates ± s.e.m. (n = 3). For gel source data, see Supplementary Fig. 1.