SUPPLEMENTAL TABLE 1. The post-translationally modified histone peptides analyzed in this study, with the simplified notation, as identified by both accurate mass and MS/MS.

Peptide (sequence; charge)^{a}	**Simplified notation**	**Theor.(*m/z*)**	**Obs.(*m/z*)**
Histone H1.4			
25-32 fragment			
$_{pr}$K$_{pr}$SAGAAK$_{pr}$R;+2	H1.4K25me0:0	478.780	478.779
$_{pr}$K$_{pr,me1:0}$SAGAAK$_{pr}$R;+2	H1.4K25me1:0	485.788	485.787
$_{pr}$K$_{pr,me1:1}$SAGAAK$_{pr}$R;+2	H1.4K25me1:1	487.798	487.798
33-53 fragment			
$_{pr}$K$_{0,pr}$ASGPPVSELITK$_{0,pr}$AVAASK$_{0,pr}$ER;+3	H1.4K33lys3:0	788.447	788.446
$_{pr}$K$_{1,pr}$ASGPPVSELITK$_{1,pr}$AVAASK$_{1,pr}$ER;+3	H1.4K33lys3:3	796.455	796.457
Histone H3			
3-8 fragment			
$_{pr}$TK$_{pr}$QTAR; +2	H3K4me0:0	408.733	408.733
$_{pr}$TK$_{pr,me1:0}$QTAR; +2	H3K4me1:0	415.741	415.742
$_{pr}$TK$_{pr,me1:1}$QTAR; +2	H3K4me1:1	417.751	417.751
9-17 fragment			
$_{pr}$K$_{pr}$STGGK$_{pr}$APR; +2	H3K9me0:0	535.304	535.306
$_{pr}$K$_{pr,me1:0}$STGGK$_{pr}$APR; +2	H3K9me1:0	542.312	542.313
$_{pr}$K$_{pr,me1:1}$STGGK$_{pr}$APR; +2	H3K9me1:1	544.322	544.323
$_{pr}$K$_{me2:0}$STGGK$_{pr}$APR; +2	H3K9me2:0	521.307	521.307
$_{pr}$K$_{me2:1}$STGGK$_{pr}$APR; +2	H3K9me2:1	523.317	523.318
$_{pr}$K$_{me2:2}$STGGK$_{pr}$APR; +2	H3K9me2:2	525.327	525.328
$_{pr}$K$_{me3:0}$STGGK$_{pr}$APR; +2	H3K9me3:0	528.315	528.313
$_{pr}$K$_{me3:1}$STGGK$_{pr}$APR;+2	H3K9me3:1	530.325	530.324
$_{pr}$K$_{me3:2}$STGGK$_{pr}$APR;+2	H3K9me3:2	532.335	532.336
$_{pr}$K$_{me3:3}$STGGK$_{pr}$APR; +2	H3K9me3:3	534.345	534.347
$_{pr}$K$_{pr,me1:0}$STGGK$_{ac}$APR; +2	H3K9me1:0K14ac1	535.304	535.305
$_{pr}$K$_{pr,me1:1}$STGGK$_{ac}$APR; +2	H3K9me1:1K14ac1	537.314	537.316
$_{pr}$K$_{me2:0}$STGGK$_{ac}$APR; +2	H3K9me2:0K14ac1	514.299	514.299
$_{pr}$K$_{me2:1}$STGGK$_{ac}$APR; +2	H3K9me2:1K14ac1	516.309	516.310
$_{pr}$K$_{me2:2}$STGGK$_{ac}$APR; +2	H3K9me2:2K14ac1	518.319	518.321
18-26 fragment			
$_{pr}$K$_{pr}$QLATK$_{pr}$AAR; +2	H3K18me0:0	577.849	577.850
$_{pr}$K$_{pr,me1:0}$QLATK$_{pr}$AAR; +2	H3K18me1:0	584.857	584.858
$_{pr}$K$_{pr,me1:1}$QLATK$_{pr}$AAR; +2	H3K18me1:1	586.867	586.870
$_{pr}$K$_{pr}$QLATK$_{ac}$AAR; +2	H3K18me0:0K23ac1	570.841	570.842
$_{pr}$K$_{ac}$QLATK$_{pr}$AAR; +2	H3K18ac1	570.841	570.842
$_{pr}$K$_{ac}$QLATK$_{ac}$AAR; +2	H3K18ac1K23ac1	563.833	563.834
27-40 fragment			
$_{pr}$K$_{pr}$SAPATGGVK$_{pr}$K$_{pr}$PHR; +3	H3K36me0:0	553.318	553.319
$_{pr}$K$_{pr}$SAPATGGVK$_{pr,me1:0}$K$_{pr}$PHR; +3	H3K36me1:0	557.990	557.990
$_{pr}$K$_{pr}$SAPATGGVK$_{pr,me1:1}$K$_{pr}$PHR; +3	H3K36me1:1	559.330	559.329
$_{pr}$K$_{pr,me1:0}$SAPATGGVK$_{pr}$K$_{pr}$PHR; +3	H3K27me1:0	557.990	557.990
$_{pr}$K$_{pr,me1:1}$SAPATGGVK$_{pr}$K$_{pr}$PHR; +3	H3K27me1:1	559.330	559.331
$_{pr}$K$_{me2:0}$SAPATGGVK$_{pr}$K$_{pr}$PHR; +3	H3K27me2:0	543.987	543.988
$_{pr}$K$_{me2:1}$SAPATGGVK$_{pr}$K$_{pr}$PHR; +3	H3K27me2:1	545.327	545.328
$_{pr}$K$_{me2:2}$SAPATGGVK$_{pr}$K$_{pr}$PHR; +3	H3K27me2:2	546.667	546.668
$_{pr}$K$_{pr}$SAPATGGVK$_{me2:0}$K$_{pr}$PHR; +3	H3K36me2:0	543.987	543.987
$_{pr}$K$_{pr}$SAPATGGVK$_{me2:1}$K$_{pr}$PHR; +3	H3K36me2:1	545.327	545.327
$_{pr}$K$_{pr}$SAPATGGVK$_{me2:2}$K$_{pr}$PHR; +3	H3K36me2:2	546.667	546.668
$_{pr}$K$_{pr,me1:0}$SAPATGGVK$_{pr,me1:0}$K$_{pr}$PHR; +3	H3K27me1:0K36me1:0	562.662	562.662
$_{pr}$K$_{pr,me1:1}$SAPATGGVK$_{pr,me1:0}$K$_{pr}$PHR; +3^{b}	H3K27me1:1K36me1:0		

${}_{pr}K_{pr,me1:0}SAPATGGVK_{pr,me1:1}K_{pr}PHR$; +3[b]	H3K27me1:0K36me1:1	564.002	564.004
${}_{pr}K_{pr,me1:1}SAPATGGVK_{pr,me1:1}K_{pr}PHR$; +3	H3K27me1:1K36me1:1	565.342	565.344
${}_{pr}K_{me3:0}SAPATGGVK_{pr}K_{pr}PHR$; +3	H3K27me3:0	548.658	548.658
${}_{pr}K_{me2:0}SAPATGGVK_{pr,me1:0}K_{pr}PHR$; +3	H3K27me2:0K36me1:0	548.658	548.660
${}_{pr}K_{pr,me1:0}SAPATGGVK_{me2:0}K_{pr}PHR$; +3	H3K27me1:0K36me2:0	548.658	548.660
${}_{pr}K_{me3:1}SAPATGGVK_{pr}K_{pr}PHR$; +3	H3K27me3:1	549.999	549.997
${}_{pr}K_{me2:1}SAPATGGVK_{pr,me1:0}K_{pr}PHR$; +3[b] ${}_{pr}K_{me2:0}SAPATGGVK_{pr,me1:1}K_{pr}PHR$; +3[b]	H3K27me2:1K36me1:0 H3K27me2:0K36me1:1	549.999	549.999
${}_{pr}K_{pr,me1:1}SAPATGGVK_{me2:0}K_{pr}PHR$; +3[b] ${}_{pr}K_{pr,me1:0}SAPATGGVK_{me2:1}K_{pr}PHR$; +3[b]	H3K27me1:1K36me2:0 H3K27me1:0K36me2:1	549.999	549.998
${}_{pr}K_{me3:2}SAPATGGVK_{pr}K_{pr}PHR$; +3	H3K27me3:2	551.339	551.339
${}_{pr}K_{me2:2}SAPATGGVK_{pr,me1:0}K_{pr}PHR$; +3[b] ${}_{pr}K_{me2:1}SAPATGGVK_{pr,me1:1}K_{pr}PHR$; +3[b]	H3K27me2:2K36me1:0 H3K27me2:1K36me1:1	551.339	551.339
${}_{pr}K_{pr,me1:1}SAPATGGVK_{me2:1}K_{pr}PHR$; +3[b] ${}_{pr}K_{pr,me1:0}SAPATGGVK_{me2:2}K_{pr}PHR$; +3[b]	H3K27me1:1K36me2:1 H3K27me1:0K36me2:2	551.339	551.339
${}_{pr}K_{me3:3}SAPATGGVK_{pr}K_{pr}PHR$; +3	H3K27me3:3	552.679	552.679
${}_{pr}K_{me2:2}SAPATGGVK_{pr,me1:1}K_{pr}PHR$; +3	H3K27me2:2K36me1:1	552.679	552.680
${}_{pr}K_{pr,me1:1}SAPATGGVK_{me2:2}K_{pr}PHR$; +3	H3K27me1:1K36me2:2	552.679	552.680
${}_{pr}K_{me3:0}SAPATGGVK_{pr,me1:0}K_{pr}PHR$; +3	H3K27me3:0K36me1:0	553.330	553.332
${}_{pr}K_{pr,me1:0}SAPATGGVK_{me3:0}K_{pr}PHR$; +3	H3K27me1:0K36me3:0	553.330	553.331
${}_{pr}K_{me3:1}SAPATGGVK_{pr,me1:0}K_{pr}PHR$; +3[b] ${}_{pr}K_{me3:0}SAPATGGVK_{pr,me1:1}K_{pr}PHR$; +3[b]	H3K27me3:1K36me1:0 H3K27me3:0K36me1:1	554.671	554.670
${}_{pr}K_{pr,me1:1}SAPATGGVK_{me3:0}K_{pr}PHR$; +3[b] ${}_{pr}K_{pr,me1:0}SAPATGGVK_{me3:1}K_{pr}PHR$; +3[b]	H3K27me1:1K36me3:0 H3K27me1:0K36me3:1	554.671	554.670
${}_{pr}K_{me3:2}SAPATGGVK_{pr,me1:0}K_{pr}PHR$; +3[b] ${}_{pr}K_{me3:1}SAPATGGVK_{pr,me1:1}K_{pr}PHR$; +3[b]	H3K27me3:2K36me1:0 H3K27me3:1K36me1:1	556.011	556.011
${}_{pr}K_{pr,me1:1}SAPATGGVK_{me3:1}K_{pr}PHR$; +3[b] ${}_{pr}K_{pr,me1:0}SAPATGGVK_{me3:2}K_{pr}PHR$; +3[b]	H3K27me1:1K36me3:1 H3K27me1:0K36me3:2	556.011	556.010
${}_{pr}K_{me3:3}SAPATGGVK_{pr,me1:0}K_{pr}PHR$; +3[b] ${}_{pr}K_{me3:2}SAPATGGVK_{pr,me1:1}K_{pr}PHR$; +3[b]	H3K27me3:3K36me1:0 H3K27me3:2K36me1:1	557.351	557.353
${}_{pr}K_{pr,me1:1}SAPATGGVK_{me3:2}K_{pr}PHR$; +3[b] ${}_{pr}K_{pr,me1:0}SAPATGGVK_{me3:3}K_{pr}PHR$; +3[b]	H3K27me1:1K36me3:2 H3K27me1:0K36me3:3	557.351	557.351
${}_{pr}K_{me3:3}SAPATGGVK_{pr,me1:1}K_{pr}PHR$; +3	H3K27me3:3K36me1:1	558.691	558.677
${}_{pr}K_{pr,me1:1}SAPATGGVK_{me3:3}K_{pr}PHR$; +3	H3K27me1:1K36me3:3	558.691	558.692
${}_{pr}K_{me2:0}SAPATGGVK_{me2:0}K_{pr}PHR$; +3	H3K27me2:0K36me2:0	534.654	534.654
${}_{pr}K_{me2:1}SAPATGGVK_{me2:0}K_{pr}PHR$; +3[b] ${}_{pr}K_{me2:0}SAPATGGVK_{me2:1}K_{pr}PHR$; +3[b]	H3K27me2:1K36me2:0 H3K27me2:0K36me2:1	535.995	535.994
${}_{pr}K_{me2:2}SAPATGGVK_{me2:0}K_{pr}PHR$; +3[b] ${}_{pr}K_{me2:1}SAPATGGVK_{me2:1}K_{pr}PHR$; +3[b] ${}_{pr}K_{me2:0}SAPATGGVK_{me2:2}K_{pr}PHR$; +3[b]	H3K27me2:2K36me2:0 H3K27me2:1K36me2:1 H3K27me2:0K36me2:2	537.335	537.335
${}_{pr}K_{me2:1}SAPATGGVK_{me2:2}K_{pr}PHR$; +3[b] ${}_{pr}K_{me2:2}SAPATGGVK_{me2:1}K_{pr}PHR$; +3[b]	H3K27me2:1K36me2:2 H3K27me2:2K36me2:1	538.675	538.676
${}_{pr}K_{me2:2}SAPATGGVK_{me2:2}K_{pr}PHR$; +3	H3K27me2:2K36me2:2	540.016	540.016
${}_{pr}K_{me3:0}SAPATGGVK_{me2:0}K_{pr}PHR$; +3	H3K27me3:0K36me2:0	539.327	539.326
${}_{pr}K_{me3:1}SAPATGGVK_{me2:0}K_{pr}PHR$; +3[b] ${}_{pr}K_{me3:0}SAPATGGVK_{me2:1}K_{pr}PHR$; +3[b]	H3K27me3:1K36me2:0 H3K27me3:0K36me2:1	540.667	540.667
${}_{pr}K_{me3:2}SAPATGGVK_{me2:0}K_{pr}PHR$; +3[b] ${}_{pr}K_{me3:1}SAPATGGVK_{me2:1}K_{pr}PHR$; +3[b] ${}_{pr}K_{me3:0}SAPATGGVK_{me2:2}K_{pr}PHR$; +3[b]	H3K27me3:2K36me2:0 H3K27me3:1K36me2:1 H3K27me3:0K36me2:2	542.007	542.007
${}_{pr}K_{me3:3}SAPATGGVK_{me2:0}K_{pr}PHR$; +3[b] ${}_{pr}K_{me3:2}SAPATGGVK_{me2:1}K_{pr}PHR$; +3[b] ${}_{pr}K_{me3:1}SAPATGGVK_{me2:2}K_{pr}PHR$; +3[b]	H3K27me3:3K36me2:0 H3K27me3:2K36me2:1 H3K27me3:1K36me2:2	543.347	543.343
${}_{pr}K_{me3:3}SAPATGGVK_{me2:1}K_{pr}PHR$; +3[b] ${}_{pr}K_{me3:2}SAPATGGVK_{me2:2}K_{pr}PHR$; +3[b]	H3K27me3:3K36me2:1 H3K27me3:2K36me2:2	544.688	544.688

$_{pr}$K$_{me3:3}$SAPATGGVK$_{me2:2}$K$_{pr}$PHR; +3	H3K27me3:3K36me2:2	546.028	546.029
73-83 fragment			
$_{pr}$EIAQDFK$_{pr}$TDLR; +2	H3K79me0:0	724.376	724.379
$_{pr}$EIAQDFK$_{pr,me1:0}$TDLR; +2	H3K79me1:0	731.383	731.387
$_{pr}$EIAQDFK$_{pr,me1:1}$TDLR; +2	H3K79me1:1	733.394	733.398
$_{pr}$EIAQDFK$_{pr,me2:0}$TDLR; +2	H3K79me2:0	710.378	710.380
$_{pr}$EIAQDFK$_{pr,me2:1}$TDLR; +2	H3K79me2:1	712.388	712.391
$_{pr}$EIAQDFK$_{pr,me2:2}$TDLR; +2	H3K79me2:2	714.399	714.402
117-128 fragment			
$_{pr}$VTIM$_{0}$PK$_{pr}$DIQLAR	H3M120met1:0	748.929	748.933
$_{pr}$VTIM$_{0,ox}$PK$_{pr}$DIQLAR	H3M120met1:0ox	756.927	756.932
$_{pr}$VTIM$_{1}$PK$_{pr}$DIQLAR	H3M120met1:1	750.940	750.944
$_{pr}$VTIM$_{1,ox}$PK$_{pr}$DIQLAR	H3M120met1:1ox	758.937	758.942
Histone H4			
1-17 fragment(4-17 for unmodified)			
$_{pr}$GK$_{pr}$GGK$_{pr}$GLGK$_{pr}$GGAK$_{pr}$R; +2	H4R3me0:0	775.955	775.956
$_{pr}$GK$_{pr}$GGK$_{pr}$GLGK$_{pr}$GGAK$_{pr}$R; +3	“ “	517.639	517.640
$_{ac}$SGR$_{me1:0}$GK$_{pr}$GGK$_{pr}$GLGK$_{pr}$GGAK$_{pr}$R; +2	H4R3me1:0	926.032	926.032
$_{ac}$SGR$_{me1:0}$GK$_{pr}$GGK$_{pr}$GLGK$_{pr}$GGAK$_{pr}$R; +3	H4R3me1:0	617.690	617.692
$_{ac}$SGR$_{me1:1}$GK$_{pr}$GGK$_{pr}$GLGK$_{pr}$GGAK$_{pr}$R; +2	H4R3me1:1	928.042	928.042
$_{ac}$SGR$_{me1:1}$GK$_{pr}$GGK$_{pr}$GLGK$_{pr}$GGAK$_{pr}$R; +3	H4R3me1:1	619.030	619.032
20-23 fragment			
$_{pr}$K$_{pr}$VLR; +1	H4K20me0:0	627.419	627.419
$_{pr}$K$_{pr}$VLR; +2	“ “	314.214	314.213
$_{pr}$K$_{pr,me1:0}$VLR; +1	H4K20me1:0	641.435	641.435
$_{pr}$K$_{pr,me1:0}$VLR; +2	“ “	321.222	321.221
$_{pr}$K$_{pr,me1:1}$VLR; +1	H4K20me1:1	645.456	645.458
$_{pr}$K$_{pr,me1:1}$VLR: +2	“ “	323.232	323.232
$_{pr}$K$_{me2:0}$VLR; +2	H4K20me2:0	300.216	300.215
$_{pr}$K$_{me2:1}$VLR; +2	H4K20me2:1	302.226	300.226
$_{pr}$K$_{me2:2}$VLR; +2	H4K20me2:2	304.237	304.237
$_{pr}$K$_{me3:0}$VLR; +2	H4K20me3:0	307.224	307.224
$_{pr}$K$_{me3:1}$VLR; +2	H4K20me3:1	309.234	309.235
$_{pr}$K$_{me3:2}$VLR; +2	H4K20me3:2	311.244	311.246
$_{pr}$K$_{me3:3}$VLR; +2	H4K20me3:3	313.255	313.257
79-92 fragment			
$_{pr}$K$_{pr}$TVTAM$_{0}$DVVYALK$_{pr}$R	H4M84met1:0	882.496	882.501
$_{pr}$K$_{pr}$TVTAM$_{0,ox}$DVVYALK$_{pr}$R	H4M84met1:0ox	890.494	890.498
$_{pr}$K$_{pr}$TVTAM$_{1}$DVVYALK$_{pr}$R	H4M84met1:1	884.506	884.511
$_{pr}$K$_{pr}$TVTAM$_{1,ox}$DVVYALK$_{pr}$R	H4M84met1:1ox	892.504	892.510

[a] PTMs identified include propionylation (pr, +56 Da), acetylation (ac) and methylation (meX:Y), where X = number of total methyl groups and Y = number of labeled methyl groups. Methionine oxidation (ox) was also accounted for certain peptides. Peptides used for determining overall histone turnover (H1.4 33-53, H3 117-128, and H4 79-92 fragment) have similar simplified notation, but the specific residue is labeled (“lys” and “met” for lysine and methionine respectively).

[b] Unable to differentiate between peptides using MS/MS data.

SUPPLEMENTAL TABLE 2. The average half-max time ($t_{1/2}$, days) of fully labeled histone methylation sites, depending on the methylation or acetylation state of another residue on the same peptide. H3K27me3:3K36me2:2 was detected in only one run, and consequently, standard error was not determined.

PTM	**$t_{1/2}$**	**Std. Error**
H3K9me1:1K14ac0	0.470	0.012
H3K9me1:1K14ac1	0.719	0.162
H3K9me2:2K14ac0	1.688	0.360
H3K9me2:2K14ac1	1.446	0.790
H3K27me1:1K36me0:0	0.909	0.320
H3K27me1:1K36me1:1	0.840	0.226
H3K27me1:1K36me2:2	1.584	0.444
H3K27me1:1K36me3:3	3.680	1.103
H3K27me2:2K36me0:0	1.515	0.011
H3K27me2:2K36me1:1	1.963	0.244
H3K27me2:2K36me2:2	4.337	1.017
H3K27me3:3K36me0:0	4.618	0.144
H3K27me3:3K36me1:1	3.849	1.499
H3K27me3:3K36me2:2	8.931	2.040
H3K27me0:0K36me1:1	0.714	0.696
H3K27me1:1K36me1:1	1.726	0.132
H3K27me2:2K36me1:1	2.223	0.586
H3K27me3:3K36me1:1	2.963	1.332
H3K27me0:0K36me2:2	0.881	0.100
H3K27me1:1K36me2:2	1.940	0.081
H3K27me2:2K36me2:2	2.847	0.346
H3K27me3:3K36me2:2	3.273	-