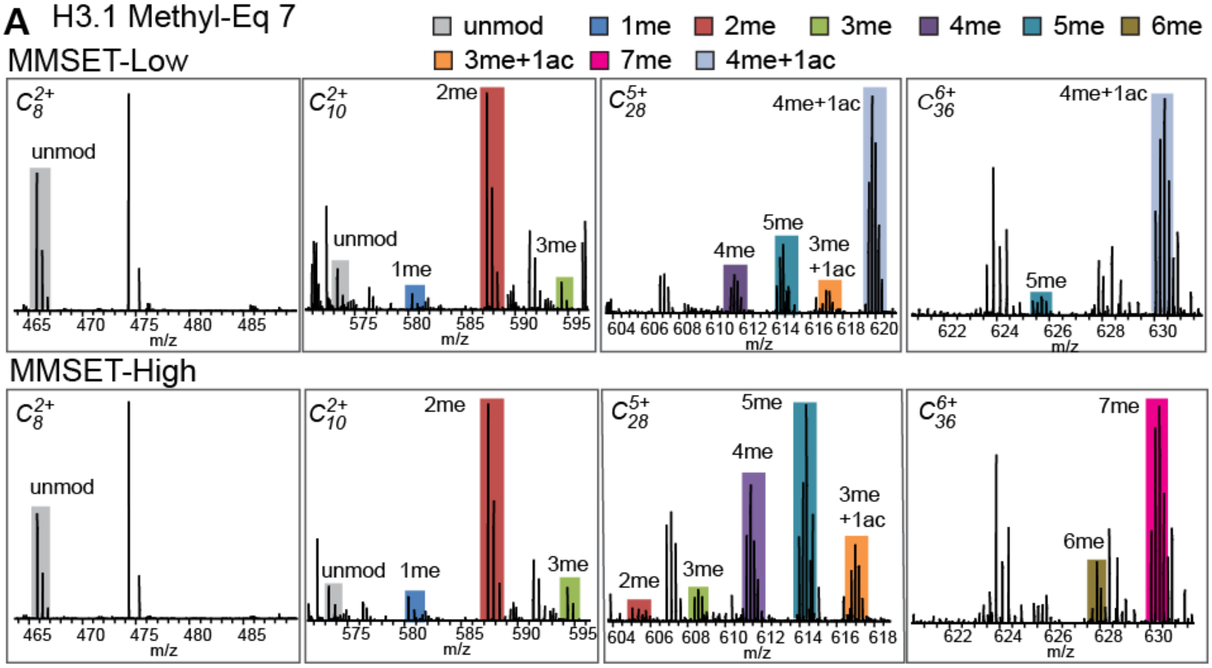
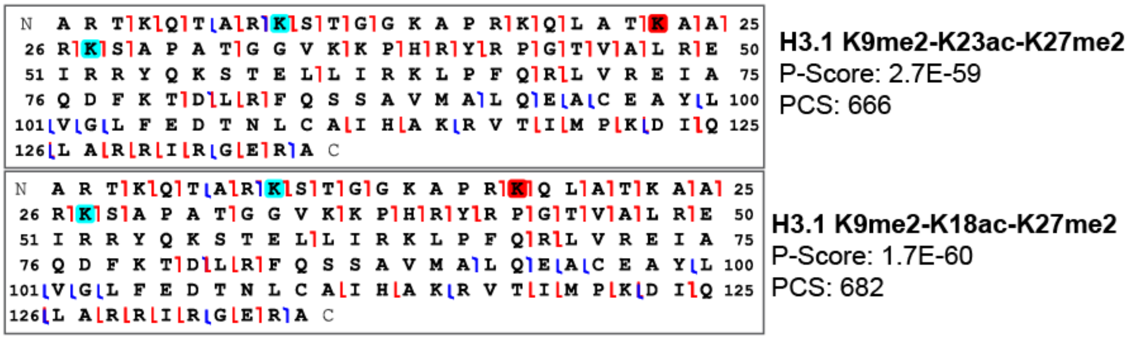
A H3.1 Methyl-Eq 7



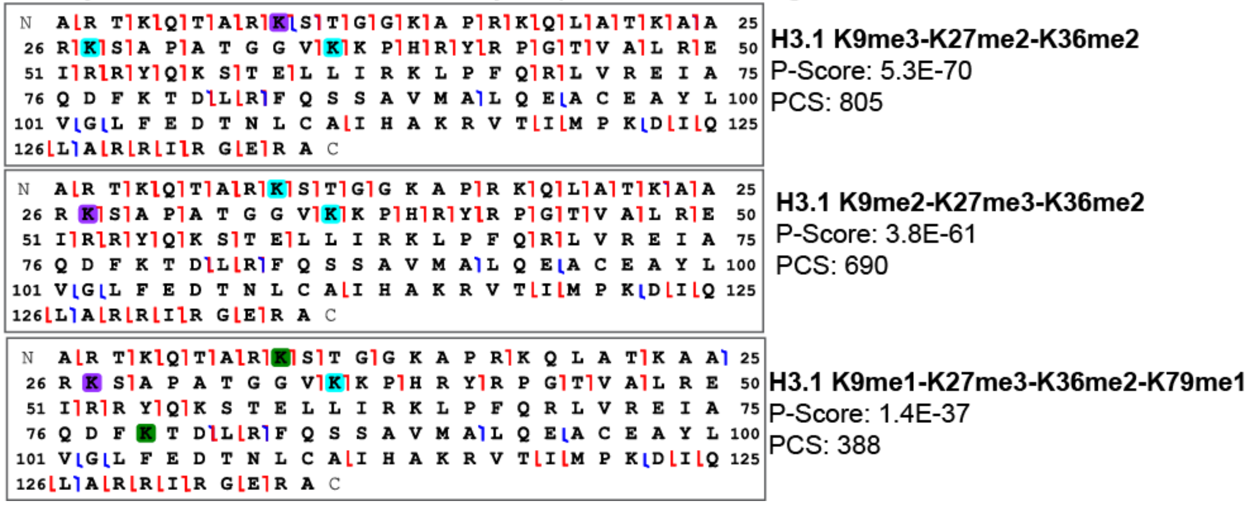
B Major H3.1 Proteoforms of Methyl-Eq 7 in MMSET-Low



H3.1 K9me2-K23ac-K27me2
P-Score: 2.7E-59
PCS: 666

H3.1 K9me2-K18ac-K27me2
P-Score: 1.7E-60
PCS: 682

C Major H3.1 Proteoforms of Methyl-Eq 7 in MMSET-High



H3.1 K9me3-K27me2-K36me2
P-Score: 5.3E-70
PCS: 805

H3.1 K9me2-K27me3-K36me2
P-Score: 3.8E-61
PCS: 690

H3.1 K9me1-K27me3-K36me2-K79me1
P-Score: 1.4E-37
PCS: 388

Fig. S6. Different proteoforms present in Methyl Equivalent 7 for H3.1 variant in MMSET-Low and MMSET-High cells. (A) Raw mass spectrometry data of *c* ions from ETD-MS^2 and their matched modifications. (B) and (C) Graphical representation of major proteoforms determined by EThcD using ProSight Lite. Green, cyan, and purple squares indicate mono-, di-, and tri-methylation respectively; red square: acetylation; red rotated-L bar: *c* ions; red L bar: *z* ions; blue rotated-L bar: *b* ions; blue L bar: *y* ions.