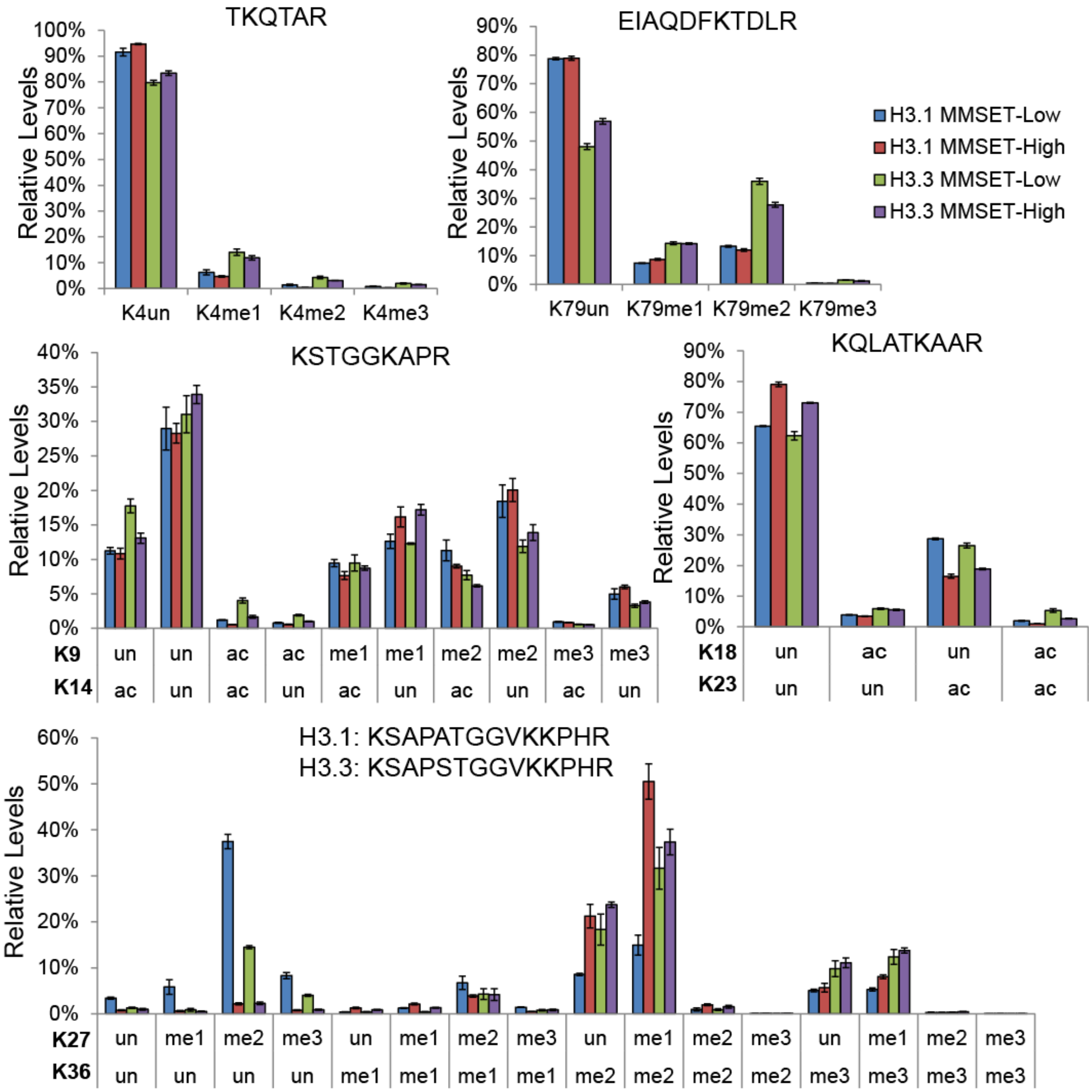

**Fig. S7.** Bottom-Up mass spectrometry quantitation of RP-HPLC purified H3.1 and H3.3 from MMSET-Low and MMSET-High cells using selective reaction monitoring (SRM) developed previously. Relative levels of each modification were normalized against total peak areas of modifications measured by SRM in each peptide listed. The relative levels of K9me2 are calculated by aggregating levels of K9me2-K14un and K9me2-K14ac (H3.1-K9me2 is ~30% and H3.3-K9me2 is ~20%).