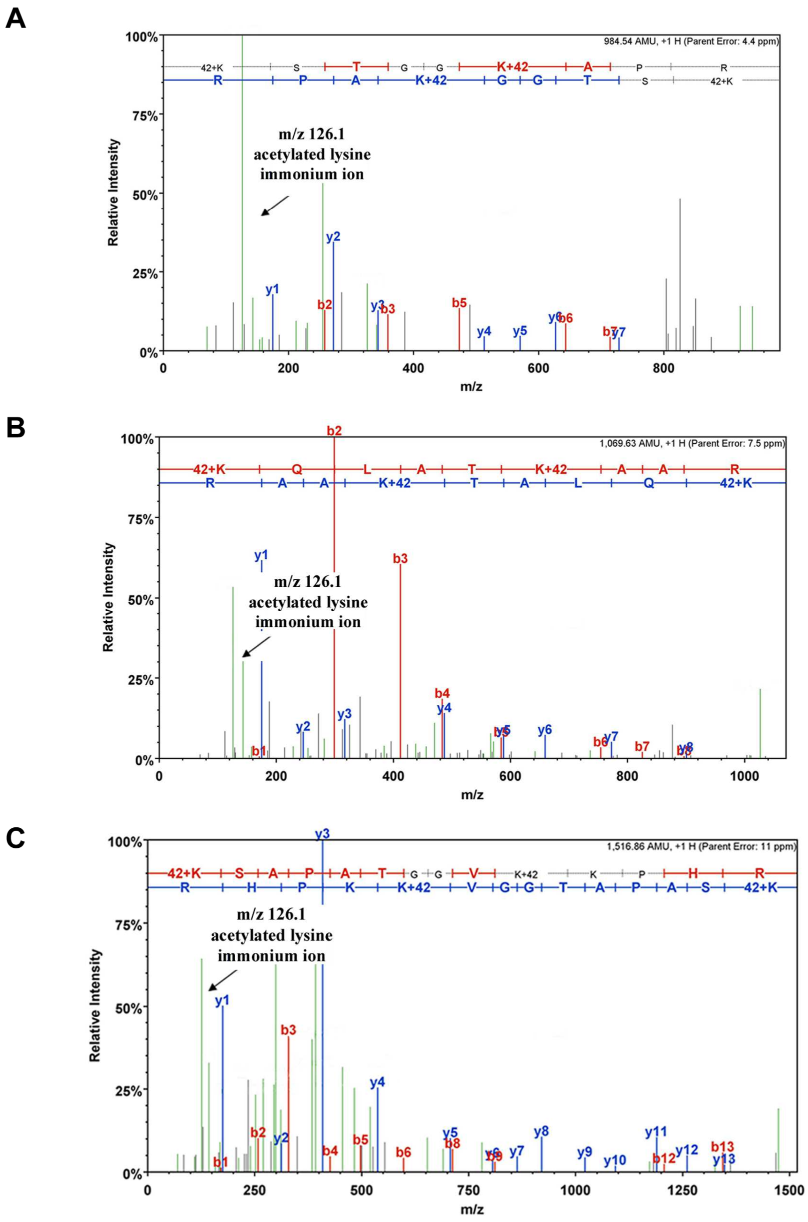

Fig. S4. MS/MS spectrum of histone H3 acetylated peptides. *A*. MS/MS spectrum of peptide ^{9}K$_{AC}$STGGK$_{AC}$APR^{17} (amino acids 9-17 of X. laevis H3 sequence) confirming acetylation on lysines 9 and 14. Confirmation is based on the Mascot ion score of 50 and coverage of theoretical y (blue) and b (red) ions including the sequence region of acetylated K9. *B*. MS/MS spectrum of peptide ^{18}K$_{AC}$QLATK$_{AC}$AAR^{26} (amino acids 18-26 of X. laevis H3 sequence) confirming acetylation on lysines 18 and 23. Confirmation is based on the Mascot ion score of 56 and coverage of theoretical y (blue) and b (red) ions including the sequence region of acetylated K18 and K23. *C*. MS/MS spectrum of peptide ^{27}K$_{AC}$SAPATGGVK$_{AC}$KPHR^{40} (amino acids 27-40 of *X. laevis* H3 sequence) confirming acetylation on lysines 27 and 36. Confirmation is based on the Mascot ion score of 118 and coverage of theoretical y (blue) and b (red) ions including the sequence region of acetylated K27and K36 (in addition to the *absence* of y and b ion coverage that would indicate acetylation at K37). For *A*, *B* and *C*, the peak at m/*z* 126 corresponds to an acetylated lysine immonium ion – NH3 and peaks corresponding to internal fragmentation are shown in green.