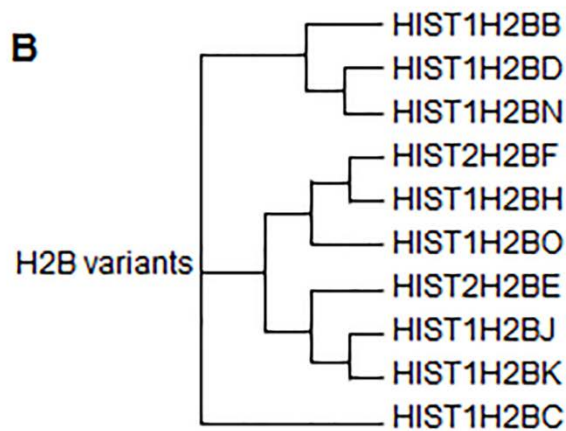


A

40 123

H2B1H-P **D**PAKSAPAPKKGSKKAVTKAQQKKGKRRKRSRKESYSVY...**S**SK
H2B1K-P **E**PAKSAPAPKKGSKKAVTKAQQKKGKRRKRSRKESYSVY...**S****A**K
H2B1C-P **E**PAKSAPAPKKGSKKAVTKAQQKKGKRRKRSRKESYSVY...**S**SK
H2B1J-P **E**PAKSAPAPKKGSKKAVTKAQQKKGKRRKRSRKESYS**I**Y...**S****A**K
H2B1O-P **D**PAKSAPAPKKGSKKAVTKAQQKKGKRRKRSRKESYS**I**Y...**S**SK
H2B1N-P **E****S**KSAPAPKKGSKKAVTKAQQKKGKRRKRSRKESYSVY...**S**SK
H2B2E-P **E**PAKSAPAPKKGSKKAVTKAQQKKGKRRKRSRKESYS**I**Y...**S**SK
H2B2F-P **D**PAKSAPAPKKGSKKAVTK**V**QKKGKRRKRSRKESYSVY...**S**SK
H2B1D-P **E****T**KSAPAPKKGSKKAVTKAQQKKGKRRKRSRKESYSVY...**S**SK
H2B1B-P **E****S**KSAPAPKKGSKK**A****I**TKAQQKKGKRRKRSRKESYS**I**Y...**S**SK



Supplemental Figure 1

Supplemental Fig. 1. Comparative analyses of the identified histone variants. **A.**

Sequence alignment of the identified H2B forms altered in iAs-mediated EMT. The amino acids that changed in the different variants are highlighted. As shown in some cases, these histone H2B variants differ by as little as a single amino acid. For example, at position 3, glutamic acid is replaced by aspartic acid in HIST1H2BH or at position 40, valine is replaced by isoleucine in HIST2H2BE. Amino acid sequence is the same between residues 41 and 124. **B.** Phylogenetic analysis of the identified human H2B variants. The phylogenetic tree was constructed with ClustalW2 based on full-length protein sequences.