

Supplemental Material to:

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A novel ubiquitin mark at the N-terminal tail of histone H2As targeted by RNF168 ubiquitin ligase

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Figure S1

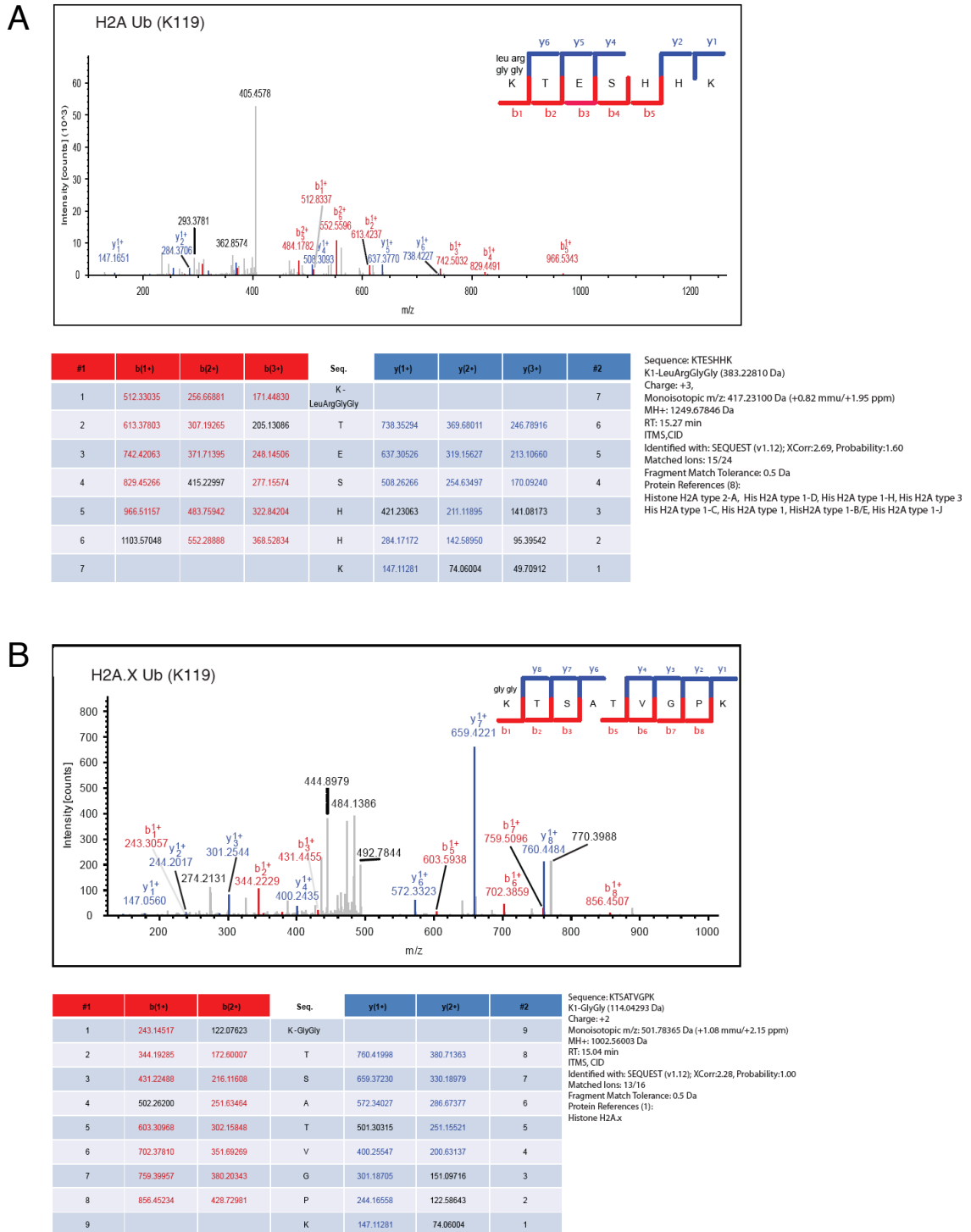


Figure S1. Identification of ubiquitinated peptides corresponding to the canonical C-terminal site in histone H2A family. Mass spectrometric analysis revealed the presence of the ubiquitinated peptides corresponding to the canonical C-terminal sites of histones H2A and H2A.X. The peptide sequences encompassing the ubiquitinated Lys residues in position 119 (for H2A and H2A.X) are indicated.

Figure S2

Hs_H2A/11-19	R	A	K	A	K	T	R	S	S
Mm_H2A/11-19	R	A	K	A	K	T	R	S	S
Rn_H2A/11-19	R	A	K	A	K	T	R	S	S
Bt_H2A/11-19	R	A	K	A	K	S	R	S	S
Xl_H2A/11-19	R	A	K	S	K	T	R	S	S
Hs_H2A.X/11-19	R	A	K	A	K	S	R	S	S
Mm_H2A.X/11-19	R	A	K	A	K	S	R	S	S
Rn_H2A.X/11-19	R	A	K	A	K	S	R	S	S
Bt_H2A.X/11-19	R	A	K	A	K	S	R	S	S
Dm_H2A.X/11-19	K	A	K	A	K	A	V	S	R

Figure S2. K13/K15 Ub mark is conserved during evolution. Sequence alignment of the new ubiquitination sites found in histones H2A and H2A.X from different organisms. ClustalX colors (reflecting the chemical properties of the amino acids) are applied.