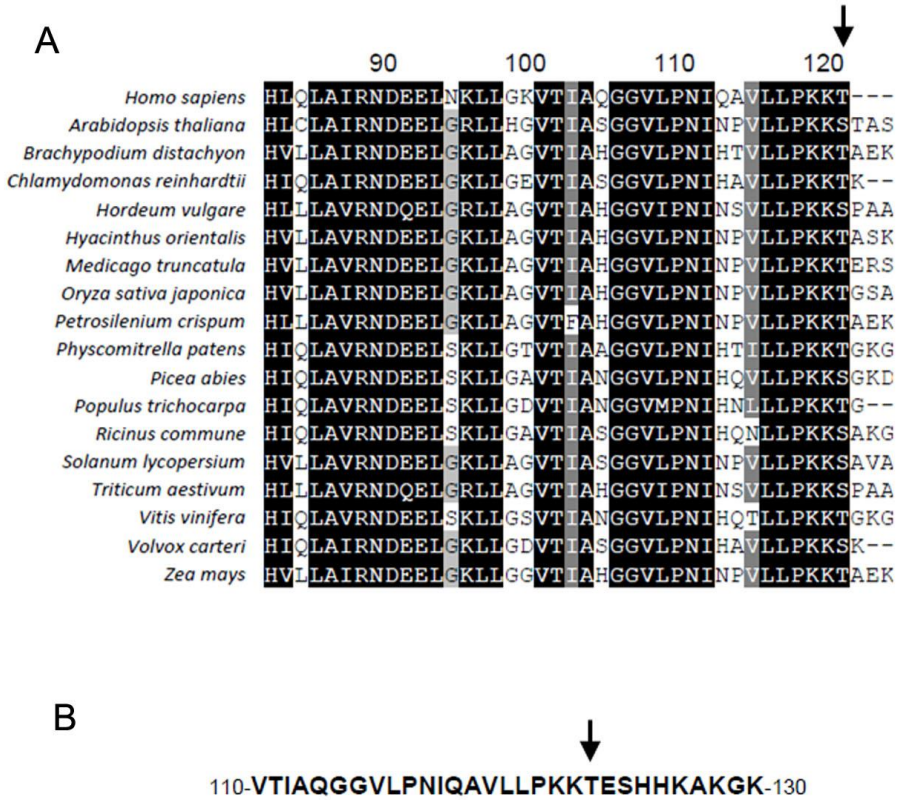
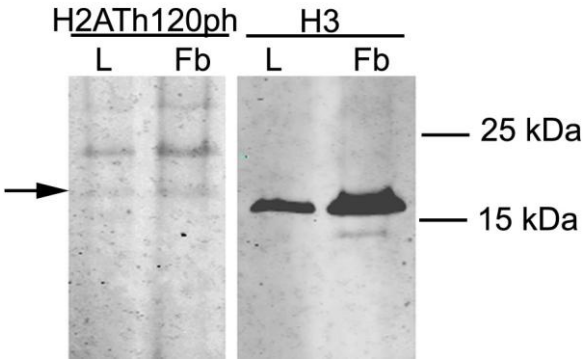
Suppl. Figures



Suppl. Figure 1

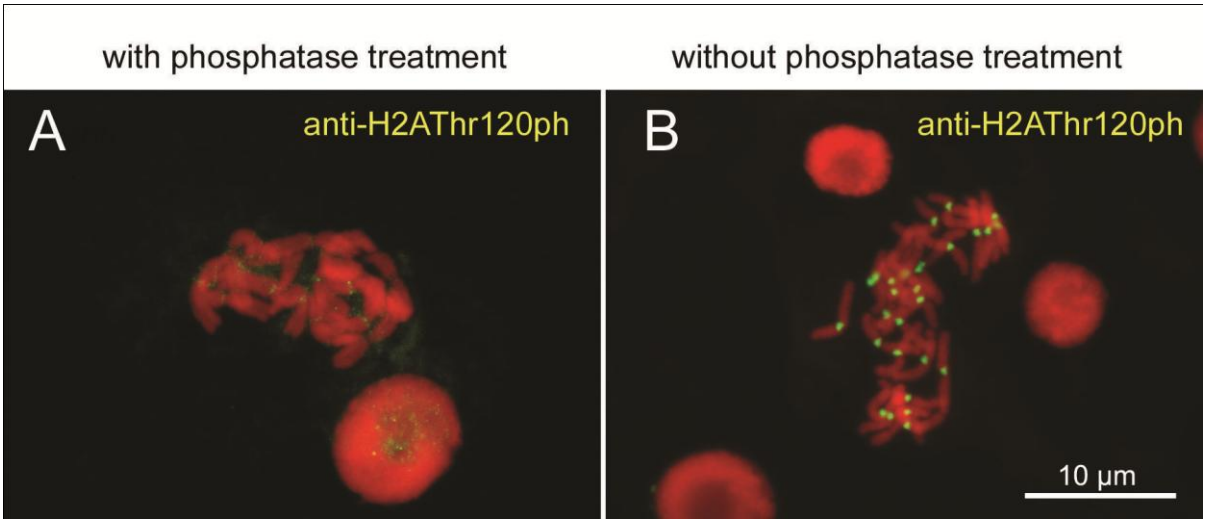
(A) Comparison of deduced protein sequences of parts of the histone H2A variants of *Homo sapiens*: NP_003500, *Arabidopsis thaliana*: NP_198119, *Brachypodium distachyon*: XP_003558214, *Chlamydomonas reinhardtii*: P50567.1, *Hordeum vulgare*: BAK07505, *Hyacinthus orientalis*: AAT08677, *Medicago truncatula:* XP_003597343, *Oryza sativa japonica:* AAT39174*, Petrosilenium crispum*: P19177.1, *Physcomitrella patens*: EDQ49957, *Picea abies*: P35063.1, *Populus trichocarpa*: XP_002316965, *Ricinus commune*: XP_002520712, *Solanum lycopersium*: P25469.1, *Triticum aestivum*: P02275.2, *Vitis vinifera*: XP_002265878, *Volvox carteri*: P16865, *Zea mays:* P40280.1.

(B) Amino acid sequence region of human histone H2A used for phospho peptide antibody production. The phosphorylated threonine is arrowed.



Suppl. Fig. 2

Western gel blot analysis of *Arabidopsis thaliana* proteins isolated from young flower buds (Fb) and leaves (L) using an antibody specific to histone H2A phosphorylated at threonine 120. Arrow indicates the histone H2A-typical size of ~15 kDa. An anti-histone H3 antibody was used as control.



Suppl. Fig. 3

Anti-histone H2AThr120ph staining of mitotic rye cells after (A) and without (B) phosphatase treatment. Treatment leads to the absence of the immunosignals.