



**Figure S2. Identification of global changes in histone H4 modifications by quantitative targeted mass spectrometry analysis. (A)** Heat map (log<sub>2</sub> of fold change) of the different histone modifications as detailed on top. Data was normalized to average signal of interphase samples. **(B)** Relative abundance of selected modifications on H4 tails from interphase or mitotic HeLa-S3 cells. The data was obtained by quantitative targeted mass spectrometry analysis. Each bar represents the percentage of the H4 peptides with the indicated modifications within the total H4 tail peptide population.