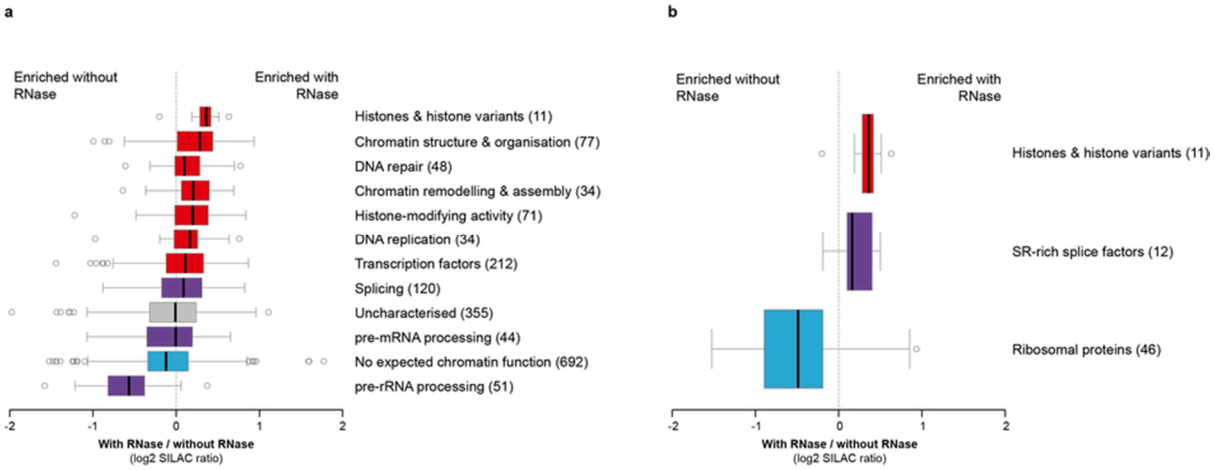

Supplementary Figure 1: The effect of RNase treatment on ChEP-isolated chromatin fractions. (**a**) Boxplot showing the impact of RNase digestion on various functional categories of proteins. Proteins with functions related to RNA processing (purple) are depleted by RNase treatment, presumably because they are cross-linked to chromatin indirectly via RNA. Proteins without expected chromatin function (i.e. contaminants, blue) are also somewhat reduced by RNase treatment, but proteins with canonical chromatin functions are not (red). (**b**) Boxplot showing that RNase treatment reduces the co-purification of ribosomes, which are typical contaminants of chromatin fractions. Note that the family of serine / arginine (SR)-rich splicing factors is not affected by RNase treatment, as these proteins generally act co-transcriptionally and are thus likely to be cross-linked directly to DNA or other chromatin factors.