



Figure 6. Histone variant phylogenies. Histone sequences from selected species were multiply aligned and neighbor-joining trees were produced using the EBI server (<http://www.ebi.ac.uk/Tools/phylogeny>). (A) Histone H3s. (B) Histone H2As. Note that there are no clear phylogenetic distinctions between RC H3 and RI H3.3, and between RC H2A and RI H2A.X. (C) H1 variants from diverse eukaryotes show a “star” phylogeny, which suggests that they are functionally interchangeable. (C, Modified from Talbert et al. 2012.)