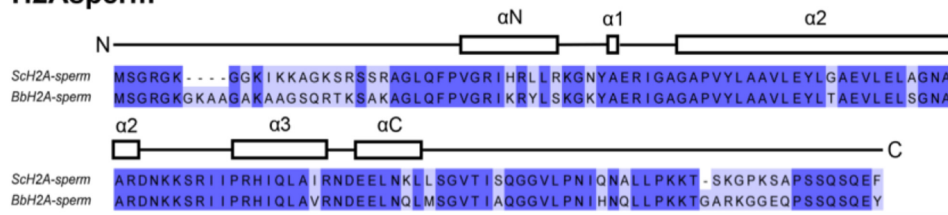
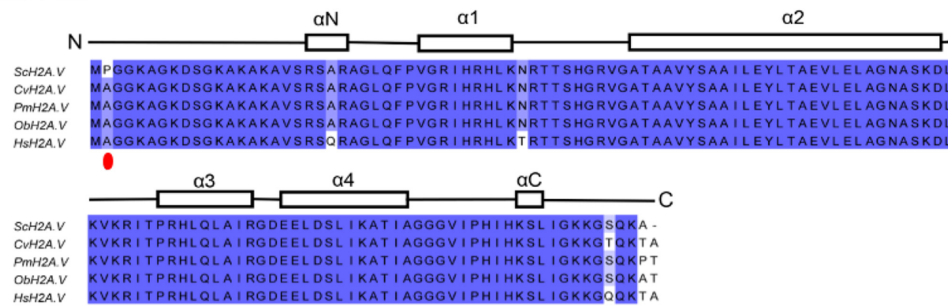


**Figure S1.** Multiple sequence alignment of H1 and H1oo amino acid sequences from selected members of molluscs and humans. Percent similarity is shown in blue and the intensity of the color are corresponding to the degree of similarity.

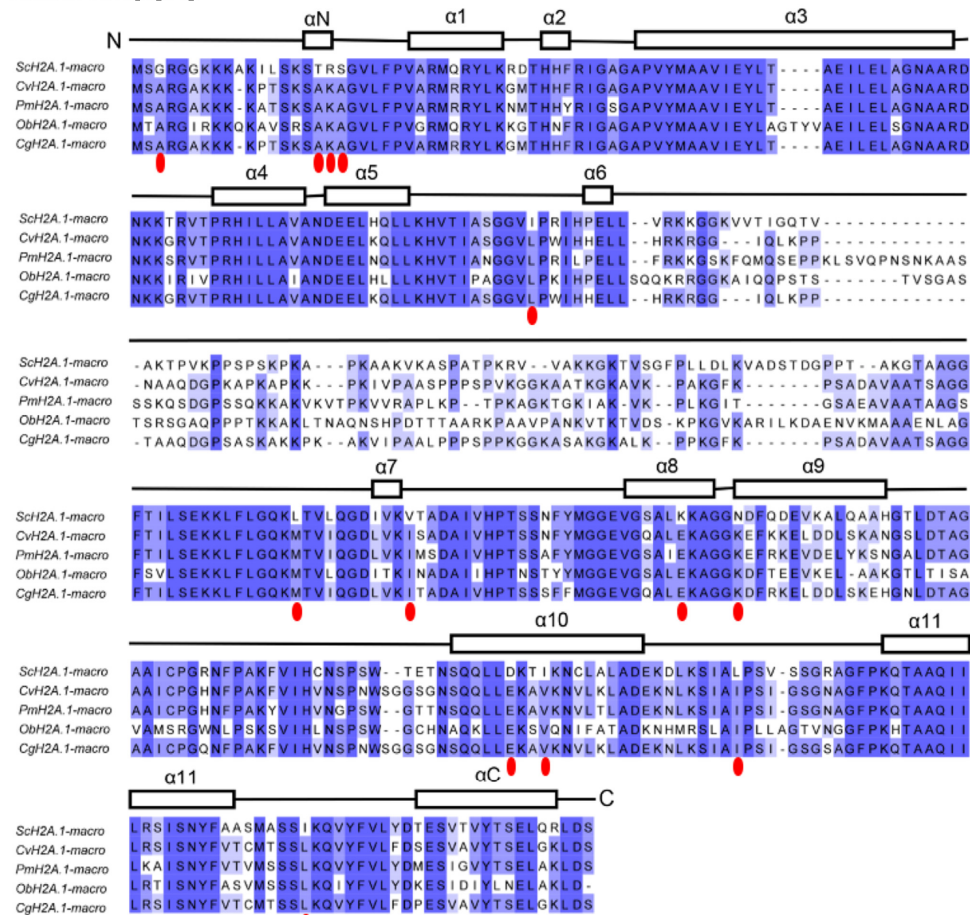
## H2Asperm



## H2A.V



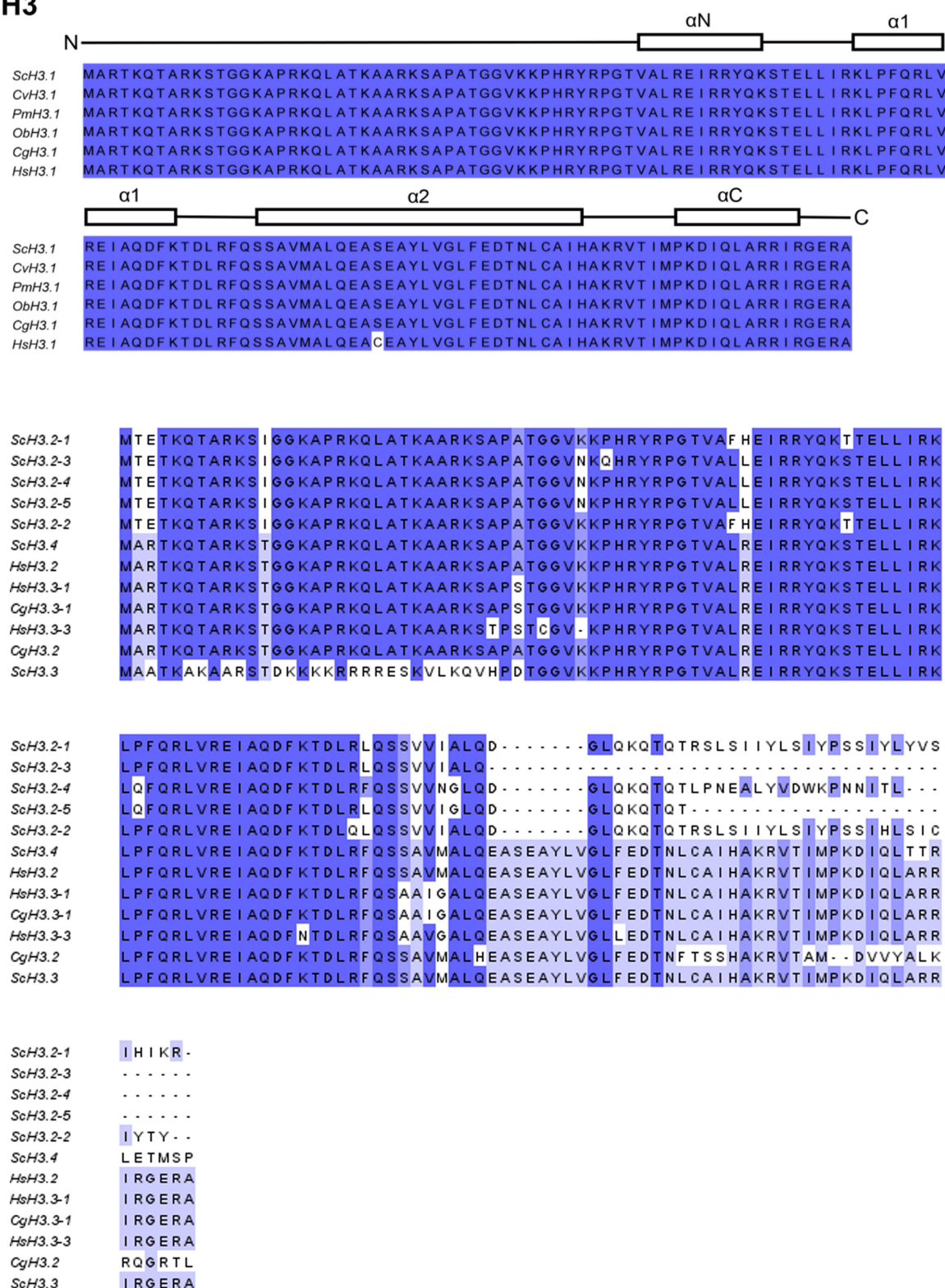
## H2A.1macro



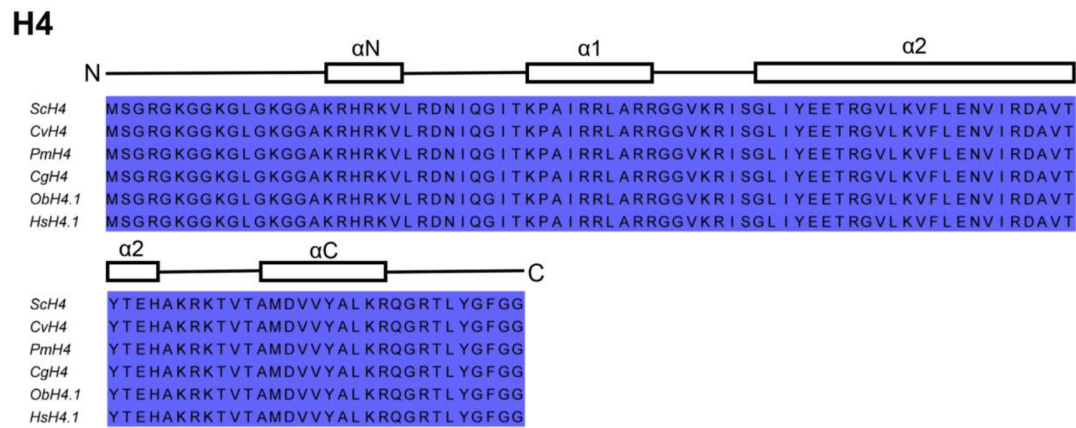
**Figure S2.** Multiple sequence alignment of H2A variants' amino acid sequences from selected members of molluscs and human. Percent similarity is shown in blue and the intensity of the color are corresponding to the degree of similarity. The amino (N) and carboxy (C) terminal ends, as well as the predicted secondary structure, are signed above the alignment. Unique amino acid changes in *S. constricta* are marked by red ovals below alignment.



# H3



**Figure S3.** Multiple sequence alignment of H3 amino acid sequences from selected members of molluscs and human. Percent similarity is shown in blue and the intensity of the color are corresponding to the degree of similarity. The amino (N) and carboxy (C) terminal ends of the protein, as well as the predicted secondary structure, are signed above the alignment.



**Figure S4.** Multiple sequence alignment of H4 amino acid sequences from selected members of molluscs and human. Percent similarity is shown in blue and the intensity of the color are corresponding to the degree of similarity. The amino (N) and carboxy (C) terminal ends of the protein, as well as the predicted secondary structure, are signed above the alignment.



**Figure S5.** Phylogenetic analysis of histone gene family-related 390-amino acid sequences across 11 animals. Species abbreviations: Hs, *Homo sapiens*; Dm, *Drosophila melanogaster*; Bb, *Branchiostoma belcheri*; Ce, *Caenorhabditis elegans*; Sp, *Strongylocentrotus purpuratus*; Sc, *Sinonovaula constricta*; Cv, *Crassostrea virginica*; Cg, *Crassostrea gigas*; Pm, *Pecten maximus*; Tg, *Tegillarca granosa*; Ob, *Octopus bimaculoides*.