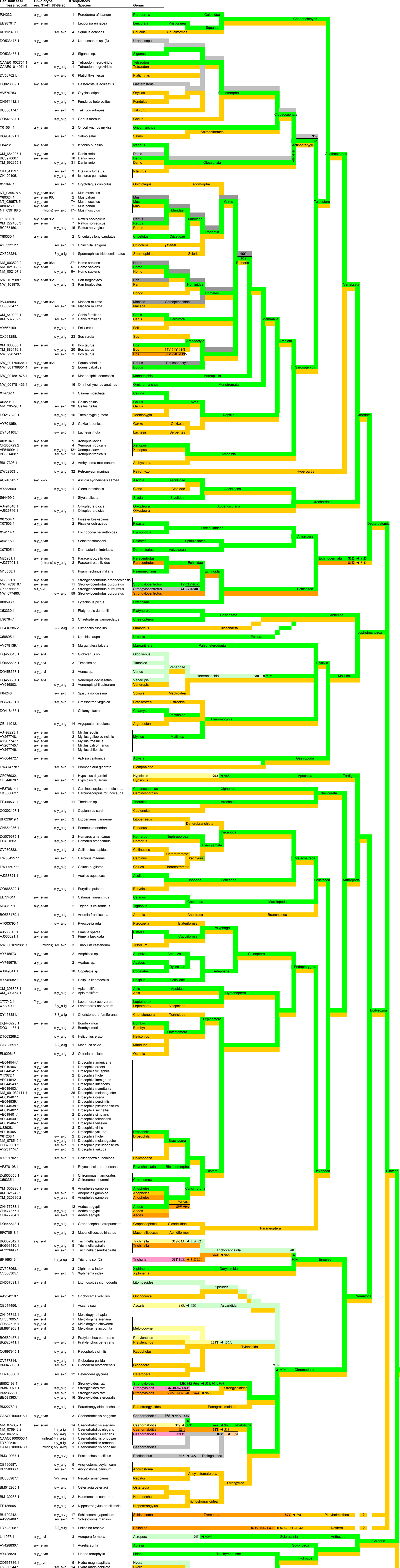
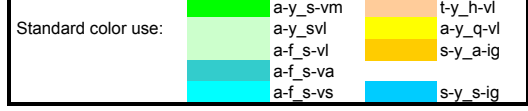


Analysis of the evolution of metazoan histone H3 forms, based on Tree Of Life phylogenetic relationships

Full protein sequences are available in table format, arranged alphabetically and by location in the tree below.

H3s which are known or expected to be replication-coupled (RC) are separated from H3s which are known or expected to be replication-independent (RI). A deduced sequence change is marked by * (from-to) pointers, by a change in color and by the value of the original residue (regular font) and the new residue (bold font). Single-codon, single-residue variations without support by similar species are marked in bracketed italics.

Duplication-with-divergence of a functional H3 type, deduced as certain (or probable), is marked by a dark separation bar and a change of color color, e.g. green-to-blue or gold-to-orange.



Base sequences: **a-y** **s-vm** **a-y** **s-vl** **a-f** **s-vl** **a-y** **q-vl** **a-f** **s-va** **a-y** **a-ig** **a-f** **s-vs** **s-y** **s-ig**

differences: x xx