

Consensus and “best” sequences of the 10 avian ERV clades

This document contains consensus sequences, the nucleic acid of the highest ReTe scoring provirus, and the nucleic acid protein interpretation (“putein”, as described in the 2007 ReTe paper) from the “best” representative gene, with the least number of stops and frameshifts, for the clades described in the paper. Zinc fingers and GPYF domains are highlighted in red. Nucleotides and amino acids in consensus sequences which occurred in at least 50% of the nucleotides or amino acids in the same column of a Clustal alignment are shown in upper case. For the best putein representative, upper case denotes that the amino acid was found in the alignment which was used to deduce the putein (described in the 2007 ReTe paper). The best representatives are shown with the assembly name and chromosomal position.

The consensus sequences are shown together with the percent internal identity of the members of the group. The consensus sequences are intended for use as proxys in alignments and BLAST searches, to reduce complexity. The lower case characters in consensus, particularly in those with a low (<50%) percent of internal identity, may be artefactual (due to imperfections of the alignment) and should be handled with caution.

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