

Supporting Information

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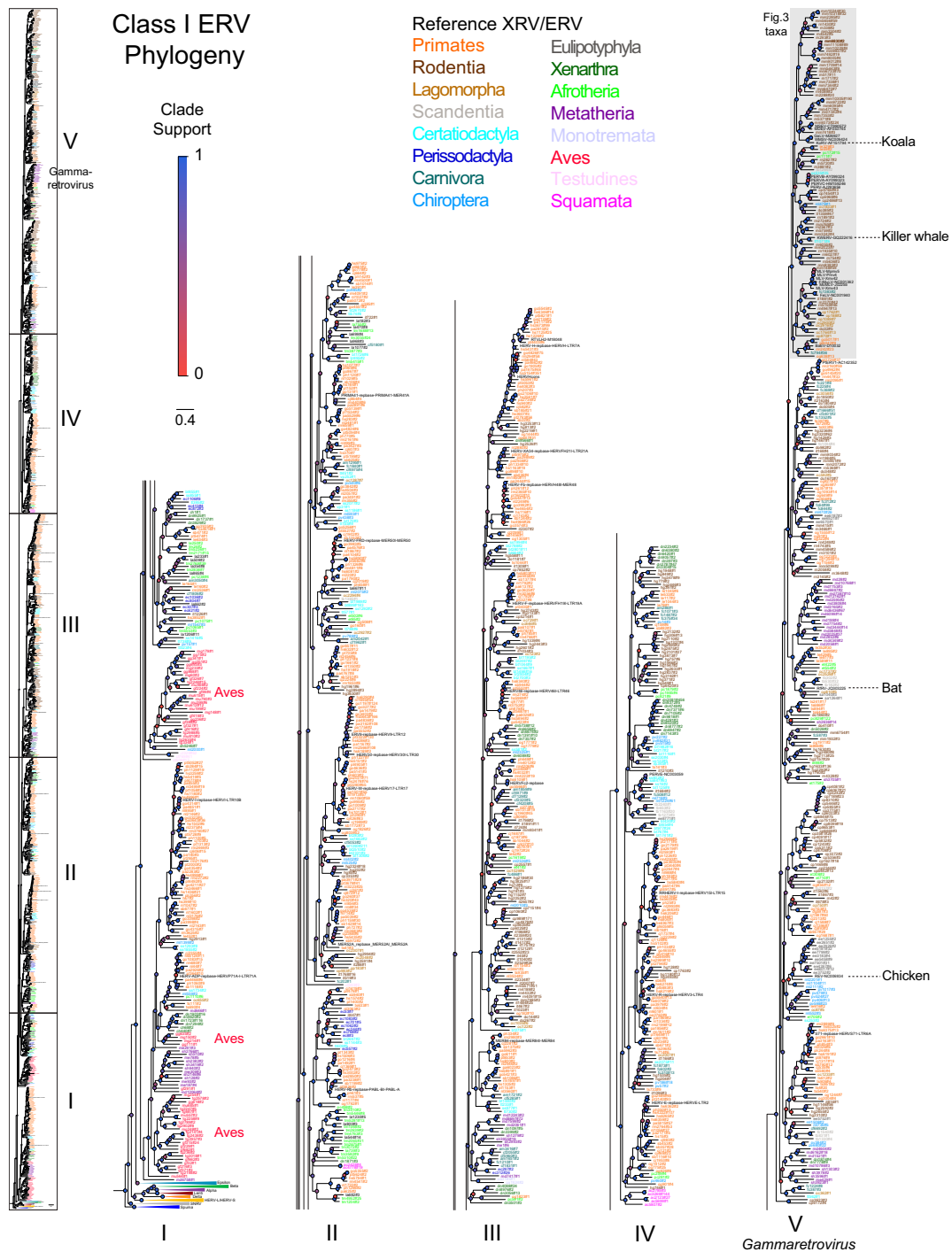


Fig. S1. Class I endogenous retrovirus (ERV) phylogeny. Phylogenetic representation of gammaretroviruses and associated class I ERVs is shown. Sequences from color-coded host genomes follow the short nomenclature outlined in Table S1. I–V represent class I ERVs and XRV from the full tree (far left). The *Gammaretrovirus* genus locates in V, and the gray highlight indicates taxa included in Fig. 3. The phylogenetic locations for sequences discussed in the text are highlighted (I, Aves; V, chicken, bat, killer whale, and koala). Taxon nomenclature hash marks precede the number of represented ERVs for each taxon. The tree was rooted on the Cer1 element (Gypsy/Ty3; GenBank accession no. U15406.1) as outgroup to the Retroviridae. Clades for retroviral genera other than gammaretroviruses/class I ERVs were collapsed for presentation at the base of the phylogeny. Colored circles indicate node support.

Other Supporting Information Files

[Table S1 \(docx\)](#)

[Table S2 \(docx\)](#)