

Supporting Information

Hayward et al. 10.1073/pnas.1315419110

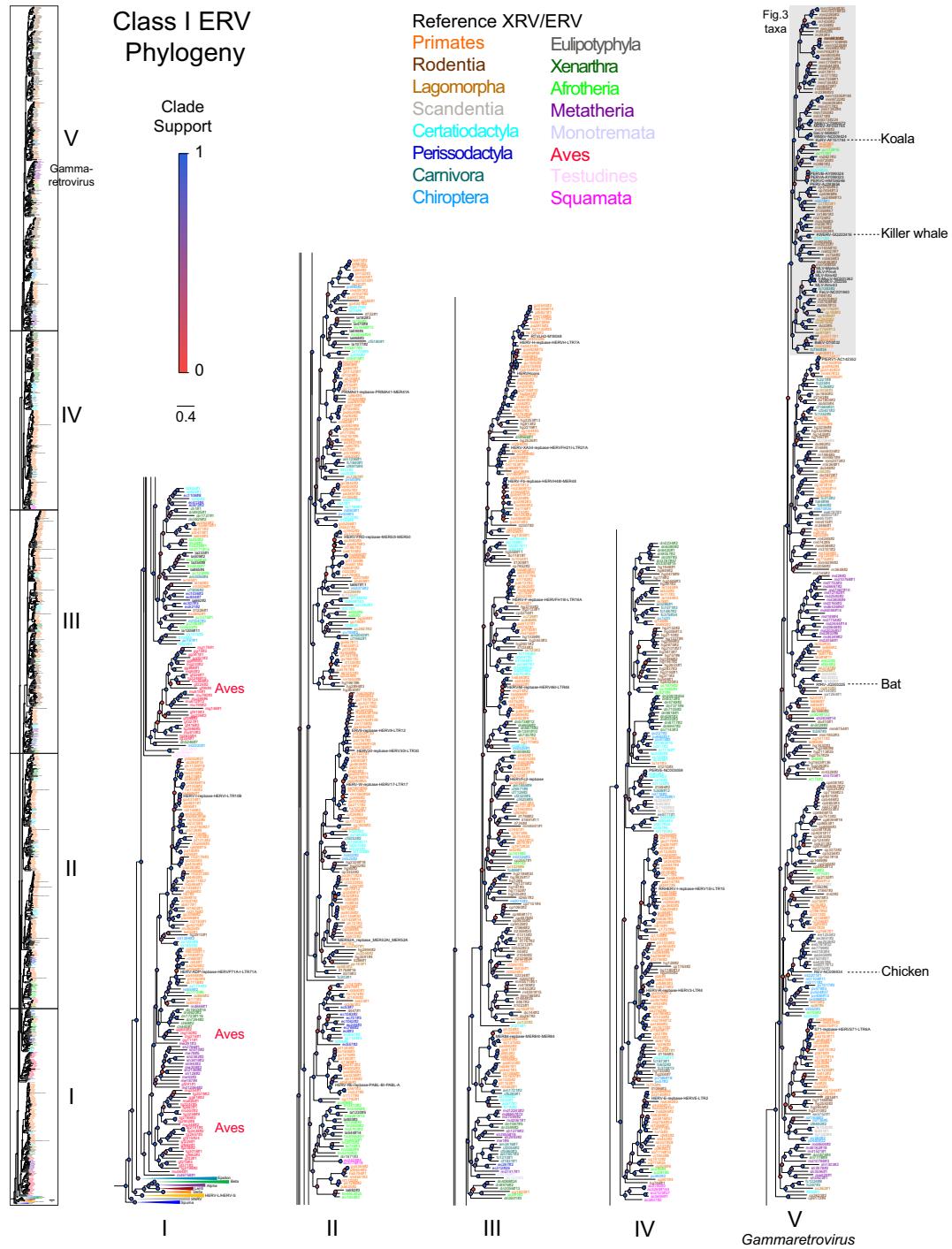


Fig. S1. Class I endogenous retrovirus (ERV) phylogeny. Phylogenetic representation of gammaretroviruses and associated class I ERVs is shown. Sequences from color-coded host genomes follow the short nomenclature outlined in Table S1. I–V represent class I ERVs and XRV from the full tree (far left). 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.

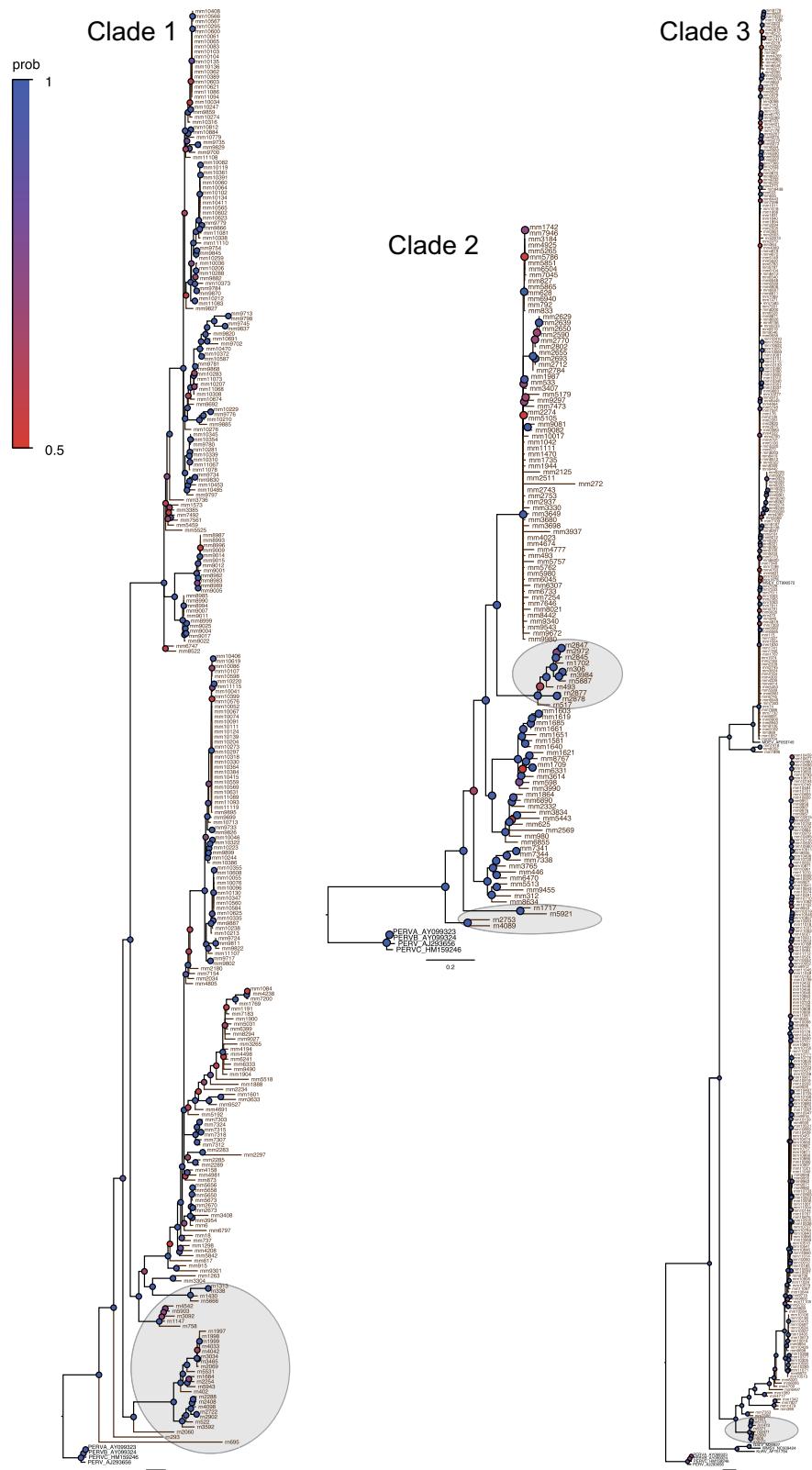


Fig. S2. Gamma-ERV clades 1–3. Expanded phylogenies of Fig. 3 clades 1–3 rooted on porcine ERV reference sequences. Sequences from color-coded host genomes follow the short nomenclature outlined in [Table S1](#). Highlighted rat ERVs lie basally in the trees and as sister clades to mouse ERVs. Colored circles indicate node support. Loci details for rat and mouse ERVs are presented in [Table S2](#).

Other Supporting Information Files

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

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