



**Figure 1. Phylogeny of AAV *rep* genes supports host-virus co-divergence.**

**(a)** AAV genome schematic (4.7 Kb), showing *rep* and *cap* genes flanked by inverted terminal repeats (ITRs).

**(b)** Rooted maximum-likelihood phylogeny of AAVs and endogenous viral elements (EVEs) based on *rep*. Brackets indicate clustering with host taxa. The inset tree (bottom right) illustrates host divergence times. Boxes next to EVE taxa denote minimum ages inferred from orthology. Asterisks indicate bootstrap support >70% (1,000 replicates). Amino acid-based support values are above branches, nucleotide-based below.

**(c)** Expanded primate AAV cladogram, showing associations with humans, Asian primates, and African primates. Format as in (b).