



Supplementary information S1 (figure) | **Phylogenetic history of human and sylvatic dengue.** The figure shows the maximum clade credibility (MCC) tree of 150 complete coding region (alignment of length 10,185 nucleotides) sequences of all four serotypes of dengue virus (DENV). The sylvatic viruses are shown in red. Note that the sequence from the putative sylvatic DENV-1 (PS-1244/1972) falls within the genetic diversity of human DENV-1 so that its status as a sylvatic virus is unclear. Molecular clock estimates (95% credible intervals) of dates of common ancestry are also shown next to key nodes and provided the timescale for the tree (x-axis). The tree was estimated using the Bayesian Markov Chain Monte Carlo approach available in the BEAST package¹ and using the general time reversible model of nucleotide substitution with a different substitution rate for each codon position, a strict molecular clock and a Bayesian skyline coalescent prior (highly comparable results were obtained using different evolutionary models; more details are available from the authors on request).

1. Drummond, A. J. & Rambaut, A. BEAST: Bayesian evolutionary analysis by sampling trees. *BMC Evol. Biol.* 7, 214 (2007).