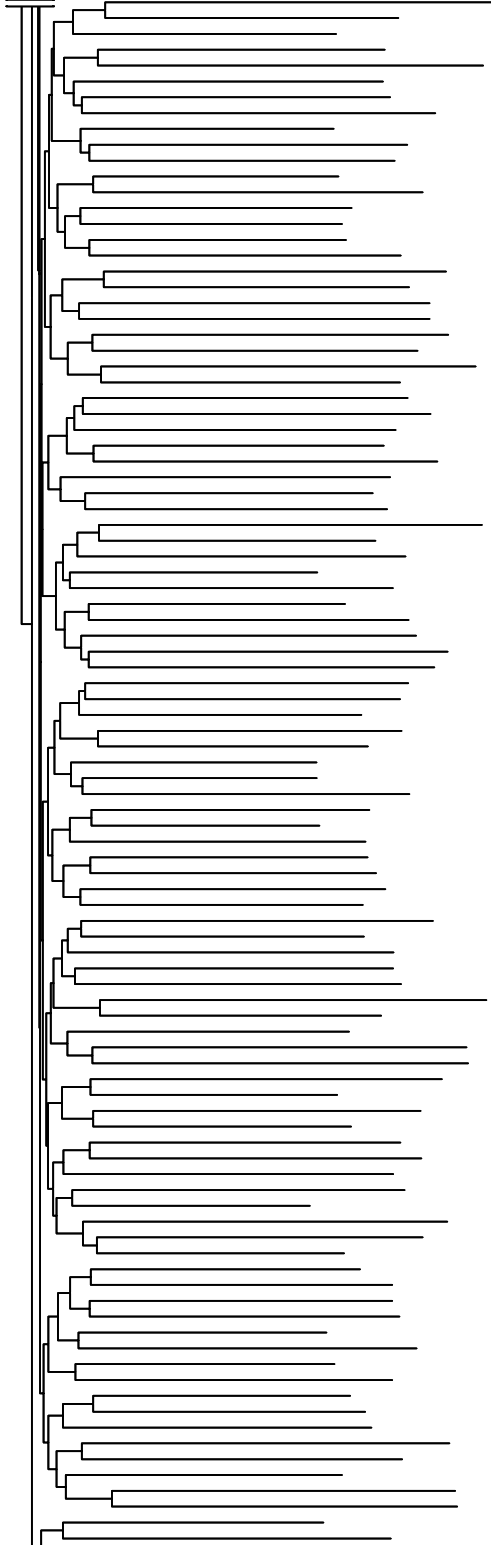
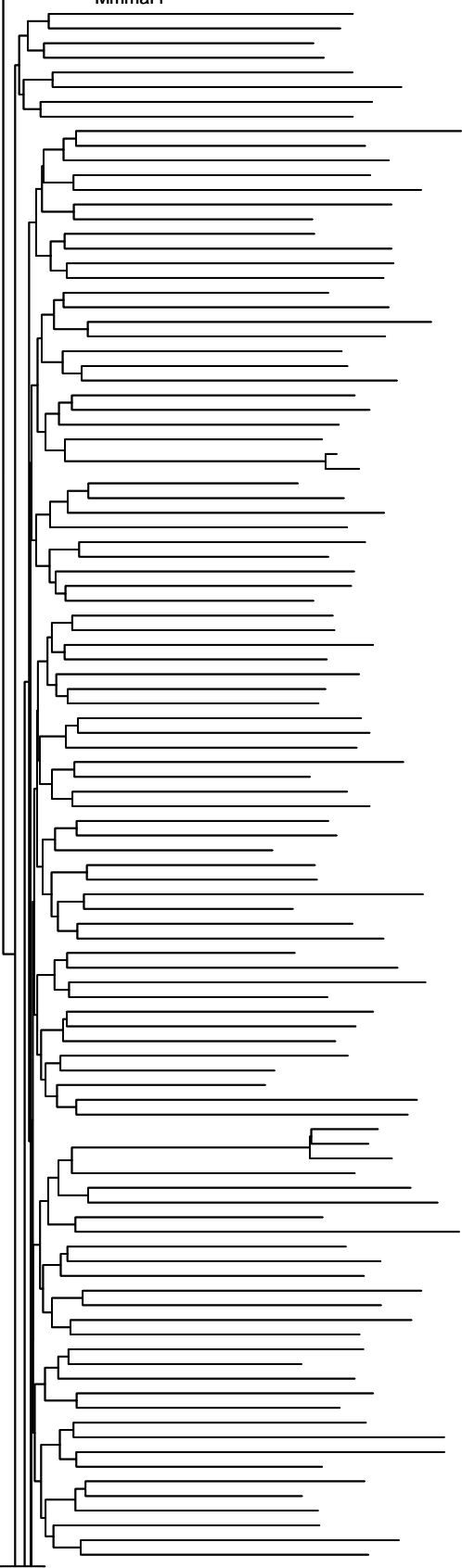


Mmmar1



Mar-Owl
Mar-Gre
Mar-Rhe
Mar-Sia
Mar-Ora
Mar-Gor
Mar-Ptr
Mar-Hsa

0.05

Fig. 5. Phylogenetic tree of 205 human *Hsmar1* transposons and the *MAR* region in eight primates. The tree was reconstructed by using the neighbor-joining algorithm and the Kimura 2-parameter nucleotide substitution model, based on the DNA sequence corresponding to the transposase gene. The tree is rooted with the consensus sequence of the mouse *Mmmar1 mariner*-like transposon. Unlabelled terminal branches correspond to *Hsmar1* transposons. The monophyletic clade of *MAR* sequences is highlighted in gray (Hsa, human; Ptr, common chimpanzee; Gor, gorilla; Ora, orangutan; Sia, siamang; Gre, African green monkey; Rhe, rhesus macaque; Owl, owl monkey). The tree is parted in two halves, at the level of the two horizontal bars interrupting deep branches of the tree.