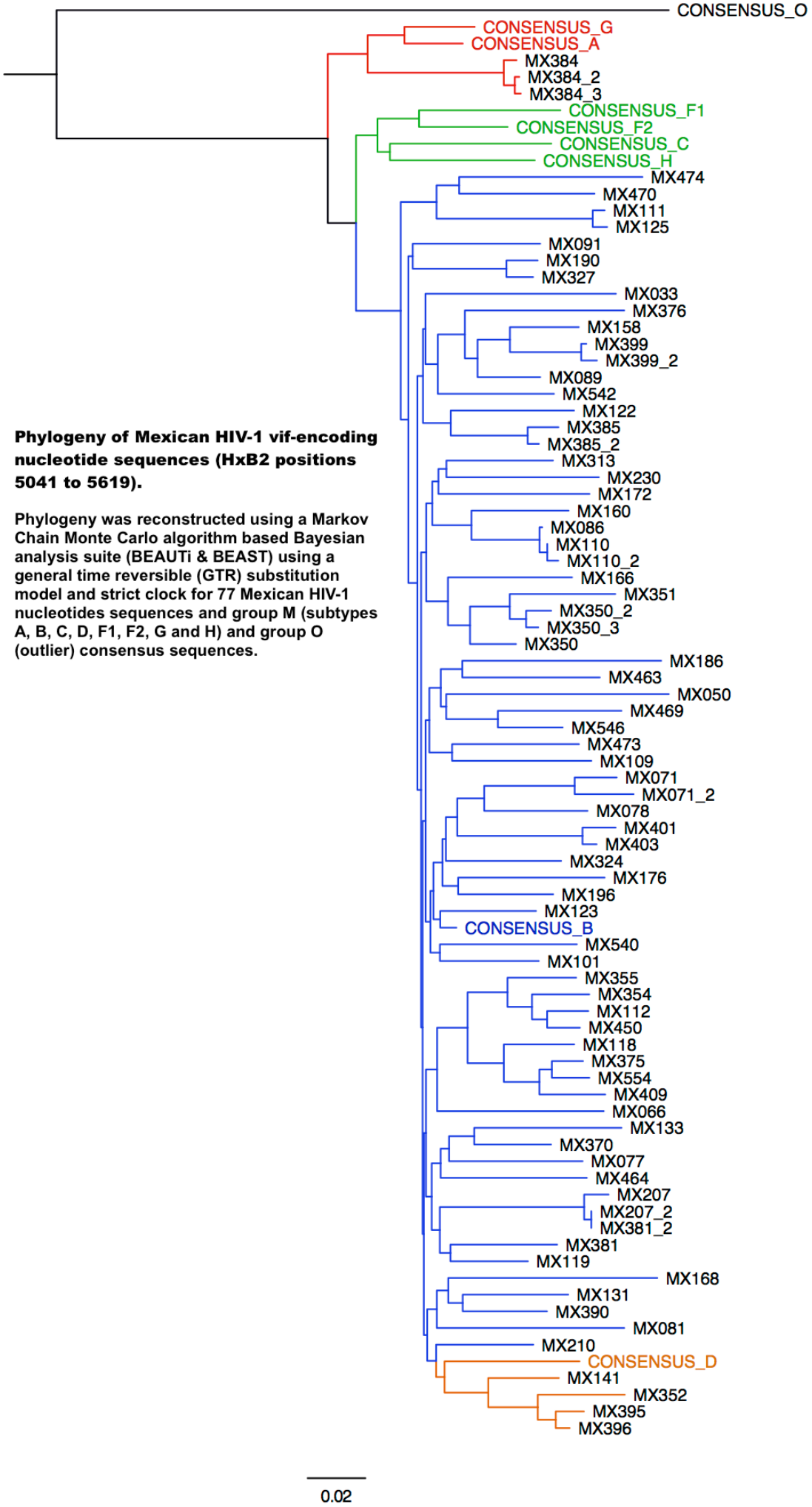

Phylogeny of Mexican HIV-1 vif-encoding nucleotide sequences (HxB2 positions 5041 to 5619).

Phylogeny was reconstructed using a Markov Chain Monte Carlo algorithm based Bayesian analysis suite (BEAUTi & BEAST) using a general time reversible (GTR) substitution model and strict clock for 77 Mexican HIV-1 nucleotides sequences and group M (subtypes A, B, C, D, F1, F2, G and H) and group O (outlier) consensus sequences.