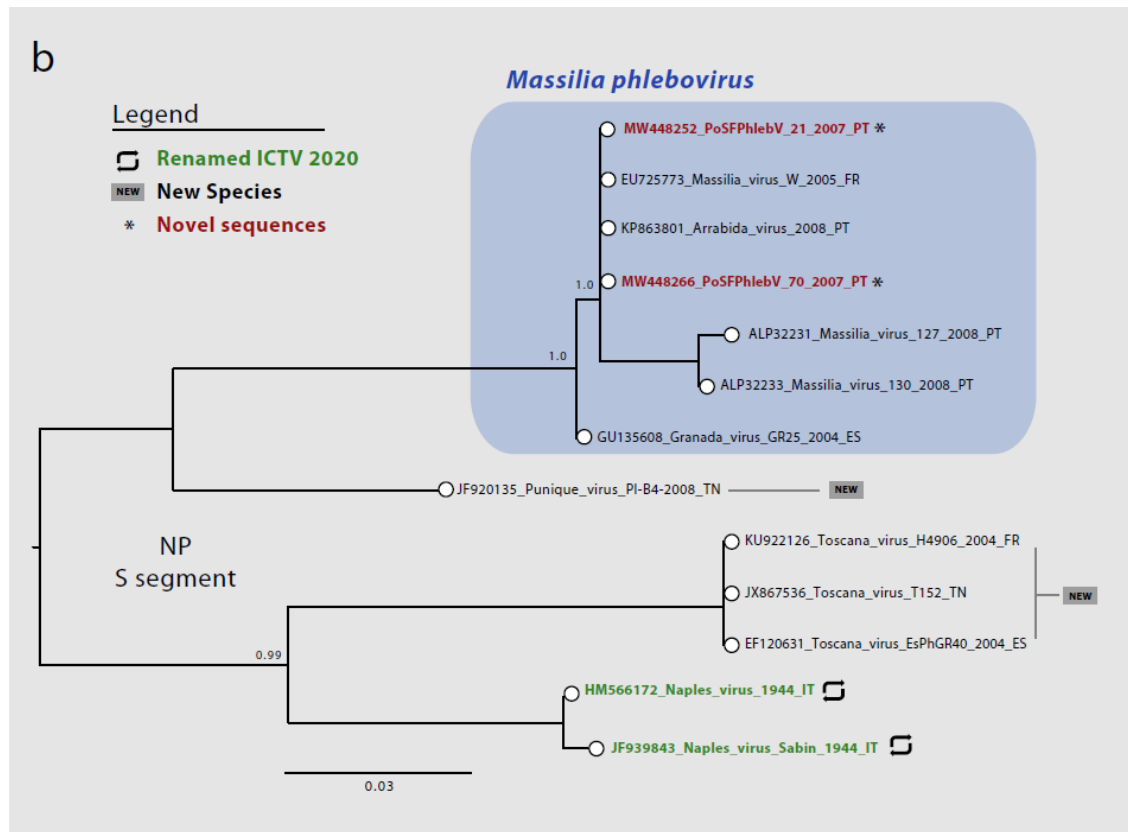
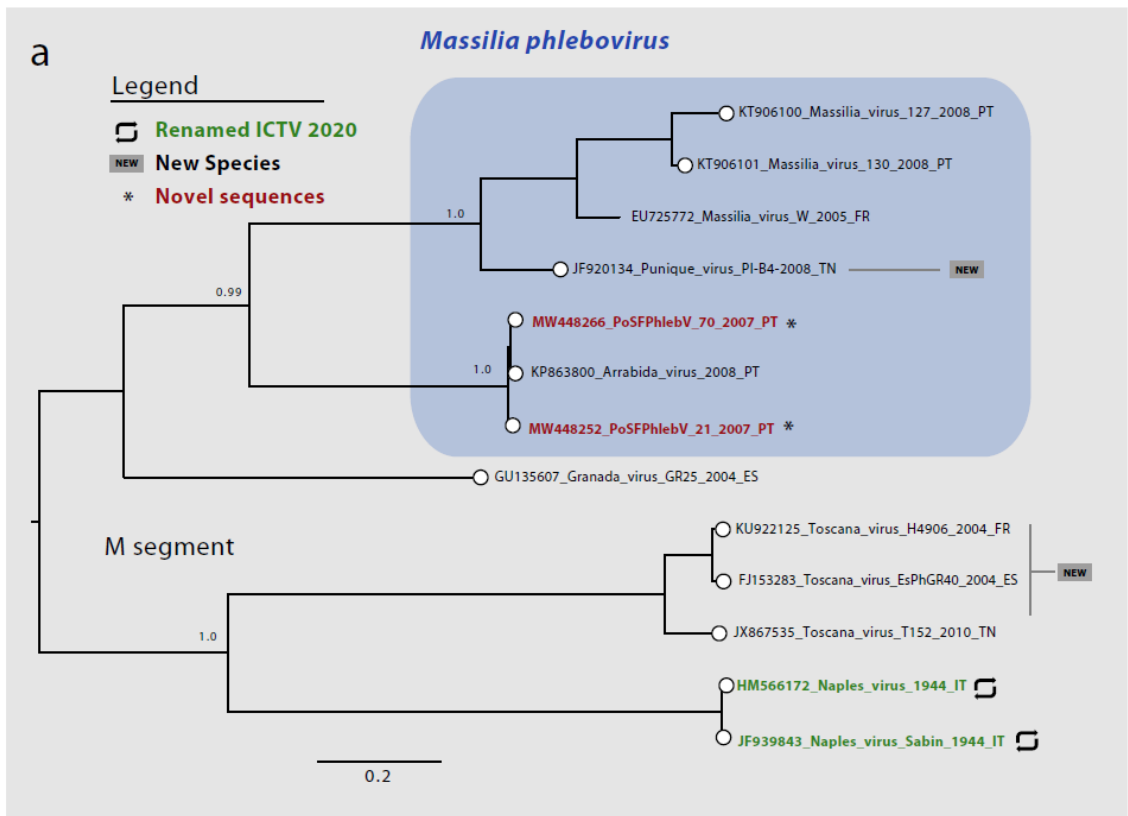
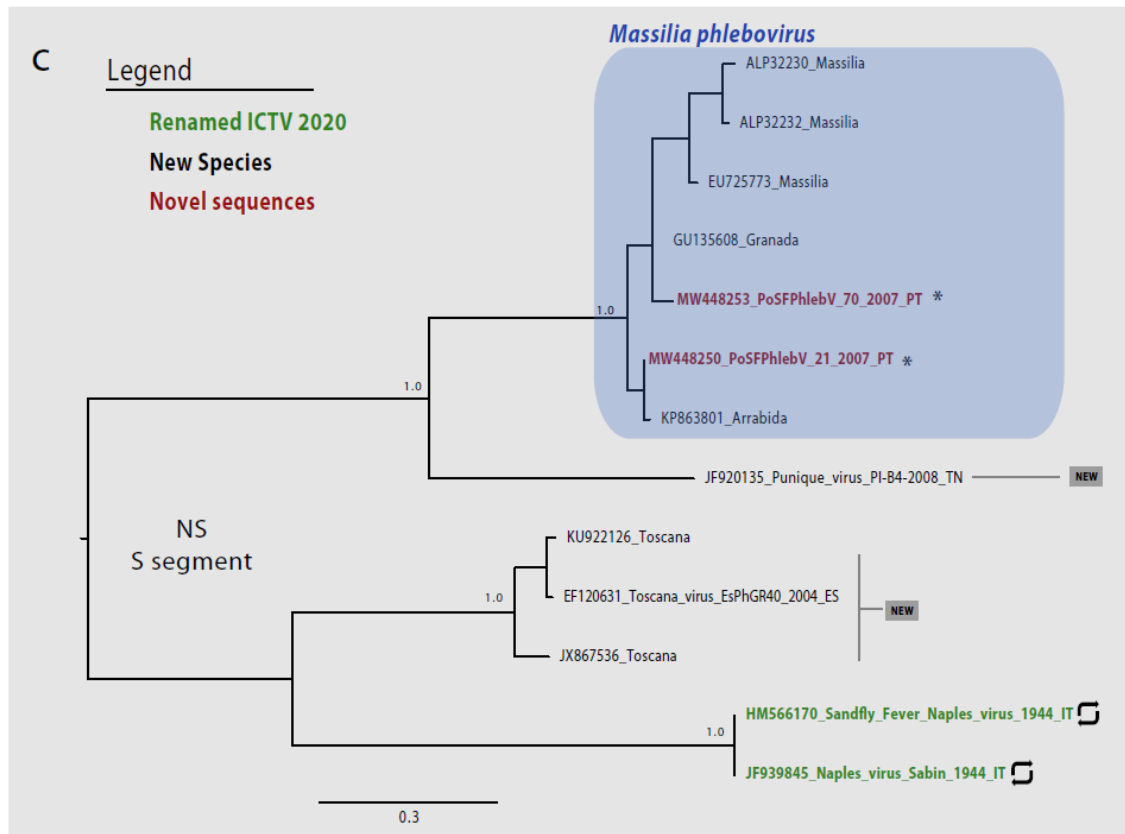


Supplementary File S3: Additional Phleboviruses' trees





Supplementary File S3: Additional Phleboviruses' trees

Maximum likelihood phylogenetic tree of phleboviruses entire amino acid sequences of: a. Glycoprotein precursor protein (segment M); b. Nucleoprotein (NP, segment S); c. Non-structural protein (NS, segment S). Sequence names in red and marked with an asterisk have been sequenced in this study. According to ICTV 2020, sequence names in green have recently had their species renamed, while those marked by "new" symbols on the right side of the tree have been assigned as new species. Names of the sequences in the tree match the IDs in the alignment made available as a supplementary file. Numbers on branches are the bootstrap support. The shaded area on the top highlights the Massilia phlebovirus cluster (please note that in a., showing the phylogenetic tree based in segment M sequences, *Punique phlebovirus* is included within Massilia phlebovirus cluster due to reassortment events).