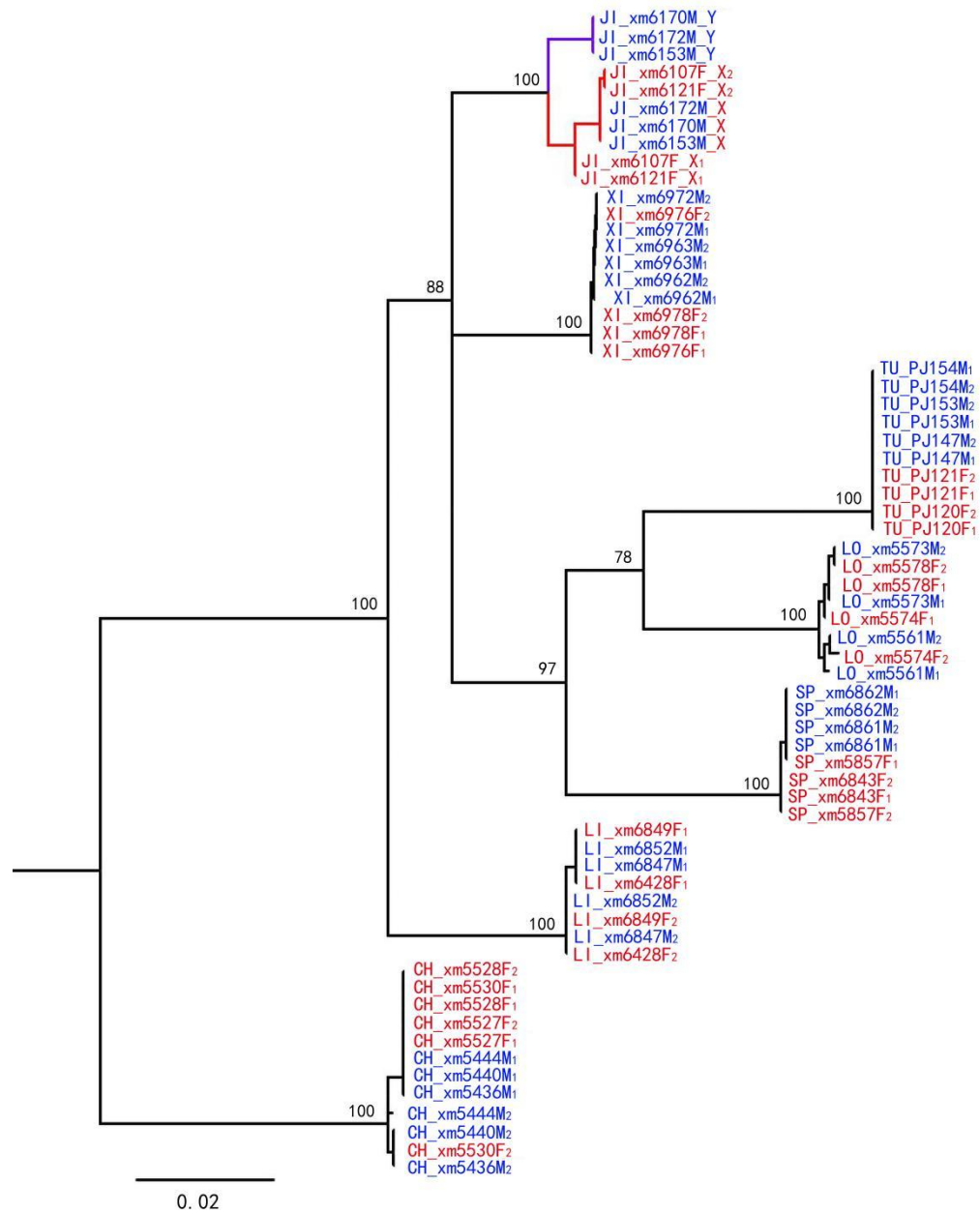


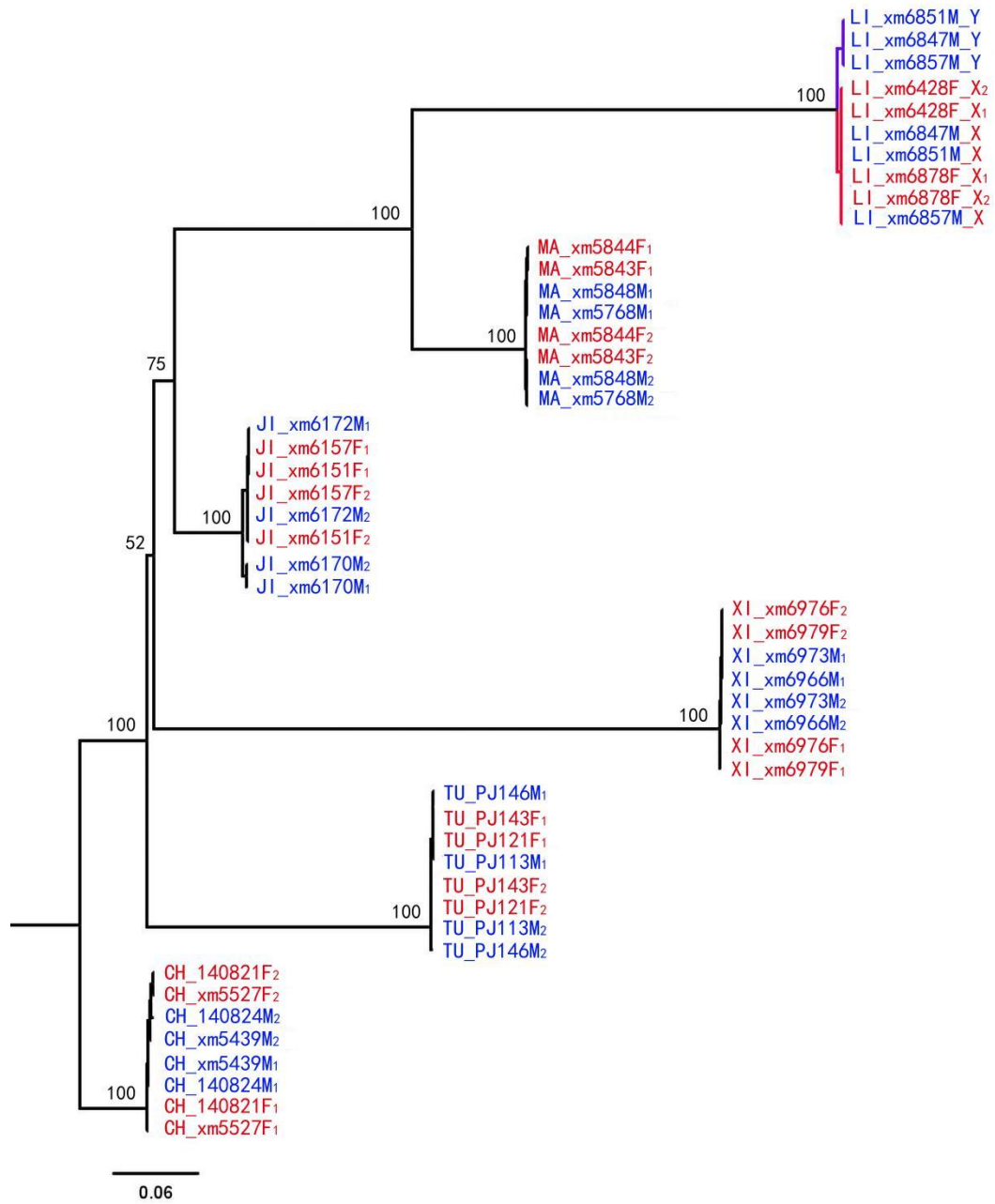
File S8

Maximum-likelihood phylogenies of five sex-linked markers and its cross-species homologous sequence in *Amolops* (JI for *A. jinjiangensis*, LI for *A. lifanensis*, LO for *A. loloensis*, MA for *A. mantzorum*, SP for *A. sp.*, TU for *A. tuberodepressus*, WU for *A. wuyiensis*, XI for *A. xinduqiao*). Bootstrap values are shown for the main branches, when above 50%. Sequence labels feature species, ID number, sex and allele. The trees are constructed using RAxML from a phased male and female sequences. Clades of Y sequences are shown in blue. Clades of X sequences are shown in red. All other sequences from males and females sequences are shown in black.

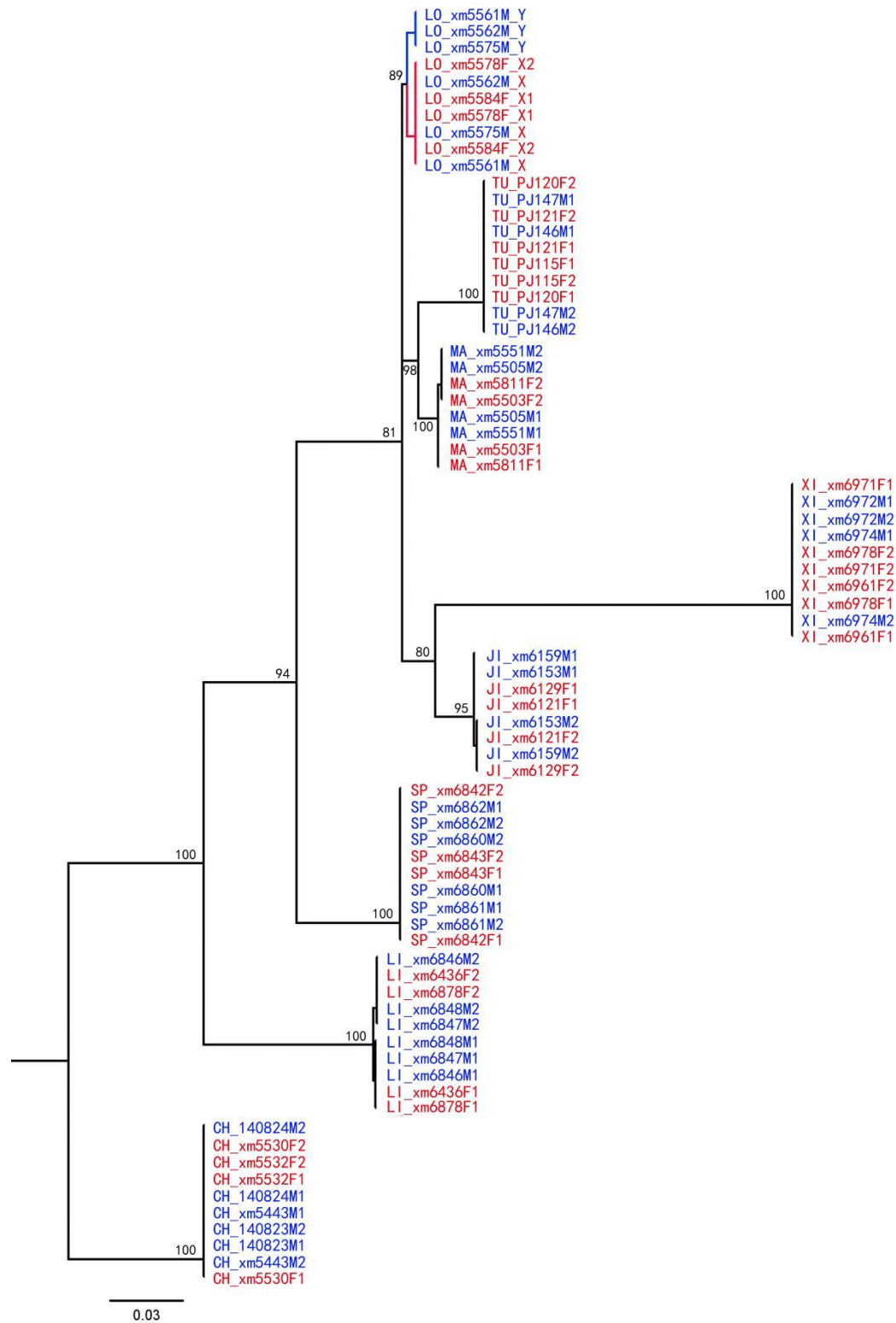
A. jinjiangensis



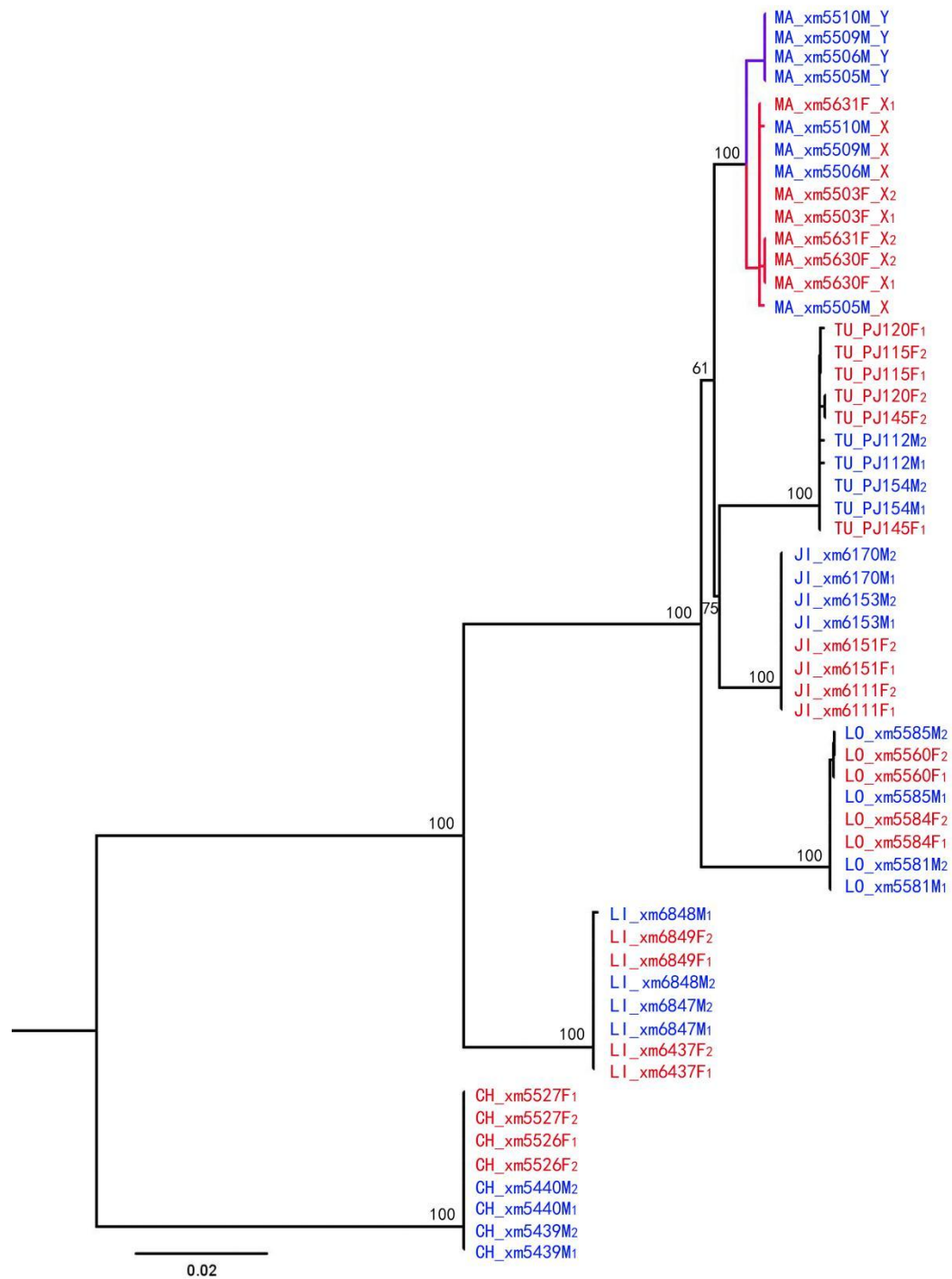
A. lifanensis



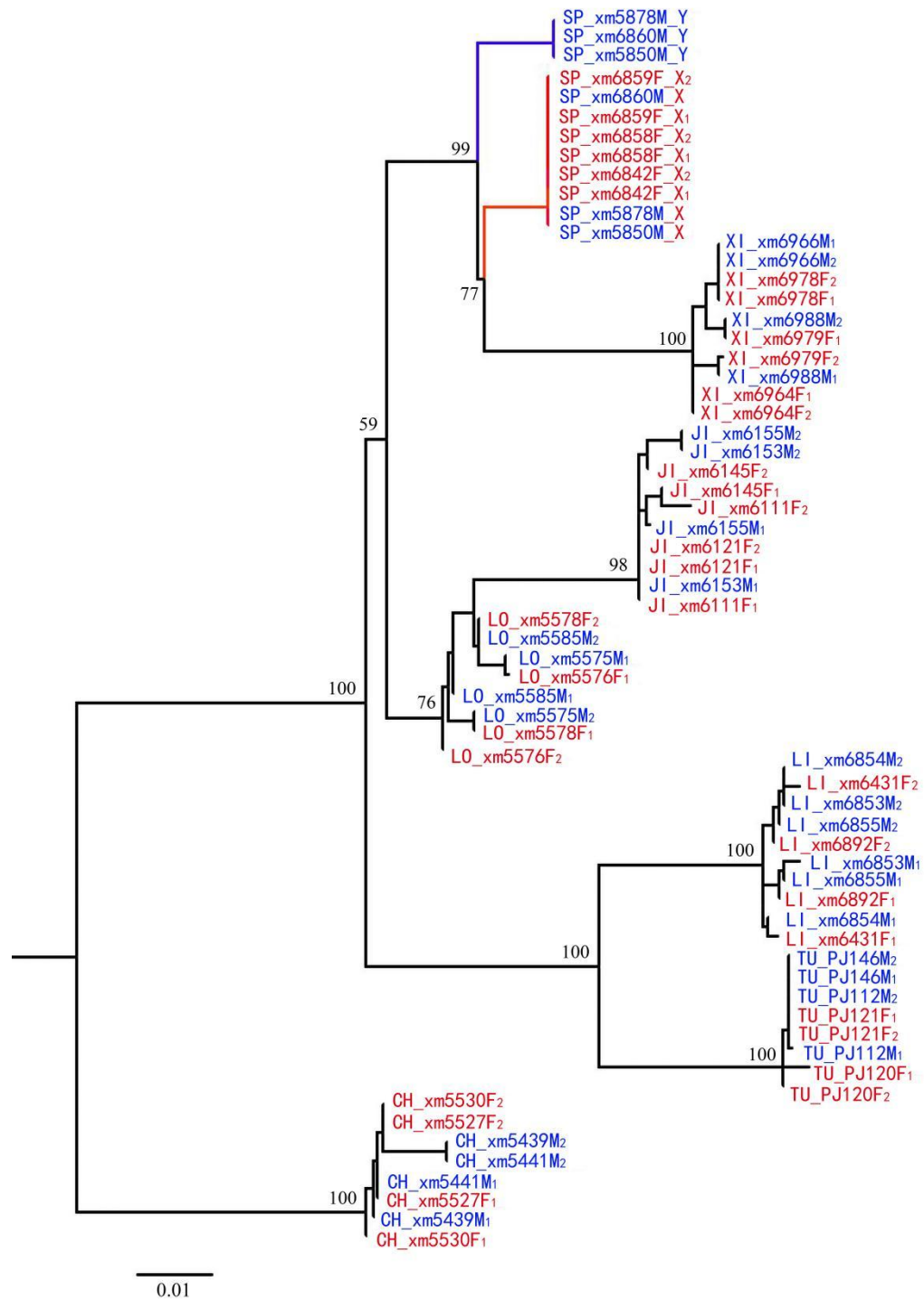
A. loloensis



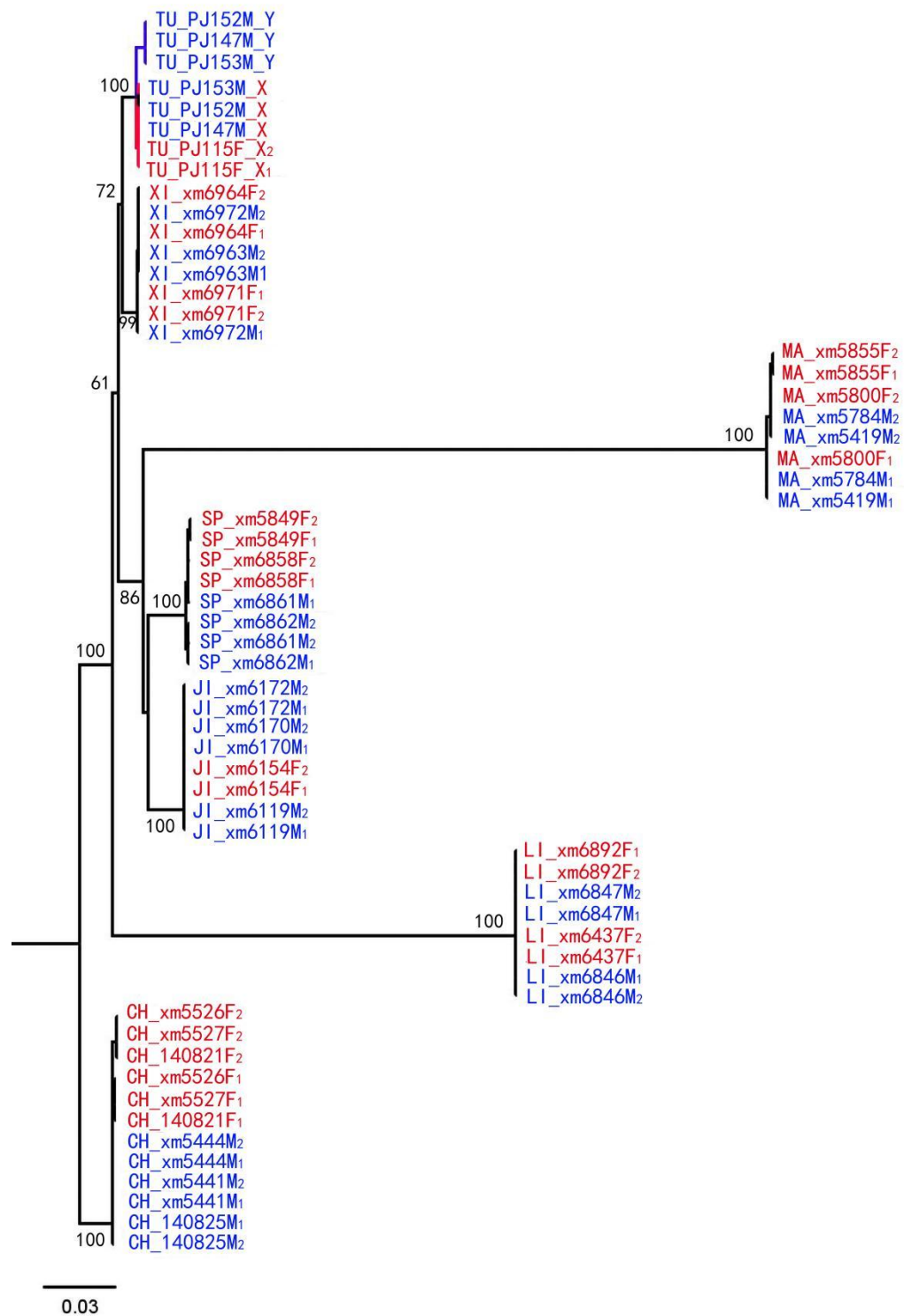
A. mantzorum



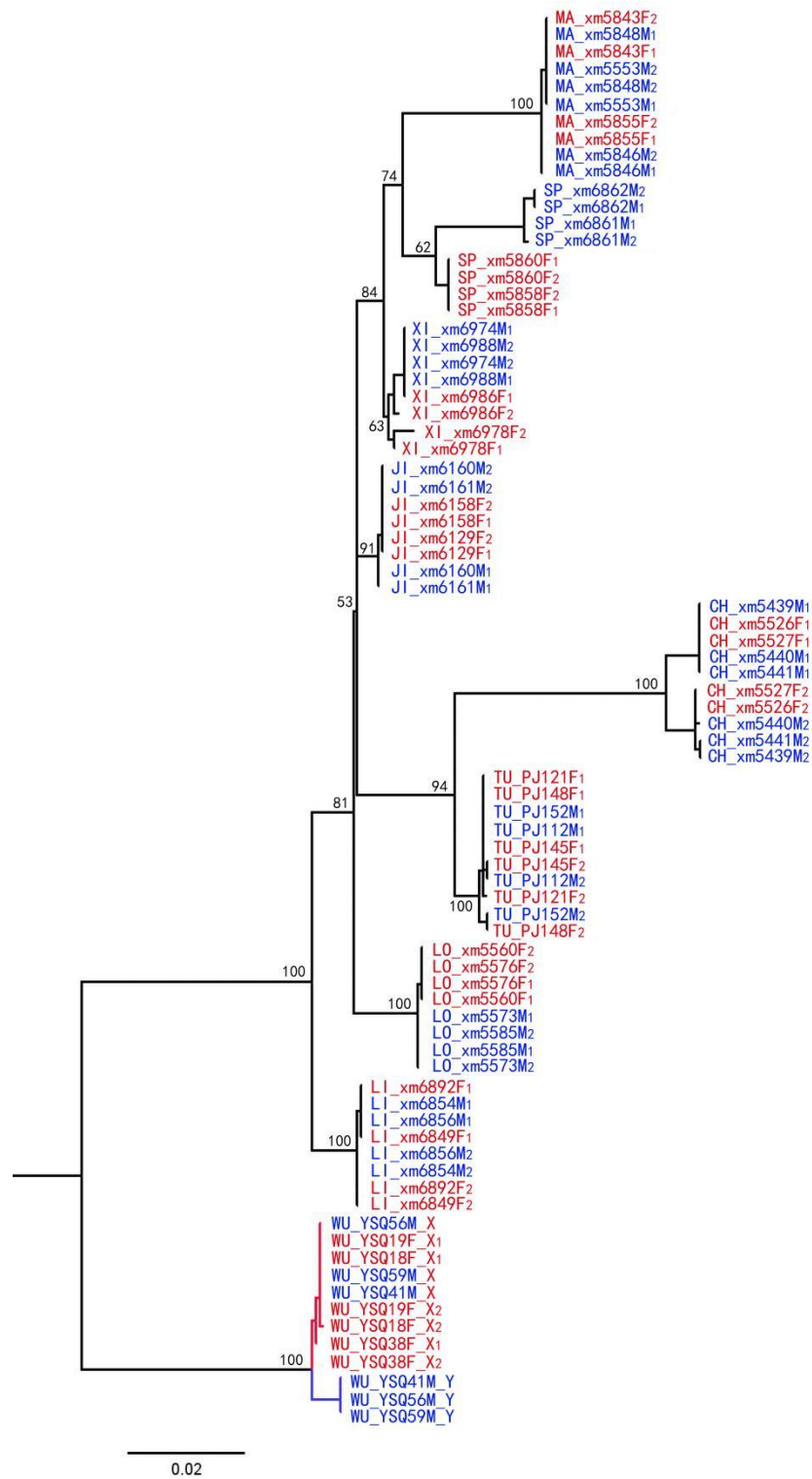
A. sp.



A. tuberodepressus



A. wuyiensis



Phylogenetic tree of the 16S rDNA sequences of the bacterial strains. The tree is rooted on the left and branches to the right. Bootstrap values are indicated at the nodes. The sequences are color-coded: red for *L. obumbratus*, blue for *L. gossypii*, and black for *L. plantarum*. The tree shows three main clusters: a large cluster of *L. obumbratus* strains (red) at the top, a cluster of *L. gossypii* strains (blue) in the middle, and a cluster of *L. plantarum* strains (black) at the bottom. The *L. obumbratus* cluster is further divided into several sub-clusters, including those with 'X' and 'Y' suffixes, and those with 'F1', 'F2', 'M1', and 'M2' suffixes. The *L. gossypii* cluster is also divided into sub-clusters with 'F1', 'F2', 'M1', and 'M2' suffixes. The *L. plantarum* cluster is divided into sub-clusters with 'F1', 'F2', 'M1', and 'M2' suffixes. A scale bar at the bottom left indicates a distance of 0.008.

0.008