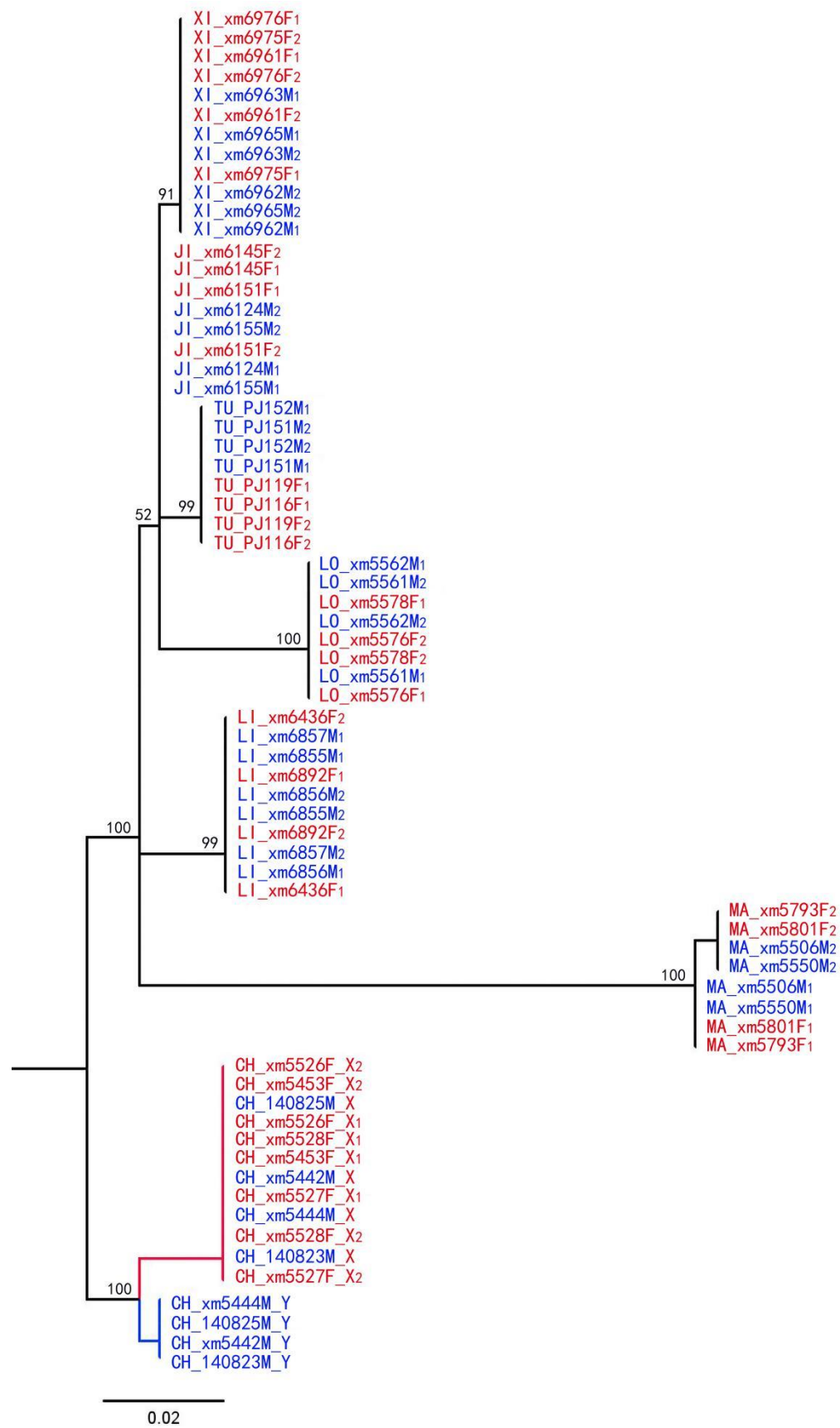


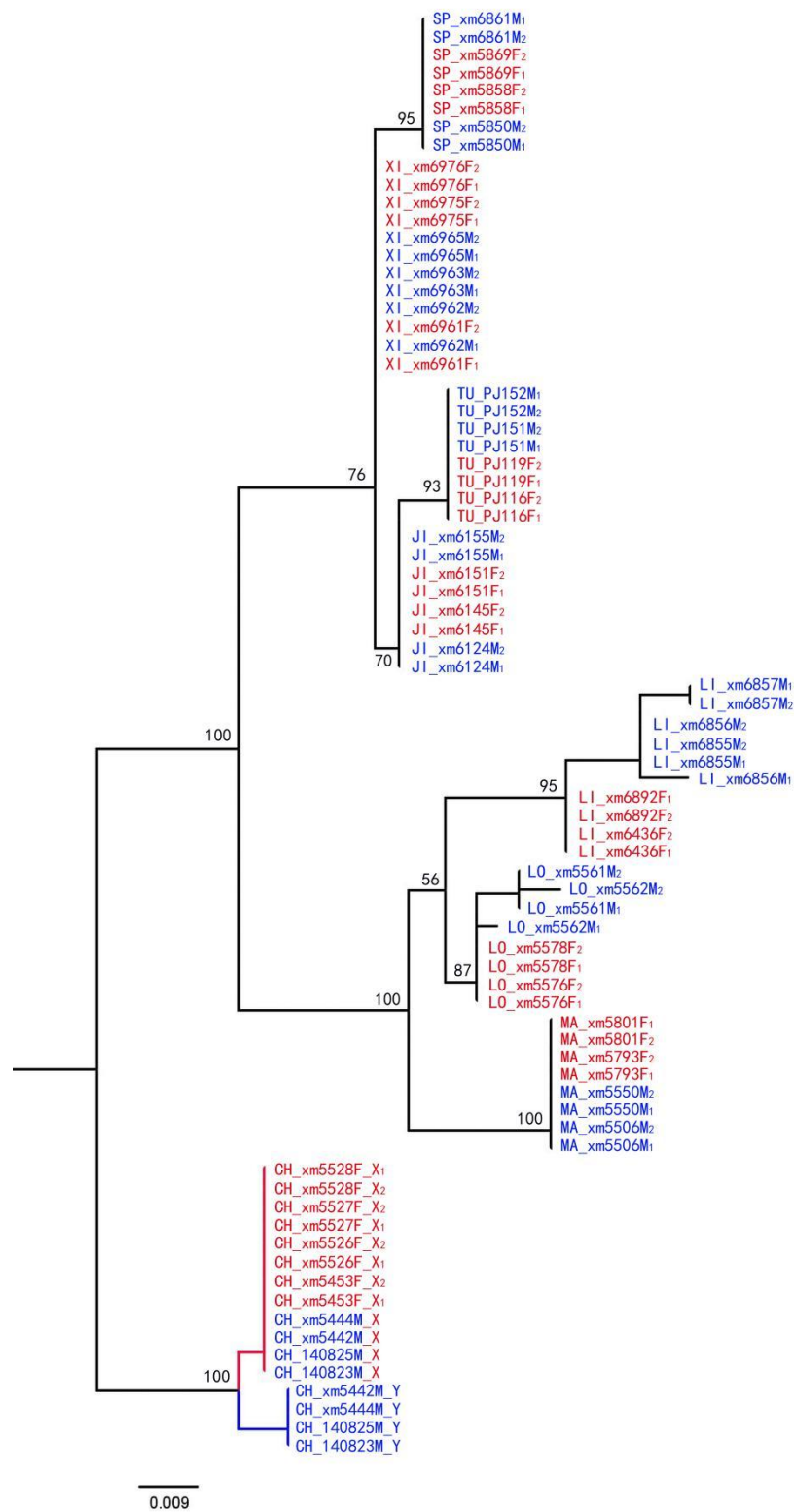
File S7

Maximum-likelihood phylogenies of single sex-linked marker and its cross-species homologous sequence in *Amolops* (CH for *A. chunganensis*, 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.

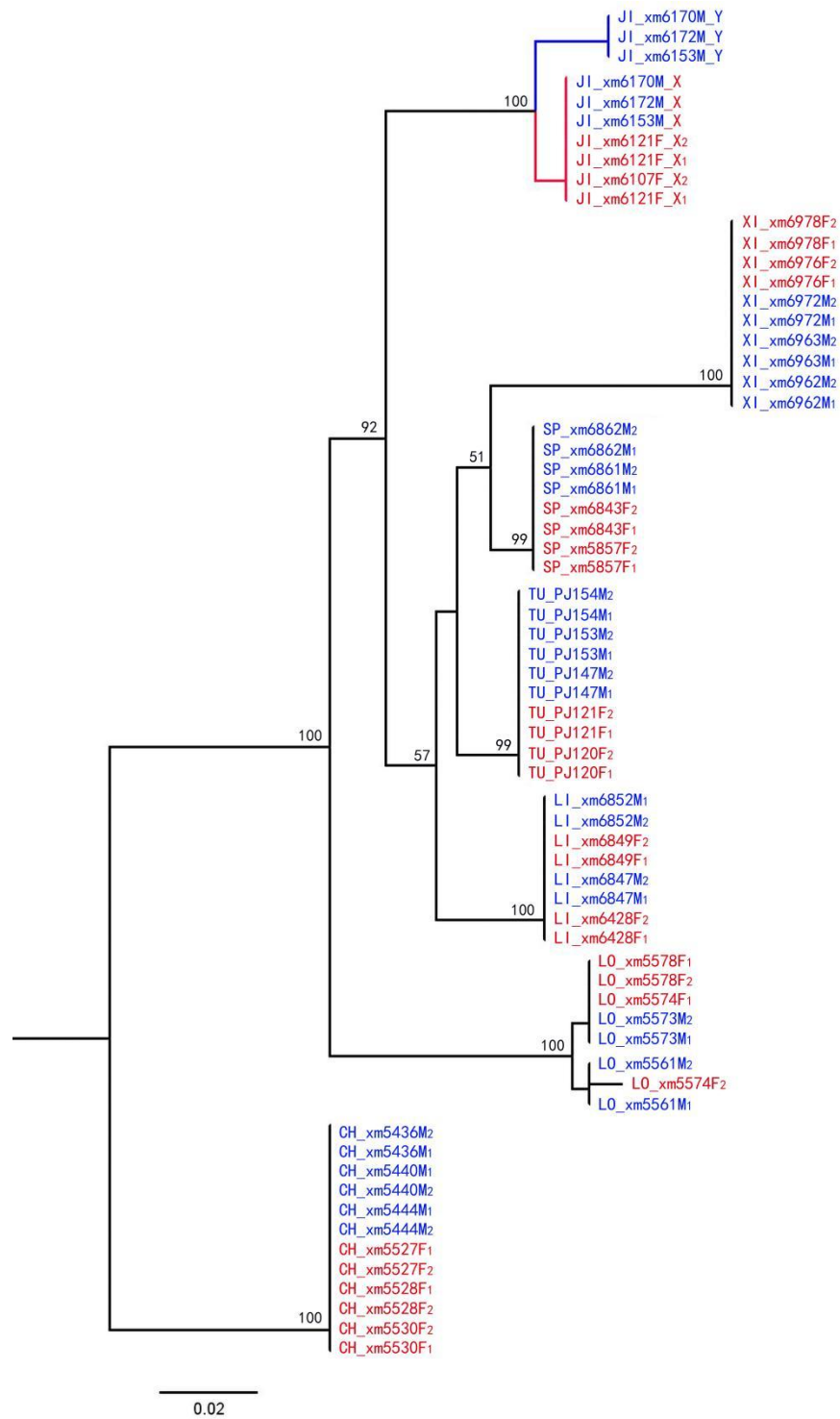
A. Chunganensis: Clocus_697780



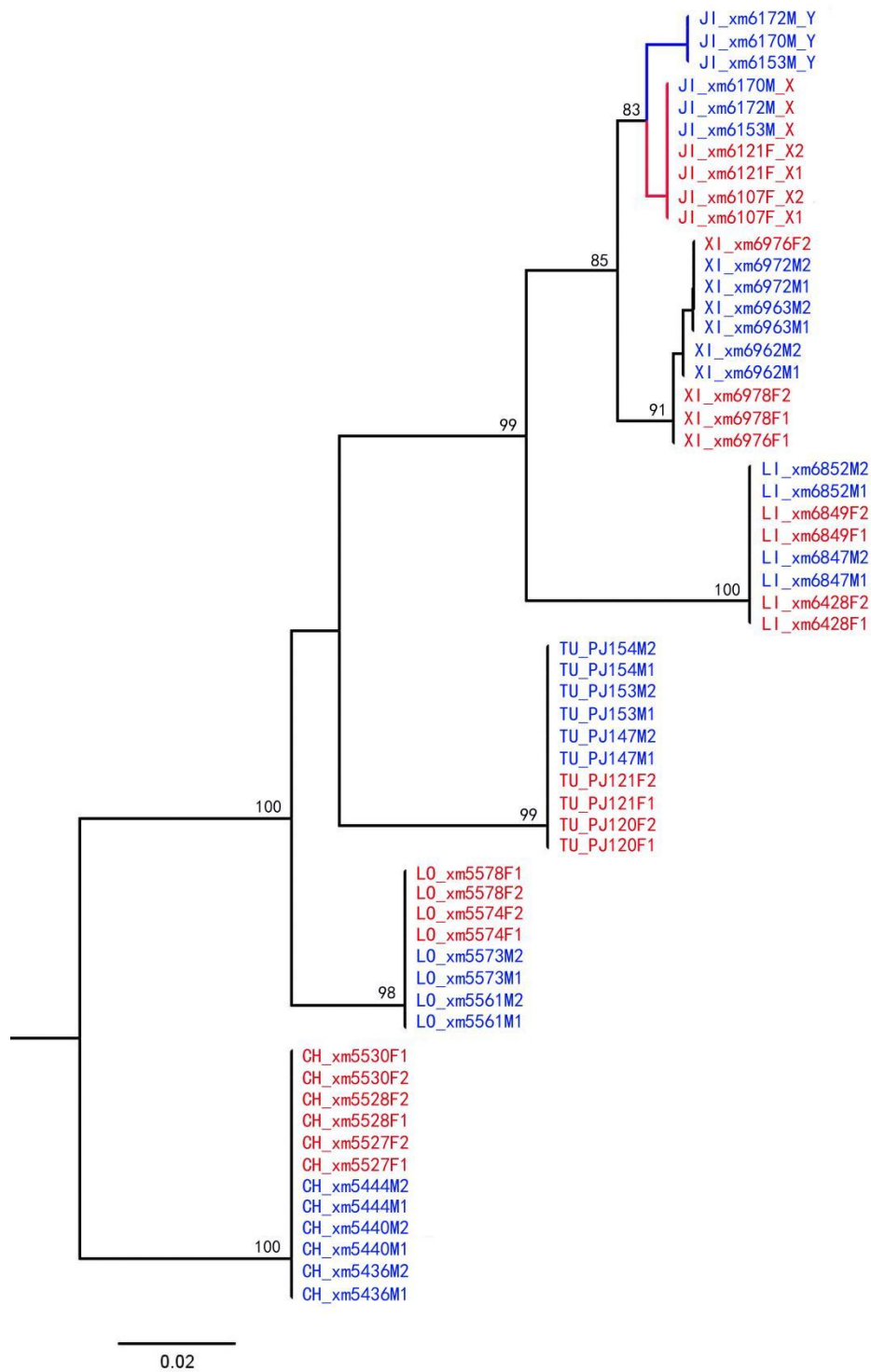
A. Chunganensis: Clocus_2189594



A. jinjiangensis: Clocus_94572



A. jinjiangensis: Clocus_263214



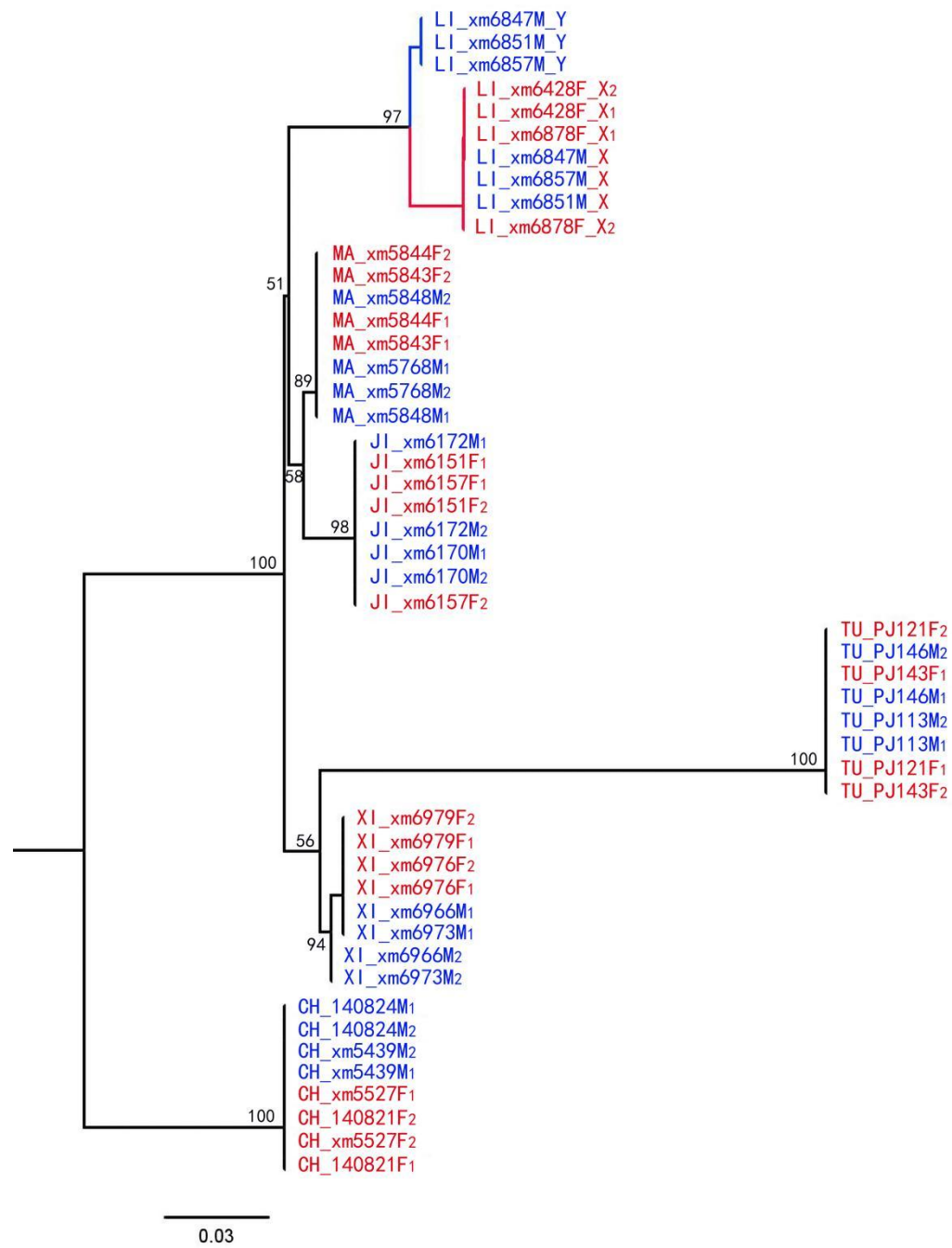
Phylogenetic tree showing relationships between various bacterial strains. The tree is rooted on the left and branches out to the right. Strains are color-coded: red for LI, MA, and JI; blue for TU, XI, and CH. Bootstrap values are indicated at the nodes. A scale bar of 0.05 is at the bottom.

Strains and their bootstrap values (from left to right):

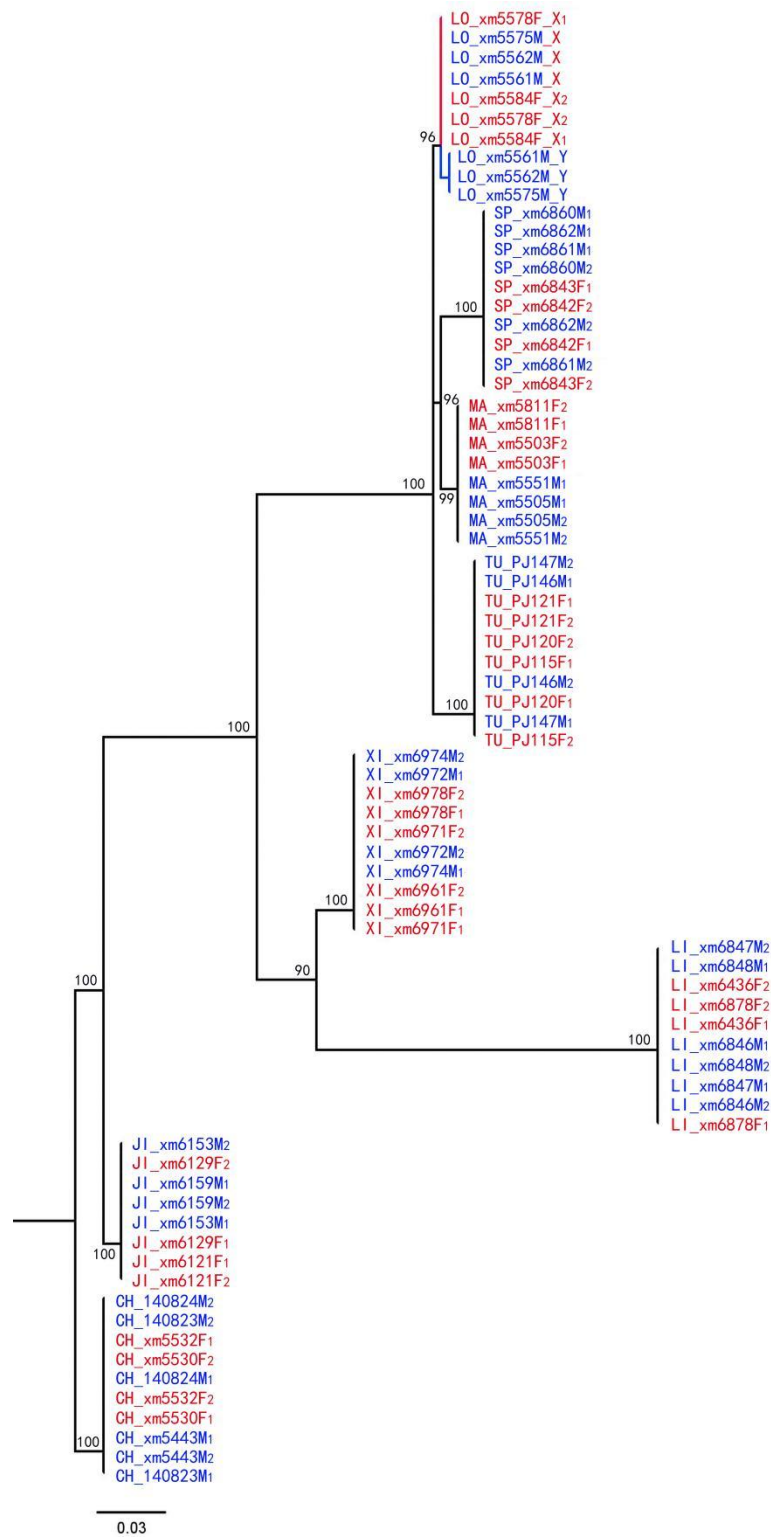
- LI_xm6847M_X (red)
- LI_xm6428F_X2 (red)
- LI_xm6878F_X1 (red)
- LI_xm6878F_X2 (red)
- LI_xm6857M_X (red)
- LI_xm6851M_X (red)
- LI_xm6428F_X1 (red)
- LI_xm6847M_Y (blue)
- LI_xm6851M_Y (blue)
- LI_xm6857M_Y (blue)
- MA_xm5843F2 (red)
- MA_xm5844F1 (red)
- MA_xm5843F1 (red)
- MA_xm5848M1 (blue)
- MA_xm5768M1 (blue)
- MA_xm5844F2 (red)
- MA_xm5848M2 (blue)
- MA_xm5768M2 (blue)
- XI_xm6973M1 (blue)
- XI_xm6966M2 (blue)
- XI_xm6966M1 (blue)
- XI_xm6979F1 (red)
- XI_xm6973M2 (blue)
- XI_xm6976F2 (red)
- XI_xm6976F1 (red)
- XI_xm6979F2 (red)
- JI_xm6157F1 (red)
- JI_xm6172M2 (blue)
- JI_xm6172M1 (blue)
- JI_xm6170M2 (blue)
- JI_xm6157F2 (red)
- JI_xm6151F2 (red)
- JI_xm6151F1 (red)
- JI_xm6170M1 (blue)
- CH_xm5527F2 (red)
- CH_140821F2 (red)
- CH_xm5527F1 (red)
- CH_140821F1 (red)
- CH_xm5439M2 (blue)
- CH_140824M1 (blue)
- CH_xm5439M1 (blue)
- CH_140824M2 (blue)

Scale bar: 0.05

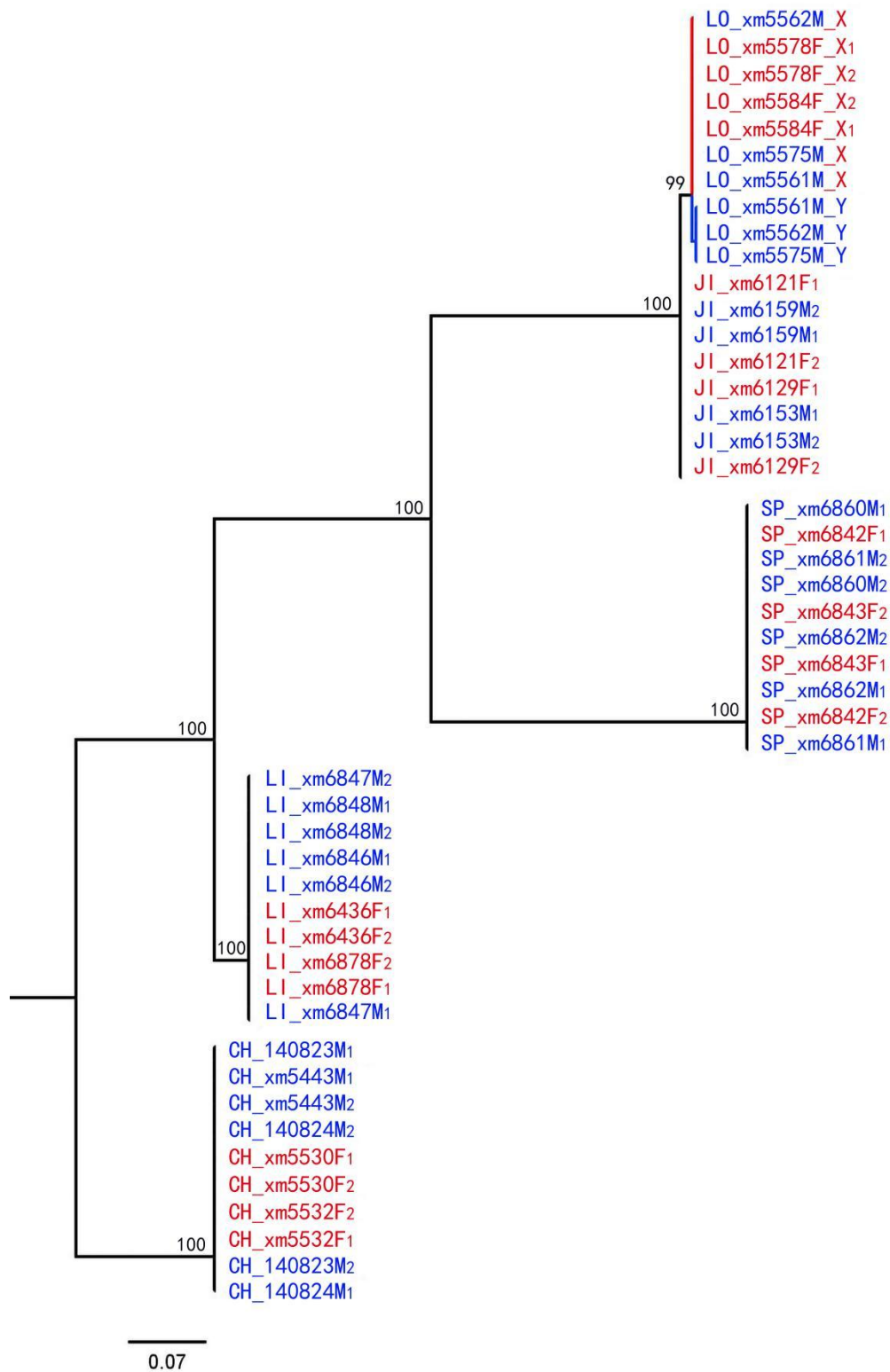
A. lifanensis: Clocus_520205



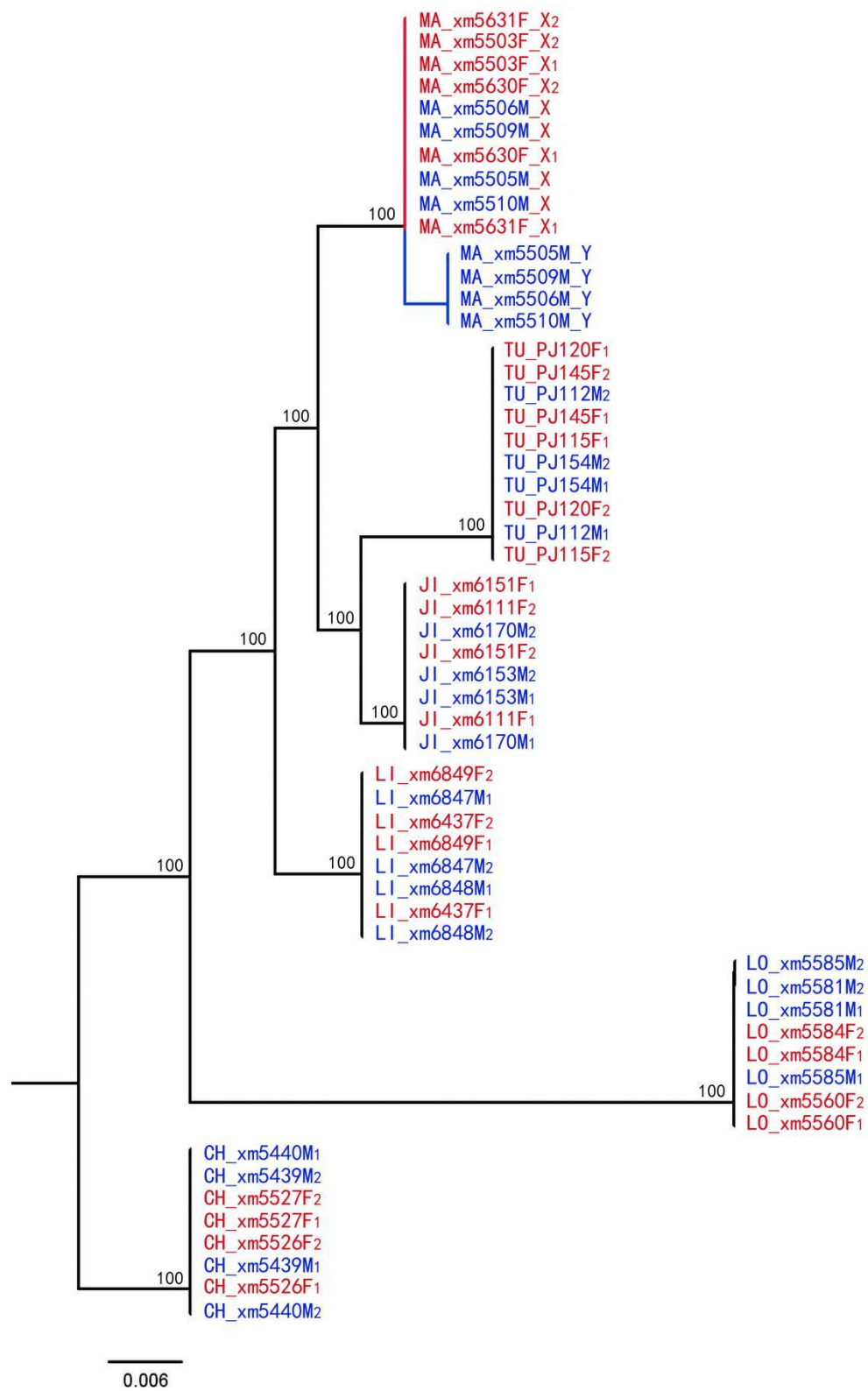
A. loloensis: Clocus_108264



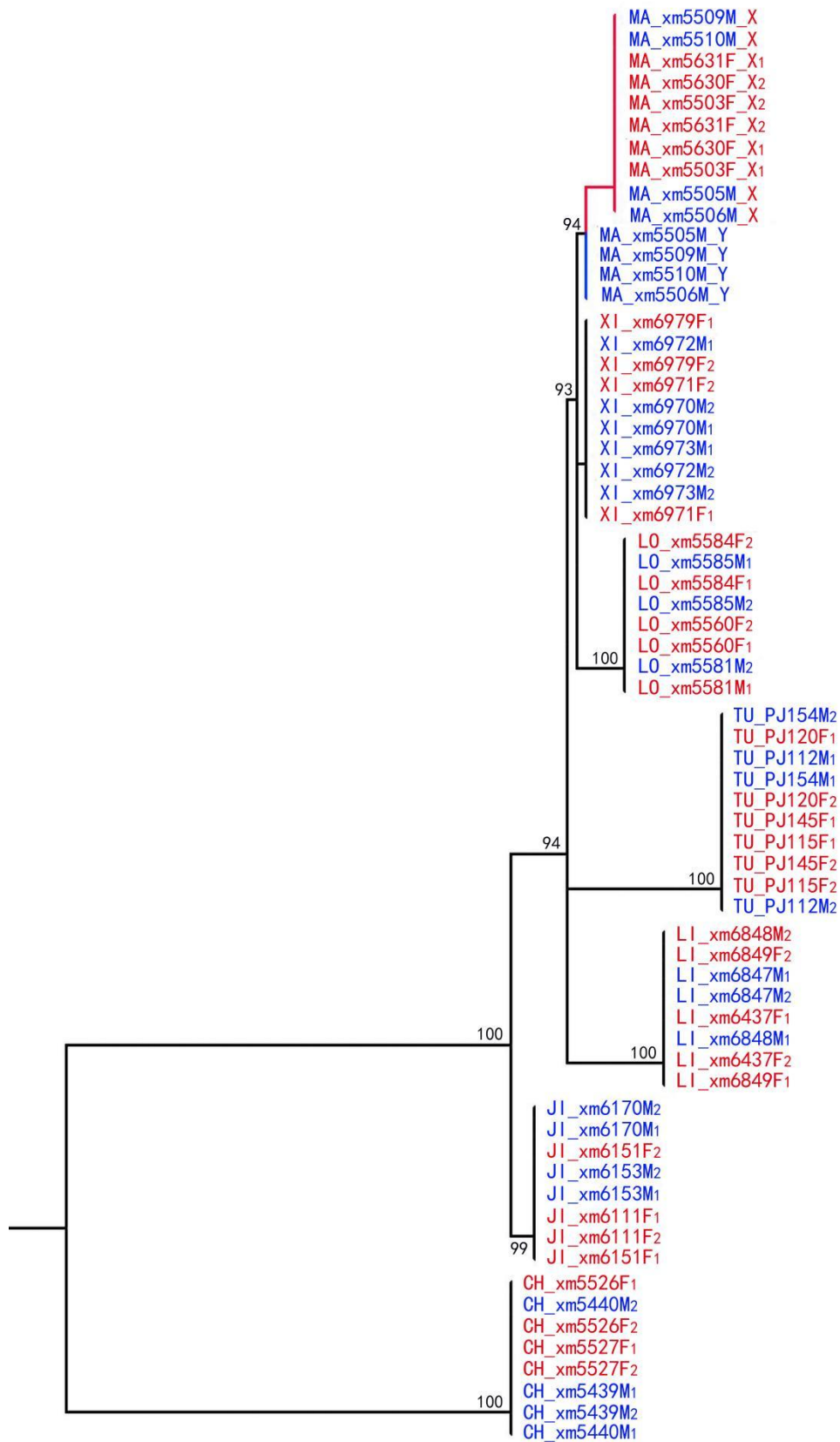
A. loloensis: Clocus_771638



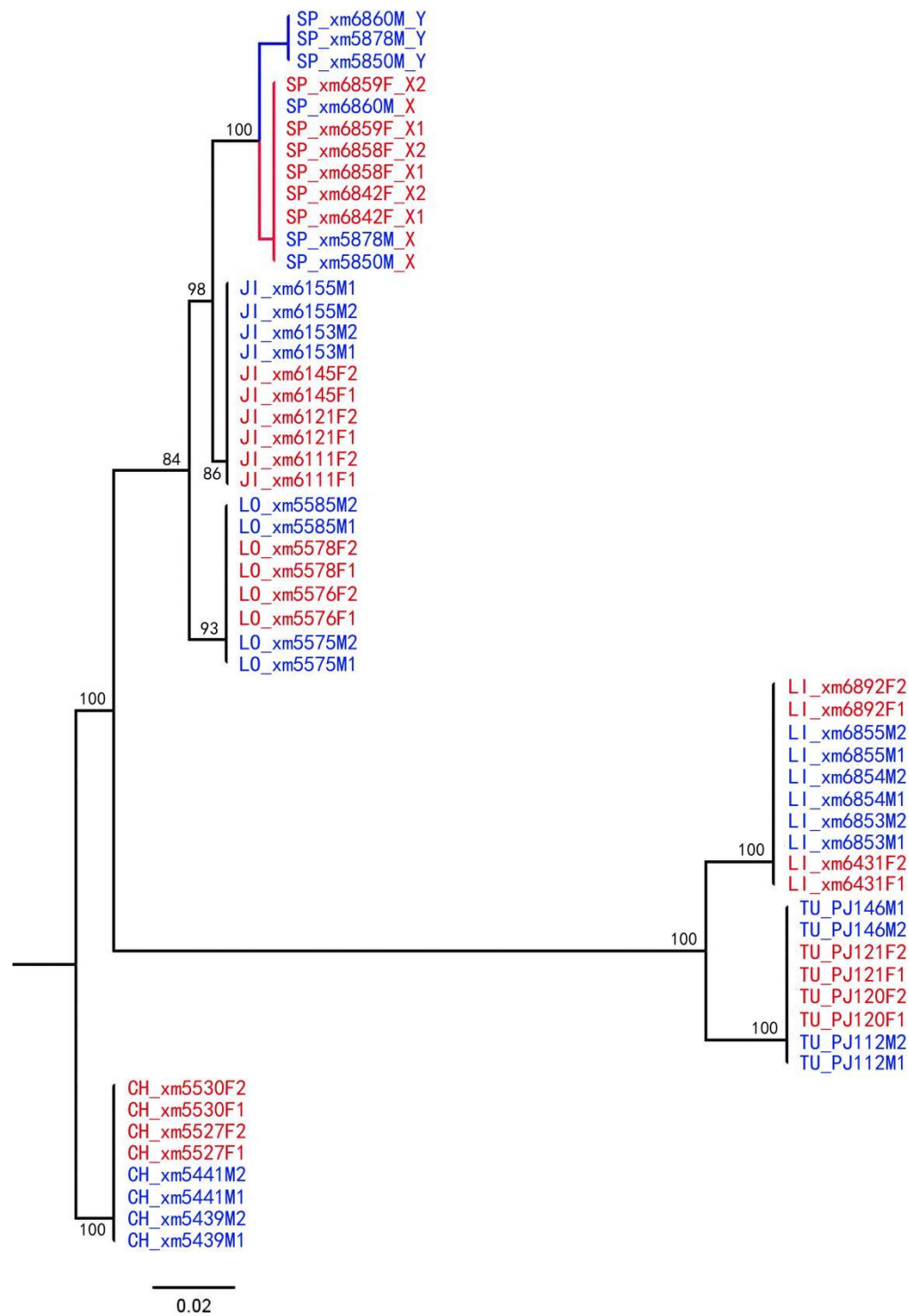
A. mantzorum: Clocus_240963



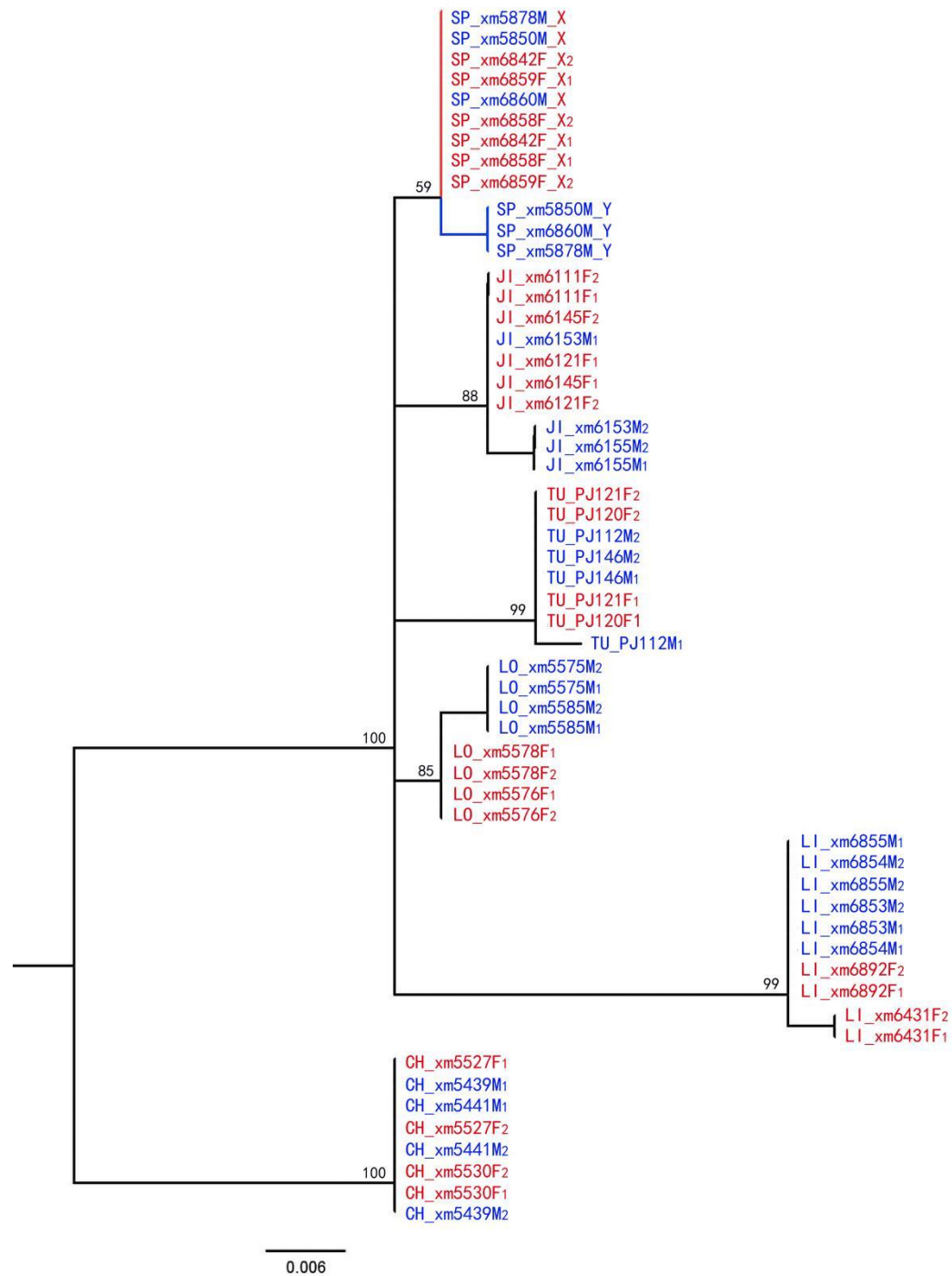
A. mantzorum: Clocus_650096



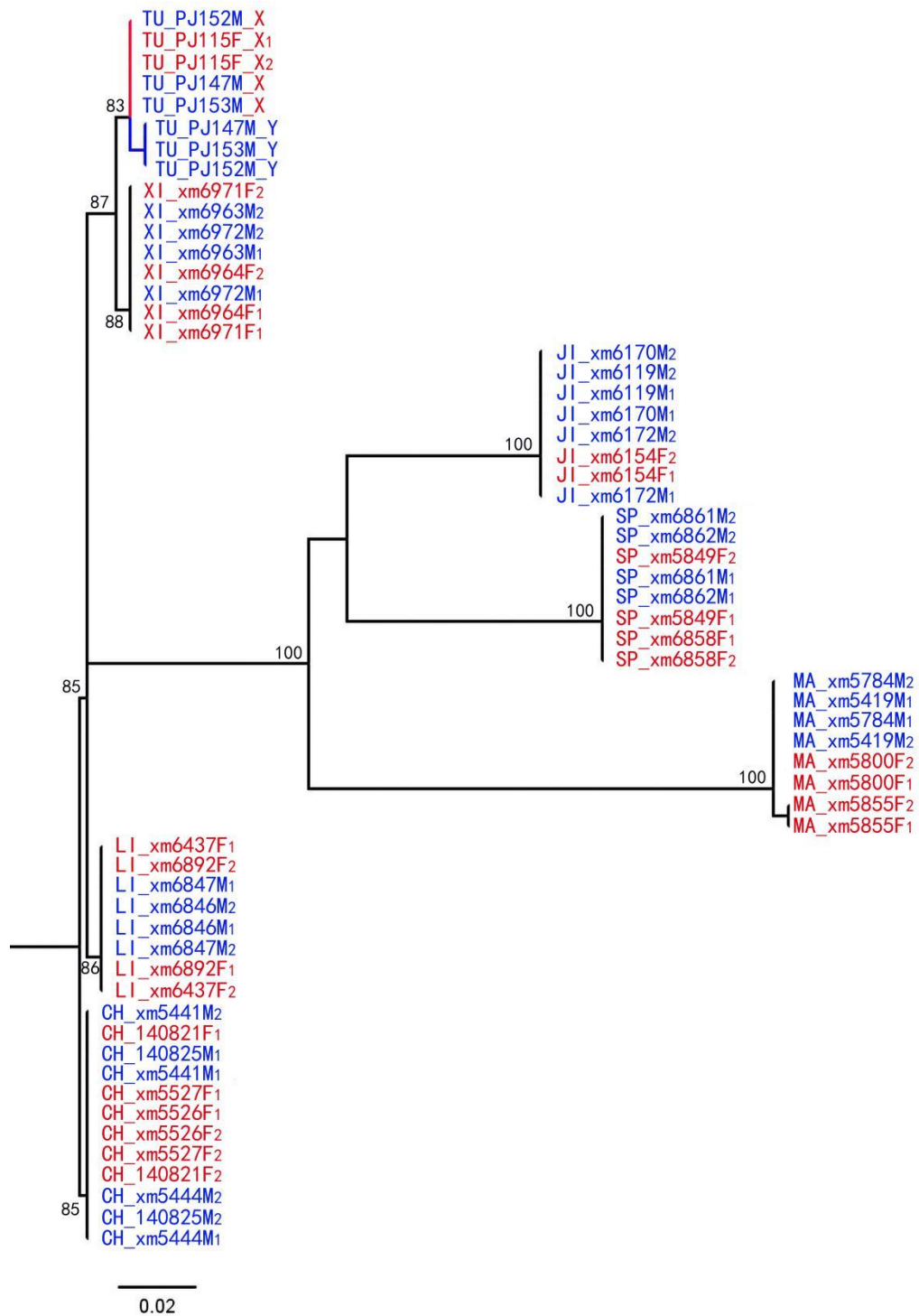
A. sp.: Clocus_46910



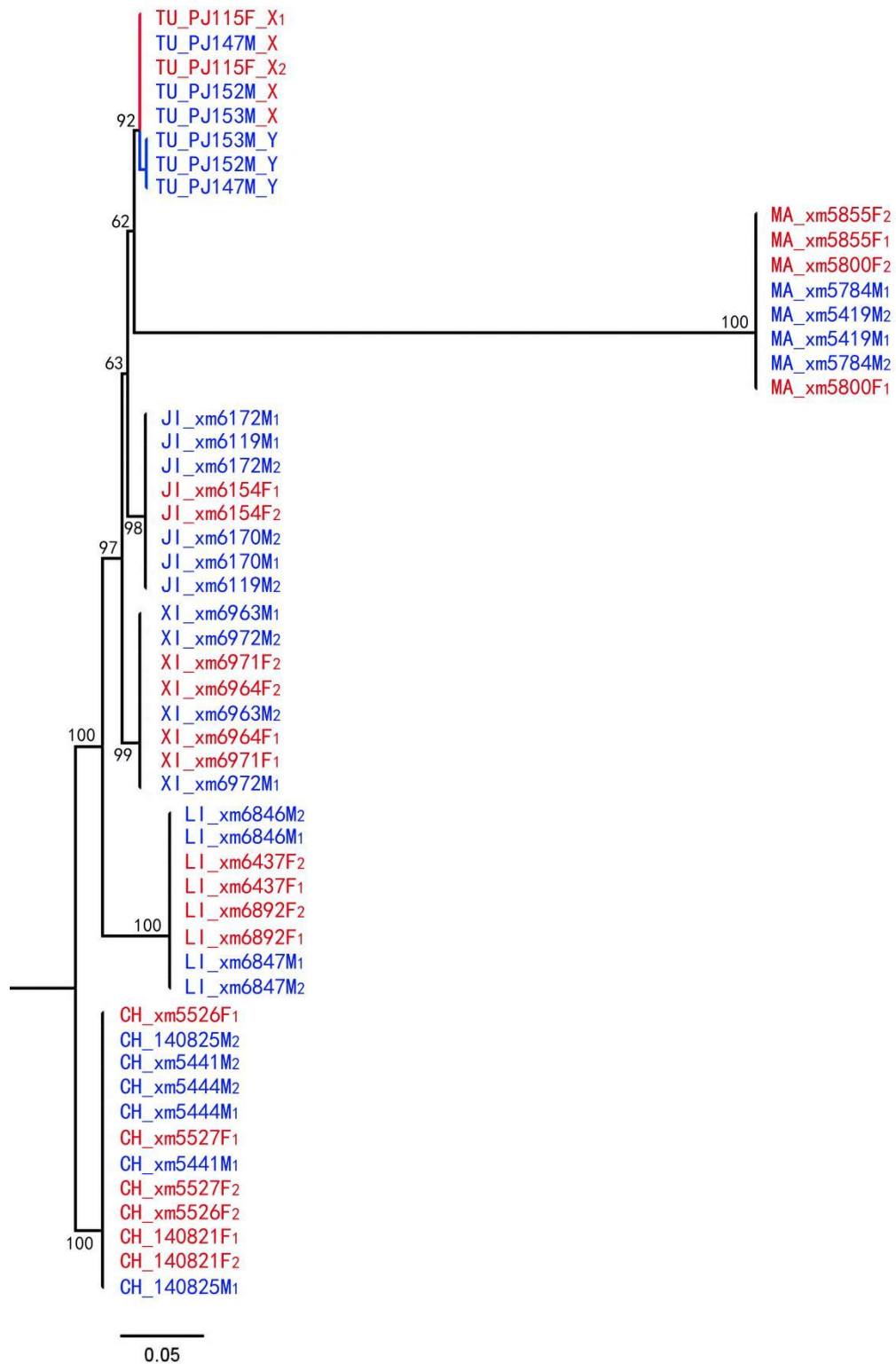
A. sp.: Clocus_271488



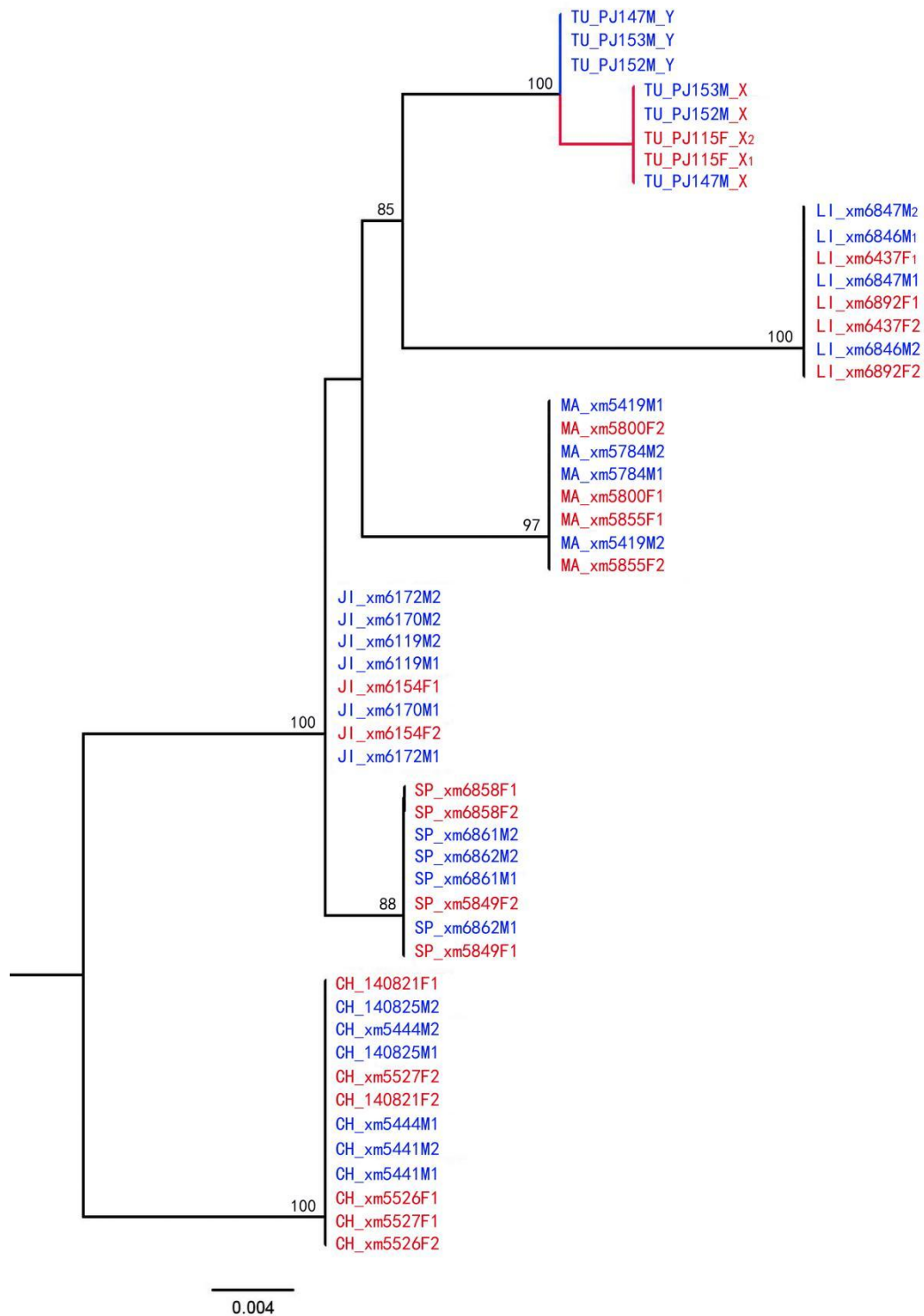
A. tuberodepressus: Clocus_312165



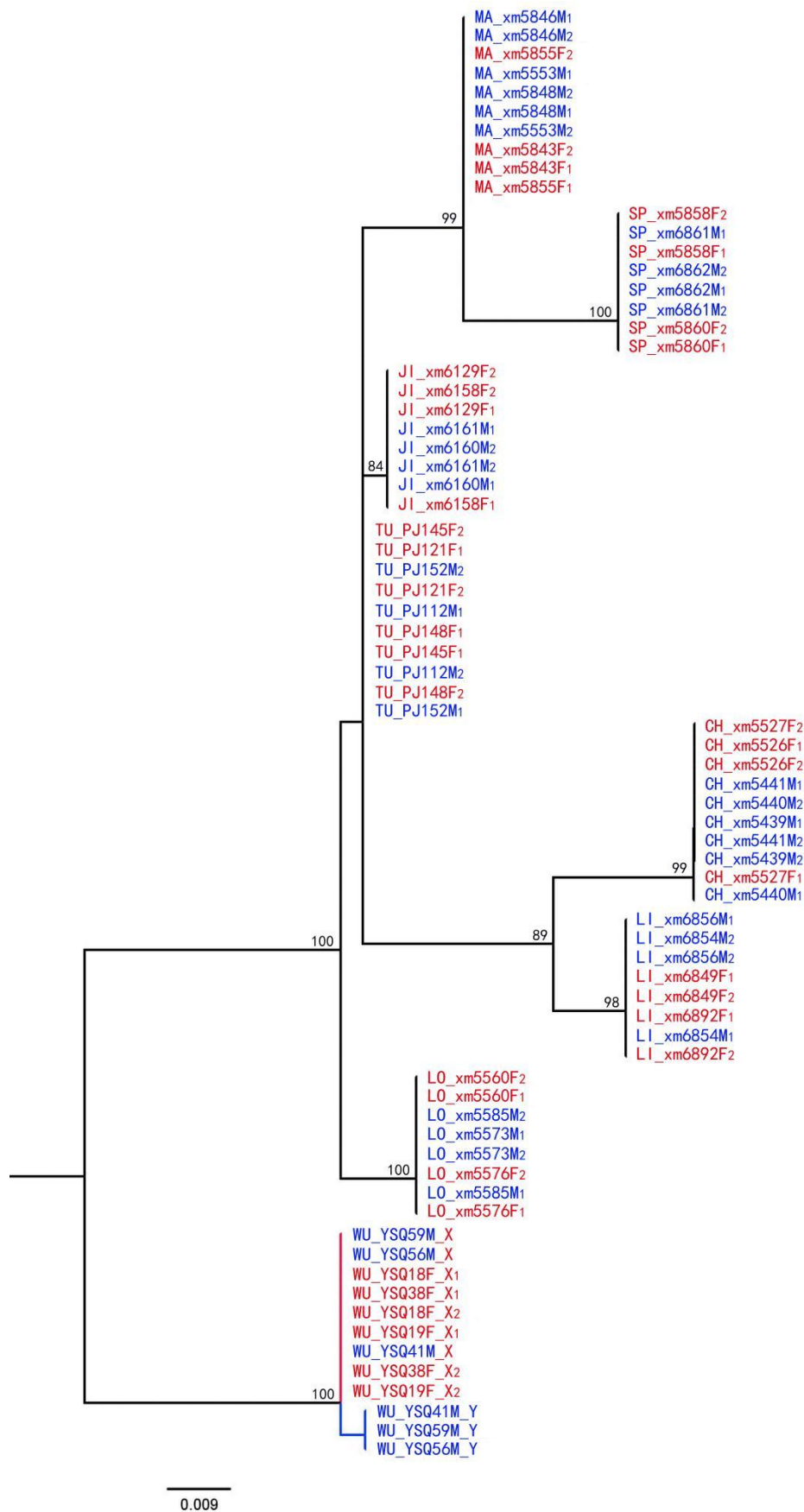
A. tuberodepressus: Clocus_657724



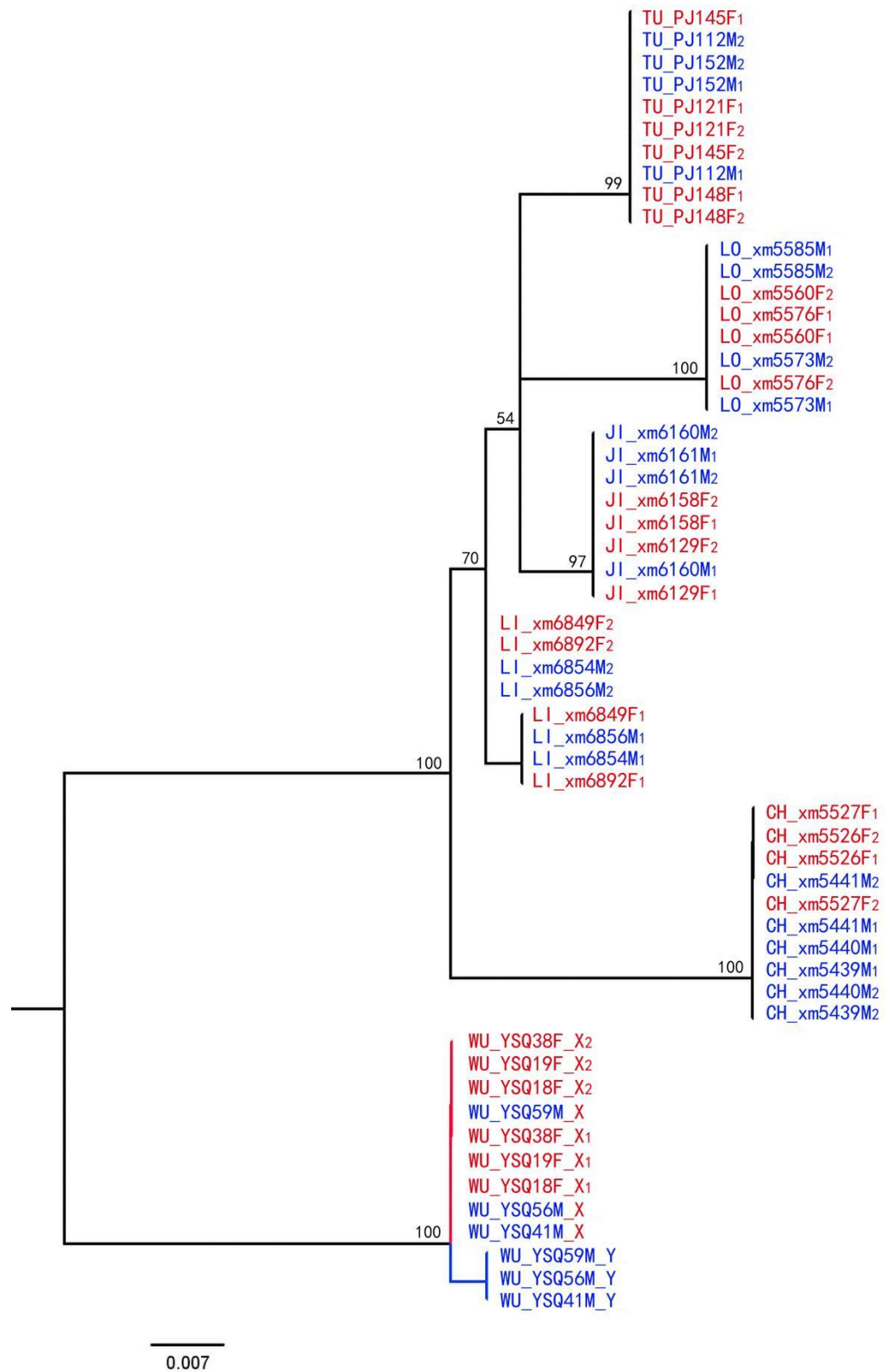
A. tuberodepressus: Clocus_934386



A. wuyiensis: Clocus_201111



A. wuyiensis: Clocus_312243



Phylogenetic tree showing relationships between various bacterial strains. The tree is rooted on the left and branches to the right. Bootstrap values of 100 are indicated at several nodes. Strains are color-coded: red for some, blue for others, and black for a few. The strains are grouped into several clusters, including those starting with XI_, LO_, JI_, TU_, LI_, and CH_. The tree shows high bootstrap support for the major branches.

Strains listed (from top to bottom):

- XI_xm6965M_X
- XI_xm6967F_X1
- XI_xm6961F_X1
- XI_xm6961F_X2
- XI_xm6970M_X
- XI_xm6967F_X2
- XI_xm6974M_X
- XI_xm6962M_X
- XI_xm6972M_X
- XI_xm6965M_Y
- XI_xm6970M_Y
- XI_xm6962M_Y
- XI_xm6974M_Y
- XI_xm6972M_Y
- LO_xm5580F1
- LO_xm5580F2
- LO_xm5574F1
- LO_xm5574F2
- LO_xm5575M1
- LO_xm5575M2
- LO_xm5592M2
- LO_xm5592M1
- JI_xm6161M2
- JI_xm6145F1
- JI_xm6161M1
- JI_xm6124M1
- JI_xm6111F2
- JI_xm6145F2
- JI_xm6160M2
- JI_xm6111F1
- JI_xm6160M1
- JI_xm6124M2
- TU_PJ153M2
- TU_PJ113M2
- TU_PJ144F2
- TU_PJ153M1
- TU_PJ144F1
- TU_PJ113M1
- TU_PJ115F1
- TU_PJ115F2
- LI_xm6849F2
- LI_xm6864M2
- LI_xm6853M1
- LI_xm6856M2
- LI_xm6878F2
- LI_xm6853M2
- LI_xm6878F1
- LI_xm6856M1
- LI_xm6849F1
- LI_xm6864M1
- CH_xm5442M1
- CH_140821F2
- CH_140821F1
- CH_140824M1
- CH_xm5449F1
- CH_xm5449F2
- CH_140824M2
- CH_xm5442M2

Phylogenetic tree showing relationships between various sequences. The tree is rooted on the left and branches to the right. Bootstrap values of 100 are indicated at several nodes. Sequences are color-coded: red for X, blue for Y, and black for M and F.

Sequences listed (from top to bottom):

- XI_xm6967F_X1
- XI_xm6961F_X2
- XI_xm6961F_X1
- XI_xm6965M_X
- XI_xm6962M_X
- XI_xm6967F_X2
- XI_xm6972M_X
- XI_xm6974M_X
- XI_xm6970M_X
- XI_xm6970M_Y
- XI_xm6974M_Y
- XI_xm6972M_Y
- XI_xm6965M_Y
- XI_xm6962M_Y
- JL_xm6145F1
- JL_xm6111F2
- JL_xm6161M1
- JL_xm6145F2
- JL_xm6124M2
- JL_xm6111F1
- JL_xm6160M2
- JL_xm6160M1
- JL_xm6161M2
- JL_xm6124M1
- LO_xm5592M1
- LO_xm5574F2
- LO_xm5592M2
- LO_xm5574F1
- LO_xm5575M1
- LO_xm5575M2
- LO_xm5580F1
- LO_xm5580F2
- TU_PJ144F2
- TU_PJ153M2
- TU_PJ144F1
- TU_PJ113M2
- TU_PJ115F1
- TU_PJ153M1
- TU_PJ113M1
- TU_PJ115F2
- LI_xm6853M2
- LI_xm6864M2
- LI_xm6878F2
- LI_xm6878F1
- LI_xm6849F1
- LI_xm6853M1
- LI_xm6864M1
- LI_xm6856M2
- LI_xm6856M1
- LI_xm6849F2
- CH_140824M1
- CH_140824M2
- CH_xm5442M1
- CH_xm5449F2
- CH_xm5442M2
- CH_xm5449F1
- CH_140821F2
- CH_140821F1

0.005