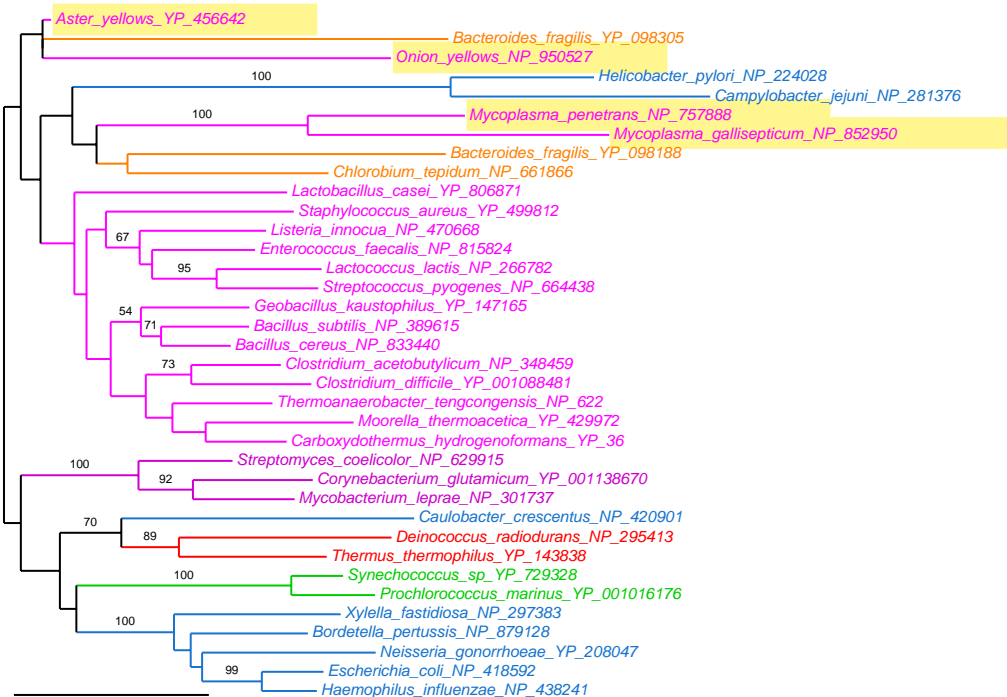
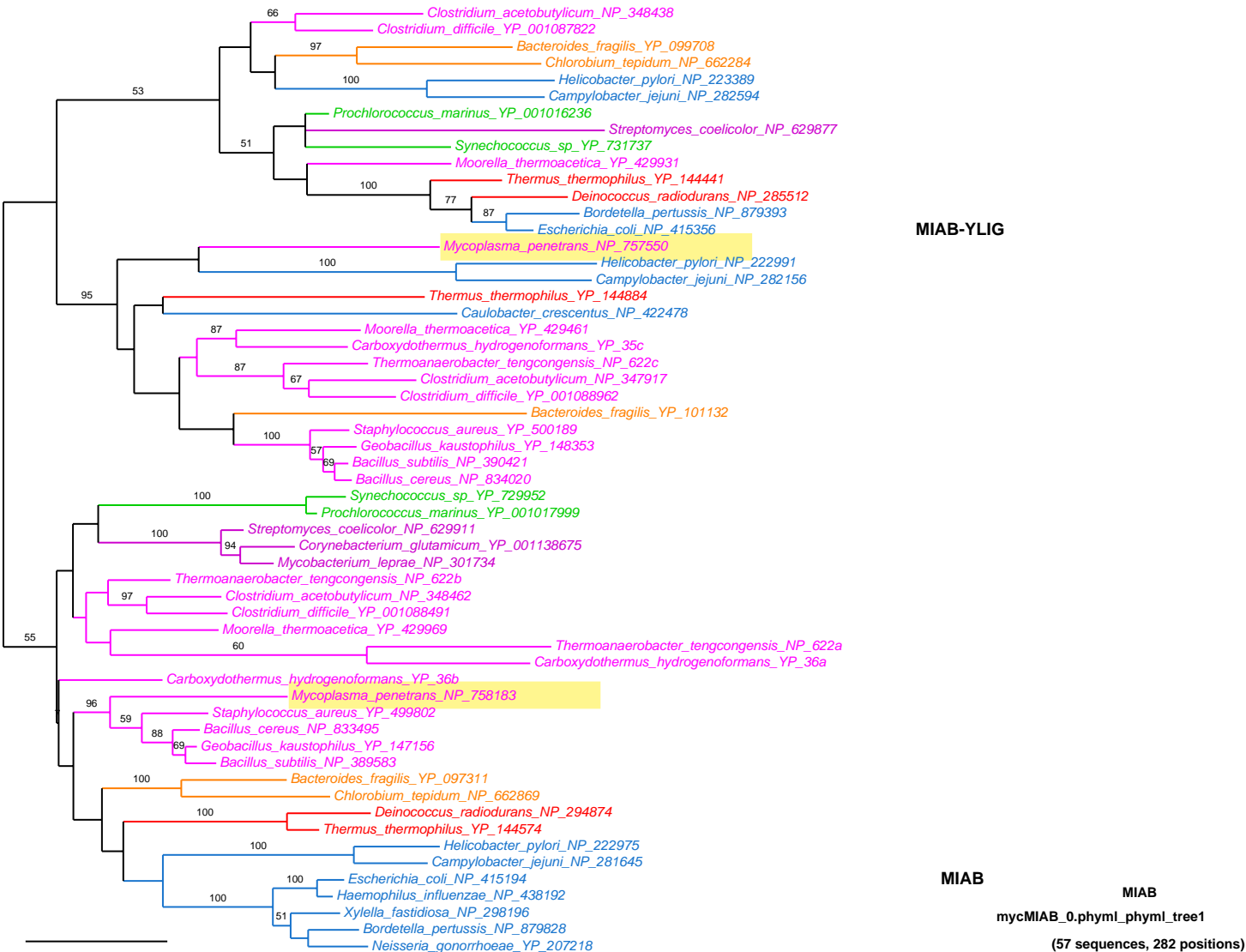


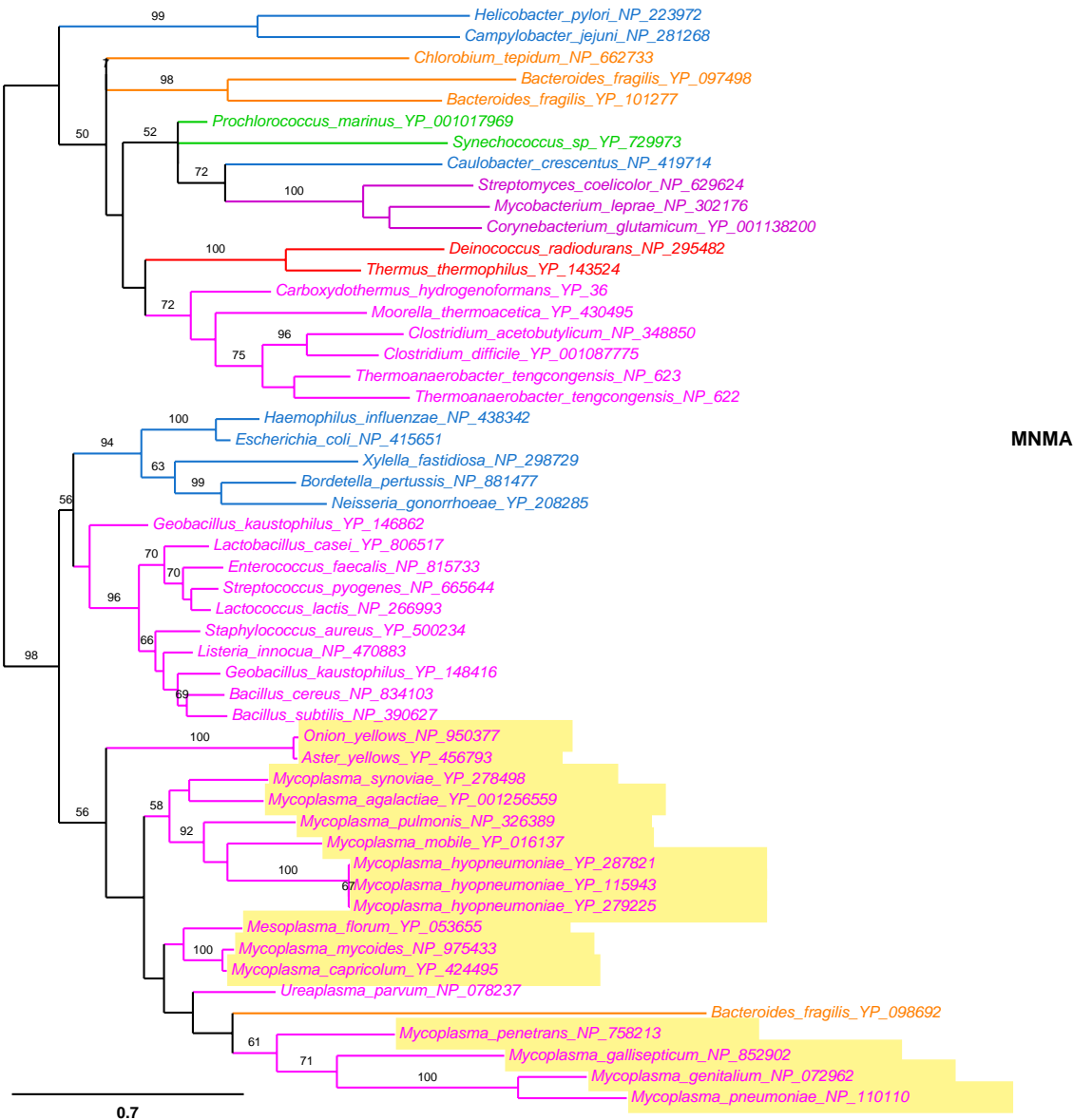
DUSA/DUSB/DUSC
 (50 sequences, 165 positions)
 mycDUSB_0.phyml_phyml_tree1



MIAA

MIAA
 mycMIAA_0.phyml_phyml_tree1
 (36 sequences, 219 positions)





MNMA
 mycMNMA_0.phyml_phyml_tree1
 (52 sequences, 254 positions)



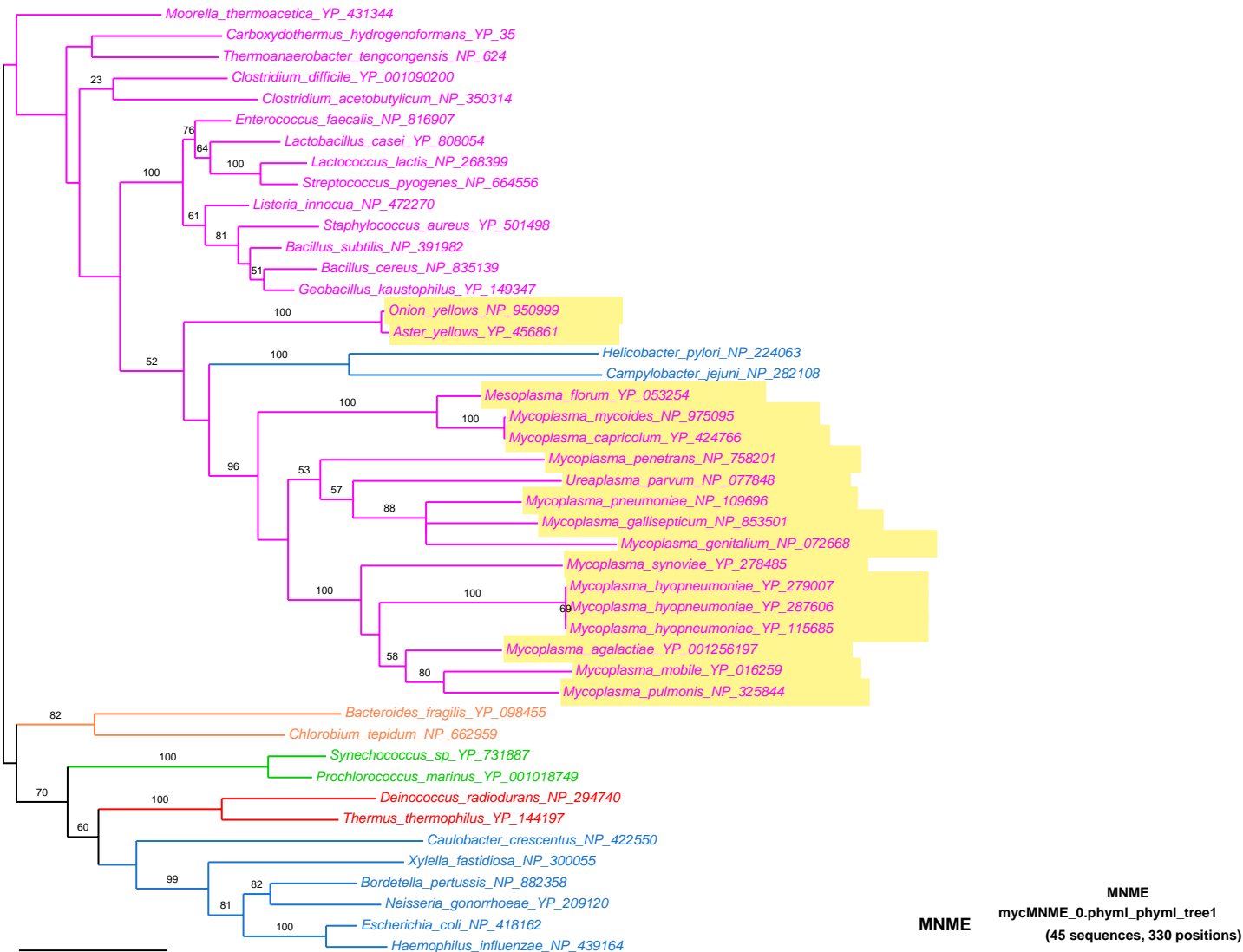
MNMB-GIDA

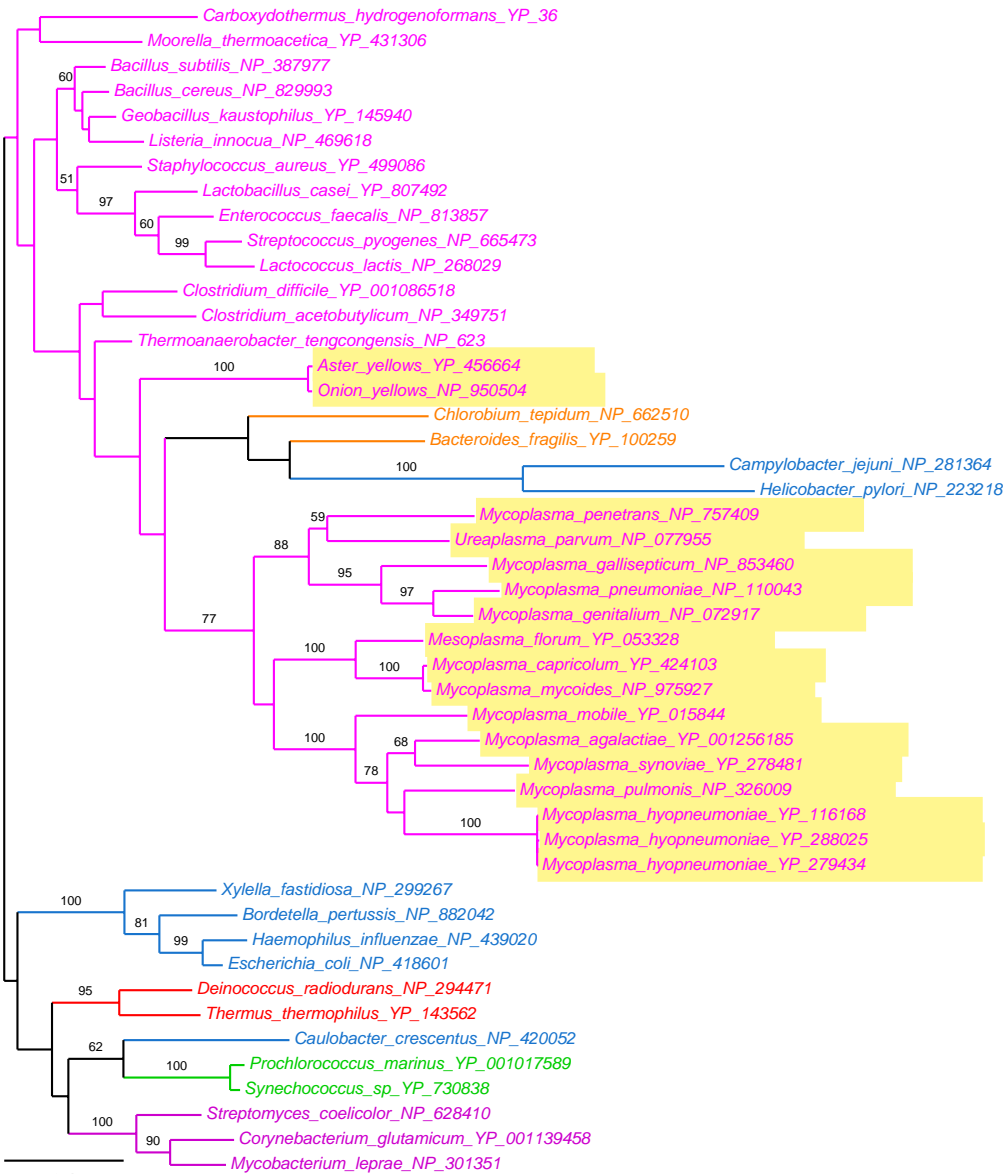
MNMB/GIDA

mycMNMB_0.phyml_phyml_tree1

(47 sequences, 551 positions)

0.3





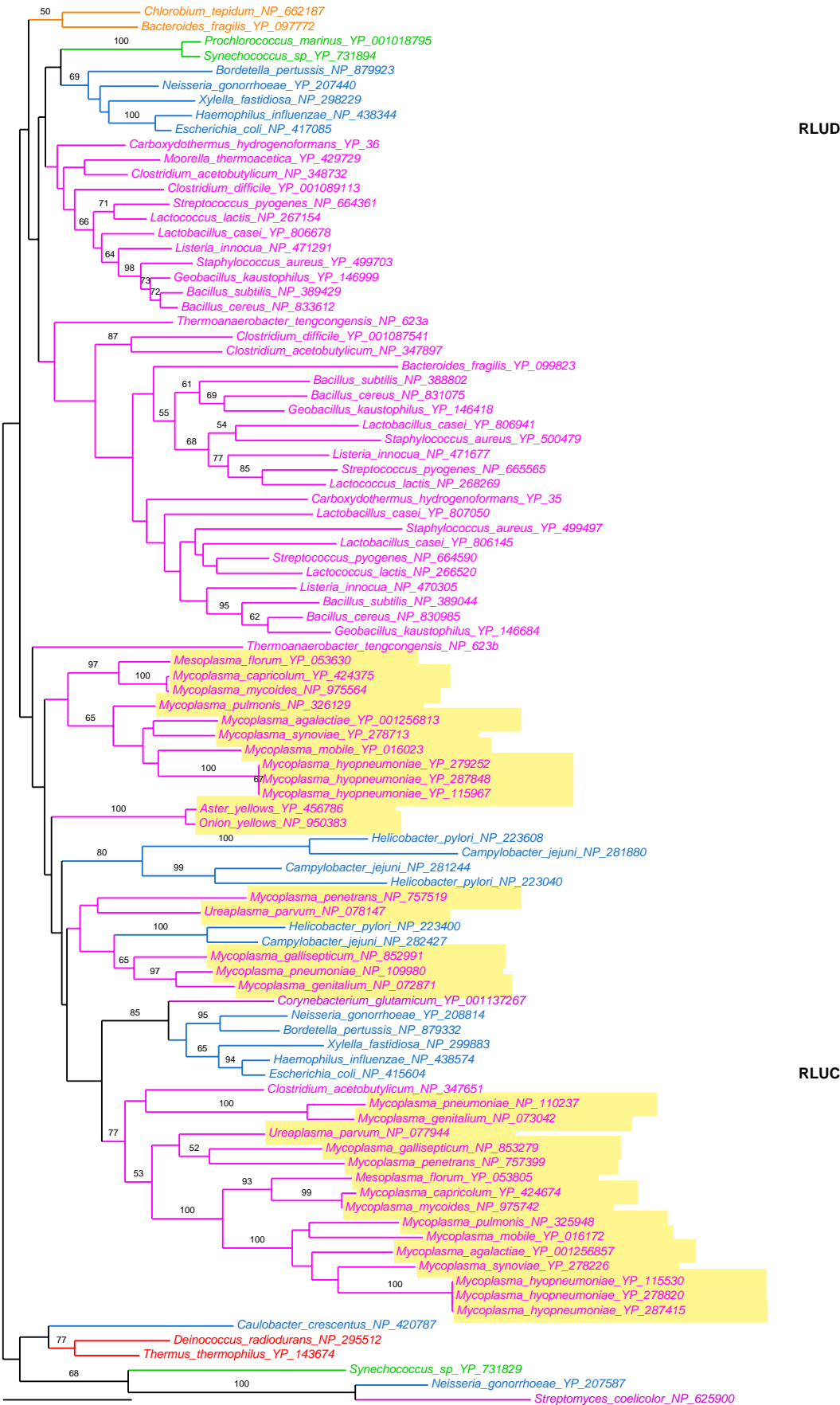
RLMB

RLMB

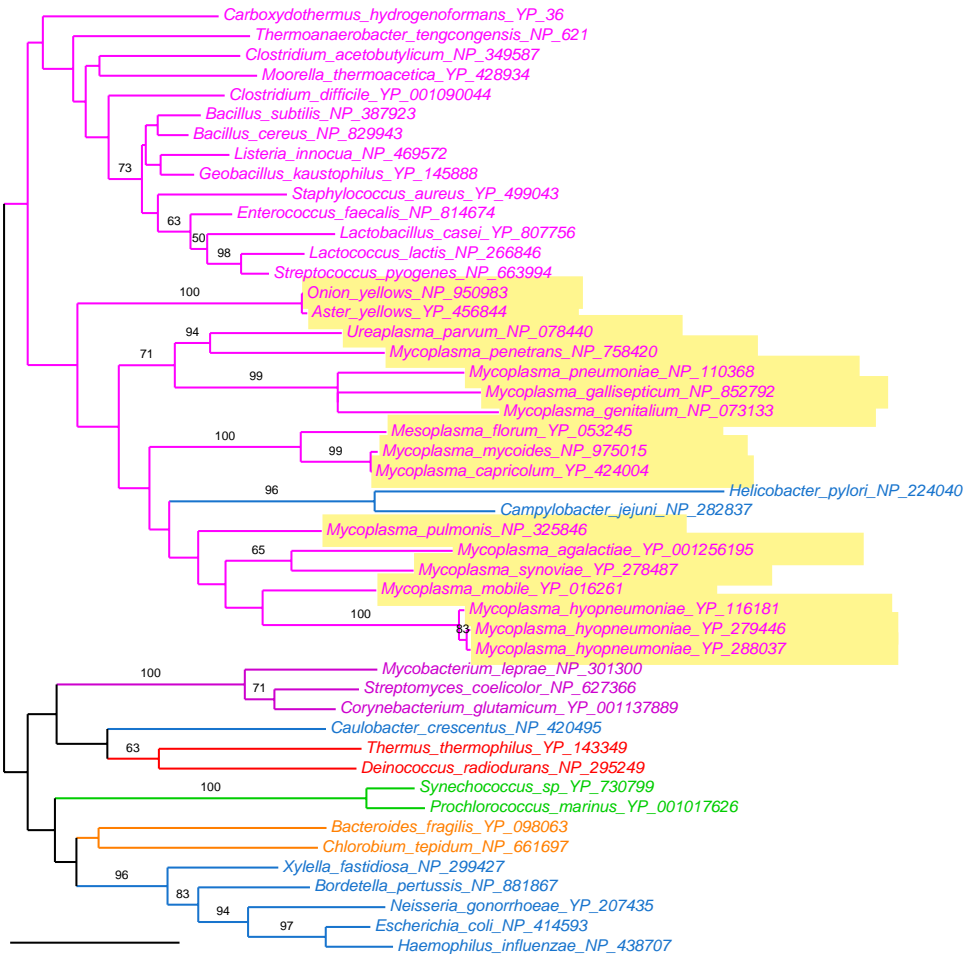
mycRLMB_0.phyml_phyml_tree1

(47 sequences, 147 positions)

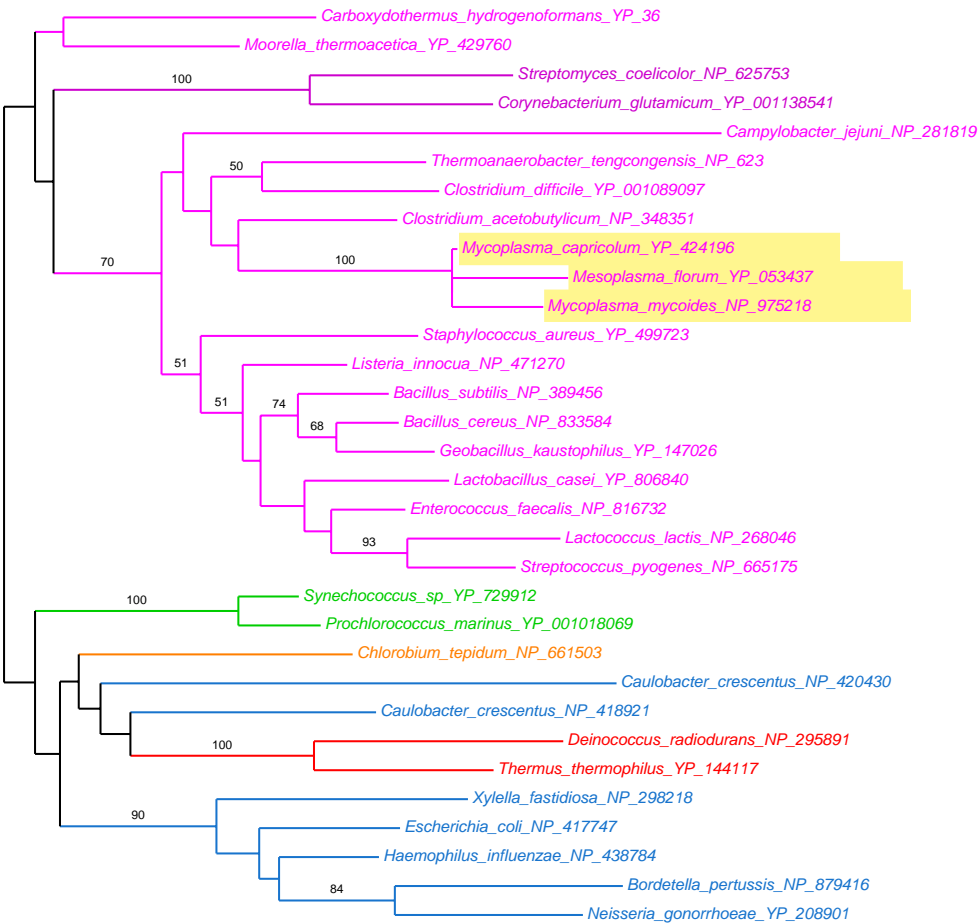
0.4



RLUC/RLUD
 mycRULCD_0.phyml_phyml_tree1
 (95 sequences, 161 positions)



RMSA
 (48 sequences, 186 positions)
 mycRMSA_0.phyml_phyml_tree1



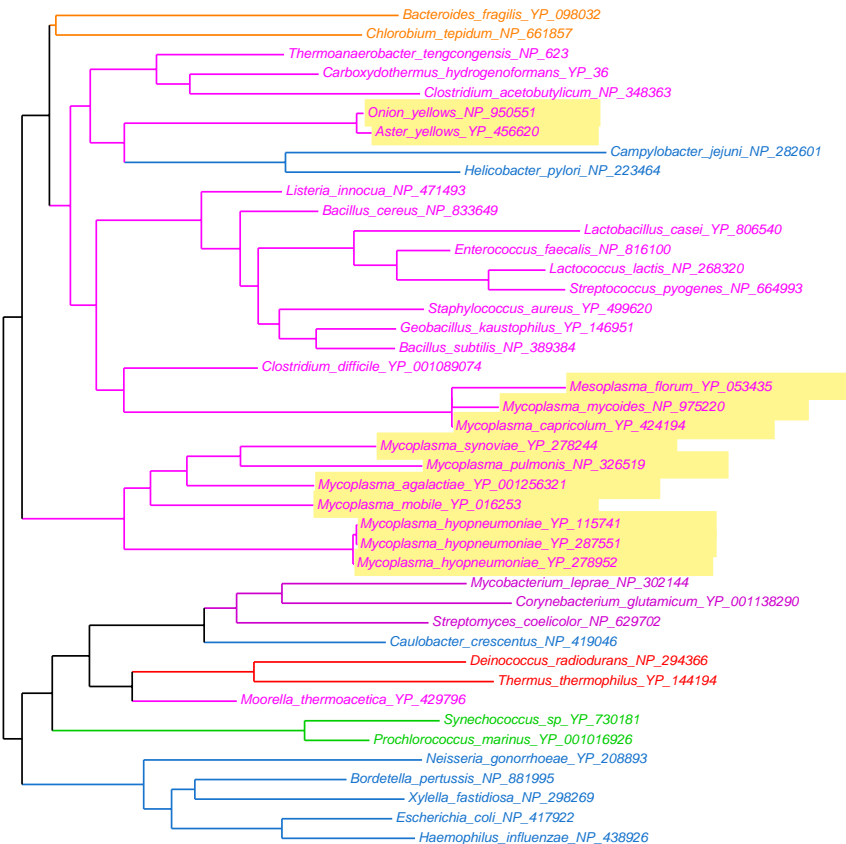
RMSB

RSMB

mycRSMB_0.phyml_phyml_tree1

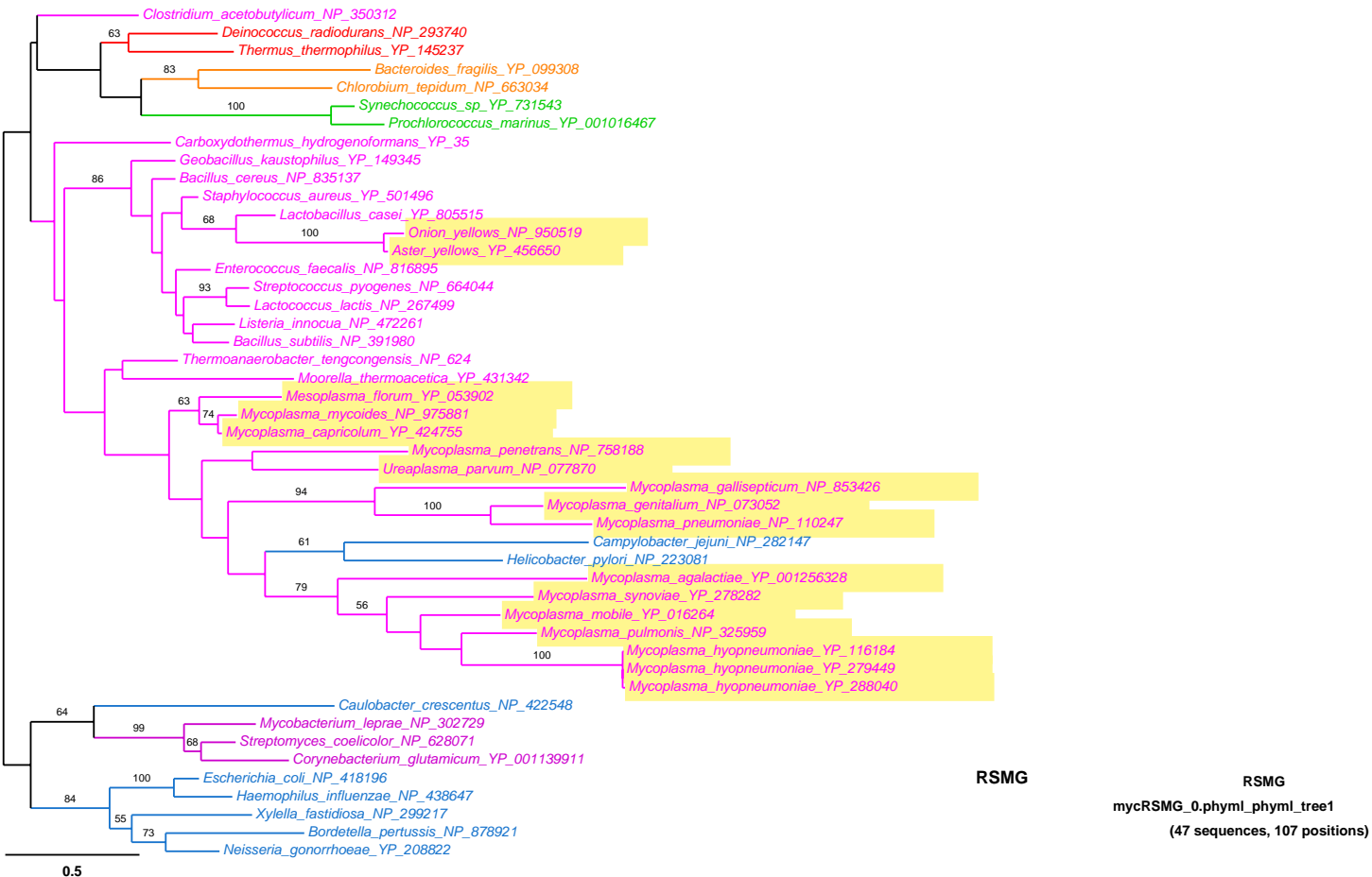
(32 sequences, 227 positions)

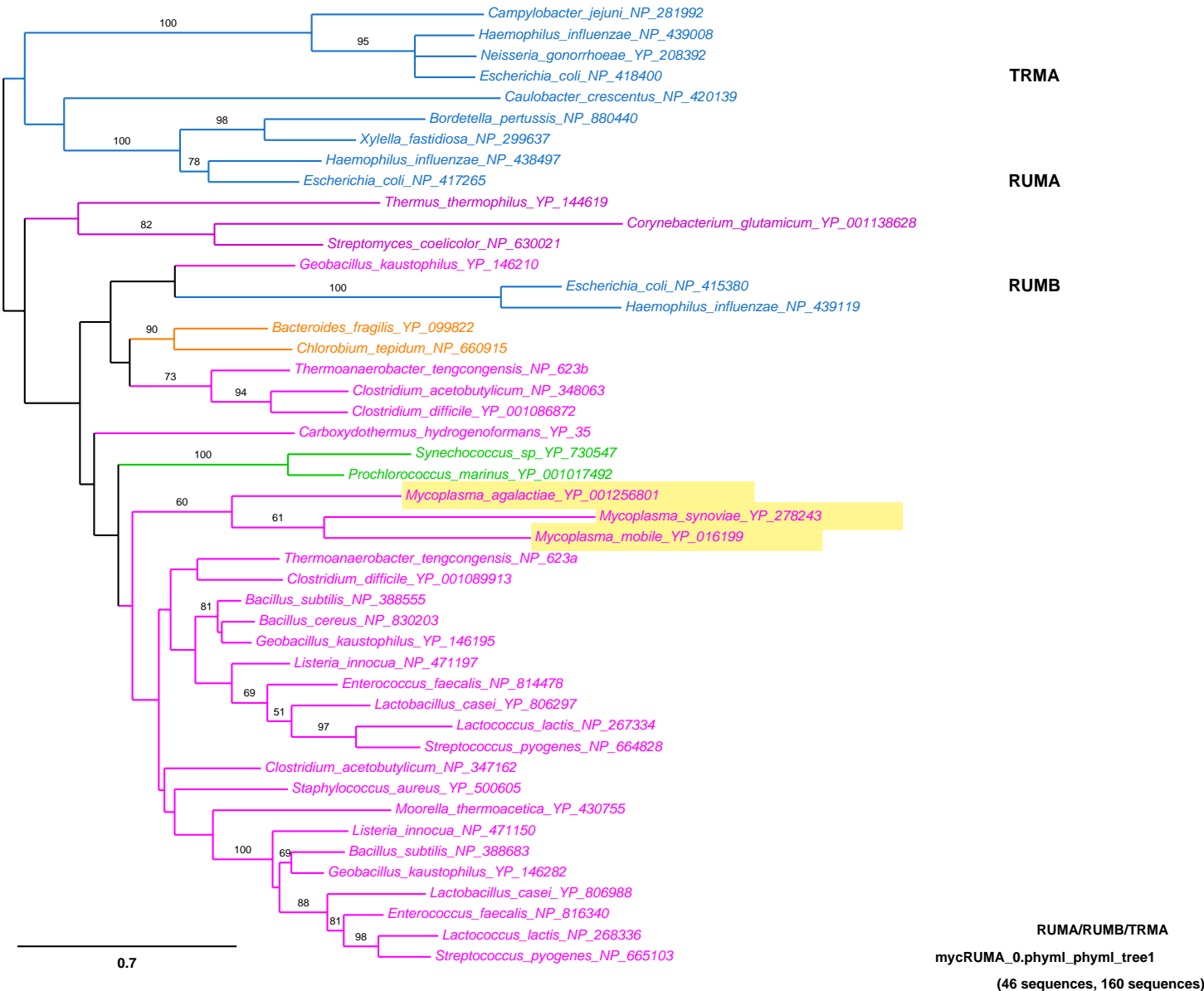
0.7

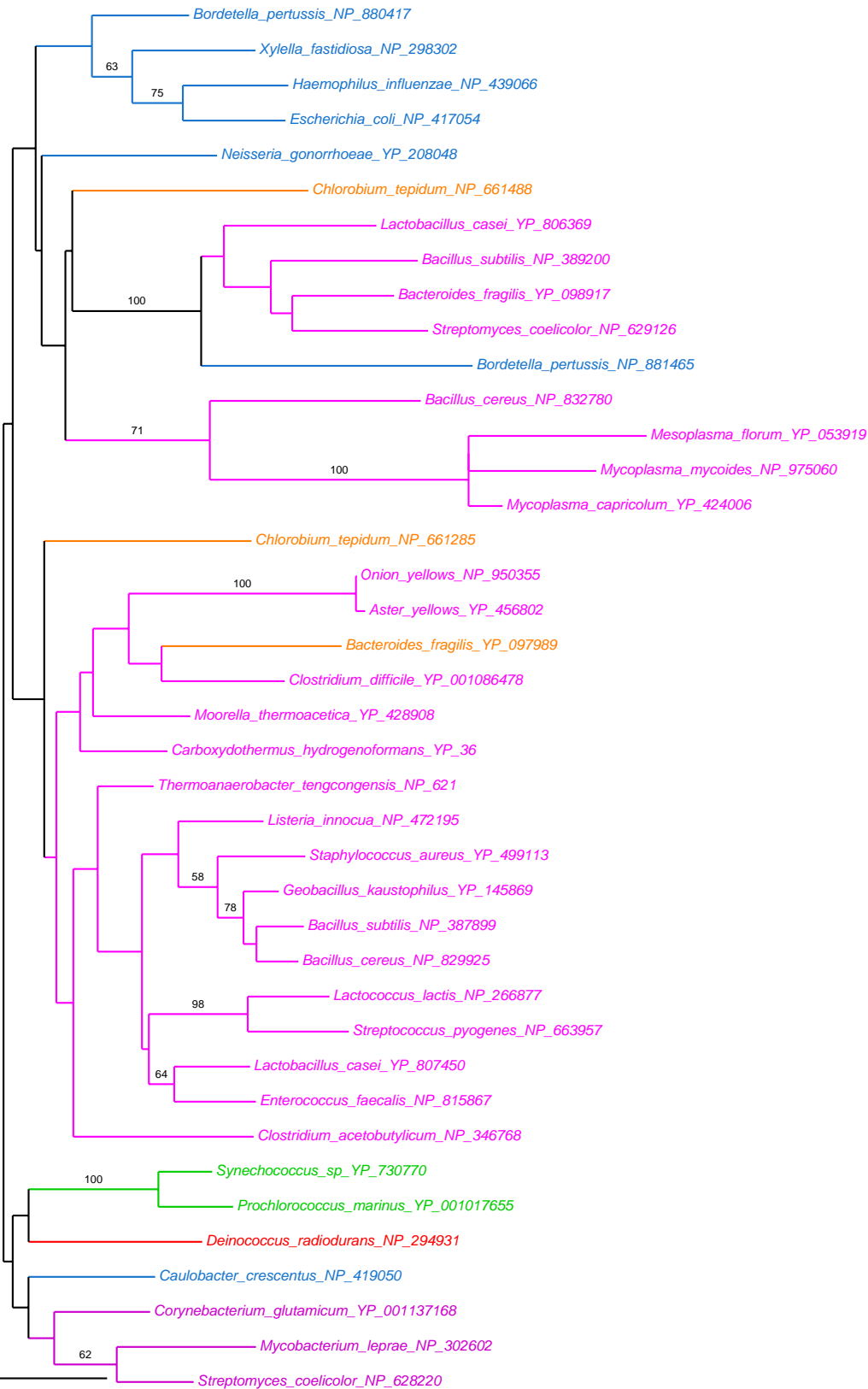


RMSD
mycRMSD_0.phyml_phyml_tree1
(43 sequences, 106 positions)

RMSD







TADA

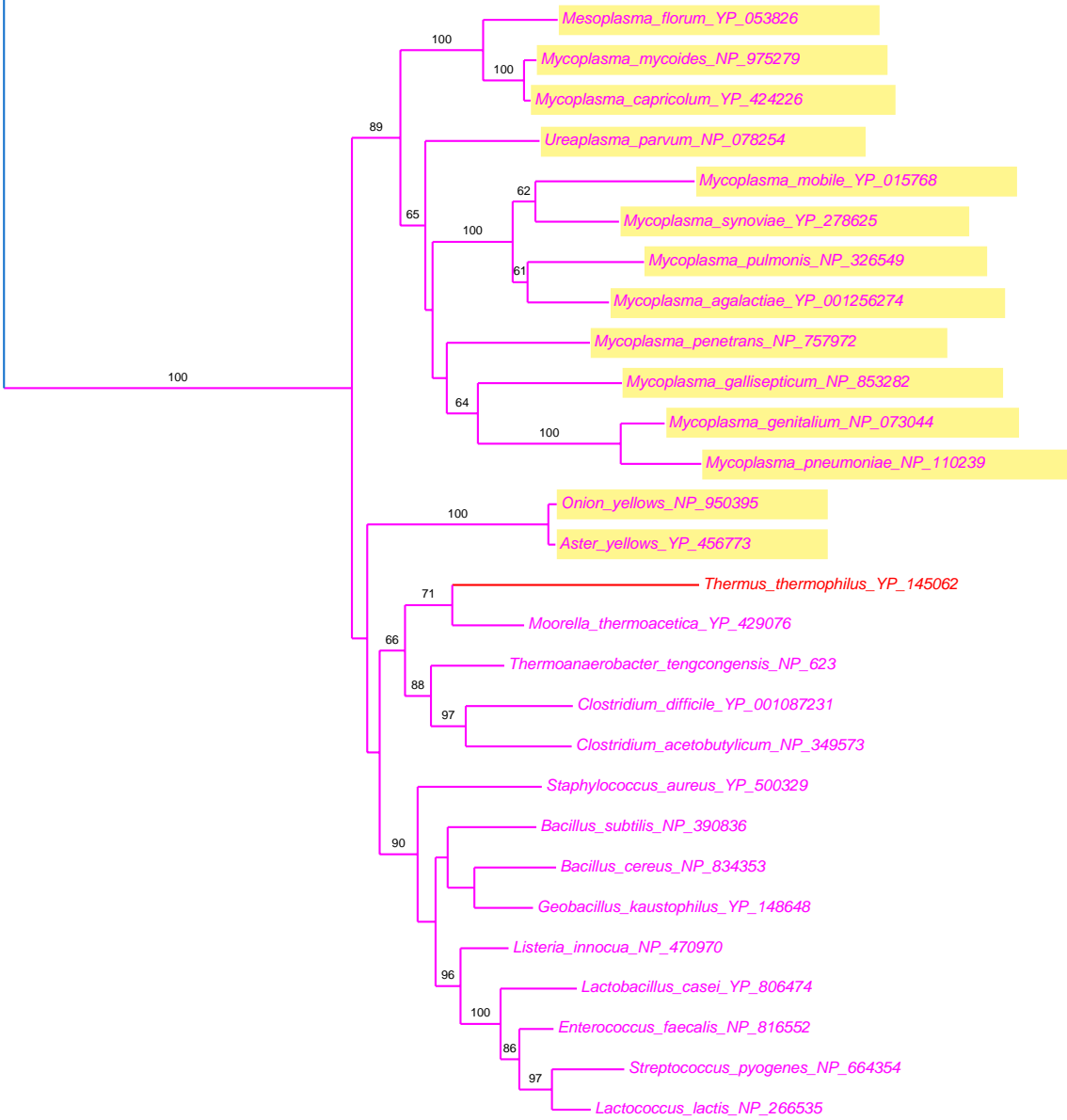
TADA

mycTADA_0.phyml_phyml_tree1

(40 sequences, 104 positions)

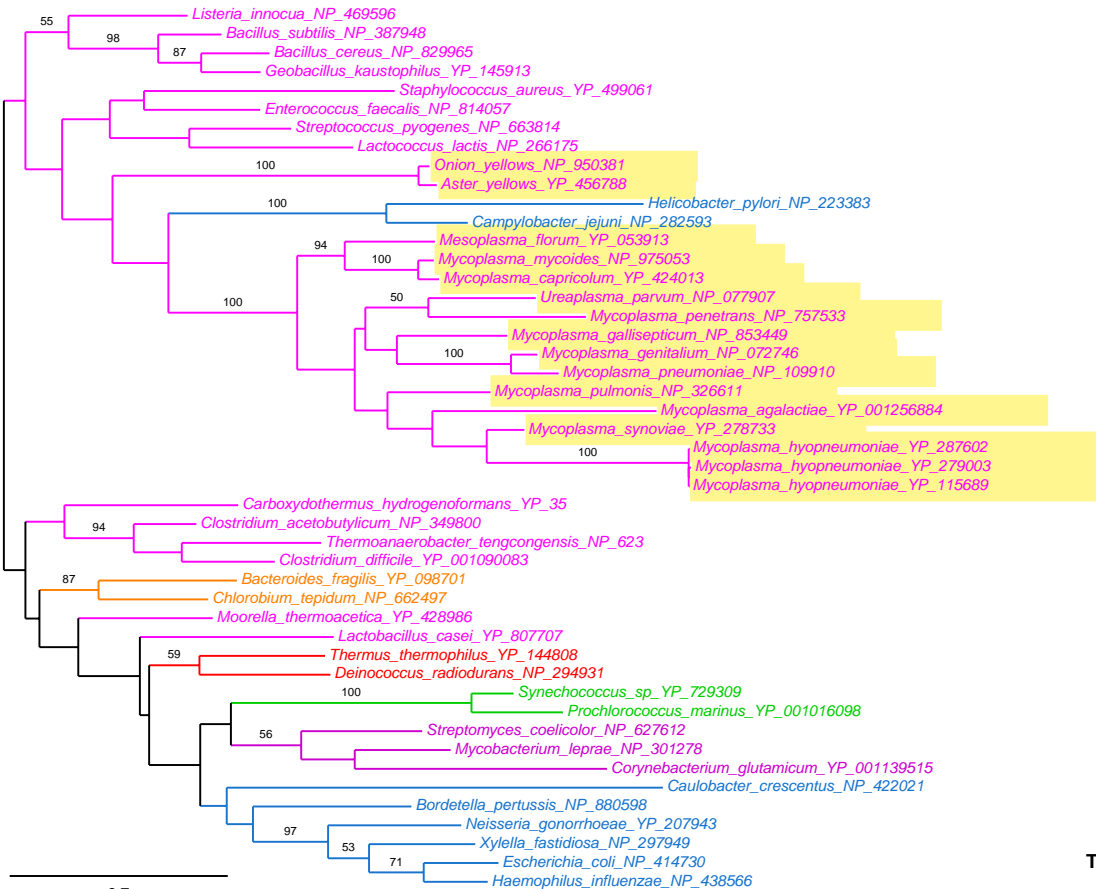
Escherichia_coli_NP_414957
Haemophilus_influenzae_YP_001291692

THII

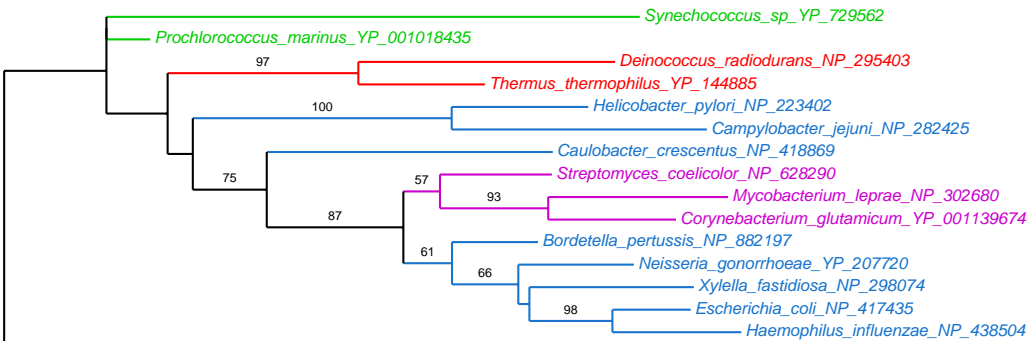


0.7

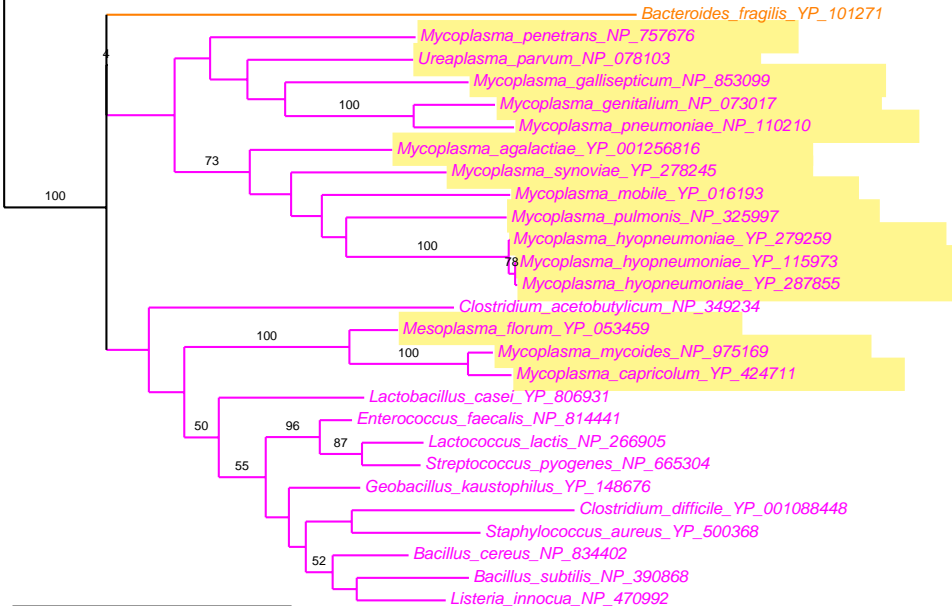
THII
mycTHII_0.phyml_phyml_tree1
(30 sequences, 296 positions)



TILS
 mycTILS_0.phyml_phyml_tree1
 (47 sequences, 131 positions)



TRMB

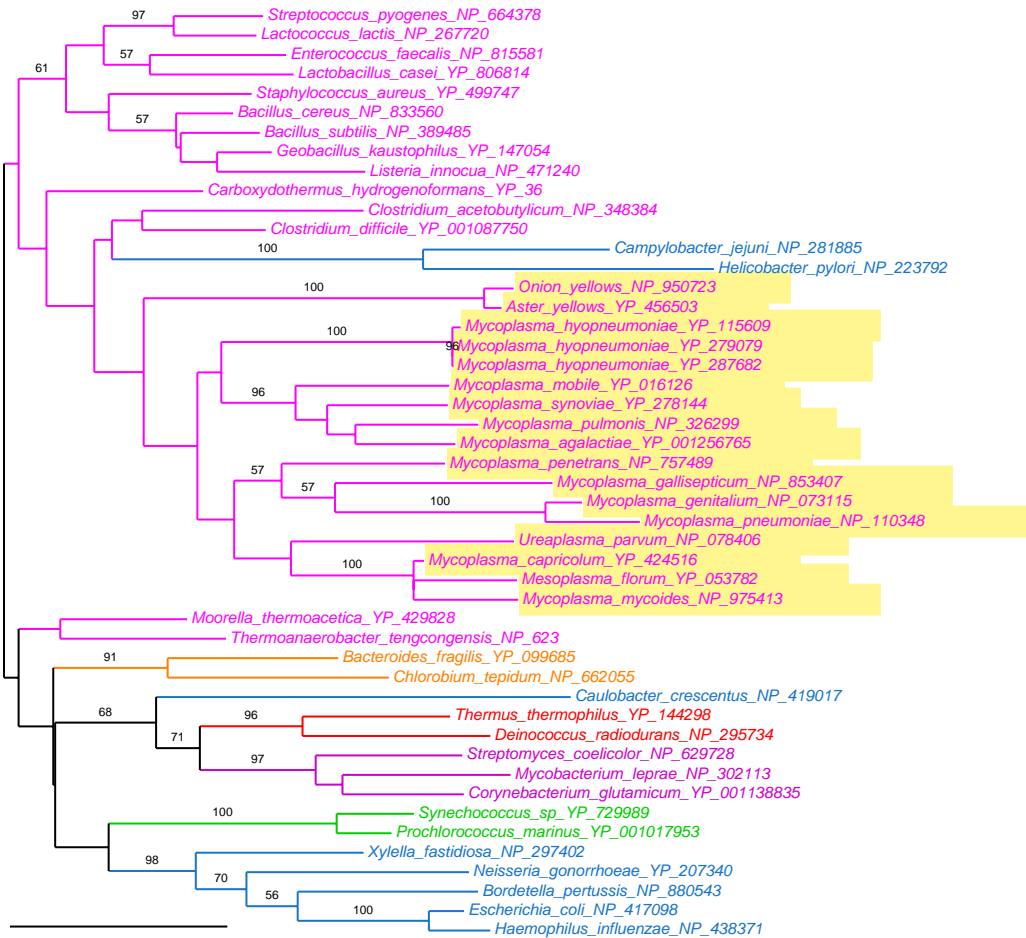


TRMB

mycTRMB_0.phyml_phyml_tree1

(42 sequences, 152 positions)

0.8

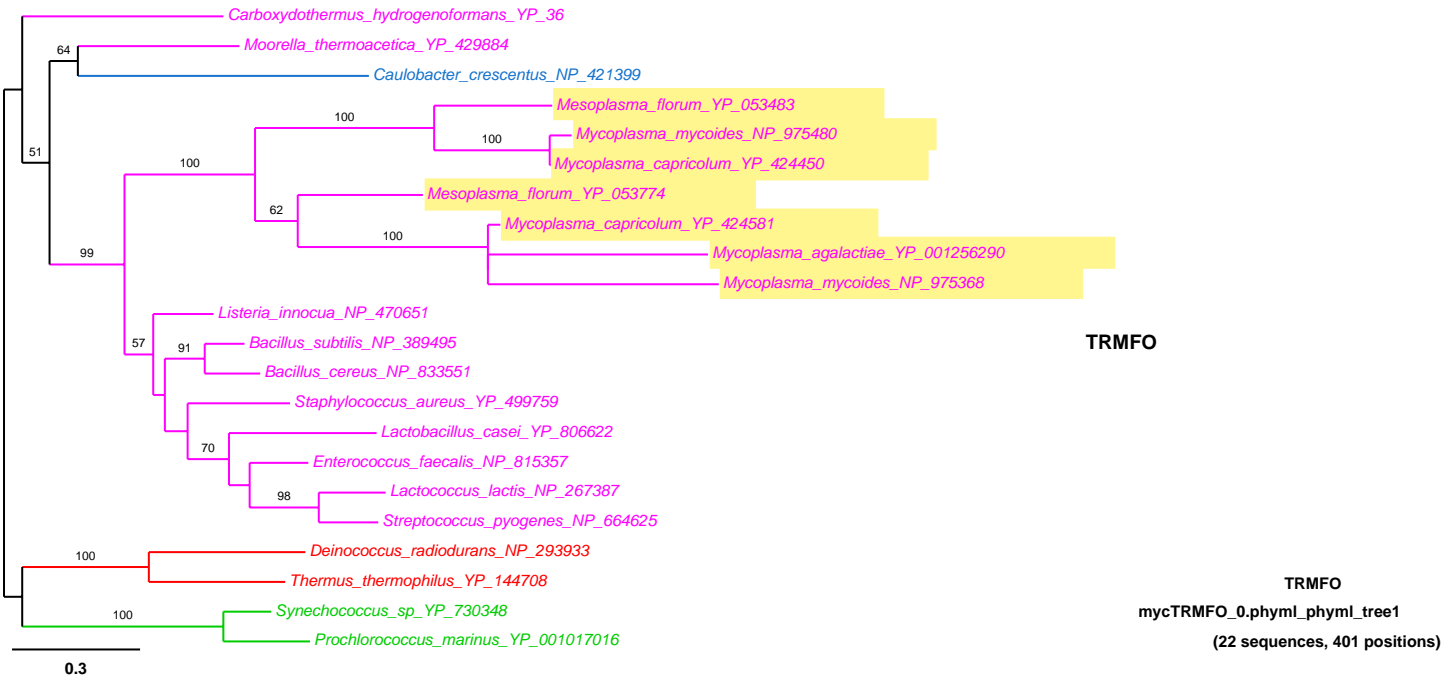


TRMD

mycTRMD_0.phyml_phyml_tree1

(48 sequences, 192 positions)

0.4

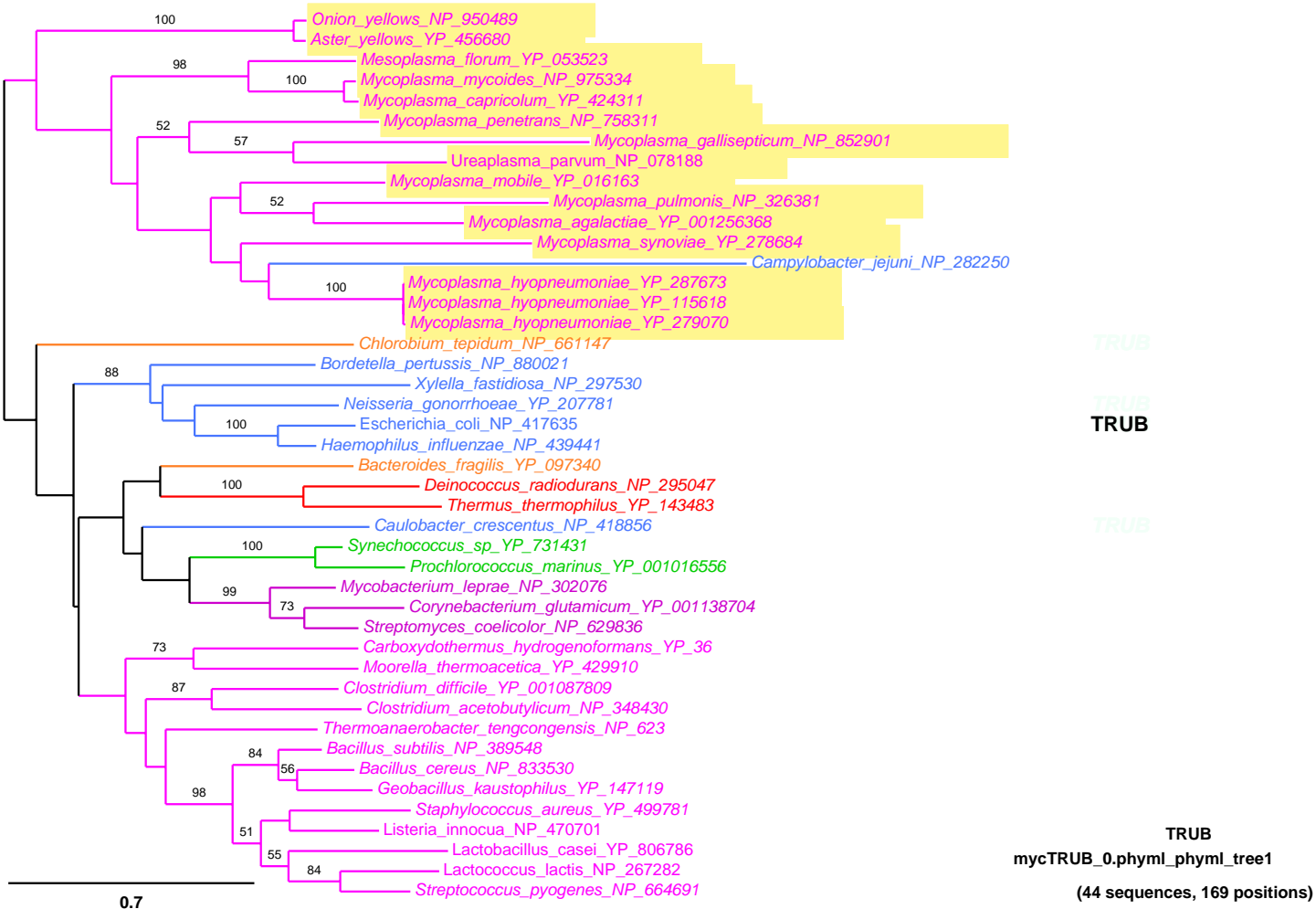


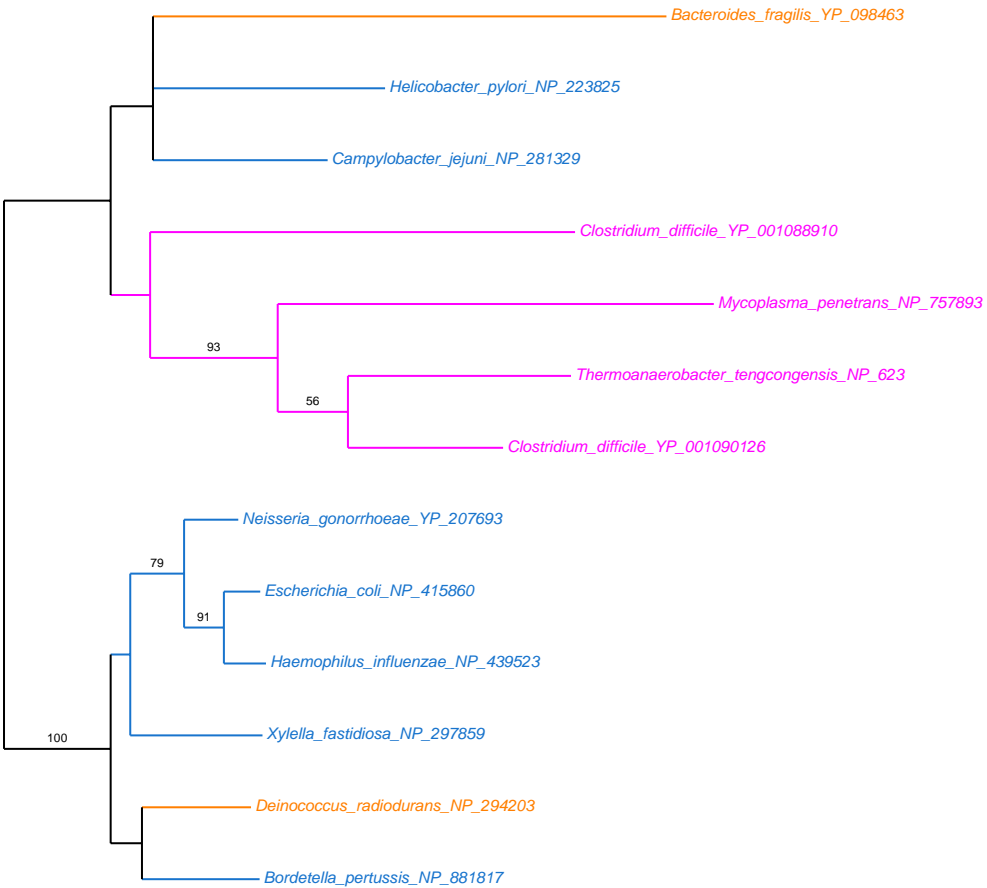


TRUA

TRUA
 mycTRUA_0.phyml_phyml_tree1
 (42 sequences, 194 positions)

0.5





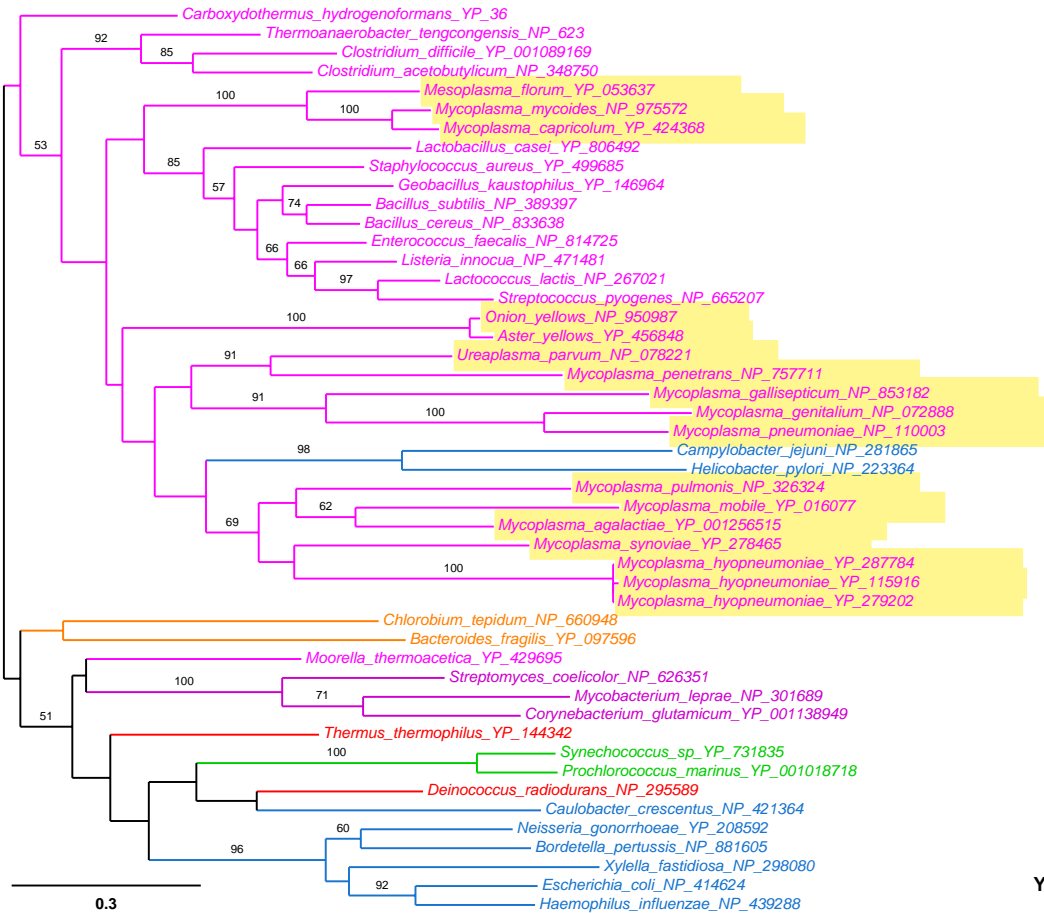
TTCA

TTCA

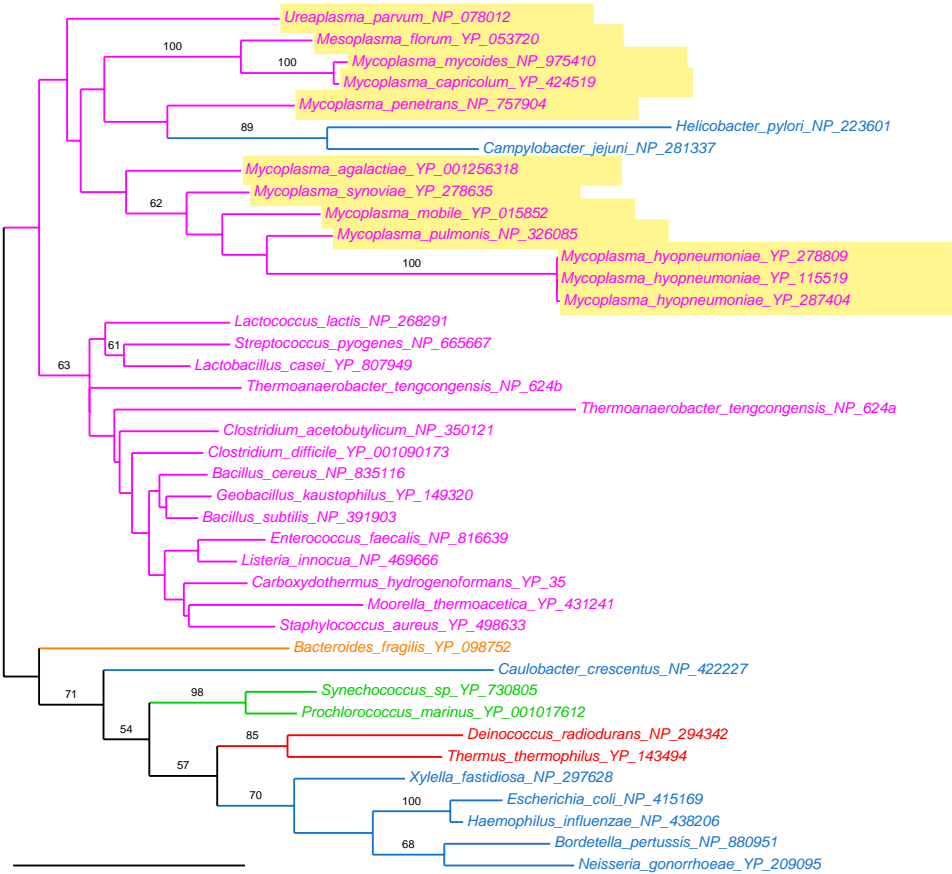
mycTTCA_0.phyml_phyml_tree1

(13 sequences, 200 positions)

0.6



YABC
 mycYABC_0.phyml_phyml_tree1
 (48 sequences, 219 positions)



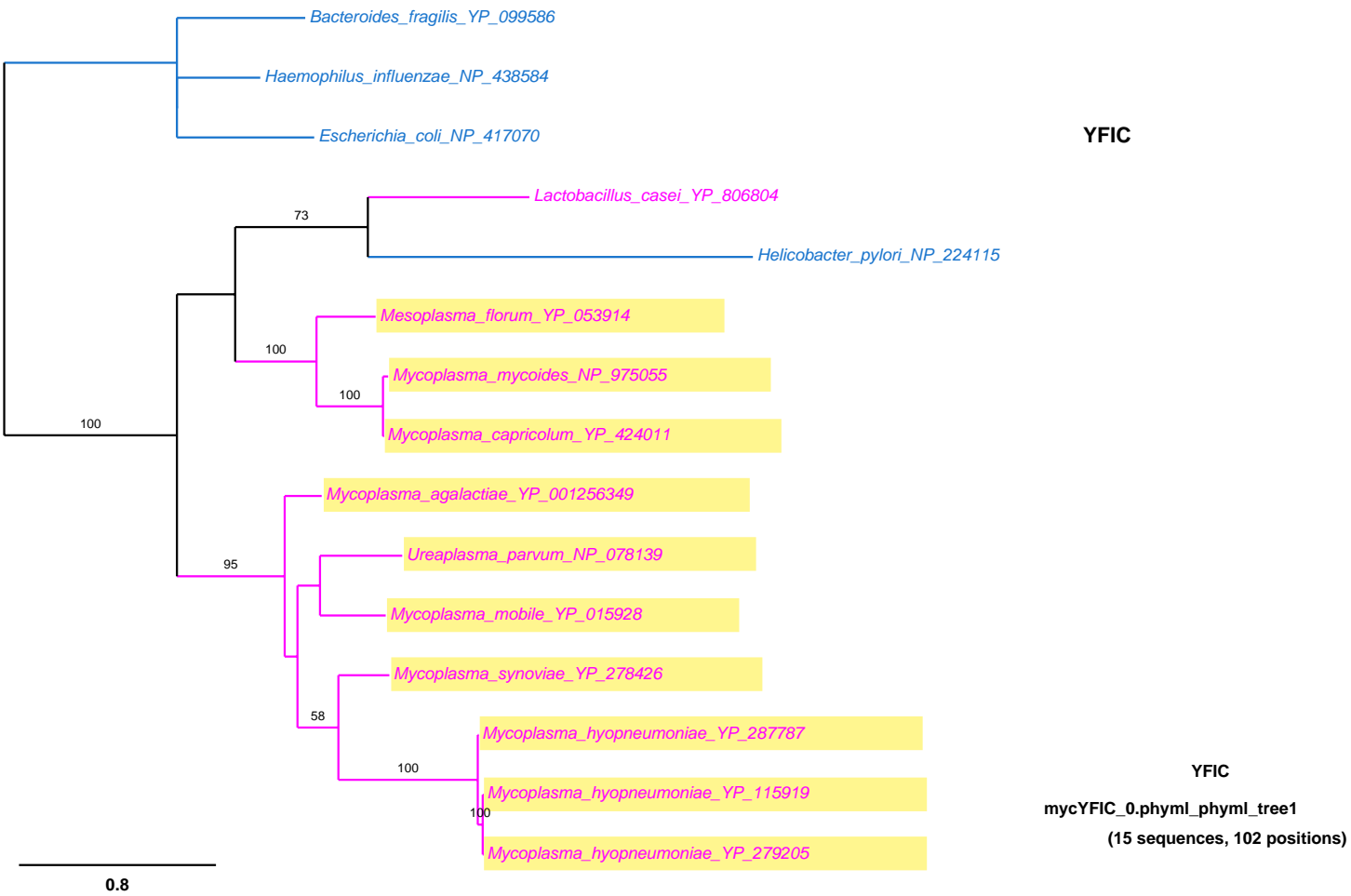
YEBA

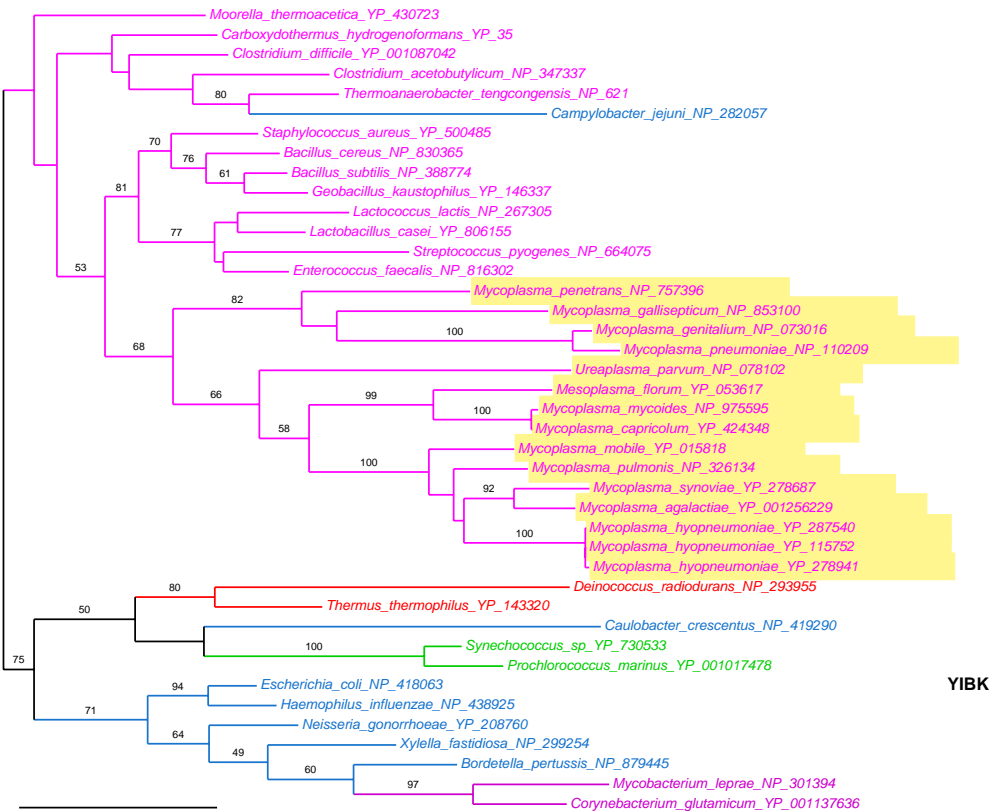
YEBA

mycYEBA_0.phyml_phyml_tree1

(40 sequences, 116 positions)

0.7

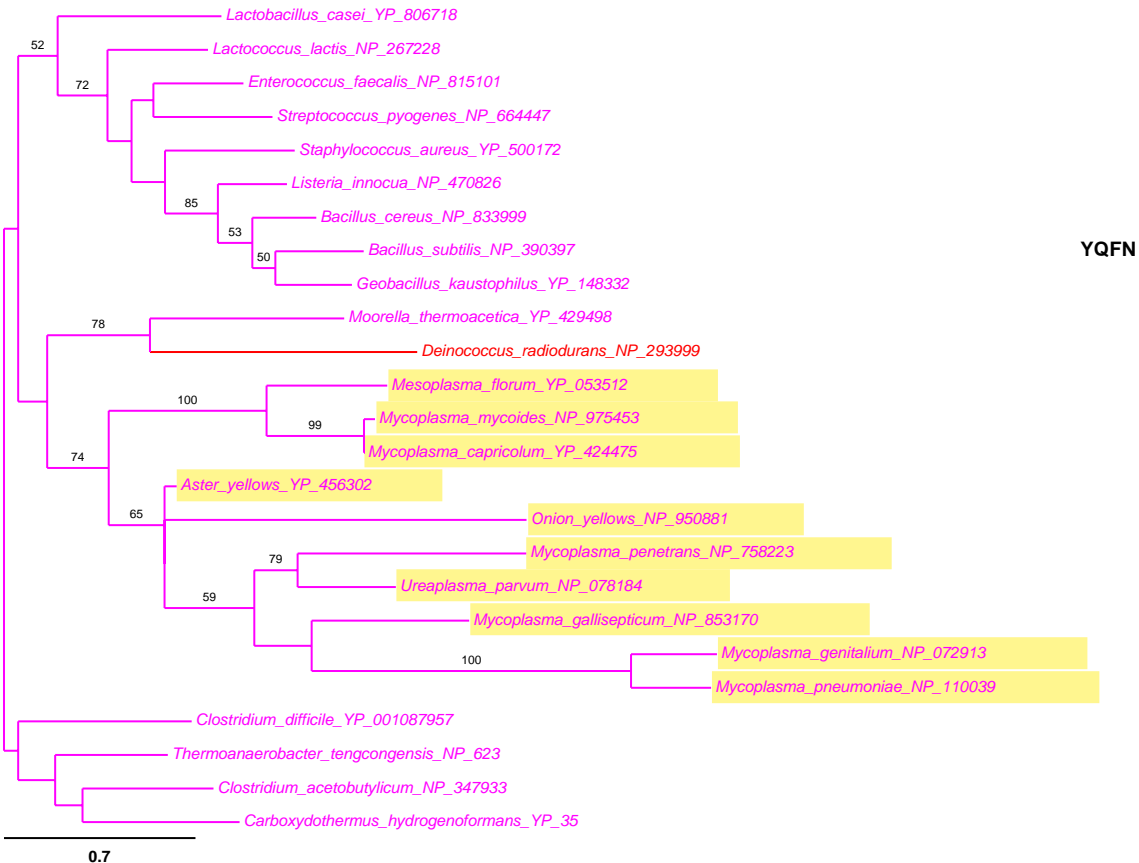




YIBK

YIBK

mycYIBK_0.phyml_phyml_tree1
(41 sequences, 128 positions)



YQFN

YQFN

mycYQFN_0.phyml_phyml_tree1

(25 sequences, 125 positions)

