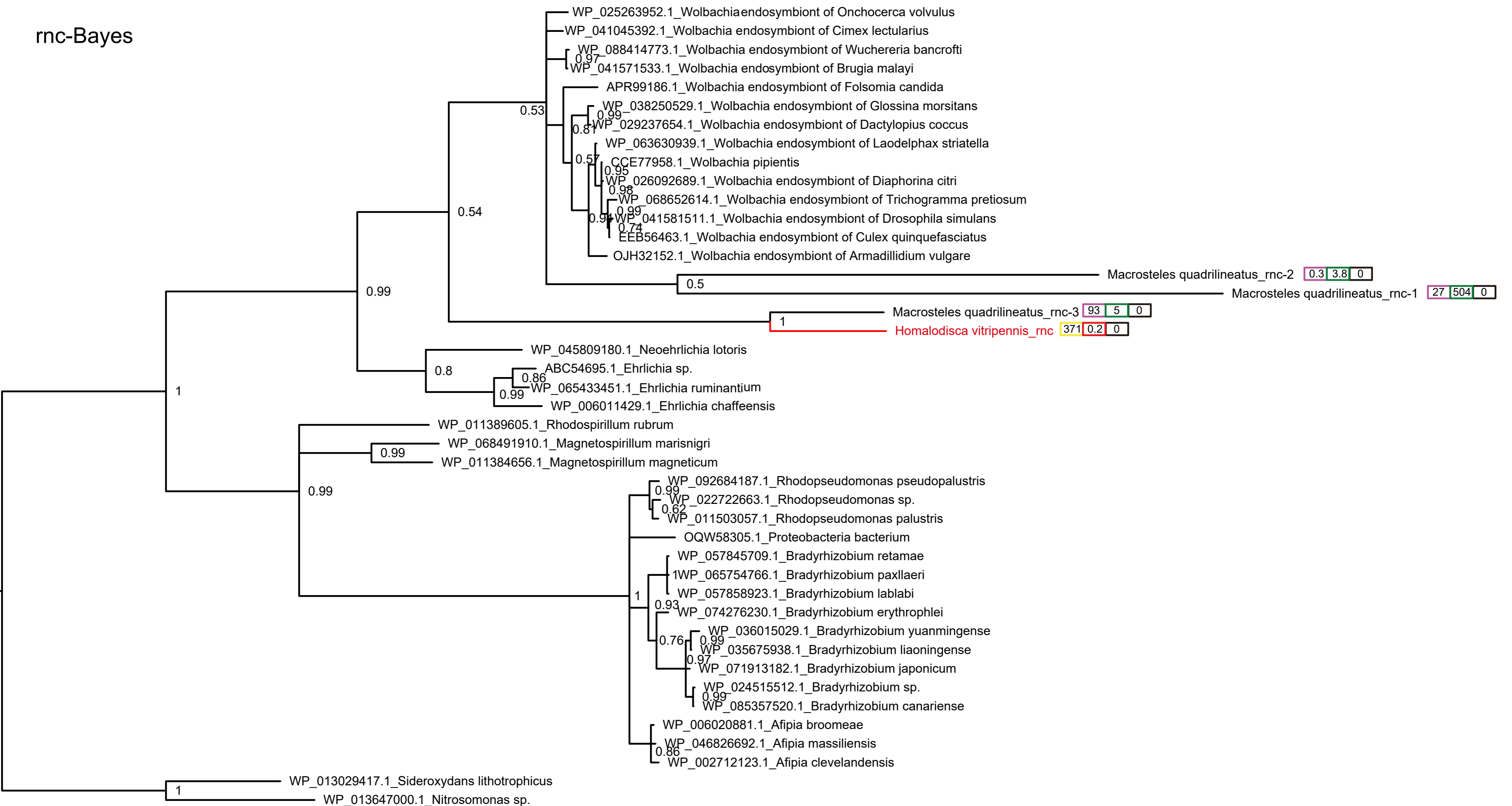


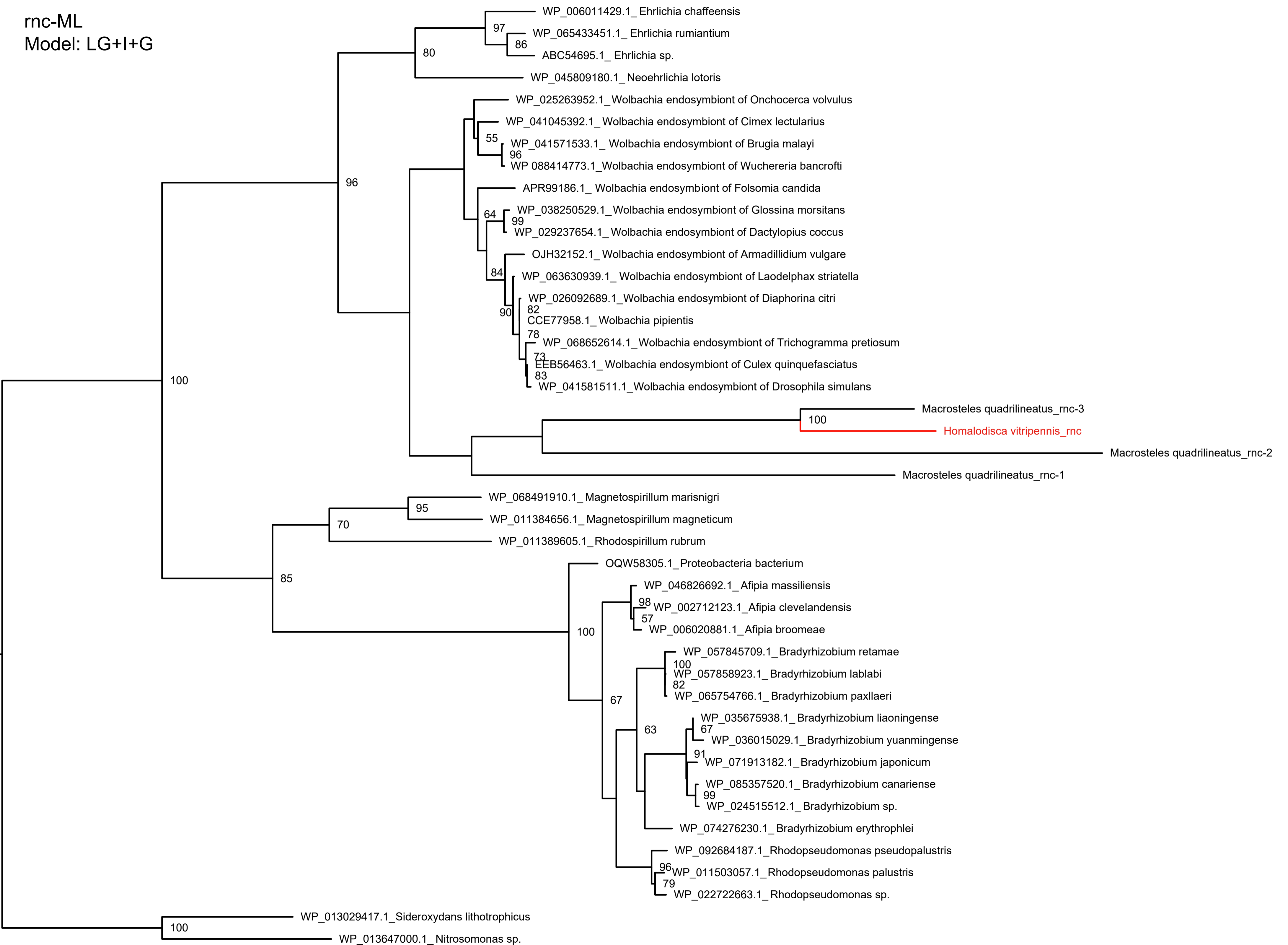
Figure S1 Bayesian and ML trees for 13 horizontally transferred genes (the highly divergent ATPase gene is excluded) and 2 duplicated mitochondrial support genes. Bayesian posterior probability and ML bootstrap value are shown for nodes with $\geq 50\%$ support. Genes from this study are shown in red. Gene expression values (FPKM) of each tissue in ALF and GWSS are shown in colored boxes: GWSS-red bacteriome (red), GWSS-yellow bacteriome (yellow), GWSS-body (black), ALF-*Sulcia* bacteriocyte (purple), ALF-*Nasuia* bacteriocyte (green), and ALF-body (black).

rnc-Bayes



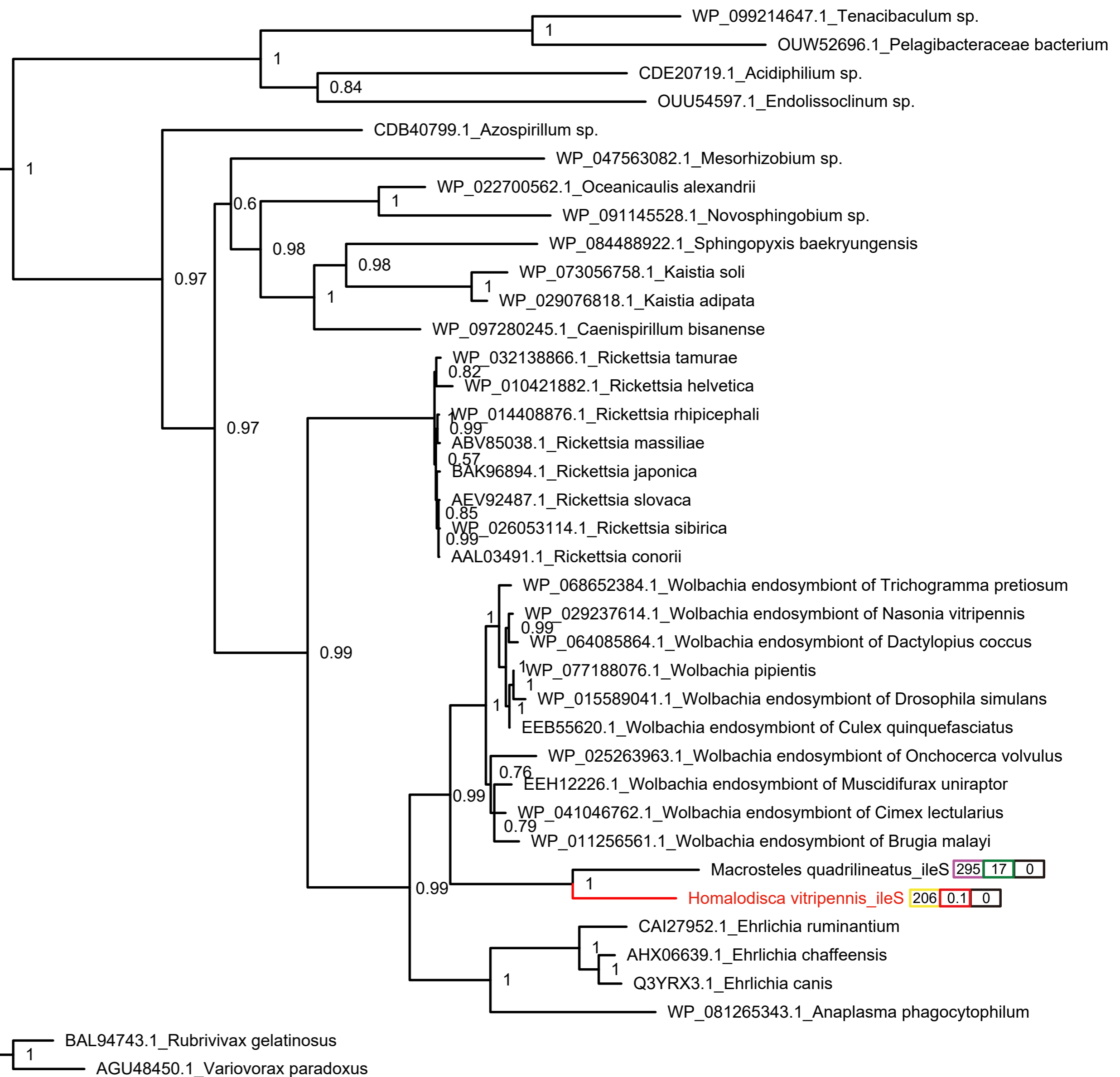
0.5

rnc-ML
Model: LG+I+G



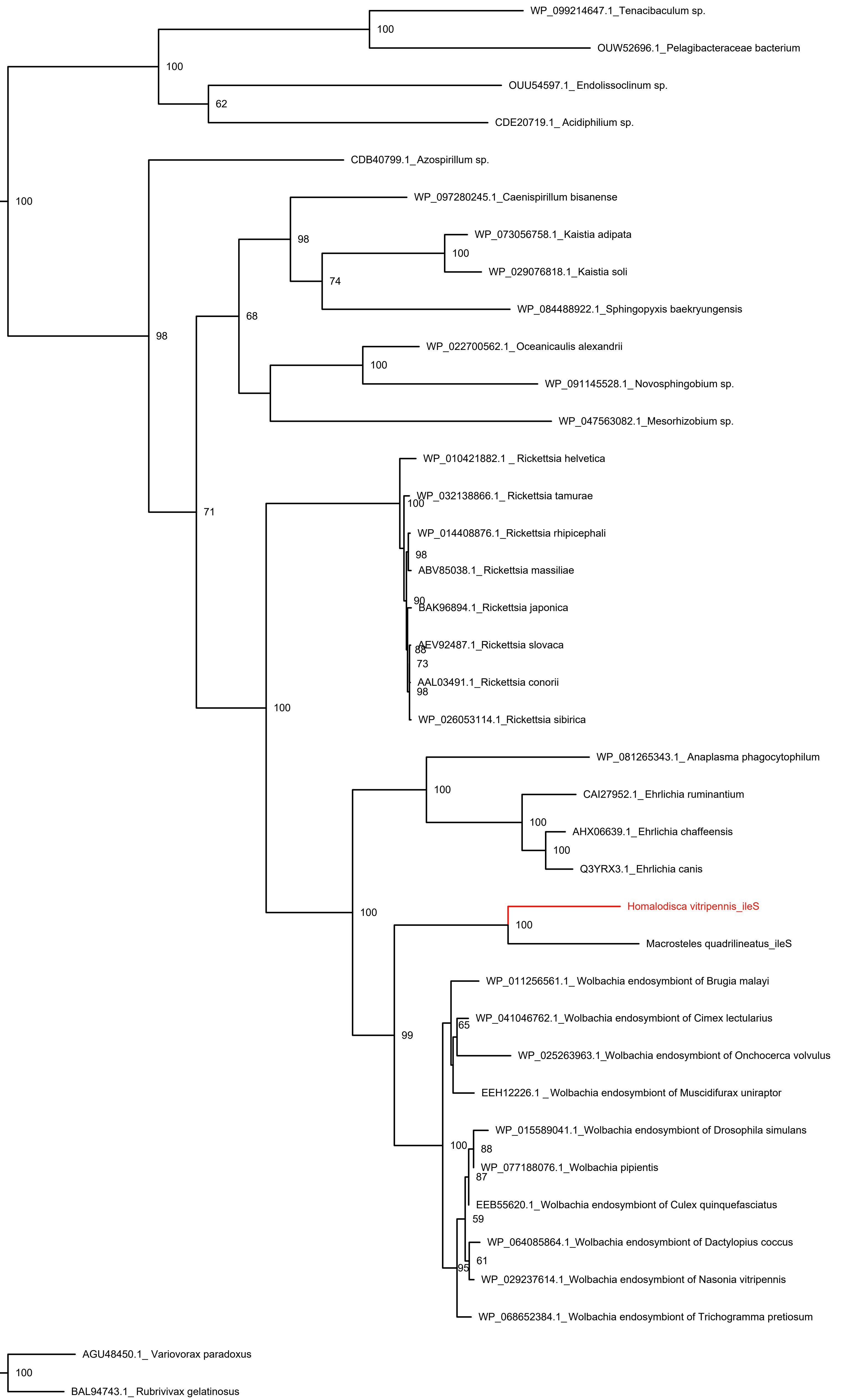
0.8

ileS-Bayes



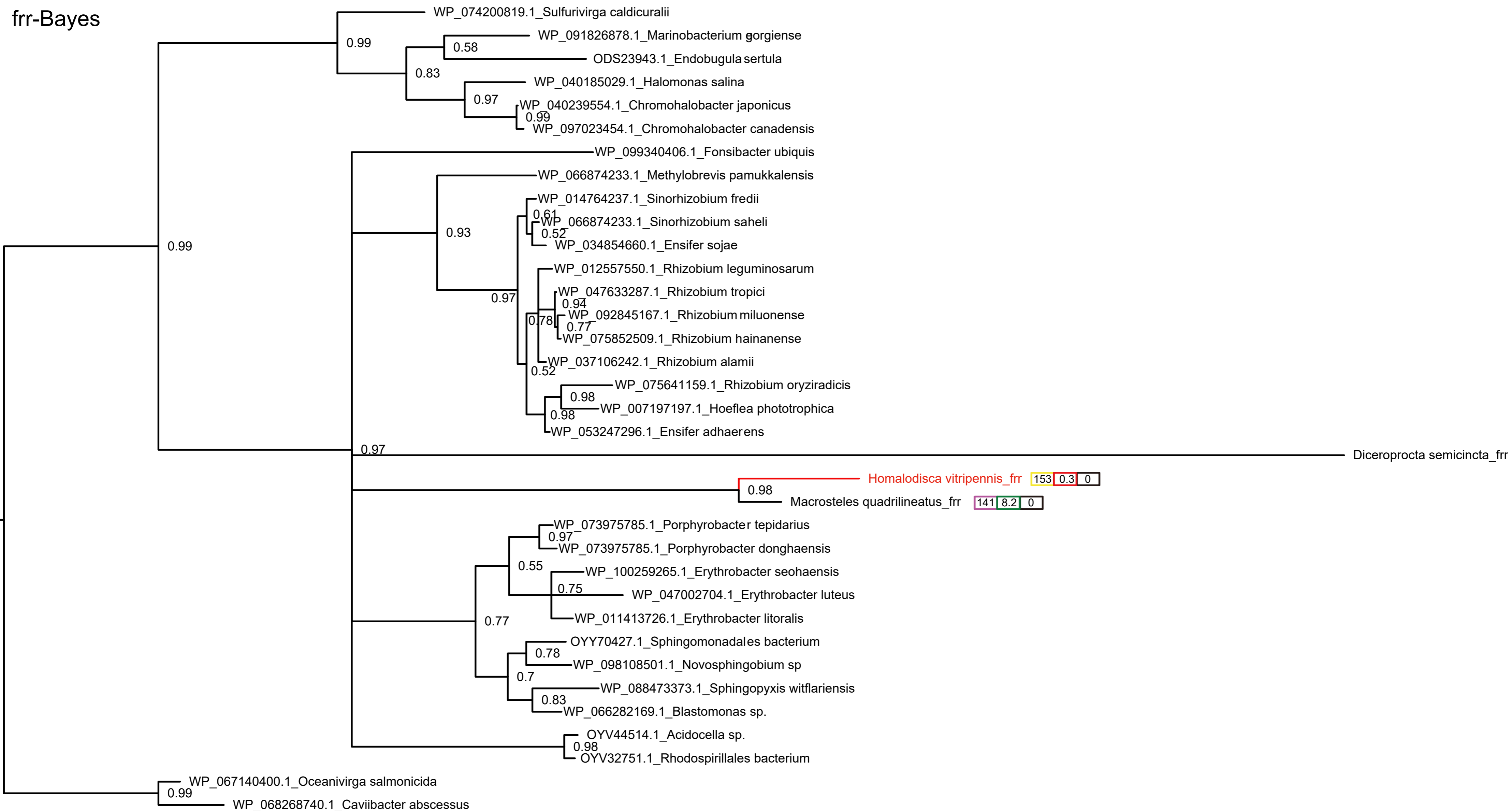
0.6

ileS-ML
Model: LG+I+G



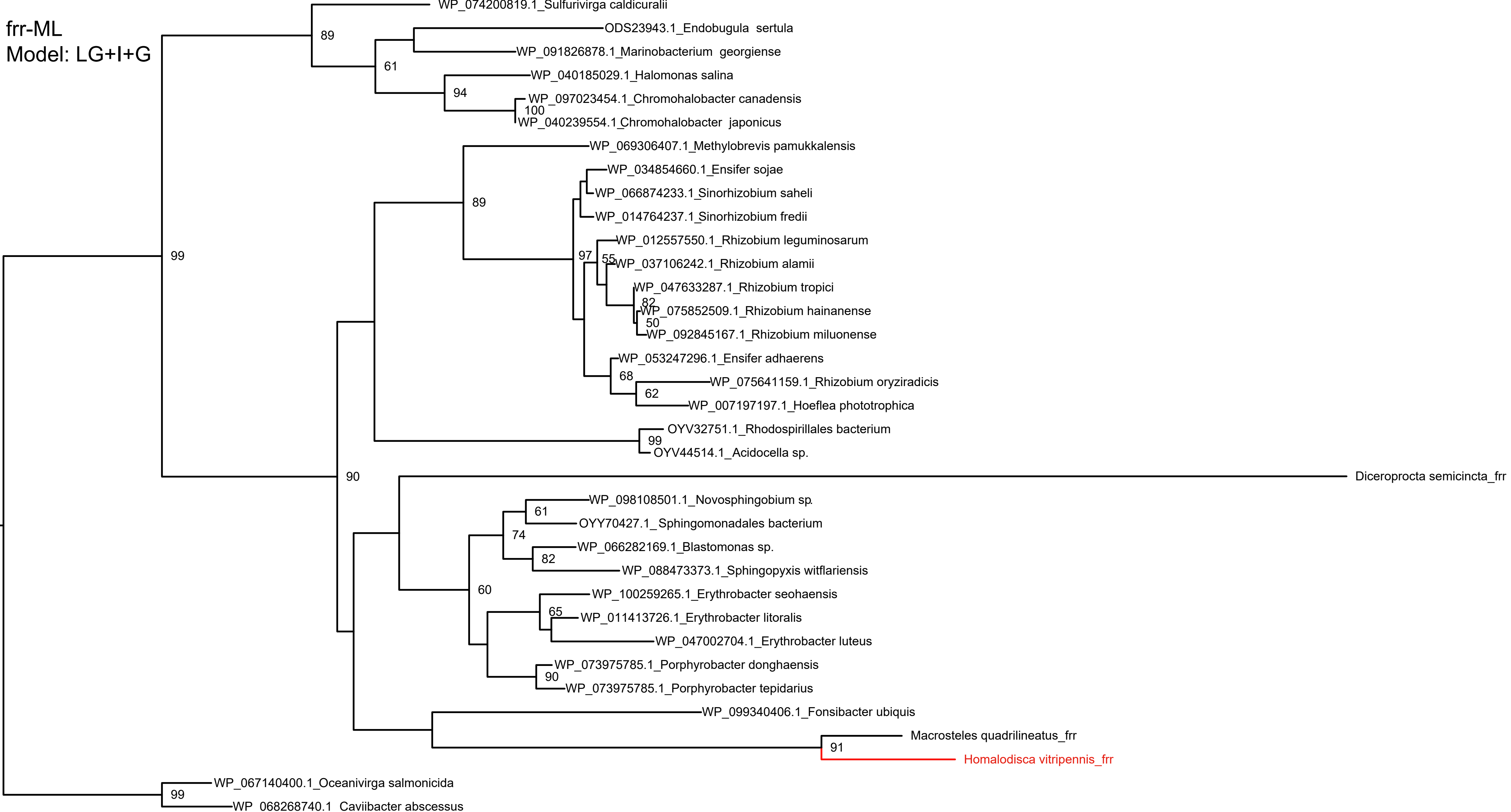
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frr-Bayes



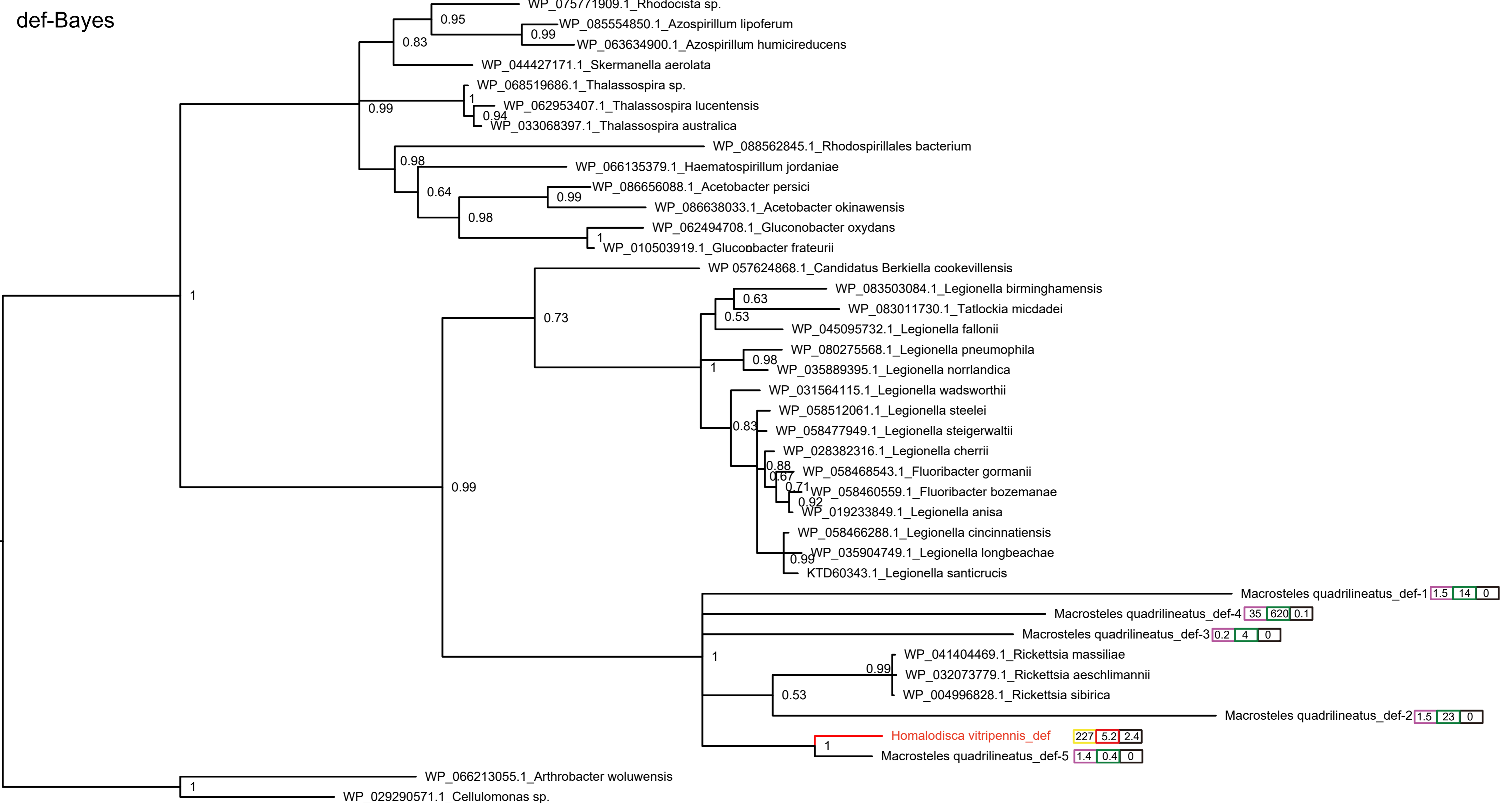
0.5

frr-ML
Model: LG+I+G

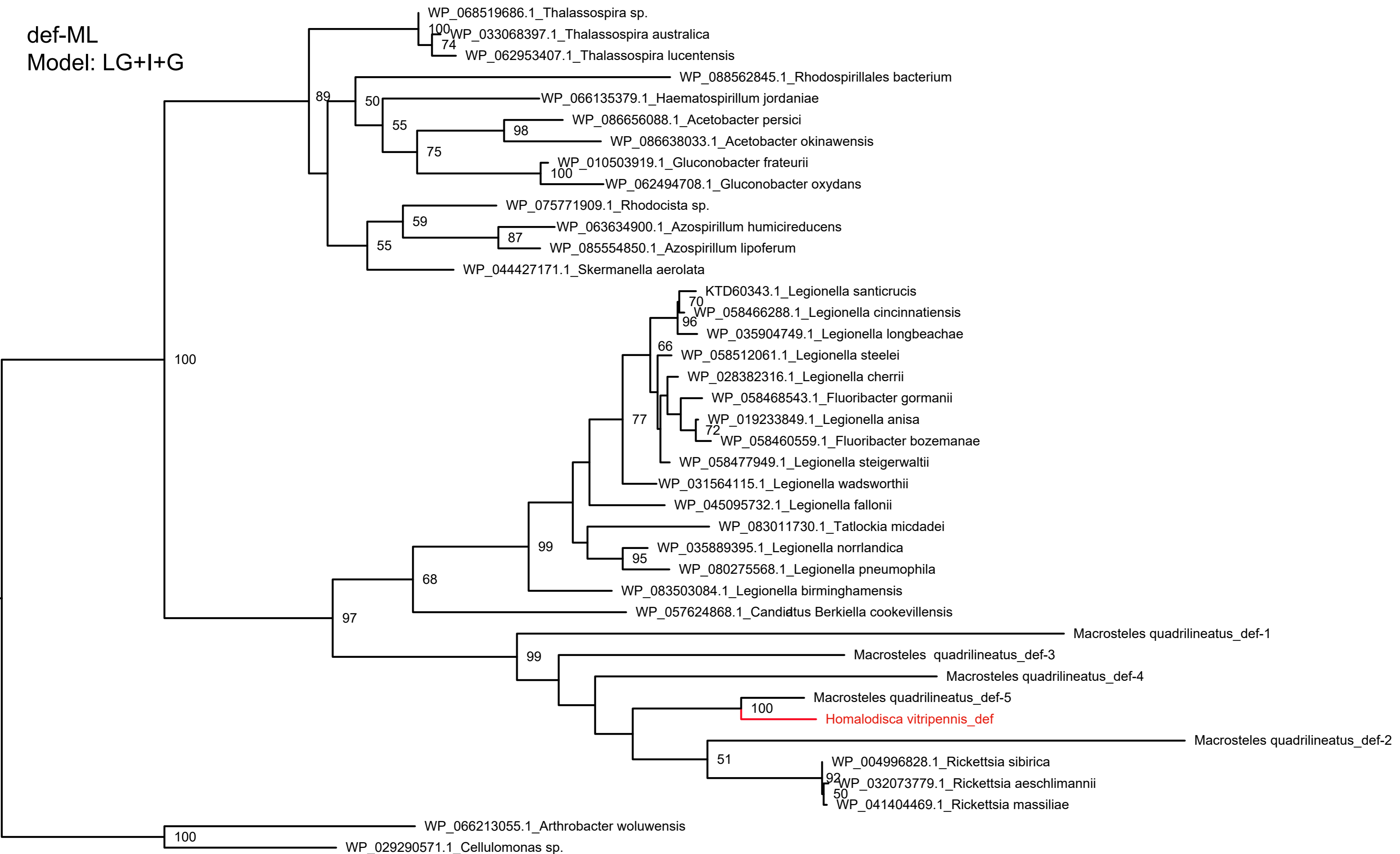


0.3

def-Bayes

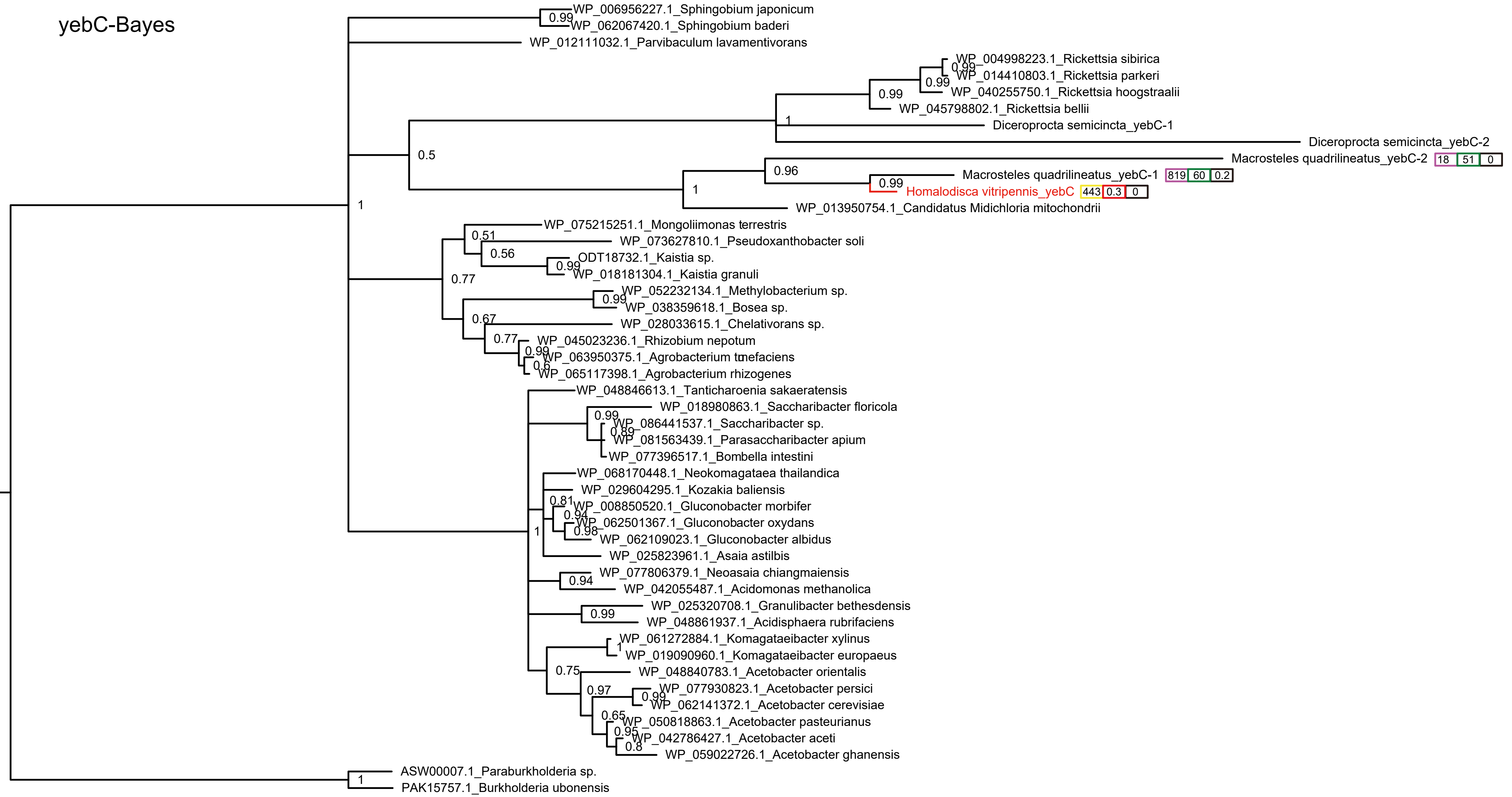


def-ML
Model: LG+I+G



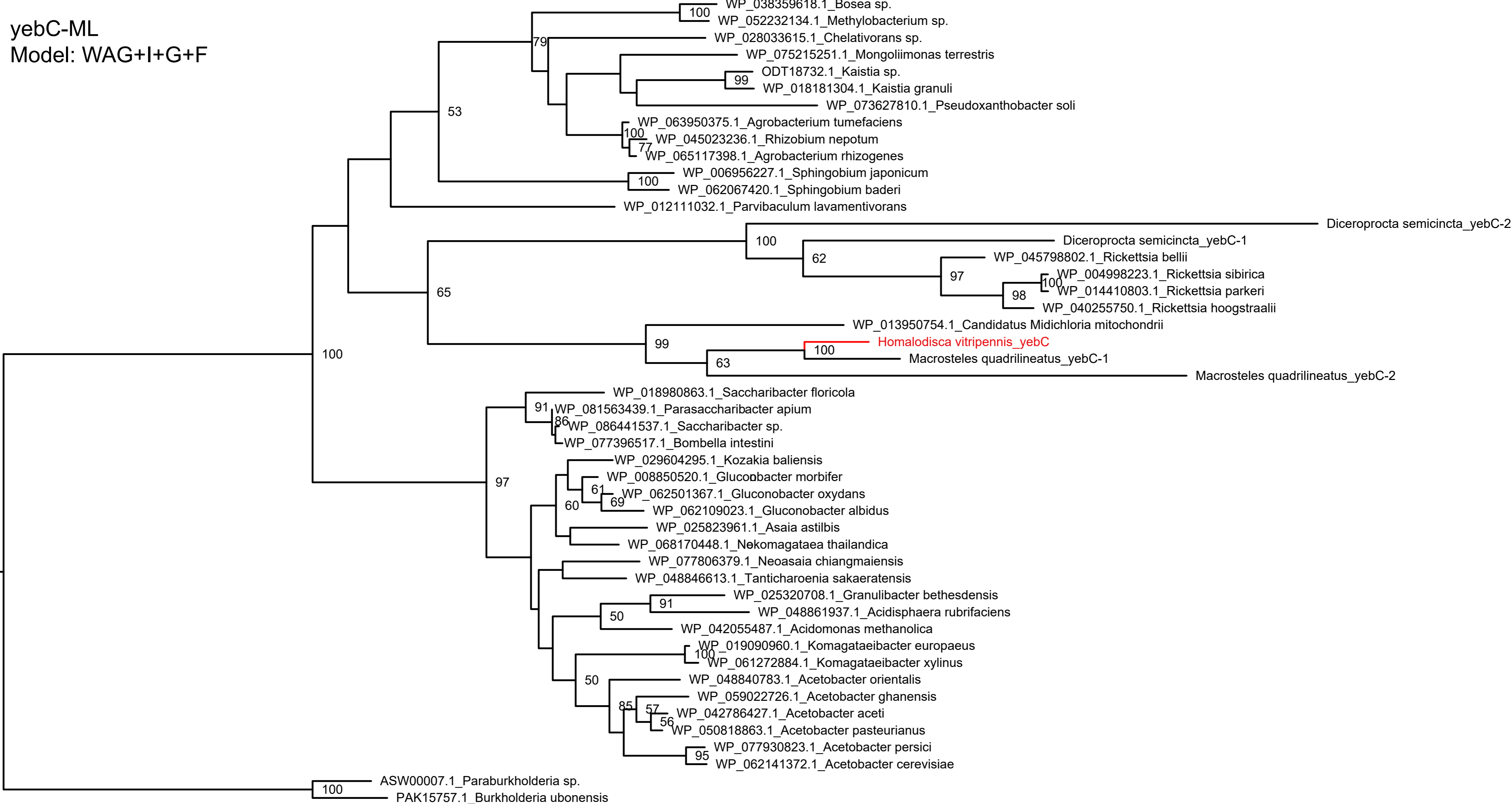
0.4

yebC-Bayes



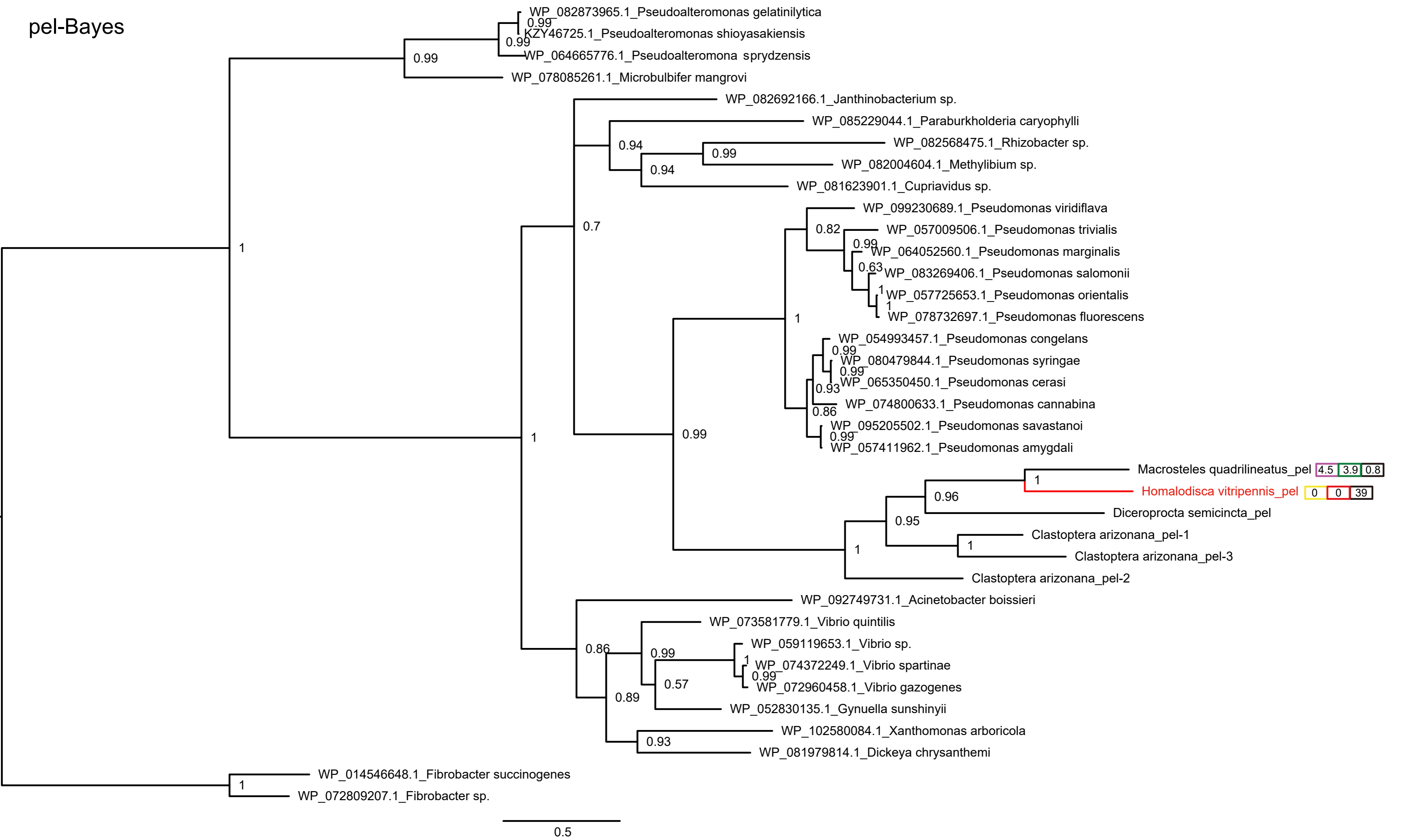
0.3

yebC-ML
Model: WAG+I+G+F

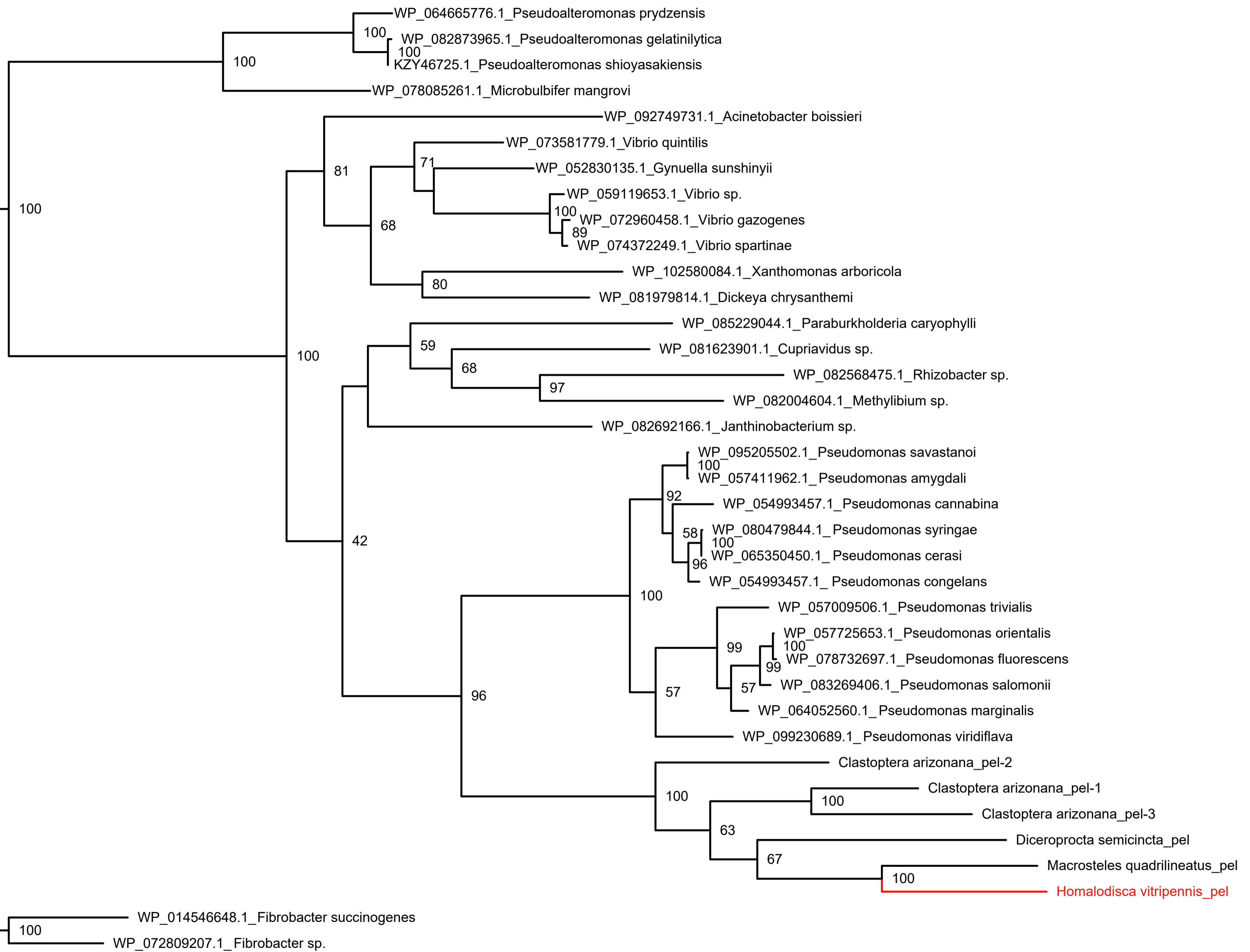


0.2

pel-Bayes

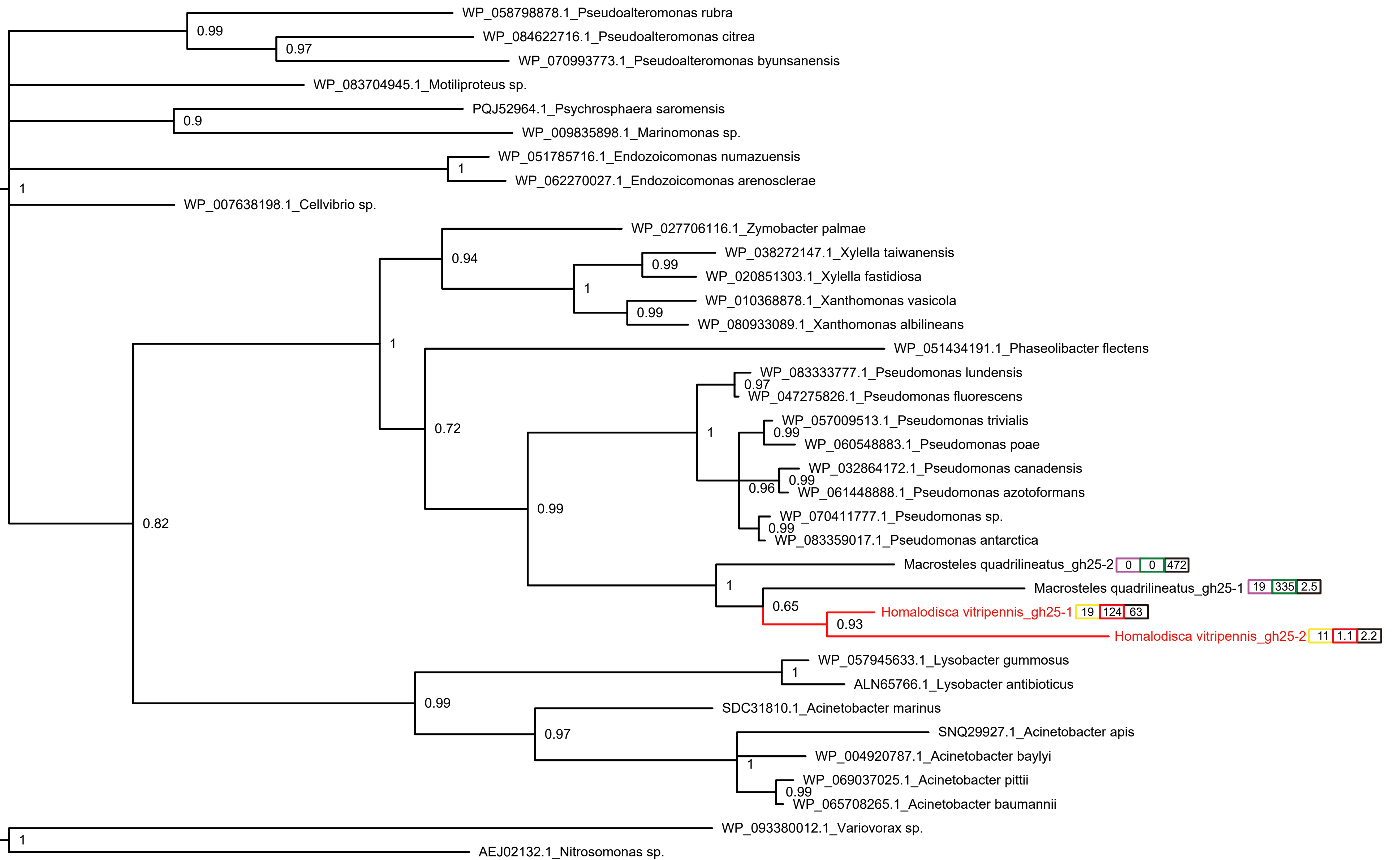


pel-ML
Model: WAG+I+G



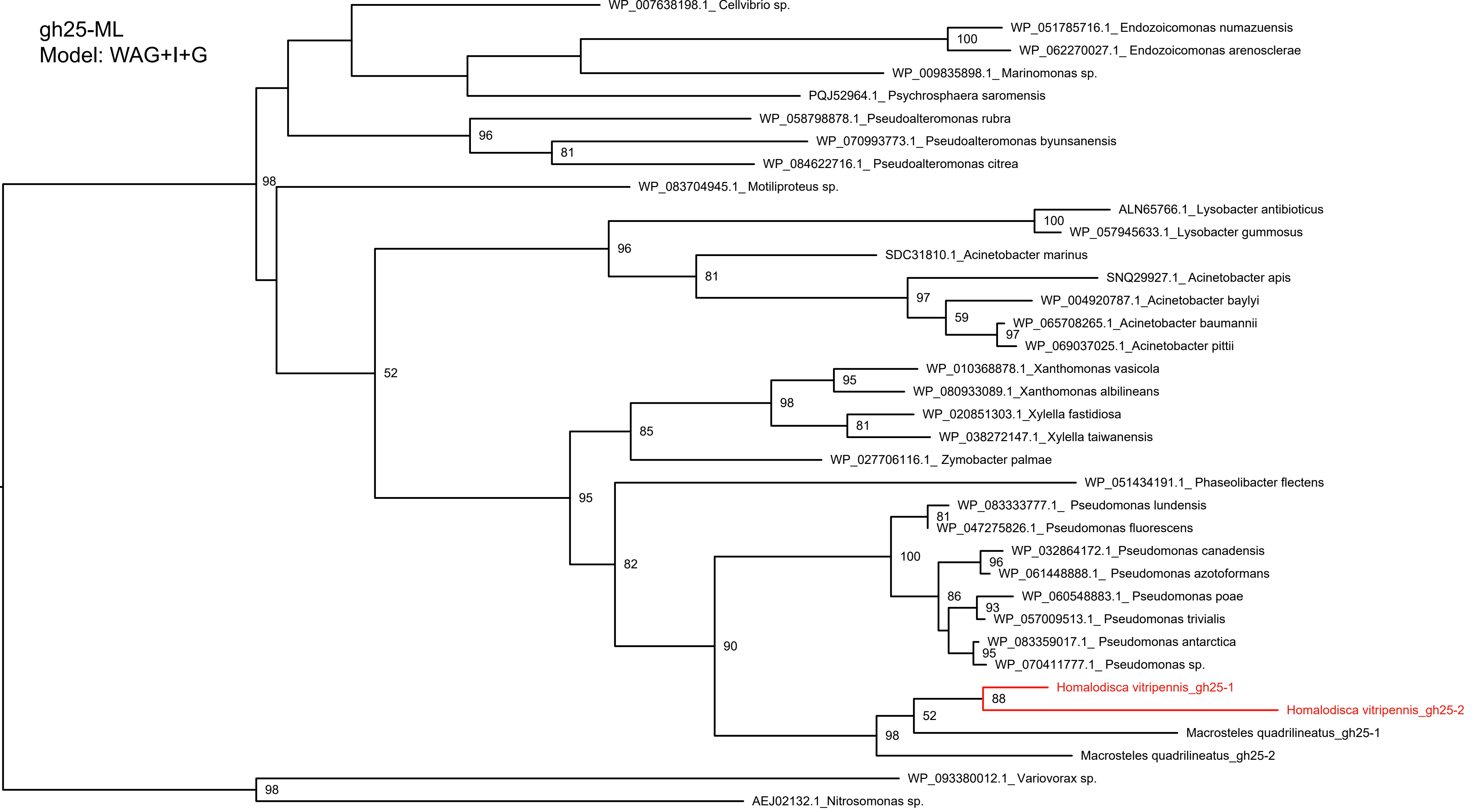
0.4

gh25-Bayes



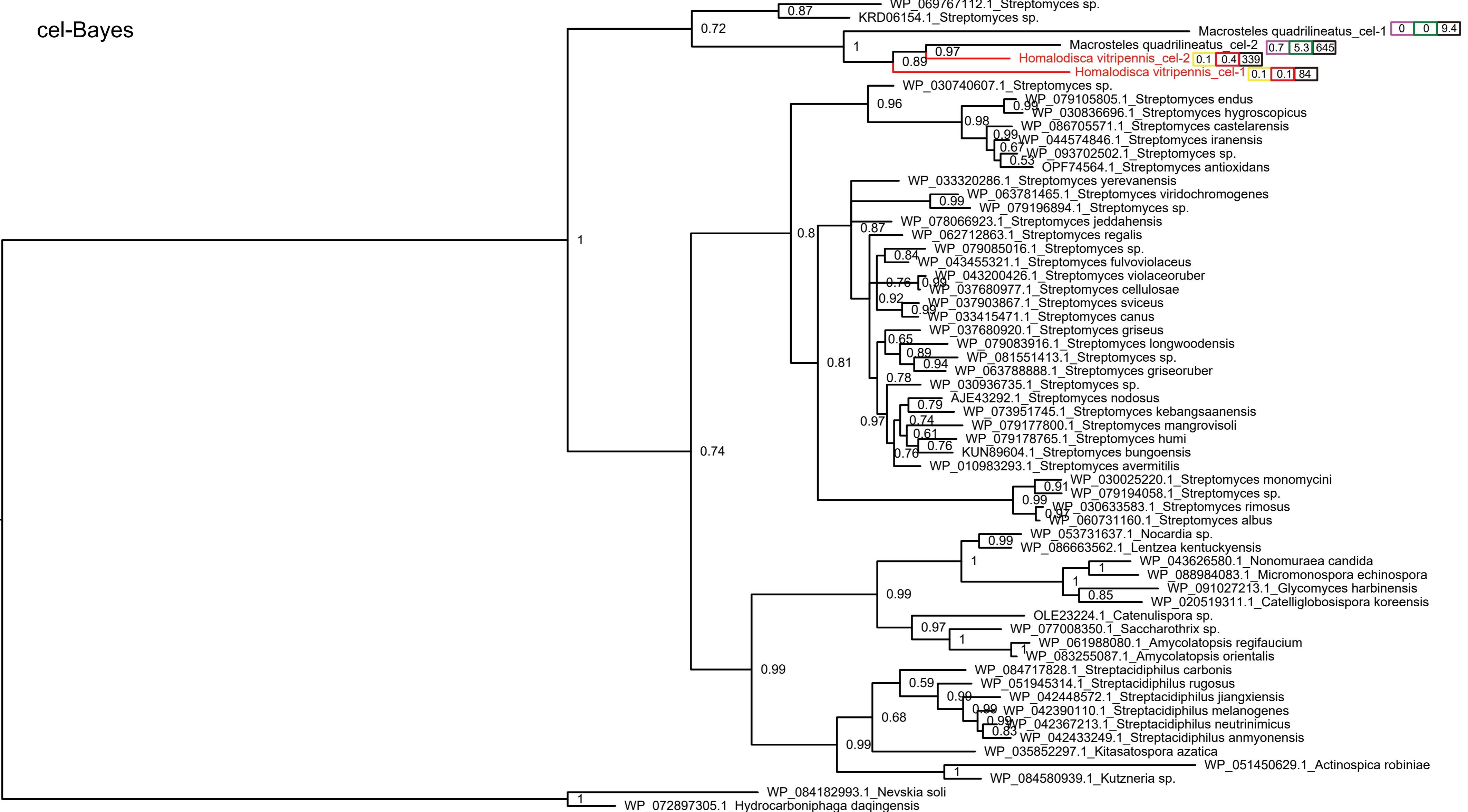
0.4

gh25-ML
Model: WAG+I+G



0.4

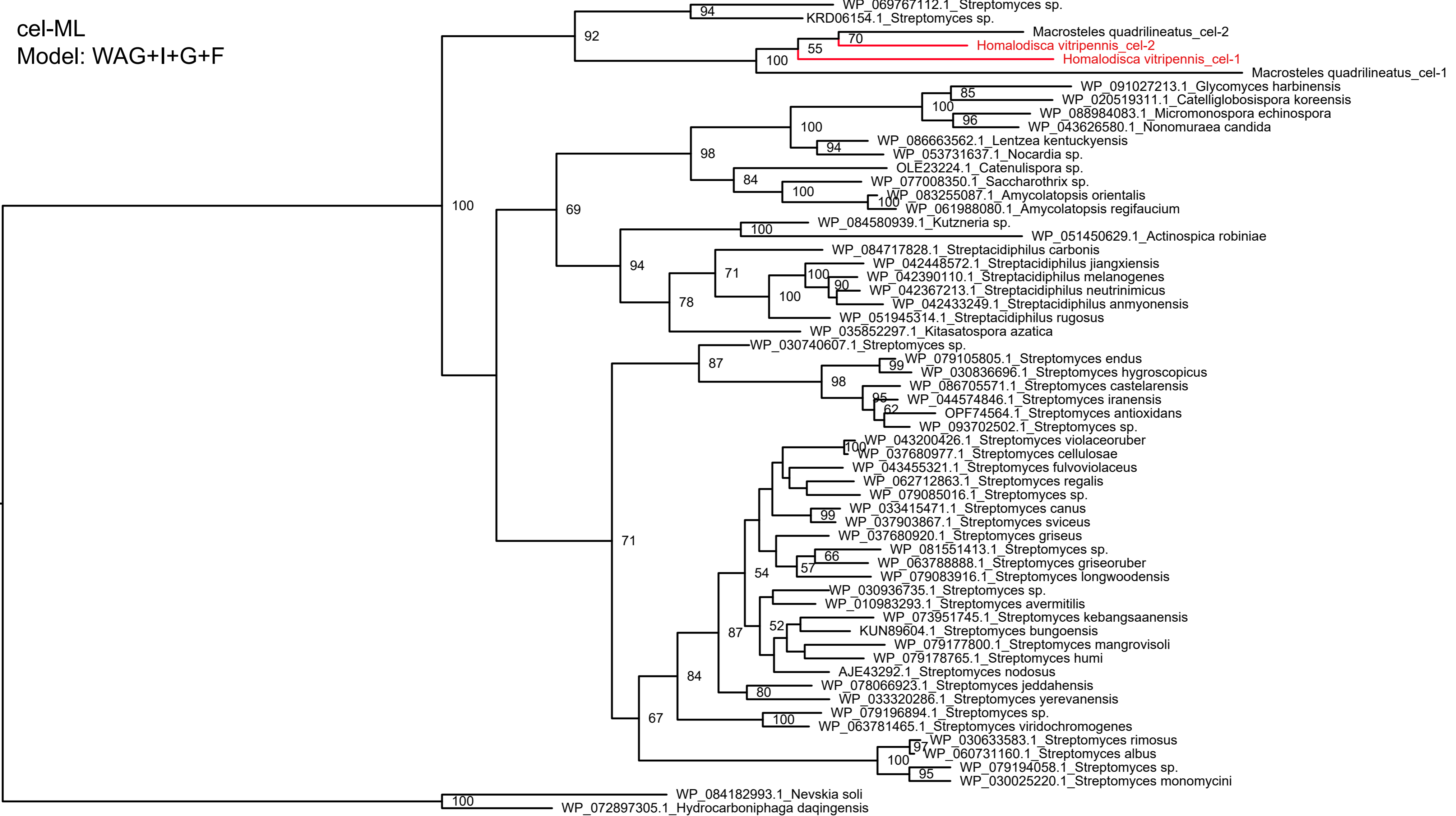
cel-Bayes



0.4

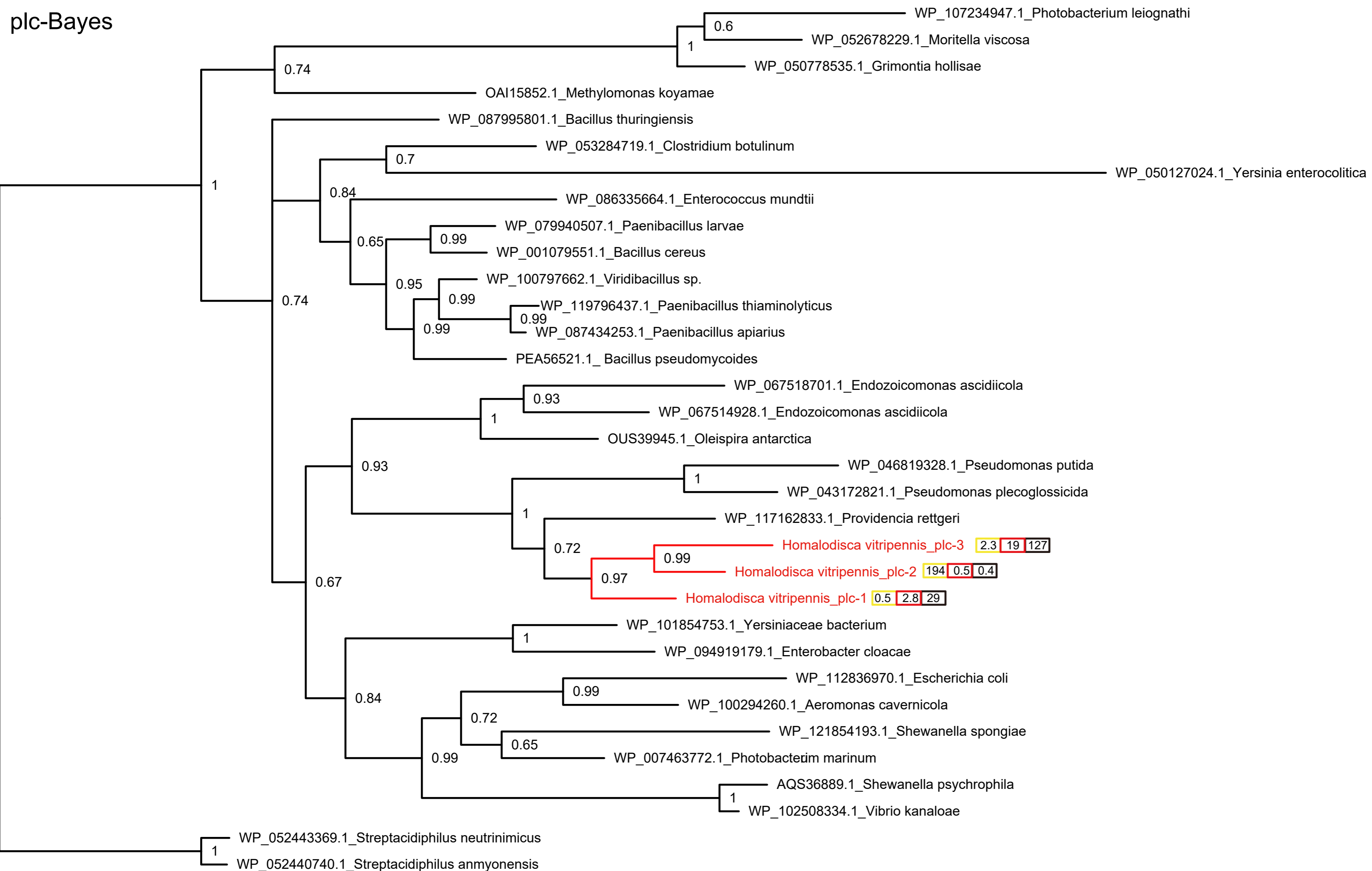
cel-ML

Model: WAG+I+G+F



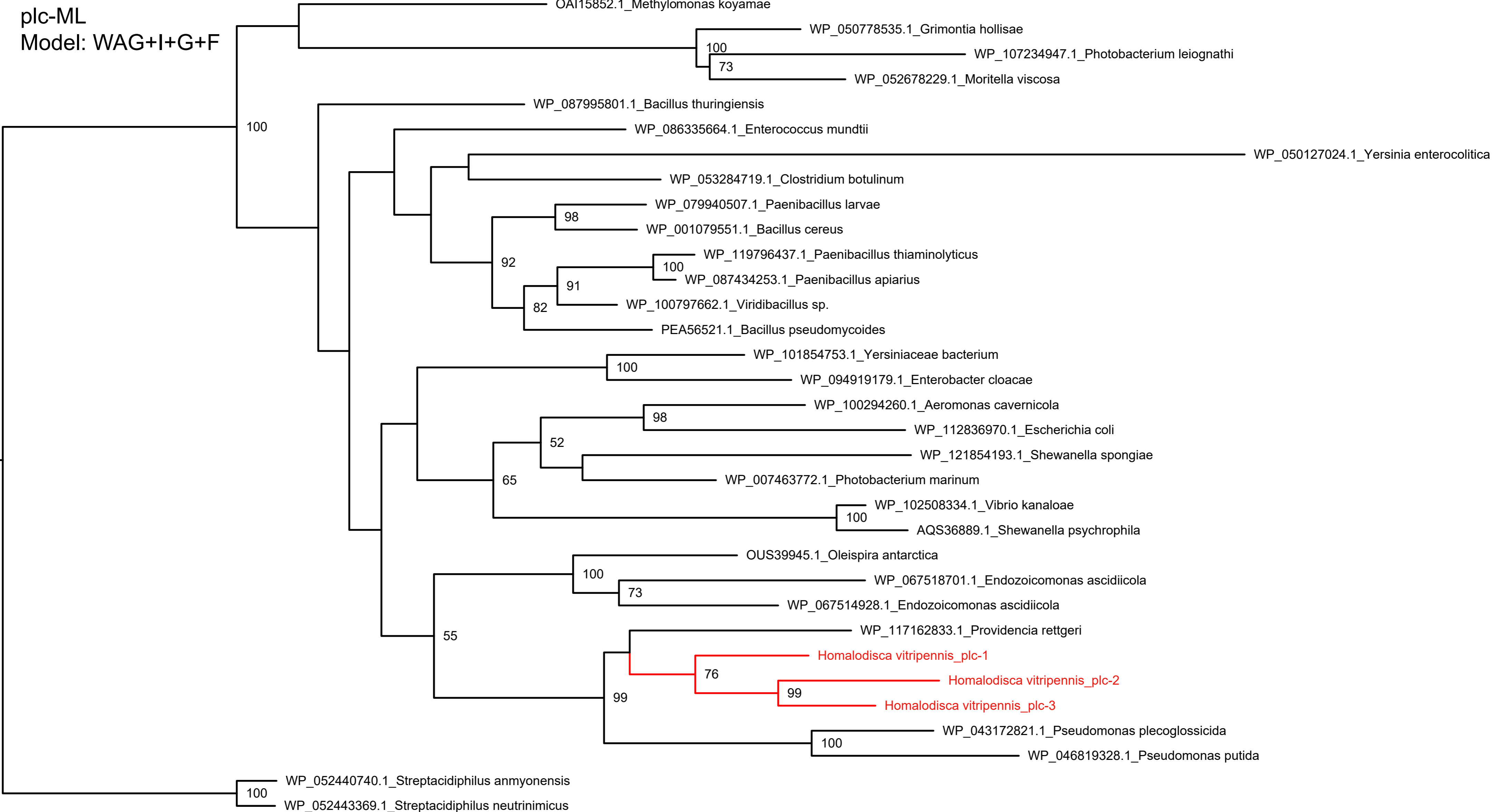
0.2

plc-Bayes



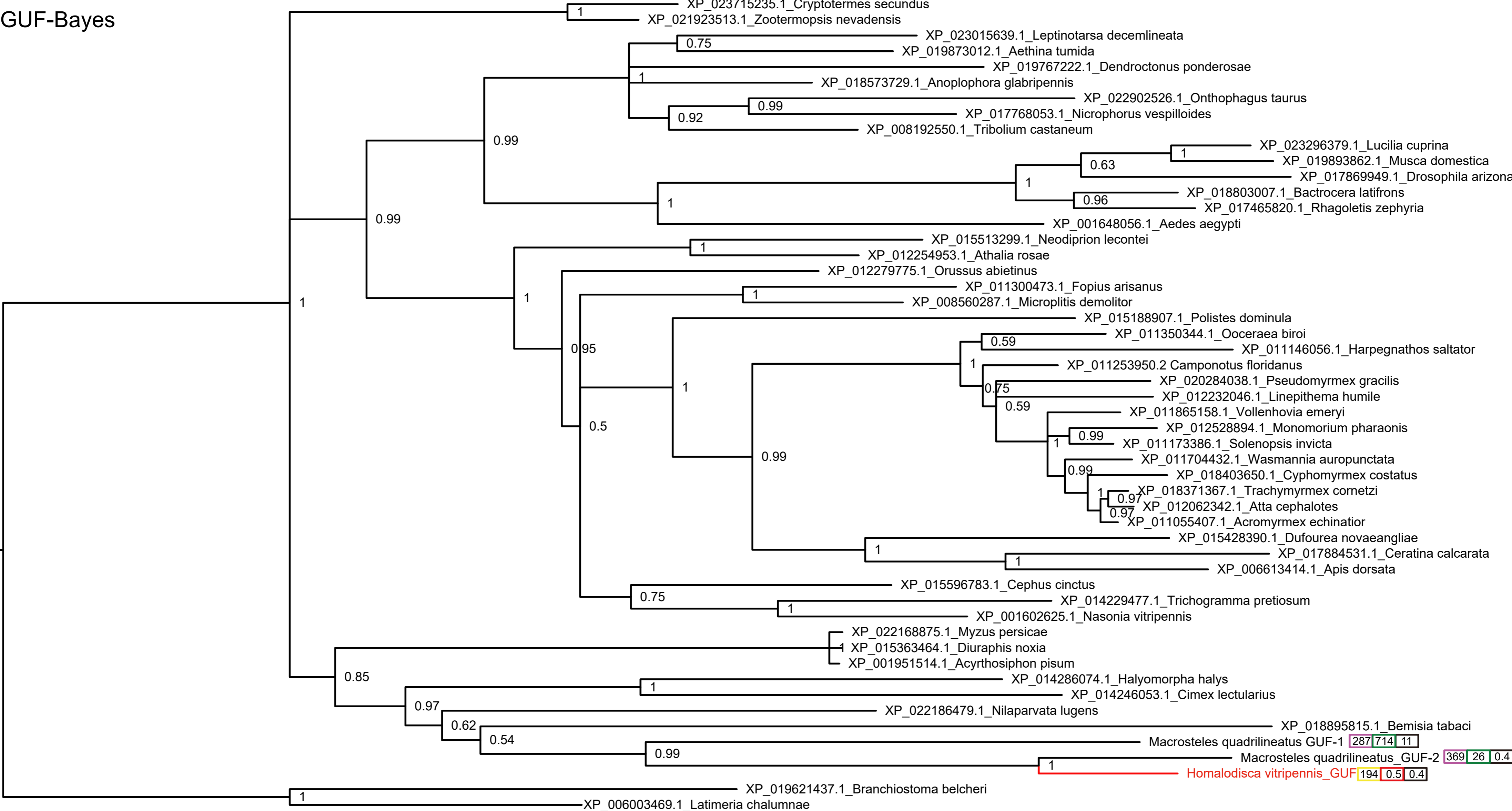
0.4

plc-ML
Model: WAG+I+G+F



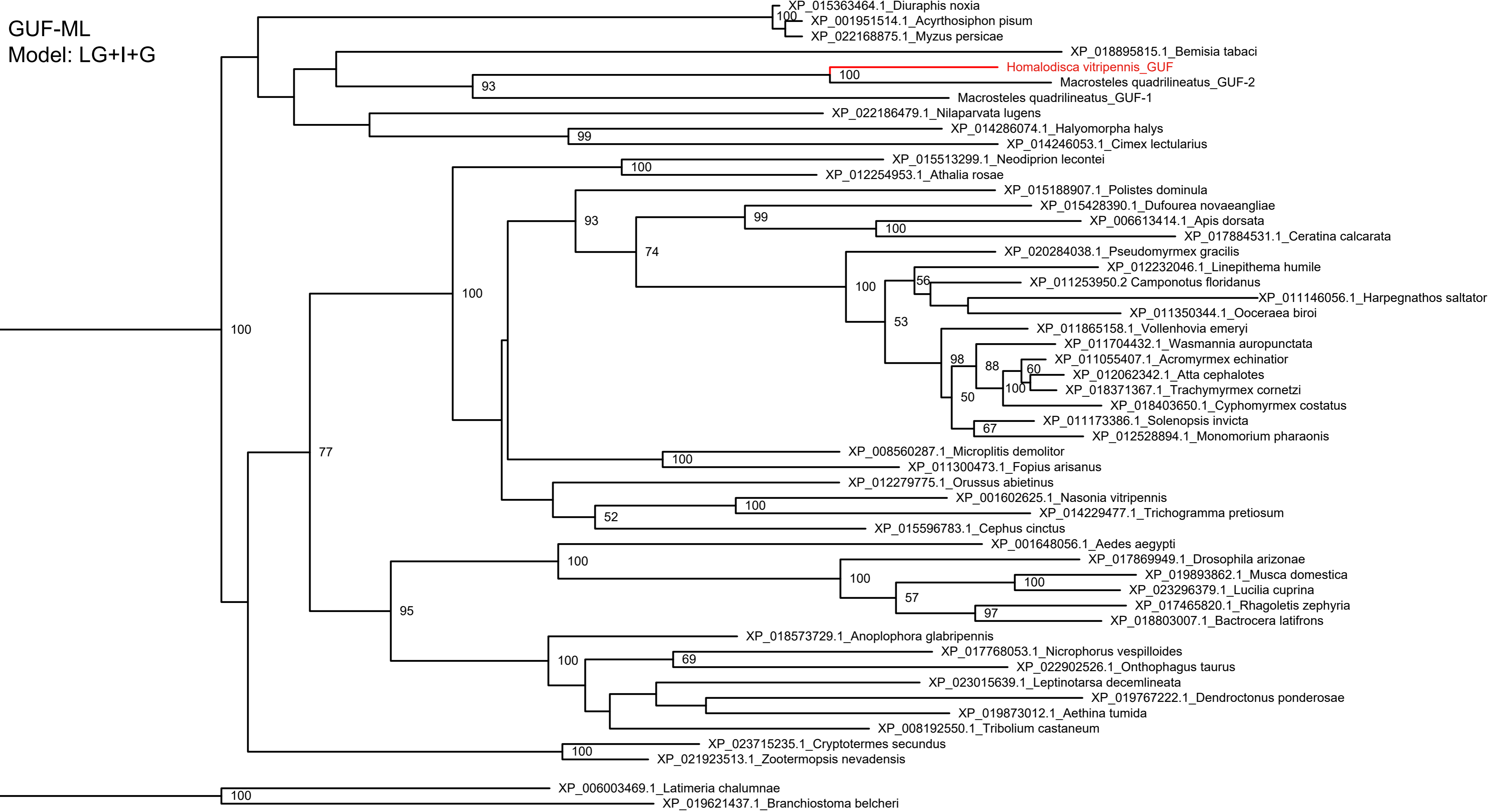
0.3

GUF-Bayes



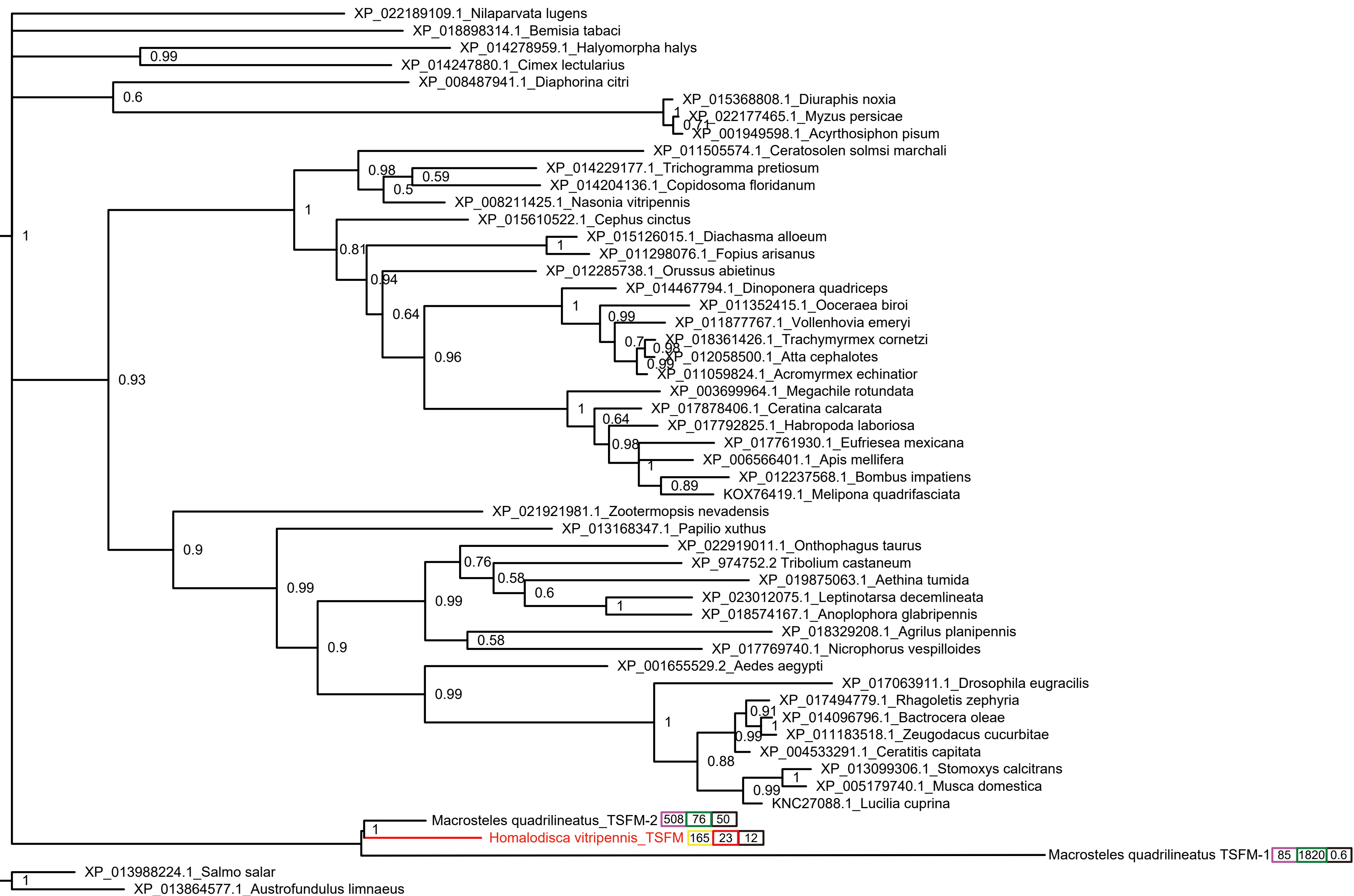
0.2

GUF-ML
Model: LG+I+G



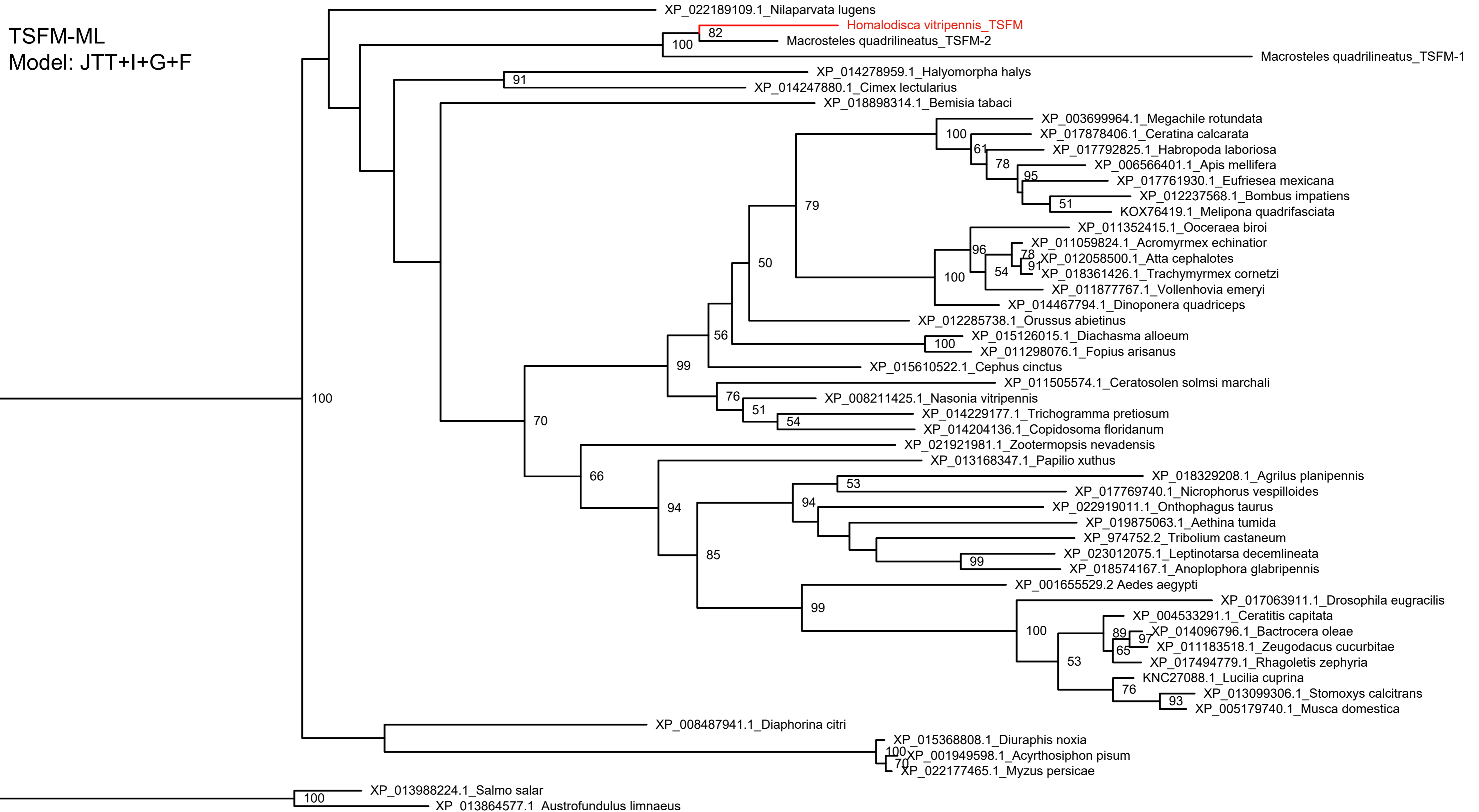
0.2

TSFM-Bayes



0.4

TSFM-ML
Model: JTT+I+G+F



0.3