

Supplementary File S1: Neighbor joining trees and 50% majority-rule bootstrap consensus neighbor joining trees for all loci. Bootstrap trees are based on 1,000 replicates. Trees are rooted with sequences from *Bahiopsis lanata* and/or *B. reticulata*. Population names for *H. petiolaris* and *H. neglectus* sequences correspond to names given in Table 6 of the main text.

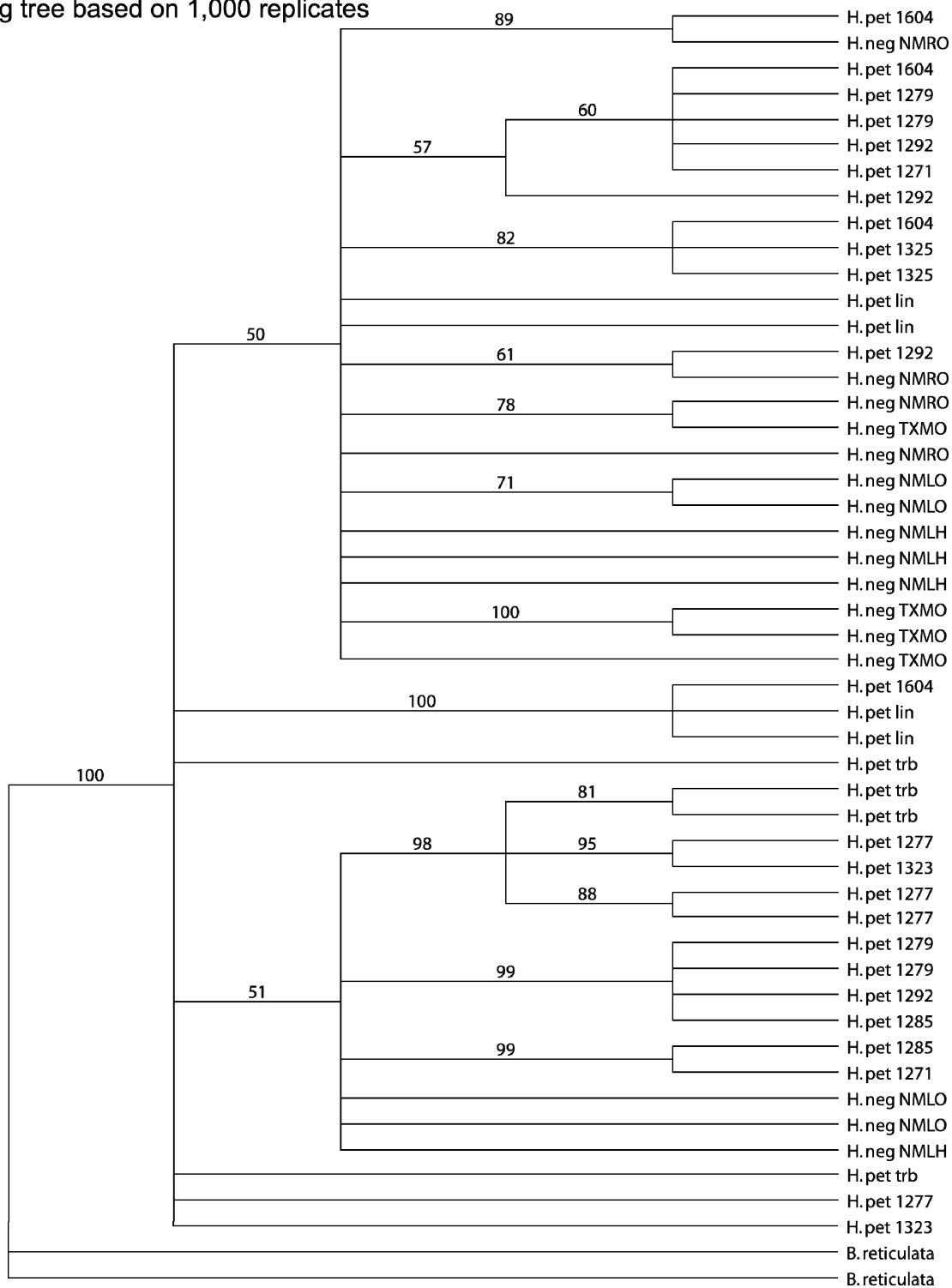
Locus (2213)
neighbor joining tree



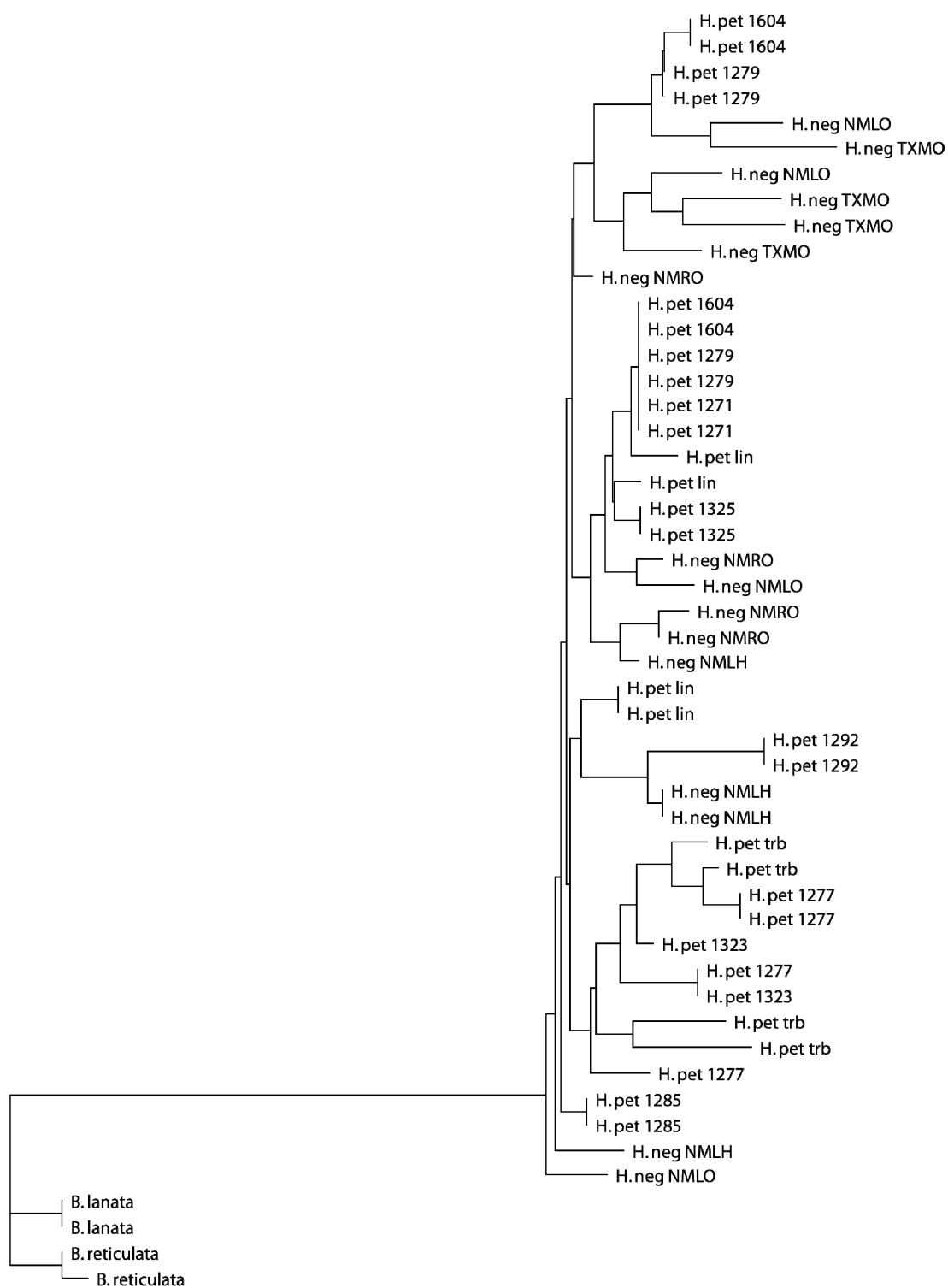
Locus (2213)

50% majority-rule bootstrap consensus neighbor

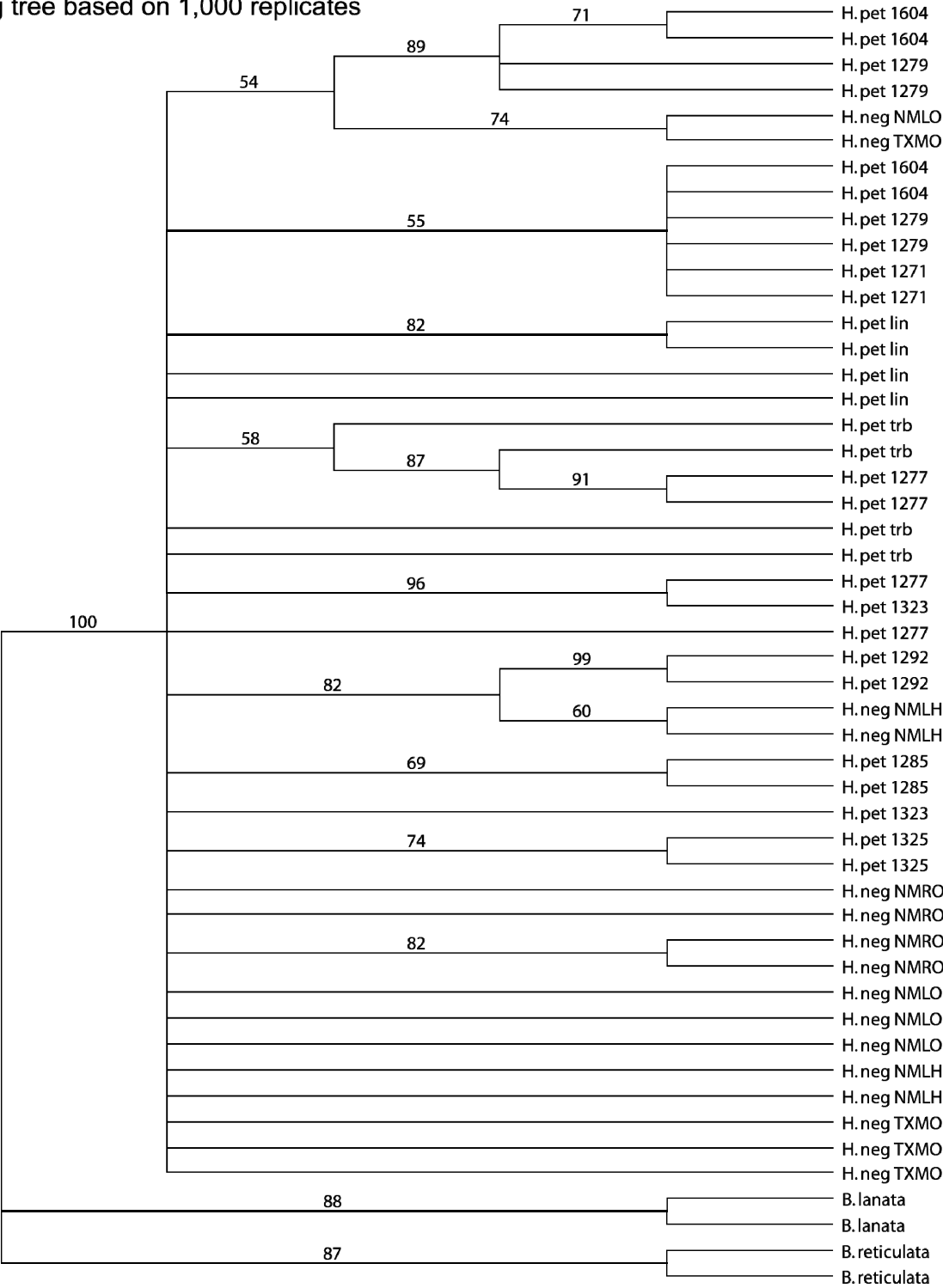
joining tree based on 1,000 replicates



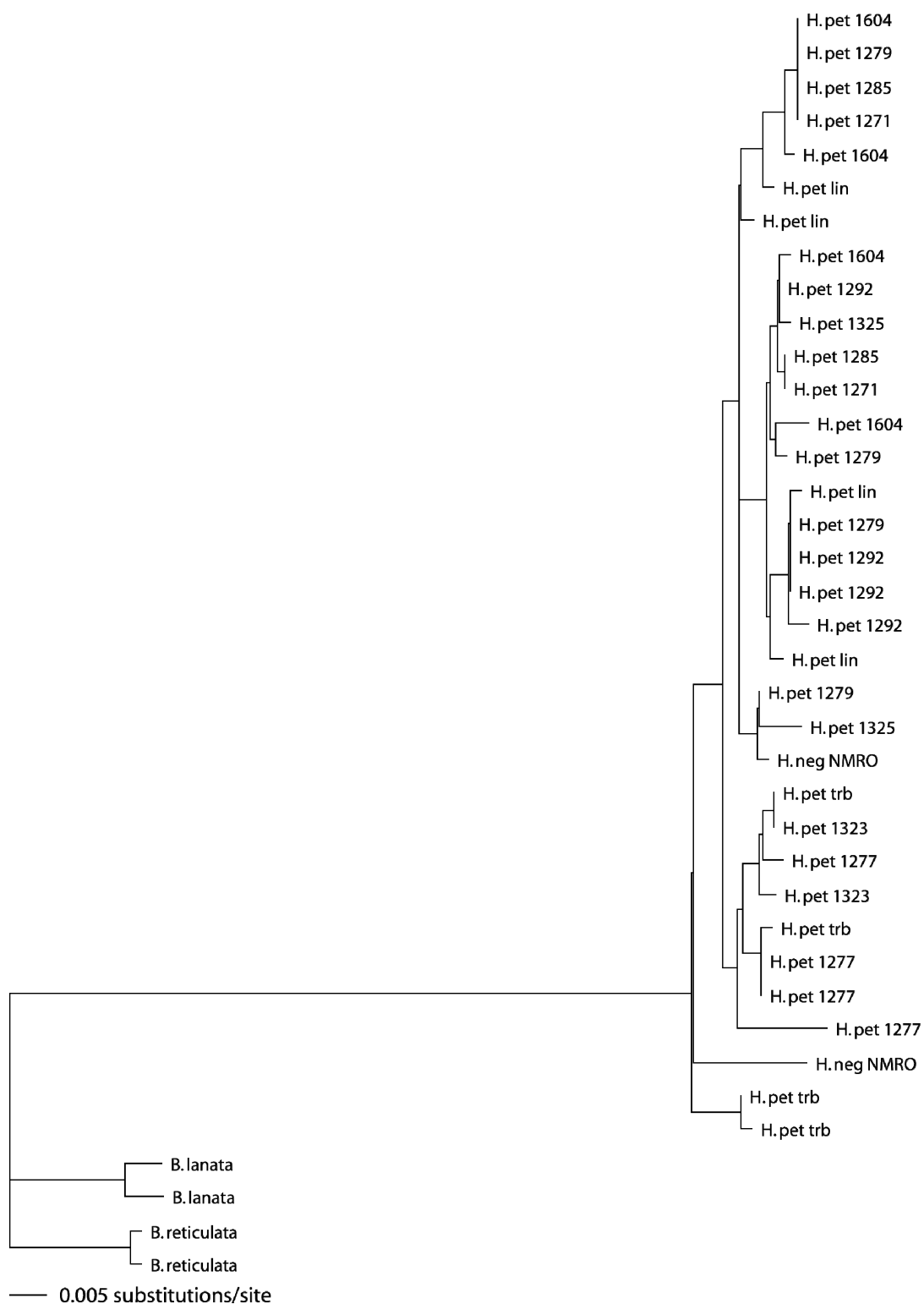
Locus JLS244
neighbor joining tree



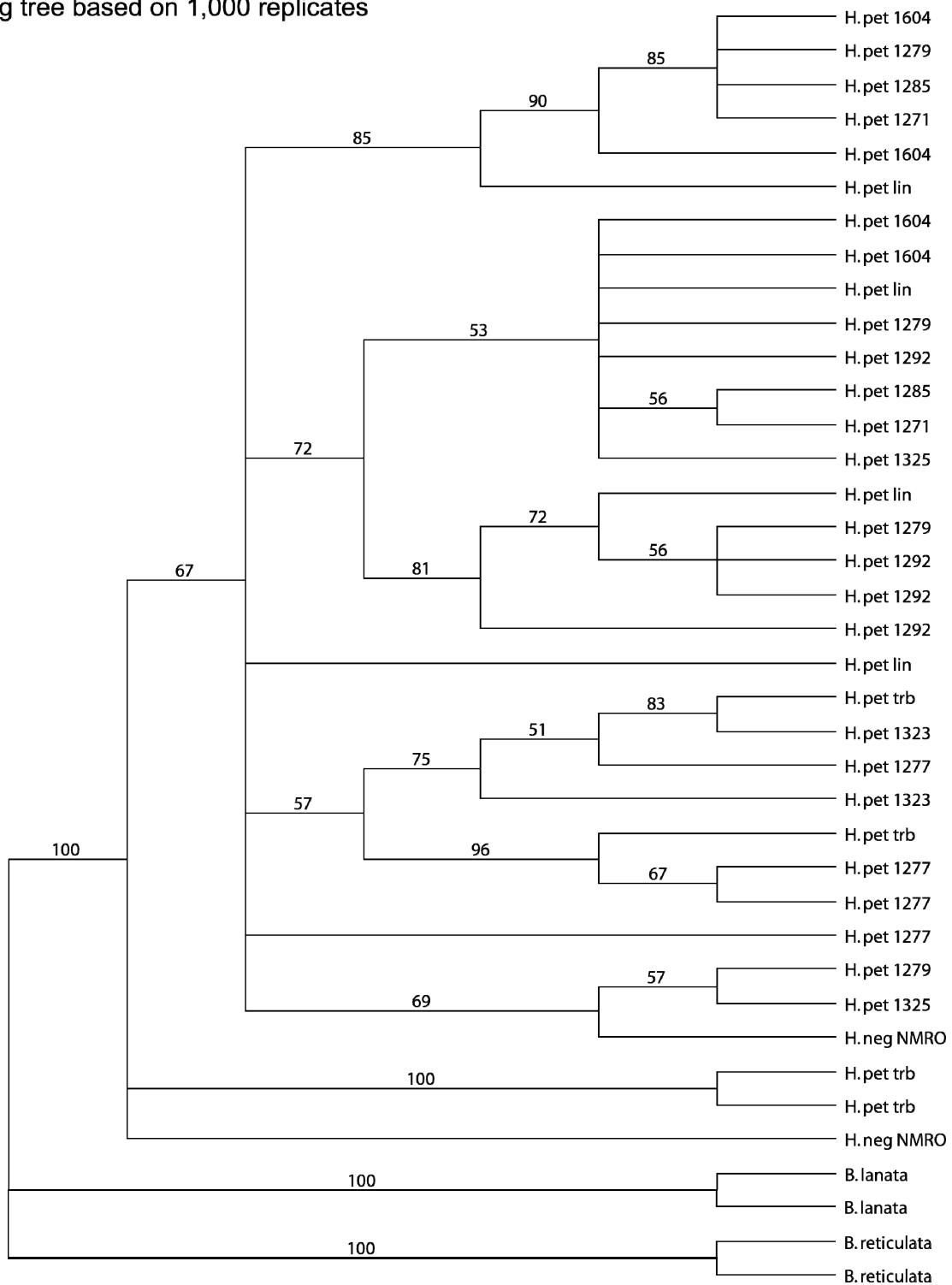
Locus JLS244
50% majority-rule bootstrap consensus neighbor
joining tree based on 1,000 replicates



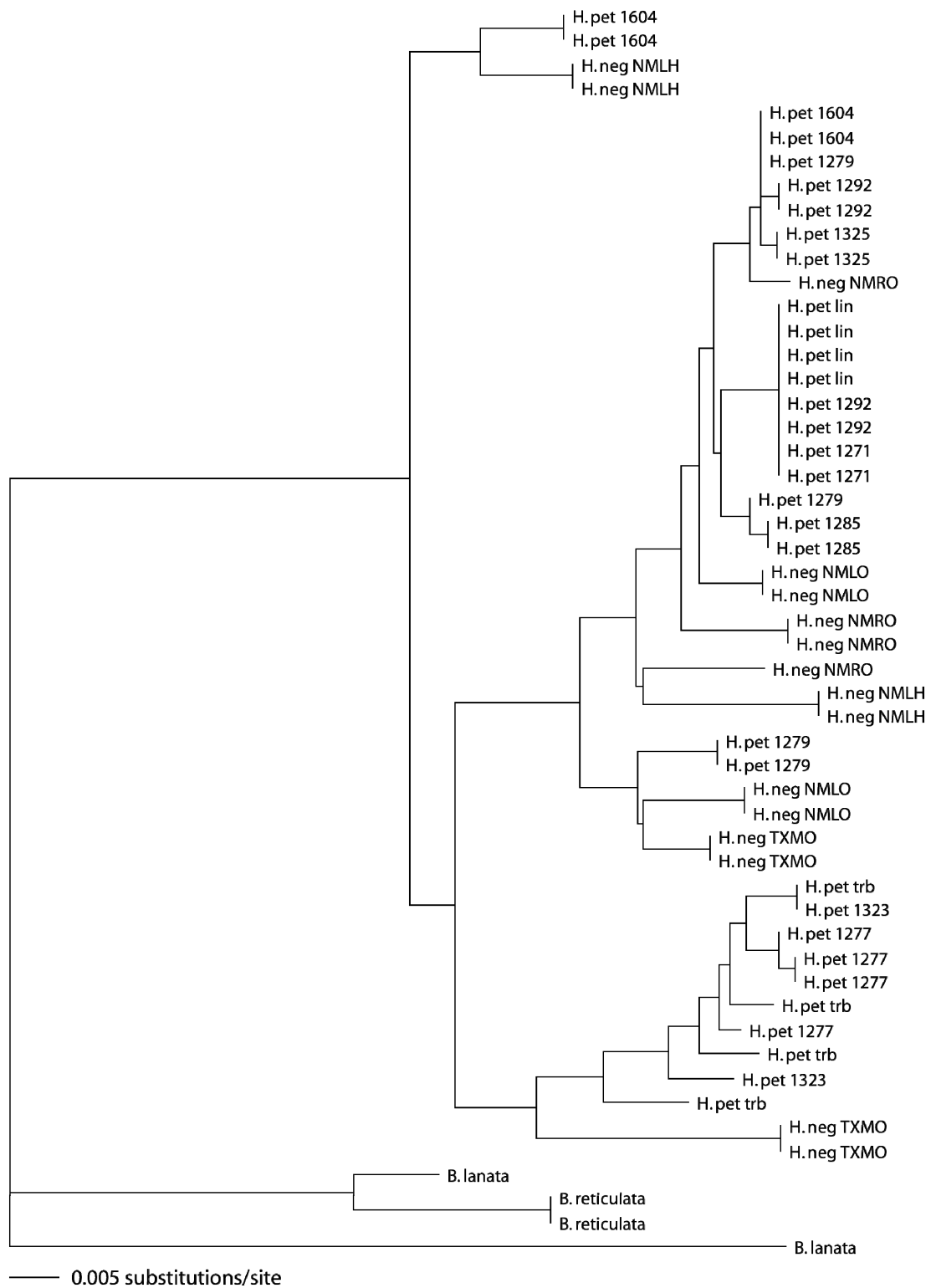
Locus JLS720
neighbor joining tree



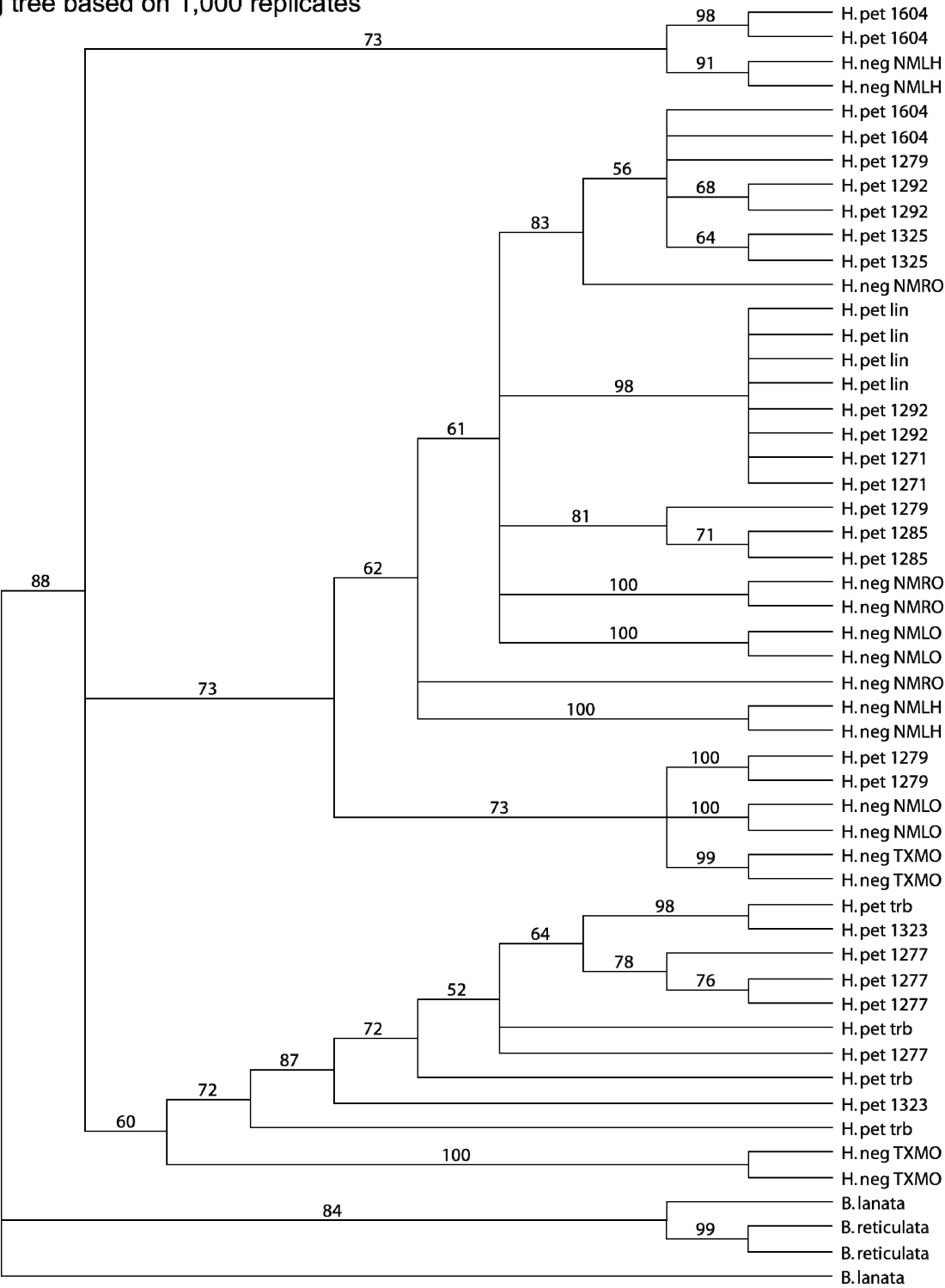
50% majority-rule bootstrap consensus neighbor joining tree based on 1,000 replicates



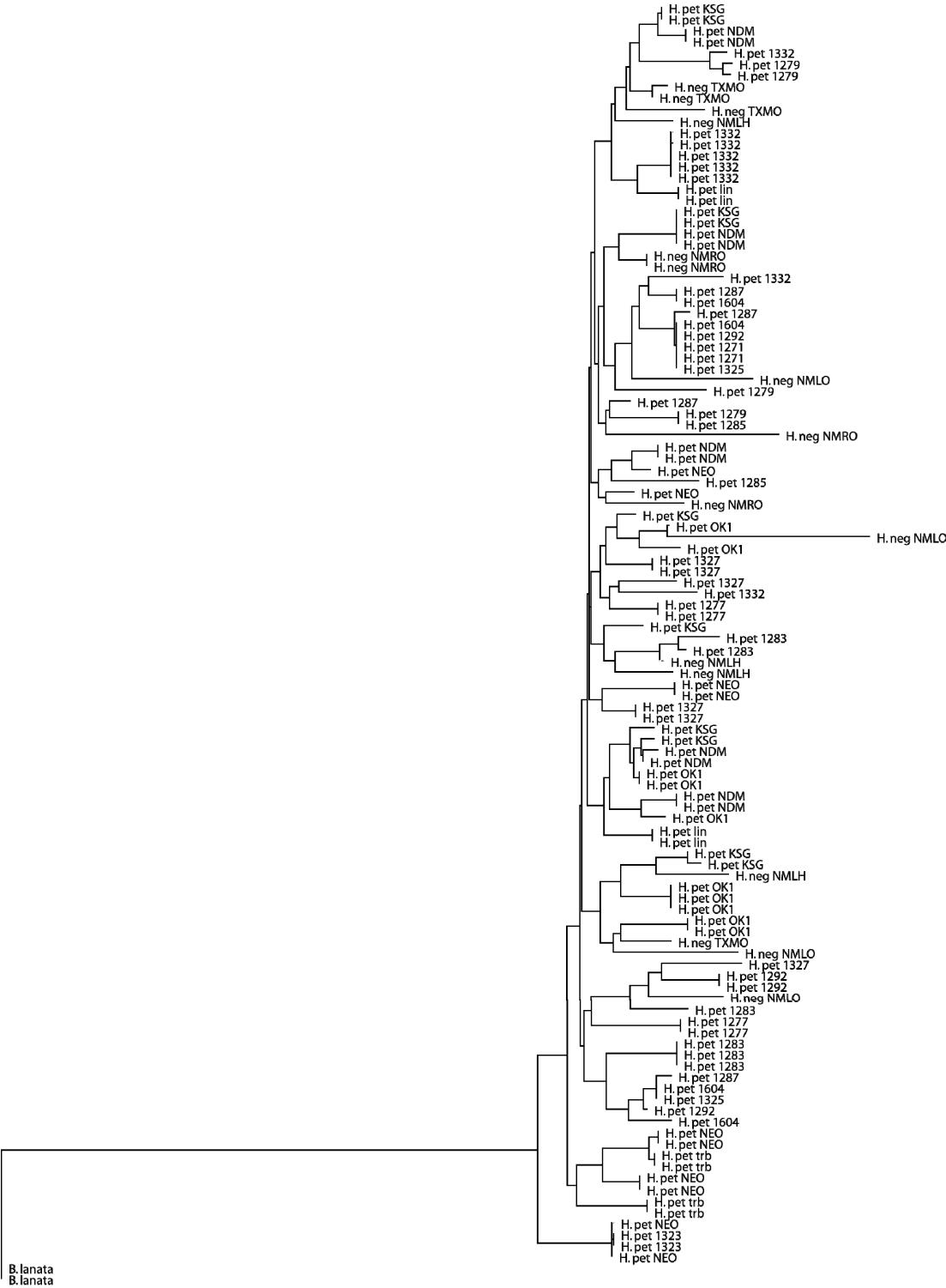
Locus JLS810R1
neighbor joining tree



Locus JLS810R1
50% majority-rule bootstrap consensus neighbor
joining tree based on 1,000 replicates

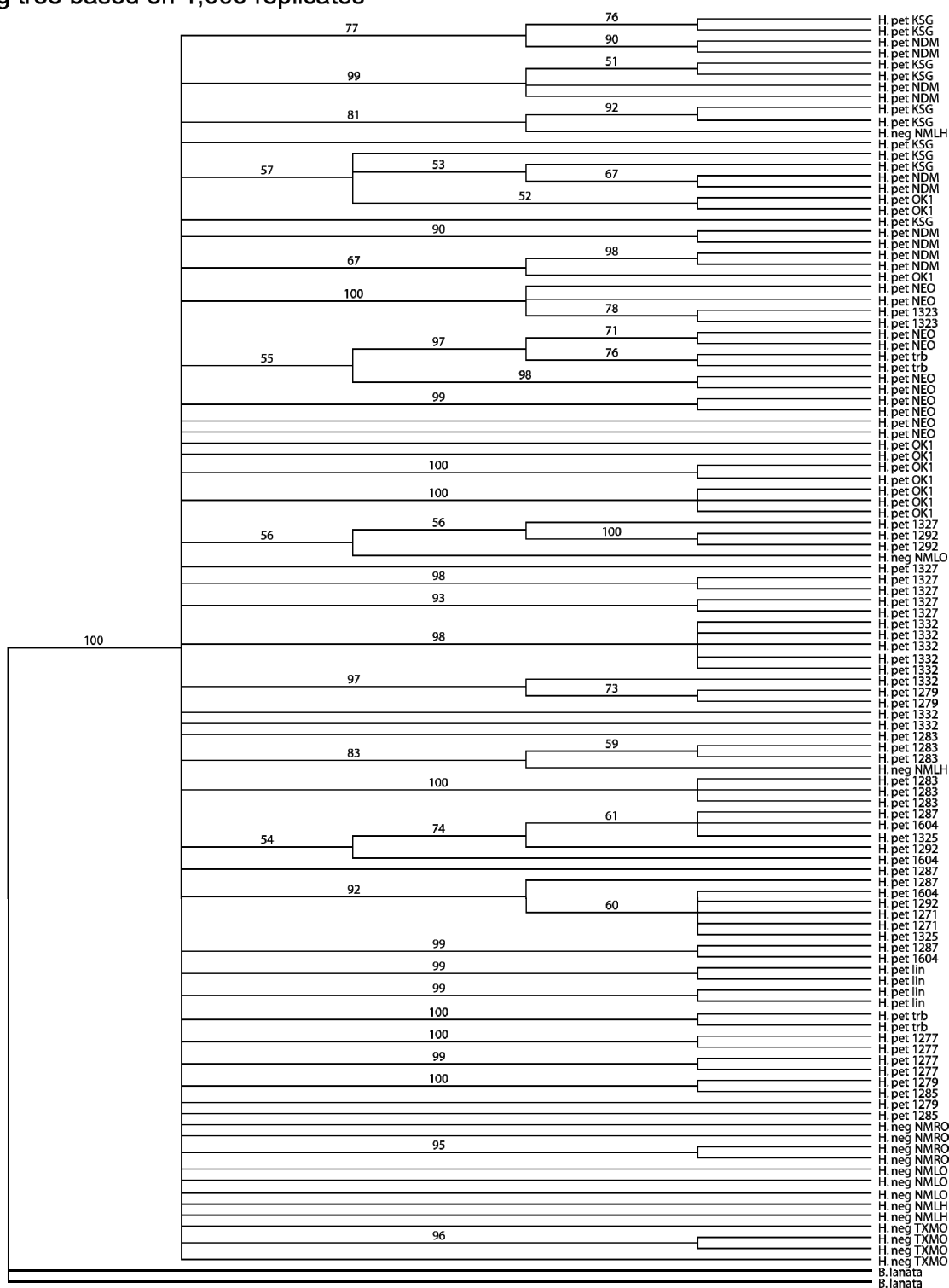


Locus JLS1040
neighbor joining tree

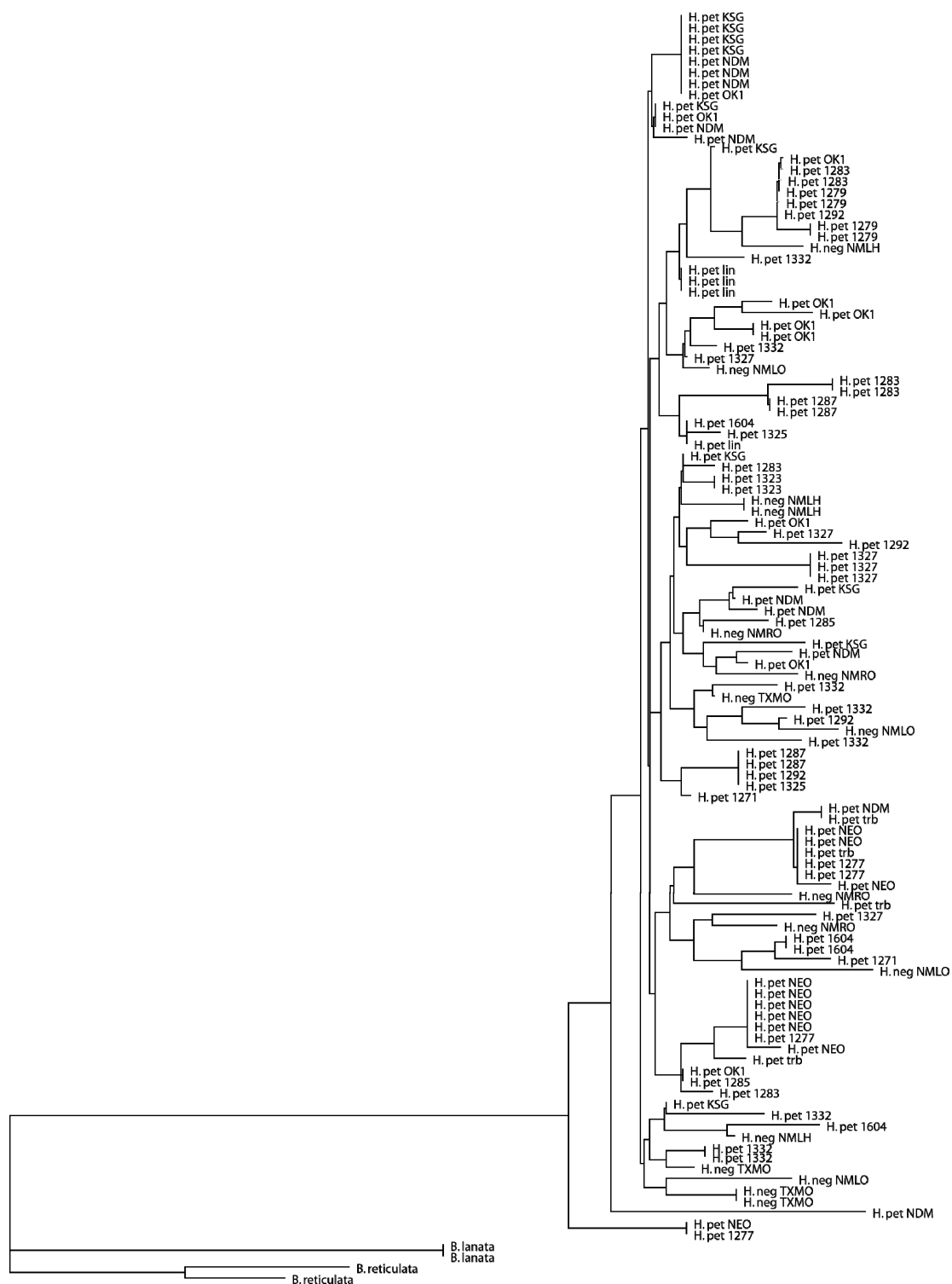


– 0.001 substitutions/site

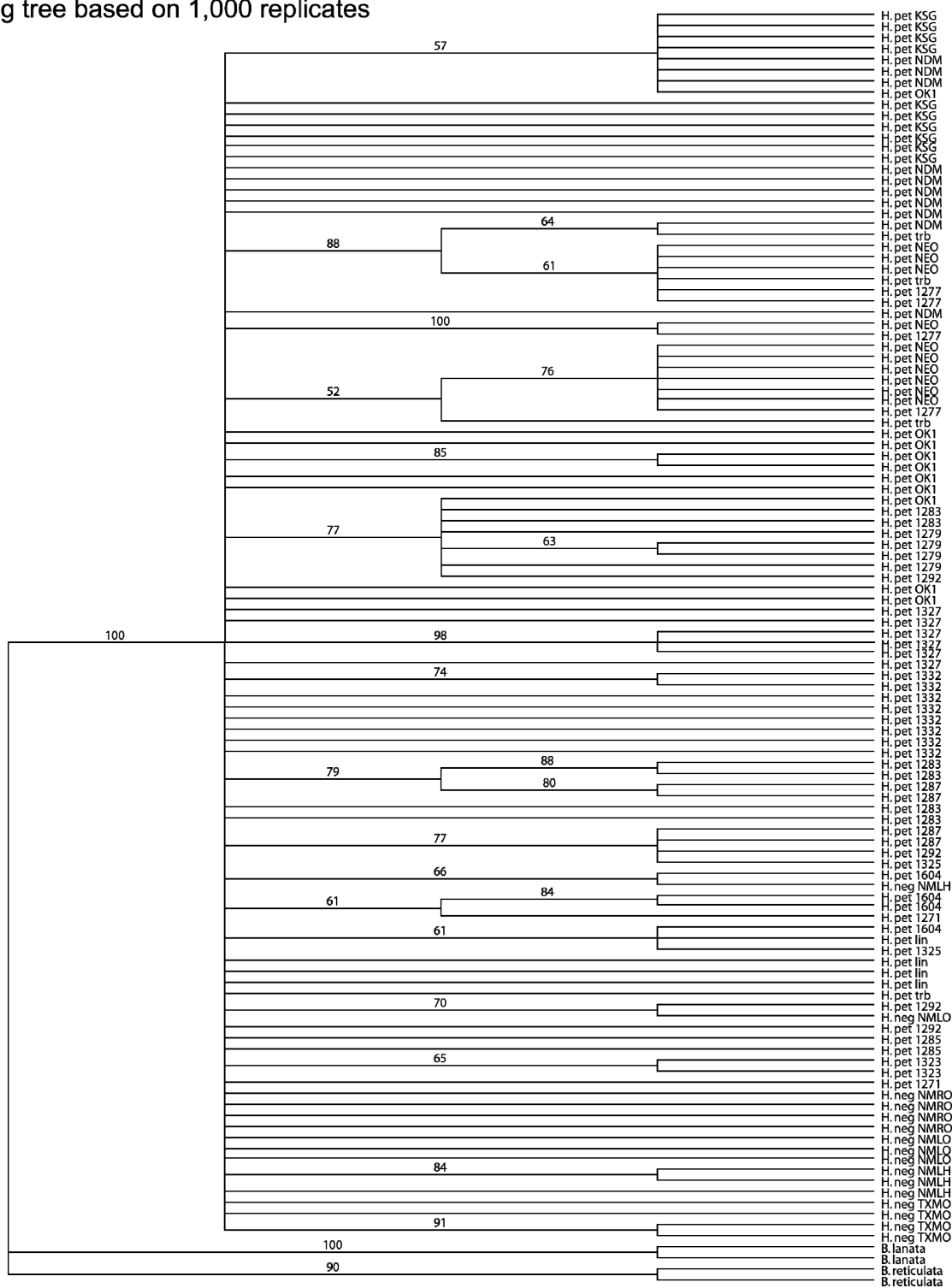
50% majority-rule bootstrap consensus neighbor
joining tree based on 1,000 replicates



Locus JLS1615
neighbor joining tree



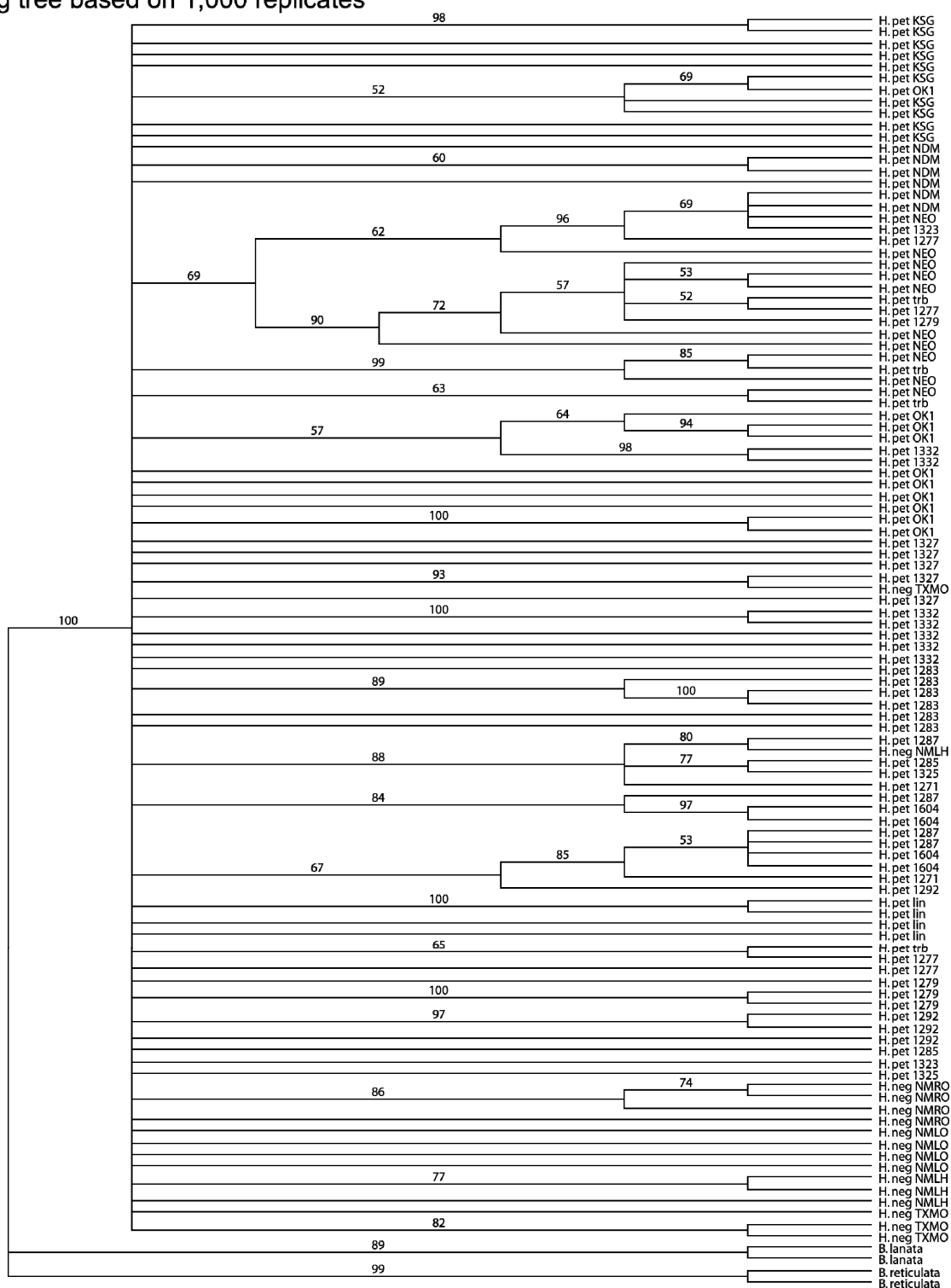
50% majority-rule bootstrap consensus neighbor joining tree based on 1,000 replicates



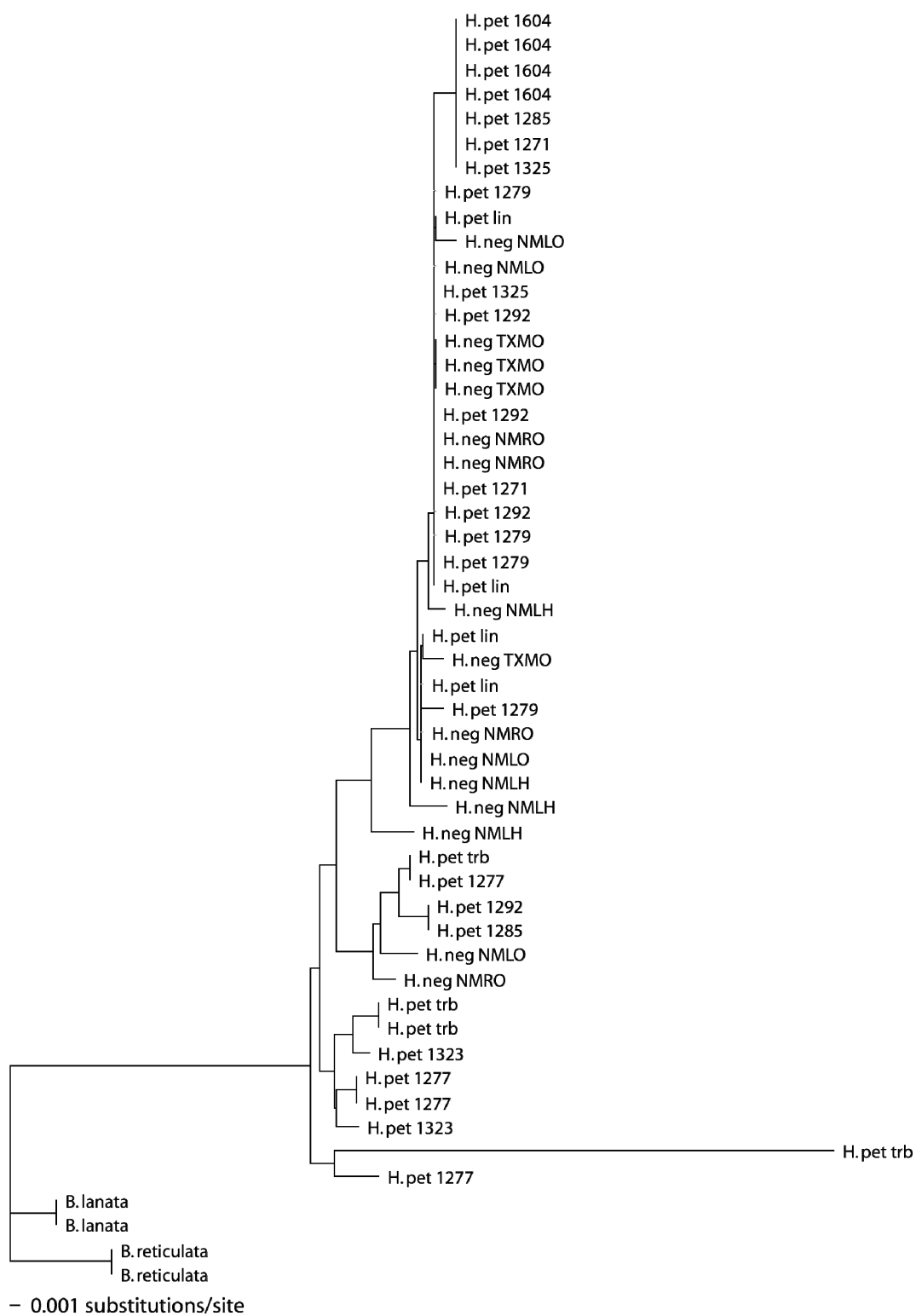
Locus JLS1747
neighbor joining tree



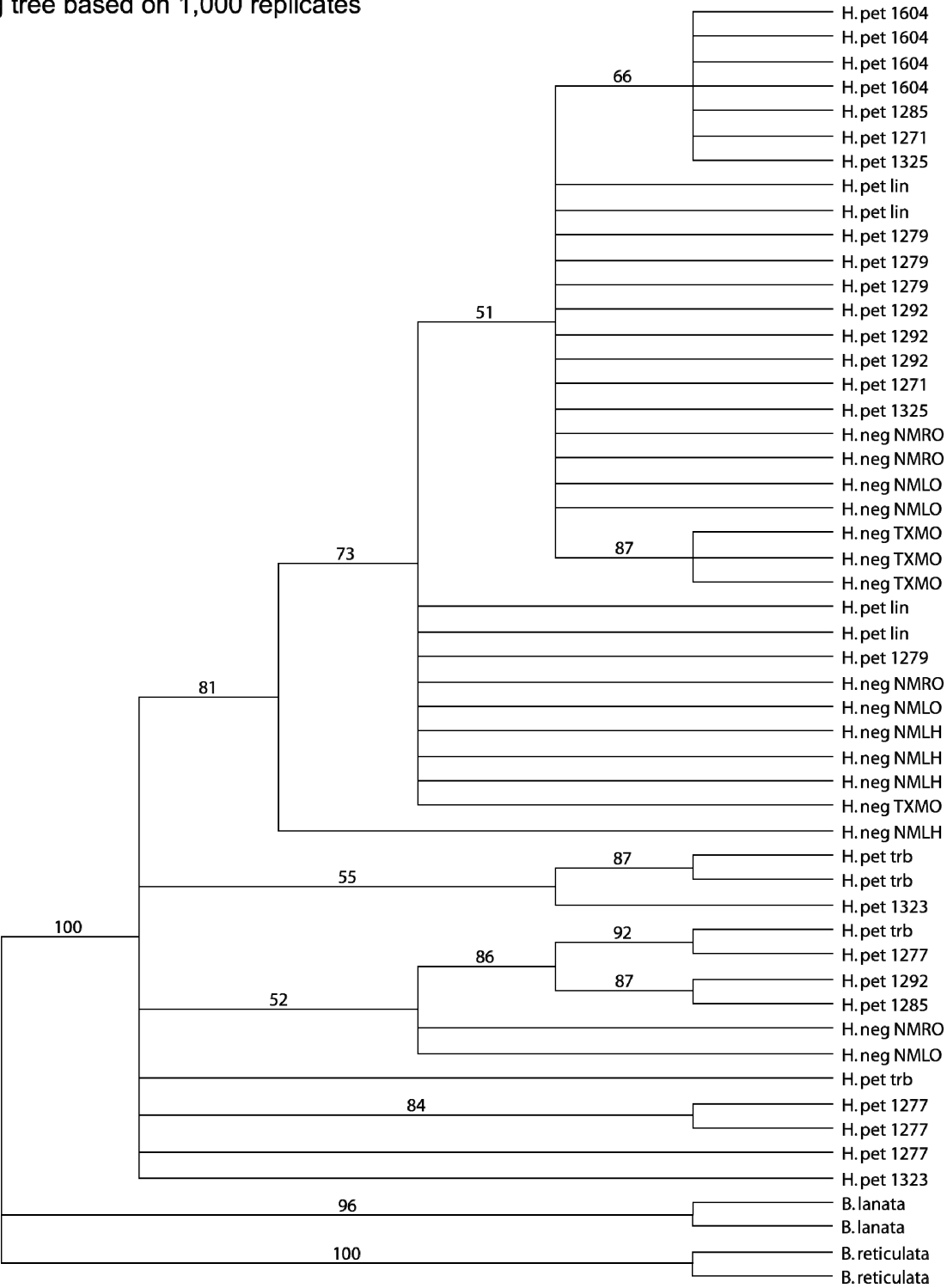
50% majority-rule bootstrap consensus neighbor joining tree based on 1,000 replicates



Locus JLS1953
neighbor joining tree



Locus JLS1953
50% majority-rule bootstrap consensus neighbor
joining tree based on 1,000 replicates



Locus JLS2899
neighbor joining tree



Locus JLS2899
50% majority-rule bootstrap consensus neighbor
joining tree based on 1,000 replicates

