

Figure S5a (see legend below figure)

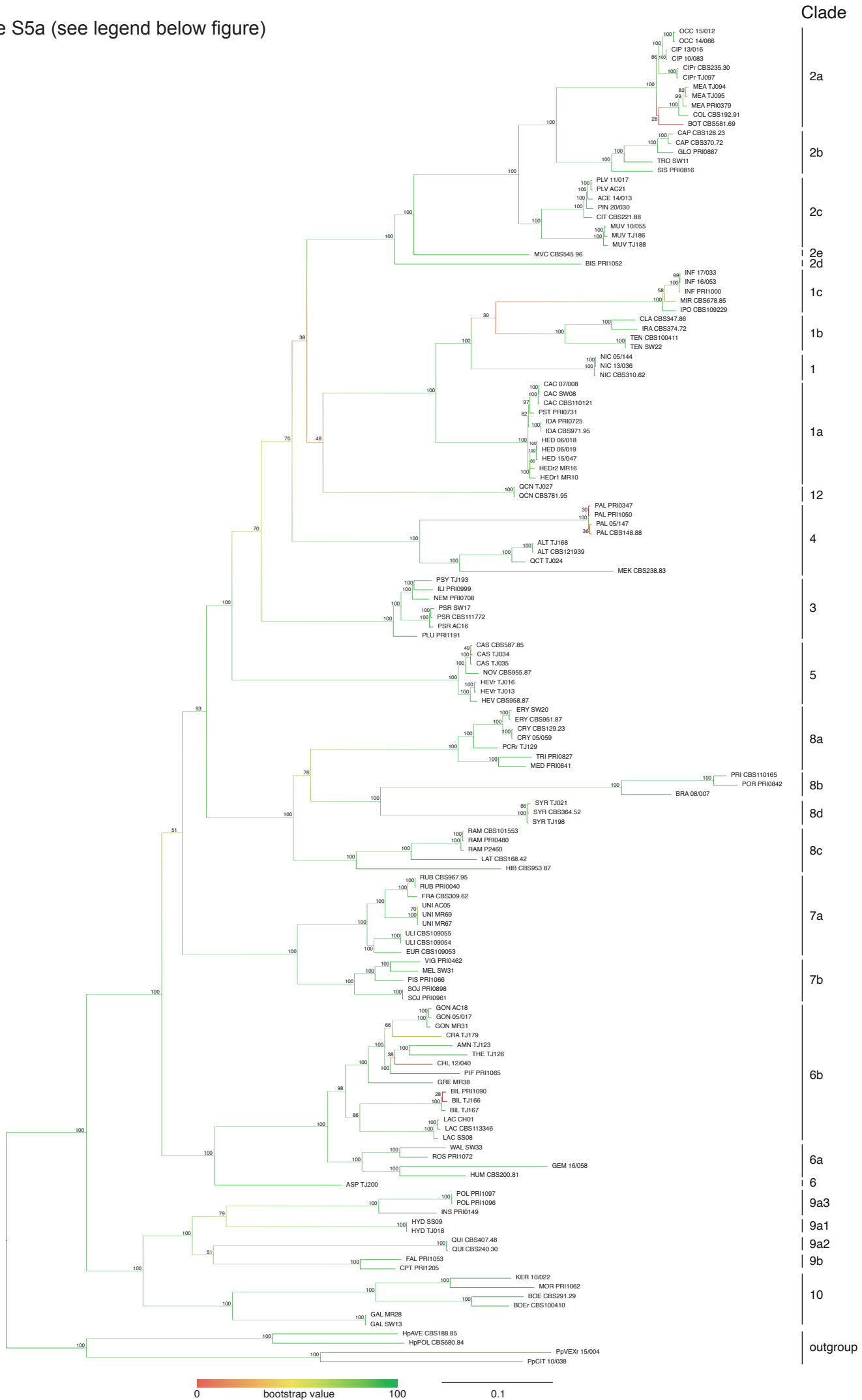


Figure S5a

Concatenation-based phylogenomic tree using RAxML on 61111 SNPs from 1610 loci that occur in 30% of a set of representative *Phytophthora* isolates from all clades. Numbers on branches indicate bootstrap values.

Figure S5b (see legend below figure)

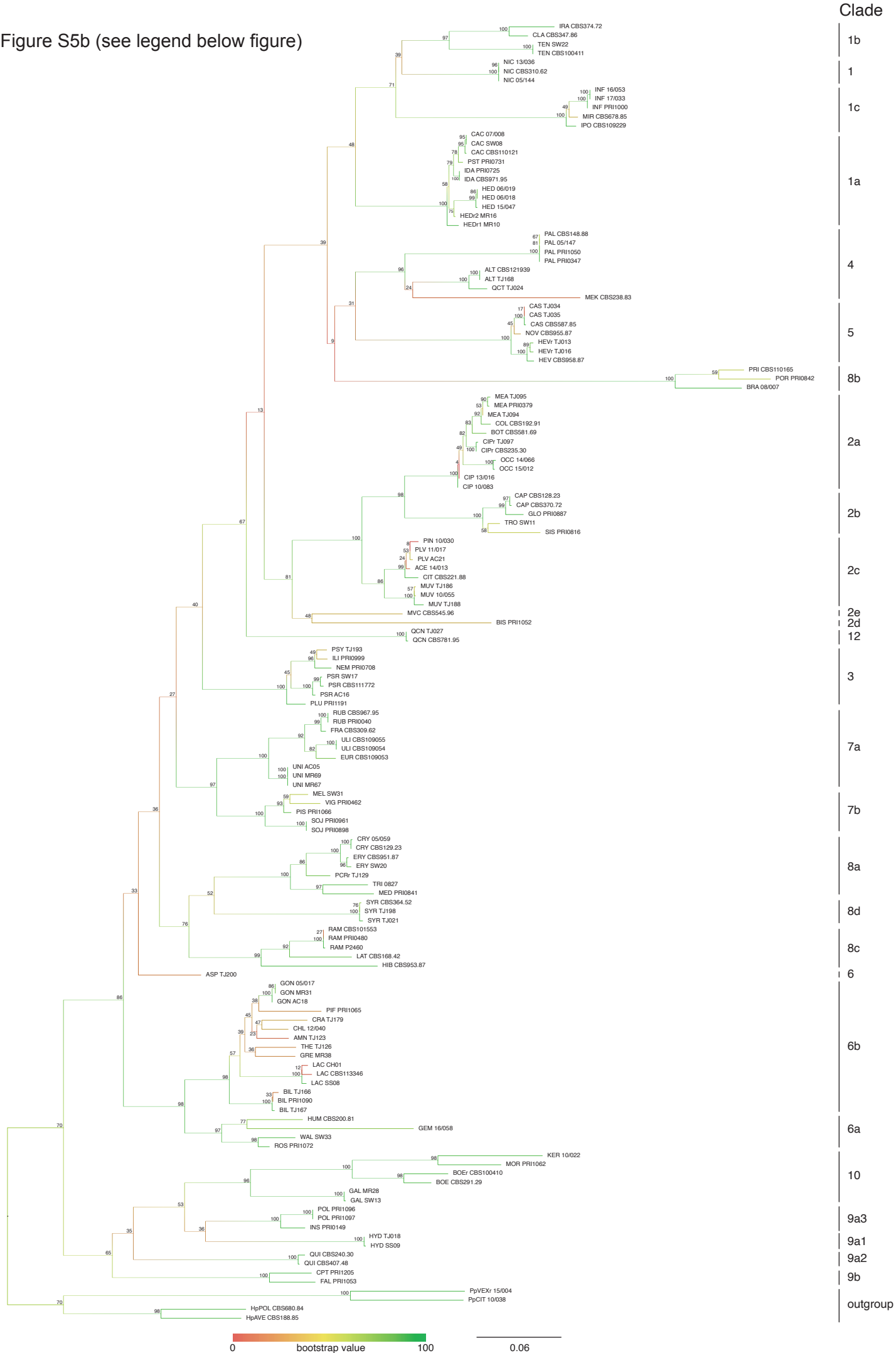


Figure S5b

Concatenation-based phylogenomic tree using RAxML on 1062 SNPs from 29 loci that occur in 80% of a set of representative *Phytophthora* isolates of all clades. Numbers on branches indicate bootstrap values.

Figure S5c (see legend below figure)

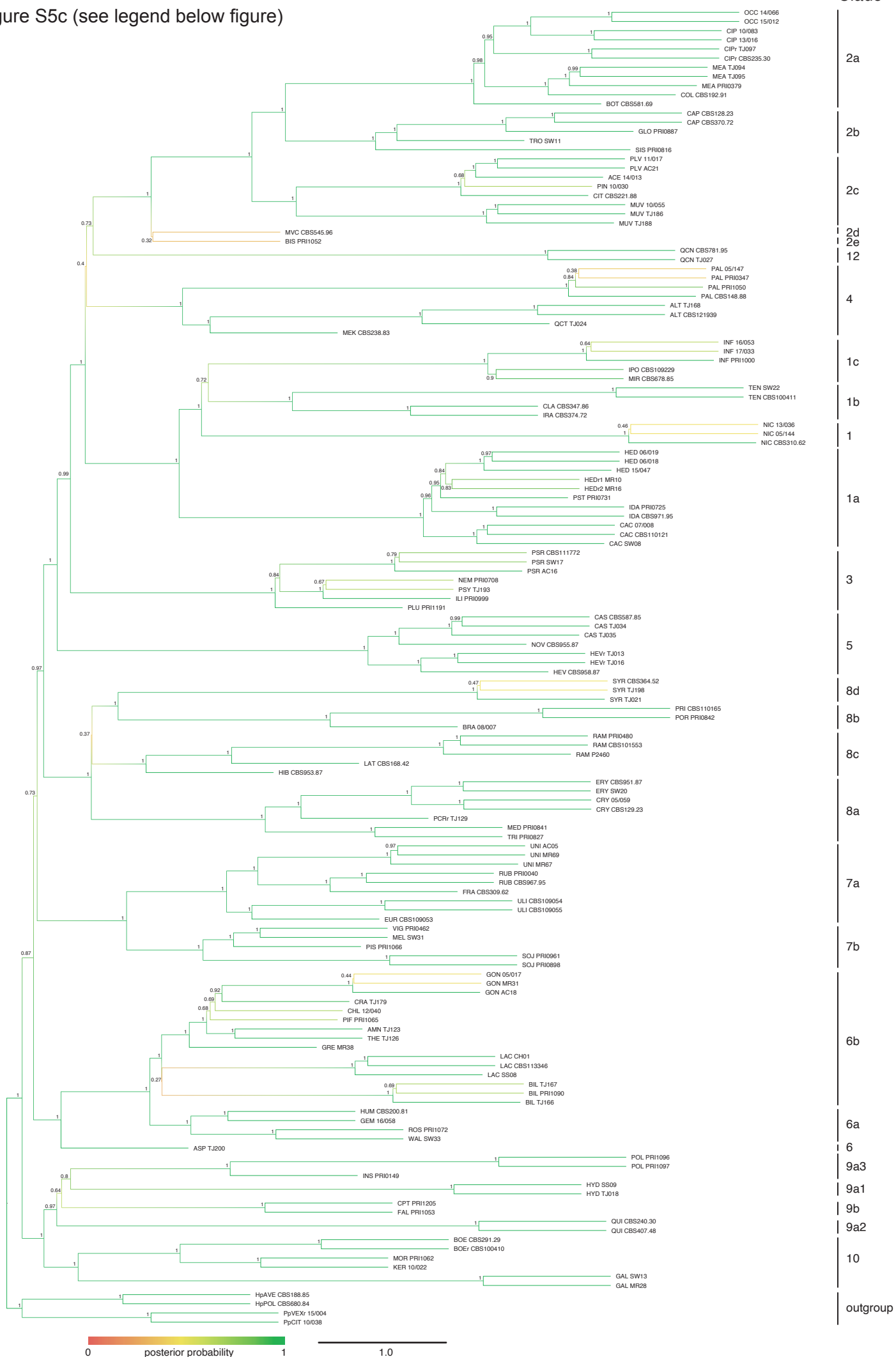


Figure S5c

Coalescence-based phylogenomic tree using ASTRALIII on 61111 SNPs from 1610 loci that occur in 30% of a set of representative *Phytophthora* isolates of all clades. Numbers on branches indicate bootstrap values.

Figure S5d (see legend below figure)

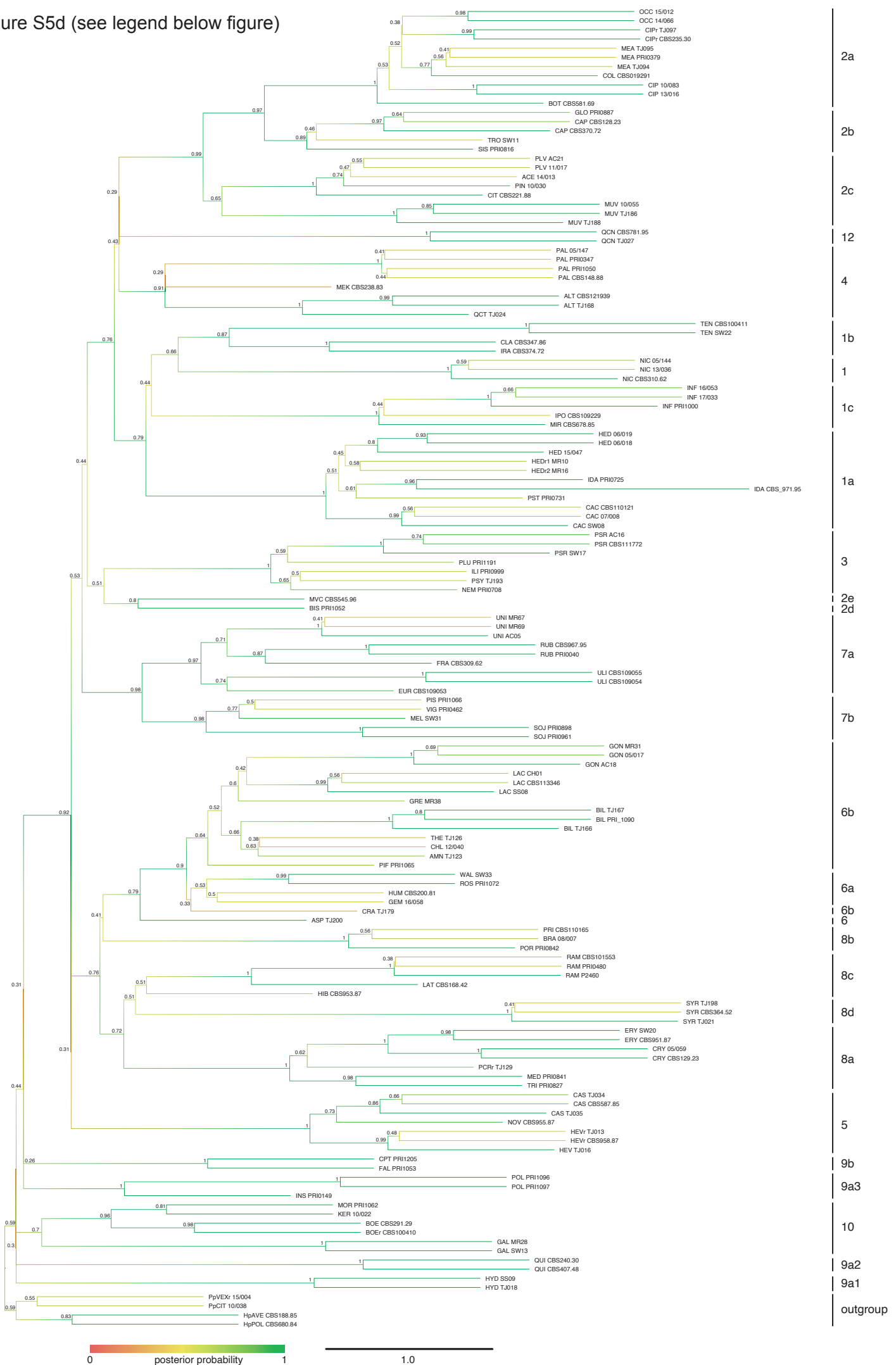


Figure S5d

Coalescence-based phylogenomic tree using ASTRALIII on 1062 SNPs from 29 loci that occur in 80% of a set of representative *Phytophthora* isolates of all clades. Numbers on branches indicate bootstrap values.