a)
Clade A

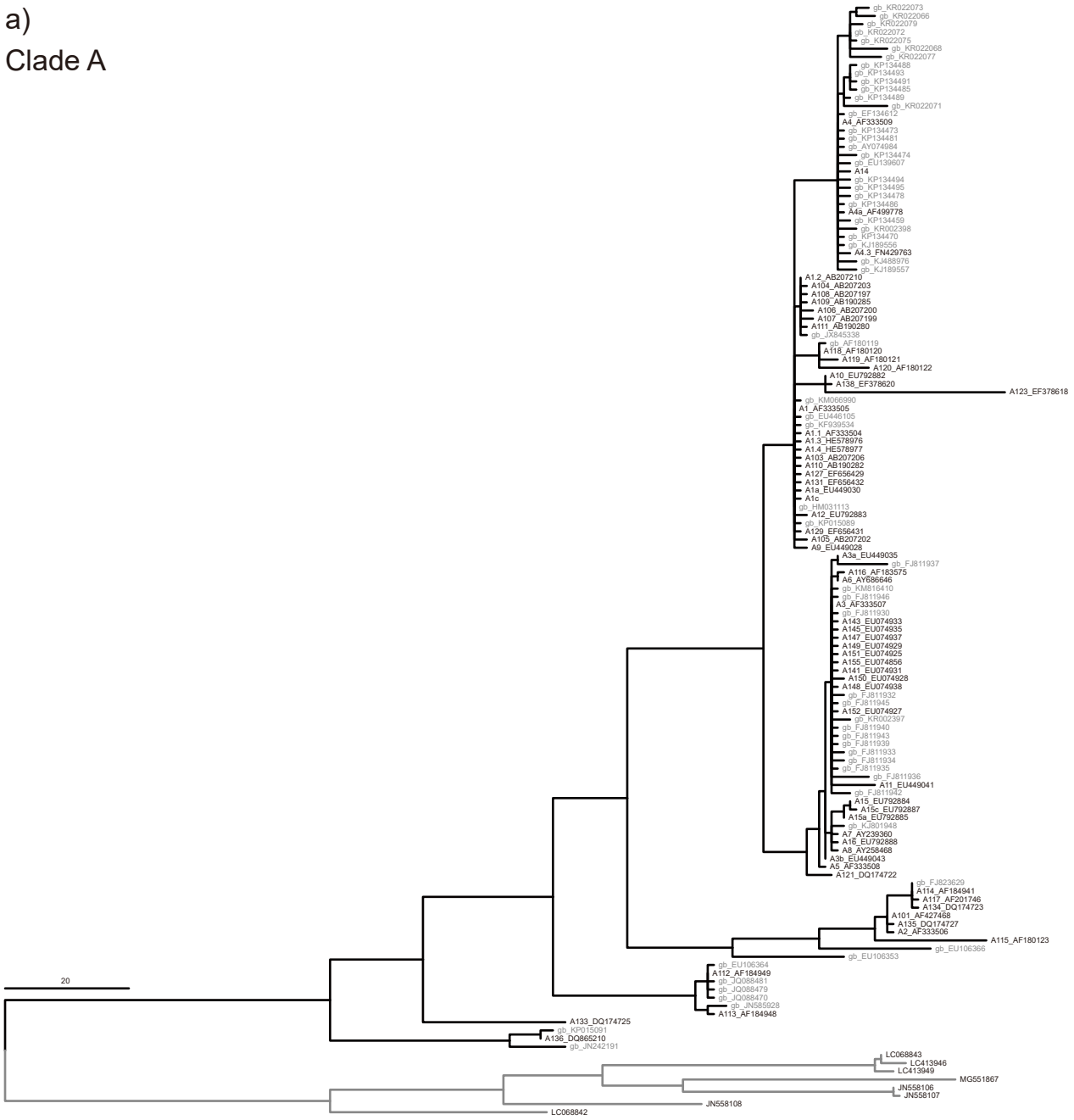


Figure S3. Maximum parsimony (MP) trees reconstructed with extended set of ITS2 sequences in each Symbiodiniaceae clade (A–I). Sequences in clade C are split into multiple groups of subclades that are each named after the reference ITS2 type (indicated by arrow) occupying or closest to the **central (i.e., putatively ancestral) node position in the haplotype network in Fig. 3**. Sequence variants corresponding to the reference core and additional GenBank entities are shown in black and grey, respectively. The scale bar represents number of informative base changes. Dinoflagellate and free-living Symbiodiniaceae species sequences were used as outgroups. a) Clade A; b) Clade B; c) Clade C1; d) Clade C3; e) Clade C15; f) Clade C17; g) Clade C1169; h) Clade C1c; i) Clade C31; j) Clade C62; k) Clade C91; l) Clade C1143; m) Clade D; n) Clade F; o) Clade E; p) Clade G; q) Clade H.

b)
Clade B

Figure S3—*continued*

c)
Clade C1

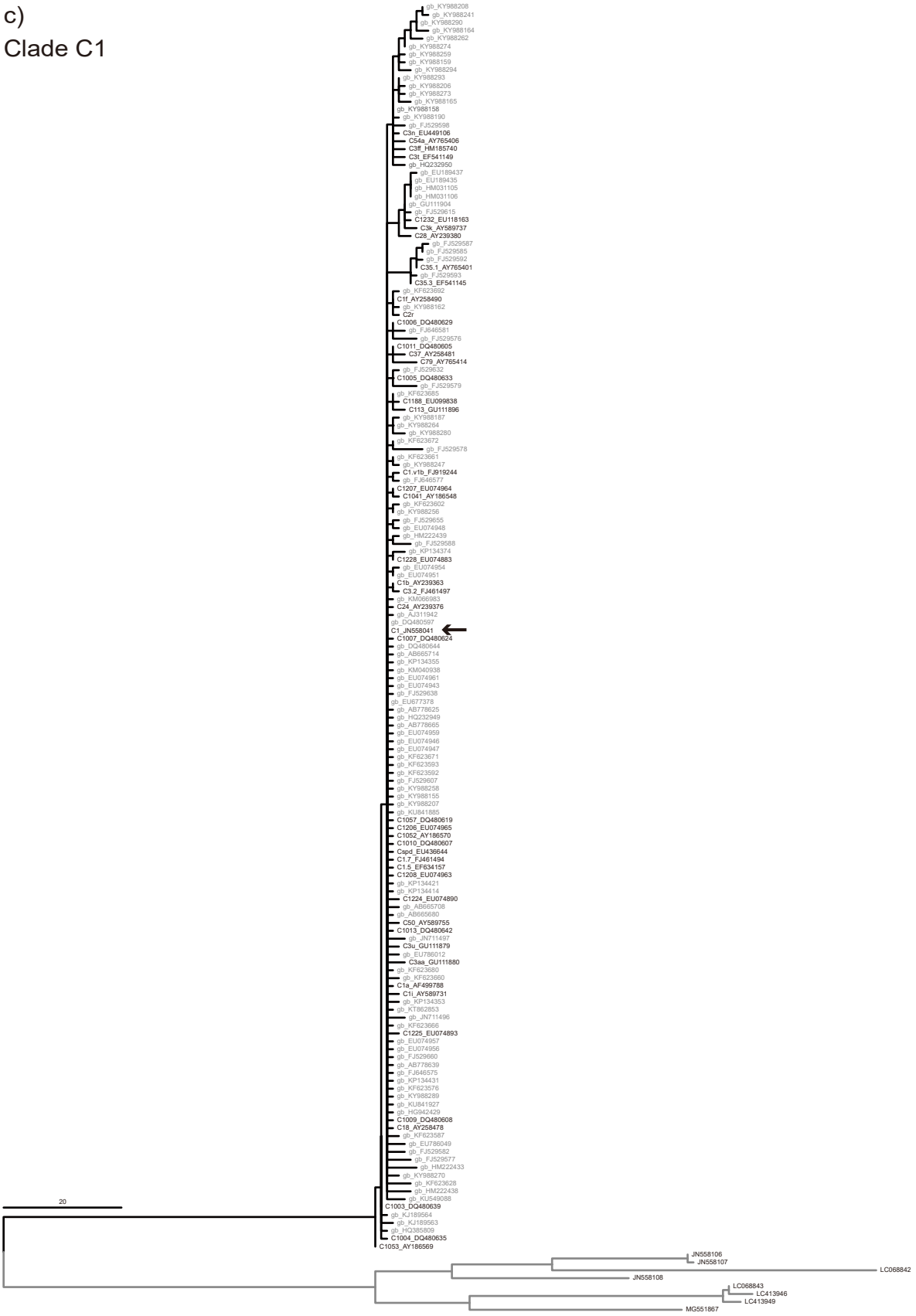


Figure S3—*continued*

d)
Clade C3

Figure S3—*continued*

e)
Clade C15

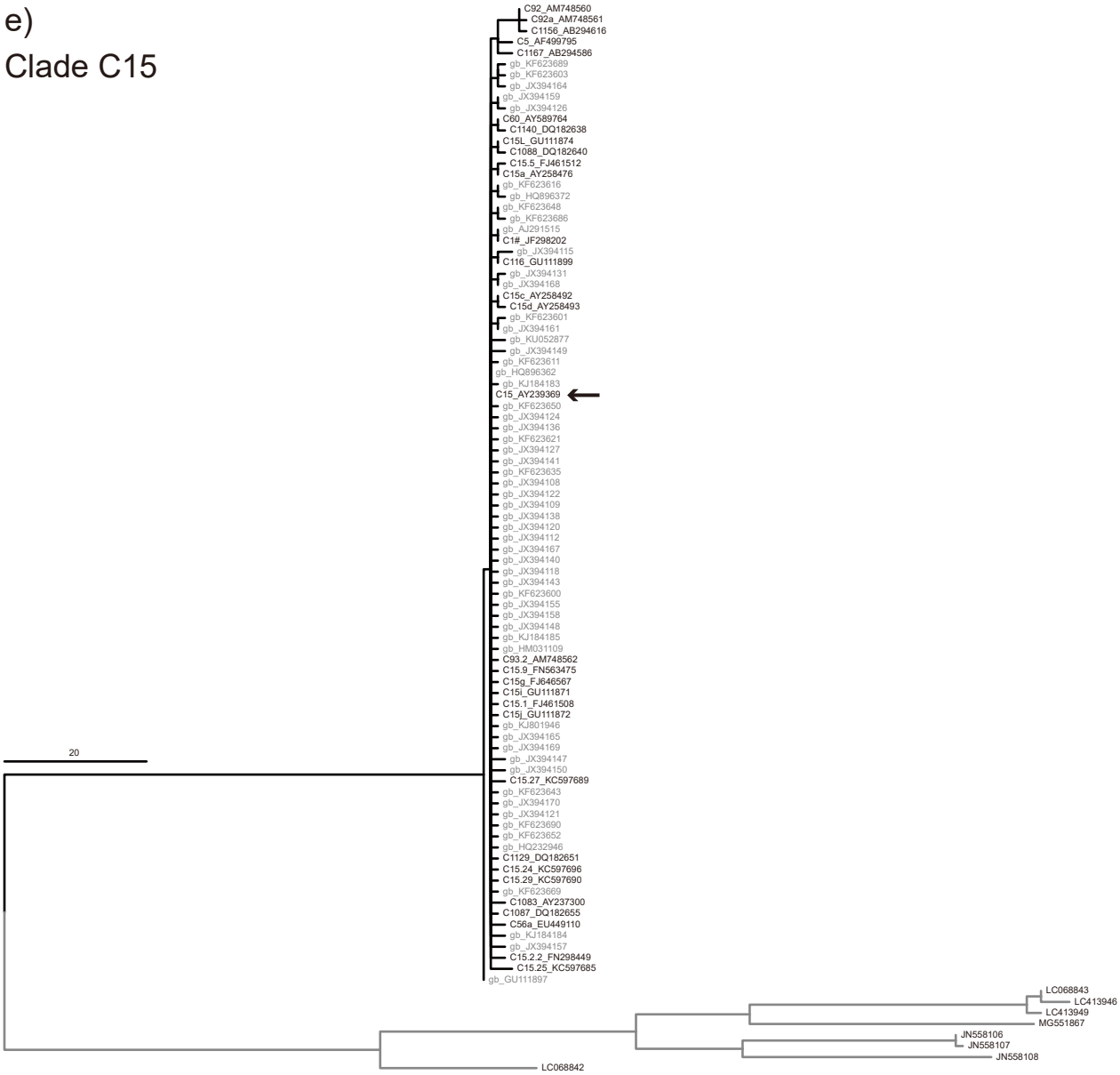


Figure S3—*continued*

f)
Clade C17

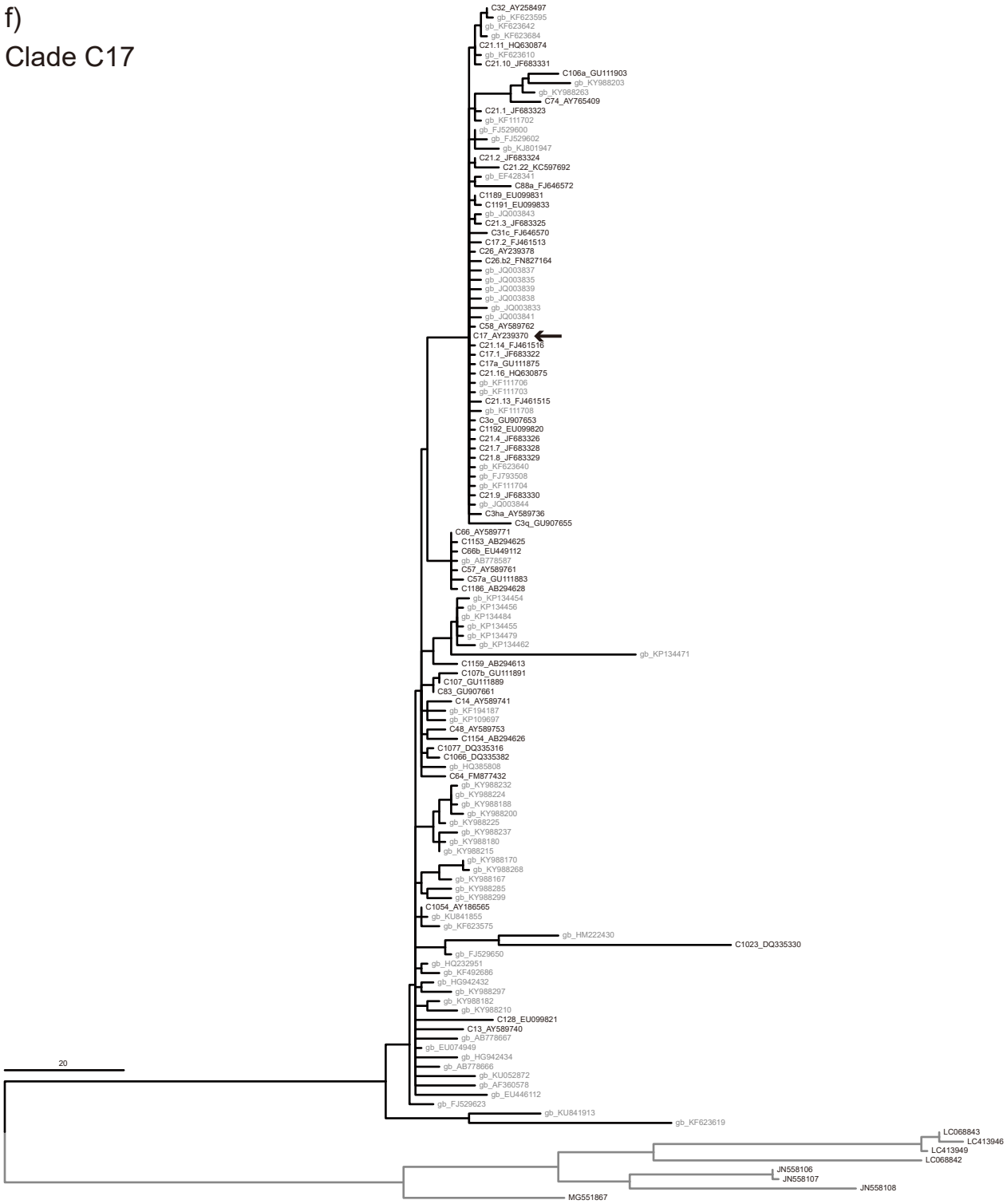


Figure S3—*continued*

g)
Clade C1169

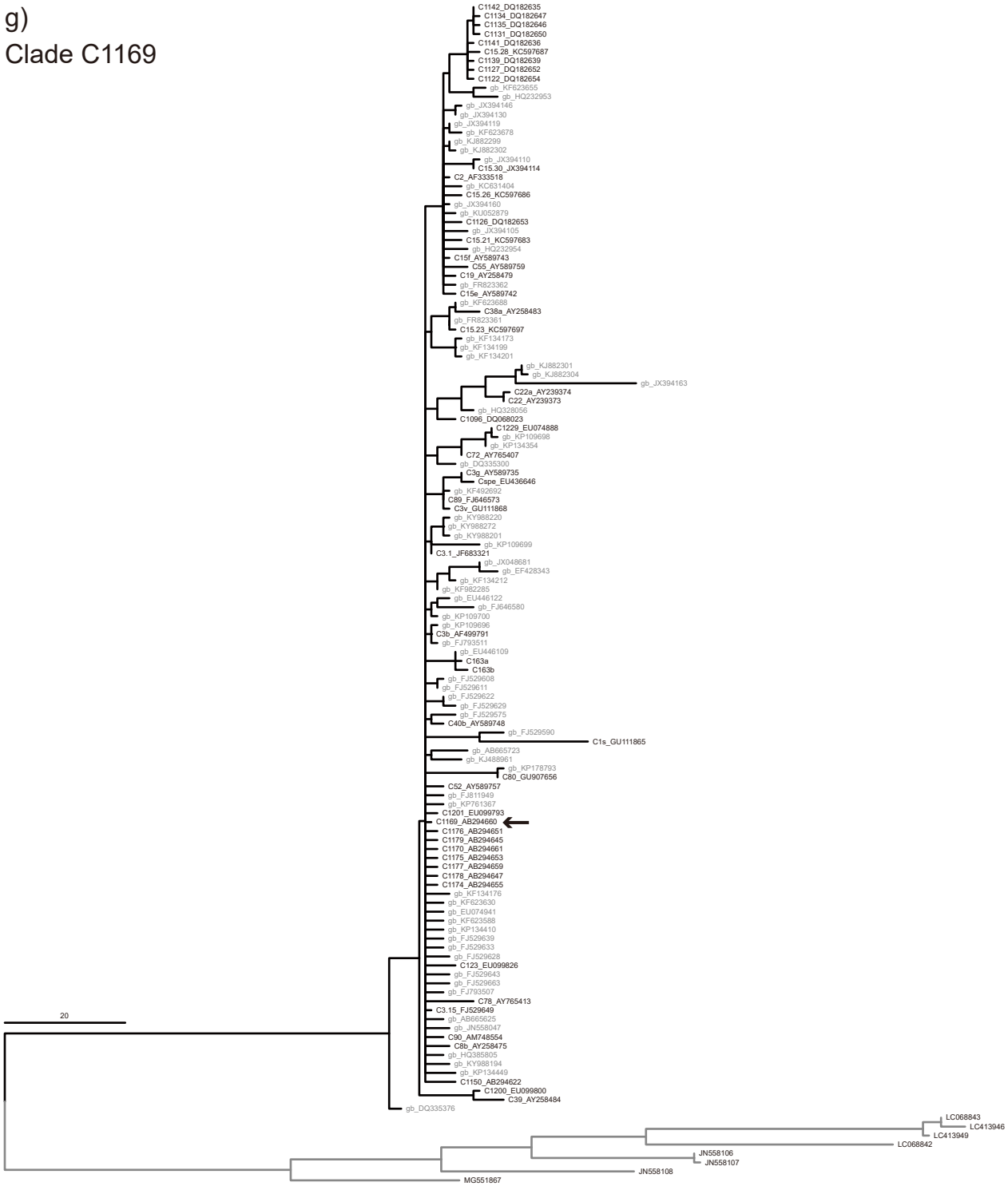
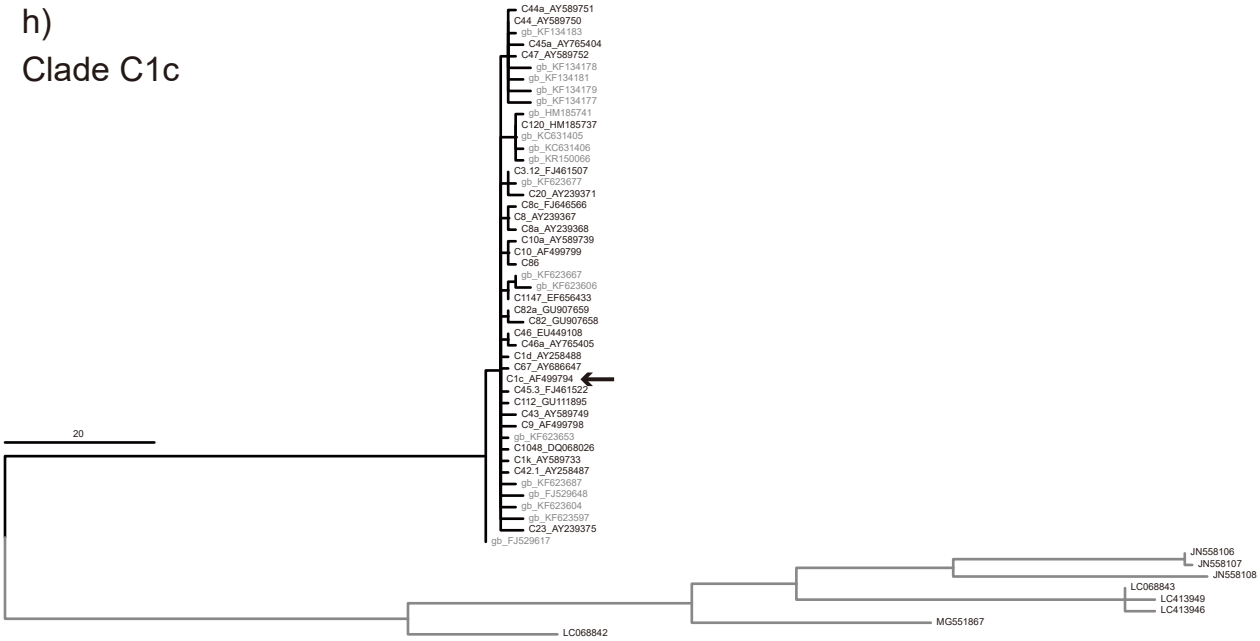


Figure S3—*continued*

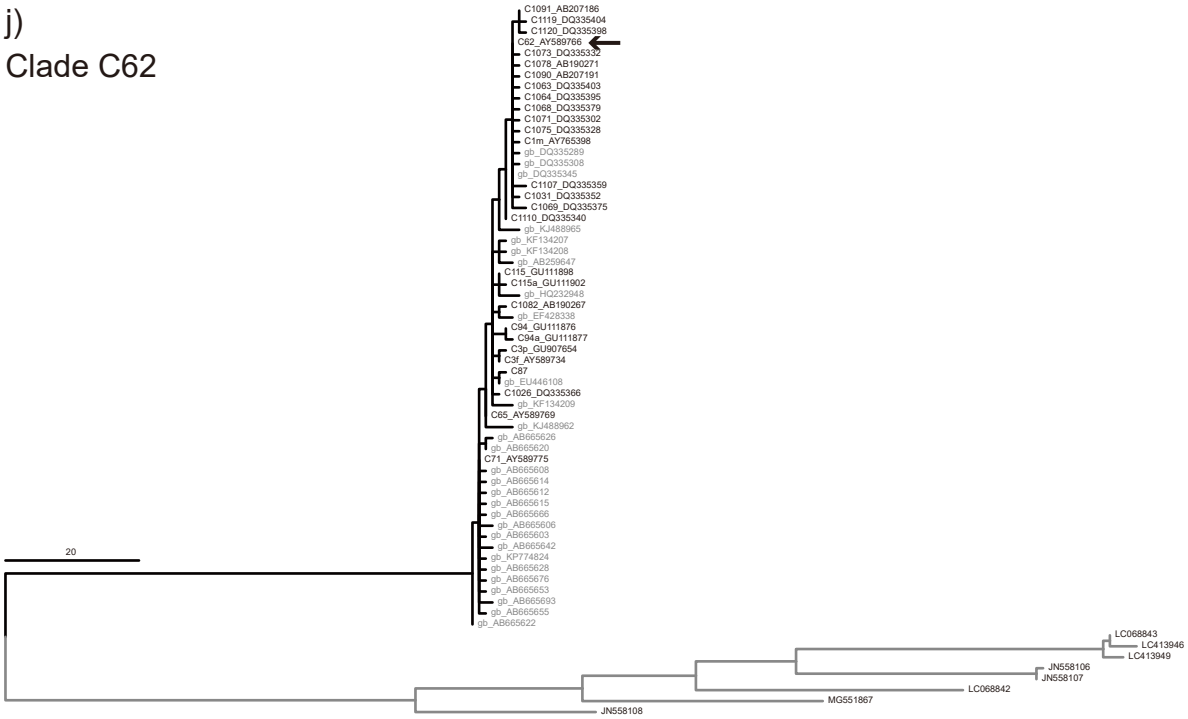
h)
Clade C1c



i)
Clade C31

Figure S3—*continued*

j)
Clade C62



k)
Clade C91

l)
Clade C1143

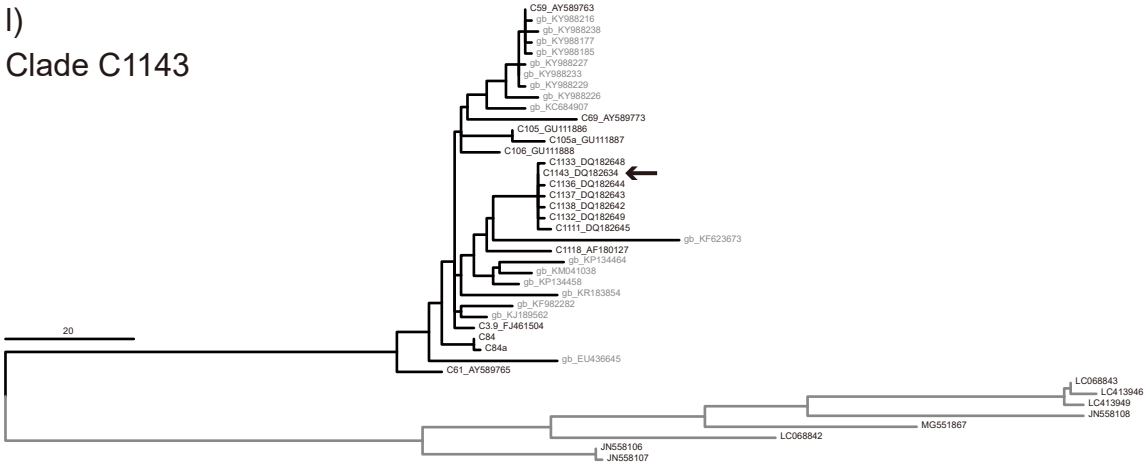


Figure S3—*continued*

m)
Clade D

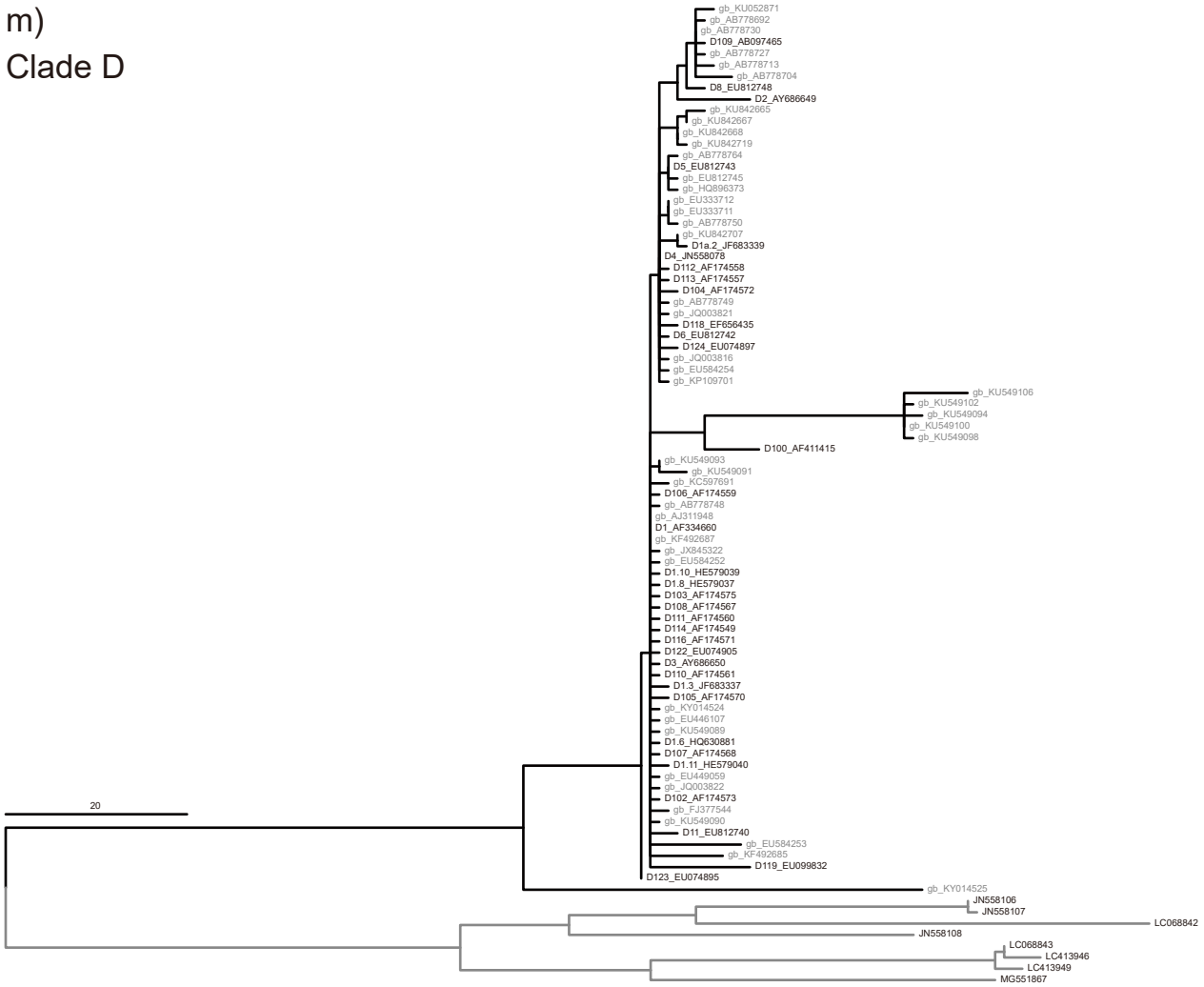


Figure S3—*continued*

n)
Clade F

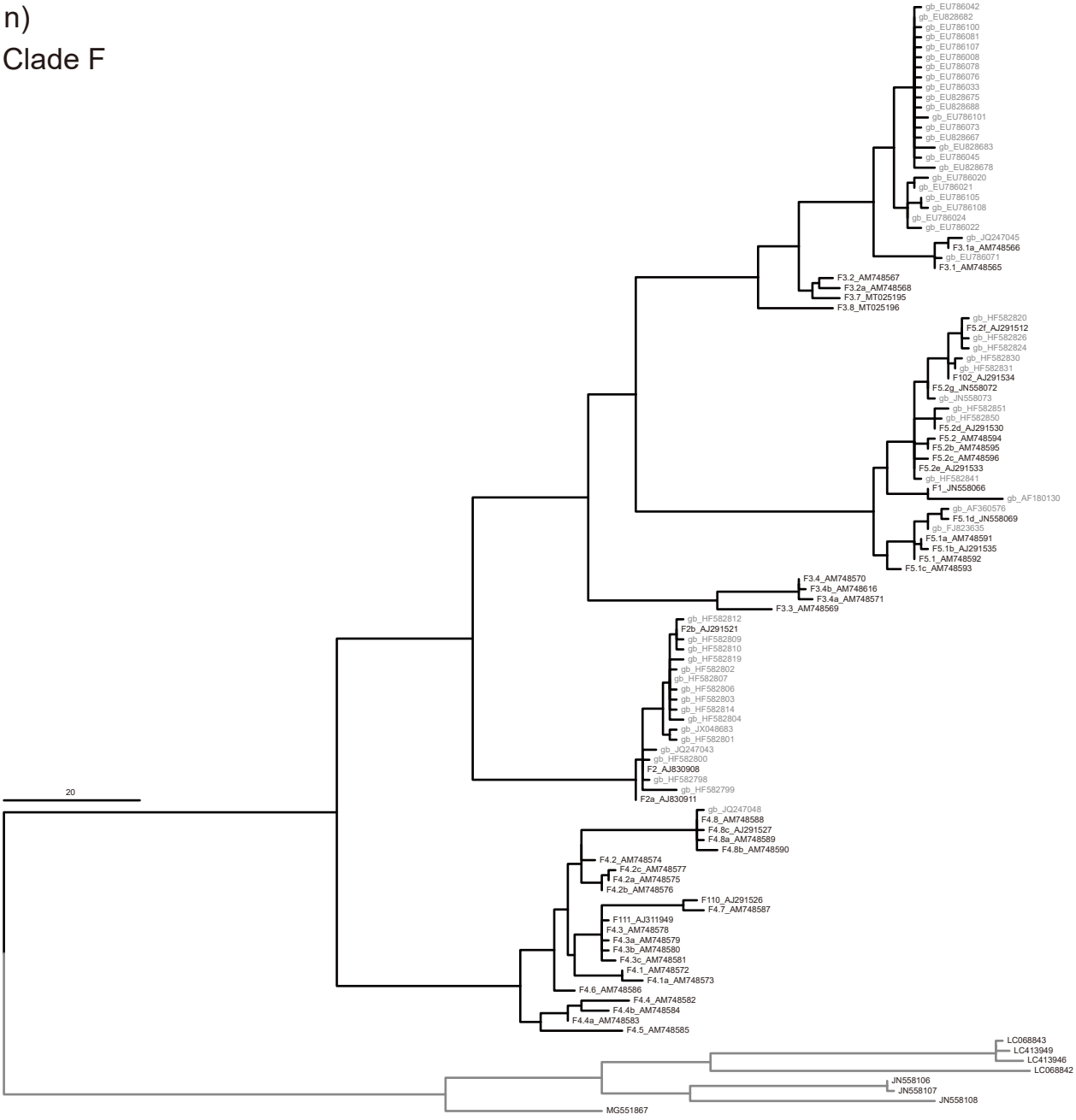


Figure S3—*continued*

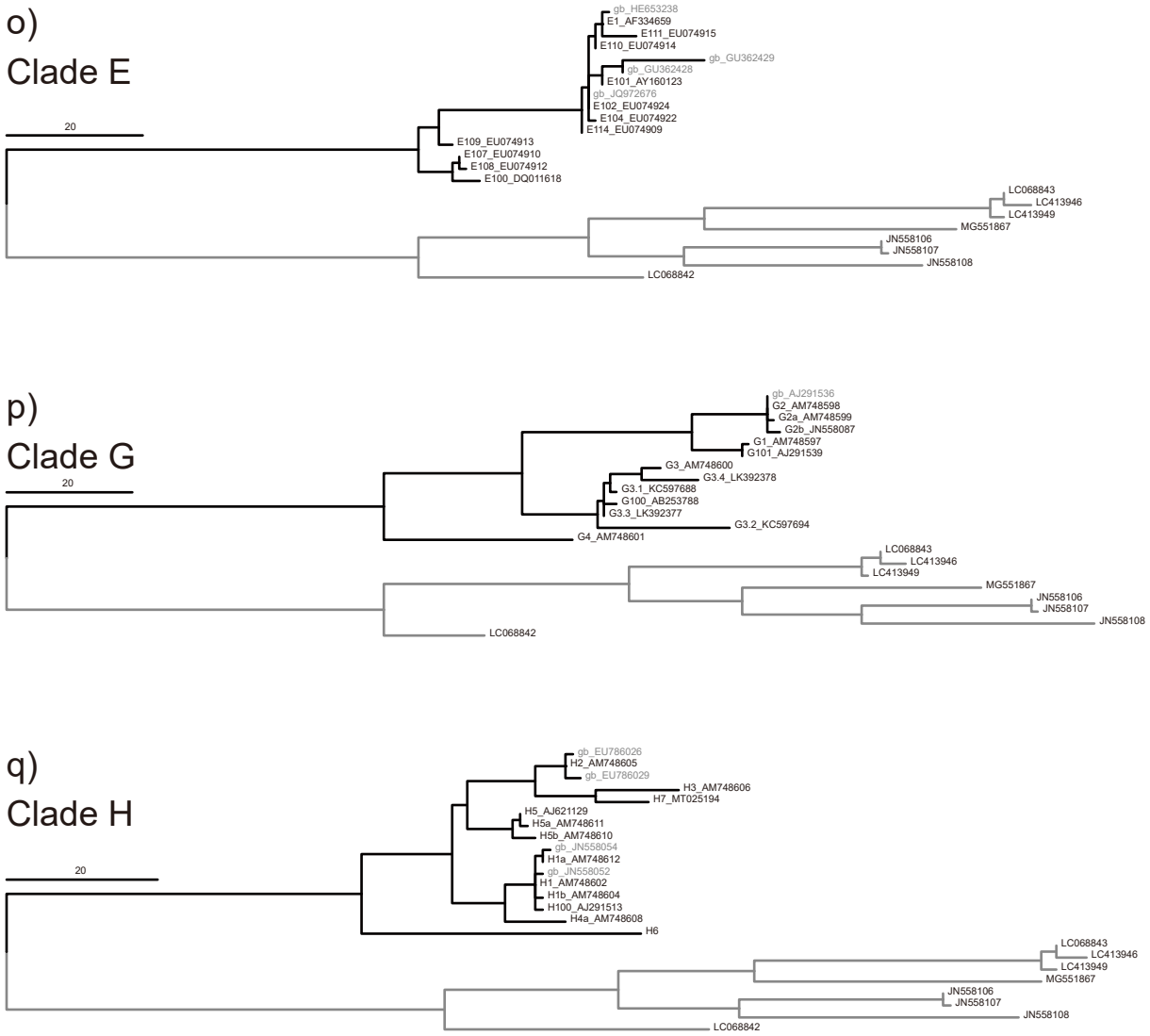


Figure S3—*continued*