

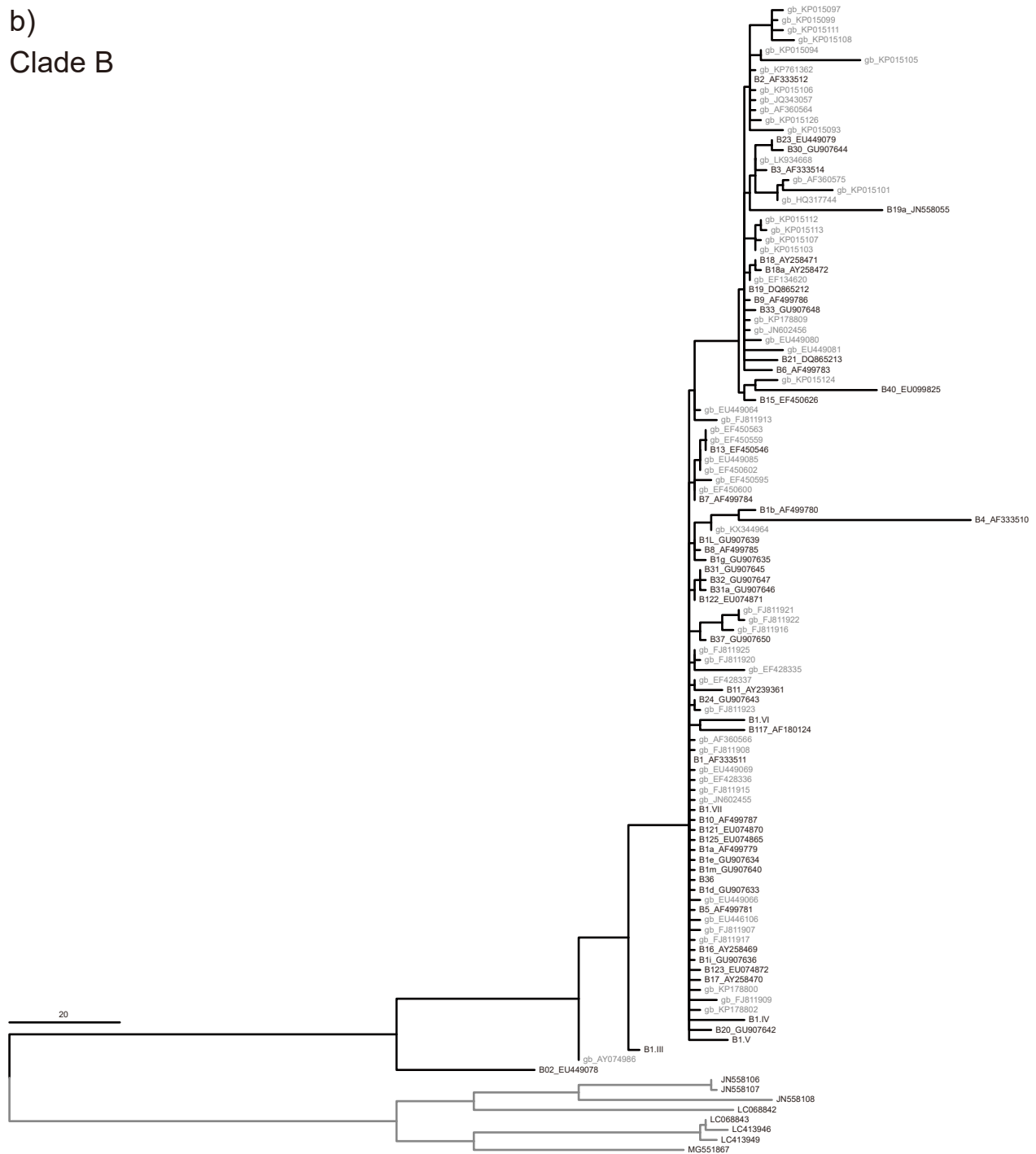
a)

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

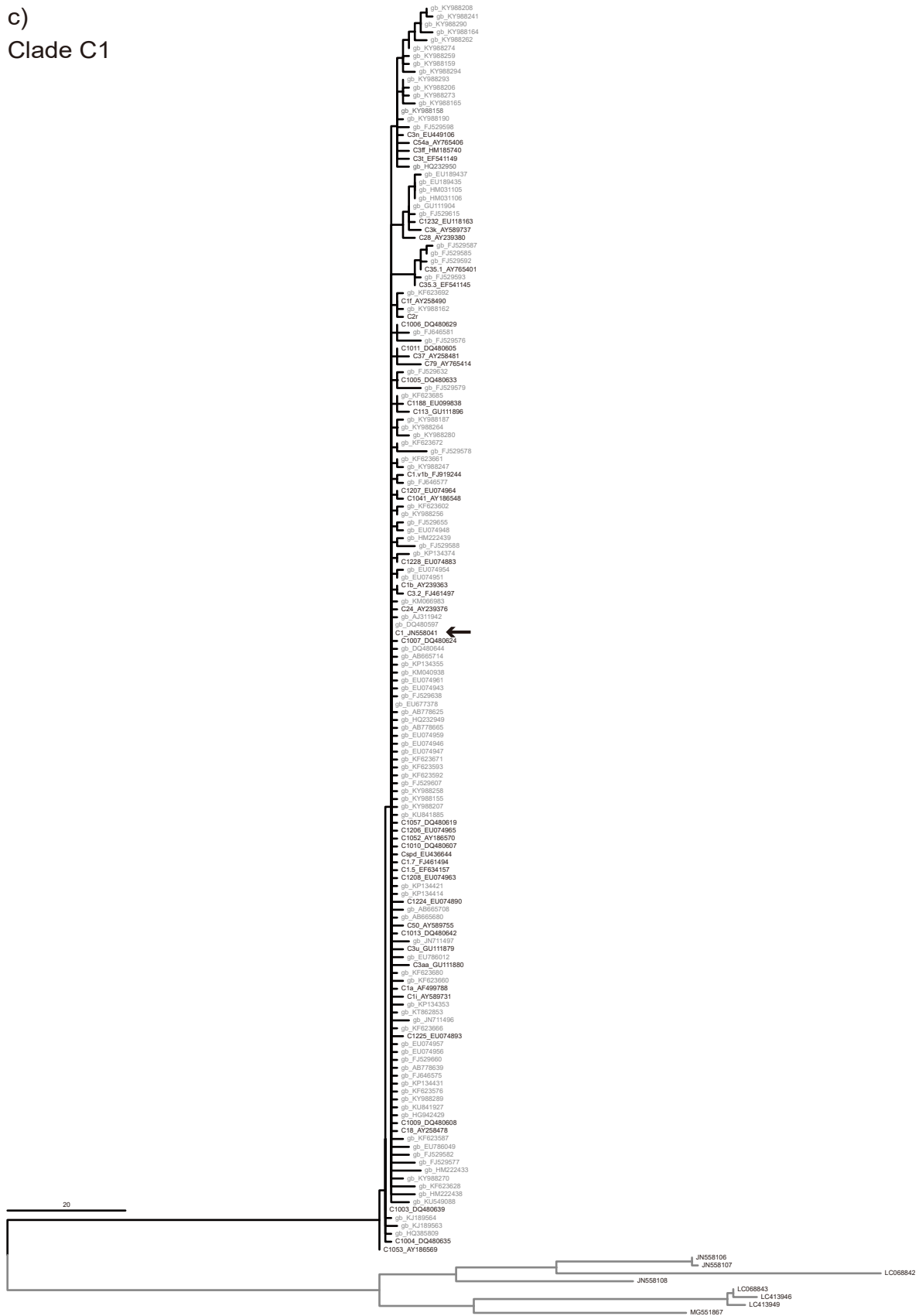


Figure S3—continued

d)
Clade C3



Figure S3—continued

e)
Clade C15

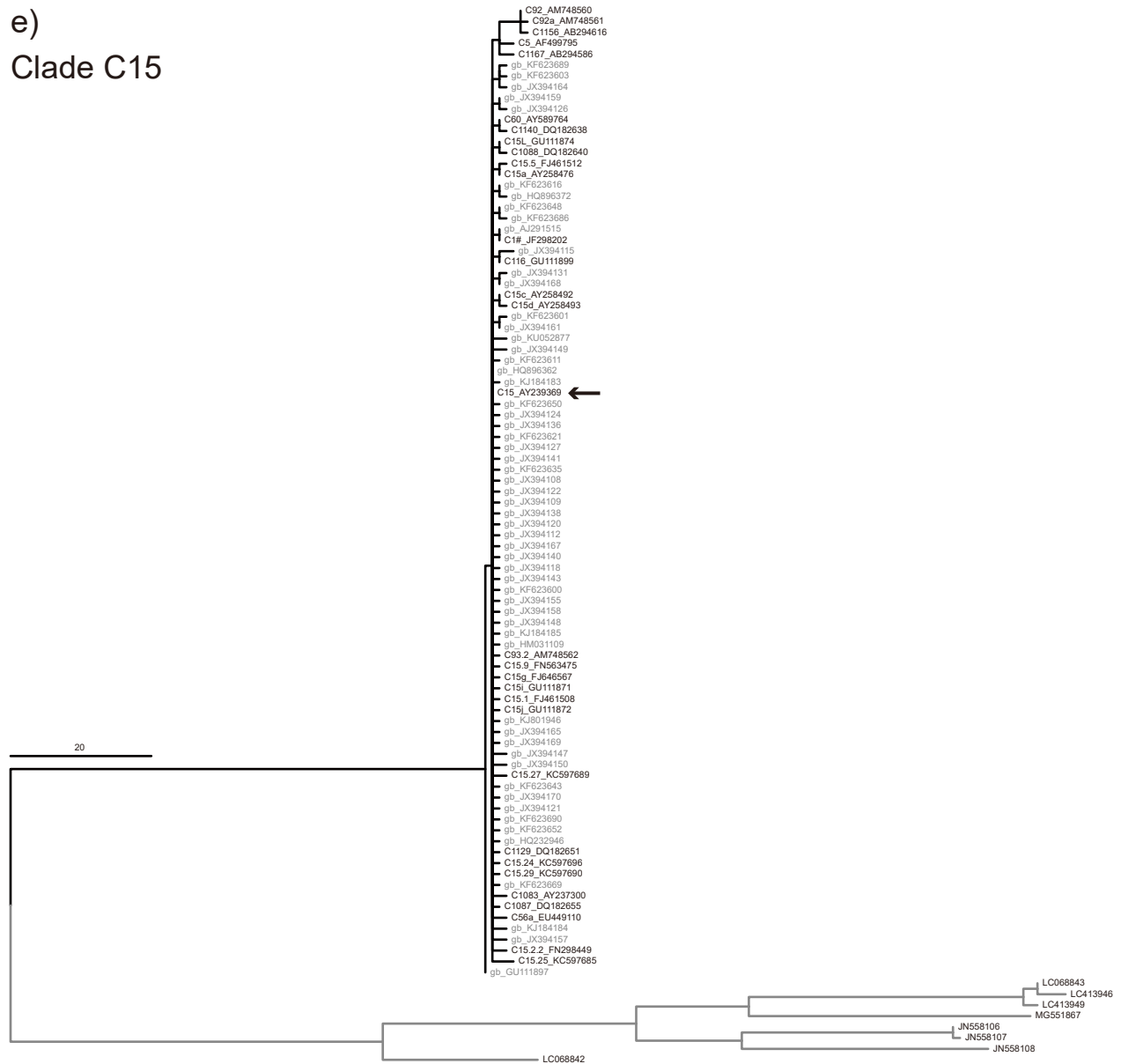


Figure S3—continued

f)
Clade C17

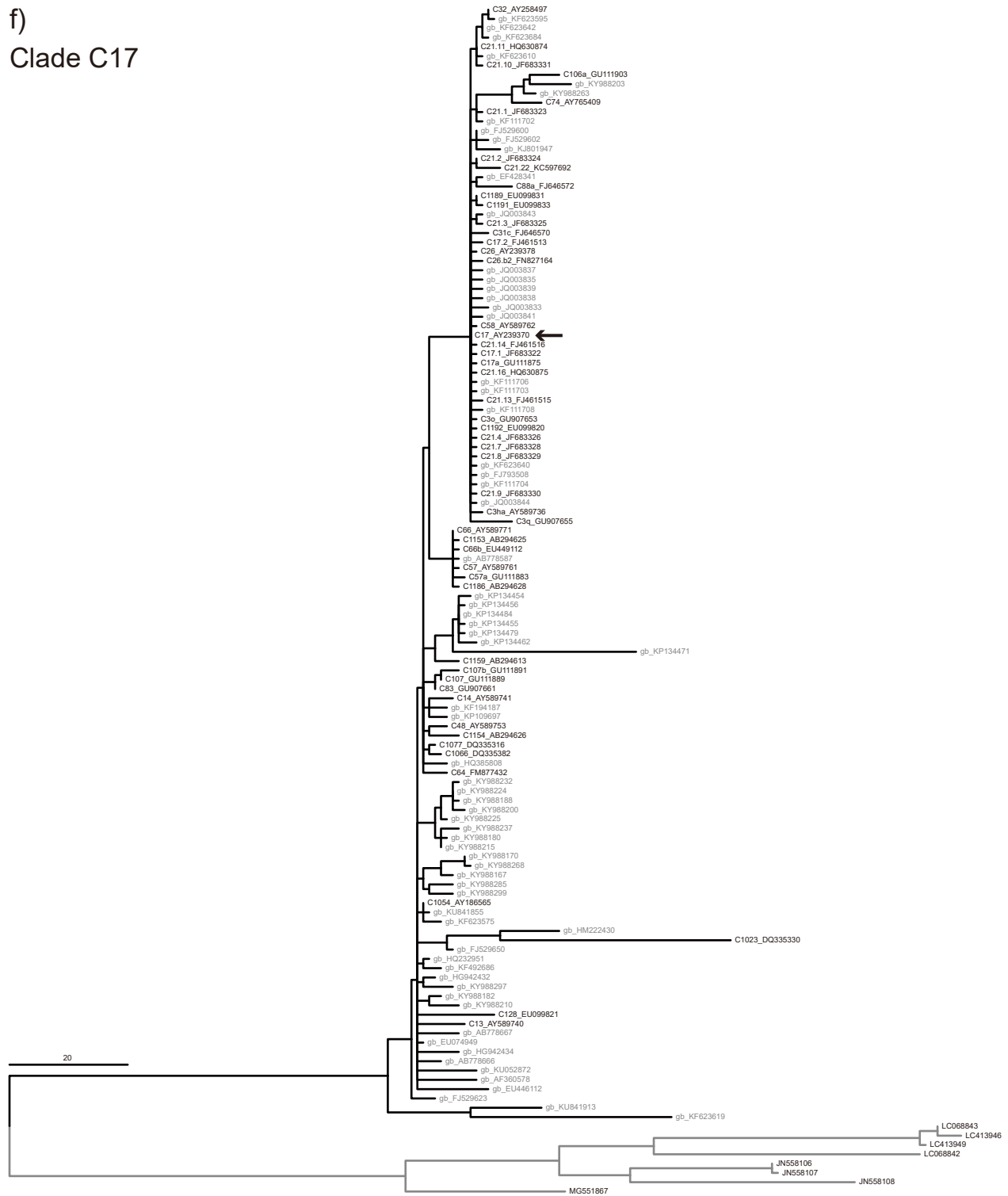


Figure S3—continued

g)
Clade C1169

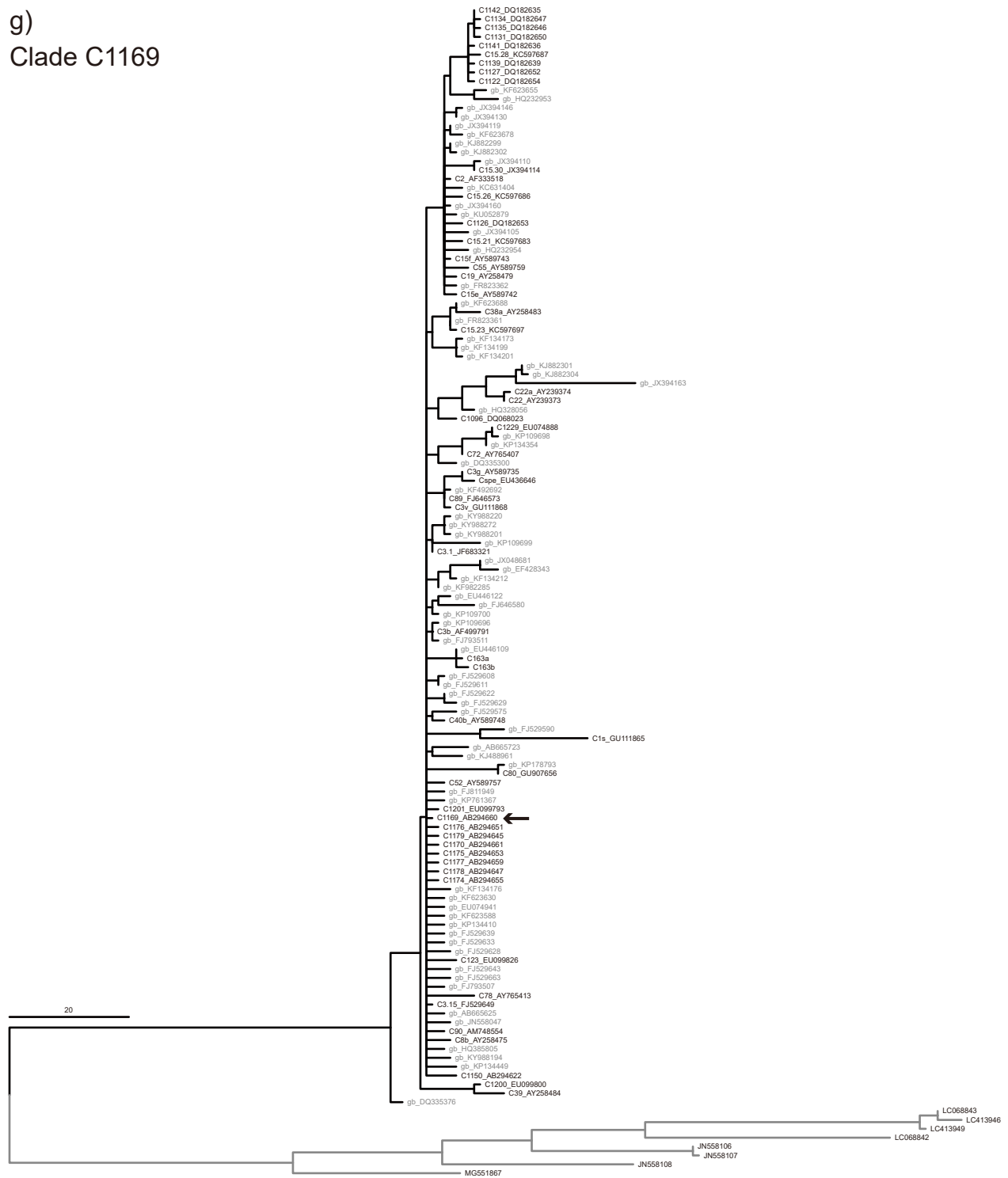
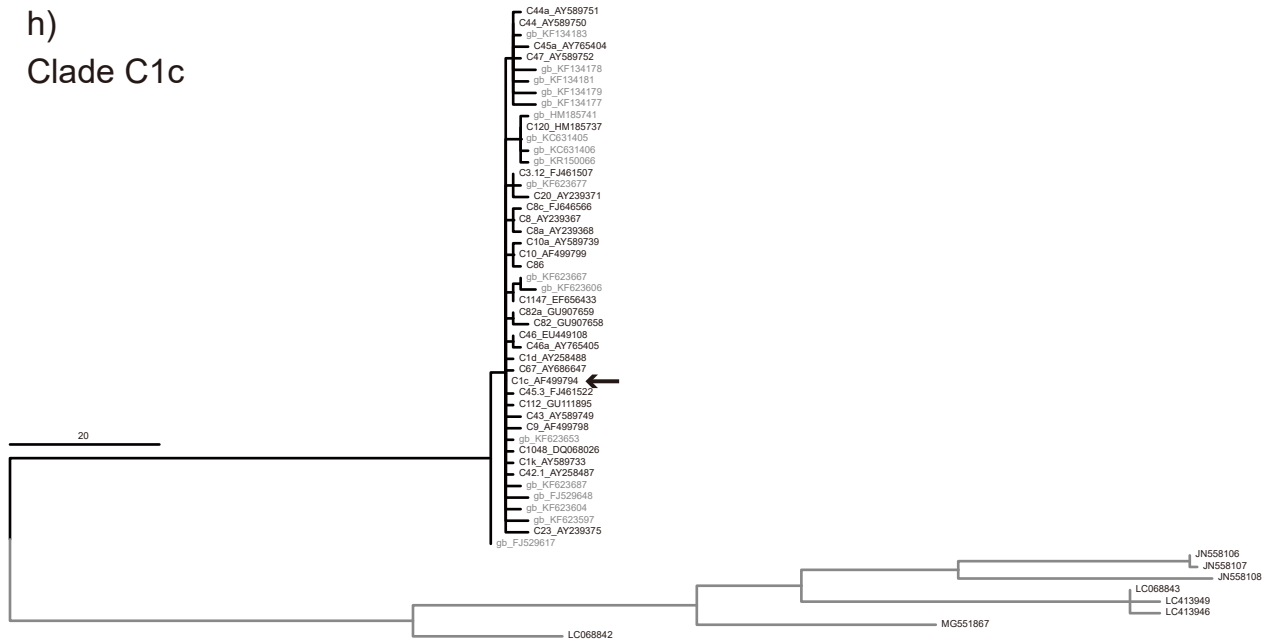


Figure S3—*continued*

h)
Clade C1c

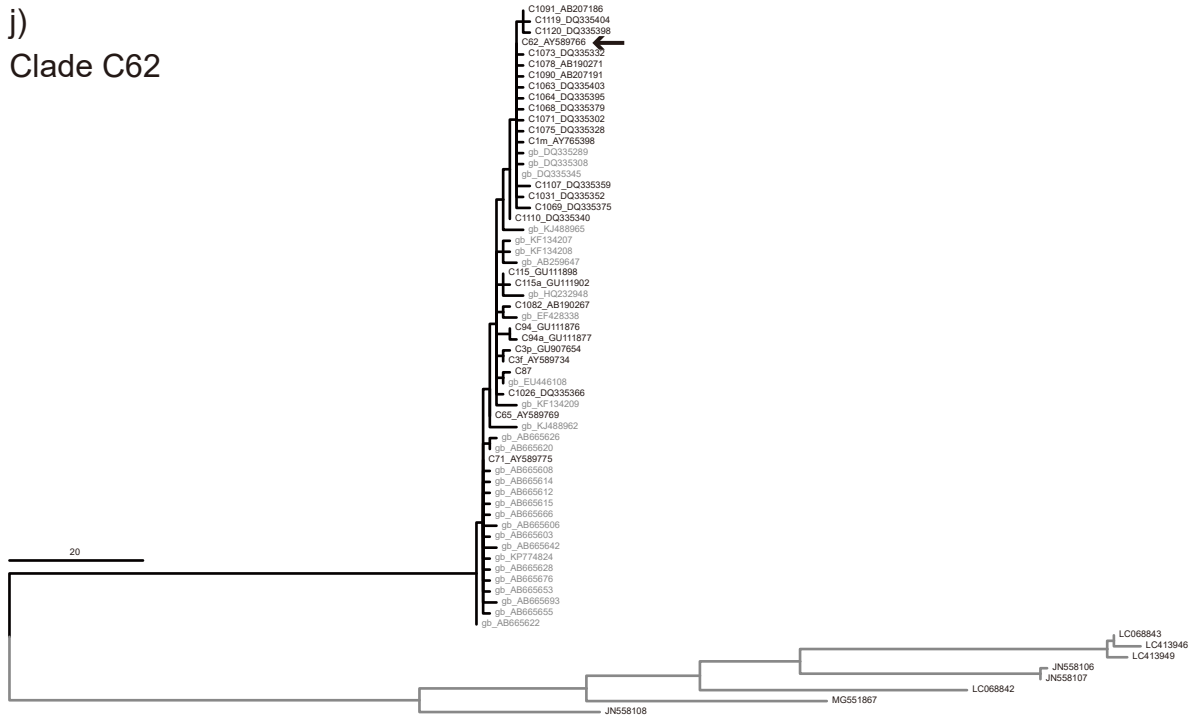


i)
Clade C31

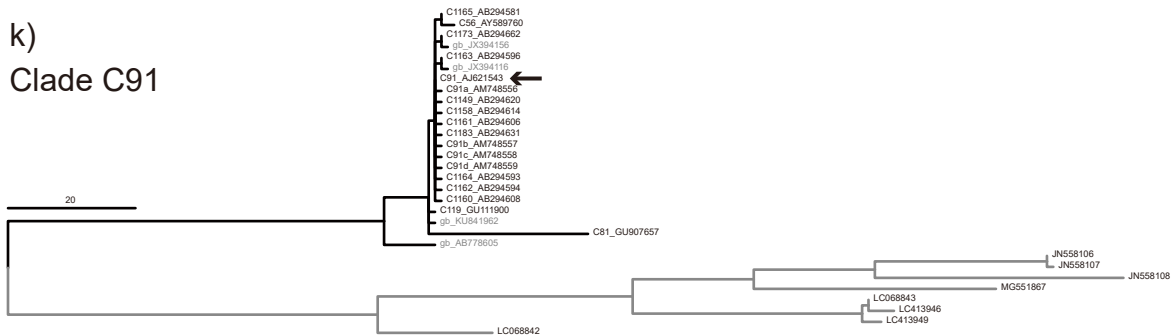


Figure S3—*continued*

j)
Clade C62



k)
Clade C91



l)
Clade C1143

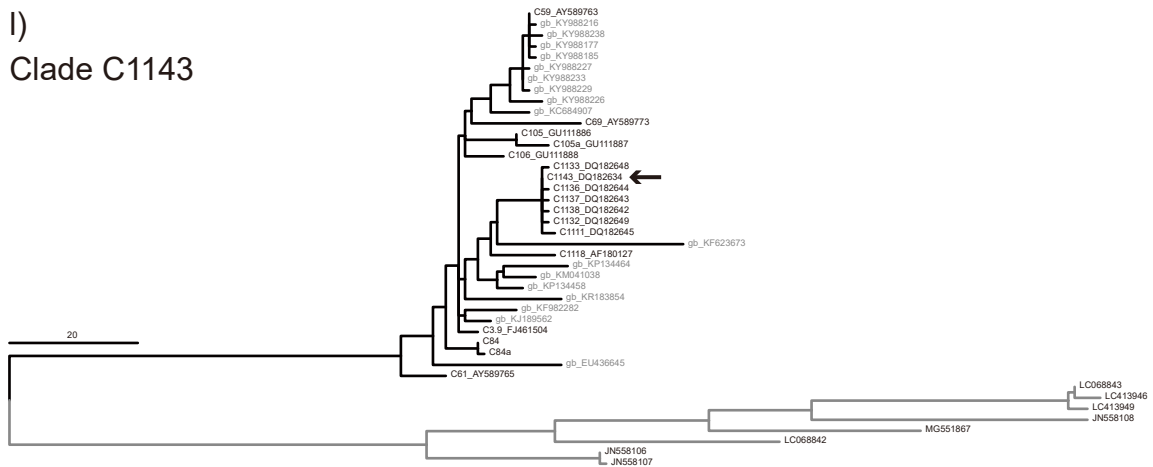


Figure S3—*continued*

m)
Clade D

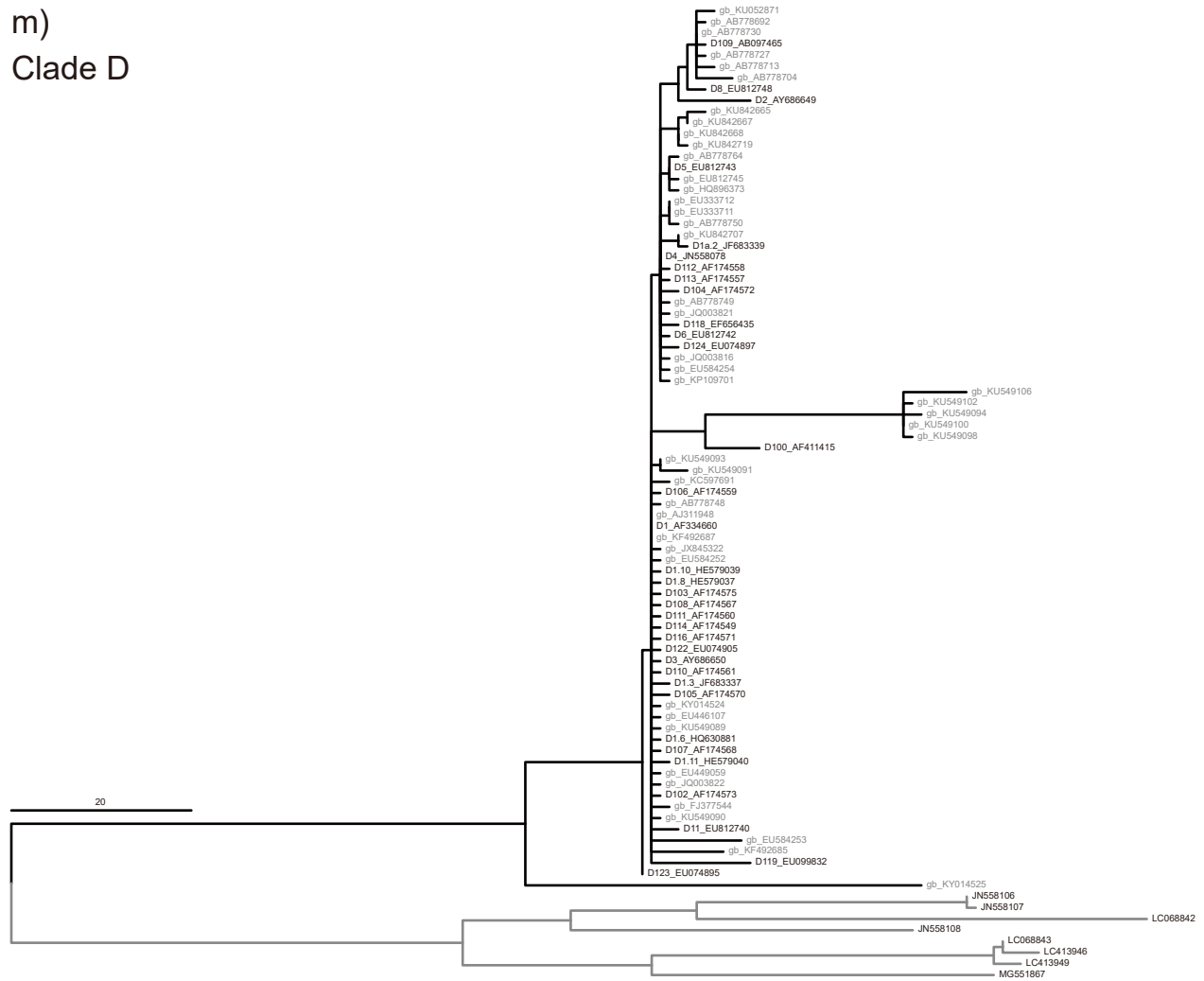


Figure S3—continued

n)
Clade F

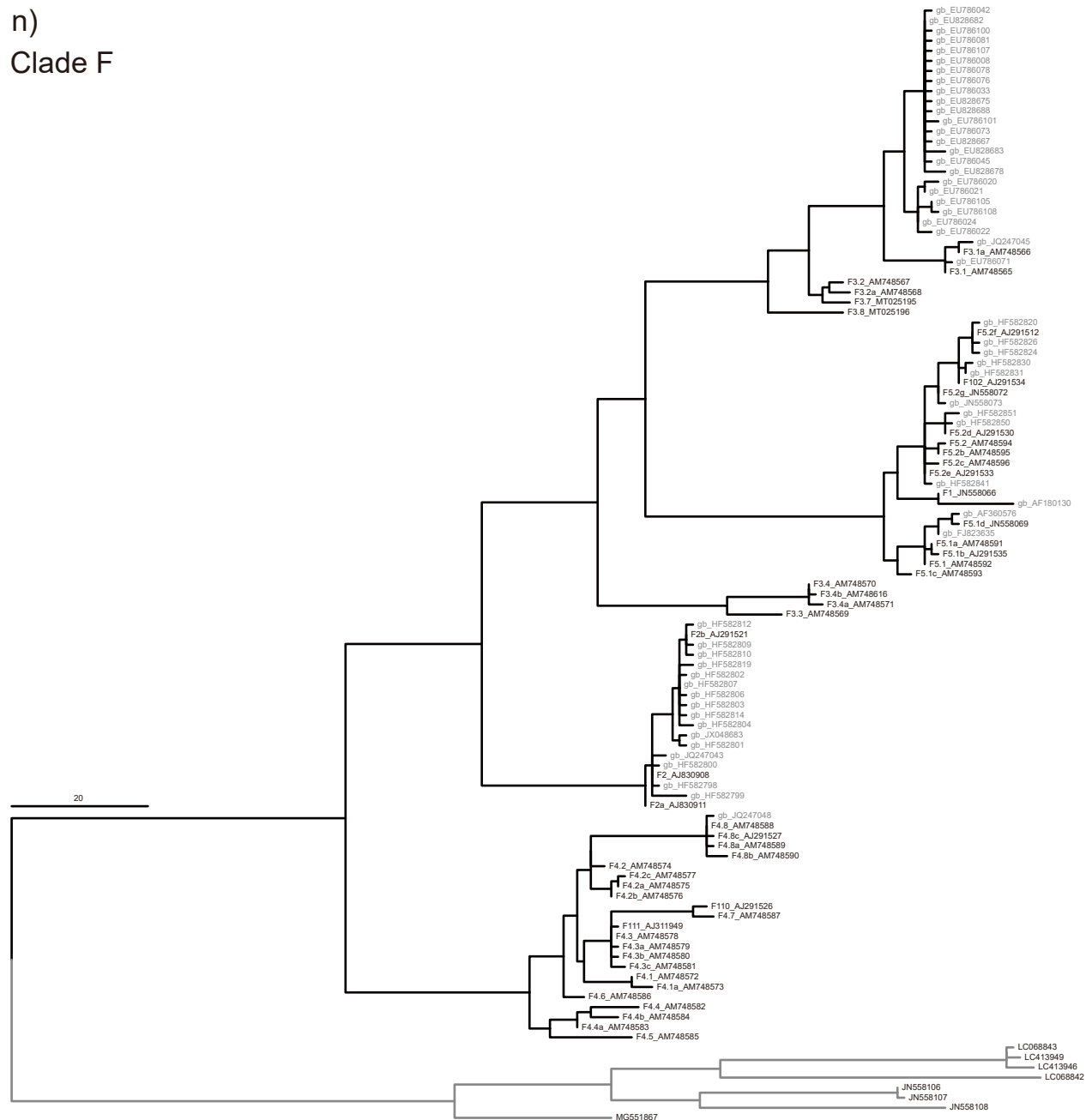


Figure S3—continued

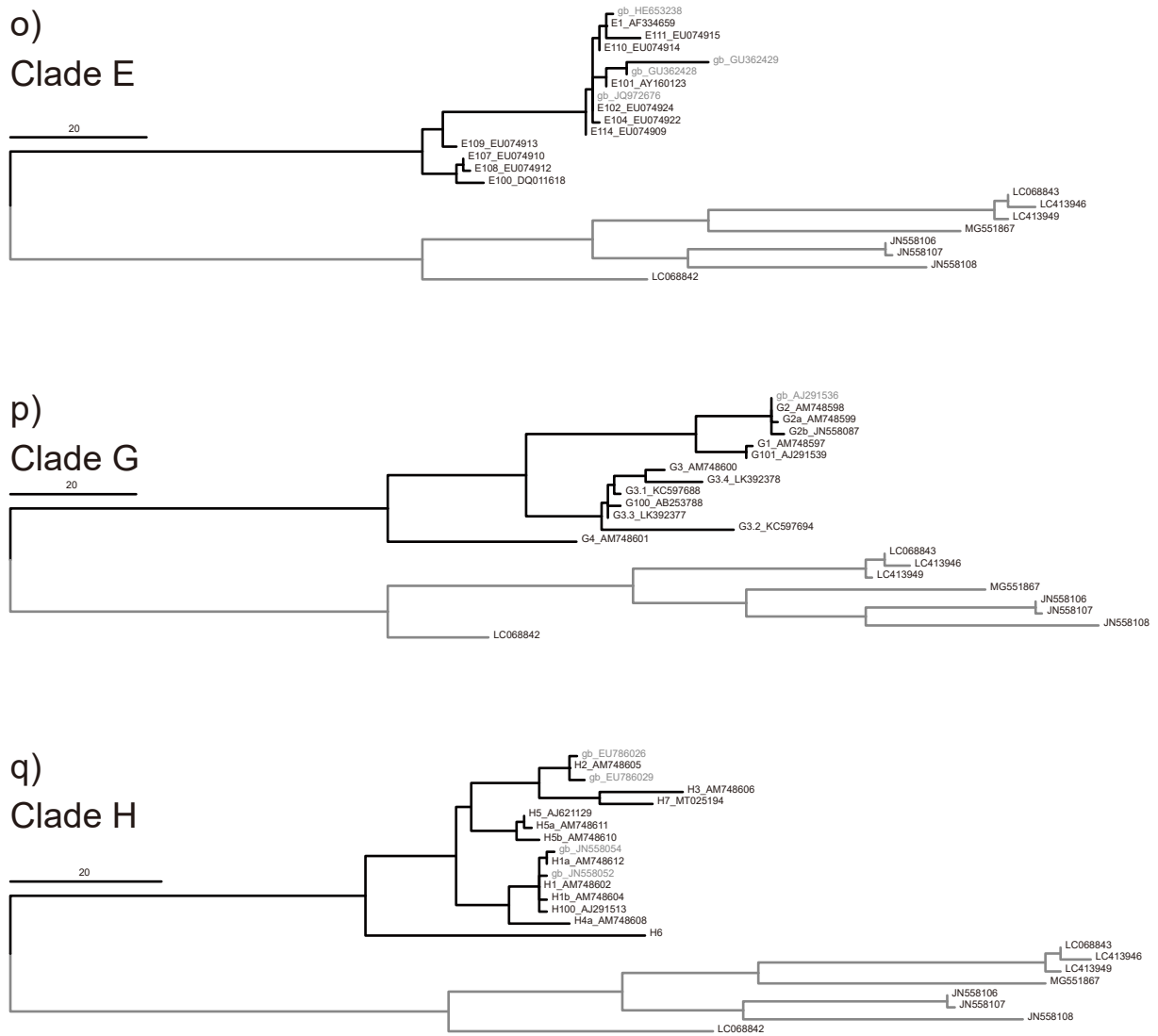


Figure S3—*continued*