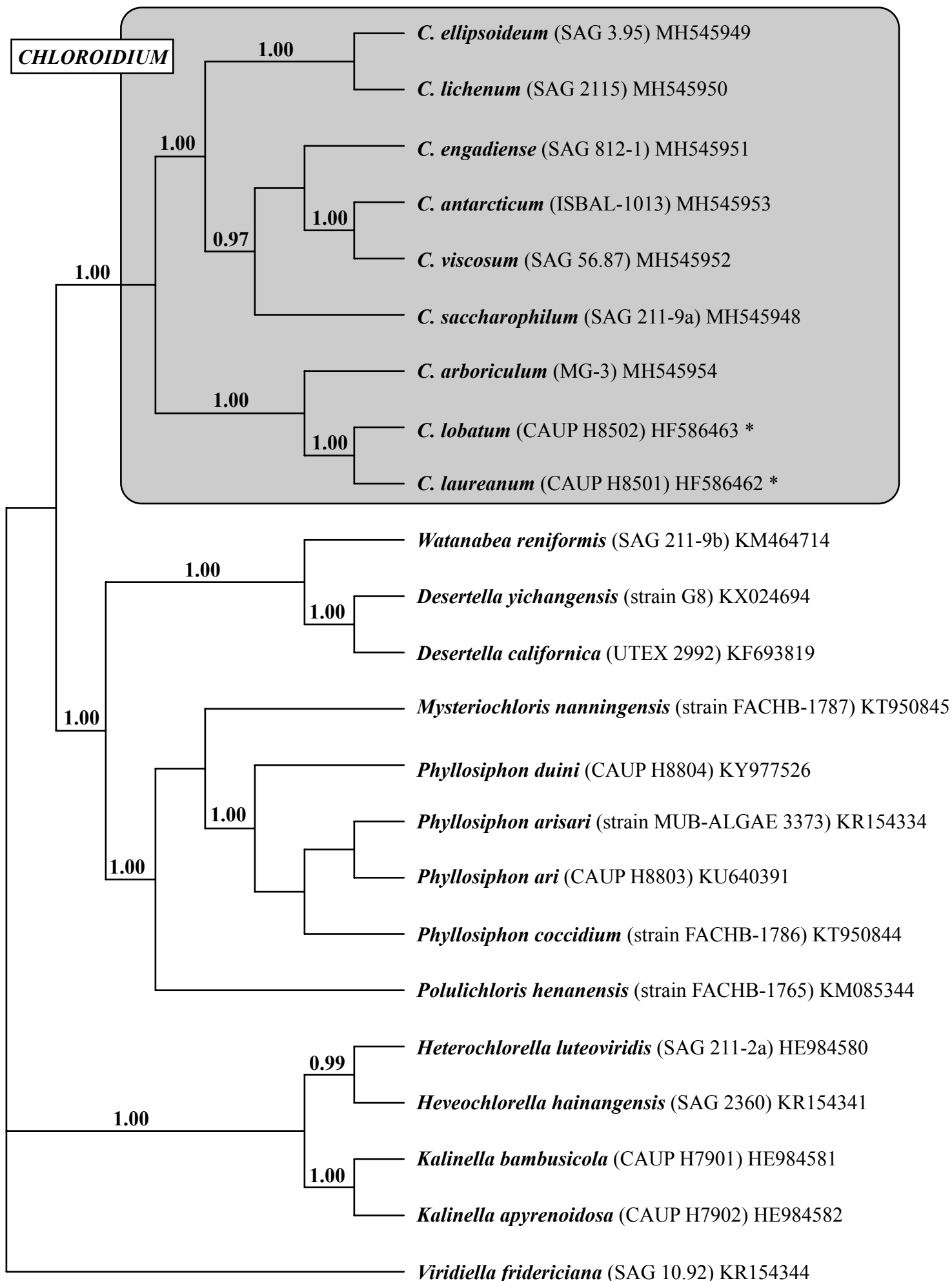
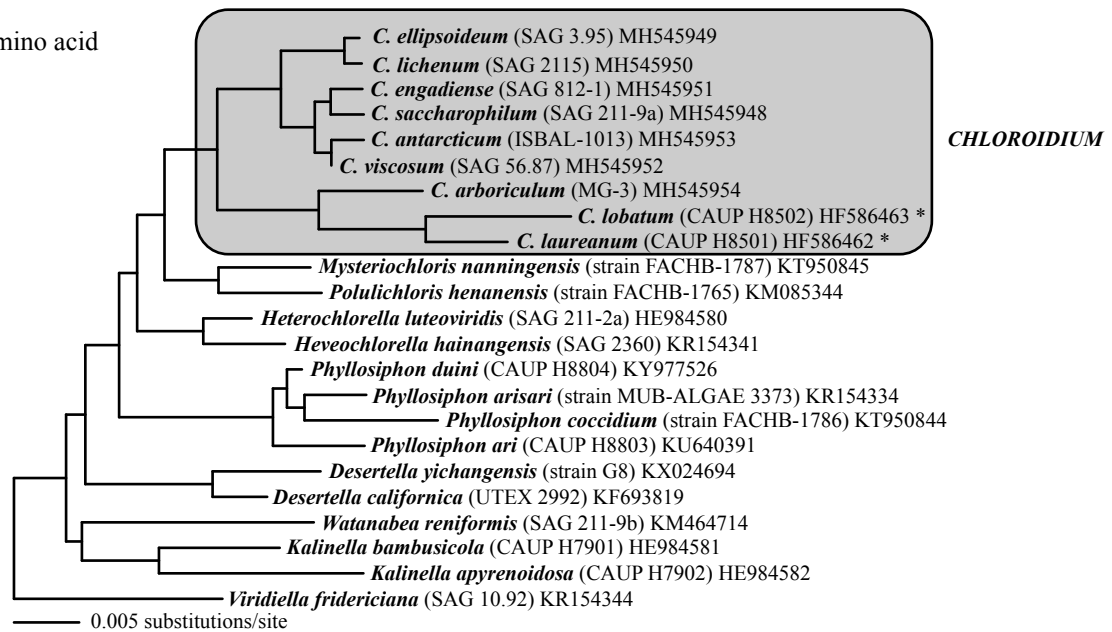


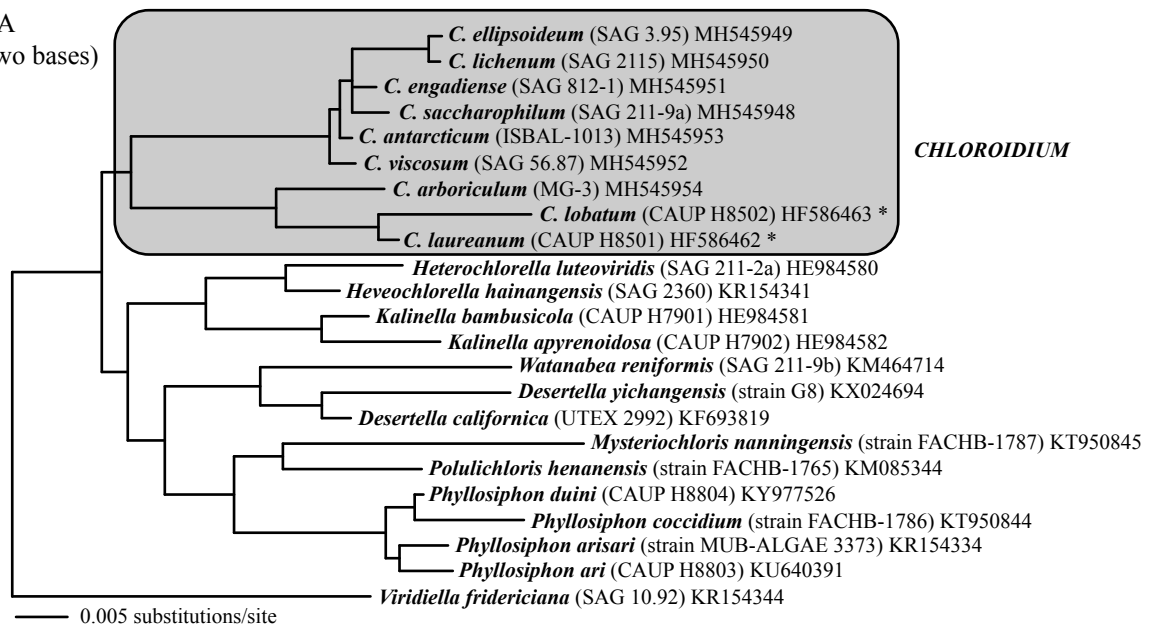
	codon 1	codon 2	codon 3
For a symmetrical tree:			
Prop. invar. sites	0,0000	0,0000	0,0000
Mean H	0,1384	0,0406	0,7877
Standard Error	0,0171	0,0107	0,0243
Hmax	1,8318	1,8861	1,6511
Iss	0,0756	0,0215	0,4771
Iss.c	0,6917	0,6917	0,6917
T	36,0655	62,7597	8,8342
DF	401	401	401
Prob (Two-tailed)	0,0000	0,0000	0,0032
95% Lower Limit	0,0420	0,0005	0,4293
95% Upper Limit	0,1091	0,0425	0,5248
For an extreme asymmetrical (and generally very unlikely) tree:			
Iss.c	0,4350	0,4350	0,4350
T	21,0401	38,7215	1,7323
DF	401	401	401
Prob (Two-tailed)	0,0000	0,0000	0,0840
95% Lower Limit	0,0420	0,0005	0,4293
95% Upper Limit	0,1091	0,0425	0,5248
symmetric	Iss.c >> Iss	Iss.c >> Iss	Iss.c > Iss
	informative	informative	little informative
asymmetric	Iss.c >> Iss	Iss.c >> Iss	Iss.c << Iss
	informative	informative	useless



A. Amino acid



B. DNA
(first two bases)



C. DNA
(all three bases)

