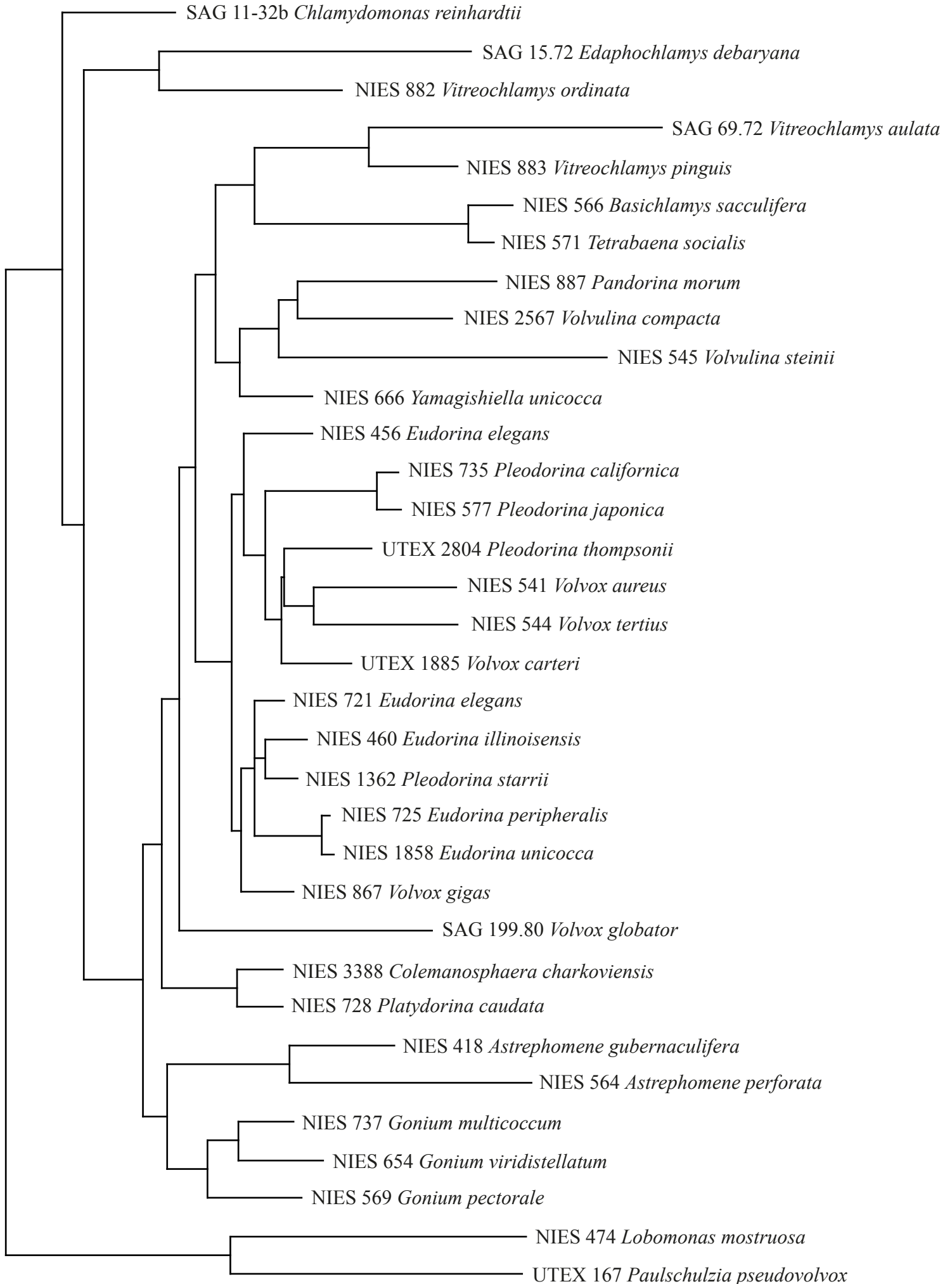


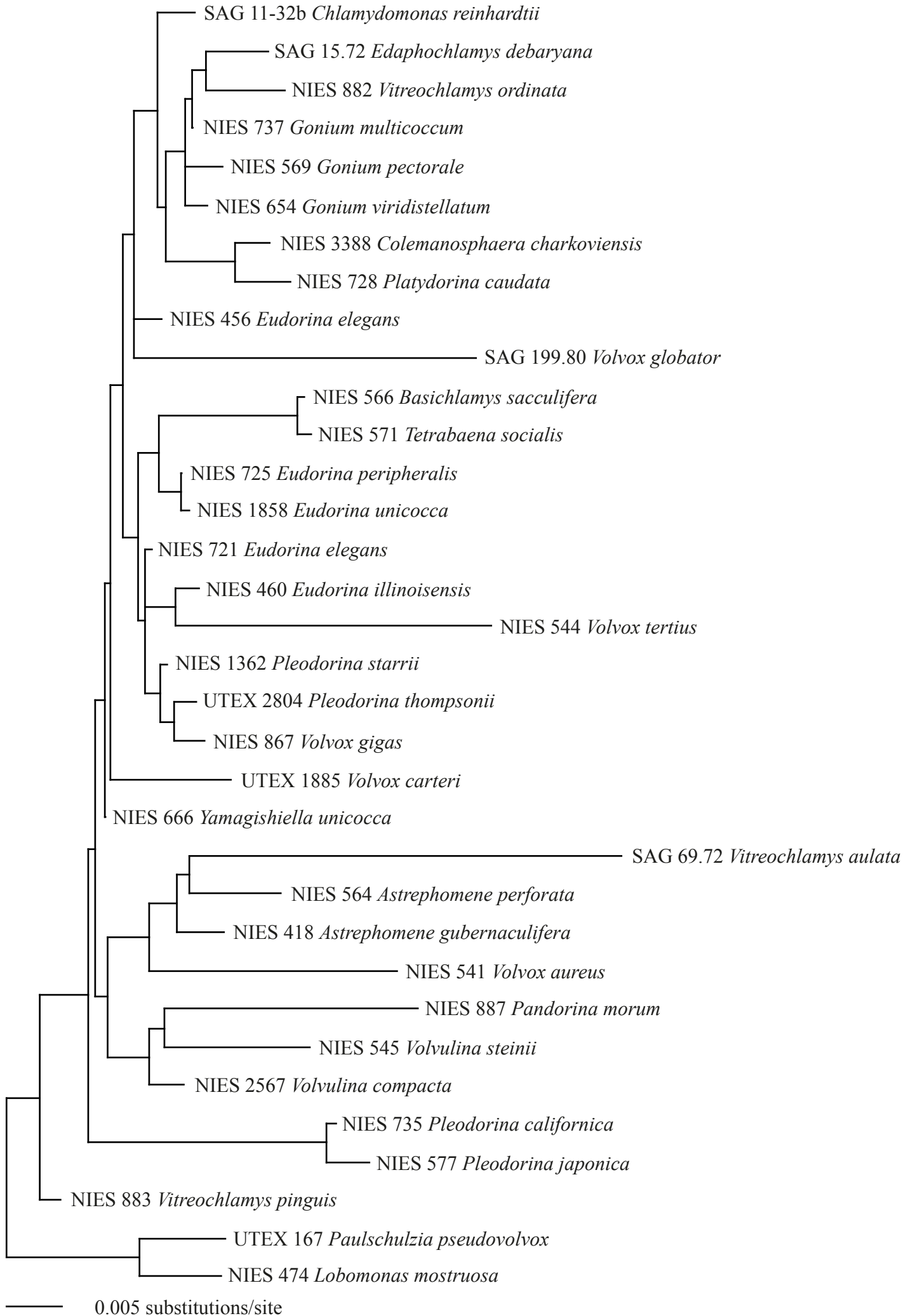
Model settings calculated with Modeltest of the datasets used by Nakada et al. (2016); third codon bases of the protein genes were excluded.

	SSU	rbcL	atpB	psaA	psaB	psbC	all
model	GTR+I+G	TrN+I+G	TrNef+I+G	GTR+I+G	TrNef+I+G	TrN+I+G	GTR+I+G
base frequencies							
freqA	0.2491	0.2617	equal	0.2383	equal	0.2260	0.2431
freqC	0.2177	0.2130	equal	0.2096	equal	0.1925	0.2196
freqG	0.2773	0.2894	equal	0.2478	equal	0.2900	0.2661
freqT	0.2559	0.2360	equal	0.3042	equal	0.2916	0.2712
rate matrix							
R(a) [A-C]	1.3071	1.0000	1.0000	2.6647	1.0000	1.0000	1.2620
R(b) [A-G]	3.1919	1.2922	0.9968	2.4031	1.8453	2.4230	2.4042
R(c) [A-T]	1.8059	1.0000	1.0000	1.2387	1.0000	1.0000	1.3757
R(d) [C-G]	0.5329	1.0000	1.0000	1.7603	1.0000	1.0000	1.1233
R(e) [C-T]	7.6650	5.9852	6.7900	10.6385	4.3715	6.7072	6.7996
R(f) [G-T]	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
I	0.7643	0.7894	0.7525	0.7577	0.7591	0.7954	0.7843
G	0.6561	0.2914	0.4478	0.6872	0.6167	0.4977	0.5779
2cdn							
variable positions	222	68	93	127	138	55	703
total positions	1743	752	752	994	996	520	5757
% variability	12.74	9.04	12.37	12.78	13.86	10.58	12.21
3cdn							
variable positions	-	333	398	528	542	265	2288
total positions	-	1128	1128	1491	1494	780	7764
% variability	-	29.52	35.28	35.41	36.28	33.97	29.47

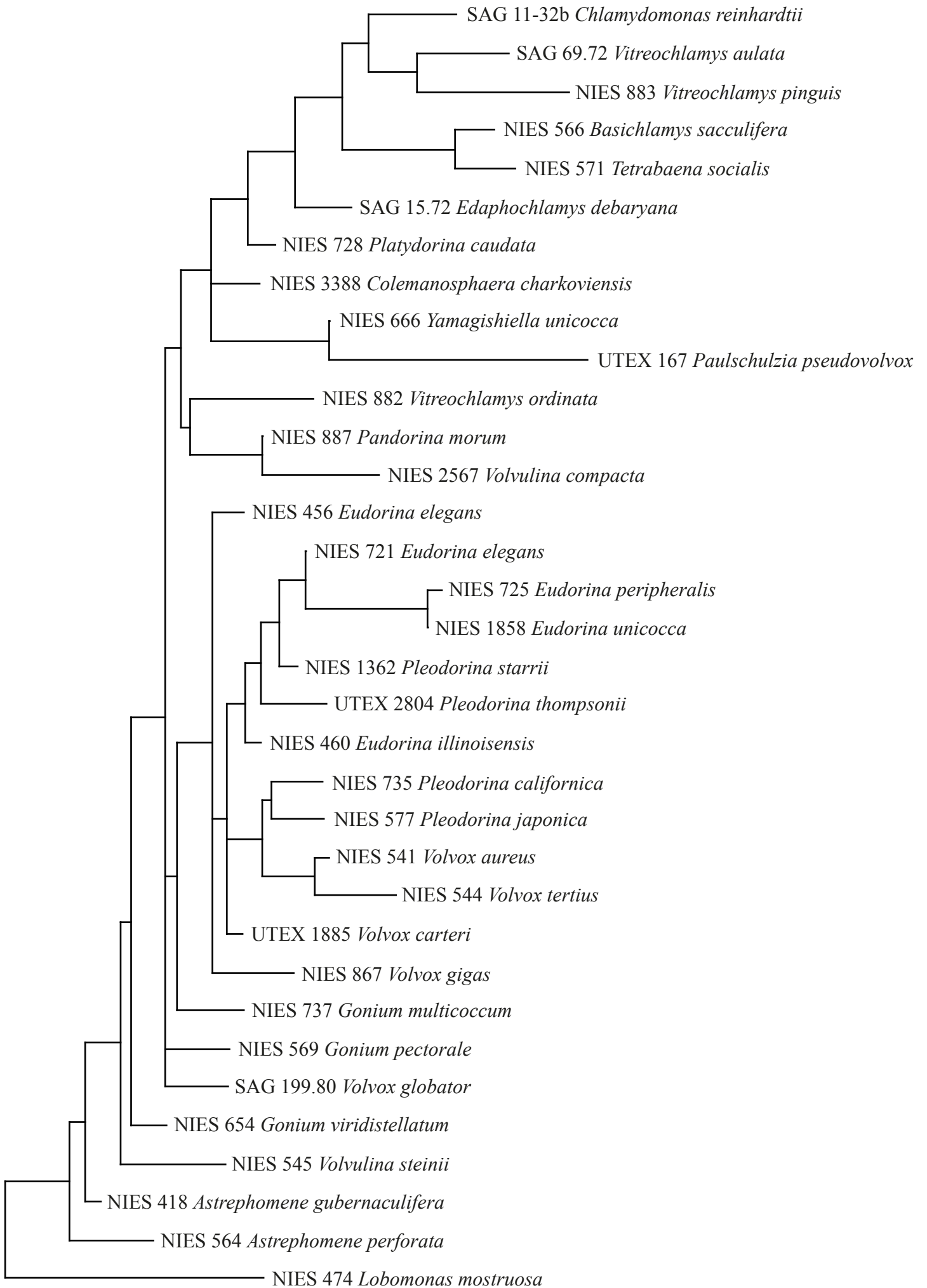
18S+rbcL+atpB+psaA+psaB+psbC (first two codons only by protein genes)



0.005 substitutions/site

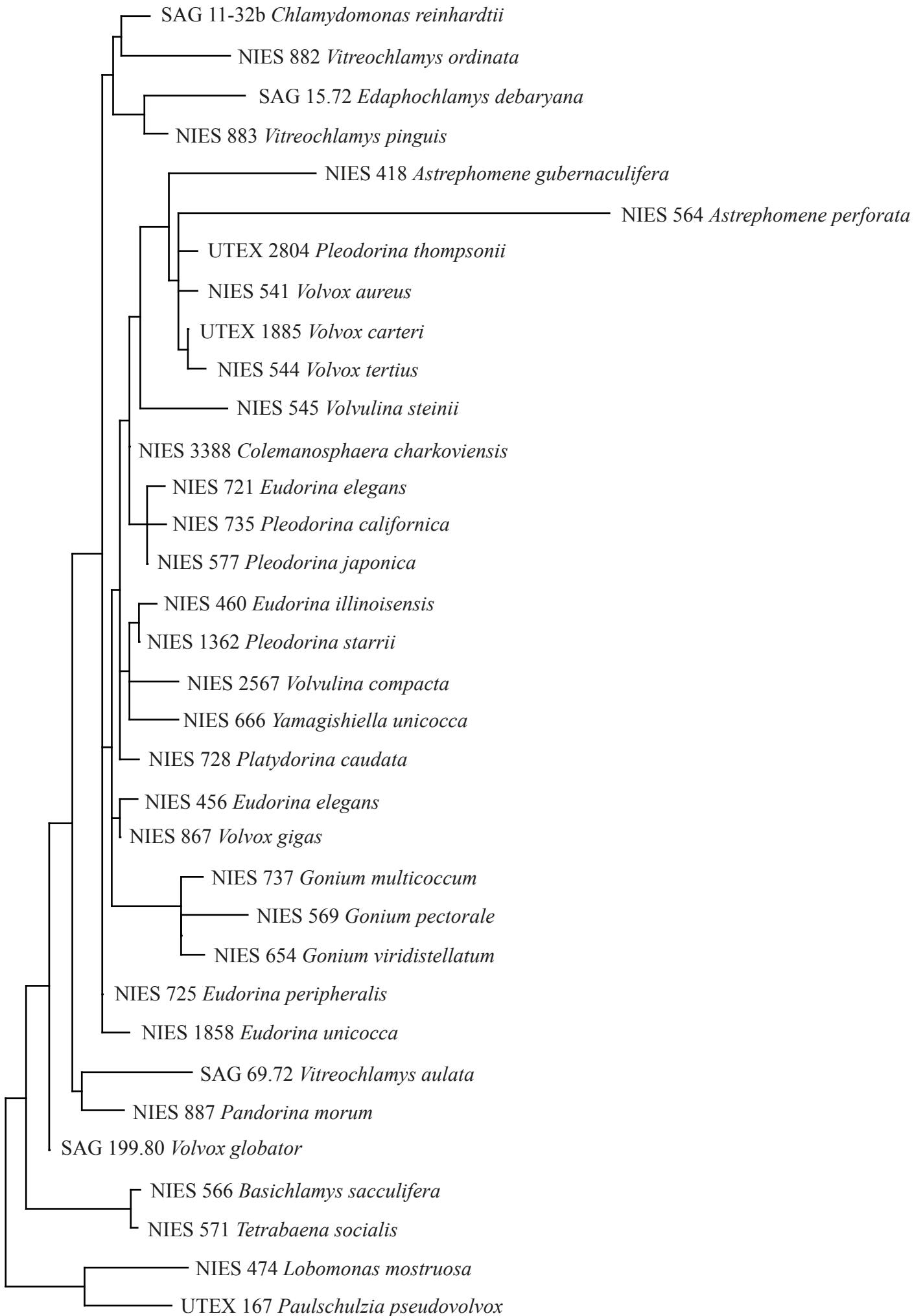


rbcl (first two codon bases only)



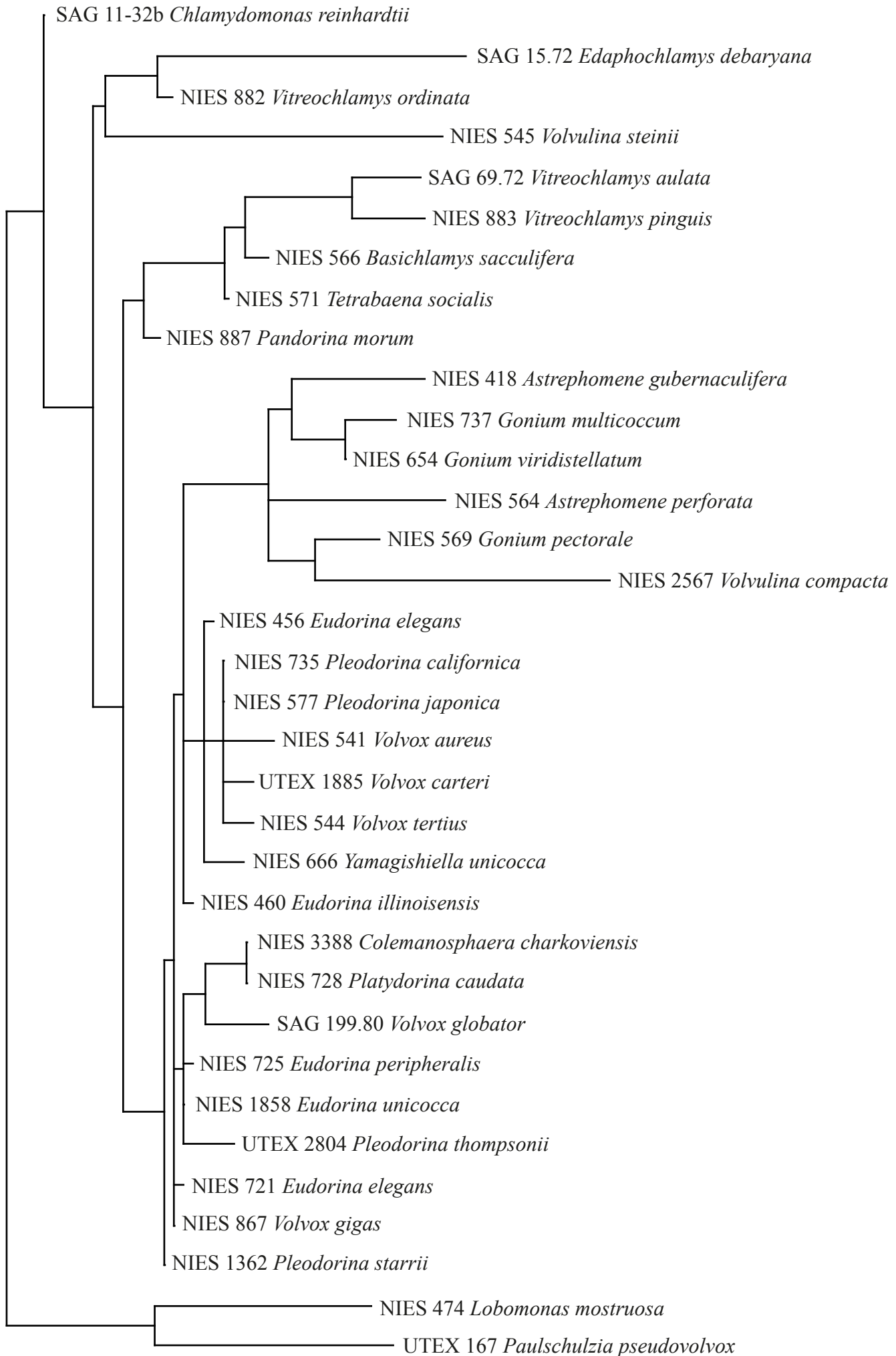
0.005 substitutions/site

atpB (first two codons only)



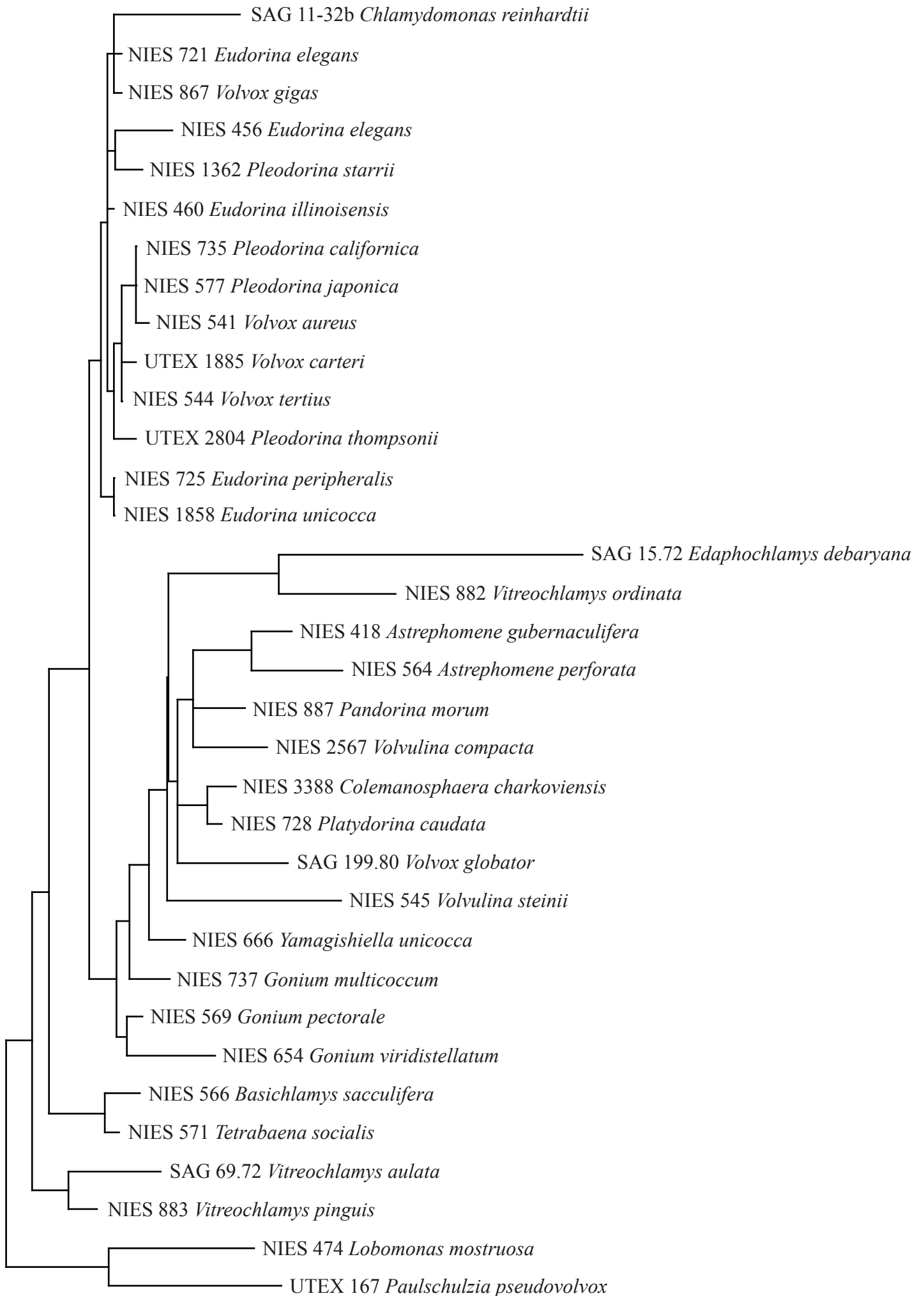
— 0.005 substitutions/site

psaA (first two codon bases only)



— 0.005 substitutions/site

psaB (first two codon bases only)



— 0.005 substitutions/site

psbC (first two codon bases only)

