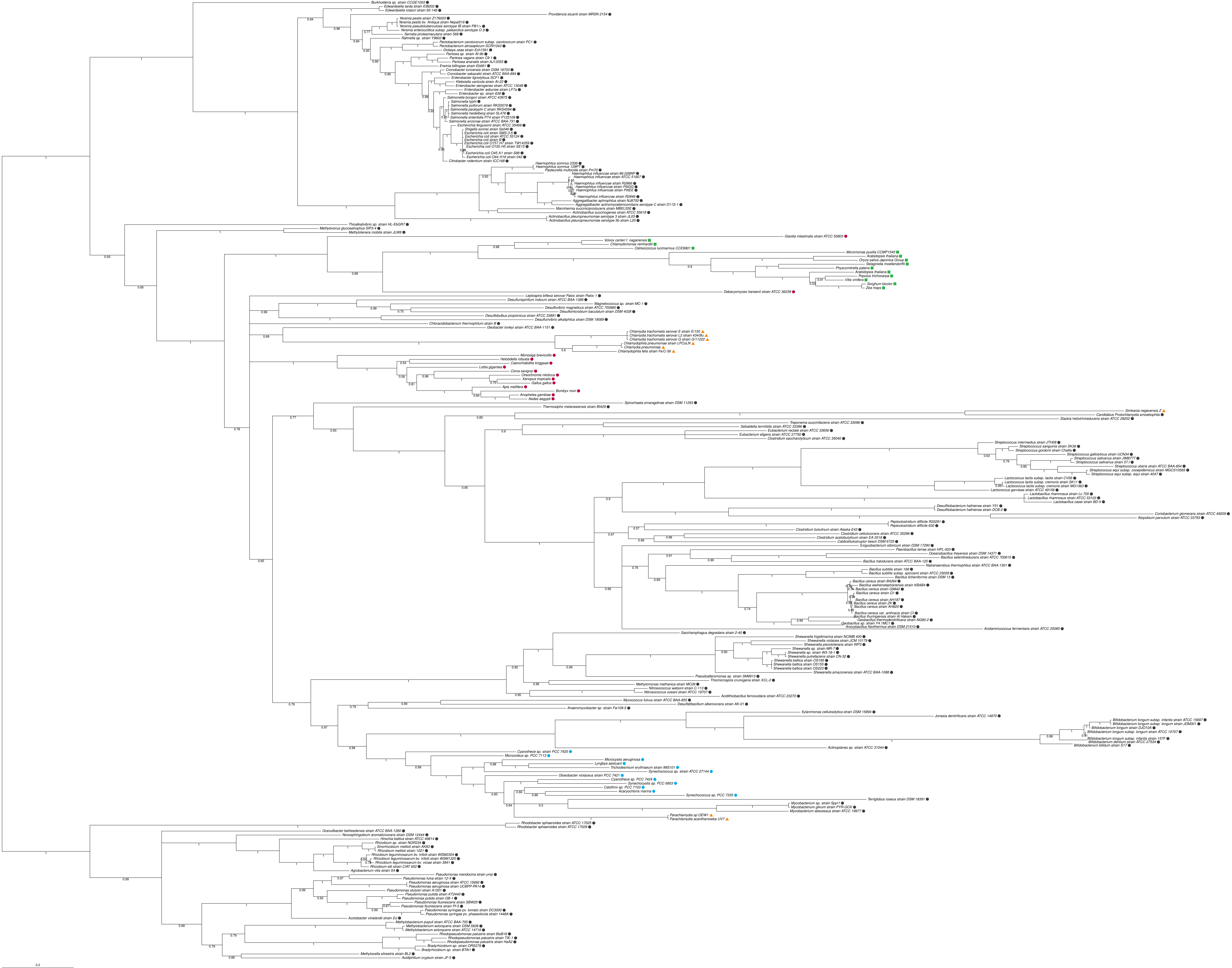


**Supplementary Figure 1: Phylogenetic analysis of the GlgC gene under the CAT+GTR model.** This is the complete tree upon which Fig. 3(a) is based. Archaeplastida sequences are denoted with green squares, *Chlamydiae* with orange triangles, *Cyanobacteria* with cyan circles, and other bacterial groups with black circles. Branch supports are Bayesian posterior probabilities, and branch lengths are proportional to the expected number of substitutions per site, as indicated by the scale bar.





**Supplementary Figure 2: Phylogenetic analysis of the GlgP gene under the CAT+GTR model.** This is the complete tree upon which Fig. 3(b) is based. Archaeplastida sequences are denoted with green squares, other eukaryotes with purple circles, *Chlamydiae* with orange triangles, *Cyanobacteria* with cyan circles, and other bacterial groups with black circles. Branch supports are Bayesian posterior probabilities, and branch lengths are proportional to the expected number of substitutions per site, as indicated by the scale bar.





**Supplementary Figure 3: Phylogenetic analysis of the GlgX gene under the CAT+GTR model.** This is the complete tree upon which Fig. 3(c) is based. Archaeplastida sequences are denoted with green squares, *Chlamydiae* with orange triangles, *Cyanobacteria* with cyan circles, and other bacterial groups with black circles. Branch supports are Bayesian posterior probabilities, and branch lengths are proportional to the expected number of substitutions per site, as indicated by the scale bar.

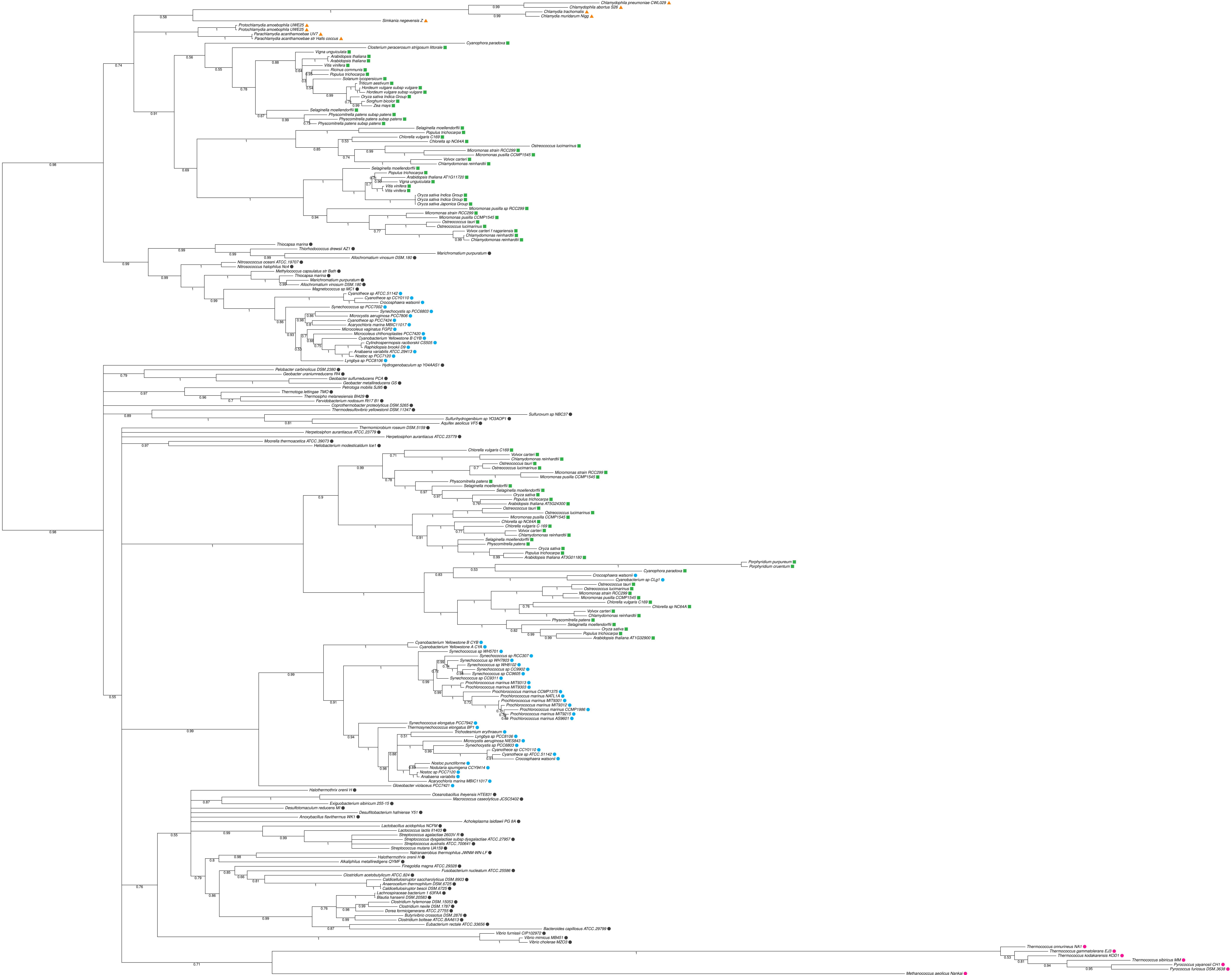




**Supplementary Figure 4: Phylogenetic analysis of the UhpC gene under the CAT+GTR model.** This is the complete tree upon which Fig. 3(d) is based.

Archaeplastida sequences are denoted with green squares, *Chlamydiae* with orange triangles, and other bacterial groups with black circles. Branch supports are Bayesian posterior probabilities, and branch lengths are proportional to the expected number of substitutions per site, as indicated by the scale bar.



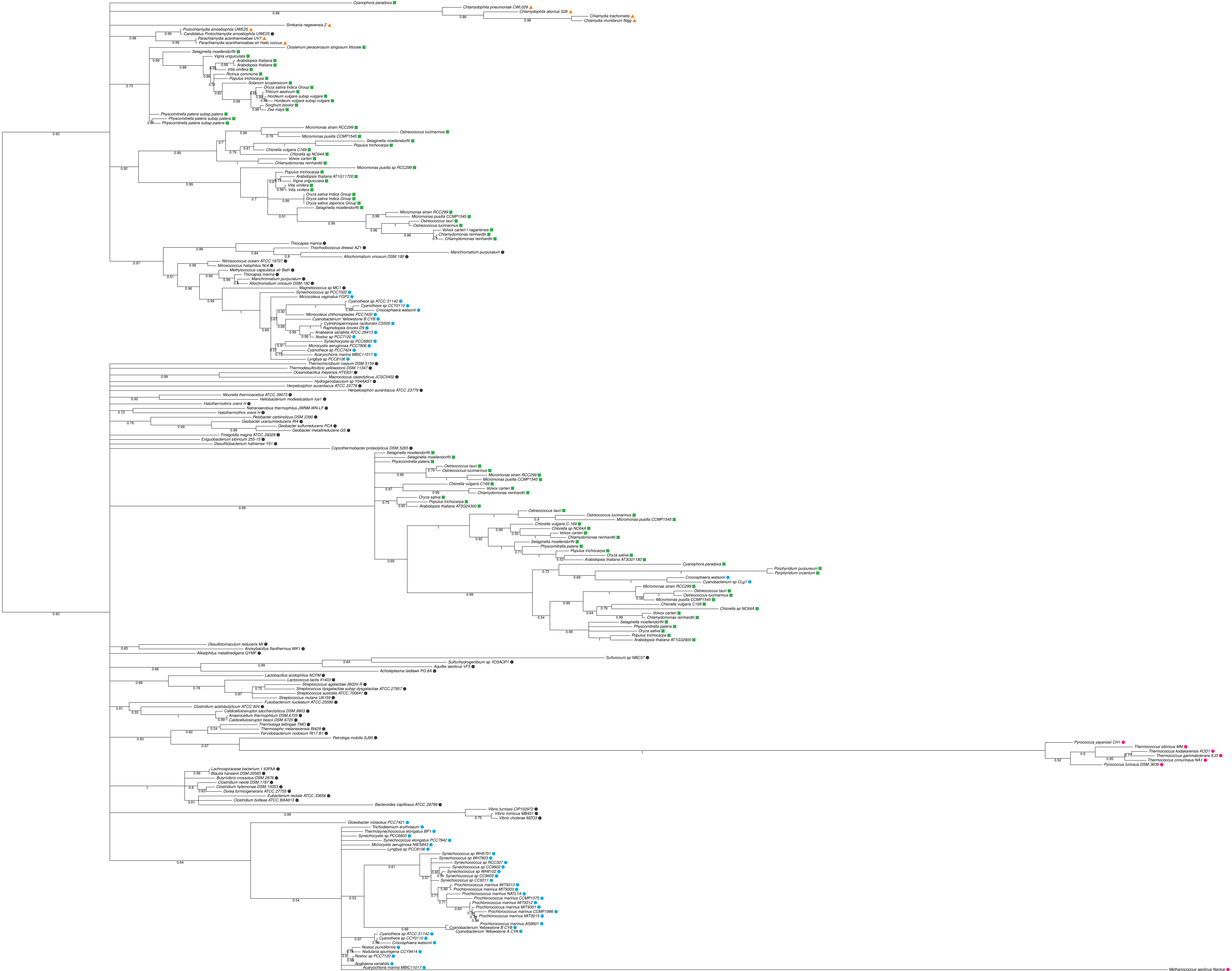


**Supplementary Figure 5: Phylogenetic analysis of the GlgA gene under the CAT+GTR model.** This is the complete tree upon which Fig. 4(a) is based. Archaeplastida sequences are denoted with green squares, *Chlamydiae* with orange triangles, *Cyanobacteria* with cyan circles, other bacterial groups with black circles, and Archaea with pink circles. Branch supports are Bayesian posterior probabilities, and branch lengths are proportional to the expected number of substitutions per site, as indicated by the scale bar.



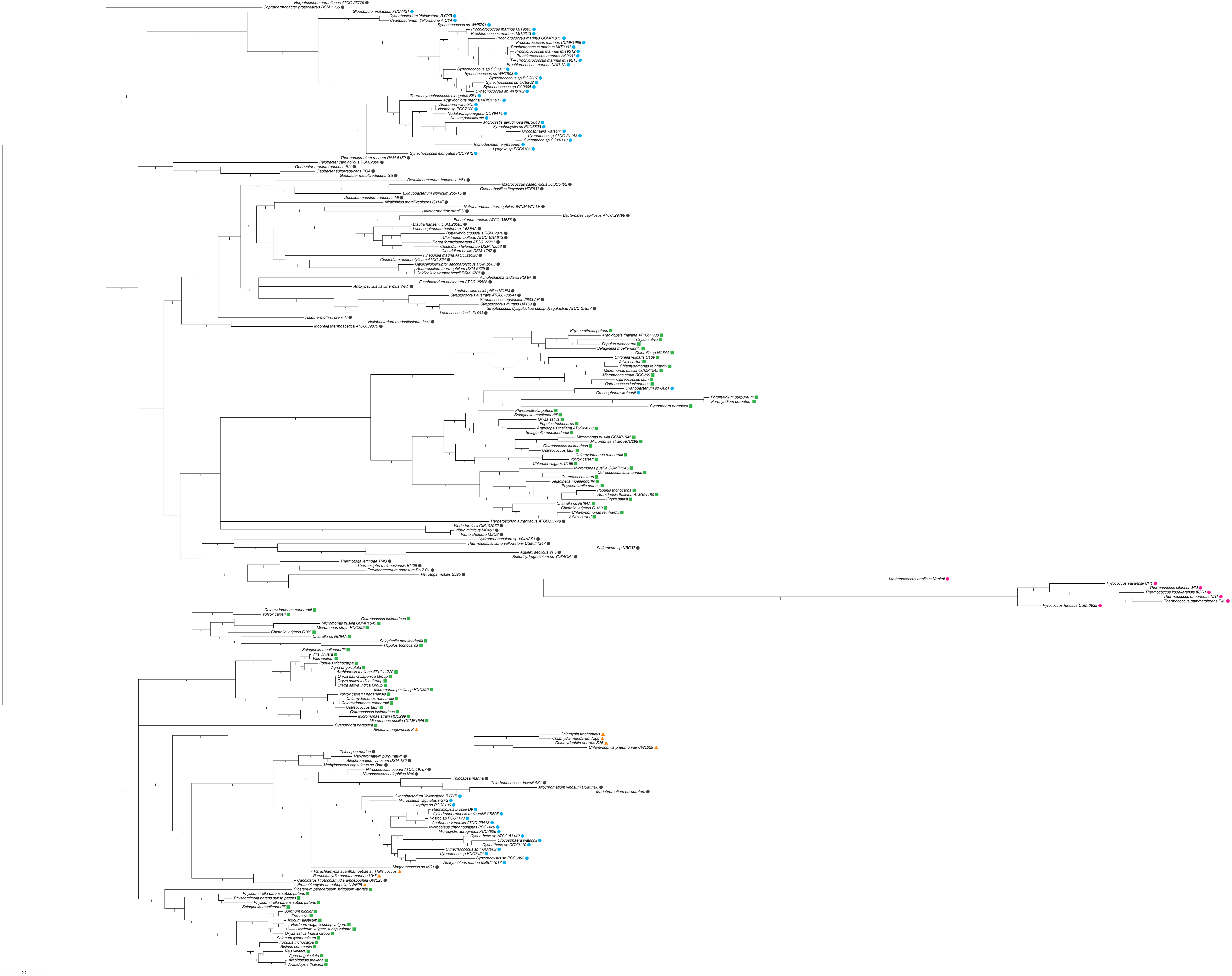


**Supplementary Figure 6: Phylogenetic analysis of the GlgA gene with only the closest outgroup clade under the CAT+GTR model.** This is the complete tree upon which Fig. 4(b) is based. Archaeplastida sequences are denoted with green squares, other eukaryotes with purple circles, *Chlamydiae* with orange triangles, *Cyanobacteria* with cyan circles, and other bacterial groups with black circles. Branch supports are Bayesian posterior probabilities, and branch lengths are proportional to the expected number of substitutions per site, as indicated by the scale bar.



**Supplementary Figure 7: Phylogenetic analysis of the Dayhoff-recoded GlgA alignment under the CAT+GTR model.** This is the complete tree upon which Fig. 4(c) is based. Archaeplastida sequences are denoted with green squares, *Chlamydiae* with orange triangles, *Cyanobacteria* with cyan circles, other bacterial groups with black circles, and Archaea with pink circles. Branch supports are Bayesian posterior probabilities, and branch lengths are proportional to the expected number of substitutions per site, as indicated by the scale bar.





**Supplementary Figure 8: Phylogenetic analysis of the GlgA gene under the nonstationary CAT+BP model.** This is the complete tree upon which Fig. 4(d) is based. Archaeplastida sequences are denoted with green squares, other eukaryotes with purple circles, *Chlamydiae* with orange triangles, *Cyanobacteria* with cyan circles, other bacterial groups with black circles, and Archaea with pink circles. Branch supports are Bayesian posterior probabilities, and branch lengths are proportional to the expected number of substitutions per site, as indicated by the scale bar.

**Supplementary Table 1: Posterior predictive simulations of compositional heterogeneity for the single gene alignments analyzed in this study.**

	Across-site composition			Across-branch composition		
	Observed	Predicted	<i>P</i> -value	Observed	Predicted	<i>P</i> -value
<b>GlgC</b>						
LG	7.78	9.71 +/- 0.1	<b>0</b>	0.0016	0.0014	0.069
CAT+GTR	7.78	7.86 +/- 0.19	0.33	0.004	0.0047 +/- 0.0009	0.63
<b>GlgP</b>						
LG	8.51	11.61 +/- 0.09	<b>0</b>	0.008	0.0026	<b>0</b>
CAT+GTR	8.51	8.91 +/- 0.09	<b>0</b>	0.008	0.0049 +/- 0.00057	<b>0</b>
<b>GlgX</b>						
LG	9.43	11.17 +/- 0.09	<b>0</b>	0.015	0.004	<b>0</b>
CAT+GTR	9.43	9.54 +/- 0.16697	0.24	0.015	0.0059 +/- 0.001	<b>0</b>
<b>UhpC</b>						
LG	8.465	9.84 +/- 0.14	<b>0</b>	0.009	0.0069 +/- 0.0007	<b>0.008</b>
CAT+GTR	8.465	8.41 +/- 0.09	0.71	0.009	0.0068 +/- 0.0008	<b>0.008</b>
<b>GlgA</b>						
LG	10.97	13.64 +/- 0.11	<b>0</b>	0.016	0.0083	<b>0.002</b>
CAT+GTR	10.97	11.49 +/- 0.16	<b>0</b>	0.016	0.009	<b>0.017</b>
CAT+GTR (closest outgroup)	8.253	8.414 +/- 0.2	0.21	0.017	0.008 +/- 0.001	<b>0</b>
CAT+GTR +Dayhoff	4.409	4.408 +/- 0.04	0.49	0.012	0.008	0.1