

Table 6. Results of maximum likelihood analyses. Analyses are distinguished by combination of alignment and outgroup(s) used. Summary statistics shown are: the final log likelihood of each analysis; their AIC, AICc and BIC scores; the total number of free parameters in the analysis; the alignment size (total number of character traits); whether or not trees were able to be successfully rooted in the maximum likelihood tree search and bootstrap analyses; and whether or not bootstraps converged in the bootstopping test.

Analysis Dataset	Outgroup(s) Used	Final Log Likelihood	AIC Score	AICc Score	BIC Score	Free Parameters (model + branch length)	Alignment Size	Search Trees Rooted	Bootstrap Trees Rooted	Bootstrap Convergence
Concatenated Alignment	Zerg_OG Tyranids_OG Xenomorphs_OG	-2544.78	5227.56	14887.56	5382.71	69	70	Rooted	Not Rooted	Yes
Concatenated Alignment	Protoss_OG Zerg_OG Tyranids_OG Xenomorphs_OG	-2544.78	5227.56	14887.56	5382.71	69	70	Not Rooted	Not Rooted	Yes
Concatenated Alignment	Protoss_OG	-2145.14	4416.27	5760.27	4557.92	63	70	Rooted	Rooted	Yes
Physiological Alignment	Zerg_OG	-636.42	1398.84	9462.84	1491.18	63	32	Rooted	--	--
Behavioral Alignment	Zerg_OG	--	--	--	--	--	--	--	--	--
Archetypal Alignment	Zerg_OG	-639.63	1405.26	9469.26	1461.36	63	18	Rooted	Rooted	No
Physiological Alignment	Protoss_OG	-627.05	1380.10	9444.10	1472.44	63	32	Rooted	Rooted	No
Behavioral Alignment	Protoss_OG	--	--	--	--	--	--	--	--	--
Archetypal Alignment	Protoss_OG	-632.35	1390.70	9454.70	1446.80	63	18	Rooted	Rooted	Yes