Table S3

Topology testing.

Topology	Uniform model			Separate model		
	AU test	KH test	SH test	AU test	KH test	SH test
(((Pr,DT)Di)(R,C)A)(Ma,U)	**0.651**	**0.627**	**0.877**	**0.678**	**0.600**	**0.884**
(((Pr,DT)Di)((R,C)A))(Ma,U)	**0.499**	**0.373**	**0.775**	**0.574**	**0.400**	**0.814**
((((Pr,DT)Di)Ma)((R,C)A)U)	**0.111**	**0.159**	**0.376**	**0.241**	**0.236**	**0.588**
((((Pr,DT)Ma)Di)((R,C)A)U)	0.02	**0.051**	**0.065**	**0.166**	**0.168**	**0.32**
(((Pr,DT)(Ma,Di))((R,C)A)U)	0.009	0.029	0.04	0.049	**0.082**	**0.156**
(((((Pr,DT)Di)Ma)(R,C)A)U)	1.00E-68	0	0.002	0.002	0.001	0.022
(((((Pr,DT)Ma)Di)(R,C)A)U)	8.00E-06	1.00E-04	0.001	0.014	0.016	0.055
((((Pr,Ma)DT)Di)((R,C)A)U)	2.00E-04	0.003	0.003	0.001	0.03	0.04
((((DT,Ma)Pr)Di)((R,C)A)U)	1.00E-78	0.001	0.001	3.00E-04	0.011	0.014
((((Pr,DT)(Ma,Di))(R,C)A)U)	1.00E-48	0	1.00E-04	0.001	0.001	0.005
(((((Ma,Pr)DT)Di)(R,C)A)U)	5.00E-65	0	0	4.00E-04	0.001	0.005
(((((Ma,DT)Pr)Di)(R,C)A)U)	2.00E-07	0	0	3.00E-56	2.00E-04	0.001

Table summarizes the p-values of three types of topology tests – the approximately unbiased test (AU), the Kishino-Hasegawa test (KH) and the Shimodaira-Hasegawa test (SH) – all performed with both the uniform or separate (protein-specific) likelihood models. Topology number 1 has the overall highest likelihood for both models. In topologies 1 and 2 the Excavata are polyphyletic, whereas the remaining topologies represent plausible hypothesis where Excavata are monophyletic. The instances in which the topology cannot be rejected at the 5% level of significance are highlighted in bold. A=Archaeplastida, C=Chromalveolata, Di=Discoba, DT=diplomonads and *Trichomas*, Ma=*Malawimonas*, Pr=Preaxostyla, R=Rhizaria, U=unikonts.