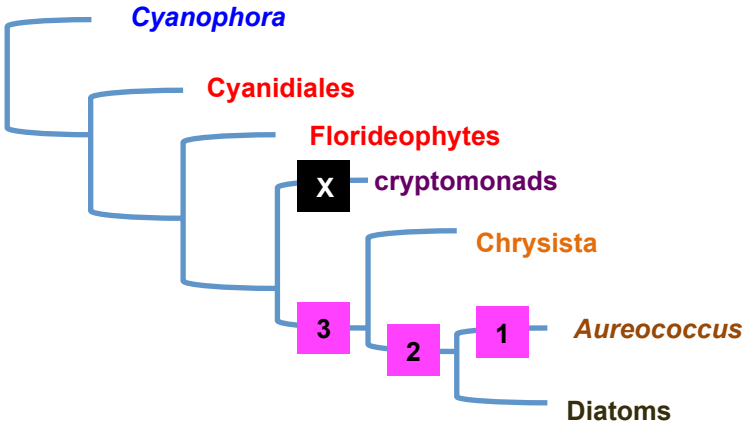
Fig. 9- figure supplement 1. Alternative topology tests of plastid genome trees. Tests were performed with the RAxML + JTT trees inferred for the gene-rich (**panel A**) and taxon-rich (**panel B**) plastid-encoded protein alignments. In each case, a schematic diagram of the tree topology obtained is given (**i**). The black box corresponds to the branch position of haptophytes in the consensus tree; alternative branching positions for the haptophyte sequences are labelled with numbered boxes. The table below (**ii**) lists the probabilities for each alternative position under eight different tests performed with CONSEL. Alternative positions that are not rejected by a topology test are shaded. All possible trees in which the haptophyte sequences branch within the ochrophytes are clearly rejected under all conditions, confirming that its plastid genome is of non-ochrophyte origin. The legend at the bottom of panel B gives full names for each test performed.

A

i)

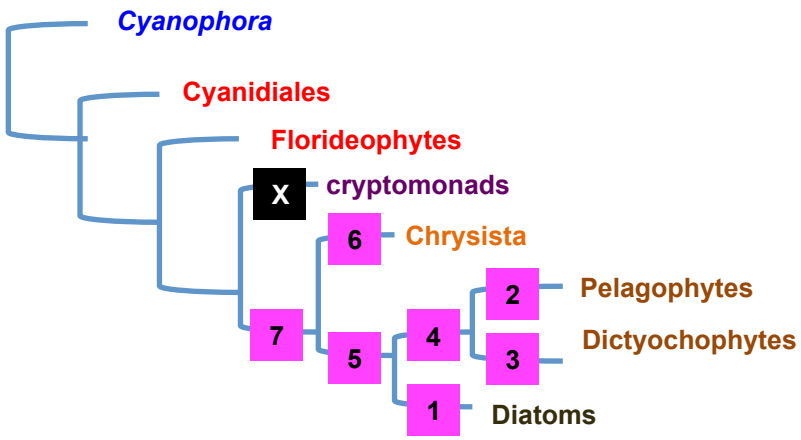


ii)

	haptophytes sister to	AU	NP	BP	PP	KH	SH	WKH	WSH
1	***Aureococcus***	0.004	8E-05	0	0	0	0	0	0
2	***Aureococcus* and diatoms**	0.001	6E-05	0	0	0	0	0	0
3	**All ochrophytes**	**0.057**	0.049	0.05	2E-23	**0.051**	**0.385**	**0.051**	**0.137**

B

i)



ii)

	haptophytes sister to	AU	NP	BP	PP	KH	SH	WKH	WSH
1	**Diatoms**	1E-95	3E-24	0	1E-94	0	0	0	0
2	**Pelagophytes**	5E-05	7E-06	0	1E-109	0	0	0	0
3	**Dictyochophytes**	6E-47	1E-16	0	5E-111	0	0	0	0
4	**Hypogyristea**	2E-06	2E-06	0	1E-106	0	0	0	0
5	**Hypogyristea + diatoms**	7E-75	2E-21	0	2E-99	9E-05	9E-05	0	0
6	**Chrysista**	2E-38	6E-15	0	1E-94	8E-05	8E-05	0	0
7	**All ochrophytes**	**0.423**	**0.418**	**0.419**	3E-04	**0.414**	**0.812**	**0.414**	**0.808**

- **AU - approximately unbiased test**
- **NP & BP - bootstrap probabilities for the selection**
- **PP - bayesian posterior probability (using BIC)**
- **KH - Kishino-Hasegawa test**
- **SH - Shimodaira-Hasegawa test**
- **WKH & WSH - weighted versions of the above two tests**