Table S4: Binomial logistic regression results for a range of datasets, excluding highly influential genes based on studentized residuals, leverage and Cook's distance and including all predictors, both ignoring and considering BS ≥ 70% support. Parameters are not transformed i.e. they represent the estimated ceteris paribus effect of the predictor on log odds. Quantities in brackets are standard errors. The genes *ycf1* and *ycf2* were uniformly removed due to their long tree and alignment length. Other genes removed are as follows: FSA AA cln, FSA AA cln BS ≥ 70: *rpl32*, high tree length. FSA nuc cln: *clpP*, poor concordance relative to length; *rps15*, relatively high tree length. FSA nuc cln BS ≥ 70: as not considering support, but *clpP* is included. MAFFT AA: *ndhJ*, high concordance relative to length; *rpl22*, high tree length; *rpl32*, high tree length. MAFFT AA BS ≥ 70: *rpoB*, highly concordant relative to length and tree length. MAFFT nuc: *clpP*, poor concordance relative to alignment and tree length. MAFFT nuc BS ≥ 70: *rps15*, poor performance relative to tree length. WAG: *rpl32*, high tree length; *rpoC2*, very high concordance. WAG BS ≥ 70: *rpoC2*, very high concordance.

	Dependent variable: Total Concordant/Total Discordant									
	FSA cln AA	FSA cln AA BS ≥ 70	FSA cln nuc	FSA cln nuc BS ≥ 70	MAFFT AA	MAFFT AA BS ≥ 70	MAFFT nuc	MAFFT nuc BS ≥ 70	WAG	WAG BS ≥ 70
alignment_length	0.002***	0.002***	0.001***	0.001***	0.002***	0.002***	0.001***	0.001***	0.002***	0.002***
	(0.0002)	(0.0002)	(0.0001)	(0.0001)	(0.0002)	(0.0002)	(0.0001)	(0.0001)	(0.0002)	(0.0002)
tree_length	0.709***	0.709***	1.133***	1.063***	0.703***	0.545***	0.760***	0.819***	0.636***	0.536***
	(0.061)	(0.061)	(0.142)	(0.113)	(0.058)	(0.049)	(0.098)	(0.093)	(0.065)	(0.051)
variance	-51.572***	-51.572***	-214.123***	-174.957***	-57.590***	-36.888***	-85.038***	-92.043***	-55.714***	-32.252***
	(11.301)	(11.301)	(60.266)	(36.877)	(9.389)	(6.835)	(22.402)	(16.402)	(11.792)	(6.856)
Constant	-2.715***	-2.715***	-1.949***	-1.927***	-2.736***	-2.580***	-1.800***	-1.840***	-2.562***	-2.517***
	(0.088)	(0.088)	(0.113)	(0.109)	(0.089)	(0.083)	(0.104)	(0.104)	(0.086)	(0.083)
Observations	76	76	75	76	74	76	76	76	75	76
Log Likelihood	-242.311	-242.311	-239.310	-241.719	-225.654	-254.021	-260.033	-257.260	-238.827	-243.560
Akaike Inf. Crit.	492.621	492.621	486.620	491.439	459.308	516.042	528.067	522.520	485.654	495.121

Note: *p<0.1; **p<0.05; ***p<0.01