

Table S3: Quasibinomial logistic regression results for all genes from a range of datasets, including all predictors, both ignoring and considering $BS \geq 70\%$ 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. Dispersion gives the estimated quasibinomial dispersion parameter.

Dependent variable: Total Concordant/Total Discordant												
	FSA cln AA		FSA cln AA		FSA cln nuc		MAFFT AA		MAFFT nuc		WAG	WAG
	BS \geq 70		BS \geq 70		BS \geq 70		BS \geq 70		BS \geq 70			BS \geq 70
alignment_length	0.001*** (0.0003)	0.001 (0.001)	0.001*** (0.0001)	0.001*** (0.0001)	0.001*** (0.0002)	0.001*** (0.0001)	0.0003*** (0.0001)	0.0004*** (0.0001)	0.0002** (0.0001)	0.0002** (0.0001)		
tree_length	0.539*** (0.122)	0.746 (0.709)	1.124*** (0.185)	1.350*** (0.199)	0.680*** (0.085)	0.702*** (0.066)	0.925*** (0.193)	1.390*** (0.256)	0.616*** (0.122)	0.736*** (0.169)		
variance	-39.588** (18.726)	-106.125 (133.489)	-245.838*** (59.407)	-374.209*** (62.058)	-62.247*** (7.986)	-63.180*** (6.008)	-145.851*** (39.803)	-371.749*** (75.183)	-53.085*** (19.897)	-99.388*** (35.646)		
Constant	-2.238*** (0.182)	-3.261*** (1.036)	-1.738*** (0.185)	-2.852*** (0.210)	-2.427*** (0.155)	-3.468*** (0.144)	-1.489*** (0.216)	-2.721*** (0.275)	-2.062*** (0.167)	-2.982*** (0.216)		
Dispersion	6.116	104.083	3.255	2.643	4.054	1.794	5.194	4.927	5.718	5.041		
Observations	79	79	79	79	79	79	79	79	79	79		

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