

**Table S2:** Binomial 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.

Dependent variable: Total Concordant/Total Discordant										
	FSA cln AA	FSA cln AA	FSA cln nuc	FSA cln nuc	MAFFT AA	MAFFT AA	MAFFT nuc	MAFFT nuc	WAG	WAG
	$BS \geq 70$		$BS \geq 70$		$BS \geq 70$		$BS \geq 70$			$BS \geq 70$
alignment_length	0.001*** (0.0001)	0.001*** (0.0001)	0.001*** (0.00004)	0.001*** (0.00004)	0.001*** (0.0001)	0.001*** (0.0001)	0.0003*** (0.00003)	0.0004*** (0.00003)	0.0002*** (0.00004)	0.0002*** (0.00004)
tree_length	0.539*** (0.049)	0.746*** (0.070)	1.124*** (0.103)	1.350*** (0.122)	0.680*** (0.042)	0.702*** (0.049)	0.925*** (0.085)	1.390*** (0.115)	0.616*** (0.051)	0.736*** (0.075)
variance	-39.588*** (7.572)	-106.125*** (13.084)	-245.838*** (32.927)	-374.209*** (38.174)	-62.247*** (3.966)	-63.180*** (4.486)	-145.851*** (17.464)	-371.749*** (33.871)	-53.085*** (8.321)	-99.388*** (15.877)
Constant	-2.238*** (0.073)	-3.261*** (0.102)	-1.738*** (0.102)	-2.852*** (0.129)	-2.427*** (0.077)	-3.468*** (0.107)	-1.489*** (0.095)	-2.721*** (0.124)	-2.062*** (0.070)	-2.982*** (0.096)
Observations	79	79	79	79	79	79	79	79	79	79
Log Likelihood	-319.263	-201.664	-283.221	-246.157	-281.726	-184.137	-348.941	-280.545	-345.767	-233.138
Akaike Inf. Crit.	646.526	411.327	574.443	500.313	571.451	376.274	705.883	569.090	699.535	474.275

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