

Table S16: Quasibinomial logistic regression results for all genes from both amino acid and nucleotide 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				
<i>glm: quasibinomial</i>				
<i>link = logit</i>				
	AA	AA BS ≥ 70	Nuc	Nuc BS ≥ 70
Length	0.0002** (0.0001)	0.0002* (0.0001)	0.0002*** (0.00004)	0.0002*** (0.00004)
Tree_Length	0.589*** (0.123)	0.701*** (0.186)	1.306*** (0.222)	1.649*** (0.266)
Root-to-tip Variance	-41.119*** (14.787)	-74.377** (31.532)	-310.777*** (73.500)	-504.933*** (91.484)
Constant	-2.012*** (0.183)	-2.968*** (0.273)	-1.618*** (0.215)	-2.732*** (0.266)
Dispersion	7.096	8.575	4.587	4.383
Observations	79	79	79	79

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