

Table S17: Quasibinomial 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 $\geq 70\%$ 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. For details of genes removed see main text.

Dependent variable: Total Concordant/Total Discordant				
<i>glm: quasibinomial</i>				
<i>link = logit</i>				
	AA	AA BS ≥ 70	Nuc	Nuc BS ≥ 70
Length	0.002 ^{***} (0.0003)	0.002 ^{***} (0.0002)	0.001 ^{***} (0.0001)	0.001 ^{***} (0.0001)
Tree_Length	0.772 ^{***} (0.129)	0.677 ^{***} (0.094)	1.138 ^{***} (0.242)	1.138 ^{***} (0.242)
Root-to-tip Variance	-98.944 ^{***} (29.067)	-76.416 ^{***} (22.918)	-234.793 ^{**} (93.245)	-234.793 ^{**} (93.245)
Constant	-2.546 ^{***} (0.156)	-3.557 ^{***} (0.126)	-1.894 ^{***} (0.189)	-1.894 ^{***} (0.189)
Dispersion	3.557	1.27	2.792	2.792
Observations	75	75	75	75

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