Table S15: 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. For details of genes removed, see main text.

	Dependent variable: Total Concordant/Total Discordant			
	logistic			
	AA	AA BS ≥ 70	Nuc	Nuc BS ≥ 70
Length	0.002***	0.002***	0.001***	0.001***
	(0.0001)	(0.0002)	(0.0001)	(0.0001)
Tree_Length	0.772***	0.677***	1.138***	1.138***
	(0.068)	(0.083)	(0.145)	(0.145)
Root-to-tip Variance	-98.944***	-76.416***	-234.793***	-234.793***
	(15.412)	(20.333)	(55.806)	(55.806)
Constant	-2.546***	-3.557***	-1.894***	-1.894***
	(0.083)	(0.111)	(0.113)	(0.113)
Observations	75	75	75	75
Log Likelihood	-257.248	-156.195	-253.832	-253.832
Akaike Inf. Crit.	522.496	320.391	515.665	515.665

Note: $^{*}p<0.1$; $^{**}p<0.05$; $^{***}p<0.01$