

Table S18: Binomial logistic regression results for amino acid and nucleotide datasets, including only alignment length and tree length, 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.

Dependent Variable: Total Concordant/Total Discordant				
	<i>logistic</i>			
	AA	AA $BS \geq 70$	Nuc	Nuc $BS \geq 70$
Length	0.0002*** (0.00004)	0.0002*** (0.00003)	0.0001*** (0.00002)	0.0001*** (0.00001)
Tree_Length	0.266*** (0.027)	0.223*** (0.032)	0.567*** (0.063)	0.412*** (0.068)
Constant	-1.756*** (0.060)	-2.575*** (0.076)	-1.187*** (0.087)	-1.867*** (0.097)
Observations	79	79	79	79
Log Likelihood	-430.988	-295.026	-390.554	-395.112
Akaike Inf. Crit.	867.975	596.053	787.109	796.225

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