Table S20: Quasibinomial logistic regression results for amino acid and nucleotide datasets, including only alignment length and tree length, 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. Dispersion gives the estimated quasibinomial dispersion parameter.

	Dependent Variable: Total Concordant/Total Discordant			
	glm: quasibinomial			
	link = logit			
	AA	AA BS ≥ 70	Nuc	Nuc BS ≥ 70
Length	0.0002^{**}	0.0002^{**}	0.0001^{***}	0.0001^{***}
	(0.0001)	(0.0001)	(0.0001)	(0.00004)
Tree_Length	0.266^{***}	0.223^{***}	0.567^{***}	0.412^{**}
	(0.076)	(0.072)	(0.166)	(0.176)
Constant	-1.756^{***}	-2.575^{***}	-1.187^{***}	-1.867^{***}
	(0.168)	(0.173)	(0.229)	(0.249)
Dispersion	7.827	5.175	6.862	6.621
Observations	79	79	79	79

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