Supplementary Information: Relative model selection of evolutionary substitution models is sensitive to multiple sequence alignment uncertainty

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Supplementary Figures

Figure S1

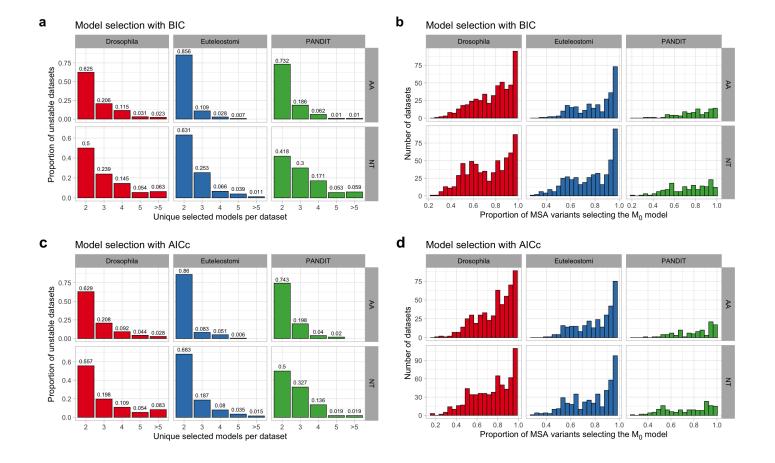


Figure S2

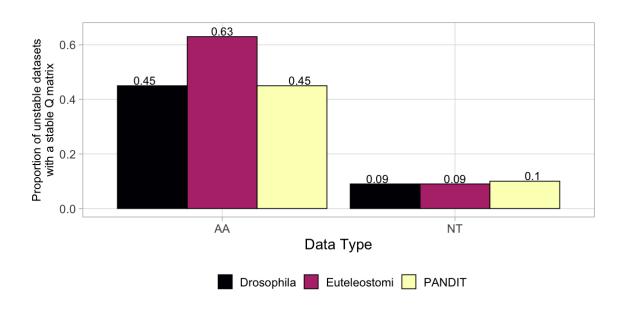
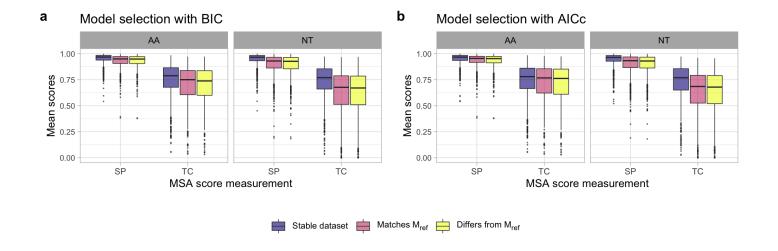


Figure S3



Supplementary Tables

Table S1

SP and TC scores comparisons among groups Model selection with BIC						
Datatype	Score type	Comparison	Effect size (99% CI)	Adjusted P-value		
AA	SP	differs-matches	-0.002 (-0.011, 0.008)	0.867		
AA	SP	stable-matches	0.023 (0.015, 0.032)	0.000		
AA	SP	stable-differs	0.025 (0.017, 0.033)	0.000		
AA	TC	differs-matches	-0.006 (-0.034, 0.021)	0.769		
AA	тс	stable-matches	0.049 (0.026, 0.073)	0.000		
AA	тс	stable-differs	0.056 (0.032, 0.079)	0.000		
NT	SP	differs-matches	-0.003 (-0.015, 0.009)	0.739		
NT	SP	stable-matches	0.05 (0.038, 0.062)	0.000		
NT	SP	stable-differs	0.053 (0.041, 0.065)	0.000		
NT	TC	differs-matches	-0.007 (-0.033, 0.019)	0.699		
NT	тс	stable-matches	0.105 (0.079, 0.132)	0.000		
NT	тс	stable-differs	0.112 (0.086, 0.139)	0.000		

Table S2

SP and TC scores comparisons among groups

Model selection with AICc

Datatype	Score type	Comparison	Effect size (99% CI)	Adjusted P-value
AA	SP	differs-matches	-0.002 (-0.012, 0.007)	0.762
AA	SP	stable-matches	0.016 (0.008, 0.025)	0.000
AA	SP	stable-differs	0.019 (0.01, 0.027)	0.000
AA	TC	differs-matches	-0.008 (-0.034, 0.018)	0.653
AA	TC	stable-matches	0.025 (0.001, 0.048)	0.006
AA	TC	stable-differs	0.033 (0.009, 0.056)	0.000
NT	SP	differs-matches	-0.002 (-0.014, 0.01)	0.831
NT	SP	stable-matches	0.044 (0.032, 0.056)	0.000
NT	SP	stable-differs	0.046 (0.034, 0.058)	0.000
NT	TC	differs-matches	-0.006 (-0.032, 0.02)	0.788
NT	TC	stable-matches	0.095 (0.068, 0.121)	0.000
NT	тс	stable-differs	0.101 (0.074, 0.127)	0.000