

Table S1. Maximum likelihood and Bayesian inference fits of 24 different nucleotide substitution models.

Model	AIC	BIC
GTR+G+I	353031.033	353643.490
GTR+G	353200.724	353800.682
GTR+I	353614.946	354214.904
HKY+G	354111.048	354661.01
T92+G	354143.419	354668.383
TN93+G	354109.835	354672.296
GTR	354109.393	354696.852
HKY+G+I	354269.828	354832.289
T92+G+I	354301.964	354839.427
TN93+G+I	354268.764	354843.724
HKY+I	354355.475	354905.437
T92+I	354387.773	354912.737
TN93+I	354353.758	354916.219
HKY	354867.021	355404.484
T92	354899.058	355411.523
TN93	354864.971	355414.933
K2+G	363159.029	363671.494
K2+G+I	363372.122	363897.085
K2+I	363391.878	363904.342
K2	363918.337	364418.303
JC+G+I	364789.547	365302.012
JC+G	364822.607	365322.572
JC+I	365137.003	365636.968
JC	365653.674	366141.141

AIC: Akaike Information Criterion; BIC: Bayesian Information Criterion