Supplemental Table 3. Maximum Likelihood fits of 24 different nucleotide substitution models

Model	Parameters	BIC	AICc	lnL	(+I)	(+G)	R	f(A)	f(T)	f(C)	f(G)	r(AT)	r(AC)	r(AG)	r(TA)	r(TC)	r(TG)	r(CA)	r(CT)	r(CG)	r(GA)	r(GT)	r(GC)
T92+G+I	685	24971.58	18612.06	-8615.17	0.22	0.42	1.79	0.279	0.279	0.221	0.221	0.05	0.039	0.143	0.05	0.143	0.039	0.05	0.18	0.039	0.18	0.05	0.039
T92+G	684	24987.55	18637.3	-8628.81	n/a	0.34	1.8	0.279	0.279	0.221	0.221	0.049	0.039	0.143	0.049	0.143	0.039	0.049	0.18	0.039	0.18	0.049	0.039
K2+G+I	684	24987.85	18637.6	-8628.96	0.23	0.45	1.78	0.25	0.25	0.25	0.25	0.045	0.045	0.16	0.045	0.16	0.045	0.045	0.16	0.045	0.16	0.045	0.045
GTR+G+I	691	25003.7	18588.58	-8597.33	0.23	0.45	1.77	0.265	0.293	0.212	0.23	0.053	0.036	0.121	0.048	0.162	0.051	0.045	0.223	0.03	0.139	0.065	0.028
K2+G	683	25004.99	18664.01	-8643.18	n/a	0.34	1.8	0.25	0.25	0.25	0.25	0.045	0.045	0.161	0.045	0.161	0.045	0.045	0.161	0.045	0.161	0.045	0.045
GTR+G	690	25019.58	18613.73	-8610.92	n/a	0.34	1.79	0.265	0.293	0.212	0.23	0.053	0.036	0.122	0.048	0.162	0.051	0.045	0.223	0.03	0.14	0.065	0.027
TN93+G+I	688	25073.91	18686.6	-8649.39	0.24	0.49	1.8	0.265	0.293	0.212	0.23	0.052	0.038	0.119	0.047	0.164	0.041	0.047	0.226	0.041	0.137	0.052	0.038
HKY+G+I	687	25080.58	18702.53	-8658.38	0.22	0.44	1.81	0.265	0.293	0.212	0.23	0.052	0.037	0.149	0.047	0.138	0.04	0.047	0.19	0.04	0.172	0.052	0.037
HKY+G	686	25093.28	18724.49	-8670.37	n/a	0.35	1.83	0.265	0.293	0.212	0.23	0.051	0.037	0.15	0.046	0.138	0.04	0.046	0.19	0.04	0.172	0.051	0.037
TN93+G	687	25094.9	18716.85	-8665.53	n/a	0.35	1.82	0.265	0.293	0.212	0.23	0.051	0.037	0.121	0.046	0.163	0.04	0.046	0.225	0.04	0.14	0.051	0.037
JC+G+I	683	25539.8	19198.82	-8910.59	0.25	0.49	0.5	0.25	0.25	0.25	0.25	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083
JC+G	682	25560.7	19228.99	-8926.69	n/a	0.36	0.5	0.25	0.25	0.25	0.25	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083
K2+I	683	26880.68	20539.69	-9581.02	0.36	n/a	1.53	0.25	0.25	0.25	0.25	0.049	0.049	0.151	0.049	0.151	0.049	0.049	0.151	0.049	0.151	0.049	0.049
T92+I	684	26887.8	20537.55	-9578.94	0.36	n/a	1.51	0.279	0.279	0.221	0.221	0.055	0.044	0.134	0.055	0.134	0.044	0.055	0.169	0.044	0.169	0.055	0.044
GTR+I	690	26907.73	20501.88	-9554.99	0.36	n/a	1.47	0.265	0.293	0.212	0.23	0.067	0.035	0.114	0.061	0.15	0.055	0.044	0.207	0.034	0.132	0.07	0.031
TN93+I	687	26945.13	20567.08	-9590.65	0.36	n/a	1.51	0.265	0.293	0.212	0.23	0.058	0.042	0.115	0.052	0.15	0.045	0.052	0.207	0.045	0.133	0.058	0.042
HKY+I	686	26964.36	20595.57	-9605.91	0.36	n/a	1.53	0.265	0.293	0.212	0.23	0.057	0.042	0.14	0.052	0.129	0.045	0.052	0.178	0.045	0.161	0.057	0.042
JC+I	682	27380.6	21048.89	-9836.64	0.36	n/a	0.5	0.25	0.25	0.25	0.25	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083
GTR	689	28321.64	21925.06	-10267.6	n/a	n/a	1.49	0.265	0.293	0.212	0.23	0.06	0.037	0.105	0.054	0.159	0.053	0.047	0.219	0.04	0.121	0.067	0.037
T92	683	28323.94	21982.96	-10302.7	n/a	n/a	1.49	0.279	0.279	0.221	0.221	0.056	0.044	0.133	0.056	0.133	0.044	0.056	0.168	0.044	0.168	0.056	0.044
K2	682	28341.05	22009.33	-10316.9	n/a	n/a	1.49	0.25	0.25	0.25	0.25	0.05	0.05	0.149	0.05	0.149	0.05	0.05	0.149	0.05	0.149	0.05	0.05
TN93	686	28357.88	21989.1	-10302.7	n/a	n/a	1.51	0.265	0.293	0.212	0.23	0.058	0.042	0.105	0.052	0.159	0.045	0.052	0.22	0.045	0.121	0.058	0.042
HKY	685	28416.33	22056.81	-10337.5	n/a	n/a	1.51	0.265	0.293	0.212	0.23	0.058	0.042	0.139	0.052	0.128	0.045	0.052	0.177	0.045	0.16	0.058	0.042
JC	681	28830.23	22507.78	-10567.1	n/a	n/a	0.5	0.25	0.25	0.25	0.25	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083	0.083

NOTE.-- Models with the lowest BIC scores (Bayesian Information Criterion) are considered to describe the substitution pattern the best. For each model, AICc value (Akaike Information Criterion, corrected), Maximum Likelihood value (lnL), and the number of parameters (including branch lengths) are also presented [1]. Non-uniformity of evolutionary rates among sites may be modeled by using a discrete Gamma distribution (+G) with 5 rate categories and by assuming that a certain fraction of sites are evolutionarily invariable (+I). Whenever applicable, estimates of gamma shape parameter and/or the estimated fraction of invariant sites are shown. Assumed or estimated values of transition/transversion bias (R) are shown for each model, as well. They are followed by nucleotide frequencies (f) and rates of base substitutions (r) for each nucleotide pair. Relative values of instantaneous r should be considered when evaluating them. For simplicity, sum of r values is made equal to 1 for each model. For estimating ML values, a tree topology was automatically computed. The analysis involved **342** nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions with less than 95% site coverage were eliminated. That is, fewer than 5% alignment gaps, missing data, and ambiguous bases were allowed at any position. There were a total of 238 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 [2].

Abbreviations: GTR: General Time Reversible; HKY: Hasegawa-Kishino-Yano; TN93: Tamura-Nei; T92: Tamura 3-parameter; K2: Kimura 2-parameter; JC: Jukes-Cantor.

1. Nei M. and Kumar S. (**2000**). *Molecular Evolution and Phylogenetics*. Oxford University Press, New York.

2. Tamura K., Peterson D., Peterson N., Stecher G., Nei M., and Kumar S. (**2011**). MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. *Molecular Biology and Evolution* **(In Press)**.