

Supplemental Table 6. 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	180	12862.591	11345.72	-5491.9	n/a	0.37	2.53	0.271	0.271	0.229	0.229	0.038	0.032	0.164	0.038	0.164	0.032	0.038	0.195	0.032	0.195	0.038	0.032
T92+G+I	181	12871.156	11345.868	-5490.96	0.04	0.39	2.53	0.271	0.271	0.229	0.229	0.038	0.032	0.164	0.038	0.164	0.032	0.038	0.195	0.032	0.195	0.038	0.032
K2+G	179	12877.38	11368.925	-5504.51	n/a	0.37	2.53	0.25	0.25	0.25	0.25	0.035	0.035	0.179	0.035	0.179	0.035	0.035	0.179	0.035	0.179	0.035	0.035
GTR+G	186	12881.434	11314.066	-5470.01	n/a	0.37	2.44	0.234	0.308	0.216	0.242	0.065	0.036	0.174	0.049	0.153	0.032	0.039	0.219	0.012	0.168	0.041	0.011
K2+G+I	180	12886.18	11369.309	-5503.7	0.04	0.39	2.53	0.25	0.25	0.25	0.25	0.035	0.035	0.179	0.035	0.179	0.035	0.035	0.179	0.035	0.179	0.035	0.035
GTR+G+I	187	12890.325	11314.542	-5469.24	0.04	0.39	2.44	0.234	0.308	0.216	0.242	0.065	0.036	0.174	0.049	0.154	0.032	0.039	0.22	0.012	0.167	0.041	0.011
HKY+G	182	12970.442	11436.739	-5535.39	n/a	0.38	2.6	0.234	0.308	0.216	0.242	0.042	0.03	0.176	0.032	0.156	0.033	0.032	0.224	0.033	0.169	0.042	0.03
TN93+G	183	12980.81	11438.69	-5535.35	n/a	0.38	2.6	0.234	0.308	0.216	0.242	0.042	0.03	0.173	0.032	0.159	0.033	0.032	0.227	0.033	0.167	0.042	0.03
HKY+G+I	183	13007.91	11465.79	-5548.9	0.04	0.4	2.59	0.234	0.308	0.216	0.242	0.043	0.03	0.175	0.032	0.156	0.033	0.032	0.223	0.033	0.169	0.043	0.03
TN93+G+I	184	13018.078	11467.542	-5548.77	0.04	0.39	2.59	0.234	0.308	0.216	0.242	0.043	0.03	0.171	0.032	0.159	0.033	0.032	0.228	0.033	0.165	0.043	0.03
JC+G	178	13368.549	11868.511	-5755.32	n/a	0.38	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+I	179	13431.587	11923.132	-5781.62	0.07	0.42	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
T92+I	180	13666.394	12149.523	-5893.8	0.16	n/a	2.2	0.271	0.271	0.229	0.229	0.042	0.036	0.158	0.042	0.158	0.036	0.042	0.187	0.036	0.187	0.042	0.036
GTR+I	186	13678.979	12111.611	-5868.78	0.16	n/a	2.16	0.234	0.308	0.216	0.242	0.068	0.039	0.161	0.052	0.154	0.036	0.042	0.22	0.015	0.155	0.046	0.013
K2+I	179	13679.34	12170.885	-5905.49	0.16	n/a	2.21	0.25	0.25	0.25	0.25	0.039	0.039	0.172	0.039	0.172	0.039	0.039	0.172	0.039	0.172	0.039	0.039
HKY+I	182	13679.844	12146.14	-5890.09	0.16	n/a	2.21	0.234	0.308	0.216	0.242	0.048	0.033	0.167	0.036	0.149	0.037	0.036	0.213	0.037	0.161	0.048	0.033
TN93+I	183	13689.514	12147.394	-5889.71	0.16	n/a	2.21	0.234	0.308	0.216	0.242	0.048	0.033	0.161	0.036	0.154	0.037	0.036	0.22	0.037	0.155	0.048	0.033
T92	179	13803.604	12295.15	-5967.63	n/a	n/a	2.13	0.271	0.271	0.229	0.229	0.043	0.036	0.156	0.043	0.156	0.036	0.043	0.185	0.036	0.185	0.043	0.036
HKY	181	13817.129	12291.842	-5963.95	n/a	n/a	2.14	0.234	0.308	0.216	0.242	0.049	0.034	0.166	0.037	0.148	0.038	0.037	0.211	0.038	0.16	0.049	0.034
K2	178	13824.965	12324.927	-5983.53	n/a	n/a	2.13	0.25	0.25	0.25	0.25	0.04	0.04	0.17	0.04	0.17	0.04	0.04	0.17	0.04	0.17	0.04	0.04
TN93	182	13826.001	12292.298	-5963.17	n/a	n/a	2.15	0.234	0.308	0.216	0.242	0.049	0.034	0.157	0.037	0.155	0.038	0.037	0.221	0.038	0.152	0.049	0.034
GTR	185	13826.701	12267.749	-5947.86	n/a	n/a	2.14	0.234	0.308	0.216	0.242	0.063	0.04	0.158	0.048	0.155	0.038	0.044	0.222	0.017	0.152	0.049	0.015
JC+I	178	14152.367	12652.329	-6147.23	0.16	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
JC	177	14297.278	12805.657	-6224.9	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 90 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 382 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).

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