

**Supplemental Table 4. 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	1107	29917.907	18602.643	-8188.316	0	0.48	2.22	0.273	0.273	0.227	0.227	0.042	0.035	0.157	0.042	0.157	0.035	0.042	0.189	0.035	0.189	0.042	0.035
K2+G	1105	29925.23	18630.388	-8204.21	n/a	0.48	2.23	0.25	0.25	0.25	0.25	0.039	0.039	0.173	0.039	0.173	0.039	0.039	0.173	0.039	0.173	0.039	0.039
GTR+G	1112	29944.803	18578.486	-8171.183	n/a	0.48	2.15	0.226	0.319	0.226	0.228	0.062	0.044	0.156	0.044	0.155	0.032	0.044	0.218	0.023	0.155	0.045	0.023
GTR+G+I	1113	29957.117	18580.59	-8171.224	0	0.48	2.15	0.226	0.319	0.226	0.228	0.062	0.044	0.156	0.044	0.155	0.032	0.044	0.218	0.023	0.155	0.045	0.023
HKY+G	1108	29974.716	18649.241	-8210.604	n/a	0.5	2.25	0.226	0.319	0.226	0.228	0.049	0.035	0.158	0.035	0.157	0.035	0.035	0.221	0.035	0.157	0.049	0.035
K2+G+I	1106	29984.496	18679.443	-8227.726	0.01	0.49	2.24	0.25	0.25	0.25	0.25	0.039	0.039	0.173	0.039	0.173	0.039	0.039	0.173	0.039	0.173	0.039	0.039
T92+G	1106	29989.668	18684.615	-8230.313	n/a	0.5	2.24	0.273	0.273	0.227	0.227	0.042	0.035	0.158	0.042	0.158	0.035	0.042	0.189	0.035	0.189	0.042	0.035
HKY+G+I	1109	29995.795	18660.11	-8215.027	0	0.5	2.25	0.226	0.319	0.226	0.228	0.049	0.035	0.158	0.035	0.157	0.035	0.035	0.221	0.035	0.157	0.049	0.035
TN93+G	1109	29996.479	18660.794	-8215.369	n/a	0.5	2.25	0.226	0.319	0.226	0.228	0.049	0.035	0.161	0.035	0.154	0.035	0.035	0.218	0.035	0.16	0.049	0.035
TN93+G+I	1110	30007.897	18662.001	-8214.962	0	0.5	2.25	0.226	0.319	0.226	0.228	0.049	0.035	0.161	0.035	0.154	0.035	0.035	0.218	0.035	0.16	0.049	0.035
JC+G	1104	30587.47	19302.838	-8541.446	n/a	0.46	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	1105	30689.22	19394.377	-8586.205	0.05	0.52	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	1106	31133.839	19828.786	-8802.398	0.14	n/a	2.01	0.273	0.273	0.227	0.227	0.045	0.038	0.152	0.045	0.152	0.038	0.045	0.183	0.038	0.183	0.045	0.038
HKY+I	1108	31160.031	19834.556	-8803.261	0.14	n/a	2.03	0.226	0.319	0.226	0.228	0.053	0.037	0.153	0.037	0.152	0.038	0.037	0.214	0.038	0.152	0.053	0.037
K2+I	1105	31160.783	19865.941	-8821.986	0.14	n/a	2.01	0.25	0.25	0.25	0.25	0.042	0.042	0.167	0.042	0.167	0.042	0.042	0.167	0.042	0.167	0.042	0.042
GTR+I	1112	31178.468	19812.151	-8788.015	0.14	n/a	1.99	0.226	0.319	0.226	0.228	0.063	0.043	0.138	0.045	0.162	0.037	0.043	0.229	0.027	0.137	0.051	0.026
TN93+I	1109	31184.576	19848.891	-8809.418	0.14	n/a	2.03	0.226	0.319	0.226	0.228	0.053	0.038	0.135	0.038	0.165	0.038	0.038	0.233	0.038	0.134	0.053	0.038
T92	1105	31384.502	20089.66	-8933.846	n/a	n/a	1.96	0.273	0.273	0.227	0.227	0.046	0.038	0.151	0.046	0.151	0.038	0.046	0.181	0.038	0.181	0.046	0.038
HKY	1107	31397.442	20082.178	-8928.083	n/a	n/a	2.01	0.226	0.319	0.226	0.228	0.053	0.038	0.152	0.038	0.151	0.038	0.038	0.213	0.038	0.151	0.053	0.038
TN93	1108	31416.186	20090.711	-8931.339	n/a	n/a	2.02	0.226	0.319	0.226	0.228	0.053	0.038	0.131	0.038	0.169	0.038	0.038	0.238	0.038	0.13	0.053	0.038
GTR	1111	31416.869	20060.763	-8913.332	n/a	n/a	1.98	0.226	0.319	0.226	0.228	0.061	0.045	0.132	0.043	0.166	0.036	0.045	0.234	0.028	0.131	0.05	0.028
K2	1104	31416.929	20132.297	-8956.175	n/a	n/a	1.96	0.25	0.25	0.25	0.25	0.042	0.042	0.166	0.042	0.166	0.042	0.042	0.166	0.042	0.166	0.042	0.042
JC+I	1104	31795.58	20510.948	-9145.501	0.14	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	1103	32049.562	20775.141	-9278.608	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 553 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 374 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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