

Supplementary Table 1. Twenty-four best fit model of nucleotide substitution for evolutionary history analysis through maximum likelihood method

Model	Parameters	BIC	AICc	$\ln L$	(+I)	(+G)	R	$f(A)$	$f(T)$	$f(C)$	$f(G)$
T92	51	1,605.8	1,285.5	-591.1	n/a	n/a	1.38	0.167	0.167	0.333	0.333
T92 + I	52	1,606	1,279.5	-587	0.15	n/a	1.61	0.167	0.167	0.333	0.333
T92 + G	52	1,606.1	1,279.5	-587.1	n/a	3.07	1.5	0.167	0.167	0.333	0.333
T92 + G + I	53	1,614.3	1,281.5	-587	0.13	200	1.55	0.167	0.167	0.333	0.333
K2	50	1,619.4	1,305.4	-602.1	n/a	n/a	1.33	0.25	0.25	0.25	0.25
HKY	53	1,622.3	1,289.5	-591.1	n/a	n/a	1.38	0.169	0.166	0.332	0.334
HKY + I	54	1,622.5	1,283.5	-587	0.14	n/a	1.59	0.169	0.166	0.332	0.334
HKY + G	54	1,622.9	1,283.9	-587.2	n/a	3.72	1.47	0.169	0.166	0.332	0.334
K2 + G	51	1,627.6	1,307.4	-602	n/a	9.49	1.35	0.25	0.25	0.25	0.25
K2 + I	51	1,627.7	1,307.4	-602	0.05	n/a	1.36	0.25	0.25	0.25	0.25
TN93	54	1,630	1,291	-590.8	n/a	n/a	1.38	0.169	0.166	0.332	0.334
TN93 + G	55	1,630.3	1,285	-586.7	n/a	3.22	1.49	0.169	0.166	0.332	0.334
JC	49	1,631.3	1,323.5	-612.2	n/a	n/a	0.5	0.25	0.25	0.25	0.25
TN93 + I	55	1,631.4	1,286.2	-587.3	0.14	n/a	1.58	0.169	0.166	0.332	0.334
HKY + G + I	55	1,631.5	1,286.2	-587.3	0.14	200	1.59	0.169	0.166	0.332	0.334
JC + I	50	1,633.3	1,319.3	-609	0.03	n/a	0.5	0.25	0.25	0.25	0.25
K2 + G + I	52	1,636.1	1,309.5	-602.1	0	5.86	1.4	0.25	0.25	0.25	0.25
TN93 + G + I	56	1,638.6	1,287.1	-586.7	0.15	200	1.6	0.169	0.166	0.332	0.334
JC + G	50	1,641	1,327	-612.9	n/a	13.38	0.5	0.25	0.25	0.25	0.25
JC + G + I	51	1,641.6	1,321.3	-609	0	14.45	0.5	0.25	0.25	0.25	0.25
GTR + I	58	1,650.4	1,286.4	-584.3	0.12	n/a	1.55	0.169	0.166	0.332	0.334
GTR + G	58	1,650.6	1,286.6	-584.4	n/a	5.53	1.46	0.169	0.166	0.332	0.334
GTR	57	1,651.7	1,293.9	-589.1	n/a	n/a	1.27	0.169	0.166	0.332	0.334
GTR + G + I	59	1,658.8	1,288.5	-584.4	0.11	200	1.52	0.169	0.166	0.332	0.334

BIC, Bayesian information criterion; AIC, corrected Akaike Information Criterion; n/a, not available.