

Type of Data Set	Model	Score	SD
Nucleotide	<i>CAT</i> + <i>GTR</i> + Γ_4	+103.01	± 9.15
	<i>CAT</i> + <i>GTR</i> + <i>COV</i> + Γ_4	+79.76	± 9.44
	<i>GTR</i> + <i>COV</i> + Γ_4	-7.22	± 6.46
	<i>CAT</i> + <i>JTT</i> + Γ_4	+17.88	± 5.87
	<i>CAT</i> + <i>MTREV</i> + Γ_4	+16.49	± 6.92
	<i>CAT</i> + <i>GTR</i> + Γ_4	+13.68	± 9.25
	<i>CAT</i> + <i>GTR</i> + <i>COV</i> + Γ_4	+1.55	± 12.97
	<i>GTR</i> + Γ_4	+1.24	± 5.14
	<i>CAT</i> + <i>JTT</i> + <i>COV</i> + Γ_4	+1.07	± 9.41
	<i>CAT</i> + Γ_4	-1.09	± 6.27
Amino Acid	<i>MTREV</i> + Γ_4	-1.38	± 4.11
	<i>CAT</i> + <i>MTREV</i> + <i>COV</i> + Γ_4	-3.25	± 7.20
	<i>UL3</i> + Γ_4	-20.10	± 10.45
	<i>UL3</i> + <i>COV</i> + Γ_4	-22.42	± 8.20
	<i>UL2</i> + Γ_4	-26.71	± 8.77
	<i>UL2</i> + <i>COV</i> + Γ_4	-27.66	± 7.40

Supplementary Table S3: **Fit of Bayesian models.** Cross-validation estimations of the fit of Bayesian models to the 33 taxa and the three concatenated gene data sets. Models applied to the nucleotide and amino-acid data-set are compared to the best fitting ML models, *GTR_{nt}* + Γ_4 and *JTT* + Γ_4 , respectively. Models are defined according to their components. Substitution model: *GTR_{nt}*, *GTR_{aa}*, *MtREV* and *JTT*, exchange rate parameters; *CAT*, *UL2* and *UL3*, site heterogeneous mixture models. Rates across sites models: + Γ_4 , discretized gamma rates (Yang 1994, [42]); +*COV*, covarion model (Tuffley and Steel 1998, [71]).