

Additional File 2. Sequence data sets used in the studies with applied substitution models in four programs.

Data set	Markers	Alignment length [bp]	Substitution models used in:			
			TreeFinder	PAUP	MrBayes ⁵	PhyloBayes
7 taxa	<i>atp6</i>	684	J3+I,HKY+I,J3+I	010020+I	Mix+:I,I,I	CAT+GTR+Γ
	<i>atp8</i>	168	TN,HKY+I,HKY+I	010022+I	Mix+:E,I,I	CAT+GTR+Γ
	<i>cox1</i>	1,584	TN+I,HKY+I,GTR+I	012210+Γ	Mix+:I,E,I	CAT+GTR+Γ
	<i>cox2</i>	684	J2+I,TN+I,HKY+Γ	010020+I	Mix+:I,I,Γ	CAT+GTR+Γ
	<i>cox3</i>	784	J3+I,HKY,J1+I	010210+I	Mix+:Γ,E,I	CAT+GTR+Γ
	<i>cytb</i>	1,140	J3+Γ,J1+I,J1+Γ	010212+Γ	Mix+:I,I,I	CAT+GTR+Γ
	<i>nd1</i>	981	HKY+I,TN+Γ+I,HKY+Γ	HKY+Γ	Mix+:Γ,I,Γ	CAT+GTR+Γ
	<i>nd2</i>	1,040	J1+Γ,J1+Γ+I,J3+Γ	012034+Γ+I	Mix+:Γ,Γ,Γ	CAT+GTR+Γ
	<i>nd3</i>	350	HKY+I,HKY+I,J3+Γ	010020+I	Mix+:I,I,I	CAT+GTR+Γ
	<i>nd4</i>	1,393	J1+Γ,J1+Γ+I,TN+Γ+I	010020+I	Mix+:Γ,I,I	CAT+GTR+Γ
	<i>nd4L</i>	297	HKY,HKY+I,HKY	012212+Γ	Mix+:E,I,E	CAT+GTR+Γ
	<i>nd5</i>	1,815	J3+Γ,HKY+Γ+I,J1+Γ+I	010232+Γ+I	Mix+:Γ,I+I,Γ+I	CAT+GTR+Γ
	<i>nd6</i>	513	HKY+Γ,J3+I,J2+Γ	012340+Γ	Mix+:Γ,I,Γ	CAT+GTR+Γ
	<i>12s rRNA</i>	971	J3+Γ	010023+Γ+I	Mix+Γ+I	GTR+Γ
	<i>16s rRNA</i>	1,567	GTR+Γ	010234+Γ	Mix+Γ	GTR+Γ
	<i>tRNA1¹</i>	560	HKY+Γ	HKY+Γ+I	Mix+Γ+I	GTR+Γ
	<i>tRNA2²</i>	983	J1+Γ	012232+Γ+I	Mix+Γ+I	GTR+Γ
	<i>control region (CR)</i>	1,478	TVM+Γ	010213+Γ+I	Mix+Γ+I	GTR+Γ
<i>ALL³</i>	16,956	GTR+Γ+I,J1+Γ+I,J1+Γ+I,HKY+Γ,J3+I,J2+Γ,J3+Γ,GTR+Γ,TVM+Γ,HKY+Γ,J1+Γ	012310+Γ	Mix+:Γ+I,Γ+I,Γ+I,Γ+I,Γ+I,Γ+I,Γ+I,Γ+I,Γ+I,Γ+I	CAT+GTR+Γ	
<i>ALL-CR⁴</i>	15,478	GTR+Γ+I,J1+Γ+I,J1+Γ+I,HKY+Γ,J3+I,J2+Γ,J3+Γ,GTR+Γ,HKY+Γ,J1+Γ	012340+Γ	Mix+:Γ+I,Γ+I,Γ+I,Γ+I,Γ+I,Γ+I,Γ+I,Γ+I	CAT+GTR+Γ	
11 taxa	<i>atp6</i>	684	HKY+Γ,J1+Γ+I,J3+Γ+I	010020+Γ+I	Mix+:Γ,I,Γ+I	CAT+GTR+Γ
	<i>atp8</i>	168	TN,HKY+I,HKY+I	010023+I	Mix+:E,I,I	CAT+GTR+Γ
	<i>cox1</i>	1,584	J3+Γ+I,HKY+I, TN+Γ+I	012310+Γ+I	Mix+:Γ+I,E,Γ	CAT+GTR+Γ
	<i>cox2</i>	684	J2+I,HKY+I,J3+Γ	HKY+Γ+I	Mix+:Γ,I,Γ	CAT+GTR+Γ
	<i>cox3</i>	784	J3+Γ,HKY+Γ+I,J1+Γ+I	010210+Γ+I	Mix+:Γ,I,Γ+I	CAT+GTR+Γ
	<i>cytb</i>	1,140	J2+Γ,J1+I,J1+Γ+I	010230+Γ+I	Mix+:I,I,I	CAT+GTR+Γ
	<i>nd1</i>	981	HKY+I,HKY+Γ+I,TVM+Γ+I	HKY+Γ+I	Mix+:I,I,Γ+I	CAT+GTR+Γ
	<i>nd2</i>	1,040	J1+Γ,J1+Γ+I,J3+Γ+I	010023+Γ+I	Mix+:Γ,Γ+I,Γ	CAT+GTR+Γ
	<i>nd3</i>	350	HKY+Γ,HKY+Γ,J1+Γ	010230+Γ+I	Mix+:Γ,Γ,Γ	CAT+GTR+Γ
	<i>nd4</i>	1,393	J1+Γ,J1+Γ+I,TN+Γ+I	010020+Γ+I	Mix+:Γ,Γ+I,Γ+I	CAT+GTR+Γ
	<i>nd4L</i>	297	HKY+Γ,HKY+I,HKY+I	012212+Γ	Mix+:E,E,I	CAT+GTR+Γ
	<i>nd5</i>	1,815	J2+Γ+I,HKY+Γ+I,J1+Γ+I	010212+Γ+I	Mix+:Γ,Γ+I,Γ+I	CAT+GTR+Γ
	<i>nd6</i>	513	J3+Γ,HKY+Γ,J2+Γ	010012+Γ+I	Mix+:Γ,Γ,Γ	CAT+GTR+Γ
	<i>12s rRNA</i>	962	GTR+Γ	010023+Γ	Mix+Γ	GTR+Γ
	<i>16s rRNA</i>	1,568	GTR+Γ	010234+Γ+I	Mix+Γ+I	GTR+Γ
	<i>tRNA1¹</i>	560	HKY+Γ	012010+Γ+I	Mix+Γ+I	GTR+Γ
	<i>tRNA2²</i>	988	J1+Γ	012032+Γ+I	Mix+Γ+I	GTR+Γ
	<i>control region (CR)</i>	1,477	J2+Γ	010213+Γ	Mix+Γ	GTR+Γ
<i>ALL³</i>	16,952	GTR+Γ+I,J1+Γ+I,GTR+Γ+I,J3+Γ,TVM+Γ,J2+Γ,J1+Γ,GTR+Γ,J2+Γ,HKY+Γ+I,J1+Γ	012314+Γ+I	Mix+:Γ+I,Γ+I,Γ+I,Γ+I,Γ+I,Γ+I,Γ+I,Γ+I,Γ+I,Γ+I	CAT+GTR+Γ	
<i>ALL-CR⁴</i>	15,475	GTR+Γ+I,J1+Γ+I,GTR+Γ+I,J3+Γ,TVM+Γ,J2+I,GTR+Γ,GTR+Γ,TVM+Γ+I,J1+Γ	012310+Γ+I	Mix+:Γ+I,Γ+I,Γ+I,Γ+I,Γ+I,Γ+I,Γ+I,Γ+I	CAT+GTR+Γ	

¹ - includes tRNA-Ala, tRNA-Asn, tRNA-Cys, tRNA-Gln, tRNA-Glu, tRNA-Pro, tRNA-Ser1 and tRNA-Tyr; ² - includes tRNA-Arg, tRNA-Asp, tRNA-Gly, tRNA-His, tRNA-Ile, tRNA-Leu1, tRNA-Leu2, tRNA-Lys, tRNA-Met, tRNA-Phe, tRNA-Ser2, tRNA-Thr, tRNA-Trp and tRNA-Val; ³ - includes all the nucleotide markers; ⁴ - the same as ³ but without CR; ⁵ - E means equal rates across sites.