

**Table S3a: jModelTest model selection on full data set.** The best model selected by jModelTest per gene or codon is displayed according to analysis.

Gene/Codon	Best model*	Best model according to	
		PhyML	MrBayes
<i>ND1</i>	TrN+I+G	TrN+I+G	GTR+I+G
<i>ND2</i>	TIM1+I+G	TrN+I+G	GTR+I+G
<i>COX1</i>	GTR+I+G	GTR+I+G	GTR+I+G
<i>COX2</i>	TVM+I+G	GTR+I+G	GTR+I+G
<i>ATP8</i>	TrN+G	TrN+G	HKY+G
<i>ATP6</i>	TrN+I+G	TrN+I+G	GTR+I+G
<i>COX3</i>	TVM+I+G	GTR+I+G	GTR+I+G
<i>ND3</i>	TPM1uf+I+G	HKY+I+G	HKY+I+G
<i>ND4L</i>	HKY+G	HKY+G	HKY+G
<i>ND4</i>	GTR+I+G	GTR+I+G	GTR+I+G
<i>ND5</i>	GTR+I+G	GTR+I+G	GTR+I+G
<i>ND6</i>	TPM1uf+G	HKY+G	HKY+G
<i>CYTB</i>	TrN+I+G	TrN+I+G	HKY+I+G
<i>CR</i>	HKY+G	HKY+G	HKY+G
12sRNA	GTR+I+G	GTR+I+G	GTR+I+G
16sRNA	GTR+G	GTR+G	GTR+G
Codon1	GTR+I+G	GTR+I+G	GTR+I+G
Codon2	GTR+I+G	GTR+I+G	GTR+I+G
Codon3	TIM1+I+G	GTR+I+G	GTR+I+G
RNAs	GTR+I+G	GTR+I+G	GTR+I+G
unpart	TVM+I+G	GTR+I+G	GTR+I+G

\* for RaxML and MrBayes GTR+I+G was chosen for both the 4 and the 5 partitions datasets.

**Table S3b: jModelTest model selection on data set excluding non-equid outgroups.** The best model selected by jModelTest per gene or codon is displayed according to analysis.

Gene/Codon	Best model*	Best model according to	
		PhyML	MrBayes
<i>ND1</i>	HKY+G	HKY+G	HKY+G
<i>ND2</i>	TPM1uf+I	HKY+I	HKY+I
<i>COX1</i>	TPM1uf+I	GTR+I	GTR+I
<i>COX2</i>	TVM+G	GTR+G	GTR+G
<i>ATP8</i>	TrN+G	TrN+G	HKY+G
<i>ATP6</i>	TrN+I	TrN+I	GTR+I
<i>COX3</i>	TPM1uf+G	HKY+G	HKY+G
<i>ND3</i>	TPM1uf+I	HKY+I	HKY+I
<i>ND4L</i>	HKY+G	HKY+G	HKY+G
<i>ND4</i>	TIM1+I	GTR+I	GTR+I
<i>ND5</i>	GTR+I+G	GTR+I+G	GTR+I+G
<i>ND6</i>	TPM1uf+G	TrN+G	GTR+G
<i>CYTB</i>	TrN+I	TrN+I	GTR+I
<i>CR</i>	TrN+G	TrN+G	HKY+G
12sRNA	TIM1+G	GTR+G	GTR+G
16sRNA	TIM+I+G	TrN+I+G	GTR+I+G
Codon1	GTR+I+G	GTR+I+G	GTR+I+G
Codon2	TIM1+I+G	GTR+I+G	GTR+I+G
Codon3	TIM1+I+G	GTR+I+G	GTR+I+G
RNAs	TIM+I+G	GTR+I+G	GTR+I+G
unpart	TVM+G	GTR+I+G	GTR+I+G

\* for RaxML and MrBayes GTR+I+G was chosen for both the 4 and the 5 partitions datasets excluding outgroups.