

**Table S3.** jModelTest selections for mitochondrial and nuclear data partitions.

| Mitochondrial sequences         |                    | Nuclear sequences               |                    |
|---------------------------------|--------------------|---------------------------------|--------------------|
| Partition <sup>1</sup>          | Model <sup>2</sup> | Partition                       | Model <sup>2</sup> |
| <i>Protein codons</i>           |                    | <i>Protein codons</i>           |                    |
| 1 <sup>st</sup> codon positions | GTR+I+ $\Gamma$    | 1 <sup>st</sup> codon positions | TIM+ $\Gamma$      |
| 2 <sup>nd</sup> codon positions | K81uf+I+ $\Gamma$  | 2 <sup>nd</sup> codon positions | TVM+ $\Gamma$      |
| 3 <sup>rd</sup> codon positions | TIM+ $\Gamma$      | 3 <sup>rd</sup> codon positions | TVMef+ $\Gamma$    |
| <i>RNA structure</i>            |                    | <i>Genes</i>                    |                    |
| Stem positions                  | SYM+I+ $\Gamma$    | <i>BRCA1</i>                    | TrN+ $\Gamma$      |
| Loop positions                  | TIM+I+ $\Gamma$    | <i>ApoB</i>                     | TrN+ $\Gamma$      |
|                                 |                    | <i>IRBP</i>                     | TVM+ $\Gamma$      |
|                                 |                    | <i>RAG1</i>                     | HKY+I+ $\Gamma$    |
|                                 |                    | <i>vWF</i>                      | K80+I+ $\Gamma$    |

<sup>1</sup> Meredith et al. (2008) modelled the nuclear data as five gene-wise partitions, whereas we employ three codon-wise partitions. Both partitioning schemes identified the same ML tree topology for Nuc<sub>17</sub> (Figure 1B). However codon-wise partitioning provides higher likelihood (in PAUP\*) with fewer free parameters (-13,107.338, df=113) than gene-wise partitioning (-13,115.969, df=184). Partitioning by both gene and codon resulted in several partitions with far more parameters requiring estimation than variable sites and hence, was considered too parameter rich.

<sup>2</sup> The most general of either the hierarchical likelihood ratio test or Akaike Information Criterion model suggestions is reported.

## Reference

Meredith RW, Westerman M, Springer MS (2008) A phylogeny and timescale for the living genera of kangaroos and kin (Macropodiformes: Marsupialia) based on nuclear DNA sequences. Aust J Zool 56: 395-410.