Supplementary Table S2. Summary of data partition selection with resulting partitions and their respective nucleotide substitution models (when applicable) for each phylogenetic method and data matrix combinations.

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| --- | --- | --- | --- | --- | --- |
| Dataset | Analysis | Partitioning method/criterion | No. of subsets | Subsets | Model |
| Matrix 1 | RAxML,  | PartitionFinder  | 4 | 1: 3rd codons; *EFT2*.1, ß-tubulin introns | HKY + I + G |
|  | MrBayes | (BIC, All) |  | 2: 1st codons; LSU | GTR + I + G |
|  |  |  |  | 3: 2nd codons | HKY + I + G |
|  |  |  |  | 4: *RPB1* intron | K80 |
| Matrix 2 | RAxML | PartitionFinder  | 11 | 1: ITS1, ITS2, ß-tubulin and *EFT2*.1 introns | GTR + G |
|  |  | (AICc, All) |  | 2: ß-tubulin 1st codon | GTR + G |
|  |  |  |  | 3: ß-tubulin and *RPB1* 2nd codons | GTR + G |
|  |  |  |  | 4: ß-tubulin and *EFT2*.1 3rd codons | GTR + G |
|  |  |  |  | 5: *EFT2*.1 1st codon | GTR + G |
|  |  |  |  | 6: *EFT2*.1 2nd codon | GTR + G |
|  |  |  |  | 7: *RPB1* 1st codon | GTR + G |
|  |  |  |  | 8: *RPB1* 3rd codon | GTR + G |
|  |  |  |  | 9: *RPB1* intron | GTR + G |
|  |  |  |  | 10: 5.8S | GTR + G |
|  |  |  |  | 11: LSU | GTR + G |
|  | MrBayes | Manually | 7 | 1: 1st codons | HKY + I |
|  |  |  |  | 2: 2nd codons | HKY + I + G |
|  |  |  |  | 3: 3rd codons | HKY + I |
|  |  |  |  | 4: introns | HKY + G |
|  |  |  |  | 5: LSU | GTR + I + G |
|  |  |  |  | 6: ITS1, ITS2 | K80 + G |
|  |  |  |  | 7: 5.8S | constant, excluded |
|  | BEAST | Manually | 6 | 1: ß-tubulin coding | HKY + I + G |
|  |  |  |  | 2: EFT2.1 coding | HKY + G |
|  |  |  |  | 3: RPB1 coding | GTR + G |
|  |  |  |  | 4: introns | HKY + G |
|  |  |  |  | 5: LSU | GTR + I + G |
|  |  |  |  | 6: ITS | HKY + G |
| Matrix 4, Matrix 6 | RAxML, | Manually | 3 | 1 1st codon | GTR + G |
|  | MrBayes |  |  | 2: 2nd codon | GTR + G |
|  |  |  |  | 3: 3rd codon | GTR + G |