Table S2**.** Best fit partitions and substitution models.

|  |  |  |
| --- | --- | --- |
| Nassariidae dataset | Set Partition (Conducted by PartitionFinder 2) | Best Model for BI (Selected by PartitionFinder 2) |
| Best Partition CDS genes | *atp6-8* | MTMAM+I+G+F |
|  | *cox1-2-3* | MTMAM+I+G+F |
|  | *cob* | MTART+I+G |
|  | *nad1-2-3-4-4L-5-6* | MTART+I+G+F |
| Best Partition to rRNA genes | *rrnS-L* | GTR+I+G |
| Nassariinae dataset | Set Partition (Conducted by PartitionFinder 2) | Best Model for BI (Selected by PartitionFinder 2) |
| Best Partition CDS genes | *atp6-8* 1th | TRN+I+G |
|  | *atp6-8* 2th | HKY+I |
|  | *atp6-8* 3th | TVM+I+G |
|  | *cox1-2-3* 1th | TRN+I+G |
|  | *cox1-2-3* 2th | TVM+I+G |
|  | *cox1-2-3* 3th | TVM+I+G |
|  | *cob* 1th | TRN+I+G |
|  | *cob* 2th | TVM+I+G |
|  | *cob* 3th | K81UF+I+G |
|  | *nad1-2-3-4-4L-5-6* 1th | GTR+I+G |
|  | *nad1-2-3-4-4L-5-6* 2th | GTR+I+G |
|  | *nad1-2-3-4-4L-5-6* 3th | TVM+I+G |
| Best Partition to rRNA genes | *rrnS-L* | GTR+I+G |