Supplementary Table S2. Sequence substitution model used for phylogenetic analysis

ML phylogeny based on Rag1

|  |  |  |
| --- | --- | --- |
| Gene | Codon position | Model |
| Rag1 | Rag1\_1 | HKY+F+G4 |
|  | Rag1\_2 | TPM2+F+G4 |
|  | Rag1\_3 | TVMe+G4 |

Concatinated dataset ML phylogeny

|  |  |  |
| --- | --- | --- |
| Gene | Codon position | Model |
| *ND*2 | nd2\_codon1 | HKY+F+I+G4 |
|  | nd2\_codon2 | GTR+F+I+G4 |
|  | nd2\_codon3 | TPM2u+F+G4 |
| *Cyt* b | cytb\_codon1 | TIMe+I+G4 |
|  | cytb\_codon2 | GTR+F+G4 |
|  | cytb\_codon3 | TIM2e+I+G4 |
| 16S | - | TIM2+F+I+G4 |
| 12S | - | TIM2+F+I+G4 |
| *Mc1r* | mc1r\_codon1 | HKY+F+G4 |
|  | mc1r\_codon2 | JC |
|  | mc1r\_codon3 | F81+F |
| Nktr | nktr\_codon1 | TN+F+I |
|  | nktr\_codon2 | K2P+G4 |
|  | nktr\_codon3 | K3P+G4 |

Concatinated dataset BI phylogeny

|  |  |  |
| --- | --- | --- |
| Gene | Codon position | Model |
| *ND*2 | nd2\_codon1 | HKY+I+G |
|  | nd2\_codon2 | GTR+ I+G |
|  | nd2\_codon3 | GTR+ I+G |
| *Cyt* b | cytb\_codon1 | GTR+ I+G |
|  | cytb\_codon2 | GTR+G |
|  | cytb\_codon3 | SYM+I+G |
| 16S | - | GTR+ I+G |
| 12S | - | GTR+ I+G |
| *Mc1r* | mc1r\_codon1 | HKY+G |
|  | mc1r\_codon2 | JC |
|  | mc1r\_codon3 | F81 |
| Nktr | nktr\_codon1 | GTR+G |
|  | nktr\_codon2 | GTR+G |
|  | nktr\_codon3 | K80+G |