Table S4. Characteristics of sequence data used in analyses including pairwise percentage identity, and numbers of constant, variable and parsimony informative characters

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | n | Pairwise ID | length | Alignment length | constant | Variable | Pars Inf. |
| 28s | 121 | 95.50% | 566 (255-592) | 604 | 477 | 121 | 78 |
| 18s | 78 | 99.30% | 920.9 (352-958) | 967 | 907 | 53 | 34 |
| COI | 112 | 85.30% | 756.7 | 770 | 377 | 393 | 339 |
|  | (475-770) |  |
| 12s-trna | 50 | 88.20% | 382.4 (331-398) | 429 | 213 | 200 | 135 |
| 16s | 90 | 84.70% | 787(337-1206) | 1383 | 561 | 729 | 516 |