**Supplementary Table 3. The index of substitution saturation (Iss) values of 5 datasets.**

| **Number** | **Gene** | **P-inva** | **Site inclusion** | **Iss** | **Iss.cSym** | **Psym** | **Iss.cAsym** | **Pasym** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| 1 | 18S rDNA | 0.30007 | A | 0.4444 | 0.7762 | 0.0000 | 0.5549 | 0.0000 |
| 2 | B | 0.1234 | 0.7322 | 0.0000 | 0.4854 | 0.0000 |
| 3 | ITS-1 | 0.16788 | A | 0.290 | 0.707 | 0.0000 | 0.379 | 0.0006 |
| 4 | B | 0.188 | 0.688 | 0.0000 | 0.359 | 0.0000 |
| 5 | 28S rDNA | 0.39806 | A | 0.3309 | 0.7806 | 0.0000 | 0.5585 | 0.0000 |
| 6 | B | 0.0547 | 0.6959 | 0.0000 | 0.4454 | 0.0000 |
| 7 | COI | 0.17485 | A, C, D | 0.494 | 0.722 | 0.0000 | 0.397 | 0.0000 |
| 8 | B, C, D | 0.155 | 0.722 | 0.0000 | 0.437 | 0.0000 |
| 9 | 0.35652 | A, C | 0.400 | 0.698 | 0.0000 | 0.371 | 0.2322 |
| 10 | B, C | 0.089 | 0.788 | 0.0000 | 0.557 | 0.0000 |
| 11 | 0.06135 | A, D | 0.800 | 0.685 | 0.0001 | 0.362 | 0.0000 |
| 12 | B, D | 0.451 | 1.385 | 0.0000 | 1.585 | 0.0000 |
| 13 | aCOI | 0.18160 | A, C, D | 0.348 | 0.722 | 0.0000 | 0.397 | 0.0153 |
| 14 | B, C, D | 0.220 | 0.696 | 0.0000 | 0.368 | 0.0000 |
| 15 | 0.25714 | A, C | 0.239 | 0.698 | 0.0000 | 0.371 | 0.0000 |
| 16 | B, C | 0.142 | 0.684 | 0.0000 | 0.255 | 0.0000 |
| 17 | 0.03662 | A, D | 0.640 | 0.685 | 0.1263 | 0.362 | 0.0000 |
| 18 | B, D | 0.553 | 0.769 | 0.000 | 0.523 | 0.4841 |

P-inva: proportion of invariant sites; Iss: an entropy-based index of substitution saturation proposed by Xia et al.; Iss.cSym: the critical Iss value assuming a symmetrical topology. Psym: probability of significant difference between Iss and Iss.cSym (two-Tailed test); Iss.cAsym: the critical Iss value assuming an asymmetrical topology; Pasym: probability of significant difference between Iss and Iss.cAsym (two-Tailed test).

Site inclusion: A. all sites; B. analyze only fully resolved sites; C. codon positions 1 and 2; D. codon position 3.