Supplementary file 10. Percentage of average Kimura 2-parameter model genetic distances between species within each family analyzed in this study (values in parentheses are range of genetic distance between species). Abbreviation: SE = Standard Error.

|  |  |  |
| --- | --- | --- |
| Column1  Family | Kimura 2-parameter model genetic distance between speciesolumn2 | |
| 16S (%) | COI (%) |
| Asteronychidae | 4.49±0.91 SE (1.64±0.61 SE to 9.42±1.50 SE) | 7.37±0.95 SE (6.56±1.08 SE to 16.88±1.88 SE) |
| Gorgonocephalidae | - | 13.35±1.51 SE (1.16±0.43 SE to 18.82±1.85 SE) |
| Euryalidae | - | 17.19±1.75 SE (3.21±0.72 SE to 23.87±1.97 SE) |
| Ophiomusaidae | - | 21.13±1.96 SE (2.15±0.61SE to 29.92±2.46 SE) |
| Ophiotomidae | - | 18.90±1.83 SE (15.83±1.77 SE to 22.61±2.02 SE) |
| Ophiacanthidae | 13.38±2.88 SE (8.43±1.34 SE to 25.94±2.54 SE) | 29.40±3.11(12.72±1.90 SE to 44.16±4.36 SE) |
| Ophiactidae | - | 18.75±1.98 SE (4.5±0.91 to 30.73±2.81) |
| Total | 8.94±1.90 SE (1.64±0.61 SE to 25.94±2.54 SE) | 18.41±1.90 SE (1.16±0.43 SE to 44.16±4.36 SE) |