**Table S3**. **Recovered clades across individual genes and concatenated analyses (All genes)**. Monophyletic clades are marked with the posterior probability, which is shaded grey if 0.95 or greater. N/A indicates that there was a missing taxon so the clade could not be recovered. A “C” preceding a taxon name in a cell indicates that a congruent clade was recovered even though the indicated taxon was missing. Taxon Abbreviations are as follows: Mic (*Micrevania*); Bra (*Brachygaster*); Pro (*Prosevania*); Tri (*Trissevania*); Eva (*Evania*); Zeu (*Zeuxevania*); Par (*Parevania*); CEv (*Evaniscus*); Dec (*Decevania*); Sem (*Semaeomyia*); Hyp (*Hyptia*); Alo (*Alobevania*); LEv (*Evaniella*); Sze (*Szepligetella*); Aca (*Acanthinevania*).

|  |  |  |
| --- | --- | --- |
|   |  | **Genera recovered** |
| **Assoc. Figure** | **Gene Region** | **Mic** | **Bra** | **Pro** | **Tri** | **Eva** | **Zeu** | **Par** | **CEv** | **Dec** | **Sem** | **Hyp** | **Alo** | **LEv** | **Sze** | **Aca** |
| **S1** | **28S** |   | **1.0** | **1.0** | **N/A** | **0.94** |   |   |   | **1.0** | **1.0** | **1.0** | **N/A** | **1.0** |   |   |
| **S2** | **16S** | **0.96** | **0.98** | **1.0** | **N/A** |   |   |   | **0.96** | **1.0** |   | **0.75** | **N/A** | **1.0** |   | **x** |
| **S3** | **COI** | **1.0** | **1.0** | **1.0** | **N/A** | **0.61** | **0.79** |   |   | **1.0** | **1.0** | **1.0** | **N/A** | **1.0** |   | **x** |
| **S4** | **CAD1** | **N/A** | **1.0** | **1.0** | **N/A** | **1.0** |   |   | **N/A** | **1.0** | **0.99** | **1.0** | **N/A** | **1.0** |   |   |
| **S5** | **CAD2** |   | **1.0** | **1.0** | **1.0** | **1.0** |   |   | **N/A** | **1.0** | **1.0** | **1.0** | **N/A** |   |   |   |
| **S6** | **RPS23** | **N/A** | **0.95** | **N/A** | **1.0** |   |   |   | **0.81** | **0.98** | **0.76** | **0.81** | **N/A** |   |   |   |
| **S7** | **AM2** | **N/A** | **N/A** | **0.99** | **N/A** | **N/A** | **N/A** | **0.94** | **N/A** | **1.0** | **N/A** | **0.99** | **N/A** |   |   |   |
| **2** | **All** |  | **1.0** | **1.0** | **1.0** | **1.0** |   |   | **1.0** | **1.0** | **1.0** | **1.0** | **N/A** | **1.0** |   |   |
|   |   | **Higher Level Clades Recovered** |
| **Assoc. Figure** | **Gene Region** | **Sze + Aca** | **LEv + Sze + Aca** | **Alo + Eva + Sze + Aca** | **CEv + Dec + Rot + Sem + Hyp** | **Zeu + Par + Pap** | **Bra + Pro** | **All but Bra/ Pro/ Mic** | **Tri + Eva** | **Tri + Evan****Zeu + Par + Pap** |
| **S1** | **28S** | **0.94** | **1.0** | **0.88** |   | **1.0** |   |   |   |  |
| **S2** | **16S** |   |   |   |   |   |   |   |   |   |
| **S3** | **COI** | **1.0** | **0.99** | **N/A** |   | **1.0** |   |   | **0.82** |  |
| **S4** | **CAD1** | **1.0** |   |   | **0.94 C (CEv)** | **1.0** |   |   | **N/A** | **N/A** |
| **S5** | **CAD2** | **1.0** | **0.91** |  | **0.66 C (CEv)** | **1.0** | **0.99** | **0.57** |  |  |
| **S6** | **RPS23** | **0.71** |  | **N/A** |  | **0.96** |  |  |  |  |
| **S7** | **AM2** | **0.75** |  | **0.72** |  | **N/A** | **N/A** |  |  |  |
| **2** | **All** | **1.0** | **1.0** | **1.0** | **1.0** | **1.0** | **1.0** | **1.0** | **1.0** | **0.98** |