

## **Supporting Information**

**Molecular phylogenetics of the predatory lineage of flower flies *Eupeodes-Scaeva* (Diptera: Syrphidae), with the description of the Neotropical genus *Austroscaeva* gen. nov.**

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Fig. S1. Maximum Likelihood tree ( $\ln L = -31,292.223746$ ) based on the combined dataset (COI, 28S and 18S) using Garli v.2.01.1067 and the structural alignment for 28S and 18S. Bootstrap support values (right) and Bayesian posterior probabilities (left) are depicted at the nodes (only  $>50$  or  $>0.5$  respectively). Asterisk (\*) denotes Bootstrap support values = 100 or Bayesian posterior probabilities = 1.



Fig. S1

Fig. S2. Bayesian phylogram based on the combined dataset (COI, 28S and 18S) using MrBayes 3.2.6 and the structural alignment for 28S and 18S. Posterior probability values higher than 0.5 are indicated on the branches.

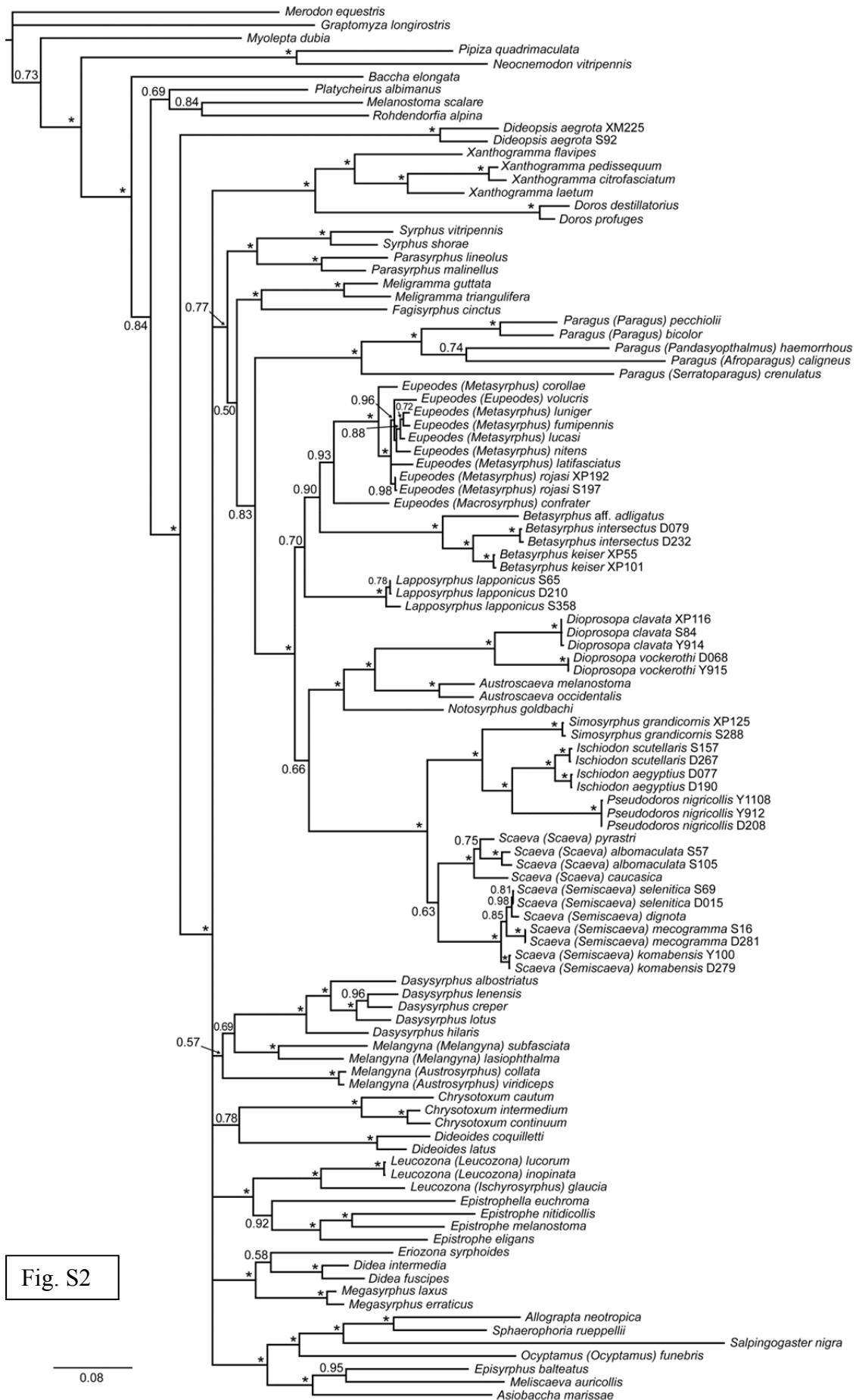


Fig. S2

0.08