

Supplementary Data 1

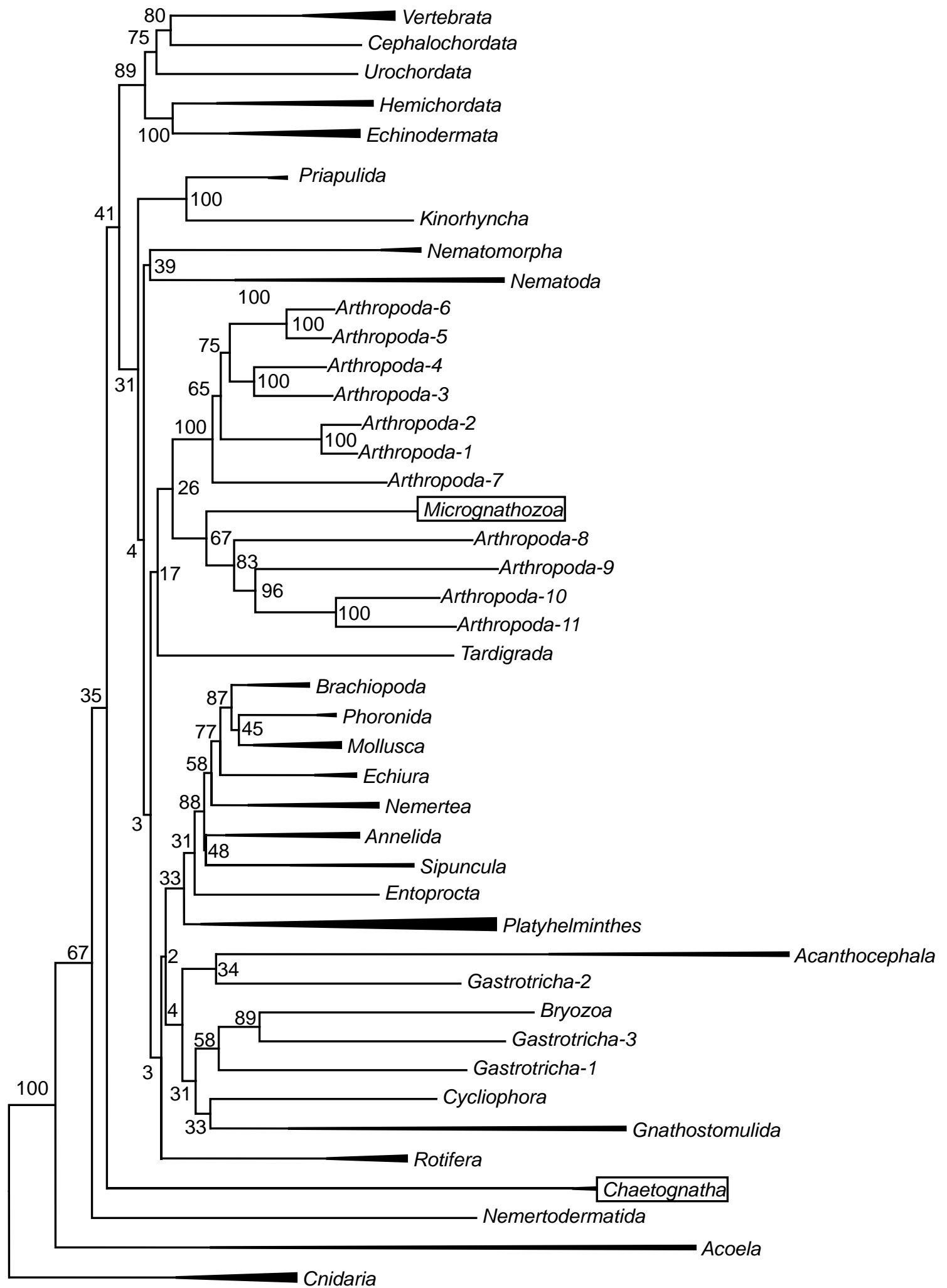
Inference methods

The results obtained with NJ (Supplementary Fig. 1A), Treefinder and PhyML (Supplementary Fig. 1B) show some groupings that never appear in the trees inferred by BI and RaxML (Fig. 1 main text) and that are contradictory to well established clades. As an example:

1. NJ (Supplementary Fig. 1A) places Micrognathozoa within the Arthropoda, while Chaetognaths appear splitting after acoelomorphs and sistergroup to the rest of bilaterians.
2. PhyML (Supplementary Fig. 1B) recovers a group made up by nemertodermatids, chaetognaths and micrognathozoans inside ecdysozoans, as sistergroup to Panarthropoda
3. Treefinder (not shown) anomalies appear mainly in the subsets trees:
 - a. *Acoelomorpha* dataset: Tardigrada at the bilaterian base, splitting after *Nemertodermatida*; *Micrognathozoa* within Arthropoda.
 - b. *Gnathifera* dataset: *Urochordata* at bilaterian base; *Micrognathozoa* within Arthropoda.
 - c. *Bryozoa* dataset: at the bilaterian base shows *Bryozoa* + ((*Cycliophora* + *Entoprocta*) + rest of bilaterians); *Micrognathozoa* within *Arthropoda*.
 - d. *Chaetognatha* dataset: *Micrognathozoa* within *Arthropoda*.

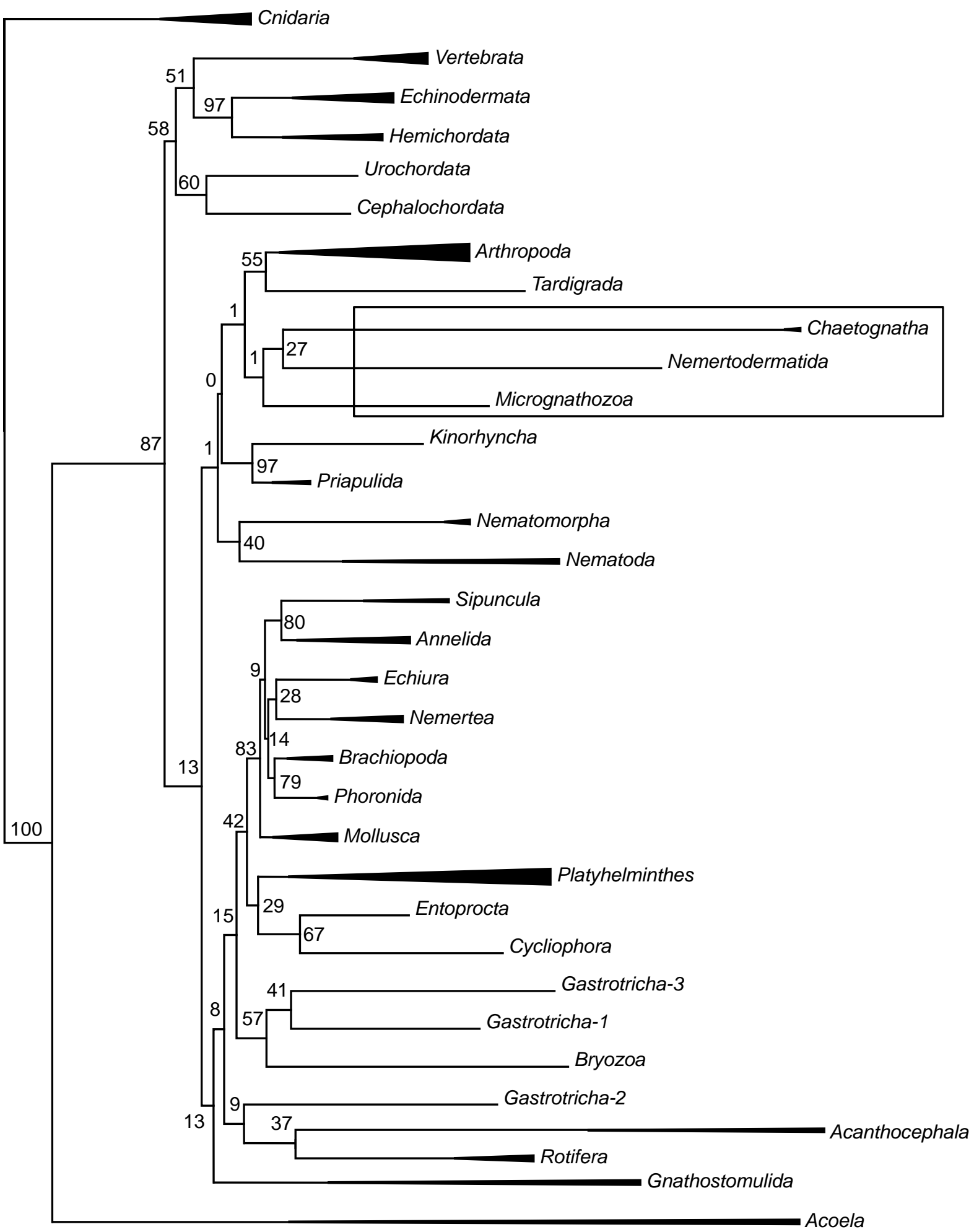
The differences found could be due to an inefficiency on the heuristic search of the first group of methods. In order to test this hypothesis we calculated with Treefinder the likelihood of the best RAxML tree with branch length optimization; the value obtained (lnL= -72,953.36) was better than the likelihood obtained by the original Treefinder search (lnL= -72,967.834). Hence, indicating that Treefinder had not been able to find the best tree.

Supplementary Figure 1. Topology obtained by NJ (A) and PhyML (B) with the All-set.



0.02

A



0.05

B