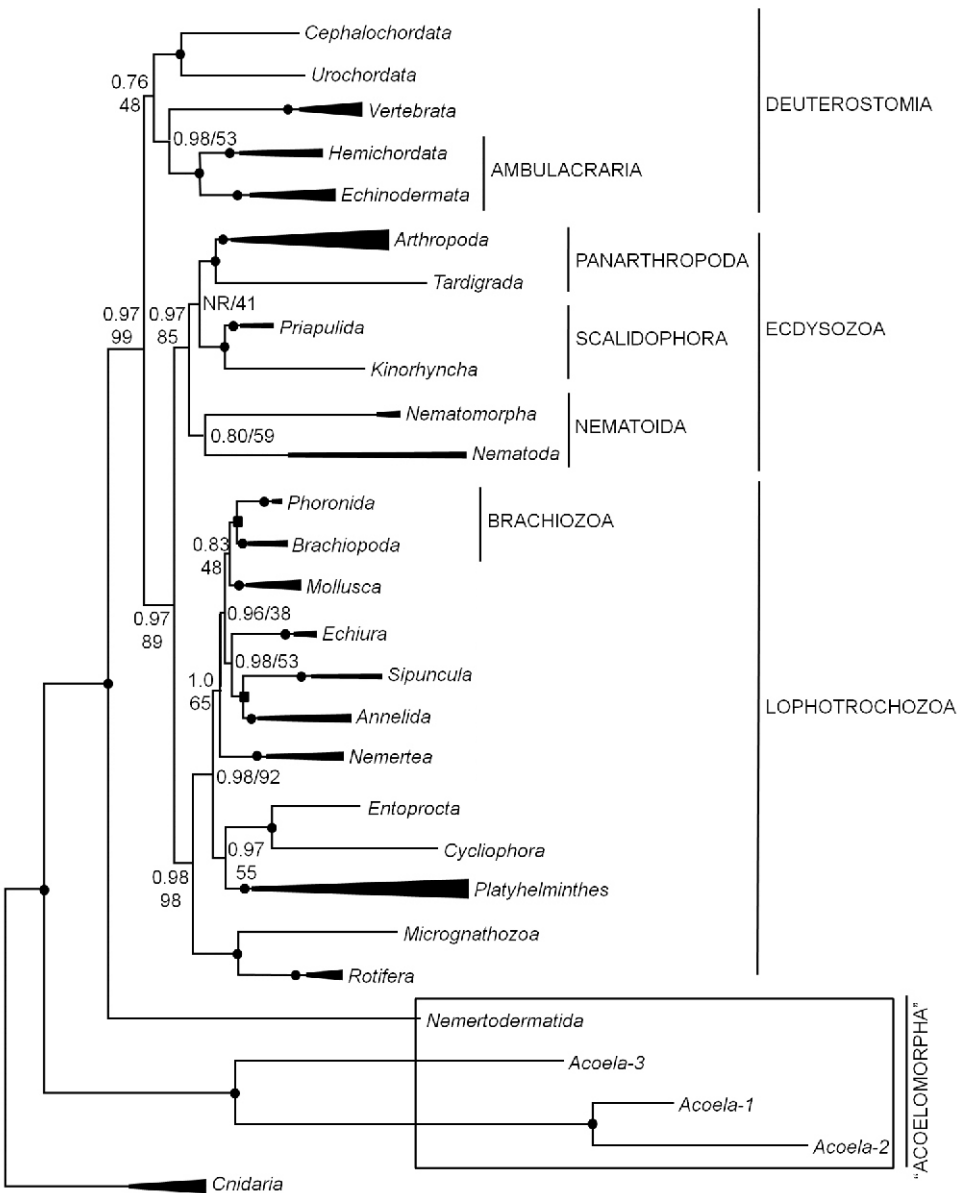


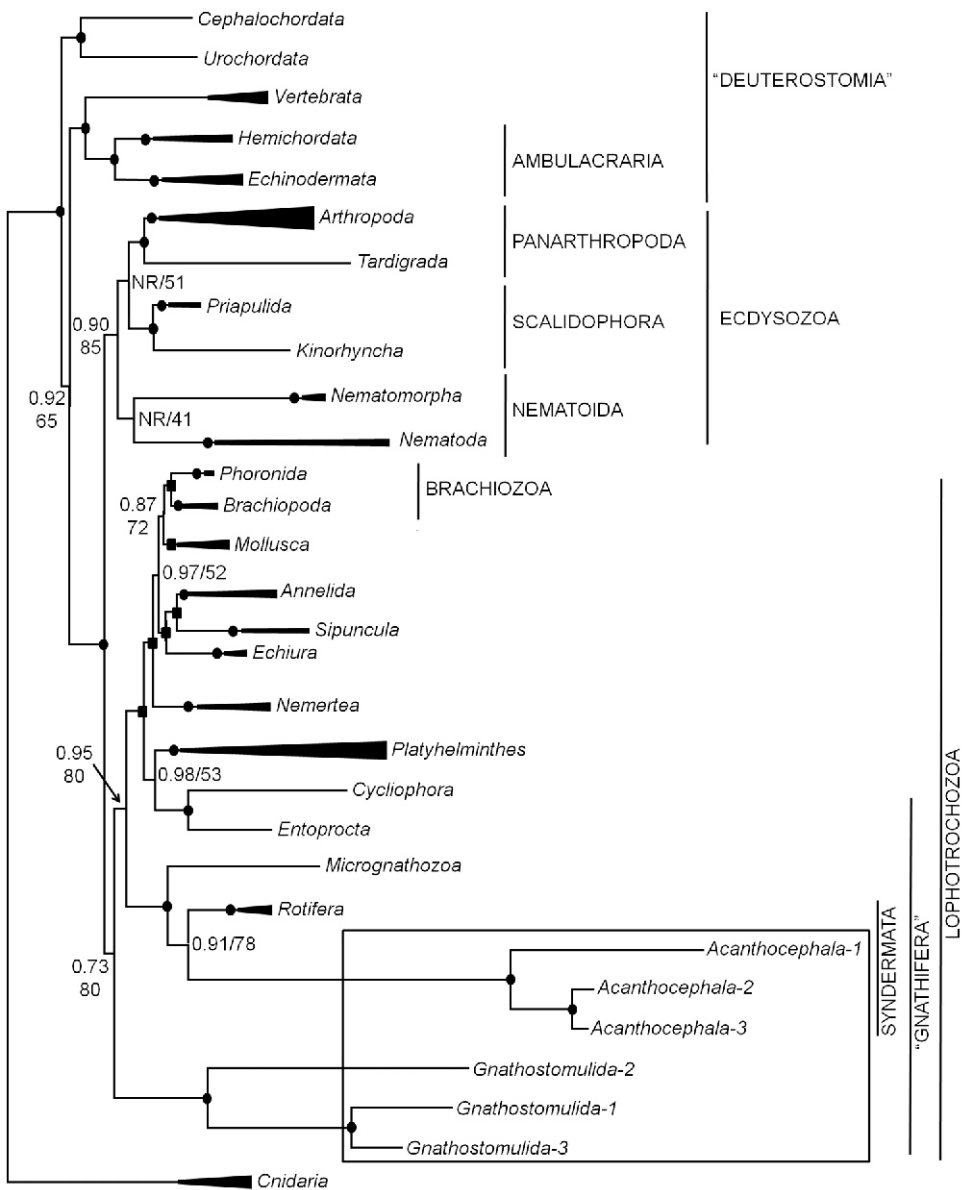
Supplementary Data 2

Bayesian and RaxML topologies (GTR + Γ + I) for the taxa subsets. Posterior probabilities (PP) and ML bootstrap values (BV) are indicated with a bullet (PP=1.0 & BV>90%) or a square (PP=1.0 & 75%<BV≤90%) on the node; lower values are indicated. For a comparison of the bootstrap values in the different trees see table 1. NR stands for a node not resolved in the BI consensus tree. Phyla of interest for each independent analysis are boxed. Monophyletic phyla are collapsed (triangle size proportional to number of representatives included), the monophyly of each phylum has maximum support (except for gastrotrichs). The scale bar indicates the number of changes per site. A: tree from Acoelomorpha dataset (Acoel-set); B: tree from Gnathifera dataset (Gna-set); C: tree from Gastrotricha dataset (Gast-set); D: tree from Bryozoa dataset (Bryo-set); E: tree from Chaetognatha dataset (Chae-set); and F: tree from the Basic-set. For species names corresponding to each terminal see Supp. Data table 1.



A

BPP/ML BS
 ● BPP:1.0 and ML BS >90%
 ■ BPP:1.0 and ML BS between 75% and 90%

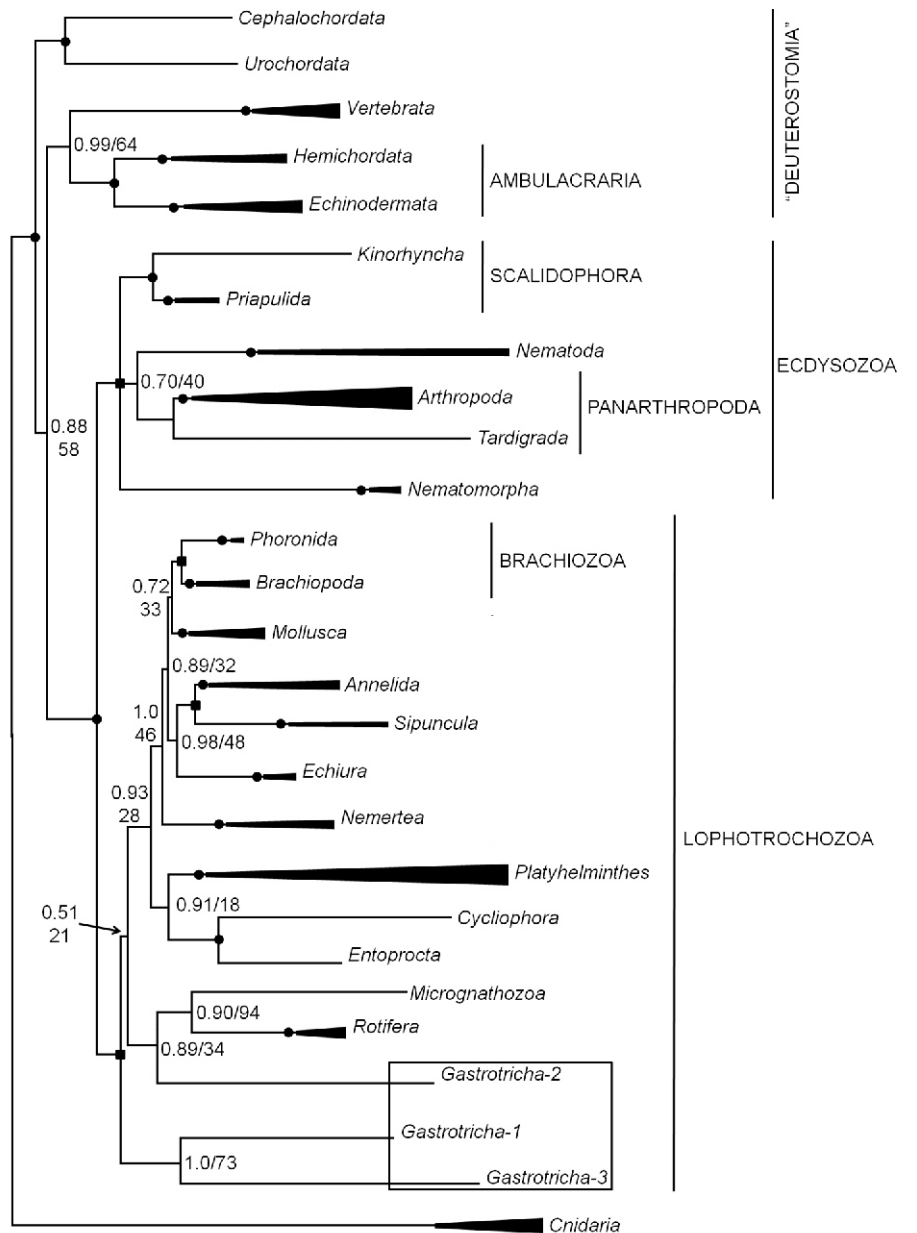


BPP/ML BS

● BPP:1.0 and ML BS >90%

■ BPP:1.0 and ML BS between 75% and 90%

B



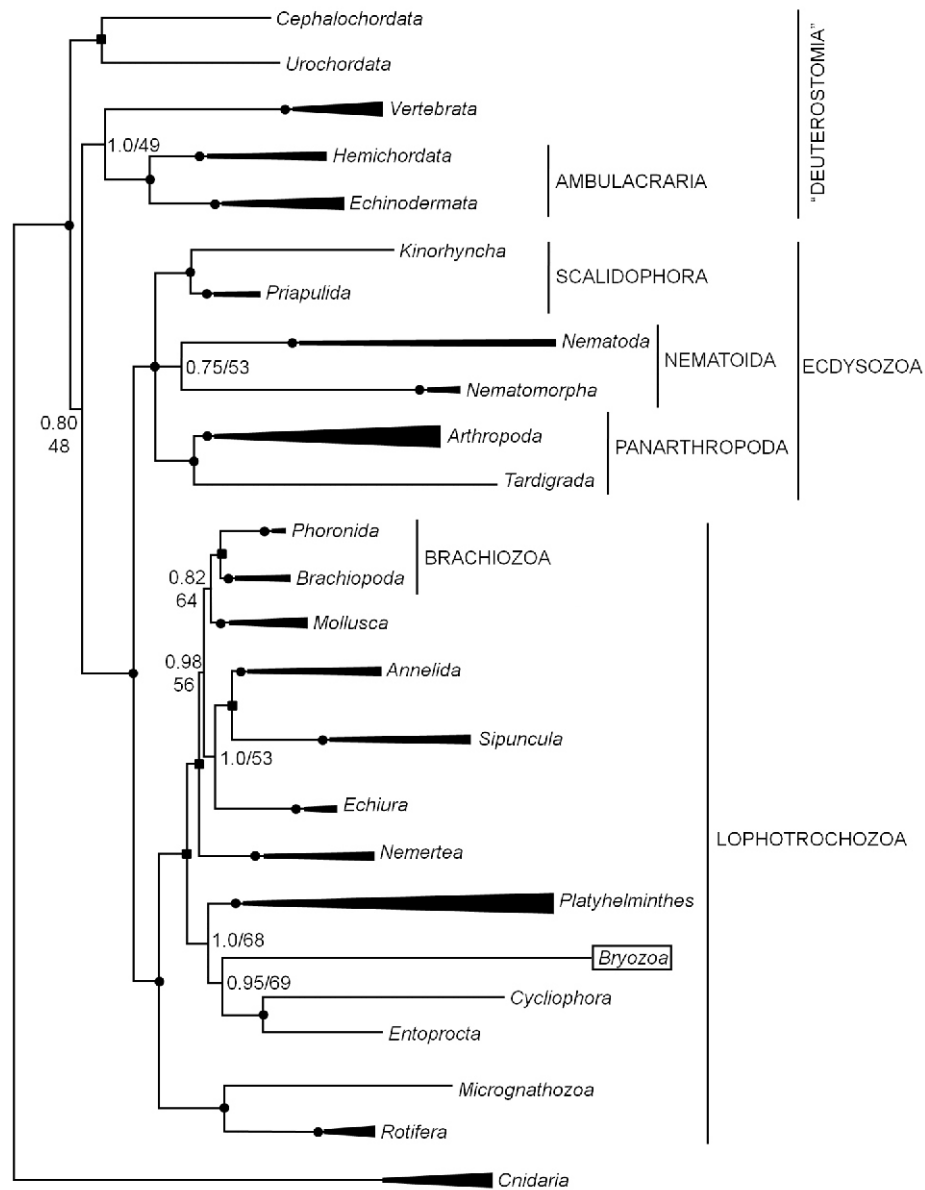
0.05

C

BPP/ML BS

● BPP:1.0 and ML BS >90%

■ BPP:1.0 and ML BS between 75% and 90%



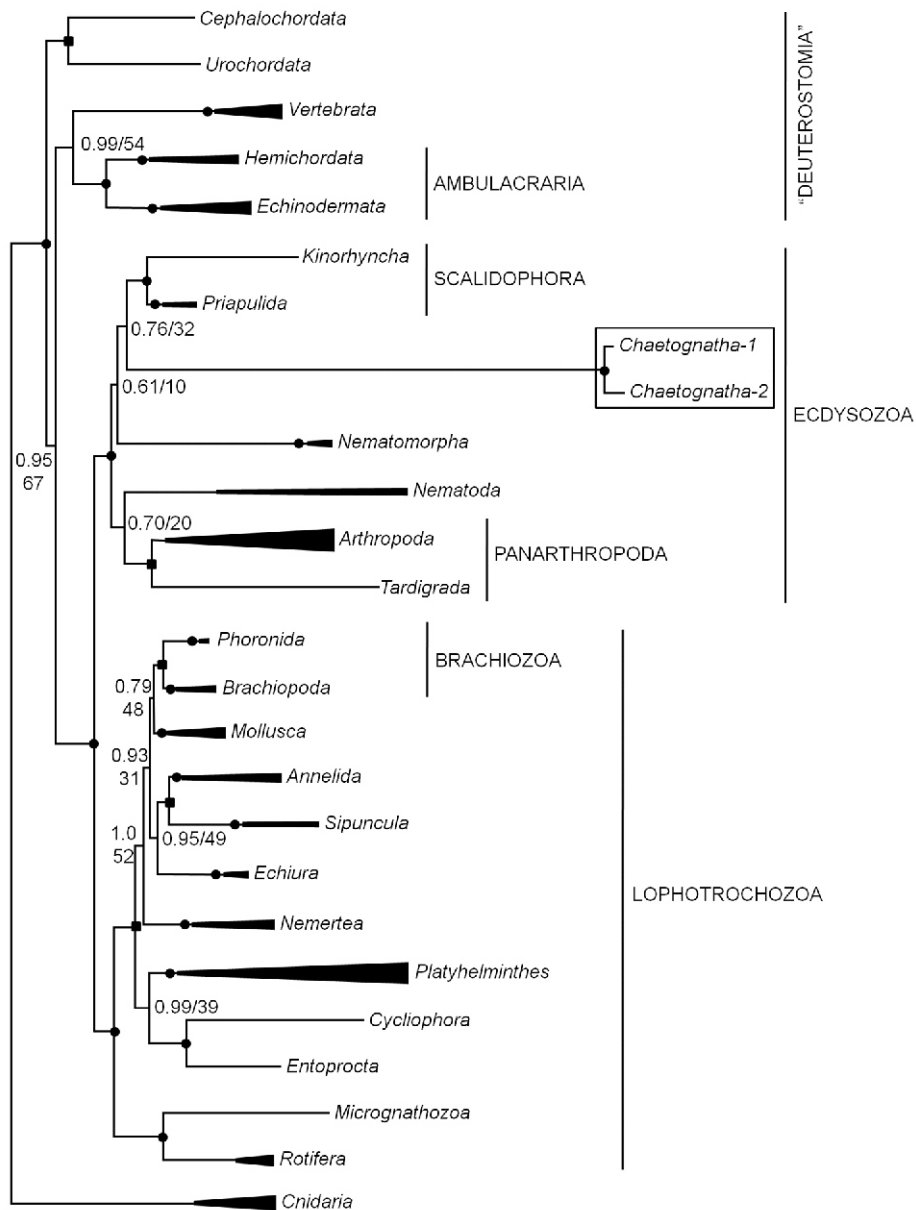
0.05

BPP/ML BS

● BPP:1.0 and ML BS >90%

■ BPP:1.0 and ML BS between 75% and 90%

D



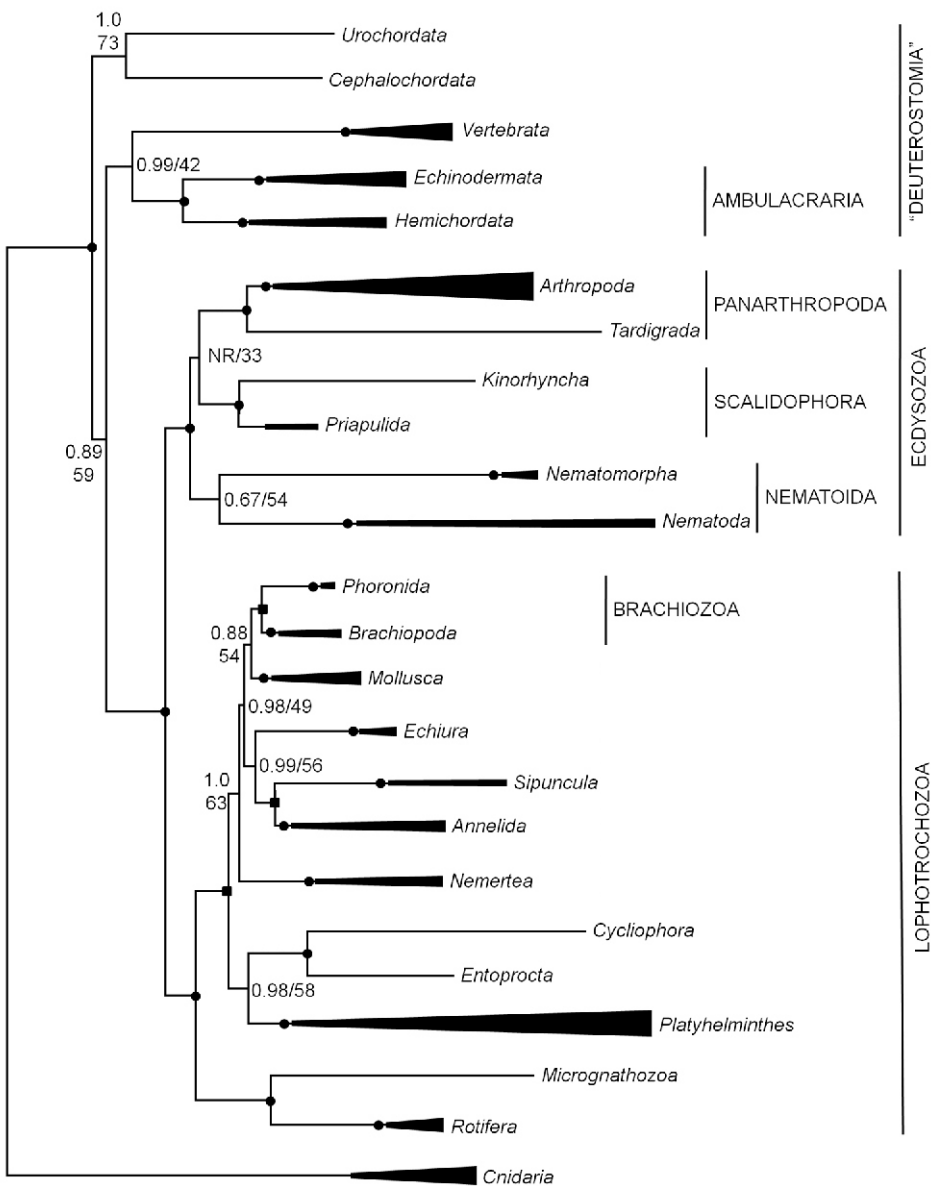
0.05

BPP/ML BS

● BPP:1.0 and ML BS >90%

■ BPP:1.0 and ML BS between 75% and 90%

E



BPP/ML BS

● BPP:1.0 and ML BS >90%

■ BPP:1.0 and ML BS between 75% and 90%