Supplementary File S3. Branch support values obtained for the cladistic analyses.
to
Neopterygian Phylogeny: the merger assay

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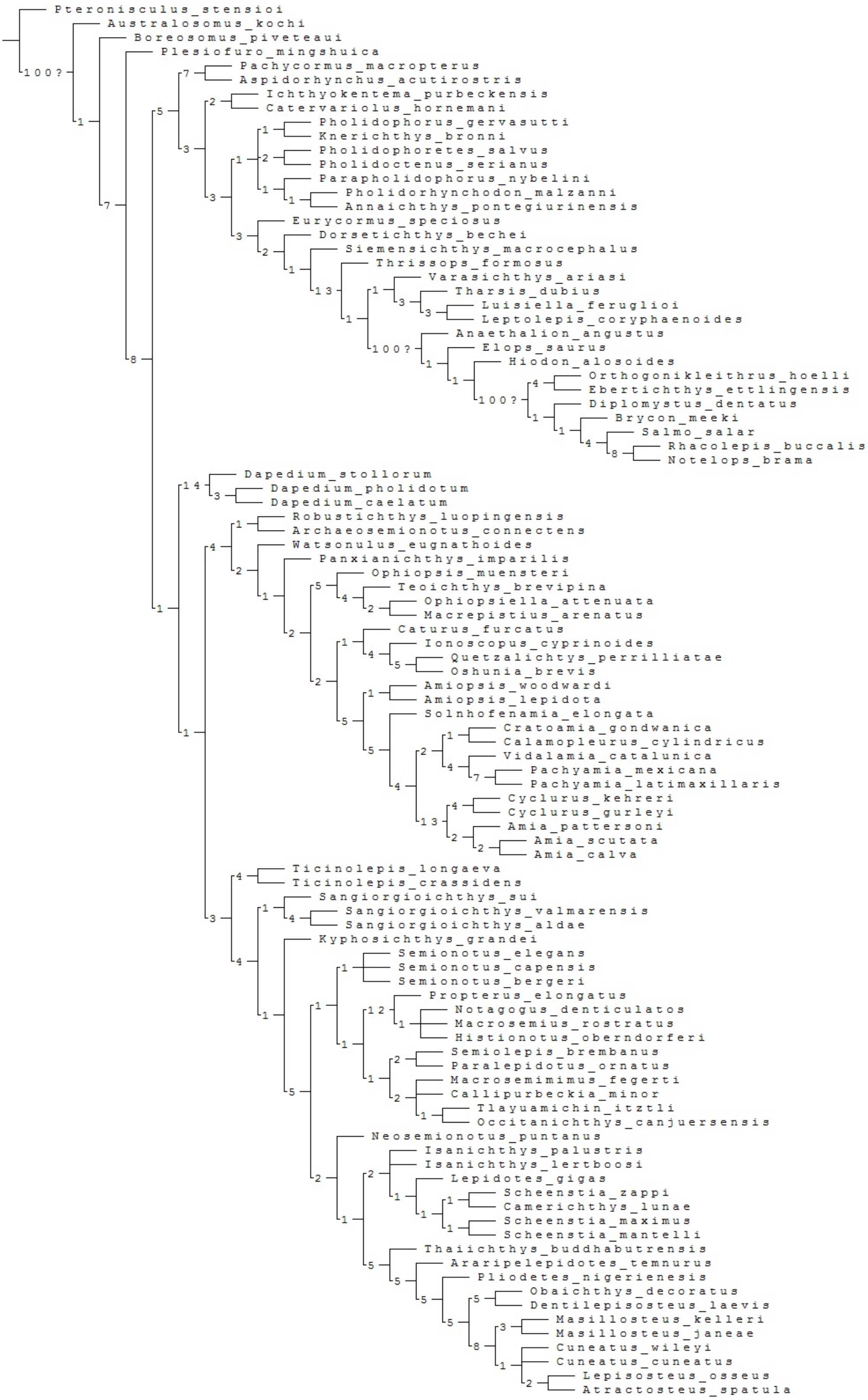
The cladistic analyses were performed with TNT under equal and implied weighting. The weighting strength was determined by using K-values of 3 and 8. Branch support was evaluated also with TNT applying bootstrap expressed as values of GC (groups present/contradicted) through 10000 replicates and calculating Bremer decay indexes for each node. Support measurements were calculated for implied (K=8 and K=3) and equal weighting analyses.

Equal weighting analyses:

Bremer supports (from 3720477 trees, cut 0)

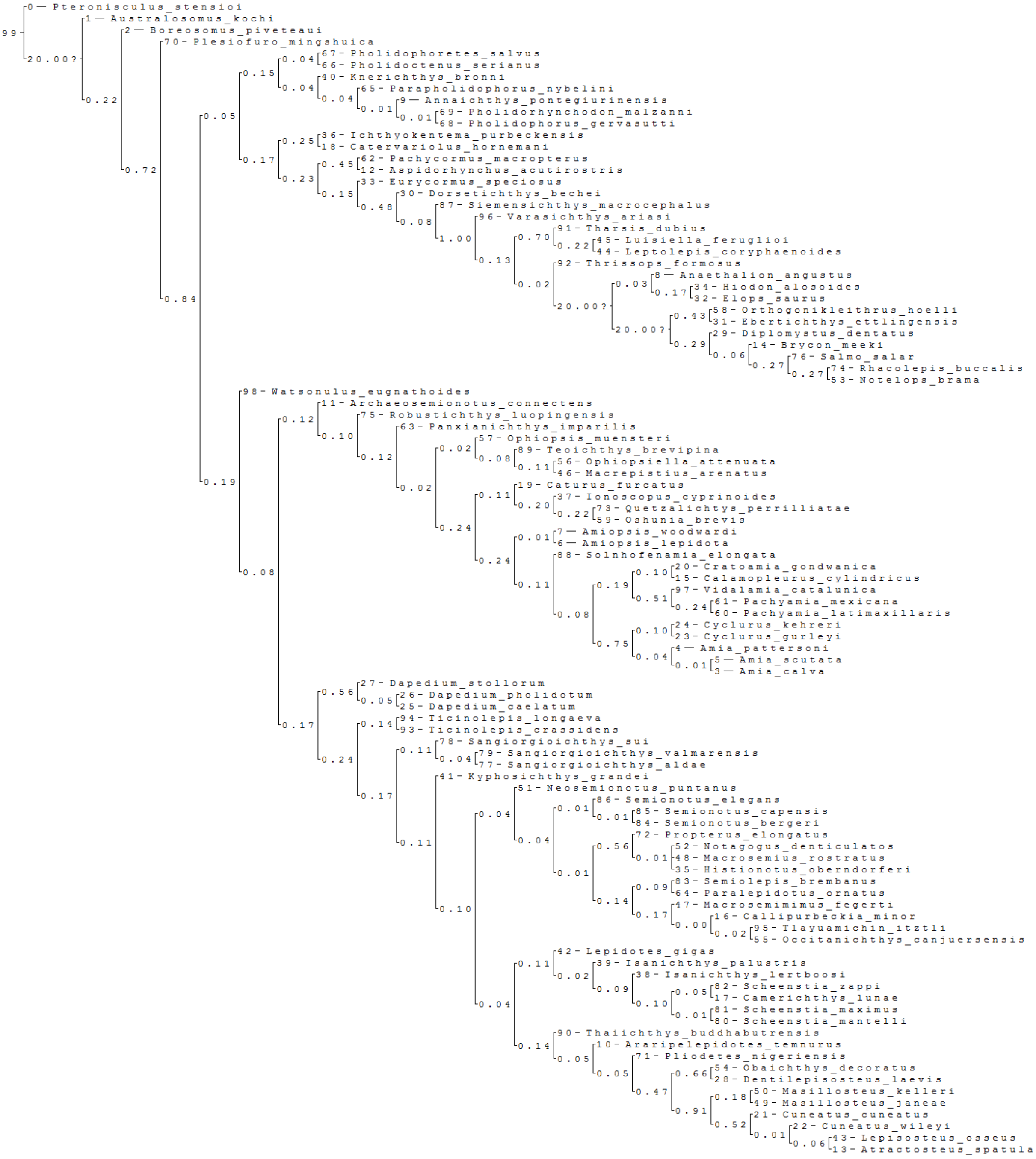


Equal weighting analyses:

GC values, 10000 replicates, cut=1 (tree 0) - Standard Bootstrap

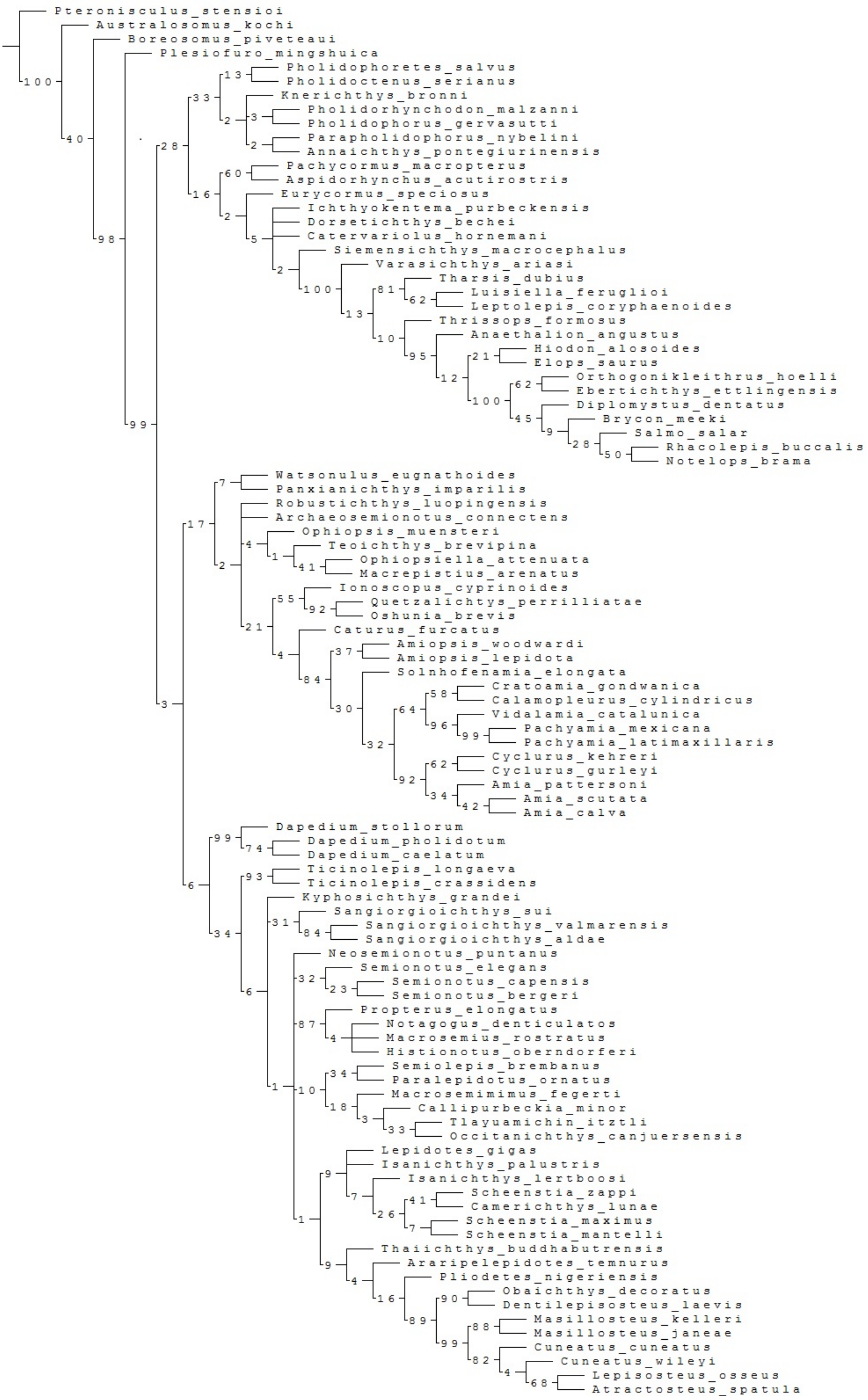
Implied weighting analyses (K = 3):

Bremer supports (from 175620 trees, cut 0.00)



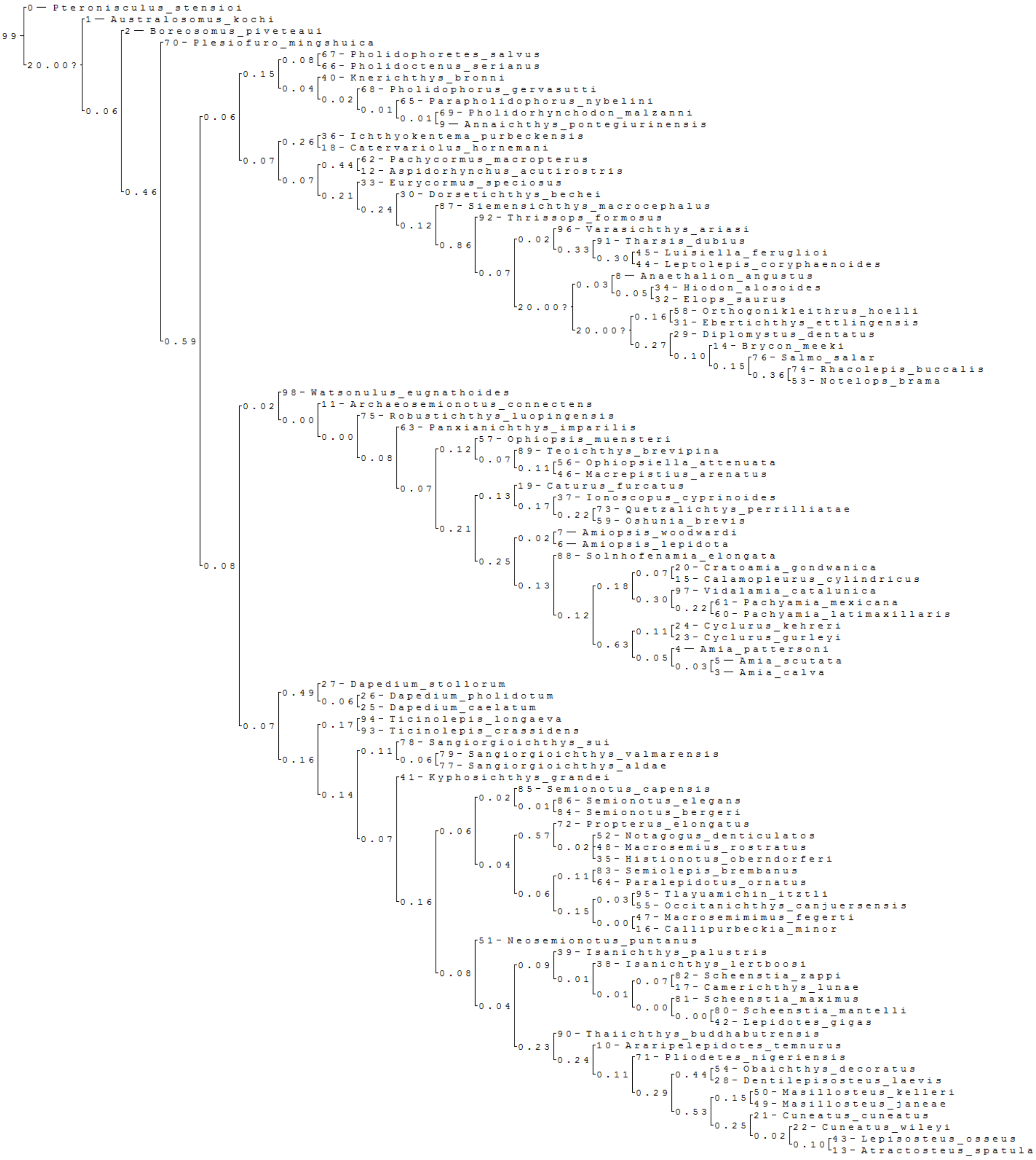
Implied weighting analyses (K = 3):

GC values, 1000 replicates, cut=1 (tree 0) - Standard Bootstrap



Implied weighting analyses (K = 8):

Bremer supports (from 176760 trees, cut 0.00)



Implied weighting analyses (K = 8):