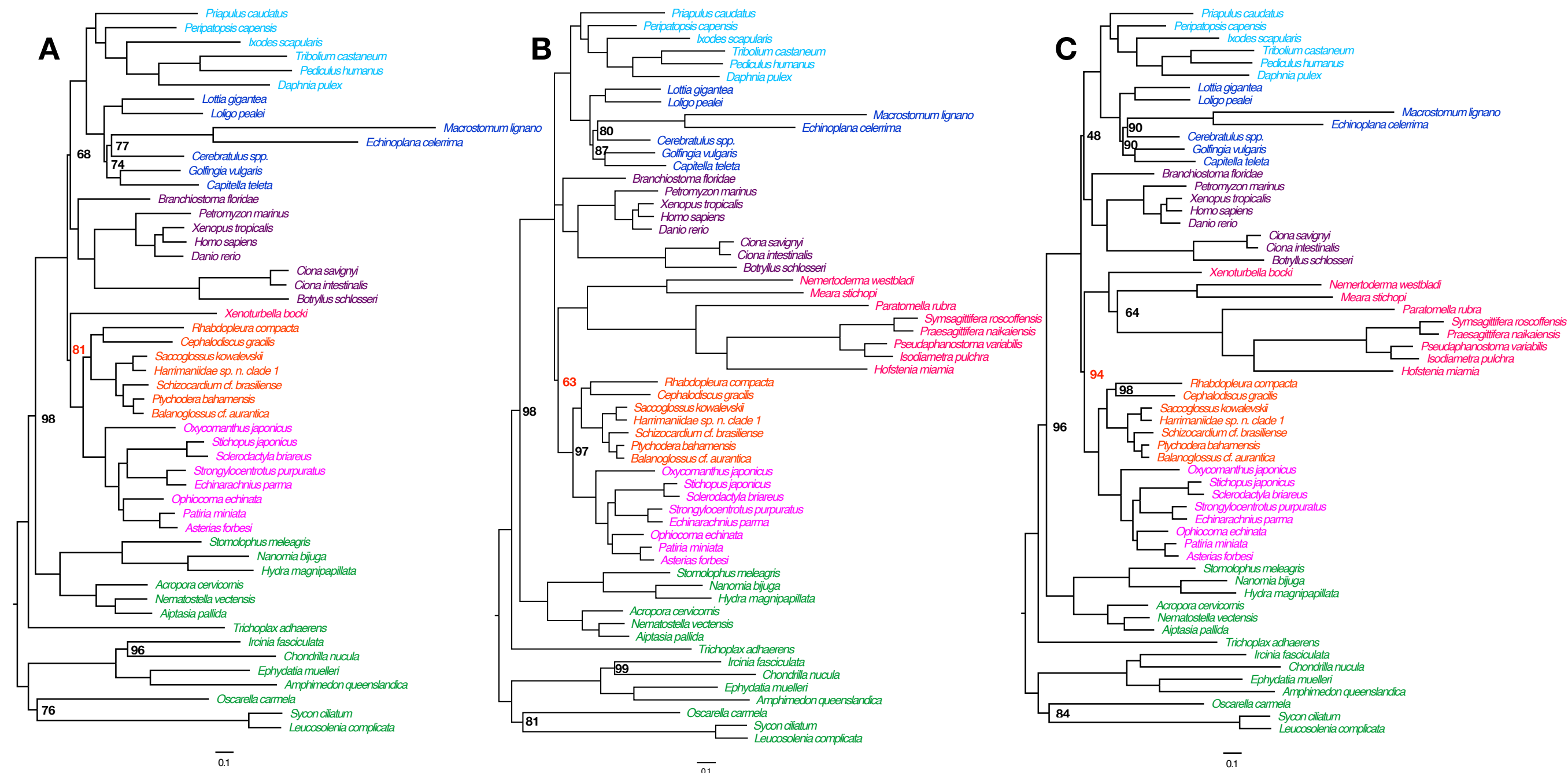


**Supplemental Information**

**Mitigating Anticipated Effects of Systematic  
Errors Supports Sister-Group Relationship  
between Xenacoelomorpha and Ambulacraria**

**Hervé Philippe, Albert J. Poustka, Marta Chiodin, Katharina J. Hoff, Christophe Dessimoz, Bartłomiej Tomiczek, Philipp H. Schiffer, Steven Müller, Daryl Domman, Matthias Horn, Heiner Kuhl, Bernd Timmermann, Noriyuki Satoh, Tomoe Hikosaka-Katayama, Hiroaki Nakano, Matthew L. Rowe, Maurice R. Elphick, Morgane Thomas-Chollier, Thomas Hankeln, Florian Mertes, Andreas Wallberg, Jonathan P. Rast, Richard R. Copley, Pedro Martinez, and Maximilian J. Telford**



**Figure S1. Phylobayes analyses of the data produced in this study. Related to Figure 1.**

A. Phylobayes jackknife analysis. This study, All genes, No Acoelomorphs, CATGTR, 50 x 30,000 amino acids Jackknife. Jackknife proportions less than 100% shown to right of node supported.

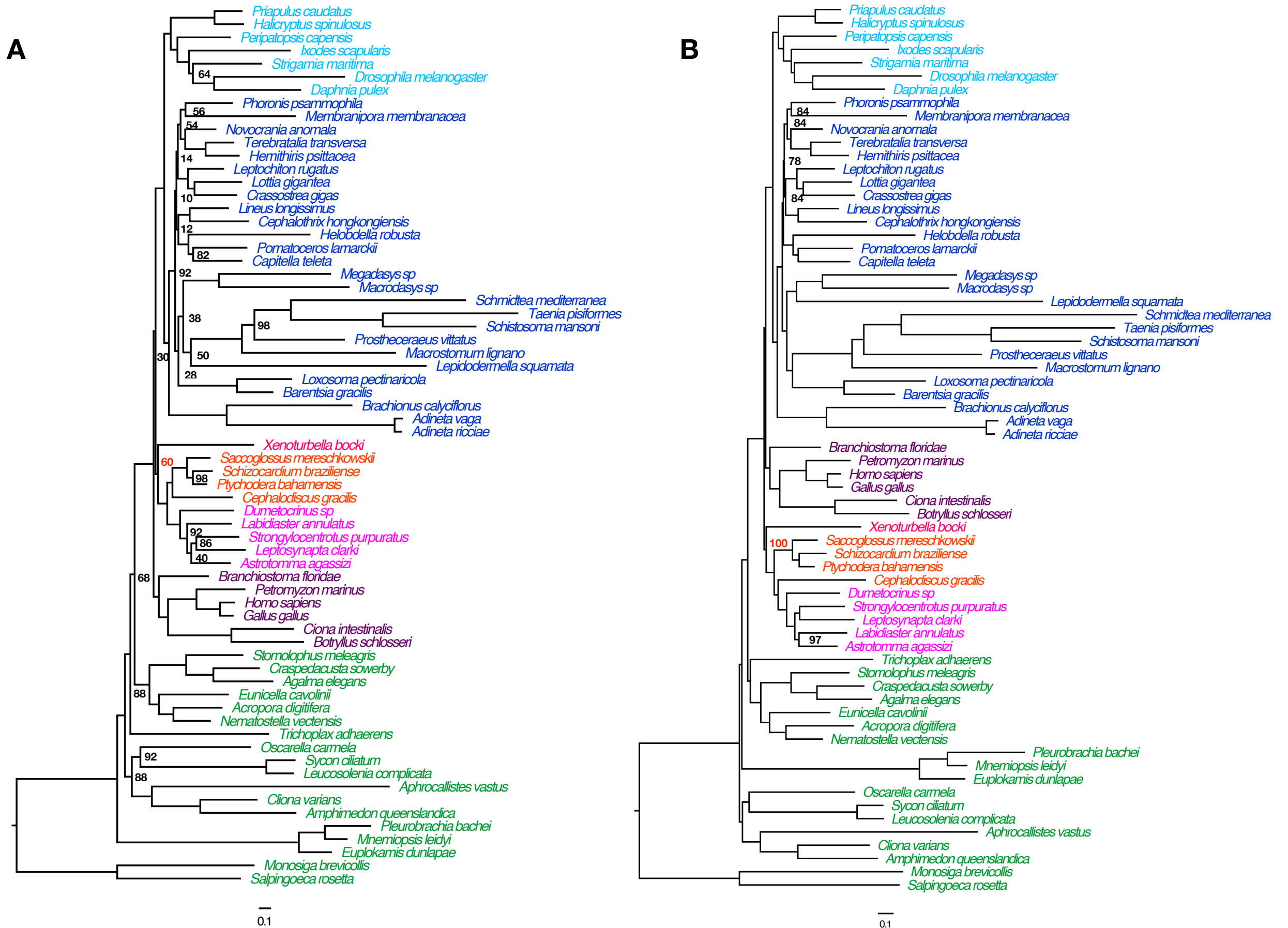
Xenambulacraria support highlighted in red.

B. Phylobayes jackknife analysis. This study, Best quarter of genes, No *Xenoturbella*, CATGTR, 50 x 30,000 amino acids Jackknife. Jackknife proportions less than 100% shown to right of node supported.

Xenambulacraria support highlighted in red.

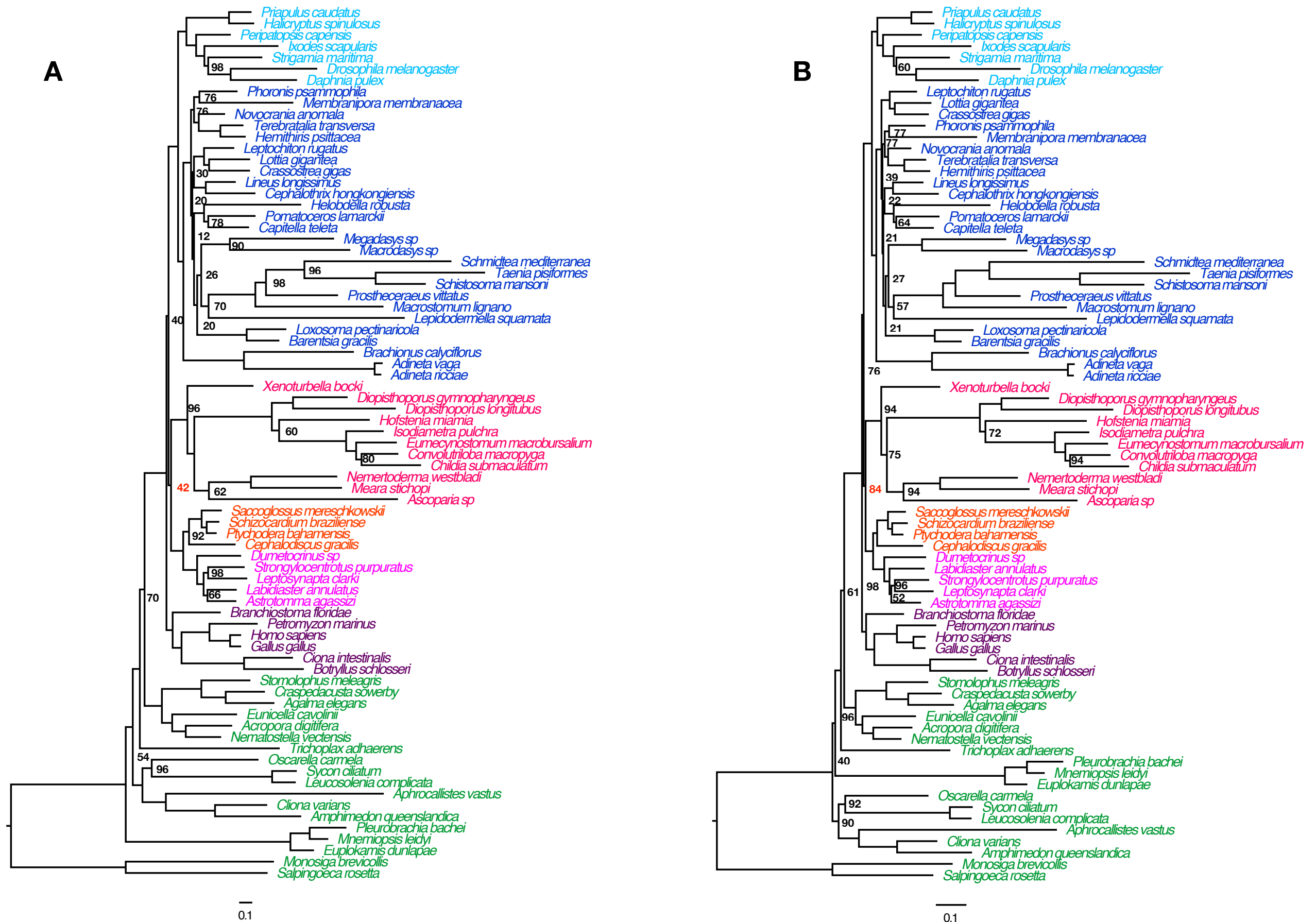
C. Phylobayes jackknife analysis. This study, Best genes, All taxa, CATGTR, 50 x 30,000 amino acids. Jackknife proportions less than 100% shown to right of node supported. Xenambulacraria support

highlighted in red.



**Figure S2. Reanalyses of data from Cannon et al. using Phylobayes. Related to Figure 1.**

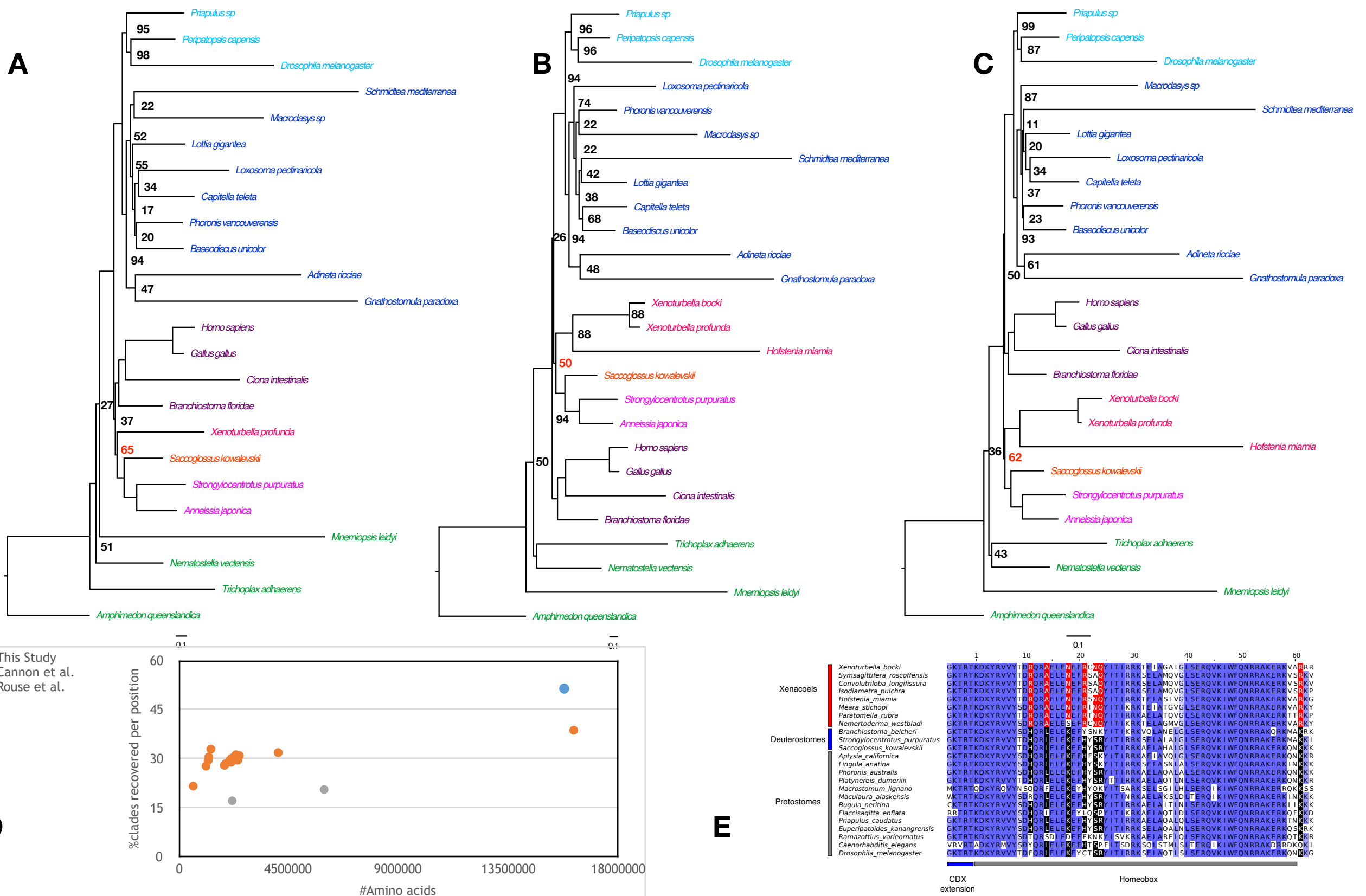
- A. Phylobayes jackknife analysis. Cannon et al. data, All genes, No Acoelomorphs, CATGTR, 50 x 30,000 amino acids. Jackknife proportions less than 100% shown to right of node supported. Xenambulacraria support highlighted in red.
- B. Phylobayes full dataset analysis. Cannon et al. data, All 212 genes, No Acoelomorphs, CATGTR. Posterior probabilities proportions less than 100% shown to right of node supported. Xenambulacraria support highlighted in red.



**Figure S3. Reanalyses of data from Cannon et al. using Phylobayes. Related to Figure 1.**

A. Phylobayes jackknife analysis. Cannon et al. data, Best genes, All taxa, CATGTR, 50 x 30,000 amino acids. Jackknife proportions less than 100% shown to right of node supported. Xenambulacraria support highlighted in red.

B. Phylobayes jackknife analysis. Cannon et al. data, All genes, All taxa, Dayhoff Recoded, CATGTR, 50 x 30,000 amino acids. Jackknife proportions less than 100% shown to right of node supported. Xenambulacraria support highlighted in red.



**Figure S4. Reanalyses of data from Rouse et al. using Phylobayes, comparison of three data sets and sequences of CDX genes supporting monophyly of Xenacoelomorpha. Related to Figure 1.**

- A. Phylobayes jackknife analysis. Rouse et al. data, All genes, No Acoelomorphs, CATGTR, 50 x 30,000 amino acids. Jackknife proportions <100% shown to right of node supported. Xenambulacraria support highlighted in red.
- B. Phylobayes jackknife analysis. Rouse et al. data, Best genes, All taxa, CATGTR, 50 x 30,000 amino acids Jackknife. Jackknife proportions <100% shown to right of node supported. Xenambulacraria support highlighted in red.
- C. Phylobayes jackknife analysis. Rouse et al. data, All genes, All taxa, Dayhoff Recoded, CATGTR, 50 x 30,000 amino acids. Jackknife proportions <100% shown to right of node supported. Xenambulacraria support highlighted in red.
- D. Comparison of size and ability to reconstruct clades of different recent data sets used to reconstruct position of xenacoelomorphs. X axis: total number of amino acids in alignment. Y axis: % of clades that are present in the tree reconstructed from the total data set that are recovered by individual genes - score is the average % across genes. Cannon et al and Rouse et al presented several different data sets as shown.
- E. Alignment of homeobox region of the CDX (Caudal) gene from bilaterians. Amino acids unique to, and supporting monophyly of Xenacoelomorpha are indicated in red.