# **ID TSAB-2018-0076 supplementary material description**

Tables:

**Table S1**: List of markers and primers with relative sequences amplified.

**Table S2**: List of datasets. Datasets utilized with description, best nucleotide model employed, analyses performed and number of specimens included.

**Table S3**: Number of tested and successfully amplified specimens per marker, and % of success.

**Table S4**: Estimates of Evolutionary Divergence between Sequences of the Central Hamersley Range, representatives of Pilbaranella species and the De Grey River specimen (468 bp). (Excel file)

**Table S5**:Subfamilies comparison. Differences and similarities among Central Hamersley Range species and lineages, Pilbaranella genus and the three Bathynellidae subfamilies. Austrobathynellinae\*: three species described, two species represented by male only. A.I= antenna I; A.II= antenna II; Th=thoracopod.

Figures:

**Fig. S1: 16S\_MrB\_tree.pdf** = 16S Bayesian tree including sequences of specimens from the Central Hamersley Range, representatives of *Pilbaranella* species, 1 specimen from the De Grey River and *Bathynella* sp from Slovenia (original file: 16S\_CP\_EG\_CA\_Slov\_44seq\_Gbl.nex.con.tre)

**Fig. S2: 28S\_MrB\_tree.pdf** = 28S Bayesian tree including sequences of specimens from the Central Hamersley Range, representatives of *Pilbaranella* species, 1 specimen from the De Grey River (original file: 28S\_CP\_EG\_CA\_49seq\_Gbl.nex.con.tre)

**Fig. S3: COI\_MrB\_tree.pdf** = COI Bayesian tree including sequences of specimens from the Central Hamersley Range, representatives of *Pilbaranella* species, 1 specimen from the De Grey River and *Bathynella* from Slovenia (original file: COI\_CP\_EG\_CA\_Slo\_63seq\_trim.nex.con.tre)

**Fig. S4: Concat\_COI\_18S\_RAxML\_tree.pdf** = COI-18S concatenate RaxML tree including representatives of specimens from the Central Hamersley Range, *Pilbaranella* species, 1 specimen from the De Grey River and genera from other countries (original file: Concat\_COI\_18S\_33seq\_RAxML\_bipartitions.result)