Having re-read this submission in full, I commend the authors on the considerable pains they have taken to improve the transparency and reproducibility of the manuscript (my major concern), and have also taken on board many of the small comments that I believe improve the interpretability of the figures. This is a compelling report and will go some considerable distance in informing the (sadly still ongoing) Nephrozoa vs Xenambulacraria debate - even if it is not decisive on the topology per se, I think the authors have used the genome and orthology analyses to compellingly argue against a "strong Nephrozoa", and the detailed analyses of neuro-peptide complement, microRNAs, and gene content also should give pause to those who interpret Nephrozoa as a well-argued conclusion.

One thing I would like to see in the final version of this manuscript is a table displaying the accession numbers of all raw reads used in the study - those for assembly, scaffolding, and annotation. Naturally the final scaffolded assembly and annotation should also be made public, whether through NCBI/ENA (preferable) or Zenodo or some other mechanism, and accession numbers for these outputs should be cited in the paper. This will make it much easier for anyone else who wishes to re-assemble or re-use these data. Similarly, it would be nice to see public access to raw reads and assemblies made from other non-Xenoturbella specimens used in this paper (I am thinking of the Paratomella assembly used in the OrthoFinder analysis).

A few other small notes:

Typo on line 126 - presumably N50 is 8.5 kb, not 8,500 kb

Discrepancy between text and table - is the final assembly span 111 Mb or 107.7 Mb?

Please cite the SRA accession numbers of the RNA seq data you used as input to Braker.

To clarify line 216: these are the orthologs present in the last common ancestor of all Metazoa? "all orthologs present in any bilaterian and any non-bilaterian" is a bit of a complicated way to say that.

I thought I'd check this claim: "The model nematode Caenorhabditis elegans is ~81% complete for the same set." and actually I got 78.5% for the C.elg N2 protein models downloaded of Ensembl Metazoa, with BUSCO5 and Metazoa odb10.

Access to the Zenodo data is embargoed for me so I cannot inspect it, but I do wonder, if it would be appropriate to also upload the draft Paratomella rubra genome & the raw reads used to derive it, to a public archive, since this is currently non-public data which was used to derive the OrthoFinder results cited in the text, if I understand right.

Line 471 - if acoels and Xenoturbella have similar levels of gene loss, then the long branches seen for acoels but not Xenoturbella in your gene presence/absence trees must be due to something other than gene loss. Furthermore, if this is just presence/absence data, it implies nothing about the rate of sequence substitution can be influencing the branch lengths. Surely therefore acoels have long branches in these trees only because they have gained many lineage-specific genes, no?

Line 513: I have to agree with the other reviewer - while you may or may not be correct in interpreting the acoel position in these analyses as an artifact, strictly, because of the non-monophyly of Xenacoelomorpha in this analysis, your analyses of gene content do support both Nephrozoa and Xenambulacraria, contradicting the text.

Line 650: you say that you used the gVolante server for BUSCO5 assessment with the cukaryote USCO reference - contradicting the text earlier when you say you used a Metazoa database. Which is it?

Supplementary figure 1 - Please describe how the blobplot was colored - was this diamond hits against uniprot, or blast against nr?

Supplementary figure 2 - Which k-mer was chosen, what reads were used as inputs, and what software was used to perform k-mer counting? Please also show the full genome-scope plot, including details of the inferred genome size and fit of the model. From the glimpse I see here the WGS reads used for the raw assembly seem to be fairly low coverage, and it would help for a more clear-eyed interpretation of the primary assembly to understand any differences in the k-mer inferred genome size and the assembled genome-size.