

## ***Interactive comment on “Species variability and connectivity in the deep sea: evaluating effects of spatial heterogeneity and hydrodynamics” by Lidia Lins et al.***

**Anonymous Referee #2**

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The title should be changed, at present it is far too general. The topic of the manuscript is free-living nematode species variability and connectivity- not species variability and connectivity. Moreover, the manuscript does not study effects of hydrodynamics as no hydrodynamic variables are measured. There are a sufficient number of ways that sediment heterogeneity may be obtained that “high” hydrodynamics can not be inferred. I’m also not sure what “high” hydrodynamics means. Finally the degree to which connectivity is analysed in the manuscript is pretty limited- connectivity between deep and shallow only measured apparently by cluster techniques. Furthermore, if I have followed the methods correctly, there are only 3 – 4 replicates from 6 and 4 stations (shallow and deep respectively) for nematodes (and it is unstated whether there is any

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replication for the other measures). I would have expected a study focussed on defining and explaining variability to have more replication and stations that that. However, the manuscript is well written and structured. The methods are well explained and the analyses are appropriate. I was surprised to see no reference to the Leduc et al paper “Nematode beta diversity on the continental slope of New Zealand: spatial patterns and environmental drivers.” I would like to see a reduction in the scope of the manuscript with a focus on the variables actually measured (food availability) and the type of organism studied. Broadening the discussion to consider how different results may have been obtained if a greater mix of phyla, size and biological traits (including dispersal) had been studied would also be useful. I don’t know that connectivity to the degree that it is analysed here is actually useful as there is no indication of space and time scales. The “connectivity” terminology should be dropped from the manuscript and instead merely discussed as a lack of clear depth-related population differences, depth-endemic lineages or isolation.

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