We thank the reviewer for his/her helpful suggestions and constructive comments. Detailed response to each comment is provided below:

For Methods: It was not indicated in Methods, how many samples from each expedition/habitat/depth range were examined. Is it possible, that distinctions in dissimilarities (and number of taxa) between habitats, depth ranges, etc. were caused by different number of examined animals or samples (smaller number is supposed to lead to higher dissimilarity within an area)? Did you try to examine correlation between distance between samples (within area, depth range, habitat) and dissimilarity values within these ranges? Can it be that some portion of dissimilarities is explained by this factor?

Reply: This comment is threefold, and each aspect was addressed separately.

i) The supplementary table TS1 was amended in order to include in the last column the number of replicated samples per station and type of data. For meiofaunal major taxa analysis three sediment cores were used for most of the stations (>75%), while for nematode analysis 50% of the stations were based on a single sample. Microbial analysis was based on 3-4 sediment cores from each station that were merged in a single sample.

ii) All analyses were based on station level and not replicated samples; hence, one value per station was incorporated in the analyses. From the results of our study it becomes apparent that the number of stations per habitat or depth range does not seem to affect dissimilarity in the way it is hypothesised by the reviewer (“smaller number is supposed to lead to higher dissimilarity within an area”). Differentiation diversity presented in Table 4 can be used as an argument for this. For example, basin and slope habitat differ in the number of stations they involve (45 and 24 stations respectively) however they were not found to differ in delta diversity, having similar within habitat dissimilarity values (42 and 38.45 respectively). In a similar way, the depth range 1000-1500 has the highest number of stations (13) and among the highest dissimilarity values (39.1), whereas the depth range <500 with only 3 stations has the lowest dissimilarity value (13.27). Similar examples can also be indicated for

within habitat or depth ranges dissimilarity at smaller scale (beta diversity).

(iii) Our study involves an extensive number of samples and stations in the Mediterranean and could therefore support a technical paper on the correlation of between samples dissimilarity and their distance. However, the focus of our study is the investigation and comparison of benthic patterns in two different marine habitats, basins and slopes. Therefore, and in view of a rather extensive manuscript, we limited the exploration and presentation of correlations only with regard to the most relevant to the study variable.

Table 2. I understand Table 2 not completely. What do overlapping lines mean?

Reply: The overlapping lines are a common way to visualize post-hot pairwise comparisons. In our case, depth ranges with common underline are not significantly different at the 95% significance level. This explanation has been added to the revised ms.

Table 2 and Figure 3. You have depths less than 1500 m (even less than 500 m) in Basins. Unfortunately, I am not familiar with bathymetry of the Mediterranean, but how can it be? Normally, depth of basins is more than 2000 m. May be, you mean some rises or seamounts, not basins? In this case, I believe, these habitats should be separated from basins.

Reply: The Mediterranean Sea has a very complicated topography with many different features such as seamounts, trenches, slopes and basins all occurring within a very narrow geographic area. It consists of two large basins, the western and the eastern, which are separated by the Straits of Sicily. Each of these two basins consists of a number of sub-basins or peripheral seas with variable depths. The eastern Mediterranean in particular, where this study is focused, consists of the Adriatic Sea (max depth 1216 m), the Ionian Basin (max depth 5093 m), the Levantine Basin (max depth 4384 m) and the Aegean Sea (max depth ~2500 m). However, all these peripheral seas consist of another series of sub-basins with smaller depths which however possess all the characteristics of the large deep-sea basins of the world oceans (i.e. they are surrounded by slopes, they are completely isolated, in terms of depth, by neighbouring basins,

they function as traps of organic matter etc.). Of course, their main difference is that these Mediterranean sub-basins occupy a relatively small area of the sea floor compared to the vast areas occupied by the Atlantic or Pacific basins. Nevertheless, for all the above reasons we believe that we should keep and treat even these shallower basins as real basins, similarly to the way they have been treated in many other previous studies (e.g. Lampadariou & Tselepides 2006, Lykousis et al. 2002). Moreover, if we were to exclude some of them, we would have to use a completely arbitrary criterion (e.g. exclude every basin which is shallower than 1000 m).

Tables 4 and 5. I do not understand, to what applies sighs "*" and "**" in this table? They stay in headings for rows, but not in some certain values of dissimilarity. Hay can I understand, which difference between dissimilarities was statistically significant?

Reply: We understand the complexity of these two tables and in the revised version of the ms we modified them according to the suggestions from all reviewers, as well as their legends and notes in order to be more easily read.

Figures 4 and 5. Number of taxa / genera depends on number of samples or number of examined individuals. That is why, I believe, that it is not correct to use indicators "Number of taxa" and "Number of genera". It seems to me, in this case, it would be better to use average values (for each area, depth range, habitat) of estimated number of taxa for samples of 200 individuals for nematodes and for some number of individuals for major taxa.

Reply: Sample size dependence of species richness is a substantial problem in comparative diversity studies and we therefore understand the concerns of the reviewer regarding the way diversity is presented in our study. However, the ES rarefaction method proposed by the reviewer as a better way of presenting our data has been heavily criticized from the start (indicative references Fager 1972, Simberlof 1972, Abele & Walters 1979, Gage & May 1993, Gray 2000, 2001, 2002 (and references therein), Magurran 2004) as an inappropriate method for comparing diversity, in particular with regard to benthic communities. During the last decade,

improved methodology has been developed by Colwell and colleagues as an efficient way for the measurement and comparison of species richness (details in Gotelli & Colwell 2001, Colwell et al 2004). These state-of-the-art statistical techniques propose sample- or individual-based rarefaction accumulation curves for comparing richness. The specific methodology has been previously used by our group in a meiobenthic copepod diversity study (Sevastou et al 2011); yet it appeared to us that this could not be used in the present study for several reasons. First, it would be awkward to apply accumulation curves, or the proposed ES rarefaction method, for major meiofaunal taxa since the individuals are not sorted to major taxa of the same taxonomic level. Apparently, this is the reason why ES, which is widely used in meiofaunal studies, has not been applied, at least to our knowledge, in studies focusing on major meiofaunal taxa. Moreover, we cannot also apply this method for the microbiological data, because abundances are not available for this benthic group. In addition, and in connection to the previous reasons, it would be rather unbalanced to present accumulation curves just for the nematode community. Having decided that accumulation curves should not be used in our study, the decision on using richness as a measure of diversity for our analyses seemed the most appropriate choice. Richness (number of species, genera or any other taxonomic level) is in general considered the simplest, more straightforward and concise index of diversity. Furthermore, and in view of a rather long manuscript, in our study it could serve both for summarizing and presenting the basic/raw information of the paper as well as an index for comparing meiofaunal communities. In addition to the number of taxa/genera/OTUs, the extrapolative, sample-independent estimators Jack1 and Chao1 were used and discussed for nematodes and microorganisms, respectively.

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