Reviewer 1

We would like to thank the reviewer for taking the time to carefully read and comment on our manuscript. Below is a point-by-point response to the questions and comments raised.

The paper reports on lipid composition in five sediment traps placed in different sites of the Southern Ocean, characterized by different productivity: two of them (M6 and P2) were in HNLC waters, while three other sites (A3, M5 and P3) were located in naturally iron-fertilized areas characterized by higher productivity. Lipid composition markedly differed among these sites, with higher proportion of labile lipids in the naturally iron-fertilized waters. For one of the sediment traps (A3 located in the Kerguelen Plateau), quantitative data on the composition of settled material were available from a previous study. These data have been used to depict the seasonal trend in lipid composition as related to the biological components (diatom cells, resting spores and faecal pellets). Samples collected during the summer period were dominated by diatom resting spores, which transferred to depth a considerable amount of lipids, dominated by the labile The study is interesting since provides the link between qualitative composition of sediment traps and the composition in lipids, which are also used as biomarkers to infer the origin of sinking material.

R1 – Q/C – 1: I have the following comment: The comparison between trap content and lipids was done for the sediment trap A3, which was deployed at relatively shallow depth as compared to the other traps. It is mentioned that the labile lipids can be degraded/ remineralized with depth. Can the 'fingerprint' of lipids derived from diatom spores be preserved in the deeper layers? The other sediment traps placed in iron-enriched areas (P3 and M5) were much deeper; is it possible to state that the composition of lipids in these deep stations still reflects the contribution of diatom spores? Or of diatoms in general? The role of diatom spores in mediating a considerable carbon flux for the benthic organism has been demonstrated for the shallower areas: can it be extended to the deep stations in the productive areas as well? I would suggest the points listed above be addressed in the discussion.

R1 – R – 1: We would like to thank the reviewer for this comment. To clarify, we have available detailed diatom counts and lipid analyses for all of the sediment trap samples, including the deeper stations P3 and M5. In the current manuscript, we thus aim to compare the trap content with lipid composition for all the samples.

We know from our previous work that diatom-resting spores account for 60% of annual carbon export from at 300m from an iron-fertilized bloom on the Kerguelen plateau (Rembaubille et al. 2015). We have observed similar patterns in deep samples (>1500m) from the productive regime at South Georgia (P3), whereby 42% of annual carbon export could be attributed to resting spores (Rembauville et al. 2016). At the productive Crozet site (M5), *Eucampia antarctica* resting spores dominate flux in the bathypelagic and are strongly correlated with total POC flux (Salter et al. 2012). This is in stark contrast to the HNLC sites from these areas, which have very few resting spores with a negligible contribution to organic carbon flux. These findings, from different island systems, provide strong evidence that diatom flux, in particular resting spores of Chaetoceros and Eucampia, are the dominant vector of organic carbon flux to the bathypelagic (>1500m) ocean following iron fertilized blooms. In the present

manuscript we are also able to demonstrate that these resting spore-dominated systems not only transfer significant amounts or organic carbon to the deep ocean, but also mediate a bathypelagic flux of labile lipids in the form of mono- and polyunsaturated fatty acids. For example, consulting Table 2 and Figure 2 in the manuscript, it is clear that the relative abundance and concentration of MUFAs and PUFAs is considerably higher in the productive sites, when compared to the HNLC sites (cf M5 and M6; P3 and P2). All of these samples are >1500m in depth. We thus take this as strong evidence that the signature of enhanced unsaturated fatty acids associated with resting spores is transferred to the bathypelagic ocean.

We acknowledge that this was perhaps not stated as explicitly as it might have been. We have rewritten the first paragraph of section 4.4 (Implications for pelagic-benthic coupling) in order to express these considerations more thoroughly (Lines 363-378).