

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 of 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).

Reviewer 2

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.

R2 – Q/C – 1: This manuscript by Rembuaville et al describes lipid fluxes and compositions for five deep-water sediment traps deployed in the Southern Ocean to evaluate relationships between Fe fertilization and organic matter (OM) flux to the seafloor and the effects of seasonality in upper ocean ecology and particle morphologies on the ON flux. The major conclusions are that labile lipid fluxes are higher at the three iron-fertilized sites than at the two lower productivity HNLC sites, that lipid fluxes are greatly attenuated with depth, and that specifics of lipid flux and composition depend on ecological factors in the upper ocean. The conclusion that diatom resting spores and zooplankton grazing on the main phytoplankton that produces fecal pellets of various morphologies are major determinants on OM and lipid flux to the seafloor at these sites, and specifics of the fluxes and types of particles varies between the site. Unfortunately there are some serious flaws with the present form of the manuscript that would require attention of the authors before proceeding further.

R2 – R – 1: We thank the reviewer for the precise synopsis of our manuscript. In the detailed comments below we aim to address the issues concerning the reviewer.

R2 – Q/C – 2: First and foremost, the lipid compositional data are actually given short shrift. Are they supposed to be in Supplemental table 1 (noted at line 137 and again at line 297), which apparently was either not included (intended or otherwise?) or simply not available to this reviewer. This would actually include the seasonal data for the plot shown in Fig 4.

R2 – R – 2: We would like to assure the reviewer that we would not reference a supplementary file containing the lipid compositional data and then intentionally exclude it from the manuscript. It seems for some reason the reviewer did not receive the supplementary tables, most probably due to an error during the submission process. The lipid data is highly complex: it is a matrix containing 2832 elements that clearly precludes a detailed discussion of all the patterns observed. We have attempted to present and discuss the lipid data we consider most pertinent to our objectives of examining the link between ecological flux vectors and organic matter composition. We agree with the reviewer that this data should be available to validate the patterns we describe, which is why we intended to present it as supplementary information. We also recognize that some of the detail in the patterns of specific compounds we don't fully describe in the manuscript might be of interest to a certain sector of the readership. As originally intended, tables of lipid fluxes and concentrations are presented as Supplementary Tables 1-5 in the revised version of the manuscript.

R2 – Q/C – 3: Without a more complete data set (indeed at line 276 “quantitative datasets on both compound and organisms fluxes are required” tells all).

R2 – R – 3: This comment is somewhat confusing. At line 276 we make a general statement that quantitative flux datasets are required for both chemical elements (in this case lipids) and biological elements (diatoms, fecal pellets etc) in order to provide a quantitative framework and examine mechanistic processes related to pelagic-benthic coupling. By “referencing a complete dataset” we assume the reviewer is revisiting their previous point concerning the lipid compositional data. As stated above, the intention was to provide this complete dataset and it is available as part of our revised submission.

R2 – Q/C – 4: The lipid compositional data that are included in the text are too sparse for the generalized conclusions that are drawn.

R2 – R – 4: We have added more quantitative references to the text, in addition to providing full supplementary tables of lipid compositional data that may be used as a reference supporting our general conclusions.

R2 – Q/C – 5: Throughout the text, and in Table 2, there is some confusion about fluxes vs concentration. E.g., at line 284, the “spring lipid flux is low (0.3 mg/m²)

...

”, but this is a rate not a flux without some time frame. Is it supposed to be per day, or over the deployment period, or annualized?

R2 – R – 5 We acknowledge that there might be some confusing terminology throughout the manuscript, which we have tried to address in the revised version (see below). It is perhaps worth clarifying that a rate, by definition, describes some change in a property as a function of time. We would therefore politely disagree with the reviewer that 0.3 mg/m² would be considered a rate, since it lacks a time component. A flux, on the other-hand, is a special kind of rate that describes the passage of some property through a defined area, integrated over a certain time interval. In sediment trap studies, it is sometimes the case that the time interval over which fluxes are integrated corresponds to the sediment trap deployment period (which is of course a unit of time), in which case it is entirely correct to write xx mg/m² over the deployment period as a flux, if the time period is specified. The collection periods for the sediment traps are of course known and were presented in Table 1 of the original version of the manuscript.

The reviewer is specifically referencing our use of the term flux at line 284. However, in the submitted version of the manuscript the units at line 284 are 0.3 mg m⁻² d⁻¹ (i.e. including the time component), not 0.3 mg m⁻² (excluding the time component) stated by the reviewer, who appears to have misquoted our original text.

R2 – Q/C – 6: At line Likewise, in Table 2, the “normalized total lipid fluxes, mg lipid/g OC” are concentrations not fluxes (it is correct that lipid flux/OC flux will give a concentration of mg lipid/g OC). (Note that in figs 2a, c, g, and e fluxes have correct units.)

R2 – Q/C – 6: The reviewer has a valid point here concerning terminology. It is of course the case that normalizing lipid fluxes to organic carbon fluxes removes both the units of area and time, resulting in two mass quantities expressed as a ratio that

can also therefore be considered as a concentration. In the original version of the manuscript we had chosen the terminology “normalized lipid flux”, but in order to avoid unnecessary confusion we follow the reviewers suggestion and have changed this to concentration throughout the manuscript.

R2 – Q/C – 7: Other comments: P 6 - were the traps treated with some sort of poison or preservative to preserve the integrity of the OM over the entire deployment period (if this is given in one of the references it was not clear)?

R2 – R – 7: Yes, the detailed processing of samples is in the references in Table 1. This has now been referenced in this section.

R2 – Q/C – 8 Line 173 - this is the first instance of the flux “units” being incorrect. See also line 185– a concentration

...

R2 – R – 8.

@line 173 - As explained above these are fluxes integrated over the deployment period. In the original text this was phrased as “The total lipid flux...” However, this is clearly causing some confusion and so the text has been modified as follows:

Total lipid fluxes integrated over the sediment trap deployment period (Table 1.)

@line 185 – As stated above we have changed our terminology from normalized lipid flux to concentration.

R2- Q/C – 9: What are the annualized primary productivity levels at the five sites? And annualized chl-a concentrations (is that what’s in fig 1?). This information is important to give some sense of the quality of the OM produced at each site, as this impacts the comparative fluxes near the seafloor.

R2 – R – 9: The chlorophyll maps presented in Figure 1 show the annual climatologies of MODIS-chl data at each site. This information has been added to the figure legend. The purpose of presenting these maps was primarily to show the different biomass regimes at the iron-fertilised and “HNLC” sites where the sediment traps were deployed. We do not have a good estimate of primary productivity levels at each site, as these would depend on using satellite data and a model to convert chlorophyll to productivity. Such algorithms are not well validated in the Southern Ocean. Furthermore, in order to achieve this one would need to estimate the surface catchment area over which the sediment traps are integrating based on particle trajectories. In order to compute particle trajectories one would need a good estimation of particle sinking speed and vertically resolved current vectors. None of these variables are well constrained at our deployment sites.

We are also not clear that annualized primary productivity levels would offer much insight concerning the quality of OM produced at each site. OM quality is related to the geochemical composition of OM. The reviewer appears to be suggesting that there might be some relationship between the magnitude of organic matter production and it’s lipid composition. We are not aware of any studies supporting this notion.

R2- Q/C – 10: Line 187- what are monounsaturated FAMES MUFAs, and polyunsaturated FAMES PUFA, but saturated FAMES are FAMES (why not Sat-FAMES or SFMES) for consistence. After all, everything measured is a FAME.

R2- R – 10: I am not sure we used the terminology described above. At line 187 we say:

“...displayed high contributions from MUFAs (57.7 mg lipid g OC-1), PUFAs (13.8 mg lipid g OC-1) and FAMES (44.6 mg lipid g OC-1)”

MUFAs are monounsaturated fatty acids (1 double bond)

PUFAs are polyunsaturated fatty acids (>1 double bond)

FAMES are saturated fatty acids.

The reviewer is correct that it is unnecessary to include the ME suffix for FAMES, although this nomenclature is sometimes encountered in the literature. However, we have followed the reviewer's suggestion and changed to FAMES to saturated fatty acids throughout the manuscript.

R2- Q/C – 11: Line 201 - isn't "unsaturated alkenols" redundant since alkenols are unsaturated by definition?

R2- R – 11: Yes, this is true. I think in a previous version we had used the terms saturated and unsaturated alcohols, the latter of course also being an alkenol. Somehow we changed the terminology to alkenol but unsaturated was not removed. Thank you for picking up on this mistake. We have corrected it throughout.

R2- Q/C – 12: Line 209 - maybe spell out the name of EPA the first time it is used.

R2- R – 12: Done.

R2- Q/C – 13: Line 252 - why does the cholesterol reflect the dominance of diatoms are the base of the food web? The references cited later (e.g., Rampen et al., 2010; line 328) shows that C27-5 is a relatively minor component of many diatoms. What about 24-methylene C2 cholesterol (C28-5,24(28)? It's hard to evaluate these statements without the data, which as noted above are missing for some reason. See also paragraph at line 326.

R2- R – 13: This was a typing mistake, $C_{27}\Delta^5$, should have been written as $C_{27}\Delta^{5,22}$, which appears to be more prevalent in Bacillariophyceae (Volkman, 2003). However, upon further reflection we have decided to remove the paragraph that links patterns in sterols to phytoplankton composition. There is too much ambiguity as many sterols are not completely diagnostic as they occur in different groups of phytoplankton.

R2- Q/C – 14: Line 266 – The conclusion that lipids are selectively degraded/remineralized during sinking relative to OC because lipid/OC ratios decrease between the shallower and the deepest traps also depends in part on the lipid/OC ratios of the starting material. Since there are apparently differences in production, or chl-a, or ecology between the Fe-fertilized sites and the HNLC sites,

what are lipid/OC ratios in the material that is initially exported out of the surface waters?

R2- R – 14: We agree with the reviewer that the composition of organic matter produced had not been explicitly mentioned. The reason being that we do not have time-series, or point measurements, of lipid/OC ratios in organic matter produced in the mixed layer that could be sensibly compared with our sediment trap measurements. As mentioned above we are not familiar with reports that changes in productivity or biomass are linked to lipid/OC ratios directly, although they may of course be linked indirectly due to patterns related to the taxonomic composition of plankton under different productivity regimes. However, we would not be able to draw any strong inferences on diatom/plankton community structure from productivity estimates and would be therefore unable to link these to variability in lipid/OC concentrations from different bloom areas. As stated in the text, the lipid flux decreases by 5 orders of magnitude between the shallowest and deep trap, which is accompanied by a loss of labile lipid classes such as MUFAs and PUFAs. These features are entirely consistent with degradation over depth. However, we now mention in the manuscript that part of the difference observed at different depths may be related in part to that lipid/OC of “starting material”

Line 331-333: *It is possible that some of the differences observed over depth may be related to the initial lipid composition of organic material produced in the photic zone by different phytoplankton taxa*

R2- Q/C – 15 Fig. 2. Are the units on the abscissa supposed to be fluxes. Under “refractory”, what is the “other” category? Table 2 – are POC and BSi annual “fluxes” with flux units? There is no discussion of BSi in the manuscript.

R2- R – 15: Yes these are fluxes integrated over the sediment trap deployment period (c.f. R2-R-5). We have added some extra information to the Figure caption to clarify this point.

Line 962-963: *Total lipid fluxes (grey bars, left axis) integrated over the sediment trap deployment periods (Table 1).....*

The “other” category is all of the other lipid compounds that were measured but do not fall into any of the listed categories. A full list of these compounds is available in the supplementary files and these files have now been referenced in the figure caption. We have also made the same correction for the table captions where the category “other” appears.

Yes the fluxes in Table 1 are integrated over the sediment trap deployment period. The table caption has been modified to clarify this point.

Line 293-294: *Information on sediment trap deployments and fluxes of particulate organic carbon (POC) integrated over the deployment period.*

Biogenic silica data has been removed.

1 **The role of diatom resting spores for pelagic-benthic coupling in the**
2 **Southern Ocean.**

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13 **Abstract**

14 Natural iron fertilization downstream of Southern Ocean island plateaus support large
15 phytoplankton blooms and promote carbon export from the mixed layer. In addition to
16 sequestering atmospheric CO₂, the biological carbon pump also supplies organic matter (OM)
17 to deep-ocean ecosystems. Although the total flux of OM arriving at the seafloor sets the
18 energy input to the system, the chemical nature of OM is also of significance. However, a
19 quantitative framework linking ecological flux vectors to OM composition is currently
20 lacking. In the present study we report the lipid composition of export fluxes collected by
21 five-moored sediment traps deployed in contrasting productivity regimes of Southern Ocean
22 island systems (Kerguelen, Crozet and South Georgia) and compile them with quantitative
23 data on diatom and faecal pellet fluxes. At the three naturally iron fertilized sites, the relative
24 contribution of labile lipids (mono- and polyunsaturated fatty acids, unsaturated fatty

25 alcohols) is 2-4 times higher than at low productivity sites. There is a strong attenuation of
26 labile components as a function of depth, irrespective of productivity. The three island
27 systems also display regional characteristics in lipid export. An enrichment of zooplankton
28 dietary sterols, such as $C_{27}\Delta^5$, at South Georgia is consistent with high zooplankton and krill
29 biomass in the region and the importance of faecal pellets to POC flux. There is a strong
30 association of diatom resting spore fluxes that dominate productive flux regimes with energy
31 rich unsaturated fatty acids. At the Kerguelen Plateau we provide a statistical framework to
32 link seasonal variation in ecological flux vectors and lipid composition over a complete
33 annual cycle. Our analyses demonstrate that ecological processes in the upper ocean, e.g.
34 resting spore formation and grazing, not only impact the magnitude and stoichiometry of the
35 Southern Ocean biological pump, but also regulate the composition of exported OM and the
36 nature of pelagic-benthic coupling.

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45 **1. Introduction**

46 The biological pump transfers organic carbon (OC) from photosynthetic production to
47 the deep ocean (Volk and Hoffert, 1985) with important implications for the sequestration of
48 atmospheric CO₂ (Sarmiento et al., 1988; Kwon et al., 2009). Only a minor fraction of the
49 carbon fixed in the sunlit ocean reaches the deep ocean and sediments (Martin et al., 1987;
50 Honjo et al., 2008), but this carbon and energy supply is essential for the functioning of deep-
51 sea benthic ecosystems (Billett et al., 1983, 2001; Ruhl and Smith, 2004; Ruhl et al., 2008) .
52 Commonly referred to as pelagic-benthic coupling (Graf, 1989), the composition, lability and
53 timing of organic matter (OM) flux arriving at the seafloor can exert a large influence on
54 benthic communities (Billett et al., 2001; Galeron et al., 2001; Mincks et al., 2005; Smith et
55 al., 2006; Wolff et al, 2011).

56 Understanding the factors influencing the functioning of the biological pump remains
57 a central question in biogeochemical oceanography (Boyd and Newton, 1995; Rivkin et al.,
58 1996; Boyd and Trull, 2007; Guidi et al., 2016). Many different approaches have been
59 adopted to study the biological pump, including carbon budgets (Emerson et al. 1997,
60 Emerson 2014), mixed layer nutrient inventories (Eppley and Peterson, 1979; Sarmiento et al.
61 2004), radionuclide disequilibria (Buesseler et al., 1992; Savoye et al., 2006), optical methods
62 (Gardner et al., 1990; Guidi et al. 2016), neutrally buoyant- (Buesseler et al. 2000; Salter et al.
63 2007) and moored-sediment traps (Berger, 1971; Honjo, 1976). Although all of these methods
64 have their own caveats, sediment traps offer the distinct advantage of collecting and
65 preserving sinking particles for subsequent biological and chemical analysis. Moored
66 sediment traps allow the direct quantification of sinking protists including dinoflagellates (e.g.
67 Harland and Pudsey, 1999), diatoms (e.g. Salter et al. 2012), coccolithophores (e.g. Ziveri et
68 al. 2007), radiolarians (e.g. Takahashi et al., 1991), silicoflagellates (Rigual-Hernández et al.,
69 2010), foraminifera (Salter et al. 2014) and zooplankton faecal pellets (Wilson et al., 2008,
70 2013). Indirect approaches use biomarkers such as lipids and amino acids to identify the

71 source (algal, zooplanktonic, bacterial) and diagenetic status (lability, degree of preservation)
72 of the exported OM (Wakeham, 1982; Wakeham et al., 1980, 1984, 1997; Kiriakoulakis et
73 al., 2001; Wakeham et al., 2009; Lee et al., 2009; Salter et al., 2010). Although it is generally
74 well-acknowledged that ecological vectors of flux are linked to the geochemical composition,
75 studies providing a coupled description of biological components and OM composition of
76 export fluxes remain relatively scarce (e. g. Budge and Parrish, 1998).

77 Southern Ocean island plateaus such as Kerguelen (Blain et al., 2007), Crozet (Pollard
78 et al., 2009) and South Georgia (Tarling et al., 2012) provide a natural source of iron to the
79 iron-poor waters of the Antarctic Circumpolar Current (de Baar et al., 1990; Martin et al.,
80 1990). Currents and the topography of the sea floor lead to enrichment of iron in waters
81 adjacent to the islands which supports large diatom-dominated phytoplankton blooms
82 (Armand et al., 2008; Korb et al., 2008; Quéguiner, 2013) that contrast with the high nutrient,
83 low chlorophyll (HNLC, Minas et al., 1986) regime that generally prevails in Antarctic
84 waters. Previous studies of Southern Ocean island plateaus have identified the significance of
85 resting spore formation by neritic diatom species (*Eucampia antarctica* var. *antarctica*,
86 *Chaetoceros Hyalochaete*, *Thalassiosira antarctica*) in response to nutrient limitation in mid-
87 summer (Salter et al., 2012; Rembauville et al., 2015, 2016a). The export of resting spores
88 generally occurs during short and intense events but they can account for a significant fraction
89 (40-60 %) of annual carbon flux out of the mixed layer at these naturally fertilized sites. This
90 process contributes to the ~2 fold increase in annual carbon export when compared to the
91 HNLC sites (Salter et al., 2012; Rembauville et al., 2015, 2016a).

92 Despite the general importance of resting spore ecology for POC export from naturally
93 iron-fertilized systems in the Southern Ocean, there are some notable differences in the nature
94 of export fluxes from Crozet, Kerguelen and South Georgia. At Crozet, in the Polar Front
95 Zone (PFZ), the abundance of foraminifers and pteropods leads to a high inorganic to organic

96 carbon export ratio (1 mol:mol, Salter et al., 2014). At Kerguelen, south of the Polar Front in
97 the Antarctic Zone (AAZ) the inorganic to organic carbon ratio is much lower (0.07) and
98 CaCO₃ flux is mainly attributed to coccoliths (Rembauville et al., 2016). At South Georgia
99 (AAZ), the faecal pellet contribution to carbon export is higher (~60 % in summer-autumn
100 Manno et al., 2015) when compared to Kerguelen (34 % of annual POC flux; Rembauville et
101 al., 2015). The strong gradients in productivity and ecosystem structure that characterize these
102 island systems offer a valuable framework to address the link between biological and
103 geochemical composition of particle export.

104 The impact of different carbon export vectors on the lability of the exported OM is
105 necessary to understand the impact of upper ocean ecology for pelagic-benthic coupling (Ruhl
106 and Smith, 2004; Ruhl et al., 2008). High biomass of meio-, micro- and macrofauna in abyssal
107 sediments of the Southern Ocean (Brandt et al., 2007) suggests a transfer of OM originating
108 from photosynthetic autotrophs down to the seafloor. This diversity and biomass is not
109 geographically homogeneous, but rather constrained by upper ocean productivity levels
110 (Wolff et al., 2011; Lins et al., 2015). In this context, the comparison of lipid biomarkers in
111 export fluxes originating from different sites in the Southern Ocean may help to understand
112 how ecological processes at the origin of export flux also shape the magnitude and lability of
113 OM supply to deep-sea benthic communities.

114 This study compiles lipid biomarker data from five annual sediment trap deployments
115 in the vicinity of Southern Ocean Island plateaus in order to (i) compare the composition of
116 lipid biomarkers in export fluxes collected in sites of various productivity levels and across
117 different depths, (ii) identify how ecological export vectors, in particular resting spores, shape
118 the lability of POC fluxes over a complete annual cycle and (iii) derive the potential
119 implications of ecological flux vectors for pelagic-benthic coupling.

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121 **2 Material and Methods**

122 **2.1 Trap deployments and sample processing**

123 We compile 5 long-term sediment trap deployments located in the vicinity of island plateaus
124 in the Southern Ocean (Fig. 1, Table 1). Two sediment traps were located upstream of the
125 islands in HNLC waters (M6 and P2 at Crozet and South Georgia, respectively) and three
126 were located in naturally iron-fertilized and productive waters characterized by enhanced
127 phytoplankton biomass (A3, M5 and P3 at Kerguelen, Crozet and South Georgia,
128 respectively). The detailed hydrological settings of deployments, preservative conditions of
129 samples and bulk chemical analyses of biogeochemical fluxes have been published previously
130 (Table 1). After the retrieval of each sediment trap, swimmers (organisms actively entering
131 the trap funnel) were manually removed from the samples and therefore do not contribute to
132 the lipid fluxes we report.

133 **2.2 Lipid analysis**

134 Lipid analyses were performed on 1/8 wet aliquots resulting from the splitting of original
135 samples. Because of the low amount of material collected in some cups, 1/8 wet aliquots were
136 combined prior to the lipid analyses (supplementary information). Some samples were lost
137 upon recovery of sediment traps and two were contaminated with fish debris and therefore not
138 included in lipid analyses. Full details of all sediment trap samples and those included in lipid
139 analyses is summarized in Supplementary Tables 1-5.

140 Lipids analyses of Crozet sediment trap samples were performed as described by
141 Kiriakoulakis et al. (2001) and Wolff et al. (2011). For the Kerguelan and South Georgia
142 samples a similar protocol was used. Briefly, separate 1/8 aliquots were spiked with an
143 internal standard (5 α (H)-cholestane), sonicated (filters; 3 x 15 min;

144 dichloromethane:methanol 9:1), transmethylated (methanolic acetyl chloride) and silylated
145 (bistrimethylsilyltrifluoroacetamide; 1 % trimethylsilane chloride; 30–50 μL ; 40°C; 0.5–1 h).
146 GC-MS analyses were carried out using a GC Trace 1300 fitted with a split-splitless injector,
147 using helium as a carrier gas (2 mL min^{-1}) and column DB-5MS (60m x 0.25mm (i.d.), film
148 thickness 0.1 μm , non-polar solution of 5% phenyl and 95% methyl silicone). The GC oven
149 was programmed after 1min from 60°C to 170°C at 6°C min^{-1} , then from 170°C to 315°C at
150 2.5 °C min^{-1} and held at 315 °C for 15 min. The eluent from the GC was transferred directly
151 to the electron impact source of a Thermoquest ISQMS single quadrupole mass spectrometer.
152 Typical operating conditions were: ionisation potential 70 eV; source temperature 215°C; trap
153 current 300 μA . Mass data were collected at a resolution of 600, cycling every second from
154 50–600 Thompsons and were processed using Xcalibur software. Compounds were identified
155 either by comparison of their mass spectra and relative retention indices with those available
156 in the literature and/or by comparison with authentic standards. Quantitative data were
157 calculated by comparison of peak areas of the internal standard with those of the compounds
158 of interest, using the total ion current (TIC) chromatogram. The relative response factors of
159 the analytes were determined individually for 36 representative fatty acids, sterols and
160 alkenones using authentic standards. Response factors for analytes where standards were
161 unavailable were assumed to be identical to those of available compounds of the same class.

162 **2.3 Statistical analyses**

163 The lipid composition of sediment trap samples from the five sites was investigated using
164 principal component analysis (PCA) and the similarity of samples was studied using
165 clustering (Ward aggregation criteria) based on lipid classes. This methodology has been used
166 previously to study the organic geochemistry of sinking particles in the ocean (Xue et al.,
167 2011). Prior to both PCA and clustering, raw lipid fluxes were transformed by calculating the
168 square root of their relative abundance within each sample. This transformation followed by

169 the calculation of the Euclidian distance is also known as the Hellinger distance, which
170 provides a good compromise between linearity and resolution in ordination analyses
171 (Legendre and Legendre, 1998; Legendre and Gallagher, 2001).

172 **3 Results**

173 **3.1 Lipid class distribution and seasonality**

174 **Total lipid fluxes integrated over the sediment trap deployment period (Table 1.)** were five
175 orders of magnitude higher in the shallow deployment at A3 (229 mg m⁻² at 289 m) compared
176 to the deep sediment trap at M6 (0.08 mg m⁻² at 3160 m, Fig. 2, Table 2). The contribution of
177 labile lipid compounds (defined as unsaturated fatty acids and alkenols, Wolff et al., 2011,
178 Table 2) to total lipid fluxes was 2-4 times higher in the naturally fertilized sites (20 -39 % at
179 A3, P3 and M5) relative to the HNLC deployments (<10 % at P2 and M6) (Table 2.).
180 Unsaturated fatty acids were dominated (>80 %) by monounsaturated fatty acids (MUFA) at
181 all sites. Semi-labile lipids (saturated fatty acids analysed as their methyl esters; FAMES,
182 branched fatty acids and alkanols (saturated alcohols); Table 2) accounted for a small fraction
183 (8-12 %) of total lipids at South Georgia, but a higher fraction (40-46 %) at Crozet. Semi-
184 labile lipids were dominated by saturated fatty acid contributions at all sites (64-80 %).
185 Sterols were the dominant lipids at South Georgia (65-82 %) and were less abundant (26-35
186 %) at the other sites.

187 The concentration total lipids, expressed as total lipid flux normalized to organic
188 carbon flux, decreased by four orders of magnitude between the shallowest (A3, 193.1 mg
189 lipid g OC⁻¹) and the deepest (M6, 0.9 mg lipid g OC⁻¹) deployment (Table 2). In the shallow
190 deployment at Kerguelen (A3) high concentrations of MUFAs (57.4 mg lipid g OC⁻¹), PUFAs
191 (13.7 mg lipid g OC⁻¹) and saturated fatty acids (44.4 mg lipid g OC⁻¹) were observed. All

192 other deployments (P3, P2, M5 and M6) had much lower concentrations of labile and semi-
193 labile compounds and were dominated by more refractory sterols (0.3 – 6.9 mg lipid g OC⁻¹).

194 Samples from Crozet (M5 and M6) were positively projected on the first axis of the
195 PCA together with saturated fatty acids, , C₂₈-C₂₉ sterols and long chain unsaturated fatty
196 acids (C₂₂, C₂₄) (Fig. 3a). Samples from South Georgia (P3 and P2) were negatively projected
197 on the first axis, close to C₂₇ sterols. Samples from Kerguelen (A3) were positively projected
198 on the second axis and mainly associated with C₁₆-C₂₀ unsaturated fatty acids.

199 Using the lipid composition, four main clusters of sediment trap samples could be
200 identified based on the largest distance break after the first node of the dendrogram (Fig. 3b).
201 Cluster A contained most of the spring and summer samples from the naturally-fertilized sites
202 of Kerguelen and Crozet (A3 and M5) characterized by the highest relative abundance of
203 labile lipids (PUFA and MUFA). Cluster B was composed of summer and winter samples
204 from A3 displaying a high abundance of alkenols. Cluster C contained spring and summer
205 samples from the naturally fertilized site of South Georgia (P3), several samples from
206 Kerguelen and Crozet and was characterized by a mixture of labile, semi-labile and refractory
207 lipids (MUFA, saturated fatty acids and sterols). Finally, cluster D was composed mostly of
208 samples from the HNLC site of South Georgia (P2) and displayed a large dominance of
209 sterols.

210 **3.2 Seasonality at A3**

211 In spring, vegetative diatoms were the most important constituents of relatively low POC
212 fluxes, followed by cylindrical faecal pellets (Fig. 4a). Lipid fluxes were dominated by 9Z-
213 hexadecenoic acid (C_{16:1} (cis-9); palmitoleic acid), hexadecanoic acid (C₁₆), eicosapentaenoic
214 acid; EPA (C_{20:5} (cis-5,8,11,14,17)), 9Z-octadecenoic acid (C_{18:1} (cis-9)), and cholesterol
215 (C₂₇Δ⁵) that altogether contributed >75% of total lipids (Fig. 4b).

216 Diatom resting spores dominated the enhanced POC fluxes during summer with a notable
217 contribution of cylindrical and ovoid faecal pellets (Fig. 4c). MUFA and PUFA classes were
218 the most significant components of lipid export. The principal compounds in these classes
219 were C_{16:1} (cis-9) (47% of total lipids), C_{18:1} (cis-9) (10%) and C_{20:5} (cis-8) (5.3%). Sterols
220 accounted for 21% of total lipids and were primarily comprised of C₂₇Δ⁵ (cholesterol) and
221 C₂₉Δ⁰ (Fig. 4d).

222 In autumn, tabular faecal pellets are the major vectors for POC flux (Fig. 4e), accompanied by
223 a shift to more significant contributions of refractory sterols to the lipid composition, notably
224 C₂₇Δ⁵. The C₁₆ fatty acid and C_{18:1} (cis-9), 11Z, 14Z, 17Z-eicosatrienoic acid (C_{20:3} (cis-11)
225 and *n*-hexadecanol (C₁₆ OH) were also important components of the lipid composition in
226 Autumn (Fig. 4f). During winter POC flux is mediated almost entirely by large faecal pellets
227 (tabular and ellipsoid shapes) (Fig. 4g) and the unsaturated alcohols eicosenol (C_{20:1} OH) and
228 octadecenol (C_{18:1} OH) were the major constituent of lipids, with smaller contributions from
229 C₁₆ fatty acids, C₂₇Δ⁵ and C_{18:1} (cis-9)), (Fig. 4h).

230

231 **4 Discussion**

232 **4.1 Geographical differences in lipid export composition across the** 233 **Southern Ocean island systems**

234 Annual lipid export at the naturally fertilized sites of Crozet and South Georgia was
235 characterized by relatively high fluxes of labile and semi-labile compounds compared to the
236 HNLC sites. Similarly, at the iron-fertilized productive site on the Kerguelen Plateau, labile
237 and semi-labile lipid classes dominate the annual flux profile. The labile lipid class was
238 dominated by MUFAs, and to a lesser extent, PUFAs. In particular, two lipid compounds
239 (C_{16:1} (cis-9) and EPA) commonly associated with diatoms (Kates and Volcani, 1966; Lee et

240 al., 1971) were important components of the labile lipid class. These observations confirm
241 that the large diatom-dominated phytoplankton blooms observed downstream of island
242 plateaus (Armand et al., 2008; Korb et al., 2010; Quéguiner, 2013), which are supported by
243 enhanced iron supply (Blain et al., 2008; Pollard et al., 2009; Nielsdóttir et al., 2012; Bowie et
244 al., 2015), result in significant export of diatom-derived labile OM out of the mixed layer.

245 The PCA and clustering analyses reveal a notable degree of regional structure and
246 highlight the prevalence of specific lipid classes in the different island systems. The first axis
247 of the PCA (23.7 % of variance) represents the location of the sediment trap deployments and
248 the second axis corresponds to the deployment depth. The P3 and P2 sites at South Georgia
249 both display ~2 times higher relative abundance of sterols compared to the Kerguelen (A3)
250 and Crozet (M5 and M6) sites. Sterols are important components of the plasma membrane
251 found in almost all eukaryotic organisms (Dufourc, 2008). Zooplankton use dietary sterols of
252 phytoplankton origin, preferentially assimilating $C_{27}\Delta^5$, or converting phytosterols to $C_{27}\Delta^5$
253 (Volkman, 1986, 2003) that are ultimately egested in faecal pellets (Bradshaw and Eglinton,
254 1993; Prahl et al., 1984). An enrichment in $C_{27}\Delta^5$ (and other C_{27} sterols such as $C_{27}\Delta^{5,22}$ and
255 $C_{27}\Delta^{22}$) in sinking OM is thus considered indicative of a high contribution of faecal material
256 (Ternois et al., 1998) to export flux. The relative abundance of $C_{27}\Delta^5$, $C_{27}\Delta^{22}$, $C_{27}\Delta^{5,22}$
257 compounds is highest in the export fluxes around South Georgia, consistent with the higher
258 contribution of faecal pellets to carbon export at South Georgia (Manno et al., 2015)
259 compared to Kerguelen (Rembauville et al., 2015). The biomass of zooplankton groups such
260 as copepods and pteropods reach some of their highest Southern Ocean abundances in the
261 northern Scotia Sea, which is also inhabited by Antarctic krill (Ward et al. 2012, Mackey et
262 al. 2012).

263

264 **4.2 Depth-related trends in lipid composition**

265 The decrease in the total lipid flux of five orders of magnitude between the shallowest
266 (289 m) and the deepest (>3000 m) deployment is consistent with the trend generally
267 observed in the global ocean (Wakeham and Lee, 1993; Wakeham et al., 1997, 2009).
268 Moreover, the strong decrease in OC-normalized lipid flux, particularly in the case of MUFA
269 and PUFA compounds, suggests that these labile lipid classes are selectively
270 degraded/remineralized during the sinking of the OM. It is possible that some of the
271 differences observed over depth may be related to the initial lipid composition of organic
272 material produced in the photic zone by different phytoplankton taxa. In the shallowest trap
273 (A3, 289 m), the high OC-normalized MUFA flux and the abundance of diatom-derived
274 essential PUFAs ($C_{16:3}$, $C_{18:6}$, $C_{20:4}$, $C_{20:5}$ and $C_{22:6}$) reflects the export of fresh and highly
275 labile diatom-derived OM (Dunstan et al., 1993). By contrast, the presence of branched *iso*-
276 and *anteiso*- C_{15} and C_{17} compounds in the deeper trap samples may be attributed to the
277 activity of bacterial reworking of the particulate OM during settling (Kaneda, 1991; Wakeham
278 et al., 1997).

279 **4.3 A quantitative framework linking seasonal variations in ecological** 280 **flux vectors to particulate lipid composition**

281 In order to advance our understanding of the role of ecosystem structure in driving the
282 composition of particle export, quantitative datasets characterizing both the chemical and
283 biological nature of fluxes are required. The dataset from the Kerguelen Plateau was selected
284 as a basis for constructing a quantitative framework linking dominant ecological flux vectors
285 the particulate lipid composition of exported particles. Kerguelen was selected as a case study
286 as we have previously reported detailed quantitative partitioning of POC fluxes between
287 diatom and faecal pellet fluxes that reveal major seasonal shifts in the importance of different

288 ecological flux vectors (Rembauville et al. 2015). The trap at Kerguelen was deployed 100 m
289 beneath the mixed layer, and is therefore also characterized by the highest concentrations and
290 fluxes of lipids (Table 2), thus providing the best possible resolution to examine seasonal
291 changes in lipid composition in relation to ecological flux vectors.

292 **4.3.1 Spring**

293 During spring on the Kerguelen Plateau the lipid flux is low ($0.3 \text{ mg m}^{-2} \text{ d}^{-1}$), as is the
294 corresponding POC flux ($\sim 0.15 \text{ mmol m}^{-2} \text{ d}^{-1}$), which is mainly driven by vegetative diatoms
295 belonging to the genera *Fragilariopsis*, *Pseudo-nitzschia* and *Thalassionema*, as well as small
296 faecal pellets (Rembauville et al., 2015). Diatoms are known predominantly to accumulate
297 unsaturated fatty acids such as $\text{C}_{16:1}$ (cis-9), EPA and $\text{C}_{18:1}$ (cis-9) (Kates and Volcani, 1966;
298 Opute, 1974; Chen, 2012; Levitan et al., 2014). Diatoms also produce saturated fatty acids,
299 mainly the C_{16} homologue (Lee et al., 1971; Matsumoto et al., 2009; Liang et al., 2014). Thus,
300 although the spring lipid flux is quite low, the major compounds ($\text{C}_{16:1}$ (cis-9), C_{16} , EPA and
301 $\text{C}_{18:1}$ (cis-9)) represent an export assemblage dominated by vegetative diatoms.

302 **4.3.2 Summer**

303 During summer POC fluxes are enhanced by an order of magnitude and are
304 characterized by intense export of diatom resting spores (*Chaetoceros Hyalochaete* spp. and
305 to a lesser extent *Thalassiosira antarctica*) that contribute 60% of the annual POC flux
306 (Rembauville et al. 2015). This resting spore flux event is associated with the highest export
307 of total lipids ($2.4 \text{ mg m}^{-2} \text{ d}^{-1}$, supplementary Table 1). The summer lipid profile is dominated
308 by $\text{C}_{16:1}$ (cis-9) and $\text{C}_{18:1}$ (cis-9), with a marked contribution of EPA. Higher total lipid
309 contents have been documented in resting spores of *Chaetoceros Hyalochaete* and
310 *Thalassiosira antarctica* when compared to vegetative cells (Doucette and Fryxell, 1983;
311 Kuwata et al., 1993). More specifically, our results are consistent with the 8-12 fold increase

312 in the content of C_{16:1} (cis-9) and C_{18:1} (cis-9) in *Chaetoceros pseudocurvisetus* resting spores
313 when compared to the vegetative stages (Kuwata et al., 1993). An increase in the cell content
314 of EPA during the formation of resting spores has also been reported for *Chaetoceros*
315 *salsugineus* (Zhukova and Aizdaicher, 2001).

316 Resting spore formation is an ecological strategy utilized by certain diatom species to
317 persist in environments where unfavorable conditions (e.g. light or nutrient limitation) occur
318 (Smetacek, 1985; French and Hargraves, 1985; McQuoid and Hobson, 1996). Lipids produce
319 more energy per unit mass than polysaccharides and can be stored in concentrated forms by
320 diatoms (Obata et al., 2013). The accumulation of energy-rich unsaturated fatty acids in the
321 resting spore, associated with a reduced metabolism (Oku and Kamatani, 1999) and sinking to
322 deeper waters (Smetacek, 1985) act in concert to increase the survival rate of the cells. In
323 order for this ecological strategy to work the cells must be reintroduced to the surface mixed
324 layer during a period favorable for growth. Nevertheless, sediment trap studies from Southern
325 Ocean island systems clearly document that a significant portion of the resting spores formed
326 in the surface are exported out of the mixed layer and reach bathypelagic depths (Salter et al.
327 2012, Rembauville et al. 2015, 2016). Consequently, the ecological survival strategy of
328 resting spore formation in diatoms can mediate large fluxes of labile lipid compounds to the
329 seafloor.

330 Cholesterol (C₂₇Δ⁵) was a significant component (>10 %) of particulate lipid
331 composition throughout the year. However, it reached its highest contribution (18 %) in
332 autumn when the contribution of faecal pellets to POC flux increased. Unlike many
333 eukaryotes, crustaceans are incapable of *de novo* biosynthesis of sterols and show a simple
334 sterol composition dominated by C₂₇Δ⁵ (Goad, 1981; Baker and Kerr, 1993; Kanazawa,
335 2001). Its presence throughout the year may thus be explained by the continuous export of
336 spherical, ovoid and cylindrical faecal pellets (Figure 4) which are typically attributed to

337 copepods, amphipods and euphausiids (Wilson et al., 2008, 2013). Notably we observed the
338 presence of a $C_{29}\Delta^0$ sterol during summer. C_{29} sterols are abundant in diatoms (Volkman,
339 2003), and can account for 60 % and 80 % of total lipids of *Navicula* sp., and *Eucampia*
340 *antarctica var antarctica*, respectively (Rampen et al., 2010), both of which showed a clear
341 seasonality with a marked summer maximum (Rembauville et al., 2015).

342 4.3.3 Winter

343 In winter, the lowest lipid fluxes were recorded and in contrast with other samples
344 were dominated by mono-unsaturated alkenols ($C_{18:1}$ OH and $C_{20:1}$ OH). These compounds are
345 generally absent in phytoplankton lipids but are an abundant component in zooplankton wax
346 ester (Lee et al., 1971), and are often utilized as a marker for zooplankton-derived OM
347 (Wakeham et al., 1997). More specifically, salp faecal pellets (tabular shape) have been
348 shown to contain important amounts of $C_{18:1}$ OH and $C_{20:1}$ OH (Matsueda et al., 1986). This is
349 in good agreement with the dominance of tabular faecal pellets in the winter POC flux at
350 Kerguelen. Tabular faecal material is present in the export flux during autumn but alkenols
351 represent a minor constituent of the lipid flux. We expect this difference is primarily related to
352 the larger contribution of diatoms to export flux (as both single cells or present in faecal
353 pellets), but it may also reflect changes in zooplankton lipid composition across the season
354 (Lee et al., 2006). Wax esters are used as energy reserve (Lee et al., 1970) but also contribute
355 to adjust buoyancy in cold and deep waters in winter (Pond and Tarling, 2011). The
356 abundance of wax ester-derived compounds we report in winter is also consistent with
357 observations from neritic areas of the Kerguelen Islands (Mayzaud et al., 2011). Another
358 indicator of a seasonal shift from diatom (spring) to faecal pellet-dominated export system
359 (autumn and winter) is the absence of long chain PUFAs in autumn and winter. It has been
360 previously reported that this energy-rich compound is preferentially assimilated by
361 zooplankton and is therefore typically absent in faecal pellets (Stübing et al., 2003).

4.4 Implications for pelagic-benthic coupling

362
363 Diatom-resting spores account for 60% of annual particulate organic carbon (POC) export at 300m
364 from the iron-fertilized bloom on the Kerguelen plateau (Rembaubille et al. 2015). Similar patterns
365 are observed in deeper trap samples (>2000m) from the productive regime at South Georgia (P3),
366 whereby 42% of annual POC export can be attributed to resting spores (Rembauville et al. 2016a). At
367 the productive Crozet site (M5), *Eucampia antarctica* winter growth stages dominate flux at 3000m
368 and are strongly correlated with total POC flux (Salter et al. 2012). These findings are in contrast to
369 sediment trap diatom assemblages from the low productivity/HNLC sites upstream of Kerguelen,
370 Crozet and South Georgia that contain much lower quantities of resting spores (<5%) with a negligible
371 contribution to POC (Salter et al. 2012, Rembauville et al. 2016a, 2017). The consistent feature from
372 Southern Ocean island systems is that the flux of diatom resting spores, in particular those of
373 *Chaetoceros* spp. and *E. antarctica*, are important vectors of POC transport to the bathypelagic
374 (>1500m). In the bathypelagic ocean (>1500m), concentrations of MUFAs and PUFAs are 2-25 times
375 higher in particulate flux originating from the productive regimes of these iron-fertilized systems
376 (Table 1; Wolff et al. 2011). These data demonstrate that resting spore flux also mediates enhanced
377 fluxes of freshly labile organic matter, in the form of unsaturated fatty acids, to the bathypelagic
378 ocean.

379
380 The oxidation of unsaturated fatty acids (MUFA and PUFA) classes produces more energy
381 than their saturated fatty acid counterparts (Levitan et al., 2014). An energy-rich food supply
382 associated with the resting spore flux appears to have an important impact on benthic systems.
383 For example, the decoupling of abundance between megafaunal invertebrates and OM input at
384 Crozet appears in part to be related to enhanced labile lipid and pigment fluxes supporting
385 higher fecundity of the dominant megafaunal invertebrate, *Peniagone crozeti* (Wolff et al.
386 2011). At South Georgia, nematode biomass is 10 times higher in deep-sea sediments
387 (>3000m) underlying iron-fertilized productivity regimes (Lins et al. 2015) whilst OM input

388 varies by considerably less (Rembauville et al. 2016). Nematode fatty acids are significantly
389 enriched C_{16:1} (cis-9) and EPA, two major lipid compounds we have shown to be statistically
390 associated with summer export events dominated by diatom resting spores. A resistance to
391 grazing (Kuwata and Tsuda, 2005) and enhanced sinking velocities of resting spores
392 compared to vegetative cells (McQuoid and Hobson, 1996) result in their effective transfer to
393 the seafloor (Rembauville et al. 2016), consistent with the fact they are a common feature of
394 sediments underlying productive regimes (Crosta et al. 1997; Armand et al. 2008; Tsukazaki
395 et al. 2013). The ecology of resting spore formation therefore acts as an efficient conduit to
396 transfer energy rich storage lipids to the sediment and they may thus play a particularly
397 important role in pelagic-benthic coupling.

398 Deep-sea ecosystems are strongly dependent on OM food supply originating from
399 photosynthesis in the surface ocean (Billett et al., 1983, 2001; Ruhl and Smith, 2004; Ruhl et
400 al., 2008). In the Southern Ocean, it has been demonstrated how the composition of the upper
401 ocean plankton community, and their associated ecological strategies, can influence climate
402 dynamics associated with the biological carbon pump (Smetacek et al. 2004; Salter et al.,
403 2012; Assmy et al., 2013; Salter et al. 2014 Rembauville et al., 2015) The present study
404 reveals how changes in major ecological flux vectors, and in particular the process of diatom
405 resting spore formation, can also influence pelagic-benthic coupling by moderating the supply
406 of energy rich storage lipids to deep-sea communities.

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748

749 **Tables**750 **Table 1: Information on sediment trap deployments and fluxes of particulate organic carbon**751 **(POC) integrated over the deployment period..**

Location and reference	Sediment trap model	Collection period	Total fluxes (mmol m ⁻²) POC
Kerguelen (Rembauville et al., 2015b)			
A3 50°38.30' S – 72°02.60' E 289 m	Technicap PPS3/3 0.125 m ²	21/10/2011 – 07/09/2012 No sample lost Total: 322 days	98
South Georgia (Rembauville et al., 2016a)			
P3 52°43.40' S - 40°08.83' W 2000 m	Mclane PARFLUX 0.5 m ²	15/01/2012 – 01/12/2012 1 sample lost Total: 291 days	41
P2 55°11.99' S - 41°07.42' W 1500 m		15/01/2012 – 01/12/2012 3 samples lost Total: 231 days	26
Crozet (Salter et al., 2012)			
M5 46°00.00' S – 56°05.00' E 3195 m	Mclane PARFLUX 0.5 m ²	28/12/2005 – 29/12/2005 No sample lost Total 360 days	40
M6 49°00.03' S – 51°30.59' E 3160 m		05/01/2005 – 03/01/2006 No sample lost Total 359 days	14

752

753

754 **Table 2:** Total annual lipid flux, relative contribution of lipid classes and lipid concentrations
755 for the five sediment trap deployments. Labile – MUFA (monounsaturated fatty acids), PUFA
756 (polyunsaturated fatty acids) and unsaturated alcohols; Semi-labile – saturated fatty acids,
757 branched fatty acids and saturated alcohols; Refractory – Sterols, Other (Wolff et al., 2011).
758 Sediment trap deployment periods are presented in Table 1. Individual compound fluxes,
759 concentrations and relative contributions are included in Supplementary Tables 1-5. A full list
760 of the compounds categorized as others can also be found in the supplementary tables.

Site	A3	P3	P2	M5	M6
Integrated lipid flux (mg m ⁻²)	228.8	3.83	2.67	1.20	0.08
Relative contribution (%)					
MUFA	29.7	18.0	8.1	18.1	5.2
PUFA	7.1	1.3	0.2	3.1	0.3
Unsaturated alcohols (alkenols)	2.3	1.1	0.6	2.2	0.5
Saturated fatty acids	23.0	9.7	5.9	26.0	30.5
Branched fatty acids	1.4	0.2	0.3	1.3	0.8
Saturated alcohols (alkanols)	8.5	2.3	1.7	13.2	14.5
Sterols	26.0	64.8	81.9	34.6	35.0
Other	2.0	2.5	1.3	1.5	13.3
Total lipid concentration (mg lipid g OC ⁻¹)	193.1	7.8	8.4	3.1	0.9
Lipid concentration (µg lipid g OC ⁻¹)					
MUFA	57403.2	1397.6	687.6	565.8	49.1
PUFA	13736.4	102.3	18.4	97.7	2.7
Unsaturated alcohols (alkenols)	4403.6	82.5	47.7	68.2	5.1
Saturated fatty acids	44359.3	755.2	497.5	810.7	289.0
Branched fatty acids	2792.1	18.7	24.5	39.6	7.4
Saturated alcohols (alkanols)	16325.6	176.2	145.2	411.7	137.0
Sterols	50261.1	5021.9	6911.4	1077.7	331.6
Other	3777.8	196.3	108.3	47.0	126.0

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763 **Figures captions.**

764 **Figure 1:** Location of the five annual sediment trap deployments in the Southern Ocean.

765 Color refers to annual surface satellite-derived chlorophyll *a* climatology (MODIS 2002-2016
766 full mission product accessed at <http://oceancolor.gsfc.nasa.gov/cms/>). Dashed and
767 continuous lines represent respectively the Subantarctic Front (SAF) and Polar Front (PF)
768 from Sallée et al., 2008. SAZ: Subantarctic Zone, PFZ: Polar Frontal Zone, AAZ: Antarctic
769 Zone.

770 **Figure 2:** Total lipid fluxes (grey bars, left axis) integrated over the sediment trap deployment
771 periods (Table 1) and the relative contribution of lipid classes (coloured bars, right axis) to
772 this total flux from five moored sediment trap deployments in the Southern Ocean. **Individual**
773 **compound fluxes, concentrations and relative contributions are included in Supplementary**
774 **Tables 1-5. A full list of the compounds categorized as others can also be found in the**
775 **supplementary tables.**

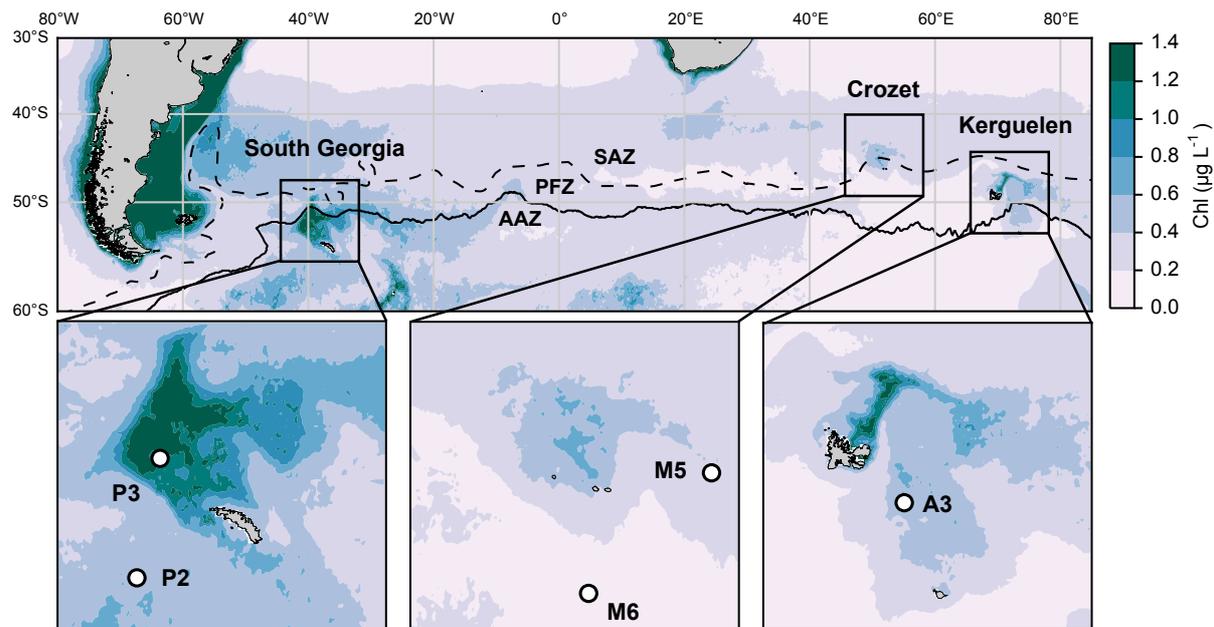
776 **Figure 3:** Association of lipid compounds with sediment trap samples. a) Principal
777 component analysis of the relative abundance of lipids ($n = 121$). Black and white symbols
778 represent respectively the naturally-fertilized and the low productivity sites. b) Clustering of
779 the sediment trap samples based on the relative abundance of lipid classes (Euclidian distance,
780 Ward aggregation criteria). Clusters A, B, C and D were defined based on the highest distance
781 break after the first node. In a) and b), color refers to the lability of lipids according to (Wolff
782 et al., 2011).

783 **Figure 4:** Seasonal evolution of carbon export vectors and associated lipid composition over
784 the central Kerguelen Plateau (A3, 289 m). Left panels: carbon export vectors from
785 Rembauville et al., 2015. Right panels: sorted relative abundance (coloured bars) and

786 cumulated relative abundance (dots) of major lipids. a) and b) cups 1-3, c) and d) cup 9, e)
787 and f) cup 11, g) and h) cup 12.

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791 **Figure 1**

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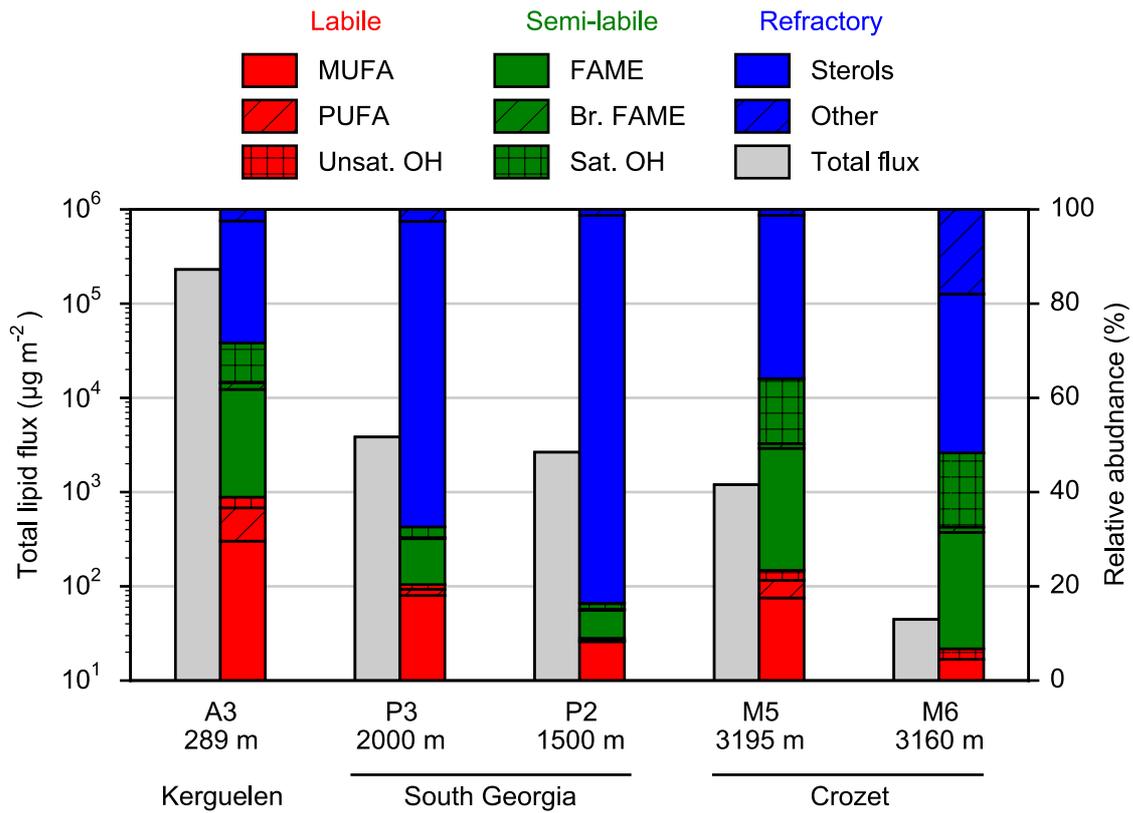
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803 **Figure 2**

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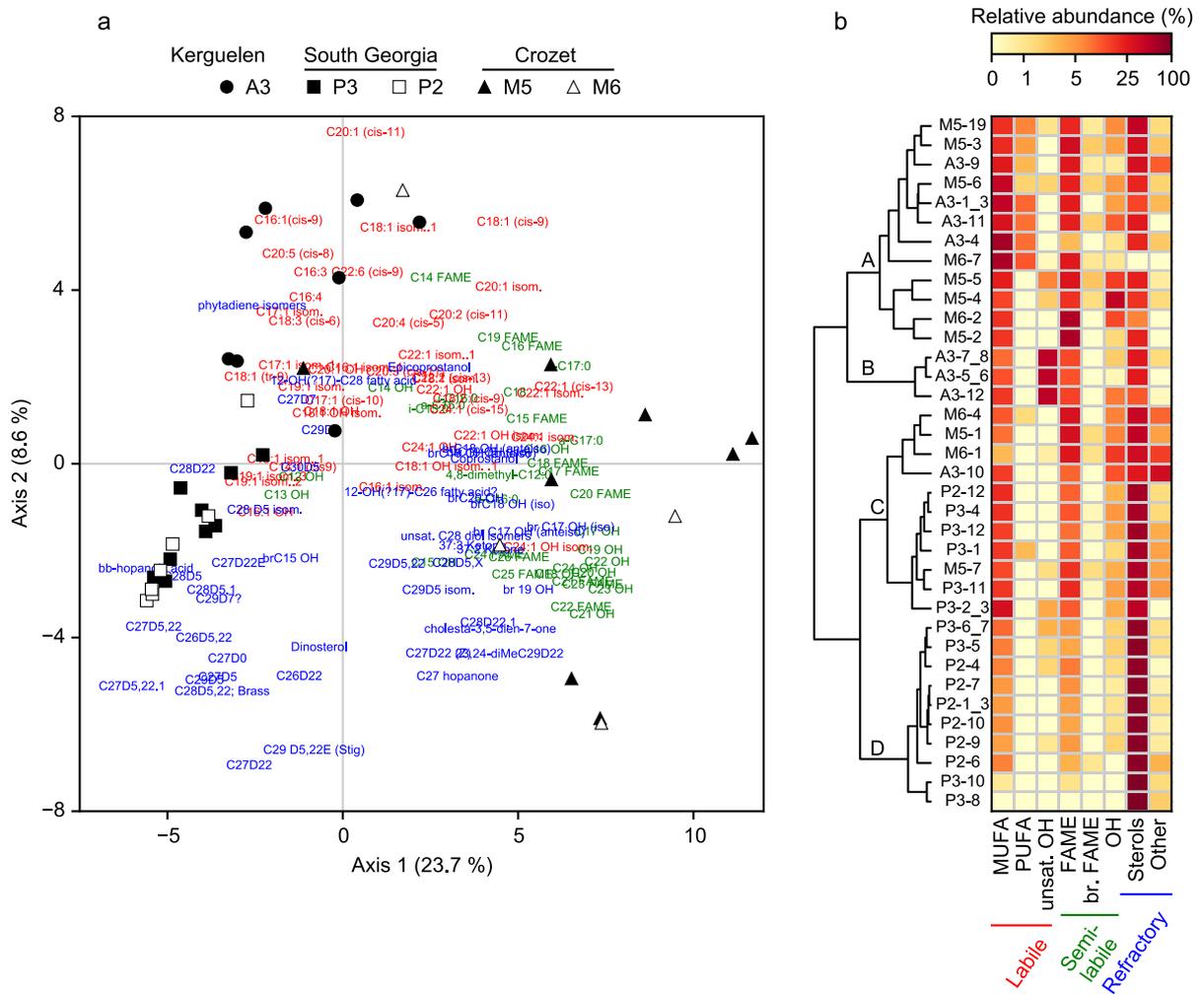
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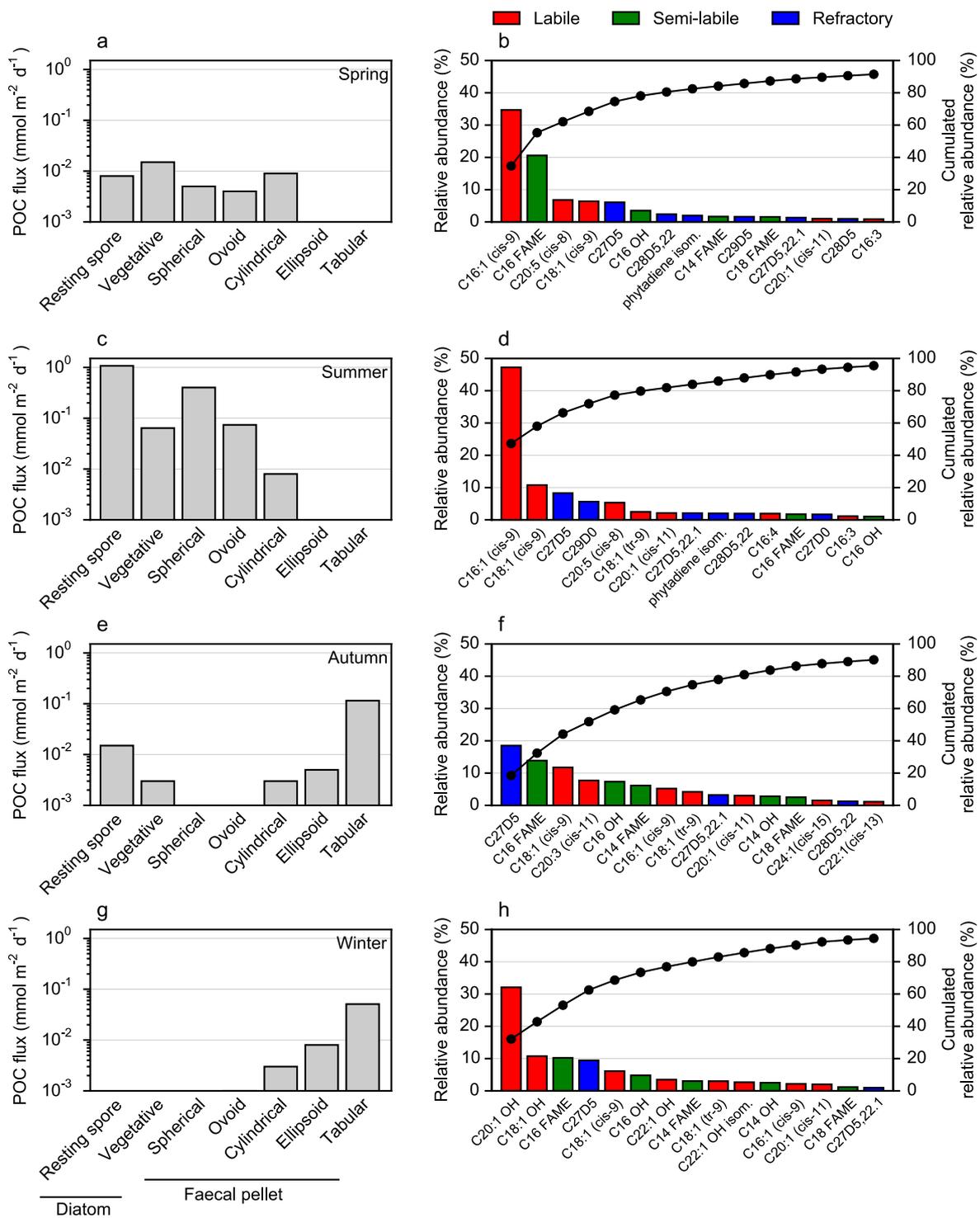
Figure 3

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823 **Figure 4**

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