*Descriptions of data*

**Daily\_int\_UV\_doses\_0.6m\_PAL1314\_kJ\_m2**

Daily doses of ultraviolet-B (UVB; 290-315 nm) and ultraviolet-A radiation (UVA; 315-400 nm) received at 0.6 m water depth at Palmer Station, Antarctica. Doses were calculated from continuous *in situ* irradiance observations made with an Ocean Optics Jaz spectrophotometer (ILX-511B detector; Ocean Optics Inc., Dunedin, FL, USA). Incident irradiances were recorded at 0.3 nm bandwidth using an upward-facing plane irradiance cosine corrector (180° field of view) and 10 m fiber optic cable. The instrument was factory calibrated prior to deployment for absolute irradiance measurements from 210-850 nm. Irradiances were recorded at 1 min. intervals. These *in situ* daily doses may be compared to incident daily UV doses recorded as part of the U.S. National Oceanic and Atmospheric Administration’s (NOAA) Antarctic UV Monitoring Network; the NOAA dosage data are available at <https://www.esrl.noaa.gov/gmd/grad/antuv/>

**Kd\_PAL1516\_Arthur\_Hbr\_Stn\_B\_20151215**

Diffuse downwelling attenuation coefficients in Napierian form (, also DAC down) for Southern Ocean waters for wavelengths 290-700 nm. Coefficients for 320-700 nm were calculated directly from depth profiles of *in situ* irradiance made with an Ocean Optics Jaz spectrophotometer at PAL-LTER Station B, Arthur Harbor, Antarctica. The station is a 75 m deep sampling location about 1 km offshore. Due to the low signal-to-noise ratio in the *in situ* irradiance observations at wavelengths < 320 nm, coefficients were estimated for 290-320 nm using an exponential model fit to observed data from the 320-370 nm interval:

To achieve minimum boat shadow while making the irradiance profile measurements, the fiber optic cable and light sensor (cosine corrector) were streamed away from the small boat in a direction that was both to windward and toward the sun; the boat was then allowed to drift downwind from the measurement location to a suitable stand-off distance. A series of concurrent surface irradiance measurements made with a LI-COR PAR sensor (model LI-193SA; LI-COR Biosciences, Lincoln, NE, USA) was used to correct the spectra made as part of these profiles for any changes in incident light intensity that occurred between measurements.

**Diatom\_cultures\_IP-DAG\_pmol\_totals**

Concentrations of intact polar diacylglycerol (IP-DAG) lipids measured in cultures of four Antarctic diatom isolates. Diatoms were isolated by Adrian Marchetti (<http://orcid.org/0000-0003-4608-4775>) from waters of the Bellingshausen Sea and grown on replete media. Cells were collected onto 0.7 µm GF/F filters. Extraction was performed using a modified Bligh and Dyer (Bligh and Dyer, 1959; <http://doi.org/10.1139/o59-099>) method described in Popendorf et al. (2013; <http://dx.doi.org/10.1007/s11745-012-3748-0>). Lipid extracts were analyzed by HPLC-ESI-MS with data dependent-MS2 acquisition on a high-resolution, accurate mass Thermo Q Exactive Hybrid Quadrupole-Orbitrap mass spectrometer (ThermoFisher Scientific, Waltham, MA, USA) coupled to an Agilent 1200 HPLC system (Agilent, Santa Clara, CA, USA). The HPLC-ESI-MS method is described in Collins et al., 2016 (<http://dx.doi.org/10.1021/acs.analchem.6b01260)>.

The LOBSTAHS lipidomics discovery software (Collins et al., 2016; <http://dx.doi.org/10.1021/acs.analchem.6b01260>) was used to putatively identify HPLC-MS features in the data. We confirmed each LOBSTAHS identification using two additional means: (1) via comparison of data-dependent MS2 spectra with those from authentic standards or published reference spectra and (2) by requiring the presence of the same compound identity in data acquired in the opposite HPLC-ESI-MS ionization mode. We confirmed all LOBSTAHS identities at the lipid class level (e.g., PC versus PE, or MGDG versus TAG) using a new, experimental LOBSTAHS feature which automatically detects diagnostic product ion fragments and constant neutral losses (as given in Popendorf et al., 2013; <http://dx.doi.org/10.1007/s11745-012-3748-0>) in the available data-dependent MS2 spectra for each sample. After identification, quantification of analytes was performed using a series of standard curves, followed by normalization to concentration of an internal standard.

Lipid identities are resolved only to the level of bulk fatty acid composition (i.e., the sum of the properties of the substituents at both the *sn*-1 and *sn*-2 positions). As a result, in some cases (e.g., PC 40:8), several different molecules having the same bulk fatty acid composition have been identified. These can be distinguished by retention time, which is given in the “Comment” field for each entry.

**PAL1314\_LMG1401\_particulate\_IP-DAG\_pmol\_L**

Concentrations of particulate intact polar diacylglycerol (IP-DAG) lipids measured in water column samples from the Drake Passage and Bellingshausen Sea. Seawater samples were retrieved from depth using standard oceanographic sampling equipment and then collected by vacuum filtration onto 0.2 µm pore size Durapore membrane filters; these were frozen immediately at –80°C. Extraction was performed using a modified Bligh and Dyer (Bligh and Dyer, 1959; <http://doi.org/10.1139/o59-099>) method described in Popendorf et al. (2013; <http://dx.doi.org/10.1007/s11745-012-3748-0>). Lipid extracts were analyzed by HPLC-ESI-MS with data dependent-MS2 acquisition on a high-resolution, accurate mass Thermo Q Exactive Hybrid Quadrupole-Orbitrap mass spectrometer (ThermoFisher Scientific, Waltham, MA, USA) coupled to an Agilent 1200 HPLC system (Agilent, Santa Clara, CA, USA). The HPLC-ESI-MS method is described in Collins et al., 2016 (<http://dx.doi.org/10.1021/acs.analchem.6b01260)>.

The LOBSTAHS lipidomics discovery software (Collins et al., 2016; <http://dx.doi.org/10.1021/acs.analchem.6b01260>) was used to putatively identify HPLC-MS features in the data. We confirmed each LOBSTAHS identification using two additional means: (1) via comparison of data-dependent MS2 spectra with those from authentic standards or published reference spectra and (2) by requiring the presence of the same compound identity in data acquired in the opposite HPLC-ESI-MS ionization mode. We confirmed all LOBSTAHS identities at the lipid class level (e.g., PC versus PE, or MGDG versus TAG) using a new, experimental LOBSTAHS feature which automatically detects diagnostic product ion fragments and constant neutral losses (as given in Popendorf et al., 2013; <http://dx.doi.org/10.1007/s11745-012-3748-0>) in the available data-dependent MS2 spectra for each sample. After identification, quantification of analytes was performed using a series of standard curves, followed by normalization to concentration of an internal standard.

Lipid identities are resolved only to the level of bulk fatty acid composition (i.e., the sum of the properties of the substituents at both the *sn*-1 and *sn*-2 positions). As a result, in some cases (e.g., DGTS\_DGTA 32:1), several different molecules having the same bulk fatty acid composition have been identified. These can be distinguished by retention time, which is given in the “Comment” field for each entry.

**Transmission\_spectra\_incubation\_vessels**

Transmission spectra from 191-800 nm for various glass and polymer incubation containers acquired using a Thermo Evolution 300 benchtop spectrophotometer. Spectra are reported for passage of light through single thicknesses of fused quartz glass, borosilicate glass, polyvinylfluoride film (PVF, sold under the brand name Tedlar), 4 mil thickness polyethylene terephthalate film (PET, sold under the brand name Mylar), and for passage through both PVF and PET films together. Transmission spectra are reported as percentages.

**Wavelength\_specific\_molar\_abs\_coefficients\_PC\_moieties**

Wavelength-specific molar decadic absorption coefficients of various phosphatidylcholine lipid standards for wavelengths 200-500 nm. Lipids were dissolved in methanol and wavelength-specific absorbances were measured in 100 mm quartz cuvettes using a dual-path UV-visible spectrophotometer (Thermo Nicolet Evolution 300; ThermoFisher Scientific). The wavelength-specific molar decadic absorption coefficients reported here (, in units of M-1 cm-1) were calculated according to the equation

where is the measured decadic absorbance at wavelength , is the pathlength (10 cm), and is the concentration of the relevant analyte (liposome standard) in units of mol L-1. HPLC-grade methanol was used as the reference solution.