Appendix: Protocol to obtain the data used in the Baffin Bay food web models.

All data were gathered in 2016 in Baffin Bay during the sea campaign on the CCGS Amundsen icebreaker and the ice camp close to Qikiqtarjuaq on Broughton Island, next to Baffin Island. (see figure 1).

At the ice camp, water column and sea ice were sampled, whereas only the water column was sampled using a CTD-rosette at 28 stations during the sea campaign. Several depths (5 and 8-10 at the ice camp and on the ship, respectively) were sampled to gain solid representation of the vertical distribution of the biological variables.

PRIMARY PRODUCTION

The primary production was measured by ^{13}C labeling at several depths in the photic zone. Water samples were separated in three acid-cleaned polycarbonate flasks and 0.5 mL of a 2.4% solution of $NaH_{13}CO_3$ (99.9 atom%^{13}C, EURISOTOP) tracer was added to all flasks inducing ^{13}C enrichment of around 10 %. After tracer addition, samples were incubated on desk. *In situ* light penetration was simulated by filters placed on each incubator and temperature maintained at 0°C. At the ice camp, samples were submitted to real *in situ* conditions as they were placed along a rope immersed in the water column. After 24h, samples were filtered on precombusted filters (500°C), dried at 60°C for 24 hours and then stored until analysis. ^{13}C enrichments on filters were measured with a CN-Sercon mass-spectrometer according to Raimbault and Garcia (2008) to quantify the rates of carbon fixation.

The same protocol was followed to estimate sea ice algae production from the first centimetre of the bottom ice core, diluted with 25-30 mL of surface sea water filtered onto 0.2 µm.

Phytoplankton taxonomy samples were taken from Niskin bottles, fixed with Acid lugol solution. Identification and cell count were made by inverted microscopy according to Utermöhl method (Utermöhl, 1958). All samples were sedimented at least 24h. A minimum of 400 cells was counted.

WATER COLUMN CHL A CONCENTRATION

Chl *a* concentration was measured on 0.2 to 1 L of seawater samples filtered on Whatman GF/F 25mm diameter filters. Immediately after, filters were soaked in 10mL of acetone 90% under dark condition and frozen (-20°C) for 24 hours. Chlorophyll *a* fluorescence was measured before and after the addition of 3 drops of 5% HCl. The method used is based on those developed by Yentsch and Menzel (1963), Holm-Hansen et al. (1965) and Lorenzen (1967). Fluorescence was converted in Chl *a* concentration using the formula:

Chlorophyll a= Fd*(A/(A-1))*(Rb-Ra)*v/V

Fd is calibration coefficient obtained with pure chlorophyll a (Sigma C6144), A is Acid ratio (Rb/Ra), Rb and Ra correspond to fluorescence of sample extract before and acidification, respectively and v is the volume extracted (10ml) and V the volume filtrated (in L).

BACTERIA

Abundance of bacteria was estimated by flow cytometry analysis following the method described by Marie et al., 1999. Cell count was performed on 1.5 mL of non-filtered seawater samples, poisoned with 15 µL of glutaraldehydes (25%) and 1/100 of solution pluronic (10%) and frozen at -80°C until analysis in laboratory.

Bacterial production was measured by H^3-Leucine incorporation (Kirchman et al., 1985) as modified by Smith and Azam (1992). Triplicates were incubated with [H^3]-Leucine (20 nmol L^{-1} final concentration.) in sterile 2.0 mL micro-tubes at surrounding temperature for at least 4 hours. Before leucine inpcorporation, 100 µL of trichloroacetic acid (TCA 50%) was added in one microtube to create a control. After the recovery of triplicates, 100 µL of TCA was added to stop incubation. Then triplicates were centrifugated and stored at -20°C until analysis. Leucine incorporation was converted into carbon production using the conversion factor of 1.5 kg C per moles of leucine (Simon and Azam, 1989).

Bacterial respiration was estimated for 3 different depths (surface, DCM, below DCM). Three L of seawater were filtered through 1 µm and distributed into 6 biological oxygen demand bottles. Three bottles were immediately fixed with $MnCl_2$ and NaOH+NaI to determine the concentration of dissolved oxygen at T0 (control). Three others bottles were incubated five days in the dark at *in situ* temperature before fixation. The bacterial respiration was determined by following the decrease in dissolved oxygen concentration. The bacterial respiration was then expressed in µg C L^{-1} d^{-1} using a respiratory quotient of 1 (Del Giorgio and Cole, 1998).

The number of bacteria infected by viruses was counted by electron microscopy. 50 mL of seawater were fixed with glutaraldehyde (final concentration 1%) and frozen at -80°C until observation. In the laboratory, aliquots were ultracentrifugated onto 400-mesh electron microscope grids with carbon-coated formvar film. Each grid was then stained for 30 s with uranyl acetate (2% wt/wt) and examined at *13 000 to *40 000 to distinguish between virus-

infected and uninfected bacteria. A bacteria was considered as infected if at least three viruses were observed within the host cell.

ZOOPLANKTON

Zooplankton community was sampled with a 200-µm mesh conical-square plankton net equipped with a KC-Denmark® flowmeter mounted on a 2*2m metal frame and deployed vertically from the surface to a maximal depth of 700m depth. A small 50-µm mesh net was mounted on the side of the frame to catch microzooplankton.

This sampler was deployed cod-end first to avoid filtration on the downward trajectory and hauled vertically from 10 m above the bottom to the surface at a speed of 30 m min−1.

After removal of fish larvae/juveniles, zooplankton samples of each net, except one of the two 200-µm mesh were preserved in a 10% buffered formalin solution.

Laboratory analysis

The samples were sieved through 1000 µm and 150 µm sieves. The two size fractions (200–1000 and >1000 µm) were resuspended in water. Individual count and identification were made for aliquots containing approximately 300 copepods. Organisms were identified to the lowest possible taxonomical level. Individual counts per aliquot were converted in abundance per square meter considering the subsampling quantities analyzed.

CILIATES AND HETEROTROPHIC FLAGELLATES

Identification and count of ciliates and heterotrophic flagellates were made by inverted microscopy. They were identified and counted is the same time that phytoplankton cells. Three transects of 26 mm were observed to count 400 cells.

Their biovolumes were computed during Imaging FlowCytobot (IFCB) image processing according to Moberg et al., (2012), following the protocol below.

At each station and for several depths, 5mL samples were analyzed using the IFCB. Samples were preserved in a cooler with ice until analysis. Before entering the IFCB the sample is screened onto 150 µm mesh in order to remove larger particles. Moreover, Milli-Q ® water was run between samples to prevent contamination. The images taken, with a resolution of 3.4 pixel per µm, were transferred to a computer for archiving and further analysis.

Grayscale images were processed to extract regions of interest (ROIs) and their associated features (*e.g.* : geometry, shape, symmetry, texture, etc.) with a MATLAB (2013b) code (Sosik and Olson, 2007) available at *https://github.com/hsosik/ifcb-analysis*. A total of 231 features were extracted

and used for automatic classification using a random forest algorithms with EcoTaxa application (Picheral et al., 2015). Reference set and validation of predictions are both done manually.

ARCTIC COD LARVAE

A double square net bearing two square-conical nets (1 m^2 aperture, 500 µm and 750 µm meshes) was deployed from the surface to depths of 75 to 103 m at 17 locations to identify the epipelagic fish assemblage and validate the acoustic signals.

The fresh standard length (SL) of individual age-0 Arctic cod was measured on the ship and their weight (W) was calculated based on $W = 0.0055\ (SL)^{3.19}$ (Geoffroy et al., 2016).

Hydroacoustic data were recorded continuously along the track of the ship with a Simrad EK60® split-beam echosounder at 38 and 120 kHz following the recording and processing methods of Bouchard et al. (2017), except that the acoustic signal was processed with background and impulsive noise removal operators (De Robertis and Higginbottom, 2007; Ryan et al., 2015) instead of a time-varied threshold. The difference in mean volume backscattering strength ΔMVBS (dB re: 1 m^{-1}) between 38 and 120 kHz was used to discriminate pelagic fish from zooplankton. Mean size (SL and W) of Arctic cod sampled by nets and the nautical area backscattering coefficient (NASC, m^2 nmi^{-2}) in echo-integration cells (0.25 nautical mile long by 3 m deep) at 38 kHz with $\Delta MVBS_{120\text{-}38}$ in the range -10 dB to 5 dB (Benoit et al., 2014; Geoffroy et al., 2016) were used to estimate age-0 Arctic cod integrated abundance (fish m^{-2}) and biomass (mg m^{-2}) from 12 m (effective sampling depth of the transducers) to 100 m.

BIOGENIC EXPORT FLUXES

Export fluxes were estimated from i) a drifting sediment trap deployed from the Amundsen from June 15 to July 9 2016 and ii) both short-term and long-term sediment traps deployed at the ice camp from mid-May to mid-July.

Drifting trap

A Technicap sequential sediment trap (12 cups) was deployed at 25 m under the ice anchored to a drifting ice floe. The carrousel of the sediment trap was programmed to rotate every 2 days to continuously collect sinking particles at a high temporal resolution.

Sample cups were labeled and filled with a filtered seawater-buffered formalin solution (5%) adjusted to a salinity of 37. After recovery, sample cups were kept in the dark until analyses back in the laboratory.

Short-term traps

Short-term sediment traps were used for measurement on fresh samples not preserved in formalin, contrary to the sequential long-term traps. Four traps were deployed under the ice at 2 m and 25 m (2 traps at 2 m; 2 traps at 25 m) in different sampling holes approximately 15 m apart for periods ranging from 2 to 7 days. Empty sample cups were labeled and fixed on each trap before they were deployed on a line and gently lowered into the water. The sampling hole was covered with Styrofoam and snow during deployment. Recoveries of the single traps were done in the morning when arriving at the ice camp. Snow and ice were removed from the ice holes and traps were pulled out of the water. Each trap was removed from the line, placed and secured on a rack, and moved under a tent to protect from wind and snow. The traps were left in the tent for approximately 3 h to allow for the material to settle. After this sedimentation period, the overflow water above the sample cup was removed from the traps in a bucket and put back in the sampling hole. Sample cups were then removed and taken to the wet lab where sample cups from the same depth were mixed together. Samples were split into several subsamples that were filtered or kept in vials/bottles.

Long-term traps

Two HydroBios multi-sediment trap were deployed at 25 m and 100 m under the ice. The sequential sediment trap were programmed to rotate every 3 days from May 17 to June 22 and every 2 days from June 25 to July 19 2016. Sample cups (12 cups) were labeled and filled with a filtered seawater-buffered formalin solution (5%) and adjusted to a salinity of 37 ‰ at the lab before deployment. The 2 traps were deployed on the same line through a large hole (75 cm x 75 cm) that had previously been made in the ice. The hole was covered during deployment with a wooden plate and snow. After recovery, sample cups were kept in the dark until analyses back in the laboratory.

Laboratory analyses

As soon as the samples were brought back in the laboratory (at the ice camp lab for short-term trap samples or at the university for long-term trap samples), subsamples for chl *a* measurements were filtered onto GF/F filters that were extracted in 90 % acetone and analyzed with a Turner Design fluorometer. Subsamples for POC measurements were filtered onto GF/F filters (pore size: 0.7 µm) pre-combusted at 500°C for 4 h, rinsed with distilled water to remove salt, exposed to 0.1 N HCl vapors for removal of inorganic carbon and dried at 60°C. POC measurements were then made on a CHN elemental analyzer. Subsamples were also used for the enumeration of diatoms cells by inverted microscopy according to the Utermöhl method. A minimum of 100 phytoplankton cells of the dominant groups were counted using phase contrast microscopy.

POC, chl a, and diatoms cell measurements were converted to daily fluxes depending on deployment time.

POC CONCENTRATION IN WATER COLUMN

From 580 to 1200mL (depending on the quantity of particulate matter) of seawater were filtered onto pre-combusted (at 500°C for 4 hours) 25 mm Whatman GF/F filters. Filters were then washed with 100µl of H_2SO_4 (0.5 N) to remove any inorganic carbon and stored until laboratory analysis. Blank filters were prepared for each set of samples by washing the filter with 600ml of <0.2µm seawater.

Determination of POC, PON and POP was carried out simultaneously on the same sample using the wet-oxidation procedure according to Raimbault et al., (1999).

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