Supplement 1. Habitat properties of the Scotian Shelf offshore banks and larval durations of resident macroinvertebrates

In this section, we provide data sources for each of the bank habitat characteristics considered in this study (Table S1.1), greater detail regarding their quantification, and reasons why certain habitat variables originally considered where not included in the analyses presented in the main text. We also provide a correlation matrix (Fig. S1.1) which provides the correlation coefficients, p-values, and scatter plots for each pair of bank habitat properties that were considered in the analyses of the main text. In general, most habitat properties were highly correlated with distance along-shelf (Fig. S1.1), which, alongside bottom temperature and peak and annual mean chlorophyll-a concentration, was largely responsible for the first principle component of the overall habitat trends across the banks (Fig. 5c, main text). Larval durations, seasons and corresponding literature sources are given in section S1.3.

Table S1.1. A list of all habitat variables initially considered before consolidation or removal.

Category	Variable	Short name	Data source
Physical	Bank area (km^2)	Area	Area calculated from DFO summer ecosystem survey strata (Doubleday & Rivard 1981) using ArcGIS 10.5 (ESRI 2016).
	Average depth (m)	AvDepth	DFO summer ecosystem survey data (Doubleday & Rivard 1981)
	Spatial variation in depth	Depth_sd	DFO summer ecosystem survey data (Doubleday & Rivard 1981)
Oceanographic	Distance of bank centroid from eastern shelf boundary, i.e., position along northeast-to-southwest current trajectory.	DistAlongShelf	Estimated via ArcGIS 10.5 (ESRI 2016).
	Distance of bank centroid from coastline, i.e., relative contribution of inner shelf vs outer shelf hydrography.	DistToCoast	Estimated via ArcGIS 10.5 (ESRI 2016).
	Average current velocities during April-October (broad larval season)	V_mean	Fisheries and Oceans Canada Oceanographic database (http://www.bio.gc.ca/science/data-donnees/base/index-en.php)
	Variance of current velocities.	V_var	Fisheries and Oceans Canada Oceanographic database (http://www.bio.gc.ca/science/data-donnees/base/index-en.php)
	Retention due to advective processes only	Ret_A	WebDrogue particle tracking program (http://www.bio.gc.ca/science/research-recherche/ocean/webdrogue/index-en.php) set to 25m, averaged across spring, summer, and fall, with no extra wind.
	Retention due to	Ret_AD	Retention calculated given equivalent

|		
advective and diffusive processes		radius of the banks, current velocity and water density data (http://www.bio.gc.ca/science/data-donnees/base/index-en.php)
Bottom temperature	BTEMP	Fisheries and Oceans Canada CLIMATE database http://www.bio.gc.ca/science/data-donnees/base/index-en.php
Annual range of bottom temperatures	BTEMP_Range	Fisheries and Oceans Canada CLIMATE database http://www.bio.gc.ca/science/data-donnees/base/index-en.php
Average annual upper water column (0-50m) temperature	TSInt_T	Fisheries and Oceans Canada CLIMATE database http://www.bio.gc.ca/science/data-donnees/base/index-en.php
Average annual upper water column (0-50m) salinity	TSInt_S	Fisheries and Oceans Canada CLIMATE database http://www.bio.gc.ca/science/data-donnees/base/index-en.php
Average annual depth-integrated (0-60m) chlorophyll-a concentration	meanchl_di	Fisheries and Oceans Canada BIOCHEM database (c/o Shelley Bond), Bedford Institute of Oceanography. P. O. Box 1006, Dartmouth, Canada, B2Y 4A2
Average depth-integrated (0-60m) chlorophyll-a concentration during the peak of the spring bloom	bloomchl_di	Fisheries and Oceans Canada BIOCHEM database (c/o Shelley Bond), Bedford Institute of Oceanography. P. O. Box 1006, Dartmouth, Canada, B2Y 4A2
Seasonality (magnitude of spring peak chlorophyll relative to the annual average)	Seasonality	bloomchl_di/ meanchl_di
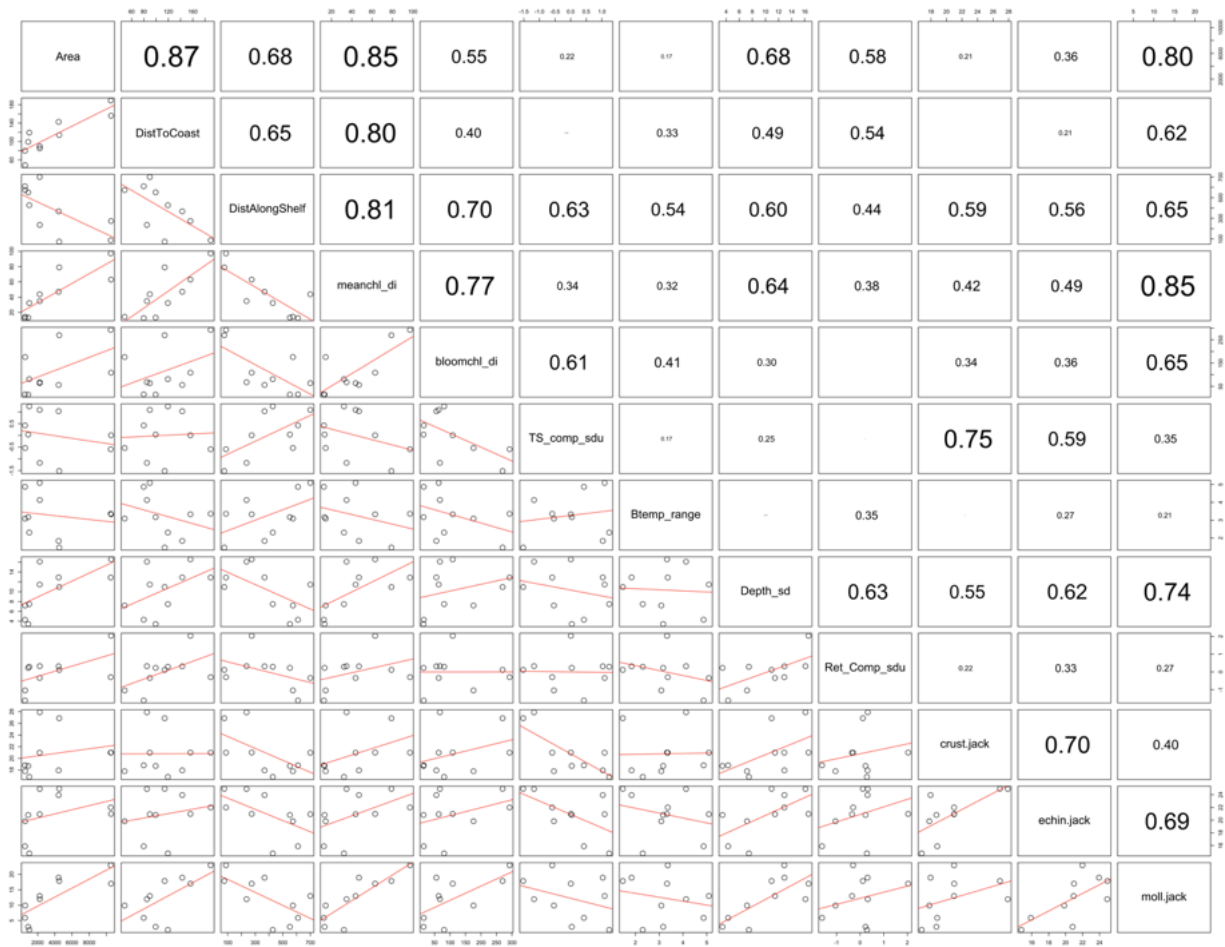
FIGURE S1.1. Correlation (font size scales with correlation coefficient) and scatter plot matrix, with corresponding linear fits (red lines), for all bank habitat characteristics considered in the main text of this study (short names given in Table S1.1). Alpha diversity estimates for the three taxonomic groups are also included: mollusks/cirripedia (moll.jack), crustaceans (crust.jack), and echinoderms (echin.jack).

S1.1. Details regarding physical habitat properties

The boundaries defined for the Fisheries and Oceans Canada annual summer ecosystem survey (Doubleday & Rivard 1981; Fig. S1.2) were used to define the banks in this study. Bank areas (within these boundaries) were measured using the "calculate geometry" function in ArcGIS Desktop 10.5 (ESRI 2016), using the World Geographic System 1984 ellipsoidal projection of the earth. The range of average depths among the banks was too small to account for a significant proportion of ecological variation among the banks; therefore, this variable was not considered in the main analyses.
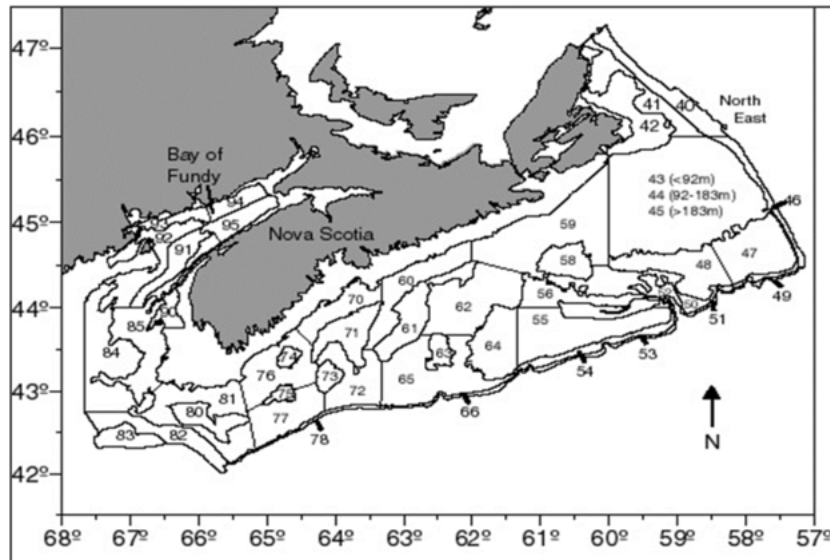
FIGURE S1.2. Two-digit numeric designations of Research Vessel (RV) survey strata (DFO, 2017 sampled annually in July by Fisheries and Oceans Canada. The banks correspond to specific strata: Banquereau (47 & 48), Misaine (43), Middle (58), Sable (55 & 56), Western (64), Emerald (63), La Have (73), Roseway (74), Baccaro (75), and Brown's (80).

S1.2. Details regarding oceanographic habitat properties

A strong inflow (estimated as ~300 000 m^3/s, on average in April-October for the upper 50 m from the current meter observations, Fig. S1.3 for locations), designated as the Nova Scotia Current, originates in the Gulf of St. Lawrence and runs from northeast to southwest from the Gulf of St. Lawrence along the Scotian Shelf; using the current meter observations off southwest Nova Scotia, we find an average outflow into the Gulf of Maine of approximately 240 000 m^3/s, in good agreement with the inflow (see also Sutcliffe et al. 1976, Chapman & Beardsley 1989, Loder et al. 2001). Data collected by these moorings are summarized in Fig. 2 (main text) and indicate that the stronger flow is to the southwest in the inner half of the shelf; weaker mean currents prevail over the outer shelf, where most of the banks we consider are located. These observations along with in situ water densities were also used to estimate horizontal mixing parameters and retention times for the 10 banks.
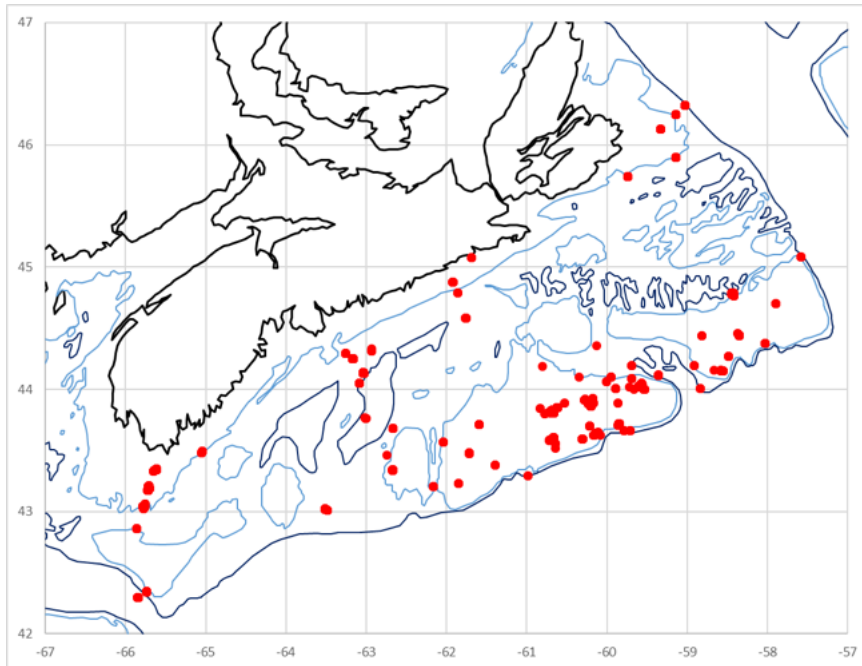
Fig. S1.3. Locations of current meter moorings of at least 15 days duration for the months of April to September on the Scotian Shelf. Approximately 750 records were considered, the majority (~500) of which were from Sable Island Bank and the result of extensive activity associated with hydrocarbon exploration. Data from these moorings are summarized in Table S1.2.

Given the dominant direction of the Nova Scotia Current (NE to SW) and its cross-shelf structure (stronger over the inner half of the shelf), we characterized the position of each bank by the distance of its centroid from the coast (DistToCoast; Fig. S1.4a), and from the northeastern edge of the shelf (DistAlongShelf; Fig. S1.4b). We hypothesized that DistAlongShelf would capture the along-shelf transport of larvae, while DistToCoast would capture cross-shelf diffusion/mixing of larvae and/or the varying influence of inshore vs offshore currents.
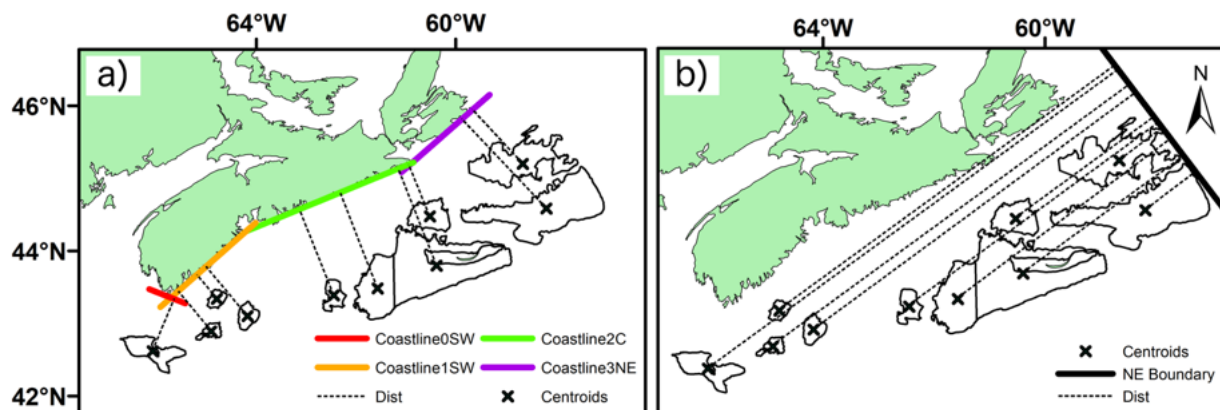

Fig. S1.4. A visual depiction of how perpendicular distance (dotted lines) of bank centroids (x) to a) the coast (defined by four lines following the curvature of the coastline), and b) to the northeastern boundary of the shelf was calculated.

Average current velocities and their temporal variances were calculated from in situ observations for each of the banks. However, these variables were weakly correlated with alpha diversity estimates (Fig. S1.1), implying limited ecological significance, at least for the purposes of this study. Further, both average and variance of current velocities were highly correlated with

average bank-specific retention times, which had a greater correlation with taxon-specific alpha diversity estimates (Fig. S1.1). For these reasons, average and variance of current velocities (summarized in Table S1.2) were not considered further in our analyses.

Table S1.2. Average speed and direction of ocean currents recorded by moorings stationed on the Scotian Shelf as shown in Fig. S1.3. The number of records is also provided.

Area	Inner shelf			Outer shelf		
	Speed	Direction	# records	Speed	Direction	# records
Inflow	0.066	192	336	NA	NA	NA
ESS	0.101	253	20	0.026	242	511
CSS	0.110	243	218	0.034	174	18
WSS	0.062	246	154	0.050	269	210

The ability of banks to retain larvae (retention) was quantified in two ways: first, using the publicly-available particle tracking program, WebDrogue (WebDrogue Drift Prediction Model v0.7, Hannah et al. 2001), which quantified retention given seasonal flow fields (no mixing or diffusive processes are accounted for explicitly), seeding each bank with passive particles and following their movement for 90 days, and second, using observations of water density, current speeds (average and variance), and equivalent radius of each bank to estimate retention given both advective and diffusive process. A point source of dye was placed at centre of each bank, the advection-diffusion equations solved and the quantity of dye remaining on each bank was calculated over time. There was a positive relationship between the two measures of retention (Fig. S1.5); the r^2 for the 10 banks was 0.46. Given the data available, it appears that the majority of our species of interest spawn in spring and summer (Table S1.7); pelagic larvae are therefore most likely to be present in the upper mixed layer (< 25 m) between spring and autumn (April-September, Table S1.7). Both advection and advection/diffusion-based estimates of retention were derived for the upper 25m and were averaged across the 6 months (April-September); these values were similar across seasons and our results from subsequent analyses did not change significantly when a particular season was used rather than the average.
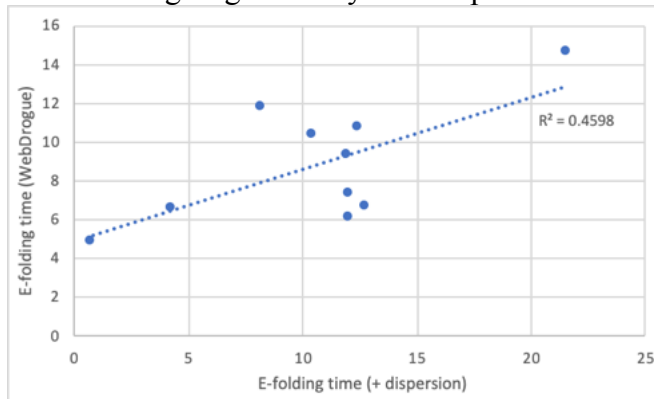

Fig. S1.5. Relationship between e-folding times as measured using WebDrogue (advective processes only, y-axis), and using equivalent radius (both advective and dispersive processes, x-axis).
Retention estimated using WebDrogue

WebDrogue v0.7 (http://www.bio.gc.ca/science/research-recherche/ocean/webdrogue/index-en.php) models the movement of particles in space and time according to local tidal, seasonal mean and wind-driven flows (Hannah et al. (2000, 2001)). This program was used to characterize the residence time of particles on the 10 banks. The seasonal

circulation patterns used in WebDrogue are derived from in-situ, smoothed temperature and salinity observations, leading to a reduction of small-scale variability.

WebDrogue provides flow fields at the surface (0-5 m average), 25 (25-35 m average) and 100 m (95-105 m average) to simulate particle trajectories. Given that vertical migration is common at the larval stage of many marine invertebrate species (Cronin & Forward 1986; Gallager et al. 1996, López-Duarte & Tankersley 2007, Tapia et al. 2010) and that the planktonic larval stage occurs mostly in the upper mixed layer (0 – 25 m), all simulations were run using the 25 m flow field. Because the in-situ density fields would reflect external forcing, no additional wind stress was specified for the runs. Fifty particles were placed within the boundaries of each bank. The number of days until only 37% of the original particles remained on the bank was recorded as the retention time (e-folding time).

Retention due to currents and mixing

To account for both mean currents and diffusive processes, a second estimate of retention was computed. Bank areas were converted to an equivalent radius, $R = Sqrt(Area/\pi)$ (Table S1.3).

Table S1.3. Area of each bank converted to equivalent radius. Banks listed from smallest to largest: Baccaro (Bc), Roseway (Rw), La Have (LH), Emerald (Em), Brown's (Bw), Middle (Md), Western (Ws), Misaine (Mi), Banquereau (Bq), and Sable (Sb).

Bank	Area (km^2)	AvDepth (m)	Depth_sd	Equivalent radius R (km)
Bc	534	87.03	4.300	13.00
Rw	551	81.49	7.190	13.20
LH	908	88.17	3.430	17.00
Em	1034	83.99	7.480	18.10
Bw	2243	81.03	11.46	26.70
Md	2253	55.47	16.11	26.80
Ws	4442	74.59	12.9	37.60
Mi	4513	81.17	10.94	37.90
Bq	10496	60.32	12.88	57.80
Sb	10537	64.00	16.58	57.90

From the Fisheries and Oceans Canada CLIMATE database (http://www.bio-iob.gc.ca/science/data-donnees/base/data-donnees/climate-climat-en.php), water density data were retrieved by month. Long-term monthly density statistics were used to best fit a linear estimate of the density gradient ($\partial\rho/\partial z$) over the average depth of each bank (Table S1.3); the Brunt-Vaisala frequency was then calculated (1). This frequency was then used to estimate the Rossby radius (2), which represents the scale an eddy would take over the bank; these eddies have the potential to mix and disperse particles over and off the bank.

(1) Brunt-Vaisala Frequency (N) = $Sqrt[(-g/\rho_{0*}\partial\rho/\partial z]$
(2) Rossby Radius = $NZ/(\pi f)$,
    where g is the acceleration due to gravity, ρ_0 the
    average density, Z the average depth of the bank,
    and f the Coriolis parameter.

Median of monthly mean current speeds (Ũ) and their standard deviations (SD) for records longer than 15 days, from 0-25 m deep were derived from Fisheries and Oceans Canada's Oceanographic database (Table S1.4). The standard deviations (SD) were determined after tides (~periods of ≤24 hours) were removed; this filtering also removed inertial period variability (~17 hours for the Scotian Shelf). The median current will carry an initial marker patch to the edge of the bank in R/Ũ seconds. This is an advective time-scale.

Table S1.4. Medians of the variable current speeds (Ũ; m s^{-1}) derived from records longer than 15 days, from 0-25 m depths, as well as their SDs, for each of the ten banks listed from smallest to largest as in Table S1.3.

Bank	Bc	Rw	LH	Em	Bw	Md	Ws	Mi	Bq	Sb
Ũ	0.153	0.131	0.061	0.061	0.141	0.074	0.067	0.095	0.174	0.077
SD	0.027	0.051	0.011	0.011	0.040	0.030	0.025	0.047	0.085	0.032

The eddy diffusivity was estimated from the eddy scale (2*Rossby radius) and median variable velocity ($K_h = 2R_0Ũ$).

The two processes, advection and dispersion, were combined by starting a point distribution with concentration 1 at the centre of the equivalent circular bank (at t=0, x=0), advecting this marker towards the edge of the bank while allowing dispersion to act. The 1-D dispersion equation (3) is solved and the spreading "dye" is advected at the median speed.

(3) Dispersion $= \partial C/\partial t - K_h * \partial^2 C/\partial x^2$

While the maximum is carried away from the centre of the bank, dispersion carries dye back towards the centre so that the e-folding time-scale will be longer than the advection time-scale. E-folding times (retention times) for each bank resulting from this analysis are listed in Table S1.5.

Table S1.5. E-folding time (retention time, in days (d)) including both dispersive and advective processes, on each of the banks, listed from smallest to largest as in Table S1.3. E-folding time as calculated using WebDrogue are also provided.

	Bw	Bc	Rw	LH	Em	Ws	Sb	Md	Bq	Mi
E-folding time (d)	12.8	0.8	4.3	12.1	12.1	12	21.6	12.5	8.2	10.5
E-folding (WebDrogue; d)	6.7	4.9	6.5	6.1	7.4	9.3	14.6	10.7	11.7	10.4

Temperature and Salinity

Bottom temperature characterizes the habitat of adults, and determines the suitability of habitat for settling larvae. Temperature is known to affect many physiological characteristics of marine animals including metabolism and growth rate, and therefore plays a significant role in determining the home range of species (Pinsky et al. 2013, Pörtner & Gutt 2016). The annual ranges of bottom temperatures were taken as a proxy of temporal habitat variability in the adult environment; this determines whether the temperature of a particular bank is suitable for a

species year-round, or only for a shorter period. Surface (0-50 m) temperature influences survival, metabolism and growth rate of pelagic larvae. Surface (0-50 m) salinity could also could influence habitat suitability for pelagic larvae and control, along with temperature, the density and stratification of the upper 50m; moreover, the temperature and salinity properties can act as a tracer of water mass movements.

Temperature and Salinity 0-50m – Larval habitat

Average annual temperature (T) and salinity (S) for the upper 50 m were obtained for each bank for all months during the time period 2005-2017. Both T and S were scaled by their effects on density (S scaled by 0.78, T by 0.15; i.e., this scaling equalized the effect of 1 unit change of S and T), since the density distribution plays a fundamental role in the residence and connectivity times of the banks.

Bottom temperature – Adult habitat

Bottom temperatures within 1 SD from the mean bottom depth, both determined from the set depths, were determined for each month of the year, and then averaged across 2005-2017 (Table S1.6). The ongoing success/presence of a particular species may depend on the annual average temperature and the magnitude of the annual cycle, so the range (max-min) of average bottom temperatures across months was also recorded (Table S1.6). There is a substantial difference among banks with Misaine at one extreme (low T 1.37, low range 1.6, a relatively cold, stable environment) and Brown's (high T 6.61, high range 5.02, a relatively warm, variable environment) at another (Table S1.6).

Table S1.6. Annual average bottom temperature within ± 1 SD of the mean depth of each bank, and the average range of bottom temperature in a year. These data were obtained for the period 2005-2017. Banks are listed from west (Bw) to east (Mi).

Bank	Annual Average T (ºC)	Range (ºC)
Bw	6.61	5.02
Bc	5.73	4.23
Rw	3.37	2.84
LH	4.94	3.19
Em	6.63	1.97
Ws	5.30	1.66
Sb	4.11	5.21
Md	2.60	5.24
Bq	2.44	4.01
Mi	1.37	1.60

Chlorophyll-a concentration

Details regarding the data source for, and calculation of annual mean chlorophyll-a concentration and long-term mean peak chlorophyll-a concentration per bank were provided in the main text. Marshall & Burgess (2015) found that community composition and species traits were strongly influenced by the temporal variability (predictability) of food availability, and that this variability can be just as important as the total amount of resources available. Consequently, we also estimated the seasonality of [chlorophyll-a] (ratio of the mean to peak concentrations). However, the variation in seasonality among the banks was too small to account for a significant proportion of variation in alpha diversity or assemblage structure for any of the taxa of concern This variable was therefore removed from the main analyses and is not discussed in the main text.

S1.3. Species pelagic larval durations and seasons within taxa

Here (Table S1.7) we provide the seasons and literature associated with pelagic larval duration estimates within each of the taxa of interest as discussed in the main text. Because local-scale (Northwest Atlantic) estimates were limited, we expanded our search to include species not resident on the Scotian Shelf, but resident in areas with similar temperature regimes (temperate). In Table S1.7, these non-local species are identified with an asterisk (*).

Bank centroid DistAlongShelf acts as a proxy for connectivity since the shelf is dominated by the NE-SW flowing NSC; a representative speed would be ~0.05 m/s. The distances between banks divided by the representative current would be a measure of their connectivity. Using this approach, we found that 9 of 45 temporal separations were within 30 d, 23 of 45 within 60 days and 35 of 45 were within 90 days. Only 10 of 45 were longer than 90 days. The temporal separations between NE/SW bank pairs ranged from 11 to 42 days and averaged 21 days. This indicates that most species with pelagic larval durations of at least 30 days would succeed in being transported among banks, especially if step-wise transport across multiple generations is considered.

Table S1.7. Larval season, period, and/or duration where data were available for some common macro-invertebrate species (within each of the three taxonomic groups of interest) resident on the Scotian Shelf offshore banks. Given that local-scale data for resident species were limited, larval durations for similar species from other temperate regions were also considered (*). Data were derived from both experimental and in situ studies of species-specific larval durations within each taxa. References are provided.

Taxonomic group	Species	Larval season	Larval duration	Reference
Crustaceans	*Lithodes maja* (Northern stone crab)	*unknown*	90 days	Dufour (1998)
	Pandalus borealis (Northern Shrimp)	April-September	90 days	Haynes & Wigley (1969); Shumway et al. (1985); Ouellet et al. (1990)
	Cancer irroratus	June-	30-90 days	Scarratt & Lowe

|				
	(Atlantic rock crab)	September		(1972)
	Chionoecetes opilio (Snow crab)	May-August+	60-240 days	Adams (1979)
	Homarus americanus (American lobster)	June-July	14-56 days	Mercaldo-Allen & Kuropat (1994); Tracey et al. (1975)
	* *Cancer magister* (Dungeness crab)	N/A	90-150 days	Shirley et al. (1987); Shanks (2009)
	* *Paralithodes glandula* (Red king crab)	N/A	90 days	Kuzmin et al. (1996); Epelbaum et al. (2006)
Echinoderms	*Cucumaria frondosa* (Sea cucumber)	April-June	43-49 days	Hamel & Mercier (1996); Shackell et al. (2013)
	Cucumaria minata (Orange sea cucumber)	N/A	14 days	Strathmann (1987)
	Isostichopus badionotus (Four-sided sea cucumber)	N/A	25 days	Zacarías-Soto et al. (2013)
	Strongylocentrotus purpuratus (Purple sea urchin)	N/A	60-90 days	Strathmann (1978)
	Sterechinus neumayeri (Antarctic sea urchin)	N/A	115 days	Bosch et al. (1987)
	Evechinus chloroticus (New Zealand sea urchin)	N/A	30 days	Wing et al. (2003)
	Asterias amurensis (Northern Pacific sea star)	N/A	40-50 days	Buttermore et al. (1994); Nozais et al. (1997)
Mollusks/ Cirripedia	*Placopecten magellanicus* (Sea scallop)	*unknown*	30-60 days	Packer et al., 1999; https://www.nefsc.noaa.gov/publications/tm/tm189/tm189.pdf
	Spisula solidissima (Surf clam)	*unknown*	21 days	http://njseagrant.org/wp-content/uploads/2014/03/atlantic-clams-surf-hard.pdf
	Arctica islandica (Ocean Quahaug)	*unknown*	18-30 days	Doall et al. (2008)

| *Mya arenaria* (Soft-shell clam)	*unknown*	10-35 days	Strathmann (1987); Zolotarev (1996)
*Crepidula fornicate (Slipper limpet)	N/A	14-21 days	Coe (1949); Dommasnes & Scham (1973)
*Adalaria proxima (Yellow false doris)	N/A	1-3 days	Lambert et al. (2003)
*Balanus glandula (Common acorn barnacle)	N/A	14-28 days	Schwindt (2007)

* Larval durations available for other temperate (similar temperature regime) species within these taxonomic groups, but from other regions where larval season may be different.

Supplement 2. Bank species accumulation curves & SAR modelling

The following subsections contain species accumulation curves for the three taxonomic groups of interest, accumulating all species observed from 2005 to 2017 (raw data, not adjusted for detection). A lack of clearly defined asymptotes of species richness after 13 years of sampling across many banks, particularly for crustaceans and mollusks/cirripedia, implies that a complete census of species has not yet been achieved. Supplement 2.4 describes our choice of SAR model.
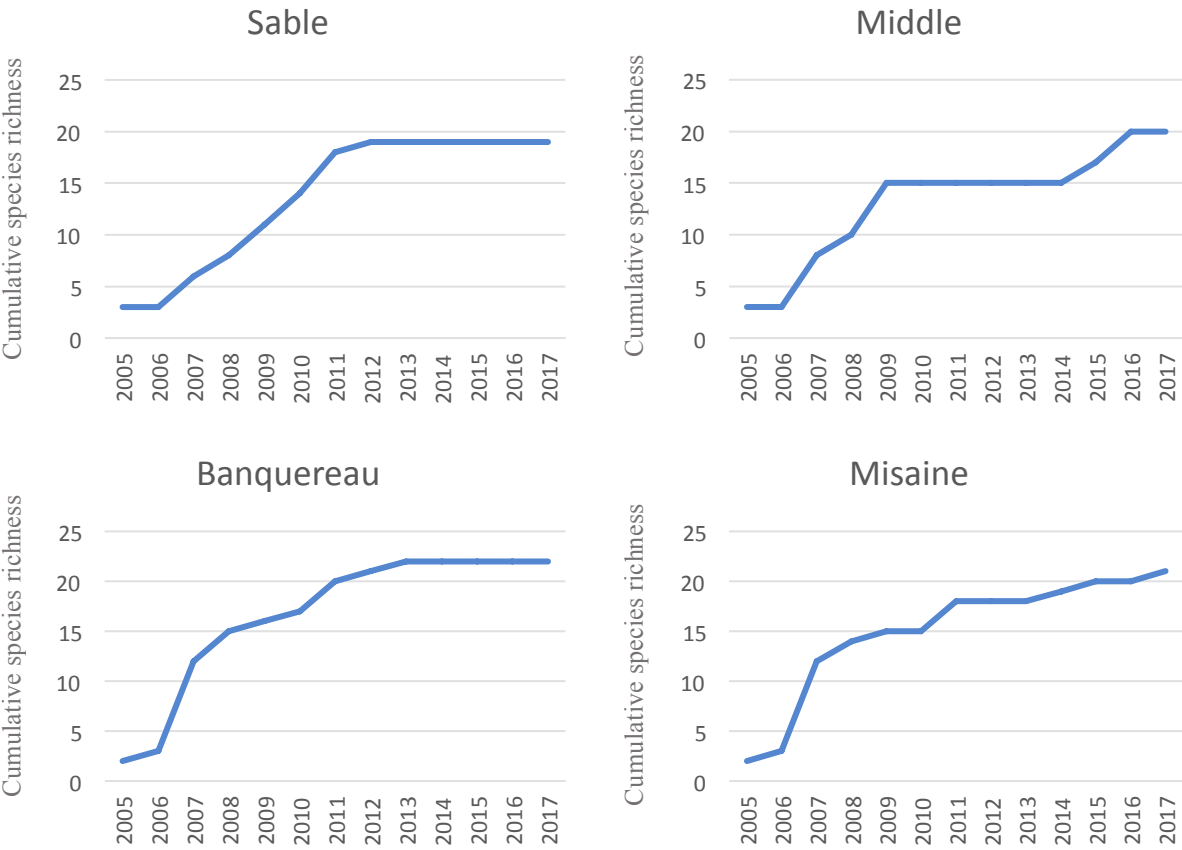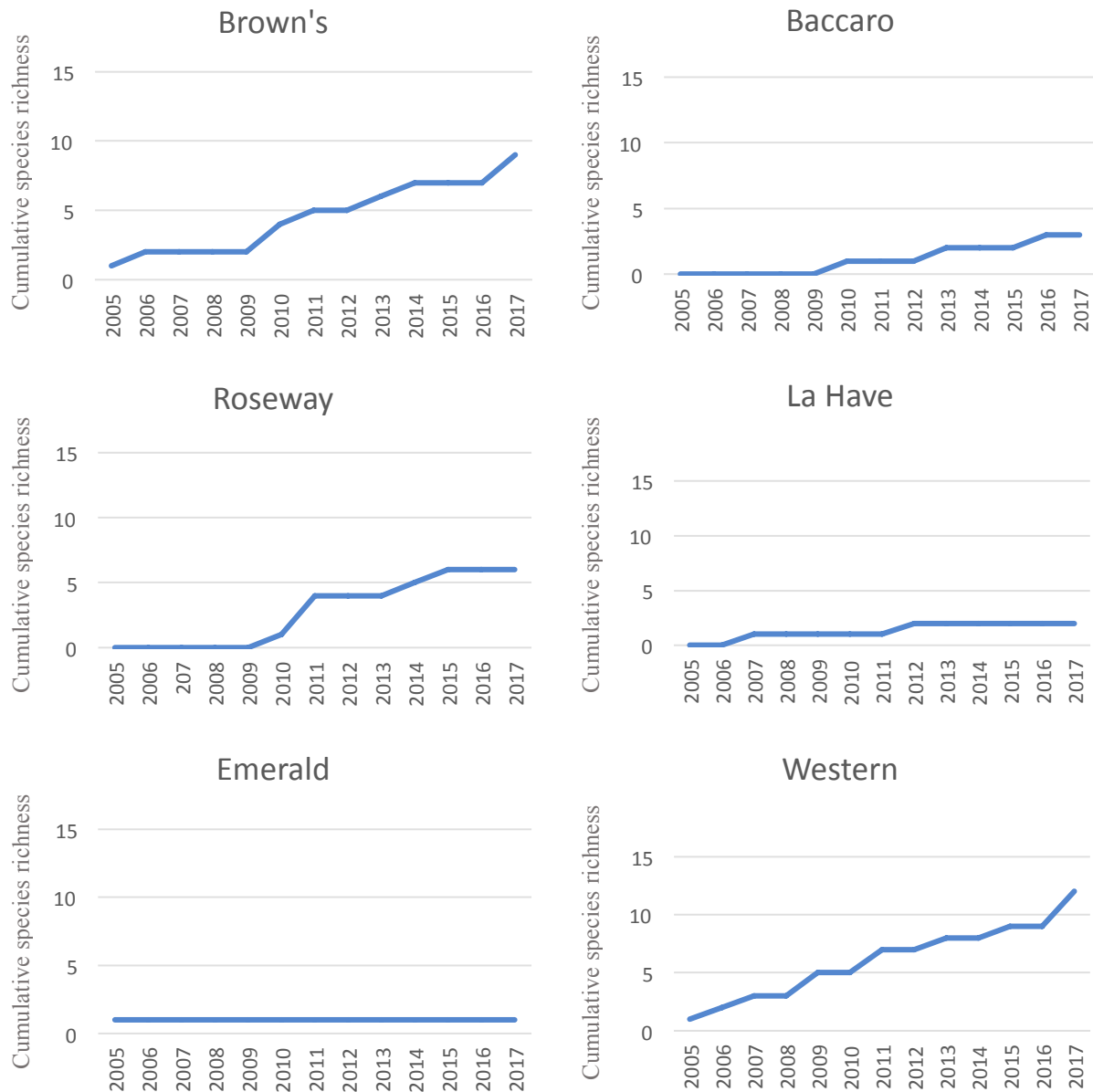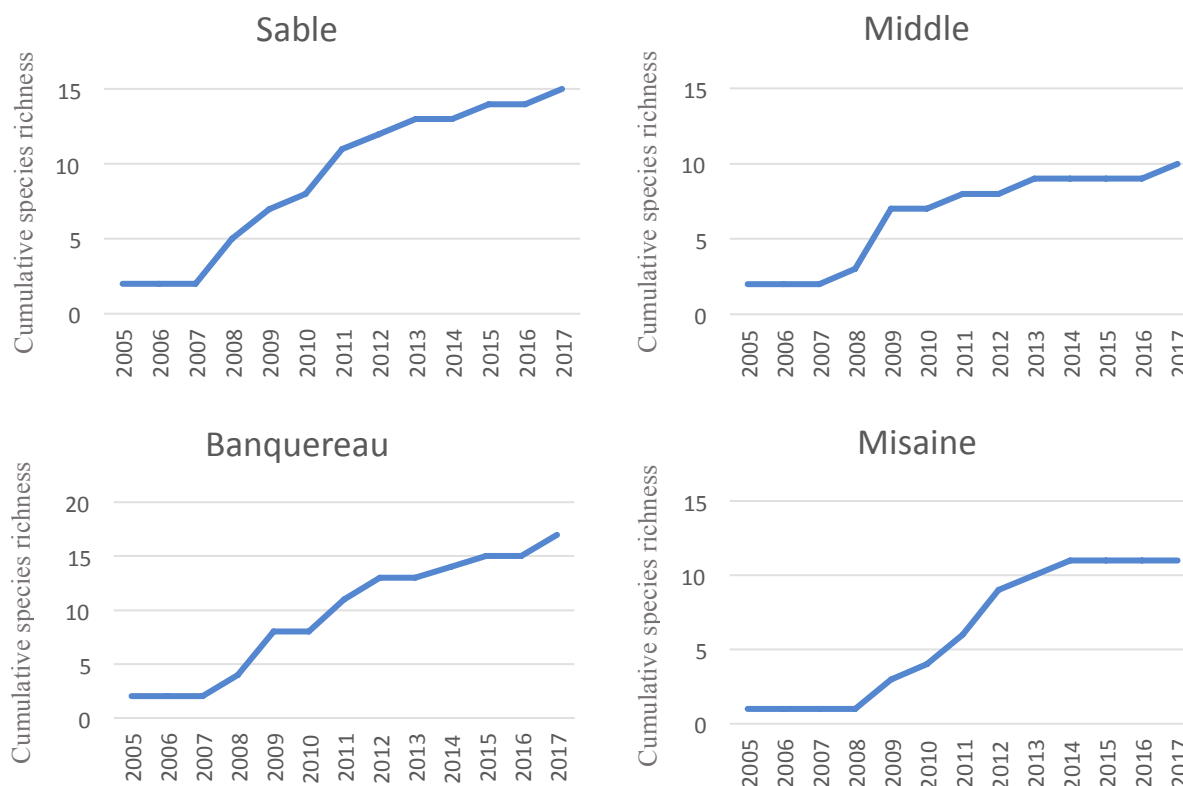
S2.1 Crustacean species accumulation curves
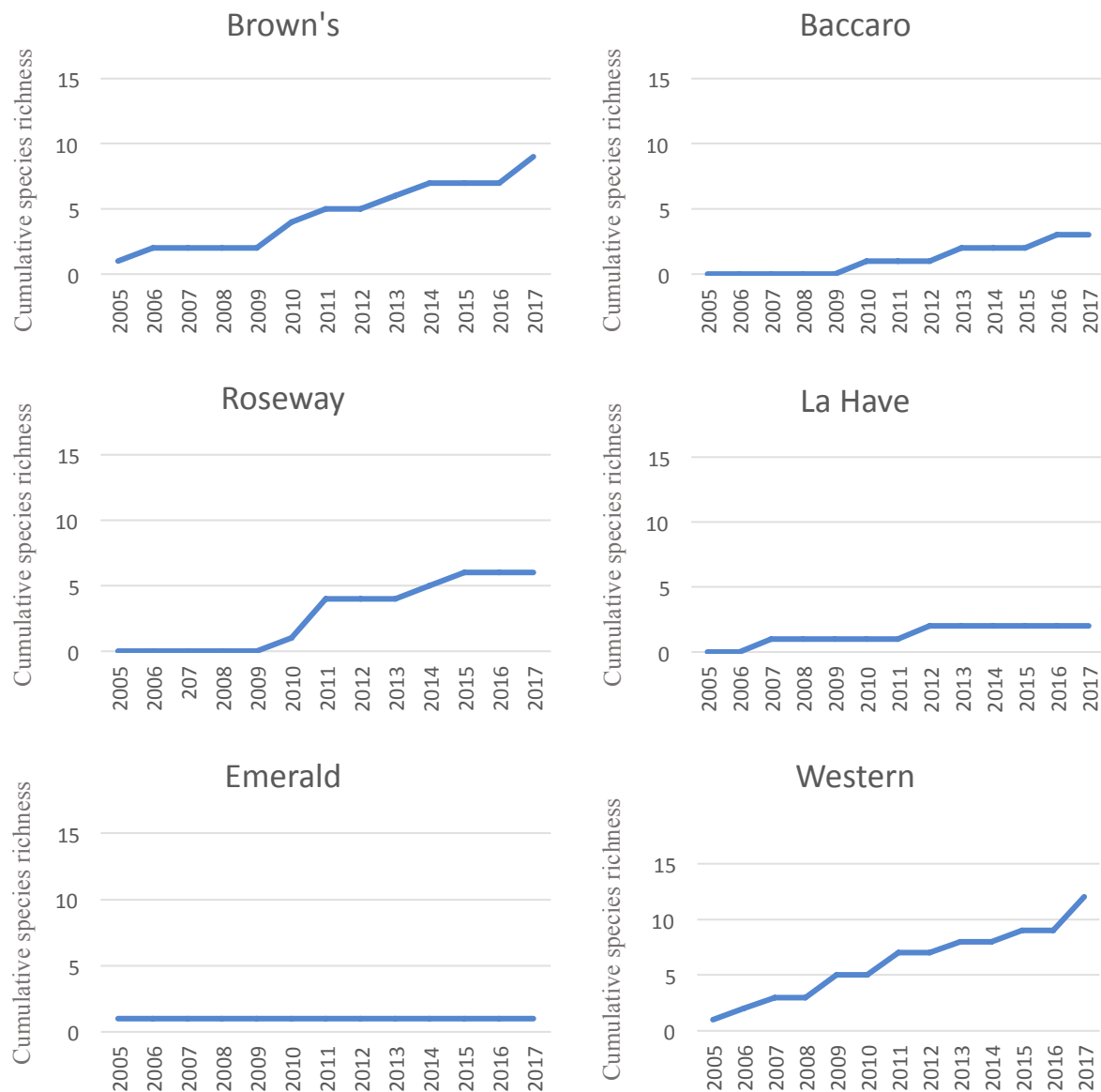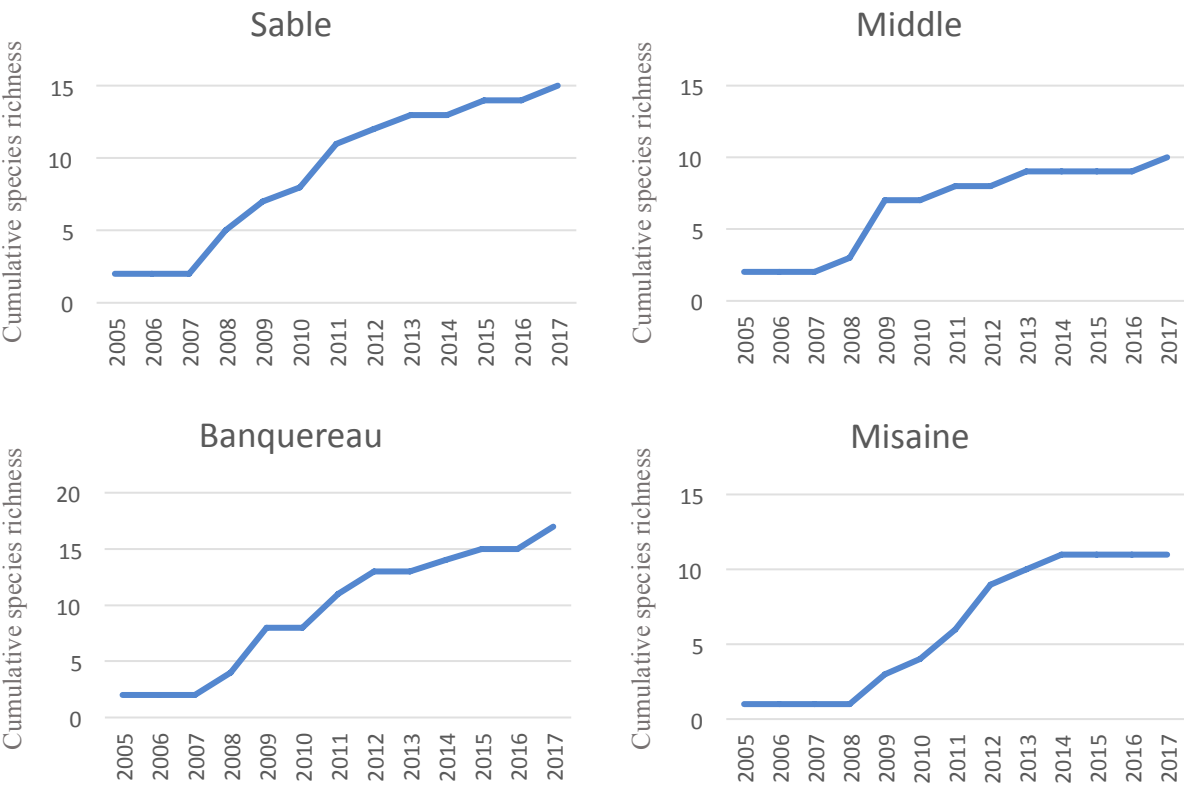
S2.2 Echinoderm species accumulation curves
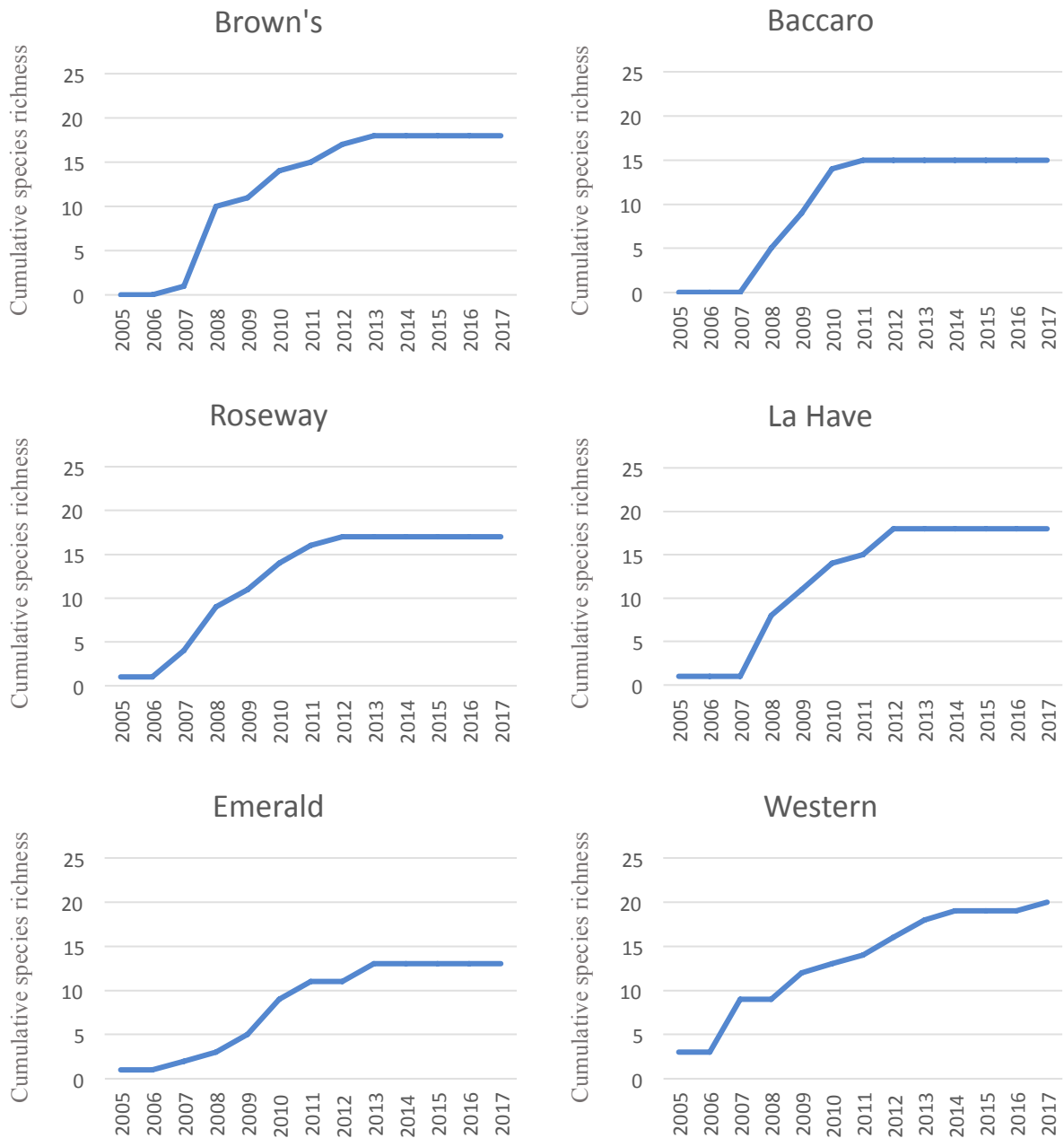
S2.3 Mollusk/Cirripedia species accumulation curves

S2.4 Modelling the SAR

To correct for species that, to date remain undetected in the survey, we used the Jaccknife1 estimate of alpha diversity (Smith & van Belle 1984). These estimates were highly correlated (R^2 = 0.79, 0.84, and 0.97 for crustaceans, echinoderms, and mollusks/cirripedia, respectively) with the raw species counts (species + genus), and the variances associated with the estimates were similar across banks.

Dengler (2009) evaluated the goodness of fit for 16 variations of SAR across a wide range of nested and island-type ecosystems and found that the power-law generally describes SARs most appropriately, and that the $\log_{10}$-transformation of alpha diversity was generally inconsequential. Self-similarity in the abundance distribution of species, and/or skewed species-abundance distributions, likely resulting from the distance-decay of the abiotic environment (Palmer, 2007), are common in nature and lead to prevalence of the power law SAR (Harte et al. 1999, Sizling & Storch, 2004, Martin & Goldenfeld 2006). Hubbell (2001) and Rosindell & Cornell (2007) also noted that the power law SAR is produced over a wide range of ecosystems at intermediate scales as a result of stochastic events of death, dispersal and speciation. We examined whether, and to what varying degree, the power-law SAR fit the patterns of variation in crustacean, echinoderm, and mollusk/cirripedia alpha diversity across the ten Scotian Shelf offshore banks.

When many rare species, i.e., those sampled only once or twice over the 2005-2017 time period, were sampled on a given bank, the standard error associated with the Jackknife1 alpha

diversity estimate (see Equations 1-2 in main text) was large relative to banks where between zero and three species were sampled resulting in an alpha diversity estimate equivalent to the species count. In order to reduce the effect of highly uncertain estimates of alpha diversity (large standard error), we chose to weight our SAR fits by the inverse of the Jackknife1 standard error estimates. This resulted in an improved SAR model fit for mollusks/cirripedia, with normally distributed residuals, compared to an unweighted SAR model (Fig. S2.1). Echinoderm and crustaceans SAR models were weak regardless of whether they were weighted or not; weighting did not significantly improve the fit or the distribution of residuals for these taxa (Fig. S2.2-3). Note that SAR models were generated using the base package in R version 3.4.3 (R Core Team 2019).
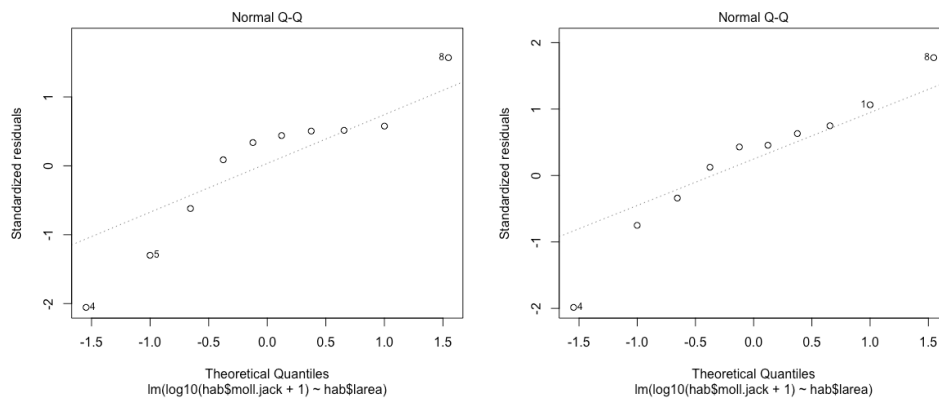

Fig. S2.1. Normal Q-Q plots for unweighted (left) and weighted (right) SAR models for the molusk taxon. Weighting the SAR by the inverse of Jackknife1 alpha diversity standard error estimates improved the fit and normalize residuals.
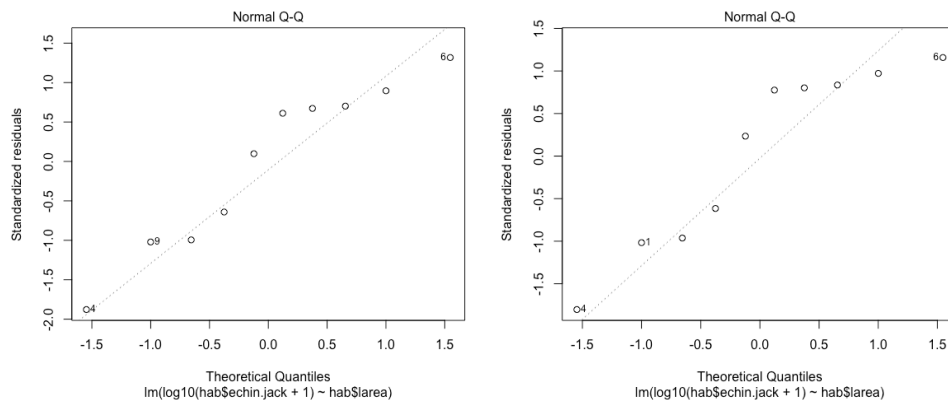

Fig. S2.2. Normal Q-Q plots for unweighted (left) and weighted (right) SAR models for the echinoderm taxon. Weighting the SAR by the inverse of Jackknife1 alpha diversity standard error estimates did not significantly improve the model.
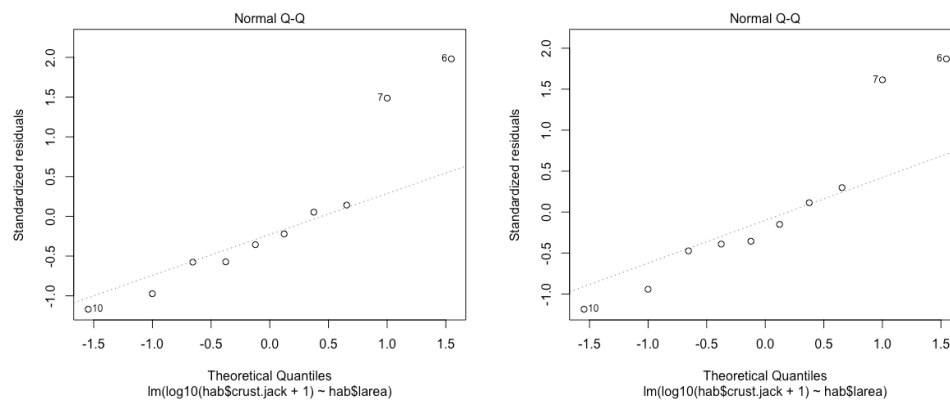
Fig. S2.3. Normal Q-Q plots for unweighted (left) and weighted (right) SAR models for the crustacean taxon. Weighting the SAR by the inverse of Jackknife1 alpha diversity standard error estimates did not significantly improve the model.

Supplement 3. Role of common vs. rare species in driving differences among assemblages

We evaluated the contribution of all species to the overall biomass of the three taxa across all banks. We found that 4 of the 29 crustacean species recorded accounted for 90% of the biomass for crustaceans (*Homarus americanus* (American lobster), *Pandalus borealis* (Northern pink shrimp), *Pandalus montagui* (Aesop shrimp), and *Chionoecetes opilio* (Snow crab), in order of decreasing biomass), 4 of 27 for echinoderms (*Cucumaria frondosa* (Sea cucumber) alone accounted for 74% of the overall biomass, *Strongylocentrotus droebachiensis* (Green sea urchin), *Leptasterias polaris* (Polar six-rayed star), and *Asterias rubens* (Common sea star) accounted for the remaining 16%), and 9 of 27 for mollusks/cirripedia (*Placopecten magellanicus* (Sea scallop), intra-class *Cirripedia* (barnacles), *Chlamys islandica* (Island scallop), *Mytilus edulis* (Common mussel), *Neptunea lyrata* (New England Neptune), *Buccinum undatum* (Waved whelk), genus *Euspira* (Northern moonsnail), *Lirabuccinum dirum* (Dire whelk), and *Modiolus modiolus* (Northern horse mussel), in order of decreasing biomass) (Figure S3.1).
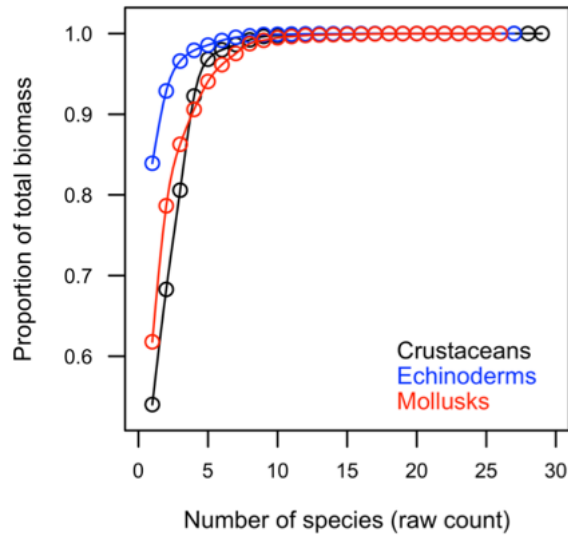
Fig. S3.1. Accumulation of biomass (proportion of the total across all banks) by species within each taxon.

These results suggested that the biomass-weighted assemblage structure used in CCA models (described in the main text) was largely reflective of inter-bank differences in the biomass of the most common species (perhaps only one species, *Cucumaria frondosa*, in the case of echinoderms). By extension, this suggested that the occurrence of rare (low-biomass or transient) species had a limited effect on assemblage similarity patterns, particularly for crustaceans and echinoderms.

Using biomass-weighted Bray-Curtis Similarity Index (BCSI º 1-BCI; Oksanen et al., 2019 range 0-1, where 1 indicates identical communities, 0 indicates no common species/species' biomasses), we found that assemblage similarity based on presence/absence of species was highly correlated ($R^2 = 0.66$; Figure S3.2) with the biomass-weighted similarity for the mollusk/cirripedia taxonomic group; the two indices were also correlated, but less strongly, for echinoderms ($R^2 = 0.53$; Figure S3.3) and crustaceans ($R^2 = 0.54$; Figure S3.4). Further, presence-absence similarities were generally much higher than biomass-weighted similarities for echinoderms and crustaceans (intercepts 0.7 and 0.6, respectively; Figures S3.3-4). Presence-absence similarities for the mollusk/cirripedia group were generally only 0.2 higher than biomass-weighted similarities for this taxon, with the two BCI's being highly correlated ($R^2 = 0.66$; Figure S3.2). This indicated that changes in biomass of common species had a lesser impact on the similarity index for mollusks/cirripedia (gradients in biomass did not cause a significant difference between the biomass-weighted 1-BCI and presence/absence 1-BCI); rather, the presence/absence of rare species (species only observed on one or two banks) had a strong influence on both indices. This higher average similarity between northeastern and southwestern assemblages of mollusks/cirripedia compared to the other two taxa (reported in the main text) was likely the result of common absences, due to the patchy distribution of mollusk/cirripedia species. The strong influence of rare species and patchy distributions, and relatively low presence/absence similarity indices for the mollusk/cirripedia taxon is in agreement with our hypothesis that mollusk/cirripedia communities are more insular/unique, while bank communities of crustaceans and echinoderms are highly similar in terms of species composition (very high presence/absence 1-BCI; Fig. S3.3- Fig. S3.4); differences in assemblage structure within these more mobile taxa are largely due to variation in the biomass of species that range across the entire shelf.
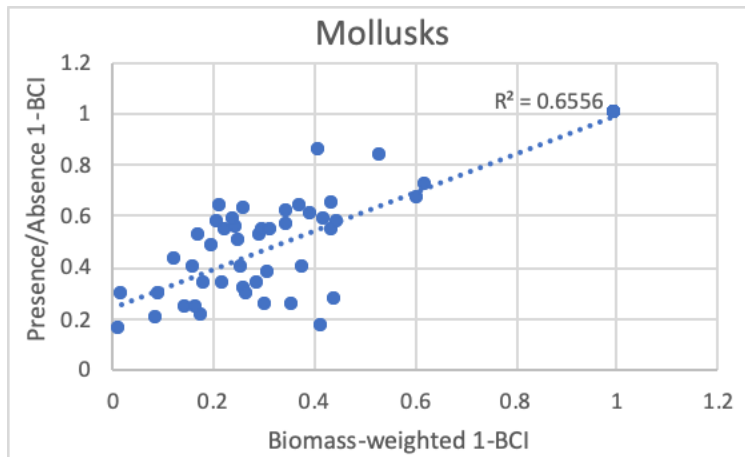
Mollusks

$R^2 = 0.6556$

Fig. S3.2. Relationship between presence-absence and biomass-weighted community similarity indices for the mollusk/cirripedia taxon.

Echinoderms
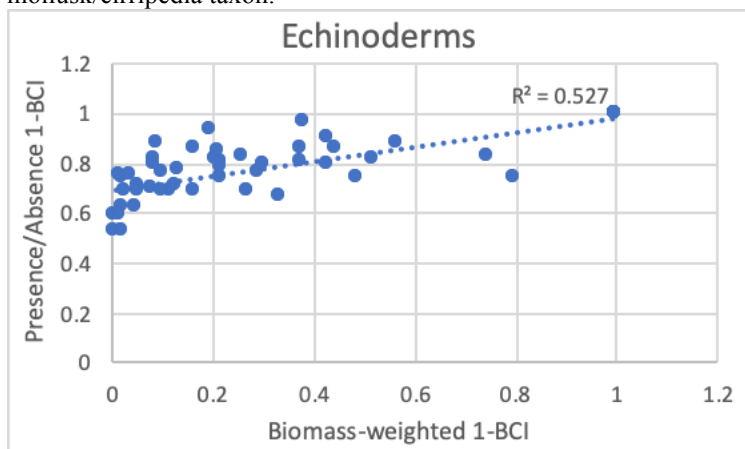
$R^2 = 0.527$

Fig. S3.3. Relationship between presence-absence and biomass-weighted community similarity indices for the echinoderm taxon.
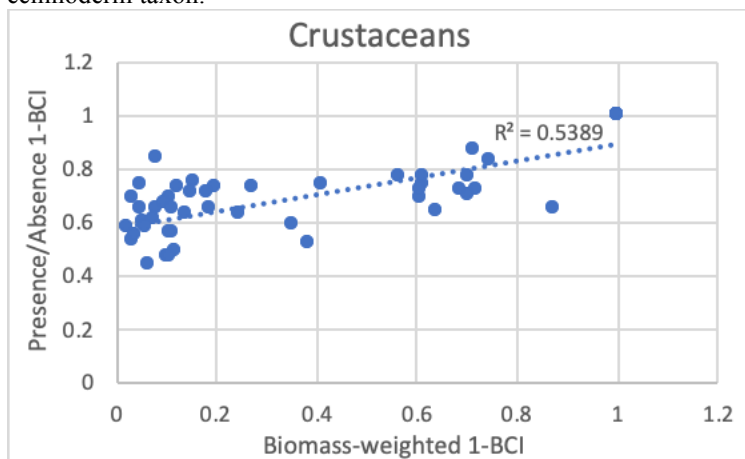
Crustaceans

$R^2 = 0.5389$

Fig. S3.4. Relationship between presence-absence and biomass-weighted community similarity indices for the crustacean taxon.

Supplement 4. Bank vs. off-bank communities

A finer partitioning of crustacean and mollusk taxa

In order to determine which species may be most responsible for the habitat preferences implied by relative proportions of biomass within taxa on and off the banks, we divided crustacean and mollusk (without barnacles) taxa into two finer partitions (shrimps and crabs/lobsters for crustaceans, and bivalves and snails/slugs for mollusks) and evaluated the spatial distribution of biomass of these groups across the shelf (Figure S4.1). Given biomass per survey tow between 2005-2017, it was evident that shrimp species were largely responsible for the higher proportion of crustacean biomass observed in deeper regions of the shelf; shrimps had greater biomass in deeper regions (6.9 ± 0.8 g per tow), particularly the deeper channels between Misaine, Middle and Banquereau Banks, than on banks (3.5 ± 0.6 g per tow; Figure S4.1). In contrast, crabs and lobsters tend to have a relatively higher biomass on banks (3.54 ± 1 g per tow) compared to deeper strata (2.84 ± 0.45 g per tow) (Figure S4.1). The majority of mollusk species, whether bivalves or snails/slugs, had higher biomass on banks compared to deeper strata (Figure S4.1). Bivalve biomass on the banks was approximately double bivalve biomass in deeper strata (1.04 ± 0.22 g per tow on banks compared to 0.56 ± 0.23 g per tow off banks). Snails/slugs (gastropods) were five times more dense (0.45 ± 0.10 g per tow) on the banks compared to deeper strata (0.09 ± 0.01 g per tow).
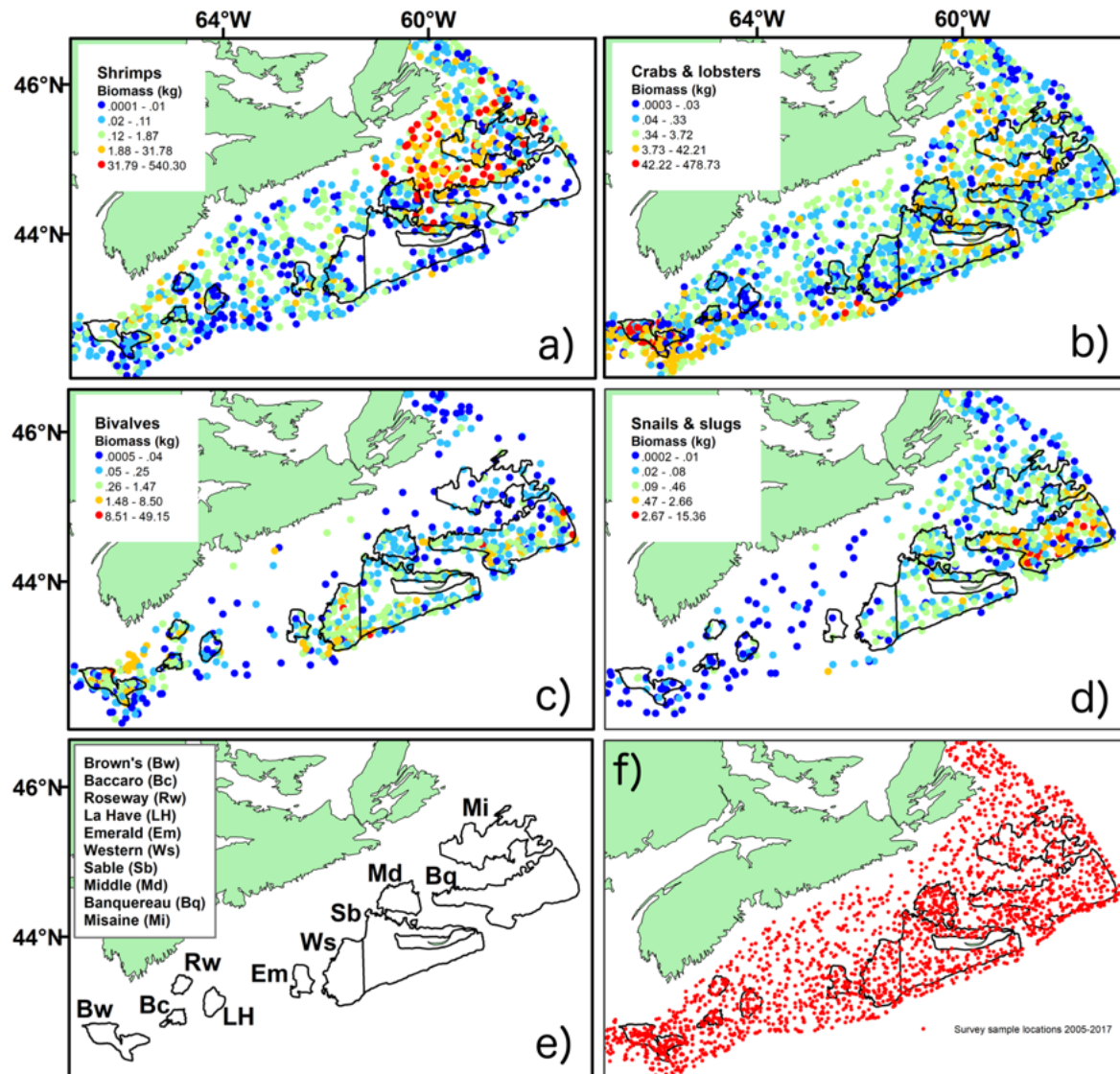
Fig. S4.1. Biomass (g per summer survey tow) of the crustacean group partitioned into shrimps (a) and crabs/lobsters (b), and biomass of the mollusk group partitioned into bivalves (c) and snails/slugs (d). Panel (e) lists the banks from west to east, and panel (f) displays the geographic location of every survey sample made between the years 2005-2017, during which macroinvertebrate species were effectively recorded.

Supplement 5. Depth distribution of common species

In general, the most common crustacean (Fig. S5.1) and echinoderm (Fig. S5.2) species were distributed (in terms of biomass (g) per survey tow) fairly evenly over a wide range of depths across the banks. Mollusks/Cirripedia species on the other hand were generally distributed over smaller ranges of depths, with the exceptions of *L. dirum* and *B. undataum*, and species tended to occupy different depths from one another (Fig. S5.3). This may explain why depth s.d. explained a larger proportion of variance in mollusk/cirripedia alpha diversity than the other two taxa; this taxon may consist of species with finer niche definition, leading to higher

alpha diversity on larger banks with a greater diversity of depths/habitat types (see Fig. 8c and Fig. 9c in main text). This suggests that mollusks/cirripedia conform more to the TIB than echinoderms or crustaceans. This supposition was supported by our finding that mollusks/cirripedia were the only taxon with a significant SAR slope (Fig. 8c in main text).
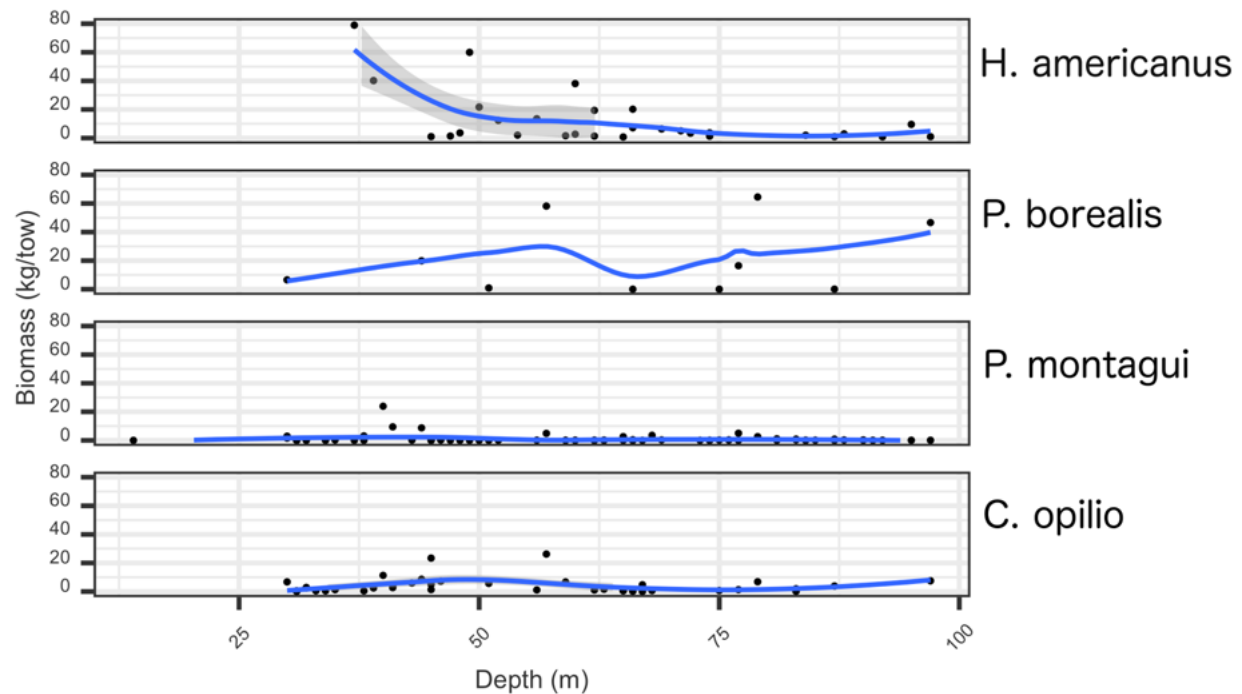

Fig. S5.1. Distribution of biomass of the most common (representing the highest proportion of total biomass) mollusk/cirripedia species by depth across all ten banks.

Fig. S5.2. Distribution of biomass of the most common (representing the highest proportion of total biomass) mollusk/cirripedia species by depth across all ten banks.

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Fig. S5.3. Distribution of biomass of the most common (representing the highest proportion of total biomass) mollusk/cirripedia species by depth across all ten banks.
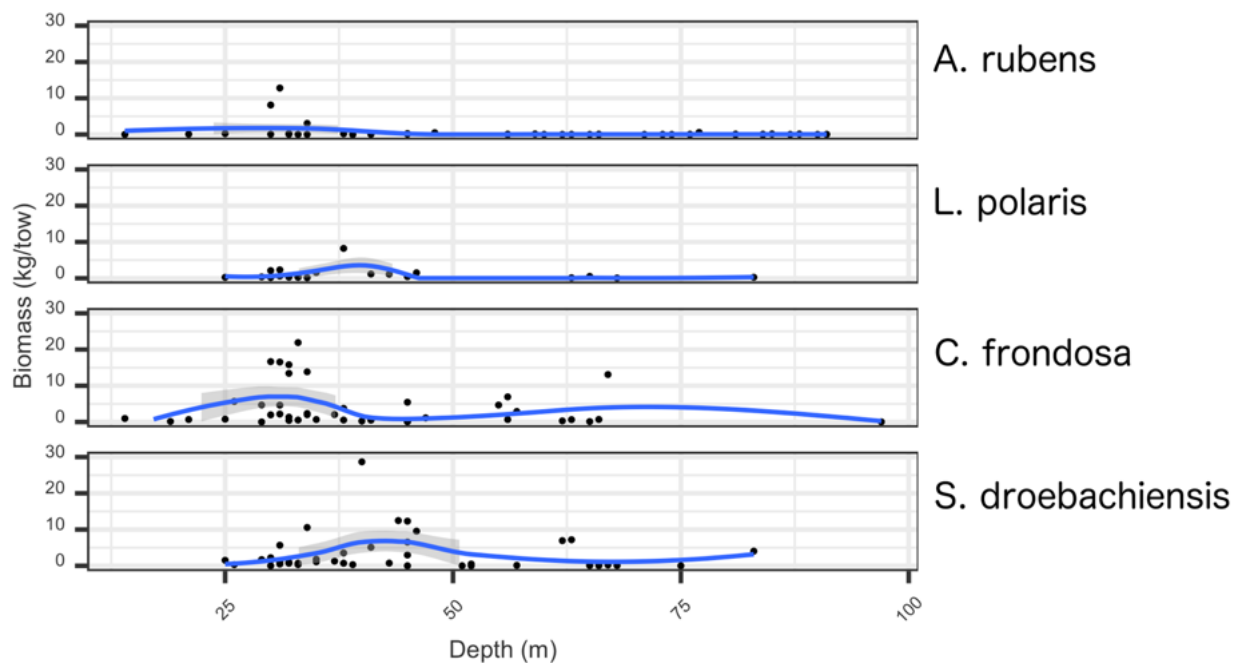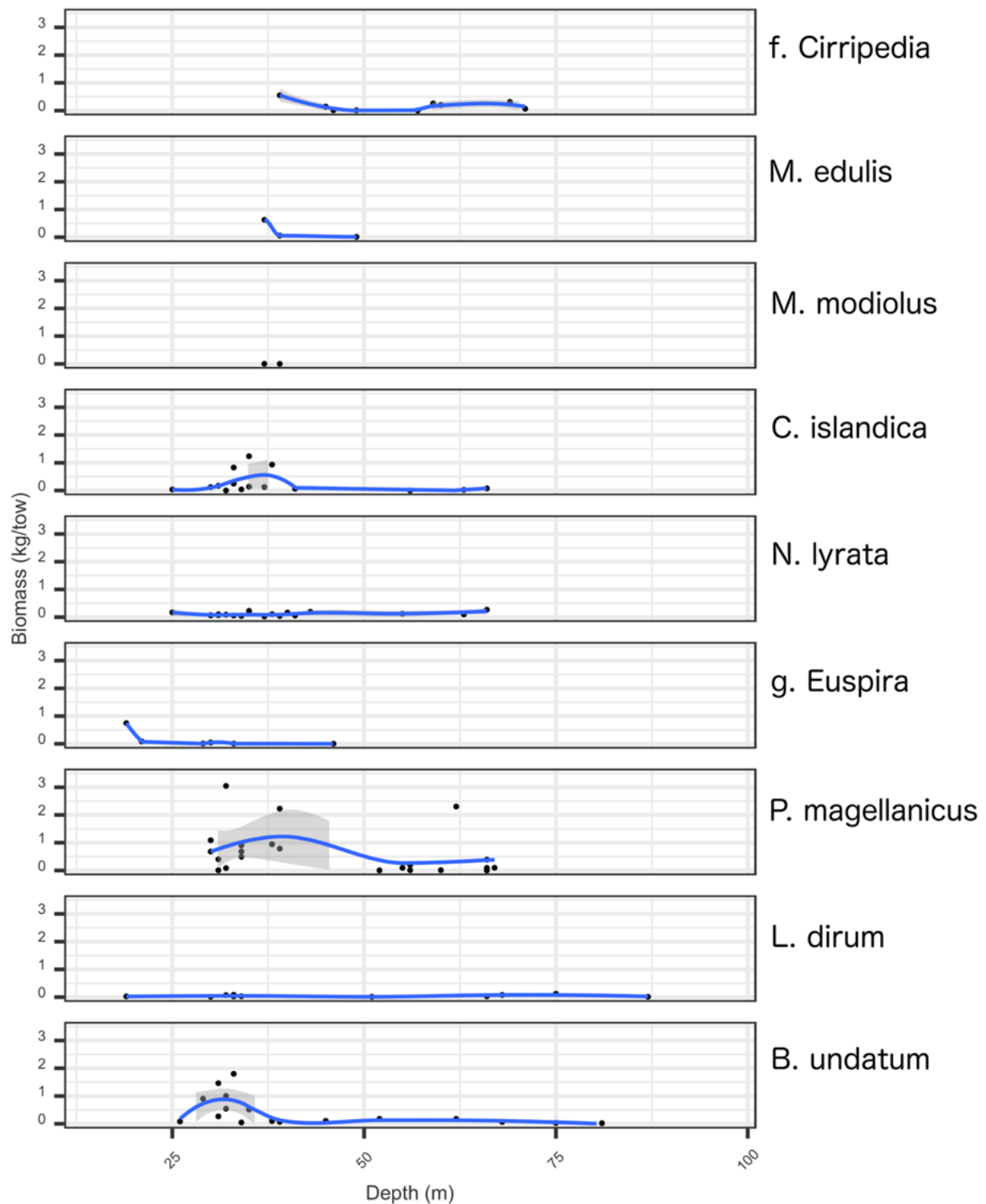

Supplement 6. Assemblage similarity from species presence/absence

Here, we compared biomass-weighted and presence/absence-based Bray-Curtis Similarity Indices (BCSI) for crustacean, echinoderm and mollusk/cirripedia bank assemblage pairs. We calculated the average between bank pairs within the NE complex, within the SW complex, and between NE/SW bank pairs. As noted in the main text, biomass-weighted BCSIs showed a clear partitioning of crustacean and mollusk/cirripedia assemblages into distinct NE and SW complexes, separated by a transition zone at Western Bank (Fig. 10a-c). This distinction between NE and SW complexes was almost non-existent for crustaceans if only species presence/absence was considered (Table S6.1), indicating that the differences between NE and SW bank assemblage complexes was largely due to differences in the biomass of a few common species (also see Supplement 3). The partitioning was weaker for echinoderms when species biomasses were considered (B-W BCSI), but not with presence/absence only (Table S6.1). For mollusks/cirripedia, the NE and SW complexes did not differ substantially from one another when biomass-weighting was employed, but were more dissimilar from one another, compared to higher similarities within complexes, when using presence/absence of species (Table S6.1).

Table S6.1. Summary of Bray-Curtis Similarity Index (BCSI) given only presence/absence of species (P/A) and weighted by species relative biomasses (B-W) for each of the three taxa of interest. Average (and corresponding standard error (SE)) BCSIs provided for all 10 banks (Entire shelf), the NE banks only (Ws, Sb, Md, Bq, Mi), the SW banks only (Bw, Bc, Rw, LH, Em), and between all NE-SW bank pairs. Biomass-weighted BCSIs are as in Fig. 10 in the main text.

	Taxon	Entire shelf (Ave, SE)	NE banks (Ave, SE)	SW banks (Ave, SE)	NE to SW banks (Ave, SE)
P/A	Crustaceans	0.65, 0.02	0.68, 0.03	0.72, 0.03	0.60, 0.02
	Echinoderms	0.76, 0.02	0.83, 0.01	0.83, 0.03	0.70, 0.02
	Mollusks/Cirripedia	0.46, 0.03	0.59, 0.03	0.52, 0.05	0.39, 0.03
B-W	Crustaceans	0.29, 0.04	0.51, 0.09	0.41, 0.09	0.15, 0.03
	Echinoderms	0.22, 0.03	0.36, 0.06	0.32, 0.06	0.12, 0.03
	Mollusks/Cirripedia	0.29, 0.02	0.37, 0.03	0.29, 0.04	0.26, 0.03

Supplement 7. Relative role of species in community similarity patterns

S7.1. Crustaceans

The canonical correspondence analysis indicated that Roseway Bank stood apart from all the other banks including the cluster of the 4 other SW banks, Brown's, Baccaro, LaHave and Emerald, and Western (Fig. 10a). We examined the relationships between these banks and Roseway to determine if particular crustacean species were responsible for the separation. The correlation matrix (below) among these 5 banks indicated that Brown's, Baccaro, LaHave, Emerald and Western were highly correlated (average r = 0.96). On the other hand, the average correlation of Roseway with these five was 0.76.

Correlation matrix using all crustacean species

	Bw	Bc	Rw	LH	Em	Ws
Bw	1	0.99	0.70	0.94	0.94	0.98
Bc	0.99	1	0.73	0.96	0.96	0.98
Rw	0.70	0.73	1	0.76	0.85	0.73
LH	0.94	0.96	0.76	1	0.97	0.94
Em	0.94	0.96	0.85	0.97	1	0.96
Ws	0.98	0.98	0.73	0.94	0.96	1

Given the strong correlations among the 4 SW banks and Western, any one of these could serve as the proxy to compare with Roseway. We selected LaHave Bank and show its relationship of biomass/tow with Roseway (Figure S7.1).
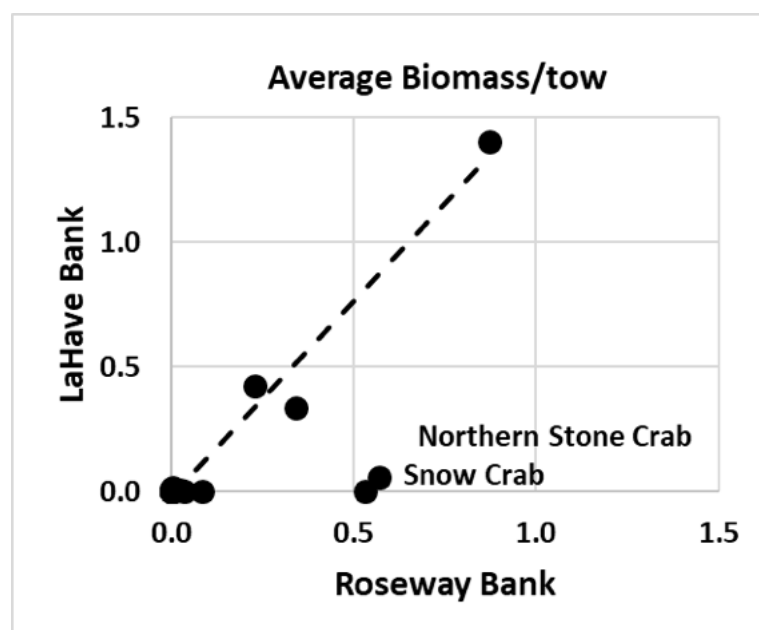

Figure S7.1. Biomass/tow of crustacean species from Roseway and LaHave Banks. The linear fit is for all species omitting Northern Stone and Snow Crab.

The matrix was recalculated omitting Northern Stone and Snow Crab (see below); we found that the average correlation of Roseway Bank crustacean species with the other 5 banks increased from 0.76 to 0.94, indicating that these species are the main cause of the large difference between Roseway Bank and the others.

Correlation matrix omitting Northern Stone Crab and Snow Crab

	Bw	Bc	Rw	LH	Em	Ws
Bw	1	1.00	0.91	0.94	0.96	0.98
Bc	1.00	1	0.93	0.96	0.98	0.98

Rw	0.91	0.93	1	0.98	0.97	0.91
LH	0.94	0.96	0.98	1	0.99	0.94
Em	0.96	0.98	0.97	0.99	1	0.97
Ws	0.98	0.98	0.91	0.94	0.97	1

S7.2. Echinoderms

The same approach was used to examine the relationships between 1) Misaine Bank and the other 4 NE banks and, 2) Emerald Bank and the other 4 SW banks. In our CCA analysis, these 2 banks appeared separated from their geographic neighbours, which tended to (Fig. 10b).

The correlation matrix of the 5 NE banks (below) indicated that all except Misaine were strongly related. Among Banquereau, Middle, Sable and Western Banks the average correlation was 0.88; whereas, the average value of these four with Misaine was 0.43. Comparing Sable Bank with Misaine we found that there were 2 candidate species that might account for the separation of Misaine from the others, namely Green Sea Urchin and Sea Cucumber (Figure S7.2).

Correlation matrix using all echinoderm species

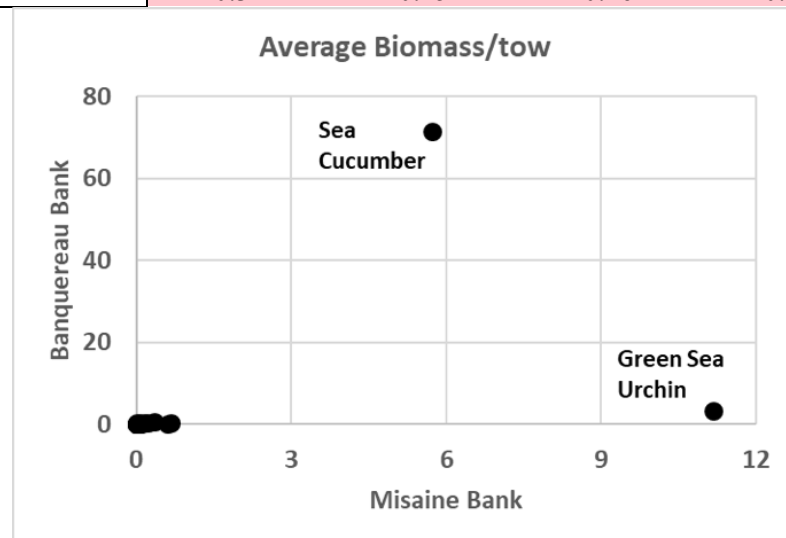|	**Ws**	**Sb**	**Md**	**Bq**	**Mi**
Ws	1	0.88	0.84	0.83	0.34
Sb	0.88	1	0.86	0.86	0.45
Md	0.84	0.86	1	1.00	0.46
Bq	0.83	0.86	1.00	1	0.46
Mi	0.34	0.45	0.46	0.46	1

Figure S7.2. Biomass/tow of echinoderm species from Misaine and Banquereau Banks.

Removing Green Sea Urchin from the species list and recalculating the correlation matrix we found that the average correlation among the 4 clustered banks remained at 0.88, while the value between Misaine and these 4 improved to 0.92. However, if sea cucumber alone were omitted, the average correlation among the 4 banks fell to 0.46 and their correlation with Misaine was also 0.46.

Removing Green sea urchin, the correlation of Misaine bank with the other 4 NE banks increased from 0.43 to 0.92 (see matrix below).

Correlation matrix omitting Green Sea Urchin

	Ws	**Sb**	**Md**	**Bq**	**Mi**
Ws	1	0.89	0.85	0.83	0.82
Sb	0.89	1	0.87	0.86	0.87
Md	0.85	0.87	1	1.00	0.99
Bq	0.83	0.86	1.00	1	0.99
Mi	0.82	0.87	0.99	0.99	1

The strong relationships (average correlation of 0.89) among the echinoderm communities of LaHave, Roseway, Baccaro and Brown's Banks were driven mainly by Sea Cucumber which accounted for on average 56% of the total biomass of these banks. Their average correlations with the Emerald Bank community, where no Sea Cucumber were found, was -0.10. Without this species, none of the banks are strongly related (average r = 0.29; see matrix below).

Correlation matrix using all echinoderm species

	Bw	*Bc*	*Rw*	*LH*	*Em*
Bw	1	0.96	0.84	0.98	-0.11
Bc	0.96	1	0.78	0.97	0.02
Rw	0.84	0.78	1	0.82	-0.20
LH	0.98	0.97	0.82	1	-0.10
Em	-0.11	0.02	-0.20	-0.10	1

S7.3. Mollusks/Cirripedia

Of the 3 taxa, more mollusk/cirripedia species contributed to the bulk of the biomass (9 species accounted for 90%) than for the other two (4 species of crustaceans, 4 of echinoderms). Consequently, the relationships among bank communities were more complex than those for the other 2 taxa where a single species might dominate the correlations among a group of banks.

S7.4. Comparison of CCA results to bank habitat PCA

We found that the bank loadings along the first CCA axis (for crustaceans and mollusks/cirripedia) were strongly and positively correlated with bank loadings along the first PCA axis from our bank habitat PCA analysis (Fig. 5c, main text). The correlation was weak for echinoderms, which is not surprising given the weak association of echinoderm assemblage structure with the NE-SW flow (which dominated the PCA).
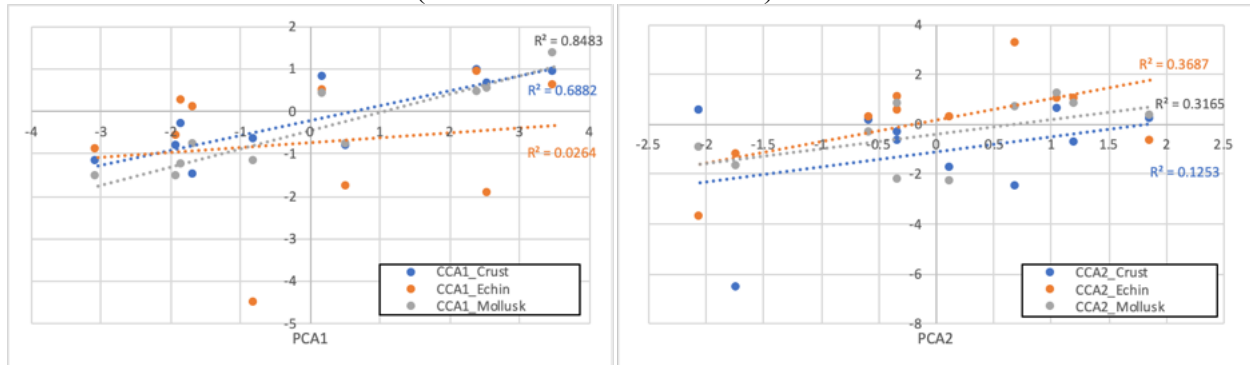

Fig. S7.3. Left: PCA1 along the x-axis shows bank loadings for the first principal component of all the most ecologically significant habitat properties (in Fig. 4, main text), and, along the y-axis, CCA1 loadings for the banks for each taxon (crustaceans (blue), echinoderms (orange), mollusks/cirripedia (blue)); Right: PCA2 along the x-axis, and CCA2 loadings for the banks along the y-axis (same colour-coding as left).

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