

Supplementary material

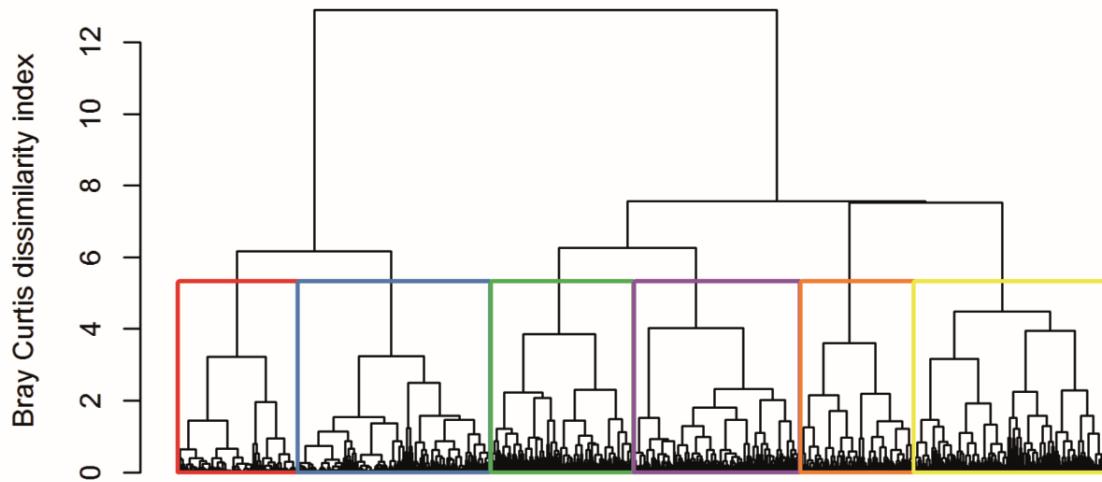


Figure S1: Dendrogram of hierarchical clustering and the cut off level determining the number of clusters/assemblages. Colors of framing is according to fish assemblage 1 to 6; red, blue, green, purple, orange and yellow respectively.

Text S1: Descriptions of community assemblages

Assemblage 1 (Fig. S2) is highly represented in the deeper area on the continental shelf called the “Kangerdlugssuaq Trough” in the North, and more widely spread along the shelf break and on the shelf area further South. Mean depth of 571 ± 164 m is significantly different from all other assemblages except assemblage 4. Mean temperature at $2.3 \pm 1.6^\circ\text{C}$ is significantly different from the other shallow assemblages 4 and 5 and the deep warmer assemblage 6. This is the assemblage with the lowest temperatures which is also reflected in the species composition consisting of highest abundance of cold-water species such as the main indicator *Boreogadus saida*. Other indicators of this group are *Lycodes eudipleurostictus*, *Raja.radiata*, *Artediellus atlanticus*, *Hippoglossoides platessoides*, *Gadus morhua*, *Lycodes reticulatus*, *Leptagonus decagonus*, *Cottunculus microps*, *Careproctus reinhardtii*, *Artediellus uncinatus*, *Lycodes esmarkii*, *Lycodes pallidus* and *Lycodes paamiuti* in ranked order (species response curve in supplementary Figs. 9-14, full species list in table S2).

Stations assigned to assemblage 2 (Fig. S2) are located along the edge and middle continental slope with mean depth of 901 ± 193 and a mean temperature of $2.9 \pm 1.19^\circ\text{C}$. Depth is significantly different from all other assemblages and temperature is significantly different from all except assemblage 1 and 3. Indicator species are *Macrourus berglax*, *Notacanthus chemnitzii*, *Bathyraja spinicauda* and *Gaidropsarus argentatus* in ranked order (species response curve in supplementary fig. 9-14, full species list in table S2).

Assemblage 3 (Fig. S2) is located in the lower parts of the middle continental slope at mean depth of 1298 ± 150 m. This is the deepest assemblage and significantly different from all other assemblages. Temperature is significantly different from assemblage 4, 5 and 6 with mean $2.9 \pm 0.7^\circ\text{C}$. The indicator species are typical deep-water species: *Alepocephalus agassizii*, *Antimora.rostrata*, *Serrivomer beanie*, *Borostomias antarcticus*, *Raja bathyphila*, *Hydrolagus affinis*, *Polyacanthonotus rissoanus*, *Raja hyperborean* *Malacosteus niger*,

Maulisia microlepis, *Dipterus linteus* in ranked order. (species response curve in supplementary fig. 9-14, full species list in table S2).

Assemblage number 4 (Fig. S2) is located at the shallower and warmer waters on the continental shelf and along the ridge and upper parts of the slope. Mean depths are 611 ± 112 m and significantly different from depths of assemblage 2, 3 and 6. Mean temperature is at $4.1 \pm 0.8^\circ\text{C}$ and significantly different from assemblage 1, 2 and 3. The three indicator species of this assemblage are *Argentina silus*, *Brosme brosme* and *Sebastes viviparous* in ranked order (species response curve in supplementary fig. 9-14, full species list in supplementary table 2).

Location of assemblage number 5 (Fig. S2) is in the shallowest areas on the shelf and along the shelf break. Mean depth is 560 ± 114 m and mean temperature is $4.0 \pm 0.7^\circ\text{C}$. Depth is significantly different from all assemblages except 6, and temperature is significantly different from assemblage 1, 2 and 3. Indicator species of the assemblage is; *Sebastes mentella*, *Sebastes marinus*, *Molva dipterygius*, *Raja fyllae*, *Anarhichas denticulatus*, *Anarhichas minor*, *Anarhichas lupus*, *Lycodes vahlii*, *Glyptocephalus cynoglossus*, *Myxine glutinosa*, and *Hippoglossus hippoglossus* in ranked order (species response curve in supplementary fig. 9-14, full species list in table S2).

Assemblage number 6 is mainly located in the middle slope (Fig. S2). The depth range of this group is wide with mean 1071 ± 234 m being significantly different from all other assemblages. Temperature range is a bit lower than within assemblage 4 and 5 and significantly different from assemblage 1, 2 and 3. Mean temperature is $3.6 \pm 0.9^\circ\text{C}$. Indicator species are *Coryphaenoides rupestris*, *Reinhardtius hippoglossoides*, *Synapobranchus kaupi*, *Trachyrhynchus murrayi*, *Coryphaenoides guentheri*, *Centroscyllium fabricii*, *Lepidion eques*, *Notoscopelus kroeyeri*, *Aphanopus carbo*, *Alepocephalus bairdii* and *Rouleina maderensis* in ranked order (species response curve in supplementary Figs. 9-14, full species list in table S2).

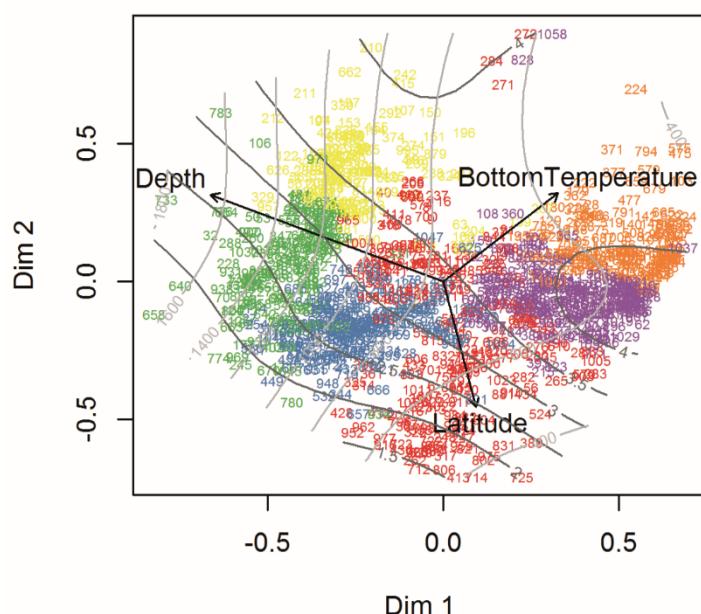


Figure S2: Non-metric multidimensional scaling (nMDS) plot of sites. Environmental variables are interpolated onto the ordination. Isolines represent depth (light grey) and bottom temperature (trawl temperature observations (TTOs)) (dark grey). Colors represent assemblages 1 to 6; red, blue, green, purple, orange and yellow respectively.

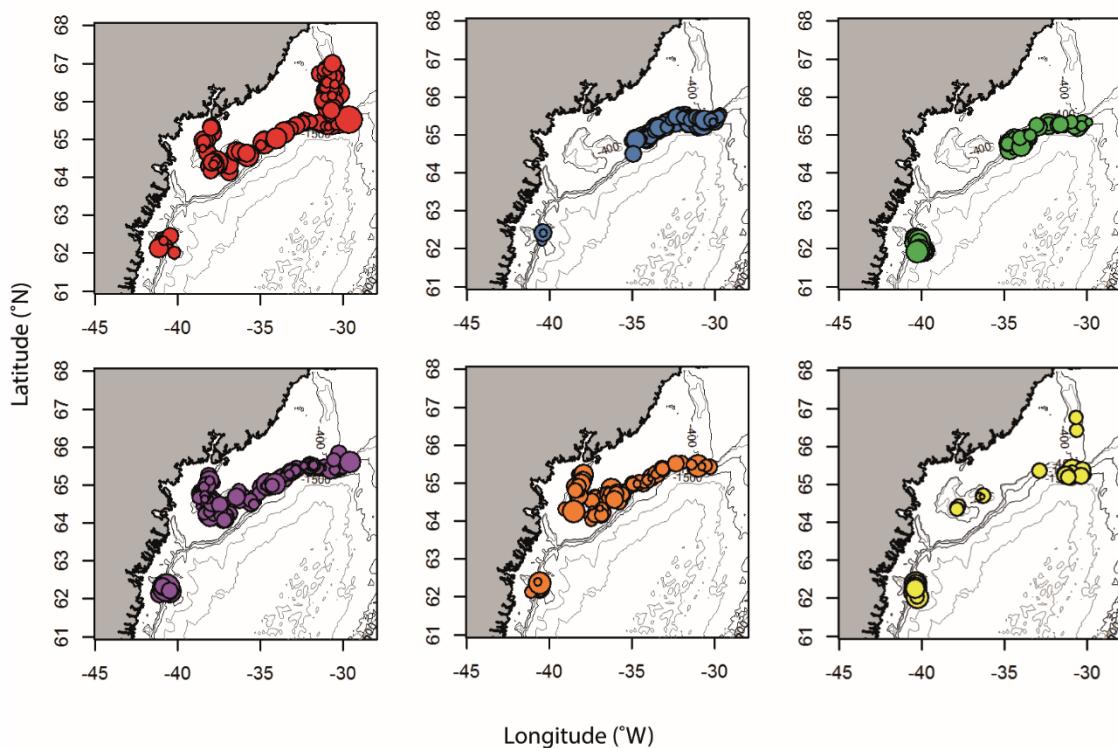


Figure S3: Maps of plotted sites according to assemblage affiliation Assemblages 1 to 6; red, blue, green, purple, orange and yellow respectively. Size of points are proportional to species richness at the site.

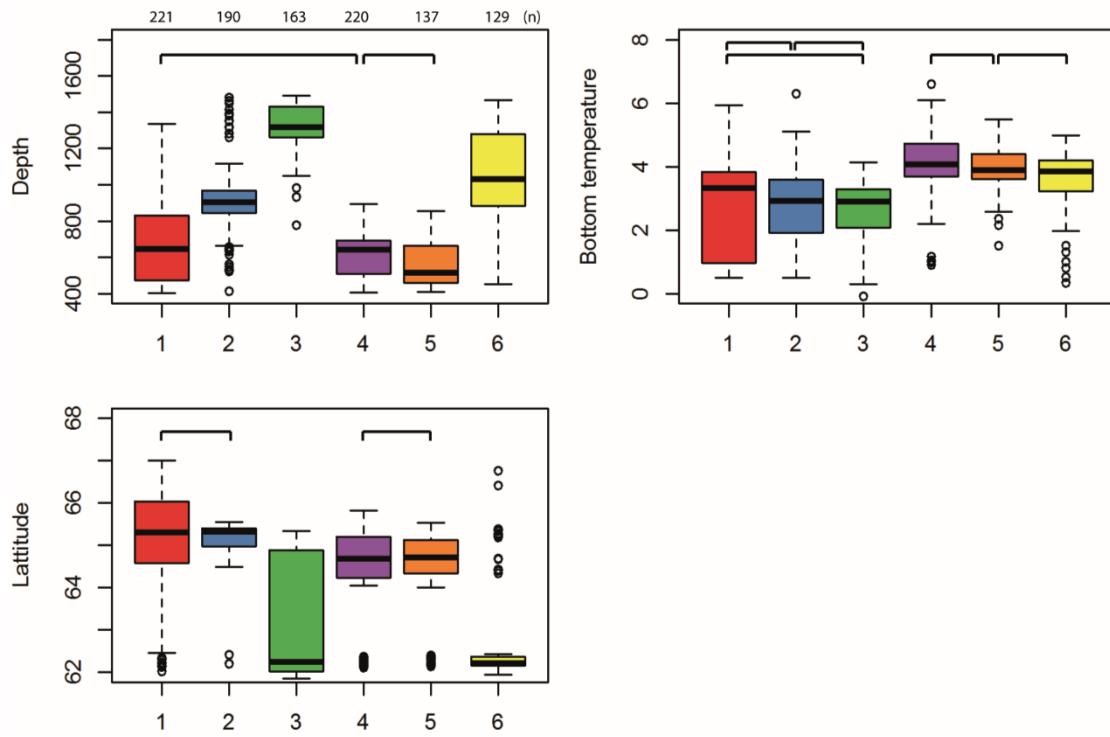


Figure S4: Box plots of depth-, Bottom temperature (trawl temperature observations (TTOs)- and latitude ranges within assemblages 1 to 6; red, blue, green, purple, orange and yellow respectively. Connecting lines above boxes indicate non-significant difference. All other assemblages are significantly different at p-value < 0.001 (Table S2). Numbers above the boxplot represents number of samples/sites for each assemblage.

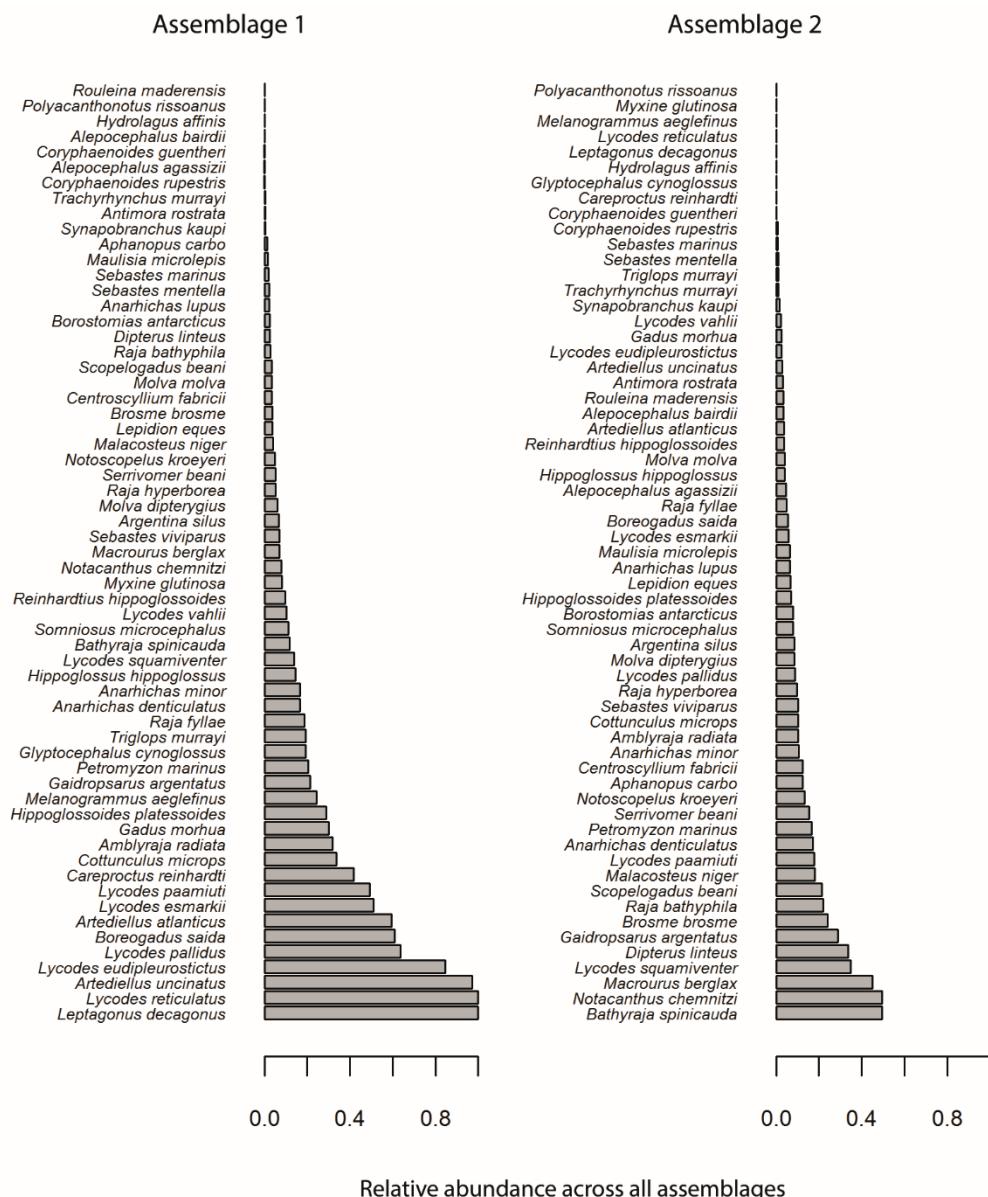


Figure S5: Species relative in assemblage 1 and 2 (relative abundance is calculated across all assemblages).

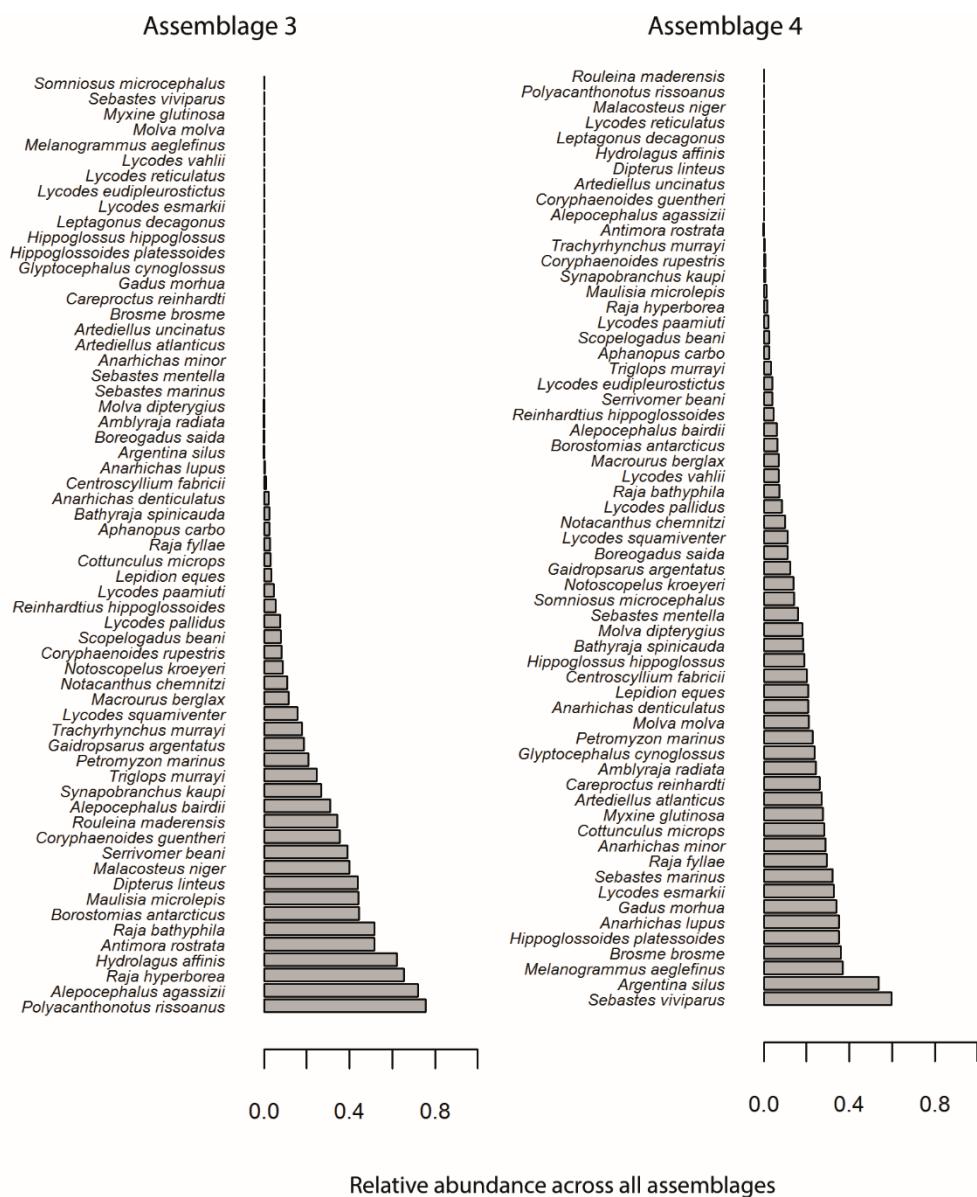


Figure S6: Species relative in assemblage 3 and 4 (relative abundance is calculated across all assemblages).

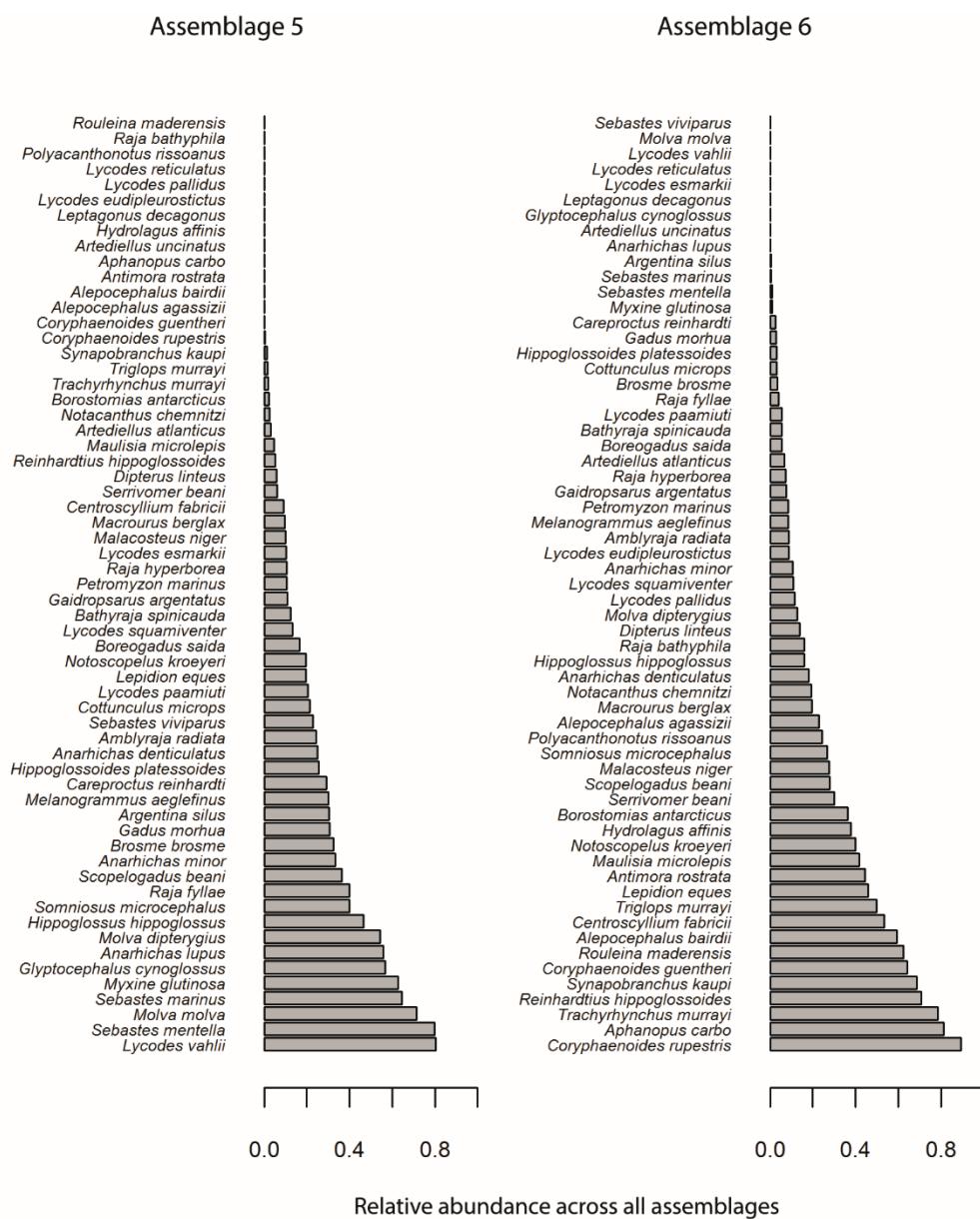


Figure S7: Species relative abundance in assemblage 5 and 6 (relative abundance is calculated across all assemblages).

Table S1: Species list with relative abundance of each species in each assemblage (1-6) Bold numbers marks significant indicator species (species with significant probability of obtaining as high an indicator values as observed over the specified iterations).

Species	Relative abundance in clusters/assemblages					
	1	2	3	4	5	6
<i>Alepocephalus agassizii</i>	0.002	0.046	0.720	0.001	0.000	0.230
<i>Alepocephalus bairdii</i>	0.000	0.035	0.309	0.062	0.000	0.595
<i>Anarhichas denticulatusS</i>	0.166	0.171	0.023	0.209	0.249	0.181
<i>Anarhichas lupus</i>	0.022	0.066	0.003	0.351	0.558	0.000
<i>Anarhichas minor</i>	0.166	0.107	0.000	0.288	0.333	0.107
<i>Antimora rostrata</i>	0.004	0.033	0.516	0.002	0.000	0.445
<i>Aphanopus carbo</i>	0.013	0.123	0.025	0.027	0.000	0.812
<i>Argentina silus</i>	0.067	0.084	0.003	0.536	0.305	0.005
<i>Artediellus atlanticus</i>	0.593	0.036	0.000	0.271	0.031	0.068
<i>Artediellus uncinatus</i>	0.971	0.029	0.000	0.000	0.000	0.000
<i>Bathyraja spinicauda</i>	0.118	0.495	0.024	0.184	0.124	0.055
<i>Boreogadus saida</i>	0.609	0.054	0.003	0.112	0.166	0.056
<i>Borostomias antarcticus</i>	0.024	0.079	0.443	0.066	0.023	0.365
<i>Brosme brosme</i>	0.037	0.242	0.000	0.361	0.325	0.035
<i>Careproctus reinhardti</i>	0.418	0.000	0.000	0.262	0.293	0.026
<i>Centroscyllium fabricii</i>	0.035	0.123	0.012	0.202	0.093	0.536
<i>Coryphaenoides guentheri</i>	0.002	0.001	0.355	0.000	0.001	0.641
<i>Coryphaenoides rupestris</i>	0.003	0.008	0.084	0.007	0.006	0.894
<i>Cottunculus microps</i>	0.335	0.104	0.032	0.282	0.214	0.032
<i>Dipterus linteus</i>	0.027	0.338	0.439	0.000	0.057	0.139

<i>Gadus morhua</i>	0.302	0.024	0.000	0.340	0.306	0.027
<i>Gaidropsarus argentatus</i>	0.214	0.290	0.186	0.124	0.109	0.077
<i>Glyptocephalus cynoglossus</i>	0.194	0.000	0.000	0.237	0.568	0.000
<i>Hippoglossoides platessoides</i>	0.290	0.071	0.000	0.352	0.256	0.031
<i>Hippoglossus hippoglossus</i>	0.145	0.040	0.000	0.189	0.465	0.162
<i>Hydrolagus affinis</i>	0.000	0.000	0.622	0.000	0.000	0.378
<i>Lepidion eques</i>	0.037	0.066	0.034	0.209	0.195	0.459
<i>Leptagonus decagonus</i>	1.000	0.000	0.000	0.000	0.000	0.000
<i>Lycodes esmarkii</i>	0.511	0.058	0.000	0.327	0.104	0.000
<i>Lycodes eudipleurostictus</i>	0.847	0.025	0.000	0.039	0.000	0.090
<i>Lycodes paamiuti</i>	0.494	0.178	0.045	0.023	0.205	0.054
<i>Lycodes pallidus</i>	0.636	0.088	0.078	0.085	0.000	0.114
<i>Lycodes reticulatus</i>	1.000	0.000	0.000	0.000	0.000	0.000
<i>Lycodes squamiventer</i>	0.139	0.348	0.159	0.111	0.135	0.108
<i>Lycodes vahlii</i>	0.104	0.022	0.000	0.071	0.803	0.000
<i>Macrourus berglax</i>	0.071	0.449	0.116	0.069	0.099	0.195
<i>Malacosteus niger</i>	0.042	0.180	0.401	0.000	0.101	0.276
<i>Maulisia microlepis</i>	0.016	0.065	0.441	0.014	0.045	0.419
<i>Melanogrammus aeglefinus</i>	0.244	0.000	0.000	0.369	0.302	0.084
<i>Molva dipterygius</i>	0.060	0.086	0.002	0.180	0.545	0.127
<i>Molva molva</i>	0.034	0.039	0.000	0.211	0.715	0.000
<i>Myxine glutinosa</i>	0.082	0.000	0.000	0.278	0.628	0.011
<i>Notacanthus chemnitzii</i>	0.080	0.494	0.108	0.100	0.024	0.194
<i>Notoscopelus kroeyeri</i>	0.049	0.132	0.088	0.138	0.195	0.398
<i>Petromyzon marinus</i>	0.206	0.165	0.209	0.229	0.107	0.084

<i>Polyacanthonotus rissoanus</i>	0.000	0.000	0.755	0.000	0.000	0.245
<i>Raja bathyphila</i>	0.028	0.221	0.516	0.075	0.000	0.160
<i>Raja fyllae</i>	0.186	0.050	0.028	0.296	0.399	0.041
<i>Raja hyperborea</i>	0.052	0.097	0.653	0.017	0.106	0.074
<i>Amblyraja radiata</i>	0.319	0.104	0.002	0.243	0.244	0.087
<i>Reinhardtius hippoglossoides</i>	0.098	0.038	0.057	0.047	0.052	0.708
<i>Rouleina maderensis</i>	0.000	0.034	0.342	0.000	0.000	0.624
<i>Scopelogadus beani</i>	0.034	0.216	0.081	0.025	0.365	0.280
<i>Sebastes marinus</i>	0.018	0.009	0.001	0.321	0.647	0.005
<i>Sebastes mentella</i>	0.021	0.009	0.001	0.161	0.799	0.009
<i>Sebastes viviparus</i>	0.070	0.103	0.000	0.598	0.229	0.000
<i>Serrivomer beani</i>	0.052	0.155	0.389	0.040	0.063	0.301
<i>Somniosus microcephalus</i>	0.112	0.080	0.000	0.141	0.399	0.267
<i>Synapobranchus kaupi</i>	0.006	0.018	0.269	0.007	0.014	0.686
<i>Trachyrhynchus murrayi</i>	0.003	0.012	0.177	0.003	0.019	0.786
<i>Triglops murrayi</i>	0.194	0.010	0.248	0.035	0.016	0.498

Table S2: Results from ANOVA analysis followed by a TukeyHSD testing for significant differences between groups in depth. Bottom temperature (trawl temperature observations (TTOs)) and latitude.

Depth

Assemblages	Difference in test scores	Lower diff. Conf. Int. 95%	Upper diff. Conf. Int. 95%	p-value
"4-5"	50.923	-0.489	102.335	0.0539
"1-5"	89.249	37.837	140.661	0.0000
"2-5"	348.484	294.878	402.090	0.0000
"6-5"	511.136	453.131	569.141	0.0000
"3-5"	738.004	683.862	792.147	0.0000
"1-4"	38.326	-6.652	83.304	0.1459

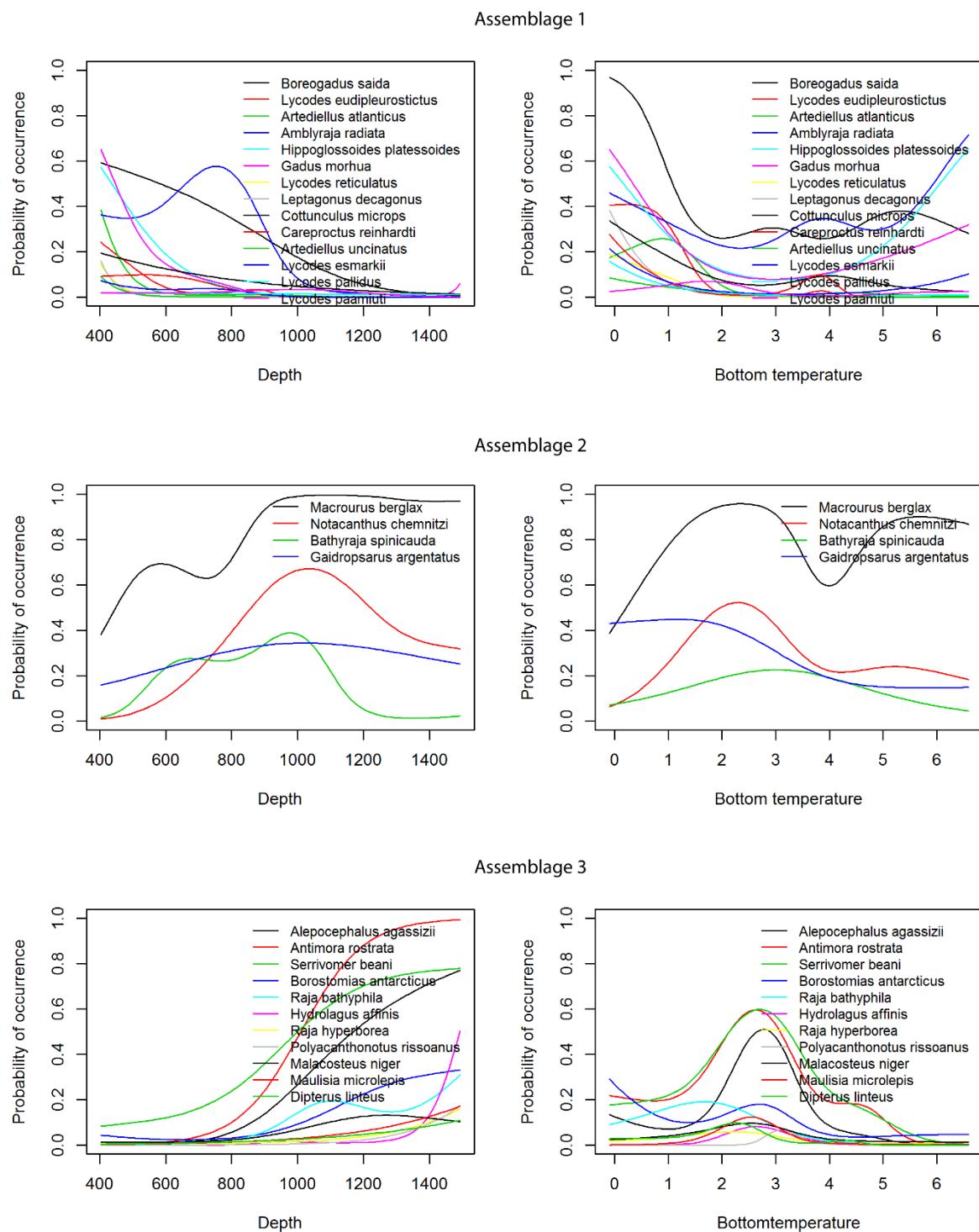
"2-4"	297.561	250.091	345.031	0.0000
"6-4"	460.213	407.826	512.600	0.0000
"3-4"	687.081	639.007	735.156	0.0000
"2-1"	259.235	211.765	306.706	0.0000
"6-1"	421.887	369.500	474.274	0.0000
"3-1"	648.755	600.681	696.830	0.0000
"6-2"	162.652	108.110	217.194	0.0000
"3-2"	389.520	339.106	439.934	0.0000
"3-6"	226.868	171.799	281.937	0.0000

Latitude

Assemblages	Difference in test scores	Lower diff. Conf. Int. 95%	Upper diff. Conf. Int. 95%	p-value
"3-6"	0.691	0.327	1.055	0.0000
"4-6"	1.633	1.287	1.980	0.0000
"5-6"	1.774	1.391	2.158	0.0000
"2-6"	2.474	2.113	2.834	0.0000
"1-6"	2.474	2.128	2.821	0.0000
"4-3"	0.943	0.625	1.261	0.0000
"5-3"	1.083	0.725	1.441	0.0000
"2-3"	1.783	1.449	2.116	0.0000
"1-3"	1.783	1.465	2.101	0.0000
"5-4"	0.141	-0.199	0.481	0.8456
"2-4"	0.840	0.526	1.154	0.0000
"1-4"	0.841	0.543	1.138	0.0000
"2-5"	0.699	0.345	1.054	0.0000
"1-5"	0.700	0.360	1.040	0.0000
"1-2"	0.001	-0.313	0.315	1.0000

Bottom temperature (trawl temperature observations (TTOs))

Assemblages	Difference in test scores	Lower diff. Conf. Int. 95%	Upper diff. Conf. Int. 95%	p-value
"1-3"	0.042	-0.263	0.347	0.9987
"2-3"	0.107	-0.213	0.426	0.9329
"6-3"	0.981	0.632	1.331	0.0000
"5-3"	1.298	0.955	1.642	0.0000
"4-3"	1.470	1.165	1.775	0.0000
"2-1"	0.064	-0.237	0.365	0.9905
"6-1"	0.939	0.607	1.271	0.0000
"5-1"	1.256	0.930	1.582	0.0000
"4-1"	1.427	1.142	1.713	0.0000
"6-2"	0.875	0.529	1.221	0.0000
"5-2"	1.192	0.852	1.532	0.0000
"4-2"	1.363	1.062	1.664	0.0000
"5-6"	0.317	-0.051	0.685	0.1377
"4-6"	0.488	0.156	0.821	0.0004
"4-5"	0.171	-0.155	0.498	0.6641



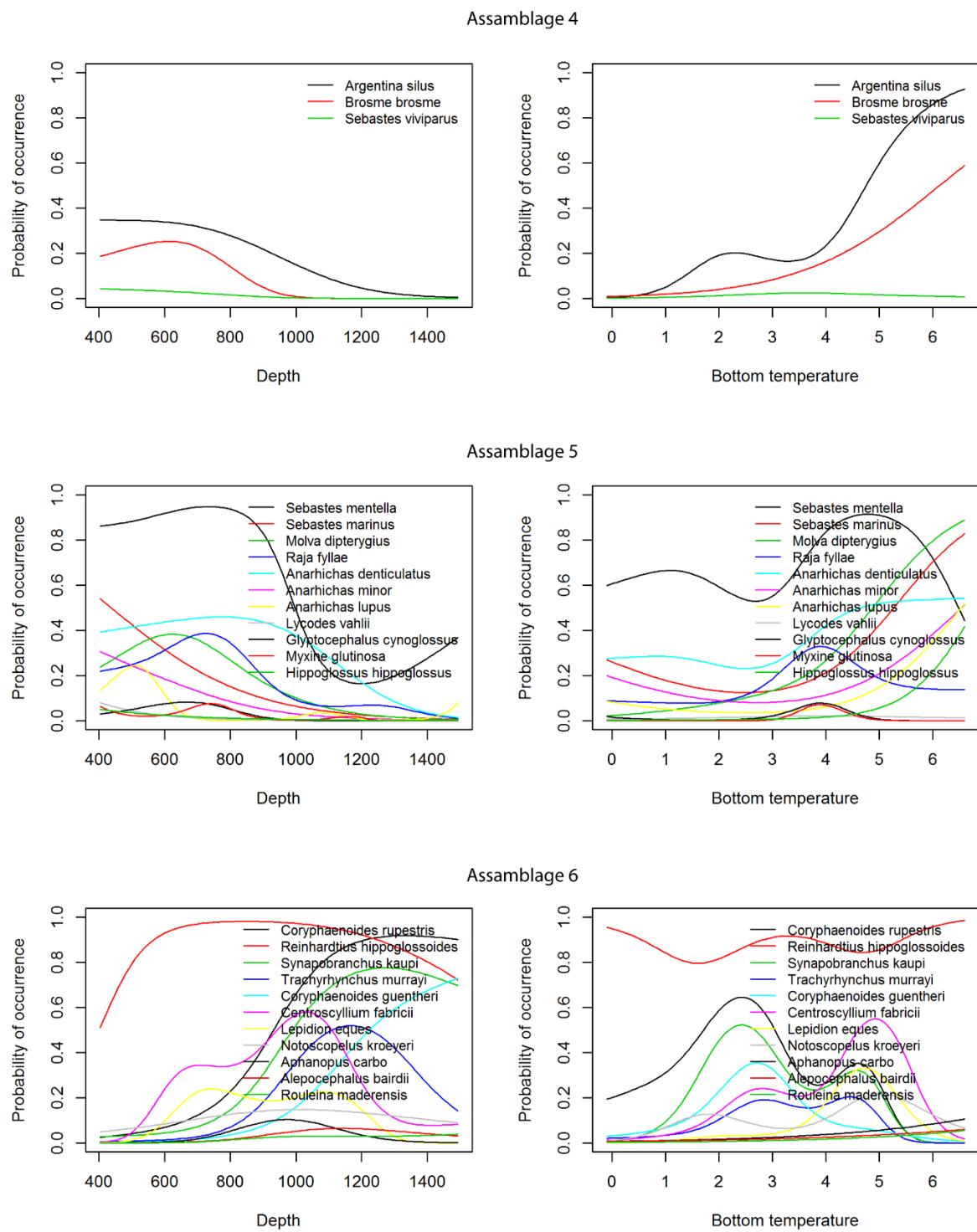


Figure S8: Species response curves of indicator species of each assemblage along the depth- and bottom temperature gradients (trawl temperature observations” (TTOs). Response curves are based on Generalized additive models (GAMs) with integrated smoothness estimation using the “goevec” package in r.

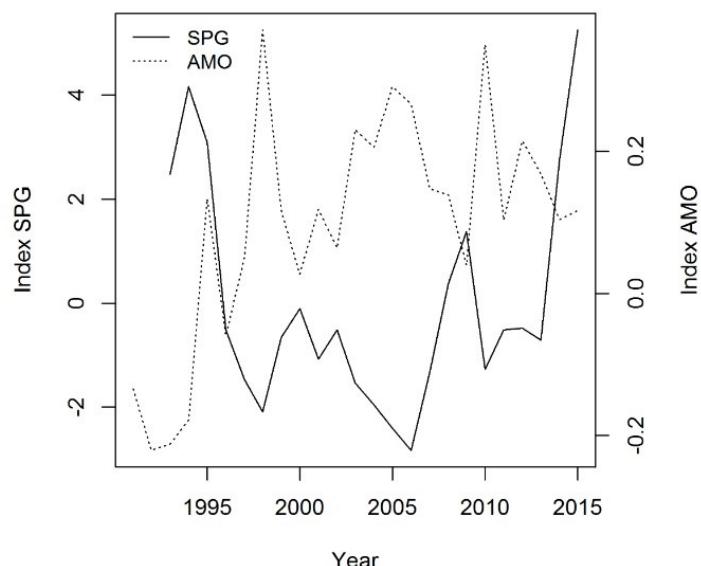


Figure S9: The Subpolar Gyre (SPG) index (solid line) and the Atlantic Multidecadal Oscillation (AMO) index (dashed line) over the study period.

Table S3: Output of Generalized Linear Model: AHOI bottom temperature as function of time (year) including an interaction term between Year (time) and Strata.

AHOI bottom temperature ~ Year + Year*Strata ~ N(0σ²)						
Predictors	Region North			Region South		
	Estimat es	CI	p	Estimat es	CI	p
(Intercept)	3.73	3.65 – 3.81	<0.001	4.64	4.59 – 4.69	<0.001
Year	0.01	0.00 – 0.01	0.034	0.02	0.02 – 0.03	<0.001
Stratum 800-1000m	-0.94	-1.05 – -0.82	<0.001	-0.49	-0.56 – -0.42	<0.001
Stratum 1000-1500m	-1.96	-2.07 – -1.84	<0.001	-1.57	-1.65 – -1.50	<0.001
Year:Stratum 800-1000m	0.00	-0.01 – 0.01	0.649	0.00	-0.00 – 0.01	0.676
Year:Stratum 1000-1500m	0.01	-0.00 – 0.01	0.315	0.00	-0.00 – 0.01	0.232
Observations	54			54		
Cox & Snell's R² / Nagelkerke's R²	0.456 / 0.993			0.347 / 0.996		

Table S4: Output of Generalized Linear Model of species richness as function of time (year) including an interaction term between strata and time (year) and the covariates latitude and longitude.

Species richness ~ Year*Strata + Longitude + Latitude ~ Poisson(λ)						
<i>Predictors</i>	Region North			Region South		
	<i>Estimate_s</i>	<i>CI</i>	<i>p</i>	<i>Estimat_{es}</i>	<i>CI</i>	<i>p</i>
(Intercept)	15.42	-3.50 – 34.35	0.110	2.22	-18.20 – 22.65	0.831
Year	-0.02	-0.02 – -0.01	0.001	-0.01	-0.03 – 0.00	0.060
Stratum 800-1000m	-0.11	-0.27 – 0.04	0.152	0.36	0.09 – 0.63	0.008
Stratum 1000-1500m	-0.43	-0.59 – -0.27	< 0.001	0.01	-0.20 – 0.23	0.913
Latitude	-0.21	-0.48 – 0.06	0.133	0.08	-0.28 – 0.45	0.655
Longitude	0.02	-0.02 – 0.06	0.276	-0.12	-0.36 – 0.11	0.300
Year:Stratum 800-1000m	-0.00	-0.02 – 0.01	0.634	-0.01	-0.03 – 0.01	0.371
Year:Stratum 1000-1500m	0.02	0.00 – 0.03	0.027	0.01	-0.01 – 0.02	0.547
Observations	408			281		
Cox & Snell's R ² / Nagelkerke's R ²	0.184 / 0.339			0.141 / 0.284		

Table S5: Output of Generalized Linear Model: Total species abundance as function of time (year) including an interaction term between strata and time (year) and the covariates latitude and longitude. Abundance data of region North and -South displayed different distribution and so the gamma- with log-link and the normal distribution was used in the models respectively.

Total species abundance ~ Year*Strata + Longitude + Latitude ~ gamma(c. λ)/ N(0σ²)						
<i>Predictors</i>	Region North			Region South		
	<i>Estimates</i>	<i>CI</i>	<i>p</i>	<i>Estimates</i>	<i>CI</i>	<i>p</i>
(Intercept)	19.21	-9.92 – 48.35	0.197	-45.41	-82.71 – -8.10	0.018
Year	-0.02	-0.03 – -0.00	0.025	-0.03	-0.05 – -0.01	0.014
Stratum 800-1000m	-0.69	-0.94 – -0.43	<0.001	1.30	0.78 – 1.82	<0.001
Stratum 1000-1500m	-1.03	-1.28 – -0.78	<0.001	0.62	0.24 – 1.01	0.002
Latitude	-0.24	-0.66 – -0.18	0.258	0.49	-0.18 – 1.16	0.151
Longitude	-0.09	-0.15 – -0.02	0.006	0.41	-0.01 – 0.83	0.054
Year:Stratum 800-1000m	0.01	-0.01 – 0.03	0.342	-0.05	-0.10 – -0.01	0.012
Year:Stratum 1000-1500m	0.01	-0.01 – 0.03	0.219	-0.02	-0.05 – 0.01	0.131
Observations	408			281		
Cox & Snell's R ² / Nagelkerke's R ²	0.121 / 0.415			0.129 / 0.357		

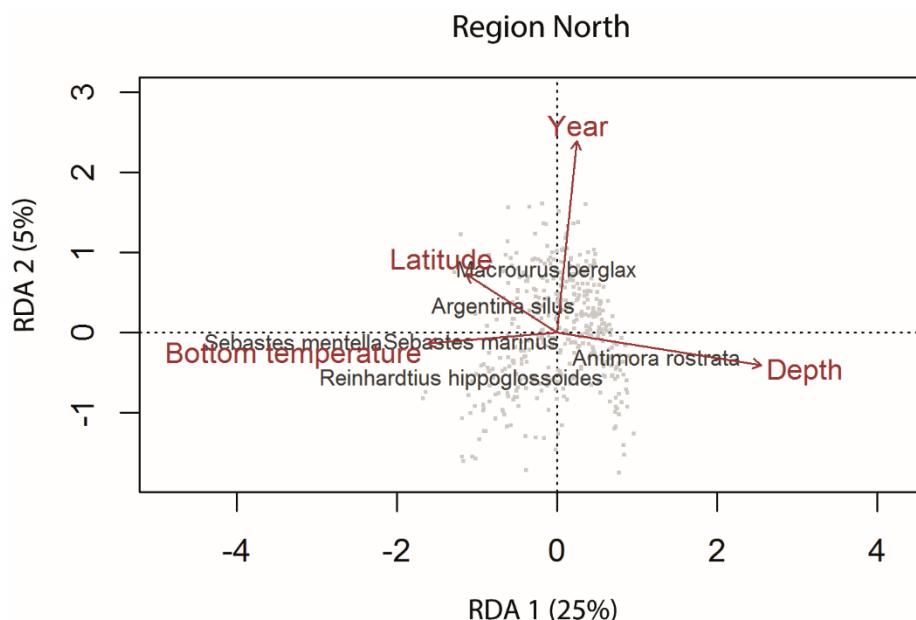


Figure S10: Redundancy analysis (RDA) triplot showing the samples (grey dots), species (black labels) and explanatory variables (red labels) of region North.

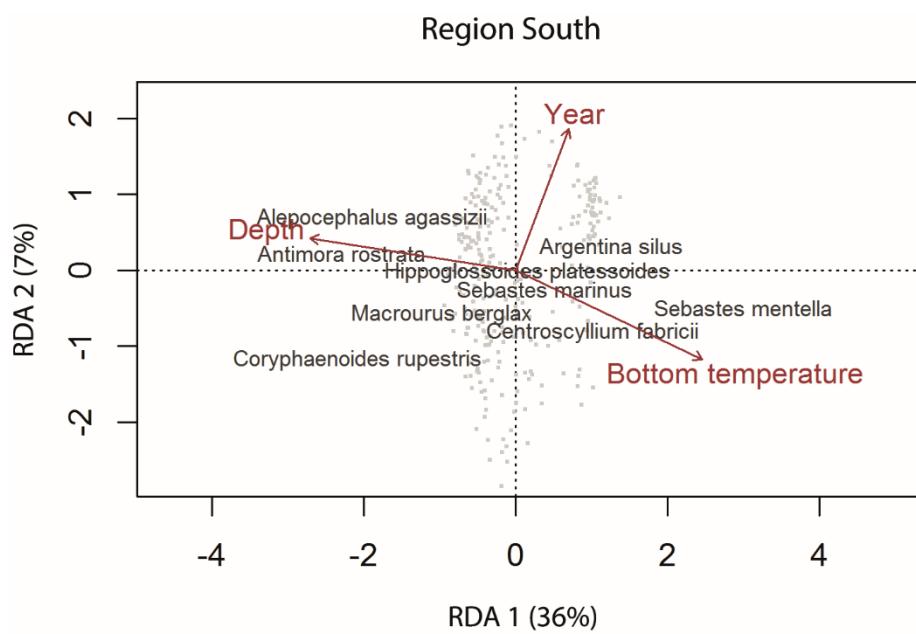


Figure S11: Redundancy analysis (RDA) triplot showing the samples (grey dots), species (black labels) and explanatory variables (red labels) of region South.

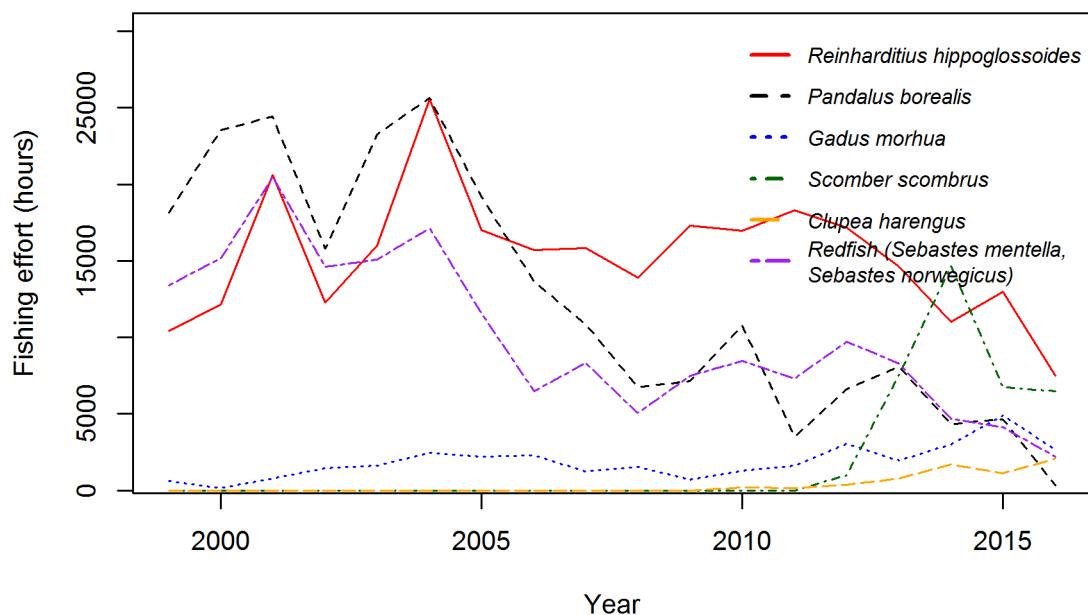


Figure S12: Fishing effort (hours) of commercial species in ICES area 14b.