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Salmon aquaculture waste effects on the distribution of epibenthic invertebrates and demersal fish and subsequent impacts on Atlantic cod dietary items

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Abstract

Open-cage fish farms are common structures in coastal waters and are known to attract wild fish. Environmental impacts from the farming of Atlantic salmon, *Salmo salar*, create concerns related to further growth of the industry. Uneaten feed pellets and faeces that are discharged from the farms leads to changes in the environments under and around the farm facilities. Sedimentation due to farm enrichment affects the organisms living on and within the sediments. This study characterizes the benthic epifaunal invertebrate and the demersal fish communities in relation to the distance from a fish farm in a fjord with hard and mixed bottom substrates in Northern Norway. A towed underwater video system was used to quantitatively assess the densities of epibenthic fauna and demersal fish species along 9 transects near the farm and 8 reference transects at greater distance to the farm. This study found that salmon aquaculture had moderate effects on the epifaunal invertebrate and demersal fish community composition in the fjord. An aggregation of flatfish species, that are known to feed on infaunal polychaetes, was observed within 500 m of the farm, where opportunistic polychaetae accumulations are abundant due to organic farm waste. Data on the diet of coastal Atlantic cod, *Gadus morhua,* caught in the same fjord, was used to compare the distribution of dietary items of cod observed in the video transects to the diet of cod caught 0-50 m from the farm and over 2 km from the farm. There was no strong overlap between the diet of cod caught in the area and the epifauna observed, but there was an interesting pattern in epifaunal distribution of the Atlantic cod dietary items. Blue mussel, *Mytilus edilus*, urchin, *Echinoidea*, crabs of the family *Lithodidae,* American plaice, *H. platessoides,* and the tunicates and sea squirts of the class *Ascidians,* all changed in their distribution along the enrichment gradient from the farm, and were all found to be attracted to the area within 500 m from of the farm. Further research needs to be done across trophic levels to understand the implications for the benthic epifaunal invertebrates and wild gadoids from salmon aquaculture.

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Abbreviations

ANOSIM – Analysis of Similarities

AICc- corrected

CAP- Analysis of principal coordinates

DistLM- Distance-based linear model

eDNA- Environmental Deoxyribonucleic Acid

EEM- Estimated marginal means

FAD- Fish aggregation device

FAO- Food and Agriculture Organization

FD- Directorate of Fisheries

GLM- Generalized linear model

GPS- Global Positioning System

IMR – Institute of Marine Research

IOE- Indicator of organic enrichment

OPC- opportunistic polychaeta complex

PERMANOVA- permutational multivariate analysis of variance

SIMPER – Similarity Percentages

TLS- Traffic light system

TPM- Total particulate material

UVS- Underwater video system

1 Introduction

1.1 Finfish aquaculture globally

The total aquaculture fish production in the world reached 82,1 million tons in 2018. This production was dominated by finfish (54 million tons), of which 7,3 million tons of fish were from marine and coastal aquaculture (FAO, 2020). The open-cage farming of Atlantic salmon (*Salmo salar*) has been a successful industry and over the past 40 years the growth has been substantial. Due to developments in cage structure, advances in knowledge about breeding, fish health, fish nutrition and a better feed efficiency, farming of fed species like the Atlantic salmon have helped the industry to work more efficiently and expand (Watson et al., 2022). Just a small number of regions in the world have the right conditions in sheltered fjords in temperate climates for open-cage Atlantic salmon farming. Scotland, Chile, Canada and Norway have dominated the industry but production also takes place in the Faroe Islands, Iceland, Ireland, Australia, and New Zealand (Martin et al., 2021).

1.2 Finfish aquaculture in Norway

The salmon farming industry in Norway has been growing rapidly since the 1980s, and until 2012 the production levels continually increased. However, after 2012 the production levels have been more or less stable and the production strategy has changed. Stagnation caused by the increased problems with salmon lice (*Lepeophtheirus salmonis)* led to the development of a new management regime (Fauchald, 2020). Today the production of fin fish is focused at larger production sites, and the sites are changed from being placed in shallow and shielded areas near land to being detached in frame moorings in more exposed areas (Holmer, 2010; Lader et al., 2017; Lekang et al., 2016). These changes have solved problems regarding water exchange but today the biomass in some fjords with aquaculture activity has caused concern as to whether the potential negative impact might be high (Watson et al., 2022).

In Norway, there are strict technical and environmental requirements for the installations and operations of fin fish farms, plus requirements for fish health and distance between sites (Norwegian standard NS-9410, 2016). Although much research has been conducted into the effects that occur in the soft sediments that predominant under most fish farms (Henderson & Ross, 1995; Kalantzi & Karakassis, 2006), very little has been conducted on the benthic epifauna that inhabitant the surface of a diverse range of seabed types that can be found near to farms. These same species may represent important habitat and potentially food sources for commercial fish species. Despite these measures, the surrounding environment including many wild marine species are still impacted. More knowledge regarding if and how salmon farming affects wild fish stocks, especially those important for coastal fisheries will be important for the development of a sustainable coexistence between the different stakeholders in the coastal region.

1.3 Finfish aquaculture in Northern Norway

In 2021, the Norwegian government presented its aquaculture strategy (Fiskeridepartementet, 2021). The goal of the strategy is to facilitate new sustainable growth for the Norwegian aquaculture industry. Much of this new growth is projected to take place in Northern Norway where there is still space available, unlike further south where less space remains for expansion (Dunlop et al., 2020). The cold-water conditions in Northern Norway are good for open-cage salmon farming. Warmer waters along the Norwegian coast due to global warming provides possibilities for farming of new species, but also provides challenges for existing production. The salmon farming industry is at risk of needing to limit production because of increasing water temperatures, more extreme weather events, changes in precipitation patterns and sea level rise (Handisyde et al., 2017).

1.4 Environmental effects of finfish aquaculture on the coastal ecosystem

With increased aquaculture production comes an increased impact on the marine environment surrounding the fish farms (Carroll et al., 2003; Uglem et al., 2014). As farmed fish in Norway are mainly raised in open sea cages, organic particles from feed and faeces are constantly discharged directly into the environment around the cages. Although the effects can be severe and acute at sheltered low flow locations, at current exposed farm sites, the risk of a significant environmental effects from dissolved nutrients is rated to low in all production aeras in Norway (Grefsrud et al., 2021). The main effects on the seabed under and around fish farms result from fecal particles and uneaten feed pellets (Brooks et al., 2002; Hargrave et al., 1997; Keeley et al., 2019). The farm waste is often easily degradable compounds and fully recovery of the seabed from waste impacts is expected to take several years (Keeley et al., 2019). The total emissions follow the farm production cycle, often with the highest emissions during the summer months when the growth is greatest. Due to lower temperatures the greatest growth of farmed salmon in northern Norway most often occurs during autumn. Emissions also increase late in the production cycle when the total biomass is increased (Sæther et al., 2013). The impacts on the benthic communities from aquaculture enrichment cannot be generalized for all substrate types. The impact degree depends on the local environmental conditions, such as current speed and direction at the different aquaculture sites and the loading of organic matter (Carroll et al., 2003).

As mentioned earlier the production sites today are relocated from sheltered locations to high current and more exposed areas. The sheltered areas are often categorized by soft bottom habitats, while the exposed high current sites often are categorized by mixed or hard bottom substrates (Dunlop et al., 2021; Hamoutene et al., 2016; Keeley et al., 2020). For soft bottom thresholds have been established on the presence of different benthic species for monitoring the degree of impact from particle emissions. Quantitative surveys of benthic species is a major part of these obligatory monitoring inspections (B- and C-surveys) (Directorate of Fisheries, 2022). As the amounts of organic emissions increases, the soft bottom benthic community will change, and can in worst case disappear (Hamoutene et al., 2018). Changes in soft benthic communities are used to set different thresholds of impact. The condition thresholds used in the assessment are “very good”, “good”, “moderate”, “bad”, and “very bad” depending on how big the changes in the benthic community are. Based on current knowledge and monitoring methods the state of the soft bottom fish farms is rated to be generally good across production areas (Grefsrud et al., 2021).

Hard and mixed bottom communities consist of organisms that are stuck on the sediments or live on surfaces where it is not possible to dig down (Wahl, 2009). These organisms are often suspension feeders like bryozoans, sponges and corals (Dunlop et al., 2020; Dunlop et al., 2021), that feed on materials like phytoplankton that can be highly diluted in the water (Gili & Coma, 1998). Suspension feeders and other sessile organisms are vulnerable to environmental changes (Sutherland et al., 2018). Sedimentation due to aquaculture production leads to changes in the diluted materials in the water and affects the suspension feeders (Laroche et al., 2021). Currently there are no standardized environmental monitoring with established thresholds for hard and mixed bottom. Based on this knowledge the state of environmental effects on solid bottom is rated to moderate (Grefsrud et al., 2021).

1.5 Monitoring methods

Since the aquaculture legislation was established in 2005 fish farmers are obliged to monitor how emissions from their fish farm affect the environment under and around the sea cages. The interaction between production, environmental monitoring and fallowing is important to minimize environmental impact and facilitate long-term good economic operations. Monitoring the seabed conditions gives an opportunity to introduce measures to fish farms where the environmental effects are unacceptable (Directorate of Fisheries, 2022) Monitoring the bottom conditions will ensure that the balance is maintained and that deviations are discovered. The basis for granting permission for the location of farms are improving due to current surveys, grab samples and mapping of the topographical bottom conditions. This knowledge base also ensures that the Directorate of Fisheries (DF) to a greater extent can allocate sites that can withstand today’s production.

The monitoring inspections are implemented in fixed frequencies based on the results from the last monitoring and are done according to Norwegian standard NS-9410 (2016). The B-survey inspection is a soft bottom inspection that is done with a handheld grab and the sediment sample is taken right under the sea cage. The C-survey inspection is a more comprehensive soft bottom inspection. The state of the seabed from the fish farm to the transition zone is measured, with the purpose of finding the extent of the impact from the fish farm (Norwegian standard NS-9410, 2016). Soft bottom monitoring is different from hard or mixed bottom monitoring as grab sampling is impossible to implement.

1.6 Visual based surveys for finfish aquaculture monitoring

Many fish farms in Norway are localized over steep bottoms consisting of solid rock, or mixed substrates, such as gravels, boulders mixed with sand and mud (Dunlop et al., 2020). B- and C-surveys are not developed for these bottom conditions where grab samples are challenging to take. According to Norwegian standard NS-9410:2016 search for representative larger soft bottom areas suitable for C-surveys near the hard bottom should be undertaken. If there are no such areas suitable for C-surveys, the government should be consulted. Organic and inorganic waste released from aquaculture that deposit at the seafloor may be used as visual indicators for aquaculture impact. Institute of Marine Research (IMR) and the DF are currently developing a guide for monitoring hard and mixed bottom around marine fish farms. The alternative method is a visual based survey where a camera is attached to a tripod and lowered down at the same stations and in the same way as in ordinary B-surveys. The method is adapted for the use of both regular grabbing equipment and video equipment at the same location and can be used on hard and mixed bottom (Hansen et al., 2019).

Direct impacts of aquaculture have been observed on the seafloor under and near fish farms around the world (Jansen et al., 2019; Staglicic et al., 2017). Indicators of organic enrichments (IOEs) like bacterial mats and opportunistic polychaete complexes (OPC) are caused by these impacts and may change the composition of benthic communities (Bannister et al., 2014; Edgar et al., 2010; Kutti et al., 2007; Tomassetti & Porrello, 2005). Barren substrates are areas with no visible epifauna present and can also be an indicator of aquaculture impact (Hamoutene et al., 2018). Opportunistic species are small size animals that are often found in organic-enriched sediments (Grassle & Grassle, 1976). Assemblages of OPCs function as a response to environmental variables, where the increase in organic emissions to the sediments is an important variable (Bannister et al., 2014). Buildups of a mixture of inorganic and organic matter on the seafloor are notable impacts from aquaculture activity and decomposing feed and feces form visible white bacterial mats (Knight et al., 2021). The presence of IOEs can be revealed by using video footage. In regions like Newfoundland, Canada, where the seafloor is mainly hard bottom, the aquaculture waste is monitored by looking at the presence of visual indicators like bacterial mats using camera system (Knight et al., 2021). The problems regarding hard substrate monitoring may be solved by modern genetic tools such as DNA metabarcoding of environmental samples (eDNA) (Keeley et al., 2021) in combination with visual surveys.

1.7 Impacts on wild fish attracted to open-cage fish farms

Fish aggregation devices (FAD's) are originally deployed to concentrate fishes and are used in both small-scale and commercial large-scale fisheries (Dempster, 2005). Today salmon farms are common artificial elements in cold coastal ecosystems that act as FAD's. The farms offer shelter for wild fish (Fréon & Dagorn, 2000), and because of this a lot of wild fish are often seen under and around fish farms (Barrett et al., 2019; Callier et al., 2018; Uglem et al., 2014). About 0,5 kg of uneaten feed and feces is generated for each kg of salmon that is produced (Svåsand et al., 2017). Most of this organic waste will accumulate in the sediments under and around the sea cages. Associated light, noise and biofouling communities are attractive to wild fish (Callier et al., 2018). The wild fishes that are attracted to the fish farms will feed on the organic waste (Uglem et al., 2014), and hazards like local eutrophication and the spreading of pathogens, drugs, heavy metals and organic pollutants are threatening the environment and the wild fish in areas with aquaculture activities (Olsvik et al., 2019). Dempster et al. (2009) observed 15 different species from 9 families around salmon farms in Norway, with the most common species being Atlantic cod (*Gadus morhua*), saithe (*Pollachius virens*) and haddock (*Melanogrammus aeglefinus*). They also found that the wild fish abundance was greater at farm sites than at paired reference sites. Dempster et al. (2010) observed 20 times greater abundance of wild fish right next to four salmon farms in Norway than at 200 m from them. The demersal fish can be affected directly through eating pellets, or indirectly through eating prey that are waste feed consumers. For demersal aquatic species that feed on the benthic fauna, a change in the sediment conditions from fish farm enrichment might affect the food access and food intake, as the distribution of species might change along with the enrichment gradient of the farm.

The wild Atlantic cod, *G. morhua*, is a commercially important gadoid that shares the coastal environment with farmed salmon in fjords with aquaculture production. The Atlantic cod is an opportunistic omnivore and its diet vary spatially and seasonally (Hanson & Chouinard, 2002; Link et al., 2009). Hedeholm et al. (2016) found that fish and crustacean prey accounted for 96% of the prey by weight of the analyzed Atlantic cod in Greenland waters. Variation of cod diet can be caused by habitat changes of that are the result of changes in environmental conditions (Demain et al., 2011). As coastal aquaculture is established in a fjord, the benthic environment within approximately 1 km of the farm can undergo significant changes from waste input (Bannister et al., 2014; Kutti et al., 2007), which can result in changes in the distribution and availability of benthic prey to Atlantic cod.

1.8 Research questions

- How does farm enrichment gradient, measured by distance to farm, affect;

- Benthic conditions?
- Epifaunal benthic communities and composition?
- Demersal fish communities and composition?

- Does the distribution and abundance of benthic epifauna dietary items of coastal Atlantic cod vary along the farm waste enrichment gradient?

2 Materials and methods

2.1 Site description

Mapping of epibenthic fauna and demersal fish and substrate conditions was conducted near an Atlantic salmon farm in Finnmark, northern Norway (Fig. 1). The Atlantic salmon farm (GEOWGS8470.N199450, E21.811017) was situated in Bergsfjorden, in the Loppa Region of Troms and Finnmark. The farm is one of 4 salmon farm sites in Bergsfjorden, with the study site being situated in the innermost area of the fjord (Fig. 1 b). The farm site is situated on the eastern side of the fjord where the seabed consists of both soft and mixed bottom substrates, and areas of hard bedrocks. Table 1 shows details of the site. The maximum allowed biomass for the farm was 3480 t. The locality was previous to this study fallowed for a period of approximately 5 years (last harvested in week 4 in 2013). The fish produced during this survey was stocked in cages between week 46 and 49 in 2018, and harvested during the period between week 27 and 38 in 2020. Details on farm production are provided in table 2.

2.2 Survey design

The area leading out from the farm cages was surveyed for patterns in benthic epifaunal and demersal fish distribution and community structure. Substrate compositions in the area were also surveyed. Reference locations further away from the farm cages were surveyed for the same patterns. The transects near the farm were run parallel to the coastline on both sides of the fish farm (video 1-8), and perpendicular to the coastline (video 9) (Fig. 1). The reference transects (video 10-17) were run further away from the farm in both directions in the fjord (Fig. 1). A total of 17 video transects were filmed on 14 and 15 October 2020. Details of the transects are presented in Table 2. The results were surveyed in relation to enrichment gradients from farm waste. Measurements of total particulate material (TPM) deposition were collected with sediment traps.

Table 1 Farm production characteristics of the salmon farm at the time of sediment trap surveys (July) and video surveys (October).

Year	Month	Max. allowed fish biomass (t)	Total feed mass (kg)
2020	July	3480	98454
2020	October	3480	0

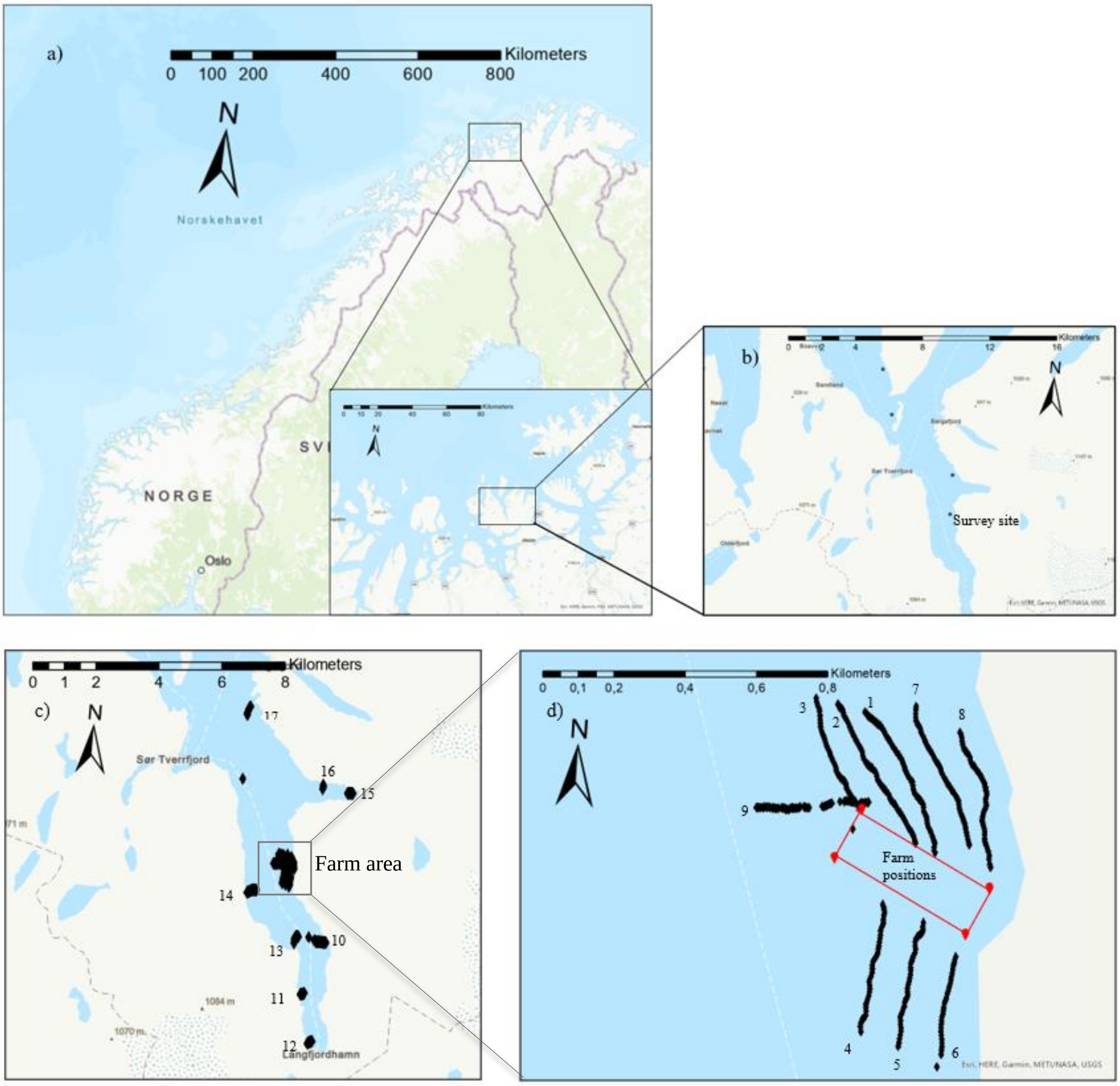

Figure 1 Map showing the location of the sampling area in Bergsfjorden. Green points indicate the Atlantic salmon farm sites in Bergsfjorden, where the innermost farm site is the survey site (b). Black lines indicate the video transects, with the transects in the square being the farm transects and the rest being reference transects (c). Red area indicates the survey farm site at the time of the video surveys (d).

2.3 Biological and environmental data collection

Sediment traps were put out to measure the flux of suspended particulate matter in the water column around the farm. The sediment traps collected suspended particulate matter at ca. 2,5 m above the seafloor. The traps were put out next to a cage, and at distances of 100, 200, 400, 700 and 1500 m from the cage for 2 d between 5 and 7 July 2020. The same number of traps were put out with the same distances to the cage for 2 days between 7 and 9 July 2020. The enrichment gradient (g/m^{2}d^{-1}) was calculated and plotted against distance to the farm. The enrichment gradient was seperated in 4 categories (6-8 g/m^{2}d^{-1}, 8-10 g/m^{2}d^{-1}, 12-14 g/m^{2}d^{-1} and 14-16 g/m^{2}d^{-1}) for analyzation.

Along transects the densities of benthic epifauna were quantitatively assessed using a towed underwater video system (UVS) (Fig. 2). The UVS consisted of an HD GoPro™ Hero, a live feed Splash-cam Delta Vision industrial underwater video camera (1/3” 960 H High Sensitivity CCS, > 750 TVL) and 2 Keldan 4X video lights (9000 lm) was mounted on a stainless-steel frame with an aerodynamic fin. The UVS was manually flown over the seafloor at ~0,3 s^{-1}. A pair of crossed Sea Beam™ lasers that was visible at the bottom of the live feed camera field of view were used as a guide for manual cable adjustments to fly the USV ~1 m above the seafloor. A GPS was recording the position of the vessel position on average every 5 s. This was used for calculation of the distance of the camera to the farm and the accumulated distance travelled along the seabed by using basic trigonometry. The depth data was recorded at the same time as the transects were filmed. Some sections were without depth data, and here the average depth of the whole transect were used.

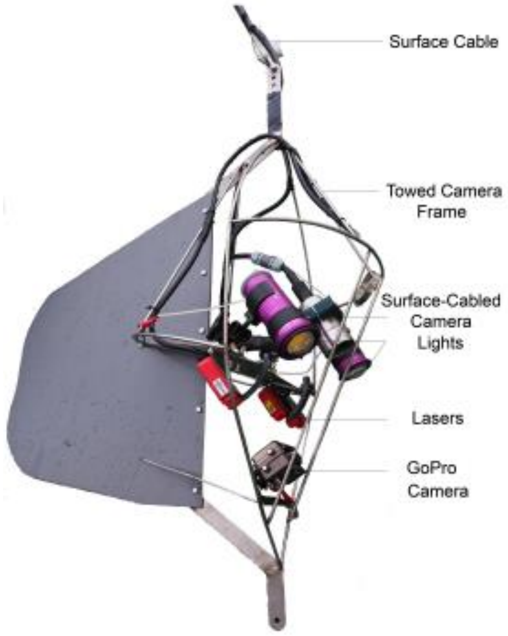

Figure 2 Diagram of the towed camera system used to record epifauna and demersal fish assemblages.

2.4 Video transect Annotation

The footage from the UVS was analyzed using the video annotation program, Video Navigator developed by IMR. The GPS position of the transects, date, time stamp and the cumulative distance travelled recorded from the boat GPS every 5 seconds was transferred to an Excel file and saved as a text file. The text file and video from each transect were added to Video Navigator for analyzing. Figure 3 shows how the videos with the paired lasers were displayed in Video Navigator. For the analysis of video sequences, the transects where subdivided into approximately 10 meter sections. For each 10 m section the epifauna and demersal fish within the 10 meters were identified and counted. Fish and epifauna were identified to the lowest achievable taxonomic level. Epifauna that were taxonomically similar and could not be distinguished were grouped in descriptive categories like “Porifera sp.”.

The seafloor area surveyed in each section was calculated by multiplying the section length (distance travelled over ground) by the average section width. By scaling the field of view with the aid of two lasers with paired lines (70 mm apart) at the beginning and end of each section the section width was determined. The average laser width in each section was multiplied by the distanced travelled in each section. In some videos the lasers were missing, here the average laser with of all transects was used. The relative density of each taxa in each section was quantified by dividing abundance by the estimated section area (m^2 per section). Within each section the percentage coverage of primary and secondary substrate types was noted. The substrate types were classified in 5 categories: sand (1), gravelly sand (2), sand and cobbles (3), sand and boulders (4) and bedrocks (5). The distance to the farm was calculated in ArcGIS Pro (version 2.9.0). Transect positions were put in a map (WGS84) (Ingeborg M Sætra, unpublished) as x y coordinates (Lat, Lon). The position of the farm was shifted ~300m south between the sediment trap surveys in July 2020 and the video transect surveys in October 2020. Therefore, there were two different farm positions for the two surveys. Based on the arrangements of the transects a polygon of the farm positions in October 2020 was deduced, this polygon is shown in Figure 1. The new farm coordinates were set as “near file” and each transect as “input files”, and the distance from each 10 m section in every transect to the farm was calculated and collected from the attribute tables. Because of many zero count samples where not epifauna or fish were observed the 10 m sections were binned into larger sample units of ~100 m for analysis to avoid overdispersion of the data.

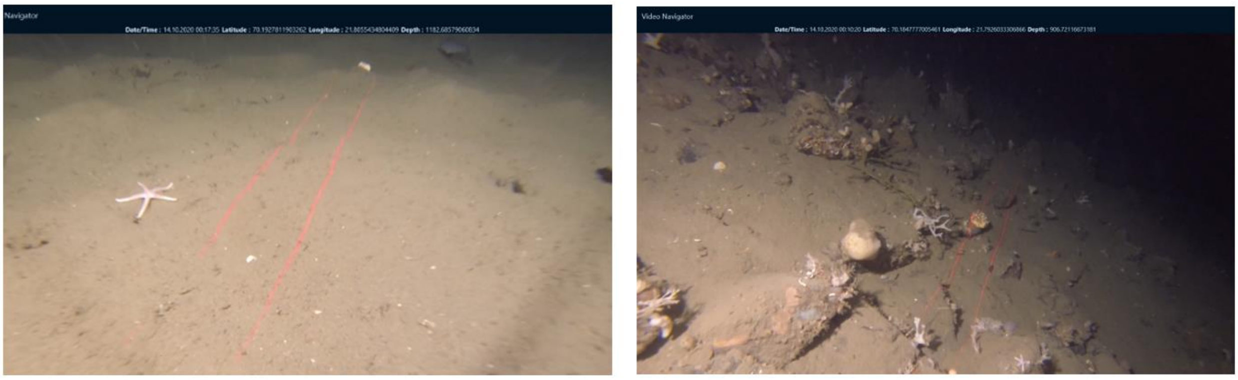

Figure 3 Images showing how the recorded videos were seen in Video Navigator. Date, longitude, latitude, and the cumulative distance travelled (as Depth) are displayed in the top of the images.

Table 2 Details of towed camera transect surveys. Positions are provided in decimal degree format (WGS84).

Date	**Video number**	**Transect start position (Lat, Lon)**	**Transect end position (Lat, Lon)**	**Transect start distance to farm (m)**	**Transect end distance to farm (m)**	**Main substrate type**	**Depth (m)**	**White bacterial mats**
14.10.2020	video 1	70.191942, 21.818580	70.195350, 21.812711	9.733	160.98	Sand (1)	60-80	present
14.10.2020	video 2	70.194800, 21.811892	70.195503, 21.810662	10.24	231.97	Sand (1)	80-90	present
14.10.2020	video 3	70.192963, 21.812731	70.195615, 21.809037	91.63	272.40	Sand and cobbles (3)	80-90	x
14.10.2020	video 4	70.190549, 21.814969	70.187326, 21.813981	218.77	553.22	Sand (1) and Bedrocks (5)	110-115	x
14.10.2020	video 5	70.190160, 21.818062	70.187012, 21.816809	243.33	584.01	Sand and cobbles (3)	65-85	x
14.10.2020	video 6	70.189358, 21.820624	70.186562, 21.819769	347.48	592.50	Gravelly sand (2), Sand and cobbles (3)	40-45	x
14.10.2020	video 7	70.195575, 21.816472	70.192189, 21.821073	94.76	159.17	Mixed	65-70	x
14.10.2020	video 8	70.194996, 21.819845	70.191660, 21.822760	157.43	191.48	Sand and cobbles (3)	40-50	x
14.10.2020	video 9	70.193100, 21.813428	70.192775, 21.805139	72.19	351.41	Mixed	90-100	present
15.10.2020	video 10	70.171580, 21.854678	70.171945, 21.844644	2489.81	2694.20	Sand and cobbles (3)	10-80	x
15.10.2020	video 11	70.156276, 21.836744	70.156755, 21.840220	4050.27	4076.59	Sand and cobbles (3)	10-50	x
15.10.2020	video 12	70.142500, 21.846020	70.143258, 21.850046	5600.61	5646.63	Sand and cobbles (3)	20-50	x
15.10.2020	video 13	70.170604, 21.828023	70.172587, 21.831300	2242.04	2435.15	Sand, cobbles and boulders (3)(4)	10-80	x
15.10.2020	video 14	70.183891, 21.785068	70.184808, 21.793028	1243.15	1537.29	Sand, cobbles and boulders (3)(4)	90	x
15.10.2020	video 15	70.214531, 21.866748	70.214403, 21.862021	2875.32	2991.04	Sand (1)	20-30	x
15.10.2020	video 16	70.216294, 21.841222	70.215033, 21.841034	2527.37	2649.30	Sand (1)	30-45	x
15.10.2020	video 17	70.236744, 21.774976	70.234230, 21.772847	4752.34	4987.93	Sand and cobbles (3)	45-80	x

2.5 Cod diet analysis

Wild Atlantic cod used for gut analyses were captured within the moorings (0-50 m) of the farm and >2 km from the farm in October 2020 by jigging, pot fishing and gill nets as part of the SalCod project. Gut analyses were conducted, and the species composition in cod stomach was assessed using eDNA with tailor blocking primers in collaboration with the Cawthron Institute in New Zealand. This was done to determine the dietary preferences of cod in the fjord.

2.6 Statistics

Histograms of the average densities of the demersal fish species and the most abundant key epifaunal taxa observed in video transects were made in Excel (version 2202). Generalized linear models (GLMs) were used to model the relationship between the average densities of the demersal fish (*G. morhua, M. aeglefinus, Pleuronectes platessa, Hippoglossus hippoglossus, Glyptocephalus cynoglossus, Hippoglossoides platessoide*s, *Sebastes and Anarhichas lupus)* and the distances and to see if the distances had significant effects on the densities of each species using RStudio (2022.02.0+443). Pairwise comparisons of estimated marginal means (EMMs) were run using emmeans (Searle et al., 1980) package to see if there were significant differences in the average densities of the species between the distances. The same analyses were done for the average densities of the key epifaunal species (Porifera, *Ascidians Ceramaster grannularis*, *Phakellia/Axinella*, *Mycale* sp. *Bryozoans*, *Hormathia digitata, Bolocera tueidae, A. rubens* and *Henricia* sp.) observed in high numbers.

The epifaunal densities were fourth root transformed prior to the multivariate analysis and used to create a Bray-Curtis similarity matrix in Primer 7 (version 7.0.13). A SIMPER analysis was performed to identify which epifaunal taxa and demersal fish characterized the biological assemblages in each distance group. The analysis achieves this by showing which taxa are responsible for the average similarity within and dissimilarity between the distances. To visualize the impact of environmental variables and individual epifaunal taxa on the variation in the epifauna community composition between transect sections where white bacterial mats were either present or absent, a canonical analysis of principal coordinates (CAP) was used. A resemblance matrix was calculated with Euclidian distance on the environmental data. Environmental variables with a correlation higher than 0,3 were presented in vector overlays. Permutational multivariate analysis of variance (PERMANOVA) was run on the transformed biological data to show which variables that had significant effect on the epifaunal community composition. A DISTance-based Linear Model (DistLM) multiple stepwise regression analysis was used to test the impact of the different environmental variables (depth, distance to farm, TPM flux, White bacterial mats, OPC and Substrate) on the assemblage structure, and to visualize the impact from the variables on the variation in the community composition between the different distance ranges. The stepwise selection procedure and corrected Akaike's information criterion (AICc) were used. A multivariate analysis, BEST, was used to select the environmental variables with the greatest explanatory power and test for differences between the unordered distances with Spearman rank and maximum 999 permutations. The BEST analysis explains what variables that best explain the patterns in the epifaunal communities, but it does not tell how much of the variation that is explained. The DistLM describes the patterns in the communities using the environmental variables and tells how much of the variation that is explained. An ANOSIM multivariate analysis was conducted with max permutations of 9999 to test for variations in the epifaunal community composition between the distance ranges (0-50 m, 50-100 m, 100-200 m, 200-500 m, 500-2000 m and >2000 m).

The crossover species that was found in both the video transects and in the diet analyses were identified (*Ascidians*, *Lithodidae*, *Corymorpha*, *Echinoidea*, *Mytilus edilus* and *Ophiodromus flexuosus*). A SIMPER analysis was performed to identify the average abundances of taxa that was found in the stomachs of the cod captured 0-50m from the farm and >2000 m from the farm. A histogram was made to show the distribution of the overlapping species in the different distances along the transects. GLMs and Pairwise comparisons emmeans (Searle et al., 1980) package were run on the average taxa densities of the cross-over taxa in the distances using RStudio (2022.02.0+443).

3 Results

3.1 Video annotation

The transects in Bergsfjorden covered bottom substrate consisting of both soft substrate (sand and gravelly sand), patchy areas and mixed bottom with sand and cobbles, and hard bottom (boulders and bedrocks). The main substrate types in each transect is presented in table 2. The conditions under the farm were highly enriched under the farm (>14,0 g/m^2d^{-1}) (Fig. 3), and the enrichment decreased gradually to 100 m from the farm. The enrichment gradient was stable from 100 to 200 m frm the farm (~ 6,0 g/m^2d^{-1}), and was gradually decreasing to 700 m from the fam (~ 4,5 g/m^2d^{-1}). From 700 m to 1500 m from the farm the enrichment gradient was slightly increasing to ~ 5,0 g/m^2d^{-1} 1500 m from the farm.

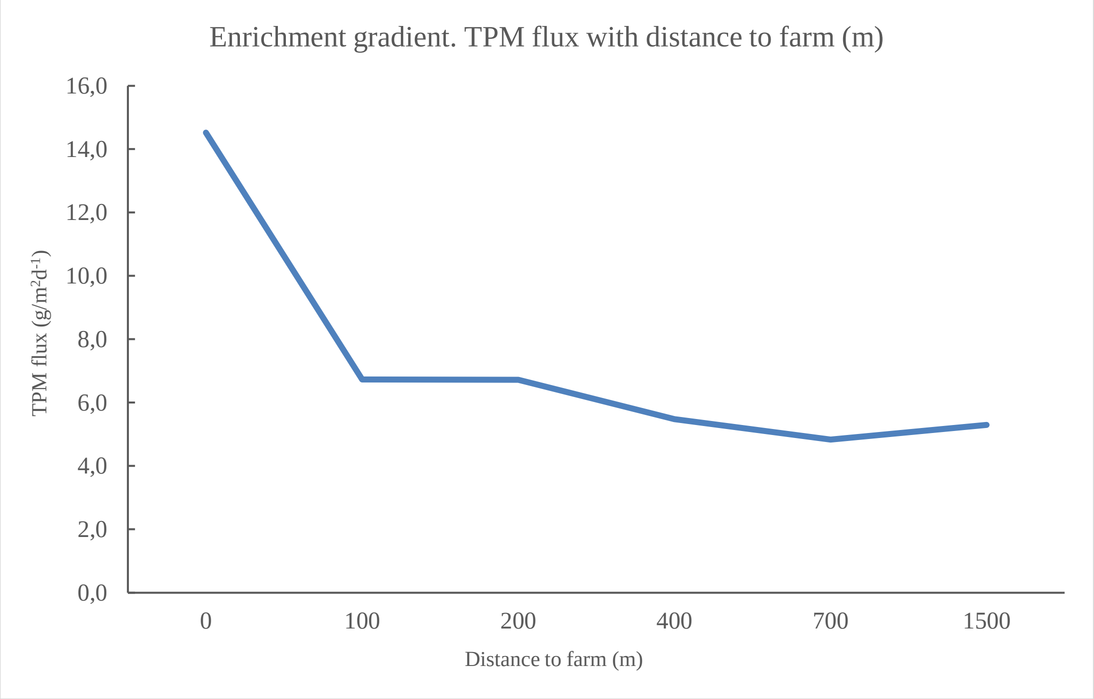

Figure 4 The total particulate material (TPM) flux plotted against distance to the farm.

3.1.1 Demersal fish

The gadoids Atlantic cod (*G. morhua*) and haddock (*M. aeglefinus*) were the most common demersal fish species observed within 2 km of the farm and at reference locations. The average densities of *G. morhua* were highest 200-500 m from the farm (~0,023 ind.m^2) and second highest 50-100 m from the farm (~0,021 ind.m^2). 100-200 m and 500- >2km from the farm the average densities of *G. morhua* were approximately the same (~0,01 ind.m^2), and the lowest average density at ~0,005 ind.m^2 was 0-50 m from the farm (Fig. 2). The densities of *M. aeglefinus* were generally high at all observed distances closer than 500 m from the farm (~0,013-0,018 ind.m^2) and >2 km from the farm (~0,0108 ind.m^2) (Fig. 2). The highest densities of *H. hippoglossus* were between 50-100 m from the farm (~0,009 ind.m^2) and declined with increasing distance from the farm. The densities of the flat fishes *P. platessa, H. hippoglossus, G. cynoglossus* and *H. platessoide*s were highest within a distance of 50-500 m from the farm. *Sebastes* was present at all observed distances, but the densities were higher at distance 200-500 m (~0.0033759 ind.m^2). *A. lupus* was not observed within 200 m of the farm and the highest densities were observed >2000 m from the farm (Fig. 2) (Appendix Table A. 52). There were no significant differences in average densities of demersal fish species between the distance ranges.

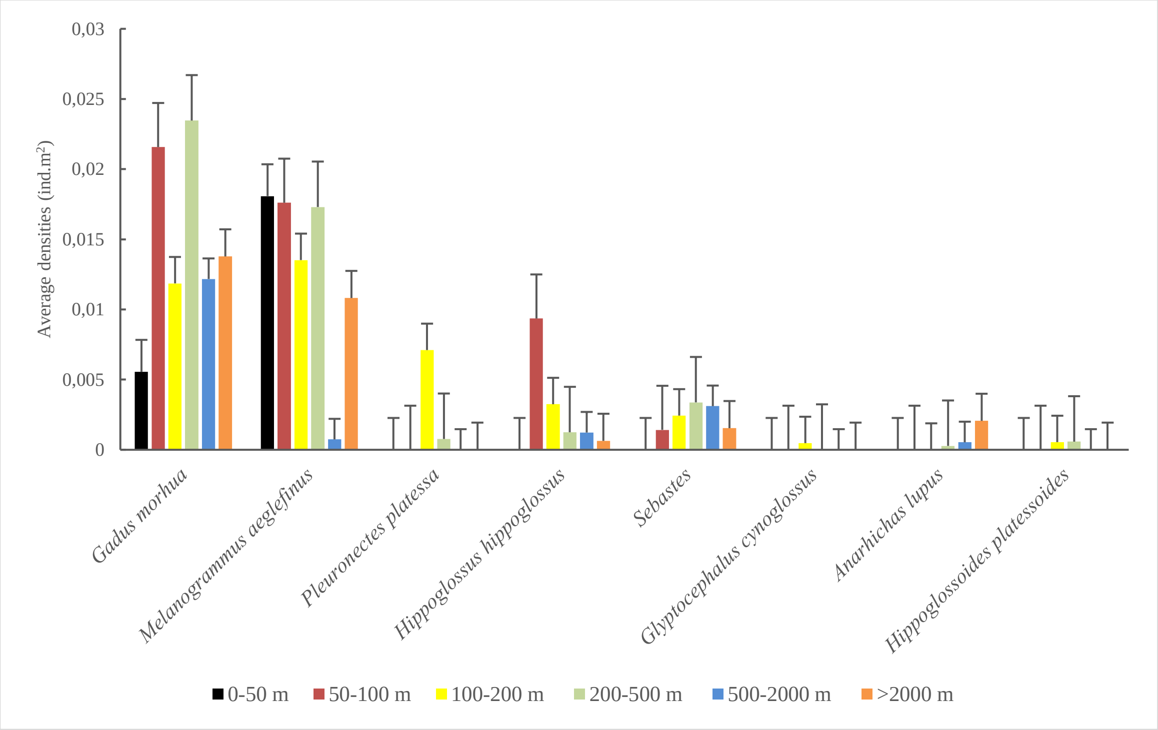

Figure 5 Histogram of average relative densities (individuals per m2) of demersal fish species observed in video transects in distances of 0-50 m, 50-100 m, 100-200 m, 200-500 m, 500-2000 m and >2000 m from the farm.

3.1.2 Key epifaunal species

Porifera sp. was the taxa with *the* highest densities within transects in Bergsfjorden (Fig.3). Distance had highly significant effects on the densities of Porifera (GLM, p=0,0001) (Appendix table A. 14). There were significant differences in Porifera densities between distances of >2000 m (~0,058 ind.m^2) and 100-200 m (p=0,0001), between >2000 m (~0,171 ind.m^2) and 200-500 m (~0,388 ind.m^2) (p=0,0027), between >2000 m and 500-2000 m (~0,188 ind.m^2) (p=0,0064) and between distance 100-200 m and 200-500 m (p=0,0005) (Appendix table A. 15). The tunicates and sea squirts of the class *Ascidians* were the second most present epifaunal taxa observed in transects. The distances had highly significant effects on the densities of Ascidians (GLM, p=0,0001) (Appendix table A. 16), and there was a significant difference in *Ascidian* densities between the distance ranges 100-200 m (~0,118 ind.m^2) and 200-500 m (~0,032 ind.m^2) (p=0,0218) (Appendix table A. 17). The asteroid *C. granularis*, the sponges *Phakellia/Axinella* and *Mycale* sp. and the *Bryozoans* were present in higher densities 500-2000 m from the farm than in the other distances, however the difference was not statistically significant. The densities of the anemone *B. tueidae* were highest (~0,015 ind.m^2) >2000 m from the farm. Distance had no significant effects on the densities of the sea anemones *Hormathia digitata* and *Bolocera tueidae,* the sea stars *A. rubens* and *Henricia* sp., *Phakellia/Axinella* and *Mycale* sp., *C. grannularis* and *Bryozoa.*

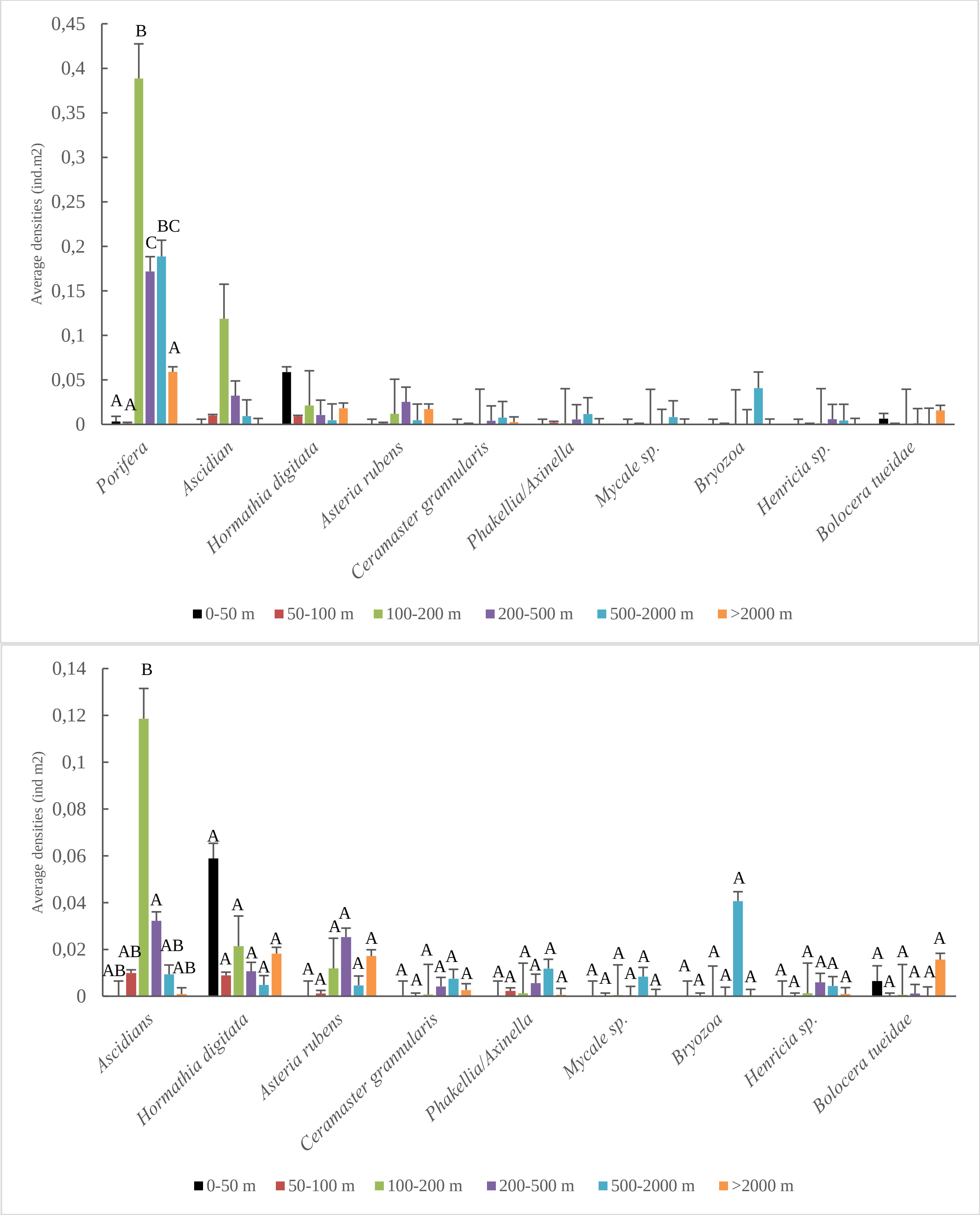

Figure 6 Histogram of average relative densities (individuals per m2) of key epifaunal invertebrate species observed in video transects in distances of 0-50 m, 50-100 m, 100-200 m, 200-500 m, 500-2000 m and >2000 m from the farm.

3.2 Epifaunal community composition

The composition of the assemblages of demersal fish and epifauna in Bergsfjorden showed a clear change with distance in a DistLM analysis. A clear clustering of composition by groups that from left to right showed decreasing distance to the farm. This corresponded to overlaid environmental variables TPM flux and Distance to farm (opposite to each other) (Fig. 7). The environmental variables with correlations higher than 0,3 were (in order of influence) TPM flux (Pseudo-F=6,2225), Distance to farm (Pseudo-F=4,59), Depth (Pseudo-F=3,9529), White bacterial mats (Pseudo-F=3,7379) and Substrate (Pseudo-F=2,2454) (Appendix Table A. 1). Results from the DistLM multiple regression model showed that these variables had significant effects on the epifaunal community composition (p=0,001 for Distance to farm p=0,001 for TPM flux p=0,002 for Depth p=0,001 for White bacterial mats p=0,031 for Substrate). Oportunistic polycchaete communities (OPC) had significant effects on the epifaunal community as well (p=0,002 for OPC). This is shown in the results from the marginal tests in the DistLM multiple regression model (Appendix table A. 1). The DistLM model explained 13,7 % of the variation in the epifaunal community composition. The composition of the assemblages of the epifauna showed separetation between the distance groups in a DistLM plot (Fig. 7). The CAP analysis showed some separation between the transect sections with white bacterial mats present and the transect sectrions without white bacterial mats present. The bacterial mats were present in transect sections that were close to the farm and with increased TPM flux (Fig. 8). The PERMANOVA test showed significant results for the effect of Depth (Pseudo-F=2,3321 p=0,001) and for OPC (Pseudo-F=2,3867 p=0,027) on the demersal fish and epifaunal community composition (Appendix table A. 4). The ANOSIM analysis detected significant differences in epifaunal composition between distances of 200-500 m and >2000 m and between 100-200 m and >2000 m (significant level=0,01%) (Appendix table A. 12). The BEST analysis showed that the best correlation between the biological and the individual environmental variables was with the variable White bacterial mats included. With White bacterial mats variable included the correlation coefficient was at 0,249 and the significance level of sample statistic was at 0,2% (Appendix table A. 13). The presence of white bacteial mats was the variable that had the strongest effect on the benthic epifaunal community composition.

The epifaunal and demersal fish community composition in transect sections with short distance to the farm (0-500 m) was mostly driven by the presence of the fish species Atlantic cod, (*G.*

morhua), haddock (*M. aeglefinus*) and the european plaice (*P. platessa*), and *Ascidians*. In the areas with greater distance from the farm (500-2000 m) the epifauna and demersal fish communities characterization were mostly driven by Porifera sp. For the transects over 2 km from the farm the composition was primarily driven by the persence of the seastars *Asterias rubens* and *Hippasteria phrygiana* (Fig. 7).

3.2.1 Demersal fish

SIMPER analysis showed that *G. morhua* was dominant in all distance groups (Fig. 5 and appendix Table A. 6-A. 10). *M. aeglefinus* was dominant 50-500 m from the farm and >2km from the farm (Fig. 5 and Appendix table A. 6- A. 8 and A. 10). The flatfish *P. platessa* and *H. Hippoglossus* both had the highest average abundance 100-200 m from the farm (Fig. 5 and Appendix table A. 7), while fish of the genus *Sebastes* were dominant 200-500 from the farm. (Fig. 5 and Appendix table A. 8- A. 9).

3.2.2 Epifaunal species

SIMPER analysis showed that Porifera was the epifauna taxa that was dominant at all distances, except 0-50 m (closest to the farm cage), but were also increasingly dominant with a greater distance from the farm (500- >2000 m) (Appendix table A. 6- A. 10). *Ascidians* were dominant in all distance ranges except 0-50 m and >2000 m from the farm (Fig. 6 and Appendix Table A. 6- A. 9). *H. digitata* was dominant at all distances and was responsible for 22 % of the average similarities between 100-200 m from the farm (Appendix Table A. 6- A. 10). *H. digitata* had the highest average densities 0-50 m from the farm (~0,058 ind.m^2) (Appendix Table A. 53). *A. rubens* was also a dominant taxa at all distances, except 0-50 m from the farm where a lower average abundance of the taxa was found (Appendix Table A. 6- A. 10). *Hippasteria phryghiana* was dominant 200-500 m and >2000 m from the farm (Appendix table A. 8 and A. 10).

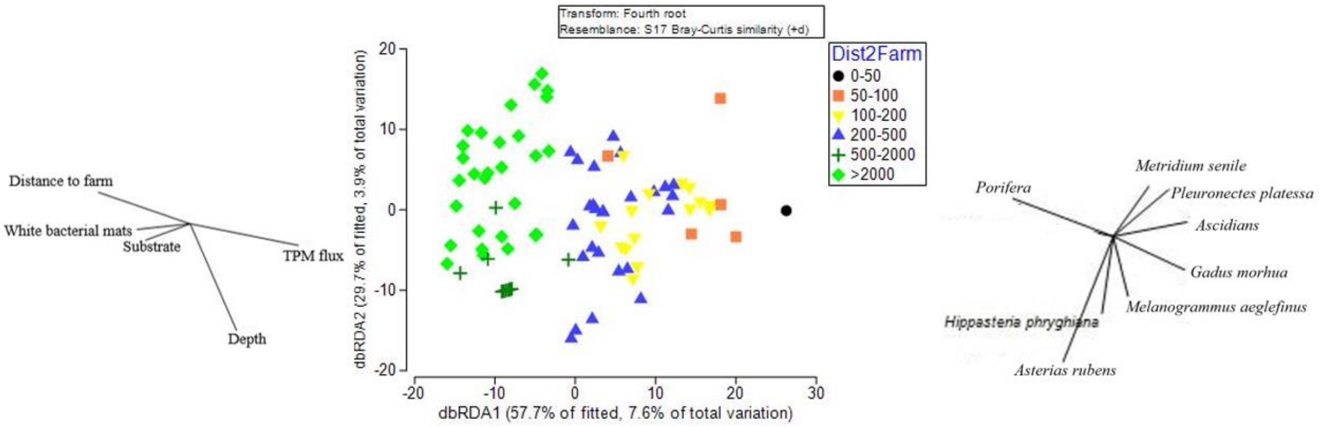

Figure 7 DISTance-based Linear Model (DistLM) multiple stepwise regression plot based on benthic epifaunal community composition at different distances from the farm. Each point represents the densities of benthic epifaunal taxa in each 100 m section of the transects. The points are coloured to represent the distance categories. Vectors overlay on the left side represent the Pearson rank correlations between the environmental characteristics (Distance to farm, TPM flux, Depth, Substrate and White bacterial mats). Vectors overlay to the right represent key epifaunal drivers of the community composition.

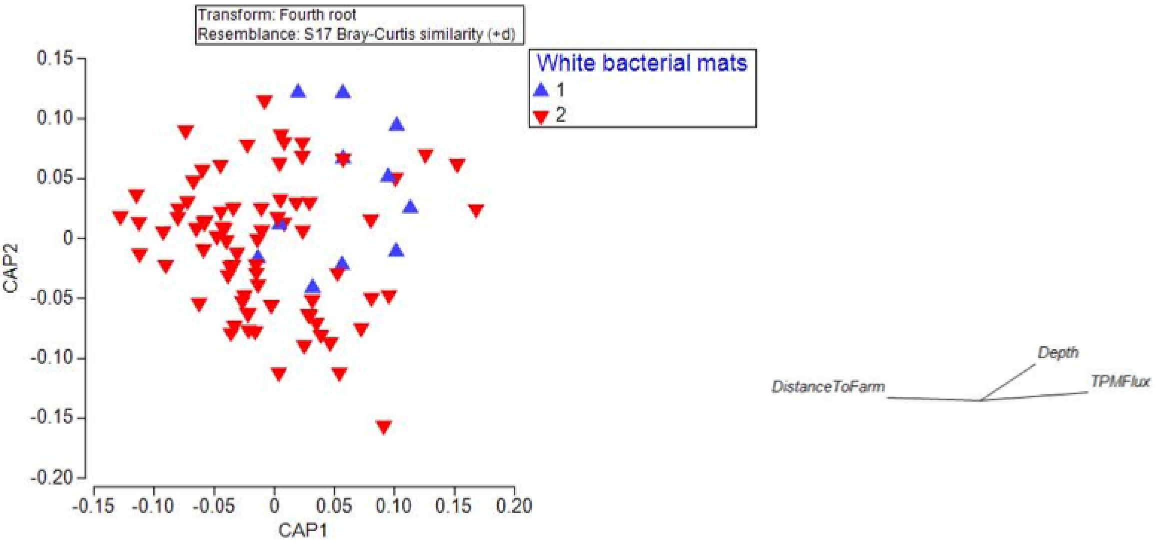

Figure 8 Canonical analysis of principal coordinates, based on Bray-Curtis dissimilarity, of the composition of epifaunal taxa in the survey sites around the farm site with white bacterial mats present (1) and not present (2). Vectors overlay represent the Pearson rank correlation between the environmental characteristics (Distance to farm, depth and TPM flux).

3.3 Distribution of cod dietary items

The taxa found in both the video transects and in cod diet analyses are presented in Table 3 and Table 4. The total SIMPER analysis table of the species detected in stomach analyses is found in the Appendix (Table A. 60). Distance had a significant effect on the densities of *Ascidians* (GLM, p=0,0001) (Appendix Table A. 16 , and the highest densities of Ascidians were observed 100-200 m (~0,118 ind.m^2) (Fig. 6). The ascidian *Ciona* sp. and the small tunicate *Oikopleura* were only detected in the stomach analysis from cod caught 0-50 m from the farm. Distance had no effect on the densities of the polychaete *Ophiodromus flexuosus*, also observed to be a cod dietary item. This polychaete was present in video transects over 2 km from the farm (Fig. 9). *Lithodidae* was observed only 200-500 m from the farm (Fig. 9). Distance had no effect on the densities of *Lithodidae* in transects. The toad crab (*Hyas coarctatus*), which belongs to the family *Lithodidae*, was only detected in the stomachs of cod caught >2 km from the farm (Table 4). Big crustaceans, *Malacostraca*, was detected in cod stomachs in cod caught both 0-50 m and >2 km from the farm (Appendix Table A. 20). Distance had no effect on the densities of the blue mussel (*Mytilus edilus*) that was present only 100-500 m from the farm (Fig. 9). The blue mussel was only detected in the cod stomach analyses in cod caught 0-50 m from the farm (Table 4). The distance groups had no effect on the densities of urchin (*Echinoidea*). The densities of *Echinoidea* were however relatively high 50-500m from the farm and none were observed in transects over 500 m from the farm (Fig. 9). In the cod stomach analyses the urchin species green urchin (*Strongylocentrotus/Echinoidea*) and pea urchin (*Echinocyamus*) were only detected in cod caught >2 km from the farm. Distance had no effect on the densities of the American plaice (*Hippoglossoides platessoides*) that was present 100-500 m from the farm (Fig. 9). *H. platessoides* was only detected in cod caught 0-50 m from the farm (Table 4).

Table 3 The mean densities recorded within each 100 m swath (ind. per m^2) of the epifaunal taxa observed in towed camera transects in the 6 distance ranges.

Taxa	0-50 m	50-100 m	100-200 m	200-500 m	500-2000 m	>2000 m
Ophiodromus flexuosus	0	0	0	0	0	0.00136952
Lithodidae	0	0	0	0.00016259	0	0
Mytilus edilus	0	0	0.00019986	0.00066291	0	0
Echinoidea	0	0.00159322	0.00200521	0.00232776	0	0
Ascidian	0	0.00994247	0.11860507	0.03220125	0.00935532	0.00091721
Hippoglossoides platessoides	0	0	0.00054266	0.00057832	0	0

Table 4 SIMPER analysis result table of the average abundance (ind. per m2) of the cross-over taxa found in cod stomachs from cod caught 0-50 m from the farm cage and >2km from the farm cage.

Taxa	**Diet group**	**Average abundance 0-50 m (ind.m^2)**	**Average abundance >2 km (ind.m^2)**
Strongylocentrotus	Epifauna	0	0.16
Echinoidea	Epifauna	0	0.11
Hyas coarctatus	Epifauna	0	0.11
Echinocyamus	Infauna	0	0.08
Ciona	Epifauna	0.09	0
Mytilus	Epifauna	0.05	0
Malacostraca_XXX	Benthic - epifauna	0.03	0.03
Oikopleura	Pelagic - zooplankton	0.02	0
Hippoglossoides	Benthic - fish	0,02	0

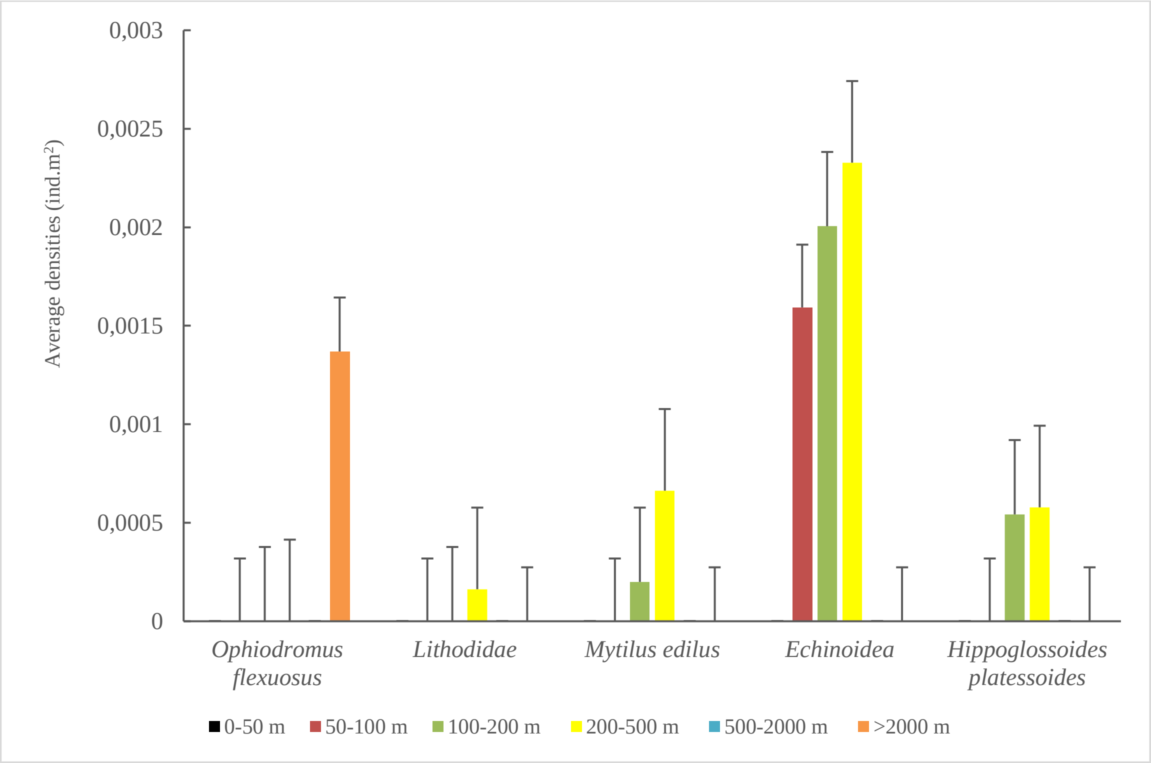

Figure 9 Histogram of average relative densities (individuals per m2) of the crossover epifaunal taxa observed in video transects in distances 0-50 m. 50-100 m. 100-200 m. 200-500 m. 500-2000 m and >2000 m from the farm.

4 Discussion

This study demonstrated that the density and community composition of benthic invertebrates and demersal fish community detected in a towed video camera system change with distance to an Atlantic salmon farm over mixed substrates in northern Norway. In addition, results showed that the distribution and abundance of benthic epifauna dietary items of coastal Atlantic cod vary along the farm waste enrichment gradient. The flatfish species *P. platessa, H. hippoglossus, G. cynoglossus* and *H. platessoide*s were all observed at their highest relative densities within 500 m of the farm, while the sponges *Phakellia/Axinella* and *Mycale* sp. were present in higher densities between 500 and 2000 m from the farm. The sea anemone *H. digitata* was most common epifaunal species within 50 m of the farm. The coastal Atlantic cod dietary items, detected by DNA metabarcoding of cod stomachs and observed in the video transects, were *M. edilus, Echinoidea, Lithodidae,* young *H. platessoide*s and *Ascidians*. All these species were all found in relatively high densities within 500 m of the fish farm.

4.1 Spatial distribution of the benthic epifaunal and demersal fish community

Infaunal polychaetes are dominate dietary items of many flatfish (Amezcua et al., 2003; Carlson et al., 1997) and have been found in high percentages in stomach analyses of Alaska plaice, *Pleuronectes quadrituberculatus*, Yellowfin sole, *Limanda aspera* and northern rock sole, *Lepidopsetta polyxystra* in the Bering Sea (Yeung et al., 2013). The distribution of the European plaice, *P. platessa* is found to be structured by the presence of polychaete reefs in Belgium (Rabaut et al., 2010). In Bergsfjorden several common coastal flatfish species showed a tendency to be close to the farm, within 500 m, where opportunistic polychaete accumulations are naturally abundant because of organic farm waste (Callier et al., 2013; Kutti et al., 2007). Therefore, it seems logical that flat fish were found in higher abundance closer to the farm where they can utilize polychaetes within and above the sediments as a food source. Opportunistic polychaetes were not observed in high abundances in video, but several polychaete species were detected in the cod stomach analyses (*Laonice*, *Capitella* and *Malacoceros* 0-50 m from the farm, and *Eunice* and *Nothria* > 2 km from the farm), indicating that the polychaete assemblages observed in the video system are an underestimation of the actual amount as many can be living as infauna within the sediment. These species are generally detected as infauna (Yeung et al., 2013). The free living polychaete *Ophiodromus flexuosus* was observed on the sediment surface in the video transects but only over 2 km from the farm.

The sponges *Phakellia/Axinella* and *Mycale* sp. were present in relatively higher densities 500-2000 m from the farm than in the other distance ranges. Dunlop et al. (2021) found that the sponges *Phakellia spp*. and *Polymastia spp*. decline in density with the enrichment gradient from salmon farms in northern Norway, thought to be the result of sensitivity to increased sedimentation. Sponges are filter feeders (Dahihande & Thakur, 2021) and can therefore be affected by farm waste and increased sedimentation clogging filter-feeder apparatus. Sutherland et al. (2018) studied the impacts on a rock-cliff epifaunal community from salmonid aquaculture activities in eastern Canada and found that various sponge taxa that were prevalent in the reference survey areas revealed a sensitivity to aquaculture-derived waste indicators and were relatively low in densities. Since it was impossible to identify many of the sponges to species level based purely on video observations (from the video transects) most were simply classified as, "Porifera sp". Porifera was found in high densities 100-200 m from the farm. The reason for the significant higher densities of Poriferas in this distance group is uncertain, but it might be important to note that a wide range of distribution and morphological adaptions in sponges was observed (Dahihande & Thakur, 2021). Different sponge species have different tolerances to particulate material. For example, some encrusting sponges are found in highly sedimented sites in southern Ireland (Bell & Barnes, 2000), and Laroche et al. (2021) found that the Polymastia sponge *Webrella brusa* is more tolerant to aquaculture enrichment than anticipated.

4.2 Factors that affect epibenthic invertebrates and demersal fish community composition

The depth in the transects in Bergsfjorden varied from <10-115 m. and for the farm transects the depth varied from ~ 40-115 m. Several studies have shown that depth is an important factor when it comes to benthic community structure in arctic fjords (Meyer et al. 2015; Kokrav et al. 2017; Steffens et al. 2006). In deeper areas there might be less current and therefore more sedimentation, which could affect the benthic community composition. The multivariate analyses conducted in this study showed that depth had a significant effect on the epifaunal and demersal fish community distribution. Substrate type is another factor that affect the benthic epifaunal community structure (Callaway et al., 2002; Dunlop et al., 2020; Dunlop et al., 2021) and was also found to have significant effect on the community distribution in this study.

The highest densities of *H. digitata* were observed 0-50 m from the farm. Dunlop et al. (2021) studied the spatial distribution of hard- and mixed bottom benthic epifauna along organic enrichment from a salmon farm in Northern Norway and found that *H. digitata* was prominent fauna at the survey site. *H. digitata* was most abundant in areas receiving <15 mg TPM m^2 d^{-1}, over 200 m from the farm. They found that *H. digitata* was common on gravel and gravelly sand substrates and was only observed in shallower waters (57-77 m). In another study *H. digitata* was associated with areas of sand (Callaway et al., 2002). In this study *H. digitata* was found in highest densities in video transect 1 on sand substrates 0-50 m from the farm. The area 0-50 m from the farm received ca. 11-14 mg TPM m^2 d^{-1}, and the depth range in transect 1 was 60-80 m, which corresponds to the findings in Dunlop et al. (2021). Dunlop et al. (2021) also found that the seastar *Asterias rubens* was more abundant near fish farms with elevated fluxes. *A rubens* has also shown to have an increased biomass around mussel farms in Canada (D'Amours et al., 2008) and salmon farms in Scotland (Wilding et al., 2012). Callaway et al. (2002) found that *A. rubens* was dominating in depth ranges of 50-100 m. In this study, the highest densities of *A. rubens* were found along video transect 5, 200-500 m from the farm in a depth range of 60-90 m. However, *A. rubens* was also observed in relatively high densities over 2 km from the farm in all video transects except for video transect 17, where no *A. rubens* were observed. As the farm was harvested 1 month prior to the video surveys there was no waste feed and feces aggregated close to the farm for *A. rubens* to feed on at the time of video surveys.

4.3 Spatial distribution of dietary items of Atlantic cod

The potential ecological impact from salmon farms on the wild cod depends on many factors such as interactions with seasons, environmental factors (current and depth), other fish species, and emissions from the farm. Fish farms are known to serve as FAD’s (Dempster et al., 2010; Dempster et al., 2009), and therefore it was expected that more demersal gadoids would be observed in the video transects. However, the video transects did not reveal any major changes in fish abundance consistent with attraction to the farm. A possible explanation for this is that the farm was destocked 1 month prior to conducting the survey, therefore there were no waste feed available. Waste feed is thought to be one of the major attractants of cod to fish farms

(Damian et al., 2011; Tuya et al., 2006). The distribution of some coastal Atlantic epifaunal dietary items in Bergsfjorden were however found to vary along the farm waste enrichment gradient.

Ascidians were found in high densities 100-200 m from the farm, a result that is in accordance with (Callier et al., 2013), who found that several tunicates had increased abundances close to a salmon farm after 2 months of impact. Biofouling ascidians are some of the main colonizers of aquaculture gear (Adams et al., 2011; Braithwaite 2007; Rosa et al., 2013). In the cod stomach analyses, the Ascidian *Ciona* sp. and the small tunicate *Oikopleura* were only detected in fish caught 0-50 m from the farm and not fish caught over 2 km from the farm. This could indicate that Ascidians were fouling on cages, moorings, or other aquaculture gear in Bergsfjorden; however, this was not able to be confirmed from seabed surveys. Blue mussels (*M. edilus*) were also identified as a dietary item but were observed 100-500 m from the farm, and the highest densities were observed 200-500 m from the farm. The blue mussel is a filter-feeder and may be attracted to the organic enrichments from the farm. A study in Maine, eastern USA on seasonal succession at an offshore fish farm cage showed that blue mussels accounted for most of the net fouling density and biomass on the cage (Greene & Grizzle, 2007). The blue mussel was only detected in cod stomachs from cod caught close to the farm, possibly as they are feeding locally or biofouling on the cages in Bergsfjorden.

In this study, urchins were only observed in close proximity to the farm (50-500 m). White et al. (2018) found that the abundances of the white urchin *Gracilechinus acutus* was 3 to 100 times greater at salmon farm sites than at reference sites in a fjord in Western Norway. *G. acutus* is shown to directly consume aquaculture waste as a trophic resource (White et al., 2017). All the urchin species detected in the eDNA stomach analyses of Atlantic cod were from cod caught over 2 km from the farm in Bergsfjorden. It is not possible to tell where the cod has been feeding, but the reason for the absence of urchins in the diet of cod caught 0-50 m from the farm might be that those fish were instead feeding on smaller fish that were aggregated around the farm structures (consistent with the FAD theory). Atlantic salmon (*S. salar*), Herring (*Clupea Harengus*), Capelin (*Mallotus villosus*) and American plaice (*H. platessoides*) were only detected in the cod stomachs of cod caught 0-50 m from the farm. *H. platessoides* was also observed in the video transects within 500 m from the farm. *Lithodidae* was only observed 200-500 m from the farm in video transects, and the cod dietary item toad crab in the *Lithodidae* family was detected in cod stomachs from cod caught over 2 km from the farm. A large crustacean species, *Malacostraca*, was detected in stomachs of cod caught both 0-50 m and over 2 km from the farm. In a study on mobile epibenthic fauna near Frøya, Mid-Norway, urchins, crabs and brittle stars are showed to be consumers of fish farm waste, and in both crabs and brittle stars, terrestrial components from salmon feed were detected up to 1 km from the study site (Woodcock et al., 2018). There were several brittle star species detected in the cod diet. The brittle star *Ophicomina nigra* was found to be abundant at distances of 250-1000 m from an Atlantic salmon farm near Frøya, mid-Norway, and showed negative tolerances to organic waste (Keeley et al., 2020). On the other hand, Gonzalez-Silvera et al. (2015) found that several brittle star species were very abundant around active aquaculture sites compared to sites without production. However, no brittle stars were observed in this study, so it was not possible to make any inferences about connections between this species in relation to cod diet and farms in this region. One reason could be that brittle stars were difficult to identify in the videos. Except from for *Ascidians*, there was no significant variation with distance from farm in the densities of dietary items of Atlantic cod in video transects. The distribution of *M. edilus, Echinoidea* and *Lithodidae* still changes with distance to farm and like *Ascidians* they are all found to be attracted to the area within 500 m of the fish farm.

There is not enough research done on the implications to the coastal Atlantic cod in a fjord with aquaculture activity to fully understand the effects from salmon aquaculture. Dempster et al. (2009) found that the distribution of cod was highest around salmon farms with shallow rocky bottoms, and Dempster et al. (2010) found that the patterns of distribution of cod varied among survey farms. The changing distribution of benthic epifaunal invertebrates and other demersal fish in a fjord with aquaculture activity will affect the wild Atlantic cod. It is possible that the tendency for ascidians to foul artificial structures that are floated up from the bottom makes them a more prominent dietary item for coastal cod.

4.4 Benthic indicators of aquaculture impact

In the present study the white bacterial mats had significant effects on the epifaunal community composition, and the BEST analysis showed that white bacteial mats was the variable that had the strongest effect on the benthic epifaunal community composition. The cages were moved between July and October 2020, which means that the most impacted areas probably were just under and around the previous farm positions. Transect 1 and 2 were run straight over the old farm positions. The transects with visual white bacterial mats were transect 1, 2 and 9, which are the transects that were closest to the old farm positions. This indicates that the area right under an close to the old farm positions were the most impacted areas. Transects going south over sediments that were previously further away from the farm should be less impacted than the transects going north over more impacted sediments. Several studies on vertical transport of aquaculture waste in fjords has been done (Bannister et al., 2016; Cromey et al., 2002; Keeley et al., 2013; Kutti et al., 2007; Valdemarsen et al., 2012) showing the importance of hydrodynamic conditions on waste transport in deep fjords. How the aquaculture waste is distributed in a fjord differ in terms of depth, current bathymetry, hydrodynamics and environmental conditions (temperature and phytoplankton concentrations) (Jansen et al., 2018).

4.5 Implications for aquaculture management and ecosystem-based aquaculture approach

Sustainable development is defined by the UN as "a development that satisfies the current needs without destroying future generations' opportunities to satisfy their needs". In the report No. 16 (2014-2015) *Forutsigbar og miljømessig bærekraftig vekst i norsk lakse- og ørretoppdrett (Predictable and environmentally sustainable growth in Norwegian salmon and trout farming)* it is determined that environmentally sustainability must be used as the most important prerequisite for regulating further growth in the aquaculture industry. The traffic light system that is used in Norway is established to regulate the aquaculture production after the environmental impact of the production. The Norwegian coastline is divided in 13 production areas with either green, yellow or red "light" indicating the environmental effect of aquaculture production based on the mortality of the wild salmon post-smolt induced by lice (Myksvoll et al., 2020; Ådlandsvik, 2015). The system is a key management tool that requires expansion to improve environmental monitoring to include aquaculture effects on other elements of the marine ecosystem such as benthic impacts and the effects on wild gadoids. Bacterial mats as a visual indicator of impact from aquaculture might be an additional indicator to the TLS, but this will need more research. Knight et al. (2021) found that use of bacterial mats as a visual indicator of aquaculture impact on hard bottom seafloor is valid, but a much less sensitive indicator than determination of the identity of the bacterial communities using DNA metabarcoding. Absence of bacterial mats do not necessarily mean absence of aquaculture impact, so the seafloor observations should be interpreted with caution. Keeley et al. (2019) observed strong benthic effects gradient from a high-capacity salmon farm on the central west coast of Norway. Despite this observation, the seafloor remained visibly unimpacted. In the present study, visual aquaculture effects were only observed in a few study transects. In July 2020, the benthic conditions at the study farm were rated to 3 (“bad”) in a B-survey, which means that there were highly affected benthic conditions near the farm in October 2020 as well. This shows that monitoring programs based on visual indicators might be problematic as monitoring methods, as organic waste can be dispersed over large areas du to water currents and make the seabed seem unimpacted. The generally impoverished epifaunal community observed in the transects provides a small foundation to assess changes to, but the changes observed were subtle. The linkage between IOE presence, organic matter deposition levels and measurable impacts in the benthic communities is not sufficiently researched (Hamoutene et al., 2015). Visual based management surveys can possibly be used as complimentary surveys but will not give a complete image of the benthic conditions. This study shows some patterns in aquaculture induced impacts on the epibenthic communities and might contribute to a better basis for further studies.

4.6 Limitations and future research

The shifting of the farm positions was performed between sediment surveys and video surveys. The previous positions could be more important drivers of the epifaunal invertebrate and demersal fish communities, but as the farm was moved only a short distance, and depth and hydrodynamics remained the same as at the previous position, the enrichment gradient calculated from the old farm positions was still valid. Still, shifting farm positions was not ideal, as the area on one side of the new farm position was in early stages of recovery before the moving. The new farm position was established on relatively unimpacted sediments and may not have had time to fully express the effects of the farming intensity. An effort has been made to interpret the results in light of this problem. Despite the challenges with the moving of the farm, towing right over the previous farm position was a unique opportunity to observe the most impacted areas of the old farm position. Video surveys were done 14 and 15 October 2020, and the feeding at the farm was ended 1 month prior to the surveys. All the salmon farms in Bergsfjorden were harvested between week 32 and 38 in 2020, and the last cage in the fjord, that was at the survey farm was harvested 16 September 2020. This may have affected the results of the study, as there were no emissions released from the farm at the survey time. Analysis of infaunal data collected along the farm enrichment gradient would have provided complementary results to the epifauna data. There were a lot of infaunal taxa detected in the cod stomach analyses, and infaunal data would give further information on the distribution of other cod dietary items buried in the sediments. However, the infaunal data was not available within the time frame of this project. The present study currently only covers one farm and time point. An expansion of the study could include several farms for a larger survey area. Implementing video surveys several times over a longer period would give valuable information on the benthic changes over time. This study gives an indication on the epibenthic community structural changes along the enrichment gradient from a fish farm. The epibenthic communities are important for the function and biodiversity in an ecosystem and need to be considered in the aquaculture management. Management tools adapted to hard and mixed bottom are important to implement in aquaculture management to ensure a good seabed recovery process.

4.7 Conclusion

This study shows that salmon farm aquaculture has moderate effects on the community composition of epifaunal invertebrates and demersal fish along an enrichment gradient. This was especially apparent in the aggregation of several flatfish near the farm that are likely to be feeding on infaunal polychaetes that are known to aggregate around fish farms, and that this persists for at least one month into the fallowing period. Although there was not a strong overlap between the diet of cod caught in the area and the epifauna comments there was some potentially important interactions. The Atlantic cod dietary items, *M. edilus, Echinoidea*, *Lithodidae* and *H. platessoides* all changed in distribution along the enrichment gradient from the farm and were all found to be attracted to the area within 500 m of the fish farm. Changes in epifaunal distribution along the enrichment gradient were also reflected in the Atlantic cod dietary item *Ascidians*, which were at a significantly higher density close to the farm. The ecological process across trophic levels needs to be researched to see the full context of salmon aquaculture induced impact on the marine environment.

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Appendix

DistLM

DistLM marginal tests

Table A. 1 DistLM marginal tests result table with factors Distance to farm. Depth. TPM flux. White bacterial mats and POC

MARGINAL TESTS				
Variable	**SS(trace)**	**Pseudo-F**	**P**	**Prop.**
DistanceToFarm	5884.7	4.59	0.001	0.051234
Depth	5104.1	3.9529	0.002	0.044438
TPMFlux	7834.8	6.2225	0.001	0.068213
White bacterial mats	4825.8	3.7279	0.002	0.042015
POC	4760.2	3.675	0.001	0.041444
Substrate	2956.1	2.2454	0.031	0.025737

DistLM sequential tests and BEST SOLUTION

Table A. 2 DistLM sequential tests

SEQUENTIAL TESTS							
Variable	**AICc**	**SS(trace)**	**Pseudo-F**	**P**	**Prop.**	**Cumul.**	**res.df**
+TPMFlux	623.14	7834.8	6.2225	0.001	0.068213	0.068213	85
+Depth	621.77	4242.1	3.4669	0.001	0.036933	0.10515	84
+POC	620.78	3691	3.0917	0.003	0.032135	0.13728	83

Table A. 3 DistLM BEST solutions

BEST SOLUTION				
AICc	**R^2**	**RSS**	**No. Vars**	**Selections**
620.78	0.13728	99091	3	4.5.12

PERMANOVA

Table A. 4 PERMANOVA table of results. Main test and pair-wise tests

Main test

Source	df	SS	MS	Pseudo-F	P(perm)	Unique perms
TPM Flux	4	3448.9	862.22	0.78719	0.784	999
Dist2Farm	5	7239.5	1447.9	1.3219	0.118	999
White bacterial mats	1	1013.9	1013.9	0.92571	0.473	997
Depth	4	10218	2554.4	2.3321	0.001	997
POC	1	2614.2	2614.2	2.3867	0.026	998
Substrate	4	4872.9	1218.2	1.1122	0.323	999
Res	67	73386	1095.3			
Total	86	1.1486E+05				

Pair-wise tests

Depth group	t	P(perm)	Unique perms	P (MC)
70-90. 10-50	1.7271	0.0038	9948	0.0061
70-90. 50-70	1.1178	0.2887	9951	0.2874
70-90. 110-120	2.3251	0.0006	9943	0.0004
70-90. 90-110	1.1112	0.293	9952	0.293
10-50. 50-70	1.1527	0.2436	9943	0.2441
10-50. 110-120	1.6555	0.0085	9948	0.0159
10-50. 90-110	1.7056	0.006	9939	0.0116
50-70. 110-120	1.4659	0.0854	9449	0.1195
50-70. 90-110	1.6573	0.0283	9957	0.0334
110-120. 90-110	1.5367	0.0509	9942	0.0656

Pair-wise tests

Distance to farm	t	P(perm)	Unique perms	P (MC)
200-500. 100-200	1.1005	0.309	997	
200-500. 50-100	0.86914	0.595	999	
200-500. >2000	1.1962	0.192	999	
200-500. 0-50	1.0371	0.381	998	
200-500. 500-2000	No test. df = 0			
100-200. 50-100	0.68157	0.798	998	
100-200. >2000	0.70896	0.821	997	
100-200. 0-50	0.81382	0.649	999	
100-200. 500-2000	No test. df = 0			
50-100. >2000	0.81699	0.612	999	
50-100. 0-50	No test. df = 0			
50-100. 500-2000	No test. df = 0			

>2000. 0-50	No test. df = 0			
>2000. 500-2000	1.8016	0.004	999	
0-50. 500-2000	No test. df = 0			

Pair-wise tests				
TPM flux	**t**	**P(perm)**	**Unique perms**	**P (MC)**
12-14. 14-16	0.57519	0.9046	9949	0.8958
12-14. 10-12	0.50484	0.9475	9944	0.9442
12-14. 8-10	0.7199	0.8134	9941	0.8104
12-14. 6-8	0.76094	0.7498	9944	0.7341
14-16. 10-12	0.89833	0.5248	8042	0.5143
14-16. 8-10	No test. df = 0			
14-16. 6-8	No test. df = 0			
10-12. 8-10	0.29711	0.9152	9947	0.9891
10-12. 6-8	0.54838	0.717	9944	0.8457
8-10. 6-8	1.3892	0.0588	9948	0.0758

Pair-wise tests				
POC	**t**	**P(perm)**	**Unique perms**	**P (MC)**
1. 2	1.6225	0.0135	9944	0.0132

Pair-wise tests				
White bacterial mats	**t**	**P(perm)**	**Unique perms**	**P (MC)**
1. 2	1.1251	0.2777	9945	0.2673

Table A. 5 PERMANOVA table of results for cod dietary items testing the difference between the distance to farm categories cage (0--50 m) and away (>2 km)

Source	df	SS	MS	Pseudo-F	P(perm)	Unique perms	P(MC)
Fjord	2	10261	5130.5	3.1218	0.0001	9878	0.0001
Dist2FarmCat	2	8140.3	4070.1	feb.66	0.0001	9878	0.0002
Res	42	69025	1643.4				
Total	46	82781					

SIMPER

SIMPER similarity tables

Group 0-50
Less than 2 samples in group

Table A. 6 SIMPER table of results for distance group 50-100 m

Group 50-100
Average similarity: 29.72

Species	**Av.Abund**	**Av.Sim**	**Sim/SD**	**Contrib%**	**Cum.%**
Gadus morhua	0.51	11.78	0.95	39.65	39.65
Ascidian	0.39	4.67	0.60	15.72	55.37
Porifera	0.40	3.72	0.61	12.52	67.89
Hormathia digitata	0.43	3.71	0.62	12.49	80.38
Melanogrammus aeglefinus	0.33	2.94	0.32	9.90	90.28
Asteria rubens	0.21	0.97	0.32	3.26	93.54
Ceramaster grannularis	0.18	0.96	0.32	3.25	96.78

Table A. 7 SIMPER table of results for distance group 100-200 m.

Group 100-200
Average similarity: 22.66

Species	**Av.Abund**	**Av.Sim**	**Sim/SD**	**Contrib%**	**Cum.%**
Hormathia digitata	0.43	4.99	0.67	22.00	22.00
Porifera	0.51	4.51	0.55	19.89	41.89
Gadus morhua	0.36	4.33	0.56	19.09	60.98
Melanogrammus aeglefinus	0.34	3.19	0.47	14.09	75.08
Asterias rubens	0.30	2.21	0.39	9.76	84.84
Ascidian	0.28	1.28	0.31	5.64	90.48
Pleuronectes platessa	0.16	0.79	0.24	3.48	93.96
Hippoglossus hippoglossus	0.17	0.66	0.24	2.91	96.88

Table A. 8 SIMPER table of results for distance group 200-500 m.

Group 200-500
Average similarity: 35.22

Species	**Av.Abund**	**Av.Sim**	**Sim/SD**	**Contrib%**	**Cum.%**
Asterias rubens	0.54	9.64	1.14	27.37	27.37
Gadus morhua	0.53	9.14	1.06	25.94	53.31
Porifera	0.66	5.59	0.65	15.86	69.17
Ascidian	0.35	2.82	0.40	8.01	77.18

Melanogrammus aeglefinus	0.31	2.63	0.41	7.48	84.66
Hormathia digitata	0.24	1.40	0.38	3.98	88.64
Hippasteria phryghiana	0.19	1.26	0.39	3.59	92.23
Sebastes	0.16	0.56	0.26	1.58	93.81
Geodia	0.12	0.39	0.22	1.09	94.91
Phakellia/Axinella	0.13	0.31	0.18	0.89	95.79

Table A. 9 SIMPER table of results for distance group 500-2000 m

Group 500-2000					
Average similarity: 40.72					
Species	**Av.Abund**	**Av.Sim**	**Sim/SD**	**Contrib%**	**Cum.%**
Porifera	1.02	20.69	2.77	50.80	50.80
Gadus morhua	0.37	4.91	0.57	12.06	62.86
Hormathia digitata	0.28	3.79	0.64	9.32	72.18
Sebastes	0.30	2.72	0.50	6.67	78.85
Ascidian	0.31	2.58	0.52	6.34	85.19
Phakellia/Axinella	0.28	1.59	0.39	3.92	89.11
Henricia sp.	0.20	1.28	0.38	3.15	92.26
Asterias rubens	0.22	1.19	0.38	2.93	95.19

Table A. 10 SIMPER table of results for distance group >2000 m

Group >2000					
Average similarity: 47.00					
Species	**Av.Abund**	**Av.Sim**	**Sim/SD**	**Contrib%**	**Cum.%**
Porifera	0.75	16.89	2.17	35.94	35.94
Asterias rubens	0.49	10.19	1.10	21.67	57.61
Hormathia digitata	0.44	7.34	0.91	15.61	73.23
Gadus morhua	0.37	5.03	0.77	10.70	83.93
Buccinum undatum	0.23	2.25	0.45	4.79	88.72
Melanogrammus aeglefinus	0.26	2.20	0.41	4.69	93.41
Hippasteria phryghiana	0.16	1.21	0.33	2.58	95.99

SIMPER Dissimilarity tables

Table A. 11 SIMPER dissimilarity tables comparing all distance groups to each other.

Groups 100-200 & 50-100

Average dissimilarity = 70.76

	Group 100-200	**Group 50-100**				
Species	**Av.Abund**	**Av.Abund**	**Av.Diss**	**Diss/SD**	**Contrib%**	**Cum.%**
Porifera	0.51	0.40	8.27	0.97	11.68	11.68
Gadus morhua	0.36	0.51	7.87	0.79	11.12	22.81
Melanogrammus aeglefinus	0.34	0.33	7.72	0.72	10.91	33.71
Ascidian	0.28	0.39	7.36	0.96	10.40	44.11
Hormathia digitata	0.43	0.43	7.15	1.04	10.11	54.22
Asteria rubens	0.30	0.21	5.08	0.98	7.18	61.41
Hippoglossus hippoglossus	0.17	0.14	4.31	0.60	6.09	67.50
Ceramaster grannularis	0.11	0.18	3.31	0.80	4.67	72.17
Mycale sp.	0.00	0.18	2.49	0.76	3.52	75.69
Pleuronectes platessa	0.16	0.00	2.47	0.52	3.49	79.18
Echinoidea	0.09	0.10	2.28	0.60	3.22	82.39
Bolocera tueidae	0.03	0.11	1.99	0.53	2.81	85.20
Metridium senile	0.12	0.00	1.94	0.38	2.73	87.94
Phakellia/Axinella	0.04	0.11	1.72	0.54	2.43	90.37
Sebastes	0.04	0.11	1.66	0.52	2.34	92.71
Hippasteria phryghiana	0.00	0.12	1.63	0.47	2.31	95.02

Groups 200-500 & >2000

Average dissimilarity = 63.55

	Group 200-500	**Group >2000**				
Species	**Av.Abund**	**Av.Abund**	**Av.Diss**	**Diss/SD**	**Contrib%**	**Cum.%**
Porifera	0.66	0.75	8.81	1.55	13.86	13.86
Hormathia digitata	0.24	0.44	5.81	1.13	9.14	23.00
Gadus morhua	0.53	0.37	5.45	1.23	8.57	31.57
Melanogrammus aeglefinus	0.31	0.26	5.16	0.96	8.12	39.69
Ascidian	0.35	0.08	5.12	0.74	8.05	47.74
Asteria rubens	0.54	0.49	4.67	1.10	7.34	55.08
Buccinum undatum	0.00	0.23	3.19	0.79	5.02	60.10
Hippasteria phryghiana	0.19	0.16	3.18	0.91	5.01	65.11
Sebastes	0.16	0.11	2.56	0.75	4.02	69.14
Ceramaster grannularis	0.12	0.10	2.24	0.62	3.53	72.66
Henricia sp.	0.13	0.10	2.19	0.67	3.45	76.11
Phakellia/Axinella	0.13	0.08	2.16	0.65	3.40	79.52
Bolocera tueidae	0.10	0.07	1.81	0.47	2.84	82.36
Geodia	0.12	0.03	1.56	0.59	2.46	84.82
Hippoglossus hippoglossus	0.06	0.07	1.55	0.50	2.43	87.25
Pleuronectes platessa	0.07	0.00	1.19	0.35	1.87	89.12
Echinoidea	0.09	0.00	1.12	0.42	1.76	90.87
Polymastia	0.04	0.05	0.98	0.39	1.54	92.41

Anarhichas lupus	0.02	0.06	0.92	0.37	1.45	93.86
Ophiodromus flexuosus	0.00	0.04	0.62	0.26	0.97	94.84
Mycale sp.	0.02	0.03	0.59	0.33	0.92	95.76
Groups 100-200 & >2000						
Average dissimilarity = 69.86						
	Group 100-200	**Group >2000**				
Species	**Av.Abund**	**Av.Abund**	**Av.Diss**	**Diss/SD**	**Contrib%**	**Cum.%**
Porifera	0.51	0.75	10.29	1.17	14.73	14.73
Asteria rubens	0.30	0.49	7.59	1.09	10.86	25.59
Hormathia digitata	0.43	0.44	7.03	1.03	10.07	35.66
Gadus morhua	0.36	0.37	6.20	1.07	8.87	44.53
Melanogrammus aeglefinus	0.34	0.26	5.90	0.94	8.45	52.98
Ascidian	0.28	0.08	4.05	0.71	5.80	58.77
Buccinum undatum	0.04	0.23	3.91	0.77	5.60	64.37
Hippasteria phryghiana	0.00	0.16	2.63	0.63	3.76	68.13
Hippoglossus hippoglossus	0.17	0.07	2.61	0.68	3.74	71.87
Ceramaster grannularis	0.11	0.10	2.54	0.58	3.63	75.50
Pleuronectes platessa	0.16	0.00	2.36	0.53	3.38	78.88
Sebastes	0.04	0.11	1.85	0.51	2.65	81.54
Metridium senile	0.12	0.00	1.84	0.38	2.64	84.17
Henricia sp.	0.05	0.10	1.61	0.54	2.31	86.48
Phakellia/Axinella	0.04	0.08	1.48	0.49	2.12	88.60
Bolocera tueidae	0.03	0.07	1.33	0.32	1.90	90.49
Echinoidea	0.09	0.00	1.04	0.38	1.48	91.98
Polymastia	0.00	0.05	0.89	0.28	1.27	93.25
Anarhichas lupus	0.00	0.06	0.83	0.31	1.18	94.43
Geodia	0.03	0.03	0.77	0.36	1.10	95.53
Groups 50-100 & >2000						
Average dissimilarity = 65.98						
	Group 50-100	**Group >2000**				
Species	**Av.Abund**	**Av.Abund**	**Av.Diss**	**Diss/SD**	**Contrib%**	**Cum.%**
Porifera	0.40	0.75	7.50	1.16	11.37	11.37
Asteria rubens	0.21	0.49	6.36	1.21	9.64	21.jan
Hormathia digitata	0.43	0.44	6.24	1.15	9.46	30.47
Melanogrammus aeglefinus	0.33	0.26	6.08	0.97	9.21	39.68
Gadus morhua	0.51	0.37	5.79	1.14	8.78	48.46
Ascidian	0.39	0.08	5.51	1.09	8.35	56.80
Buccinum undatum	0.00	0.23	3.37	0.80	5.11	61.91
Hippasteria phryghiana	0.12	0.16	3.06	0.82	4.63	66.55
Hippoglossus hippoglossus	0.14	0.07	3.04	0.59	4.61	71.16
Ceramaster grannularis	0.18	0.10	2.90	0.85	4.40	75.56
Sebastes	0.11	0.11	2.39	0.68	3.62	79.18
Mycale sp.	0.18	0.03	2.37	0.83	3.59	82.78
Bolocera tueidae	0.11	0.07	2.23	0.52	3.38	86.16
Phakellia/Axinella	0.11	0.08	2.07	0.65	3.14	89.30
Echinoidea	0.10	0.00	1.32	0.49	2.00	91.30

Henricia sp.	0.00	0.10	1.25	0.49	1.89	93.19
Mytilus edilus	0.09	0.00	1.05	0.49	1.59	94.78
Polymastia	0.00	0.05	0.77	0.31	1.17	95.96
			Groups 200-500 & 0-50			
			Average dissimilarity = 79.37			
	Group 200-500	**Group 0-50**				
Species	**Av.Abund**	**Av.Abund**	**Av.Diss**	**Diss/SD**	**Contrib%**	**Cum.%**
Asteria rubens	0.54	0.00	13.21	1.46	16.64	16.64
Porifera	0.66	0.00	12.14	1.05	15.30	31.94
Ascidian	0.35	0.00	9.45	0.63	11.91	43.85
Melanogrammus aeglefinus	0.31	0.00	7.25	0.72	9.14	52.99
Gadus morhua	0.53	0.54	6.79	0.80	8.55	61.54
Hormathia digitata	0.24	0.00	4.37	0.70	5.51	67.04
Hippasteria phryghiana	0.19	0.00	3.60	0.73	4.54	71.58
Pleuronectes platessa	0.07	0.00	2.40	0.35	3.03	74.61
Sebastes	0.16	0.00	2.40	0.59	3.02	77.63
Ceramaster grannularis	0.12	0.00	2.11	0.46	2.66	80.29
Phakellia/Axinella	0.13	0.00	2.06	0.47	2.60	82.89
Henricia sp.	0.13	0.00	2.05	0.44	2.59	85.48
Geodia	0.12	0.00	1.99	0.52	2.51	87.99
Echinoidea	0.09	0.00	1.75	0.41	2.20	90.19
Hippoglossus hippoglossus	0.06	0.00	1.70	0.33	2.14	92.33
Bolocera tueidae	0.10	0.00	1.64	0.46	2.07	94.40
Solaster endeca	0.04	0.00	0.88	0.28	1.10	95.50
			Groups 100-200 & 0-50			
			Average dissimilarity = 83.75			
	Group 100-200	**Group 0-50**				
Species	**Av.Abund**	**Av.Abund**	**Av.Diss**	**Diss/SD**	**Contrib%**	**Cum.%**
Gadus morhua	0.36	0.54	21.40	0.65	25.55	25.55
Porifera	0.51	0.00	12.25	0.80	14.63	40.18
Hormathia digitata	0.43	0.00	9.72	0.98	11.61	51.78
Melanogrammus aeglefinus	0.34	0.00	8.12	0.73	9.69	61.48
Asteria rubens	0.30	0.00	6.62	0.71	7.91	69.38
Ascidian	0.28	0.00	5.79	0.57	6.92	76.30
Pleuronectes platessa	0.16	0.00	4.15	0.50	4.95	81.25
Metridium senile	0.12	0.00	3.40	0.38	4.06	85.32
Hippoglossus hippoglossus	0.17	0.00	3.05	0.56	3.65	88.96
Ceramaster grannularis	0.11	0.00	2.80	0.40	3.34	92.30
Echinoidea	0.09	0.00	1.60	0.37	1.91	94.21
Hippoglossoides platessoides	0.04	0.00	0.78	0.26	0.93	95.14
			Groups 50-100 & 0-50			
			Average dissimilarity = 73.44			
	Group 50-100	**Group 0-50**				
Species	**Av.Abund**	**Av.Abund**	**Av.Diss**	**Diss/SD**	**Contrib%**	**Cum.%**
Melanogrammus aeglefinus	0.33	0.00	11.60	0.66	15.80	15.80
Ascidian	0.39	0.00	9.98	0.91	13.59	29.39

Hormathia digitata	0.43	0.00	8.83	0.94	12.02	41.40
Porifera	0.40	0.00	8.05	1.06	10.95	52.36
Gadus morhua	0.51	0.54	6.12	1.45	8.33	60.69
Hippoglossus hippoglossus	0.14	0.00	5.16	0.45	7.03	67.72
Asteria rubens	0.21	0.00	4.00	0.72	5.44	73.16
Ceramaster grannularis	0.18	0.00	3.56	0.73	4.85	78.01
Mycale sp.	0.18	0.00	3.48	0.73	4.74	82.75
Bolocera tueidae	0.11	0.00	2.47	0.45	3.37	86.12
Hippasteria phryghiana	0.12	0.00	2.29	0.45	3.11	89.23
Echinoidea	0.10	0.00	2.17	0.45	2.95	92.18
Sebastes	0.11	0.00	2.05	0.45	2.80	94.98
Phakellia/Axinella	0.11	0.00	2.05	0.45	2.79	97.77

Groups >2000 & 0-50

Average dissimilarity = 85.14

	Group >2000	**Group 0-50**				
Species	**Av.Abund**	**Av.Abund**	**Av.Diss**	**Diss/SD**	**Contrib%**	**Cum.%**
Porifera	0.75	0.00	18.70	2.61	21.97	21.97
Asteria rubens	0.49	0.00	13.20	1.61	15.51	37.47
Hormathia digitata	0.44	0.00	11.25	1.27	13.21	50.68
Gadus morhua	0.37	0.54	7.89	1.08	9.27	59.95
Melanogrammus aeglefinus	0.26	0.00	6.19	0.72	7.27	67.22
Buccinum undatum	0.23	0.00	5.62	0.81	6.60	73.82
Hippasteria phryghiana	0.16	0.00	3.87	0.67	4.55	78.37
Sebastes	0.11	0.00	2.40	0.49	2.81	81.18
Ceramaster grannularis	0.10	0.00	2.10	0.41	2.46	83.64
Henricia sp.	0.10	0.00	1.86	0.49	2.19	85.83
Phakellia/Axinella	0.08	0.00	1.73	0.43	2.04	87.87
Ascidian	0.08	0.00	1.51	0.43	1.77	89.64
Hippoglossus hippoglossus	0.07	0.00	1.46	0.38	1.71	91.35
Polymastia	0.05	0.00	1.37	0.30	1.61	92.96
Bolocera tueidae	0.07	0.00	1.32	0.24	1.55	94.51
Anarhichas lupus	0.06	0.00	1.15	0.32	1.35	95.86

Groups 200-500 & 500-2000

Average dissimilarity = 67.60

	Group 200-500	**Group 500-2000**				
Species	**Av.Abund**	**Av.Abund**	**Av.Diss**	**Diss/SD**	**Contrib%**	**Cum.%**
Porifera	0.66	1.02	10.34	1.35	15.29	15.29
Asteria rubens	0.54	0.22	6.14	1.19	9.08	24.38
Ascidian	0.35	0.31	5.77	0.88	8.54	32.92
Gadus morhua	0.53	0.37	5.41	1.09	8.00	40.92
Melanogrammus aeglefinus	0.31	0.09	4.41	0.84	6.52	47.44
Hormathia digitata	0.24	0.28	4.36	1.13	6.44	53.88
Sebastes	0.16	0.30	4.12	0.93	6.10	59.99
Phakellia/Axinella	0.13	0.28	3.63	0.88	5.38	65.36
Henricia sp.	0.13	0.20	3.08	0.87	4.56	69.92
Lithodidae	0.00	0.28	2.86	0.58	4.24	74.16

Ceramaster grannularis	0.12	0.09	2.32	0.65	3.43	77.59
Hippasteria phryghiana	0.19	0.00	2.24	0.73	3.31	80.90
Mycale sp.	0.02	0.19	2.05	0.65	3.03	83.93
Geodia	0.12	0.09	2.01	0.70	2.97	86.90
Hippoglossus hippoglossus	0.06	0.05	1.27	0.45	1.88	88.77
Pleuronectes platessa	0.07	0.00	1.17	0.34	1.74	90.51
Echinoidea	0.09	0.00	1.10	0.41	1.62	92.13
Bolocera tueidae	0.10	0.00	1.06	0.46	1.57	93.70
Polymastia	0.04	0.05	0.90	0.42	1.33	95.03

Groups 100-200 & 500-2000

Average dissimilarity = 73.88

	Group 100-200	**Group 500-2000**				
Species	**Av.Abund**	**Av.Abund**	**Av.Diss**	**Diss/SD**	**Contrib%**	**Cum.%**
Porifera	0.51	1.02	13.25	1.22	17.93	17.93
Gadus morhua	0.36	0.37	6.63	0.79	8.97	26.90
Hormathia digitata	0.43	0.28	6.24	1.12	8.44	35.35
Ascidian	0.28	0.31	5.76	0.94	7.79	43.14
Melanogrammus aeglefinus	0.34	0.09	4.99	0.90	6.76	49.90
Asteria rubens	0.30	0.22	4.87	0.96	6.59	56.49
Sebastes	0.04	0.30	4.62	0.78	6.25	62.74
Phakellia/Axinella	0.04	0.28	3.61	0.78	4.88	67.62
Lithodidae	0.00	0.28	3.16	0.57	4.28	71.91
Henricia sp.	0.05	0.20	3.01	0.76	4.07	75.98
Ceramaster grannularis	0.11	0.09	2.65	0.60	3.59	79.56
Pleuronectes platessa	0.16	0.00	2.32	0.52	3.14	82.71
Hippoglossus hippoglossus	0.17	0.05	2.28	0.65	3.08	85.79
Mycale sp.	0.00	0.19	2.10	0.61	2.85	88.63
Metridium senile	0.12	0.00	1.81	0.37	2.46	91.09
Geodia	0.03	0.09	1.52	0.54	2.06	93.15
Echinoidea	0.09	0.00	1.02	0.38	1.38	94.52
Buccinum undatum	0.04	0.05	0.96	0.41	1.30	95.83

Groups 50-100 & 500-2000

Average dissimilarity = 66.90

	Group 50-100	**Group 500-2000**				
Species	**Av.Abund**	**Av.Abund**	**Av.Diss**	**Diss/SD**	**Contrib%**	**Cum.%**
Porifera	0.40	1.02	10.40	1.25	15.55	15.55
Melanogrammus aeglefinus	0.33	0.09	5.65	0.83	8.45	24.00
Hormathia digitata	0.43	0.28	5.55	1.24	8.30	32.30
Gadus morhua	0.51	0.37	5.48	1.08	8.18	40.49
Ascidian	0.39	0.31	5.39	1.02	8.06	48.55
Sebastes	0.11	0.30	4.24	0.91	6.34	54.89
Phakellia/Axinella	0.11	0.28	3.69	0.89	5.52	60.41
Asteria rubens	0.21	0.22	3.57	0.98	5.34	65.75
Mycale sp.	0.18	0.19	3.20	0.96	4.78	70.53
Lithodidae	0.00	0.28	2.99	0.58	4.47	75.00
Ceramaster grannularis	0.18	0.09	2.84	0.83	4.24	79.24

Hippoglossus hippoglossus	0.14	0.05	2.82	0.53	4.21	83.45
Henricia sp.	0.00	0.20	2.59	0.76	3.87	87.32
Bolocera tueidae	0.11	0.00	1.48	0.48	2.21	89.54
Hippasteria phryghiana	0.12	0.00	1.44	0.48	2.15	91.68
Echinoidea	0.10	0.00	1.30	0.48	1.94	93.62
Geodia	0.00	0.09	1.16	0.49	1.74	95.36

Groups >2000 & 500-2000

Average dissimilarity = 61.17

	Group >2000	**Group 500-2000**				
Species	**Av.Abund**	**Av.Abund**	**Av.Diss**	**Diss/SD**	**Contrib%**	**Cum.%**
Porifera	0.75	1.02	6.15	1.27	10.05	10.05
Asteria rubens	0.49	0.22	6.03	1.23	9.86	19.91
Gadus morhua	0.37	0.37	5.32	1.10	8.70	28.61
Hormathia digitata	0.44	0.28	4.93	1.21	8.06	36.67
Sebastes	0.11	0.30	4.17	0.97	6.82	43.49
Ascidian	0.08	0.31	3.99	0.97	6.53	50.02
Melanogrammus aeglefinus	0.26	0.09	3.85	0.84	6.29	56.31
Phakellia/Axinella	0.08	0.28	3.53	0.90	5.77	62.08
Buccinum undatum	0.23	0.05	3.29	0.83	5.38	67.46
Lithodidae	0.03	0.28	3.09	0.63	5.06	72.51
Henricia sp.	0.10	0.20	2.90	0.89	4.74	77.26
Ceramaster grannularis	0.10	0.09	2.24	0.63	3.66	80.92
Hippasteria phryghiana	0.16	0.00	2.23	0.67	3.65	84.57
Mycale sp.	0.03	0.19	2.14	0.68	3.50	88.07
Geodia	0.03	0.09	1.37	0.55	2.24	90.32
Polymastia	0.05	0.05	1.27	0.44	2.07	92.39
Hippoglossus hippoglossus	0.07	0.05	1.26	0.49	2.05	94.44
Anarhichas lupus	0.06	0.05	1.10	0.44	1.81	96.25

Groups 0-50 & 500-2000

Average dissimilarity = 83.63

	Group 0-50	**Group 500-2000**				
Species	**Av.Abund**	**Av.Abund**	**Av.Diss**	**Diss/SD**	**Contrib%**	**Cum.%**
Porifera	0.00	1.02	24.65	2.35	29.47	29.47
Gadus morhua	0.54	0.37	8.46	1.28	10.12	39.59
Hormathia digitata	0.00	0.28	7.27	0.99	8.69	48.28
Sebastes	0.00	0.30	6.78	0.80	8.10	56.38
Ascidian	0.00	0.31	6.21	0.86	7.43	63.81
Phakellia/Axinella	0.00	0.28	4.80	0.76	5.74	69.55
Lithodidae	0.00	0.28	4.19	0.56	5.01	74.55
Henricia sp.	0.00	0.20	4.09	0.73	4.89	79.44
Asteria rubens	0.00	0.22	3.95	0.73	4.72	84.16
Mycale sp.	0.00	0.19	2.76	0.60	3.30	87.46
Melanogrammus aeglefinus	0.00	0.09	2.54	0.43	3.03	90.50
Ceramaster grannularis	0.00	0.09	2.53	0.46	3.02	93.52
Geodia	0.00	0.09	1.75	0.47	2.10	95.62

ANOSIM

Tests for differences between unordered Dist2Farm groups
Global Test
Sample statistic (R): 0.18
Significance level of sample statistic: 0.01%
Number of permutations: 9999 (Random sample from a large number)
Number of permuted statistics greater than or equal to R: 0

Table A. 12 ANOSIM result table. Differences in epifaunal taxa distribution between the distance groups

Groups	**R Statistic**	**Significance Level %**	**Possible Permutations**	**Actual Permutations**	**Number >=Observed**
200-500, 100-200	0.111	2.8	Very large	9999	277
200-500, 50-100	0	49.5	169911	9999	4951
200-500, >2000	0.154	0.01	Very large	9999	0
200-500, 0-50	0.136	33.3	27	27	9
200-500, 500-2000	0.111	5.7	254186856	9999	569
100-200, 50-100	-0.133	90.8	15504	9999	9080
100-200, >2000	0.302	0.01	Very large	9999	0
100-200, 0-50	-0.086	62.5	16	16	10
100-200, 500-2000	0.133	4.2	3268760	9999	414
50-100, >2000	0.328	2.4	324632	9999	234
50-100, 0-50	-0.24	100	6	6	6
50-100, 500-2000	0.185	6.8	3003	3003	203
>2000, 0-50	0.619	6.5	31	31	2
>2000, 500-2000	0.242	1	847660528	9999	97
0-50, 500-2000	0.507	9.1	11	11	1

BEST

Global Test
Sample statistic (Rho): 0.249
Significance level of sample statistic: 0.2%
Number of permutations: 999 (Random sample)
Number of permuted statistics greater than or equal to Rho: 1

Table A. 13 BEST results table showing the correlations between the biological abundance data and environmental variables

No.Vars	**Correlations**	**Selections**
1	0.249	White bacterial mats
2	0.172	Whitebacterial mats. Substrate
3	0.169	TPMFlux. White bacterial mats. Substrate
2	0.157	TPMFlux. White bacterial mats

2	0.155	TPMFlux. Substrate
1	0.134	TPMFlux
1	0.093	Substrate
4	-0.025	Depth. TPMFlux. White bacterial mats. Substrate
3	-0.025	Depth. TPMFlux. Substrate
3	-0.025	Depth. TPMFlux. White bacterial mats

GLM

Table A. 14 Generalized linear model (GLM) of the effect from Distance group on the average densities of Porifera

			Porifera		
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**	
Distance group	-0.29231	-0.29231	-4.788	1.68e-06	***

Table A. 15 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Porifera.

			Porifera		
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	2. 2.8958	4.532	Inf	0.639	0.9881
>2000 - (100-200)	-1.8864	0.274	Inf	-6.881	<.0001
>2000 - (200-500)	-1.0702	0.287	Inf	-3.725	0.0027
>2000 - (50-100)	3.9477	4.948	Inf	0.798	0.9680
>2000 - (500-2000)	-1.1638	0.333	Inf	-3.493	0.0064
(0-50) - (100-200)	-4.7822	4.527	Inf	1.056	0.8985
(0-50) - (200-500)	-3.9661	4.528	Inf	-0.876	0.9523
(0-50) - (50-100)	1.0519	6.701	Inf	0.157	1.0000
(0-50) - (500-2000)	-4.0596	4.531	Inf	-0.896	0.9476
(100-200) - (200-500)	0.8161	0.196	Inf	4.154	0.0005
(100-200) - (50-100)	5.8341	4.943	Inf	1.180	0.8465
(100-200) - (500-2000)	0.7225	0.259	Inf	2.790	0.0590
(200-500) - (50-100)	5.0179	4.944	Inf	1.015	0.9131
(200-500) - (500-2000)	-0.0936	0.273	Inf	-0.343	0.9994
(50-100) - (500-2000)	-5.1115	4.947	Inf	-1.033	0.9068

Table A. 16 Generalized linear model (GLM) of the effect from Distance group on the average densities of Ascidia sp.

			Ascidian		
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**	
Distance group	-0.5986	0.1382	-4.332	1.47e-05	***

Table A. 17 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Ascidia sp.

Ascidian					
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	10.3084	895.399	Inf	0.012	1.0000
>2000 - (100-200)	-4.8622	1.969	Inf	-2.470	0.1332
>2000 - (200-500)	-3.5584	1.987	Inf	-1.791	0.4716
>2000 - (50-100)	-2.3832	2.573	Inf	-0.926	0.9399
>2000 - (500-2000)	-2.3224	2.205	Inf	-1.053	0.8997
(0-50) - (100-200)	-15.1706	895.397	Inf	-0.017	1.0000
(0-50) - (200-500)	-13.8668	895.397	Inf	-0.015	1.0000
(0-50) - (50-100)	-12.6916	895.399	Inf	-0.014	1.0000
(0-50) - (500-2000)	-12.6308	895.398	Inf	-0.014	1.0000
(100-200) - (200-500)	1.3038	0.417	Inf	3.127	0.0218
(100-200) - (50-100)	2.4790	1.687	Inf	1.470	0.6837
(100-200) - (500-2000)	2.5399	1.044	Inf	2.434	0.1446
(200-500) - (50-100)	1.1752	1.708	Inf	0.688	0.9833
(200-500) - (500-2000)	1.2361	1.077	Inf	1.147	0.8614
(50-100) - (500-2000)	0.0609	1.958	Inf	0.031	1.0000

Table A. 18 Generalized linear model (GLM) of the effect from Distance group on the average densities of Ceramster grannularis.

		Ceramaster grannularis		
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	0.2062	0.4862	0.424	0.67147

Table A. 19 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Ceramster grannularis.

		Ceramaster grannularis			
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	15.370	6616.14	Inf	0.002	1
>2000 - (100-200)	1.313	3.13	Inf	0.419	0.9984
>2000 - (200-500)	0.458	1.5	Inf	-0.304	0.9997
>2000 - (50-100)	15.37	4270.7	Inf	0.004	1
>2000 - (500-2000)	-1.042	1.62	Inf	-0.644	0.9876
(0-50) - (100-200)	-14.057	6616.14	Inf	-0.002	1
(0-50) - (200-500)	-15.828	6616.14	Inf	-0.002	1
(0-50) - (50-100)	0	7874.78	Inf	0	1
(0-50) - (500-2000)	-16.411	6616.14	Inf	-0.002	1
(100-200) - (200-500)	-1.771	3.07	Inf	-0.576	0.9926
(100-200) - (50-100)	14.057	4270.7	Inf	0.003	1
(100-200) - (500-2000)	-2.354	3.13	Inf	-0.753	0.9752
(200-500) - (50-100)	15.828	4270.7	Inf	0.004	1
(200-500) - (500-2000)	-0.583	1.5	Inf	-0.39	0.9988

(50-100) - (500-2000)	-16.411	4270.7	Inf	-0.004	1

Table A. 20 Generalized linear model (GLM) of the effect from Distance group on the average densities of Phakellia/Axinella.

Phakellia/Axinella				
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	-0.03499	0.42555	-0.082	0.93447

Table A. 21 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of the sponges Phakellia/Axinella.

Phakellia/Axinella					
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	12.961	4012.89	Inf	0.003	1
>2000 - (100-200)	-0.648	3.21	Inf	-0.202	1
>2000 - (200-500)	-2.151	2.48	Inf	-0.869	0.9538
>2000 - (50-100)	-1.239	4.22	Inf	-0.293	0.9997
>2000 - (500-2000)	-2.903	2.5	Inf	-1.162	0.8548
(0-50) - (100-200)	-13.609	4012.89	Inf	-0.003	1
(0-50) - (200-500)	-15.112	4012.89	Inf	-0.004	1
(0-50) - (50-100)	-14.2	4012.89	Inf	-0.004	1
(0-50) - (500-2000)	-15.863	4012.89	Inf	-0.004	1
(100-200) - (200-500)	-1.503	2.37	Inf	-0.635	0.9884
(100-200) - (50-100)	-0.591	4.16	Inf	-0.142	1
(100-200) - (500-2000)	-2.255	2.39	Inf	-0.943	0.9353
(200-500) - (50-100)	0.912	3.62	Inf	0.252	0.9999
(200-500) - (500-2000)	-0.752	1.24	Inf	-0.607	0.9906
(50-100) - (500-2000)	-1.663	3.64	Inf	-0.457	0.9975

Table A. 22 Generalized linear model (GLM) of the effect from Distance group on the average densities of Henricia sp.

Henricia sp.				
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	-0.07253	0.47671	-0.152	0.8791

Table A. 23 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of the seastar Henricia sp.

Henricia sp.					
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	14.364	6616.14	Inf	0.002	1
>2000 - (100-200)	-0.268	2.9	Inf	-0.093	1
>2000 - (200-500)	-1.809	2.07	Inf	-0.874	0.9528
>2000 - (50-100)	14.364	4270.7	Inf	0.003	1

>2000 - (500-2000)	-1.51	2.41	Inf	-0.626	0.9892
(0-50) - (100-200)	-14.632	6616.14	Inf	-0.002	1
(0-50) - (200-500)	-16.173	6616.14	Inf	-0.002	1
(0-50) - (50-100)	0	7874.78	Inf	0	1
(0-50) - (500-2000)	-15.875	6616.14	Inf	-0.002	1
(100-200) - (200-500)	-1.541	2.33	Inf	-0.66	0.9862
(100-200) - (50-100)	14.632	4270.7	Inf	0.003	1
(100-200) - (500-2000)	-1.242	2.64	Inf	-0.47	0.9972
(200-500) - (50-100)	16.173	4270.7	Inf	0.004	1
(200-500) - (500-2000)	0.298	1.7	Inf	0.176	1
(50-100) - (500-2000)	-15.875	4270.7	Inf	-0.004	1

Table A. 24 Generalized linear model (GLM) of the effect from Distance group on the average densities of Asterias rubens.

Asterias rubens				
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	0.0795	0.2065	0.385	0.7

Table A. 25 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of the seastar Asterias rubens.

Asterias rubens					
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	15.237	2433.942	Inf	0.006	1
>2000 - (100-200)	0.368	0.846	Inf	0.435	0.998
>2000 - (200-500)	-0.399	0.599	Inf	-0.666	0.0956
>2000 - (50-100)	2.714	4.963	Inf	0.547	0.9942
>2000 - (500-2000)	1.305	1.514	Inf	0.862	0.9554
(0-50) - (100-200)	-14.869	2433.942	Inf	-0.006	1
(0-50) - (200-500)	-15.636	2433.942	Inf	-0.006	1
(0-50) - (50-100)	-12.523	2433.942	Inf	-0.005	1
(0-50) - (500-2000)	-13.932	2433.942	Inf	-0.006	1
(100-200) - (200-500)	-0.767	0.815	Inf	-0.941	0.9359
(100-200) - (50-100)	2.346	4.994	Inf	0.47	0.9972
(100-200) - (500-2000)	0.937	1.612	Inf	0.582	0.9923
(200-500) - (50-100)	3.113	4.958	Inf	0.628	0.989
(200-500) - (500-2000)	1.704	1.497	Inf	1.138	0.8654
(50-100) - (500-2000)	-1.409	5.149	Inf	-0.274	0.9998

Table A. 26 Generalized linear model (GLM) of the effect from Distance group on the average densities of Hormathia digitata.

Hormathia digitata				
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	-0.08224	0.20521	-0.401	0.689

Table A. 27 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of the sea anemone Hormathia digitata.

Hormathia digitata					
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	-1.173	1.151	Inf	-1.019	0.9118
>2000 - (100-200)	-0.161	0.69	Inf	-0.234	0.9999
>2000 - (200-500)	0.538	0.751	Inf	0.717	0.98
>2000 - (50-100)	0.712	1.817	Inf	0.392	0.9988
>2000 - (500-2000)	1.33	1.486	Inf	0.895	0.9479
(0-50) - (100-200)	1.012	1.19	Inf	0.85	0.9579
(0-50) - (200-500)	1.712	1.227	Inf	1.395	0.7922
(0-50) - (50-100)	1.885	2.06	Inf	0.915	0.9427
(0-50) - (500-2000)	2.503	1.774	Inf	1.411	0.7206
(100-200) - (200-500)	0.7	0.809	Inf	0.864	0.9549
(100-200) - (50-100)	0.873	1.842	Inf	0.474	0.997
(100-200) - (500-2000)	1.491	1.516	Inf	0.983	0.9234
(200-500) - (50-100)	0.174	1.866	Inf	0.093	1
(200-500) - (500-2000)	0.791	1.545	Inf	0.512	0.9957
(50-100) - (500-2000)	0.618	2.264	Inf	0.273	0.9998

Table A. 28 Generalized linear model (GLM) of the effect from Distance group on the average densities of Echinoidea.

Echinoidea				
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	-0.4960	0.7482	-0.663	0.5074

Table A. 29 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Echinoidea.

Echinoidea					
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	0	30421,78	Inf	0	1
>2000 - (100-200)	-18,091	6802,52	Inf	-0,003	1
>2000 - (200-500)	-18,240	6802,52	Inf	-0,003	1
>2000 - (50-100)	-17,861	6802,52	Inf	-0,003	1
>2000 - (500-2000)	0	13202,83	Inf	0	1
(0-50) - (100-200)	-18,091	29651,48	Inf	-0,001	1
(0-50) - (200-500)	-18,24	29651,48	Inf	-0,001	1
(0-50) - (50-100)	17,861	29651,48	Inf	-0,001	1
(0-50) - (500-2000)	0	31737,22	Inf	0	1
(100-200) - (200-500)	-0,149	2,17	Inf	-0,069	1
(100-200) - (50-100)	0,230	4,52	Inf	0,051	1
(100-200) - (500-2000)	18,091	11315,49	Inf	0,002	1

(200-500) - (50-100)	0,379	4,37	Inf	0,087	1
(200-500) - (500-2000)	18240	11315,49	Inf	0,002	1
(50-100) - (500-2000)	17,861	11315,49	Inf	0,002	1

Table A. 30 Generalized linear model (GLM) of the effect from Distance group on the average densities of Bolocera tueidae.

	Bolocera tueidae			
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	1.1594	0.6698	1.731	0.08344

Table A. 31Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Bolcera tueidae.

	Bolocera tueidae				
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	0.877	3.24	Inf	0.271	0.9998
>2000 - (100-200)	3.165	3.07	Inf	1.032	0.9073
>2000 - (200-500)	2.582	1.89	Inf	1.367	0.7469
>2000 - (50-100)	17.144	4270.7	Inf	0.004	1
>2000 - (500-2000)	17.144	2524.83	Inf	0.007	1
(0-50) - (100-200)	2.288	4.41	Inf	0.519	0.9955
(0-50) - (200-500)	1.705	3.69	Inf	0.462	0.9974
(0-50) - (50-100)	16.267	4270.7	Inf	0.004	1
(0-50) - (500-2000)	16.267	2524.83	Inf	0.006	1
(100-200) - (200-500)	-0.583	3.54	Inf	-0.165	1
(100-200) - (50-100)	13.979	4270.7	Inf	0.003	1
(100-200) - (500-2000)	13.979	2524.83	Inf	0.006	1
(200-500) - (50-100)	14.562	4270.7	Inf	0.003	1
(200-500) - (500-2000)	14.562	2524.83	Inf	0.006	1
(50-100) - (500-2000)	0	4961.21	Inf	0	1

Table A. 32 Generalized linear model (GLM) of the effect from Distance group on the average densities of Bryozoa.

	Bryozoa			
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	0.3515	0.413	0.851	0.3947

Table A. 33 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Bryozoa.

	Bryozoa				
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	14.86	17984.53	Inf	0.001	1
>2000 - (100-200)	14.86	5422.54	Inf	0.003	1

>2000 - (200-500)	14.87	4379.1	Inf	0.003	1
>2000 - (50-100)	15.86	11608.97	Inf	0.001	1
>2000 - (500-2000)	-5.24	4.07	Inf	-1.289	0.7911
(0-50) - (100-200)	0	18784.23	Inf	0	1
(0-50) - (200-500)	0	18510	Inf	0	1
(0-50) - (50-100)	0	21405.88	Inf	0	1
(0-50) - (500-2000)	-20.1	17984.53	Inf	-0.001	1
(100-200) - (200-500)	0	6969.97	Inf	0	1
(100-200) - (50-100)	0	12812.97	Inf	0	1
(100-200) - (500-2000)	-20.1	5422.54	Inf	-0.004	1
(200-500) - (50-100)	0	12407.44	Inf	0	1
(200-500) - (500-2000)	-20.1	4379.1	Inf	-0.005	1
(50-100) - (500-2000)	-20.1	11608.97	Inf	-0.002	1

Table A. 34 Generalized linear model (GLM) of the effect from Distance group on the average densities of Mycale.

	Mycale			
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	0.2255	0.769	0.293	0.7693

Table A. 35 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Mycale.

	Mycale				
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	13.97	10908.17	Inf	0.001	1
>2000 - (100-200)	-0.736	5.16	Inf	-0.143	1
>2000 - (200-500)	-0.381	5.08	Inf	-0.075	1
>2000 - (50-100)	13.97	7041.19	Inf	0.002	1
>2000 - (500-2000)	-3.545	3.97	Inf	-0.893	0.9483
(0-50) - (100-200)	-14.706	10908.17	Inf	-0.001	1
(0-50) - (200-500)	-14.351	10908.17	Inf	-0.001	1
(0-50) - (50-100)	0	12983.32	Inf	0	1
(0-50) - (500-2000)	-17.514	4.83	Inf	-0.002	1
(100-200) - (200-500)	0.355	7041.19	Inf	0.074	1
(100-200) - (50-100)	14.706	3.64	Inf	0.002	1
(100-200) - (500-2000)	-2.808	7041.19	Inf	-0.772	0.9722
(200-500) - (50-100)	14.351	3.52	Inf	0.002	1
(200-500) - (500-2000)	-3.163	7041.19	Inf	-0.899	0.947
(50-100) - (500-2000)	-17.514	1.958	Inf	-0.002	1

Table A. 36 Generalized linear model (GLM) of the effect from Distance group on the average densities of Gadus morhua.

Gadus morhua

Coefficients	Estimate	Std.Error	z value	Pr(>|z|)
Distance group	-0.04089	0.20037	-0.204	0.838

Table A. 37 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Gadus morhua.

		Gadus morhua			
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	0.9063	17984.53	Inf	0.001	1
>2000 - (100-200)	0.15	5422.54	Inf	0.003	1
>2000 - (200-500)	-0.5325	4.01	Inf	0.502	0.9961
>2000 - (50-100)	-0.4485	11608.97	Inf	0.001	1
>2000 - (500-2000)	0.1239	4.46	Inf	0.302	0.9997
(0-50) - (100-200)	-0.7563	18784.23	Inf	0	1
(0-50) - (200-500)	-1.4388	17984.53	Inf	0.302	1
(0-50) - (50-100)	-1.3548	21405.88	Inf	0	1
(0-50) - (500-2000)	-0.7824	17984.53	Inf	-0.001	1
(100-200) - (200-500)	-0.6825	5422.54	Inf	0	1
(100-200) - (50-100)	-0.5986	12812.97	Inf	-0.001	1
(100-200) - (500-2000)	-0.0261	5422.54	Inf	-0.003	1
(200-500) - (50-100)	0.084	11608.97	Inf	0.001	1
(200-500) - (500-2000)	0.6564	5.7	Inf	-0.116	1
(50-100) - (500-2000)	0.5725	11608.97	Inf	-0.001	1

Table A. 38 Generalized linear model (GLM) of the effect from Distance group on the average densities of Anarhicas lupus.

		Anarhichas lupus		
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	1.186	1.808	0.656	0.512

Table A. 39 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Anarhichsa lupus.

		Anarhichas lupus			
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	17,117	17984,53	Inf	0,001	1
>2000 - (100-200)	17,117	5422,54	Inf	0,003	1
>2000 - (200-500)	2,012	4,01	Inf	0,502	0,9961
>2000 - (50-100)	17,117	11608,97	Inf	0,001	1
>2000 - (500-2000)	1,348	4,46	Inf	0,302	0,9997
(0-50) - (100-200)	0	18784,23	Inf	0	1
(0-50) - (200-500)	-15,104	17984,53	Inf	0,302	1
(0-50) - (50-100)	0	21405,88	Inf	0	1
(0-50) - (500-2000)	-15,768	17984,53	Inf	-0,001	1
(100-200) - (200-500)	-15,104	5422,54	Inf	0	1

(100-200) - (50-100)	0	12812,97	Inf	-0,001	1
(100-200) - (500-2000)	-15,768	5422,54	Inf	-0,003	1
(200-500) - (50-100)	15,104	11608,97	Inf	0,001	1
(200-500) - (500-2000)	-0,664	5,7	Inf	-0,116	1
(50-100) - (500-2000)	-15,768	11608,97	Inf	-0,001	1

Table A. 40 Generalized linear model (GLM) of the effect from Distance group on the average densities of Hippoglossus hippoglossus.

	Hippoglossus hippoglossus			
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	-0,5108	0,6059	-0,843	0,3993

Table A. 41 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Hippoglossus hippoglossus.

		Hippoglossus hippoglossus			
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	12.9360	4012.89	Inf	0.003	1
>2000 - (100-200)	-1.6354	2.72	Inf	-0.6	0.991
>2000 - (200-500)	-0.68	2.95	Inf	-0.23	0.9999
>2000 - (50-100)	-2.6945	2.92	Inf	-0.923	0.9407
>2000 - (500-2000)	-0.6652	3.67	Inf	-0.181	1
(0-50) - (100-200)	-14.5714	4012.89	Inf	-0.004	1
(0-50) - (200-500)	-13.6159	4012.89	Inf	-0.003	1
(0-50) - (50-100)	-15.6304	4012.89	Inf	-0.004	1
(0-50) - (500-2000)	-13.6012	4012.89	Inf	-0.003	1
(100-200) - (200-500)	0.9554	2.24	Inf	0.426	0.9982
(100-200) - (50-100)	-1.059	2.2	Inf	-0.481	0.9968
(100-200) - (500-2000)	0.9702	3.12	Inf	0.31	0.9996
(200-500) - (50-100)	-2.0145	2.48	Inf	-0.813	0.9652
(200-500) - (500-2000)	0.0147	3.33	Inf	0.004	1
(50-100) - (500-2000)	2.0292	3.3	Inf	0.616	0.9899

Table A. 42 Generalized linear model (GLM) of the effect from Distance group on the average densities of Pleuronectes platessa.

	Pleuronectes platessa			
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	-0,05248	0,6509	-1,108	0,268

Table A. 43 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Pleuronectes platessa.

		Pleuronectes platessa			
Contrasts	**Estimate**	**SE**	**df**	**z,ratio**	**p,value**

>2000 - (0-50)	0,00	30421,78	Inf	0	1
>2000 - (100-200)	-19,36	6802,52	Inf	-0,003	1
>2000 - (200-500)	-17,13	6802,52	Inf	-0,003	1
>2000 - (50-100)	0	20312,85	Inf	0	1
>2000 - (500-2000)	0	13202,83	Inf	0	1
(0-50) - (100-200)	-19,36	29651,48	Inf	-0,001	1
(0-50) - (200-500)	-17,13	29651,48	Inf	-0,001	1
(0-50) - (50-100)	0	35292,32	Inf	0	1
(0-50) - (500-2000)	0	31737,22	Inf	0	1
(100-200) - (200-500)	2,22	2,45	Inf	0,908	0,9446
(100-200) - (50-100)	19,36	1939,95	Inf	0,001	1
(100-200) - (500-2000)	19,36	11315,49	Inf	0,002	1
(200-500) - (50-100)	17,13	19139,95	Inf	0,001	1
(200-500) - (500-2000)	17,13	11315,49	Inf	0,002	1
(50-100) - (500-2000)	0	22234,61	Inf	0	1

Table A. 44 Generalized linear model (GLM) of the effect from Distance group on the average densities of Glyptocephalus cynoglossus.

	Glyptocephalus cynoglossus			
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	-0,8051	2,7709	-0,291	0,771

Table A. 45 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Glyptocephalus cynoglossus.

		Glyptocephalus cynoglossus			
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	0	136341	Inf	0	1
>2000 - (100-200)	-19,6	30487	Inf	-0,001	1
>2000 - (200-500)	0	44457	Inf	0	1
>2000 - (50-100)	0	91036	Inf	0	1
>2000 - (500-2000)	0	59171	Inf	0	1
(0-50) - (100-200)	-19,6	132889	Inf	0	1
(0-50) - (200-500)	0	136771	Inf	0	1
(0-50) - (50-100)	0	158169	Inf	0	1
(0-50) - (500-2000)	0	142236	Inf	0	1
(100-200) - (200-500)	19,6	32357	Inf	0	1
(100-200) - (50-100)	19,6	85779	Inf	0	1
(100-200) - (500-2000)	19,6	50713	Inf	0	1
(200-500) - (50-100)	0	91679	Inf	0	1
(200-500) - (500-2000)	0	60156	Inf	0	1
(50-100) - (500-2000)	0	99649	Inf	0	1

Table A. 46 Generalized linear model (GLM) of the effect from Distance group on the average densities of Sebastes.

		Sebastes		
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	-0,06764	0,51809	-0,131	0,8961

Table A. 47 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Sebastes.

			Sebastes		
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	0,2955	0,2632	Inf	1,123	0,8721
>2000 - (100-200)	-0,1319	0,081	Inf	-1,628	0,5798
>2000 - (200-500)	-0,1575	0,0716	Inf	-2,201	0,2373
>2000 - (50-100)	-0,0128	0,1517	Inf	-0,084	1
>2000 - (500-2000)	-0,1757	0,0931	Inf	-1,887	0,4104
(0-50) - (100-200)	-0,4274	0,2657	Inf	-1,608	0,5929
(0-50) - (200-500)	-0,4531	0,263	Inf	-1,723	0,5167
(0-50) - (50-100)	-0,3083	0,2951	Inf	-1,045	0,9027
(0-50) - (500-2000)	-0,4712	0,2697	Inf	-1,747	0,5003
(100-200) - (200-500)	-0,0256	0,0804	Inf	-0,319	0,9996
(100-200) - (50-100)	0,1191	0,1561	Inf	0,763	0,9736
(100-200) - (500-2000)	-0,0438	0,1001	Inf	-0,437	0,998
(200-500) - (50-100)	0,1448	0,1514	Inf	0,956	0,9316
(200-500) - (500-2000)	-0,0182	0,0926	Inf	-0,196	1
(50-100) - (500-2000)	-0,1629	0,1627	Inf	-1,001	0,9176

Table A. 48 Generalized linear model (GLM) of the effect from Distance group on the average densities of Melanogrammus aeglefinus.

		Melanogrammus aeglefinus		
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	-0,1527	0,2256	-0,677	0,498603

Table A. 49 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Melanogrammus aeglefinus.

			Melanogrammus aeglefinus		
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	-0,5141	2,003	Inf	-0,257	0,9998
>2000 - (100-200)	-0,2235	0,879	Inf	-0,254	0,9999
>2000 - (200-500)	-0,4702	0,744	Inf	-0,632	0,9886
>2000 - (50-100)	-0,4876	1,379	Inf	-0,354	0,9993
>2000 - (500-2000)	2,6837	3,67	Inf	0,731	0,9781
(0-50) - (100-200)	0,2906	2,034	Inf	0,143	1
(0-50) - (200-500)	0,044	1,979	Inf	0,022	1

(0-50) - (50-100)	0,0266	2,295	Inf	0,012	1
(0-50) - (500-2000)	3,1978	4,103	Inf	0,779	0,9711
(100-200) - (200-500)	-0,2467	0,823	Inf	-0,3	0,9997
(100-200) - (50-100)	-0,2641	1,423	Inf	-0,186	1
(100-200) - (500-2000)	2,9072	3,687	Inf	0,788	0,9696
(200-500) - (50-100)	-0,0174	1,344	Inf	-0,013	1
(200-500) - (500-2000)	3,1539	1,657	Inf	0,862	0,9553
(50-100) - (500-2000)	3,1713	3,837	Inf	0,826	0,9627

Table A. 50 Generalized linear model (GLM) of the effect from Distance group on the average densities of Hippoglossoides platessoides.

	Hippoglodssoides platessoides			
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	-0,5108	0,6059	-0,843	0,3993

Table A. 51 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Hippoglossoides platessoides.

	Hippoglossoides platessoides				
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	12,9360	4012,89	Inf	0,003	1
>2000 - (100-200)	-1,6354	2,72	Inf	-0,6	0,991
>2000 - (200-500)	-0,68	2,95	Inf	-0,23	0,9999
>2000 - (50-100)	-2,6945	2,92	Inf	-0,923	0,9407
>2000 - (500-2000)	-0,6652	3,67	Inf	-0,181	1
(0-50) - (100-200)	-14,5714	4012,89	Inf	-0,004	1
(0-50) - (200-500)	-13,6159	4012,89	Inf	-0,003	1
(0-50) - (50-100)	-15,6304	4012,89	Inf	-0,004	1
(0-50) - (500-2000)	-13,6012	4012,89	Inf	-0,003	1
(100-200) - (200-500)	0,9554	2,24	Inf	0,426	0,9982
(100-200) - (50-100)	-1,059	2,2	Inf	-0,481	0,9968
(100-200) - (500-2000)	0,9702	3,12	Inf	0,31	0,9996
(200-500) - (50-100)	-2,0145	2,48	Inf	-0,813	0,9652
(200-500) - (500-2000)	0,0147	3,33	Inf	0,004	1
(50-100) - (500-2000)	2,0292	3,3	Inf	0,616	0,9899

Table A. 52 Demersal fish species observed in towed camera transects in the 6 distance categories and corresponding mean fish densities recorded within each section (ind. m^2).

Fish species	**0-50 m**	**50-100 m**	**100-200 m**	**200-500 m**	**500-2000 m**	**>2000 m**
Gadus morhua	0.00556534	0.02157154	0.01185587	0.02346113	0.01216924	0.01377462
Melanogrammus aeglefinus	0.01807773	0.01760408	0.0135187	0.0173003	0.00073849	0.01081069
Pleuronectes platessa	0	0	0.00710458	0.00077006	0	0
Hippoglossus hippoglossus	0	0.00935206	0.00324321	0.00124747	0.00122923	0.00063201
Sebastes	0	0.00141812	0.00243514	0.0033759	0.00310819	0.0015387

Glyptocephalus cynoglossus	0	0	0.00047019	0	0	0
Anarhichas lupus	0	0	0	0.00027509	0.00053439	0.00205793
Hippoglossoides platessoides	0	0	0.00054266	0.00057832	0	0

Table A. 53 The most abundant key epifaunal taxa observed in towed camera transects in the 6 distance categories and corresponding mean taxa densities recorded within each swath (ind. m2).

Taxa	**0-50 m**	**50-100 m**	**100-200 m**	**200-500 m**	**500-2000 m**	**>2000 m**
***Porifera* sp.**	0.003255442	0.001137064	0.388582375	0.171808784	0.188665458	0.05891844
Ascidians	0	0.009942472	0.118605065	0.032201251	0.009355321	0.000917206
Hormathia digitata	0.058856217	0.008934593	0.021392962	0.010627888	0.004817762	0.018209599
Asteria rubens	0	0.001137064	0.011876334	0.025246346	0.004652078	0.017155981
Ceramaster grannularis	0	0	0.000713528	0.004192004	0.007512441	0.002651141
Phakellia/Axinella	0	0.002237453	0.001238747	0.005568375	0.011806596	0.000647956
***Mycale* sp.**	0	0	0.000502215	0.000352101	0.00832639	0.000240468
Bryozoa	0	0	0	0	0.040669437	0.000215475
***Henricia* sp.**	0	0	0.001268283	0.00592085	0.004393336	0.000970075
Bolocera tueidae	0.006501245	0	0.000659975	0.001182123	0	0.015632916

GLM

Table A. 54 Generalized linear model (GLM) of the effect from Distance group on the average densities of Lithodidae.

	Lithodidae			
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	-0,2501	3,6129	-0,069	0,945

Table A. 55 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Hippoglossoides Lithodidae.

	Lithodidae				
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	0	136341	Inf	0	1
>2000 - (100-200)	0	50347	Inf	0	1
>2000 - (200-500)	-18,6	30487	Inf	-0,001	1
>2000 - (50-100)	0	91036	Inf	0	1
>2000 - (500-2000)	0	59171	Inf	0	1
(0-50) - (100-200)	0	138798	Inf	0	1
(0-50) - (200-500)	-18,6	132889	Inf	0	1
(0-50) - (50-100)	0	158169	Inf	0	1
(0-50) - (500-2000)	0	142236	Inf	0	1
(100-200) - (200-500)	-18,6	40067	Inf	0	1
(100-200) - (50-100)	0	9494676	Inf	0	1
(100-200) - (500-2000)	0	64631	Inf	0	1

(200-500) - (50-100)	18,6	85779	Inf	0	1
(200-500) - (500-2000)	18,6	50713	Inf	0	1
(50-100) - (500-2000)	0	99649	Inf	0	1

Table A. 56 Generalized linear model (GLM) of the effect from Distance group on the average densities of Mytilus edilus.

Mytilus edilus				
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	-0,3382	1,6353	0,207	0,836

Table A. 57 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Hippoglossoides Mytilus edilus.

Mytilus edilus					
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**
>2000 - (0-50)	0	50157,04	Inf	0	1
>2000 - (100-200)	-16,8	11215,46	Inf	-0,001	1
>2000 - (200-500)	-18	11215,45	Inf	-0,002	1
>2000 - (50-100)	0	33490,23	Inf	0	1
>2000 - (500-2000)	0	21767,78	Inf	0	1
(0-50) - (100-200)	-16,8	48887,03	Inf	0	1
(0-50) - (200-500)	-16,8	48887,03	Inf	0	1
(0-50) - (50-100)	0	58187,21	Inf	0	1
(0-50) - (500-2000)	0	52325,82	Inf	0	1
(100-200) - (200-500)	-1,2	6,02	Inf	-0,199	1
(100-200) - (50-100)	16,8	31556,44	Inf	0,001	1
(100-200) - (500-2000)	16,8	18656,09	Inf	0,001	1
(200-500) - (50-100)	18	31556,44	Inf	0,001	1
(200-500) - (500-2000)	18	18656,09	Inf	0,001	1
(50-100) - (500-2000)	0	36658,68	Inf	0	1

Table A. 58 Generalized linear model (GLM) of the effect from Distance group on the average densities of Ophiodromus flexosus.

Ophiodromus flexuosus				
Coefficients	**Estimate**	**Std.Error**	**z value**	**Pr(>|z|)**
Distance group	16,7	6819,5	0,002	0,998

Table A. 59 Pairwise comparisons of generalized linear models (GLM) on effect from distance to an Atlantic salmon (Salmo salar) open cage fish farm on the average densities of Hippoglossoides Pohioromus flexosus.

Ophiodromus flexuosus					
Contrasts	**Estimate**	**SE**	**df**	**z.ratio**	**p.value**

>2000 - (0-50)	18,7		48887	Inf	0	1
>2000 - (100-200)		18,7	14740	Inf	0,001	1
>2000 - (200-500)	18,7		11904	Inf	0,002	1
>2000 - (50-100)		18,7	31556	Inf	0,001	1
>2000 - (500-2000)	18,7		18656	Inf	0,001	1
(0-50) - (100-200)		0	51061	Inf	0	1
(0-50) - (200-500)		0	50315	Inf	0	1
(0-50) - (50-100)		0	58187	Inf	0	1
(0-50) - (500-2000)		0	52326	Inf	0	1
(100-200) - (200-500)	0		18946	Inf	0	1
(100-200) - (50-100)		0	34829	Inf	0	1
(100-200) - (500-2000)		0	23776	Inf	0	1
(200-500) - (50-100)		0	33727	Inf	0	1
(200-500) - (500-2000)		0	22130	Inf	0	1
(50-100) - (500-2000)		0	36659	Inf	0	1

Species	**Diet group**	**Species**	**Av.Abund 0-50 m**	**Av.Abund (>2 km)**	**Av.Diss**	**Diss/SD**	**Contrib%**	**Cum.%**
Ophiopholis	Benthic - epifauna	Brittle star	0	**0.43**	8.05	1.14	8.51	8.51
Pandalus	Benthic - shrimp	Shrimp	0	**0.3**	5.71	0.76	6.03	14.54
Siphonophorae_XX	Pelagic - zooplankton	Salp	0.14	**0.18**	3.89	1.12	4.12	18.66
Cryptosporidium	Parasite	Crypto	0.07	**0.14**	3.65	0.59	3.86	22.51
Trisopterus esmarkii	Pelagic - fish	Norway pout	0	**0.19**	3.47	0.74	3.67	26.19
Laonice	Benthic - infauna	Large spionid polychaete	**0.13**	0	3.07	0.42	3.25	29.43
Eukaryota_XXXXXX	Unknowen	Eukaryote	**0.16**	0.04	2.97	0.69	3.14	32.57
Strongylocentrotus	Benthic - epifauna	Green urchin	0	**0.16**	2.9	0.67	3.07	35.64
Streptophyta_XXXX	Terrestrial	Plants	**0.12**	0.02	2.88	0.47	3.04	38.69
Chromadorea_XXX	Parasite	Roundworm	**0.05**	0.1	2.35	0.71	2.48	41.17
Flabelligeridae_X	Benthic - infauna	Cage worm	0.03	**0.07**	2.3	0.51	2.43	43.6
Apicomplexa_XXXX	Parasite	Parasitic alveolates (fungus)	**0.09**	0.06	2	0.66	2.11	45.71
Echinoidea_XXX	Benthic - epifauna	Green urchin	0	**0.11**	1.91	0.54	2.02	47.73
Hyas coarctatus	Benthic - epifauna	Toad crab	0	**0.11**	1.68	0.62	1.77	49.5
Echinocyamus	Benthic - infauna	Pea / green urchin	0	**0.08**	1.49	0.51	1.58	51.07
Salmo	Pelagic - fish	Salmon	**0.09**	0	1.36	0.38	1.43	52.51
Obelia	Benthic - epifauna	Hydroid	**0.06**	0.03	1.35	0.49	1.43	53.94
Clupea	Pelagic - fish	Herring	**0.07**	0	1.3	0.29	1.37	55.31
Myxidium intestinalis	Parasite	Parasite in Saithe	**0.06**	0	1.27	0.29	1.34	56.65
Ciona	Benthic - epifauna	Ciona	**0.09**	0	1.18	0.41	1.24	57.9
Ophiothrix	Benthic - epifauna	Brittle star	0	**0.07**	1.17	0.61	1.24	59.13
Platyhelminthes_XXXX	Benthic - infauna	Flatworm	**0.06**	0	1.15	0.49	1.22	60.35
Stenocypria	Benthic - infauna	Ostracod	0	**0.06**	1.13	0.34	1.19	61.54
Halecium	Benthic - epifauna	Herring-bone hydroid	**0.04**	0.02	1.11	0.44	1.18	62.72
Semaeostomeae_XX	Pelagic - zooplankton	Jellyfish	0.02	**0.04**	1.06	0.54	1.12	63.84
Mallotus villosus	Pelagic - fish	Capelin	**0.05**	0	1.06	0.34	1.12	64.96
Perlophiura	Benthic - epifauna	Brittle star	0	**0.06**	1.05	0.59	1.11	66.07
Nanomia	Pelagic - zooplankton	Salp	0.01	**0.04**	0.98	0.5	1.04	67.11
Thyasiridae_X	Benthic - infauna	Small bivalve	**0.03**	0	0.93	0.28	0.98	68.1
Gymnodinioides	Unknowen	Ciliate	0	**0.04**	0.9	0.34	0.95	69.04
Ophiuroidea_XXX	Benthic - epifauna	Brittle star	0	**0.05**	0.89	0.78	0.94	69.99
Acartia	Terrestrial	Storage mite	0	**0.06**	0.82	0.35	0.86	70.85
Capitella	Benthic - infauna	Capitella	**0.07**	0	0.76	0.3	0.8	71.65
Golfingiida_XX	Benthic - infauna	Penut worm	0	**0.04**	0.72	0.34	0.76	72.41
Sylon	Parasite	Parasite in shrmp (Pandalina)	0	**0.05**	0.72	0.52	0.76	73.17
Gaidropsarus	Benthic - fish	3-bearded rockling	0	**0.04**	0.72	0.49	0.76	73.92
Undinula	Pelagic - zooplankton	Calanoid copepod	0	**0.04**	0.69	0.34	0.73	74.66
Fagales_XX	Terrestrial	Plant - peas	0	**0.02**	0.67	0.33	0.71	75.36
Hyperia galba	Pelagic - zooplankton	Amphipod	0	**0.02**	0.66	0.33	0.7	76.07
Calanus	Pelagic - zooplankton	Copepod	**0.03**	0.01	0.64	0.35	0.68	76.75
Mytilus	Benthic - epifauna	Blue mussel	**0.05**	0	0.64	0.3	0.68	77.43
Betula	Terrestrial	Birch tree	0	0.05	0.63	0.35	0.67	78.1
Hysterothylacium	Parasite	Roundworm	0	0.04	0.62	0.55	0.66	78.75
Mammalia_XXX	Terrestrial	NA	0.02	0	0.62	0.28	0.66	79.41
Spumellaria_XX	Benthic - infauna	Radiolarian	0.03	0	0.6	0.29	0.64	80.05
Ramphogordius	Benthic - infauna	Nemertean worm	0	0.03	0.6	0.34	0.63	80.68
Eunice	Benthic - infauna	Erant polychaete	0	0.03	0.58	0.34	0.62	81.3

Ptilota	Benthic - epiphyte	Red algae	0	0.03	0.57	0.34	0.6	81.9
Malacostraca_XXX	Benthic - epifauna	Crustacia	0.03	0.03	0.57	0.67	0.6	82.51
Cladonia	Unknowen	Eukaryote	0.02	0	0.55	0.28	0.59	83.09
Nothria	Benthic - infauna	Erant polychaete	0	0.03	0.54	0.34	0.57	83.67
Oikopleura	Pelagic - zooplankton	Small tunicate	0.02	0	0.54	0.28	0.57	84.24
Hippoglossoides	Benthic - fish	American plaice	0.02	0	0.52	0.28	0.55	84.79
Trebouxiophyceae_XXX	Benthic - epiphyte	Grean algae	0.01	0.02	0.51	0.44	0.54	85.32
Cladosporium	Unknowen	Eukaryote	0.03	0	0.5	0.29	0.53	85.85
Gonepteryx	Terrestrial	Butterfly	0.04	0	0.49	0.3	0.51	86.36
Insecta_XXX	Terrestrial	Insect	0.04	0	0.44	0.3	0.47	86.83
Poecilostomatoida_XX	Pelagic - zooplankton	Copepod	0	0.02	0.4	0.34	0.43	87.26
Malassezia	Fungus	Fungi	0	0.02	0.4	0.34	0.42	87.68
Malacoceros	Benthic - infauna	Erant polychaete	0.04	0	0.39	0.3	0.41	88.1
Selenidium	Parasite	Single-celled parasite	0.04	0	0.39	0.3	0.41	88.51
Metridia	Pelagic - zooplankton	Copepod	0.01	0	0.38	0.28	0.4	88.91
Paracalanus	Pelagic - zooplankton	Copepod	0	0.02	0.37	0.34	0.39	89.3
Syndiniales_XX	Parasite	Dynoflagelate	0.03	0	0.37	0.3	0.39	89.69
Crangon	Benthic - shrimp	Shrimp	0.01	0	0.36	0.28	0.38	90.07