MASTER THESIS

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Community composition and depth distribution of benthic scavenging amphipods (Lysianassoidea) in sub-Arctic fjords

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Abstract

Scavengers are found in all environments, and the dominant ones in the benthic habitat are fish and amphipods.

Here we report the findings of an integrated study of lysianassoid amphipods of a sub-Arctic fjord system, Saltfjord-Skjerstadfjord, combining morphological and molecular species identification (COI barcoding) methods to examine more than 30,000 specimens from baited traps. Lysianassoid amphipods constitute a major part of the benthic scavenging guild inhabiting the Saltfjord-Skjerstadfjord ecosystem and a strong differentiation and some genetic diversity in the amphipod community composition is shown in the study area.

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1. INTRODUCTION

In the marine environment, food sources can be limited for benthic organisms, therefore, they depend primarily on episodic events of food inputs, and use different feeding strategies depending on the food source (Nixon, 1981; Blankenship & Levin, 2007).

Food sources, coming from surface waters, descend in the form of particulate organic matter (e.g., cellular debris, bacteria, phytoplankton etc.) or as decomposing plant and animal remains (Nixon, 1981; Pape *et al*., 2013). This downward flux of organic matter is key for benthic communities, and during this process, a fraction of the organic matter settles on the seabed. In fact, the quantity of organic matter decreases as it is progressively broken down in the pelagic zone by zooplankton and bacteria before it sinks to deeper areas (Smith *et al.*, 1989).

Due to this lack of food sources, scavenging opportunities arise in the benthos but are less predictable in time and space than in shallow waters (Slattery & Oliver, 1986). Scavengers present a high ability to localize potential food resources and consume large quantities of food within a short period of time (Dahl, 1979; Blankenship & Levin, 2007; Legeżyńska, 2008). For instance, some of the most commonly reported scavenging fauna (e.g., decapods, amphipods and ophiuroids) feed on sporadic nekton carcasses (e.g., mobile consumers that have died of natural causes or have been discarded during fishing practices) that sink to the seafloor (King *et al*., 2007). These benthic scavengers play a crucial role in remineralization, nutrient cycling and benthic-pelagic exchange in marine habitats (Ehrnsten *et al*, 2019), although food web models have often underestimated the importance of scavenging feeding (Wilson & Wolkovich, 2011).

Scavengers are found in all environments (King *et al*., 2007), and the dominant ones in the benthic habitat are fish and amphipods (Dahl, 1979). These organisms are in most cases, carrion-feeders, and they can be found at all depths, but carrion is a more important energy input in the deep-sea than in shallow-water environments (Smith & Baco, 2003), where opportunistic predators prevail over specialized scavengers (Britton & Morton, 1994; Davenport *et al*., 2016). However, it has been shown that most scavengers are also predators, therefore facultative scavengers. For instance, video footage from Dunlop *et al*. (2021) showed hagfish (Myxinidae), which were thought to be obligate scavengers, preying on bony fish and sharks. Another fish species that inhabits benthic environments and plays an important role in carrion removal is the Atlantic cod (*Gadus morhua*), whose behavior can indeed attract other cod. On the other hand, amphipods, especially lysianassoids, which are known for their scavenging activity, can also prey on other marine organisms (e.g., Copepoda) (Slattery & Oliver, 1986).

According to various authors, trophic diversity is related to species diversity, and the type of habitat and food availability determine which feeding strategies are dominant (Dauby *et al.*,2001; De Broyer *et al*., 2004; Włodarska-Kowalczuk *et al*., 2019). In the case of lysianassoid amphipods, their occurrence in different shallow and deep-water habitats depends to a great extent on food availability (Slattery & Oliver, 1986). Lysianassoid amphipods are closely associated to the sea floor as part of the benthic boundary layer, and their distribution may be affected by the environmental factors in their habitat. While some species are members of the sedimentary macrofauna (e.g., epifauna) or live attached to hosts such as bryozoans, others use their high swimming ability to disperse in the hyperbenthos to feed (Bett, 2019). However, habitat heterogeneity decreases with depth (Buhl-Mortensen *et* al., 2012), as well as food sources. A range of bathymetric profiles where habitat complexity can be studied are provided by fjord ecosystems. The habitat-diversity hypothesis states that habitat complexity has a positive correlation with species diversity (Whittaker *et al*., 2001), but deeper habitats such as soft-sediment fjord basins are more homogeneous habitats where species diversity and resources availability are significantly reduced.

Most recently, human activities have increased the availability of carrion into the benthos (e.g., fishing, whaling discards) (Blankenship & Levin, 2007; Wilson & Wolkovich, 2011; Davenport *et al*., 2016) and the response from marine scavengers to these food falls has attracted significant attention, as well as the behavior of shallow-water benthic marine scavengers which are also involved in the trophic transfer of scavenged material (Bergmann *et al*., 2002; Davenport *et al*., 2016). Several studies have attempted to estimate the abundance, distribution, and composition of shallow-water scavenging species by conducting baited trap experiments (e.g., Sainte-Marie, 1986; Bergmann *et al*., 2002; Premke *et al*., 2006).

The scavenging fauna that is most frequently sampled using baited traps are lysianassoid amphipods (Witte, 1999). They occur in a wide variety of shallow and benthic habitats, and they have several types of adaptations to a scavenging mode of life. For instance, their rapid response to bait is an indicator of their ability to detect and locate carrion that has been shown to rely on chemoreception (Meador, 1989; Sainte-Marie, 1992). Certain amino acids which are found in many marine organisms (e.g., betaurine, taurine etc.) (Meador, 1989) are the ones attracting the amphipods that swim up current towards the bait (Havermans & Smetacek, 2018).

The presence of lysianassoid amphipod assemblages in the benthos has been well documented in the Arctic (Christiansen & Diel-Christiansen, 1993; Havermans et al. 2013; Brix *et* al., 2018; Dunlop *et al.*, 2021), in Antarctic waters (De Broyer *et al.*, 2004; Smale *et* al., 2007; Havermans *et al.*, 2010) and to a lesser extent, in sub-Arctic regions (Christiansen & Diel-Christiansen, 1993). Older studies only provide occurrence data, but research on lysianasoids has gone much further, and the most recent research provides data on species diversity and distribution in relation to abiotic factors (e.g., hydrography, season, bottom type etc.) (Percy, 1975; Legeżyńska, J., 2001; Semprucci *et al.*, 2019) over different spatial scales (Conlan *et al.*, 2013) and biotic factors such as the presence of predators (Dunlop *et al.*, 2021). As part of benthic communities, scavenging amphipods can be potential prey to fish such as Atlantic cod (Dunlop *et al.*, 2021), tusk (*Brosme* brosme) (Bergstad & Knutsen, 2004) and other demersal fish. Besides, Atlantic cod can act as both, a predator for benthic amphipods, or a competitor when food resources are scarce and there is easily accessible carrion.

Benthic macrofauna shows significant differences in biomass and species diversity between deep and shallow environments, especially within fjord systems where abiotic factors such as topography (e.g., sills, troughs) shape the habitats from the mouth of the fjord to offshore waters and hence, the composition of macrofaunal communities (Buhl-Mortensen, 1996). Fjords, unlike deep sea ecosystems in the open ocean, are confined ecosystems (Kwong *et al.*, 2019), thus benthic macrofaunal communities in deep fjord basins are more sheltered (e.g., shallow sills) and might result in less diverse fauna due to restricted access and specific environmental conditions (Kokarev *et al.*, 2021).

This study investigates a particular fjord system in northern Norway which is formed by two adjacent fjords (Saltfjord and Skerstadfjord) connected by a small strait and a shallow sill (Eliassen *et al.*, 2001), which can act as a barrier to benthic organisms (Buhl-Mortensen, 1996). Kokarev *et al.* (2021) examined this fjord system and concluded that macrofaunal communities differed significantly between fjords, mainly because of the hydrological isolation of Skjerstadfjord. Their sampling design was based on grab samples, which mainly accounted for the infauna community composition, where the scavenging amphipod fauna was not properly addressed. However, these scavenging functional guild might be specifically important for nutrient recycling in the deep basins, but knowledge about their distribution in the fjords is scarce. We assume that also the scavenging species composition might differ among fjords as a result of the variation in hydrological conditions, food availability and predation pressure.

The dispersal of amphipods is not only limited by environmental barriers, but also by their brooding reproduction mode (Lörz *et al.*, 2021). Unlike most benthic invertebrates, amphipod larvae do not have a planktonic phase, but female adults retain the eggs in a brood pouch until juveniles hatch directly (Highsmith, 1985). Presumably, brooders are species with a restricted dispersal range, but existing evidence indicates that many brooder species have a high dispersal ability ('Rockall paradox'; Levin, 1984; Johannesson, 1988) and colonization rates depending on the traveled distance (Johannesson, 1988). According to their geographic distribution, brooding species are more abundant at higher latitudes ('Thorson's rule'; Thorson, 1950). In these regions, cold temperate and polar waters can slow down the metabolic rate of pelagic larvae, but benthic species without pelagic development like amphipods, carry their own offspring (brooding) avoiding a delayed growth (Thorson, 1950). Nevertheless, there is still a lack of knowledge about zonation patterns and dispersal barriers in lysiannasoids.

Despite the environmental barriers and low dispersal rates, amphipods have wide geographical distributions (Havermans *et al*., 2013; Lörz *et al.*, 2021) and high species richness (Guerra-García *et al*., 2014). Although many morphologically identified species have been reported to be widespread, they may comprise various cryptic species (France & Kocher, 1996; Havermans *et al*., 2013). For instance, the giant bentho-pelagic deep-sea amphipod *Eurythenes gryllus*, which can be found in all oceans of the world (France & Kocher, 1996), comprises at least 9 species-level lineages due to speciation events triggered by low rates of gene flow and hence, the isolation of populations (Havermans *et al*.,2013).

The delimitation of amphipod species is a complex task (Coleman, 2015). To overcome this , we have studied the identification of amphipod morphospecies with modern molecular tools. The use of the molecular marker cytochrome oxidase c subunit I (COI) gene, allows us to delineate species and recognize potentially cryptic species, as it has successfully been done in previous studies of amphipod assemblages (Browne *et* al., 2007; Baird *et al*., 2011; Knox *et al*., 2012).

In this study, we investigate the distribution pattern and the community composition of scavenging amphipods in two sub-Arctic fjords. The specific objectives of this study are:

(1) Morphological identification of scavenging amphipod species in Saltfjord and Skjerstadfjord (2) to determine whether the distribution pattern of recorded species is associated with fjord habitat and depth. (3) Seasonal variability of amphipod abundance shown in the Arctic (Nygård *et* al., 2012; Dalpadado *et al.*, 2016) is studied in one sub-Arctic fjord, Saltfjord.

(4) Use of different bait types were used to examine whether the composition of scavenging amphipods is disrupted by additional food sources such as artificial feed used salmon farming or not.

(5) To assess genetic diversity of amphipod species in the study fjords and verify morphological identification using molecular tools (COI gene).

(6) To reveal first insights into potential isolation of populations. Simultaneously, a more in depth analysis of populations differentiation in a dominant lysianassoid species was carried out in the master thesis of Jørgen Hetzler (Hetzler 2022 [Unpublished]).

2. MATERIALS AND METHODS

2.1. Study site

Our study was carried out in two fjords, Saltfjord and Skjerstadfiord, which are separated by the Salstraumen tidal current (Fig. 1). The geography of the fjord system has been described in the previous section (see page 3).

In each location, a transect was sampled from the deepest parts of the fjord basin (350 m /500 m) to shallower depths (30 m). The transect in Saltfjord comprised four stations and it was 3.52 km long, while In Skjerstadfjord, the transect comprised five stations along 3.23 km.

The sampling was divided into summer and winter sampling. Summer sampling was conducted in April, May and June 2021 in both fjords, while winter sampling took place in November 2021 and February 2022, exclusively in Saltfjord (for sampling dates see Table S1). Three replicates were taken in each station in both seasons, and for all replicates baited traps were deployed for approximately 24 h at a time.

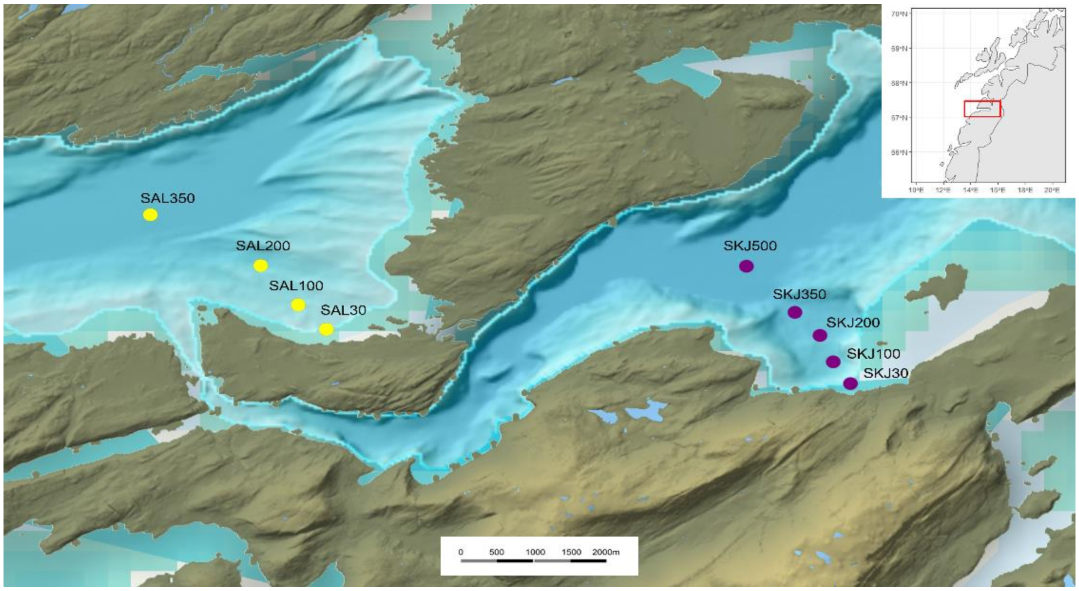

FIG. 1 | SAMPLING LOCATION
Map of the study region. Saltfjord stations are indicated in yellow (SAL) and Skjerstadfjord stations in purple (SKJ). Depth of all stations is shown in each label. Bathymetry map data source: norgeskart.no.

2.2. Sampling gear

Scavenging amphipod traps and CTD

All stations were sampled in the two fjords with the Nord University research boat *Tanteyen*. Two traps attached to a benthic lander were deployed at each station (Fig. 2). The design of the amphipod traps was based on a previous study, and it consisted of a plastic PVC tube with a diameter of 14 cm and height of 38 cm ± 2 which had a mesh (1 mm) attached to one of the openings. The traps were open from both sides, and on the other side of the tube, a funnel and a mesh were attached using rope. The mesh size on this side was bigger, and it would stop other scavengers from entering the traps. This design enabled amphipods entering the traps and prevented them from escaping, regardless of the size.

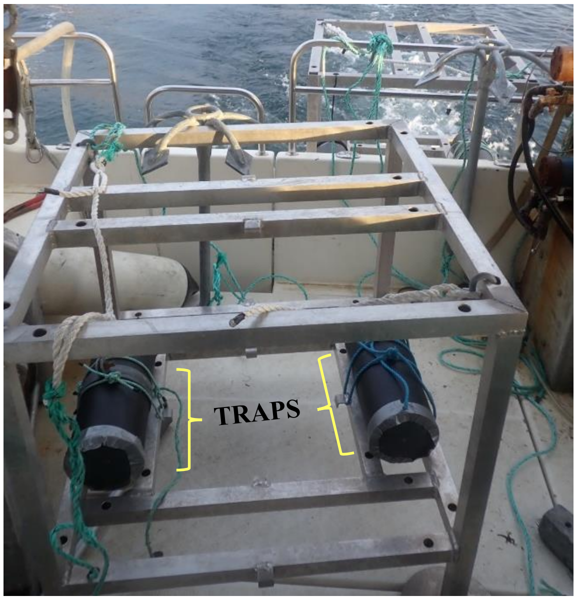

FIG. 2 | TRAP DESIGN
Amphipod traps attached to a benthic lander with rubber straps ready for deployment.

The traps were deployed at 25 cm above the sediment, and they were baited with either herring (50 ± 3 g) or aquaculture feed (50 ± 1.9 g). The bait was placed into bait boxes with small holes that allowed the amphipods to locate the bait with their chemoreceptors (Sainte-Marie, 1992), preventing them from feeding on the bait. Atlantic herring (*Clupea harengus*) was used as bait because previous experiments have already shown that scavenging amphipods are readily attracted to this oily fish (Schmid *et al.*, 2017). All traps were numbered to differentiate the samples and sort them properly in buckets after their retrieval.

Temperature and salinity measurements were taken with a CTD in certain points of the transects (Figures 7 and 10) in both fjords, and in both seasons in Saltfjord.

2.3. Handling of samples and morphological species identification

Sample size was highly variable, and samples were always split into two groups, one for morphological identification and another one for barcoding analysis. If sample size was too small (< 10 individuals), amphipods were only preserved for barcoding analysis.

After rinsing the samples with seawater and a sieve (65µm), the total wet weight (g) per sample was recorded (Table S1). When the total wet weight of a sample exceeded 100g, subsampling was carried out to reduce workload.

A fraction of each sample was used for morphological and barcoding analyses, 10%, respectively. Amphipods were stored separately to perform different downstream species identification analyses. Individuals were sorted and stored in 4% buffered formaldehyde for morphological identification and stored in the freezer for barcoding analysis based on the COI gene.

Sample individuals morphologically (Fig. 3) examined were counted and sorted by species. All amphipods from this study belonged to the superfamily Lysianassoidea (Ahyong *et al*., 2022), and they were identified to the lowest taxonomic level possible under a stereo microscope, using identification keys for lysianassoid amphipods (Sars, 1895; Stephensen, 1935).

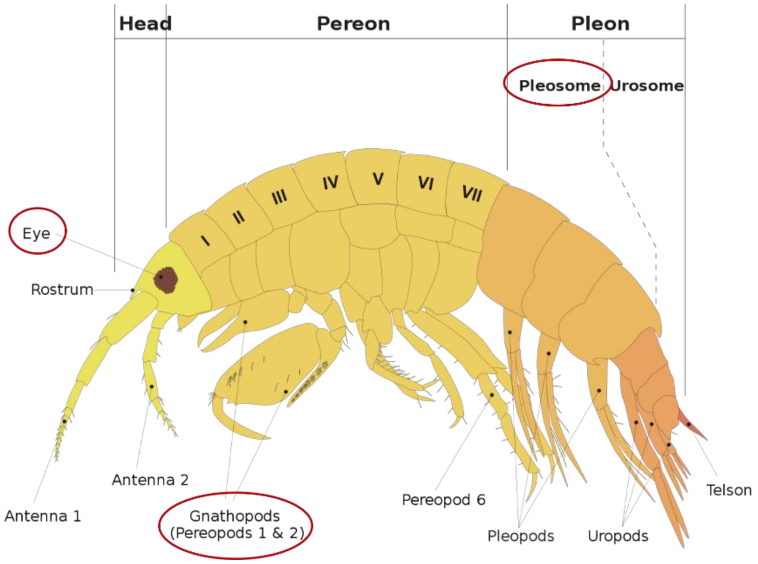

FIG. 3 | MORPHOLOGICAL STRUCTURE OF AN AMPHIPOD
Outline of the left aspect of an amphipod body. The most distinguishing body parts examined to differentiate lysianassoid amphipods in this study are circled in red. From left to right: eye shape, gnathopods 1 and 2 morphology, and shape of the last pleosome plates. Bodyplan of an amphipod source: © Hans Hillewaert.

2.4. Statistical analyses

Amphipod community data between fjords and depths were analyzed using R-statistical environment (Team, 2013). The total number of individuals per trap was recorded and used as a proxy for abundance (individuals/trap), although this was not an indication of the abundances in the vicinity of the stations. The most abundant amphipod species were considered in the statistical analyses, while the rarest species belonging to different taxa which were not relevant in this study were disregarded.

An analysis of non-parametric multidimensional scaling (NMDS) together with a dendrogram were used to visually examine whether fjords and depth structured amphipod communities in the Saltfjord-Skjerstadfjord system. For calculating the Bray-Curtis distance, the original, untransformed data was used. An analysis of similarities (ANOSIM) was performed to support the visualization of the results in the NMDS.

A permutational multivariate analysis of variance (PERMANOVA) was using the factors fjord, depth, bait, and season to assess the differences in amphipod communities in the different sampling sites and stations. Data on seasonality was studied separately because it only corresponded to one of the sampled fjords, Saltfjord.

Ultimately, several Kruskal–Wallis tests were performed to examine the differences in amphipod abundances within depths and bait types. Pairwise comparisons were performed as well to determine which factor combinations had the highest significance.

2.5. COI barcoding of lysianassoid amphipods

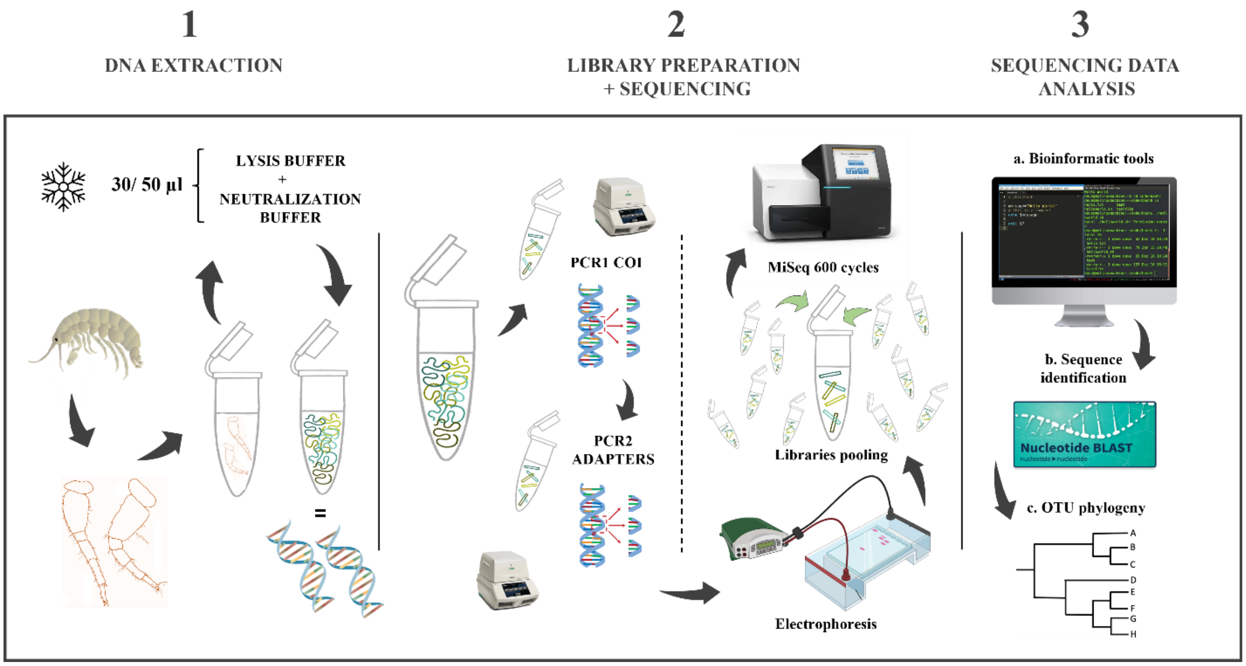

FIG. 4 | GRAPHICAL ABSTRACT OF THE PROCEDURES FOLLOWED IN THE COI BARCODING ANALYSIS
Workflow for taxonomic assignment of lysianassoid amphipods using high throughput DNA barcoding.

Individuals used in the barcoding analysis were chosen according to morphologically identified species and sample size of each sampled station. In order to have a representative picture of the amphipod community where at least all morphospecies would be depicted, individuals were randomly picked from the samples stored in the freezer. The number of selected individuals per station and total number of samples are shown on Table 1.

Amphipods were thawed and stored in 96% ethanol prior to DNA extraction. Every specimen was stored in a single Eppendorf tube to prevent cross contamination between samples. The procedures followed during the COI barcoding analyses are outlined in Fig. 4.

2.5.1. DNA extraction

All samples were labelled individually according to sampling station and identified morphospecies.

DNA extraction was performed using the HotSHOT protocol (Montero-Pau *et* al., 2008) from only pereopods 5-7 from one side of the amphipods, providing intact voucher specimens which could be traced back if needed.

TABLE 1 | NUMBER OF INDIVIDUALS PER SPECIES AND SAMPLING STATION FOR COI BARCODE ANALYSIS

Number of individuals per identified morphospecies by sampling station in Saltfjord and Skjerstadfjord. (all sampled specimens were used).*

	Station ID	***T. cicada***	***O. obtusa***	***S. hopei***	***Morphospecies 4***
Saltfjord	SAL30	8*	0	0	1*
	SAL100	21*	0	0	0
	SAL200	15	15	4*	0
	SAL350	20	20	20	0
Skjerstadfjord	SKJ30	2*	0	0	0
	SKJ100	15	15	0	1*
	SKJ200	0	20	0	0
	SKJ350	0	20	0	0
	SKJ500	0	20	0	0
Total	217				

First, amphipod pereopods (5-7) were rinsed in pure water for 30 minutes, and afterwards they were dried off and added to a lysis buffer solution (50 µl for *Tmetonyx cicada* and 30 µl for the other species). Then the thermomixer was pre-heated to 95ºC, and samples were homogenized at 700 rpm for 30 minutes. Samples were kept on ice for 5 minutes and finally they were mixed with neutralization buffer using the same volume as indicated above, depending on the species.

Isolated DNA was stored in the fridge at 4ºC for a short period of time, and at -20ºC in the freezer for long term storage before moving to the next step.

2.5.2. Library preparation and sequencing

The libraries for sequencing were prepared via 2-step amplification protocol, where primers in the first PCR target COI fragment and contain heterogeneity spacer and Illumina sequencing priming regions for the primers in the second PCR. In the 2nd PCR primers target llumina sequencing priming regions and contain dual barcodes and flow-cell linker sequences (more details in e.g., Holm et al. 2019).

First, polymerase chain reaction 1 (PCR1) amplification of a 705 bp fragment from the mitochondrial COI gene was carried out using primers LCO1490-JJ (5′-CHACWAAYCATAAAGATATYGG-3′) and HCO2198-JJ (5′-AWACTTCVGGRTGVCCAAARAATCA-3′) from Astrin and Stüben (2008). PCR amplification was performed in 14 µL volumes containing 9 µL master mix (7 µL ASM, 0.02 µL $MgCl_2$, 0.8 µL of forward and reverse primers with concentration of 10 µM each and 0.4 µL water) and 5 µL of DNA sample. PCR1 was carried out under the following conditions: 94ºC for 3 min, followed by 36 cycles of 94ºC for 30 s, annealing at 52.5ºC for 30 s, and 72ºC for 1 min, with a final elongation step at 72ºC for 8 min. After that, 2 µL of the PCR1 product were diluted with 38 µL water (1:20 dilution) in 96-well plates.

A second PCR was carried out for adapters ligation to the DNA fragments in 20 µL volumes. Each volume contained 17 µL of the prepared master mix (10 µL ASM, 0.02 µL $MgCl_2$ and 7 µL water), 1 µL of diluted DNA product from PCR1 and 1 µL of each barcode adapter. The second PCR step was carried out under similar conditions to the first PCR step except the elongation time was increased to 8 min and the annealing temperature to 59ºC, while the number of cycles was reduced to 18.

PCR2 products were checked by electrophoresis on agarose gel. Samples which did not show any band on the gel went through the same procedure another time.

Prepared amplicon libraries were pooled according to their band brightness on the agarose gel into several subpools (e.g., 1 µL for extremely bright, 3 µL for very bright+, 6 µL for bright, 9 µL for weak, 12 µL for very weak and 15 µL for nearly invisible) (Table S4). The subpools were cleaned with magnetic beads Mag-Bind® TotalPure NGS (Omega Bio-tek) with 0.6x ratio to the sample and further assessed on Tape Station using High Sensitivity D1000 reagents (Agilent Technologies). Quantified subpools were pooled together into a common COI pool in molarities proportional to the number of individual libraries in subpools in a way to achieve equimolar concentration for each library. The pool of amplicons converted into sequencing libraries was sent to Oslo sequencing centre for 300 bp paired end sequencing (v3 chemistry) on an Illumina MiSeq.

2.5.3. COI metabarcoding analyses

Sequences with an average length of 270 bp were obtained. The overall quality examination of the reads, trimming and mapping to operational taxonomic units (OTUs) were carried out following recommendation from the online metabarcoding pipeline *Bioinformatic Methods for Biodiversity Metabarcoding* (https://learnmetabarcoding.github.io/LearnMetabarcoding/index.html).

(1) *Read processing*

Raw data was imported in FASTQ format, and a quality control check was performed with multiQC v1.12. All information was exported as a table included in the supplementary material (see Table S1). Forward and reverse sequences were trimmed to a common length with *cutadapt*. This software cleaned the data by removing the adapter and primer sequences from the amplicon reads. This process was followed by the generation of another multiQC report providing information of the trimmed sequences (Table S1).

Mate-pairing of reads was performed using the tool PEAR. Reads in either the forward or reverse file without a mate pair in the other file were discarded.

(2) *Filtering amplicons*

Reads were filtered using a Phred quality score of 13 or higher. Phred scores indicated the quality of the identification of the bases generated in the sequencing process.

The analysis continued with dereplication, using *vsearch* by discarding all replicate reads, redusing the data size. This new dataset was comprised by unique amplicon sequences, and it will be referred as Amplicon Sequence Variants (ASVs).

Once this set of sequences was obtained, several steps to filter out possible errors were followed. Denoising was performed using the UNOISE3 algorithm, which excluded infrequent reads. This means that a proportion of the previously obtained ASVs was removed, and a total of 2722 sequences were kept.

Finally, chimera filtering was performed. This step removes ASVs composed by fragments coming from different true sources due to annealing of DNA strands which are not the correct mirror of one another. Fortunately, no chimeras were found possibly by high quality filtering.

(3) ASVs, OTUs and read mapping

Once all data was processed from raw reads to ASVs, ASVs were grouped into OTUs. *Greedy clustering* was the OTU delimitation method used in this study, with a 97% similarity threshold. Each ASV was examined individually and joined an OTU cluster based on the frequency of reads. Once a final set of OTUs and an associated record of ASVs within each OUT were obtained, read mapping was carried out.

Finally, representative OTU sequences were obtained by matching reads to the OTUs. All occurrences of all ASVs within each OTU were added up into one row, and a matrix of read counts per sample together with the final set of biological sequences (OTUs) was created.

2.5.4. OTU phylogeny and taxonomic assignments

Identification of the representative OTU sequences was performed using the publicly online database GeneBank. A BLASTn search was carried out to assign taxonomy to the OTUs.

From the obtained OTUs, only the ones that corresponded to sequences of the COI gene were directly used to make a phylogenetic tree. OTUs were aligned with MAFFT (Katoh *et al.*, 2019) in Geneious 9.1.3 (Biomatters), and a phylogenetic maximum likelihood tree was build using GTR+I+R substitution model. Sequences of the same barcode region with known taxonomy were added to the tree as a reference, to see if the phylogeny matched that taxonomy.

3. Results

3.1. Ecological analyses

3.1.1. Spatial species composition of scavenging amphipods

A total of 31313 individuals were sampled in the study fjords for their morphological identification. According to the sampling site, the number of individuals collected between the two locations, Saltfjord and Skjerstadfjord, was very similar (9184 and 10185 respectively) despite one more station was sampled in Skjerstadfjord. A greater number of individuals was recorded in Saltfjord during the winter, 11944 amphipods.

A total of 4 amphipod species were found, belonging to the same superfamily, Lysianassoidea. The 3 most abundant species (Fig. 5*),* *Tmetonyx cicada*, *Scopelocheirus hopei* and *Orchomenella obtusa* occurred in large numbers in the sampled stations, while only 9 individuals of the rarest species, *initially identified as morphospecies 4*, were found in both fjords. However, most of the traps retrieved from the shallowest stations (30 m), were empty in both fjords or had other organisms attached to them (Gastropoda and Echinoderms).

The count of amphipods sampled in the baited traps was considered a proxy of amphipod abundance (individuas/ trap).

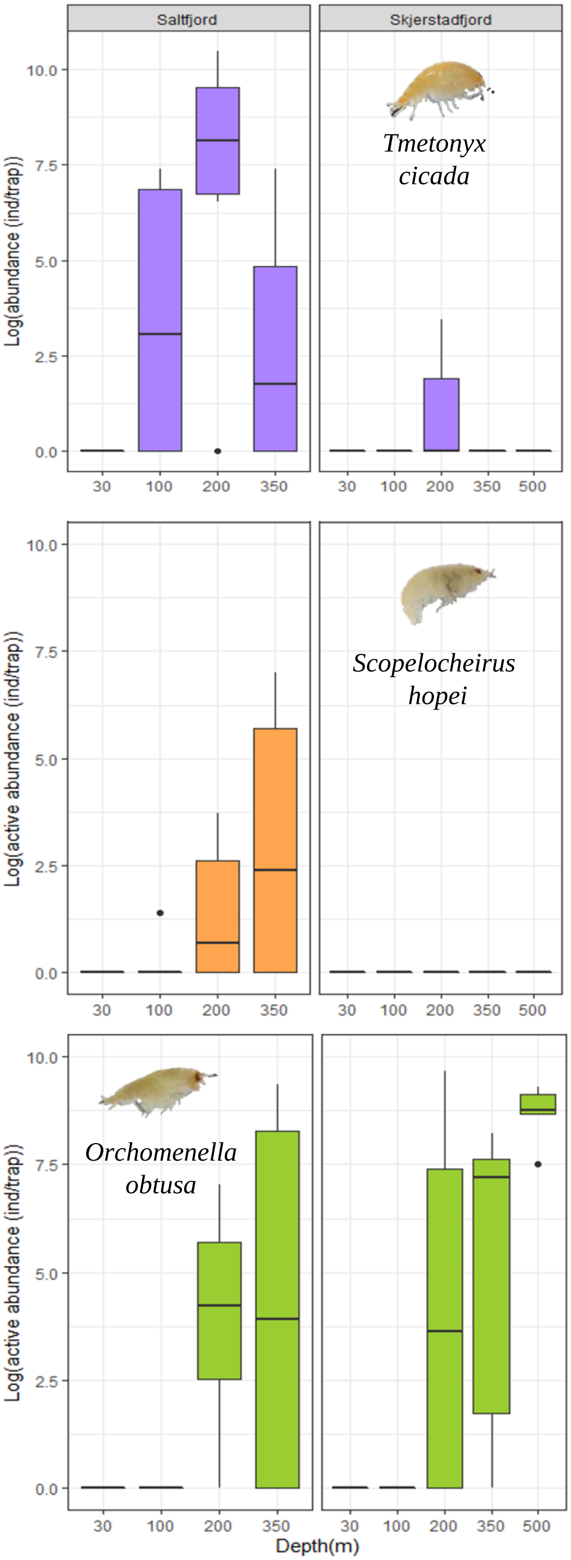

FIG. 5 | BOXPLOTS OF THE MOST ABUNDANT AMPHIPOD SPECIES ABUNDANCE
Variation in amphipods active abundance (individuals/ trap) for the most dominant amphipod species in Saltfjord and Skjerstadfjord during spring-summer Error bars indicate standard error. Abundance values are log transformed. Zero values are shown with a black line.

Tmetonyx cicada and *Orchomenella obtusa* were found in both fjords, but *Scopelocheirus hopei* was restricted to one area, Saltfjord, where the number of individuals increased with depth (Fig. 5).

The number of *Tmetonyx cicada* individuals was higher at intermediate depths (200 m) in both locations. In contrast to *S. hopei*, *T. cicada* did not show a pattern in abundance along the depth gradient, but it occurred in high numbers at 100 and 350 m in Saltfjord. *T. cicada* abundance was significantly different between depths (Kruskal–Wallis, $p = 0.02$) in Saltfjord, and a pairwise comparison revealed the most significantly different depths were 30 and 200 m.

Orchomenella obtusa occurred at 200 m in both fjords and this species exhibited higher abundances than the other two at the deepest depths. There were significant differences between the sampling depths in *O. obtusa* in both locations: Saltfjord (Kruskal–Wallis, $p = 0.0007$) and Skjerstadfjord (Kruskal–Wallis, $p = 0.01$). The only depths at which there were not significant differences in Saltfjord were at 200 and 350 m.

The Kruskal–Wallis test was also applied to the *S. hopei* abundance, and it did not show significant differences between depths ($p = 0.1152$)

O. obtusa and *S. hopei* individuals were usually smaller than *T.cicada* individuals. Furthermore, during the winter sampling many *T. cicada* individuals were big ovigerous females and *O. obtusa* juveniles were very abundant.

Another scavenging crustacean that was found in the region, was the ostracod *Vargula norvegica* (Baird, 1860). It only occurred at 100 m depth in Skjerstadfjord, but was not included in the data analysis. Abundances of *V. norvegica* ranged between 50 and 100 individuals/trap.

Samples showed a clear separation in the nMDS plot (Fig. 6A) between the fjords, Saltfjord and Skjerstadfjord, and the different depths. A non-parametric multivariate analysis of variance (PERMANOVA) showed significant differences in the amphipod abundances and species composition between the two fjords (Table 2).

Furthermore, the ANOSIM test also indicated that there were statistically significant differences between the samples based on the groupings ‘fjord’ ($R = 0.5147$, $p < 0.05$) and ‘depth’ ($R = 0.3591$, $p < 0.05$).

Almost all samples from Saltfjord were clustered together on the left side of the nMDS plot while Skjerstadfjord samples were grouped on the right. However, samples from the deepest stations in Saltfjord (350 m) overlaped with the samples from Skjerstadfjord. This could be explained by a shift in the dominant species, which occured at 350 m in Saltfjord. Here, *T.cicada*, *S. hopei* and *O.obtusa* coexisted, but *O. obtusa* abundance was the highest, as in Skjerstadfjord (Fig. 5).

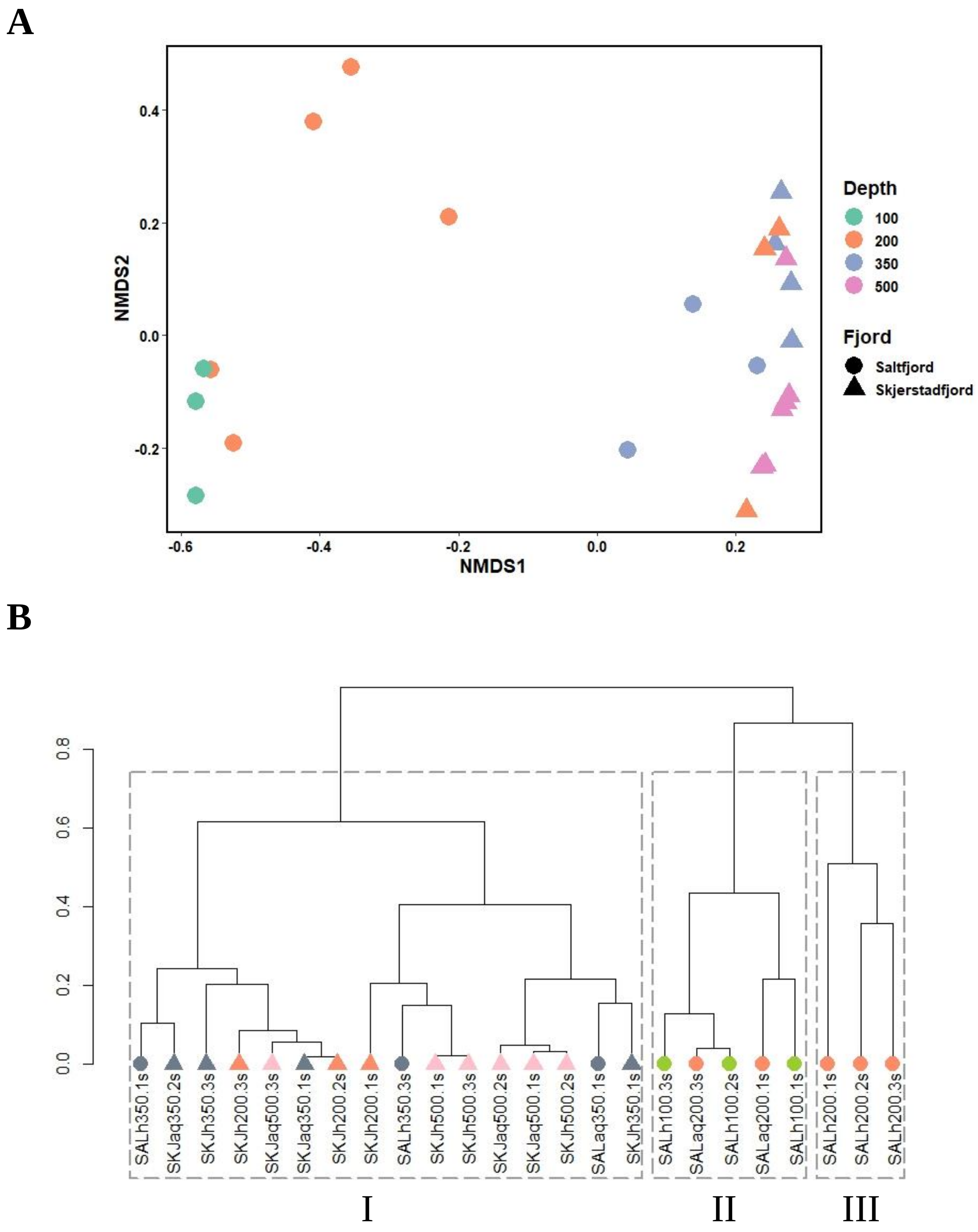

FIG. 6 | NDMS PLOT AND CLUSTER DENDROGRAM OF THE SAMPLING STATIONS

(A) nMDS plot showing the classification of 24 samples based on the abundance of all amphipod species; Bray–Curtis similarity measure. Distance groups correspond to fjords, indicated by shape, and depth, indicated by colors. Replicates of samples with no individuals were excluded. Stress: 0.068. (B) Dendrogram based on Bray Curtis dissimilarities estimated among 24 samples. Labels show the information of the sampling site. The symbols correspond to the same shapes and colors as the symbols in the nMDS plot. The letters correspond to the location (SAL: Saltfjord, SKJ: Skjerstadfjorden) and the following numbers to the depth.

High levels of variation were shown within the fjords, especially in Saltfjord. There was a strong separation between the shallower and the deeper stations (Fig. 6A). Even intermediate stations (100m and 200m) which were closer with each other in the sampling, were clustered separately.

In addition, the cluster dendrogram (Fig. 6B) showed the hierarchical relationship between samples, and the labels in each node indicated the location of each sample. Two large groups and a smaller one, framed with dashed lines, were distinguished at 62% similarity. Group I comprised all samples from Skjerstadfjord, and they were clustered together with samples from Saltfjord of the deepest stations, as stated above for the nMDS. Groups II and III comprised the shallower and deeper samples from Saltfjord respectively.

3.1.2. Environmental variables in the study area

The results of the CTD measurements (temperature and salinity) are shown in Fig. X.

Saltfjord is influenced by warmer and more saline Atlantic water masses which are overlayered by water masses from the Norwegian Coastal Current (Mitchelson-Jacob & Sundby, 2001). During the first sampling in Saltfjord, the maximum temperature record was 7.7ºC at 190 m, and it remained steady until the deepest point in the fjord, 350 m. Salinity increased gradually reaching a bottom salinity value of 34.91 psu, at 200 m depth (Fig. 7).

The adjacent fjord, Skjerstadfjord, which is almost completely enclosed and influenced by freshwater runoff, shows different hydrological features. In spite of its narrow opening, there is a considerable deep water exchange because of the tidal inflow (Kokarev *et al*., 2021). Its bottom water masses were colder (5.1ºC) and less saline (33.38 psu) than in Saltfjord (Fig. 7). Furthermore, surface waters are more affected by the freshwater runoff intensifies during the summer due to the snow melting. On the contrary, bottom waters are very homogeneous due to vertical mixing.

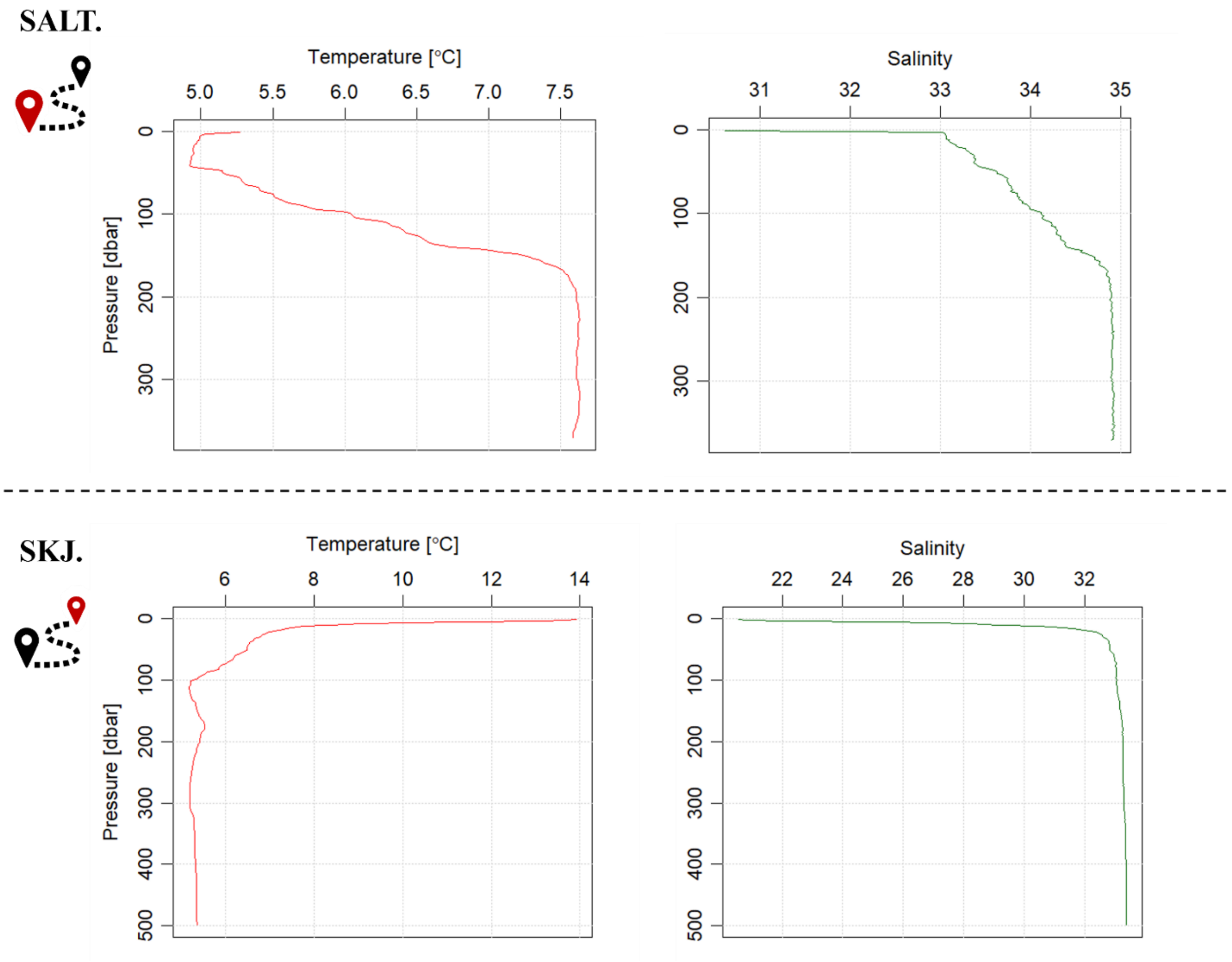

FIG. 7 | CTD TEMPERATURE AND SALINITY PROFILES OF SALTFJORD AND SKJERSTADFJORD
Temperature (ºC) and salinity (psu) profiles of Saltfjord and Skjerstadfjord when sampling was carried out. (A) TS profile of Saltfjord in April; (B) TS profile of Skjerstadfjord in June.

3.1.3. Attraction to bait

In spite of their scavenging feeding habits, *T. cicada*, *S. hopei* and *O.obtusa* were attracted to both bait types, herring and standard aquaculture feed. The amphipods occurred in almost all baited traps, but not at all depths (Fig. 8).

In Saltfjord, all species showed higher abundances in the traps baited with herring, although many individuals were also attracted to standard aquaculture feed. In Skjerstadfjord, the highest abundances were shown by the *O. obtusa* species, whose abundance in the aquaculture feed baited traps was higher at 200 m and 350 m than in the traps baited with herring.

A non-parametric multivariate analysis of variance (PERMANOVA) showed that differences in abundances between bait type were not statistically significant ($p > 0.05$) (Table 2) .

However, independent Kruskal Wallis tests showed significant differences in *T. cicada* abundance between bait types ($p < 0.05$) in Saltfjord.

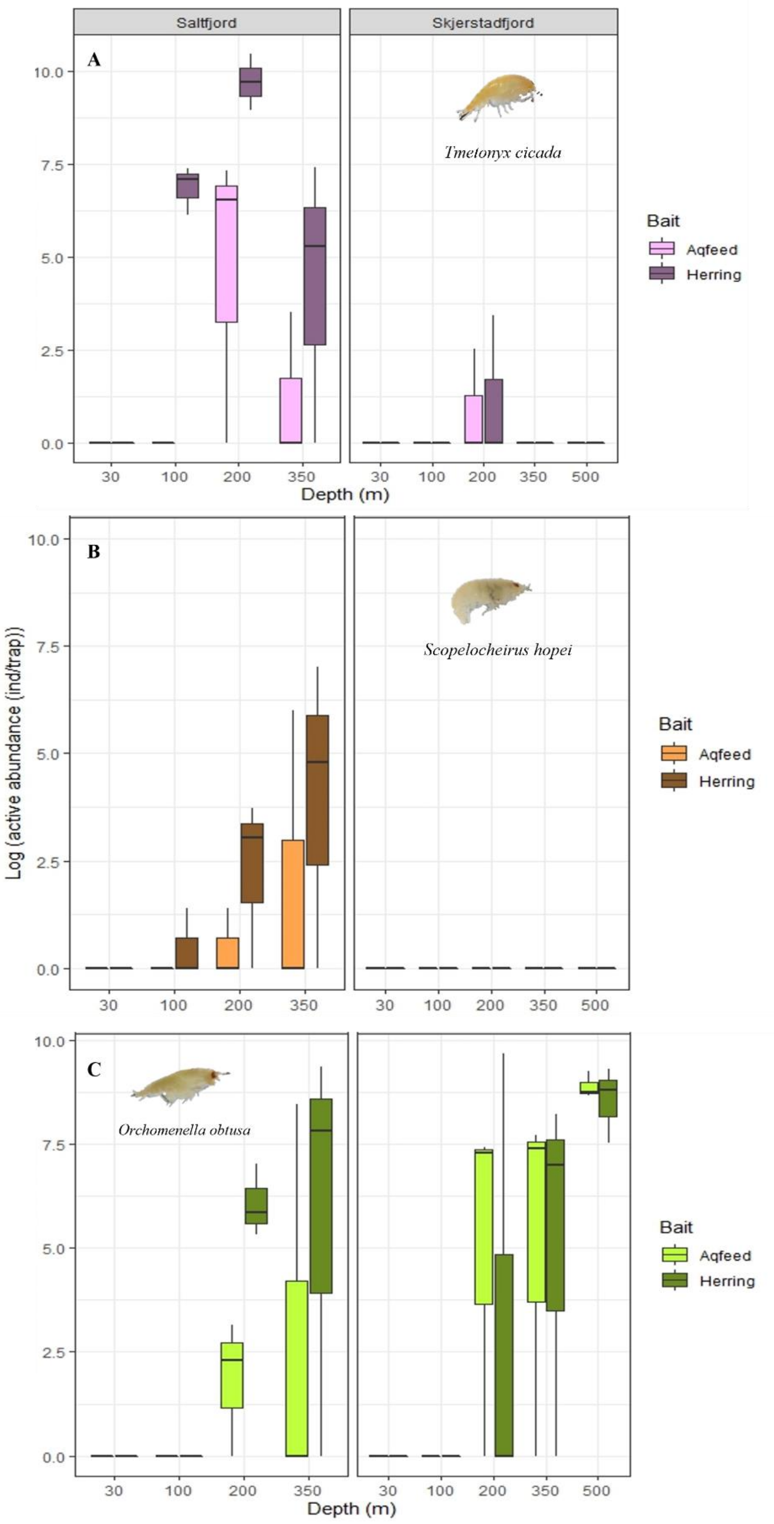

FIG. 8 | BOXPLOT OF AMPHIPOD SPECIES ABUNDANCE ACCORDING TO BAIT ATTENDANCE

Boxplots of bait attendance for all amphipod species at each sampled depth in spring. The active abundance was used to determine the bait attendance for the different species. Abundance values are log(x+1) transformed. Error bars indicate standard error. Zero values are shown with a black line.

3.1.4. Seasonal species composition of scavenging amphipods

At all stations in Saltfjord, sampling was carried out in spring and early winter. There was an increase in amphipod abundances for all species during the winter (Fig. 9), and *T. cicada* and *O. obtusa* occurred at shallower depths for the first time, 30 and 100 m respectively.

The mean total weight of the retrieved samples was higher in the winter sampling (136.5 ± 5.4 g) than in the summer (112 ± 2.4 g), and the size of female individuals was larger because many of them they were carrying their eggs in the marsupium. Environmental data was also retrieved along the depth gradient in Saltfjord during winter (Fig. 10). Salinity did not seem to change over the seasons, but the temperature profile in November showed a more prominent thermocline at 150 m depth.

PERMANOVA results (Table 3) showed that seasonality had a significant effect ($p < 0.05$) on the amphipod abundances in Saltfjord.

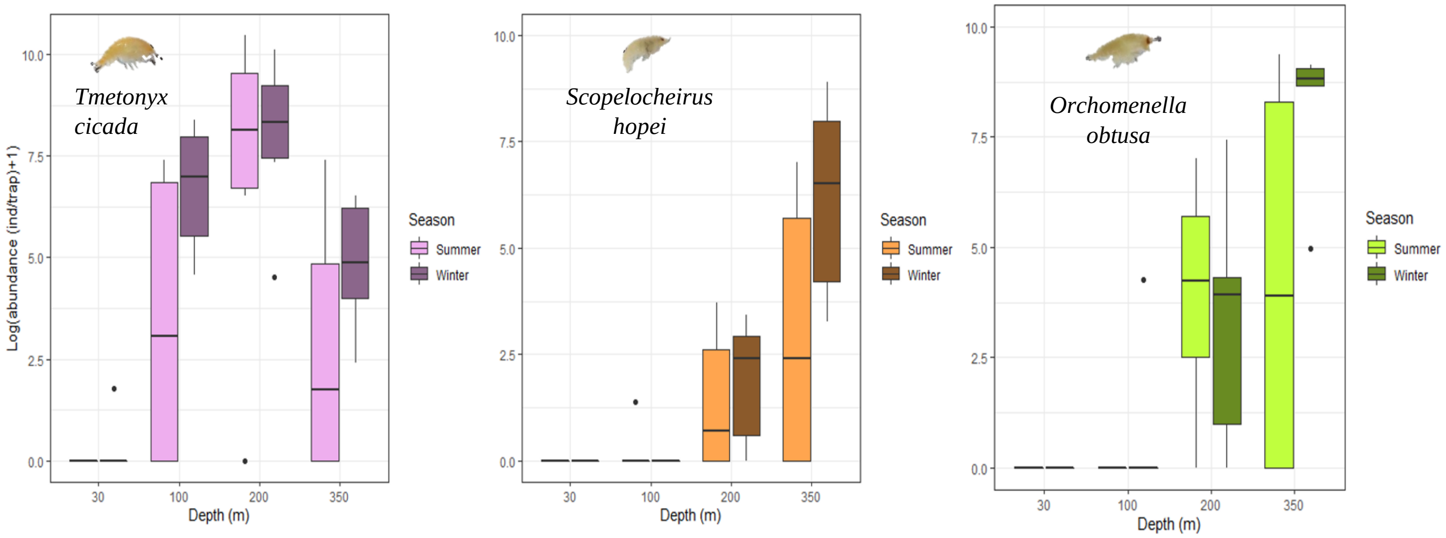

FIG. 9 | BOXPLOT OF AMPHIPOD SPECIES ABUNDANCE IN EACH SEASON.
Seasonal variation of amphipod species active abundance in Saltfjord along the sampled depth gradient (30 – 350 m). Abundance values are log transformed. Error bars indicate standard error.

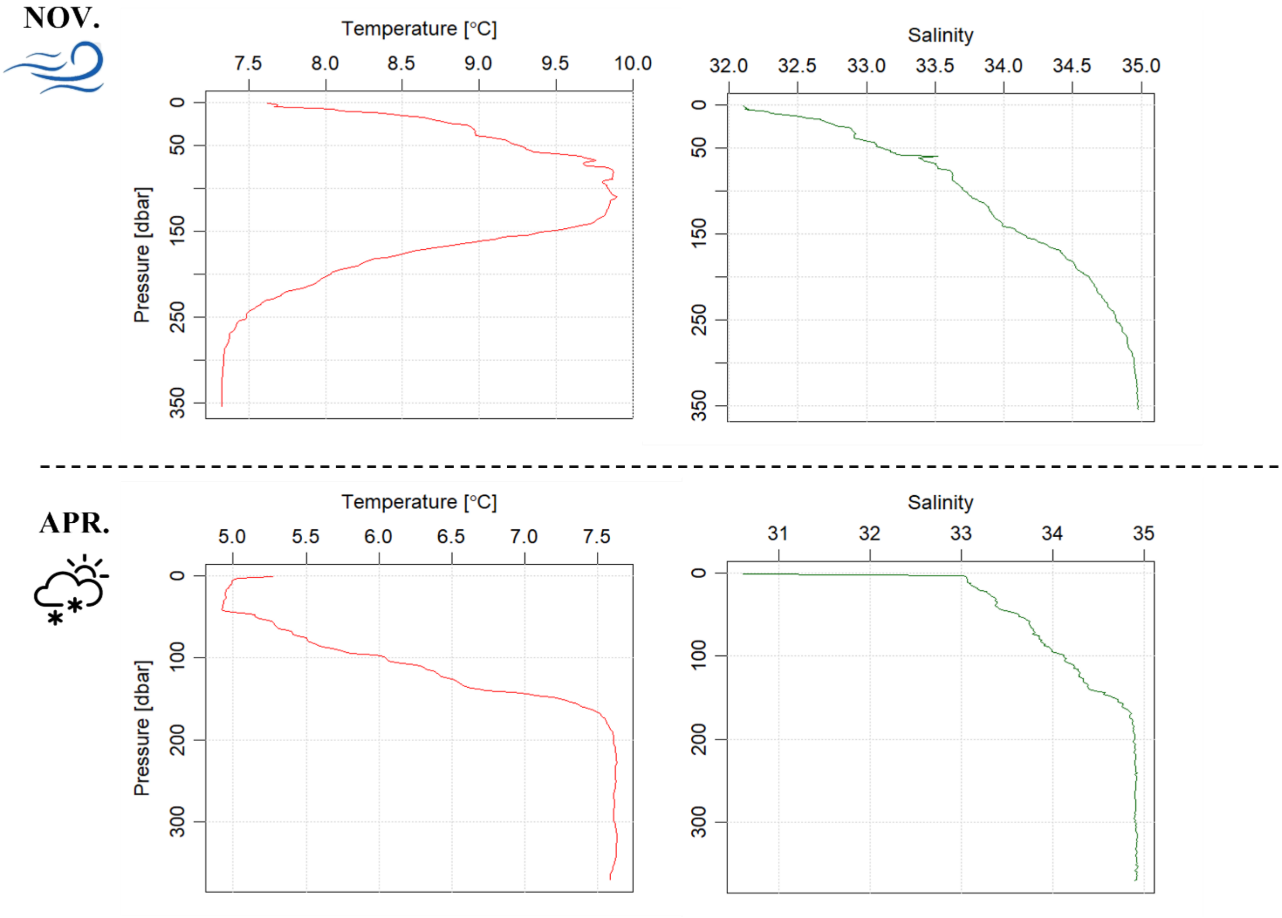

FIG. 10 | CTD TEMPERATURE AND SALINITY PROFILES OF SALTFJORD THROUGHOUT THE YEAR

Temperature (ºC) and salinity (psu) profiles of Saltfjord when sampling was carried out. (A) Temperature and salinity profiles of Saltfjord in November (above) and in April (below).

TABLE 2 | PERMUTATIONAL MULTIVARIATE ANALYSIS OF VARIANCE (PERMANOVA) FOR AMPHIPOD DISTRIBUTION IN SALTFJORD AND SKJERSTADFJORD

PERMANOVA for amphipod species distribution from catches along a depth gradient (30, 100, 200 and 350 m) in Saltfjord and Skjerstadfjord. 'Fj': Fjord; 'De':Depth; 'Ba':Bait.

Source	*df*	*SS*	*F*	*P(perm)*	*P(MC)*
Fjord	1	8314.5289	4.3537	0.0325	0.0317
Depth	3	36922.8309	6.4445	0.0008	0.0005
Bait	1	927.2408	0.4855	0.5397	0.5696
Fj*De	3	7673.0814	1.3393	0.2576	0.2536
Fj*Ba	1	2993.3847	1.5674	0.1907	0.2131
De*Ba	3	846.6219	0.1478	0.9850	0.9798
Fj*De*Ba	3	2149.2380	0.3751	0.8485	0.8529
Residual	32	61112.9089			
Total	47	120939.8355			

TABLE 3 | PERMUTATIONAL MULTIVARIATE ANALYSIS OF VARIANCE (PERMANOVA) FOR AMPHIPOD DISTRIBUTION IN SUMMER AND WINTER

PERMANOVA for amphipod species distribution along a depth gradient (30, 100, 200 and 350 m) in the summer and in the winter in Saltfjord. 'Fj': Fjord; 'De':Depth; 'Ba':Bait.

Source	*df*	*SS*	*F*	*P(perm)*	*P(MC)*
Season	1	11439.8677	7.8951	0.0051	0.0031
Depth	3	60062.2387	13.8171	0.0001	0.0001
Bait	1	1067.2722	0.7366	0.4375	0.4483
Se*De	3	4851.7033	1.1161	0.3448	0.3477
Se*Ba	1	2802.2467	1.9339	0.1428	0.1465
De*Ba	3	2327.0646	0.5353	0.7421	0.7460
Se*De*Ba	3	983.5813	0.2263	0.9655	0.9593
Residual	32	46367.4817			
Total	47	129901.4563			

3.2. Genetic variation and species identification of lysianassoid amphipods

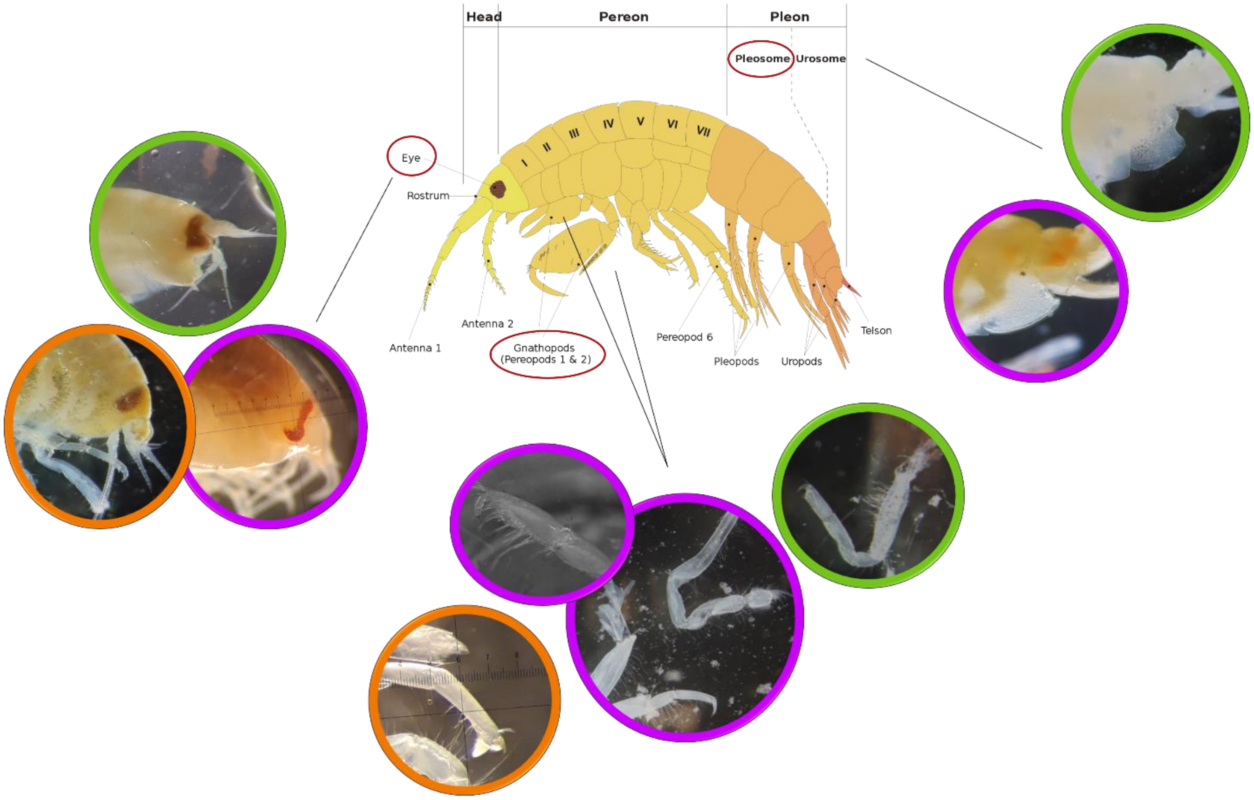

FIG. 11 | CHARACTERISTIC MORPHOLOGICAL FEATURES OF IDENTIFIED AMPHIPOD SPECIES

Body plan of an amphipod. Surrounding labels circled in red correspond to the most representative morphological features examined in the collected specimens. Color code is based on identified species: purple for T. cicada, orange for S.hopei and green for O.obtusa.

Amphipods were examined individually prior to the COI barcoding analysis. Fig. 11 shows the most characteristic morphological features that were examined in order to identify each species and compare their morphological identification to the COI barcoding outcome.

From the sequenced COI library, a total of 8,194,676 reads (4,097,338 forward and reverse) were analyzed and the average number of reads per sample was 18,882. A 58.7% of reads remained on average after trimming and adapter removal. Read lengths of the analyzed COI sequences ranged from 272 to 278 bp after removing the adapters and primers (see Table S2).

Sequence data analysis of 217 individuals revealed 24 OTUs. Of the obtained OTUs, six were discarded because they did not have a sensible hit on BLASTn (see Table S3), while the rest were COI OTUs which matched the refence sequences in the GenBank database with a 100% of query cover. It is important to note that there was a 18S hit to *O. obtusa* and another species, *Orchomenella gerulicorbis*, probably due to cross-contamination with samples of another ongoing project that overlapped during the library preparation.

The identified species that matched the recovered OTUs were assigned to each of the samples according to the maximum number of reads per sample per OTU. Out of the 217 examined samples, only 20 were mismatches between their morphological and the genetic identification.

The phylogenetic tree analysis of these COI OTUs (Fig.13) reveals the structure of the data based on the similarity of the COI region sequences among local amphipods.

Little genetic variation was found in specimens belonging to *S. hopei* and *O. obtusa* species which were depicted only by one OTU each, 4 and 1 respectively. Conversely, many different OTUs corresponded to *T. cicada*. OTUs 12 and 22 had a lower query cover percentage but also matched to the *T. cicada* species.

All Skjerstadfjord samples identified as *T.cicada* were represented by the OTU2 as the maximum number of reads per OTU2 in those samples was noticeably higher (μ= 3,983), compared to lower values for other OTUs. However, *T.cicada* samples from Saltfjord were not only depicted by OTU2 (83% of samples) but also OTU3 (17%). All the other *T. cicada* OTUs were secondary hits with few reads in the samples.

A new species was shown in the BLASTn search due to a mismatch, *Anonyx lilljeborgi*, OTU5. This species matched the only two specimens which had been morphologically identified as *Thyphosites longipes*, with lack of certainty. The rest of the mismatches in BLASTn were shown by morphologically identified *O. obtusa* specimens which matched to *O. gerulicorbis* 18S sequences. This mismatch was discarded because *O. gerulicorbis* has just been recorded at abyssal depths in the North Pacific Gyre (Shulenberger & Barnard, 1976).

FIG. 13 | PHYLOGENETIC TREE OF BARCODES

Phylogenetic tree of 18 COI barcodes collected from lysianassid amphipods and 4 known COI barcode sequences (marked with a blue star). These sequences were taken from NCBI and they belong to the assumed morphologically identified species (T. cicada, S.hopei, O.obtusa and T. longipes). A color code is used to identify the species each OTU represents; yellow for S. hopei, green for O. obtusa, purple for T. cicada and no fill color for Orchomenella gerulicorbis. OTU 22 and OTU 12 faded color shows the match had <100% of query cover. The maximum likelihood tree was done using GTR+I+R substitution model. Alignment is done using MAFFT.

4. Discussion

Lysianassoid amphipods constitute a major part of the benthic scavenging guild inhabiting the Saltfjord-Skjerstadfjord ecosystem, which is also made up of other scavengers typical from the NE Atlantic (e.g., Atlantic hagfish, galatheid crabs, decapod shrimp) (Sweetman *et al*., 2014).

The fjords in this study are characterized by distinct benthic communities (Kokarev *et al*., 2021), accordingly, a closer analysis of the amphipod fauna showed that species composition differed between fjords, and also that their distribution within the fjords was affected by, depth whose effect on the amphipod community might be explained by different hypothesis discussed below:

(a) Spatial distribution pattern favored by environmental fjord conditions

Although the superfamily Lysianassoidea is one of the key amphipod taxa regarding species richness (Seefeldt *et al*., 2018), only four species of lysianassoids, *Tmetonyx cicada*, *Scopelocheirus hopei*, *Orchomenella obtusa* and *Anonyx lilljeborgi* were found in our study. All these species have wide geographical distributions (Christiansen & Diel-Christiansen, 1993; Kaim-Malka, 2003) and depth ranges, but they usually occur in high numbers in the Norwegian and North seas (GBIF.org, 2020). Other studies carried out in Norwegian fjords have shown a distinction in the structure of benthic communities between shallow and deep areas, and their findings conclude that changes in habitat characteristics with depth play a major role in the benthos (Holte & Cochrane, 2004; Sen *et al*., 2022).

In Saltfjord, the most abundant species was *Tmetonyx cicada*, which is a member of the arcto-boreal fauna, and it has been recorded at shelf and mid-to-upper-slope depths (Lampitt *et al*., 1983). This species shows a wide bathymetric range (50 - 3200 m), as well as *S. hopei* (40 - 2500 m) (Ruffo, 1989), whereas *O. obtusa* does not show a clear depth range in the literature, but it has been recorded at 100 and 200 m depths in other studies (Christiansen & Diel-Christiansen, 1993; Anderson & Bell, 2014; Sweetman *et al*., 2014). Our sampling showed *O. obtusa* occurred at the deepest points of the basins in both fjords. This could be linked to the bottom water conditions which are very stable (Fig. X) and similar to previous studies were *O. obtusa* individuals have been sampled (Vader, 1971; Christiansen & Diel-Christiansen, 1993).

In Skjerstadfjord, higher abundance of *O.obtusa* and the absence of *S. hopei* individuals indicated that there was an isolation event because of the small trait by which the two fjords are connected. However, there is evidence that supports deep water exchange between the fjords (Kokarev *et* al., 2021) and this might not be the reason why this disaggregation occurs, instead, certain amphipod species are likely to colonize Skjerstadfjord regardless of the geomorphology of the fjord system.

Anonyx lilljeborgi was the least abundant species found in our sampling, and some authors consider this species to be found in areas with an Atlantic influence down to a depth of several hundred meters (Gurjanova, 1962) but its presence in this study was negligible compared to the other species.

(b) Predation pressure as a limiting factor for amphipod colonization of shallow waters

Predation on amphipods at baits by bathyal fish and large predatory crustaceans has been documented (Havermans & Smetacek, 2018). Heterogeneity in foraging activity of benthic fish in the study area (personal observation) has implications for understanding amphipod community structure. Habitat segregation in *T. cicada*, *S. hopei* and *O.obtusa* may have been caused by feeding habits of fish such as Atlantic cod and/or tusk, two of the most common demersal fish species found in the area.

If predation pressure in the Saltfjord-Skjerstadfjord system constrained lysianassoid amphipods to deeper depths, their lower abundances at shallow depths could be explained by amphipods escaping feeding events and relocating to avoid predators.

Furthermore, if amphipods were frequently consumed prey items based on their size (bigger individuals have a larger biomass), targeted individuals would be brooding amphipods or individuals close to maturity, what would have a negative impact on amphipod populations. In order to study the effect of predation on lysianassoids *in situ*, baited underwater camera systems could be used in these fjords.

(c) Scavenging activity: food availability in the benthos affects lysianassoid feeding behavior

Lysianassoidea exhibit a variety of lifestyles; the superfamily includes scavengers, as well as free-living detritivores and predators (Kraft *et al*., 2013).

The reaction to the presence of food differs depending on the species. For instance, *T. cicada* and *O. obtusa* can endure prolonged starvation periods, up to two months, by reducing their metabolic rates (Christiansen & Diel-Christiansen, 1993). This is an energy saving adaptation which depends on the size of individuals; larger body volumes have relatively lower metabolic rates (Christiansen & Diel-Christiansen, 1993). Another common strategy, known as ventral dilation, is storing food in the foregut right after feeding (Sainte-Marie, 1992).

But this is not the case for *S. hopei,* its alimentary strategy differs from the other amphipod species found in this study. *S. hopei* is thought to be a generalist scavenger and the individuals feed continuously because the storage of their digestive apparatus is limited is limited and they do not have ventral dilation (Kaim-Malka, 2003).

The alimentary spectrum of the species *T. cicada* and *O. obtusa* also differs from *S. hopei*. The latter can feed on different marine organisms (e.g., Echinoidea, fish, other species of lysianassoids etc.) (Kaim-Malka, 2003) while *T. cicada* and *O. obtusa* prey selectively on demersal and pelagic crustaceans. Besides, the smaller age classes of *T. cicada* and *O. obtusa* can feed on detritus besides carrion (Christiansen & Diel-Christiansen, 1993).

The similarities between *T. cicada* and *O. obtusa* feeding habits can be indicative of similar organic matter inputs and food availability in both fjords. However, the wide alimentary spectrum of *S. hopei* could imply that this species would thrive in Skjerstadfjord as well, but it was not found there.

Seasonal variations in the input of organic matter to the benthos have been recorded (Navarro & Thompson, 1995; Soerensen *et al*., 2017). Towards higher latitudes, seasonality marks a major shift in organic matter input. During spring, most of the biomass accumulates and reaches the bottom during high primary production events (Christiansen & Diel-Christiansen, 1993; Gray & Elliott, 2009). Amphipod composition in Saltfjord differed throughout the year, and higher abundances of all amphipod species were recorded during the winter. Since food resources may be scarce in the winter due to a lesser organic matter input, scavenging amphipods might be more rapidly attracted to bait in order to meet their energetic demands.

The main drawback using baited traps and limited periods of exposition to examine the composition of scavenging amphipods in this study might have affected the abundance of the collected individuals. However, this is the most commonly used sampling technique for freely swimming lysianassoid species (Legeżyńska *et al.*, 2000).

It appears from this study that scavenging amphipods can be attracted to both, herring and standard aquaculture feed, although *T.cicada.*showed significantly higher abundance in traps baited with herring. Nevertheless, *O. obtusa and S.* hopei abundances were just slightly higher with herring. There are very few quantitative available data on fish farm impacts on scavenging amphipods, however, reductions of biodiversity of crustacean assemblages near fish farms have been documented (Zhulay *et al*., 2015), and lysianassoid amphipods are one of the most common taxonomic groups found close to fish farms (Hall-Spencer & Bamber, 2007; Zhulay *et al*., 2015). The effect of organic wastes and the use of products in salmon farming (e.g., sea-lice treatments which are toxic to crustaceans) can significantly impact benthic amphipods (Zhulay *et al.*, 2015) and probably higher trophic levels in the subsequent transfer of energy from scavenged material.

Ironically, some amphipod species have shown a good potential for utilization in marine fish aquaculture (Baeza-Rojano *et al*., 2014; Jiménez-Prada *et al*., 2021). They exhibit several biological and ecological characteristics which makes them ideal candidates for this purpose. However, only amphipods of certain families (e.g., Caprellidae, Hyalidae, Gammaridae) (Baeza-Rojano *et al*., 2014; Vargas-Abúndez *et al*., 2021), may serve as an alternative resource for aquaculture diet applications. Scavenging amphipods of the Lysianassoidea superfamily may not be suitable candidates because of their feeding mode and their low lipid reserves (Christiansen & Diel-Christiansen, 1993), but the culture of these amphipods could be considered since they can be prey for commercial species such as Atlantic cod.

Given the importance of lysianassoid amphipods, molecular technologies have helped us to increase our knowledge about these scavengers and assess their ecology correctly (Havermans *et al*., 2010).

In our molecular analysis, the data verified the morphological identification of all amphipod species found in the samples fjords, *T. cicada*, *O. obtusa* and *S. hopei,* except for the rarest one, *A. lilljeborgi*.

As barcode ID focused only on COI of arthropods, inconsistent results retrieved from the sequencing analysis which resulted in mismatches with COI OTU sequences, were reported as contamination events (see Table S3). The principal reason for this lies in the sensitivity of the methods used (e.g., picking up small traces of non-target sequences).

In *O. obtusa* and *S. hopei* species, a genetic homogeneity was found among specimens from Saltfjord and Skjerstadfjord, indicating a widespread distribution in the sub-Arctic fjords. However, *T. cicada* seemed to have more genetic diversity than the other species and this could be the evidence of a significant population structure or cryptic species.

The fact that amphipod communities in Saltfjord and Skjerstadfjord might share an available pool of species from offshore waters could indicate that the colonization process of amphipod species into this fjord system has not been completed yet. Nevertheless, Buhl-Jensen (1986) found that species richness of benthic amphipods on the continental shelf was generally higher than at comparable depths in adjacent fjords.

5. Conclusions

A strong differentiation in the amphipod community composition is shown in the study area. It is possible that the underlying factors of these patterns are a combination of the ones mentioned above (environmental conditions, food supply, predation pressure and life cycles) and some others which have not been included in the objectives of this study (e.g., offshore pool of species, sex ratio etc.).

This study brings more clarity and understanding in the genetic diversity of the lysianassoid amphipods inhabiting these sub-Arctic fjords..

It should be stressed, however, that our results do not provide comprehensive information on the scavenging fauna in the examined localities as the trap types used and the periods of their exposition might have affected the diversity and abundance of the animals collected.

Finally, our results show that the amphipod fauna of the Saltfjord-Skjerstadfjord ecosystem is still widely unexplored, and that further studies, particularly molecular studies about the genetic diversity of *T. cicada* should be carried out.

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Supplementary material

TABLE S1 | SAMPLING DESIGN OVERVIEW

Sampled locations (Saltfjord and Skerstadfjord), sampling seasons, stations ID (each station has 3 replicates; only replicate 1 is shown in this table), depth category ('depth category' is used in the main text but the actual depths were not exact throughout the sampling), coordinates of the sampling stations (it was intended that all replicates had the same coordinates), deployment and retrieval dates, and time.

	Season	***Station ID***	***Depth category (m)***	***Total weight (g)***	***Latitude***	***Longitude***	***Date***	***Deployment time***	***Retrieval date***	***Retrieval time***
Saltfjord	Summer	SAL30.1s	30	0	67.14,369	14.39,990	16.04.2021	13:15	17.04.2021	12:40
	Summer	SAL100.1s	100	60.4	67.14,717	14.33,170	16.04.2022	13:00	17.04.2021	12:30
	Summer	SAL200.1s	200	189.5	67.15,087	14.28,253	16.04.2023	12:05	17.04.2021	12:05
	Summer	SAL350.1s	350	183	67.15,651	14.26,080	16.04.2024	11:50	17.04.2021	11:45
Skjerstadfjord	Summer	SKJ30.1s	30	0	67.14.866	14.53.986	19.05.2021	11:55	20.05.2021	12:15
	Summer	SKJ100.1s	100	12.78	67.14.921	14.53.674	19.05.2022	11:50	20.05.2021	12:05
	Summer	SKJ200.1s	200	313.7	67.14.981	14.52.928	19.05.2023	11:45	20.05.2021	11:30
	Summer	SKJ350.1s	350	103.2	67.14.883	14.51.696	19.05.2024	10:47	20.05.2021	10:25
	Summer	SKJ500.1s	500	243.6	67.14.877	14.50.937	19.05.2025	10:28	20.05.2021	10:10
Saltfjord	Winter	SAL30.1w	30	0	67.15,751	14.36,115	3.11.2021	10:38	4.11.2021	9:52
	Winter	SAL100.1w	100	144.51	67.14,697	14.39,247	3.11.2022	10:45	4.11.2021	9:41
	Winter	SAL200.1w	200	105.48	67.15,143	14.36,235	3.11.2023	10:59	4.11.2021	9:33
	Winter	SAL350.1w	350	169.49	67.15,115	14.38,223	3.11.2024	11:10	4.11.2021	9:19

TABLE S2 | RESULTS FROM THE MULTIQC REPORT OF THE FORWARD AND REVERSE READS ACROSS ALL SEQUENCED SAMPLES BEFORE AND AFTER ADAPTOR/ QUALITY TRIMMING

Number of raw reads and eneral statistics from the filtered reads after sequencing. Sample names indicate the sampling site (K: Skjerstadfjorden, SAL: Saltfjorden). Column labels indicate the % of total base pairs trimmed (BP trimmed) and the average read length (bp)

Sequencing ID (F1)	***Nº raw reads (F1)***	***Sample ID (forward/R1)***	***Read Length***	***% Failed***	***Sequencing ID (F2)***	***Nº raw reads (F2)***	***Sample ID (reverse/ R2)***	***% BP Trimmed***	***Read Length***
SAL1_S1_L001_R1_001.fastq.gz	1245	K10_S116_L001_trim_R1	276 bp	45%	SAL1_S1_L001_R2_001.fastq.gz	1245	K1_S169_L001_trim_R2	42.70%	273 bp
SAL31_S2_L001_R1_001.fastq.gz	14180	K11_S124_L001_trim_R1	276 bp	45%	SAL31_S2_L001_R2_001.fastq.gz	14180	K11_S124_L001_trim_R2	43.30%	273 bp
SAL66_S3_L001_R1_001.fastq.gz	1140	K12_S132_L001_trim_R1	276 bp	45%	SAL66_S3_L001_R2_001.fastq.gz	1140	K10_S116_L001_trim_R2	43.20%	273 bp
SAL81_S4_L001_R1_001.fastq.gz	4685	K13_S140_L001_trim_R1	276 bp	45%	K10_S116_L001_R2_001.fastq.gz	4685	K13_S140_L001_trim_R2	44.30%	274 bp
SAL106_S5_L001_R1_001.fastq.gz	86604	K14_S147_L001_trim_R1	276 bp	45%	SAL106_S5_L001_R2_001.fastq.gz	86604	K12_S132_L001_trim_R2	43.10%	273 bp
SAL121_S6_L001_R1_001.fastq.gz	15511	K15_S155_L001_trim_R1	276 bp	55%	K11_S124_L001_R2_001.fastq.gz	15511	K15_S155_L001_trim_R2	43.70%	273 bp
SAL10_S7_L001_R1_001.fastq.gz	21538	K16_S163_L001_trim_R1	276 bp	55%	SAL10_S7_L001_R2_001.fastq.gz	21538	K14_S147_L001_trim_R2	43.60%	273 bp
SAL18_S8_L001_R1_001.fastq.gz	16502	K17_S171_L001_trim_R1	276 bp	55%	K12_S132_L001_R2_001.fastq.gz	16502	K17_S171_L001_trim_R2	42.20%	273 bp

SAL26_S9_L001_R1_001.fastq.gz	21726	K18_S117_L001_trim_R1	276 bp	45%	SAL26_S9_L001_R2_001.fastq.gz	21726	K16_S163_L001_trim_R2	43.20%	273 bp
SAL42_S10_L001_R1_001.fastq.gz	25193	K19_S125_L001_trim_R1	276 bp	45%	K13_S140_L001_R2_001.fastq.gz	25193	K19_S125_L001_trim_R2	46.00%	273 bp
SAL50_S11_L001_R1_001.fastq.gz	12404	K1_S169_L001_trim_R1	276 bp	45%	SAL50_S11_L001_R2_001.fastq.gz	12404	K18_S117_L001_trim_R2	46.20%	273 bp
SAL69_S12_L001_R1_001.fastq.gz	13565	K20_S133_L001_trim_R1	276 bp	64%	K2_S170_L001_R2_001.fastq.gz	13565	K2_S170_L001_trim_R2	42.30%	273 bp
SAL77_S13_L001_R1_001.fastq.gz	25940	K21_S141_L001_trim_R1	276 bp	55%	SAL77_S13_L001_R2_001.fastq.gz	25940	K21_S141_L001_trim_R2	42.20%	273 bp
SAL58_S14_L001_R1_001.fastq.gz	45168	K22_S148_L001_trim_R1	276 bp	55%	K22_S148_L001_R2_001.fastq.gz	45168	K20_S133_L001_trim_R2	42.20%	273 bp
SAL2_S15_L001_R1_001.fastq.gz	50	K23_S156_L001_trim_R1	276 bp	55%	SAL2_S15_L001_R2_001.fastq.gz	50	K23_S156_L001_trim_R2	43.50%	273 bp
SAL32_S16_L001_R1_001.fastq.gz	5578	K24_S164_L001_trim_R1	276 bp	55%	K23_S156_L001_R2_001.fastq.gz	5578	K22_S148_L001_trim_R2	42.70%	273 bp
SAL67_S17_L001_R1_001.fastq.gz	31833	K25_S172_L001_trim_R1	276 bp	55%	SAL67_S17_L001_R2_001.fastq.gz	31833	K25_S172_L001_trim_R2	43.10%	273 bp
SAL82_S18_L001_R1_001.fastq.gz	19334	K26_S118_L001_trim_R1	276 bp	55%	K24_S164_L001_R2_001.fastq.gz	19334	K24_S164_L001_trim_R2	42.90%	273 bp
SAL107_S19_L001_R1_001.fastq.gz	13956	K27_S126_L001_trim_R1	276 bp	55%	SAL107_S19_L001_R2_001.fastq.gz	13956	K27_S126_L001_trim_R2	42.90%	273 bp

SAL122_S20_L001_R1_001.fastq.gz	11408	K28_S134_L001_trim_R1	277 bp	55%	K25_S172_L001_R2_001.fastq.gz	11408	K26_S118_L001_trim_R2	30.30%	276 bp
SAL11_S21_L001_R1_001.fastq.gz	17653	K29_S142_L001_trim_R1	276 bp	55%	SAL11_S21_L001_R2_001.fastq.gz	17653	K29_S142_L001_trim_R2	42.00%	273 bp
SAL19_S22_L001_R1_001.fastq.gz	1678	K2_S170_L001_trim_R1	276 bp	45%	K26_S118_L001_R2_001.fastq.gz	1678	K28_S134_L001_trim_R2	42.80%	273 bp
SAL27_S23_L001_R1_001.fastq.gz	20454	K30_S149_L001_trim_R1	276 bp	55%	SAL27_S23_L001_R2_001.fastq.gz	20454	K30_S149_L001_trim_R2	42.60%	273 bp
SAL43_S24_L001_R1_001.fastq.gz	13219	K31_S157_L001_trim_R1	277 bp	55%	K27_S126_L001_R2_001.fastq.gz	13219	K3_S162_L001_trim_R2	28.60%	276 bp
SAL51_S25_L001_R1_001.fastq.gz	38	K32_S213_L001_trim_R1	276 bp	64%	SAL51_S25_L001_R2_001.fastq.gz	38	K32_S213_L001_trim_R2	44.00%	273 bp
SAL70_S26_L001_R1_001.fastq.gz	15021	K33_S165_L001_trim_R1	276 bp	55%	K28_S134_L001_R2_001.fastq.gz	15021	K31_S157_L001_trim_R2	42.60%	273 bp
SAL78_S27_L001_R1_001.fastq.gz	17980	K34_S173_L001_trim_R1	276 bp	64%	SAL78_S27_L001_R2_001.fastq.gz	17980	K34_S173_L001_trim_R2	43.20%	273 bp
SAL60_S28_L001_R1_001.fastq.gz	10207	K35_S119_L001_trim_R1	276 bp	64%	K29_S142_L001_R2_001.fastq.gz	10207	K33_S165_L001_trim_R2	42.90%	273 bp
SAL3_S29_L001_R1_001.fastq.gz	337	K36_S127_L001_trim_R1	278 bp	27%	SAL3_S29_L001_R2_001.fastq.gz	337	K36_S127_L001_trim_R2	9.70%	279 bp
SAL33_S30_L001_R1_001.fastq.gz	15399	K37_S135_L001_trim_R1	278 bp	36%	K3_S162_L001_R2_001.fastq.gz	15399	K35_S119_L001_trim_R2	14.20%	278 bp

SAL68_S31_L001_R1_001.fastq.gz	588	K39_S150_L001_trim_R1	277 bp	45%	SAL68_S31_L001_R2_001.fastq.gz	588	K39_S150_L001_trim_R2	20.50%	278 bp
SAL83_S32_L001_R1_001.fastq.gz	14788	K3_S162_L001_trim_R1	276 bp	45%	K39_S150_L001_R2_001.fastq.gz	14788	K37_S135_L001_trim_R2	42.90%	273 bp
SAL108_S33_L001_R1_001.fastq.gz	10168	K40_S158_L001_trim_R1	277 bp	45%	SAL108_S33_L001_R2_001.fastq.gz	10168	K4_S154_L001_trim_R2	42.90%	273 bp
SAL123_S34_L001_R1_001.fastq.gz	21621	K41_S166_L001_trim_R1	278 bp	55%	K4_S154_L001_R2_001.fastq.gz	21621	K41_S166_L001_trim_R2	24.30%	277 bp
SAL12_S35_L001_R1_001.fastq.gz	19416	K42_S174_L001_trim_R1	277 bp	45%	SAL12_S35_L001_R2_001.fastq.gz	19416	K40_S158_L001_trim_R2	20.50%	277 bp
SAL20_S36_L001_R1_001.fastq.gz	10986	K43_S120_L001_trim_R1	276 bp	64%	K40_S158_L001_R2_001.fastq.gz	10986	K43_S120_L001_trim_R2	43.00%	273 bp
SAL28_S37_L001_R1_001.fastq.gz	19207	K44_S128_L001_trim_R1	276 bp	45%	SAL28_S37_L001_R2_001.fastq.gz	19207	K42_S174_L001_trim_R2	42.80%	276 bp
SAL44_S38_L001_R1_001.fastq.gz	16283	K45_S136_L001_trim_R1	277 bp	36%	K41_S166_L001_R2_001.fastq.gz	16283	K45_S136_L001_trim_R2	25.70%	275 bp
SAL52_S39_L001_R1_001.fastq.gz	27786	K46_S143_L001_trim_R1	277 bp	55%	SAL52_S39_L001_R2_001.fastq.gz	27786	K44_S128_L001_trim_R2	44.70%	273 bp
SAL59_S40_L001_R1_001.fastq.gz	1646	K47_S151_L001_trim_R1	276 bp	55%	K42_S174_L001_R2_001.fastq.gz	1646	K47_S151_L001_trim_R2	35.20%	276 bp
SAL71_S41_L001_R1_001.fastq.gz	27437	K48_S159_L001_trim_R1	277 bp	45%	SAL71_S41_L001_R2_001.fastq.gz	27437	K46_S143_L001_trim_R2	29.20%	274 bp

SAL79_S42_L001_R1_001.fastq.gz	11369	K49_S167_L001_trim_R1	277 bp	45%	K43_S120_L001_R2_001.fastq.gz	11369	K49_S167_L001_trim_R2	28.10%	276 bp
SAL4_S43_L001_R1_001.fastq.gz	23232	K4_S154_L001_trim_R1	276 bp	45%	SAL4_S43_L001_R2_001.fastq.gz	23232	K48_S159_L001_trim_R2	32.90%	277 bp
SAL101_S44_L001_R1_001.fastq.gz	587	K50_S175_L001_trim_R1	277 bp	36%	K44_S128_L001_R2_001.fastq.gz	587	K5_S146_L001_trim_R2	8.20%	276 bp
SAL84_S45_L001_R1_001.fastq.gz	27260	K51_S176_L001_trim_R1	276 bp	55%	SAL84_S45_L001_R2_001.fastq.gz	27260	K51_S176_L001_trim_R2	54.20%	274 bp
SAL109_S46_L001_R1_001.fastq.gz	13646	K52_S178_L001_trim_R1	276 bp	55%	K45_S136_L001_R2_001.fastq.gz	13646	K50_S175_L001_trim_R2	38.70%	274 bp
SAL124_S47_L001_R1_001.fastq.gz	32	K53_S180_L001_trim_R1	276 bp	55%	SAL124_S47_L001_R2_001.fastq.gz	32	K53_S180_L001_trim_R2	41.20%	273 bp
SAL13_S48_L001_R1_001.fastq.gz	3897	K54_S182_L001_trim_R1	276 bp	55%	K5_S146_L001_R2_001.fastq.gz	3897	K52_S178_L001_trim_R2	40.20%	274 bp
SAL21_S49_L001_R1_001.fastq.gz	26872	K55_S183_L001_trim_R1	276 bp	36%	SAL21_S49_L001_R2_001.fastq.gz	26872	K55_S183_L001_trim_R2	44.40%	275 bp
SAL29_S50_L001_R1_001.fastq.gz	16022	K56_S185_L001_trim_R1	276 bp	55%	K51_S176_L001_R2_001.fastq.gz	16022	K54_S182_L001_trim_R2	33.60%	275 bp
SAL45_S51_L001_R1_001.fastq.gz	16833	K57_S187_L001_trim_R1	276 bp	64%	SAL45_S51_L001_R2_001.fastq.gz	16833	K57_S187_L001_trim_R2	44.00%	273 bp
SAL53_S52_L001_R1_001.fastq.gz	199	K58_S189_L001_trim_R1	276 bp	64%	K52_S178_L001_R2_001.fastq.gz	199	K56_S185_L001_trim_R2	43.30%	273 bp

SAL61_S53_L001_R1_001.fastq.gz	27100	K59_S191_L001_trim_R1	276 bp	64%	SAL61_S53_L001_R2_001.fastq.gz	27100	K59_S191_L001_trim_R2	43.60%	273 bp
SAL72_S54_L001_R1_001.fastq.gz	24862	K5_S146_L001_trim_R1	276 bp	45%	K53_S180_L001_R2_001.fastq.gz	24862	K58_S189_L001_trim_R2	42.60%	273 bp
SAL80_S55_L001_R1_001.fastq.gz	16651	K60_S193_L001_trim_R1	276 bp	36%	SAL80_S55_L001_R2_001.fastq.gz	16651	K6_S139_L001_trim_R2	42.80%	273 bp
SAL34_S56_L001_R1_001.fastq.gz	19111	K61_S195_L001_trim_R1	276 bp	55%	K54_S182_L001_R2_001.fastq.gz	19111	K61_S195_L001_trim_R2	43.30%	273 bp
SAL5_S57_L001_R1_001.fastq.gz	882	K62_S197_L001_trim_R1	276 bp	64%	SAL5_S57_L001_R2_001.fastq.gz	882	K60_S193_L001_trim_R2	31.80%	277 bp
SAL35_S58_L001_R1_001.fastq.gz	20072	K63_S198_L001_trim_R1	276 bp	64%	K63_S198_L001_R2_001.fastq.gz	20072	K63_S198_L001_trim_R2	44.00%	273 bp
SAL102_S59_L001_R1_001.fastq.gz	263	K64_S200_L001_trim_R1	276 bp	55%	SAL102_S59_L001_R2_001.fastq.gz	263	K62_S197_L001_trim_R2	43.40%	273 bp
SAL110_S60_L001_R1_001.fastq.gz	27727	K65_S202_L001_trim_R1	276 bp	55%	K64_S200_L001_R2_001.fastq.gz	27727	K65_S202_L001_trim_R2	43.80%	273 bp
SAL125_S61_L001_R1_001.fastq.gz	4620	K66_S204_L001_trim_R1	276 bp	64%	SAL125_S61_L001_R2_001.fastq.gz	4620	K64_S200_L001_trim_R2	43.20%	273 bp
SAL14_S62_L001_R1_001.fastq.gz	41	K67_S205_L001_trim_R1	276 bp	55%	K65_S202_L001_R2_001.fastq.gz	41	K67_S205_L001_trim_R2	43.30%	273 bp
SAL22_S63_L001_R1_001.fastq.gz	23429	K68_S207_L001_trim_R1	276 bp	55%	SAL22_S63_L001_R2_001.fastq.gz	23429	K66_S204_L001_trim_R2	43.30%	273 bp

SAL30_S64_L001_R1_001.fastq.gz	20037	K69_S209_L001_trim_R1	276 bp	55%	K66_S204_L001_R2_001.fastq.gz	20037	K69_S209_L001_trim_R2	43.60%	273 bp
SAL46_S65_L001_R1_001.fastq.gz	5949	K6_S139_L001_trim_R1	276 bp	45%	SAL46_S65_L001_R2_001.fastq.gz	5949	K68_S207_L001_trim_R2	43.40%	273 bp
SAL54_S66_L001_R1_001.fastq.gz	2489	K70_S211_L001_trim_R1	276 bp	64%	K71_S212_L001_R2_001.fastq.gz	2489	K7_S131_L001_trim_R2	43.70%	273 bp
SAL62_S67_L001_R1_001.fastq.gz	26818	K71_S212_L001_trim_R1	276 bp	55%	SAL62_S67_L001_R2_001.fastq.gz	26818	K71_S212_L001_trim_R2	43.70%	273 bp
SAL73_S68_L001_R1_001.fastq.gz	19493	K72_S214_L001_trim_R1	276 bp	64%	K72_S214_L001_R2_001.fastq.gz	19493	K70_S211_L001_trim_R2	42.90%	273 bp
SAL89_S69_L001_R1_001.fastq.gz	19679	K72ii_S210_L001_trim_R1	276 bp	64%	SAL89_S69_L001_R2_001.fastq.gz	19679	K72ii_S210_L001_trim_R2	43.20%	273 bp
SAL85_S70_L001_R1_001.fastq.gz	5084	K73_S216_L001_trim_R1	276 bp	64%	K72ii_S210_L001_R2_001.fastq.gz	5084	K72_S214_L001_trim_R2	44.00%	273 bp
SAL6_S71_L001_R1_001.fastq.gz	804	K74_S217_L001_trim_R1	276 bp	55%	SAL6_S71_L001_R2_001.fastq.gz	804	K74_S217_L001_trim_R2	43.30%	273 bp
SAL36_S72_L001_R1_001.fastq.gz	16966	K75_S177_L001_trim_R1	276 bp	64%	K73_S216_L001_R2_001.fastq.gz	16966	K73_S216_L001_trim_R2	43.30%	273 bp
SAL103_S73_L001_R1_001.fastq.gz	1963	K76_S179_L001_trim_R1	276 bp	64%	SAL103_S73_L001_R2_001.fastq.gz	1963	K76_S179_L001_trim_R2	43.50%	273 bp
SAL86_S74_L001_R1_001.fastq.gz	24071	K77_S181_L001_trim_R1	276 bp	64%	K79_S184_L001_R2_001.fastq.gz	24071	K75_S177_L001_trim_R2	43.20%	273 bp

SAL111_S75_L001_R1_001.fastq.gz	19023	K79_S184_L001_trim_R1	276 bp	64%	SAL111_S75_L001_R2_001.fastq.gz	19023	K79_S184_L001_trim_R2	43.50%	273 bp
SAL126_S76_L001_R1_001.fastq.gz	27	K7_S131_L001_trim_R1	276 bp	45%	K80_S186_L001_R2_001.fastq.gz	27	K77_S181_L001_trim_R2	42.80%	273 bp
SAL15_S77_L001_R1_001.fastq.gz	19910	K80_S186_L001_trim_R1	276 bp	55%	SAL15_S77_L001_R2_001.fastq.gz	19910	K80_S186_L001_trim_R2	44.00%	273 bp
SAL23_S78_L001_R1_001.fastq.gz	29594	K81_S188_L001_trim_R1	276 bp	64%	K81_S188_L001_R2_001.fastq.gz	29594	K8_S123_L001_trim_R2	44.70%	273 bp
SAL39_S79_L001_R1_001.fastq.gz	23494	K82_S190_L001_trim_R1	277 bp	45%	SAL39_S79_L001_R2_001.fastq.gz	23494	K82_S190_L001_trim_R2	48.20%	274 bp
SAL47_S80_L001_R1_001.fastq.gz	19778	K83_S192_L001_trim_R1	276 bp	64%	K82_S190_L001_R2_001.fastq.gz	19778	K81_S188_L001_trim_R2	42.80%	273 bp
SAL55_S81_L001_R1_001.fastq.gz	5308	K84_S194_L001_trim_R1	276 bp	64%	SAL55_S81_L001_R2_001.fastq.gz	5308	K84_S194_L001_trim_R2	43.50%	273 bp
SAL63_S82_L001_R1_001.fastq.gz	5258	K85_S196_L001_trim_R1	277 bp	55%	K83_S192_L001_R2_001.fastq.gz	5258	K83_S192_L001_trim_R2	27.60%	276 bp
SAL74_S83_L001_R1_001.fastq.gz	29105	K87_S199_L001_trim_R1	276 bp	55%	SAL74_S83_L001_R2_001.fastq.gz	29105	K87_S199_L001_trim_R2	43.00%	273 bp
SAL90_S84_L001_R1_001.fastq.gz	12250	K88_S201_L001_trim_R1	276 bp	64%	K84_S194_L001_R2_001.fastq.gz	12250	K85_S196_L001_trim_R2	43.40%	273 bp
SAL7_S85_L001_R1_001.fastq.gz	3867	K89_S203_L001_trim_R1	276 bp	55%	SAL7_S85_L001_R2_001.fastq.gz	3867	K89_S203_L001_trim_R2	43.70%	273 bp

SAL37_S86_L001_R1_001.fastq.gz	13999	K8_S123_L001_trim_R1	276 bp	45%	K85_S196_L001_R2_001.fastq.gz	13999	K88_S201_L001_trim_R2	43.30%	273 bp
SAL104_S87_L001_R1_001.fastq.gz	1094	K90_S206_L001_trim_R1	276 bp	64%	SAL104_S87_L001_R2_001.fastq.gz	1094	K9_S115_L001_trim_R2	27.60%	275 bp
SAL87_S88_L001_R1_001.fastq.gz	22305	K91_S208_L001_trim_R1	276 bp	64%	K90_S206_L001_R2_001.fastq.gz	22305	K91_S208_L001_trim_R2	43.30%	273 bp
SAL112_S89_L001_R1_001.fastq.gz	15411	K9_S115_L001_trim_R1	276 bp	45%	SAL112_S89_L001_R2_001.fastq.gz	15411	K90_S206_L001_trim_R2	44.10%	273 bp
SAL127_S90_L001_R1_001.fastq.gz	7684	SAL100_S168_L001_trim_R1	277 bp	45%	K91_S208_L001_R2_001.fastq.gz	7684	SAL10_S7_L001_trim_R2	32.30%	276 bp
SAL16_S91_L001_R1_001.fastq.gz	5574	SAL101_S44_L001_trim_R1	276 bp	45%	SAL16_S91_L001_R2_001.fastq.gz	5574	SAL1_S1_L001_trim_R2	40.50%	273 bp
SAL24_S92_L001_R1_001.fastq.gz	28691	SAL102_S59_L001_trim_R1	276 bp	45%	SAL100_S168_L001_R2_001.fastq.gz	28691	SAL100_S168_L001_trim_R2	40.80%	273 bp
SAL40_S93_L001_R1_001.fastq.gz	14781	SAL103_S73_L001_trim_R1	276 bp	45%	SAL40_S93_L001_R2_001.fastq.gz	14781	SAL101_S44_L001_trim_R2	44.30%	273 bp
SAL48_S94_L001_R1_001.fastq.gz	19469	SAL104_S87_L001_trim_R1	276 bp	45%	SAL101_S44_L001_R2_001.fastq.gz	19469	SAL102_S59_L001_trim_R2	42.00%	273 bp
SAL56_S95_L001_R1_001.fastq.gz	20226	SAL105_S101_L001_trim_R1	276 bp	45%	SAL56_S95_L001_R2_001.fastq.gz	20226	SAL103_S73_L001_trim_R2	41.10%	273 bp
SAL75_S96_L001_R1_001.fastq.gz	16038	SAL106_S5_L001_trim_R1	276 bp	64%	SAL109_S46_L001_R2_001.fastq.gz	16038	SAL104_S87_L001_trim_R2	43.00%	273 bp

SAL91_S97_L001_R1_001.fastq.gz	2536	SAL107_S19_L001_trim_R1	276 bp	55%	SAL91_S97_L001_R2_001.fastq.gz	2536	SAL105_S101_L001_trim_R2	43.20%	273 bp
SAL64_S98_L001_R1_001.fastq.gz	28987	SAL108_S33_L001_trim_R1	276 bp	55%	SAL110_S60_L001_R2_001.fastq.gz	28987	SAL106_S5_L001_trim_R2	42.60%	273 bp
SAL8_S99_L001_R1_001.fastq.gz	2716	SAL109_S46_L001_trim_R1	276 bp	64%	SAL8_S99_L001_R2_001.fastq.gz	2716	SAL107_S19_L001_trim_R2	42.50%	273 bp
SAL38_S100_L001_R1_001.fastq.gz	16915	SAL10_S7_L001_trim_R1	276 bp	45%	SAL114_S114_L001_R2_001.fastq.gz	16915	SAL108_S33_L001_trim_R2	43.80%	273 bp
SAL105_S101_L001_R1_001.fastq.gz	961	SAL110_S60_L001_trim_R1	276 bp	64%	SAL105_S101_L001_R2_001.fastq.gz	961	SAL109_S46_L001_trim_R2	42.90%	273 bp
SAL88_S102_L001_R1_001.fastq.gz	26893	SAL111_S75_L001_trim_R1	276 bp	55%	SAL115_S122_L001_R2_001.fastq.gz	26893	SAL111_S75_L001_trim_R2	42.80%	273 bp
SAL113_S103_L001_R1_001.fastq.gz	16356	SAL112_S89_L001_trim_R1	276 bp	55%	SAL113_S103_L001_R2_001.fastq.gz	16356	SAL11_S21_L001_trim_R2	42.90%	273 bp
SAL128_S104_L001_R1_001.fastq.gz	9677	SAL113_S103_L001_trim_R1	276 bp	55%	SAL116_S130_L001_R2_001.fastq.gz	9677	SAL113_S103_L001_trim_R2	43.20%	273 bp
SAL17_S105_L001_R1_001.fastq.gz	2287	SAL114_S114_L001_trim_R1	276 bp	45%	SAL17_S105_L001_R2_001.fastq.gz	2287	SAL110_S60_L001_trim_R2	42.40%	273 bp
SAL25_S106_L001_R1_001.fastq.gz	30537	SAL115_S122_L001_trim_R1	276 bp	55%	SAL117_S138_L001_R2_001.fastq.gz	30537	SAL115_S122_L001_trim_R2	31.70%	274 bp
SAL41_S107_L001_R1_001.fastq.gz	26295	SAL116_S130_L001_trim_R1	276 bp	45%	SAL41_S107_L001_R2_001.fastq.gz	26295	SAL112_S89_L001_trim_R2	43.30%	273 bp

SAL49_S108_L001_R1_001.fastq.gz	49	SAL117_S138_L001_trim_R1	276 bp	45%	SAL121_S6_L001_R2_001.fastq.gz	49	SAL117_S138_L001_trim_R2	43.20%	273 bp
SAL57_S109_L001_R1_001.fastq.gz	21405	SAL118_S145_L001_trim_R1	276 bp	45%	SAL57_S109_L001_R2_001.fastq.gz	21405	SAL114_S114_L001_trim_R2	43.00%	273 bp
SAL65_S110_L001_R1_001.fastq.gz	14620	SAL119_S153_L001_trim_R1	276 bp	36%	SAL122_S20_L001_R2_001.fastq.gz	14620	SAL119_S153_L001_trim_R2	41.90%	273 bp
SAL76_S111_L001_R1_001.fastq.gz	22217	SAL11_S21_L001_trim_R1	276 bp	45%	SAL76_S111_L001_R2_001.fastq.gz	22217	SAL116_S130_L001_trim_R2	41.80%	273 bp
SAL92_S112_L001_R1_001.fastq.gz	22965	SAL120_S161_L001_trim_R1	276 bp	55%	SAL123_S34_L001_R2_001.fastq.gz	22965	SAL120_S161_L001_trim_R2	43.10%	273 bp
SAL93_S113_L001_R1_001.fastq.gz	19379	SAL121_S6_L001_trim_R1	276 bp	55%	SAL93_S113_L001_R2_001.fastq.gz	19379	SAL118_S145_L001_trim_R2	41.50%	273 bp
SAL114_S114_L001_R1_001.fastq.gz	8574	SAL122_S20_L001_trim_R1	276 bp	55%	SAL126_S76_L001_R2_001.fastq.gz	8574	SAL122_S20_L001_trim_R2	42.30%	273 bp
K9_S115_L001_R1_001.fastq.gz	53	SAL123_S34_L001_trim_R1	276 bp	55%	K9_S115_L001_R2_001.fastq.gz	53	SAL12_S35_L001_trim_R2	42.70%	273 bp
K10_S116_L001_R1_001.fastq.gz	27647	SAL124_S47_L001_trim_R1	277 bp	45%	SAL127_S90_L001_R2_001.fastq.gz	27647	SAL124_S47_L001_trim_R2	22.00%	277 bp
K18_S117_L001_R1_001.fastq.gz	854	SAL125_S61_L001_trim_R1	276 bp	45%	K18_S117_L001_R2_001.fastq.gz	854	SAL121_S6_L001_trim_R2	42.60%	273 bp
K26_S118_L001_R1_001.fastq.gz	20037	SAL126_S76_L001_trim_R1	276 bp	27%	SAL128_S104_L001_R2_001.fastq.gz	20037	SAL126_S76_L001_trim_R2	40.10%	274 bp

K35_S119_L001_R1_001.fastq.gz	14719	SAL127_S90_L001_trim_R1	276 bp	45%	K35_S119_L001_R2_001.fastq.gz	14719	SAL123_S34_L001_trim_R2	42.40%	273 bp
K43_S120_L001_R1_001.fastq.gz	12194	SAL128_S104_L001_trim_R1	276 bp	45%	SAL13_S48_L001_R2_001.fastq.gz	12194	SAL128_S104_L001_trim_R2	42.30%	273 bp
SAL94_S121_L001_R1_001.fastq.gz	13914	SAL12_S35_L001_trim_R1	276 bp	45%	SAL94_S121_L001_R2_001.fastq.gz	13914	SAL125_S61_L001_trim_R2	42.40%	273 bp
SAL115_S122_L001_R1_001.fastq.gz	50	SAL13_S48_L001_trim_R1	276 bp	45%	SAL14_S62_L001_R2_001.fastq.gz	50	SAL13_S48_L001_trim_R2	44.10%	273 bp
K8_S123_L001_R1_001.fastq.gz	34606	SAL14_S62_L001_trim_R1	277 bp	55%	K8_S123_L001_R2_001.fastq.gz	34606	SAL127_S90_L001_trim_R2	43.00%	273 bp
K11_S124_L001_R1_001.fastq.gz	30056	SAL15_S77_L001_trim_R1	276 bp	55%	SAL18_S8_L001_R2_001.fastq.gz	30056	SAL15_S77_L001_trim_R2	43.20%	273 bp
K19_S125_L001_R1_001.fastq.gz	538	SAL16_S91_L001_trim_R1	276 bp	45%	K19_S125_L001_R2_001.fastq.gz	538	SAL14_S62_L001_trim_R2	34.00%	276 bp
K27_S126_L001_R1_001.fastq.gz	17964	SAL17_S105_L001_trim_R1	276 bp	55%	SAL19_S22_L001_R2_001.fastq.gz	17964	SAL17_S105_L001_trim_R2	43.10%	273 bp
K36_S127_L001_R1_001.fastq.gz	23	SAL18_S8_L001_trim_R1	276 bp	55%	K36_S127_L001_R2_001.fastq.gz	23	SAL16_S91_L001_trim_R2	43.70%	273 bp
K44_S128_L001_R1_001.fastq.gz	163	SAL19_S22_L001_trim_R1	276 bp	45%	SAL20_S36_L001_R2_001.fastq.gz	163	SAL19_S22_L001_trim_R2	42.10%	273 bp
SAL95_S129_L001_R1_001.fastq.gz	15498	SAL1_S1_L001_trim_R1	276 bp	45%	SAL95_S129_L001_R2_001.fastq.gz	15498	SAL18_S8_L001_trim_R2	42.50%	273 bp

SAL116_S130_L001_R1_001.fastq.gz	5817	SAL20_S36_L001_trim_R1	276 bp	45 %	SAL23_S78_L001_R2_001.fastq.gz	5817	SAL2_S15_L001_trim_R2	42.70%	273 bp
K7_S131_L001_R1_001.fastq.gz	34141	SAL21_S49_L001_trim_R1	276 bp	45 %	K7_S131_L001_R2_001.fastq.gz	34141	SAL21_S49_L001_trim_R2	42.30%	273 bp
K12_S132_L001_R1_001.fastq.gz	29907	SAL22_S63_L001_trim_R1	276 bp	45 %	SAL24_S92_L001_R2_001.fastq.gz	29907	SAL20_S36_L001_trim_R2	43.30%	273 bp
K20_S133_L001_R1_001.fastq.gz	25143	SAL23_S78_L001_trim_R1	276 bp	45 %	K20_S133_L001_R2_001.fastq.gz	25143	SAL23_S78_L001_trim_R2	42.80%	273 bp
K28_S134_L001_R1_001.fastq.gz	210	SAL24_S92_L001_trim_R1	276 bp	45 %	SAL25_S106_L001_R2_001.fastq.gz	210	SAL22_S63_L001_trim_R2	42.00%	273 bp
K37_S135_L001_R1_001.fastq.gz	34	SAL25_S106_L001_trim_R1	276 bp	45 %	K37_S135_L001_R2_001.fastq.gz	34	SAL25_S106_L001_trim_R2	42.50%	273 bp
K45_S136_L001_R1_001.fastq.gz	16	SAL26_S9_L001_trim_R1	276 bp	45 %	SAL29_S50_L001_R2_001.fastq.gz	16	SAL24_S92_L001_trim_R2	42.40%	273 bp
SAL96_S137_L001_R1_001.fastq.gz	12746	SAL27_S23_L001_trim_R1	276 bp	45 %	SAL96_S137_L001_R2_001.fastq.gz	12746	SAL27_S23_L001_trim_R2	42.80%	273 bp
SAL117_S138_L001_R1_001.fastq.gz	8238	SAL28_S37_L001_trim_R1	276 bp	45 %	SAL30_S64_L001_R2_001.fastq.gz	8238	SAL26_S9_L001_trim_R2	42.50%	273 bp
K6_S139_L001_R1_001.fastq.gz	27075	SAL29_S50_L001_trim_R1	276 bp	45 %	K6_S139_L001_R2_001.fastq.gz	27075	SAL29_S50_L001_trim_R2	42.80%	273 bp
K13_S140_L001_R1_001.fastq.gz	71	SAL2_S15_L001_trim_R1	276 bp	45 %	SAL32_S16_L001_R2_001.fastq.gz	71	SAL28_S37_L001_trim_R2	32.80%	274 bp

K21_S141_L001_R1_001.fastq.gz	28925	SAL30_S64_L001_trim_R1	276 bp	45%	K21_S141_L001_R2_001.fastq.gz	28925	SAL3_S29_L001_trim_R2	45.40%	273 bp
K29_S142_L001_R1_001.fastq.gz	44170	SAL31_S2_L001_trim_R1	276 bp	55%	SAL33_S30_L001_R2_001.fastq.gz	44170	SAL31_S2_L001_trim_R2	42.90%	273 bp
K46_S143_L001_R1_001.fastq.gz	68	SAL32_S16_L001_trim_R1	276 bp	55%	K46_S143_L001_R2_001.fastq.gz	68	SAL30_S64_L001_trim_R2	42.60%	273 bp
SAL97_S144_L001_R1_001.fastq.gz	14668	SAL33_S30_L001_trim_R1	276 bp	55%	SAL34_S56_L001_R2_001.fastq.gz	14668	SAL33_S30_L001_trim_R2	42.20%	273 bp
SAL118_S145_L001_R1_001.fastq.gz	78	SAL34_S56_L001_trim_R1	276 bp	55%	SAL118_S145_L001_R2_001.fastq.gz	78	SAL32_S16_L001_trim_R2	42.40%	273 bp
K5_S146_L001_R1_001.fastq.gz	45917	SAL35_S58_L001_trim_R1	276 bp	55%	SAL35_S58_L001_R2_001.fastq.gz	45917	SAL35_S58_L001_trim_R2	42.70%	273 bp
K14_S147_L001_R1_001.fastq.gz	15369	SAL36_S72_L001_trim_R1	276 bp	55%	K14_S147_L001_R2_001.fastq.gz	15369	SAL34_S56_L001_trim_R2	42.50%	273 bp
K22_S148_L001_R1_001.fastq.gz	12398	SAL37_S86_L001_trim_R1	276 bp	55%	SAL36_S72_L001_R2_001.fastq.gz	12398	SAL37_S86_L001_trim_R2	43.20%	273 bp
K30_S149_L001_R1_001.fastq.gz	72314	SAL38_S100_L001_trim_R1	276 bp	55%	K30_S149_L001_R2_001.fastq.gz	72314	SAL36_S72_L001_trim_R2	42.40%	273 bp
K39_S150_L001_R1_001.fastq.gz	37	SAL39_S79_L001_trim_R1	276 bp	64%	SAL37_S86_L001_R2_001.fastq.gz	37	SAL39_S79_L001_trim_R2	42.70%	273 bp
K47_S151_L001_R1_001.fastq.gz	39	SAL3_S29_L001_trim_R1	276 bp	45%	K47_S151_L001_R2_001.fastq.gz	39	SAL38_S100_L001_trim_R2	43.40%	273 bp

SAL98_S152_L001_R1_001.fastq.gz	12712	SAL40_S93_L001_trim_R1	276 bp	64%	SAL38_S100_L001_R2_001.fastq.gz	12712	SAL4_S43_L001_trim_R2	43.10%	273 bp
SAL119_S153_L001_R1_001.fastq.gz	10792	SAL41_S107_L001_trim_R1	276 bp	64%	SAL119_S153_L001_R2_001.fastq.gz	10792	SAL41_S107_L001_trim_R2	43.10%	273 bp
K4_S154_L001_R1_001.fastq.gz	47313	SAL42_S10_L001_trim_R1	276 bp	64%	SAL42_S10_L001_R2_001.fastq.gz	47313	SAL40_S93_L001_trim_R2	42.80%	273 bp
K15_S155_L001_R1_001.fastq.gz	16507	SAL43_S24_L001_trim_R1	276 bp	64%	K15_S155_L001_R2_001.fastq.gz	16507	SAL43_S24_L001_trim_R2	42.90%	273 bp
K23_S156_L001_R1_001.fastq.gz	13580	SAL44_S38_L001_trim_R1	276 bp	55%	SAL43_S24_L001_R2_001.fastq.gz	13580	SAL42_S10_L001_trim_R2	43.00%	273 bp
K31_S157_L001_R1_001.fastq.gz	170	SAL45_S51_L001_trim_R1	276 bp	64%	K31_S157_L001_R2_001.fastq.gz	170	SAL45_S51_L001_trim_R2	44.00%	273 bp
K40_S158_L001_R1_001.fastq.gz	44	SAL46_S65_L001_trim_R1	276 bp	45%	SAL44_S38_L001_R2_001.fastq.gz	44	SAL44_S38_L001_trim_R2	41.50%	273 bp
K48_S159_L001_R1_001.fastq.gz	37	SAL47_S80_L001_trim_R1	276 bp	45%	K48_S159_L001_R2_001.fastq.gz	37	SAL47_S80_L001_trim_R2	43.80%	273 bp
SAL99_S160_L001_R1_001.fastq.gz	14929	SAL48_S94_L001_trim_R1	276 bp	45%	SAL47_S80_L001_R2_001.fastq.gz	14929	SAL46_S65_L001_trim_R2	42.80%	273 bp
SAL120_S161_L001_R1_001.fastq.gz	32542	SAL49_S108_L001_trim_R1	276 bp	45%	SAL120_S161_L001_R2_001.fastq.gz	32542	SAL49_S108_L001_trim_R2	38.60%	275 bp
K3_S162_L001_R1_001.fastq.gz	19590	SAL4_S43_L001_trim_R1	276 bp	45%	SAL48_S94_L001_R2_001.fastq.gz	19590	SAL48_S94_L001_trim_R2	42.70%	273 bp

K16_S163_L001_R1_001.fastq.gz	17357	SAL50_S11_L001_trim_R1	276 bp	55%	K16_S163_L001_R2_001.fastq.gz	17357	SAL5_S57_L001_trim_R2	43.70%	273 bp
K24_S164_L001_R1_001.fastq.gz	23042	SAL51_S25_L001_trim_R1	277 bp	45%	SAL49_S108_L001_R2_001.fastq.gz	23042	SAL51_S25_L001_trim_R2	37.80%	274 bp
K33_S165_L001_R1_001.fastq.gz	71204	SAL52_S39_L001_trim_R1	276 bp	55%	K33_S165_L001_R2_001.fastq.gz	71204	SAL50_S11_L001_trim_R2	42.80%	273 bp
K41_S166_L001_R1_001.fastq.gz	95	SAL53_S52_L001_trim_R1	276 bp	45%	SAL53_S52_L001_R2_001.fastq.gz	95	SAL53_S52_L001_trim_R2	45.00%	273 bp
K49_S167_L001_R1_001.fastq.gz	67	SAL54_S66_L001_trim_R1	276 bp	45%	K49_S167_L001_R2_001.fastq.gz	67	SAL52_S39_L001_trim_R2	43.60%	273 bp
SAL100_S168_L001_R1_001.fastq.gz	29	SAL55_S81_L001_trim_R1	276 bp	55%	SAL54_S66_L001_R2_001.fastq.gz	29	SAL55_S81_L001_trim_R2	43.10%	273 bp
K1_S169_L001_R1_001.fastq.gz	26909	SAL56_S95_L001_trim_R1	276 bp	55%	K1_S169_L001_R2_001.fastq.gz	26909	SAL54_S66_L001_trim_R2	42.20%	273 bp
K2_S170_L001_R1_001.fastq.gz	25836	SAL57_S109_L001_trim_R1	276 bp	55%	SAL58_S14_L001_R2_001.fastq.gz	25836	SAL57_S109_L001_trim_R2	43.10%	273 bp
K17_S171_L001_R1_001.fastq.gz	38582	SAL58_S14_L001_trim_R1	276 bp	45%	K17_S171_L001_R2_001.fastq.gz	38582	SAL56_S95_L001_trim_R2	42.90%	273 bp
K25_S172_L001_R1_001.fastq.gz	21684	SAL59_S40_L001_trim_R1	276 bp	45%	SAL59_S40_L001_R2_001.fastq.gz	21684	SAL59_S40_L001_trim_R2	42.10%	273 bp
K34_S173_L001_R1_001.fastq.gz	41580	SAL5_S57_L001_trim_R1	276 bp	45%	K34_S173_L001_R2_001.fastq.gz	41580	SAL58_S14_L001_trim_R2	43.00%	273 bp

K42_S174_L001_R1_001.fastq.gz	31	SAL60_S28_L001_trim_R1	276 bp	45%	SAL60_S28_L001_R2_001.fastq.gz	31	SAL6_S71_L001_trim_R2	43.30%	273 bp
K50_S175_L001_R1_001.fastq.gz	19	SAL61_S53_L001_trim_R1	276 bp	45%	K50_S175_L001_R2_001.fastq.gz	19	SAL61_S53_L001_trim_R2	42.90%	273 bp
K51_S176_L001_R1_001.fastq.gz	88	SAL62_S67_L001_trim_R1	276 bp	55%	SAL63_S82_L001_R2_001.fastq.gz	88	SAL60_S28_L001_trim_R2	42.90%	273 bp
K75_S177_L001_R1_001.fastq.gz	15461	SAL63_S82_L001_trim_R1	276 bp	45%	K75_S177_L001_R2_001.fastq.gz	15461	SAL63_S82_L001_trim_R2	42.80%	273 bp
K52_S178_L001_R1_001.fastq.gz	180	SAL64_S98_L001_trim_R1	276 bp	64%	SAL64_S98_L001_R2_001.fastq.gz	180	SAL62_S67_L001_trim_R2	43.70%	273 bp
K76_S179_L001_R1_001.fastq.gz	133140	SAL65_S110_L001_trim_R1	276 bp	55%	K76_S179_L001_R2_001.fastq.gz	133140	SAL65_S110_L001_trim_R2	43.40%	273 bp
K53_S180_L001_R1_001.fastq.gz	212	SAL66_S3_L001_trim_R1	276 bp	45%	SAL65_S110_L001_R2_001.fastq.gz	212	SAL64_S98_L001_trim_R2	40.90%	274 bp
K77_S181_L001_R1_001.fastq.gz	45904	SAL67_S17_L001_trim_R1	276 bp	64%	K77_S181_L001_R2_001.fastq.gz	45904	SAL67_S17_L001_trim_R2	43.30%	273 bp
K54_S182_L001_R1_001.fastq.gz	175	SAL68_S31_L001_trim_R1	276 bp	45%	SAL69_S12_L001_R2_001.fastq.gz	175	SAL66_S3_L001_trim_R2	42.90%	273 bp
K55_S183_L001_R1_001.fastq.gz	106	SAL69_S12_L001_trim_R1	276 bp	64%	K55_S183_L001_R2_001.fastq.gz	106	SAL69_S12_L001_trim_R2	42.70%	273 bp
K79_S184_L001_R1_001.fastq.gz	143057	SAL6_S71_L001_trim_R1	276 bp	45%	SAL70_S26_L001_R2_001.fastq.gz	143057	SAL68_S31_L001_trim_R2	41.80%	273 bp

K56_S185_L001_R1_001.fastq.gz	182	SAL70_S26_L001_trim_R1	276 bp	55%	K56_S185_L001_R2_001.fastq.gz	182	SAL7_S85_L001_trim_R2	42.90%	273 bp
K80_S186_L001_R1_001.fastq.gz	217079	SAL71_S41_L001_trim_R1	276 bp	55%	SAL72_S54_L001_R2_001.fastq.gz	217079	SAL71_S41_L001_trim_R2	43.40%	273 bp
K57_S187_L001_R1_001.fastq.gz	28626	SAL72_S54_L001_trim_R1	276 bp	55%	K57_S187_L001_R2_001.fastq.gz	28626	SAL70_S26_L001_trim_R2	43.70%	273 bp
K81_S188_L001_R1_001.fastq.gz	40303	SAL73_S68_L001_trim_R1	276 bp	55%	SAL73_S68_L001_R2_001.fastq.gz	40303	SAL73_S68_L001_trim_R2	42.80%	273 bp
K58_S189_L001_R1_001.fastq.gz	24238	SAL74_S83_L001_trim_R1	276 bp	64%	K58_S189_L001_R2_001.fastq.gz	24238	SAL72_S54_L001_trim_R2	42.30%	273 bp
K82_S190_L001_R1_001.fastq.gz	84	SAL75_S96_L001_trim_R1	276 bp	55%	SAL75_S96_L001_R2_001.fastq.gz	84	SAL75_S96_L001_trim_R2	43.10%	273 bp
K59_S191_L001_R1_001.fastq.gz	17338	SAL76_S111_L001_trim_R1	276 bp	55%	K59_S191_L001_R2_001.fastq.gz	17338	SAL74_S83_L001_trim_R2	42.20%	273 bp
K83_S192_L001_R1_001.fastq.gz	43163	SAL77_S13_L001_trim_R1	276 bp	64%	SAL79_S42_L001_R2_001.fastq.gz	43163	SAL77_S13_L001_trim_R2	42.20%	274 bp
K60_S193_L001_R1_001.fastq.gz	23	SAL78_S27_L001_trim_R1	276 bp	64%	K60_S193_L001_R2_001.fastq.gz	23	SAL76_S111_L001_trim_R2	42.90%	273 bp
K84_S194_L001_R1_001.fastq.gz	46305	SAL79_S42_L001_trim_R1	276 bp	55%	SAL81_S4_L001_R2_001.fastq.gz	46305	SAL79_S42_L001_trim_R2	42.70%	273 bp
K61_S195_L001_R1_001.fastq.gz	15656	SAL7_S85_L001_trim_R1	276 bp	36%	K61_S195_L001_R2_001.fastq.gz	15656	SAL78_S27_L001_trim_R2	42.30%	273 bp

K85_S196_L001_R1_001.fastq.gz	42	SAL80_S55_L001_trim_R1	276 bp	64%	SAL82_S18_L001_R2_001.fastq.gz	42	SAL8_S99_L001_trim_R2	42.80%	273 bp
K62_S197_L001_R1_001.fastq.gz	44823	SAL81_S4_L001_trim_R1	276 bp	45%	K62_S197_L001_R2_001.fastq.gz	44823	SAL81_S4_L001_trim_R2	42.70%	273 bp
K63_S198_L001_R1_001.fastq.gz	40780	SAL82_S18_L001_trim_R1	276 bp	64%	SAL83_S32_L001_R2_001.fastq.gz	40780	SAL80_S55_L001_trim_R2	43.10%	273 bp
K87_S199_L001_R1_001.fastq.gz	44312	SAL83_S32_L001_trim_R1	276 bp	64%	K87_S199_L001_R2_001.fastq.gz	44312	SAL83_S32_L001_trim_R2	43.50%	273 bp
K64_S200_L001_R1_001.fastq.gz	17292	SAL84_S45_L001_trim_R1	276 bp	55%	SAL85_S70_L001_R2_001.fastq.gz	17292	SAL82_S18_L001_trim_R2	43.30%	273 bp
K88_S201_L001_R1_001.fastq.gz	38211	SAL85_S70_L001_trim_R1	276 bp	45%	K88_S201_L001_R2_001.fastq.gz	38211	SAL85_S70_L001_trim_R2	43.00%	273 bp
K65_S202_L001_R1_001.fastq.gz	15062	SAL86_S74_L001_trim_R1	276 bp	55%	SAL86_S74_L001_R2_001.fastq.gz	15062	SAL84_S45_L001_trim_R2	42.00%	273 bp
K89_S203_L001_R1_001.fastq.gz	11806	SAL87_S88_L001_trim_R1	276 bp	55%	K89_S203_L001_R2_001.fastq.gz	11806	SAL87_S88_L001_trim_R2	42.70%	273 bp
K66_S204_L001_R1_001.fastq.gz	30077	SAL88_S102_L001_trim_R1	276 bp	64%	SAL87_S88_L001_R2_001.fastq.gz	30077	SAL86_S74_L001_trim_R2	42.30%	273 bp
K67_S205_L001_R1_001.fastq.gz	11712	SAL89_S69_L001_trim_R1	276 bp	45%	K67_S205_L001_R2_001.fastq.gz	11712	SAL89_S69_L001_trim_R2	43.00%	273 bp
K90_S206_L001_R1_001.fastq.gz	21802	SAL8_S99_L001_trim_R1	276 bp	45%	SAL88_S102_L001_R2_001.fastq.gz	21802	SAL88_S102_L001_trim_R2	44.50%	273 bp

K68_S207_L001_R1_001.fastq.gz	12447	SAL90_S84_L001_trim_R1	276 bp	55%	K68_S207_L001_R2_001.fastq.gz	12447	SAL90_S84_L001_trim_R2	42.90%	273 bp
K91_S208_L001_R1_001.fastq.gz	32341	SAL91_S97_L001_trim_R1	276 bp	36%	SAL90_S84_L001_R2_001.fastq.gz	32341	SAL91_S97_L001_trim_R2	44.70%	273 bp
K69_S209_L001_R1_001.fastq.gz	18865	SAL92_S112_L001_trim_R1	276 bp	55%	K69_S209_L001_R2_001.fastq.gz	18865	SAL92_S112_L001_trim_R2	42.60%	273 bp
K72ii_S210_L001_R1_001.fastq.gz	43753	SAL93_S113_L001_trim_R1	276 bp	45%	SAL92_S112_L001_R2_001.fastq.gz	43753	SAL93_S113_L001_trim_R2	43.00%	273 bp
K70_S211_L001_R1_001.fastq.gz	18879	SAL94_S121_L001_trim_R1	276 bp	55%	K70_S211_L001_R2_001.fastq.gz	18879	SAL94_S121_L001_trim_R2	42.80%	273 bp
K71_S212_L001_R1_001.fastq.gz	86058	SAL95_S129_L001_trim_R1	276 bp	64%	SAL97_S144_L001_R2_001.fastq.gz	86058	SAL95_S129_L001_trim_R2	43.10%	273 bp
K32_S213_L001_R1_001.fastq.gz	24089	SAL96_S137_L001_trim_R1	276 bp	55%	K32_S213_L001_R2_001.fastq.gz	24089	SAL96_S137_L001_trim_R2	43.00%	273 bp
K72_S214_L001_R1_001.fastq.gz	18372	SAL97_S144_L001_trim_R1	276 bp	45%	SAL98_S152_L001_R2_001.fastq.gz	18372	SAL97_S144_L001_trim_R2	43.90%	273 bp
SAL9ii_S215_L001_R1_001.fastq.gz	35177	SAL98_S152_L001_trim_R1	276 bp	55%	SAL9ii_S215_L001_R2_001.fastq.gz	35177	SAL98_S152_L001_trim_R2	43.10%	273 bp
K73_S216_L001_R1_001.fastq.gz	17586	SAL99_S160_L001_trim_R1	276 bp	64%	SAL99_S160_L001_R2_001.fastq.gz	17586	SAL99_S160_L001_trim_R2	42.50%	273 bp
K74_S217_L001_R1_001.fastq.gz	18397	SAL9ii_S215_L001_trim_R1	276 bp	64%	K74_S217_L001_R2_001.fastq.gz	18397	SAL9ii_S215_L001_trim_R2	42.80%	273 bp

TABLE S3 | DISCONTIGUOUS MEGABLAST RESULTS FROM NCBI DATABASE

BLASTn results from the open- access NCBI database of the OTU sequences. Identified species names are given in the 'Blast species' column. Percent identity (Per identity %) and query cover describe how similar the query sequence is to the target sequence in the database and how much of the query sequence is covered by the target sequence

OTU_ID	***Blast species***		***Hit accession***	***E-value***	***query cover, %***	***Per identity, %***	***Note***
otu1	Orchomenella obtusa	Orchomenella obtusa voucher Crust 19785V cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	MG935152	2E-136	100	100	
otu2	Tmetonyx cicada	Tmetonyx cicada voucher BIOUG<CAN>:10BPBS-0099 cytochrome oxidase subunit 1 (COI) gene	HQ919145	2E-105	100	91.97	
otu3	Tmetonyx cicada	Tmetonyx cicada voucher BIOUG<CAN>:10BPBS-0099 cytochrome oxidase subunit 1 (COI) gene	HQ919145	3E-109	100	93.07	
otu4	Scopelocheirus hopei	Scopelocheirus hopei voucher Crust 18871V cytochrome oxidase subunit 1 (COI) gene, partial cds	MG935125	5E-132	100	98.56	
otu5	Anonyx lilljeborgi	Anonyx lilljeborgi voucher NUN-0197 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochon	MG321071	1E-119	99	95.32	
otu6		no sensible hit (too short length cover)					
otu7	Tmetonyx cicada	Tmetonyx cicada voucher BIOUG<CAN>:10BPBS-0099 cytochrome oxidase subunit 1 (COI) gene	HQ919145	1E-95	100	89.13	

otu8	Tmetonyx cicada	Tmetonyx cicada voucher BIOUG<CAN>:10BPBS-0099 cytochrome oxidase subunit 1 (COI) gene	HQ919145	2E-98	100	88.74	
otu9		no sensible hit (too short length cover)					
otu10		no sensible hit (too short length cover)					
otu11		no sig hit					
otu12	Amphipoda sp.	Amphipoda sp. LysC074 cytochrome oxidase subunit 1 (COI) gene, partial cds	MG264799	1E-83	95	86.6	Tmetonix cicada 85.8%
otu13	Homo sapiens	Homo sapiens chromosome 2 clone VMRC59-129A11	AC278679	0	100	98.3	
otu14	Tmetonyx cicada	Tmetonyx cicada voucher BIOUG<CAN>:10BPBS-0099 cytochrome oxidase subunit	HQ919145	2E-106	100	90.78	
otu15	Tmetonyx cicada	Tmetonyx cicada voucher BIOUG<CAN>:10BPBS-0099 cytochrome oxidase subunit	HQ919145	3E-116	100	94.89	
otu16	Tmetonyx cicada	Tmetonyx cicada voucher BIOUG<CAN>:10BPBS-0099 cytochrome oxidase subunit	HQ919145	5E-94	100	88.77	
otu17	Tmetonyx cicada	Tmetonyx cicada voucher BIOUG<CAN>:10BPBS-0099 cytochrome oxidase subunit	HQ919145	1E-113	100	94.53	
otu18	Tmetonyx cicada	Tmetonyx cicada voucher BIOUG<CAN>:10BPBS-0099 cytochrome oxidase subunit	HQ919145	9E-116	100	94.57	

otu19	Tmetonyx cicada	Tmetonyx cicada voucher BIOUG<CAN>:10BPBS-0099 cytochrome oxidase subunit	HQ919145	6E-112	100	92.15	
otu20	Tmetonyx cicada	Tmetonyx cicada voucher BIOUG<CAN>:10BPBS-0099 cytochrome oxidase subunit	HQ919145	3E-109	100	92.75	
otu21	Orchomenella gerulicorbis	Orchomenella gerulicorbis isolate 2 18S ribosomal RNA gene, partial sequence	KP347455.	9E-135	93	100	Same identity to Lysianassoidea sp., Abyssorchonomene sp.
otu22	Tmetonyx cicada	Tmetonyx cicada voucher BIOUG<CAN>:10BPBS-0099 cytochrome oxidase subunit	HQ919145	2E-74	80	89.19	
otu23	Tmetonyx cicada	Tmetonyx cicada voucher BIOUG<CAN>:10BPBS-0099 cytochrome oxidase subunit	HQ919145	2E-105	100	90.44	
otu24	Tmetonyx cicada	Tmetonyx cicada voucher BIOUG<CAN>:10BPBS-0099 cytochrome oxidase subunit	HQ919145	4E-82	100	85.3	

TABLE S4 | LIBRARIES PREPARATION FOR DNA POOLING ACCORDING TO THEIR BAND BRIGHTNESS

Amplicon samples were divided into groups according to the brightness shown on the agarose gel (each brightness indicates the volume needed for the DNA pooling). Nearly invisible - 15µl , Very weak – 12 µl, Weak – 9 µl, Bright - 6 µl, Super bright - 3 µl, SuperD bright - 1 µl

ID	*Morph species*	*Location*	*Description*	*Pooling (µl)*	*Barcode combination*
SAL1	T. cicada	Saltfjorden	brigth	6	D501 - D701
SAL2	T. cicada	Saltfjorden	weak	9	D502 - D701
SAL3	T. cicada	Saltfjorden	weak	9	D503 - D701
SAL4	T. cicada	Saltfjorden	super bright	3	D504 - D701
SAL5	T. cicada	Saltfjorden	bright	6	D505 - D701
SAL6	T. cicada	Saltfjorden	bright	6	D506 - D701
SAL7	T. cicada	Saltfjorden	SB	3	D507 - D701
SAL8	T. cicada	Saltfjorden	SB	3	D508 - D701
SAL31	O.obtusa	Saltfjorden	SB	3	D501 - D702
SAL32	O.obtusa	Saltfjorden	SB	3	D502 - D702
SAL33	O.obtusa	Saltfjorden	SB	3	D503 - D702
SAL34	O.obtusa	Saltfjorden	SB	3	D504- D702
SAL35	O.obtusa	Saltfjorden	SB	3	D505 - D702
SAL36	O.obtusa	Saltfjorden	SB	3	D506 - D702
SAL37	O.obtusa	Saltfjorden	SB	3	D507 - D702
SAL38	O.obtusa	Saltfjorden	SB	3	D508 - D702
SAL66	S.hopei	Saltfjorden	very weak	12	D501 - D703
SAL67	S.hopei	Saltfjorden	bright	6	D502 - D703
SAL68	S.hopei	Saltfjorden	very weak	12	D503 - D703
SAL101	S.hopei	Saltfjorden	nearly invisible	15	D504 - D703
SAL102	S.hopei	Saltfjorden	nearly invisible	15	D505 - D703
SAL103	S.hopei	Saltfjorden	bright	6	D506 - D703
SAL104	S.hopei	Saltfjorden	weak	9	D507 - D703
SAL105	S.hopei	Saltfjorden	weak	9	D508 - D703

SAL81	T. cicada	Saltfjorden	nearly invisible	15	D501 - D707
SAL82	T. cicada	Saltfjorden	bright	6	D502 - D707
SAL83	T. cicada	Saltfjorden	bright	6	D503 - D707
SAL84	T. cicada	Saltfjorden	bright	6	D504 - D707
SAL85	T. cicada	Saltfjorden	weak	9	D505- D707
SAL86	T. cicada	Saltfjorden	bright	6	D506 - D707
SAL87	T. cicada	Saltfjorden	bright	6	D507 - D707
SAL88	T. cicada	Saltfjorden	bright	6	D508 - D707
SAL106	S.hopei	Saltfjorden	nearly invisible	15	D501 - D708
SAL107	S.hopei	Saltfjorden	weak	9	D502 - D708
SAL108	S.hopei	Saltfjorden	weak	9	D503 - D708
SAL109	S.hopei	Saltfjorden	weak	9	D504 - D708
SAL110	S.hopei	Saltfjorden	bright	6	D505 - D708
SAL111	S.hopei	Saltfjorden	bright	6	D506 - D708
SAL112	S.hopei	Saltfjorden	bright	6	D507 - D708
SAL113	S.hopei	Saltfjorden	bright	6	D508 - D708
SAL121	O.obtusa	Saltfjorden	bright	6	D501 - D709
SAL122	O.obtusa	Saltfjorden	bright	6	D502 - D709
SAL123	O.obtusa	Saltfjorden	bright	6	D503 - D709
SAL124	O.obtusa	Saltfjorden	SB	3	D504 - D709
SAL125	O.obtusa	Saltfjorden	weak	9	D505 - D709
SAL126	O.obtusa	Saltfjorden	weak	9	D506 - D709
SAL127	O.obtusa	Saltfjorden	SDB	1	D507 - D709
SAL128	O.obtusa	Saltfjorden	SDB	1	D508 - D709
SAL10	T.cicada	Saltfjorden	SDB	1	D501 - i7_13
SAL11	T.cicada	Saltfjorden	very weak	12	D502 - i7_13
SAL12	T.cicada	Saltfjorden	bright	6	D503 - i7_13
SAL13	T.cicada	Saltfjorden	weak	9	D504 - i7_13
SAL14	T.cicada	Saltfjorden	bright	6	D505 - i7_13
SAL15	T.cicada	Saltfjorden	SDB	1	D506 - i7_13
SAL16	T.cicada	Saltfjorden	bright	6	D507 - i7_13

SAL17	T.cicada	Saltfjorden	very weak	12	D508 - i7_13
SAL18	T.cicada	Saltfjorden	SDB	1	D501 - i7_14
SAL19	T.cicada	Saltfjorden	very weak	12	D502 - i7_14
SAL20	T.cicada	Saltfjorden	bright	6	D503 - i7_14
SAL21	T.cicada	Saltfjorden	SB	3	D504 - i7_14
SAL22	T.cicada	Saltfjorden	SB	3	D505 - i7_14
SAL23	T.cicada	Saltfjorden	SB	3	D506 - i7_14
SAL24	T.cicada	Saltfjorden	SB	3	D507 - i7_14
SAL25	T.cicada	Saltfjorden	SB	3	D508 - i7_14
SAL26	T.cicada	Saltfjorden	bright	6	D501 - i7_15
SAL27	T.cicada	Saltfjorden	bright	6	D502 - i7_15
SAL28	T.cicada	Saltfjorden	bright	6	D503 - i7_15
SAL29	T.cicada	Saltfjorden	bright	6	D504 - i7_15
SAL30	T.cicada	Saltfjorden	bright	6	D505 - i7_15
SAL39	O.obtusa	Saltfjorden	bright	6	D506 - i7_15
SAL40	O.obtusa	Saltfjorden	SDB	1	D507 - i7_15
SAL41	O.obtusa	Saltfjorden	weak	9	D508 - i7_15
SAL42	O.obtusa	Saltfjorden	weak	9	D501 - i7_17
SAL43	O.obtusa	Saltfjorden	SDB	1	D502 - i7_17
SAL44	O.obtusa	Saltfjorden	bright	6	D503 - i7_17
SAL45	O.obtusa	Saltfjorden	SDB	1	D504 - i7_17
SAL46	T.cicada	Saltfjorden	weak	9	D505 - i7_17
SAL47	T.cicada	Saltfjorden	SDB	1	D506 - i7_17
SAL48	T.cicada	Saltfjorden	SB	3	D507 - i7_17
SAL49	T.cicada	Saltfjorden	very weak	12	D508 - i7_17
SAL50	T.cicada	Saltfjorden	SDB	1	D501 - i7_18
SAL51	T.cicada	Saltfjorden	very weak	12	D502 - i7_18
SAL52	T.cicada	Saltfjorden	SB	3	D503 - i7_18
SAL53	T.cicada	Saltfjorden	weak	9	D504 - i7_18
SAL54	T.cicada	Saltfjorden	weak	9	D505 - i7_18
SAL55	T.cicada	Saltfjorden	weak	9	D506 - i7_18

SAL56	T.cicada	Saltfjorden	SB	3	D507 - i7_18
SAL57	T.cicada	Saltfjorden	SB	3	D508 - i7_18
SAL58	T.cicada	Saltfjorden	SB	3	D501- i7_19
SAL59	T.cicada	Saltfjorden	bright	6	D503 - i7_19
SAL60	T.cicada	Saltfjorden	very weak	12	D502- i7_19
SAL61	T.cicada	Saltfjorden	SB	3	D504 - i7_19
SAL62	T.cicada	Saltfjorden	SB	3	D505 - i7_19
SAL63	T.cicada	Saltfjorden	bright	6	D506 - i7_19
SAL64	T.cicada	Saltfjorden	very weak	12	D507- i7_19
SAL65	T.cicada	Saltfjorden	bright	6	D508 - i7_19
SAL69	O.obtusa	Saltfjorden	weak	9	D501 - i7_21
SAL70	O.obtusa	Saltfjorden	bright	6	D502 - i7_21
SAL71	O.obtusa	Saltfjorden	SB	3	D503 - i7_21
SAL72	O.obtusa	Saltfjorden	SB	3	D504 - i7_21
SAL73	O.obtusa	Saltfjorden	bright	6	D505 - i7_21
SAL74	O.obtusa	Saltfjorden	bright	6	D506 - i7_21
SAL75	O.obtusa	Saltfjorden	bright	6	D507 - i7_21
SAL76	O.obtusa	Saltfjorden	bright	6	D508 - i7_21
SAL77	O.obtusa	Saltfjorden	weak	9	D501 - i7_22
SAL78	O.obtusa	Saltfjorden	bright	6	D502 - i7_22
SAL79	O.obtusa	Saltfjorden	bright	6	D503 - i7_22
SAL80	O.obtusa	Saltfjorden	bright	6	D504 - i7_22
SAL89	T.cicada	Saltfjorden	SB	3	D505 - i7_22
SAL90	T.cicada	Saltfjorden	SDB	1	D506 - i7_22
SAL91	T.cicada	Saltfjorden	bright	6	D507 - i7_22
SAL92	T.cicada	Saltfjorden	SB	3	D508 - i7_22
SAL93	T.cicada	Saltfjorden	weak	9	i5_09 - D705
SAL94	T.cicada	Saltfjorden	SDB	1	i5_10 - D705
SAL95	T.cicada	Saltfjorden	bright	6	i5_13 - D705
SAL96	T.cicada	Saltfjorden	bright	6	i5_14 - D705
SAL97	T.cicada	Saltfjorden	SDB	1	i5_15 - D705

SAL98	T.cicada	Saltfjorden	weak	9	i5_16 - D705
SAL99	T.cicada	Saltfjorden	bright	6	i5_17 - D705
SAL100	T.cicada	Saltfjorden	very weak	12	i5_18 - D705
SAL114	S.hopei	Saltfjorden	bright	6	i5_09 - D706
SAL115	S.hopei	Saltfjorden	nearly invisible	15	i5_10 - D706
SAL116	S.hopei	Saltfjorden	weak	9	i5_13 - D706
SAL117	S.hopei	Saltfjorden	bright	6	i5_14 - D706
SAL118	S.hopei	Saltfjorden	nearly invisible	15	i5_15 - D706
SAL119	S.hopei	Saltfjorden	weak	9	i5_16 - D706
SAL120	S.hopei	Saltfjorden	bright	6	i5_17 - D706
K1	T.cicada	Skjerst	SB	3	i5_18 - D706
K9	T.cicada	Skjerst	SB	3	i5_09 - D707
K8	T.cicada	Skjerst	SB	3	i5_10 - D707
K7	T.cicada	Skjerst	SB	3	i5_13 - D707
K6	T.cicada	Skjerst	SB	3	i5_14 - D707
K5	T.cicada	Skjerst	SB	3	i5_15 - D707
K4	T.cicada	Skjerst	SB	3	i5_16 - D707
K3	T.cicada	Skjerst	bright	6	i5_17 - D707
K2	T.cicada	Skjerst	bright	6	i5_18 - D707
K10	T.cicada	Skjerst	SB	3	i5_09 - D708
K11	T.cicada	Skjerst	SB	3	i5_10 - D708
K12	T.cicada	Skjerst	SB	3	i5_13 - D708
K13	T.cicada	Skjerst	weak	9	i5_14 - D708
K14	T.cicada	Skjerst	SDB	1	i5_15 - D708
K15	T.cicada	Skjerst	SDB	1	i5_16 - D708
K16	T.cicada	Skjerst	SDB	1	i5_17 - D708
K17	O.obtusa	Skjerst	SB	3	i5_18 - D708
K18	O.obtusa	Skjerst	bright	6	i5_09 - D709
K19	O.obtusa	Skjerst	bright	6	i5_10 - D709
K20	O.obtusa	Skjerst	SB	3	i5_13 - D709
K21	O.obtusa	Skjerst	SB	3	i5_14 - D709

K22	O.obtusa	Skjerst	SDB	1	i5_15 - D709
K23	O.obtusa	Skjerst	SDB	1	i5_16 - D709
K24	O.obtusa	Skjerst	SDB	1	i5_17 - D709
K25	O.obtusa	Skjerst	SDB	1	i5_18 - D709
K26	O.obtusa	Skjerst	bright	6	i5_09 - D710
K27	O.obtusa	Skjerst	SDB	1	i5_10 - D710
K28	O.obtusa	Skjerst	bright	6	i5_13 - D710
K29	O.obtusa	Skjerst	SB	3	i5_14 - D710
K30	O.obtusa	Skjerst	SB	3	i5_15 - D710
K31	O.obtusa	Skjerst	bright	6	i5_16 - D710
K33	O.obtusa	Skjerst	SB	3	i5_17 - D710
K34	O.obtusa	Skjerst	SB	3	i5_18 - D710
K35	O.obtusa	Skjerst	SDB	1	i5_09 - D711
K36	O.obtusa	Skjerst	nearly invisible	15	i5_10 - D711
K37	O.obtusa	Skjerst	nearly invisible	15	i5_10 - D711
K39	O.obtusa	Skjerst	weak	9	i5_13 - D711
K40	O.obtusa	Skjerst	weak	9	i5_16 - D711
K41	O.obtusa	Skjerst	nearly invisible	15	i5_17 - D711
K42	O.obtusa	Skjerst	very weak	12	i5_18 - D711
K43	O.obtusa	Skjerst	SDB	1	i5_09 - D712
K44	O.obtusa	Skjerst	SB	3	i5_10 - D712
K45	O.obtusa	Skjerst	very weak	12	i5_13 - D712
K46	O.obtusa	Skjerst	bright	6	i5_14 - D712
K47	O.obtusa	Skjerst	bright	6	i5_15 - D712
K48	O.obtusa	Skjerst	bright	6	i5_16 - D712
K49	O.obtusa	Skjerst	weak	9	i5_17 - D712
K50	O.obtusa	Skjerst	SB	3	i5_18 - D712
K51	O.obtusa	Skjerst	SB	3	i5_19 - D701
K52	O.obtusa	Skjerst	SB	3	i5_19 - D703
K53	O.obtusa	Skjerst	SB	3	i5_19 - D705
K54	O.obtusa	Skjerst	SB	3	i5_19 - D707

K55	O.obtusa	Skjerst	bright	6	i5_19 - i7_13
K56	O.obtusa	Skjerst	nearly invisible	15	i5_19 - i7_15
K57	O.obtusa	Skjerst	weak	9	i5_19 - i7_18
K58	O.obtusa	Skjerst	weak	9	i5_19 - i7_21
K59	O.obtusa	Skjerst	weak	9	i5_20 - D701
K60	O.obtusa	Skjerst	nearly invisible	15	i5_20 - D703
K61	O.obtusa	Skjerst	SDB	1	i5_20 - D705
K62	O.obtusa	Skjerst	SB	3	i5_20 - D707
K63	O.obtusa	Skjerst	SB	3	i5_20 - i7_13
K64	O.obtusa	Skjerst	SDB	1	i5_20 - i7_15
K65	O.obtusa	Skjerst	SDB	1	i5_20 - i7_18
K66	O.obtusa	Skjerst	SB	3	i5_20 - i7_21
K67	O.obtusa	Skjerst	SDB	1	i5_21 - D701
K68	O.obtusa	Skjerst	SDB	1	i5_21 - D703
K69	O.obtusa	Skjerst	bright	6	i5_21 - D705
K70	O.obtusa	Skjerst	weak	9	i5_21 - D707
K71	O.obtusa	Skjerst	very weak	12	i5_21 - i7_13
K72	O.obtusa	Skerst200	SDB	1	i5_21 - i7_15
K73	O.obtusa	Skjerst	bright	6	i5_21 - i7_18
K74	O.obtusa	Skjerst	SDB	1	i5_21 - i7_21
K75	O.obtusa	Skjerst	SDB	1	i5_19 - D702
K76	O.obtusa	Skjerst	nearly invisible	15	i5_19 - D704
K77	O.obtusa	Skjerst	SB	3	i5_19 - D706
K79	O.obtusa	Skjerst	very weak	12	i5_19 - i7_14
K80	O.obtusa	Skjerst	SB	3	i5_19 - i7_17
K81	O.obtusa	Skjerst	nearly invisible	15	i5_19 - i7_19
K82	O.obtusa	Skjerst	bright	6	i5_19 - i7_22
K83	O.obtusa	Skjerst	SB	3	i5_20 - D702
K84	O.obtusa	Skjerst	SB	3	i5_20 - D704
K85	O.obtusa	Skjerst	bright	6	i5_20 - D706

K87	O.obtusa	Skjerst	SB	3	i5_20 - i7_14
K88	O.obtusa	Skjerst	bright	6	i5_20 - i7_17
K89	O.obtusa	Skjerst	bright	6	i5_20 - i7_19
K90	O.obtusa	Skjerst	bright	6	i5_21 - D702
K91	O.obtusa	Skjerst	SB	3	i5_21 - D704
K72ii	O.obtusa	Skjerst500	SB	3	i5_21 - D706
K32	T.longipes	Skjerst	bright	6	i5_21 - i7_14
SAL9ii	T.longipes	Saltfjorden	bright	6	i5_21 - i7_17