

“Who did you eat before I ate you?”: a metagenomic analysis of gut contents of the Arctic lamprey (*Lethenteron camtschaticum*) during its feeding phase (Gulf of Ob, Kara Sea)

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Abstract

Shotgun metagenomic sequencing was applied to analyse gut contents of two Arctic lamprey (*Lethenteron camtschaticum*) specimens collected in the Gulf of Ob (Kara Sea, Russia) in August 2018. After stringent bioinformatic filtering to remove human, lamprey and bacterial DNA, we developed a combined ranking index that incorporates prior knowledge of the regional fish fauna to minimise classification artefacts. Fish DNA from the genus *Coregonus* dominated both samples, accounting for the majority of reliably identified sequences after normalisation, establishing whitefishes as the primary hosts in this Arctic estuary. Traces of ninespine stickleback (*Pungitius pungitius*), Arctic char (*Salvelinus alpinus*) and Gadidae were also detected. The presence of exotic taxa was attributed to incomplete reference databases, while stickleback DNA likely reached the lamprey gut via secondary consumption. Diet composition differed markedly from that reported in the Bering Sea (Shink et al., 2019), reflecting regional host availability. Despite the exploratory nature of this study, our findings demonstrate the utility of shotgun metagenomics for investigating lamprey feeding ecology, emphasise the critical need for curated, region-specific reference databases, and show that combining molecular data with regional faunal knowledge enables reliable interpretation of complex metagenomic datasets in data-limited systems.

Introduction

Lampreys (Petromyzontiformes) are an ancient group of jawless vertebrates comprising about 45 species, of which adults of parasitic species attach to fishes, feeding on their blood and soft tissues (Hardisty & Potter, 1971; Renaud, 2011). In the northern Pacific, the most common anadromous lampreys are the Arctic lamprey (*Lethenteron camtschaticum*) and the Pacific lamprey (*Entosphenus tridentatus*) (Orlov et al., 2008; Parin et al., 2014). The Arctic lamprey is also widespread in the seas of the Arctic Ocean, including the Gulf of Ob (Kara Sea), where it spends its marine feeding phase (Atlas of Fishes..., 2020; Atlas of Freshwater Fishes..., 2003). Despite its ecological importance, data on the species composition of its hosts remain fragmentary, largely because direct observation in nature is logistically challenging and traditional visual analysis of gut contents is hampered by rapid tissue digestion and the fluid nature of ingested material (Cochran, 2009).

Based on oral apparatus morphology and dentition, the Arctic lamprey is classified as a flesh-feeding predator, possessing powerful lingual laminae and large velar tentacles that exclude small particles from the pharynx (Potter & Hilliard, 1987; Renaud et al., 2009; Quintella et al., 2021). This positions its trophic role closer to that of a predator than a classical haematophagous parasite. Understanding its feeding ecology is relevant not only for basic biology but also for fisheries management and conservation, as wounding surveys on Pacific salmon have provided indirect evidence of lamprey predation (Golub & Golub, 2019; Shevlyakov & Parensky, 2010, 2011), and the parasite fauna of adult Arctic lamprey confirms its trophic role in marine food webs (Katahira et al., 2014).

Comparative studies of the two dominant North Pacific lamprey species reveal differences in habitat use that reflect species-specific trophic strategies. The Arctic lamprey is most abundant in the northwestern Pacific, inhabiting mainly the upper 100-m pelagic layer and feeding on salmonids, herring and other pelagic fishes. In contrast, the Pacific lamprey occurs both pelagically and near the bottom at depths up to 500 m, attacking a wider range of demersal and pelagic fishes (Orlov et al., 2007, 2008; Orlov & Baitalyuk, 2015). Recent large-scale studies on Pacific lamprey have documented host use across 16 fish species (Weitkamp et al., 2023), but comparable data for Arctic lamprey in the European Arctic have remained absent.

In recent decades, molecular methods have transformed dietary studies. DNA metabarcoding is widely applied (Pompanon et al., 2012) but can introduce primer-dependent biases (Deagle et al., 2019). Shotgun metagenomic sequencing offers an alternative, unbiased approach (Berry et al., 2015). Metabarcoding has been used to characterise the diet of Arctic lamprey in the eastern Bering Sea, revealing dominance of capelin, Pacific herring and Pacific sand lance, with only minor salmonid contributions (Shink et al., 2019). For sea lamprey (*Petromyzon marinus*), known hosts include dozens of teleost and cartilaginous fishes, as well as cetaceans (Silva et al., 2014). For Pacific lamprey in the northwestern Pacific, direct evidence of feeding on Pacific salmon and walleye pollock has recently been obtained (Kirillova et al., 2024). However, no molecular dietary data exist for Arctic lamprey in the European Arctic, leaving a significant geographic gap.

The Gulf of Ob is the largest Arctic estuary, characterised by high biological productivity and a fish community dominated by whitefishes (*Coregonus* spp.), which comprise at least seven species (Atlas of Fishes..., 2020; Atlas of Freshwater Fishes..., 2003). Earlier observations from freshwater lakes in Canada and Alaska documented Arctic lamprey feeding on whitefishes and sticklebacks (Heard, 1966; Nursall & Buchwald, 1972), suggesting similar trophic relationships may exist in the Gulf of Ob. Given the region's distinct fish fauna compared to the Bering Sea, dietary data from this system are essential for understanding regional plasticity in host selection.

The aim of this exploratory study was to apply shotgun metagenomic sequencing to determine the taxonomic composition of fish DNA in the intestines of two Arctic lamprey specimens captured during the feeding period in the Gulf of Ob, and to interpret the results in the context of the species' ecology, regional fish fauna, and potential pathways of DNA entry (including secondary consumption). Despite the limited sample size, this work provides the first molecular insight into the diet of Arctic lamprey in the European Arctic and establishes a methodological framework for future studies.

Material and methods

Sample collection and preservation

Gut contents were obtained from two Arctic lamprey specimens (LC_1 and LC_2) captured by standard research trawl on August 24, 2018, in the Gulf of Ob, Kara Sea (69°06'50.5" N, 76°19'55.3" E, Fig. 1). The

intestinal contents were extracted, preserved in 96% ethanol and stored at – 20°C until processing. Visual inspection revealed no intact hard remains (bones, scales or otoliths); the material comprised a semi-digested reddish-brown paste, consistent with blood and macerated muscle tissue.

DNA extraction and sequencing

Total DNA was extracted from approximately 500 mg of gut content homogenate using the DNeasy PowerSoil Kit (Qiagen, Hilden, Germany) following the manufacturer's protocol for difficult samples; negative extraction controls were processed in parallel. Libraries were prepared using the commercial shotgun sequencing kit for the SURFSeq-5000 platform according to the standard protocol. Approximately 60 Gb of raw paired-end data were generated across both samples.

Bioinformatic processing and quality filtering

Read quality was assessed with FastQC (v0.12.1), and adapter trimming and quality filtering were performed with Fastp (v0.24.1) using a minimum Phred score ≥ 20 , automatic adapter detection and removal, and a minimum post-trimming read length of 130 bp. Post-trimming quality was re-assessed with FastQC and summarised with MultiQC (v1.29).

To remove potential human DNA contamination, reads were mapped to the human reference genome GRCh38 (primary assembly, excluding alternative haplotypes) using bwa-mem2 (v2.2.1); unmapped reads were extracted with samtools (v1.21). Host lamprey DNA was removed by mapping remaining reads to the sea lamprey *Petromyzon marinus* genome (RefSeq assembly GCF_010993605.1). Bacterial sequences were then eliminated using Kraken2 (v2.14) with the PlusPFP database, retaining only reads not classified as Bacteria (taxid 2 and descendants). Final quality was confirmed with FastQC. After all filtering steps, the final datasets retained approximately 22% (LC_1) and 49% (LC_2) of the original paired-end reads, with detailed filtering statistics presented in Table 1 (see Results).

Taxonomic analysis with DIAMOND

Cleaned reads were analysed with DIAMOND (v2.1.11) in blastx mode against a custom protein database of Osteichthyes constructed from NCBI RefSeq. The database included all available protein sequences for priority genera (*Coregonus* and *Lethenteron*) and up to 500,000 sequences for other Osteichthyes taxa to balance completeness and computational efficiency. Search parameters were: e-value $\leq 1e^{-5}$, minimum bitscore ≥ 50 , identity $\geq 60\%$, and minimum alignment length ≥ 30 amino acids. Only the single best hit per read was retained. Protein identifiers were mapped to taxonomic names and results were aggregated at the genus level, as short reads (150 bp) are insufficient for reliable species-level assignment.

Taxon ranking and artifact filtering

To assess the biological significance of detected genera and minimise the influence of classification artefacts, we developed a combined ranking index analogous to approaches used in stable isotope mixing models (Harvey et al., 2008). For each genus i , the product of its relative shares across the two samples was calculated as $P_i = p_{i1} \times p_{i2}$, with minor proportional values and absences adjusted to avoid zero products. This product rewards genera consistently present in both samples while penalising those appearing in only one.

A confidence coefficient k_i was then assigned based on published ichthyological data for the Gulf of Ob (Atlas of Fishes..., 2020): $k = 1$ for genera with confirmed regional presence (*Coregonus*, *Pungitius*, *Salvelinus*, *Oncorhynchus*); $k = 0.5$ for genera absent from the region but belonging to families represented locally (e.g., *Microgadus*, *Melanogrammus* as probable Gadidae); and $k = 0.1$ for all others, considered likely misclassifications. The final ranking index was calculated as $R_i = P_i \times k_i$.

For example, *Etheostoma* (8.23% in LC_1, < 0.01% in LC_2) yielded $R = 0.0041$, effectively excluding it from interpretation, whereas *Coregonus* (11.24% and 34.54%) yielded $R = 388.2$, ranking it as the most significant taxon. After ranking, proportions were normalised to include only taxa with confirmed or probable regional presence; the resulting dietary contributions are presented in the Results section (Table 4).

Diversity indices and statistical analysis

For taxonomic orders, alpha diversity was assessed using the Shannon index

$$H' = - \sum_{i=1}^S p_i \ln p_i,$$

and Pielou's evenness

$$J' = \frac{H'}{\ln S},$$

where p_i is the proportion of reads assigned to order i and S is the total number of orders detected.

Differences in taxon abundances between samples were evaluated using a chi-square test applied to the normalised proportions of taxa with confirmed regional presence. All statistical analyses and visualisations were performed in R (v4.2.0) using the tidyverse package and in Python with seaborn.

Results

Read filtering and data quality

Raw read counts were 109.7 million (LC_1) and 90.2 million (LC_2). Quality trimming with Fastp retained the vast majority of reads in both samples (see Table 1 for detailed percentages). Subsequent mapping to the human reference genome removed comparable fractions across samples, whereas removal of host lamprey DNA revealed substantial inter-sample variability: 54.2% of remaining reads in LC_1 were eliminated compared to only 6.7% in LC_2. Bacterial sequences constituted only a minor fraction in both samples (< 3%). After all filtering steps, the final datasets comprised 24.08 million reads (21.96% of original) for LC_1 and 44.12 million reads (48.94% of original) for LC_2. Complete stepwise filtering statistics are summarised in Table 1 and visualised in Fig. 2.

Table 1
Read filtering statistics for both samples

Sample	Raw reads (M)	After Fastp (M)	After human removal (M)	After lamprey removal (M)	After bacterial removal (M)	Final (%)
LC_1	109.653	104.523	54.082	24.738	24.078	21.96
LC_2	90.154	87.600	47.832	44.637	44.120	48.94

Taxonomic composition at the order level

DIAMOND analysis against the Osteichthyes protein database classified 6.18 million reads (LC_1) and 6.17 million reads (LC_2) as fish, identifying 59 and 47 fish orders, respectively. Shannon diversity ($H' = 2.84$ vs. 1.93) and Pielou's evenness ($J' = 0.48$ vs. 0.35) both indicated that LC_1 had a more evenly distributed taxonomic composition, while LC_2 exhibited stronger dominance by fewer groups.

Diet composition at the genus level: raw data

As shown in Table 2, the raw genus-level assignments revealed a wide range of taxa, but many of them – such as *Etheostoma*, *Pagrus*, *Metynnis*, *Centroberyx* and *Misgurnus* – are not native to the Gulf of Ob and were later treated as bioinformatic artifacts. Among the reliably detected groups, the family Coregonidae (genus *Coregonus*) dominated both samples, with markedly higher representation in LC_2 than in LC_1. Gadidae (represented by *Microgadus* and related genera) also appeared, though primarily in one sample.

Table 2
Top 20 fish taxa identified in the gut of Arctic lamprey *Lethenteron camtschaticum* (% of all classified fish reads)

Order	Family	Genus	LC_1 (%)	LC_2 (%)
Salmoniformes	Salmonidae	<i>Coregonus</i>	11.24	34.54
Perciformes	Percidae	<i>Etheostoma</i>	8.23	< 0.01
Gadiformes	Gadidae	<i>Microgadus</i>	6.92	< 0.01
Spariformes	Sparidae	<i>Pagrus</i>	5.17	5.68
Characiformes	Serrasalminidae	<i>Metynnis</i>	4.17	7.52
Beryciformes	Berycidae	<i>Centroberyx</i>	3.62	15.51
Perciformes	Percidae	<i>Ammocrypta</i>	2.78	–
Atheriniformes	Atherinopsidae	<i>Leuresthes</i>	2.44	3.60
Gasterosteiformes	Gasterosteidae	<i>Pungitius</i>	2.36	2.94
Perciformes	Percidae	<i>Percina</i>	2.34	–
Cypriniformes	Cobitidae	<i>Misgurnus</i>	1.96	5.12
Trachiniformes	Ammodytidae	<i>Ammodytes</i>	1.88	< 0.01
Cypriniformes	Cyprinidae	<i>Danio</i>	1.43	3.40
Gadiformes	Gadidae	<i>Melanogrammus</i>	1.41	0.39
Cypriniformes	Cyprinidae	<i>Hypophthalmichthys</i>	1.35	< 0.01
Perciformes	Lutjanidae	<i>Lutjanus</i>	1.25	–
Cypriniformes	Cyprinidae	<i>Garra</i>	1.22	4.43
Osteoglossiformes	Mormyridae	<i>Paramormyrops</i>	0.98	3.83
Salmoniformes	Salmonidae	<i>Salvelinus</i>	0.89	4.68
Salmoniformes	Salmonidae	<i>Oncorhynchus</i>	0.45	0.02

Note: The sum of percentages in the table does not equal 100, as only the 20 most abundant genera are shown. Dashes (–) indicate absence; <0.01% indicates presence below 0.01%.

Application of the ranking index and identification of reliable dietary components

Application of the ranking index (R_i) effectively penalised genera appearing in only one sample or lacking regional occurrence. The index highlighted *Coregonus*, *Pungitius*, *Salvelinus*, *Oncorhynchus* and representatives of Gadidae as the most significant taxa (Table 3). After normalisation to taxa with

confirmed or probable regional presence, *Coregonus* accounted for 64.2% in LC_1 and 81.8% in LC_2, confirming whitefishes as the primary dietary component. *Pungitius* contributed 13.5% and 7.0%, *Salvelinus* 5.1% and 11.1%, while Gadidae were present only in LC_1 (14.6%); *Oncorhynchus* was minor in both samples (Table 4 or Fig. 3).

Table 3
Application of the ranking index (R_i) to selected genera

Genus	LC_1 (%)	LC_2 (%)	P_i	k_i	R_i	Interpretation
<i>Coregonus</i>	11.24	34.54	388.20	1	388.20	Confirmed prey
<i>Pungitius</i>	2.36	2.94	6.94	1	6.94	Secondary consumption
<i>Salvelinus</i>	0.89	4.68	4.17	1	4.17	Confirmed prey
<i>Oncorhynchus</i>	0.45	0.02	0.009	1	0.009	Confirmed prey (minor)
<i>Microgadus</i>	6.92	< 0.01	0.035	0.5	0.017	Probable Gadidae
<i>Pagrus</i>	5.17	5.68	29.37	0.1	2.94	Artifact
<i>Etheostoma</i>	8.23	< 0.01	0.041	0.1	0.004	Artifact

Table 4
Normalized proportions of taxa with high probability of reflecting actual trophic links

Taxon	LC_1 (%)	LC_2 (%)
<i>Coregonus</i> spp.	64.2	81.8
<i>Pungitius pungitius</i>	13.5	7.0
<i>Salvelinus alpinus</i>	5.1	11.1
<i>Oncorhynchus gorbuscha</i>	2.6	0.1
Gadidae (presumably)	14.6	–

Comparison between samples

The two samples showed marked differences in the relative contributions of the main taxa, as summarised in Table 4. In both specimens, whitefishes (*Coregonus*) were the dominant dietary component, yet their share was considerably higher in LC_2 than in LC_1. LC_1 displayed a more heterogeneous diet, with notable contributions from gadids, sticklebacks and Pacific salmon, whereas these groups were either absent or only marginally represented in LC_2. In contrast, Arctic char (*Salvelinus*) was more prominent in LC_2.

Comparison with other regions

The diet composition observed in the Gulf of Ob differed markedly from that reported for Arctic lamprey in the Bering Sea (Shink et al., 2019). In the Bering Sea, the diet was dominated by capelin, Pacific herring and Pacific sand lance, with only minor contributions from salmonids and sticklebacks. In contrast, the Gulf of Ob samples were overwhelmingly dominated by whitefishes (*Coregonus* spp.), reflecting the distinct fish community structure of the two regions.

Discussion

Methodological considerations

The high proportion of human DNA detected in both samples (see Table 1) is a recognised challenge in shotgun metagenomics of field-collected samples (Deiner et al., 2017; Littlefair et al., 2020). Sources include contamination from researchers, environmental DNA and laboratory reagents. Stringent mapping to the human genome successfully removed the majority of these reads. The substantial inter-sample variability in host lamprey DNA content (54.2% removal in LC_1 versus 6.7% in LC_2) likely reflects variation in sloughed epithelial cells, differential preservation of host versus prey DNA, or differences in feeding history. Importantly, the dietary signal remained consistent across samples, indicating that filtering did not selectively remove prey DNA.

The appearance of exotic taxa in initial DIAMOND results illustrates a major limitation: the incompleteness and taxonomic bias of reference databases, which are skewed toward well-studied and economically important species, while Arctic taxa—particularly *Coregonus*—are underrepresented (Weigand et al., 2019; Marques et al., 2021). To mitigate this, we developed a ranking index that integrates bioinformatic data with regional faunal knowledge. Although effective, this approach is inherently subjective, as *k* values depend on expert knowledge; for less-studied systems, structured elicitation or Bayesian frameworks would be preferable (Kuhnert et al., 2010; Little et al., 2018).

Overall, our results underscore the critical need for curated, region-specific reference databases and demonstrate that combining molecular data with regional faunal knowledge enables reliable interpretation even in data-limited systems.

Coregonus as the primary host in the Gulf of Ob

The dominance of *Coregonus* DNA in both samples (Table 4) establishes whitefishes as the primary dietary component of Arctic lamprey in the Gulf of Ob. This finding is consistent with earlier observations from freshwater lakes in Canada and Alaska (Heard, 1966; Nursall & Buchwald, 1972) and aligns with the species' classification as a flesh-feeding predator (Quintella et al., 2021; Renaud et al., 2009), as whitefishes are large-bodied fish providing substantial nutritional reward per feeding event.

Preference for large hosts is well documented across lamprey species (Farmer & Beamish, 1973; Swink, 1991; Bence et al., 2003) and matches the pattern observed for Pacific lamprey, which targets fish of comparable size (Kirillova et al., 2024) and shows strong host association with abundant large-bodied

species such as Pacific Hake in the Northeast Pacific (Weitkamp et al., 2023). Our results mirror this pattern, supporting the view of lampreys as opportunistic generalists (Clemens et al., 2019; Weitkamp et al., 2023) whose diet reflects local host availability rather than strict prey preferences.

Regional dietary plasticity and comparison with the Bering Sea

The marked difference in diet composition between the Gulf of Ob and the Bering Sea (Fig. 2; see also Introduction and Results) underscores the regional plasticity of Arctic lamprey feeding ecology. In the Bering Sea, the diet is dominated by small pelagic forage fishes, whereas in the Gulf of Ob it is overwhelmingly based on whitefishes. This contrast directly reflects the distinct fish community structures of the two regions: The Gulf of Ob is a large Arctic estuary numerically dominated by *Coregonus* spp. (Atlas of Fishes..., 2020), while the Bering Sea supports a more diverse assemblage of capelin, herring and sand lance (Shink et al., 2019).

Such regional plasticity is consistent with observations for other lamprey species. Sea lamprey (*Petromyzon marinus*) uses a wide range of hosts, varying regionally (Silva et al., 2014). Pacific lamprey similarly shows broad host use across its range, from gadids in the Bering Sea to Pacific Hake off the U.S. West Coast and salmonids in the northwestern Pacific (Orlov et al., 2008; Murauskas et al., 2013; Weitkamp et al., 2023; Kirillova et al., 2024). The ability to switch among available hosts is considered a key behavioural flexibility that allows lampreys to persist under changing ecological conditions and may lead to host switching when preferred species decline (Hume et al., 2013; Adams & Jones, 2021). Our results add to this body of evidence, demonstrating that Arctic lamprey in the European Arctic similarly adapts to the locally most abundant large-bodied fish.

Variability between samples

The two samples exhibited notable differences in dietary composition (Table 4), with LC_1 showing a more diverse and evenly distributed diet compared to the strongly whitefish-dominated LC_2. Such individual variation is consistent with observations for other lamprey species, which can switch between hosts depending on availability and individual feeding history (Silva et al., 2014; Happel et al., 2017). For example, fatty acid profiles of sea lamprey in the Great Lakes indicate a broad range of hosts and considerable inter-individual dietary variation (Happel et al., 2017). In the Gulf of Ob, LC_1 may represent an individual that recently switched among different prey types, whereas LC_2 appears to have fed almost exclusively on whitefish. However, given the limited sample size, robust inference about population-level dietary variation is precluded, and larger datasets are needed to characterise the full spectrum of individual specialisation within the population.

Methodological trade-offs: shotgun metagenomics vs. metabarcoding

The shotgun approach used in this study enabled unbiased detection of fish DNA without primer-dependent biases, but its effectiveness was constrained by reference database incompleteness, as

illustrated by the appearance of exotic taxa. This trade-off mirrors the broader limitation of molecular dietary methods: metabarcoding offers high sensitivity and taxonomic resolution for targeted markers, yet primer choice can systematically bias diversity estimates (Pompanon et al., 2012; Deagle et al., 2019), while shotgun metagenomics avoids such bias but depends heavily on reference completeness (Leray et al., 2021). For future studies of lamprey diet, we suggest a hybrid strategy: initial shotgun sequencing for unbiased discovery of major host groups, followed by targeted metabarcoding for species-level resolution of key taxa. Integration with stable isotope analysis and fatty acid profiling would further validate trophic links (Quintella et al., 2021).

Several limitations of this exploratory study must be acknowledged. The sample size ($n = 2$) from a single location and time point precludes population-level inference; the lack of quantitative host abundance data prevents assessment of prey selection; database biases and the risk of secondary consumption (discussed above) complicate taxonomic assignment; and genus-level resolution limits host species identification. These constraints are inherent to the methodological approach and the study's exploratory design.

To address these limitations, future research should focus on:

1. **Larger-scale sampling:** Collection of ≥ 30 specimens from multiple sites and seasons to characterise dietary variation and host selection patterns.
2. **Multi-method integration:** Combining shotgun metagenomics with DNA metabarcoding for higher taxonomic resolution, stable isotope analysis to confirm trophic position, and fatty acid profiling to distinguish dietary sources (Quintella et al., 2021).
3. **Improved reference databases:** Targeted sequencing of Arctic fish species—especially *Coregonus* spp. and gadids—to populate reference databases and reduce misclassification (Weigand et al., 2019).
4. **Quantitative host availability surveys:** Concurrent assessment of fish community composition to evaluate prey selection via electivity indices.
5. **Long-term monitoring:** Annual sampling to assess how climate-driven changes in fish community composition affect lamprey diet and host availability.

Declarations

Ethical approval

The specimens examined in this study were collected as bycatch during a standard research trawl survey conducted in the Gulf of Ob (Kara Sea) on 24 August 2018. No animals were captured or sacrificed specifically for this research. Sampling of biological material from bycatch is permitted under Russian fisheries legislation for scientific and control purposes. As the material originated from fishing waste and was not obtained through procedures requiring separate ethical oversight, formal approval from an ethics committee was not required. The study was conducted in accordance with institutional

and national guidelines for the use of animals in research, and all applicable international norms were observed.

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Author Contribution

AK and AB, general idea and manuscript preparation; AK, data analyses; AB, field works.

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Figures



Figure 1

Map of the Kara Sea and sample collection site (red dot).

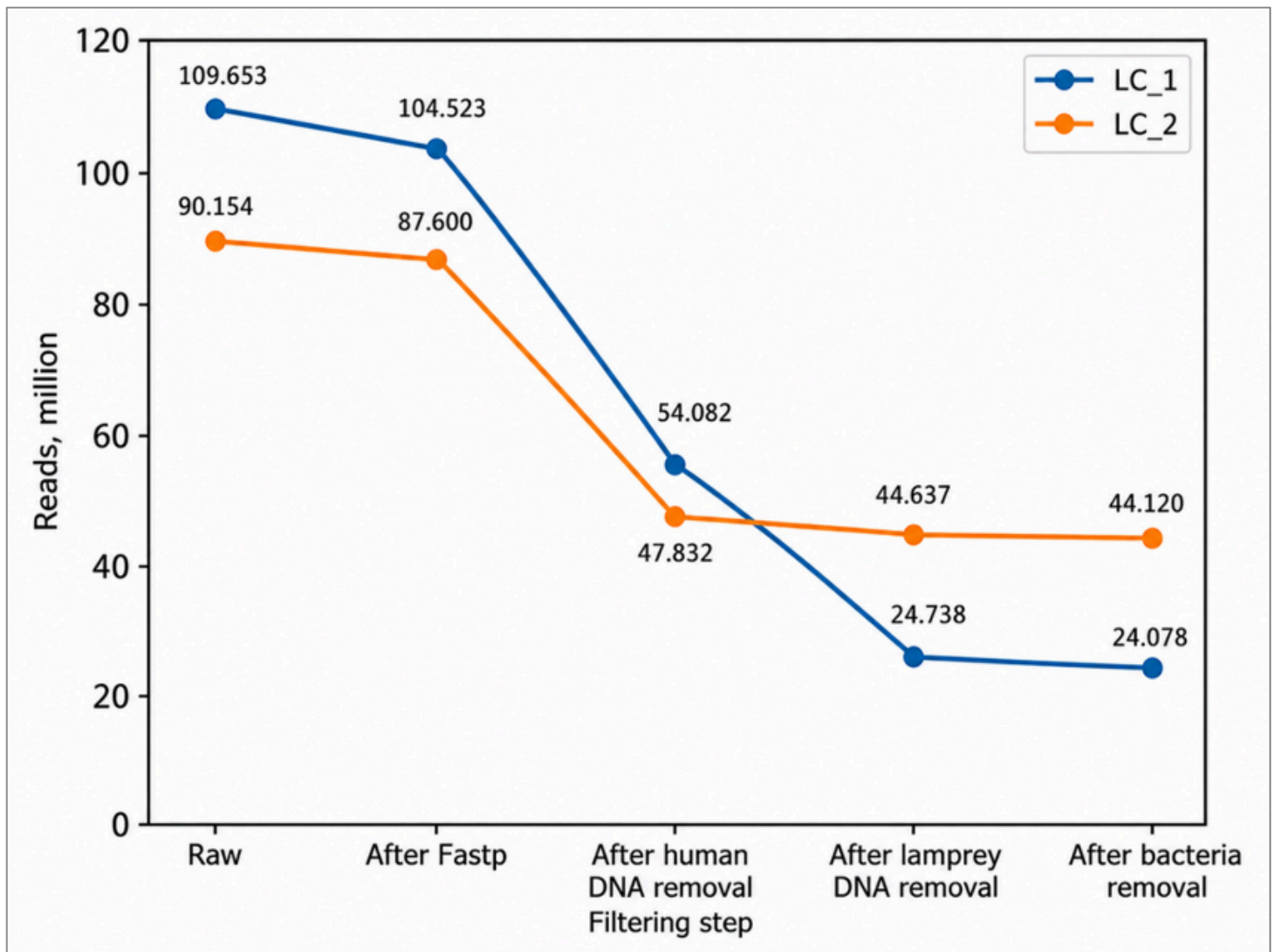


Figure 2

Dynamics of read filtering (millions of paired-end reads). Dots show the number of reads remaining after each filtering step for samples LC_1 and LC_2.

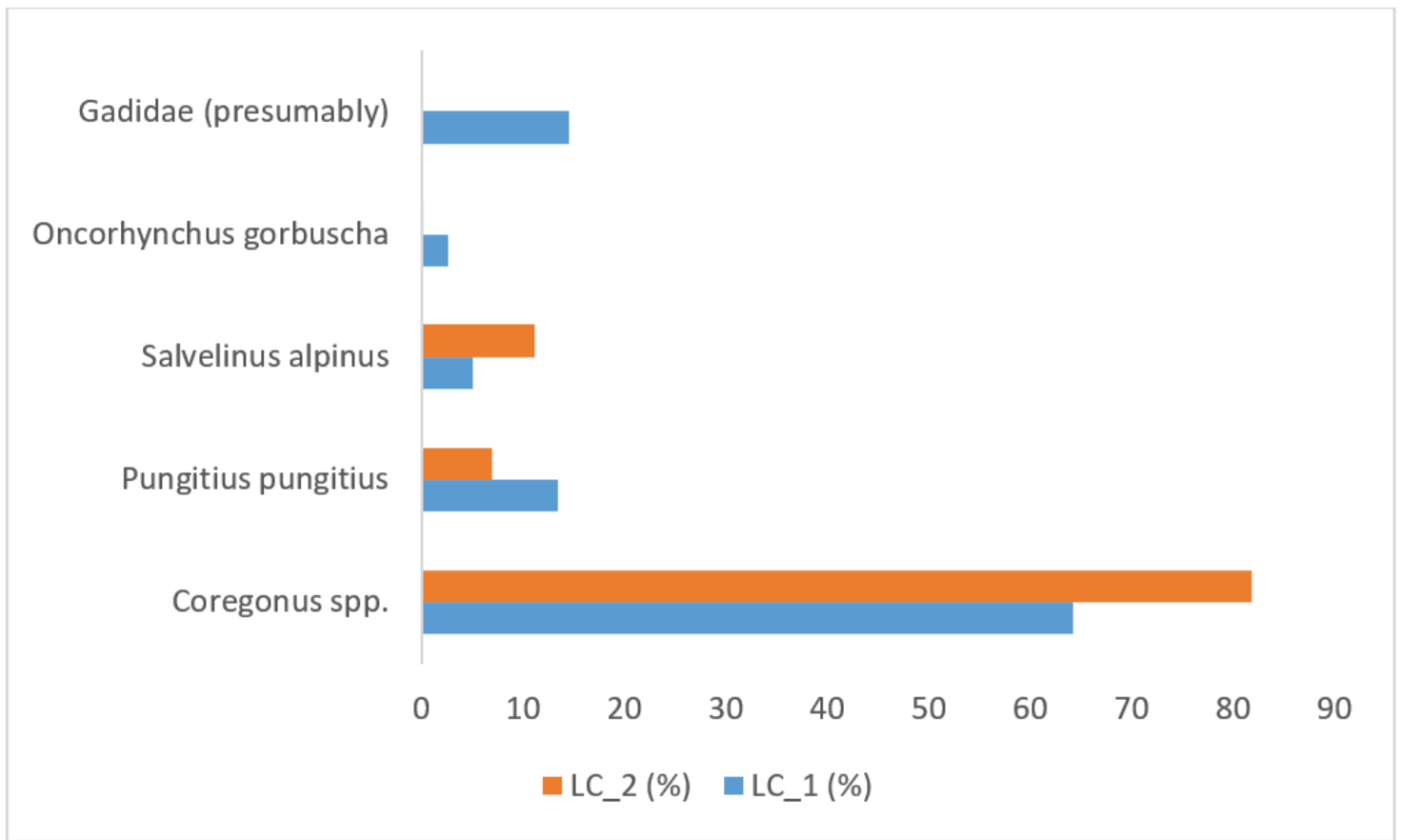


Figure 3

Normalized diet composition (%) of Arctic lamprey (*Lethenteron camtschaticum*) specimens LC_1 and LC_2 from the Gulf of Ob, showing the relative contributions of major fish taxa after bioinformatic filtering.