# Text S1

## Details of the PCR reactions

Each PCR consisted of a total volume of 50 µl, including 25 µl MyFi TM Mix (Bioline, MA, USA), 1 µl of each primer, 21 µl of molecular grade water, and 2 µl of template DNA. Cycling conditions were 95°C for 2 min, followed by 40 cycles of 95°C for 20 s, 52°C for 20 s, and 72°C for 20 s, followed by a final 72°C for 10 min. All PCRs were run on an Eppendorf Mastercycler (Eppendorf, Hamburg, Germany). Five µl of amplicon product was visualized on a 1.5% agarose gel electrophoresis stained with 3 µl Red Safe DNA Loading Dye (iNtRON Biotechnology Inc, Kyungki-Do, Korea) per sample using UV illumination to determine amplification success of targeted genes (~450 bp product for 18s rRNA and ~350 bp for COI). Out of the 47 samples amplified, two did not yield a product for the 18s rRNA (BI-F-04, OI-03) and 5 did not yield a product for COI (BI-F-06, BI-F-04, BI-F-13, FI-07, OOI-02), but all samples were included in further analysis regardless.

Table S1. Pairwise test results of PERMANOVA of untransformed epifauna abundance data using distance group as main factor. Utilizes unrestricted permutation of raw data with 9999 permutations. Significant P(perm)-values (<0.01) in bold font.

| Groups | t | Unique P(perm) | perms |
|---|---|---|---|
| 201-600m, 0-200m | 1.3542 | 0.0956 | 9947 |
| 201-600m, >2000 | 1.9373 | **0.0058** | 9949 |
| 201-600m, 601-2000m | 1.9051 | 0.0131 | 9941 |
| 0-200m, >2000m | 2.1372 | **0.0003** | 9930 |
| 0-200m, 601-2000m | 2.3512 | **0.0003** | 9927 |
| >2000, 601-2000m | 2.9267 | **0.0001** | 9937 |

Table S2. Similarity percentage (SIMPER) results comparing benthic epifauna communities assessed by towed video surveys based on square-root-transformed abundance data. All differences between groups are shown. Overall dissimilarity between the 'Near' (< 200m) and 'Away' (601m - 2000m) was 78%. Av. Abund = average abundance, Av. Diss = average dissimilarity, Diss/SD = ratio of average contribution divided by standard deviation, Contrib. % = percent contribution.

| | **0-200m** | **601-2000m** | | | | |
|---|---|---|---|---|---|---|
| **Species** | **Av.Abund** | **Av.Abund** | **Av.Diss** | **Diss/SD** | **Contrib%** | **Cum.%** |
| Porifera | 0.41 | **0.81** | 17.06 | 1.25 | 21.74 | 21.74 |
| Ascidian | **0.29** | 0.20 | 8.92 | 0.75 | 11.36 | 33.09 |
| *Hormathia digitata* | **0.32** | 0.19 | 8.22 | 0.91 | 10.47 | 43.57 |
| *Ceramaster grannularis* | 0.03 | **0.23** | 6.03 | 0.73 | 7.68 | 60.84 |
| *Asteria rubens* | **0.19** | 0.11 | 5.43 | 0.65 | 6.91 | 67.76 |
| *Phakellia/Axinella sp.* | 0.07 | **0.15** | 3.51 | 0.66 | 4.47 | 72.23 |
| Bryozoa | 0.00 | **0.19** | 3.20 | 0.51 | 4.07 | 76.30 |
| *Henricia* sp. | 0.02 | **0.15** | 3.13 | 0.63 | 3.98 | 80.29 |
| *Hippoglossus hippoglossus* | **0.12** | 0.03 | 2.77 | 0.47 | 3.52 | 83.81 |
| *Mycale sp.* | 0.03 | **0.14** | 2.71 | 0.61 | 3.45 | 87.26 |
| *Pleuronectes platessa* | **0.08** | 0.00 | 1.77 | 0.35 | 2.25 | 89.51 |
| *Geodia* sp. | **0.06** | 0.00 | 1.21 | 0.26 | 1.54 | 91.06 |

Table S3. Pairwise test results of PERMANOVA of untransformed macrofauna count data using distance group as main factor. Utilizes unrestricted permutation of raw data with 9999 permutations. Frakk = Frakkfjord, Older = Olderfjord, Lang = Langfjord.

| **Groups** | **t** | **P(perm)** | **Unique perms** |
|---|---|---|---|
| Frakkfjord, Older | 1.1919 | 0.1165 | 210 |
| Frakkfjord, **Farm** | 1.745 | 0.003 | 1707 |
| Frakkfjord, Near | 1.595 | 0.0002 | 2909 |
| Frakkfjord, Lang-Inner | 1.6271 | 0.0038 | 210 |
| Older, **Farm** | 1.8994 | 0.0091 | 330 |
| Older, Near | 1.3978 | 0.009 | 495 |
| Older, Lang-Inner | 1.8607 | 0.0301 | 35 |
| **Farm**, Near | 1.9127 | 0.0007 | 5034 |
| **Farm**, Lang-Inner | 1.7854 | 0.0051 | 329 |
| Near, Lang-Inner | 1.2376 | 0.1124 | 493 |

Table S4. Similarity percentage (SIMPER) results comparing benthic macrofaunal communities based on square-root-transformed abundance data. Differences between groups are shown to a 60% level. Overall dissimilarity between beside the 'Farmmf' (within 150m) and 'Away' (>600m) was 81%. Av. Abund = average abundance, Av. Diss = average dissimilarity, Diss/SD = ratio of average contribution divided by standard deviation, Contrib. % = percent contribution.

| | **Away** | **Farm** | | | |
|---|---|---|---|---|---|
| **Species** | **Av.Abund** | **Av.Abund** | **Av.Diss** | **Diss/SD** | **Contrib%** |
| *Capitella capitata* | 0.08 | **17.36** | 8.46 | 0.82 | **10.42** |
| *Ophryotrocha lobifera* | 0.00 | **7.36** | 4.63 | 0.82 | **5.71** |
| *Galathowenia oculata* | **6.67** | 0.53 | 3.17 | 1.25 | **3.90** |
| Calanoida | **6.87** | 6.85 | 1.97 | 1.21 | **2.43** |
| *Chaetozone sp.* | **3.17** | 2.49 | 1.72 | 1.48 | **2.12** |
| *Spio limicola* | **3.64** | 0.84 | 1.56 | 1.23 | **1.92** |
| *Prionospio cirrifera* | **2.72** | 0.00 | 1.28 | 1.80 | **1.57** |
| *Owenia polaris* | **2.75** | 0.14 | 1.26 | 1.19 | **1.56** |
| *Paramphinome jeffreysii* | **3.05** | 1.95 | 1.26 | 1.07 | **1.55** |
| *Scoloplos armiger* | **2.40** | 1.92 | 1.09 | 1.29 | **1.34** |
| *Heteromastus filiformis* | **2.23** | 1.74 | 1.05 | 1.25 | **1.29** |
| *Chaetozone setosa kompl.* | 0.79 | **1.94** | 1.03 | 0.72 | **1.27** |
| *Crenella decussata* | **1.98** | 0.38 | 0.92 | 1.12 | **1.13** |
| *Maldane sarsi* | **1.61** | 0.52 | 0.88 | 0.93 | **1.08** |
| *Pseudopolydora nordica* | **1.69** | 0.49 | 0.83 | 0.69 | **1.02** |
| *Ophiura sp. juv.* | **1.70** | 0.46 | 0.80 | 0.98 | 0.99 |
| *Pholoe assimilis* | 1.35 | **1.91** | 0.77 | 1.27 | 0.95 |
| *Cossura pygodactylata* | 1.07 | **1.56** | 0.77 | 1.16 | 0.94 |
| *Phascolion strombus* | **1.64** | 1.00 | 0.74 | 1.29 | 0.91 |
| *Nothria conchylega* | **1.54** | 0.25 | 0.72 | 1.03 | 0.89 |
| *Yoldiella lenticula* | **1.22** | 0.00 | 0.72 | 0.51 | 0.88 |
| *Ophryotrocha maculata* | 0.00 | **1.55** | 0.70 | 0.48 | 0.86 |
| Golfingiidae | **1.34** | 0.29 | 0.66 | 0.92 | 0.81 |
| Eteone flava/longa | 1.19 | **1.22** | 0.64 | 1.28 | 0.79 |
| *Chaetoderma nitidulum* | **1.48** | 0.55 | 0.64 | 1.35 | 0.79 |
| *Musculus sp. juv.* | **1.34** | 0.20 | 0.63 | 1.09 | 0.78 |
| Nemertea | **1.57** | 0.87 | 0.62 | 1.21 | 0.77 |
| *Scoletoma sp.* | **0.96** | 0.35 | 0.62 | 0.62 | 0.76 |
| *Nephtys ciliata* | **1.20** | 0.55 | 0.62 | 1.17 | 0.76 |
| *Diplocirrus glaucus* | **1.21** | 0.49 | 0.61 | 1.01 | 0.75 |
| Maldanidae | **1.27** | 0.14 | 0.60 | 0.98 | 0.74 |
| *Labidoplax buskii* | **1.30** | 0.35 | 0.59 | 1.23 | 0.73 |
| *Yoldiella solidula* | **1.11** | 0.14 | 0.57 | 0.70 | 0.70 |
| *Thyasira sarsii* | 0.08 | **1.22** | 0.57 | 0.65 | 0.70 |
| *Ennucula tenuis* | **1.41** | 1.09 | 0.53 | 1.19 | 0.65 |
| *Malacoceros vulgaris* | 0.00 | **0.90** | 0.51 | 0.70 | 0.63 |
| *Dipolydora cf. coeca* | **1.19** | 0.00 | 0.51 | 0.85 | 0.63 |

| | | | | | |
|---|---|---|---|---|---|
| *Philine denticulata* | 0.08 | **1.12** | 0.48 | 0.79 | 0.60 |
| *Praxillella praetermissa* | 0.68 | **0.70** | 0.48 | 0.83 | 0.59 |
| *Macoma calcarea* | 0.00 | **1.07** | 0.46 | 0.61 | 0.57 |
| *Laphania boecki* | 0.43 | **0.69** | 0.42 | 0.58 | 0.52 |
| *Goniada maculata* | **0.84** | 0.43 | 0.42 | 0.92 | 0.52 |
| *Photis tenuicornis* | **0.78** | 0.00 | 0.41 | 0.73 | 0.50 |
| *Paradoneis andreae* | **0.88** | 0.00 | 0.40 | 0.56 | 0.49 |
| Sabellidae | **0.88** | 0.00 | 0.38 | 0.83 | 0.46 |
| *Echinocardium flavescens* | **0.83** | 0.00 | 0.38 | 1.32 | 0.46 |
| *Pholoe baltica* | **0.76** | 0.14 | 0.37 | 0.84 | 0.46 |

Table S5. PERMANOVA table of results for dietary composition of all 47 cod based on combined 18S and CO1 analysis of homogenized stomach content. ASV read abundance were compositionally transformed and merged at the species level and then fourth root transformed to place greater emphasis on taxa with lower read abundance scores

| Source | df | SS | MS | Pseudo-F | P(perm) | Unique perms | P(MC) |
|---|---|---|---|---|---|---|---|
| Fjord | 2 | 2630 | 1315 | 0.93199 | 0.526 | 9919 | 0.5022 |
| SizeGrp | 2 | 3394.1 | 1697.1 | 1.2028 | 0.2557 | 9917 | 0.2717 |
| FjordxSizeGrp** | 2 | 3617.7 | 1808.9 | 1.282 | 0.2084 | 9913 | 0.2353 |
| Res | 18 | 25397 | 1411 | | | | |
| Total | 24 | 37335 | | | | | |

Table S6. PERMANOVA table of results for dietary composition of the 28 Langfjord cod based on combined 18S and CO1 analysis of homogenized stomach content. ASV read abundance were compositionally transformed and merged at the species level and then fourth root transformed to place greater emphasis on taxa with lower read abundance scores

| Source | df | SS | MS | Pseudo-F | P(perm) | perms | P(MC) |
|---|---|---|---|---|---|---|---|
| Dist2FarmGrp | 2 | 5940.1 | 2970 | 1.7304 | 0.026 | 9898 | 0.0449 |
| SizeGrp | 2 | 2740.3 | 1370.1 | 0.7983 | 0.7236 | 9896 | 0.6879 |
| CodStock | 2 | 5549.8 | 2774.9 | 1.6168 | 0.0404 | 9899 | 0.067 |
| Res | 21 | 36043 | 1716.3 | | | | |
| Total | 27 | 51151 | | | | | |

Table S7. PERMANOVA pairwise test results for fixed term ‘Dist2FarmGrp’ in analysis provided in Table S.2. Fish caught in outer fjord significantly different to both inner and those caught next to the farm.

| Groups | t | P(perm) | Unique perms | P(MC) |
|---|---|---|---|---|
| 0-150m, >8000m | 1.4417 | 0.0274 | 9919 | **0.0472** |
| 0-150m, 601-2000m | 0.78325 | 0.7766 | 9938 | 0.7287 |
| >8000m, 601-2000m | 1.9694 | **0.0008** | 9936 | **0.0053** |

Table S8. PERMANOVA pairwise test results for fixed term ‘CodStock’ in analysis provided in Table S.2. Mildly significant result due to differences between Coastal cod and cod of mixed genetic origin.

| Groups | t | P(perm) | Unique perms | P(MC) |
|---|---|---|---|---|
| NEA, Coastal | 1.0193 | 0.4026 | 9915 | 0.3841 |
| NEA, Mixed | 1.2714 | 0.1641 | 9413 | 0.1841 |
| Coastal, Mix | 1.498 | 0.0106 | 9941 | **0.0411** |

Table S9. Similarity percentage (SIMPER) results comparing taxa identified in cod stomachs from fish caught beside the Farm and >8000m away in Langfjord area based on square-root-transformed combined 18S and CO1 read abundance data. Overall dissimilarity between the 'Near' and 'Away' was 76.8%. Av. Abund = average abundance, Av. Diss = average dissimilarity, Diss/SD = ratio of average contribution divided by standard deviation, Contrib. % = percent contribution. 'X' denotes higher order taxonomic resolution.

| | | **Farm** | **Outer** | | | |
|---|---|---|---|---|---|---|
| **Taxa** | **Common name** | **Av.Abund** | **Av.Abund** | **Av.Diss** | **Diss/SD** | **Contrib%** |
| Ophiopholis aculeata | Brittle star | 0.00 | **0.51** | 5.01 | 1.10 | 6.53 |
| Merluccius merluccius | European Hake | **0.47** | 0.53 | 4.80 | 1.20 | 6.25 |
| Merlangius merlangus | Whiting | 0.23 | **0.43** | 4.49 | 1.09 | 5.85 |
| Haplotaxida_XXX | Oligochaete worm | 0.44 | **0.69** | 3.92 | 1.14 | 5.10 |
| Pandalus montagui | Shrimp | 0.00 | **0.35** | 3.57 | 0.81 | 4.64 |
| Metazoa_XXXXXX | Metazoan | 0.20 | **0.22** | 2.25 | 1.17 | 2.93 |
| Cryptosporidium_X | Crypto | 0.08 | **0.17** | 2.21 | 0.61 | 2.87 |
| Siphonophorae_XXX | Salp | 0.15 | **0.22** | 2.15 | 1.31 | 2.80 |
| Actinopteri_XXXX | Fish group | 0.20 | **0.34** | 2.14 | 1.25 | 2.78 |
| *Trisopterus esmarkii* | Norway pout | 0.00 | **0.23** | 2.05 | 0.78 | 2.67 |
| *Melanogrammus aeglefinus* | Haddock | **0.21** | 0.00 | 1.93 | 0.54 | 2.51 |
| Eukaryota_XXXXXXX | Eukaryote | **0.17** | 0.05 | 1.84 | 0.63 | 2.39 |
| Streptophyta_XXXXX | Plants | **0.13** | 0.02 | 1.65 | 0.44 | 2.15 |
| Chromadorea_XXXX | Roundworm | 0.06 | **0.12** | 1.48 | 0.73 | 1.92 |
| *Laonice cirrata* | Large spionid polychaete | **0.15** | 0.00 | 1.48 | 0.42 | 1.92 |
| *Strongylocentrotus droebachiensis* | Green urchin | 0.00 | **0.15** | 1.41 | 0.74 | 1.83 |
| Apicomplexa_XXXXX | Parasitic alveolates (fungus) | **0.09** | 0.07 | 1.26 | 0.64 | 1.65 |
| Echinoidea_XXXX | Urchin | 0.00 | **0.13** | 1.19 | 0.57 | 1.55 |
| Flabelligeridae_XX | Cage worm | 0.03 | **0.08** | 1.11 | 0.57 | 1.44 |
| *Hyas coarctatus* | Toad crab | 0.00 | **0.13** | 1.10 | 0.64 | 1.44 |
| *Echinocyamus pusillus* | Pea / green urchin | 0.00 | **0.10** | 0.95 | 0.52 | 1.24 |
| *Clupea harengus* | Herring | **0.07** | 0.00 | 0.85 | 0.28 | 1.10 |
| *Salmo salar* | Salmon | **0.10** | 0.00 | 0.79 | 0.38 | 1.02 |
| *Strongylocentrotus pallidus* | Green urchin | 0.00 | 0.08 | 0.79 | 0.35 | 1.02 |
| *Ciona intestinalis* | Ciona | **0.10** | 0.00 | 0.75 | 0.38 | 0.98 |
| *Ophiothrix oerstedii* | Brittle star | 0.00 | **0.08** | 0.73 | 0.62 | 0.96 |
| Stenocypria_X | Ostracod | 0.00 | **0.07** | 0.73 | 0.35 | 0.94 |
| *Perlophiura profundissima* | Brittle star | 0.00 | **0.07** | 0.68 | 0.60 | 0.88 |
| *Myxidium gadi* | Myxosporean | **0.06** | 0.00 | 0.65 | 0.28 | 0.85 |
| *Halecium labrosum* | Herring-bone hydroid | **0.05** | 0.03 | 0.64 | 0.44 | 0.83 |
| Platyhelminthes_XXXXX | Flatworm | **0.06** | 0.00 | 0.61 | 0.45 | 0.79 |
| *Acartia clausii* | Storage mite | 0.00 | **0.08** | 0.59 | 0.35 | 0.76 |
| Semaeostomeae_XXX | Jellyfish | 0.03 | **0.05** | 0.58 | 0.60 | 0.75 |
| Ophiuroidea_XXXX | Brittle star | 0.00 | **0.06** | 0.56 | 0.79 | 0.73 |
| *Capitella_X* | Capitella | **0.08** | 0.00 | 0.54 | 0.29 | 0.70 |
| Gymnodinioides_X | Ciliate | 0.00 | **0.04** | 0.52 | 0.34 | 0.68 |

| | | | | | | |
|---|---|---|---|---|---|---|
| *Nanomia cara* | Salp | 0.02 | **0.04** | 0.51 | 0.56 | 0.67 |
| *Obelia dichotoma* | Hydroid | 0.03 | 0.03 | 0.48 | 0.49 | 0.63 |
| Golfingiida_XXX | Peanut worm | 0.00 | **0.04** | 0.47 | 0.34 | 0.62 |
| *Mallotus villosus* | Capelin | **0.05** | 0.00 | 0.47 | 0.38 | 0.61 |
| *Undinula vulgaris* | Calanoid copepod | 0.00 | **0.04** | 0.47 | 0.34 | 0.61 |
| *Sylon hippolytes* | Parasite in shrimp (Pandalina) | 0.00 | **0.06** | 0.47 | 0.52 | 0.61 |
| Betula_X | Birch tree | 0.00 | **0.06** | 0.45 | 0.35 | 0.59 |
| *Gaidropsarus vulgaris* | 3-bearded rockling | 0.00 | **0.05** | 0.43 | 0.50 | 0.56 |
| *Mytilus trossulus* | Blue mussel | **0.06** | 0.00 | 0.42 | 0.29 | 0.55 |
| Calanus_X | Copepod | **0.04** | 0.01 | 0.40 | 0.36 | 0.52 |
| Hysterothylacium_X | Roundworm | 0.00 | **0.04** | 0.40 | 0.56 | 0.52 |
| *Ramphogordius lacteus* | Nemertean worm | 0.00 | **0.04** | 0.40 | 0.34 | 0.51 |
| Thyasiridae_XX | Small bivalve | **0.04** | 0.00 | 0.40 | 0.28 | 0.51 |
| Spumellaria_XXX | Radiolarian | **0.03** | 0.00 | 0.39 | 0.28 | 0.51 |
| Malacostraca_XXXX | Crustacia | 0.03 | 0.03 | 0.39 | 0.64 | 0.51 |
| *Eunice*_X | Errant polychaete | 0.00 | **0.04** | 0.38 | 0.34 | 0.50 |
| Mammalia_XXXX | NA | **0.03** | 0.00 | 0.37 | 0.28 | 0.48 |
| *Obelia*_X | Hydroid | **0.05** | 0.00 | 0.36 | 0.29 | 0.47 |
| *Nothria* conchylega CMC02 | Errant polychaete | 0.00 | **0.03** | 0.36 | 0.34 | 0.46 |
| Ptilota gunneri | Red algae | 0.00 | **0.04** | 0.35 | 0.35 | 0.46 |
| Cladosporium_X | Eukaryote | **0.03** | 0.00 | 0.32 | 0.28 | 0.42 |
| *Gonepteryx cleopatra* | Butterfly | **0.04** | 0.00 | 0.32 | 0.29 | 0.42 |
| Trebouxiophyceae_XXXX | Grean algae | 0.01 | 0.02 | 0.30 | 0.44 | 0.39 |
| Insecta_XXXX | Insect | **0.04** | 0.00 | 0.29 | 0.29 | 0.38 |
| *Malacoceros fuliginosus* | Errant polychaete | **0.04** | 0.00 | 0.28 | 0.29 | 0.36 |
| *Selenidium serpulae* | Single-celled parasite | **0.04** | 0.00 | 0.28 | 0.29 | 0.36 |
| Fagales_XXX | Plant - peas | 0.00 | **0.02** | 0.27 | 0.34 | 0.35 |
| Poecilostomatoida_XXX | Copepod | 0.00 | **0.03** | 0.27 | 0.34 | 0.35 |
| *Hyperia galba* | Amphipod | 0.00 | 0.02 | 0.27 | 0.34 | 0.35 |
| Syndiniales_XXX | Dynoflagelate | **0.04** | 0.00 | 0.26 | 0.29 | 0.34 |

Table S10. Dietary assignments of cod (absolute numbers and percentages) for the three fjords based on liver FATM's.

| Liver | | | Number of fish | | |
|---|---|---|---|---|---|
| | | Number of fish | Pellet diet | Pelagic diet | Benthic diet |
| Langfjord | Beside farm | 11 | 7 | 2 | 2 |
| Langfjord | Inside | 6 | | 6 | |
| Langfjord | Outside | 9 | | 8 | 1 |
| Frakkfjord | | 11 | | 10 | 1 |
| Olderfjord | | 6 | | 6 | |
| | | 43 | | | |
| | | | % of diet (estimated from FA profile) | | |
| | | Number of fish | Pellet diet | Pelagic diet | Benthic diet |
| Langfjord | Beside farm | 11 | 64 | 18 | 18 |
| Langfjord | Inside | 6 | | 100 | |
| Langfjord | Outside | 9 | | 89 | 11 |
| Frakkfjord | | 11 | | 91 | 9 |
| Olderfjord | | 6 | | 100 | |

Table S11. Dietary assignments of cod (absolute numbers and percentages) for the three fjords based on stomach FATM's.

| Stomach | | | Number of fish | | |
|---|---|---|---|---|---|
| | | Number of fish | Pellet diet | Pelagic diet | Benthic diet |
| Langfjord | Beside farm | 12 | 5 | 1 | 4 |
| Langfjord | Inside | 6 | | 5 | 1 |
| Langfjord | Outside | 9 | | 0 | 9 |
| Frakkfjord | | 13 | | 1 | 12 |
| Olderfjord | | 6 | | 3 | 3 |
| | | 46 | | | |
| | | | % of diet (estimated from FA profile) | | |
| | | Number of fish | Pellet diet | Pelagic diet | Benthic diet |
| Langfjord | Beside farm | 12 | 42 | 8 | 33 |
| Langfjord | Inside | 6 | | 83 | 17 |
| Langfjord | Outside | 9 | | | 100 |
| Frakkfjord | | 13 | | 8 | 92 |
| Olderfjord | | 6 | | 50 | 50 |

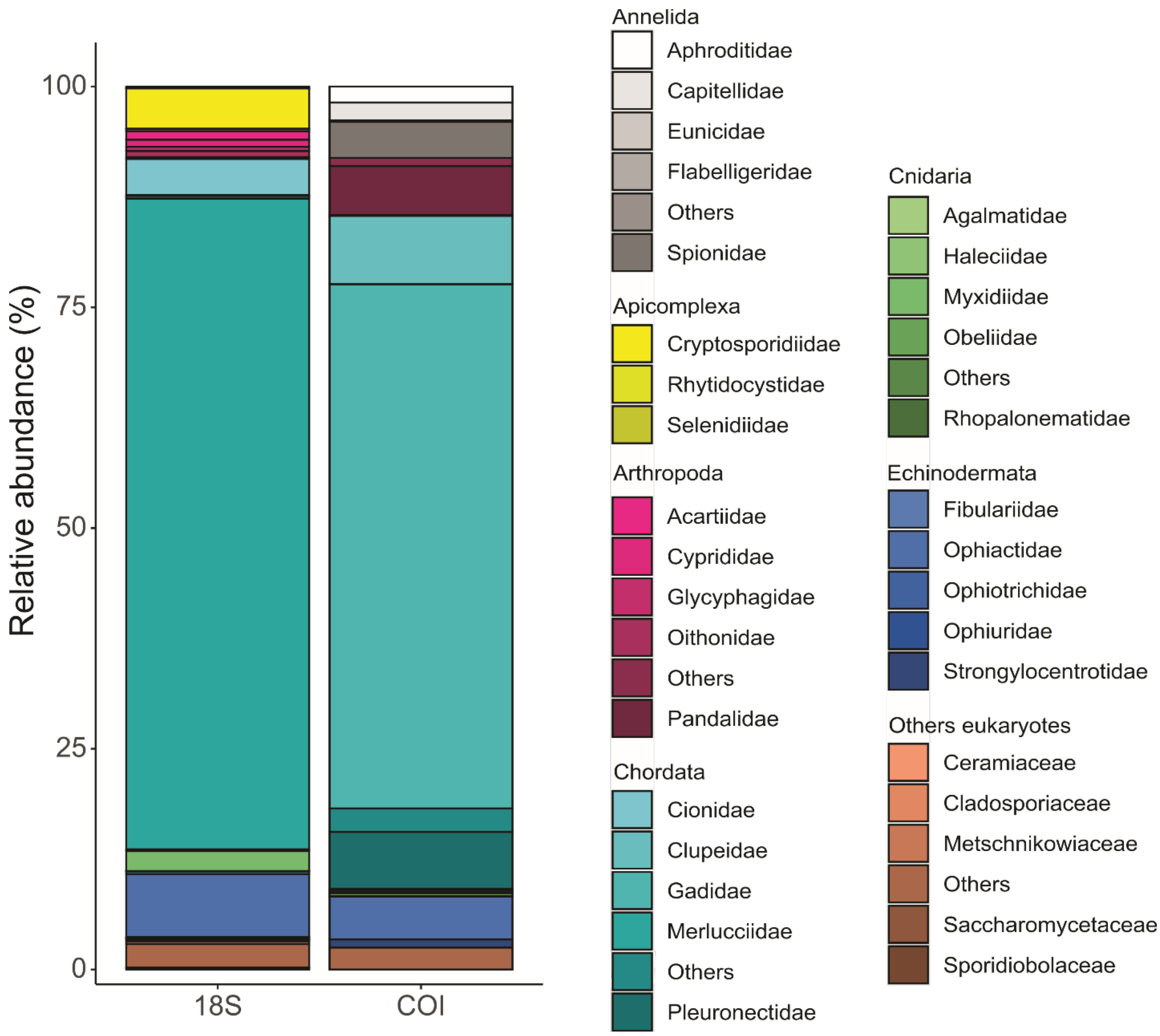


Figure S1. Barplot showing the main taxonomic groupings found in the cod stomach samples for 18S and CO1 environmental DNA.

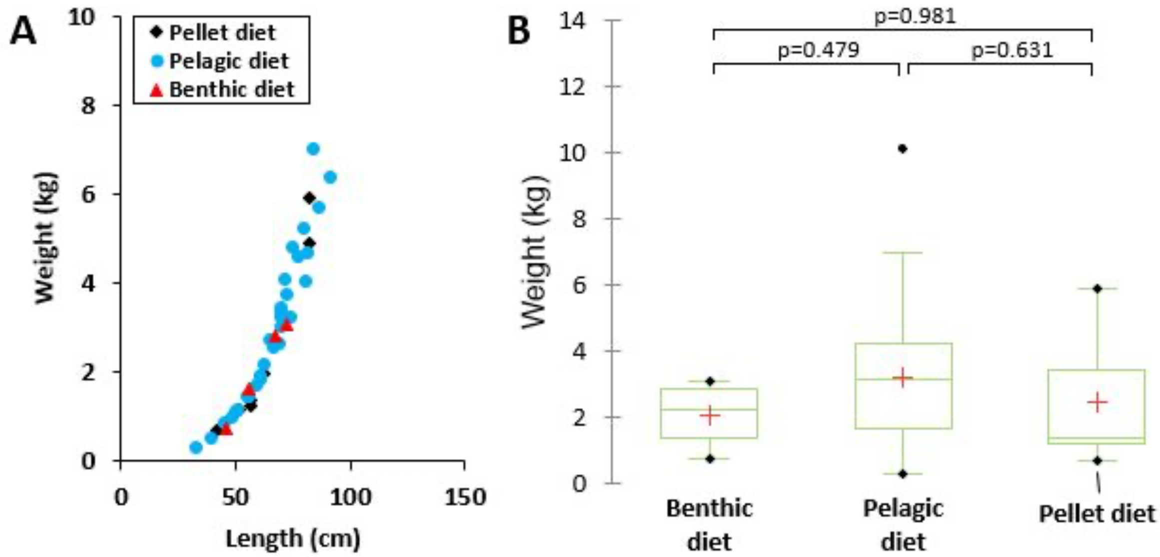


Figure S2. A. Bivariate plots of Length (cm) and weight (kg) of Atlantic cod caught at three Finnmark fjords in 2019 (all fjords are pooled together). B. Kruskal-Wallis analysis of the weight of the diet groups. Samples are classified as salmon pellet diet, pelagic diet and benthic diet according to Table 2.

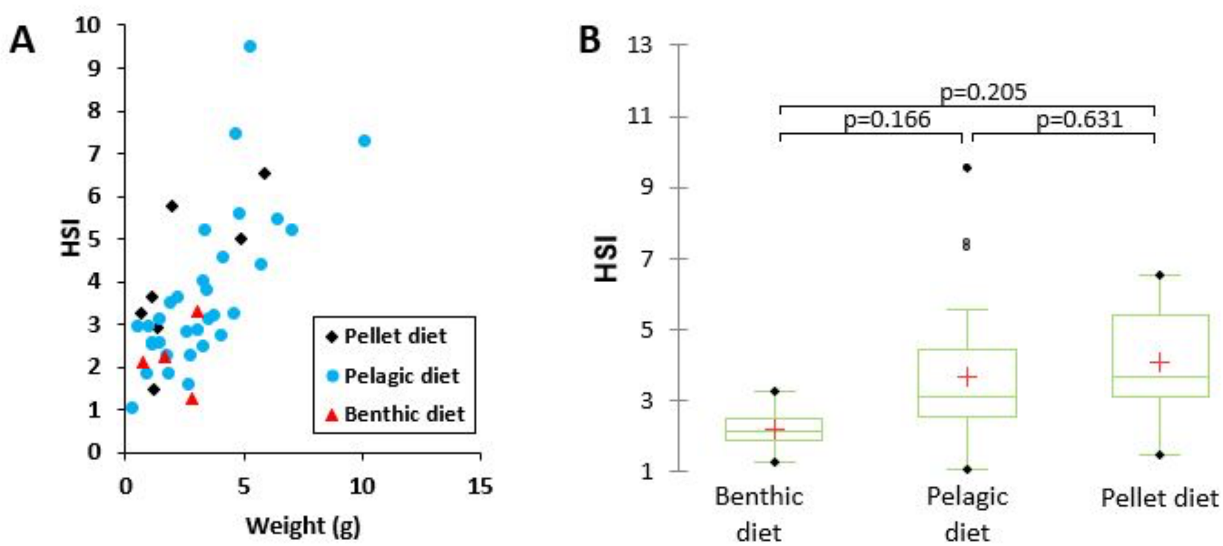


Figure S3. A. Bivariate plots of weight against hepatosomatic index for Atlantic cod caught at three Finnmark fjords in 2019 (all fjords are pooled together). Linear regression analysis of all samples (Y=0.6293X + 1,7597, R2=0.498, P<0.0001). B. Kruskal-Wallis analysis of the HSI of the diet groups Samples are visualised as salmon pellet diet, pelagic diet and benthic diet according to Table 2.

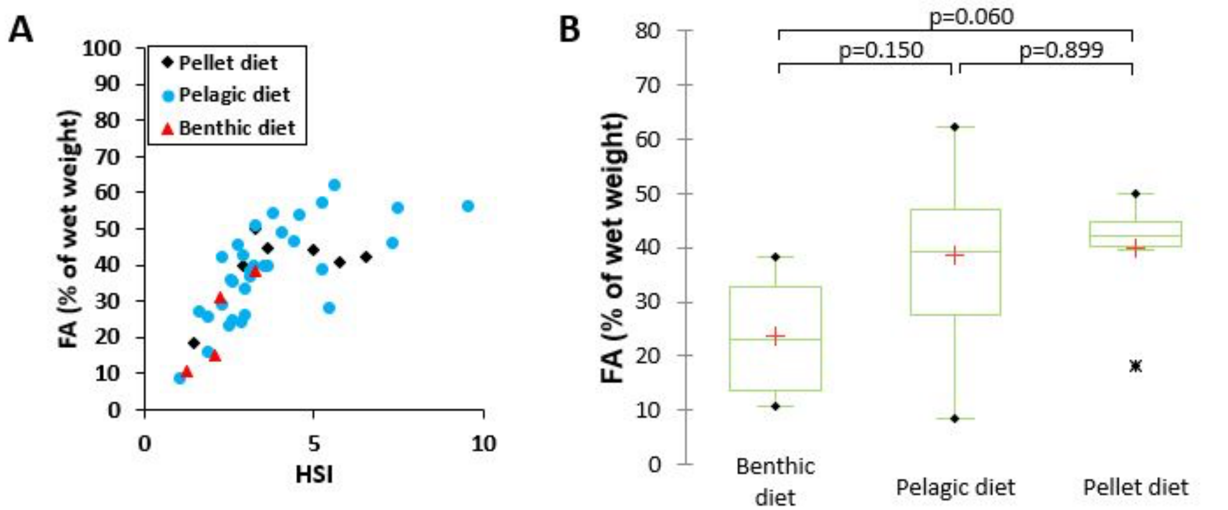


Figure S4. Bivariate plots of hepatosomatic index against FA amount in the liver (% of wet weight) for Atlantic cod caught at three Finnmark fjords in 2019 (all fjords are pooled together). Linear regression analysis of all samples (Y=0.498X + 19.39, R2=0.471, P<0.0001). B. Kruskal-Wallis analysis of the FA (%) of the diet groups. The samples are visualised as salmon pellet diet, pelagic diet and benthic diet according to Table 2.

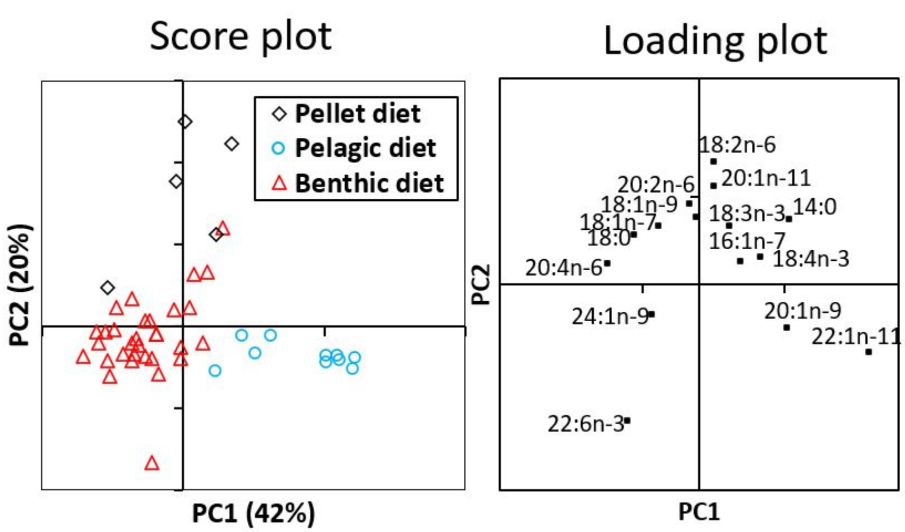


Figure S5. PCA (score and loading plot) of 51 FAs from 46 cod stomach samples. The two first axes explain 63% of the total variation (axis 1 = 42%, axis 2 =20%). The Loading plot presents the 15 fatty acids with highest contribution in the PCA.