A project in Analytical Chemistry: Quantitative analysis and comparison of fatty acid compositions of fish from the North Sea – You are what you eat?

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Master thesis

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Table of Content

Abstract

Fatty acid (FA) and lipid characterization are useful for several purposes when trying to understand marine eco-systems, environmental effects on cell membranes and nutritional quality of fish as food and raw material. As the world population grows larger, the demand for food is also growing. Application of unused resources and rest raw materials from the ocean to produce fish feed for farmed fish is increasingly important and requires analysis of FA content to ensure that the feed meets the fish' requirements for particular FAs. Fatty acids in fish are often reflected by what their diet consists of and analysing fatty acids can be helpful when trying to unravel diets of marine species. Fatty acid trophic marker (FATM) is a well-established tool to study trophic interactions. Fatty acid trophic markers as a tool can be used in conjunction with more traditional gut analysis and stable isotopes, but also on its own, to investigate diets of fish and marine organisms.

In this master project, fatty acid profiles of 30 species of fish from the North Sea was determined, for liver and muscle tissues. Derivatization of fatty acids and extraction of fatty acid methyl esters (FAME) was done by a one-step methylation method, or direct methylation. FAME were quantified using gas chromatography and internal standards. Optimization of the direct methylation method was achieved using factorial design. Variables investigated were reaction time, timing for introducing non-polar solvent and number of extractions. Results from the design show that the number of extractions can be reduced from 2 to 1, which reduces the time usage for the method.

Fatty acid profiles were explored using principal component analysis (PCA), which visualizes the data in a meaningful way and helps discern similarities and differences between the species. Similarities of pelagic fish muscle and cod fish liver samples were observed. These FA profiles are dominated by *Calanus* FATMs 22:1(n-11) and 20:1(n-9). Differences in benthic and pelagic feeders were found to be elevated levels of 20:4(n-6) and (n-7) FAs and the absence of *Calanus* FATMs for benthic fish. This clearly illustrates the use of FATMs to show consumption of herbivorous copepods such as *Calanus,* and separate pelagically feeding fish from those that feed benthically. One of the cod fish, poor cod, was found to be more similar to benthic feeders in FA profile than to other cod fish and pelagic feeders.

Many of the species analysed were shown to have no reports on FA profiles after searches in literature and may have been analysed for the first time in this project. The data produced on FA profiles and compositions in this project will eventually be included in a national database that IMR plans to build.

Sammendrag

Fettsyre (FA)- og lipidkarakterisering er nyttig for flere ulike grunner: å forstå marine økosystemer, miljøpåvirkninger på cellemembraner og kvalitet av næringsinnhold i fisk som skal spises eller brukes som råmaterial. Ettersom folketallet i verden stiger, stiger også etterspørselen etter mat. Utnyttelse av ubrukte ressurser og restråstoff fra havet for å produsere fiskefôr er viktigere og viktigere, og krever analyse av fettsyreinnhold for å sikre riktig kost for oppdrettsfisken. Fettsyrene i fisk er ofte reflektert av maten de spiser, og kan dermed være et nyttig verktøy for å forklare dietten til marine organismer. Fettsyrer som trofiske markører (FATM) er et veletablert verktøy for å studere trofisk interaksjon. Disse kan brukes sammen med tradisjonelle analyser av mageinnhold, eller alene, for å undersøke dietten til fisker og marine organismer.

I dette masterprosjektet ble fettsyreprofiler fra 30 fisker fra Nordsjøen bestemt, for både muskel- og leverprøver. Derivat av fettsyre metylester (FAME) og ekstraksjon av disse ble gjort med en et-stegs metode kalt direkte metanolyse. FAME ble kvantifisert ved bruk av gasskromatografi og intern standard. En optimalisering av metoden ble utført og oppnådd, ved bruk av faktorial forsøksdesign. Parameterne som ble undersøkt var reaksjonstid, tidspunkt for tilsetting av ikke-polart løsemiddel og antall ekstraksjoner. Resultatet fra designet viste at antall ekstraksjoner kunne reduseres fra 2 til 1, noe som redusere tidsbruken i metoden.

Fettsyreprofilene ble utforsket ved bruk av prinsipiell komponent analyse (PCA), som visualiserer store mengder data på en meningsfull måte og brukes for å avdekke likheter og ulikheter mellom artene. Det blir observert likheter mellom fettsyreprofilene til pelagiske fiskemuskler og profilene til lever av torskefisker. Disse profilene er alle dominerte av *Calanus* FATM 22:1(n-11) og 20:1(n-9). Ulikheter mellom fisker som spiser bentisk og fisker som spiser pelagisk ble undersøkt, og er i hovedsak økt nivå av 20:4(n-6) og (n-7) FA, samt svært lave nivåer av *Calanus* FATM for bentiske fisk. Denne sammenligningen viser hvordan FATM kan brukes til å avdekke en diett bestående av *Calanus* og skille fiske som spiser pelagisk fra de som spiser bentisk. En av torskefiskene, sypike, har en FA-profil som er ganske ulik de andre torskefiskene, men svært lik de bentiske flyndrene.

For flere av fiskeartene som ble analysert i prosjektet finnes det ingen FA-profiler i litteraturen. Dette betyr at noen av fiskene kan ha blitt analysert for første gang. FA-profilene og sammensetningene produsert i dette prosjektet, vil bli inkludert i en nasjonal database av fettsyreprofiler som er planlagt etablert av Havforskningsinstituttet.

List of abbreviations

DM	Direct methylation
FA	Fatty acid
FAME	Fatty acid methyl esters
FATM	Fatty acid trophic marker
FFA	Free fatty acid
FID	Flame ionization detector
GC	Gas chromatography
IS	Internal standard
MUFA	Monounsaturated fatty acid
NL	Neutral lipid
PC	Phosphatidylcholine
PCA	Principal component analysis
PE	Phosphatidylethanolamine
PI	Phosphatidylinositol
PL	Polar lipid
PPL	Phospholipid
PS	Phosphatidylserine
PUFA	Poly unsaturated fatty acid
RF	Response factor
RSD	Relative standard deviation
SD	Standard deviation
SFA	Saturated fatty acid
SM	Sphingomyelin
TAG	Triacylglycerol

1. Introduction

1.1. Background

Fish is an important and valuable resource, not only directly as food on the table, but also as supplements for our diets and fish feed for farmed fish. Omega-3 fatty acids (FAs), or (n-3) FAs, have become an increasingly popular supplement and its intake has shown promising effects on human health (Bergé and Barnathan, 2005). Marine fish contains large abundances of these beneficial fatty acids. Fish such as mackerel and salmon are natural sources of (n-3) FAs, as a result of their fatty fillets. Just as these FAs are important for the human diet, they are important for the diets of fish. FAs in fish are often reflected by what their diet consists of, and the use of fatty acids can be helpful when trying to unravel diets of marine species. The FAs found in fish are diverse and play important roles such as for use in phospholipids in cell membranes or in triacyl glycerides for energy storage. FA and lipid characterization are useful for several purposes: understanding marine eco-systems, environmental effects on cell membranes and nutritional quality of fish as food and raw material. As the world population grows larger, the demand for food is also growing. Application of unused resources and rest raw materials from the ocean to produce fish feed for farmed fish is increasingly important and requires analysis of FA content to ensure that the feed meets the fish' requirements for particular FAs.

Marine primary producers lay down a pattern of fatty acids, which can in some cases be transferred conservatively to primary consumers (Dalsgaard et al., 2003) and up the aquatic food web. This makes fatty acids applicable for use as trophic markers. Trophic markers are compounds that are transferred from one trophic level to the next and can be identified both qualitatively and quantitatively. Fatty acid trophic markers FATM, is a well-established tool to study trophic interactions. FATMs can be used in conjunction with more traditional gut analysis and stable isotopes, but also on its own, to investigate diets of fish and marine organisms.

The Institute of Marine Research (IMR) plans to build a national database of FA compositions from the marine environment. This thesis will contribute to this work by analysing fish from the North Sea, caught in 2010, 2011 and 2013. Such a database can serve as a public tool for comparing FA profiles and findings from national and international studies. Fatty acid compositions of muscle and liver tissue of 30 different species will be analysed by direct methylation and gas chromatography. The fish analysed are of many different types and families, and trophic levels, and therefore include a broad spectre of different habitats and prey, and ultimately, different diets.

Aims of the thesis

A full factorial experimental design will be conducted with the aim of optimizing the direct methylation method, investigating the effects of three variables and their interactions. The goal for this design is to investigate whether any of the variables can be optimized to make the method less time consuming without adverse effects on the yields.

FAs will be trans-esterified to their FAME derivatives by the means of a direct methylation and analysed using gas chromatography, using an internal standard for quantification. The practical work for this thesis will be conducted at the Chemistry laboratory at the Institute of Marine Research in Bergen, where these methods are used and performed daily. The resulting FA profiles of the fish will be explored by the means of principal component analysis, which is a mathematical method used to compress data and show similarities and correlations in a way that is meaningful and easy to interpret. Use of multivariate statistical methods such as this can graphically present large dataset, while still keeping large amounts of the variance within the data. FATMs will be investigated to elude information about the preys, habitats and diets of the fish analysed.

Several of the fish analysed have no reports of FA compositions in the literature and will possibly be analysed in this manner for the first time. All the FA compositions will eventually be incorporated into the database planned by IMR.

1.2. Marine fish habitats and environments

The North Sea is shelf sea of the North Atlantic (Emeis et al., 2015) where two thirds of the area are shallower than 100 meters, with an average depth of 90 meters. The deepest part of the sea reaches 725 meters in the Norwegian trench. Figure 1 shows a map of the North Sea. The seabed is sandy, but muddy in the deeper areas (Havforskningsinstituttet, 2019b). The North Sea is home to a large fauna, and large fishing banks of with species such as mackerel, saithe and Atlantic cod. It is "one of the world's most productive areas for fish and a large number of commercially important species are caught in this area" (Walday and Kroglund, 2017).

Included in this large fauna are widely different types of fish, from cod to flatfish and from mackerels to sand eels. The fish, fish types and habitats of those analysed for this thesis are presented briefly in the next sections.

Figure 1: Map of the North Sea. Adapted from: (Halava, 2010)

1.2.1. Demersal fish

Most fish in the Cod family, or of the *Gadus* genus, are demersal and benthopelagic. The demersal zone consists of the part of the water column near the seabed and is just above the benthos. Demersal fish are fish that live and feed on or near the bottom of the sea and they comprise both benthic and benthopelagic fish. A wide variety of fish families are represented in the demersal zone including cartilaginous and bony fish (Bergstad, 2009). Many of the fish analysed in this project belong to the demersal zone and is well represented in the data set.

Most demersal fish are carnivores that eat predominantly other fish, benthos, or zooplankton. Since the production of benthic food is slow, many of the species in the demersal zone rely mostly on the pelagic production by feeding on migrating nekton and zooplankton (Bergstad, 2009). Sand eels play a key role in the food web in that they are prey for a wide range of species such as cod, whiting, pollack, saithe, megrim, plaice and sole (Hart, 2001). Tables 1 to 5 show lists of species that are included in the analyses for this thesis, fish types or families are highlighted in bold and scientific names are given in parentheses.

Table 1: List of demersal fish analysed for the thesis.

Cod fish	Flatfish
Saithe (*Pollachius virens)*	Lemon sole (*Microstomus kitt*)
Pollack (*Pollachius pollachius*)	Megrim (*Lepidorhombus whiffiagonis*)
Poor cod (*Trisopterus minutus*)	Common dab (*Limanda limanda*)
Silvery pout (*Gadiculus argenteus*)	European plaice (*Pleuronectes platessa*)
Whiting (*Merlangius merlangus*)	
Blue whiting (*Micromesistius poutassou*)	
Cartilaginous fish	**Scorpaenidae**
Blackmouth catshark (*Galeus melastomus*)	Norway redfish (*Sebastes viviparus*)
Spiny dogfish (*Squalus acanthias*)	Grey gurnard (*Eutrigla gurnardus*)
Thorny skate (*Amblyraja radiata*)	
Merlucciidae	**Anarhichadidae**
European hake (*Merluccius merluccius*)	Atlantic wolffish (*Anarhichas lupus*)
Callionymidae	**Lotidae**
Spotted dragonet (*Callionymus maculatus*)	Four-bearded rockling (*Enchelyopus cimbrius*)
	Phycidae
	Greater fork-beard (*Phycis blennoides*)

Cartilaginous fish consist of sharks, skates, ray and ghost sharks. These fish have skeletons made of cartilage instead of bone, making them lighter than bony fish (Havforskningsinstituttet, 2019a). The European hake is both demersal and pelagic, as it cycles from being demersal by day and pelagic by night (Fishbase, 2021b). Both the four bearded rockling and greater fork-beard are species of cod like families.

1.2.2. Pelagic fish environment

Pelagic fish are fish that live in the open water column, not near the bottom nor the seashore, and swim steadily for long periods. Pelagic fish have a central position in the marine food web, from which they are responsible for much of the energy going up the food web from algae and copepods to fish (Cushing et al., 2019). Types of fish vary from forage fish to larger predators. Two important pelagic fish of the North Sea are Atlantic herring and Atlantic mackerel. Herring feed mainly on *Calanus,* which are herbivorous calanoid copepods, a zooplankton. Mackerel also feed on copepods among other plankton animals (Cushing et al., 2019). They are both planktivores with similar body adaptations to live in the open seas, but they belong to very different taxonomic groups (Hart, 2001).

Table 2: List of pelagic fish analysed for the thesis.

Scombridae
Atlantic mackerel (*Scomber scombrus*)

Carangidae
Atlantic horse mackerel (*Trachurus trachurus*)

Clupeidae
Atlantic herring (*Clupea harengus*)

Belonidae
Garfish (*Belone belone*)

1.2.3. Mesopelagic fish

Mesopelagic fish are fish that live in the intermediate pelagic water masses between the epipelagic zone (0-200m) and the bathypelagic zone (1000 m). Many species display vertical migration behaviours and the most apparent is migration to the epipelagic zone at dusk to prey and descending back down hundreds of meters to their daytime depth (Staby and Salvanes, 2019). Two mesopelagic fish are included in this thesis, the two Argentines (Table 3): Argentine and greater argentine.

Table 3: List of mesopelagic fish analysed for the thesis.

Argentinidae
Greater argentine (*Argentina silus*)
Argentine (*Argentina sphyraena*)

1.2.4. Sand eels

Sand eel is a term used for the species in the Ammodytidae family. The sand eels live at the sea bottom, spending a major part of their time buried. Despite their name, they are not true eels. In the North Sea there are five different species of sand eels, two of which are included in this project (Table 4) (Havforskningsinstituttet, 2020).

Table 4: List of sand eels analysed for the thesis.

Ammodytidae
Greater sand eel (*Hyperoplus immaculatus*)
Lesser sand eel (*Ammodytes marinus*)

The lesser sand eel is an important part of the marine food web as they are prey of many larger fish, and they form a link between zooplankton and higher trophic levels (MacDonald et al., 2019).

1.2.5. The fishes

Table 5 shows pictures of the fish and gives some general information about the different fish analysed in the thesis.

Table 5: Information on depth, range and biology, with pictures for all the species analysed. All the information, data and pictures are adapted from FishBase (Froese and Pauly, 2021) and retrieved on the same date.

Species	
Cod fish (Gadidae)	
Silvery pout (*Gadiculus argenteus*) Depth range: 100-1000 m Common length: 10 cm Occurs in large schools over mud, muddy sand, gravel and rock bottoms. Feeds on small crustaceans and maybe worms. Preyed upon by larger fish.	
Norway pout (*Trisopterus esmarkii*) Depth range: 50- 300 m Common length: 19 cm Benthopelagic to pelagic over muddy bottoms. Feeds mostly on copepods and other planktonic crustaceans, but also small fish.	

Species	
Poor cod (*Trisopterus minutus*) Depth range: 1- 440 m Common length: 20 cm Occurs mostly in the Atlantic on muddy or sandy bottoms. Feeds on crustaceans (copepods), small fish and polychaetes.	
Blue whiting (*Micromesistius poutassou*) Depth range: 150 – 3000 m Common length: 22 cm Found over the continental slope and shelf to more than 1000m, but more common at 300-400 m. Feeds mostly on small crustaceans but large individuals also prey on small fish and cephalopods.	
Whiting (*Merlangius merlangus*) Depth range: 10-200 m Common length: 23.5 cm Occurs mainly on mud and gravel bottoms. Feeds on shimps, crabs, small fish and polychaetes.	
Saithe (*Pollachius virens)* Depth range: 37-364 m Common length: 60 cm Occurring inshore and offshore, smaller fish feed on small crustaceans, while larger fish prey dominantly upon fishes.	
Pollack (*Pollachius pollachius*) Depth range: 40-200 m Common length: 75 cm Juveniles are pelagic and may form schools with saithe. Larger individuals move to open sea.	
Flatfish	
Lemon sole (*Microstomus kitt*) Lives most often on stony bottoms. Feeds on a variety of small invertebrates, but polychaetes dominate the diet.	
Common dab (*Limanda limanda*) Adults live mainly on sandy bottoms, from a few meters to about 100 m depth. Feed mainly on crustaceans and small fishes.	
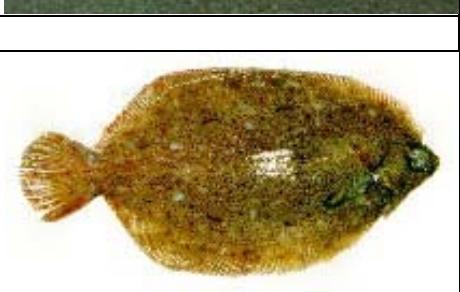
Species	
Megrim (*Lepidorhombus whiffiagonis*) Common length: 25 cm Adults occur on soft bottoms. Feeds on small bottom-living fishes, squids and crustaceans.	
European plaice (*Pleuronectes platessa*) Common length: 40 cm Adults live on mixed bottoms, the older the deeper the occurrence. Feed mainly on mollusks and polychaetes.	
Cartilaginous fish	
Blackmouth catshark (*Galeus melastomus*) Depth range: 150 – 1200 m Common length: 50 cm Found on the outer continental shelves and upper slopes. Feed mainly on bottom invertebrates but also on small pelagic bony fishes and other small elasmobranchs.	
Spiny dogfish (*Squalus acanthias*) Depth range: 0 – 1460 m Common length: 100 cm Possibly the most abundant living shark. Usually near the bottom, but also in midwater and at the surface. Feeds on a diversity of prey, from comb jellyfish, squid, mackerel and herring to benthic fishes, shrimps and crabs.	
Thorny skate (*Amblyraja radiata*) Depth range: 5 – 1540 m Cold temperature species found in offshore waters on all kinds of bottoms, mainly sandy and muddy. Feed mainly on fish, crustaceans and polychaete worms. Diet changes with increasing body size.	
Merlucciidae	
European hake (*Merluccius merluccius*) Depth range: 30 – 1075 m Common length: 45 cm Adults live close to the bottom during daytime but move off-bottom at night. Adults feed mainly on fish (small hakes, herrings, cod fishes). The young feed on crustaceans.	

Species	
Scorpaenidae	
Norway redfish (*Sebastes viviparus*) Depth range: 50 – 300 m Common length: 25 cm Inhabit rocky bottoms, close to shore. Live in shoals and moves closer to the shore in the summer. Feed on various small crustaceans and young fishes.	
Grey gurnard (*Eutrigla gurnardus*) Depth range: 10 – 340 m Common length: 30 cm Common on sandy grounds, sometimes on rocky and muddy bottoms. Feeds on crustaceans, mostly shrimps and shore crabs, and fishes (gobies, flatfish, young herring and sand eels).	
Anarhichadidae	
Atlantic wolffish (*Anarhichas lupus*) Depth range: 1 – 600 m Inhabit rocky bottoms, sometimes over sand or mud. Feeds on fishes, hard-shelled molluscs, crabs and lobsters. Solitary in habit.	
Callionymidae	
Spotted dragonet (*Callionymus maculatus*) Depth range: 45 – 650 m Max length: 16.5 cm "Benthic over sandy bottoms. Feeds on small bottom invertebrates, mainly worms, snails and crustaceans."	
Lotidae	
Four-bearded rockling (*Enchelyopus cimbrius*) Depth range: 20 – 650 m Common length: 30 cm Sedentary bottom dwellers on muddy sand between patches of hard substrate, or on the soft, smooth ground of deep sinks on the continental slopes of both sides of the North Atlantic. Feed on flatfishes, amphipods, decapods, copepods, mysids, shrimps, isopods and other small crustaceans.	
Phycidae	
Greater fork-beard (*Phycis blennoides*) Depth range: 10 – 1200 m Common length: less than 45 cm "Found over sand and mud bottoms. Feed mainly on crustaceans and fishes."	
Scombridae	

Species	
Species	
Atlantic mackerel (*Scomber scombrus*) Depth range: 0 – 1000 m Common length: 30 cm "Abundant in cold and temperate shelf areas, forms large schools near the surface. Feeds on zooplankton and small fish."	
Carangidae	
Atlantic horse mackerel (*Trachurus trachurus*) Depth range: 0 – 1050 m Common length: 22 cm "Adults form large schools in coastal areas with sandy substrate. They feed on fish, crustaceans, and cephalopods."	
Clupeidae	
Atlantic herring (*Clupea harengus*) Depth range: 0 – 364 m Common length: 30 cm "Juveniles (up to 2 years) shoal close inshore, while adults are found more offshore. Feed mainly on copepods finding food by visual sense."	
Belonidae	
Garfish (*Belone belone*) Depth range: 0 - ? m Common length: 45 cm "Lives close to the surface and has a migratory pattern similar to the mackerel. Feeds on small fishes, particularly clupeids."	
Argentinidae	
Greater argentine (*Argentina silus*) Depth range: 140 – 1440 m Max length: 70 cm "Probably form schools close to the bottom. Feeds on planktonic invertebrates including euphausiids, amphipods, chaetognaths, squids and ctenophores, also small fishes."	
Argentine (*Argentina sphyraena*) Depth range: 50 – 700 m Common length: 20 cm "Relatively common on the continental shelf and upper slope, probably schools near the bottom. Feeds on bottom-living polychaetes, molluscs and crustaceans, also on pelagic invertebrates and fishes."	
Ammodytidae	
Greater sand eel (*Hyperoplus immaculatus*) Max length: 35 cm "Inhabits inshore and offshore, although only juveniles appear to occur close inshore. Feeds initially on zooplankton, but for lengths greater than 10 to 15 cm small fish, such as clupeids and ammodytids dominate the diet"	

Species	
Lesser sand eel (*Ammodytes marinus*) Depth range: 10 – 150 m Max length: 25 cm "This schooling species is usually territorial and burrowing. Feed on plankton."	

1.2.6. Physical measurements of fish condition

Physical measurements of fish can be used to say something about the physical health of individuals or whole population of fish. Analysis of length to weight ratio is believed to be a good indicator of general fitness of a specimen, where the heavier fish of a given length is assumed to be healthier. Physical measurements and derived indices can be used for comparing conditions such as food density or climate of populations or gonad maturity timing and duration.

Some studies have confirmed the relationship between the Fulton conditioning factor, and total lipid content of fish, and its use as a measure of energy reserves. (*e.g*., Herbinger and Friars, 1991; Chellappa et al., 1995). Energy reserves are stored in the form of lipids, and one of the building blocks of lipids are fatty acids. The condition factor will be compared with total FA content in tissue, to investigate how well this index can help describe the energy storage of the fish analysed. Two other indices will also be used and compared to FA content of the fish.

The gonadosomatic index, GSI, is the calculation of the gonad mass as proportion of the total body mass.

$$GSI = \frac{Gonad\ weight}{Total\ tissue\ weight} x\ 100 \qquad \text{Equation 1}$$

It is a tool used to measure sexual maturity of animals in correlation to ovary development and testes development (Mishra and Saksena, 2012).

The hepatosomatic index, HSI, is defined as liver weight and fish weight ratio. This is used as an indicator of energy reserves in the liver (Hismayasari et al., 2015).

$$HSI = \frac{Liver\ weight}{Total\ tissue\ weight} x\ 100 \qquad \text{Equation 2}$$

Condition factors based on length and weight is readily produced because there is no time-consuming work needed to make the required measurements, compared to indices such as GSI and HSI. "Fulton's conditioning factor is widely used in fisheries and general fish biology studies. This factor is calculated from the relationship between the weight of a fish and its length, with the intention of describing the "condition of that individual" (Nash et al., 2006).

$$K = \frac{W}{L^3} \qquad \text{Equation 3}$$

Where K = Fulton's conditioning factor, W = weight of the fish and L = length.

1.3. Lipids

Lipids are broadly defined as hydrophobic or amphiphilic small molecules. Lipids can also be defined as naturally occurring molecules that have limited solubility in water and can be isolated from organisms by extraction with a nonpolar organic solvent. Lipids are classified into two general types: those that contain an ester linkage and those that do not (McMurry, 2011). W.W. Christie has proposed the

following definition: "Lipids are fatty acids and their derivatives, and substances related biochemically or functionally to these compounds" (Christie, 1989).

Lipids are essential materials in cell membranes but is also utilized as a major form of metabolic energy. Neutral lipids such as triacylglycerols and wax esters can be stored to either provide energy or for incorporation into phospholipids, which is one of the important building blocks of cell membranes (Bergé and Barnathan, 2005). Lipids comprise many types of compounds, and the most relevant lipids will be presented in this chapter.

1.3.1. Fatty acids

Fatty acids (FAs) are carboxylic acids with a long aliphatic chain of carbons. They are the simplest form of lipids. FAs are distinguished by the number of carbons in the chain and their degree of hydrogen saturation, as well as branching in the chain. This categorises them into different classes: saturated fatty acids (SFA), monounsaturated fatty acids (MUFA), polyunsaturated fatty acids (PUFA) and branched fatty acids. SFAs do not contain any double bonds in the carbon chain, while MUFAs and PUFA contain one or more, respectively. Figure 2 shows examples of different types of FAs.
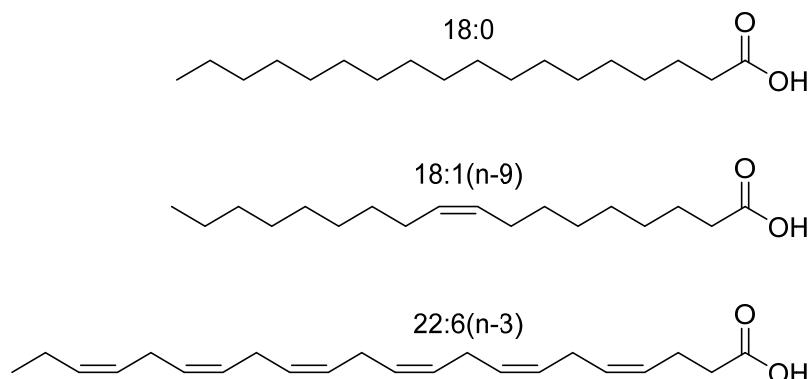
Figure 2: Examples of fatty acids with different levels of saturation.

Another classification of FAs is by cis- and trans-isomerism. This relates only to unsaturated FAs and occurs at a C-C bond adjacent to a C=C bonding. An example of such isomerism is oleic acid and elaidic acid, both 18:1(n-9) FAs, but oleic acid is the cis-isomer and elaidic acid is the trans-isomer. In Figure 3, elaidic acid and oleic acid are illustrated. Oleic acid has a cis configuration in carbon no. nine resulting in a different isomer. The different isomers have different physical and chemical properties, as is apparent with oleic acid and elaidic acid, with melting points at 13.4 and 45 °C, respectively.
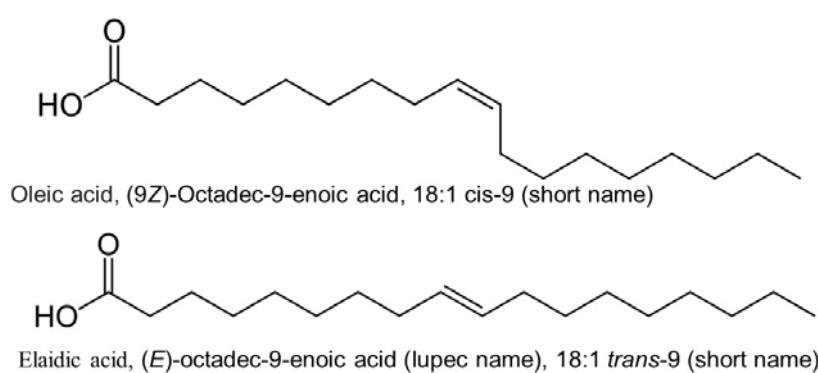
Figure 3: Example of cis-trans isomerism in fatty acids.

For the most common biosyntheses of fatty acids, it is nearly always the cis isomers that are produced. So, for this thesis all the FAs are cis-isomers, and therefore cis/trans geometry is not specified.

<u>Nomenclature for naming fatty acids:</u>

The name of an FA follows the formula: C:D (n-x), where C is the number of carbons, D is the number of double bonds, n represents the methyl carbon of the FA-chain and x represents the number of the carbon where the first double bond occurs (counted from the n-carbon, not the carboxylic carbon). The n-position is often referred to as the ω-position (omega) (Rustan and Drevon, 2005). Example: stearic acid (Figure 3) has 18 carbons, 1 double bond and the double bond occurs at the 9th carbon in the chain (counting from the methyl carbon), which results in the name 18:1(n-9).

1.3.2. Triacylglycerol (TAG)

Triacylglycerols (TAG) are tri-esters of glycerol with three fatty acids (McMurry, 2011). TAG, along with wax esters, make up most of the neutral lipids in marine species. TAG is stored for two purposes: oxidation to provide energy (ATP) or incorporation into phospholipids. TAG is the major form of energy storage in animals. Fish store their fats at different places, and the distinction between fat and lean fish is determined by the amount of energy storage in muscles (fillet). Lean fish typically store their fat in the liver. Fattier fish like mackerel have more energy reserves in their muscle.

TAGs are characterized by the three fatty acids. TAGs containing three similar FAs are referred to as a "simple triacylglycerol" or homotriglycerides. Mixed TAG contains two or three different FAs. In a simple TAG such as stearin, the three FAs are stearic acid, illustrated in Figure 4. Diacylglycerols and monoacylglycerols, which contain two fatty acids and one fatty acid, respectively, are "rarely present at greater than trace levels in fresh animal and plant tissues" (Christie, 1989).

The fatty acid composition of TAG in marine species differs from others in that they contain higher proportions of C20 and C22 PUFAs (Christie, 1989).
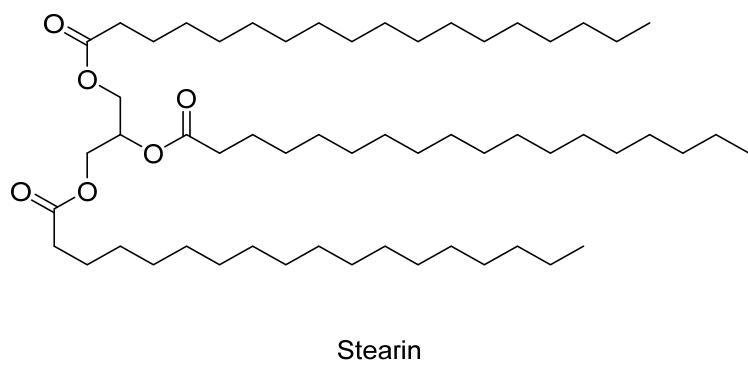
Stearin

Figure 4: Chemical structure of stearin.

1.3.3. Phospholipids (PPL)

Phospholipids (PPL) are esters of two fatty acids and one phosphoric acid. They are key components of all cell membranes. Because of its amphiphilic nature, PPLs can create a lipid bilayer (McMurry, 2011). This occurs when the non-polar end of a PPL is facing the non-polar end of another PPL, with the polar ends facing the opposite way in either direction. The non-polar end, consisting of the fatty acids, is referred to as the hydrophobic tail. The polar end, consisting of the phosphate group, is referred to as the hydrophilic head. This hydrophobic interior creates a barrier that is impermeable to water and polar molecules, and separate contents of the cell from the outside (Bergé and Barnathan, 2005).

PPLs are sorted into two main groups, diacylglyceride structures and phosphosphingolipids. Diacylglyceride structured PPLs are sorted into different classes depending on the substituent on the phosphate group. Figure 5 shows the structure of the most common diacylglyceride PPLs; phosphatidic

acid (PA), phosphatidylcholine (PC), phosphatidylethanolamin (PE), phosphatidylserine (PS) andphosphatidylinositol (PI).
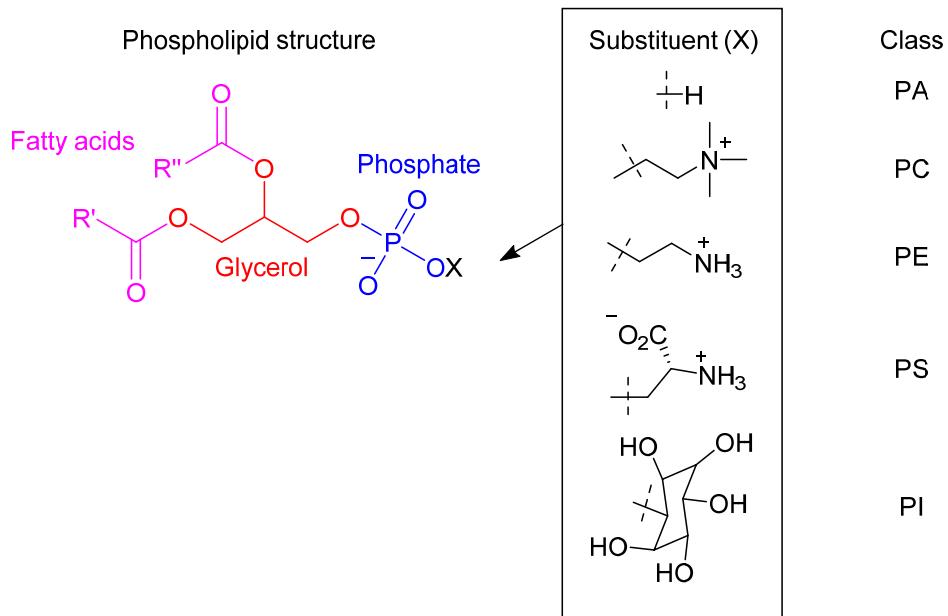
Figure 5: Basic structure of diacylglyceride PPL with examples of different substituents.

1.3.4. Sterols

Sterols, also known as steroid alcohols, are also a type of lipid. An important sterol is cholesterol, which alongside phospholipids, are important for the structure of animal cell membranes (Bramley, 1997). Hydroxyl groups of the cholesterols interact with water surrounding the cell membrane, much like the phospholipid. The steroid and the hydrocarbon chain are imbedded into the membrane alongside the fatty acids of the other lipids. Through interaction with these, cholesterol increases the packing of the cell membrane. It also maintains the membrane integrity so that animal cells do not need to build cell walls. The chemical structure of cholesterol is shown in Figure 6.
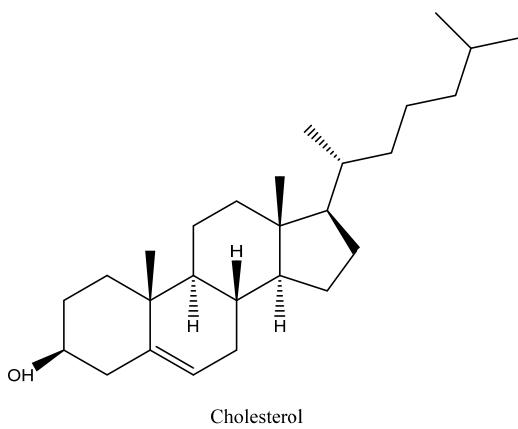
Cholesterol

Figure 6: Chemical structure of cholesterol.

1.3.5. Wax esters

Wax esters are esters of fatty acids and long chained fatty alcohols, illustrated in Figure 7. Wax esters have various functions such as energy storage and waterproofing (Christie, 1989). Significant amounts of wax ester storages can be found in marine copepods. These zooplanktons use highly unsaturated TAGs to make wax esters for storage. Lee and Hirota (1973) found that copepods living in polar and

temperate waters, accumulate much of their bodyweight as wax esters to survive unproductive winters. Fatty acids used in marine wax ester are typical marine fatty acids, with a carbon length of 14-22 (Sargent et al., 1977).

22:1(n-11) alcohol
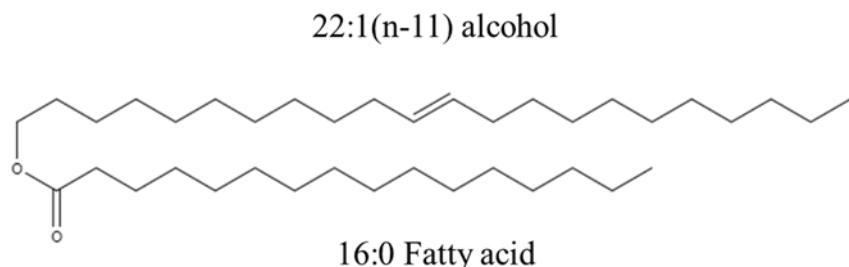
16:0 Fatty acid

Figure 7: Chemical structure of a wax ester of 16:0 alcohol and 22:1(n-) fatty acid.

1.3.6. Sphingolipids

Sphingolipids are made up of a sphingoid backbone to which a fatty acid is attached through an amid bond and a head group at the primary hydroxyl (Figure 7). The simplest sphingolipid, with hydrogen as the substituent, is a ceramide. Sphingolipids have several functions in animals, such as cell structuring and as cell signalling modulators and mediators, etc. (Merrill, 2008).
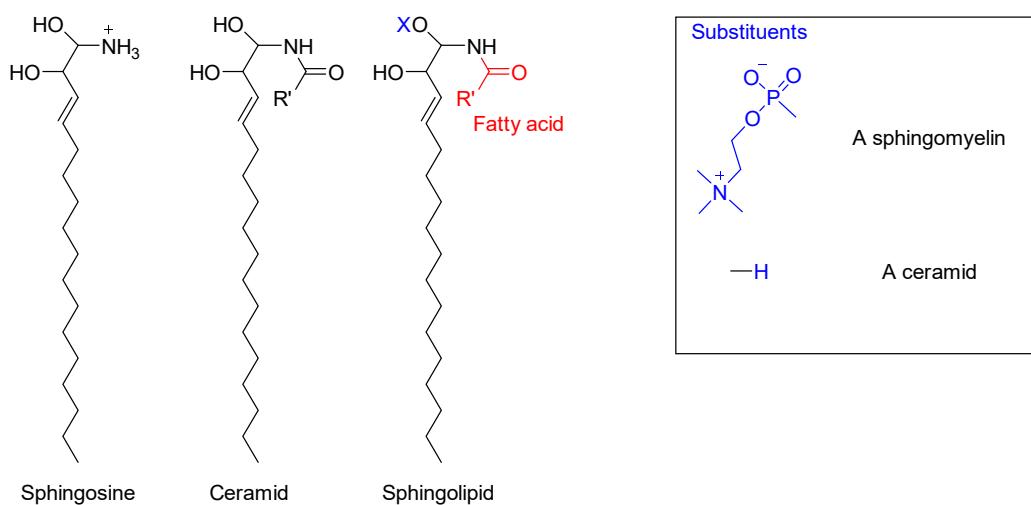
Figure 8: Sphingolipid structure with examples of substituents.

1.3.7. Biosynthesis of Fatty Acids

The *de novo* biosynthesis of FA generally follows Type I Fatty acid synthase with the major product being mainly 16:0, but 14:0, 18:0 and 20:0 can occur. In the marine food web, primary producers such as phytoplankton and macroalgae, lay down the basic FA pattern. Phytoplankton is the major energy provider in pelagic food webs, while macroalgae contribute mostly to benthic areas. In pelagic food webs, phytoplankton are predominantly *Bacillariophyceae* (diatoms), *Dinophyceae* (dinoflagellates) and *Prymnesiophyceae*. Metabolic energy provided by the phytoplankton are transferred up the pelagic food web by herbivorous and omnivorous planktivorous species (Dalsgaard et al., 2003). Herbivorous calanoid copepods play an important role in the food web as they transfer metabolic energy from primary producers to higher trophic levels, but they are also important producers of specific fatty acids themselves (Dalsgaard et al., 2003). The ability of microalgae to biosynthesize 18:2(n-6) and 18:3(n-3) contributes to an important part of FAs within marine food webs. These FAs and their derivatives (20:5(n-3) and 22:6(n-3)) are essential for heterotrophic organisms (Dalsgaard et al., 2003). Unlike animals, the marine primary producers possess enzymes that enables them to desaturate 18:1(n-9) further into 18:2(n-6) and 18:3(n-3), before further elongation into their longer chained derivatives. The typical

FAs from this process are found in dinoflagellates, with 18:4(n-3) and 22:6(n-3) being dominant (Dalsgaard et al., 2003). Figure 9 shows the pathways of FA biosynthesis for A) marine algae and B) herbivorous calanoid copepods. Fatty acids of (n-3) are found in large amounts in PPL of marine fish, but the fish cannot synthesize 22:6(n-3) *de novo* or from shorter precursors. This makes the 22:6(n-3) and 20:5(n-3) FAs, essential dietary constituents for marine fish (Sargent et al., 1999).

FAs produced by marine heterotrophic bacteria can be distinguished from eukaryotes by producing large amount of odd-numbered and branched chained FA and iso and anteiso-C_{15} and C_{17} (Dalsgaard et al., 2003). FATM specific to the different species is discussed in further detail in the next section.
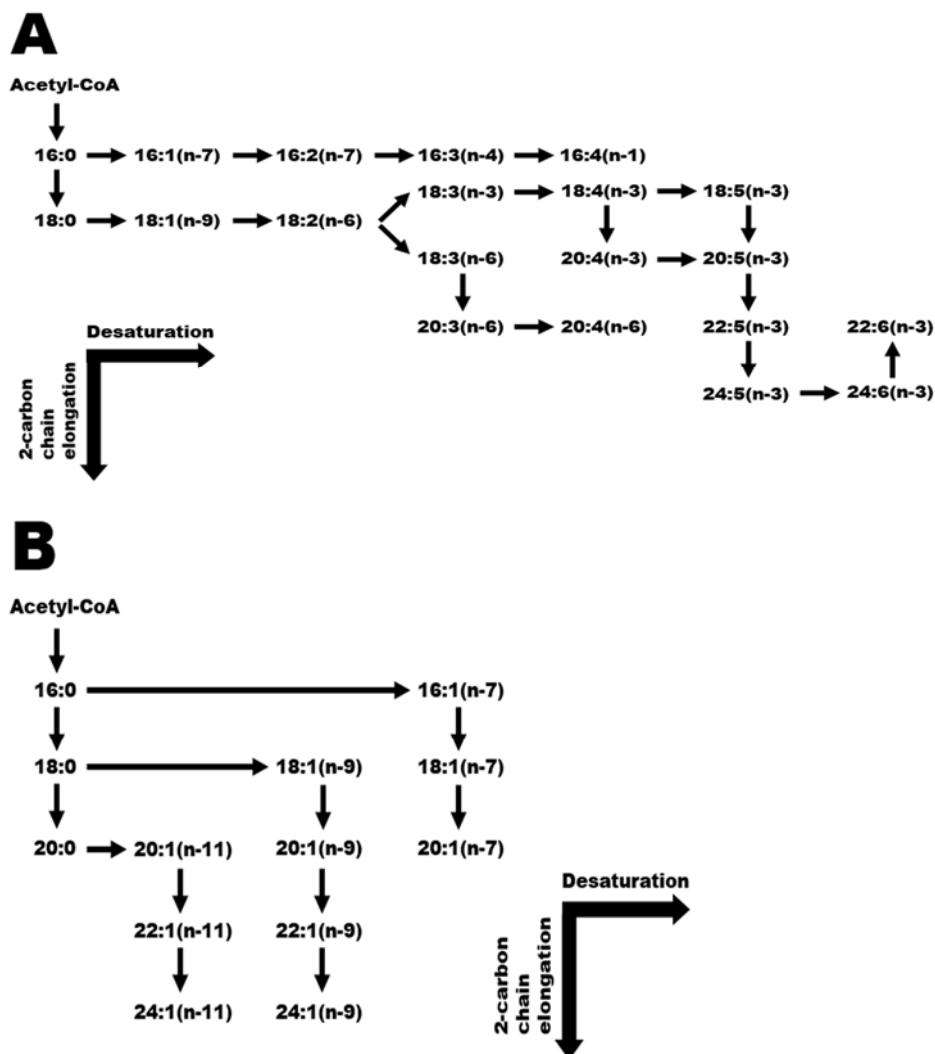
Figure 9: Pathways for FA biosynthesis in A) marine algae and B) herbivorous calanoid copepods. Adapted from: (Dalsgaard et al., 2003).

1.3.8. Fatty acids as trophic markers

FAs as trophic markers (FATM) is "based on that the observation that marine primary producers lay down certain fatty acid patterns that may, be transferred conservatively to, and hence can be recognized in, primary consumers" (Dalsgaard et al., 2003). Dalsgaard et al. described the characteristics of the "perfect trophic marker" in their 2003 review: "The perfect trophic marker is a compound whose origin can be uniquely and easily identified, that is inert and nonharmful to the organisms, that is not selectively processed during food uptake and incorporation, and that is metabolically stable and hence transferred from one trophic level to the next in both a qualitative and quantitative manner" (Dalsgaard et al., 2003).

As discussed in the previous section, primary producers have different pathways and means of biosynthesizing FAs. Previous work has shown that some of these FA patterns can be used as trophic markers. One of the advantages of using FATM instead of gut analysis is that more traditional gut content analysis, provide information only on recent feeding, while FAs provide information on the dietary intake and the food constituents over a longer period of time (Dalsgaard et al., 2003). Some problems related to gut analysis are overcome by FATM, but FATM are limited by other constraints. An example of this is that "no single FA can be assigned uniquely to any one species.." (Dalsgaard et al., 2003).

Marine bacteria mainly produce FA for incorporation into PPL. FA from marine bacteria is often saturated and monounsaturated C_{10}-C_{20}, and rarely polyunsaturated. FATM related to marine bacteria are therefore: odd numbered SFA (15:0 and 17:0), branched FA and odd numbered MUFA (Dalsgaard et al., 2003).

As mentioned in the previous section, phytoplankton in the pelagic environment are dominated by the three groups: diatoms, dinoflagellates and *Prymnesiophyceae.* There are multiple relationships that can help determine which of the microalgae that is dominating in a diet. When the ratio of 16:1(n-7) to 16:0 is greater than 1, paired with a high value of $\sum C_{16}/\sum C_{18}$ and a high value of 20:5(n-3)/22:6(n-3), it is a sign of diatoms dominating the diet. Low value of 20:5(n-3)/22:6(n-3) and a high value of 18:5(n-3)/18:3(n-3) indicates the dominance of dinoflagellates. The ratio of 20:5(n-3)/22:6(n-3) may potentially also be applied to determine degree of carnivory, as 22:6(n-3) is highly conserved through the food web, and the ratio will start to decrease (Dalsgaard et al., 2003).

FATM related to Macro algae such as *Chlorophyceae* are 16:4(n-3), 18:2(n-6) and 18:3(n-3), and high values indicate a dominance of green algae in the diet. PUFA in terrestrial plants consist predominantly of 18:2(n-6) and 18:3(n-3) and have FA profiles like those of green algae (Dalsgaard et al., 2003).

It is generally accepted that herbivorous calanoid copepods incorporate phytoplankton FATM largely unaltered. These copepods accumulate large lipid reserves, largely in the form of WE, to account for periods of poor food access. Calanoid copepods are one of the few known organisms with the ability to biosynthesize *de novo* considerable amounts of MUFA and fatty alcohols with 20 and 22 carbons. (Dalsgaard et al., 2003) Calanoid copepods have a central role in the marine food web and acts as a link between primary producers and higher trophic levels. The ability to produce C_{20} and C_{22} MUFA *de novo* leads to 20:1(n-9), 22:1(n-11) and 22:1(n-9) being useful FATMs to determine the intake of these copepods higher up in the food web (Dalsgaard et al., 2003). The fatty alcohols from the wax esters are in most cases oxidised into their corresponding FAs after being digested by fish. Table 6 shows a summary of the FATMs considered for this thesis, not all of them will be discussed as they may not all be relevant.

Table 6: List of common FATM used for analyses of the fish samples. FATMs gathered from (Dalsgaard et al., 2003).

	FATM	Comments
Terrestrial	18:1(n-9) + 18:2(n-6) + 18:3(n-3)	
Bacterial	$\sum$Odd numbered SFA + odd numbered branched + odd numbered MUFA: Iso 15:0, Antiso 15:0, 15:0, Iso 17:0, Antiso 17:0, 17:0, 15:1(n-x), 17:1(n-10), 17:1(n-8), 17:1(n-7) and 17:1(n-4).	
Bacterial	$\sum$Branched FA: Iso 15:0, Antiso 15:0, Iso 17:0, Antiso 17:0, $\sum$iso 18:0, branched 17:1 and 16:1(n-10) 7Me	
Bacterial	$\sum$Odd numbered MUFA:	

	20:0, 22:0, branched 17:1, 16:1(n-10) 7Me, 14:1(n-7), 14:1(n-5) and 15:1(n-x)	
Diatom	16:1(n-7)/16:0	>1 = diatoms
Diatom	∑C16/∑C18:	>1 = diatoms
	(16:0, 16:1(n-11), 16:1(n-9), 16:1(n-7), 16:1(n-5), 16:2(n-4), 16:3(n-4), 16:2(n-7), 16:2(n-6) and 16:4(n-3)) divided by (iso 18, 18:0, 18:1(n-11), 18:1(n-9), 18:1(n-7), 18:1(n-5), 18:1(n-4), 18:4(n-1), 18:5(n-1), 18:2(n-4), 18:2(n-6), 18:3(n-6), 18:3(n-3), 18:4(n-3) and 18:5(n-3))	
Diatom	∑C16 PUFA (n-1 + n-7 + n-6):	
	16:4(n-1), 16:2(n-4), 16:3(n-4), 16:2(n-7), 16:2(n-7) and 16:4(n-3)	
Diatom / dinoflagellate	∑C16 PUFA/∑C18 PUFA:	>1 = diatoms
	(16:4(n-1), 16:2(n-4), 16:3(n-4), 16:2(n-7), 16:2(n-7) and 16:4(n-3)) divided by ∑C18 PUFA	<1 = dinoflagellate
Dinoflagellate	∑C18 PUFA	
	18:4(n-1), 18:5(n-1), 18:2(n-4), 18:2(n-6), 18:3(n-6), 18:3(n-3), 18:4(n-3) and 18:5(n-3)	
Dinoflagellate	22:6(n-3)	
Diatom / dinoflagellate	20:5(n-3)/22:6(n-3)	>1 = diatoms <1 = dinoflagellate
Diatoms	16:1(n-7) + 16:4(n-1) + 20:5(n-3)	
Dinoflagellate	18:3(n-3) + 18:4(n-3)	
Dinoflagellate	16:4(n-3) + 18:5(n-3)	
	22:5(n-3) + 22:6(n-3)	
Calanus copepods	20:1(n-9) + 22:1(n-11) + 22:1(n-9)	

1.3.9. Lipid and fatty acid analysis

For lipid and FA analysis, two main methods are used for sample preparation: direct methylation and lipid extraction. Uberth and Henninger (1992) and Indarti et al. (2005) compared one-step methylation with the more traditional method of extraction/methylation and the results showed that the two methods achieved the same FA profile, but the yield of FA was higher in the one-step method (Meier et al., 2006). The prepared samples are analysed with gas chromatography.

Analysis of FAs by gas chromatography is typically carried out by analysing their corresponding fatty acid methyl ester (FAME) derivates. FAs are usually bound to larger lipid molecules and must be liberated from these and esterified into smaller molecules such as methyl esters. The method used is called direct methylation (DM). This method liberates the FAs from lipids and convert them to FAMEs by an esterification reaction. (Figure 10). These two steps are combined by alcoholising lipids directly by acid in a methanolic solution (Meier et al., 2006).
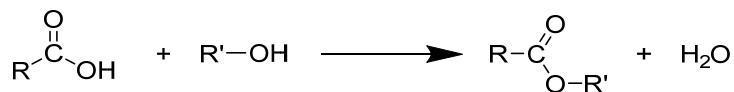
Figure 10: Trans esterification reaction.

The FAMEs are extracted from the solution by creating a two-phase system and extracting the non-polar phase. The procedure for this method is explained in Section 2.4. The water content should not exceed 10% of the methanol volume. Therefore, the methylation reagent is added in a large excess to ensure that sample with relatively high-water content do not exceed 10% of the methanol volume. From Uberth and Henninger (1992) it was found that small amounts of water do not interfere with the formation of methyl esters using methanol-HCl, which also was confirmed by Meier et al. (2006).

1.4. Gas chromatography

1.4.1. Introduction

Gas chromatography is a well-established technique for separating and analysing volatile compounds (Miller, 2005). The analyte is transported through a column by an inert gaseous mobile phase. Open tubular columns with stationary phase coated on the inner walls are the most used columns in GC. Typical column lengths vary from 15 to 100 metres with inner diameters varying from 0.1 – 0.5 mm (Harris, 2015). Separation in GC is highly dependent on the volatility of the analytes, but it also depends on the stationary phase chemistry. The mobile phase does not take part in the separation since its only function is to carry the analyte through the column. For this reason, inert gases such as helium, nitrogen or hydrogen are chosen as the carrier gas.

Interaction between analyte and stationary phase affects the retention of a compound. As the compounds of the sample elute from the column, they are detected by the detector. A wide variety of detectors are available for GC, such as flame ionization detector, thermal conductivity detector, flame photometric detector, etc. Each detector uses different methods to detect compounds and therefore have different areas of use.

1.4.2. Principles of chromatography

The distribution between the stationary and the mobile phase is described by the retention factor, k (Ettre, 1993):

$$k = \frac{amount\ of\ component\ in\ stationary\ phase}{amount\ of\ component\ in\ mobile\ phase} = \frac{n_S}{n_M} \qquad\qquad \text{Equation 4}$$

Where n_S is the number of molecules in the stationary phase and n_M is the number of molecules in the mobile phase.
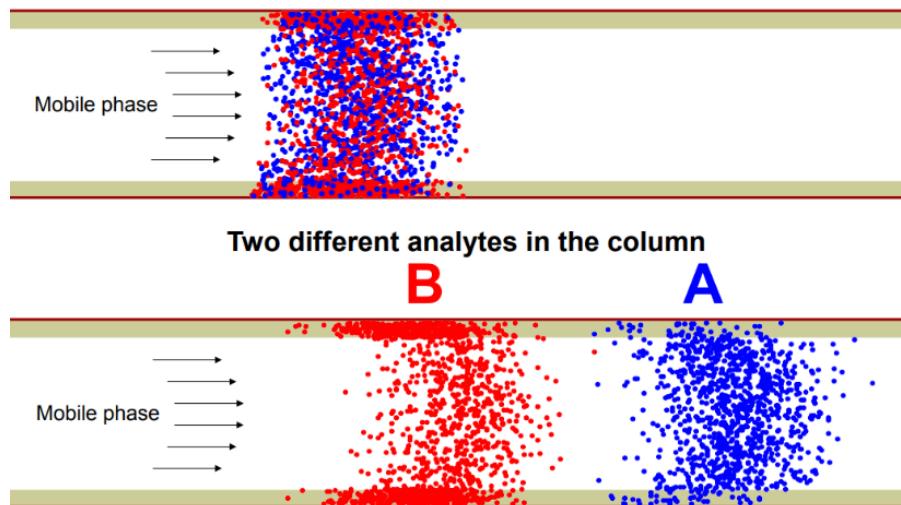
Figure 11: Illustration of a capillary column with two analytes, A and B, separating in the column based on their affinities to the stationary phase. Adapted from a lecture by Svein Mjøs.

Compounds with higher retention spends more time in the stationary phase and is by this, separated from compounds with lower retention. This is shown in Figure 11, where the stationary phase is marked in beige. If k = 0, the compounds move with the same speed as the mobile phase.
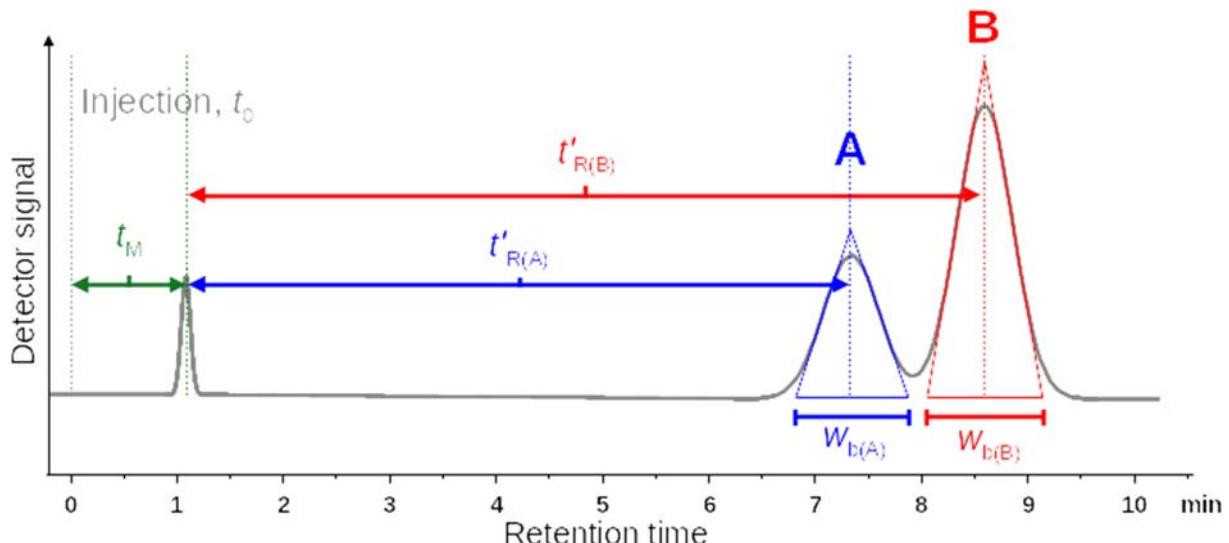
Figure 12: Illustration of a chromatogram.

An illustration of a chromatogram is shown in Figure 12. The hold-up time, t_M, is highlighted in green and this is the time it takes for the inert mobile phase to elute. Adjusted retention times, t'_R, of analytes are then calculated by subtracting the hold-up time from the total retention time and given with prime to indicate that the time has been adjusted for the hold-up time (Ettre, 1993):

$$t'_R = t_R - t_M \qquad \text{Equation 5}$$

With these measurements, the retention factor, k, can be calculated by the following equation (Ettre, 1993):

$$k = \frac{t'_R}{t_M} \qquad \text{Equation 6}$$

Where t'_r is the adjusted retention time and t_M is the holdup time. The resolution between two peaks can be described by the retention times and peak width (Ettre, 1993):

18

$$R_S = \frac{\Delta t_R}{\overline{w}_b} = \frac{t_{R(B)} - t_{R(A)}}{0.5 \cdot (w_{b(A)} + w_{b(B)})} \qquad \text{Equation 7}$$

Where R_S is the chromatographic resolution between the two peaks A and B and $w_{b(A)}$ and $w_{b(A)}$ are the average peak widths at the baseline. A resolution of 1.5 is regarded as sufficient for accurate quantification. Resolution in chromatography is dictated by three factors: retention, selectivity, and efficiency. Efficiency is measured as the number of theoretical plates and is a measure of how much peaks spread compared to time spent in the column. This is based on the plate model, where the column is divided into theoretical plates and the analyte moves down the column from one plate to the next.

$$N = \left(\frac{t_R}{\sigma}\right)^2 = 16\left(\frac{t_R}{w_b}\right)^2 \qquad \text{Equation 8}$$

Where N is the plate number, σ is the peak width given as standard deviation and w_b is the peak width at the base line (4σ by definition) (Ettre, 1993). High values of N, or more plates, correspond to narrow peaks with high retention times, and ultimately better resolution. Plate height, H, is a measure of column length, L, needed per plate (Ettre, 1993):

$$H = \frac{L}{N} \qquad \text{Equation 9}$$

Selectivity in chromatography is measured by how different retention factors are (Ettre, 1993):

$$\alpha = \frac{k_B}{k_A} \qquad \text{Equation 10}$$

Where α is the separation factor. The separation factor is always calculated by dividing the k of the most retained compound by the k of the less retained compound and will by therefore never be less than 1.

The three factors affecting chromatographic resolution is summarized in the Purnell Equation. Equation 11 is colour-marked, where the different contribution of the factors is highlighted.

$$R_S = \frac{\sqrt{N_B}}{4}\left(\frac{\alpha-1}{\alpha}\right)\left(\frac{k_B}{k_B+1}\right) \qquad \text{Equation 11}$$

The first factor (green) corresponds to efficiency, the second factor (blue) corresponds to selectivity and the last factor (red) corresponds to retention.

Band broadening in chromatography is a general term for describing the widening of peaks as compounds move through the column. The band broadening leads to loss of theoretical plates (Eq. 8) and increased plate height (Eq. 9).

Four factors decide the plate height: resistance to mass transfer, longitudinal diffusion, multipath effect also known as eddy diffusion, and extra-column effects. The Van Deemter equation expresses the plate height as a function of these factors (van Deemter et al., 1956):

$$H = A + \frac{B}{u} + C \cdot u \qquad \text{Equation 12}$$

Where the A term refers to eddy diffusion, the B term refers to longitudinal diffusion, the C term refers to resistance to mass transfer and u is the mobile phase velocity.

The C term (resistance to mass transfer) "concerns the transfer of solute into and out of the stationary phase, that is, sorption and desorption" (Miller, 2005). The solute molecules that are in the stationary phase do not move, but the solute molecules in the mobile phase move ahead and broadens the zone of solute molecules (Miller, 2005). Low diffusion between the two phases will increase the C-term and increase the band broadening of the peaks.

The B term (longitudinal diffusion) is molecular diffusion because of difference of concentration of solute molecules in the mobile phase. Molecules diffuse from high concentration regions to those of

lower concentration. This term is increased with low flow rates, since less time spent in the column gives less time for this diffusion to occur (Miller, 2005).

The A term (eddy diffusion) refers to different paths a fluid can travel when flowing through a packed column. These paths have slightly different lengths and slight differences in hold-up time, and this will lead to spreading of the molecules and broadening of the peak. When using an open tubular (capillary) column, this term equals zero.

Extra column effects are not included in the Van Deemter equation because they occur outside of the column, for example in the injection or at the detector. If the molecules enter the column as a broad band, they will remain broad until eluted.

From the Van Deemter equation it is shown that higher mobile phase velocities decrease the B term but increase the C term. High diffusion between stationary phase and mobile phase is desirable, but longitudinal diffusion is not. Unfortunately, the direction of diffusion cannot be controlled but the column dimensions, such as column diameter can be controlled. In Van Deemter plots, the plate height contribution of the A, B and C terms is plotted against mobile phase velocity. The minimum indicates the optimal velocity, which gives the lowest plate height. An example of a Van Deemter plot is shown in Figure 13, where differences between carrier gases are shown.
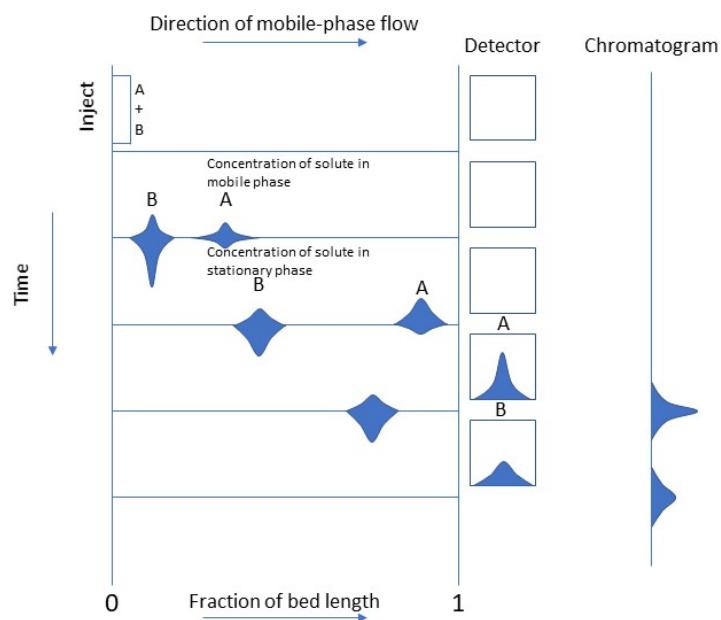
Figure 13: Schematic representation of a chromatographic process. Redrawn and adapted from: (Miller, 2005)

The general process of gas chromatography, from the injection of the analytes to the output of the signal in the software, is shown as a schematic in Figure 13.

1.4.3. Column and stationary phase
Columns used in GC are typically distinguished into two groups: open tubular columns, also known as capillary columns, and packed column. For this project, a fused silicon open tubular (FSOT) column was utilized. Characteristics of the stationary phase in GC is not as important as in high performance liquid chromatography, but it still makes an impact on the separation. When analysing FAMEs, polar stationary phases such as polyethene glycol are common. More polar FAMEs have higher affinity to the OH-groups of the stationary phase and therefore elute after less polar FAMEs.

1.4.4. Mobile phase

Mobile phase in GC is usually a choice between three gases: nitrogen (N_2), helium (He) and hydrogen (H_2). These gases are chosen for their inertness and must be very pure. The most popular choice is helium (Harris, 2015). The Van Deemter plot in Figure 14 shows the average linear velocity plotted against the theoretical plate height. Higher velocities result in lower retention times, but as the graph shows, increasing the velocity also have impact on the plate height. Increasing the carrier gas velocity (beyond optimal) results in slightly poorer resolution caused by increased plate height, but is often tolerated in return of faster analyses (Harris, 2015). These advantages matter less when programmed temperature GC (PTGC) is utilized, since the viscosity of the gas increases as the temperature rises and the flow rate decreases (if operated at constant pressure). In PTGC, the carrier gas velocity has less impact on the retention times, which are basically controlled by the temperature rate (Mjøs and Waktola, 2015).

The detector can also influence the choice of carrier gas, but in the case of a flame ionization detector, nitrogen, helium, and hydrogen all work. N_2 used as carrier gas with an FID increases its detection limits, but when H_2 or He is used, N_2 is used in the detector as a makeup gas (Miller, 2005).
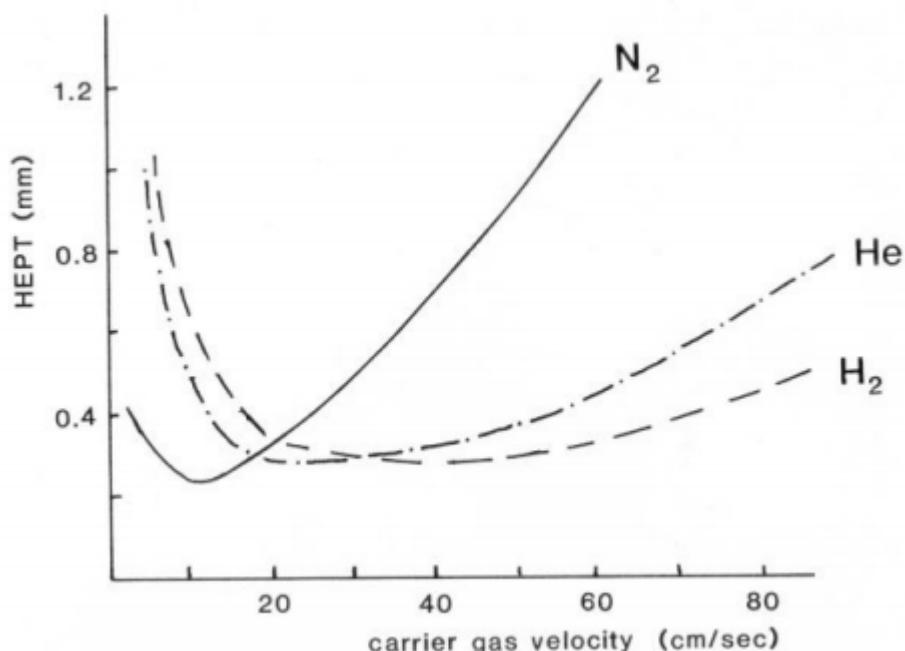
Figure 14: Plot of theoretical plate height against carrier gas velocity (Van Deemter curve) for H_2, He and N_2. Adapted from (Christie, 1989).

1.4.5. Temperature programming

Temperature programming (or programmed temperature **PT** GC) in GC is a process in which the oven temperature is increased during the run, as opposed to isothermal GC where the temperature is kept constant. PTGC allows for better separation of mixtures of compounds with large differences in boiling points, decrease in time of analysis and a lower limit of detection (Miller, 2005).

1.4.6. Injection

The "split-splitless"-injector is the most used in GC. This injector has a split that can adjust the fraction of sample going into the column. The injector has three gas flow lines: carrier gas inlet, septum purge and split flow out. When the split is open, a fraction of the sample is sent out through the split and a fraction of the sample is sent to the column. When the split is closed, referred to as "splitless", the whole sample is sent to the column.

1.4.7. Flame ionization detector

A flame ionization detector (FID) uses ions to detect compounds in the sample. A small oxygen-hydrogen flame burns the eluate to create ions. The ions are collected and make a small current, which is then amplified and sent to the data system (Miller, 2005). FID can detect almost all organic compounds, which makes it very versatile. Exceptions where FID cannot detect compounds are inorganic compounds, (H_2O, NO_2 and SO_2) and fixed gases (O_2, H_2, N_2). The last part is advantageous because it allows for the carrier gas to go through without detection. Water is often associated with producing badly tailed peaks in GC and since FID does not detect water this may also be advantageous. It is a rugged, low-cost, and easy to maintain detection method, with good stability and linearity (Miller, 2005).

1.4.8. Separation of Fatty Acids Methyl Esters in GC

The separation of FAME in GC is based primarily on boiling point. Running isothermal GC with samples that contain a large number of different FAME, will result in poor separation. Instead, the temperature program gradually increases the oven temperature. This allows for the most volatile compounds to elute first at lower temperatures and the less volatile compounds elute last at higher temperatures. Interaction with the stationary phase also affect elution. More unsaturated FAME are more polar than their saturated analogues, and with a polar stationary phase unsaturated FAME will elute later than their saturated analogues. This happens because of interaction between electrons in the double bonds and the OH-groups of the stationary phase. This is clearly illustrated by 16:1 (n-7) which elute after 16:0, despite being more volatile. Increased level of desaturation also increases polarity.

The retention patterns of FAME on polar columns can be summarized as:

1. Number of carbon dictates volatility: lower number carbon FAME elute before higher.
2. Level of saturation dictates polarity and volatility: unsaturated FAME are more volatile and more polar. Higher polarity increases affinity to stationary phase: Saturated FAME elute before its unsaturated analogue with the same number of carbons.

Samples of FA will naturally contain cholesterol. Cholesterol can cause carry-over problems when analysing FAs with GC. For this reason, an extra-long program is applied to elute cholesterol completely (Meier et al., 2006).

1.5. Quantitative analysis and internal standard

1.5.1. Internal standard

An internal standard (IS) is a compound that is added to the sample in known amounts. The internal standard must be different than the analytes, in order to compare the signal of the standard to the analytes for quantification. An internal standard should be chemically similar to the analyte, to account for matrix effects. The use of an internal standard is especially useful when the instrument response or signal can differ between runs. Since the internal standard is added to the analyte and undergo the same chemical treatment, it will account for any loss of analyte along the way. In GC, the sample amounts injected are so small that they are not reproduceable, but since the internal standard is added with a known concentration, the correct quantification of the analyte can be derived (Harris, 2015).

1.6. Statistics

1.6.1 Statistical formulas

Simple statistical formulas used for calculations of the results are listed here. Calculations related to experimental designs are introduced in Section 2.6.

Arithmetic mean:

$$\bar{x} = \frac{1}{n}\sum_{i=1}^{n} x_i \qquad \text{Equation 13}$$

Standard deviation for a sample of a population using the n-1 method:

$$s = \sqrt{\frac{\sum(x - \bar{x})^2}{(n-1)}} \qquad\qquad \text{Equation 14}$$

Relative standard deviation:

$$RSD = \frac{s}{\bar{x}} * 100 \qquad\qquad \text{Equation 15}$$

T-test used in this thesis: Independent two-sample t-test equal size and variance, where H_0: mean of both populations are equal and H_A = mean of both populations are not equal. Significance level of $\alpha = 0.05$.

1.6.2. Experimental design

A factorial design allows one to study the effect of each factor on the response value, as well as the interactions between factors. Factorial experiments vary all the factors in contrast to the one-factor-at-the-time experiments. This allows for greater efficiency and more information from fewer experiments and a lower cost. Another advantage of factorial design is its ability to detect if one factor is different for a different level of another factor.

In the setup of an experimental design, the different factor must first be determined, and the number of factors will determine how many experiments are to be performed. Each factor is given a high and a low level. The design matrix will then show all the information needed to perform the design. For example: an experimental design with two factors A and B. Both factors are given a high and low level, denoted as 1 and -1 respectively. The notation for factorial design experiments is such as L^K where L denotes the number of levels and K denotes the number of factors. In the example the resulting denotation would be a 2^2-full factorial design. This denotation also tells the user how many experiments are needed: 2^2 = 2 x 2 = 4. The next step is to set up the design matrix. The matrix is made up of k columns and contains the same number of rows as the number of experiments, in this case four. -1 and 1 are plotted into the design matrix in so-called "standard order". This method calls for alternating -1 and 1, starting with -1, in column one. Column two starts off with -1 repeating twice and alternates with two in a row of opposite signs until every place is filled. "Standard order" follows the general rule: "In general, the i-th column (X_i) starts with 2^{i-1} repeats of -1 followed by 2^{i-1} repeats of +1" (NIST/Sematech, 2003). Tables 7 and 8 show the levels and design matrix for the example.

Table 7: Levels for factors.

		Factors	
		A	B
Levels	High	1	1
	Low	-1	-1

Table 8: Design matrix example.

Experiment	A	B
1	-1	-1
2	1	-1
3	-1	1
4	1	1

A full factorial design will have no confounding patterns, or overlap, between the main effects and interactions. As the number of factors increases, a fractional factorial design is often preferred. In such a design, a subset from the full design is chosen so that the number of experiment runs are reduced. For example, a 2^{5-2} is ¼ of a full 2^5 design, and only 8 runs are required compared to the original 32. A fractional factorial design results in confounding effects or interactions, which mean they cannot be determined independently. To calculate the main effect of a factor, simply calculate the average response of all the runs of A at a high level and the average response of all the runs of A at a low level. Finally, subtract the low-level average from the high-level average.

1.6.3. Principal Component Analysis

Principal component analysis is a mathematical method used to compress large amounts of data. This method is used in explorative analysis, where the main goal is to interpret the data. It seeks to describe the systematic variation in the data with as few latent variables as possible. The latent variables used is referred to as principal components (PCs). The first principal component is a linear combination of the original variables and explains as much variation as possible. The next PC explains as much of the

remaining variation and is orthogonal to the first PC. The third PC will then explain the variation left and be orthogonal to PC1 and PC2. The number of PC that can be extracted is equal to the rank of the matrix (Nortvedt, 1996). A brief explanation of PCA is given below:

Consider a matrix **M.** The matrix **M** is centred to $\mathbf{X_c}$ by subtracting the mean $\bar{x}$ from every sample such that the origin of the coordinate system now lies on the mean. The first PC $\mathbf{p_1}$ is directed in the orientation where the samples have the most variation. The next PC $\mathbf{p_2}$ is found in a similar manner, except for the condition that it must be orthogonal to $\mathbf{p_1}$. One can keep extracting PCs in the same manner. (Nortvedt, 1996). An example of two PCs is shown in Figure 15.

To interpret results from PCA, the score vectors and loading vectors are plotted. The score plot shows information about the objects, and the loadings shows information about the variables. It is usually the two PCs that together explain the variance that is most relevant to plot together (Nortvedt, 1996). These are plotted in an xy-scatter plot, for example: scores of PC1 against scores of PC2 and loadings of PC1 against loadings against PC2. Distance between objects in a score plot is a measure of similarity, meaning that objects close in the plot are also close in the original matrix. In a loadings plot, variables that lie in the same directions are positively correlated, variables that lie in opposite directions are negatively correlated and variables that lie 90° apart are non-correlated.
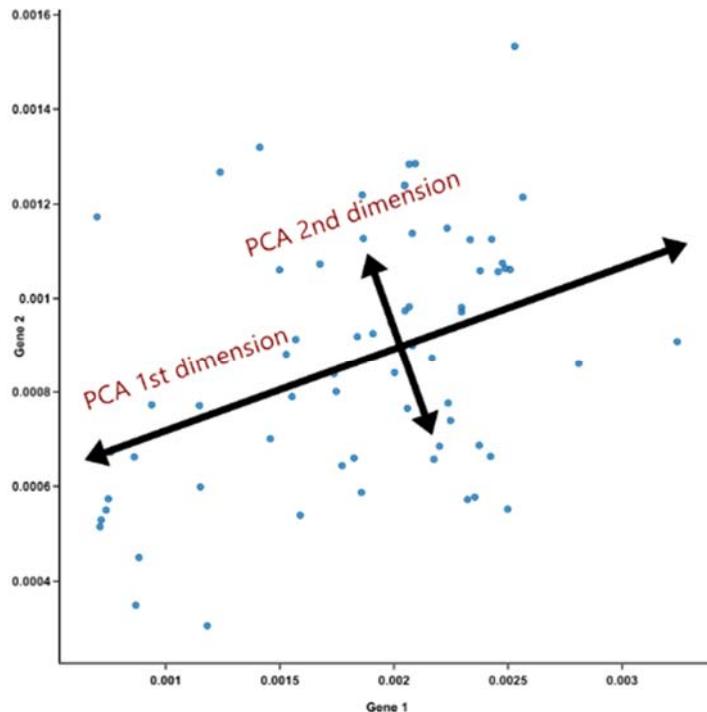
Figure 15: Example of two principal components. Adapted from: (Ngo, 2018)

2 Methods and materials

2.1. Samples

The samples were of fish caught in the North Sea in the years 2010, 2011 and 2013. Samples were frozen with liquid nitrogen in situ and thereafter stored at -80°C. The data collected per fish varies but may include length, weight, liver weight, gonad weight, gender, and additional remarks. Complete data for every individual fish can be found in Appendix II. Figure 16 shows a picture of a lesser sand eel larvae weighed in a 16 ml glass sample tube and ready for methylation.

Figure 16: Lesser sand eel larvae in sample tube.

2.2 Weighing samples

All samples were weighed directly into a 16 ml sample tube with the internal standard added in advance. Liver samples are generally fattier than muscle for most fish, and this is reflected in the aliquot weight of the two tissues. The direct methylation method calls for approximately 50 mg for liver and 100 mg for muscle.

Table 9: Target aliquot weight of liver and muscle samples.

Tissue	Aliquot weight (mg)	Internal standard used
Liver	50	IS1
Muscle	100	IS2

2.3. Internal standards

The fatty acid, 19:0 or nonadecanoic acid, was used as the internal standard. The nonadecanoic acid (as a free fatty acid) was diluted in chloroform. Two different dilutions were used (Table 10), one for higher fatty content tissue (IS1) and one for lean tissue (IS2). 19:0 was used as the internal standard because it rarely occurs in marine environments. This allows for a standard that is similar in nature to the analytes and will undergo the same chemical reactions.

Table 10: Concentrations of 19:0 internal standards.

Name	Weight 19:0 (mg)	Volume chloroform (mL)	Concentration (μg/mL)
IS1	100	10	10
IS2	10	10	1

IS2 was made by diluting IS1 by a factor of 10. The amount added to sample tubes were 100 µl regardless of the concentration. Standard added to the sample tubes were left to dry overnight, to evaporate the chloroform completely, and covered in aluminium foil to avoid dust entering the tube. 100 µl was measured using a Hamilton syringe and the syringe was washed with chloroform before and after use. Table 11 shows a list of internal standards used for the project and Table 9 shows which concentration of IS that was used for the different tissues.

Table 11: Concentrations of internal standards used for analysis.

Date	Weight 19:0 (mg)*	Volume chloroform (mL)	Concentration IS1 (µg/100 µL)	Concentration IS2 (µg/100 µL)
23.09.19	99.4	10	994	99.40
09.10.19	243.8	25	975.2	97.52
19.05.20	246.66	25	986.64	98.664

*The mass has different significant numbers because of the different balances used.

2.4. Direct methylation
The method used was a modified version of the method from Meier, S. et al (2006).

1. The sample was added 1 mL methylation reagent and put in a heating cabinet (100°C, 2 hours).
2. Half of the content in the reaction tube was evaporated. 0.5 mL distilled water and 2 mL hexane was added. The solution was homogenized and centrifuged (2000 rpm, 5 min.).
3. The upper phase (hexane) was extracted to a new 16 mL tube and added another 2 mL hexane for a second extraction.
4. The extracts were transferred to GC-vials and analysed.

Modification: the original method calls for 2 extractions of 2 mL hexane, whereas the modified method only used 1 extraction where 4 mL hexane is added.

When weighing liver samples, liquid nitrogen was utilized to keep the tissue from defrosting before entering the glass tubes. The extracted samples were stored in a freezer (-20°C) until GC-analysis was completed.

2.5. Preparing samples for gas chromatography analysis
The extracts were transferred to 1.5 mL GC-vials. A couple of test concentrations were prepared before the final analysis by GC. Fattier samples, *e.g*., saithe liver, must be more dilute than saithe muscle, and similar for fish with unknown fatty content, test concentrations are necessary.

2.6. Experimental design
The goal of the experimental design was to investigate whether any of the variables could be altered to make the method less time consuming and more efficient. Out of the three variables chosen, two of them could be considered to save time if reduced. A full (2^3) factorial design was conducted with 8 experiments by the design matrix in Table 13 and with the variables as shown in Table 12.

Table 12: High and low levels of the three variables.

	-1	+1
X1	1 hour in oven	2 hours in oven
X2	Hexane pre oven	Hexane post oven
X3	1 extraction	2 extractions

The first variable, X1, represents time spent in the heating oven. The second variable, X2, represents when the hexane was introduced to the sample tube. The third variable, X3, represents how many extractions that were performed.

Table 13: Experiment matrix with interactions.

Exp. number	Main effects			Interactions			
	X1	X2	X3	X1X2	X1X3	X2X3	X1X2X3
1	-1	-1	-1	+1	+1	+1	-1
2	+1	-1	-1	-1	-1	+1	+1
3	-1	+1	-1	-1	+1	-1	+1
4	+1	+1	-1	+1	-1	-1	-1
5	-1	-1	+1	+1	-1	-1	+1
6	+1	-1	+1	-1	+1	-1	-1
7	-1	+1	+1	-1	-1	+1	-1
8	+1	+1	+1	+1	+1	+1	+1

The amount of hexane added to all samples should be 4 ml in total. To achieve this, samples that demanded a low level of X2 and X3 were added 4 ml in one go. But samples that demanded a low level of X2 and a high level of X3 were added 2 ml hexane pre oven and 2 ml again after the first extraction. Samples that required high level of X2 and low level of X3, were added 4 ml before the oven.

The experiment with all high levels (experiment 8) was replicated 5 times to produce a standard deviation (SD) and a relative standard deviation (RSD) for the samples. The RSD is useful for getting an idea of the precision of the method. As the 5 replicates are from the same sample, they should be quite similar. An RSD of around 0.05 or less is to be expected from this method.

The design was done with samples of saithe from the North Sea caught in 2010. It was run twice, once for muscle tissue and once for liver tissue. Samples of both tissues were taken from the same specimen.

Calculating effects:

$$K_x = \frac{\sum Y(+)}{n(+)} - \frac{\sum Y(-)}{n(-)} \qquad \text{Equation 16}$$

Where K_x is the effect, Y is the response factor, and n is the number of experiments. The effect is the difference between the mean response of the experiments with high level and the experiments with low level.

$$KN_x = \frac{K_x}{(\sum Y)/n} * 100\% \qquad \text{Equation 17}$$

To compare different experiments, it is useful to normalize the effect to the mean of the response. This will show the significance of the effects relative to the mean (Meier et al., 2006).

2.7. Gas chromatography settings and equipment

Two instruments were used for analysis for this project:

1) Agilent 7890A with 7683B ALS (SSL/FID).
2) Agilent 7890B with 7693 ALS with 2 towers (2xSSL/2xFID).

Both instruments used the same GC column and temperature program. The column was a CP-WAX 52CB with length 25 m, internal diameter 0.25 mm and film thickness of 0.2 μm (Agilent p/n CP7713I). The temperature program was as follows: total run time 75 min, initial temperature 90 °C, ramp to 150 °C (30 °C/min), hold time 0 min, ramp to 240 °C (2.5 °C/min) and hold time 35 min.

Helium (99.9999%) was used as mobile phase at 1 mL/min for 45 min, followed by a flow increase to 3 mL/min which was held for 30 min. Injector and detector settings are shown in Table 14 and 15, respectively.

	Front SS Inlet He (7890B)	Back SS Inlet He (7890B)	Front SS Inlet He (7890A)
Mode:	Pulsed Splitless	Pulsed Splitless	Pulsed splitless
Heater On	280 °C	280 °C	280 °C
Pressure On	12.165 psi	13.309 psi	12.165 psi
Total Flow On	44 mL/min	44 mL/min	44 mL/min
Septum Purge Flow On	3 mL/min	3 mL/min	3 mL/min
Gas Saver On	20 After 10 min mL/min	20 after 10 min mL/min	20 after 10 min mL/min
Injection Pulse Pressure	25 psi Until 2 min	27.35 psi until 2 min	25 psi until 2 min
Purge Flow to Split Vent	40 mL/min at 2 min	40 mL/min at 2 min	40 mL/min at 2 min

Table 15: Detector settings were the same for all three detectors

	FID
Makeup	N_2
Heater on	300 °C
H_2 Flow on	35 mL/min
Air Flow on	400 mL/min
Makeup Flow on	30 mL/min

Software: OpenLab EZChrom

2.8. Quantitative analysis and calculations

2.8.1. Standards

The quantification was carried out by correcting all the peaks from the GC for the response factor and then calculating the mass of each peak through known concentration of internal standard. The calculations are shown in section 2.8.2. below. To calculate the response factor, a FAME standard with known concentrations and content was analysed, where 18:0 is used as a reference with a response factor set to 1. The response factors of the other FAME were then calculated relative to 18:0. The response factors of the FAME not present in the standard were estimated according to identity and the retention time relative to the standard FAME (Meier et al., 2006). These FAME standards were run after every 10th sample to check for instrument drift. In addition to FAME standards, cholesterol standards and blank hexane samples were run in each sequence. The cholesterol standard was useful when identifying peaks of cholesterol artefacts. For the calculation of the response factors, the averages from all the reference mixtures in the sequence were used. The FAME reference used in this project was GLC-463 (NU-CHEK-PREP) and the contents of this standard can be found in Appendix IV.

2.8.2. Peak identification

Peaks were identified by comparing retention times with a FAME standard. Retention times of peaks that were easily identified, such as 14:0, 16:0, 18:0 and 22:6(n-3), were used to make a linear regression in order to correct the retention times for the "method". This "method" had the name of every peak and a corresponding time. This lets the user setup the method for the first sample of the run, and then the method will automatically integrate the chromatograms. Minor manual tweaks and changes were necessary, as around 175 peaks were identified in the chromatograms. Areas and retention times were exported to two separate excel-files and treated further.

2.8.3. Response factors and calculations

The response factor, RF is calculated from the following equation:

$$RF_A = \frac{A_A}{A_{IS}} * \frac{m_{IS}}{m_A} \qquad \text{Equation 18}$$

Where RF_A is the response factor for analyte A, A_A is the area of analyte, A_{IS} is the area of the internal standard, m_{IS} is the mass of internal standard and m_A is the mass of the analyte, A.

Equation 19 was used to calculate mass of fatty acid once the response factors were known:

$$m_A = \frac{A_A}{A_{IS}} * \frac{m_{IS}}{RF_A} \qquad \text{Equation 19}$$

Correcting the integration value for the response factor was done with the following equation:

$$A_{corr} = \frac{A_A}{RF_A} \qquad \text{Equation 20}$$

Normalising integration values for total amount of fatty acid was done according to the following equation:

$$A_{norm} = \frac{A_{corrected}}{\sum FA_{corrected}} * 100 \qquad \text{Equation 21}$$

Where A_{norm} is the corrected integration value as % of sum FAs and $\sum FA_{corrected}$ is the sum of all integration values of relevant FAs.

Calculating mass of total fatty acid in sample was done by:

$$Amount\ FA\ in\ sample(\mu g) = \frac{\sum FA_{corrected}}{A_{IS19:0(corrected)}} * m_{IS19:0(\mu g)} \qquad \text{Equation 22}$$

Mass of total fatty acid in sample per wet weight was calculated by:

$$Amount\ of\ FA\ in\ sample\ (mg)/wet\ weight(100mg) = \frac{\frac{amount\ FA_{Sample}}{1000}}{Sample\ weight\ (mg)} * 100 \qquad \text{Equation 23}$$

2.8.4. Applying statistical methods in Excel and Sirius

Principal component analysis (PCA) was executed in the software SIRIUS. All FA contributing > 0.5 %, in addition to some FA that are relevant FATM, were used in PCA. The data was weighted and mean centred in the software prior to applying PCA. This method was applied to results from direct methylation and the results from the factorial design. PCA was used for explorative analyses of the data and to investigate similarities and differences in FA profiles of the different species. FATM profiles was also investigated using these methods.

In a PCA, the variables with the highest absolute standard deviation will have the largest influence. Thus, in fatty acid profiles with large differences in the abundance, the PCA may only explain the relationships between the most abundant FA. This problem is solved, in some degree, by weighting the variables. Common practice is to use a weighting technique called "standardisation", where the values are divided by the standard deviation of the variable, giving every variable a standard deviation of 1. This leads to all the variables having the same weight in the PCA.

The variation of each variable is a result of both biological variation and uncertainty of the analysis. Since the same internal standard and analytical equipment is used for all FAs, one can assume that uncertainty (measured as relative standard deviation) is approximately equal for every variable. If the uncertainty related to the analysis is equal for every variable, variables that carries information about biological differences must have a higher total standard deviation, since:

$$s_{tot}^2 = s_{biological}^2 + s_{analytical}^2 \qquad \text{Equation 24}$$

It is therefore appropriate to give the variables with the highest relative standard deviation most weight. This is achieved by dividing the values for each variable by the variable mean, which converts the standard deviation to relative standard deviation (RSD). The variables with the highest RSD are then given the most weight in the PCA.

In this work, standardization was applied in the method evaluation based on experimental design. All the samples were in that case from the same fish and tissue, so there was no biological variation. Division by mean was applied in studies where samples of different biological origin were compared.

3. Results

3.1. Fish measurements

Conditioning factors, hepatosomatic index (HSI) and gonadosomatic index (GSI) for all the fish is shown in Table 16. HSI and GSI values showing only +/-, and no values indicate that the liver or gonad weight was not measured, and so calculations were not possible.

Fulton's conditioning factor has an average of 0.8 ± 0.3 for all the fishes, with the highest value of 1.6 ± 0.1 for Norway redfish and the lowest value of 0.1 ± 0.03 for garfish. This shows that there is large variation for the factor, both between the species, but there is also variation within each species. HSI has an average of 3.9 ± 2.7, with the highest value of 10.6 ± 2.2 for saithe and the lowest value of 1.3 ± 0.5 for lemon sole. HSI is the percentage the liver weight contributes to the total weight of the fish. GSI has an average of 3.6 ± 3.5, with the lowest value of 0.3 ± 0.2 for saithe and the highest value of 8.2 ± 5.6 for hake. GSI is the weight ratio between the gonad and the rest of the body, in percentage.

Table 16: Fulton's conditioning factor, hepatosomatic index and gonadosomatic index for the fish analysed.

Species	n	Year	Length (cm)	Weight (g)	Liver weight (g)	Gonad weight (g)	Fulton	HSI	GSI
Cod fish									
Silvery pout	10	2010	9 ± 1	6 ± 1	±	±	0.9 ± 0.1	±	±
Norway pout	10	2010	17 ± 1	38 ± 5	4 ± 1	±	0.8 ± 0.1	9.7 ± 2.6	±
Poor cod	10	2010	17 ± 1	39 ± 8	±	±	0.8 ± 0.1	±	±
Blue whiting	10	2011	23 ± 1	73 ± 6	3 ± 1	±	0.6 ± 0.04	4.4 ± 1.9	±
Whiting	10	2010	39 ± 6	556 ± 362	14 ± 7	31 ± 50	0.8 ± 0.1	2.5 ± 1.2	3.1 ± 3.6
Saithe	10	2010	76 ± 12	4442 ± 2489	480 ± 303	14 ± 11	1 ± 0.1	10.6 ± 2.2	0.3 ± 0.2
Pollack	10	2011	67 ± 6	3165 ± 649	142 ± 47	27 ± 26	1 ± 0.1	4.6 ± 1.6	0.9 ± 1
Flatfish									
Lemon sole	10	2013	29 ± 2	249 ± 59	3 ± 1	±	1 ± 0.1	1.3 ± 0.5	±
Common dab	10	2013	28 ± 2	253 ± 53	9 ± 2	±	1.1 ± 0.1	3.7 ± 0.4	±
Megrim	10	2010	40 ± 4	729 ± 213	11 ± 5	±	1.2 ± 0.2	1.4 ± 0.4	±
European plaice	10	2010	42 ± 4	843 ± 269	13 ± 5	±	1.1 ± 0.1	1.6 ± 0.4	±
Cartilaginous fish									
Blackmouth catshark	10	2013	58 ± 8	602 ± 272	53 ± 31	±	0.3 ± 0.04	8.1 ± 2.4	±
Spiny dogfish	6	2013	77 ± 5	1913 ± 346	±	±	0.4 ± 0.02	8.7 ± 2.1	±
Thorny skate	9	2013	40 ± 4	523 ± 167	17 ± 10	12 ± 8	0.8 ± 0.2	3 ± 1	±
European hake	10	2010	73 ± 8	2654 ± 933	93 ± 55	223 ± 220	0.7 ± 0.04	3.2 ± 0.9	8.2 ± 5.6
Scorpaenidae									
Norway redfish	10	2011	23 ± 3	207 ± 82	169 ± 55	±	1.6 ± 0.1	±	±
Grey gurnard	10	2010	35 ± 2	380 ± 45	9 ± 4	±	0.9 ± 0.1	2.3 ± 0.9	±
Anarhichadidae									
Atlantic wolffish	8	2013	65 ± 13	3824 ± 2425	129 ± 109	45 ± 63	1.1 ± 0.1	3 ± 1.4	1.9 ± 2.3
Callionymidae									
Spotted dragonet	10	2011	10 ± 2	7 ± 2	±	±	0.7 ± 0.3	±	±
Lotidae									
Four bearded rockling	1	2011	20 ± 1	28 ± 9	±	±	0.3 ± 0.1	±	±
Phycidae									
Greater fork-beard	2	2011	26 ± 8	140 ± 127	16 ±	±	0.7 ± 0.1	7.1 ±	±
Pelagic fish									
Atlantic mackerel	10	2010	32 ± 2	298 ± 67	5 ± 1	2 ± 2	0.9 ± 0.1	1.8 ± 0.2	0.6 ± 0.4
Atlantic horse mackerel	10	2010	37 ± 2	454 ± 72	9 ± 3	14 ± 9	0.9 ± 0.1	2 ± 0.5	3.4 ± 2.3
Atlantic herring	10	2010	30 ± 2	227 ± 43	4 ± 2	16 ± 22	0.8 ± 0.1	1.7 ± 0.6	6.0 ± 7.0
Garfish	7	2013	60 ± 5	270 ± 70	9 ± 1	2 ± 2	0.1 ± 0.03	3.4 ± 1	0.7 ± 0.4
Argentinidae									
Greater Argentine	10	2010	27 ± 1	141 ± 14	2 ± 0	±	0.7 ± 0.1	1.3 ± 0.3	±
Argentine	10	2010	20 ± 1	45 ± 8	±	3 ± 0	0.6 ± 0.1	±	6.9 ± 2.3
Ammodytidae									
Greater sand eel	1	2011	95 ±	2 ±	2 ±	±	0.3 ±	2.1 ±	±
Lesser sand eel	4	2013	22 ± 2	30 ± 7	±	±	0.3 ± 0.02	±	±
Lesser sand eel (larvae)	10	2013	3-5						
							Average	**0.8 ± 0.3**	**3.9 ± 2.7**	**3.6 ± 3.5**

3.2. Experimental design

Normalized main effects and interactions were calculated for muscle and liver samples. The results are shown in Table 17 and the yields of all the experiments shown in Table 18. Complete results are found in Appendix I. From the validation of this method, conducted by Meier et al. (2006), time spent in oven had no significant effect in any of the tissues analysed with the levels chosen to 1 or 3 hours, and the method showed overall robustness of the direct methylation procedure. Normalised effects are calculated for six different responses: total FA, total SFA, total MUFA, total PUFA, 20:5(n-3) and 22:6(n-3) (all responses given as mg/100 mg wet weight).

Table 17: Calculated effects from the experimental design.

Normalised effects KN$_x$

	X1 Oven time	X2 Hexane	X3 Extractions	X1X2	X1X3 Interactions	X2X3
*						
Total FA						
Liver	**4.12**	1.67	2.48	-2.63	0.42	-0.43
Muscle	-1.57	-0.32	-1.08	-0.90	-1.20	-1.69
Total SFA						
Liver	**3.89**	1.86	3.04	-2.76	0.66	-0.70

Muscle	-1.57	-0.32	-1.08	-0.90	-1.20	-1.69
Total MUFA						
Liver	**3.96**	1.76	2.54	-2.61	0.50	-0.73
Muscle	-3.06	-0.45	0.51	-2.12	-5.13	-1.51
Total PUFA						
Liver	**4.43**	1.42	1.99	-2.58	0.16	0.17
Muscle	-1.21	-0.45	-1.49	-0.85	-0.34	-1.86
20:5 (n-3)						
Liver	**4.50**	1.57	1.94	-2.64	0.16	0.27
Muscle	-3.22	1.21	-2.99	-0.48	2.12	-1.64
22:6 (n-3)						
Liver	**4.59**	1.63	2.48	-3.06	0.17	-0.04
Muscle	-0.39	**-5.24**	-3.40	-1.56	-2.20	-6.21

*The responses Total FA, SFA, MUFA, PUFA, 20:5(n-3) and 22:6(n-3) are mg FA/100 mg wet weight sample. Significant effects are marked in bold face.

Table 18: Yield of total FA for the resulting experiments of the design for liver and muscle samples.

Experiment	X1	X2	X3	X1X2	X1X3	X2X3	Total FA liver	Total FA muscle
1	-1	-1	-1	1	1	1	53.30	0.59
2	1	-1	-1	-1	-1	1	61.34	0.60
3	-1	1	-1	-1	1	-1	59.41	0.62
4	1	1	-1	1	-1	-1	60.28	0.60
5	-1	-1	1	1	-1	-1	56.71	0.62
6	1	-1	1	-1	1	-1	64.91	0.59
7	-1	1	1	-1	-1	1	60.94	0.60
8	1	1	1	1	1	1	63.66	0.56
						Mean	60.07	0.60
						SD	3.71	0.02
						RSD	6.17	3.21

Total FA given as mg FA/100 mg wet weight.

With regards to the responses, X1 was the only significant main effect. X1 has a normalized effect of 4.12 for liver samples. The average yields of experiments with the low levels and high levels for X1, was 57.59 ± 3.35 and 62.55 ± 2.12 mg FA/100 mg wet weight, respectively, for liver samples. A student t-test ($\alpha = 0.05$) found the difference to be statistically significant, with a p-value of 0.047. For the muscle samples, the experiments with the low levels and the high levels of X1 yielded 0.61 ± 0.02 and 0.59 ± 0.02 mg FA/100 mg wet weight, respectively. The difference between the levels for muscle samples was not statistically different with a p-value of 0.184 from a student's t-test ($\alpha = 0.05$).

The two other main effects, X2 and X3 was insignificant with regards to the responses total FA, total SFA, total MUFA, total PUFA and 20:5(n-3), but X2 showed a significant effect of -5.24 for 22:6(n-3).

3.3. Direct methylation: Amount of FA in tissue

Amount of FA and cholesterol (mg per 100 mg wet weight) for every species is given in Table 19. The values are given as means of the population, except where no measurement uncertainty is given, which means that the population is equal to 1. Included in the results are values from previous work from a bachelor's project in 2017.

The results show clearly that most fish store small amounts of fat in their muscle tissue, except mackerel, herring and horse mackerel which store 9.61 ± 6.92, 4.73 ± 2.88 and 2.44 ± 1.22 mg/100 mg wet weight, respectively. The rest of the fish analysed store around 1-2% fat in their muscle tissue, with fat storage

varying in their livers, up to about 70% for saithe and Norway pout, but biological variation within species occurs. The poor cod stores relativity low amounts of fat in their liver, compared to the other cod fish.

Table 19: Amount of FA and cholesterol per 100 mg wet weight in all species after GC-analysis.

Species	n	Amount of FA (mg/100mg wet weight)						Amount of Chol (mg/100mg wet weight)					
		Muscle			Liver			Muscle			Liver		
Silvery pout[a]	10	0.5	±	0.1	39.8	±	13.4	0.11	±	0.01	0.13	±	0.02
Norway pout[a]	10	0.70	±	0.13	70.79	±	5.35	0.06	±	0.01	0.18	±	0.03
Poor cod	10	0.47	±	0.05	12.69	±	5.67	0.04	±	0.00	0.25	±	0.04
Blue whiting	10	0.62	±	0.05	43.20	±	12.82	0.05	±	0.01	0.26	±	0.03
Whiting[a]	10	0.45	±	0.06	39.84	±	13.45	0.05	±	0.00	0.39	±	0.06
Saithe[a]	10	0.62	±	0.10	70.14	±	5.17	0.57	±	0.91	1.97	±	1.29
Pollack	10	1.00	±	1.14	51.97	±	10.85	0.19	±	0.43	0.28	±	0.04
Lemon sole	10	0.45	±	0.04	3.58	±	1.63	0.05	±	0.01	0.21	±	0.04
Common dab	10	n.d.[b]			15.09	±	6.46	n.d.			0.54	±	0.15
Megrim	10	1.48	±	1.68	24.66	±	9.28	0.06	±	0.01	1.19	±	0.41
European plaice[a]	10	0.47	±	0.09	8.73	±	5.84	0.05	±	0.01	0.68	±	0.34
Blackmouth catshark	10	0.71	±	0.33	53.65	±	10.72	0.05	±	0.01	0.46	±	0.09
European hake[a]	6	0.83	±	0.31	36.13	±	10.81	0.04	±	0.01	0.31	±	0.11
Spiny dogfish	9	1.79	±	0.75	37.73	±	6.00	0.04	±	0.01	0.56	±	0.26
Thorny skate	10	0.44	±	0.04	16.64	±	10.76	0.04	±	0.01	0.37	±	0.20
Norway redfish	10	0.83	±	0.36	15.67	±	4.45	0.05	±	0.01	0.78	±	0.34
Grey gurnard	10	1.51	±	0.77	13.94	±	9.55	0.05	±	0.01	0.41	±	0.13
Atlantic wolffish	8	0.71	±	0.27	14.82	±	6.47	0.05	±	0.01	0.29	±	0.11
Spotted dragonet	10	0.63	±	0.16	11.85	±	13.49	0.06	±	0.01	0.29	±	0.07
Four bearded rockling	2	n.d.			11.71	±	2.13	n.d.			0.29	±	0.06
Greater fork-beard	1	n.d.			4.49	±		n.d.			0.35	±	
Atlantic mackerel	10	9.61	±	6.92	10.05	±	4.85	0.06	±	0.02	0.30	±	0.05
Atlantic horse mackerel	10	2.44	±	1.22	9.06	±	2.46	0.05	±	0.01	0.23	±	0.03
Atlantic herring	10	4.73	±	2.88	13.37	±	4.82	0.07	±	0.01	0.53	±	0.18
Garfish	7	1.27	±	0.55	7.58	±	4.49	0.12	±	0.03	0.33	±	0.04
Greater Argentine	10	0.96	±	0.37	7.49	±	1.19	0.08	±	0.02	0.28	±	0.04
Argentine	10	0.91	±	0.29	4.39	±	1.02	0.09	±	0.02	0.34	±	0.08
Greater sand eel	1	n.d.			38.72	±		n.d.			1.43	±	
Lesser sand eel	4	n.d.			18.17	±	11.39	n.d.			0.62	±	0.20
Lesser sand eel* (larvae)	10	11.65	±	2.14				1.60	±	0.16			

[a]Results included from the 2017 bachelor's projects of Sigurd Korsnes, Marie Syverstad and Charlotte Nakken. [b]Not determined. *Whole fish analysed.

Amounts of cholesterol seems to be very similar for all species, which may reflect the role that cholesterol has as an essential part of cell membranes. The levels are slightly higher for liver samples, with an average 0.43 ± 0.28 mg/100 mg wet weight, compared to the muscle samples with an average of 0.09 ± 0.11 mg/100 mg wet weight. Larvae of greater sand eel was not included for this average, as it was analysed as a whole.

3.4. Fatty acid profiles
FA profiles are displayed with values reported as % of total FA, values given as means of the populations. 85 FAs were identified from GC-analysis and used to calculate total FA content, and the complete compositions can be found in Appendix III. For illustration purposes, the fish have been grouped into six different groups. FA profiles of each group is presented in two bar charts, one for liver samples and one for muscle samples. The FA profiles contain 24 FAs, most of which account for > 0.5 % of total FA and some FAs contributing less than 0.5% have been included for use as FATMs. Table

20 shows the FAs used for the profiles. For some of the FATMs used, many of the FAs included are insignificant contributions to total FA, and so they have been calculated from the entire composition and the FAs are not included in the profiles. Bacterial FATMs, for example, contain many insignificant FA, with respect to total FA contribution. Tables of FA profiles for each species is shown in Table 21 and 22, for liver and muscle samples, respectively.

Figure 17 – Figure 22 shows the FA profiles of all the species, grouped into six categories. Bar charts are not ideal for displaying differences and similarities when the number of objects and variables increases, which is one reasons for grouping the fish into categories, enabling quick comparison of FA profiles of a few number of fish. The two profile charts of cod fish are examples of this, as the muscle profiles are quite uniform, so the differences become more apparent, as opposed to the liver profiles where there are larger differences. These differences and similarities become more apparent when the data matrix is subject to a PCA.

Table 20: FAs included in the profiles.

Fatty acids
14:0
16:0
18:0
16:1(n-9)
16:1(n-7)
18:1(n-11)
18:1(n-9)
18:1(n-7)
20:1(n-11)
20:1(n-9)
22:1(n-11)
22:1(n-9)
24:1(n-9)
18:2(n-6)
20:4(n-6)
22:4(n-6)
22:5(n-6)
18:3(n-3)
18:4(n-3)
20:4(n-3)
20:5(n-3)
22:5(n-3)
22:6(n-3)
24:5(n-3)

Cod fish: Figure 17 shows FA profiles of the cod fish, for liver and muscle samples. Muscle FA profiles are very similar to each other for cod fish. The dominant FAs for cod fish muscle are 16:0, 18:1(n-9), 20:5(n-3) and 22:6(n-3). Results from DM (Table 19) show that the % of FA in muscle for cod fish are low in fatty content (<1%). Lean muscle tissue is generally low in energy storing lipids such as TAG and WE. Silvery pout has relatively low amount of 22:6(n-3), compared to the other cod fish for muscle samples. FA profiles of the livers from cod fish are more diverse in FA, and since up to levels 70% wet weight of liver samples were FA content, this is to be expected. Liver profiles shows a general trend that is quite similar for all the cod fish but there are some differences within the FAs. Poor cod have higher levels of 20:5(n-3) and 22:6(n-3), and low levels of 22:1(n-11) and 20:1(n-9), compared to the other fish. Poor cod also have elevated levels of 18:1(n-7) and 20:4(n-6). Silvery pout and Norway pout contain the highest levels of 22:1(n-11) and 20:1(n-9), which are the main *Calanus* FATMs. Saithe is separated from the other cod fish in terms of 18:1 (n-9) levels, with relatively high amounts, and the two pouts have relatively low values here.

Pelagic fish: Figure 18 shows the FA profiles for the pelagic fish. The muscle samples of the pelagic fish are not as similar to each other as those of the cod fish. Results from DM showed that the pelagic fish store more fat in their muscle and this may be a result of that. FA profiles of pelagic fish for the muscle samples shows some of the same trends as the cod fish, relatively high levels of 22:6(n-3) compared to 20:5(n-3), and high levels of 16:0. Levels of 22:1(n-11) and 20:1(n-9) are higher in this group than for the cod fish muscles (except garfish), which can be a result of generally higher fatty content in the pelagic muscle samples, and so more its diet will be reflected compared to leaner muscle tissues. Atlantic mackerel is the fish in this dataset with the fattiest muscle tissue, with 9.62 ± 6.2 mg FA/100mg wet weight. As seen in the profiles of the cod fish (Figure 17), the differences for pelagic fish are larger within the liver samples than within the muscle samples. 22:6(n-3) levels in the livers of the pelagic group are similar to those of cod fish, garfish and herring have higher levels than the other. Garfish, mackerel, and horse mackerel have higher values of 18:1(n-9) in the liver than the other fish in the pelagic group, and most of the cod fish.

Flatfish and other benthic fish: Figure 19 shows the FA profiles of the group flatfish and other benthic fish. This group is comprised of known benthic fish. This group, much like the pelagic group, is comprised of different types of fish, and bar charts shows that there are some differences between them. The liver samples are relatively low in 22:6(n-3), except for lemon sole, and they have relatively high levels of 16:0, 16:1(n-7) and 18:1(n-9). Wolffish has higher levels of 20:5(n-3) than 22:6(n-3) in the liver samples, which could indicate more diatoms compared to dinoflagellates in its diet. Megrim shows

higher levels of 16:1(n-7), which is also a typical diatom FATM. The high levels of 18:1(n-9) could indicate that these fish feed on Chlorophyceae (green algae). The liver samples have low levels of the *Calanus* FATMs 22:1(n-11) and 20:1(n-9). The muscle samples show some of the same trends as the cod fish, and are dominated by 16:0, 18:1(n-9), 20:5(n-3) and 22:6(n-3), with some of the fish showing relatively high levels 20:4(n-6).

Mesopelagic fish: Figure 20 shows the profiles of the two mesopelagic fish. This group only contains the two Argentines: Greater argentine and argentine. Although in the same family, these fish are not that similar in terms of FA profiles, as the greater argentine is much more similar to the benthic fish and the argentine is more similar in profile to the poor cod, with higher levels of 20:4(n-6). These types of fish feed near the seabed, which may explain why the liver FA profile of the greater argentine is so similar to that of the benthic fish (Staby and Salvanes, 2019).

Cartilaginous fish: Figure 21 shows the profiles for the cartilaginous fish. Blackmouth catshark and spiny dogfish are quite similar to cod fish in terms of FA profile of the liver, and is dominated by *Calanus* FATM, unlike the thorny skate that have higher levels of 22:6(n-3) and low amounts of *Calanus* FATM. Spiny dogfish feed on juvenile cod fish and herring (Havforskningsinstituttet, 2018), which may reflect why the FA profile is so similar to that of the cod fish. The thorny skate liver has higher levels of 20:4(n-6), similar to the flatfish sole and plaice and the benthic wolffish, which is not surprising as skates usually are benthic fish.

Miscellaneous fish: FA profiles of the last group miscellaneous fish are shown in Figure 22. FA profiles for this group are, unsurprisingly, not all that similar to each other, since they are fish of different families, types and habitats. The group has more species included for liver samples than for muscle samples, which is unfortunate for the results, as comparison between muscle and liver tissue is not possible. However, most fish stores most of their fats in their liver and information about FATM coming through their diets will most likely be found in this tissue (Dalsgaard et al., 2003). Given that these fish do not store fat in the muscle as seen with the mackerel, the liver samples alone could still elude information about their diets. This group contains a very interesting species: larvae of lesser sand eel, which is a prey for many of the other species and was found whole inside the gut of the spiny dogfish that was analysed. The complete larvae were analysed, and for this reason, this species is included in plots for both the liver samples and the muscle samples. The larvae have higher levels of 22:6(n-3) than the other fish in the group, but when considering that the entire fish was analysed, this may be deceiving when compared to pure muscle and liver samples. Spotted dragonet, fourbearded rockling and greater fork beard have high levels of 20:4(n-6) in the liver, similar to the previously mentioned flatfish, wolffish, argentine and skate. The same three fish also have very low levels of *Calanus* FATMs, which could indicate that they feed on the seabed.

Table 21: FA profiles for liver samples. Amount of FA given as mg FA/100 mg wet weight. FAs given as % of total FA.

Species	Silvery pout	Norway pout	Poor cod	Blue whiting	Whiting	Saithe	Pollack	Lemon sole	Common dab	Megrim	European plaice	Blackmouth cathshark	European hake
LIVER													
Population	10	10	10	9	10	10	10	10	10	10	10	10	10
Amount of FA	59.0 ± 7.7	70.8 ± 5.4	12.69 ± 5.67	43.20 ± 12.82	39.8 ± 13.4	70.1 ± 5.2	51.97 ± 10.85	3.58 ± 1.63	15.09 ± 6.46	24.66 ± 9.28	8.7 ± 5.8	53.65 ± 10.72	36.1 ± 10.8
14:0	5.05 ± 0.27	5.77 ± 0.32	2.23 ± 0.43	4.98 ± 0.81	5.28 ± 1.00	4.33 ± 0.83	3.73 ± 0.52	3.30 ± 0.89	2.44 ± 0.20	6.09 ± 0.49	4.53 ± 0.64	4.58 ± 0.81	6.87 ± 0.52
16:0	11.07 ± 0.96	11.04 ± 0.89	14.06 ± 1.38	15.32 ± 1.88	12.05 ± 0.69	14.69 ± 1.20	13.10 ± 0.73	17.15 ± 2.77	19.19 ± 2.42	12.13 ± 0.87	21.78 ± 2.83	13.18 ± 0.50	14.28 ± 0.94
18:0	1.79 ± 0.28	1.90 ± 0.33	4.33 ± 0.75	2.17 ± 0.63	2.42 ± 0.64	3.18 ± 0.51	3.39 ± 0.34	3.05 ± 1.33	1.25 ± 0.39	1.25 ± 0.24	1.82 ± 0.34	1.93 ± 0.31	1.33 ± 0.16
∑SFA	19.25 ± 1.28	19.83 ± 1.13	24.76 ± 1.52	24.38 ± 1.95	21.42 ± 1.44	23.39 ± 1.24	21.54 ± 0.90	27.78 ± 2.33	24.05 ± 2.51	20.85 ± 0.89	30.98 ± 2.09	21.97 ± 0.61	24.33 ± 1.34
16:1 (n-9)	0.17 ± 0.02	0.18 ± 0.03	0.51 ± 0.07	0.18 ± 0.03	0.45 ± 0.13	0.23 ± 0.04	0.30 ± 0.08	0.87 ± 0.36	0.84 ± 0.61	0.60 ± 0.17	0.61 ± 0.07	0.22 ± 0.03	0.31 ± 0.04
16:1 (n-7)	2.86 ± 0.21	4.07 ± 0.58	4.60 ± 0.49	4.67 ± 0.32	4.05 ± 0.93	4.46 ± 0.49	5.26 ± 0.42	8.36 ± 6.25	21.96 ± 5.09	9.39 ± 1.81	17.34 ± 5.08	6.31 ± 0.53	5.18 ± 0.53
18:1 (n-9)	5.65 ± 1.00	4.81 ± 0.60	10.97 ± 1.82	10.29 ± 2.72	8.06 ± 1.44	15.08 ± 5.58	11.78 ± 2.14	9.08 ± 2.96	21.86 ± 2.30	16.75 ± 1.32	17.08 ± 4.43	11.80 ± 1.19	7.25 ± 1.76
18:1 (n-7)	0.93 ± 0.08	1.38 ± 0.19	5.62 ± 0.61	2.76 ± 0.63	2.02 ± 0.25	3.22 ± 1.00	3.01 ± 0.32	3.45 ± 0.42	3.08 ± 0.87	2.94 ± 0.42	4.27 ± 0.42	2.99 ± 0.95	1.82 ± 0.26
20:1 (n-11)	1.45 ± 0.09	1.88 ± 0.25	0.89 ± 0.19	1.98 ± 0.45	2.63 ± 0.40	1.65 ± 0.40	2.00 ± 0.35	0.22 ± 0.11	0.29 ± 0.05	1.24 ± 0.22	0.69 ± 0.17	1.82 ± 0.16	3.10 ± 0.57
20:1 (n-9)	11.34 ± 0.73	12.67 ± 1.75	1.55 ± 0.58	8.29 ± 1.96	9.81 ± 1.62	7.85 ± 1.89	9.23 ± 1.02	0.57 ± 0.25	1.46 ± 0.43	5.76 ± 0.79	2.57 ± 0.23	7.82 ± 1.26	11.30 ± 1.38
22:1 (n-11)	23.27 ± 2.31	16.37 ± 2.21	0.77 ± 0.73	14.62 ± 3.66	11.10 ± 2.58	8.44 ± 2.29	10.14 ± 1.16	0.23 ± 0.14	1.29 ± 0.63	4.27 ± 1.42	0.37 ± 0.08	11.79 ± 2.85	10.83 ± 2.49
22:1 (n-9)	1.15 ± 0.12	0.88 ± 0.08	0.16 ± 0.09	0.89 ± 0.20	0.78 ± 0.23	0.60 ± 0.12	0.60 ± 0.09	0.18 ± 0.08	0.45 ± 0.12	0.75 ± 0.17	0.52 ± 0.08	1.08 ± 0.21	0.94 ± 0.19
24:1 (n-9)	0.98 ± 0.14	0.59 ± 0.07	0.70 ± 0.50	0.94 ± 0.32	0.77 ± 0.31	0.60 ± 0.15	0.45 ± 0.09	1.52 ± 0.47	0.77 ± 0.25	0.49 ± 0.12	0.81 ± 0.41	0.73 ± 0.08	0.91 ± 0.17
∑MUFA	49.83 ± 1.85	45.60 ± 2.70	30.07 ± 2.58	47.25 ± 4.19	44.78 ± 3.34	45.12 ± 3.13	46.93 ± 1.89	28.67 ± 8.80	56.01 ± 3.89	48.80 ± 2.94	48.43 ± 8.40	48.23 ± 2.42	45.83 ± 3.00
18:2 (n-6)	2.23 ± 0.20	1.38 ± 0.16	1.05 ± 0.08	1.30 ± 0.10	1.44 ± 0.22	1.30 ± 0.19	1.28 ± 0.11	0.67 ± 0.17	0.90 ± 0.23	1.05 ± 0.26	0.23 ± 0.05	1.22 ± 0.11	1.75 ± 0.33
20:4 (n-6)	0.28 ± 0.02	0.30 ± 0.05	2.47 ± 0.49	0.68 ± 0.16	0.56 ± 0.34	0.47 ± 0.09	0.51 ± 0.03	3.63 ± 1.33	0.51 ± 0.13	0.47 ± 0.13	2.08 ± 0.98	0.59 ± 0.20	0.62 ± 0.09
22:4 (n-6)	0.13 ± 0.03	0.11 ± 0.02	0.50 ± 0.11	0.22 ± 0.04	0.49 ± 0.29	0.06 ± 0.05	0.13 ± 0.03	0.98 ± 0.22	0.48 ± 0.08	0.45 ± 0.18	0.74 ± 0.22	0.34 ± 0.12	0.32 ± 0.10
22:5 (n-6)	0.12 ± 0.01	0.11 ± 0.02	0.37 ± 0.05	0.18 ± 0.02	0.25 ± 0.07	0.18 ± 0.05	0.18 ± 0.02	0.64 ± 0.36	0.12 ± 0.03	0.19 ± 0.05	0.26 ± 0.12	0.40 ± 0.07	0.36 ± 0.11
18:3 (n-3)	1.44 ± 0.07	1.14 ± 0.27	0.49 ± 0.05	0.94 ± 0.14	1.03 ± 0.20	0.94 ± 0.25	0.83 ± 0.10	0.16 ± 0.06	0.33 ± 0.09	0.67 ± 0.19	0.08 ± 0.02	0.72 ± 0.12	1.13 ± 0.15
18:4 (n-3)	4.92 ± 0.19	4.76 ± 1.07	0.72 ± 0.17	2.30 ± 0.66	2.35 ± 0.84	2.50 ± 1.04	2.56 ± 0.25	0.33 ± 0.08	0.99 ± 0.29	1.43 ± 0.34	0.14 ± 0.08	1.36 ± 0.35	1.95 ± 0.63
20:4 (n-3)	0.83 ± 0.08	0.75 ± 0.11	0.42 ± 0.05	0.65 ± 0.09	0.93 ± 0.11	0.72 ± 0.17	0.68 ± 0.07	0.33 ± 0.08	0.39 ± 0.14	1.46 ± 0.22	0.15 ± 0.10	0.80 ± 0.10	0.75 ± 0.11
20:5 (n-3)	5.62 ± 0.47	8.93 ± 1.61	14.26 ± 2.79	7.93 ± 1.24	7.37 ± 1.55	8.43 ± 0.81	8.43 ± 0.48	10.26 ± 2.81	5.37 ± 1.07	5.59 ± 0.82	6.34 ± 2.83	4.39 ± 0.65	4.79 ± 0.92
22:5 (n-3)	0.88 ± 0.07	1.00 ± 0.13	2.44 ± 0.54	0.74 ± 0.12	2.10 ± 0.49	1.04 ± 0.31	1.29 ± 0.17	2.71 ± 0.60	0.74 ± 0.20	2.59 ± 0.40	1.75 ± 0.97	1.71 ± 0.35	1.62 ± 0.28
22:6 (n-3)	10.91 ± 0.39	10.52 ± 1.05	19.34 ± 3.00	9.92 ± 1.65	13.31 ± 3.39	12.49 ± 1.46	11.40 ± 0.89	20.48 ± 5.25	8.12 ± 2.59	12.68 ± 1.25	7.49 ± 3.65	14.94 ± 1.97	13.17 ± 2.21
24:5 (n-3)	0.71 ± 0.05	0.62 ± 0.05	0.18 ± 0.09	0.37 ± 0.13	0.52 ± 0.15	0.34 ± 0.12	0.53 ± 0.06	0.11 ± 0.04	0.10 ± 0.06	0.26 ± 0.04	0.08 ± 0.07	0.43 ± 0.08	0.40 ± 0.07
∑PUFA	30.58 ± 0.73	34.01 ± 1.87	44.45 ± 3.41	27.38 ± 3.19	33.19 ± 4.05	31.28 ± 3.27	30.77 ± 1.64	41.74 ± 9.71	19.08 ± 4.48	29.28 ± 2.99	20.52 ± 9.44	29.11 ± 2.19	29.15 ± 3.91
∑PUFA(n-6)	3.24 ± 0.22	2.34 ± 0.25	5.16 ± 0.63	2.90 ± 0.26	3.25 ± 0.51	2.41 ± 0.31	2.57 ± 0.15	6.37 ± 1.68	2.22 ± 0.46	2.70 ± 0.64	3.65 ± 1.44	3.04 ± 0.37	3.65 ± 0.52
∑PUFA(n-3)	26.26 ± 0.72	28.73 ± 1.80	38.65 ± 3.35	23.69 ± 3.13	28.45 ± 4.34	27.28 ± 2.91	26.75 ± 1.54	34.94 ± 8.43	16.50 ± 4.02	25.80 ± 2.56	16.35 ± 7.77	25.22 ± 1.97	24.46 ± 3.54

Table 21 Continued.

Species	Spiny dogfish	Thorny skate	Norway redfish	Grey gurnard	Atlantic wolffish	Spotted dragonet	Four-bearded rockling	Greater fork beard	Atlantic mackerel	Atlantic horse mackerel	Atlantic herring	Garfish	Greater argentine
LIVER Population	6	10	9	10	7	10	2	1	9	10	9	7	10
Amount of FA	37.73 ± 6.00	16.64 ± 10.76	15.67 ± 4.45	13.94 ± 9.55	14.82 ± 6.47	11.85 ± 13.49	11.71 ± 2.13	4.49 ±	10.05 ± 4.85	9.06 ± 2.46	13.37 ± 4.82	7.58 ± 4.49	7.49 ± 1.19
14:0	3.23 ± 0.64	2.20 ± 1.47	1.72 ± 0.19	3.03 ± 0.43	2.12 ± 0.32	5.28 ± 2.05	1.61 ± 0.38	2.06 ±	1.24 ± 0.43	2.92 ± 0.55	4.46 ± 0.31	0.79 ± 0.14	1.82 ± 0.30
16:0	13.29 ± 1.33	13.82 ± 1.15	12.78 ± 1.73	17.30 ± 0.80	16.14 ± 1.45	14.33 ± 2.18	13.42 ± 0.04	13.64 ±	14.00 ± 4.21	18.31 ± 2.52	11.94 ± 2.39	18.69 ± 1.83	16.98 ± 1.31
18:0	2.59 ± 0.38	3.68 ± 0.95	3.18 ± 0.84	4.38 ± 1.02	3.21 ± 0.52	5.36 ± 1.40	2.82 ± 0.41	4.56 ±	3.20 ± 0.77	5.84 ± 1.13	1.94 ± 0.60	6.46 ± 0.79	4.41 ± 0.63
∑SFA	21.32 ± 1.41	23.12 ± 1.27	19.33 ± 2.02	25.90 ± 1.41	24.21 ± 2.12	30.91 ± 3.66	21.56 ± 0.12	24.55 ±	20.23 ± 4.32	28.40 ± 3.15	20.48 ± 3.10	27.78 ± 1.88	24.23 ± 1.54
16:1 (n-9)	0.16 ± 0.02	0.31 ± 0.07	0.34 ± 0.09	0.30 ± 0.07	0.67 ± 0.24	0.65 ± 0.26	2.97 ± 3.19	0.42 ±	0.33 ± 0.07	0.22 ± 0.07	0.33 ± 0.12	0.38 ± 0.08	0.20 ± 0.03
16:1 (n-7)	3.17 ± 0.17	4.68 ± 0.80	6.60 ± 1.19	10.52 ± 2.51	12.21 ± 2.76	5.61 ± 2.47	2.33 ± 3.22	3.80 ±	2.06 ± 0.59	5.84 ± 1.20	3.13 ± 0.60	7.11 ± 2.99	3.60 ± 0.62
18:1 (n-9)	10.50 ± 1.74	8.40 ± 1.02	20.69 ± 5.36	22.51 ± 6.52	30.42 ± 10.04	4.88 ± 2.42	11.30 ± 1.11	11.10 ±	19.54 ± 7.26	25.40 ± 4.89	10.46 ± 2.72	19.26 ± 6.47	37.46 ± 4.21
18:1 (n-7)	2.07 ± 0.36	4.48 ± 1.46	5.33 ± 0.92	3.32 ± 0.41	6.02 ± 1.33	4.48 ± 0.56	6.22 ± 0.18	6.89 ±	5.05 ± 1.49	2.36 ± 0.32	2.39 ± 0.28	3.34 ± 0.61	3.39 ± 0.41
20:1 (n-11)	1.11 ± 0.14	1.10 ± 0.23	1.07 ± 0.42	1.41 ± 0.51	0.79 ± 0.53	1.01 ± 0.54	0.44 ± 0.02	1.85 ±	1.55 ± 0.79	1.15 ± 0.57	2.07 ± 1.15	0.33 ± 0.11	0.32 ± 0.12
20:1 (n-9)	10.73 ± 1.10	3.13 ± 3.01	5.14 ± 2.01	3.12 ± 0.63	0.81 ± 0.17	0.41 ± 0.14	1.06 ± 0.00	1.89 ±	3.44 ± 0.63	2.92 ± 0.93	5.05 ± 1.45	0.92 ± 0.14	2.62 ± 0.90
22:1 (n-11)	13.98 ± 1.31	2.22 ± 2.54	7.41 ± 2.65	2.94 ± 1.00	0.14 ± 0.07	0.36 ± 0.12	0.13 ± 0.01	1.13 ±	4.93 ± 2.37	3.73 ± 1.61	4.61 ± 1.80	0.51 ± 0.21	2.37 ± 1.20
22:1 (n-9)	3.91 ± 0.75	0.37 ± 0.20	0.71 ± 0.18	0.73 ± 0.19	0.26 ± 0.21	0.18 ± 0.05	0.12 ± 0.09	0.28 ±	0.82 ± 0.09	0.23 ± 0.07	0.38 ± 0.14	0.07 ± 0.01	0.67 ± 0.24
24:1 (n-9)	1.24 ± 0.13	0.51 ± 0.17	0.63 ± 0.18	0.96 ± 0.53	0.32 ± 0.27	0.76 ± 0.54	0.31 ± 0.22	1.47 ±	1.07 ± 0.38	0.57 ± 0.10	0.88 ± 0.19	1.25 ± 0.62	0.65 ± 0.15
∑MUFA	50.56 ± 1.16	29.06 ± 4.17	53.34 ± 3.00	50.09 ± 7.86	55.79 ± 9.10	22.80 ± 5.96	29.07 ± 1.05	34.18 ±	42.18 ± 6.47	43.88 ± 4.84	33.63 ± 5.16	37.10 ± 9.75	57.13 ± 3.57
18:2 (n-6)	1.45 ± 0.07	1.47 ± 0.42	1.18 ± 0.11	0.67 ± 0.33	0.27 ± 0.09	0.73 ± 0.12	1.19 ± 0.02	1.00 ±	1.07 ± 0.36	0.74 ± 0.17	1.42 ± 0.24	1.17 ± 0.68	0.59 ± 0.19
20:4 (n-6)	0.61 ± 0.10	2.26 ± 1.17	0.99 ± 0.15	0.74 ± 0.56	2.57 ± 2.16	3.72 ± 1.87	2.48 ± 0.03	4.00 ±	1.12 ± 0.23	0.69 ± 0.11	0.81 ± 0.25	1.03 ± 0.64	0.67 ± 0.17
22:4 (n-6)	0.52 ± 0.07	0.58 ± 0.27	0.30 ± 0.13	0.11 ± 0.06	0.37 ± 0.32	0.71 ± 0.39	0.47 ± 0.08	0.81 ±	0.08 ± 0.05	0.09 ± 0.04	0.08 ± 0.05	0.81 ± 0.40	0.18 ± 0.08
22:5 (n-6)	0.39 ± 0.12	0.62 ± 0.31	0.13 ± 0.01	0.14 ± 0.06	0.18 ± 0.15	0.53 ± 0.19	0.29 ± 0.00	0.35 ±	0.36 ± 0.12	0.22 ± 0.04	0.32 ± 0.05	0.27 ± 0.06	0.14 ± 0.04
18:3 (n-3)	0.82 ± 0.10	0.61 ± 0.30	0.62 ± 0.08	0.36 ± 0.14	0.12 ± 0.05	0.31 ± 0.13	0.47 ± 0.01	0.31 ±	0.74 ± 0.33	0.47 ± 0.16	1.08 ± 0.27	0.59 ± 0.28	0.25 ± 0.08
18:4 (n-3)	2.34 ± 0.77	1.61 ± 1.31	0.92 ± 0.33	0.55 ± 0.22	0.54 ± 0.25	0.67 ± 0.25	0.75 ± 0.07	0.27 ±	1.02 ± 0.59	1.02 ± 0.55	2.14 ± 0.67	0.33 ± 0.08	0.19 ± 0.09
20:4 (n-3)	1.23 ± 0.19	0.49 ± 0.17	0.93 ± 0.12	0.73 ± 0.17	0.41 ± 0.20	0.44 ± 0.12	0.68 ± 0.01	0.43 ±	2.52 ± 1.09	1.10 ± 0.37	1.64 ± 0.58	0.79 ± 0.12	0.51 ± 0.18
20:5 (n-3)	4.85 ± 0.86	10.12 ± 3.61	9.83 ± 2.27	5.92 ± 1.81	7.70 ± 3.85	12.28 ± 2.61	19.37 ± 0.07	10.79 ±	7.93 ± 2.50	5.53 ± 1.20	11.32 ± 1.32	4.80 ± 1.68	4.62 ± 0.97
22:5 (n-3)	1.44 ± 0.22	2.50 ± 0.74	1.77 ± 0.31	1.17 ± 0.20	0.66 ± 0.22	3.06 ± 1.05	2.25 ± 0.08	2.60 ±	3.75 ± 1.13	1.66 ± 0.39	1.67 ± 0.44	3.46 ± 0.59	1.22 ± 0.37
22:6 (n-3)	10.94 ± 1.27	24.10 ± 3.84	6.89 ± 0.86	11.51 ± 4.02	3.98 ± 1.48	17.99 ± 5.70	18.07 ± 0.43	17.71 ±	15.90 ± 3.48	14.17 ± 2.43	21.73 ± 3.74	20.00 ± 6.31	9.15 ± 1.93
24:5 (n-3)	0.26 ± 0.08	0.17 ± 0.13	0.36 ± 0.15	0.20 ± 0.09	0.10 ± 0.24	0.24 ± 0.12	0.16 ± 0.16	0.14 ±	0.27 ± 0.16	0.25 ± 0.13	0.51 ± 0.10	0.18 ± 0.13	0.11 ± 0.11
∑PUFA	27.36 ± 2.51	47.18 ± 4.24	26.29 ± 3.47	23.30 ± 7.58	18.89 ± 9.32	45.10 ± 8.52	48.88 ± 1.07	40.65 ±	36.86 ± 8.46	27.28 ± 4.58	45.06 ± 3.43	34.58 ± 9.47	18.35 ± 4.01
∑PUFA(n-6)	3.70 ± 0.33	5.86 ± 1.39	3.10 ± 0.35	1.91 ± 0.99	3.88 ± 2.97	6.29 ± 2.13	5.57 ± 0.18	7.14 ±	3.16 ± 0.71	2.04 ± 0.32	3.14 ± 0.30	3.68 ± 1.68	1.82 ± 0.52
∑PUFA(n-3)	22.67 ± 2.60	40.34 ± 3.73	22.11 ± 2.97	20.94 ± 6.53	14.06 ± 6.27	38.04 ± 6.92	42.86 ± 0.88	33.07 ±	33.24 ± 7.67	24.77 ± 4.16	41.08 ± 3.25	30.61 ± 8.32	16.37 ± 3.49

37

Table 21 Continued.

Species	Argentine	Greater sand eel	Lesser sand eel	Lesser sand eel (larvae)
LIVER				
Population	9	1	4	10
Amount of FA	4.39 ± 1.02	38.72 ±	18.17 ± 11.39	11.65 ± 2.14
14:0	1.91 ± 0.40	2.30 ±	3.45 ± 1.35	2.29 ± 0.55
16:0	15.47 ± 2.64	18.85 ±	14.40 ± 1.09	15.31 ± 0.65
18:0	3.50 ± 0.70	2.04 ±	1.80 ± 0.41	3.89 ± 0.48
∑SFA	**23.64 ± 2.89**	**24.82 ±**	**21.66 ± 0.71**	**23.80 ± 0.59**
16:1 (n-9)	0.42 ± 0.07	0.41 ±	0.23 ± 0.07	0.27 ± 0.03
16:1 (n-7)	3.42 ± 1.47	13.80 ±	5.59 ± 0.91	2.78 ± 0.73
18:1 (n-9)	18.43 ± 3.62	19.17 ±	9.22 ± 3.21	5.18 ± 0.49
18:1 (n-7)	3.70 ± 0.24	3.06 ±	1.95 ± 0.65	2.10 ± 0.18
20:1 (n-11)	0.47 ± 0.16	0.43 ±	0.59 ± 0.08	0.43 ± 0.11
20:1 (n-9)	1.35 ± 0.71	3.35 ±	7.93 ± 3.13	3.49 ± 1.47
22:1 (n-11)	0.88 ± 0.55	4.56 ±	8.34 ± 4.04	3.12 ± 1.93
22:1 (n-9)	0.47 ± 0.24	0.66 ±	0.84 ± 0.20	0.34 ± 0.13
24:1 (n-9)	1.36 ± 0.17	0.52 ±	1.03 ± 0.75	2.04 ± 0.22
∑MUFA	**34.48 ± 4.69**	**48.35 ±**	**39.29 ± 4.42**	**22.44 ± 3.57**
18:2 (n-6)	0.92 ± 0.26	1.27 ±	1.65 ± 0.18	2.10 ± 0.37
20:4 (n-6)	2.49 ± 0.74	0.28 ±	0.60 ± 0.20	0.77 ± 0.12
22:4 (n-6)	0.63 ± 0.20	0.97 ±	0.81 ± 0.30	0.40 ± 0.08
22:5 (n-6)	0.37 ± 0.07	0.07 ±	0.10 ± 0.12	0.42 ± 0.13
18:3 (n-3)	0.37 ± 0.17	2.00 ±	0.87 ± 0.19	0.80 ± 0.12
18:4 (n-3)	0.28 ± 0.13	2.03 ±	4.75 ± 2.22	1.69 ± 0.45
20:4 (n-3)	0.82 ± 0.36	1.29 ±	0.98 ± 0.05	0.46 ± 0.08
20:5 (n-3)	9.20 ± 2.07	8.29 ±	9.37 ± 0.59	12.19 ± 1.06
22:5 (n-3)	3.50 ± 0.55	0.51 ±	0.80 ± 0.14	1.09 ± 0.06
22:6 (n-3)	21.03 ± 3.93	7.48 ±	13.98 ± 6.74	30.82 ± 2.81
24:5 (n-3)	0.25 ± 0.15	0.13 ±	0.38 ± 0.07	0.23 ± 0.09
∑PUFA	**41.29 ± 6.71**	**25.76 ±**	**36.79 ± 3.99**	**52.67 ± 3.05**
∑PUFA(n-6)	4.81 ± 0.92	**2.96 ±**	3.61 ± 0.65	4.25 ± 0.32
∑PUFA(n-3)	36.14 ± 6.28	22.26 ±	32.23 ± 4.13	47.76 ± 3.20

Table 22: FA profiles for muscle samples. Amount of FA given as mg FA/100 mg wet weight. FAs given as % of total FA.

Species	Silvery pout	Norway pout	Poor cod	Blue whiting	Whiting	Saithe	Pollack	Lemon sole	Megrim	European plaice	Blackmouth cathshark	Spiny dogfish
MUSCLE Population	2	10	8	10	10	10	9	10	10	10	10	6
Amount of FA	0.8 ± 0.2	0.7 ± 0.1	0.47 ± 0.05	0.62 ± 0.05	0.5 ± 0.1	0.6 ± 0.1	1.00 ± 1.14	0.45 ± 0.04	1.48 ± 1.68	0.5 ± 0.1	0.71 ± 0.33	1.79 ± 0.75
14:0	2.24 ± 0.36	1.90 ± 0.21	0.66 ± 0.06	1.37 ± 0.31	0.95 ± 0.18	1.39 ± 0.35	1.28 ± 0.39	2.13 ± 0.35	3.95 ± 1.23	2.06 ± 0.19	2.76 ± 1.46	1.32 ± 0.50
16:0	19.01 ± 0.17	19.08 ± 0.86	17.57 ± 0.58	17.68 ± 0.45	17.93 ± 0.99	17.75 ± 1.02	15.95 ± 0.90	16.19 ± 1.24	15.52 ± 2.20	15.68 ± 1.05	16.61 ± 1.79	16.66 ± 0.86
18:0	4.04 ± 0.06	3.39 ± 0.22	4.94 ± 0.21	3.81 ± 0.29	5.07 ± 0.31	5.01 ± 0.42	4.92 ± 1.47	5.22 ± 0.35	2.77 ± 0.67	4.54 ± 0.32	4.89 ± 1.30	3.73 ± 0.86
∑SFA	27.08 ± 0.40	25.17 ± 0.80	25.32 ± 0.54	24.08 ± 0.53	24.65 ± 1.08	25.06 ± 0.89	23.28 ± 1.14	26.74 ± 0.92	23.88 ± 1.60	25.44 ± 0.67	26.49 ± 1.69	24.14 ± 0.67
16:1 (n-9)	0.30 ± 0.00	0.22 ± 0.03	0.27 ± 0.03	0.18 ± 0.02	0.20 ± 0.02	0.22 ± 0.03	0.35 ± 0.23	0.40 ± 0.13	0.35 ± 0.03	0.60 ± 0.10	0.24 ± 0.03	0.27 ± 0.02
16:1 (n-7)	2.34 ± 0.43	1.20 ± 0.21	1.08 ± 0.16	1.22 ± 0.23	0.79 ± 0.14	0.98 ± 0.34	1.37 ± 0.29	2.63 ± 0.72	3.57 ± 1.51	4.62 ± 0.60	2.85 ± 1.24	2.67 ± 0.70
18:1 (n-11)	0.61 ± 0.07	0.97 ± 0.13	0.36 ± 0.11	0.52 ± 0.08	1.46 ± 0.37	1.17 ± 0.26	1.15 ± 0.30	0.32 ± 0.17	1.63 ± 0.32	0.28 ± 0.18	0.70 ± 0.14	1.54 ± 0.22
18:1 (n-9)	9.66 ± 1.16	3.80 ± 0.38	5.39 ± 0.43	6.05 ± 0.69	4.48 ± 0.45	5.91 ± 1.03	6.91 ± 5.12	5.83 ± 0.86	7.55 ± 1.86	6.03 ± 1.13	6.76 ± 0.41	12.50 ± 1.42
18:1 (n-7)	2.23 ± 0.05	1.23 ± 0.09	2.51 ± 0.30	2.10 ± 0.27	1.38 ± 0.15	2.04 ± 0.32	1.63 ± 0.26	2.32 ± 0.55	1.59 ± 0.36	2.69 ± 0.50	4.26 ± 0.95	2.91 ± 0.31
20:1 (n-11)	0.55 ± 0.14	0.67 ± 0.11	0.42 ± 0.07	0.50 ± 0.10	0.69 ± 0.08	0.45 ± 0.15	0.53 ± 0.14	0.53 ± 0.29	1.08 ± 0.39	0.86 ± 0.24	0.66 ± 0.17	2.19 ± 0.33
20:1 (n-9)	1.61 ± 0.44	3.17 ± 0.84	0.77 ± 0.10	1.54 ± 0.48	2.31 ± 0.37	2.03 ± 0.64	2.57 ± 0.44	0.86 ± 0.31	5.29 ± 2.21	1.61 ± 0.15	4.18 ± 1.85	4.85 ± 0.63
22:1 (n-11)	1.55 ± 0.69	3.33 ± 1.26	0.30 ± 0.07	1.61 ± 0.98	0.97 ± 0.27	0.95 ± 0.70	1.28 ± 0.56	0.27 ± 0.12	5.25 ± 2.55	0.38 ± 0.13	5.46 ± 3.56	2.74 ± 0.46
22:1 (n-9)	0.72 ± 0.16	0.29 ± 0.07	0.14 ± 0.01	0.22 ± 0.06	0.14 ± 0.02	0.12 ± 0.05	0.20 ± 0.19	0.11 ± 0.03	0.47 ± 0.15	0.22 ± 0.03	0.45 ± 0.20	1.51 ± 0.27
24:1 (n-9)	1.62 ± 0.00	1.30 ± 0.22	1.48 ± 0.20	1.59 ± 0.29	1.24 ± 0.19	1.16 ± 0.10	1.79 ± 2.20	2.00 ± 0.17	1.10 ± 0.43	1.41 ± 0.29	0.64 ± 0.13	0.34 ± 0.13
∑MUFA	23.02 ± 2.85	17.08 ± 2.58	14.95 ± 0.84	16.99 ± 2.13	14.37 ± 1.37	15.81 ± 2.05	19.46 ± 7.38	18.24 ± 2.80	30.24 ± 7.38	21.46 ± 1.69	28.22 ± 6.14	34.02 ± 2.44
18:2 (n-6)	0.87 ± 0.19	1.09 ± 0.15	0.46 ± 0.02	1.12 ± 0.12	0.69 ± 0.15	0.90 ± 0.13	0.84 ± 0.35	0.57 ± 0.10	1.00 ± 0.18	0.46 ± 0.04	1.17 ± 0.15	1.58 ± 0.18
20:4 (n-6)	3.01 ± 0.55	0.82 ± 0.10	3.21 ± 0.68	1.34 ± 0.07	1.53 ± 0.42	1.64 ± 0.27	1.52 ± 0.44	5.48 ± 1.74	1.18 ± 0.42	5.84 ± 1.10	2.37 ± 0.59	2.81 ± 0.65
22:4 (n-6)	0.90 ± 0.29	0.15 ± 0.03	0.42 ± 0.12	0.10 ± 0.01	0.14 ± 0.03	0.13 ± 0.09	0.13 ± 0.03	1.11 ± 0.39	0.24 ± 0.06	2.03 ± 0.33	0.62 ± 0.20	0.56 ± 0.10
22:5 (n-6)	0.70 ± 0.07	0.48 ± 0.05	0.75 ± 0.12	0.56 ± 0.03	0.62 ± 0.11	0.57 ± 0.09	0.48 ± 0.18	1.03 ± 0.68	0.49 ± 0.15	0.80 ± 0.07	0.51 ± 0.12	0.63 ± 0.09
18:3 (n-3)	0.45 ± 0.05	0.47 ± 0.07	0.16 ± 0.02	0.49 ± 0.08	0.27 ± 0.06	0.37 ± 0.09	0.34 ± 0.15	0.12 ± 0.03	0.65 ± 0.25	0.13 ± 0.04	0.42 ± 0.20	0.67 ± 0.21
18:4 (n-3)	0.52 ± 0.02	1.46 ± 0.20	0.30 ± 0.06	0.83 ± 0.21	0.49 ± 0.19	0.71 ± 0.34	0.75 ± 0.29	0.23 ± 0.07	1.85 ± 0.91	0.17 ± 0.12	0.99 ± 0.83	0.90 ± 0.39
20:4 (n-3)	0.69 ± 0.07	0.55 ± 0.04	0.24 ± 0.01	0.43 ± 0.06	0.44 ± 0.05	0.61 ± 0.10	0.48 ± 0.17	0.27 ± 0.06	0.87 ± 0.19	0.26 ± 0.10	0.54 ± 0.08	0.58 ± 0.27
20:5 (n-3)	11.72 ± 1.88	9.97 ± 0.79	11.13 ± 0.92	10.70 ± 1.11	9.21 ± 1.01	11.50 ± 1.56	10.98 ± 2.98	12.90 ± 1.76	7.92 ± 1.20	18.45 ± 1.97	5.96 ± 1.50	4.75 ± 1.78
22:5 (n-3)	2.58 ± 0.01	1.60 ± 0.22	1.99 ± 0.30	1.20 ± 0.08	1.51 ± 0.13	1.48 ± 0.39	1.60 ± 0.39	3.44 ± 0.47	2.28 ± 0.25	4.80 ± 1.18	4.71 ± 1.58	2.14 ± 0.29
22:6 (n-3)	26.67 ± 2.09	38.53 ± 1.99	39.06 ± 2.30	40.23 ± 3.36	44.64 ± 2.69	39.70 ± 2.48	37.62 ± 4.98	27.26 ± 3.58	25.92 ± 6.54	18.14 ± 3.35	24.98 ± 5.75	24.68 ± 3.34
24:5 (n-3)	0.21 ± 0.07	0.76 ± 0.16	0.27 ± 0.13	0.39 ± 0.05	0.49 ± 0.09	0.27 ± 0.19	0.42 ± 0.10	0.23 ± 0.03	0.54 ± 0.06	0.16 ± 0.10	0.37 ± 0.22	0.12 ± 0.10
∑PUFA	49.83 ± 3.24	57.46 ± 2.01	59.41 ± 0.90	58.46 ± 2.39	60.88 ± 1.46	59.02 ± 1.71	56.69 ± 7.95	54.19 ± 3.12	45.15 ± 5.91	53.00 ± 1.81	44.90 ± 4.73	41.35 ± 2.35
∑PUFA(n-6)	5.81 ± 0.56	2.83 ± 0.27	5.23 ± 0.90	3.42 ± 0.17	3.23 ± 0.54	3.58 ± 0.29	3.28 ± 0.98	8.64 ± 2.15	3.42 ± 0.44	9.58 ± 1.26	5.16 ± 0.87	6.21 ± 0.53
∑PUFA(n-3)	43.61 ± 3.83	53.98 ± 2.01	53.92 ± 1.50	54.73 ± 2.46	57.38 ± 1.67	55.09 ± 1.79	52.71 ± 7.57	45.15 ± 3.21	40.91 ± 5.71	42.80 ± 2.07	38.57 ± 4.63	34.35 ± 2.27

Table 22 Continued.

Species	Thorny skate	European hake	Norway redfish	Grey gurnard	Atlantic wolffish	Spotted dragonet	Atlantic mackerel	Atlantic horse mackerel	Atlantic herring	Garfish	Greater argentine	Argentine	Lesser sand eel (larvae)
MUSCLE													
Population	10	10	10	10	8	10	10	9	8	7	9	8	10
Amount of FA	0.44 ± 0.04	0.8 ± 0.3	0.83 ± 0.36	1.51 ± 0.77	0.71 ± 0.27	0.63 ± 0.16	9.61 ± 6.92	2.44 ± 1.22	4.73 ± 2.88	1.27 ± 0.55	0.96 ± 0.37	0.91 ± 0.29	11.65 ± 2.14
14:0	0.74 ± 0.41	2.95 ± 0.56	2.81 ± 0.86	3.08 ± 1.24	1.83 ± 0.59	1.76 ± 0.73	5.78 ± 2.02	5.32 ± 1.38	6.28 ± 1.62	1.34 ± 0.53	1.86 ± 0.74	2.29 ± 0.86	2.29 ± 0.55
16:0	21.79 ± 0.98	16.25 ± 1.22	16.53 ± 1.95	16.64 ± 1.28	15.15 ± 1.25	14.97 ± 1.37	14.50 ± 2.63	16.64 ± 1.32	13.28 ± 1.87	18.43 ± 0.84	19.77 ± 0.99	18.97 ± 1.30	15.31 ± 0.65
18:0	4.98 ± 0.47	3.47 ± 0.69	4.52 ± 0.67	4.44 ± 0.96	4.09 ± 0.49	5.59 ± 0.62	2.96 ± 1.32	4.10 ± 0.79	1.58 ± 0.71	6.06 ± 0.91	3.58 ± 0.23	3.58 ± 0.30	3.89 ± 0.48
∑SFA	**30.43 ± 1.26**	**23.98 ± 1.73**	**25.57 ± 1.79**	**25.77 ± 1.09**	**24.72 ± 0.74**	**26.06 ± 1.58**	**25.31 ± 1.99**	**27.88 ± 1.00**	**22.93 ± 1.08**	**27.84 ± 1.07**	**26.71 ± 0.54**	**26.88 ± 0.75**	**23.80 ± 0.59**
16:1 (n-9)	0.43 ± 0.08	0.27 ± 0.02	0.19 ± 0.03	0.29 ± 0.04	0.64 ± 0.11	0.33 ± 0.07	0.24 ± 0.04	0.20 ± 0.03	0.17 ± 0.02	0.37 ± 0.07	0.18 ± 0.02	0.26 ± 0.03	0.27 ± 0.03
16:1 (n-7)	1.55 ± 0.39	2.94 ± 0.20	2.95 ± 0.72	4.72 ± 1.61	4.85 ± 1.87	2.11 ± 0.85	2.87 ± 0.67	3.80 ± 0.64	2.86 ± 0.64	2.82 ± 0.82	1.60 ± 0.59	1.94 ± 0.58	2.78 ± 0.73
18:1 (n-11)	0.41 ± 0.26	1.61 ± 0.18	0.73 ± 0.39	1.09 ± 0.46	0.43 ± 0.63	0.25 ± 0.22	0.35 ± 0.10	0.42 ± 0.09	0.45 ± 0.08	0.73 ± 0.93	0.27 ± 0.07	0.49 ± 0.14	0.64 ± 0.08
18:1 (n-9)	6.01 ± 0.76	7.30 ± 1.71	5.80 ± 1.09	12.46 ± 2.47	8.18 ± 3.12	4.13 ± 1.12	8.16 ± 4.49	12.22 ± 2.69	4.02 ± 0.54	7.76 ± 1.73	13.18 ± 3.92	9.50 ± 0.96	5.18 ± 0.49
18:1 (n-7)	3.03 ± 0.40	1.74 ± 0.28	2.01 ± 0.15	2.77 ± 0.43	4.08 ± 1.09	2.87 ± 0.38	1.89 ± 0.78	2.01 ± 0.31	1.07 ± 0.19	2.31 ± 0.30	2.14 ± 0.39	2.06 ± 0.32	2.10 ± 0.18
20:1 (n-11)	0.25 ± 0.10	2.10 ± 0.41	0.70 ± 0.51	0.88 ± 0.37	1.34 ± 0.69	1.05 ± 0.38	0.64 ± 0.20	0.90 ± 0.34	1.07 ± 0.24	0.25 ± 0.09	0.38 ± 0.11	0.46 ± 0.22	0.43 ± 0.11
20:1 (n-9)	1.01 ± 0.96	7.31 ± 1.52	4.72 ± 1.67	3.34 ± 1.26	0.97 ± 0.14	0.82 ± 1.05	5.95 ± 2.31	4.91 ± 1.58	8.38 ± 1.91	0.95 ± 0.35	2.61 ± 0.87	1.62 ± 0.60	3.49 ± 1.47
22:1 (n-11)	0.43 ± 0.53	8.68 ± 2.74	5.85 ± 2.62	2.46 ± 1.07	0.40 ± 0.09	0.76 ± 1.13	10.50 ± 5.29	7.89 ± 3.13	18.63 ± 4.81	0.61 ± 0.30	3.44 ± 1.37	1.83 ± 0.94	3.12 ± 1.93
22:1 (n-9)	0.58 ± 0.20	0.76 ± 0.22	0.53 ± 0.18	0.40 ± 0.15	0.39 ± 0.16	0.18 ± 0.10	0.70 ± 0.20	0.45 ± 0.14	0.74 ± 0.15	0.11 ± 0.02	0.61 ± 0.24	0.88 ± 0.36	0.34 ± 0.13
24:1 (n-9)	1.04 ± 0.43	1.81 ± 0.20	1.55 ± 0.25	0.96 ± 0.32	0.82 ± 0.23	0.92 ± 0.23	0.83 ± 0.23	0.93 ± 0.13	0.97 ± 0.15	1.56 ± 0.43	0.96 ± 0.31	1.21 ± 0.14	2.04 ± 0.22
∑MUFA	**17.56 ± 2.45**	**35.65 ± 6.35**	**26.95 ± 6.58**	**31.10 ± 6.74**	**25.37 ± 6.07**	**16.67 ± 4.51**	**33.87 ± 7.16**	**35.26 ± 5.78**	**39.89 ± 7.83**	**19.25 ± 3.09**	**27.00 ± 7.09**	**22.52 ± 4.11**	**22.44 ± 3.57**
18:2 (n-6)	1.31 ± 0.37	1.08 ± 0.15	1.52 ± 0.23	1.06 ± 0.17	0.49 ± 0.10	0.63 ± 0.09	1.55 ± 0.25	1.26 ± 0.12	1.20 ± 0.30	1.36 ± 0.46	0.97 ± 0.07	0.85 ± 0.11	2.10 ± 0.37
20:4 (n-6)	3.55 ± 0.79	1.05 ± 0.13	1.84 ± 0.41	1.34 ± 0.42	6.88 ± 1.98	4.57 ± 1.15	0.71 ± 0.40	0.85 ± 0.18	0.58 ± 0.29	1.60 ± 0.43	1.19 ± 0.10	1.71 ± 0.39	0.77 ± 0.12
22:4 (n-6)	0.70 ± 0.17	0.16 ± 0.05	0.17 ± 0.03	0.25 ± 0.07	0.44 ± 0.10	0.82 ± 0.18	0.14 ± 0.04	0.14 ± 0.07	0.04 ± 0.01	0.47 ± 0.18	0.23 ± 0.05	0.63 ± 0.20	0.40 ± 0.08
22:5 (n-6)	0.50 ± 0.06	0.53 ± 0.08	0.58 ± 0.09	0.51 ± 0.19	0.61 ± 0.12	1.05 ± 0.20	0.43 ± 0.16	0.38 ± 0.08	0.22 ± 0.02	0.52 ± 0.11	0.51 ± 0.08	0.63 ± 0.09	0.42 ± 0.13
18:3 (n-3)	0.26 ± 0.13	0.59 ± 0.09	0.39 ± 0.08	0.54 ± 0.20	0.20 ± 0.04	0.24 ± 0.11	1.31 ± 0.37	0.79 ± 0.14	0.90 ± 0.29	0.68 ± 0.30	0.49 ± 0.07	0.54 ± 0.08	0.80 ± 0.12
18:4 (n-3)	0.30 ± 0.27	0.97 ± 0.13	0.94 ± 0.27	1.15 ± 0.56	0.87 ± 0.34	0.56 ± 0.32	4.54 ± 2.00	2.19 ± 0.61	2.85 ± 1.20	0.72 ± 0.45	0.55 ± 0.14	0.65 ± 0.28	1.69 ± 0.45
20:4 (n-3)	0.40 ± 0.20	0.47 ± 0.05	0.42 ± 0.08	0.69 ± 0.18	0.41 ± 0.07	0.32 ± 0.12	1.01 ± 0.17	0.87 ± 0.11	0.52 ± 0.14	0.66 ± 0.25	0.61 ± 0.06	0.64 ± 0.07	0.46 ± 0.08
20:5 (n-3)	8.66 ± 0.99	6.46 ± 0.73	9.39 ± 1.34	7.91 ± 0.72	17.30 ± 2.70	14.79 ± 1.57	7.28 ± 0.84	6.54 ± 1.00	7.88 ± 1.30	7.35 ± 1.29	8.12 ± 0.79	10.40 ± 0.75	12.19 ± 1.06
22:5 (n-3)	3.39 ± 0.54	1.37 ± 0.11	1.49 ± 0.10	1.85 ± 0.08	1.42 ± 0.17	2.64 ± 0.35	1.27 ± 0.30	1.76 ± 0.23	0.77 ± 0.07	2.80 ± 0.37	1.73 ± 0.19	2.42 ± 0.31	1.09 ± 0.06
22:6 (n-3)	30.96 ± 2.12	25.50 ± 4.75	27.75 ± 4.88	25.26 ± 7.07	17.42 ± 3.21	27.74 ± 4.36	18.67 ± 7.49	18.78 ± 4.66	18.77 ± 6.83	34.25 ± 3.21	30.07 ± 7.04	29.80 ± 4.65	30.82 ± 2.81
24:5 (n-3)	0.28 ± 0.08	0.55 ± 0.12	0.54 ± 0.06	0.32 ± 0.05	0.14 ± 0.06	0.32 ± 0.06	0.52 ± 0.25	0.50 ± 0.17	0.35 ± 0.28	0.12 ± 0.08	0.33 ± 0.04	0.35 ± 0.06	0.23 ± 0.09
∑PUFA	**51.76 ± 1.70**	**40.08 ± 5.00**	**47.01 ± 5.10**	**42.64 ± 6.10**	**49.07 ± 5.68**	**56.61 ± 4.38**	**40.20 ± 6.36**	**36.34 ± 5.97**	**36.60 ± 7.04**	**52.40 ± 2.19**	**45.84 ± 7.25**	**49.96 ± 4.21**	**52.67 ± 3.05**
∑PUFA(n-6)	**6.53 ± 0.82**	**3.14 ± 0.29**	4.62 ± 0.29	3.55 ± 0.57	9.17 ± 2.05	7.55 ± 1.23	3.37 ± 0.54	3.06 ± 0.25	2.52 ± 0.28	**4.42 ± 0.61**	3.21 ± 0.20	4.16 ± 0.61	4.25 ± 0.32
∑PUFA(n-3)	44.57 ± 1.72	**36.35 ± 4.88**	41.51 ± 5.12	38.26 ± 5.93	38.62 ± 5.25	48.54 ± 3.89	35.81 ± 6.07	32.43 ± 5.79	32.74 ± 6.93	47.42 ± 2.38	42.34 ± 7.45	45.35 ± 4.34	47.76 ± 3.20

40
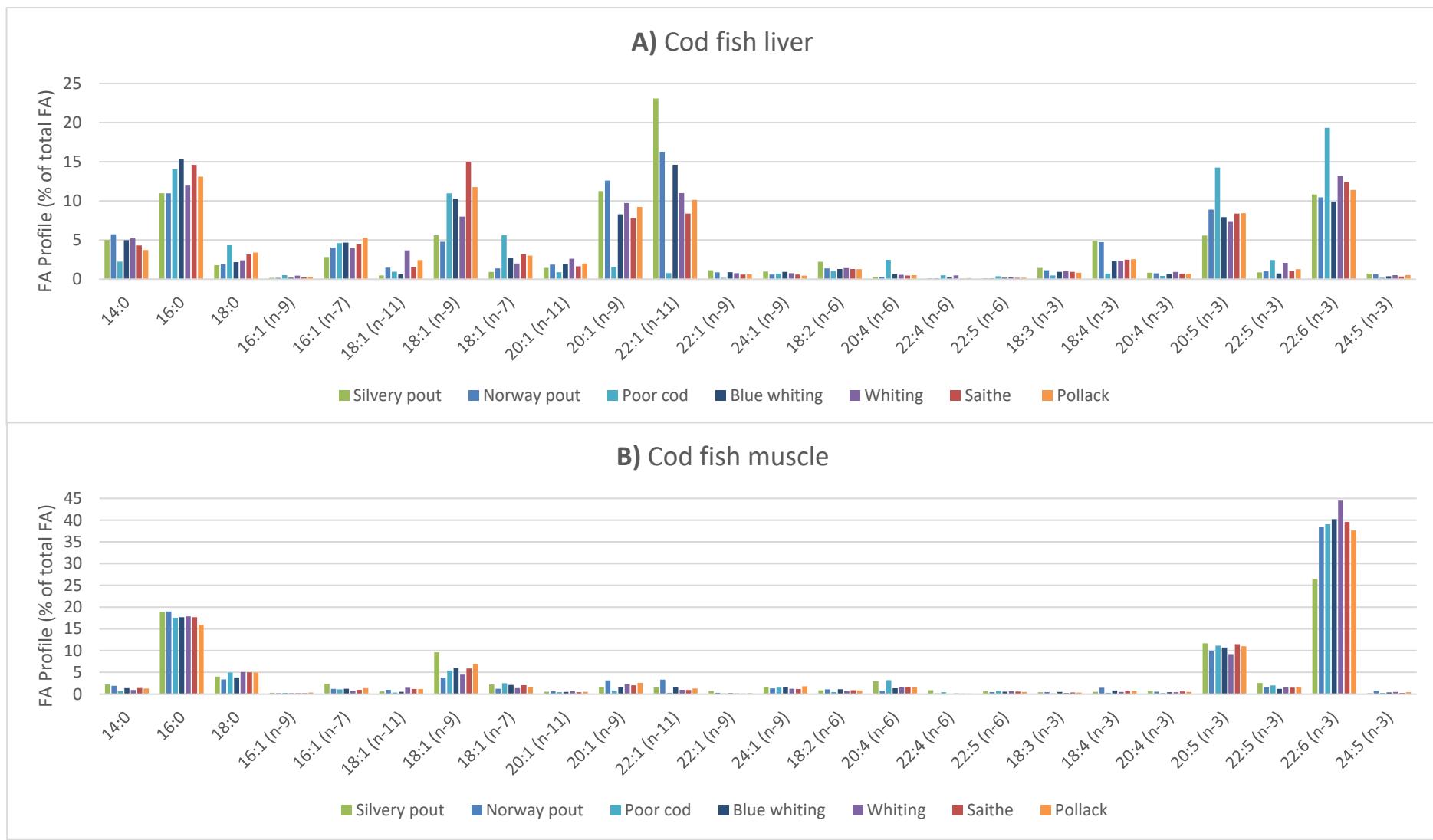
Figure 17: FA profiles for A) liver and B) muscle samples for cod fish.
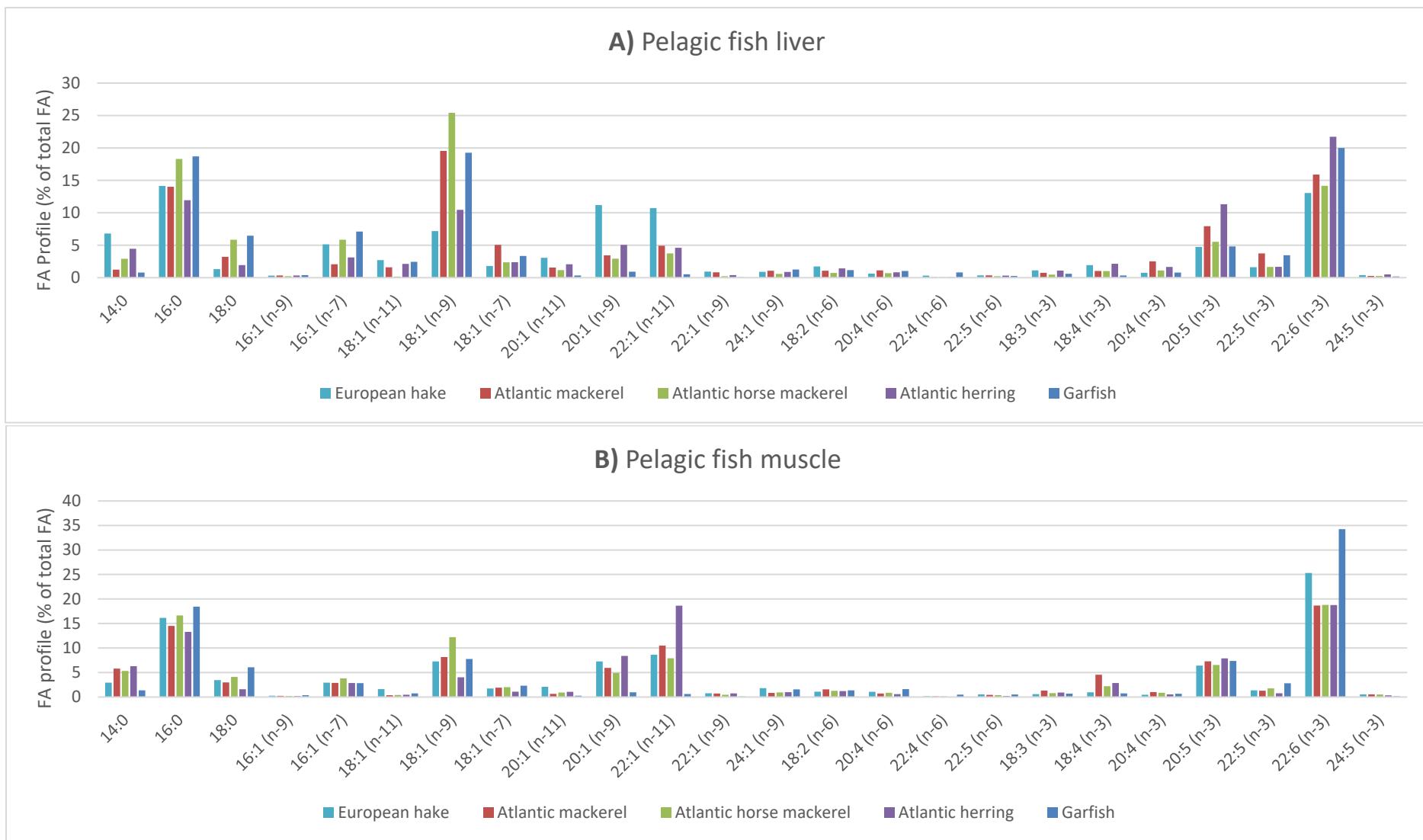
Figure 18: FA profiles of A) liver and B) muscle samples for pelagic fish.
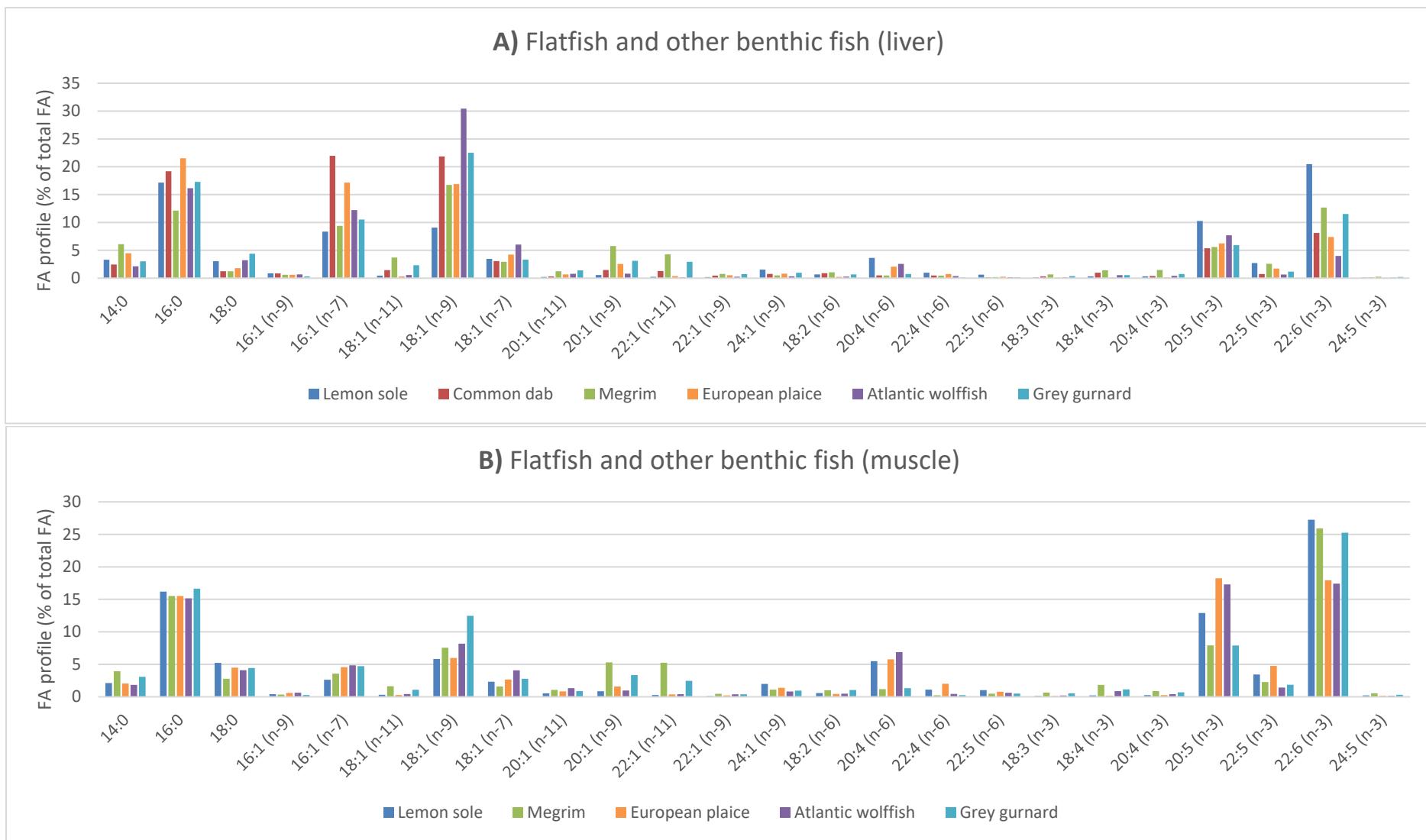
Figure 19: FA profiles of A) liver and B) muscle samples for flatfish and other benthic fish.
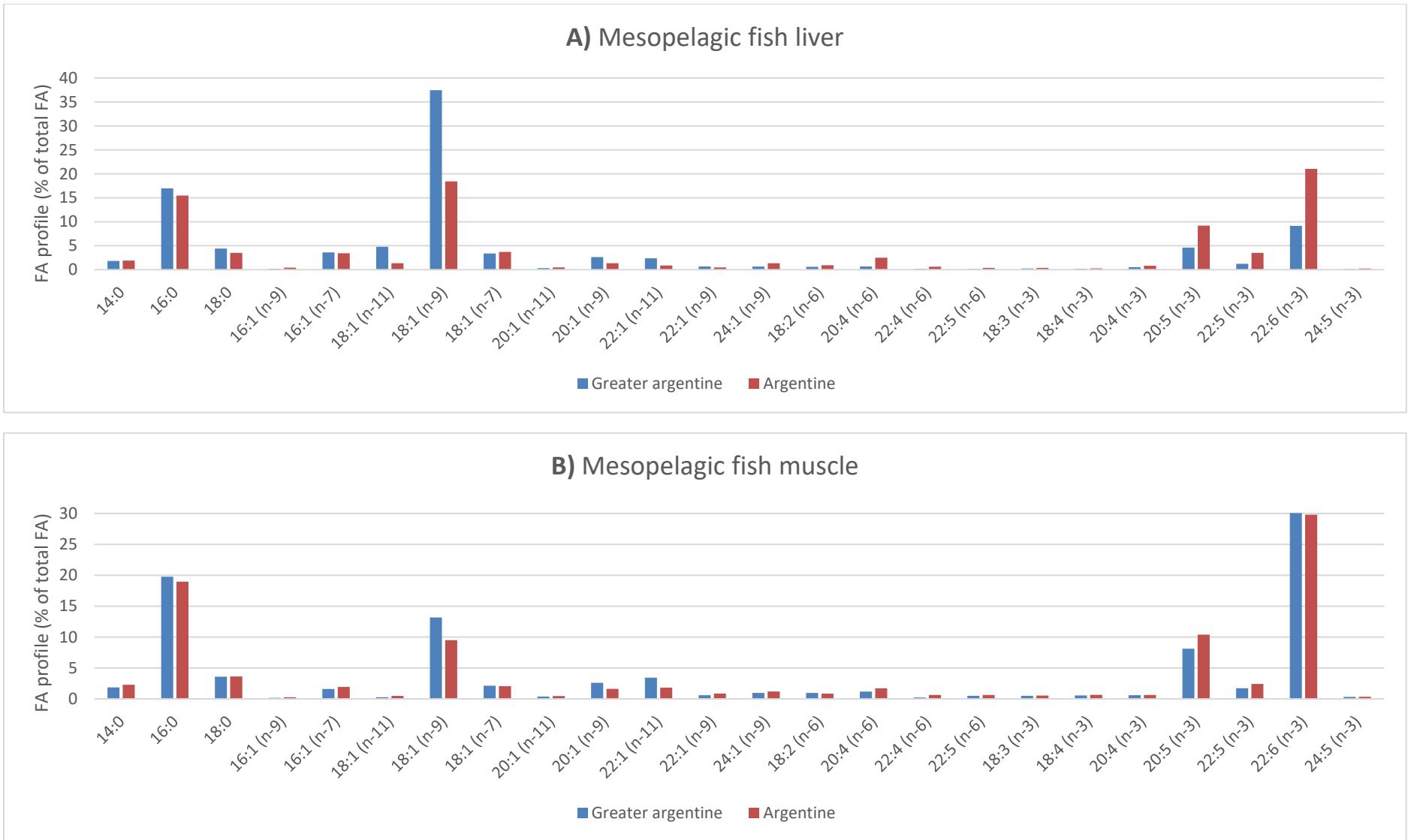
Figure 20: FA profiles of A) liver and B) muscle samples for mesopelagic fish.
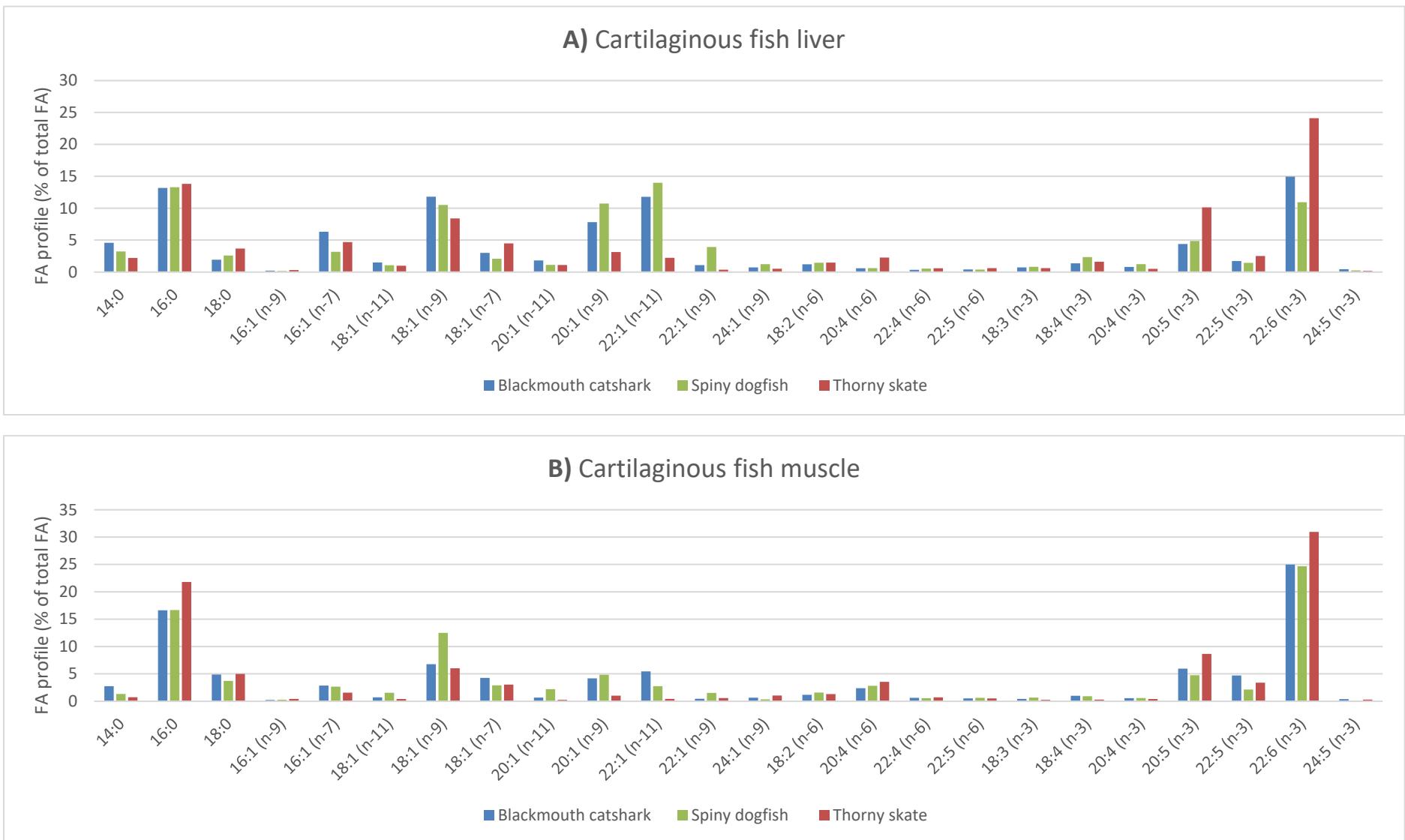
Figure 21: FA profiles of A) liver and B) muscle samples for cartilaginous fish.
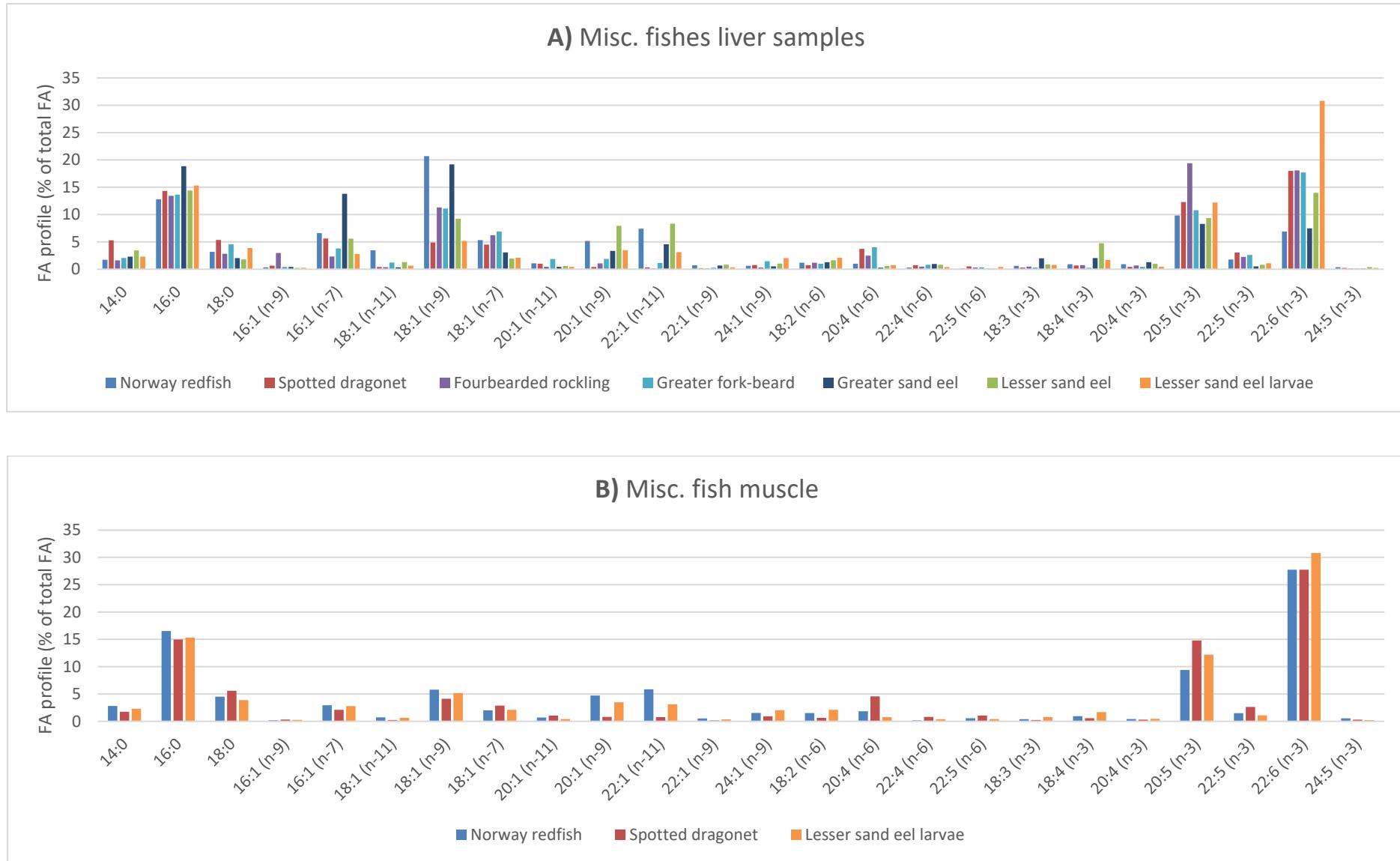
Figure 22: FA profiles of A) liver and B) muscle samples for the miscellaneous fish.

Figure 23 shows the distribution between SFA, MUFA and PUFA for the two tissues. Muscle tissues are generally highest in PUFAs. The four pelagic fish mackerel, horse mackerel, herring and hake have more even distributions of ∑SFA, ∑MUFA and ∑PUFA, compared to the rest of the fish. Cod fish muscle generally has higher levels of ∑SFA than ∑MUFA in the muscle, with almost identical distributions. For the liver samples, there is much more variation in the distributions between the fish. Cod fish have generally high levels of ∑MUFA, except for poor cod, for which ∑PUFA is much higher. European hake has a similar distribution to the cod fish.
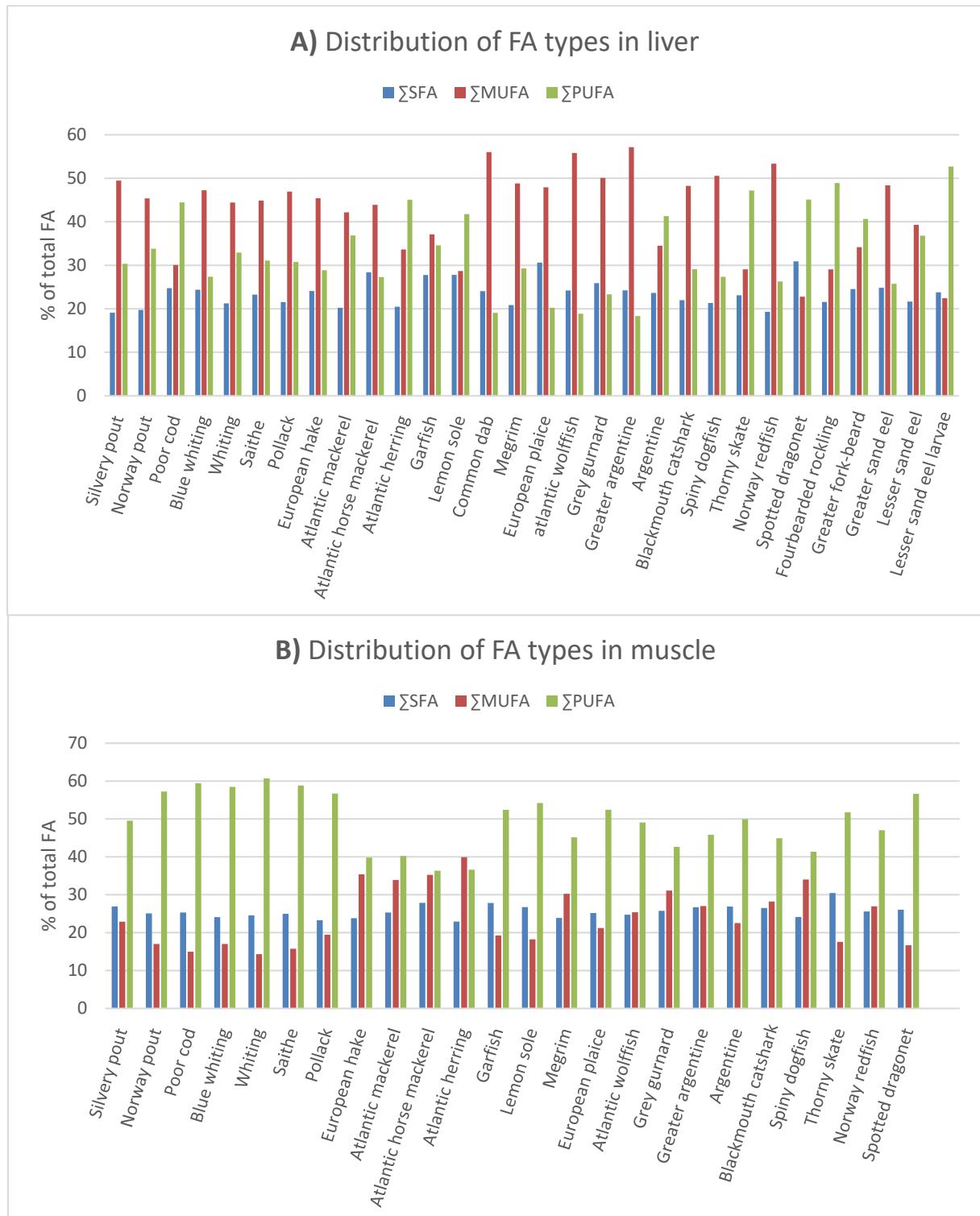
Figure 23: Distribution of ∑SFA, ∑MUFA and ∑PUFA in A) liver samples and B) muscle samples.
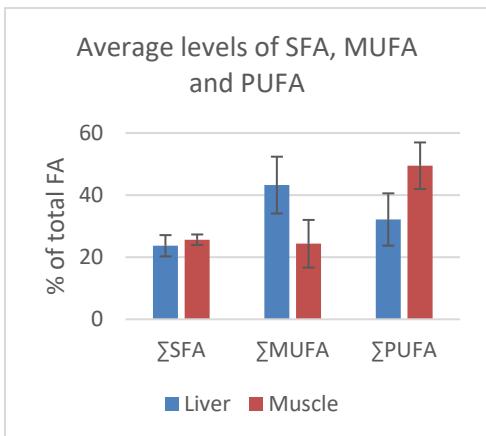
The average levels of ∑SFA, ∑MUFA and ∑PUFA of all the fish analysed is shown in Figure 24, with error bars corresponding to the standard deviations. ∑SFA shows the least variation, especially for muscle samples, while ∑MUFA and ∑PUFA varies greatly between the species.

Figure 25 shows the distribution of MUFAs (n-11), (n-9) and (n-7). Cod fish livers are generally lower in (n-7) MUFAs than (n-11) and (n-9) MUFAs and is largely attributed to the high levels of *Calanus* FATMs 22:1(n-11) and 20:1(n-9). Poor cod is again very different from the other cod fish, with almost no (n-11) MUFA content.

Figure 24: Average levels of ∑SFA, ∑MUFA and ∑PUFA, error bars show the standard deviations.
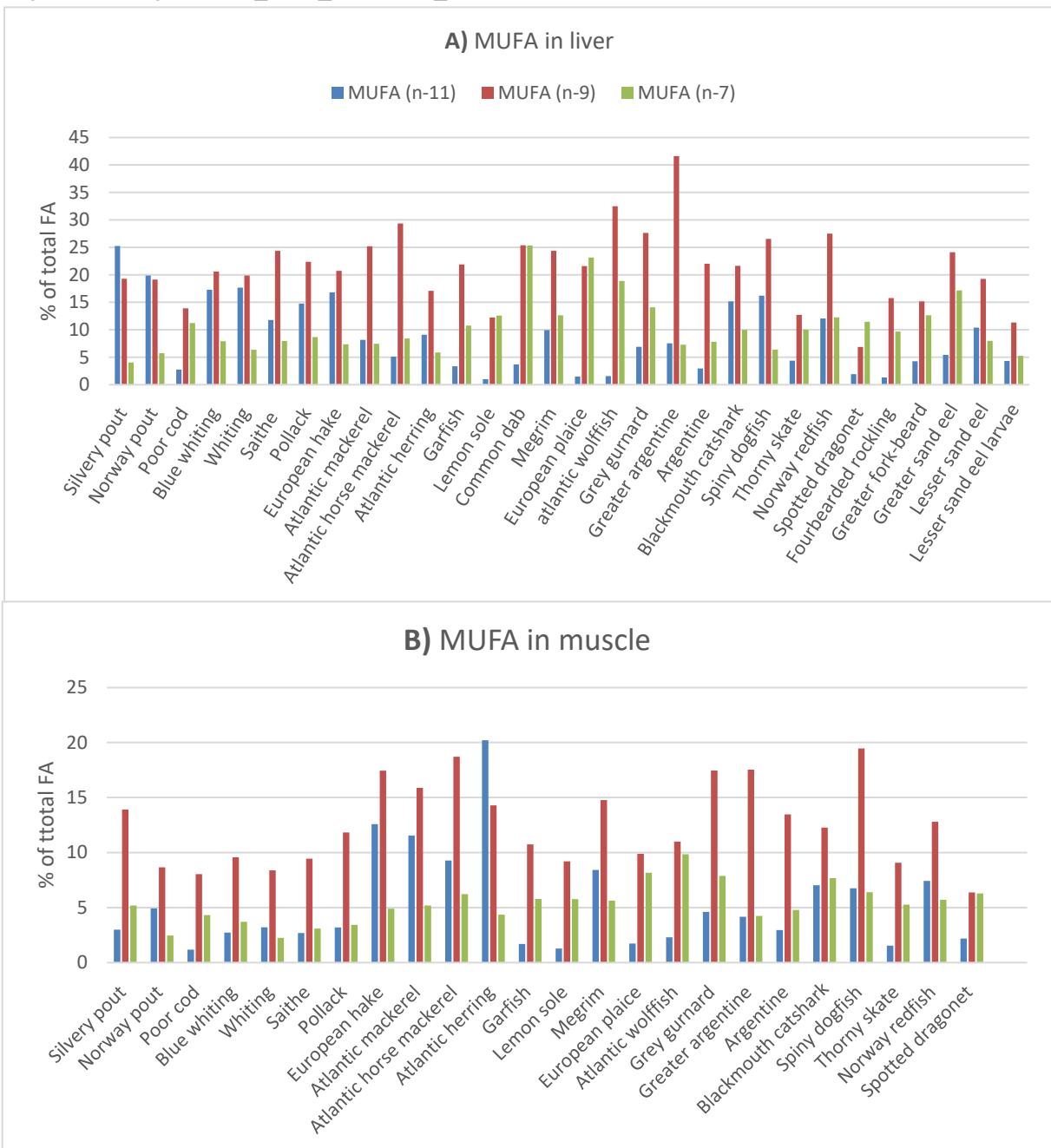
Figure 25: Levels of MUFAs (n-11), (n-9) and (n-7) for A) liver and B) muscle samples.

For the distribution of MUFAs in muscle tissue, hake, mackerel, horse mackerel and herring (especially) stand out with higher levels of (n-11) MUFAs compared to the rest of the fish. Generally, (n-9) MUFAs are the most abundant MUFA in the muscle samples. Plaice and wolffish have relatively high levels of (n-7) MUFAs, almost the same amount as (n-9).

Ratios of $\sum$(n-3) and $\sum$(n-6) PUFAs, with sums given as % of total FA, are shown in Figure 26. As the figure shows, the ratios are generally high, especially for cod fish muscle tissue showing ratios up to 19. The cod fish Norway pout, blue whiting, saithe and pollack, and hake stands out from the rest as they have much higher ratios in the muscle tissue compared to liver. The benthic fish sole, plaice and wolffish display the lowest ratios, which coincide with the observations of the profiles, having elevated levels of 20:4(n-6) and lower levels of 22:6(n-3).
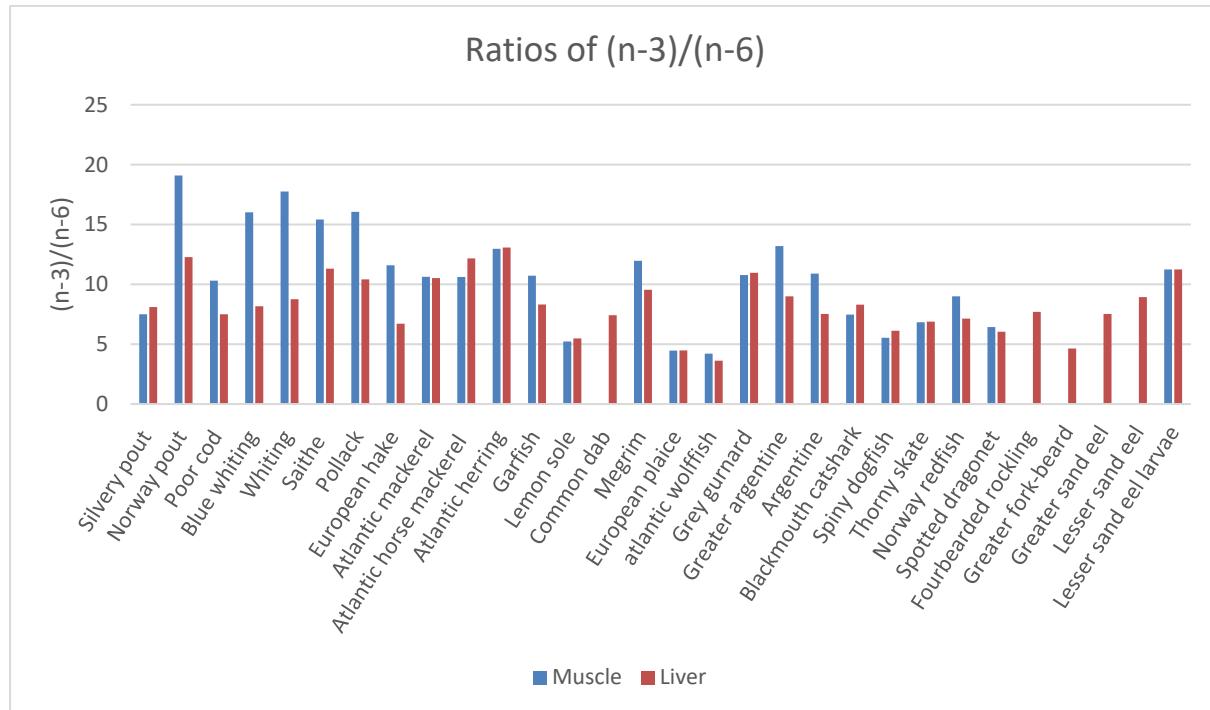
Figure 26: Ratios of (n-3) FAs to (n-6) FAs in muscle and liver samples.

4. Discussion

4.1. Optimization of the derivatization

PCA was applied to the results from the experimental design for the purposes of explorative analysis. Figure 27 and 28 shows biplots from the resulting PCAs. All variables were standardized prior to the PCA. As the responses all are fractions of the response total FA, it is no surprise that they lie close in proximity in the biplot. These responses are included to investigate whether any of the variables correlate with changes in yield for a specific category of FA, *i.e.*, SFA, MUFA or PUFA.

For an effect to be significant, its value should be larger than the majority of the effects. None of the interactions were significant. X1, time in oven, is the only variable that was significant for the responses total FA, SFA, MUFA and PUFA, and 20:5(n-3) in liver tissue but shows no significance for the muscle tissue. For the response of 22:6(n-3), X1 again was significant, but for this specific FA, X2, hexane before or after the oven, also indicated that it could be significant for muscle tissue. A student's t-test (α = 0.05), however, shows that there is no significant difference between the low and high group for X2 with p-values of 0.4 and 0.2 for 22:6(n-3) and 20:5(n-3), respectively. Since there is negligible difference when performing 1 or 2 extractions, it can be justified to reduce the number from 2 to 1 to save time during the procedure. As this result pertains only to that specific FA, it did not justify any change for the method. Introducing hexane before samples are put in the oven makes no difference for the time use

in the method. The results are also contradictory between muscle and liver samples for X2, and the biplot for muscle samples in Figure 28 shows that X2 is non correlated to the response FA. The muscle samples contain small amounts of fatty acid content compared to the saithe liver. Homogeneity can often be an issue with stringy muscle samples, and it cannot be excluded that there was a homogeneity issue or analytical error. RSD of the replicated experiment for this FA is 5.3 % which is the expected analytical measurement uncertainty from this method. The muscle samples have about 100 times less mg FA/100 mg wet weight in the tissue than in the liver (for this species) and emulsion often occurs when centrifuging lean muscle samples during the procedure, making the extraction-stage more difficult, which could impact the procedure. The use of an internal standard should however account for any loss of analyte.
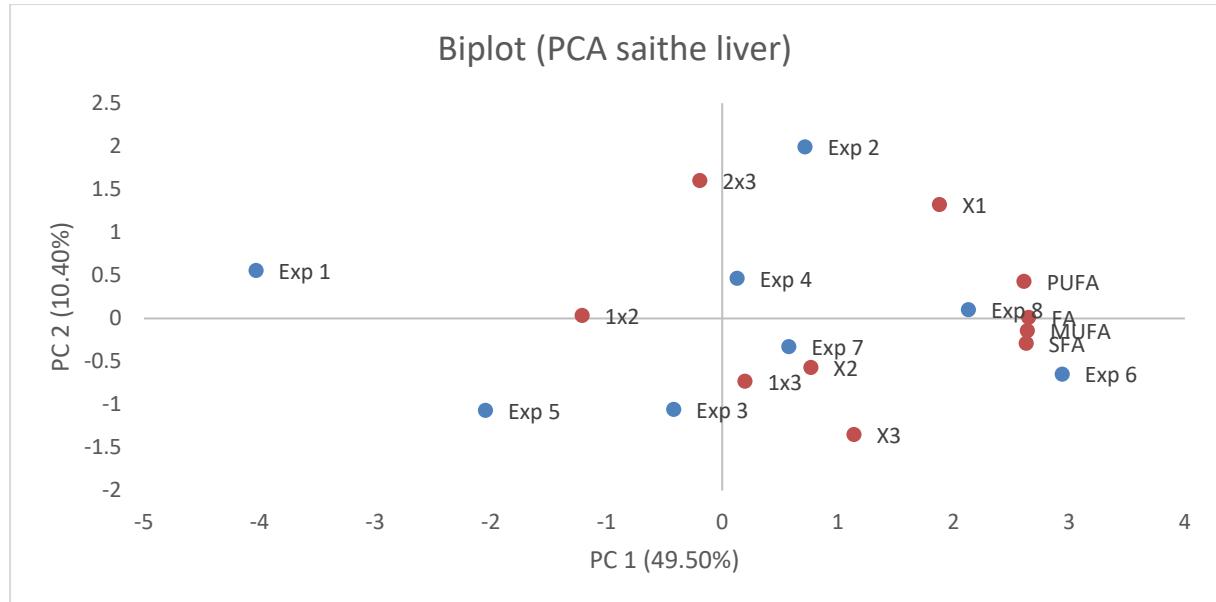
Figure 27: Biplot of the two first components from PCA of experimental design with the responses FA, SFA, MUFA and PUFA, all as mg FA/100 mg wet weight. The score values are blue, and the loading values are red.

The biplot from PCA of liver samples (Figure 27), shows that experiments 6 and 8 are the most optimal with respect to total FA and that experiment 1 has a strong negative correlation to experiments 6 and 8. Experiments 6 and 8 both have high levels of X1 and X2, whereas experiment 1 has low levels for all the variables. This shows that the conditions that are least optimal with respect to the response are those of experiment 1. The biplot shows that X1 is the variable that is most strongly correlated to the responses, which coincides with the calculated main effects in Table 17. A comparison of results between experiments of 1 hour and 2 hours, respectively, yielded different significance for different tissues. For liver samples a student t-test (α = 0.05) resulted in a significant p-value of 0.47 which would indicate that the two groups are different.

For the muscle samples, experiment 3 and 5 are the most optimal with regards to the response, and experiment 8 is the least optimal. This is almost opposite to the findings for the liver samples. None of the variables, however, show positive correlations to the responses. For muscle, all the effects are negative, meaning that high levels would have a negative impact on the yield.
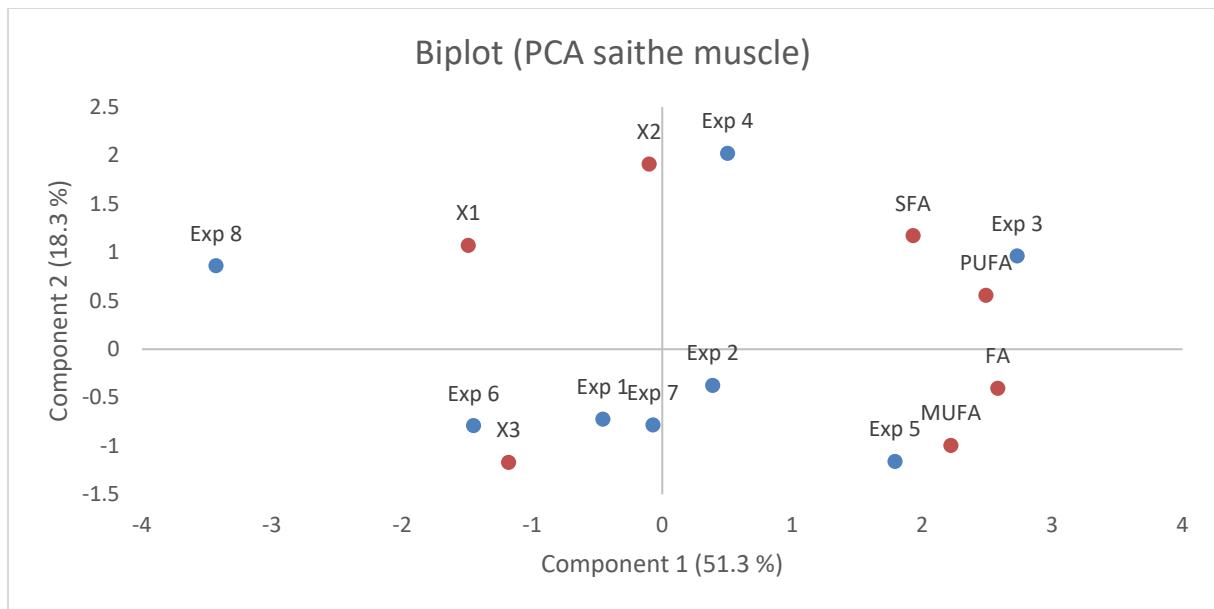
Figure 28: Biplot of the two first components from PCA of the experimental design with the responses FA, SFA, MUFA and PUFA, all as mg FA/100 mg wet weight. The score values are blue, and the loading values are red.

Replication of experiment 8 for the two tissues resulted in RSDs of 5.01 and 2.27% for muscle and liver tissue, respectively. A significant effect should be larger than the experimental errors (Nortvedt, 1996), considering this, X1 was the only effect that was considerably larger than the RSD (2.27 % for liver samples), with an effect of 4.12 for the response (liver samples). The only effect for the muscle samples that was larger than the RSD for the given tissue was X2 with regards to 22:6(n-3) for muscle samples, but as shown, the yields were not statistically different for the high and low levels for this variable. The reason for putting this variable in the design was not to investigate whether it could save time or not, it was to investigate whether it produced a higher yield or not when changing when the solvent was added. As this was not the case, the original method was not modified with regards to this variable.

The effect of X3, one or two extractions, was negligible and there was no statistical difference whether one or two extractions were performed. Comparing the high and low levels of X3 a with student's t-test ($\alpha = 0.05$) yielded p-values of 0.29 and 0.38, for liver and muscle, respectively. Since the effect of X3 is negligible, it was decided to modify the original method and reduce the number of extractions to 1. The extraction is one of the more time-consuming operations in this method, the operator must manually extract all sample, and so this helps optimizing the time usage, and indirectly the cost of performing the analysis.

4.2. Fatty acid and cholesterol content

The results of FA and cholesterol (mg/100 mg wet weight) shown in Table 19, shows that most of the fish analysed, store most of their fats in the liver, except for mackerel which is known to have fattier fillets. For some fish, there are large variations within the species. Spotted dragonet, for example, has an RSD of 113% for the liver samples. This variation may be attributed to analytical uncertainty or biological variation. As shown in the result for the experimental design, 4 and 5 replicates of the same samples had an RSD of around 2.3 % and 5% for the liver and muscle samples, respectively. This indicates that the large variation may lie within the samples could be caused by biological variation. Homogeneity of the samples is a very important aspect in analysis of biological tissues. Samples acquired from different regions of the same tissue may have different compositions. Unrepresentative sampling can cause large variation between the results, on top of biological variation. Differences in total FA content between genders of the fish were investigated for species with large variation between samples, but yielded no statistical difference between the male and the female groups when compared using a student's t-test ($\alpha = 0.05$). Cholesterol levels for muscle samples varies between fish, with an

average of 0.15±0.32 mg/100mg wet weight, and an RSD of 218%. Calculating cholesterol as a ratio between amount cholesterol and amount FA yielded much less variation, with an RSD of 66%. A scatterplot of FA amounts and cholesterol amounts showed no correlation between these two. This becomes apparent when comparing cholesterol levels of the fish with very high and low FA content in the muscle tissue. Mackerel has the highest FA content in the muscle and has the same cholesterol content as lemon sole that has the least amount of FA content in muscle tissue. Cholesterol breaks down during the methylation stage, and can be quantified, with high accuracy, by identifying the peaks of the decompositions and summing these. (Meier et al., 2006). Cholesterol levels for the liver samples vary less, with an average of 0.47±0.35 mg/100mg wet weight, and an RSD of 75%. Ratios between FA and cholesterol amounts also shows no correlation for liver tissue.

4.3. Fatty acid profiles

PCA was applied to the liver and muscle FA profiles. PCA is a great tool to visualise large amounts of data and helps to discern the similarities and differences between the fish. As there are many fish analysed in this project, it is not appropriate to dive deeply into trophic interactions between all of them. Instead, the focus of trophic interaction will be between the cod fish, pelagic fish and flatfish. These three groups represent fish that feed pelagically and fish that are benthic feeders. They also cover multiple trophic levels, from the small pouts to the larger saithe. Comparing the benthic flatfish to cod fish and pelagic fish is interesting as it could clearly show the differences in dietary habits. Many of the fish analysed in this thesis showed no reports in the literatures on FA profiles, which gives no background literature to compare with, but this also helps to show the usefulness of the database planned by the IMR. Table 24 shows a list of literature that will be compared to some of the FA profiles from this project.

The dendrograms in Figures 29 and 30 uses Euclidean distances to classify objects, and similar objects are linked together. The closer to the bottom the link is, the closer they are. The y-axis is dissimilarity. Variable correlations are not accounted for in such plots. Dendrograms are a fast way of classifying objects and to identify possible clusters. The dendrogram of liver samples shows that the most similar fish are pollack and saithe, whiting and hake, and poor cod and greater fork-beard. The dendrogram can be broken down into three main groups, the one in the middle contains most of the cod fish, and the one to the right contains a mix of all fish types. These two groups are more similar to each other than to the big group on the left, which contain a mix of fish types but no cod fish. This plot shows a clear dissimilarity between poor cod and the other cod fish, as was observed in the FA profiles for the cod fish. For muscle samples, the dissimilarities between all fish are generally lower compared to liver samples. All the cod fish are clustered in one group, except for silvery pout. The muscle tissue of the pelagic fish herring is far more similar to mackerel and horse mackerel than for liver samples. Again, there are three groups. The group in the middle contains a variety of fish and fish types, and the one to the right contains pelagic fish and two benthic fish. Plots like dendrograms can be used as a tool to identify clusters, but the PCA will better explain the relationships between the species as it will also explain variable variation and show correlations.
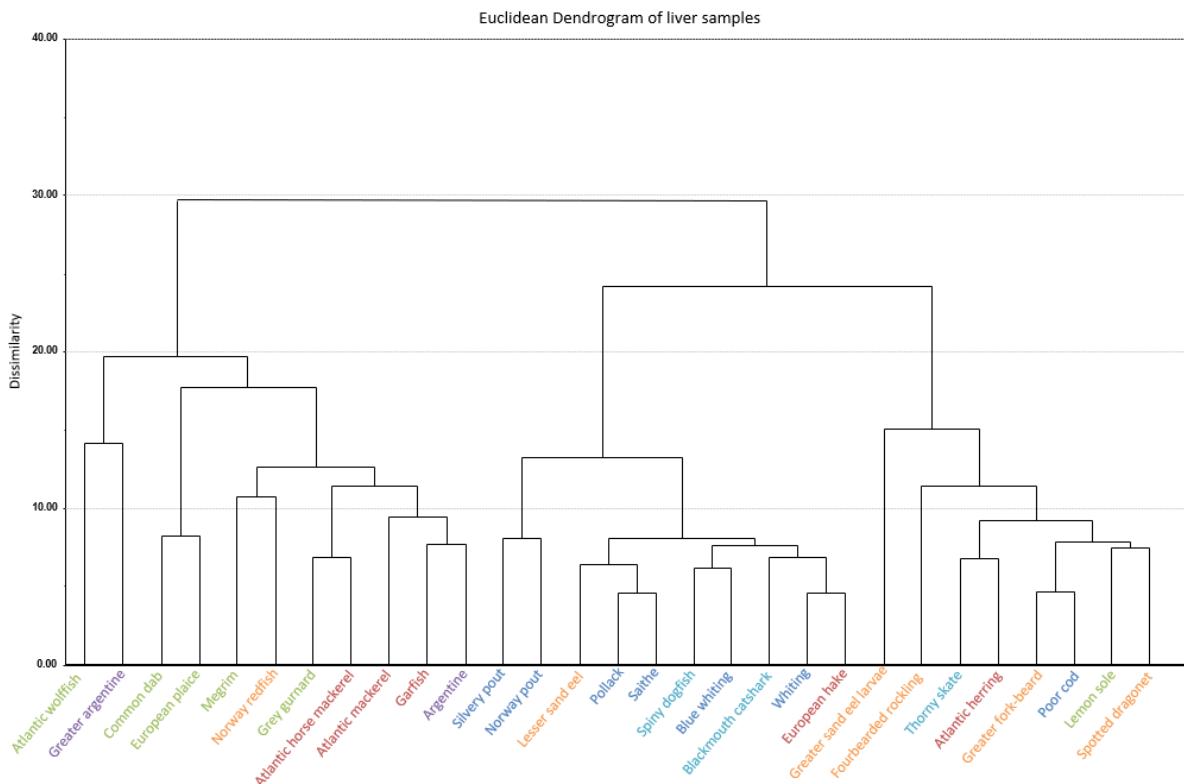
Figure 29: Dendrogram for the liver FA profiles.
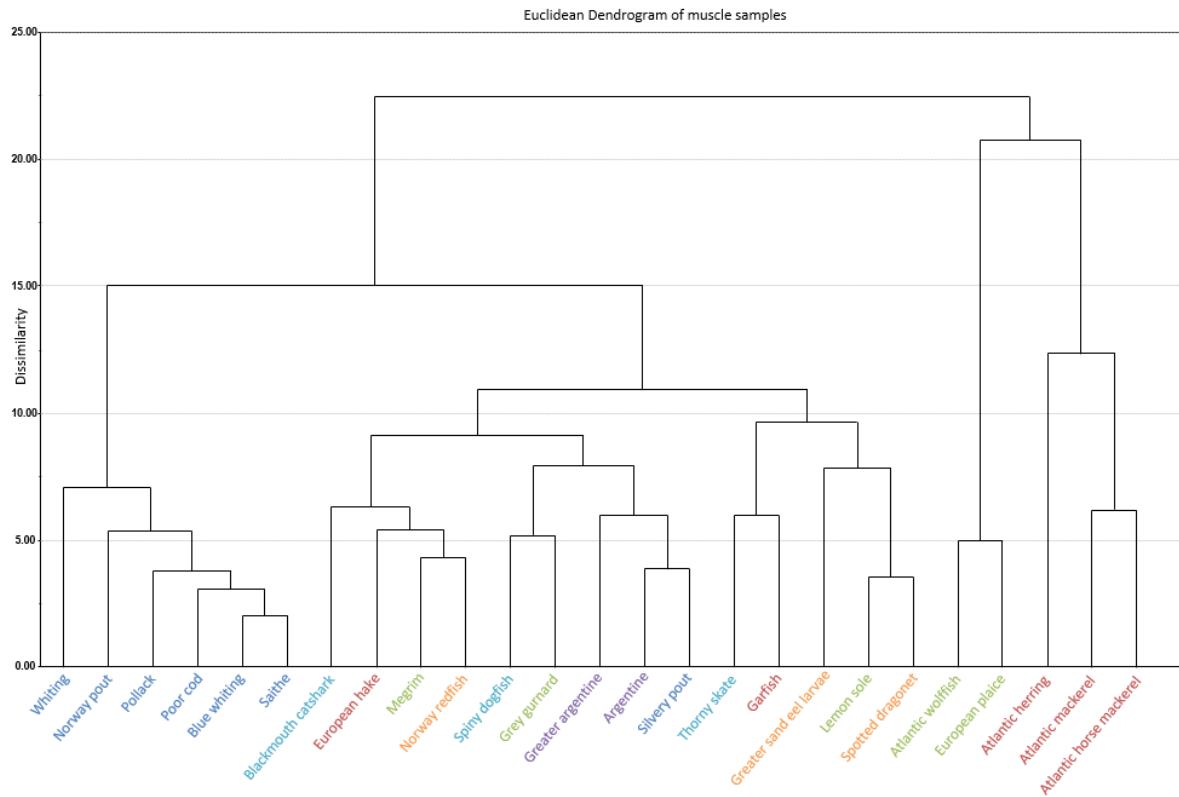
Figure 30: Dendrogram for the muscle FA profiles.

4.3.1. Principal component analysis

Table 23: Abbreviations used for PCA plots.

Abbreviation	Species	Abbreviation	Species
SP	Silvery pout	NRf	Norway redfish
NP	Norway pout	GG	Grey gurnard
PC	Poor cod	AWf	Atlantic wolffish
BW	Blue whiting	SpD	Spotted dragonet
Wh	Whiting	FbR	Four-bearded rockling
Pol	Pollack	GFB	Greater fork beard
Sa	Saithe	AMa	Atlantic mackerel
Ls	Lemon sole	AHMa	Atlantic horse mackerel
Cd	Common dab	AHe	Atlantic herring
Me	Megrim	Ga	Garfish
EuP	European plaice	GrA	Greater argentine
BC	Blackmouth catshark	Arg	Argentine
EuH	European hake	GSE	Greater sand eel
SD	Spiny dogfish	LSE	Lesser sand eel
TS	Thorny skate	LSEl	Lesser sand eel larvae

To make the plots from the PCAs easier to read, abbreviations have been utilized, which are listed in Table 23. By the nature of the weighting chosen for the PCAs, by dividing variables by absolute mean, the standard deviation is converted to RSD. This allows for the variables with the highest relative standard deviation to carry the most weight. Figure 31 shows a score plot and loadings plot from PCA of liver samples. For this PCA, component 1 explains 42.0 % of the variance and component 2 explains 12.2 % of the variance in the data. The cod fish saithe, pollack, whiting and blue whiting are grouped together with herring, blackmouth catshark, hake, and lesser sand eel, indicating that these have similar FA profiles. Further up component 1 lies spiny dogfish, and the two cod fish, Norway pout and silvery pout. They are slightly more separated, compared to the first group, along both components but indicate similarities in FA profiles. The first component has high positive contributions of 18:4(n-3) and C20 and C22 MUFAs, which are positively correlated. For the fish in these two groups, this means that higher scores in component 1, are associated higher content of 22:1(n-11) and 20:1(n-9), and this coincides with the FA profile comparisons for the cod fish. 20:1(n-9) has a strong positive correlation to 22:1(n-11), both of which are typical *Calanus* FATM (Dalsgaard et al., 2003). As these fish move up the y-axis, they become more associated with the main positive contributes of component 2, which are 16:1(n-9) and 20:4(n-6).

In the middle of the plot, mackerel, greater sand eel, megrim and Norway redfish are grouped together. The highest negative contributions to component 2 come from 18:1(n-9), 18:1(n-11) and 16:1(n-7). This shows that the four fish are associated with high levels of these FAs. The cosine of the angle between megrim and silvery pout is 0.097, and this group of fish are non-correlated to the two groups associated with high levels of 22:1(n-11). Wolffish, plaice, garfish and common dab are quite similar in FA profiles as seen in the score plot. The main negative contributions for component 1 come from 20:4(n-6) and 16:1(n-9), which mean that these four fish are associated with high levels of 16:1(n-7), 18:1(n-9), 16:1(n-9) and 20:4(n-6) and shows negative correlations to groups containing cod fish. The common dab lies in between the plaice, wolffish and garfish, and horse mackerel and gurnard. The fish in the second quadrant are mostly spread out along the first component, and since the main negative contributions of component 1 are the same as the main positive contributions of component 2, lower scores in the first and higher scores in the second component ultimately indicate higher levels of 16:1(n-9) and 20:4(n-6). None of the fish have 16:1(n-9) levels that exceeds 1%, except the four bearded rockling and has among the highest levels of 20:4(n-6). The two mesopelagic fish, argentine and greater argentine are almost non-correlated, cosine of the angle between them is 0.19.
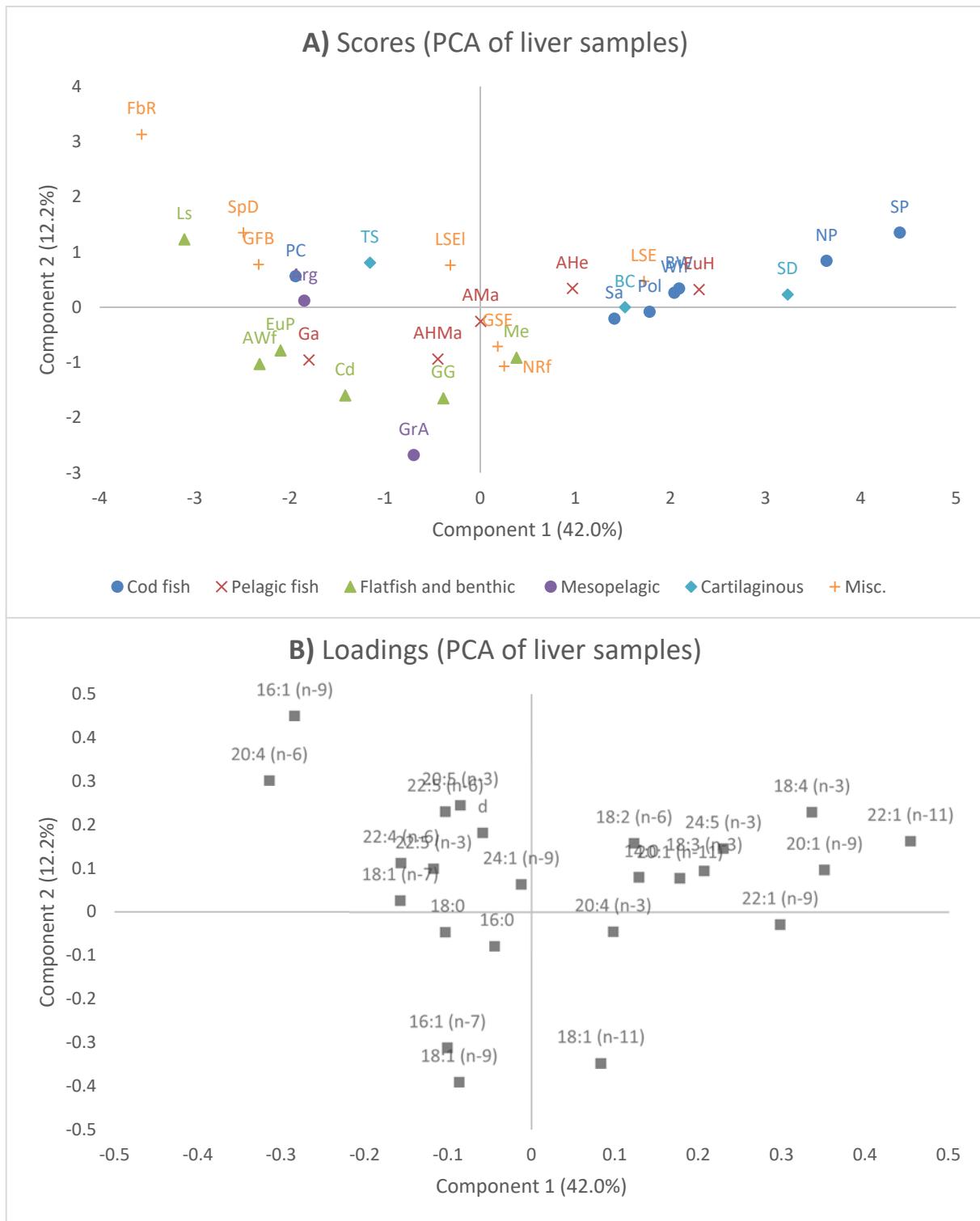
Figure 31: A) Scores- and **B)** loadings plots from PCA of FA profiles for liver samples.

Figure 32 shows a score plot and loadings plot from PCA of muscle samples. Component 1 and 2 explain 50.1% and 16.4% of the variance in the data, respectively. The four "pelagic" fish are spread apart, with hake and horse mackerel lying close together and mackerel and herring lying close together. The main positive contributions of component 1 comes from 20:1(n-11), 18:4(n-3) and 20:1(n-9) (descending order), which is similar to that of PCA for liver samples. Mackerel and herring are associated with high levels of these FAs, and especially 22:1(n-11). The high levels of 22:1(n-11) compared to other muscle samples was also observed in the FA profile (Figure 18). Megrim lies close to the hake and horse mackerel, and as shown in the FA profiles, contains considerably higher amounts of 22:1(n-11)

55

compared to the other flatfish and benthic fish. Towards the middle of the plot lie the two cartilaginous fish blackmouth catshark and spiny dogfish, which have similar FA profiles in muscle tissues. The main positive contributes for component 2 are 22:4(n-6), 20:4(n-6), 22:1(n-11) and 16:1(n-7). Below the two cartilaginous fish, lies a group of fish consisting of grey gurnard, great argentine, Norway redfish, larvae of greater sand eel and Norway pout. This group is associated with negative contributions from component 2 and 20:1(n-11), 18:4(n-3) and 20:1(n-9) from component 1, in very small degree.
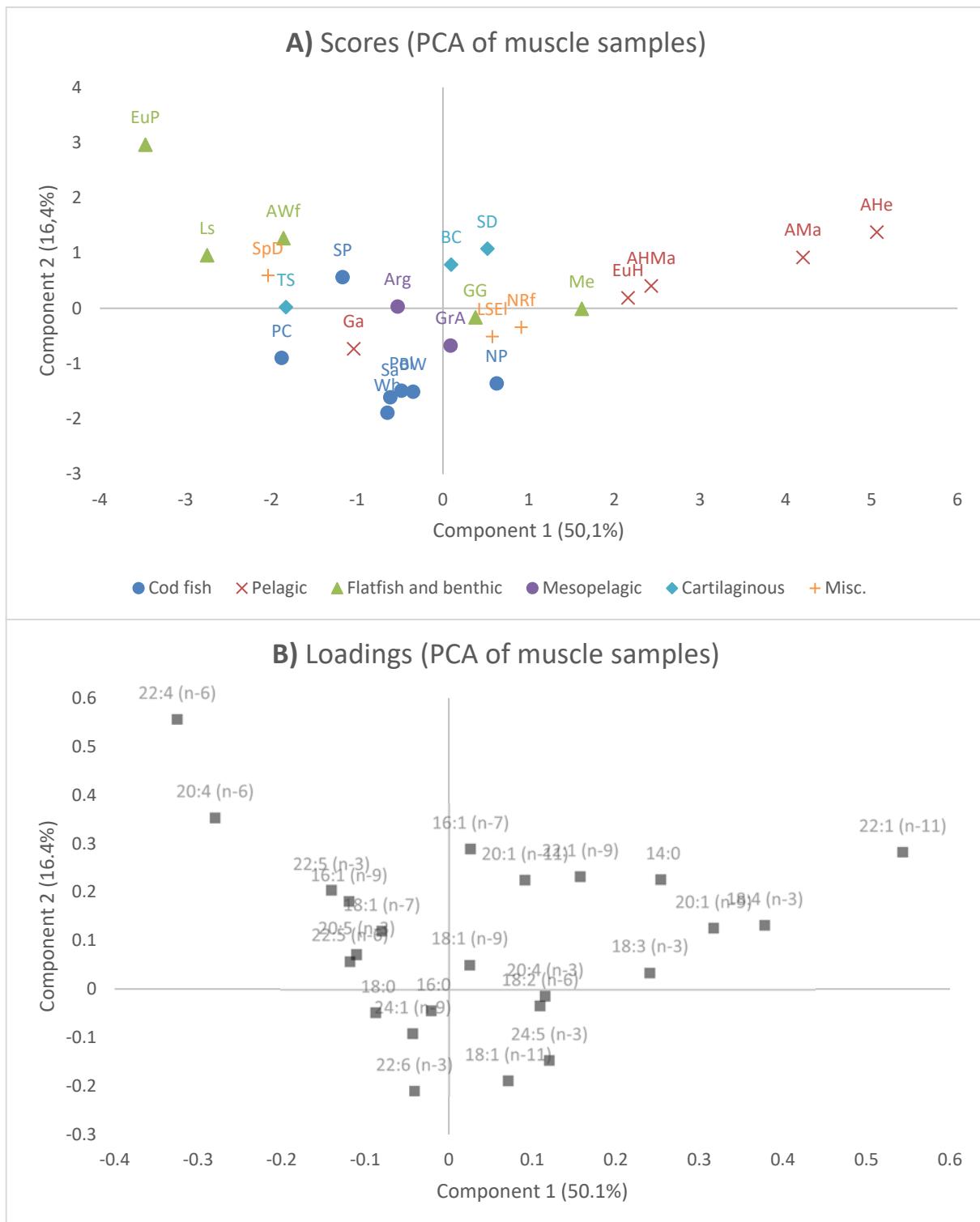
Figure 32: **A)** Scores- and **B)** loadings plots from PCA of FA profiles for muscle samples.

As seen in the PCA for liver samples, cod fish are mostly grouped together, except for silvery pout, poor cod and Norway pout. This shows that the four cod fish whiting, saithe, pollack and blue whiting have similar FA profiles. These are in the third quadrant of the score plot and are associated with the main negative contributions of component 2, which are 22:6(n-3) and 18:1(n-11). Both contributes little compared to the positive contributions, indicating that these FAs are not very well explained by the component, and this may largely be attributed to generally high levels of 22:6(n-3). The RSD of 22:6(n-3) for all muscle samples is 27%, which is the third lowest behind 18:0 and 16:0, both of which contribute very little to the two components. This shows low variation in the levels of these three FA along with 20:5(n-3) which also showed generally high levels for muscle samples), and that the main difference in FA profiles in muscle samples do not lie within these. The two cod fish poor cod and silvery pout are associated with the main negative contributions for component 1 which are 22:4(n-6) and 20:4(n-6). These two cod fish lie in the third and second quadrant, respectively, with thorny skate in between them. In the top left corner of the second quadrant lies the plaice and is clearly associated with high levels of 22:4(n-6) and 20:4(n-6), as are the sole and wolffish. The two main differences between FA profiles of muscle samples seems to occur in either high levels of the *Calanus* FATMs 22:1(n-11) and 20:1(n-9), and high levels of 22:4(n-6) and 20:4(n-6).

SFAs 14:0, 16:0 and 18:0 contribute much less to the principal components than MUFAs and PUFAs, as illustrated in the loadings plots for the PCAs. Shorter chained dietary SFAs such as 14:0 and 16:0 enter the biosynthetic pathway and are further modified to longer-chained SFA and MUFA in *Calanus* copepods (Sargent and Henderson, 1986). Fish can, like most other organisms, biosynthesize SFA with up to 18 carbons *de novo* and further desaturate these into MUFA following the common lipid pathway (Dalsgaard et al., 2003). SFA is not preferentially incorporated into PPL in the way that PUFA is.
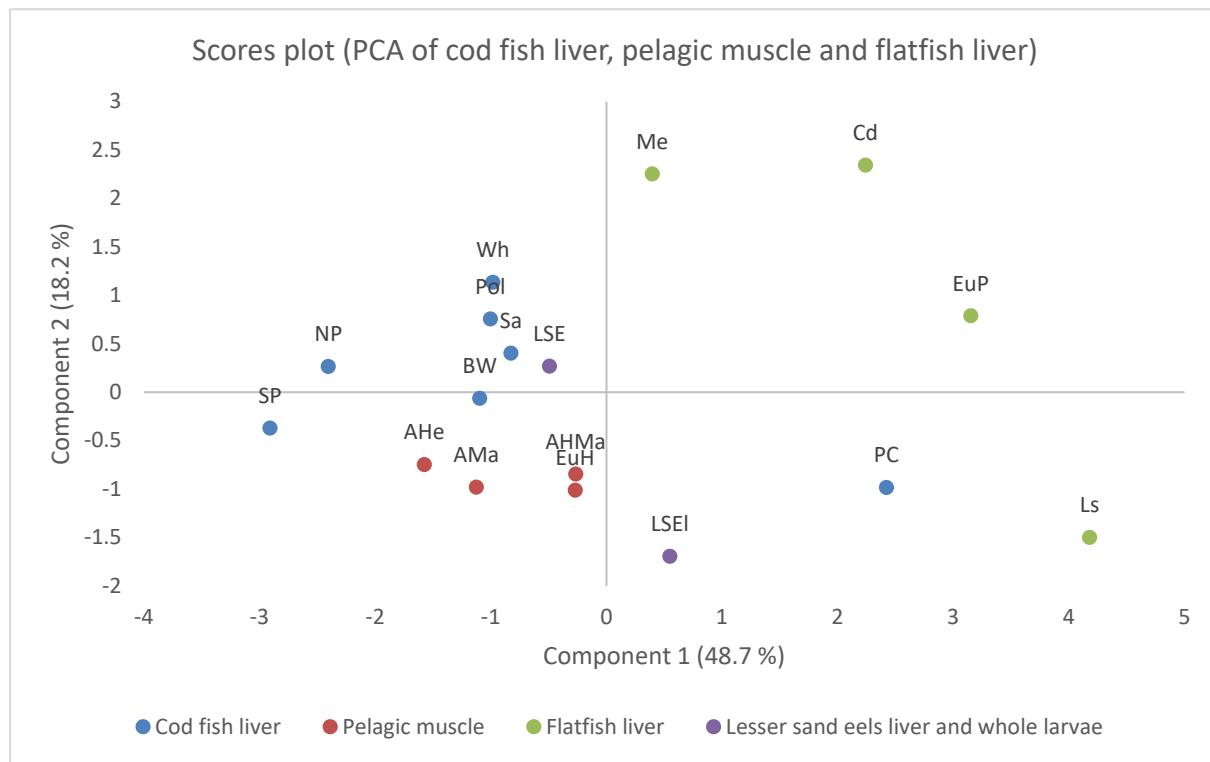
Figure 33: Scores plot from PCA of FA profiles for cod liver, pelagic muscle and flatfish liver samples.
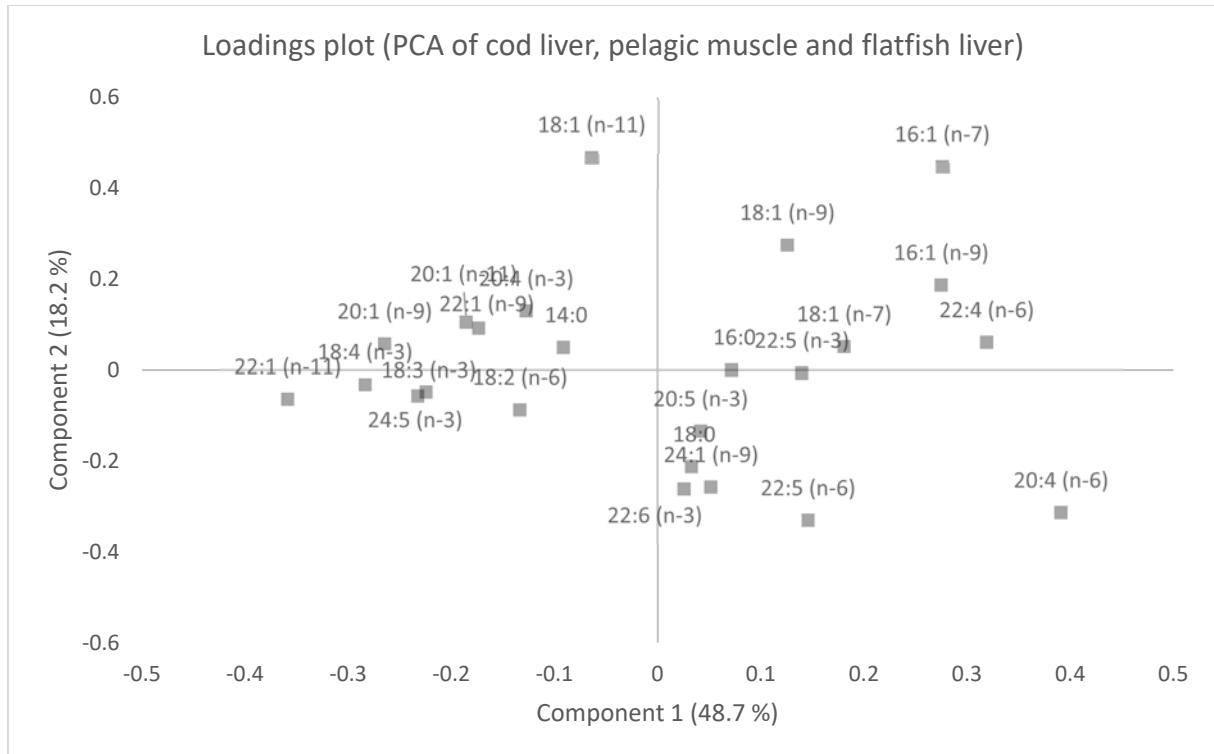
Figure 34: Loadings plot from PCA of FA profiles of cod liver, pelagic muscle and flatfish liver samples.

4.3.2. Trophic interactions and differences in FA profiles between cod fish, pelagic fish and flatfish

To investigate the similarities between the pelagic fish muscle and cod fish, a PCA was conducted on a dataset consisting of cod fish livers, muscle samples of the four pelagic fish mackerel, horse mackerel, herring and hake, in addition to these, liver samples of flatfish were also included. This was done to compare fish that are known to feed on the seabed to fish that feed pelagically. When comparing FA profiles of muscle and liver it is important to keep in mind that most fish have very lean muscle. MUFAs are virtually not present in fish PPL, suggesting that they are used preferably for TAG and fat storage, rather than involved in membrane functions (Sargent and Whittle, 1981). As seen in the profiles of the fish analysed, 22:6(n-3) levels are generally higher in muscle tissue. This is a result of 22:6(n-3) being conserved up the food web and preferentially incorporated into PPL (Dalsgaard et al., 2003). In the case of this PCA, the profiles showed that the pelagic muscle samples were similar to the profiles of the cod fish livers, and also contained higher levels of *Calanus* MUFAs. Figures 33 and 34 show the scores plot and loadings plot, respectively, for this PCA. The pelagic muscle samples lie very close to the liver samples of cod, illustrating clearly that they have similar FA profiles. The flatfish are not close together, but they lie in the opposite direction along component 1 compared to the other fish, showing the difference in diets. Benthic feeders are generally higher in 20:4(n-6) but have more complex and mixed diets compared to those of pelagic feeders (Kelly and Scheibling, 2012). To further discuss similarities and dissimilarities of FA profiles for the cod fish, pelagic fish and flatfish, studies of their diets must be included.

Whole Norway pout was found inside the belly of the pollack, and whiting analysed in this project. Norway pout and other smaller fish, such as sand eels, are known preys to whiting and larger fish (Hislop et al., 1991). As the PCA shows, the two smaller cod fish are much closer together in score plots, whereas the bigger cod fish are clustered together with the pelagic fish, and lesser sand eel. In a stomach analysis, Norway pout was also found in the saithe in the North Sea (Du Buit, 1991). Larger cod fish such as pollock and saithe will also feed on blue whiting and herring (Havforskningsinstituttet, 2019c). This illustrates the three trophic levels within the cod fish analysed for this thesis. The smallest fish, silvery

pout and Norway pout are eaten by larger cod fish such as whiting, poor cod and blue whiting, which in return are eaten by saithe and pollock (illustrated in Figure 35). And as the results show, the silvery pout and Norway pout are specialized in consuming *Calanus*. Interestingly, the poor cod have a drastically different FA profile compared to the other cod and pelagic fish. No reports were found of FA profiles of the poor cod, but stomach analyses of poor cod from the Faroe bank shows that their diets consisted mostly of prey living on or near the bottom, and particularly shrimps and galatheids (Magnussen and Magnussen, 2009). In the north eastern North Sea, polychaetes occurred in 83% of the poor cod stomachs analysed (Albert, 1993), which is also one of the main prey of flatfish in the southern bight of the North Sea (Amara et al., 2001, Fishbase, 2021a). Since no stomach analysis has been conducted in this project, a direct dietary overlap between poor cod and flatfish cannot be concluded, but the results and literature mentioned shows that they both consume polychaetes as a main part of their diet, and this can help explain why the poor cod is so dissimilar to the cod fish, and more similar to flatfish in the FA profile. The flatfish are known benthic feeders, and feed on the seabed, and are associated with higher levels in n-6 PUFAs 20:4(n-6) and 22:4(n-6) and C16 MUFAs. The PCA shows that the larger cod fish feed more pelagically, alongside and on the smaller pelagic fish mackerel and herring. Herring is an important prey of large cod fish such as the saithe and pollack (Cormon et al., 2016), as well as for the hake (Fishbase, 2021b). Stomach analyses of hake from Celtic sea showed the diet to consist of whiting, poor cod, Norway pout, as well as mackerel and horse mackerel (Du Buit, 1996). The European hake has been reported to be demersal by day and pelagic by night (Fishbase, 2021b) and is well adapted to live both demersally and pelagically (Bergstad, 2009). From the PCA, it is evident that hake feed on many of the same prey as the cod fish.

Mackerel and herring are the two of the most important pelagic fish stocks. In an article by Bachiller et al. (2016) about feeding ecology of mackerel, herring and blue whiting, it was found through stomach sampling that mackerel and blue whiting tend to have low dietary overlap. They found that the diet of mackerel and herring was dominated by *Calanus* copepods and that the two species had overlapping diets. The blue whiting was found to rely more on larger prey items such as amphipods. Interestingly, amphipods store both WE and TAG that are rich in 20:1 and 22:1 MUFA, indicating that they either deposit WE directly from preying on *Calanus* or they possess the ability to biosynthesize these FAs *de novo* (Dalsgaard et al., 2003). Assuming that amphipods cannot biosynthesize these FA, *Calanus* FATM can be transferred up the food chain through amphipods into blue whiting, giving similar FA profile as the mackerel and herring. The biggest difference between FA profiles of mackerel and blue whiting is that the mackerel have higher levels of 22:6(n-3), which is a typical dinoflagellate FATM, but as the results show, 22:6(n-3) tends to be high in muscle samples as it is incorporated into PPL (Dalsgaard et al., 2003). Dalsgaard et al. (2003) found through review of literature that the FA composition of NL usually reflects the trophic influences in "end" predator better that composition of PL, but if the intention is to study FA profiles of a potential prey, total lipid is preferable, *i.e.*, FA in PL such as PPL can elude information about the predator.
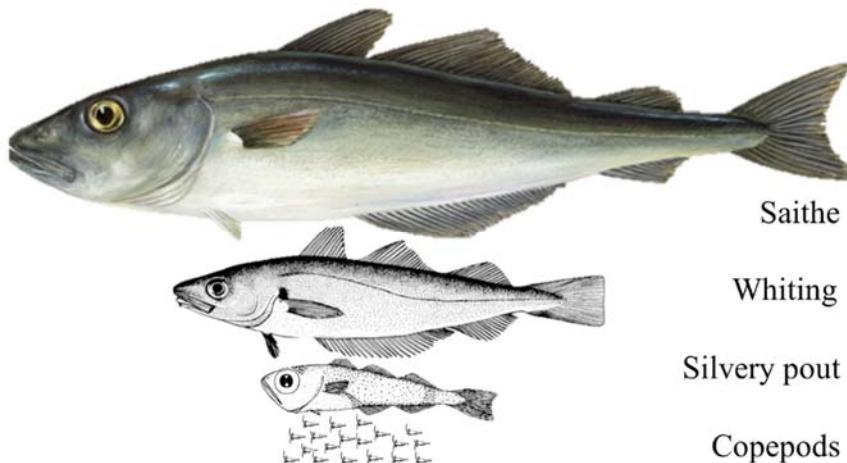
Figure 35: Illustration the trophic levels within the cod fish. Illustrations adapted from (MSC, 2021, FAO, 2021, Watson, 1982, Harris, 2001)

FA profiles and FATMs are cannot perfectly describe the diet of a fish, but alongside stomach analysis, and historical data, FATMs can elude differences in diet and maybe show deviations from what the diet was expected to consist of. Some FATMs are very useful, such as C20 and C22 MUFAs for *Calanus*, which is well-documented (Dalsgaard et al., 2003). Central prey of the pelagic food web such as *Calanus,* which are preyed on by Norway pout, which again is preyed on by whiting, which again is preyed on by saithe, shows the usefulness of the FATMs, when discussing FA profiles and diets.

4.4 Comparing content of fatty acids of different categories

Comparison of SFA levels in muscle and liver tissue shows that they are quite similar but tend to be higher in the muscle tissue for most fish. A students t-test gave a significant p-value of 0.018 when comparing the two groups, indicating that there is statistically significant difference between them. Furthermore, comparing SFA in muscle and liver for pelagic fish yielded a p-value of 0.5, which indicates that SFA levels are similar in the two tissues for these fish. The overall average levels of SFA are 25.6±1.7 % and 23.7±3.4 % for muscle, and liver, respectively. This gives RSDs of 6.6% and 14.4% for the two tissues and gives the indication that the variation is bigger within the liver samples. These comparisons were made with fish that has both muscle and liver tissue, and so those that just have liver samples are excluded. A similar comparison for MUFAs shows once again that MUFA levels generally are higher in liver samples, with an average of 43.2 ± 9.2%, compared to 24.3 ± 7.7 % for the muscle samples. RSDs are higher, compared to SFA levels, indicating larger variation within the fish than for SFA (31.5% for muscle and 21.2% for liver). PUFA levels are generally higher in muscle tissue with an average of 49.5 ± 7.5% and RSD of 15.1%, compared to an average of 32.2 ± 8.5% and RSD of 26.3% for liver samples. These results show that SFA levels vary much less than those of MUFA and PUFA, especially in muscle tissue but still vary less in liver tissue compared to the variation in MUFA and PUFA levels.

The ratios of (n-3) to (n-6) FAs are generally high for all fish analysed. PUFAs are important FAs for polar lipids in biomembranes of fish, and the high levels of n-3 FAs have been attributed to the fluidity of the membranes. (n-3) FAs may ensure functional integrity of biomembranes at lower temperatures, but has also been related to structural role rather than that of determining fluidity of the membrane (Dalsgaard et al., 2003). Figure 26 shows the ratios for muscle and liver samples. For the cod fish, the ratios are higher in muscle tissue than liver, generally for the other fish the ratios are similar between the two tissues.

60

4.5. Comparing the FA profiles of previous work

Table 24: Review of literature on FA profiles of the species of fish analysed.

Cod fish	*Lipid and fatty acid data*
***Silvery pout* (Gadiculus argenteus)**	No reports found
Norway pout	(van Oevelen et al., 2018)
***Poor cod* (Trisopterus minutus)**	No reports found
***Blue whiting* (Micromesistius poutassou)**	(Guil-Guerrero et al., 2011, Petursdottir et al., 2012)
***Whiting* (Merlangius merlangus)**	(Ghanawi and McAdam, 2020)
***Pollack* (Pollachius pollachius)**	No reports found
***Saithe* (Pollachius virens)**	(Budge et al., 2020, Budge et al., 2016, Arechavala-Lopez et al., 2015, Skog et al., 2003, McGill and Moffat, 1992)
Merlucciidae	
***European hake* (Merluccius merluccius)**	(Guil-Guerrero et al., 2011, Kucukgulmez et al., 2008, Soriguer et al., 1997, Mendez, 1997, Mendez and Gonzalez, 1997, Lloret et al., 2008)
Argentinidae	
***Argentine* (Argentina sphyraena)**	No reports found
***Greater argentine* (Argentina silus)**	No reports found
Scorpaenidae	
***Norway redfish* (Sebastes viviparus)**	(Bromaghin et al., 2013, Joensen and Grahl-Nielsen, 2000, Joensen and Grahl-Nielsen, 2001, Joensen and Grahl-Nielsen, 2004, Petursdottir et al., 2008a, Petursdottir et al., 2008b)
***Grey gurnard* (Eutrigla gurnardus)**	No reports found
Pelagic fish	
Scombridae	
***Atlantic mackerel* (Scomber scombrus)**	(Hemre et al., 1997, Romotowska et al., 2016, Guizani and Moujahed, 2015, Cardona et al., 2015, El Oudiani et al., 2019)
Carangidae	
***Atlantic horse mackerel* (Trachurus trachurus)**	(Bandarra et al., 2001, Celik, 2008, Orban et al., 2011)
Clupeidae	
***Atlantic herring* (Clupea harengus)**	(Ackman et al., 1975, Aidos et al., 2002, Aro et al., 2000, HAMRE et al., 2003, Henderson and ALMATAR, 1989, Jensen et al., 2007, Keinanen et al., 2017, Linko et al., 1985, Murzina et al., 2012, Navarro and Sargent, 1992, Rojbek et al., 2014)
Belonidae	
***Garfish* (Belone belone)**	(Cardona et al., 2015, Kocatepe and Turan, 2012, Tufan et al., 2018)
Flatfish	
***Lemon sole* (Microstomus kitt)**	No reports found
***Megrim* (Lepidorhombus whiffiagonis)**	(Barbosa et al., 2018)
***Common dab* (Limanda limanda)**	(Lund, I. (2007).
***European plaice* (Pleuronectes platessa)**	(Dickeycollas and Geffen, 1992, Kakela et al., 2009, Owen et al., 1972, Rainuzzo et al., 1992)
Anarhichadidae	
***Atlantic wolffish* (Anarhichas lupus)**	No reports found

Lotidae	
Four-bearded rockling (Enchelyopus cimbrius)	No reports found
Phycidae	
Greater fork-beard (Phycis blennoides)	No reports found
Cartilaginous fish	
Blackmouth catshark (Galeus melastomus)	(Hornung et al., 1994)
Spiny dogfish (Squalus acanthias)	(Kang et al., 1997, Kang et al., 1998, Sargent et al., 1971, Sargent et al., 1972, Stefanov et al., 1997)
Thorny skate (Amblyraja radiata)	No reports found
Callionymidae	
Spotted dragonet (Callionymus maculatus)	No reports found
Sand eels	
Ammodytidae	
Lesser sand eel (Ammodytes marinus)	(Dalsgaard and St John, 2004, Danielsen et al., 2016)

The review of literature on FA profiles and compositions on the fish analysed in this thesis is listed in Table 24. For many of the species, no reports on FA or lipid data could be found. This illustrates one of the reasons why IMR want to build a database of FA data, to be a resource for others to use and compare results with. The literature for cod fish and pelagic fish compared to the results obtained in this thesis.

Guil-Guerrero et al. (2011) analysed the FA content in liver samples from Atlantic mackerel and blue whiting, among other fish, bought at a fish market in Spain. The blue whiting had considerably higher content of 22:6(n-3) and 18:1(n-9). It is interesting that 18:1(n-9) was elevated at this FA have been shown to increase during starvation, but also as an indicator for herbivorous versus carnivorous feeding and is not unambiguous for marking either of the two (Dalsgaard et al., 2003). The study did not include 22:1(n-11), which would have been interesting to compare, as *Calanus* is constitute an important role in northern and arctic seas (Falk-Petersen et al., 2009). Ghanawi and McAdam (2020) analysed muscle of whiting from the east coast of Scotland, sampled near fish farms and compared them to reference whiting. The fish feeding in proximity to fish farms had elevated levels of PUFAs and much higher ratios of (n-3)/n-6). The FA profile for the muscle samples of the reference whiting was almost identical to FA profiles obtained in this project. No liver samples were analysed. Arechavala-Lopez et al. (2015) determined the FA profiles and compared saithe that was feeding close to salmon farms and unaggregated saithe. Both profiles are similar to the profile obtained in this project, but the analyses showed that the profiles were statistically different for the two groups of saithe. The farm-aggravated saithe had increased levels of MUFAs and PUFAs, while the unaggregated saithe had higher levels of SFAs. Hake was included in the fish liver analysed by Guil-Guerrero et al. (2011) but Mediterranean as opposed to European as analysed in this project. Mediterranean hake had higher levels of 18:1(n-9) compared to the European hake, and low levels of 20:1(n-9). This reflects the dietary differences of the fish from two widely different habitats, indicating that Calanus copepods capable of synthesising C20 and C22 MUFAs are not as abundant in the Mediterranean as it is in the North Sea. Total lipid analyses of mackerel from the Icelandic waters by Romotowska et al. (2016) showed the seasonal variation in the FA profiles. As total lipid was analysed it is not directly comparable to the muscle samples analysed in this project. El Oudiani et al. (2019) analysed muscle samples of mackerel from the middle east which had twice as high levels of 22:6(n-3), which could be a result of a more dinoflagellate dominated diet compared to that of the mackerel from the North Sea.

4.6. Fatty acid trophic markers

FATMs introduced in Section 1.3.8. are shown in Figure 36 – 41. The main differences will be discussed. All the FATMs are listed in Table 6.
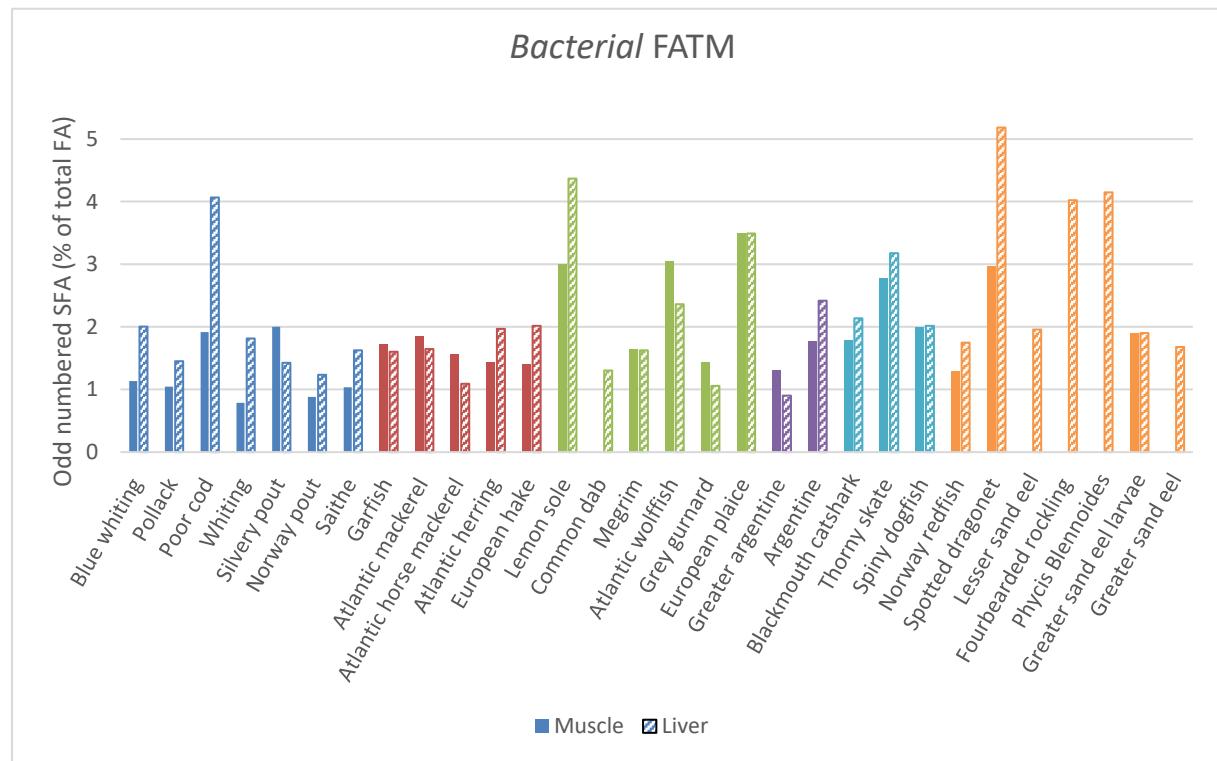
Figure 36: Bacterial FATM "odd numbered SFA" for all species.

Levels of two bacterial FATMs are shown in Figures 36 and 37. Lemon sole, plaice, spotted dragonet, four bearded rocking and greater fork-beard show the highest levels of these bacterial FATM, indicating a higher proportion of bacteria in the diet or in their preys, depending on their trophic level. Muscle samples contain smaller amounts compared to the liver, except for the plaice which contains equal levels of the FATM in muscle and liver tissue. For the second bacterial FATM, odd numbered MUFA, again the lemon sole, plaice, and dragonet with the addition of lesser sand eel, have the highest levels. Four bearded rockling and greater fork-beard have lower levels of this FATM compared to the first bacterial FATM. The presence of bacterial FATMs are typical for fish that feed on the seabed (Dalsgaard et al., 2003) such as the flatfish analysed in this project. This is illustrated here. Once again, the poor cod stands out from the other cod fish and as shown in the PCAs, its FA profile is similar in some cases to those of benthic feeders.
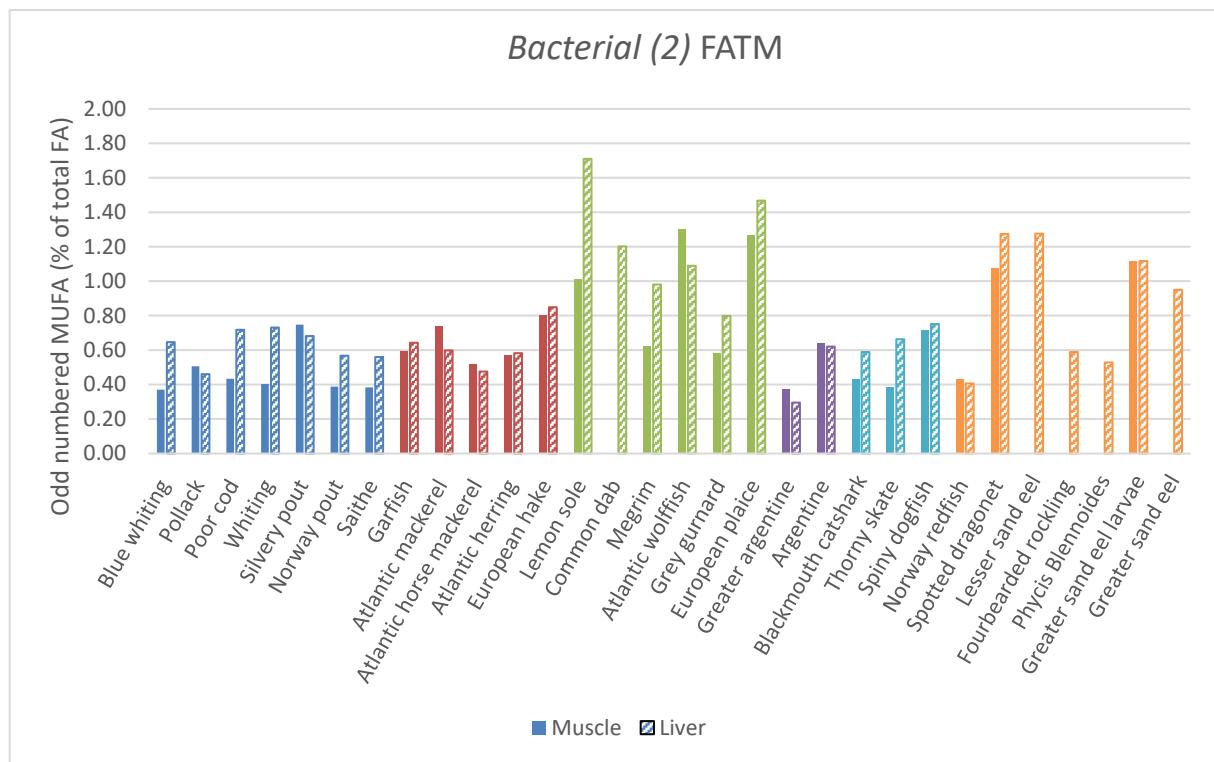
Figure 37: Bacterial FATM "odd numbered MUFA" for all species.

As seen from the FA profiles and PCAs, the cod fish are rich in Calanus FATMs, 20:1(n-9). 22:1(n-11) and 22:1(n-9). The pelagic fish, except garfish, also contain considerable amounts of these FATMs along with the cartilaginous catshark and spiny dogfish. The hake contains considerable amounts in both liver and muscle samples, separating it slight from rest. As demonstrated by the PCAs, mackerel and herring muscle samples are similar in profile to those of the liver samples in cod fish, and so the muscle samples for these two fish are richer in *Calanus* FATMs than liver samples. The lesser sand eel also contains considerable amounts of these FATMs. The fish that had the highest levels of the bacterial FATMs, have relatively low amounts of *Calanus* FATMs, and vice versa showing the difference of pelagic and benthic feeding. Figure 38 shows 20:1(n-9) levels plotted against 22:1(n-11) levels. There is a clear positive correlation between the two FAs, as was also observed in the PCAs. From the PCAs, it was shown that 18:4(n-3) has a positive correlation with the *Calanus* FATMs. 18:4(n-3) is a typical dinoflagellate FATM and dinoflagellate are also rich in 18:5(n-3) but is not observed in any of the fish as it is readily elongated into longer (n-3) FAs (Dalsgaard et al., 2003). Atlantic herring has the highest values of both *Calanus* FATM of the muscle samples as seen in the plot. Herring is a pelagic fish, and in the pelagic food web, herbivorous calanoid copepods are important for transferring energy up to higher trophic levels.
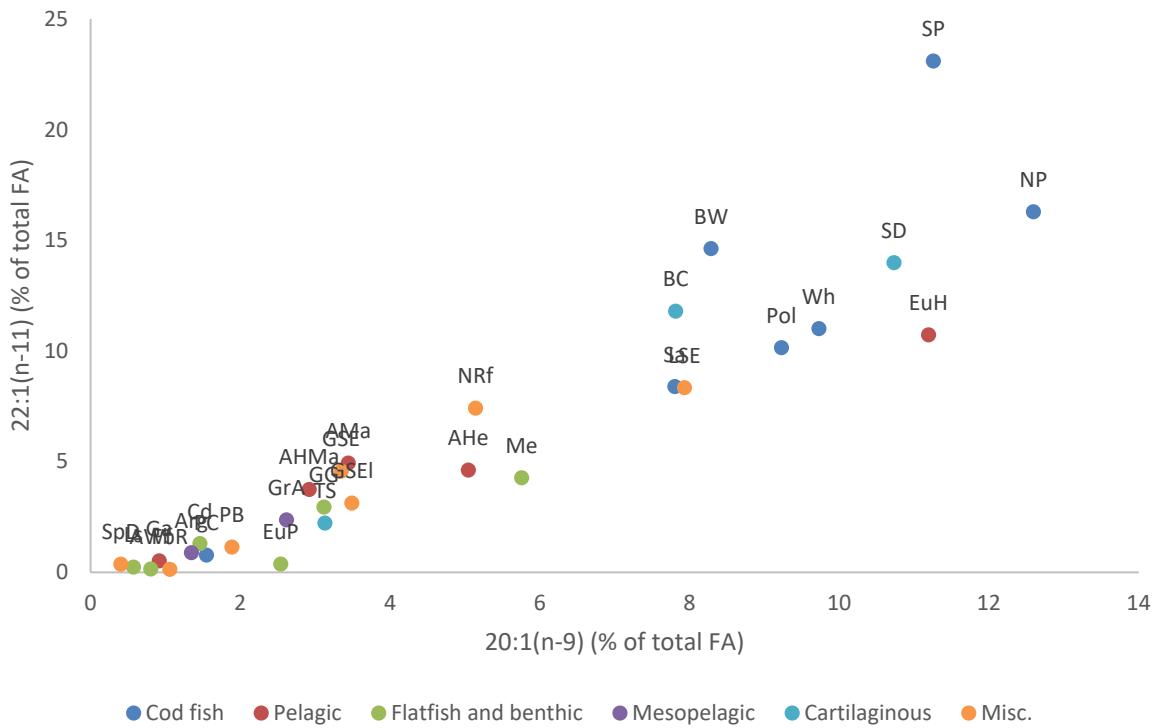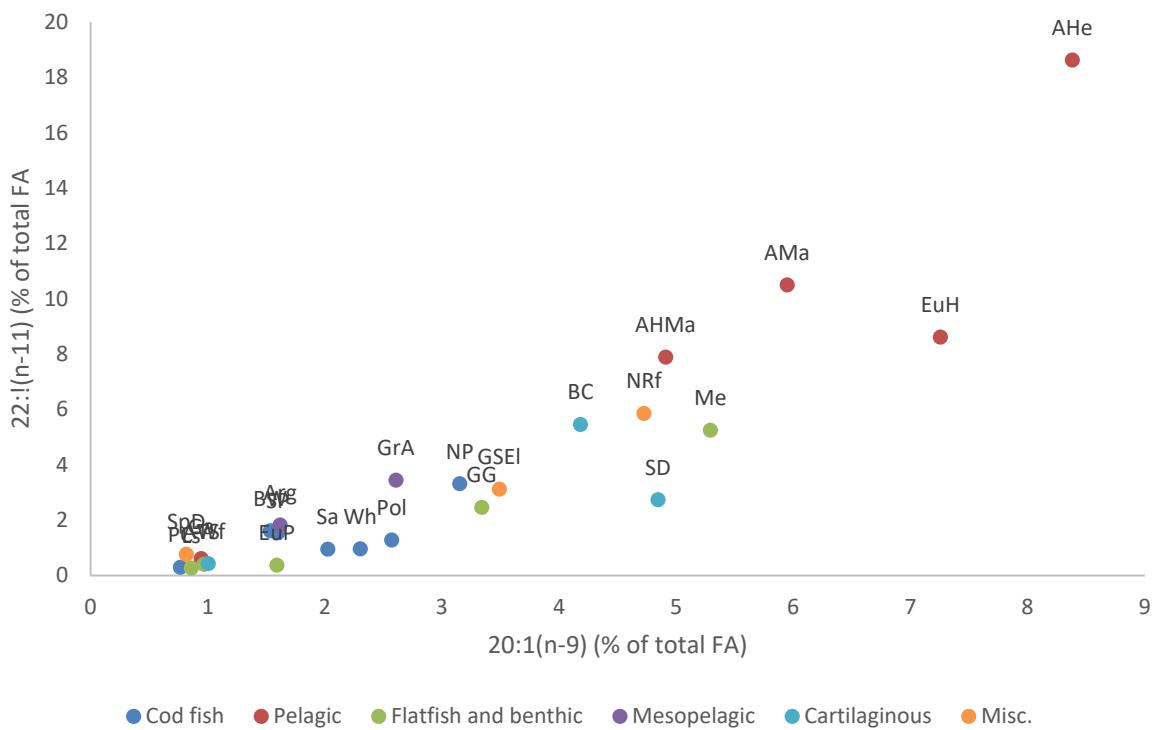
Figure 38: *Calanus* FATMs 22:1(n-11) and 20:1(n-9) plotted against each other for **A)** liver and **B)** muscle samples.
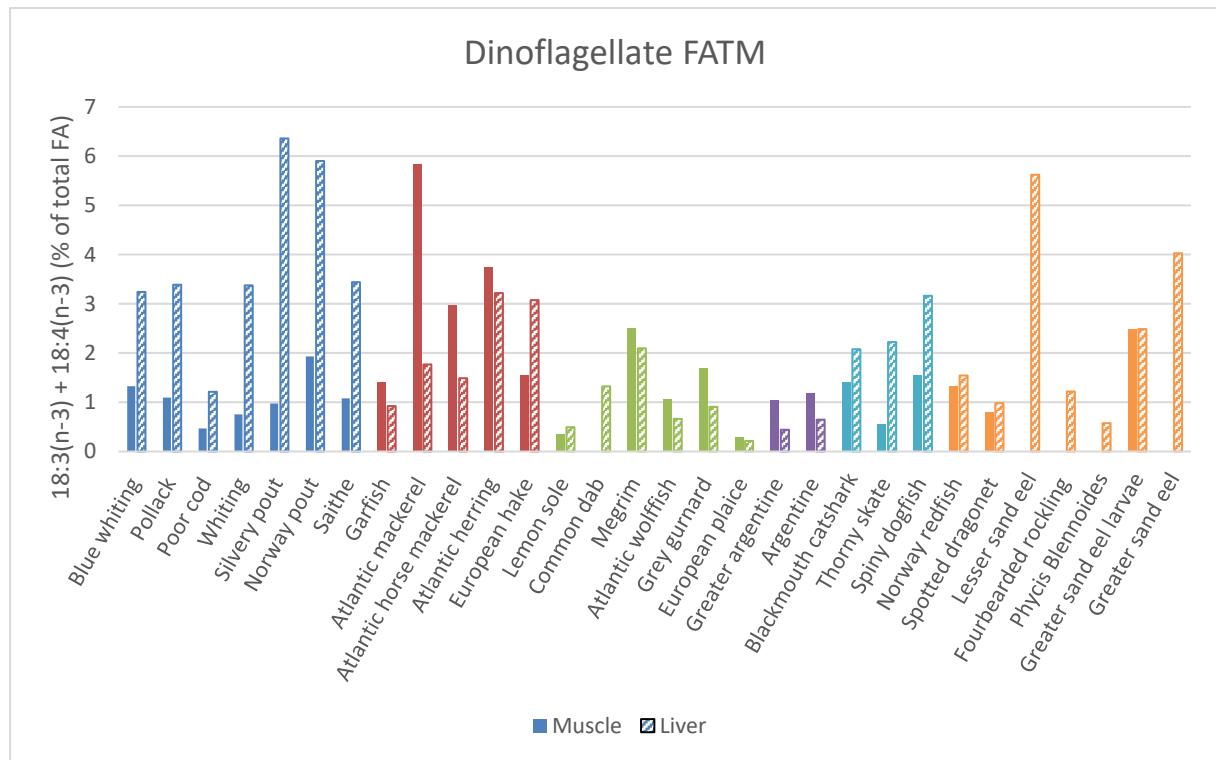
Figure 39: Sum of dinoflagellate FATMs 18:3(n-3) and 18:4(n-3) for all species.

Dinoflagellate FATMs are shown in Figure 39. The cod fish show high levels of dinoflagellate FATM, alongside mackerel, herring, and sand eels. Among the rest of the fish, plaice, catshark, spiny dogfish and lesser sand eel also have relatively high levels of dinoflagellate FATMs. The plaice have very low levels of the 18:3(n-3) + 18:4(n-3).
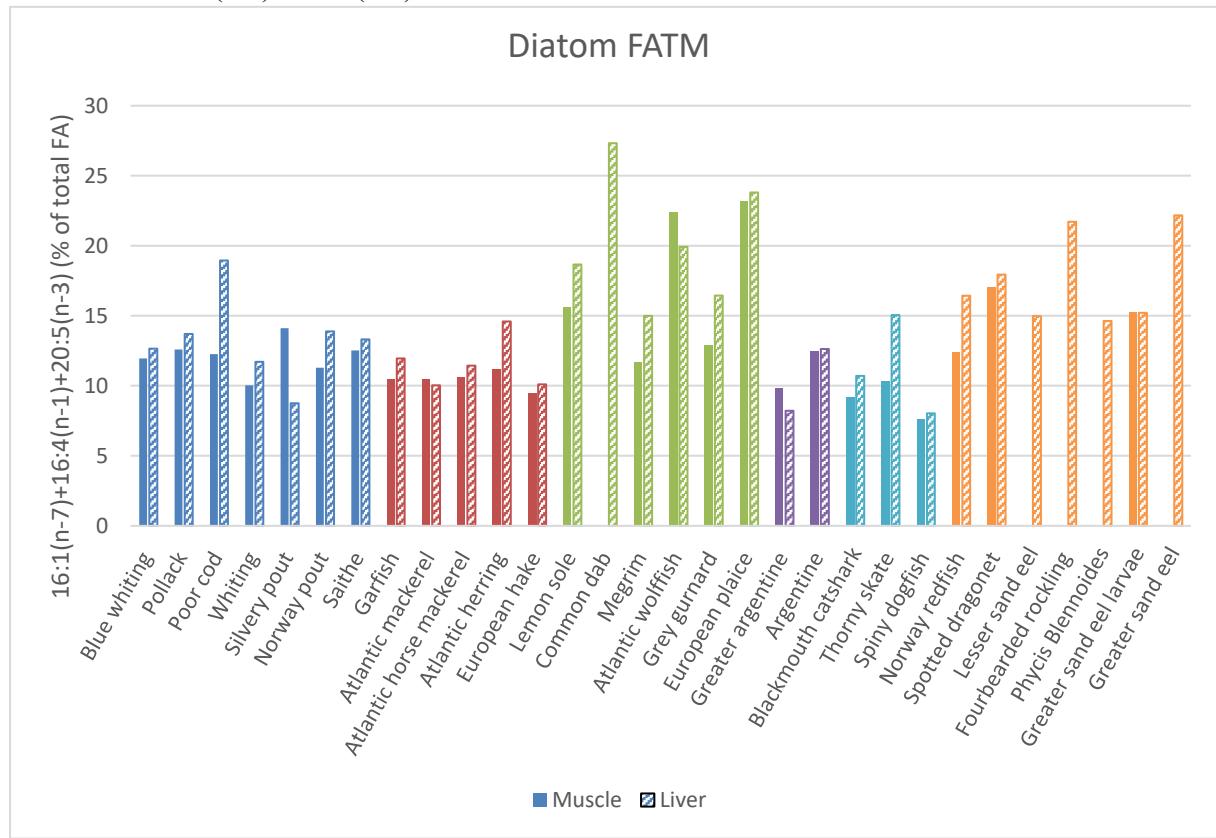
Figure 40: Sum of diatom FATMs 16:1(n-7), 16:4(n-1) and 20:5(n-3) for all species.

Diatom FATMs 16:1(n-7), 16:4(n-1) and 20:5(n-3) is shown in figure 40. Poor cod together with the benthic fish have the highest levels of these FATMs. While it may not conclude a diet dominated by diatoms, it gives the indication of a stronger presence of diatoms in their diets compared to the cod fish and fish that feed pelagically.

Plot of 22:6(n-3) against 20:5(n-3) is shown in Figure 41. For the muscle samples, the cod fish are clustered together, except for silvery pout and whiting. The pelagic fish are clustered together as well, except for garfish. This changes for the liver samples, where the cod are still clustered together, but many other species are also in the cluster. The poor cod is no longer located near the other cod fish, while the silvery pout and whiting now are. The pelagic fish are spread out more. Flatfish and benthic fish lie almost on a line up the x-axis, with similar levels of 20:5(n-3) but increasing levels of 22:6(n-3). Interestingly, the lesser sand eel larvae have much higher levels of 22:6(n-3) than other species, this can be attributed to the fact that the whole sample was analysed. The liver samples also show a trend of increasing levels of 22:6(n-3) with not much increase in 20:5(n-3) levels.
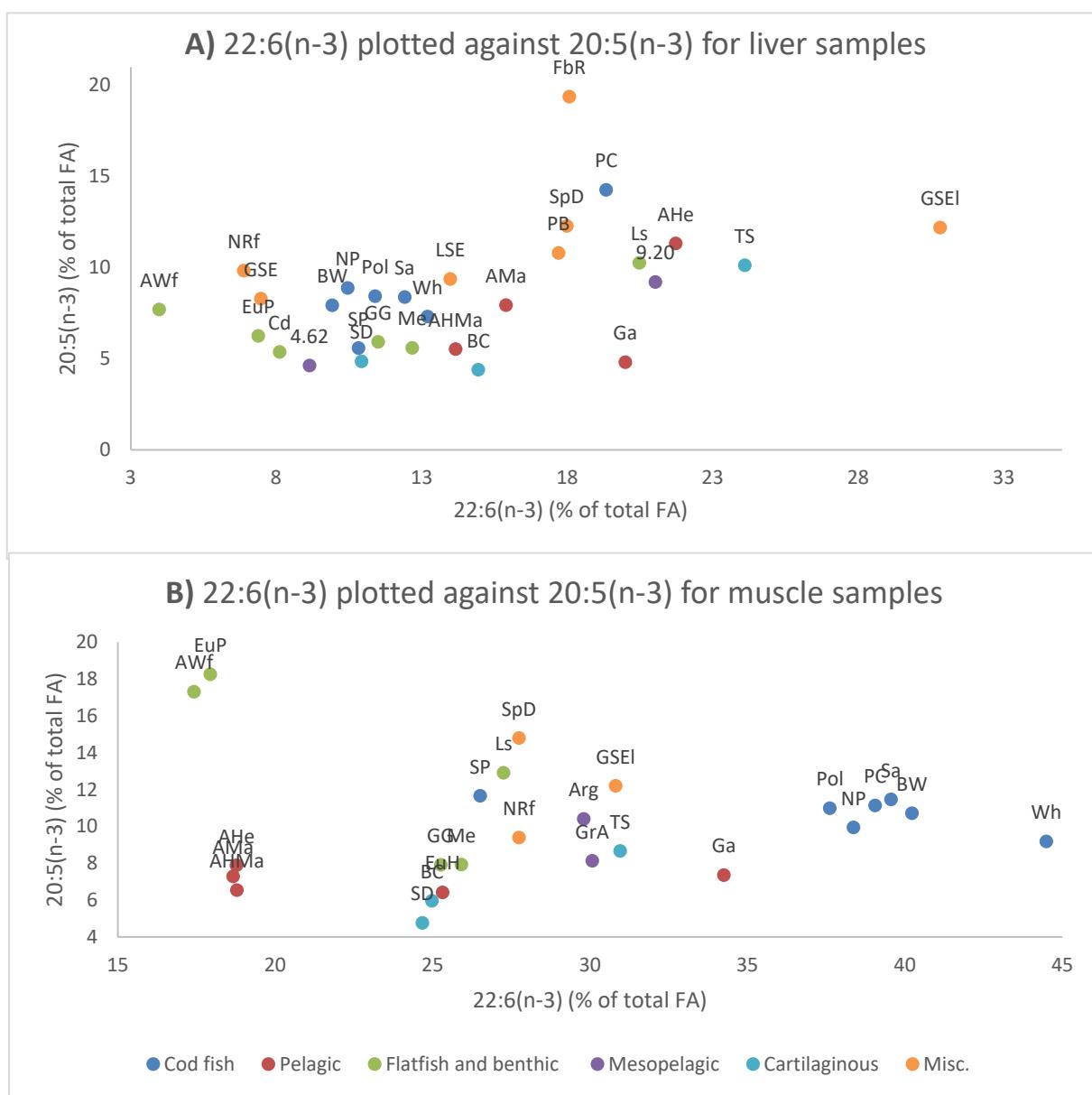
Figure 41: 22:6(n-3) plotted against 20:5(n-3) for **A)** liver and **B)** muscle samples.

4.7. Comparing fatty acid contents to fish data

High values of Fulton's condition factor can in some cases be used as an indication of overall health of fish, and as displayed in Table 16, this index vary greatly between the species, but there is also some variation within each species. As mention in Section 1.2.6., some studies have applied the conditioning factor as a way of estimating energy storage (Herbinger and Friars, 1991). Figure 42 show a plot of Fulton's condition factor plotted against FA content in liver. The fish in this dataset shows no correlation between the conditioning factor and amount FA. It should be mentioned that the study by Herbinger and Friars (1991) used the conditioning factor compared to total lipid content, which may yield different results than comparing it directly to liver and muscle FA content. They analysed immature Atlantic salmon, not adult fish.
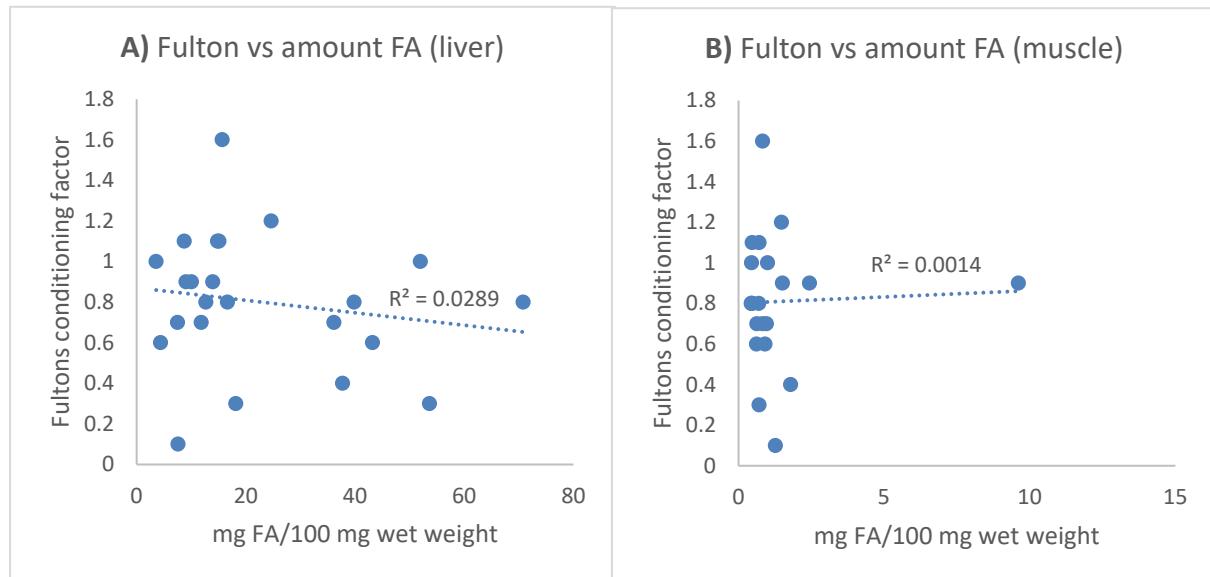
Figure 42: Fulton's conditioning factor plotted against amount of FA for **A)** liver and **B)** muscle samples.

4.8. Comparing fatty acid contents to trophic level

Table 25: Values used for trophic levels, sorted in rising order. Values adapted from (Jiming, 1982).

Species	Tropic level
Lesser sand eel	3.3
Norway pout	3.4
Greater sand eel	3.5
Atlantic herring	3.5
Atlantic mackerel	3.5
European plaice	3.7
Common dab	3.7
Blue whiting	3.7
Grey gurnard	3.8
Whiting	4.3
Pollack	4.4
Spiny dogfish	4.4
Saithe	4.5
Megrim	4.5
European hake	4.6

To investigate if certain groups of FAs accumulate as the trophic levels of the fish increases, values of trophic levels were adopted from (Jiming, 1982), and the fish used for making these plots were only those that had values included in this study. Table 25 shows the values used. It is common that fish retain essential FAs such as 20:4(n-6), 20:5(n-3) and 22:6(n-3), and so it would be natural that the sum of these FA would increase with increasing trophic level. Figure 43 shows the sum of these FAs (as % of total FA) plotted against trophic level. There is no correlation between the sum and trophic level. For liver samples it has a negative tendency, while for muscle samples it has a positive tendency, but for both cases the correlation is extremely low. It should be mentioned that the adapted values of trophic levels may not be accurate for the fish in this project, and this may contribute to inaccuracy in the plots.
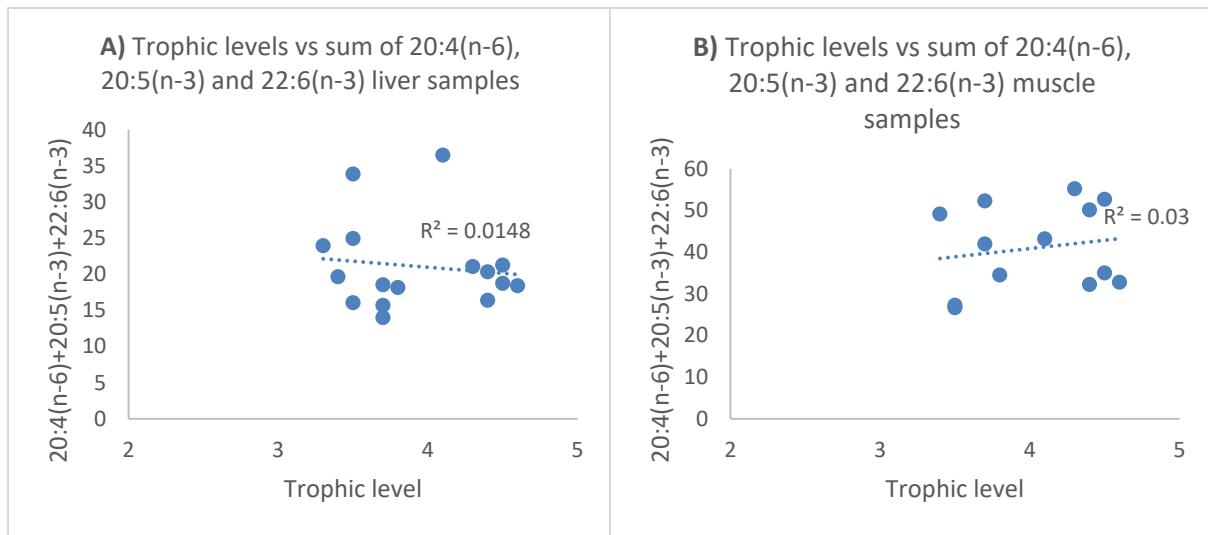
Figure 43: Trophic levels plotted against sums of 20:4(n-6), 20:5(n-3) and 22:6(n-3), given as % of total FA.

4.9. Sources of error

4.9.1. Homogeneity

Homogeneity in samples was challenging to achieve, especially for muscle tissue. Although none of the samples are from the same fish, the results from DM shows a large variation in amount fatty acids. RSDs are high for both muscle and liver samples. The factorial design experiment with all high levels were duplicated five times to establish a standard deviation and this resulted in RSDs around 5% which is standard for this method. This result shows that the high RSDs not necessarily stem from analytical error, which leaves biological or sampling variation.

4.9.2. Weighing

Sample tissue stuck on the side walls can leave fatty oils in the upper part of the tube that is not subjected to the methylation reagent, resulting in too low FA mass per wet weight of sample.

If the samples defrost too much, the fats can leave the tissue that has defrosted, resulting in less homogeneity in the sample and ultimately, less FA in the tissue on the top of the sample that is sampled for analysis. Samples are kept in NUNC sample tubes which are quite narrow, which means that to avoid removing the entire sample from the tube, the top of the sample is used. The aliquot is removed from the sample with a spatula and introduced to the weighing glass. To prevent defrosting of liver samples (which are high in fatty content), liquid nitrogen was utilized. Bits of sample were taken from the NUNC tube and placed in liquid nitrogen shortly after it was taken out of the freezer, and quickly placed back.

4.9.3. Integration of peaks in chromatography

The integration is mostly automated by the computer software, but there are known problem areas where one must manually integrate the peaks. An example of this is the overlapping peaks of iso 17:0 and branched 17:1. Often these peaks will overlap such that the user must manually draw the line between them. This allows for human error, but as long the manual integration is performed consistently for all chromatograms, this should not increase analytical variation between samples. Samples analysed for this project contain generally low amounts of these FA (<0.5% of total FA).

4.9.4. Replicates of samples

It would have been beneficial to analyse multiple replicates of the fish to obtain good estimates of the averages, especially for species with large variations between individuals. This would have allowed for the determination of whether the variation is biological or analytical. Analysing multiple replicates is time consuming and considering the number of samples analysed, even adding one replicate to every sample would increase the amount of work substantially. Adding more replicates only to species with

high variation would have been a more feasible approach, but would probably reduce the number of species that could have been analysed.

5. Conclusions

Optimization of the direct methylation method was achieved by using a 2^3 full factorial design, with the three variables 1) reaction time, 2) introducing solvent before or after putting samples in oven and 3) number of extractions. The results showed that the number of extractions in the method could be reduced to 1, and that the reaction time in the oven was the only significant effect. Following these results, the method was performed as per Meier (2006) but reducing the number of extractions. FAME-extracts prepared by the direct methylation method were analysed using GC-FID and quantified by using an internal standard.

FA compositions for liver and muscle tissues of 30 fish from the North Sea were determined and the results were investigated by means of multivariate statistics. Principal component analysis was used to investigate similarities and differences in FA profiles and potential fatty acid trophic markers. The importance of the *Calanus* in the pelagic food web of the North Sea was observed through the FA profiles and PCAs. These FATMs were dominating in liver samples of the cod fish (expect poor cod). Muscle profiles of pelagic fish mackerel, herring, horse mackerel and hake were also dominated by *Calanus* FATMs, and PCAs of cod liver and these pelagic muscle profiles showed them to be very similar, indicating that these fish may have similar diets and feed on each other. Flatfish was also included in this PCA, which illustrated the difference between pelagic feeders and benthic feeders. Main differences of dietary FAs between benthic feed compared to pelagic feeders are 1) lower levels of *Calanus FATMs* 22:1(n-11) and 20:1(n-9), 2) benthic feeders tend to have higher levels of 20:4(n-6), 22:4(n-6), 16:1(n-7) and 16:1(n-9), 3) generally lower in (n-3).

A review of literature showed that 12 of the 30 species analysed had no reports on FA compositions or profiles, and of the fish reported, many of them were not from the North Sea, which means that some of these fish may have been analysed for FA compositions for the first time.

The results from this project will be further used in a future project by IMR. The results will also be included in a planned database by IMR.

6. Future work

The fauna of the oceans is filled with species and resources where little is known about the FA composition. Making FA compositions of the fish in our seas available to all scientists could be very useful for future research when trying to unravel trophic interactions or investigating the utilization of new raw material for marine ingredients or health food products. Future work would include analysing more species, but also including lipid classification and total lipid analyses and analysing species from multiple seasons to investigate the effects of ocean temperatures on FA compositions.

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Appendices

Appendix I: Experimental Design

Table A1: Overview of responses from factorial design with liver samples.

Experiment	X1	X2	X3	X1X2	X1X3	X2X3	% FA	% SFA	% MUFA	% PUFA
1	-1	-1	-1	1	1	1	53,30	10,89	23,81	18,02
2	1	-1	-1	-1	-1	1	61,34	12,45	27,41	20,79
3	-1	1	-1	-1	1	-1	59,41	12,29	26,88	19,58
4	1	1	-1	1	-1	-1	60,28	12,32	27,02	20,24
5	-1	-1	1	1	-1	-1	56,71	11,73	25,63	18,70
6	1	-1	1	-1	1	-1	64,91	13,46	29,11	21,56
7	-1	1	1	-1	-1	1	60,94	12,62	27,26	20,36
8	1	1	1	1	1	1	63,66	13,14	28,59	21,18
						Mean	60,07	12,36	26,96	20,05
						SD	3,71	0,80	1,66	1,22
						RSD	6,17	6,46	6,15	6,08

Table A2: Overview of responses from factorial design with muscle samples.

Experiment	X1	X2	X3	X1X2	X1X3	X2X3	% FA	% SFA	% MUFA	% PUFA
1	-1	-1	-1	1	1	1	0,59	0,14	0,09	0,35
2	1	-1	-1	-1	-1	1	0,60	0,14	0,10	0,36
3	-1	1	-1	-1	1	-1	0,62	0,15	0,10	0,37
4	1	1	-1	1	-1	-1	0,60	0,15	0,09	0,36
5	-1	-1	1	1	-1	-1	0,62	0,15	0,10	0,36
6	1	-1	1	-1	1	-1	0,59	0,14	0,09	0,35
7	-1	1	1	-1	-1	1	0,60	0,14	0,10	0,35
8	1	1	1	1	1	1	0,56	0,14	0,08	0,34
						Mean	0,60	0,14	0,09	0,36
						SD	0,02	0,004	0,01	0,01
						RSD	3,21	2,59	7,03	3,10

Table A3: Replications of the experiments with all high levels.

Experiment #	Liver (% FA / 100 mg wet weight)	Muscle (% FA / 100 mg wet weight)
8-1	*Evaporated in oven*	0,58
8-2	61,97	0,55
8-3	64,44	0,57
8-4	63,03	0,52
8-5	65,20	0,58
Mean	63,66	0,56
SD	1,44	0,03
RSD	2,27	5,01

Table A4: Comparisons of low and high levels for each variable for muscle samples.

X1	Experiment	X1	X2	X3	X1X2	X1X3	X2X3	FA / 100 mg wet weight	
Low level	1	-1	-1	-1	1	1	1	0,59	
	3	-1	1	-1	-1	1	-1	0,62	
	5	-1	-1	1	1	-1	-1	0,62	
	7	-1	1	1	-1	-1	1	0,60	
							Mean	**0,61**	
							SD	0,02	
							RSD	2,51	
High level	2	1	-1	-1	-1	-1	1	0,60	
	4	1	1	-1	1	-1	-1	0,60	
	6	1	-1	1	-1	1	-1	0,59	
	8	1	1	1	1	1	1	0,56	
							Mean	**0,59**	**T-Test***
							SD	0,02	0,184
							RSD	3,37	
X2									
Low level	1	-1	-1	-1	1	1	1	0,59	
	2	1	-1	-1	-1	-1	1	0,60	
	5	-1	-1	1	1	-1	-1	0,62	
	6	1	-1	1	-1	1	-1	0,59	
							Mean	0,60	
							SD	0,01	
							RSD	2,15	
High level	3	-1	1	-1	-1	1	-1	0,62	
	4	1	1	-1	1	-1	-1	0,60	
	7	-1	1	1	-1	-1	1	0,60	
	8	1	1	1	1	1	1	0,56	
							Mean	0,60	**T-Test***
							SD	0,03	0,803
							RSD	4,39	
X3									
Low level	1	-1	-1	-1	1	1	1	0,59	
	2	1	-1	-1	-1	-1	1	0,60	
	3	-1	1	-1	-1	1	-1	0,62	
	4	1	1	-1	1	-1	-1	0,60	
							Mean	0,60	
							SD	0,01	
							RSD	2,23	
High level	5	-1	-1	1	1	-1	-1	0,62	
	6	1	-1	1	-1	1	-1	0,59	
	7	-1	1	1	-1	-1	1	0,60	
	8	1	1	1	1	1	1	0,56	
							Mean	0,59	**T-Test***
							SD	0,02	0,384
							RSD	4,03	

*Two-sample equal variance, two tailed student t-test with α = 0,05, displayed value = p-value.

Table A5: Comparisons of low and high levels for each variable for liver samples.

X1	Experiment	X1	X2	X3	X1X2	X1X3	X2X3	FA / 100 mg wet weight		
Low level	1	-1	-1	-1	1	1	1	53,30		
	3	-1	1	-1	-1	1	-1	59,41		
	5	-1	-1	1	1	-1	-1	56,71		
	7	-1	1	1	-1	-1	1	60,94		
							Mean	**57,59**		
							SD	3,35		
							RSD	5,82		
High level	2	1	-1	-1	-1	-1	1	61,34		
	4	1	1	-1	1	-1	-1	60,28		
	6	1	-1	1	-1	1	-1	64,91		
	8	1	1	1	1	1	1	63,66		
							Mean	**62,55**	**T-Test***	
							SD	2,12	0,047	
							RSD	3,38		
X2										
Low level	1	-1	-1	-1	1	1	1	53,30		
	2	1	-1	-1	-1	-1	1	61,34		
	5	-1	-1	1	1	-1	-1	56,71		
	6	1	-1	1	-1	1	-1	64,91		
							Mean	**59,06**		
							SD	5,10		
							RSD	8,64		
High level	3	-1	1	-1	-1	1	-1	59,41		
	4	1	1	-1	1	-1	-1	60,28		
	7	-1	1	1	-1	-1	1	60,94		
	8	1	1	1	1	1	1	63,66		
							Mean	**61,07**	**T-Test***	
							SD	1,84	0,487	
							RSD	3,01		
X3										
Low level	1	-1	-1	-1	1	1	1	53,30		
	2	1	-1	-1	-1	-1	1	61,34		
	3	-1	1	-1	-1	1	-1	59,41		
	4	1	1	-1	1	-1	-1	60,28		
							Mean	**58,58**		
							SD	3,61		
							RSD	6,16		
High level	5	-1	-1	1	1	-1	-1	56,71		
	6	1	-1	1	-1	1	-1	64,91		
	7	-1	1	1	-1	-1	1	60,94		
	8	1	1	1	1	1	1	63,66		
							Mean	**61,56**	**T-Test***	
							SD	3,63	0,289	
							RSD	5,90		

*Two-sample equal variance, two tailed student t-test with $\alpha = 0,05$, displayed value = p-value.

Appendix II: Fish data

Table A.6: Sample list with common names in English and Norwegian, and scientific names. Year refers to the year the species was caught, the code refers to the ID the fish was given, and n refers to the number of fish sampled.

Common name (English)	Common name (Norwegian)	Latin name	n	Code	Year
Silvery pout	Sølv torsk	Gadiculus argentus	10	D	2010
Norway pout	Øyepål	Trisopterus esmarkii	10	B	2010
Poor cod	Sypike	Trisopterus minutus	10	A	2010
Blue whiting	Kolmule	Micromesistius poutassou	10	S	2011
Whiting	Hvitting	Merlangius merlangus	10	K	2010
Saithe	Sei	Pollachius virens	10	N	2010
Pollack	Lyr	Pollachius pollachius	10	I	2011
Lemon sole	Lomre	Microstomus kitt	10	A	2013
Common dab	Sandflyndre	*Limanda limanda*	10	F	2013
Megrim	Glassvar	Lepidorhombus whiffiagonis	10	G	2010
European plaice	Rødspette	Pleuronectes platessa	10	F	2010
Blackmouth catshark	Hågjel	Galeus melastomus	10	S	2013
European hake	Lysing	Merluccius merluccius	10	E	2010
Spiny dogfish	Pigghå	Squalus acanthias	6	BS	2013
Thorny skate	Kloskate	Raja radiata	9	GS/H	2013
Norway redfish	Lusuer	Sebastes viviparus	10	R	2011
Grey gurnard	Knurr	Eutrigla gurnardus	10	H	2010
Atlantic wolffish	Grå steinbit	Anarhichas lupus	8	KS	2013
Spotted dragonet	Flekket fløyfisk	Callionymus marculatus	10	D	2011
Four-bearded rockling	Tangbrosme	Enchelyopus cimbrius	2	E	2011
Greater fork-beard	Skjell brosme	Phycis blennoides	2	E	2011
Atlantic mackerel	Makrell	Scomber scombrus	10	R	2010
Atlantic horse mackerel	Taggmakrell	Trachurus trachurus	10	L	2010
Atlantic herring	Sild	Clupea harengrus	10	J	2010
Garfish	Hornfisk	Belone belone	7	QS	2013
Greater argentine	Vassild	Argentina silus	10	M	2010
Argentine	Strømsild	Argentina sphyraena	10	O	2010
Greater sand eel	Uflekket storsil	Hyperoplus immaculatus	1	E	2011
Lesser sand eel	Havsil	Ammodytes marinus	4	HS	2013
Lesser sand eel larvae	Topis larver	Ammodytes marinus	10		2013

Table A.7: Fish data for silvery pout.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks		GSI	HSI	Fulton
40386	Sølvtorsk	D1	10	7.5														0.8
	silvery pout	D2	9	5.3														0.7
		D3	9	6.1														0.8
		D4	8	5.2														1.0
		D5	9	6.5														0.9
		D6	9	5.8														0.8
		D7	9	8.1														1.1
		D8	8	5.1														1.0
		D9	9	7.5														1.0
		D10	9	5.8														0.8
	MEAN		9	6														0.9
	STD		1	1														0.1
	RSD		6	17														15.0

Table A.8: Fish data for Norway pout.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks		GSI	HSI	Fulton
25.07.2010	Øyepål	B1	18	45	5.5		1										12.2	0.8
	norway pout	B2	19	47	4.8		2										10.2	0.7
		B3	18	41	2.4		2										5.9	0.7
		B4	16	33	2.8		2										8.5	0.8
		B5	16	36	3		2										8.3	0.9
		B6	16	33	3.5		2										10.6	0.8
		B7	17	41	4.5		2										11.0	0.8
		B8	16	32	4.4		2										13.8	0.8
		B9	16	36	3.9		2										10.8	0.9
		B10	17	39	2.2		2										5.6	0.8
	MEAN		17	38	4		1.9										9.7	0.8
	STD		1	5	1		0.3										2.6	0.1
	RSD		7	14	30		16.6										26.9	8.1

Table A.9: Fish data for poor cod.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks		GSI	HSI	Fulton
25.07.2010	Sypike	A1	17	43			1											0.9
	Poor cod	A2	18	52			1											0.9
		A3	17	41			1											0.8
		A4	19	48			1											0.7
		A5	17	41			1											0.8
		A6	16	36			2											0.9
		A7	16	31			1											0.8
		A8	15	27			2											0.8
		A9	15	29			2											0.9
		A10	17	39			2											0.8
	MEAN		17	39			1.4											0.8
	STD		1	8			0.5											0.1
	RSD		7	21			36.9											7.4

Table A.10: Fish data for blue whiting.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks		GSI	HSI	Fulton
22.07.2011	Kolmule	S1	24	87	3.4		2		x	x	x		x				3.9	0.6
	Blue whiting	S2	23	71.4	4		2		x	x	x		x				5.6	0.6
		S3	23	68.2	2.2		1		x	x	x		x				3.2	0.6
		S4	23.5	73.2	2.8		1		x	x	x		x				3.8	0.6
		S5	23	70.1	3.8		2		x	x	x		x				5.4	0.6
		S6	23	72.2	2.3		2		x	x	x		x				3.2	0.6
		S7	24	70.5	1.8		1		x	x	x		x				2.6	0.5
		S8	23	65.3	1.5		1		x	x	x		x				2.3	0.5
		S9	23	75.4	4.7		1		x	x	x		x				6.2	0.6
		S10	23	75.8	6.2		2		x	x	x		x				8.2	0.6
	MEAN		23.3	72.9	3.3												4.4	0.6
	STD		0.4	5.9	1.5												1.9	0.04
	RSD		1.8	8.0	44.5												42.0	6.7

86

Table A.11: Fish data for whiting.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
26.07.2010	Hvitting	K1	56	1525	22.7	127	1.3							5 whole øyepål frozen	8.3	1.5	0.9
	Whiting	K2	39	450	5.6		2.1									1.2	0.8
		K3	37	455	19.5		2.1									4.3	0.9
		K4	36	435	14.7		2.1									3.4	0.9
		K1	34	335	9	2.9	1.1								0.9	2.7	0.9
		K2	38	460	20.2		1.1									4.4	0.8
		K3	43	770	23.4	44.9	1.3								5.8	3.0	1.0
		K4	35	340	7.5	3.6	1.1								1.1	2.2	0.8
		K1	37	380	5.1	3	1.1								0.8	1.3	0.8
		K2	37	405	7.6	3.3	1.1								0.8	1.9	0.8
	MEAN		39	556	14	31	1.4								2.9	2.6	0.8
	STD		6	362	7	50	0.5								3.3	1.2	0.1
	RSD		16	65	54	162	32.1								111.9	44.9	8.6

Table A.12: Fish data for saithe.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
28.07.2010	sei	N1	77	4080	518.6	27.6	2.1								0.7	12.7	0.9
	saithe	N2	74	3775	467	9.2	1.1								0.2	12.4	0.9
		N3	74	3655	305	21.6	1.1								0.6	8.3	0.9
		N4	73	4020	562.3	10.5	2.1								0.3	14.0	1.0
29.07.2010		N5	108	11390	1284	36.1	2.1								0.3	11.3	0.9
		N6	69	3200	256.1	6.2	2.1								0.2	8.0	1.0
		N7	68	3150	377	2.8	2.1								0.1	12.0	1.0
		N8	73	4245	431.6	13.1	2.1								0.3	10.2	1.1
		N9	76	4120	382.2	7.8	2.1								0.2	9.3	0.9
		N10	66	2780	218	1.7	1.1								0.1	7.8	1.0
	MEAN		76	4442	480	13.7									0.3	10.6	1.0
	STD		12	2489	303	11.3									0.2	2.2	0.1
	RSD		16	56	63	82.5									67.9	20.6	6.6

Table A.13: Fish data for pollack.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
17.07.2011	Lyr	I1	74	3740	143.3		1		x	x	x		x	5 øyepål in belly		3.8	0.9
22.07.2011	Pollack	I2	61	2760	171.1	7	2		x	x	x		x	Brain and muscle switched	0.3	6.2	1.2
		I3	67	3450	250	20.8	1		x	x	x		x		0.6	7.2	1.1
		I4	64	2750	132.4	3.5	2		x	x	x		x		0.1	4.8	1.0
		I5	70	3260	105	26.8	1		x	x	x		x		0.8	3.2	1.0
		I6	78	4560	125	46.9	1		x	x	x		x		1.0	2.7	1.0
		I7	57	2280	145	15.7	1		x	x	x		x		0.7	6.4	1.2
		I8	65	3010	162	25.7	1		x	x	x		x		0.9	5.4	1.1
		I9	68	3200	104	12.6	2		x	x	x		x		0.4	3.3	1.0
		I10	63	2640	81	87	2		x	x	x		x		3.3	3.1	1.1
	MEAN		66.70	3165.00	141.88	27.33									0.9	4.6	1.1
	STD		6.18	648.70	46.95	25.79									0.9	1.6	0.1
	RSD		9.27	20.50	33.09	94.37									105.6	35.0	10.1

Table A.14: Fish data for lemon sole.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
08.08.2013	Lomre	A-S1	28	220	2.3		1/2		x	x	x		x	Ready to spawn, small amounts of food in stom		1.0	1.0
	Lemon sole	A-S2	29	240	1.9		2		x	x	x		x			0.8	1.0
		A-S3	30	310	4.3		1/2		x	x	x		x			1.4	1.1
		A-S4	27	225	4.2		1/2		x	x	x		x			1.9	1.1
		A-S5	29	260	2.1		2		x	x	x		x			0.8	1.1
		A-S6	30	305	5.2		1		x	x	x		x			1.7	1.1
		A-S7	33	360	2.7		2		x	x	x		x			0.8	1.0
		A-S8	27	200	4.2		1/2		x	x	x		x			2.1	1.0
		A-S9	26	190	3.4		1/2		x	x	x		x			1.8	1.1
		A-S10	27	180	1.3		2		x	x	x		x			0.7	0.9
	MEAN		29	249	3.2		2									1.3	1.0
	STD		2	59	1.3		0									0.5	0.1
	RSD		7	24	40.6		25									41.2	7.4

Table A.15: Fish data for common dab.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks / Lots of tobis in belly	GSI	HSI	Fulton
07.07.2013	Sandflyndre	F-S1	30.5	322	12.4		1		x	x	x		x			3.9	1.1
	Common dab	F-S2	34	362	13.4		1		x	x	x		x	Dark skin, illness?		3.7	0.9
		F-S3	27	241	10		1/1		x	x	x		x	Dark skin, illness?		4.1	1.2
		F-S4	28	251	8.8		1/1		x	x	x		x	Parasite in liver		3.5	1.1
		F-S5	27	197	5.8		1/1		x	x	x		x			2.9	1.0
		F-S6	28	245	9.4		2		x	x	x		x			3.8	1.1
		F-S7	27	227	9		1/1		x	x	x		x			4.0	1.2
		F-S8	25.5	190	7.7		1		x	x	x		x			4.1	1.1
		F-S9	28.5	259	8.1		1/1		x	x	x		x			3.1	1.1
		F-S10	27.5	239	9.5		1/1		x	x	x		x			4.0	1.1
	MEAN		28	253	9.4		1									3.7	1.1
	STD		2	53	2.2		1									0.4	0.1
	RSD		8	21	23.3		40									10.8	7.8

Table A.16: Fish data for megrim.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
25.07.2010	Glassvar	G1	45	925	15.6		1									1.69	1.02
	Megrim	G2	43	945	16.3		1									1.72	1.19
		G3	45	1095	17.1		1									1.56	1.20
		G4	38	630	7.6		1									1.21	1.15
		G5	40	830	18		2									2.17	1.30
		G6	40	545	6.3		2									1.16	0.85
		G7	39	710	9.8		1									1.38	1.20
		G8	37	660	8.8		1									1.33	1.30
		G9	37	470	4.8		2									1.02	0.93
		G10	32	480	4.5		1									0.94	1.46
	MEAN		40	729	11		1.3									1.4	1.2
	STD		4	213	5		0.5									0.4	0.2
	RSD		10	29	49		37.2									26.4	15.9

Table A.17: Fish data for European plaice.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
24.07.2010	Rødspette	F1	47	1415	14		1.2		x	x	x		x			0.99	1.36
	European plaice	F2	47	1105	16		1.2		x	x	x		x			1.45	1.06
		F3	45	930	17.8		1.2		x	x	x		x	Tumor in liver		1.91	1.02
		F4	38	640	10		1.1		x	x	x		x			1.56	1.17
		F5	37	620	9		1.2		x	x	x		x			1.45	1.22
		F6	40	620	9.5		1.2		x	x	x		x			1.53	0.97
		F7	39	730	18		1.2		x	x	x		x			2.47	1.23
		F8	40	680	9		1.1		x	x	x		x			1.32	1.06
		F9	47	1030	22		1.2		x	x	x		x	Tumor in liver		2.14	0.99
		F10	40	660	8.4		1.1		x	x	x		x	Tumor in liver		1.27	1.03
		11	37	520	4.5		1.1									0.87	1.03
		12	34	445	7		1.1									1.57	1.13
		13	34	425	3.7		1.1									0.87	1.08
	MEAN		42.0	843.0	13.4		1.2									1.6	1.1
	STD		4.0	269.1	4.9		0.0									0.4	0.1
	RSD		9.6	31.9	36.3		4.1									27.3	11.5

Table A.18: Fish data for blackmouth catshark

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade	Belly Freeze	Remarks	GSI	HSI	Fulton
17.07.2013	Hågjel	S-S1	67	910	102		2		x	x	x		x			11.21	0.30
	Blackmouth catshark	S-S2	65	995	72		2		x	x	x		x	Whole fish in belly		7.24	0.36
		S-S3	48	230	12.3		1		x	x	x		x			5.35	0.21
		S-S4	57	540	52.4		1		x	x	x		x			9.70	0.29
		S-S5	59	650	69.4		2		x	x	x		x			10.68	0.32
		S-S6	63	810	80		2		x	x	x		x			9.88	0.32
		S-S7	49	305	14.7		1		x	x	x		x			4.82	0.26
		S-S8	56	470	38.4		2		x	x	x		x			8.17	0.27
		S-S9	47	310	15.8		1		x	x	x		x			5.10	0.30
		S-S10	65	800	70		2		x	x	x		x			8.75	0.29
	MEAN		58	602	52.70		1.60									8.09	0.29
	STD		8	272	31.21		0.52									2.37	0.04
	RSD		13	45	59.23		32.27									29.30	14.18

Table A.19: Fish data for spiny dogfish.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks		GSI	HSI	Fulton
07.07.2013	Pigghå	B-S1	79	2250	164				x	x	x		x	Belly full of lesser sand eel larvae		7.29		0.46
	Spiny dogfish	B-S2	77	1910	192				x	x	x		x	Belly full of lesser sand eel larvae		10.05		0.42
		B-S3	78	1930	163				x	x	x		x	Belly full of lesser sand eel larvae		8.45		0.41
		B-S4	78	1910	208				x	x	x		x	Belly full of lesser sand eel larvae		10.89		0.40
		B-S5	82	2200	222				x	x	x		x	Belly full of lesser sand eel larvae		10.09		0.40
		B-S6	67	1280	67				x	x	x		x	Belly full of lesser sand eel larvae + dark liver		5.23		0.43
	MEAN		77	1913	169.33											8.67		0.42
	STD		5	346	55.36											2.13		0.02
	RSD		7	18	32.69											24.54		5.08

Table A.20: Fish data for thorny skate.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
08.08.2013	Kloskate	G-S1	43	588	21.5		1		x	x	x		x			3.66	0.74
08.08.2013	Thorny skate	G-S2	39	521	17.9		1		x	x	x		x			3.44	0.88
09.07.2013		G-S3	37	351	7.8		2		x	x	x		-			2.22	0.69
09.07.2013		H5	40	743	40		1		x	x	x		x			5.38	1.16
10.07.2013		H3	47	813	25		2		x	x	x		x	NIVA sampled		3.08	0.78
10.07.2013		H4	41	465	10		2		x	x	x		x	NIVA sampled		2.15	0.67
10.07.2013		H5	32	242	8		1		x	x	x		x	NIVA sampled		3.31	0.74
10.07.2013		G-S9	40	534	13.5		2		x	x	x		x	NIVA sampled		2.53	0.83
13.07.2013		G-S11	36.5	472	7.8	6.3	2		x	x	x		x	NIVA sampled	1.33	1.65	0.97
13.07.2013		G-S12	42	502	15.5	18	1		x	x	x		x	NIVA sampled	3.59	3.09	0.68
	MEAN		40	523	16.70	12.15									2.46	3.05	0.82
	STD		4	167	10.15	8.27									1.59	1.04	0.15
	RSD		10	32	60.77	68.09									64.70	34.13	18.93

Table A.21: Fish data for European hake.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
24.07.2010	Lysing	E1	68	2035	61	177	1.2		x	x	x		x		8.7	3.0	0.6
	European hake	E2	80	3415	100	204	1.2		x	x	x		x		6.0	2.9	0.7
		E3	83	4310	177	798	1.2		x	x	x		x		18.5	4.1	0.8
		E4	70	2270	59	136	1.2		x	x	x		x		6.0	2.6	0.7
		E5	66	1800	51	69	2.3		x	x	x		x		3.8	2.8	0.6
		E6	66	1845	38	61	2.3		x	x	x		x		3.3	2.1	0.6
		E7	64	1750	-	109	1.2		x	x	x		x		6.2		0.7
		E8	83	3470	107	230	1.2		x	x	x		x		6.6	3.1	0.6
		E9	79	3550	187	350	1.2		x	x	x		x	Inverted stomach	9.9	5.3	0.7
		E10	68	2095	58	100	2.3		x	x	x		x		4.8	2.8	0.7
	MEAN		73	2654	93	223	1.5								7.4	3.2	0.7
	STD		8	933	55	220	0.5								4.4	0.9	0.04
	RSD		10	35	59	98	34.7								59.5	29.8	6.5

Table A.22: Fish data for Norway redfish.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
21.07.2011	Lusuer	R1	21.5	169			2		x	x	x		x				1.70
	Norway redfish	R2	23	182			1		x	x	x		x				1.50
		R3	20.5	137			2		x	x	x		x				1.59
		R4	24	206			1		x	x	x		x				1.49
		R5	27	329			1		x	x	x		x				1.67
		R6	22	181			2		x	x	x		x				1.70
		R7	28.5	380			2		x	x	x		x				1.64
		R8	21	144			2		x	x	x		x				1.55
		R9	23	192			2		x	x	x		x				1.58
		R10	21	146			2		x	x	x		x				1.58
	MEAN		23.15	207													1.60
	STD		2.68	82													0.08
	RSD		11.57	40													4.80

Table A.23: Fish data for grey gurnard.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
24.07.2010	Knurr	H1	34	375	3.5		1		x	x	x		x			0.93	0.95
	Grey gurnard	H2	37	350	9.8		2		x	x	x		x			2.80	0.69
		H3	33	330	8.1		?		x	x	x		x			2.45	0.92
		H4	37	495	14.3		1		x	x	x		x			2.89	0.98
		H5	33	375	15.3		1		x	x	x		x			4.08	1.04
		H6	35	360	5.9		2		x	x	x		x			1.64	0.84
		H7	35	405	7.3		1		x	x	x		x			1.80	0.94
		H8	35	380	6.7		1		x	x	x		x			1.76	0.89
		H9	34	365	9.4		2		x	x	x		x			2.58	0.93
		H10	32	360	7.6		1		x	x	x		x			2.11	1.10
	MEAN		35	380	9		1.3									2.3	0.9
	STD		2	45	4		0.5									0.9	0.1
	RSD		5	12	41		37.5									37.6	12.0

Table A.24: Fish data for Atlantic wolffish.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
10.07.2013	Grå steinbit	K-S1	42	685	13	25	1		x	x	x		x		3.65	1.90	0.92
10.07.2013		K-S2	55	1560	20	1.5	2		x	x	x		x		0.10	1.28	0.94
11.07.2013		K-S3		8285	331		1		x	x	x		x			4.00	
11.07.2013		K-S4	62	2490	99	113	1		x	x	x		x		4.54	3.98	1.04
11.07.2013		K-S5	72	4065	43	7.6	2		x	x	x		x		0.19	1.06	1.09
11.07.2013		K-S6	77	4510	159	4	2		x	x	x		x		0.09	3.53	0.99
11.07.2013		K-S7	78	5740	213	8	2		x	x	x		x		0.14	3.71	1.21
11.07.2013		K-S8	72	3260	151	155	1		x	x	x		x		4.75	4.63	0.87
	MEAN		65	3824	128.63	44.87									1.92	3.01	1.01
	STD		13	2425	108.81	62.54									2.26	1.38	0.11
	RSD		20	63	84.59	139.37									117.76	45.84	11.36

Table A.25: Fish data for spotted dragonet.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
16.07.2011	Flekket fløyfisk	D1	11	6	-	-	-	-	x	x	x		-				0.45
	Spotted dragonet	D2	13	10													0.46
16.07.2011		D3	12	9													0.52
		D4	10	6													0.60
		D5	12	10													0.58
		D6	8	5													0.98
		D7	6	3													1.39
		D8	10	7													0.70
		D9	8	4													0.78
17.07.2011		D10	11	8.2													0.62
	MEAN		10.10	6.82													0.71
	STD		2.18	2.45													0.29
	RSD		21.62	35.95													40.65

Table A.26: Fish data for four bearded rockling.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
	Tang-brosme	E2	19.5	21.3					x	x	x		x				0.3
	Four bearded rockling	E3	20.5	34.6					x	x	x		x				0.4
	MEAN		20.0	28.0													0.3
	STD		0.7	9.4													0.1
	RSD		3.5	33.6													23.5

Table A.27: Fish data for greater fork beard.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
	Skjell-brosme	E4	20	50			1		x	x	x		x				0.6
	Greater fork beard	E5	32	230	16.4		1		x	x	x		x			7.1	0.7
	MEAN		26.0	140.0													0.7
	STD		8.5	127.3													0.1
	RSD		32.6	90.9													8.2

Table A.28: Fish data for Atlantic mackerel.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
30.07.2010	Makrell	R1	38	455	7.7	5.9	1.4								1.30	1.69	0.83
Atlantic mackerel		R2	32	305	5.6	2.6	1.3								0.85	1.84	0.93
		R3	33	305	5.3	1.7	2.2							Full of "Kveis"	0.56	1.74	0.85
		R4	32	297	4.8	0.3	2.1								0.10	1.62	0.91
		R5	30	232	4.3	1.7	1.3								0.73	1.85	0.86
		R6	33	311	4.3	0.2	2.1								0.06	1.38	0.87
		R7	30	192	3.4	1	2.1								0.52	1.77	0.71
		R8	32	290	4.3	1.5	1.3								0.52	1.48	0.89
		R9	32.5	301	6	3	1.3								1.00	1.99	0.88
		R10	32	290	6.5	0.4	2.3								0.14	2.24	0.89
	MEAN		32	298	5	2	1.7								0.6	1.8	0.9
	STD		2	67	1	2	0.4								0.4	0.2	0.1
	RSD		7	23	24	94	25.7								70.3	14.0	6.9

Table A.29: Fish data for Atlantic horse mackerel.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Indvolde	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
26.07.2010	Taggmakrell	L1	37	398	6.1		2	22								1.5	0.8
Atlantic horse mackerel		L2	39	528	12.2		1	31.2								2.3	0.9
		L3	36	381	7.3	23.3	1	10.2							6.1	1.9	0.8
		L4	41	584	7.1	7.8	1	31.3							1.3	1.2	0.8
		L5	36	391	7.4		2	24.2								1.9	0.8
		L6	37	492	9.6	13.2	1	23.4							2.7	2.0	1.0
		L7	38	517	13.8	9.5	2	25							1.8	2.7	0.9
		L8	35	393	8	4	1	17.5							1.0	2.0	0.9
		L9	35	406	6	13.7	2	15.4							3.4	1.5	0.9
		L10	35	452	11.4	28.3	1	16.9							6.3	2.5	1.1
	MEAN		37	454	9	14	1.4	21.7							3.2	2.0	0.9
	STD		2	72	3	9	0.5	6.8							2.2	0.5	0.1
	RSD		5	16	31	61	36.9	31.3							67.1	23.7	9.1

Table A.30: Fish data for Atlantic herring.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
30.07.2010	Sild	J1	34.5	254	5.4	15.5	1.4	7							6.1	2.1	0.6
	Atlantic herring	J2	29	175	2.3	1.6	2.3	7							0.9	1.3	0.7
		J3	28	171	2	1.4	1.2	3							0.8	1.2	0.8
		J4	28.5	195	2.9	4.1	1.3	3							2.1	1.5	0.8
		J5	28	191	3.3	5.5	1.4	3							2.9	1.7	0.9
		J6	30.5	245	4.9	10.4	1.3	9							4.2	2.0	0.9
		J7	30	239	3	9.7	2.4	6							4.1	1.3	0.9
		J8	32	269	6.8	28.6	1.4								10.6	2.5	0.8
		J9	28.5	230	5.4	8.7	1.3	7							3.8	2.3	1.0
		J10	31	302	2.4	72.5	2.5	8							24.0	0.8	1.0
	MEAN		30	227	3.8	15.8	1.7	5.9							6.0	1.7	0.8
	STD		2	43	1.6	21.5	0.5	2.3							7.0	0.6	0.1
	RSD		7	19	42.9	135.9	31.7	39.3							116.8	33.7	14.0

Table A.31: Fish data for garfish.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade	Belly Freeze	Remarks	GSI	HSI	Fulton
15.07.2013	Hornfisk	Q-S1	56	340	8.1	1.5	2		x	x	x		x		0.44	2.38	0.19
	Garfish	Q-S2	62	245	7.5		2		x	x	x		x			3.06	0.10
		Q-S3	69	395	7.8	5	1		x	x	x		x		1.27	1.97	0.12
		Q-S4	57	205	9	2	1		x	x	x		x		0.98	4.39	0.11
		Q-S5	60	245	10		2		x	x	x		x	Multiple fish had a lot of visceral fat		4.08	0.11
		Q-S6	56	220	9.5	1.1	2		x	x	x		x		0.50	4.32	0.13
		Q-S7	62	240	8	1.2	1		x	x	x		x	Ready to spawn, eggs sampled	0.50	3.33	0.10
	MEAN		60	270	8.56	2.16									0.74	3.36	0.12
	STD		5	70	0.95	1.63									0.37	0.95	0.03
	RSD		8	26	11.06	75.27									49.72	28.38	25.84

Table A.32: Fish data for greater argentine.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
28.07.2010	Vassild	M1	26	130	2.4											1.85	0.74
	Greater argentine	M2	27	140	2.3											1.64	0.71
		M3	26	140	1.6											1.14	0.80
		M4	28	145	2.1											1.45	0.66
		M5	27	150	1.5											1.00	0.76
		M6	26	135	2.1		2									1.56	0.77
		M7	28	160	2		1									1.25	0.73
		M8	27	135	1.1		2									0.81	0.69
		M9	25	115	1.2		2									1.04	0.74
		M10	29	160	1.8		2									1.13	0.66
	MEAN		27	141	2		1.8									1.3	0.7
	STD		1	14	0		0.4									0.3	0.05
	RSD		4	10	25		24.8									25.3	6.4

Table A.33: Fish data for argentine.

Date	Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks	GSI	HSI	Fulton
27.07.2010	Strømsild	O1	21	51			2							Visceral fat			0.55
	Argentine	O2	20	47			1							Visceral fat, big oocytes, flowing?			0.59
		O3	19	36			2							Visceral fat			0.52
		O4	19	46		3.6	1							Visceral fat, big oocytes, flowing?	7.83		0.67
		O5	19	36			1							Visceral fat, big oocytes, flowing?			0.52
		O6	18	35			1							Large amount of visceral fat			0.60
		O7	19	42			2							Large amount of visceral fat			0.61
		O8	21	51			1							Visceral fat			0.55
		O9	22	62		3.1	1							Visceral fat, big oocytes, flowing?	5.00		0.58
		O10	19	43			1							Large amount of visceral fat			0.63
	MEAN		20	45		3	1.3								6.4		0.6
	STD		1	8		0	0.5								2.0		0.05
	RSD		6	19		11	37.2								31.2		8.0

Table A.34: Fish data for greater sand eel.

Greater sand eel		Fish	Length	Weight	Liver weight	Gonade	Gender	Age	Muscle	Liver	Brain	Gonade	Belly	Remarks			
Date	Species	Nr.	(cm)	(g)	(g)	(g)	Stad.		Cryo	Cryo	Cryo	Cryo	Freeze		GSI	HSI	Fulton
	Uflekket storsil	E1	32	95	2		1		x	x	x		x			2.1	0.3

97

Table A.35: Fish data for lesser sand eel.

Date	Lesser sand eel Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Muscle Cryo	Liver Cryo	Brain Cryo	Gonade Cryo	Belly Freeze	Remarks		GSI	HSI	Fulton
09.07.2013	Havsil	H-S1	23	32.8					x	x	x		-	Brain labeled as belly				0.27
09.07.2013		H-S6	21	27									H2L	Belly frozen in Nunc-tube				0.29
09.07.2013		H-S7	23	38									H2B	Belly frozen in Nunc-tube				0.31
09.07.2013		H-S8	20	23									H2M	Belly frozen in Nunc-tube				0.29
	MEAN		22	30														0.29
	STD		2	7														0.02
	RSD		7	22														6.05

Table A.36: Fish data for lesser sand eel larvae

Date	Lesser sand eel larvae Species	Fish Nr.	Length (cm)	Weight (g)	Liver weight (g)	Gonade (g)	Gender Stad.	Age	Hel yngel Cryo				Remarks	GSI	HSI	Fulton
													10 indviduals sampled, whole larvae			
07.07.2013	Tobis	Tobis	3-5 cm										A number of the different species has been feeding on these			

Appendix III: Complete fatty acid compositions (% of total fatty acids)

Table A.33: FA composition of blue whiting

Species	Blue whiting				
Tissue	Muscle			Liver		
Population	10			9		
Amount of FA (mg/100 mg wet weight)	0,62	±	0,05	43,20	±	12,82
Amount of Chol (mg/100 mg wet weight)	0,05	±	0,01	0,26	±	0,03
14:0	1,37	±	0,31	4,98	±	0,81
Iso 15:0	0,06	±	0,02	0,24	±	0,03
Antiso 15:0	0,01	±	0,01	0,02	±	0,02
15:0	0,26	±	0,03	0,46	±	0,04
Iso 16:0	0,02	±	0,01	0,10	±	0,01
16:0	17,68	±	0,45	15,32	±	1,88
Iso 17:0	0,19	±	0,03	0,29	±	0,05
Antiso 17:0	0,07	±	0,02	0,12	±	0,03
17:0	0,21	±	0,03	0,23	±	0,05
iso 18:0	0,14	±	0,03	0,12	±	0,03
iso 18:0	0,02	±	0,01	0,03	±	0,04
18:0	3,81	±	0,29	2,17	±	0,63
iso 19:0	0,00	±	0,00	0,03	±	0,01
antiso 19:0	0,01	±	0,00	0,00	±	0,00
i-20:0	0,00	±	0,01	0,03	±	0,01
20:0	0,03	±	0,01	0,12	±	0,01
21:0	0,02	±	0,01	0,00	±	0,01
22:0	0,03	±	0,02	0,06	±	0,01
24:0	0,12	±	0,06	0,05	±	0,04
4,8,12-Me 13:0	0,09	±	0,02	0,27	±	0,09
∑pristanic	0,02	±	0,02	0,00	±	0,00
∑phytanic	0,10	±	0,02	0,00	±	0,00
Forgrenet 17:1	0,08	±	0,01	0,12	±	0,02
16:1 n-10, 7Me	0,18	±	0,03	0,22	±	0,06
∑SFA	24,08	±	0,53	24,38	±	1,95
14:1 (n-7)	0,00	±	0,00	0,04	±	0,01
14:1 (n-5)	0,03	±	0,02	0,07	±	0,01
15:1 n-x	0,01	±	0,03	0,02	±	0,01
15:1 (n-5)	0,00	±	0,00	0,00	±	0,00
16:1 (n-11)	0,10	±	0,02	0,06	±	0,01
16:1 (n-9)	0,18	±	0,02	0,18	±	0,03
16:1 (n-7)	1,22	±	0,23	4,67	±	0,32
16:1 (n-5)	0,22	±	0,03	0,24	±	0,02
17:1 (n-10)	0,02	±	0,00	0,17	±	0,09
17:1 (n-8)	0,18	±	0,02	0,33	±	0,05
17:1 (n-7)	0,02	±	0,02	0,03	±	0,00
17:1 (n-6)	0,02	±	0,01	0,05	±	0,01
17:1 (n-4)	0,10	±	0,02	0,09	±	0,03
18:1 (n-11)	0,52	±	0,08	0,62	±	0,15
18:1 (n-9)	6,05	±	0,69	10,29	±	2,72
18:1 (n-7)	2,10	±	0,27	2,76	±	0,63
18:1 (n-5)	0,18	±	0,04	0,35	±	0,05
18:1 (n-4)	0,01	±	0,01	0,01	±	0,01
19:1 (n-x2)	0,04	±	0,02	0,08	±	0,06
20:1 (n-11)	0,50	±	0,10	1,98	±	0,45
20:1 (n-9)	1,54	±	0,48	8,29	±	1,96
20:1 (n-7)	0,04	±	0,01	0,22	±	0,02
20:1 (n-5)	0,18	±	0,11	0,06	±	0,02
22:1 (n-11)	1,61	±	0,98	14,62	±	3,66
22:1 (n-9)	0,22	±	0,06	0,89	±	0,20
22:1 (n-7)	0,08	±	0,02	0,14	±	0,02
24:1 (n-9)	1,59	±	0,29	0,94	±	0,32
24:1 (n-7)	0,24	±	0,10	0,06	±	0,03
∑MUFA	16,99	±	2,13	47,25	±	4,19
16:4 (n-1)	0,02	±	0,02	0,05	±	0,13
18:4 (n-1)	0,04	±	0,01	0,11	±	0,03
18:5 (n-1)	0,01	±	0,01	0,00	±	0,00
16:2 (n-4)	0,09	±	0,02	0,37	±	0,10
16:3 (n-4)	0,03	±	0,01	0,03	±	0,09
18:2 (n-4)	0,05	±	0,01	0,11	±	0,02
16:2 (n-7)	0,05	±	0,02	0,05	±	0,02
18:2 (n-7)	0,02	±	0,00	0,06	±	0,01
16:2 (n-6)	0,01	±	0,02	0,02	±	0,01
18:2 (n-6)	1,12	±	0,12	1,30	±	0,10
18:3 (n-6)	0,04	±	0,01	0,11	±	0,02
20:2 (n-6)	0,16	±	0,03	0,29	±	0,02
20:3 (n-6)	0,06	±	0,01	0,06	±	0,01
20:4 (n-6)	1,34	±	0,07	0,68	±	0,16
22:2 (n-6)	0,02	±	0,02	0,04	±	0,01
22:4 (n-6)	0,10	±	0,01	0,22	±	0,04
22:5 (n-6)	0,56	±	0,03	0,18	±	0,02
16:4 (n-3)	0,00	±	0,01	0,04	±	0,02
18:3 (n-3)	0,49	±	0,08	0,94	±	0,14
18:4 (n-3)	0,83	±	0,21	2,30	±	0,66
18:5 (n-3)	0,00	±	0,00	0,00	±	0,00
20:3 (n-3)	0,13	±	0,03	0,26	±	0,07
20:4 (n-3)	0,43	±	0,06	0,65	±	0,09
20:5 (n-3)	10,70	±	1,11	7,93	±	1,24
21:5 (n-3)	0,21	±	0,03	0,34	±	0,08
22:3 (n-3)	0,00	±	0,00	0,02	±	0,00
22:4 (n-3)	0,03	±	0,01	0,08	±	0,02
22:5 (n-3)	1,20	±	0,08	0,74	±	0,12
22:6 (n-3)	40,23	±	3,36	9,92	±	1,65
24:5 (n-3)	0,39	±	0,05	0,37	±	0,13
24:6 (n-3)	0,08	±	0,04	0,10	±	0,04
20:2 D5,11 (NMI)	0,12	±	0,03	0,07	±	0,02
20:2 D5,13 (NMI)	0,00	±	0,00	0,00	±	0,00
20:3 D5,11,14 (NMI)	0,01	±	0,01	0,05	±	0,03
20:4 D5,11,14,17 (NMI)	0,01	±	0,01	0,02	±	0,01
22:2 D7,13 (NMI)	0,00	±	0,00	0,01	±	0,01
22:2 D7,15 (NMI)	0,00	±	0,00	0,01	±	0,01
22:2 NMI	0,01	±	0,01	0,04	±	0,01
∑PUFA	58,46	±	2,39	27,38	±	3,19
∑PUFA(n-6)	3,42	±	0,17	2,90	±	0,26
∑PUFA(n-3)	54,73	±	2,46	23,69	±	3,13
∑NMI	0,15	±	0,04	0,18	±	0,04
∑DMA	0,21	±	0,05	0,31	±	0,16
∑Chol	8,68	±	1,09	0,66	±	0,24
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3)	7,65	±	0,77	12,53	±	2,65
∑Odd-numbered SFA	1,13	±	0,12	2,00	±	0,19
∑Branched FA	0,75	±	0,07	1,16	±	0,12
∑Odd-numbered MUFA	0,37	±	0,04	0,65	±	0,09
16:1(n-7)/16:0	0,07	±	0,01	0,31	±	0,05
∑C16/ ∑C18	1,28	±	0,10	1,00	±	0,09
∑C16 PUFA (n-1 + n-7 + n-6)	0,20	±	0,05	0,57	±	0,27
∑C16 PUFA/ ∑C18 PUFA	0,08	±	0,02	0,11	±	0,04
20:5(n-3)/22:6(n-3)	0,27	±	0,04	0,80	±	0,08
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	11,94	±	1,22	12,65	±	1,20
18:3 (n-3) + 18:4 (n-3)	1,32	±	0,27	3,24	±	0,78
16:4 (n-3) + 18:5 (n-3)	0,00	±	0,01	0,05	±	0,02
22:5 (n-3) + 22:6 (n-3)	41,42	±	3,34	10,66	±	1,66
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	3,37	±	1,50	23,80	±	5,74
MUFA (n-11)	2,73	±	1,09	17,28	±	4,08
MUFA (n-9)	9,56	±	1,02	20,59	±	1,64
MUFA (n-7)	3,71	±	0,43	7,91	±	0,58

Table: A.34: FA composition of poor cod

Specoes	Poor cod				
Tissue	Muscle			Liver		
Population	8			10		
Amount of FA (mg/100 mg wet weight)	0,47	±	0,05	12,69	±	5,67
Amount of Chol (mg/100 mg wet weight)	0,04	±	0,00	0,25	±	0,04
14:0	0,66	±	0,06	2,23	±	0,43
Iso 15:0	0,08	±	0,02	0,33	±	0,05
Antiso 15:0	0,02	±	0,01	0,06	±	0,01
15:0	0,36	±	0,05	0,75	±	0,09
Iso 16:0	0,08	±	0,02	0,20	±	0,16
16:0	17,57	±	0,58	14,06	±	1,38
Iso 17:0	0,35	±	0,06	0,79	±	0,09
Antiso 17:0	0,16	±	0,03	0,41	±	0,05
17:0	0,51	±	0,07	0,80	±	0,18
iso 18:0	0,13	±	0,01	0,19	±	0,02
iso 18:0	0,10	±	0,02	0,14	±	0,03
18:0	4,94	±	0,21	4,33	±	0,75
iso 19:0	0,06	±	0,01	0,07	±	0,02
antiso 19:0	0,05	±	0,01	0,07	±	0,01
i-20:0	0,03	±	0,00	0,06	±	0,02
20:0	0,06	±	0,01	0,11	±	0,02
21:0	0,04	±	0,01	0,05	±	0,03
22:0	0,08	±	0,01	0,07	±	0,01
24:0	0,06	±	0,01	0,04	±	0,01
4,8,12-Me 13:0	0,04	±	0,02	0,09	±	0,10
∑pristanic	0,00	±	0,00	0,00	±	0,00
∑phytanic	0,00	±	0,00	0,00	±	0,00
Forgrenet 17:1	0,06	±	0,01	0,21	±	0,02
16:1 n-10, 7Me	0,12	±	0,02	0,22	±	0,05
∑SFA	25,32	±	0,54	24,76	±	1,52
14:1 (n-7)	0,00	±	0,00	0,03	±	0,01
14:1 (n-5)	0,04	±	0,02	0,05	±	0,02
15:1 n-x	0,06	±	0,01	0,03	±	0,00
15:1 (n-5)	0,00	±	0,00	0,02	±	0,00
16:1 (n-11)	0,10	±	0,02	0,13	±	0,03
16:1 (n-9)	0,27	±	0,03	0,51	±	0,07
16:1 (n-7)	1,08	±	0,16	4,60	±	0,49
16:1 (n-5)	0,22	±	0,04	0,27	±	0,04
17:1 (n-10)	0,03	±	0,01	0,06	±	0,01
17:1 (n-8)	0,25	±	0,05	0,72	±	0,15
17:1 (n-7)	0,03	±	0,01	0,05	±	0,01
17:1 (n-6)	0,03	±	0,01	0,08	±	0,02
17:1 (n-4)	0,07	±	0,01	0,07	±	0,01
18:1 (n-11)	0,36	±	0,11	0,95	±	0,35
18:1 (n-9)	5,39	±	0,43	10,97	±	1,82
18:1 (n-7)	2,51	±	0,30	5,62	±	0,61
18:1 (n-5)	0,26	±	0,05	0,61	±	0,13
18:1 (n-4)	0,03	±	0,01	0,07	±	0,02
19:1 (n-x2)	0,05	±	0,02	0,11	±	0,03
20:1 (n-11)	0,42	±	0,07	0,89	±	0,19
20:1 (n-9)	0,77	±	0,10	1,55	±	0,58
20:1 (n-7)	0,22	±	0,06	0,67	±	0,15
20:1 (n-5)	0,37	±	0,13	0,11	±	0,03
22:1 (n-11)	0,30	±	0,07	0,77	±	0,73
22:1 (n-9)	0,14	±	0,01	0,16	±	0,09
22:1 (n-7)	0,15	±	0,02	0,12	±	0,03
24:1 (n-9)	1,48	±	0,20	0,70	±	0,50
24:1 (n-7)	0,33	±	0,11	0,13	±	0,07
∑MUFA	14,95	±	0,84	30,07	±	2,58
16:4 (n-1)	0,04	±	0,02	0,08	±	0,06
18:4 (n-1)	0,03	±	0,02	0,06	±	0,03
18:5 (n-1)	0,00	±	0,00	0,00	±	0,00
16:2 (n-4)	0,03	±	0,01	0,11	±	0,07
16:3 (n-4)	0,01	±	0,01	0,04	±	0,04
18:2 (n-4)	0,07	±	0,01	0,18	±	0,02
16:2 (n-7)	0,04	±	0,00	0,02	±	0,01
18:2 (n-7)	0,04	±	0,00	0,14	±	0,03
16:2 (n-6)	0,01	±	0,00	0,03	±	0,00
18:2 (n-6)	0,46	±	0,02	1,05	±	0,08
18:3 (n-6)	0,01	±	0,01	0,06	±	0,03
20:2 (n-6)	0,29	±	0,04	0,62	±	0,10
20:3 (n-6)	0,05	±	0,02	0,03	±	0,01
20:4 (n-6)	3,21	±	0,68	2,47	±	0,49
22:2 (n-6)	0,01	±	0,00	0,03	±	0,01
22:4 (n-6)	0,42	±	0,12	0,50	±	0,11
22:5 (n-6)	0,75	±	0,12	0,37	±	0,05
16:4 (n-3)	0,00	±	0,00	0,03	±	0,01
18:3 (n-3)	0,16	±	0,02	0,49	±	0,05
18:4 (n-3)	0,30	±	0,06	0,72	±	0,17
18:5 (n-3)	0,00	±	0,00	0,00	±	0,00
20:3 (n-3)	0,10	±	0,01	0,24	±	0,04
20:4 (n-3)	0,24	±	0,01	0,42	±	0,05
20:5 (n-3)	11,13	±	0,92	14,26	±	2,79
21:5 (n-3)	0,20	±	0,03	0,30	±	0,05
22:3 (n-3)	0,00	±	0,00	0,00	±	0,00
22:4 (n-3)	0,03	±	0,00	0,04	±	0,02
22:5 (n-3)	1,99	±	0,30	2,44	±	0,54
22:6 (n-3)	39,06	±	2,30	19,34	±	3,00
24:5 (n-3)	0,27	±	0,13	0,18	±	0,09
24:6 (n-3)	0,44	±	0,10	0,19	±	0,08
20:2 D5,11 (NMI)	0,16	±	0,02	0,24	±	0,07
20:2 D5,13 (NMI)	0,00	±	0,00	0,08	±	0,05
20:3 D5,11,14 (NMI)	0,01	±	0,01	0,03	±	0,01
20:4 D5,11,14,17 (NMI)	0,01	±	0,01	0,01	±	0,01
22:2 D7,13 (NMI)	0,01	±	0,02	0,00	±	0,00
22:2 D7,15 (NMI)	0,04	±	0,01	0,08	±	0,03
22:2 NMI	0,00	±	0,00	0,02	±	0,02
∑PUFA	59,41	±	0,90	44,45	±	3,41
∑PUFA(n-6)	5,23	±	0,90	5,16	±	0,63
∑PUFA(n-3)	53,92	±	1,50	38,65	±	3,35
∑NMI	0,23	±	0,04	0,45	±	0,12
∑DMA	0,27	±	0,09	0,09	±	0,02
∑Chol	8,89	±	0,81	2,68	±	1,84
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3)	6,01	±	0,43	12,51	±	1,81
∑Odd-numbered SFA	1,92	±	0,28	4,07	±	0,50
∑Branched FA	1,02	±	0,15	2,35	±	0,20
∑Odd-numbered MUFA	0,43	±	0,03	0,72	±	0,07
16:1(n-7)/16:0	0,06	±	0,01	0,33	±	0,04
∑C16/ ∑C18	1,31	±	0,07	0,78	±	0,08
∑C16 PUFA (n-1 + n-7 + n-6)	0,13	±	0,02	0,32	±	0,18
∑C16 PUFA/ ∑C18 PUFA	0,12	±	0,01	0,12	±	0,06
20:5(n-3)/22:6(n-3)	0,29	±	0,04	0,76	±	0,18
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	12,25	±	1,02	18,94	±	2,64
18:3 (n-3) + 18:4 (n-3)	0,47	±	0,08	1,21	±	0,22
16:4 (n-3) + 18:5 (n-3)	0,00	±	0,00	0,03	±	0,01
22:5 (n-3) + 22:6 (n-3)	41,05	±	2,04	21,78	±	3,35
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	1,20	±	0,15	2,49	±	1,38
MUFA (n-11)	1,18	±	0,18	2,75	±	1,08
MUFA (n-9)	8,04	±	0,42	13,90	±	1,75
MUFA (n-7)	4,32	±	0,56	11,23	±	0,86

Table A.35: FA composition of pollack.

Species	Pollack					
Tissue	Muscle			Liver		
Population	9			10		
Amount of FA (mg/100 mg wet weight)	1,00	±	1,14	51,97	±	10,85
Amount of Chol (mg/100 mg wet weight)	0,19	±	0,43	0,28	±	0,04
14:0	1,28	±	0,39	3,73	±	0,52
Iso 15:0	0,04	±	0,01	0,14	±	0,04
Antiso 15:0	0,00	±	0,00	0,01	±	0,01
15:0	0,21	±	0,05	0,29	±	0,04
Iso 16:0	0,02	±	0,01	0,07	±	0,01
16:0	15,95	±	0,90	13,10	±	0,73
Iso 17:0	0,18	±	0,02	0,23	±	0,02
Antiso 17:0	0,08	±	0,04	0,09	±	0,02
17:0	0,18	±	0,03	0,19	±	0,03
iso 18:0	0,07	±	0,03	0,06	±	0,01
iso 18:0	0,04	±	0,03	0,01	±	0,00
18:0	4,92	±	1,47	3,39	±	0,34
iso 19:0	0,01	±	0,03	0,02	±	0,00
antiso 19:0	0,01	±	0,01	0,01	±	0,01
i-20:0	0,02	±	0,02	0,02	±	0,01
20:0	0,05	±	0,04	0,09	±	0,01
21:0	0,02	±	0,00	0,02	±	0,01
22:0	0,08	±	0,05	0,04	±	0,01
24:0	0,12	±	0,07	0,01	±	0,00
4,8,12-Me 13:0	0,16	±	0,06	0,32	±	0,08
∑pristanic	0,00	±	0,00	0,00	±	0,00
∑phytanic	0,00	±	0,00	0,00	±	0,00
Forgrenet 17:1	0,06	±	0,01	0,06	±	0,02
16:1 n-10, 7Me	0,22	±	0,05	0,17	±	0,03
∑SFA	23,28	±	1,14	21,54	±	0,90
14:1 (n-7)	0,00	±	0,00	0,03	±	0,01
14:1 (n-5)	0,06	±	0,05	0,05	±	0,00
15:1 n-x	0,03	±	0,05	0,03	±	0,00
15:1 (n-5)	0,00	±	0,00	0,01	±	0,00
16:1 (n-11)	0,23	±	0,12	0,18	±	0,04
16:1 (n-9)	0,35	±	0,23	0,30	±	0,08
16:1 (n-7)	1,37	±	0,29	5,26	±	0,42
16:1 (n-5)	0,20	±	0,06	0,15	±	0,05
17:1 (n-10)	0,02	±	0,01	0,09	±	0,14
17:1 (n-8)	0,14	±	0,03	0,30	±	0,02
17:1 (n-7)	0,05	±	0,04	0,03	±	0,01
17:1 (n-6)	0,01	±	0,00	0,03	±	0,01
17:1 (n-4)	0,11	±	0,04	0,05	±	0,01
18:1 (n-11)	1,15	±	0,30	2,44	±	0,53
18:1 (n-9)	6,91	±	5,12	11,78	±	2,14
18:1 (n-7)	1,63	±	0,26	3,01	±	0,32
18:1 (n-5)	0,15	±	0,04	0,30	±	0,02
18:1 (n-4)	0,00	±	0,00	0,02	±	0,01
19:1 (n-x2)	0,08	±	0,02	0,11	±	0,04
20:1 (n-11)	0,53	±	0,14	2,00	±	0,35
20:1 (n-9)	2,57	±	0,44	9,23	±	1,02
20:1 (n-7)	0,05	±	0,04	0,17	±	0,02
20:1 (n-5)	0,21	±	0,08	0,03	±	0,02
22:1 (n-11)	1,28	±	0,56	10,14	±	1,16
22:1 (n-9)	0,20	±	0,19	0,60	±	0,09
22:1 (n-7)	0,05	±	0,04	0,08	±	0,02
24:1 (n-9)	1,79	±	2,20	0,45	±	0,09
24:1 (n-7)	0,29	±	0,42	0,08	±	0,02
∑MUFA	19,46	±	7,38	46,93	±	1,89
16:4 (n-1)	0,24	±	0,43	0,01	±	0,00
18:4 (n-1)	0,07	±	0,03	0,20	±	0,02
18:5 (n-1)	0,01	±	0,01	0,01	±	0,00
16:2 (n-4)	0,14	±	0,06	0,50	±	0,07
16:3 (n-4)	0,07	±	0,03	0,33	±	0,18
18:2 (n-4)	0,10	±	0,02	0,24	±	0,02
16:2 (n-7)	0,06	±	0,11	0,10	±	0,01
18:2 (n-7)	0,03	±	0,03	0,06	±	0,01
16:2 (n-6)	0,06	±	0,03	0,04	±	0,01
18:2 (n-6)	0,84	±	0,35	1,28	±	0,11
18:3 (n-6)	0,05	±	0,02	0,13	±	0,01
20:2 (n-6)	0,14	±	0,04	0,23	±	0,01
20:3 (n-6)	0,07	±	0,02	0,06	±	0,00
20:4 (n-6)	1,52	±	0,44	0,51	±	0,03
22:2 (n-6)	0,00	±	0,01	0,01	±	0,00
22:4 (n-6)	0,13	±	0,03	0,13	±	0,03
22:5 (n-6)	0,48	±	0,18	0,18	±	0,02
16:4 (n-3)	0,00	±	0,01	0,05	±	0,01
18:3 (n-3)	0,34	±	0,15	0,83	±	0,10
18:4 (n-3)	0,75	±	0,29	2,56	±	0,25
18:5 (n-3)	0,00	±	0,00	0,00	±	0,00
20:3 (n-3)	0,08	±	0,02	0,17	±	0,02
20:4 (n-3)	0,48	±	0,17	0,68	±	0,07
20:5 (n-3)	10,98	±	2,98	8,43	±	0,48
21:5 (n-3)	0,26	±	0,06	0,55	±	0,04
22:3 (n-3)	0,00	±	0,00	0,01	±	0,00
22:4 (n-3)	0,04	±	0,01	0,13	±	0,00
22:5 (n-3)	1,60	±	0,39	1,29	±	0,17
22:6 (n-3)	37,62	±	4,98	11,40	±	0,89
24:5 (n-3)	0,42	±	0,10	0,53	±	0,06
24:6 (n-3)	0,12	±	0,16	0,14	±	0,01
20:2 D5,11 (NMI)	0,14	±	0,06	0,07	±	0,01
20:2 D5,13 (NMI)	0,00	±	0,01	0,04	±	0,03
20:3 D5,11,14 (NMI)	0,02	±	0,02	0,01	±	0,01
20:4 D5,11,14,17 (NMI)	0,02	±	0,01	0,01	±	0,00
22:2 D7,13 (NMI)	0,02	±	0,02	0,01	±	0,01
22:2 D7,15 (NMI)	0,00	±	0,00	0,00	±	0,01
22:2 NMI	0,04	±	0,01	0,04	±	0,01
∑PUFA	56,69	±	7,95	30,77	±	1,64
∑PUFA(n-6)	3,28	±	0,98	2,57	±	0,12
∑PUFA(n-3)	52,71	±	7,57	26,75	±	1,54
∑NMI	0,23	±	0,07	0,17	±	0,04
∑DMA	0,44	±	0,81	0,57	±	0,09
∑Chol	9,94	±	8,69	0,56	±	0,13
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3)	8,09	±	4,74	13,88	±	2,09
∑Odd-numbered SFA	1,04	±	0,10	1,45	±	0,23
∑Branched FA	0,71	±	0,08	0,77	±	0,11
∑Odd-numbered MUFA	0,51	±	0,17	0,46	±	0,05
16:1(n-7)/16:0	0,09	±	0,02	0,40	±	0,04
∑C16/ ∑C18	1,15	±	0,25	0,77	±	0,09
∑C16 PUFA (n-1 + n-7 + n-6)	0,57	±	0,47	1,02	±	0,25
∑C16 PUFA/ ∑C18 PUFA	0,78	±	1,83	0,19	±	0,05
20:5(n-3)/22:6(n-3)	0,29	±	0,08	0,74	±	0,06
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	12,59	±	2,83	13,70	±	0,78
18:3 (n-3) + 18:4 (n-3)	1,10	±	0,43	3,39	±	0,31
16:4 (n-3) + 18:5 (n-3)	0,00	±	0,01	0,05	±	0,01
22:5 (n-3) + 22:6 (n-3)	39,21	±	5,30	12,69	±	1,01
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	4,05	±	0,69	19,97	±	2,02
MUFA (n-11)	3,19	±	0,78	14,76	±	1,36
MUFA (n-9)	11,83	±	7,95	22,35	±	1,52
MUFA (n-7)	3,44	±	0,55	8,66	±	0,43

Table A.36: FA composition of greater argentine.

Species	Greater argentine					
Tissue	Muscle			Liver		
Population	9			10		
Amount of FA (mg/100 mg wet weight)	0,96	±	0,37	7,49	±	1,19
Amount of Chol (mg/100 mg wet weight)	0,08	±	0,02	0,28	±	0,04
14:0	1,86	±	0,74	1,82	±	0,30
Iso 15:0	0,09	±	0,03	0,06	±	0,03
Antiso 15:0	0,00	±	0,01	0,01	±	0,01
15:0	0,29	±	0,05	0,12	±	0,05
Iso 16:0	0,03	±	0,02	0,04	±	0,02
16:0	19,77	±	0,99	16,98	±	1,31
Iso 17:0	0,23	±	0,07	0,21	±	0,07
Antiso 17:0	0,08	±	0,03	0,08	±	0,03
17:0	0,26	±	0,02	0,12	±	0,04
iso 18:0	0,17	±	0,02	0,11	±	0,04
iso 18:0	0,02	±	0,01	0,01	±	0,01
18:0	3,58	±	0,23	4,41	±	0,63
iso 19:0	0,01	±	0,02	0,03	±	0,02
antiso 19:0	0,02	±	0,01	0,00	±	0,01
i-20:0	0,02	±	0,02	0,03	±	0,01
20:0	0,06	±	0,02	0,09	±	0,02
21:0	0,03	±	0,01	0,05	±	0,01
22:0	0,06	±	0,02	0,05	±	0,02
24:0	0,11	±	0,05	0,01	±	0,01
4,8,12-Me 13:0	0,09	±	0,02	0,07	±	0,03
∑pristanic	0,00	±	0,00	0,00	±	0,00
∑phytanic	0,00	±	0,00	0,00	±	0,00
Forgrenet 17:1	0,06	±	0,03	0,02	±	0,01
16:1 n-10, 7Me	0,17	±	0,03	0,09	±	0,03
∑SFA	26,71	±	0,54	24,23	±	1,54
14:1 (n-7)	0,00	±	0,00	0,01	±	0,00
14:1 (n-5)	0,02	±	0,01	0,03	±	0,01
15:1 n-x	0,00	±	0,00	0,00	±	0,00
15:1 (n-5)	0,00	±	0,00	0,00	±	0,00
16:1 (n-11)	0,08	±	0,01	0,05	±	0,02
16:1 (n-9)	0,18	±	0,02	0,20	±	0,03
16:1 (n-7)	1,60	±	0,59	3,60	±	0,62
16:1 (n-5)	0,17	±	0,02	0,06	±	0,02
17:1 (n-10)	0,02	±	0,01	0,02	±	0,01
17:1 (n-8)	0,26	±	0,07	0,26	±	0,07
17:1 (n-7)	0,02	±	0,01	0,00	±	0,00
17:1 (n-6)	0,01	±	0,01	0,01	±	0,01
17:1 (n-4)	0,06	±	0,02	0,02	±	0,01
18:1 (n-11)	0,27	±	0,07	4,78	±	5,26
18:1 (n-9)	13,18	±	3,92	37,46	±	4,21
18:1 (n-7)	2,14	±	0,39	3,39	±	0,41
18:1 (n-5)	0,22	±	0,03	0,24	±	0,06
18:1 (n-4)	0,01	±	0,01	0,02	±	0,01
19:1 (n-x2)	0,03	±	0,02	0,01	±	0,01
20:1 (n-11)	0,38	±	0,11	0,32	±	0,12
20:1 (n-9)	2,61	±	0,87	2,62	±	0,90
20:1 (n-7)	0,19	±	0,09	0,17	±	0,09
20:1 (n-5)	0,25	±	0,09	0,05	±	0,02
22:1 (n-11)	3,44	±	1,37	2,37	±	1,20
22:1 (n-9)	0,61	±	0,24	0,67	±	0,24
22:1 (n-7)	0,07	±	0,03	0,05	±	0,03
24:1 (n-9)	0,96	±	0,31	0,65	±	0,15
24:1 (n-7)	0,22	±	0,29	0,06	±	0,01
∑MUFA	27,00	±	7,09	57,13	±	3,57
16:4 (n-1)	0,05	±	0,06	0,00	±	0,00
18:4 (n-1)	0,04	±	0,02	0,03	±	0,02
18:5 (n-1)	0,00	±	0,00	0,01	±	0,01
16:2 (n-4)	0,08	±	0,04	0,03	±	0,02
16:3 (n-4)	0,02	±	0,02	0,00	±	0,01
18:2 (n-4)	0,06	±	0,03	0,04	±	0,03
16:2 (n-7)	0,00	±	0,01	0,00	±	0,00
18:2 (n-7)	0,04	±	0,02	0,05	±	0,01
16:2 (n-6)	0,02	±	0,01	0,00	±	0,00
18:2 (n-6)	0,97	±	0,07	0,59	±	0,19
18:3 (n-6)	0,03	±	0,01	0,03	±	0,01
20:2 (n-6)	0,20	±	0,06	0,16	±	0,06
20:3 (n-6)	0,06	±	0,01	0,04	±	0,01
20:4 (n-6)	1,19	±	0,10	0,67	±	0,17
22:2 (n-6)	0,01	±	0,01	0,01	±	0,01
22:4 (n-6)	0,23	±	0,05	0,18	±	0,08
22:5 (n-6)	0,51	±	0,08	0,14	±	0,04
16:4 (n-3)	0,00	±	0,00	0,00	±	0,01
18:3 (n-3)	0,49	±	0,07	0,25	±	0,08
18:4 (n-3)	0,55	±	0,14	0,19	±	0,09
18:5 (n-3)	0,00	±	0,00	0,00	±	0,00
20:3 (n-3)	0,15	±	0,04	0,13	±	0,06
20:4 (n-3)	0,61	±	0,06	0,51	±	0,18
20:5 (n-3)	8,12	±	0,79	4,62	±	0,97
21:5 (n-3)	0,19	±	0,03	0,13	±	0,04
22:3 (n-3)	0,00	±	0,00	0,01	±	0,01
22:4 (n-3)	0,02	±	0,01	0,02	±	0,01
22:5 (n-3)	1,73	±	0,19	1,22	±	0,37
22:6 (n-3)	30,07	±	7,04	9,15	±	1,93
24:5 (n-3)	0,33	±	0,04	0,11	±	0,11
24:6 (n-3)	0,06	±	0,03	0,02	±	0,03
20:2 D5,11 (NMI)	0,19	±	0,03	0,29	±	0,06
20:2 D5,13 (NMI)	0,01	±	0,01	0,01	±	0,02
20:3 D5,11,14 (NMI)	0,01	±	0,01	0,01	±	0,02
20:4 D5,11,14,17 (NMI)	0,00	±	0,01	0,00	±	0,00
22:2 D7,13 (NMI)	0,00	±	0,01	0,00	±	0,00
22:2 D7,15 (NMI)	0,00	±	0,01	0,00	±	0,00
22:2 NMI	0,01	±	0,01	0,00	±	0,01
∑PUFA	45,84	±	7,25	18,35	±	4,01
∑PUFA(n-6)	3,21	±	0,20	1,82	±	0,52
∑PUFA(n-3)	42,34	±	7,45	16,37	±	3,49
∑NMI	0,22	±	0,05	0,31	±	0,04
∑DMA	0,02	±	0,02	0,02	±	0,02
∑Chol	9,13	±	1,53	3,90	±	0,83
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3)	14,64	±	3,98	38,30	±	4,06
∑Odd-numbered SFA	1,31	±	0,28	0,90	±	0,29
∑Branched FA	0,83	±	0,15	0,60	±	0,20
∑Odd-numbered MUFA	0,37	±	0,07	0,29	±	0,07
16:1(n-7)/16:0	0,08	±	0,03	0,21	±	0,03
∑C16/ ∑C18	1,05	±	0,21	0,41	±	0,03
∑C16 PUFA (n-1 + n-7 + n-6)	0,18	±	0,13	0,04	±	0,03
∑C16 PUFA/ ∑C18 PUFA	0,08	±	0,05	0,03	±	0,01
20:5(n-3)/22:6(n-3)	0,29	±	0,08	0,51	±	0,04
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	9,78	±	0,72	8,22	±	0,65
18:3 (n-3) + 18:4 (n-3)	1,05	±	0,21	0,44	±	0,15
16:4 (n-3) + 18:5 (n-3)	0,00	±	0,00	0,00	±	0,01
22:5 (n-3) + 22:6 (n-3)	31,80	±	7,20	10,36	±	2,19
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	6,66	±	2,42	5,65	±	2,22
MUFA (n-11)	4,17	±	1,53	7,52	±	4,78
MUFA (n-9)	17,53	±	4,67	41,60	±	3,68
MUFA (n-7)	4,24	±	1,04	7,28	±	0,68

Table A.37: FA composition of blackmouth catshark.

Species	Blackmouth catshark					
Tissue	Muscle			Liver		
Population	10			10		
Amount of FA (mg/100 mg wet weight)	0,71	±	0,33	53,65	±	10,72
Amount of Chol (mg/100 mg wet weight)	0,05	±	0,01	0,46	±	0,09
14:0	2,76	±	1,46	4,58	±	0,81
Iso 15:0	0,22	±	0,04	0,24	±	0,02
Antiso 15:0	0,07	±	0,03	0,06	±	0,01
15:0	0,23	±	0,06	0,47	±	0,06
Iso 16:0	0,07	±	0,02	0,13	±	0,04
16:0	16,61	±	1,79	13,18	±	0,50
Iso 17:0	0,28	±	0,05	0,42	±	0,11
Antiso 17:0	0,18	±	0,06	0,16	±	0,06
17:0	0,33	±	0,08	0,25	±	0,08
iso 18:0	0,34	±	0,09	0,23	±	0,07
iso 18:0	0,05	±	0,02	0,02	±	0,02
18:0	4,89	±	1,30	1,93	±	0,31
iso 19:0	0,02	±	0,01	0,02	±	0,00
antiso 19:0	0,04	±	0,01	0,01	±	0,02
i-20:0	0,03	±	0,01	0,02	±	0,01
20:0	0,08	±	0,03	0,14	±	0,02
21:0	0,03	±	0,01	0,03	±	0,01
22:0	0,12	±	0,04	0,04	±	0,03
24:0	0,14	±	0,05	0,02	±	0,00
4,8,12-Me 13:0	0,11	±	0,07	0,16	±	0,04
∑pristanic	0,06	±	0,03	0,08	±	0,02
∑phytanic	0,06	±	0,03	0,16	±	0,08
Forgrenet 17:1	0,05	±	0,02	0,09	±	0,02
16:1 n-10, 7Me	0,11	±	0,03	0,19	±	0,03
∑SFA	26,49	±	1,69	21,97	±	0,61
14:1 (n-7)	0,04	±	0,02	0,02	±	0,00
14:1 (n-5)	0,03	±	0,02	0,10	±	0,02
15:1 n-x	0,00	±	0,00	0,01	±	0,01
15:1 (n-5)	0,00	±	0,00	0,01	±	0,00
16:1 (n-11)	0,21	±	0,06	0,06	±	0,01
16:1 (n-9)	0,24	±	0,03	0,22	±	0,03
16:1 (n-7)	2,85	±	1,24	6,31	±	0,53
16:1 (n-5)	0,26	±	0,03	0,21	±	0,02
17:1 (n-10)	0,04	±	0,01	0,03	±	0,01
17:1 (n-8)	0,21	±	0,03	0,39	±	0,09
17:1 (n-7)	0,04	±	0,01	0,04	±	0,00
17:1 (n-6)	0,03	±	0,01	0,04	±	0,01
17:1 (n-4)	0,18	±	0,05	0,06	±	0,01
18:1 (n-11)	0,70	±	0,14	1,49	±	0,29
18:1 (n-9)	6,76	±	0,41	11,80	±	1,19
18:1 (n-7)	4,26	±	0,95	2,99	±	0,95
18:1 (n-5)	0,33	±	0,03	0,31	±	0,02
18:1 (n-4)	0,02	±	0,01	0,03	±	0,01
19:1 (n-x2)	0,05	±	0,03	0,17	±	0,04
20:1 (n-11)	0,66	±	0,17	1,82	±	0,16
20:1 (n-9)	4,18	±	1,85	7,82	±	1,26
20:1 (n-7)	0,13	±	0,05	0,34	±	0,11
20:1 (n-5)	0,08	±	0,04	0,07	±	0,02
22:1 (n-11)	5,46	±	3,56	11,79	±	2,85
22:1 (n-9)	0,45	±	0,20	1,08	±	0,21
22:1 (n-7)	0,12	±	0,05	0,15	±	0,01
24:1 (n-9)	0,64	±	0,13	0,73	±	0,08
24:1 (n-7)	0,23	±	0,08	0,14	±	0,03
∑MUFA	28,22	±	6,14	48,23	±	2,42
16:4 (n-1)	0,40	±	0,28	0,02	±	0,01
18:4 (n-1)	0,08	±	0,05	0,18	±	0,05
18:5 (n-1)	0,02	±	0,01	0,00	±	0,01
16:2 (n-4)	0,23	±	0,17	0,32	±	0,06
16:3 (n-4)	0,16	±	0,13	0,14	±	0,04
18:2 (n-4)	0,13	±	0,02	0,08	±	0,08
16:2 (n-7)	0,09	±	0,04	0,05	±	0,01
18:2 (n-7)	0,06	±	0,01	0,06	±	0,01
16:2 (n-6)	0,06	±	0,05	0,03	±	0,00
18:2 (n-6)	1,17	±	0,15	1,22	±	0,11
18:3 (n-6)	0,05	±	0,04	0,13	±	0,05
20:2 (n-6)	0,26	±	0,03	0,25	±	0,06
20:3 (n-6)	0,10	±	0,02	0,06	±	0,01
20:4 (n-6)	2,37	±	0,59	0,59	±	0,20
22:2 (n-6)	0,01	±	0,01	0,03	±	0,01
22:4 (n-6)	0,62	±	0,20	0,34	±	0,12
22:5 (n-6)	0,51	±	0,12	0,40	±	0,07
16:4 (n-3)	0,03	±	0,04	0,06	±	0,01
18:3 (n-3)	0,42	±	0,20	0,72	±	0,12
18:4 (n-3)	0,99	±	0,83	1,36	±	0,35
18:5 (n-3)	0,01	±	0,01	0,00	±	0,00
20:3 (n-3)	0,11	±	0,02	0,13	±	0,06
20:4 (n-3)	0,54	±	0,08	0,80	±	0,10
20:5 (n-3)	5,96	±	1,50	4,39	±	0,65
21:5 (n-3)	0,22	±	0,11	0,32	±	0,03
22:3 (n-3)	0,01	±	0,01	0,02	±	0,02
22:4 (n-3)	0,09	±	0,04	0,12	±	0,02
22:5 (n-3)	4,71	±	1,58	1,71	±	0,35
22:6 (n-3)	24,98	±	5,75	14,94	±	1,97
24:5 (n-3)	0,37	±	0,22	0,43	±	0,08
24:6 (n-3)	0,13	±	0,04	0,21	±	0,04
20:2 D5,11 (NMI)	0,13	±	0,02	0,06	±	0,03
20:2 D5,13 (NMI)	0,01	±	0,01	0,02	±	0,02
20:3 D5,11,14 (NMI)	0,03	±	0,02	0,06	±	0,03
20:4 D5,11,14,17 (NMI)	0,01	±	0,01	0,01	±	0,00
22:2 D7,13 (NMI)	0,02	±	0,01	0,03	±	0,03
22:2 D7,15 (NMI)	0,01	±	0,01	0,02	±	0,02
22:2 NMI	0,01	±	0,01	0,06	±	0,01
∑PUFA	44,90	±	4,73	29,11	±	2,19
∑PUFA(n-6)	5,16	±	0,87	3,04	±	0,37
∑PUFA(n-3)	38,57	±	4,63	25,22	±	1,97
∑NMI	0,22	±	0,04	0,24	±	0,05
∑DMA	0,66	±	0,24	0,29	±	0,09
∑Chol	7,41	±	1,90	0,90	±	0,32
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3))	8,35	±	0,56	13,74	±	1,13
∑Odd-numbered SFA	1,78	±	0,25	2,14	±	0,40
∑Branched FA	1,30	±	0,20	1,41	±	0,21
∑Odd-numbered MUFA	0,43	±	0,08	0,59	±	0,04
16:1(n-7)/16:0	0,18	±	0,10	0,48	±	0,04
∑C16/ ∑C18	1,03	±	0,06	0,92	±	0,07
∑C16 PUFA (n-1 + n-7 + n-6)	0,96	±	0,62	0,61	±	0,11
∑C16 PUFA/ ∑C18 PUFA	0,31	±	0,09	0,17	±	0,03
20:5(n-3)/22:6(n-3)	0,27	±	0,16	0,30	±	0,07
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	9,21	±	2,96	10,71	±	1,08
18:3 (n-3) + 18:4 (n-3)	1,41	±	1,03	2,08	±	0,47
16:4 (n-3) + 18:5 (n-3)	0,03	±	0,05	0,06	±	0,01
22:5 (n-3) + 22:6 (n-3)	29,69	±	7,18	16,66	±	2,23
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	10,09	±	5,59	20,69	±	4,27
MUFA (n-11)	7,03	±	3,62	15,16	±	3,03
MUFA (n-9)	12,27	±	2,27	21,65	±	0,69
MUFA (n-7)	7,68	±	0,59	9,98	±	1,09

Table A.38: FA composition of lemon sole.

Species	Lemon sole					
Tissue	Muscle			Liver		
Population	10			10		
Amount of FA (mg/100 mg wet weight)	0,45	±	0,04	3,58	±	1,63
Amount of Chol (mg/100 mg wet weight)	0,05	±	0,01	0,21	±	0,04
14:0	2,13	±	0,35	3,30	±	0,89
Iso 15:0	0,12	±	0,11	0,25	±	0,10
Antiso 15:0	0,04	±	0,02	0,05	±	0,02
15:0	0,76	±	0,18	0,74	±	0,30
Iso 16:0	0,08	±	0,01	0,34	±	0,09
16:0	16,19	±	1,24	17,15	±	2,77
Iso 17:0	0,56	±	0,14	1,18	±	0,24
Antiso 17:0	0,17	±	0,05	0,44	±	0,16
17:0	0,58	±	0,07	0,62	±	0,40
iso 18:0	0,18	±	0,05	0,25	±	0,12
iso 18:0	0,06	±	0,02	0,05	±	0,02
18:0	5,22	±	0,35	3,05	±	1,33
iso 19:0	0,03	±	0,01	0,03	±	0,02
antiso 19:0	0,06	±	0,01	0,04	±	0,01
i-20:0	0,07	±	0,02	0,06	±	0,02
20:0	0,09	±	0,02	0,04	±	0,01
21:0	0,04	±	0,01	0,09	±	0,03
22:0	0,21	±	0,08	0,03	±	0,03
24:0	0,16	±	0,03	0,07	±	0,03
4,8,12-Me 13:0	0,03	±	0,02	0,04	±	0,02
∑pristanic	0,01	±	0,01	0,08	±	0,02
∑phytanic	0,12	±	0,06	0,16	±	0,13
Forgrenet 17:1	0,13	±	0,05	0,32	±	0,08
16:1 n-10, 7Me	0,55	±	0,15	1,13	±	0,26
∑SFA	26,74	±	0,92	27,78	±	2,33
14:1 (n-7)	0,02	±	0,01	0,04	±	0,03
14:1 (n-5)	0,03	±	0,01	0,13	±	0,16
15:1 n-x	0,00	±	0,01	0,02	±	0,01
15:1 (n-5)	0,00	±	0,00	0,01	±	0,01
16:1 (n-11)	0,15	±	0,04	0,09	±	0,04
16:1 (n-9)	0,40	±	0,13	0,87	±	0,36
16:1 (n-7)	2,63	±	0,72	8,36	±	6,25
16:1 (n-5)	0,43	±	0,13	0,34	±	0,09
17:1 (n-10)	0,14	±	0,05	0,16	±	0,08
17:1 (n-8)	0,45	±	0,12	0,73	±	0,15
17:1 (n-7)	0,05	±	0,01	0,03	±	0,02
17:1 (n-6)	0,06	±	0,02	0,09	±	0,04
17:1 (n-4)	0,12	±	0,03	0,15	±	0,04
18:1 (n-11)	0,32	±	0,17	0,46	±	0,22
18:1 (n-9)	5,83	±	0,86	9,08	±	2,96
18:1 (n-7)	2,32	±	0,55	3,45	±	0,42
18:1 (n-5)	0,37	±	0,14	0,78	±	0,13
18:1 (n-4)	0,05	±	0,03	0,11	±	0,02
19:1 (n-x2)	0,17	±	0,06	0,22	±	0,04
20:1 (n-11)	0,53	±	0,29	0,22	±	0,11
20:1 (n-9)	0,86	±	0,31	0,57	±	0,25
20:1 (n-7)	0,40	±	0,14	0,35	±	0,15
20:1 (n-5)	0,18	±	0,04	0,12	±	0,03
22:1 (n-11)	0,27	±	0,12	0,23	±	0,14
22:1 (n-9)	0,11	±	0,03	0,18	±	0,08
22:1 (n-7)	0,21	±	0,10	0,17	±	0,04
24:1 (n-9)	2,00	±	0,17	1,52	±	0,47
24:1 (n-7)	0,13	±	0,07	0,19	±	0,06
∑MUFA	18,24	±	2,80	28,67	±	8,80
16:4 (n-1)	0,08	±	0,01	0,05	±	0,02
18:4 (n-1)	0,03	±	0,01	0,04	±	0,01
18:5 (n-1)	0,00	±	0,00	0,00	±	0,01
16:2 (n-4)	0,05	±	0,02	0,06	±	0,01
16:3 (n-4)	0,01	±	0,01	0,01	±	0,00
18:2 (n-4)	0,09	±	0,03	0,12	±	0,03
16:2 (n-7)	0,07	±	0,02	0,01	±	0,01
18:2 (n-7)	0,07	±	0,03	0,14	±	0,03
16:2 (n-6)	0,01	±	0,00	0,07	±	0,07
18:2 (n-6)	0,57	±	0,10	0,67	±	0,17
18:3 (n-6)	0,03	±	0,01	0,03	±	0,01
20:2 (n-6)	0,29	±	0,08	0,25	±	0,04
20:3 (n-6)	0,11	±	0,06	0,06	±	0,04
20:4 (n-6)	5,48	±	1,74	3,63	±	1,33
22:2 (n-6)	0,02	±	0,01	0,04	±	0,03
22:4 (n-6)	1,11	±	0,39	0,98	±	0,22
22:5 (n-6)	1,03	±	0,68	0,64	±	0,36
16:4 (n-3)	0,01	±	0,01	0,02	±	0,01
18:3 (n-3)	0,12	±	0,03	0,16	±	0,06
18:4 (n-3)	0,23	±	0,07	0,33	±	0,08
18:5 (n-3)	0,00	±	0,00	0,00	±	0,00
20:3 (n-3)	0,09	±	0,03	0,12	±	0,03
20:4 (n-3)	0,27	±	0,06	0,33	±	0,08
20:5 (n-3)	12,90	±	1,76	10,26	±	2,81
21:5 (n-3)	0,22	±	0,06	0,21	±	0,03
22:3 (n-3)	0,02	±	0,01	0,01	±	0,01
22:4 (n-3)	0,03	±	0,01	0,03	±	0,02
22:5 (n-3)	3,44	±	0,47	2,71	±	0,60
22:6 (n-3)	27,26	±	3,58	20,48	±	5,25
24:5 (n-3)	0,23	±	0,03	0,11	±	0,04
24:6 (n-3)	0,34	±	0,25	0,17	±	0,05
20:2 D5,11 (NMI)	0,16	±	0,04	0,14	±	0,04
20:2 D5,13 (NMI)	0,03	±	0,04	0,00	±	0,01
20:3 D5,11,14 (NMI)	0,11	±	0,04	0,04	±	0,02
20:4 D5,11,14,17 (NMI)	0,01	±	0,01	0,06	±	0,02
22:2 D7,13 (NMI)	0,18	±	0,20	0,08	±	0,10
22:2 D7,15 (NMI)	0,05	±	0,02	0,01	±	0,01
22:2 NMI	0,03	±	0,01	0,04	±	0,02
∑PUFA	54,19	±	3,12	41,74	±	9,71
∑PUFA(n-6)	8,64	±	2,15	6,37	±	1,68
∑PUFA(n-3)	45,15	±	3,21	34,94	±	8,43
∑NMI	0,54	±	0,29	0,38	±	0,09
∑DMA	0,58	±	0,08	0,10	±	0,01
∑Chol	10,21	±	1,33	6,73	±	2,40
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3))	6,53	±	0,93	9,91	±	2,78
∑Odd-numbered SFA	3,00	±	0,52	4,37	±	1,17
∑Branched FA	1,82	±	0,38	3,66	±	0,83
∑Odd-numbered MUFA	1,02	±	0,23	1,71	±	0,33
16:1(n-7)/16:0	0,16	±	0,05	0,46	±	0,28
∑C16/ ∑C18	1,30	±	0,13	1,44	±	0,40
∑C16 PUFA (n-1 + n-7 + n-6)	0,23	±	0,05	0,22	±	0,07
∑C16 PUFA/ ∑C18 PUFA	0,21	±	0,03	0,17	±	0,09
20:5(n-3)/22:6(n-3)	0,48	±	0,10	0,50	±	0,06
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	15,61	±	1,74	18,66	±	4,04
18:3 (n-3) + 18:4 (n-3)	0,35	±	0,10	0,49	±	0,13
16:4 (n-3) + 18:5 (n-3)	0,01	±	0,01	0,02	±	0,01
22:5 (n-3) + 22:6 (n-3)	30,70	±	3,31	23,19	±	5,72
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	1,24	±	0,43	0,99	±	0,47
MUFA (n-11)	1,27	±	0,53	1,00	±	0,47
MUFA (n-9)	9,20	±	1,06	12,23	±	2,94
MUFA (n-7)	5,76	±	1,12	12,59	±	6,04

Table A.39: FA composition of garfish.

Species	Garfish					
Tissue	Muscle			Liver		
Population	7			7		
Amount of FA (mg/100 mg wet weight)	1,27	±	0,55	7,58	±	4,49
Amount of Chol (mg/100 mg wet weight)	0,12	±	0,03	0,33	±	0,04
14:0	1,34	±	0,53	0,79	±	0,14
Iso 15:0	0,10	±	0,03	0,06	±	0,03
Antiso 15:0	0,03	±	0,01	0,01	±	0,00
15:0	0,34	±	0,07	0,23	±	0,10
Iso 16:0	0,05	±	0,01	0,05	±	0,03
16:0	18,43	±	0,84	18,69	±	1,83
Iso 17:0	0,31	±	0,06	0,38	±	0,08
Antiso 17:0	0,12	±	0,02	0,13	±	0,05
17:0	0,41	±	0,07	0,33	±	0,16
iso 18:0	0,15	±	0,07	0,13	±	0,04
iso 18:0	0,06	±	0,04	0,02	±	0,02
18:0	6,06	±	0,91	6,46	±	0,79
iso 19:0	0,04	±	0,03	0,08	±	0,05
antiso 19:0	0,03	±	0,00	0,02	±	0,01
i-20:0	0,04	±	0,01	0,05	±	0,01
20:0	0,10	±	0,02	0,10	±	0,02
21:0	0,03	±	0,01	0,07	±	0,04
22:0	0,07	±	0,03	0,07	±	0,05
24:0	0,14	±	0,05	0,10	±	0,03
4,8,12-Me 13:0	0,03	±	0,01	0,04	±	0,03
∑pristanic	0,01	±	0,01	0,00	±	0,00
∑phytanic	0,09	±	0,03	0,07	±	0,01
Forgrenet 17:1	0,09	±	0,02	0,09	±	0,05
16:1 n-10, 7Me	0,29	±	0,06	0,34	±	0,06
∑SFA	27,84	±	1,07	27,78	±	1,88
14:1 (n-7)	0,01	±	0,00	0,01	±	0,01
14:1 (n-5)	0,04	±	0,01	0,03	±	0,02
15:1 n-x	0,00	±	0,00	0,00	±	0,00
15:1 (n-5)	0,00	±	0,00	0,02	±	0,03
16:1 (n-11)	0,09	±	0,02	0,06	±	0,01
16:1 (n-9)	0,37	±	0,07	0,38	±	0,08
16:1 (n-7)	2,82	±	0,82	7,11	±	2,99
16:1 (n-5)	0,19	±	0,04	0,13	±	0,04
17:1 (n-10)	0,04	±	0,01	0,02	±	0,01
17:1 (n-8)	0,25	±	0,06	0,39	±	0,07
17:1 (n-7)	0,07	±	0,04	0,02	±	0,01
17:1 (n-6)	0,01	±	0,01	0,01	±	0,01
17:1 (n-4)	0,06	±	0,02	0,03	±	0,01
18:1 (n-11)	0,73	±	0,93	2,45	±	1,59
18:1 (n-9)	7,76	±	1,73	19,26	±	6,47
18:1 (n-7)	2,31	±	0,30	3,34	±	0,61
18:1 (n-5)	0,24	±	0,04	0,29	±	0,04
18:1 (n-4)	0,03	±	0,02	0,03	±	0,01
19:1 (n-x2)	0,08	±	0,06	0,11	±	0,08
20:1 (n-11)	0,25	±	0,09	0,33	±	0,11
20:1 (n-9)	0,95	±	0,35	0,92	±	0,14
20:1 (n-7)	0,17	±	0,07	0,14	±	0,05
20:1 (n-5)	0,11	±	0,07	0,04	±	0,01
22:1 (n-11)	0,61	±	0,30	0,51	±	0,21
22:1 (n-9)	0,11	±	0,02	0,07	±	0,01
22:1 (n-7)	0,16	±	0,08	0,07	±	0,07
24:1 (n-9)	1,56	±	0,43	1,25	±	0,62
24:1 (n-7)	0,23	±	0,14	0,09	±	0,02
∑MUFA	19,25	±	3,09	37,10	±	9,75
16:4 (n-1)	0,28	±	0,20	0,05	±	0,08
18:4 (n-1)	0,02	±	0,01	0,02	±	0,01
18:5 (n-1)	0,00	±	0,00	0,00	±	0,00
16:2 (n-4)	0,06	±	0,03	0,03	±	0,01
16:3 (n-4)	0,01	±	0,01	0,00	±	0,00
18:2 (n-4)	0,09	±	0,02	0,07	±	0,01
16:2 (n-7)	0,02	±	0,01	0,01	±	0,00
18:2 (n-7)	0,07	±	0,02	0,10	±	0,02
16:2 (n-6)	0,04	±	0,03	0,02	±	0,02
18:2 (n-6)	1,36	±	0,46	1,17	±	0,68
18:3 (n-6)	0,06	±	0,01	0,04	±	0,01
20:2 (n-6)	0,29	±	0,03	0,27	±	0,10
20:3 (n-6)	0,06	±	0,00	0,06	±	0,02
20:4 (n-6)	1,60	±	0,43	1,03	±	0,64
22:2 (n-6)	0,03	±	0,01	0,02	±	0,01
22:4 (n-6)	0,47	±	0,18	0,81	±	0,40
22:5 (n-6)	0,52	±	0,11	0,27	±	0,06
16:4 (n-3)	0,01	±	0,01	0,00	±	0,00
18:3 (n-3)	0,68	±	0,30	0,59	±	0,28
18:4 (n-3)	0,72	±	0,45	0,33	±	0,08
18:5 (n-3)	0,00	±	0,00	0,00	±	0,00
20:3 (n-3)	0,19	±	0,04	0,18	±	0,05
20:4 (n-3)	0,66	±	0,25	0,79	±	0,12
20:5 (n-3)	7,35	±	1,29	4,80	±	1,68
21:5 (n-3)	0,34	±	0,16	0,12	±	0,02
22:3 (n-3)	0,01	±	0,00	0,01	±	0,01
22:4 (n-3)	0,07	±	0,02	0,07	±	0,04
22:5 (n-3)	2,80	±	0,37	3,46	±	0,59
22:6 (n-3)	34,25	±	3,21	20,00	±	6,31
24:5 (n-3)	0,12	±	0,08	0,18	±	0,13
24:6 (n-3)	0,20	±	0,12	0,10	±	0,08
20:2 D5,11 (NMI)	0,10	±	0,02	0,16	±	0,05
20:2 D5,13 (NMI)	0,01	±	0,01	0,04	±	0,08
20:3 D5,11,14 (NMI)	0,02	±	0,02	0,02	±	0,01
20:4 D5,11,14,17 (NMI)	0,02	±	0,01	0,02	±	0,01
22:2 D7,13 (NMI)	0,01	±	0,01	0,00	±	0,00
22:2 D7,15 (NMI)	0,00	±	0,01	0,00	±	0,00
22:2 NMI	0,02	±	0,02	0,07	±	0,01
∑PUFA	52,40	±	2,19	34,58	±	9,47
∑PUFA(n-6)	4,42	±	0,61	3,68	±	1,68
∑PUFA(n-3)	47,42	±	2,38	30,61	±	8,32
∑NMI	0,18	±	0,05	0,32	±	0,09
∑DMA	0,71	±	0,23	0,11	±	0,08
∑Chol	10,94	±	4,67	6,08	±	4,24
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3))	9,80	±	2,40	21,02	±	6,37
∑Odd-numbered SFA	1,73	±	0,28	1,60	±	0,38
∑Branched FA	1,14	±	0,18	1,15	±	0,25
∑Odd-numbered MUFA	0,60	±	0,09	0,64	±	0,10
16:1(n-7)/16:0	0,16	±	0,05	0,38	±	0,15
∑C16/ ∑C18	1,10	±	0,15	0,79	±	0,15
∑C16 PUFA (n-1 + n-7 + n-6)	0,42	±	0,17	0,11	±	0,08
∑C16 PUFA/ ∑C18 PUFA	0,17	±	0,15	0,05	±	0,04
20:5(n-3)/22:6(n-3)	0,22	±	0,05	0,24	±	0,02
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	10,45	±	1,58	11,96	±	1,60
18:3 (n-3) + 18:4 (n-3)	1,40	±	0,72	0,92	±	0,34
16:4 (n-3) + 18:5 (n-3)	0,01	±	0,01	0,00	±	0,00
22:5 (n-3) + 22:6 (n-3)	37,06	±	2,89	23,45	±	6,52
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	1,66	±	0,66	1,50	±	0,35
MUFA (n-11)	1,68	±	0,75	3,35	±	1,74
MUFA (n-9)	10,74	±	1,73	21,88	±	5,98
MUFA (n-7)	5,78	±	0,87	10,76	±	2,94

Table A.40: FA composition of thorny skate

Species	Thorny skate					
Tissue	Muscle			Liver		
Population	10			10		
Amount of FA (mg/100 mg wet weight)	0,44	±	0,04	16,64	±	10,76
Amount of Chol (mg/100 mg wet weight)	0,04	±	0,01	0,37	±	0,20
14:0	0,74	±	0,41	2,20	±	1,47
Iso 15:0	0,13	±	0,02	0,24	±	0,05
Antiso 15:0	0,02	±	0,01	0,06	±	0,01
15:0	0,32	±	0,07	0,51	±	0,07
Iso 16:0	0,05	±	0,02	0,12	±	0,07
16:0	21,79	±	0,98	13,82	±	1,15
Iso 17:0	0,35	±	0,09	0,62	±	0,15
Antiso 17:0	0,23	±	0,05	0,22	±	0,10
17:0	0,89	±	0,21	0,77	±	0,26
iso 18:0	0,44	±	0,10	0,24	±	0,07
iso 18:0	0,09	±	0,02	0,11	±	0,05
18:0	4,98	±	0,47	3,68	±	0,95
iso 19:0	0,04	±	0,01	0,05	±	0,07
antiso 19:0	0,06	±	0,01	0,06	±	0,03
i-20:0	0,01	±	0,02	0,06	±	0,02
20:0	0,06	±	0,01	0,09	±	0,03
21:0	0,03	±	0,02	0,05	±	0,04
22:0	0,09	±	0,03	0,12	±	0,06
24:0	0,11	±	0,07	0,10	±	0,05
4,8,12-Me 13:0	0,02	±	0,02	0,11	±	0,10
∑pristanic	0,01	±	0,01	0,03	±	0,03
∑phytanic	0,03	±	0,01	0,10	±	0,04
Forgrenet 17:1	0,07	±	0,03	0,14	±	0,03
16:1 n-10, 7Me	0,12	±	0,03	0,25	±	0,07
∑SFA	30,43	±	1,26	23,12	±	1,27
14:1 (n-7)	0,01	±	0,00	0,01	±	0,01
14:1 (n-5)	0,03	±	0,01	0,03	±	0,02
15:1 n-x	0,01	±	0,02	0,01	±	0,01
15:1 (n-5)	0,00	±	0,00	0,01	±	0,00
16:1 (n-11)	0,46	±	0,07	0,09	±	0,03
16:1 (n-9)	0,43	±	0,08	0,31	±	0,07
16:1 (n-7)	1,55	±	0,39	4,68	±	0,80
16:1 (n-5)	0,30	±	0,02	0,26	±	0,02
17:1 (n-10)	0,08	±	0,01	0,08	±	0,01
17:1 (n-8)	0,32	±	0,08	0,50	±	0,18
17:1 (n-7)	0,08	±	0,03	0,04	±	0,01
17:1 (n-6)	0,03	±	0,01	0,06	±	0,02
17:1 (n-4)	0,33	±	0,06	0,13	±	0,05
18:1 (n-11)	0,41	±	0,26	0,98	±	0,52
18:1 (n-9)	6,01	±	0,76	8,40	±	1,02
18:1 (n-7)	3,03	±	0,40	4,48	±	1,46
18:1 (n-5)	0,31	±	0,04	0,60	±	0,13
18:1 (n-4)	0,03	±	0,02	0,06	±	0,02
19:1 (n-x2)	0,04	±	0,03	0,16	±	0,09
20:1 (n-11)	0,25	±	0,10	1,10	±	0,23
20:1 (n-9)	1,01	±	0,96	3,13	±	3,01
20:1 (n-7)	0,16	±	0,03	0,59	±	0,24
20:1 (n-5)	0,21	±	0,06	0,08	±	0,03
22:1 (n-11)	0,43	±	0,53	2,22	±	2,54
22:1 (n-9)	0,58	±	0,20	0,37	±	0,20
22:1 (n-7)	0,19	±	0,09	0,12	±	0,05
24:1 (n-9)	1,04	±	0,43	0,51	±	0,17
24:1 (n-7)	0,24	±	0,13	0,08	±	0,02
∑MUFA	17,56	±	2,45	29,06	±	4,17
16:4 (n-1)	0,11	±	0,06	0,24	±	0,11
18:4 (n-1)	0,02	±	0,02	0,09	±	0,04
18:5 (n-1)	0,01	±	0,01	0,02	±	0,03
16:2 (n-4)	0,05	±	0,04	0,17	±	0,13
16:3 (n-4)	0,02	±	0,02	0,08	±	0,08
18:2 (n-4)	0,08	±	0,02	0,22	±	0,04
16:2 (n-7)	0,32	±	0,05	0,03	±	0,02
18:2 (n-7)	0,05	±	0,01	0,14	±	0,05
16:2 (n-6)	0,04	±	0,02	0,05	±	0,01
18:2 (n-6)	1,31	±	0,37	1,47	±	0,42
18:3 (n-6)	0,03	±	0,02	0,12	±	0,05
20:2 (n-6)	0,25	±	0,03	0,62	±	0,20
20:3 (n-6)	0,10	±	0,02	0,10	±	0,01
20:4 (n-6)	3,55	±	0,79	2,26	±	1,17
22:2 (n-6)	0,04	±	0,02	0,04	±	0,02
22:4 (n-6)	0,70	±	0,17	0,58	±	0,27
22:5 (n-6)	0,50	±	0,06	0,62	±	0,31
16:4 (n-3)	0,00	±	0,00	0,01	±	0,01
18:3 (n-3)	0,26	±	0,13	0,61	±	0,30
18:4 (n-3)	0,30	±	0,27	1,61	±	1,31
18:5 (n-3)	0,00	±	0,00	0,00	±	0,00
20:3 (n-3)	0,08	±	0,02	0,22	±	0,06
20:4 (n-3)	0,40	±	0,20	0,49	±	0,17
20:5 (n-3)	8,66	±	0,99	10,12	±	3,61
21:5 (n-3)	0,15	±	0,05	0,37	±	0,10
22:3 (n-3)	0,00	±	0,00	0,01	±	0,01
22:4 (n-3)	0,03	±	0,03	0,06	±	0,05
22:5 (n-3)	3,39	±	0,54	2,50	±	0,74
22:6 (n-3)	30,96	±	2,12	24,10	±	3,84
24:5 (n-3)	0,28	±	0,08	0,17	±	0,13
24:6 (n-3)	0,05	±	0,04	0,07	±	0,05
20:2 D5,11 (NMI)	0,13	±	0,02	0,11	±	0,06
20:2 D5,13 (NMI)	0,00	±	0,00	0,08	±	0,05
20:3 D5,11,14 (NMI)	0,04	±	0,04	0,11	±	0,05
20:4 D5,11,14,17 (NMI)	0,01	±	0,01	0,02	±	0,02
22:2 D7,13 (NMI)	0,05	±	0,01	0,22	±	0,12
22:2 D7,15 (NMI)	0,03	±	0,01	0,08	±	0,06
22:2 NMI	0,02	±	0,01	0,03	±	0,01
∑PUFA	51,76	±	1,70	47,18	±	4,24
∑PUFA(n-6)	6,53	±	0,82	5,86	±	1,39
∑PUFA(n-3)	44,57	±	1,72	40,34	±	3,73
∑NMI	0,27	±	0,05	0,64	±	0,28
∑DMA	0,54	±	0,11	0,26	±	0,18
∑Chol	9,90	±	2,21	3,06	±	2,04
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3))	7,58	±	0,84	10,48	±	0,76
∑Odd-numbered SFA	2,77	±	0,46	3,18	±	0,70
∑Branched FA	1,44	±	0,16	1,88	±	0,34
∑Odd-numbered MUFA	0,38	±	0,06	0,66	±	0,07
16:1(n-7)/16:0	0,07	±	0,02	0,34	±	0,07
∑C16/ ∑C18	1,45	±	0,10	0,86	±	0,08
∑C16 PUFA (n-1 + n-7 + n-6)	0,54	±	0,10	0,59	±	0,32
∑C16 PUFA/ ∑C18 PUFA	0,29	±	0,08	0,15	±	0,04
20:5(n-3)/22:6(n-3)	0,28	±	0,03	0,43	±	0,18
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	10,32	±	1,09	15,05	±	4,00
18:3 (n-3) + 18:4 (n-3)	0,56	±	0,38	2,22	±	1,58
16:4 (n-3) + 18:5 (n-3)	0,00	±	0,00	0,01	±	0,01
22:5 (n-3) + 22:6 (n-3)	34,35	±	2,00	26,61	±	4,20
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	2,02	±	1,60	5,72	±	5,71
MUFA (n-11)	1,54	±	0,91	4,38	±	2,79
MUFA (n-9)	9,07	±	1,54	12,72	±	2,81
MUFA (n-7)	5,26	±	0,48	10,00	±	1,49

Table A.41: FA composition of greater sand eel

Species	Greater sand eel			
Tissue	Muscle		Liver	
Population			1	
Amount of FA (mg/100 mg wet weig	±		38,72	±
Amount of Chol (mg/100 mg wet we	±		1,43	±
14:0	±		2,30	±
Iso 15:0	±		0,20	±
Antiso 15:0	±		0,03	±
15:0	±		0,24	±
Iso 16:0	±		0,09	±
16:0	±		18,85	±
Iso 17:0	±		0,45	±
Antiso 17:0	±		0,17	±
17:0	±		0,11	±
iso 18:0	±		0,06	±
iso 18:0	±		0,07	±
18:0	±		2,04	±
iso 19:0	±		0,00	±
antiso 19:0	±		0,01	±
i-20:0	±		0,04	±
20:0	±		0,06	±
21:0	±		0,02	±
22:0	±		0,04	±
24:0	±		0,02	±
4,8,12-Me 13:0	±		0,23	±
∑pristanic	±		0,18	±
∑phytanic	±		0,13	±
Forgrenet 17:1	±		0,10	±
16:1 n-10, 7Me	±		0,42	±
∑SFA	±		24,82	±
14:1 (n-7)	±		0,00	±
14:1 (n-5)	±		0,31	±
15:1 n-x	±		0,01	±
15:1 (n-5)	±		0,01	±
16:1 (n-11)	±		0,09	±
16:1 (n-9)	±		0,41	±
16:1 (n-7)	±		13,80	±
16:1 (n-5)	±		0,27	±
17:1 (n-10)	±		0,01	±
17:1 (n-8)	±		0,31	±
17:1 (n-7)	±		0,01	±
17:1 (n-6)	±		0,06	±
17:1 (n-4)	±		0,11	±
18:1 (n-11)	±		0,35	±
18:1 (n-9)	±		19,17	±
18:1 (n-7)	±		3,06	±
18:1 (n-5)	±		0,47	±
18:1 (n-4)	±		0,07	±
19:1 (n-x2)	±		0,00	±
20:1 (n-11)	±		0,43	±
20:1 (n-9)	±		3,35	±
20:1 (n-7)	±		0,12	±
20:1 (n-5)	±		0,03	±
22:1 (n-11)	±		4,56	±
22:1 (n-9)	±		0,66	±
22:1 (n-7)	±		0,08	±
24:1 (n-9)	±		0,52	±
24:1 (n-7)	±		0,08	±
∑MUFA	±		48,35	±
16:4 (n-1)	±		0,08	±
18:4 (n-1)	±		0,06	±
18:5 (n-1)	±		0,01	±
16:2 (n-4)	±		0,17	±
16:3 (n-4)	±		0,04	±
18:2 (n-4)	±		0,08	±
16:2 (n-7)	±		0,02	±
18:2 (n-7)	±		0,07	±
16:2 (n-6)	±		0,05	±
18:2 (n-6)	±		1,27	±
18:3 (n-6)	±		0,05	±
20:2 (n-6)	±		0,21	±
20:3 (n-6)	±		0,04	±
20:4 (n-6)	±		0,28	±
22:2 (n-6)	±		0,02	±
22:4 (n-6)	±		0,97	±
22:5 (n-6)	±		0,07	±
16:4 (n-3)	±		0,02	±
18:3 (n-3)	±		2,00	±
18:4 (n-3)	±		2,03	±
18:5 (n-3)	±		0,00	±
20:3 (n-3)	±		0,23	±
20:4 (n-3)	±		1,29	±
20:5 (n-3)	±		8,29	±
21:5 (n-3)	±		0,20	±
22:3 (n-3)	±		0,01	±
22:4 (n-3)	±		0,03	±
22:5 (n-3)	±		0,51	±
22:6 (n-3)	±		7,48	±
24:5 (n-3)	±		0,13	±
24:6 (n-3)	±		0,05	±
20:2 D5,11 (NMI)	±		0,09	±
20:2 D5,13 (NMI)	±		0,00	±
20:3 D5,11,14 (NMI)	±		0,12	±
20:4 D5,11,14,17 (NMI)	±		0,02	±
22:2 D7,13 (NMI)	±		0,00	±
22:2 D7,15 (NMI)	±		0,00	±
22:2 NMI	±		0,05	±
∑PUFA	±		25,76	±
∑PUFA(n-6)	±		2,96	±
∑PUFA(n-3)	±		22,26	±
∑NMI	±		0,27	±
∑DMA	±		0,04	±
∑Chol	±		3,70	±
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-	±		22,44	±
∑Odd-numbered SFA	±		1,68	±
∑Branched FA	±		1,52	±
∑Odd-numbered MUFA	±		0,95	±
16:1(n-7)/16:0	±		0,73	±
∑C16/ ∑C18	±		1,10	±
∑C16 PUFA (n-1 + n-7 + n-6)	±		0,38	±
∑C16 PUFA/ ∑C18 PUFA	±		0,07	±
20:5(n-3)/22:6(n-3)	±		1,11	±
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	±		22,17	±
18:3 (n-3) + 18:4 (n-3)	±		4,03	±
16:4 (n-3) + 18:5 (n-3)	±		0,02	±
22:5 (n-3) + 22:6 (n-3)	±		7,99	±
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	±		8,57	±
MUFA (n-11)	±		5,43	±
MUFA (n-9)	±		24,11	±
MUFA (n-7)	±		17,15	±

Table A.42: FA composition Atlantic wolffish.

Species	Atlantic wolffish					
Tissue	Muscle			Liver		
Population	8			7		
Amount of FA (mg/100 mg wet weight)	0,71	±	0,27	14,82	±	6,47
Amount of Chol (mg/100 mg wet weight)	0,05	±	0,01	0,29	±	0,11
14:0	1,83	±	0,59	2,12	±	0,32
Iso 15:0	0,17	±	0,10	0,12	±	0,09
Antiso 15:0	0,06	±	0,04	0,01	±	0,02
15:0	0,60	±	0,08	0,24	±	0,12
Iso 16:0	0,13	±	0,06	0,13	±	0,06
16:0	15,15	±	1,25	16,14	±	1,45
Iso 17:0	0,65	±	0,11	0,68	±	0,25
Antiso 17:0	0,24	±	0,05	0,21	±	**0,10**
17:0	0,51	±	0,05	0,21	±	**0,11**
iso 18:0	0,20	±	0,08	0,14	±	0,06
iso 18:0	0,09	±	0,04	0,03	±	0,02
18:0	4,09	±	0,49	3,21	±	0,52
iso 19:0	0,18	±	0,27	0,68	±	1,06
antiso 19:0	0,06	±	0,01	0,04	±	0,01
i-20:0	0,10	±	0,02	0,07	±	0,04
20:0	0,12	±	0,04	0,09	±	0,03
21:0	0,04	±	0,01	0,03	±	0,04
22:0	0,41	±	0,14	0,04	±	0,08
24:0	0,08	±	0,04	0,00	±	0,00
4,8,12-Me 13:0	0,08	±	0,05	0,11	±	0,07
∑pristanic	0,01	±	0,01	0,01	±	0,02
∑phytanic	0,10	±	0,03	0,33	±	0,32
Forgrenet 17:1	0,15	±	0,03	0,11	±	0,05
16:1 n-10, 7Me	0,51	±	0,06	0,55	±	0,16
∑SFA	24,72	±	0,74	24,21	±	2,12
14:1 (n-7)	0,02	±	0,04	0,06	±	0,03
14:1 (n-5)	0,07	±	0,04	0,22	±	0,09
15:1 n-x	0,02	±	0,02	0,02	±	0,01
15:1 (n-5)	0,00	±	0,00	0,03	±	0,01
16:1 (n-11)	0,13	±	0,02	0,07	±	0,03
16:1 (n-9)	0,64	±	0,11	0,67	±	0,24
16:1 (n-7)	4,85	±	1,87	12,21	±	2,76
16:1 (n-5)	0,47	±	0,16	0,20	±	0,13
17:1 (n-10)	0,14	±	0,04	0,10	±	0,07
17:1 (n-8)	0,46	±	0,12	0,69	±	0,17
17:1 (n-7)	0,07	±	0,02	0,02	±	0,01
17:1 (n-6)	0,08	±	0,02	0,05	±	0,03
17:1 (n-4)	0,13	±	0,04	0,07	±	0,06
18:1 (n-11)	0,43	±	0,63	0,56	±	0,49
18:1 (n-9)	8,18	±	3,12	30,42	±	10,04
18:1 (n-7)	4,08	±	1,09	6,02	±	1,33
18:1 (n-5)	0,39	±	0,04	0,57	±	0,13
18:1 (n-4)	0,06	±	0,03	0,04	±	0,04
19:1 (n-x2)	0,16	±	0,31	0,30	±	0,13
20:1 (n-11)	1,34	±	0,69	0,79	±	0,53
20:1 (n-9)	0,97	±	0,14	0,81	±	0,17
20:1 (n-7)	0,60	±	0,36	0,44	±	0,13
20:1 (n-5)	0,26	±	0,49	0,59	±	0,56
22:1 (n-11)	0,40	±	0,09	0,14	±	0,07
22:1 (n-9)	0,39	±	0,16	0,26	±	0,21
22:1 (n-7)	0,11	±	0,02	0,08	±	0,09
24:1 (n-9)	0,82	±	0,23	0,32	±	0,27
24:1 (n-7)	0,12	±	0,08	0,04	±	0,02
∑MUFA	25,37	±	6,07	55,79	±	9,10
16:4 (n-1)	0,22	±	0,07	0,01	±	0,02
18:4 (n-1)	0,14	±	0,05	0,14	±	0,08
18:5 (n-1)	0,04	±	0,02	0,00	±	0,01
16:2 (n-4)	0,17	±	0,12	0,09	±	0,07
16:3 (n-4)	0,14	±	0,18	0,04	±	0,05
18:2 (n-4)	0,23	±	0,09	0,18	±	0,10
16:2 (n-7)	0,07	±	0,06	0,16	±	0,19
18:2 (n-7)	0,28	±	0,24	0,32	±	0,24
16:2 (n-6)	0,07	±	0,03	0,03	±	0,01
18:2 (n-6)	0,49	±	0,10	0,27	±	0,09
18:3 (n-6)	0,06	±	0,02	0,07	±	0,11
20:2 (n-6)	0,46	±	0,09	0,32	±	0,16
20:3 (n-6)	0,12	±	0,02	0,06	±	0,04
20:4 (n-6)	6,88	±	1,98	2,57	±	2,16
22:2 (n-6)	0,03	±	0,01	0,01	±	0,01
22:4 (n-6)	0,44	±	0,10	0,37	±	0,32
22:5 (n-6)	0,61	±	0,12	0,18	±	0,15
16:4 (n-3)	0,01	±	0,01	0,02	±	0,01
18:3 (n-3)	0,20	±	0,04	0,12	±	0,05
18:4 (n-3)	0,87	±	0,34	0,54	±	0,25
18:5 (n-3)	0,00	±	0,00	0,00	±	0,00
20:3 (n-3)	0,19	±	0,05	0,12	±	0,07
20:4 (n-3)	0,41	±	0,07	0,41	±	0,20
20:5 (n-3)	17,30	±	2,70	7,70	±	3,85
21:5 (n-3)	0,39	±	0,11	0,28	±	0,10
22:3 (n-3)	0,01	±	0,01	0,01	±	0,02
22:4 (n-3)	0,03	±	0,01	0,03	±	0,03
22:5 (n-3)	1,42	±	0,17	0,66	±	0,22
22:6 (n-3)	17,42	±	3,21	3,98	±	1,48
24:5 (n-3)	0,14	±	0,06	0,10	±	0,24
24:6 (n-3)	0,20	±	0,08	0,10	±	0,12
20:2 D5,11 (NMI)	0,90	±	0,42	0,81	±	0,49
20:2 D5,13 (NMI)	0,10	±	0,22	0,05	±	0,05
20:3 D5,11,14 (NMI)	0,19	±	0,05	0,02	±	0,03
20:4 D5,11,14,17 (NMI)	0,09	±	0,03	0,04	±	0,03
22:2 D7,13 (NMI)	0,12	±	0,06	0,07	±	0,04
22:2 D7,15 (NMI)	0,22	±	0,11	0,06	±	0,07
22:2 NMI	0,03	±	0,01	0,03	±	0,03
∑PUFA	49,07	±	5,68	18,89	±	9,32
∑PUFA(n-6)	9,17	±	2,05	3,88	±	2,97
∑PUFA(n-3)	38,62	±	5,25	14,06	±	6,27
∑NMI	1,64	±	0,57	1,08	±	0,64
∑DMA	0,45	±	0,21	0,20	±	0,05
∑Chol	7,44	±	2,09	2,67	±	2,44
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3)	8,87	±	3,23	30,82	±	9,93
∑Odd-numbered SFA	3,04	±	0,32	2,36	±	0,89
∑Branched FA	2,07	±	0,28	1,86	±	0,61
∑Odd-numbered MUFA	1,30	±	0,20	1,09	±	0,22
16:1(n-7)/16:0	0,33	±	0,15	0,75	±	0,15
∑C16/ ∑C18	1,13	±	0,14	0,71	±	0,11
∑C16 PUFA (n-1 + n-7 + n-6)	0,69	±	0,28	0,34	±	0,15
∑C16 PUFA/ ∑C18 PUFA	0,33	±	0,07	0,37	±	0,44
20:5(n-3)/22:6(n-3)	1,01	±	0,14	1,89	±	0,49
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	22,37	±	1,77	19,92	±	2,95
18:3 (n-3) + 18:4 (n-3)	1,08	±	0,36	0,66	±	0,29
16:4 (n-3) + 18:5 (n-3)	0,01	±	0,01	0,02	±	0,01
22:5 (n-3) + 22:6 (n-3)	18,85	±	3,23	4,64	±	1,69
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	1,76	±	0,25	1,21	±	0,43
MUFA (n-11)	2,30	±	0,82	1,56	±	0,90
MUFA (n-9)	11,00	±	3,08	32,47	±	9,42
MUFA (n-7)	9,85	±	2,99	18,88	±	2,09

Table A.43: FA composition of Norway redfish.

Species	Norway redfish					
Tissue	Muscle			Liver		
Population	10			9		
Amount of FA (mg/100 mg wet weight)	0,83	±	0,36	15,67	±	4,45
Amount of Chol (mg/100 mg wet weight)	0,05	±	0,01	0,78	±	0,34
14:0	2,81	±	0,86	1,72	±	0,19
Iso 15:0	0,09	±	0,01	0,10	±	0,01
Antiso 15:0	0,02	±	0,01	0,00	±	0,00
15:0	0,28	±	0,04	0,24	±	0,03
Iso 16:0	0,04	±	0,02	0,12	±	0,03
16:0	16,53	±	1,95	12,78	±	1,73
Iso 17:0	0,19	±	0,02	0,41	±	0,07
Antiso 17:0	0,08	±	0,01	0,20	±	0,05
17:0	0,24	±	0,03	0,19	±	0,06
iso 18:0	0,13	±	0,03	0,14	±	0,07
iso 18:0	0,04	±	0,02	0,02	±	0,01
18:0	4,52	±	0,67	3,18	±	0,84
iso 19:0	0,01	±	0,01	0,02	±	0,02
antiso 19:0	0,02	±	0,01	0,01	±	0,01
i-20:0	0,01	±	0,01	0,02	±	0,01
20:0	0,12	±	0,02	0,08	±	0,01
21:0	0,02	±	0,01	0,04	±	0,01
22:0	0,13	±	0,06	0,04	±	0,02
24:0	0,29	±	0,18	0,02	±	0,02
4,8,12-Me 13:0	0,22	±	0,07	0,38	±	0,12
∑pristanic	0,04	±	0,02	0,13	±	0,07
∑phytanic	0,09	±	0,01	0,29	±	0,09
Forgrenet 17:1	0,04	±	0,01	0,05	±	0,02
16:1 n-10, 7Me	0,08	±	0,02	0,19	±	0,06
∑SFA	25,57	±	1,79	19,33	±	2,02
14:1 (n-7)	0,01	±	0,01	0,00	±	0,00
14:1 (n-5)	0,04	±	0,01	0,03	±	0,01
15:1 n-x	0,02	±	0,01	0,01	±	0,01
15:1 (n-5)	0,00	±	0,00	0,00	±	0,00
16:1 (n-11)	0,13	±	0,02	0,13	±	0,03
16:1 (n-9)	0,19	±	0,03	0,34	±	0,09
16:1 (n-7)	2,95	±	0,72	6,60	±	1,19
16:1 (n-5)	0,19	±	0,02	0,15	±	0,02
17:1 (n-10)	0,03	±	0,00	0,03	±	0,01
17:1 (n-8)	0,20	±	0,03	0,49	±	0,10
17:1 (n-7)	0,05	±	0,01	0,03	±	0,01
17:1 (n-6)	0,02	±	0,01	0,03	±	0,01
17:1 (n-4)	0,08	±	0,01	0,04	±	0,01
18:1 (n-11)	0,73	±	0,39	3,46	±	0,50
18:1 (n-9)	5,80	±	1,09	20,69	±	5,36
18:1 (n-7)	2,01	±	0,15	5,33	±	0,92
18:1 (n-5)	0,27	±	0,03	0,50	±	0,06
18:1 (n-4)	0,01	±	0,01	0,02	±	0,02
19:1 (n-x2)	0,04	±	0,03	0,17	±	0,04
20:1 (n-11)	0,70	±	0,51	1,07	±	0,42
20:1 (n-9)	4,72	±	1,67	5,14	±	2,01
20:1 (n-7)	0,11	±	0,04	0,13	±	0,05
20:1 (n-5)	0,13	±	0,02	0,04	±	0,03
22:1 (n-11)	5,85	±	2,62	7,41	±	2,65
22:1 (n-9)	0,53	±	0,18	0,71	±	0,18
22:1 (n-7)	0,13	±	0,03	0,10	±	0,02
24:1 (n-9)	1,55	±	0,25	0,63	±	0,18
24:1 (n-7)	0,44	±	0,15	0,06	±	0,03
∑MUFA	26,95	±	6,58	53,34	±	3,00
16:4 (n-1)	0,06	±	0,02	0,01	±	0,01
18:4 (n-1)	0,09	±	0,03	0,25	±	0,09
18:5 (n-1)	0,03	±	0,01	0,00	±	0,01
16:2 (n-4)	0,29	±	0,11	0,27	±	0,08
16:3 (n-4)	0,22	±	0,10	0,14	±	0,07
18:2 (n-4)	0,11	±	0,02	0,29	±	0,18
16:2 (n-7)	0,06	±	0,03	0,04	±	0,02
18:2 (n-7)	0,03	±	0,01	0,08	±	0,01
16:2 (n-6)	0,05	±	0,03	0,03	±	0,01
18:2 (n-6)	1,52	±	0,23	1,18	±	0,11
18:3 (n-6)	0,09	±	0,03	0,18	±	0,18
20:2 (n-6)	0,18	±	0,10	0,20	±	0,02
20:3 (n-6)	0,09	±	0,01	0,08	±	0,03
20:4 (n-6)	1,84	±	0,41	0,99	±	0,15
22:2 (n-6)	0,08	±	0,15	0,01	±	0,00
22:4 (n-6)	0,17	±	0,03	0,30	±	0,13
22:5 (n-6)	0,58	±	0,09	0,13	±	0,01
16:4 (n-3)	0,00	±	0,01	0,02	±	0,01
18:3 (n-3)	0,39	±	0,08	0,62	±	0,08
18:4 (n-3)	0,94	±	0,27	0,92	±	0,33
18:5 (n-3)	0,00	±	0,00	0,00	±	0,00
20:3 (n-3)	0,09	±	0,02	0,15	±	0,02
20:4 (n-3)	0,42	±	0,08	0,93	±	0,12
20:5 (n-3)	9,39	±	1,34	9,83	±	2,27
21:5 (n-3)	0,30	±	0,06	0,43	±	0,12
22:3 (n-3)	0,01	±	0,01	0,00	±	0,00
22:4 (n-3)	0,08	±	0,02	0,09	±	0,01
22:5 (n-3)	1,49	±	0,10	1,77	±	0,31
22:6 (n-3)	27,75	±	4,88	6,89	±	0,86
24:5 (n-3)	0,54	±	0,06	0,36	±	0,15
24:6 (n-3)	0,10	±	0,04	0,11	±	0,05
20:2 D5,11 (NMI)	0,09	±	0,01	0,14	±	0,05
20:2 D5,13 (NMI)	0,00	±	0,00	0,02	±	0,02
20:3 D5,11,14 (NMI)	0,02	±	0,01	0,01	±	0,01
20:4 D5,11,14,17 (NMI)	0,01	±	0,01	0,00	±	0,01
22:2 D7,13 (NMI)	0,01	±	0,01	0,01	±	0,01
22:2 D7,15 (NMI)	0,01	±	0,01	0,00	±	0,01
22:2 NMI	0,01	±	0,00	0,04	±	0,03
∑PUFA	47,01	±	5,10	26,29	±	3,47
∑PUFA(n-6)	4,62	±	0,29	3,10	±	0,35
∑PUFA(n-3)	41,51	±	5,12	22,11	±	2,97
∑NMI	0,15	±	0,02	0,22	±	0,05
∑DMA	0,53	±	0,17	0,18	±	0,08
∑Chol	6,79	±	1,63	5,28	±	2,45
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3))	7,71	±	1,12	22,49	±	5,21
∑Odd-numbered SFA	1,29	±	0,11	1,75	±	0,24
∑Branched FA	0,67	±	0,09	1,10	±	0,23
∑Odd-numbered MUFA	0,43	±	0,10	0,41	±	0,08
16:1(n-7)/16:0	0,19	±	0,07	0,52	±	0,06
ΣC16/ ΣC18	1,24	±	0,14	0,56	±	0,07
ΣC16 PUFA (n-1 + n-7 + n-6)	0,67	±	0,23	0,50	±	0,18
ΣC16 PUFA/ ΣC18 PUFA	0,21	±	0,05	0,14	±	0,03
20:5(n-3)/22:6(n-3)	0,34	±	0,06	1,45	±	0,36
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	12,40	±	1,16	16,44	±	1,66
18:3 (n-3) + 18:4 (n-3)	1,33	±	0,35	1,54	±	0,40
16:4 (n-3) + 18:5 (n-3)	0,00	±	0,01	0,02	±	0,01
22:5 (n-3) + 22:6 (n-3)	29,23	±	4,85	8,65	±	1,09
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	11,11	±	4,44	13,26	±	4,26
MUFA (n-11)	7,42	±	3,41	12,06	±	2,92
MUFA (n-9)	12,79	±	2,50	27,50	±	3,90
MUFA (n-7)	5,70	±	0,71	12,26	±	1,58

Table A.44: FA composition of common dab.

Species	Common dab					
Tissue	Muscle			Liver		
Population				10		
Amount of FA (mg/100 mg wet weight)		±		15,09	±	6,46
Amount of Chol (mg/100 mg wet weight)		±		0,54	±	0,15
14:0		±		2,44	±	0,20
Iso 15:0		±		0,12	±	0,04
Antiso 15:0		±		0,01	±	0,01
15:0		±		0,23	±	0,05
Iso 16:0		±		0,07	±	0,02
16:0		±		19,19	±	2,42
Iso 17:0		±		0,29	±	0,06
Antiso 17:0		±		0,08	±	0,02
17:0		±		0,05	±	0,01
iso 18:0		±		0,12	±	0,04
iso 18:0		±		0,01	±	0,00
18:0		±		1,25	±	0,39
iso 19:0		±		0,02	±	0,01
antiso 19:0		±		0,00	±	0,01
i-20:0		±		0,02	±	0,01
20:0		±		0,07	±	0,02
21:0		±		0,03	±	0,02
22:0		±		0,02	±	0,01
24:0		±		0,04	±	0,04
4,8,12-Me 13:0		±		0,06	±	0,01
∑pristanic		±		0,00	±	0,00
∑phytanic		±		0,00	±	0,00
Forgrenet 17:1		±		0,19	±	0,04
16:1 n-10, 7Me		±		0,53	±	0,09
∑SFA		±		24,05	±	2,51
14:1 (n-7)		±		0,05	±	0,02
14:1 (n-5)		±		0,34	±	0,08
15:1 n-x		±		0,01	±	0,01
15:1 (n-5)		±		0,01	±	0,01
16:1 (n-11)		±		0,65	±	0,31
16:1 (n-9)		±		0,84	±	0,61
16:1 (n-7)		±		21,96	±	5,09
16:1 (n-5)		±		0,19	±	0,03
17:1 (n-10)		±		0,05	±	0,03
17:1 (n-8)		±		0,40	±	0,09
17:1 (n-7)		±		0,02	±	0,01
17:1 (n-6)		±		0,02	±	0,01
17:1 (n-4)		±		0,04	±	0,01
18:1 (n-11)		±		1,45	±	0,80
18:1 (n-9)		±		21,86	±	2,30
18:1 (n-7)		±		3,08	±	0,87
18:1 (n-5)		±		0,34	±	0,06
18:1 (n-4)		±		0,03	±	0,02
19:1 (n-x2)		±		0,13	±	0,02
20:1 (n-11)		±		0,29	±	0,05
20:1 (n-9)		±		1,46	±	0,43
20:1 (n-7)		±		0,12	±	0,04
20:1 (n-5)		±		0,03	±	0,01
22:1 (n-11)		±		1,29	±	0,63
22:1 (n-9)		±		0,45	±	0,12
22:1 (n-7)		±		0,04	±	0,02
24:1 (n-9)		±		0,77	±	0,25
24:1 (n-7)		±		0,09	±	0,05
∑MUFA		±		56,01	±	3,89
16:4 (n-1)		±		0,00	±	0,00
18:4 (n-1)		±		0,04	±	0,02
18:5 (n-1)		±		0,01	±	0,01
16:2 (n-4)		±		0,09	±	0,03
16:3 (n-4)		±		0,06	±	0,03
18:2 (n-4)		±		0,07	±	0,04
16:2 (n-7)		±		0,02	±	0,01
18:2 (n-7)		±		0,06	±	0,02
16:2 (n-6)		±		0,03	±	0,02
18:2 (n-6)		±		0,90	±	0,23
18:3 (n-6)		±		0,06	±	0,02
20:2 (n-6)		±		0,09	±	0,02
20:3 (n-6)		±		0,04	±	0,01
20:4 (n-6)		±		0,51	±	0,13
22:2 (n-6)		±		0,02	±	0,01
22:4 (n-6)		±		0,48	±	0,08
22:5 (n-6)		±		0,12	±	0,03
16:4 (n-3)		±		0,04	±	0,01
18:3 (n-3)		±		0,33	±	0,09
18:4 (n-3)		±		0,99	±	0,29
18:5 (n-3)		±		0,00	±	0,00
20:3 (n-3)		±		0,10	±	0,04
20:4 (n-3)		±		0,39	±	0,14
20:5 (n-3)		±		5,37	±	1,07
21:5 (n-3)		±		0,15	±	0,05
22:3 (n-3)		±		0,02	±	0,01
22:4 (n-3)		±		0,02	±	0,01
22:5 (n-3)		±		0,74	±	0,20
22:6 (n-3)		±		8,12	±	2,59
24:5 (n-3)		±		0,10	±	0,06
24:6 (n-3)		±		0,14	±	0,05
20:2 D5,11 (NMI)		±		0,13	±	0,04
20:2 D5,13 (NMI)		±		0,02	±	0,02
20:3 D5,11,14 (NMI)		±		0,03	±	0,02
20:4 D5,11,14,17 (NMI)		±		0,02	±	0,00
22:2 D7,13 (NMI)		±		0,01	±	0,01
22:2 D7,15 (NMI)		±		0,00	±	0,00
22:2 NMI		±		0,02	±	0,01
∑PUFA		±		19,08	±	4,48
∑PUFA(n-6)		±		2,22	±	0,46
∑PUFA(n-3)		±		16,50	±	4,02
∑NMI		±		0,24	±	0,03
∑DMA		±		0,10	±	0,04
∑Chol		±		4,38	±	2,39
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3))		±		23,09	±	2,28
∑Odd-numbered SFA		±		1,30	±	0,30
∑Branched FA		±		1,35	±	0,28
∑Odd-numbered MUFA		±		1,20	±	0,16
16:1(n-7)/16:0		±		1,15	±	0,26
ΣC16/ ΣC18		±		1,43	±	0,30
ΣC16 PUFA (n-1 + n-7 + n-6)		±		0,24	±	0,09
ΣC16 PUFA/ ΣC18 PUFA		±		0,10	±	0,02
20:5(n-3)/22:6(n-3)		±		0,69	±	0,12
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)		±		27,33	±	4,46
18:3 (n-3) + 18:4 (n-3)		±		1,32	±	0,37
16:4 (n-3) + 18:5 (n-3)		±		0,04	±	0,01
22:5 (n-3) + 22:6 (n-3)		±		8,86	±	2,77
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)		±		3,20	±	1,13
MUFA (n-11)		±		3,68	±	1,01
MUFA (n-9)		±		25,38	±	2,33
MUFA (n-7)		±		25,35	±	4,36

Table A.45: FA composition of spotted dragonet.

Species	Spotted dragonet					
Tissue	Muscle			Liver		
Population	10			10		
Amount of FA (mg/100 mg wet weight)	0,63	±	0,16	11,85	±	13,49
Amount of Chol (mg/100 mg wet weight)	0,06	±	0,01	0,29	±	0,07
14:0	1,76	±	0,73	5,28	±	2,05
Iso 15:0	0,19	±	0,06	0,55	±	0,13
Antiso 15:0	0,05	±	0,03	0,10	±	0,08
15:0	0,50	±	0,07	0,98	±	0,12
Iso 16:0	0,17	±	0,07	0,49	±	0,10
16:0	14,97	±	1,37	14,33	±	2,18
Iso 17:0	0,69	±	0,25	1,30	±	0,17
Antiso 17:0	0,25	±	0,08	0,55	±	0,14
17:0	0,65	±	0,10	0,86	±	0,19
iso 18:0	0,27	±	0,07	0,32	±	0,07
iso 18:0	0,08	±	0,02	0,10	±	0,03
18:0	5,59	±	0,62	5,36	±	1,40
iso 19:0	0,03	±	0,02	0,09	±	0,06
antiso 19:0	0,10	±	0,02	0,06	±	0,02
i-20:0	0,04	±	0,03	0,07	±	0,01
20:0	0,17	±	0,06	0,16	±	0,07
21:0	0,07	±	0,01	0,14	±	0,12
22:0	0,35	±	0,09	0,09	±	0,03
24:0	0,13	±	0,07	0,06	±	0,03
4,8,12-Me 13:0	0,05	±	0,03	0,07	±	0,04
∑pristanic	0,00	±	0,00	0,00	±	0,00
∑phytanic	0,00	±	0,00	0,00	±	0,00
Forgrenet 17:1	0,11	±	0,06	0,15	±	0,03
16:1 n-10, 7Me	0,34	±	0,08	0,67	±	0,16
∑SFA	26,06	±	1,58	30,91	±	3,66
14:1 (n-7)	0,02	±	0,01	0,06	±	0,04
14:1 (n-5)	0,05	±	0,03	0,10	±	0,10
15:1 n-x	0,04	±	0,05	0,04	±	0,02
15:1 (n-5)	0,00	±	0,00	0,02	±	0,02
16:1 (n-11)	0,12	±	0,04	0,14	±	0,04
16:1 (n-9)	0,33	±	0,07	0,65	±	0,26
16:1 (n-7)	2,11	±	0,85	5,61	±	2,47
16:1 (n-5)	0,34	±	0,04	0,51	±	0,06
17:1 (n-10)	0,05	±	0,01	0,07	±	0,04
17:1 (n-8)	0,35	±	0,10	0,58	±	0,27
17:1 (n-7)	0,08	±	0,02	0,08	±	0,02
17:1 (n-6)	0,05	±	0,01	0,11	±	0,01
17:1 (n-4)	0,09	±	0,02	0,08	±	0,02
18:1 (n-11)	0,25	±	0,22	0,41	±	0,11
18:1 (n-9)	4,13	±	1,12	4,88	±	2,42
18:1 (n-7)	2,87	±	0,38	4,48	±	0,56
18:1 (n-5)	0,35	±	0,08	0,56	±	0,14
18:1 (n-4)	0,04	±	0,02	0,06	±	0,03
19:1 (n-x2)	0,16	±	0,04	0,27	±	0,10
20:1 (n-11)	1,05	±	0,38	1,01	±	0,54
20:1 (n-9)	0,82	±	1,05	0,41	±	0,14
20:1 (n-7)	0,46	±	0,21	0,55	±	0,32
20:1 (n-5)	0,28	±	0,10	0,16	±	0,10
22:1 (n-11)	0,76	±	1,13	0,36	±	0,12
22:1 (n-9)	0,18	±	0,10	0,18	±	0,05
22:1 (n-7)	0,53	±	0,18	0,42	±	0,19
24:1 (n-9)	0,92	±	0,23	0,76	±	0,54
24:1 (n-7)	0,21	±	0,08	0,25	±	0,10
∑MUFA	16,67	±	4,51	22,80	±	5,96
16:4 (n-1)	0,12	±	0,04	0,05	±	0,04
18:4 (n-1)	0,07	±	0,03	0,11	±	0,06
18:5 (n-1)	0,00	±	0,01	0,02	±	0,04
16:2 (n-4)	0,08	±	0,05	0,16	±	0,08
16:3 (n-4)	0,03	±	0,03	0,08	±	0,07
18:2 (n-4)	0,14	±	0,03	0,22	±	0,05
16:2 (n-7)	0,01	±	0,01	0,04	±	0,02
18:2 (n-7)	0,07	±	0,04	0,10	±	0,03
16:2 (n-6)	0,06	±	0,02	0,08	±	0,04
18:2 (n-6)	0,63	±	0,09	0,73	±	0,12
18:3 (n-6)	0,03	±	0,01	0,06	±	0,02
20:2 (n-6)	0,26	±	0,07	0,32	±	0,09
20:3 (n-6)	0,10	±	0,02	0,09	±	0,02
20:4 (n-6)	4,57	±	1,15	3,72	±	1,87
22:2 (n-6)	0,02	±	0,01	0,05	±	0,03
22:4 (n-6)	0,82	±	0,18	0,71	±	0,39
22:5 (n-6)	1,05	±	0,20	0,53	±	0,19
16:4 (n-3)	0,00	±	0,01	0,03	±	0,01
18:3 (n-3)	0,24	±	0,11	0,31	±	0,13
18:4 (n-3)	0,56	±	0,32	0,67	±	0,25
18:5 (n-3)	0,01	±	0,01	0,01	±	0,02
20:3 (n-3)	0,11	±	0,04	0,18	±	0,03
20:4 (n-3)	0,32	±	0,12	0,44	±	0,12
20:5 (n-3)	14,79	±	1,57	12,28	±	2,61
21:5 (n-3)	0,27	±	0,07	0,35	±	0,11
22:3 (n-3)	0,01	±	0,01	0,01	±	0,01
22:4 (n-3)	0,03	±	0,03	0,03	±	0,01
22:5 (n-3)	2,64	±	0,35	3,06	±	1,05
22:6 (n-3)	27,74	±	4,36	17,99	±	5,70
24:5 (n-3)	0,32	±	0,06	0,24	±	0,12
24:6 (n-3)	1,50	±	0,48	2,45	±	1,12
20:2 D5,11 (NMI)	0,21	±	0,06	0,24	±	0,08
20:2 D5,13 (NMI)	0,01	±	0,01	0,04	±	0,03
20:3 D5,11,14 (NMI)	0,09	±	0,09	0,05	±	0,05
20:4 D5,11,14,17 (NMI)	0,04	±	0,01	0,04	±	0,01
22:2 D7,13 (NMI)	0,11	±	0,05	0,12	±	0,08
22:2 D7,15 (NMI)	0,10	±	0,04	0,01	±	0,03
22:2 NMI	0,04	±	0,01	0,05	±	0,03
∑PUFA	56,61	±	4,38	45,10	±	8,52
∑PUFA(n-6)	7,55	±	1,23	6,29	±	2,13
∑PUFA(n-3)	48,54	±	3,89	38,04	±	6,92
∑NMI	0,60	±	0,15	0,56	±	0,11
∑DMA	0,25	±	0,09	0,16	±	0,06
∑Chol	10,36	±	1,80	7,04	±	5,79
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3))	5,00	±	1,31	5,92	±	2,61
∑Odd-numbered SFA	2,96	±	0,68	5,18	±	0,72
∑Branched FA	1,98	±	0,56	3,74	±	0,49
∑Odd-numbered MUFA	1,08	±	0,15	1,28	±	0,18
16:1(n-7)/16:0	0,14	±	0,07	0,38	±	0,14
∑C16/ ∑C18	1,19	±	0,15	1,17	±	0,10
∑C16 PUFA (n-1 + n-7 + n-6)	0,30	±	0,14	0,44	±	0,16
∑C16 PUFA/ ∑C18 PUFA	0,18	±	0,03	0,21	±	0,05
20:5(n-3)/22:6(n-3)	0,54	±	0,09	0,72	±	0,19
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	17,02	±	1,61	17,94	±	2,30
18:3 (n-3) + 18:4 (n-3)	0,81	±	0,43	0,98	±	0,34
16:4 (n-3) + 18:5 (n-3)	0,01	±	0,01	0,04	±	0,02
22:5 (n-3) + 22:6 (n-3)	30,38	±	4,07	21,05	±	5,31
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	1,76	±	2,27	0,95	±	0,28
MUFA (n-11)	2,18	±	1,48	1,91	±	0,65
MUFA (n-9)	6,38	±	2,17	6,87	±	2,10
MUFA (n-7)	6,29	±	1,29	11,45	±	3,04

Table A.46: FA composition of grey gurnard.

Species	Grey gurnard					
Tissue	Muscle			Liver		
Population	10			10		
Amount of FA (mg/100 mg wet weight)	1,51	±	0,77	13,94	±	9,55
Amount of Chol (mg/100 mg wet weight)	0,05	±	0,01	0,41	±	0,13
14:0	3,08	±	1,24	3,03	±	0,43
Iso 15:0	0,14	±	0,05	0,11	±	0,05
Antiso 15:0	0,04	±	0,02	0,01	±	0,02
15:0	0,33	±	0,09	0,20	±	0,14
Iso 16:0	0,04	±	0,02	0,04	±	0,03
16:0	16,64	±	1,28	17,30	±	0,80
Iso 17:0	0,14	±	0,07	0,22	±	0,08
Antiso 17:0	0,09	±	0,02	0,07	±	0,03
17:0	0,22	±	0,04	0,12	±	0,08
iso 18:0	0,18	±	0,04	0,09	±	0,04
iso 18:0	0,03	±	0,01	0,01	±	0,01
18:0	4,44	±	0,96	4,38	±	1,02
iso 19:0	0,08	±	0,02	0,11	±	0,06
antiso 19:0	0,02	±	0,01	0,00	±	0,01
i-20:0	0,02	±	0,01	0,02	±	0,02
20:0	0,10	±	0,01	0,11	±	0,02
21:0	0,02	±	0,01	0,04	±	0,03
22:0	0,05	±	0,01	0,03	±	0,02
24:0	0,10	±	0,03	0,02	±	0,03
4,8,12-Me 13:0	0,16	±	0,07	0,26	±	0,07
∑pristanic	0,00	±	0,00	0,00	±	0,00
∑phytanic	0,00	±	0,00	0,00	±	0,00
Forgrenet 17:1	0,10	±	0,11	0,06	±	0,02
16:1 n-10, 7Me	0,16	±	0,04	0,20	±	0,04
∑SFA	25,77	±	1,09	25,90	±	1,41
14:1 (n-7)	0,01	±	0,01	0,01	±	0,01
14:1 (n-5)	0,15	±	0,08	0,39	±	0,20
15:1 n-x	0,01	±	0,01	0,01	±	0,01
15:1 (n-5)	0,00	±	0,00	0,01	±	0,01
16:1 (n-11)	0,17	±	0,04	0,23	±	0,05
16:1 (n-9)	0,29	±	0,04	0,30	±	0,07
16:1 (n-7)	4,72	±	1,61	10,52	±	2,51
16:1 (n-5)	0,22	±	0,03	0,20	±	0,06
17:1 (n-10)	0,03	±	0,01	0,02	±	0,01
17:1 (n-8)	0,28	±	0,09	0,26	±	0,08
17:1 (n-7)	0,07	±	0,04	0,02	±	0,01
17:1 (n-6)	0,01	±	0,01	0,02	±	0,01
17:1 (n-4)	0,08	±	0,01	0,04	±	0,02
18:1 (n-11)	1,09	±	0,46	2,32	±	0,67
18:1 (n-9)	12,46	±	2,47	22,51	±	6,52
18:1 (n-7)	2,77	±	0,43	3,32	±	0,41
18:1 (n-5)	0,24	±	0,05	0,33	±	0,05
18:1 (n-4)	0,00	±	0,01	0,01	±	0,01
19:1 (n-x2)	0,07	±	0,03	0,10	±	0,06
20:1 (n-11)	0,88	±	0,37	1,41	±	0,51
20:1 (n-9)	3,34	±	1,26	3,12	±	0,63
20:1 (n-7)	0,14	±	0,05	0,09	±	0,03
20:1 (n-5)	0,08	±	0,03	0,12	±	0,09
22:1 (n-11)	2,46	±	1,07	2,94	±	1,00
22:1 (n-9)	0,40	±	0,15	0,73	±	0,19
22:1 (n-7)	0,07	±	0,02	0,05	±	0,03
24:1 (n-9)	0,96	±	0,32	0,96	±	0,53
24:1 (n-7)	0,09	±	0,06	0,07	±	0,06
∑MUFA	31,10	±	6,74	50,09	±	7,86
16:4 (n-1)	0,23	±	0,06	0,00	±	0,00
18:4 (n-1)	0,09	±	0,06	0,07	±	0,04
18:5 (n-1)	0,01	±	0,01	0,01	±	0,01
16:2 (n-4)	0,21	±	0,12	0,12	±	0,04
16:3 (n-4)	0,10	±	0,07	0,04	±	0,02
18:2 (n-4)	0,08	±	0,05	0,08	±	0,04
16:2 (n-7)	0,04	±	0,02	0,04	±	0,01
18:2 (n-7)	0,07	±	0,01	0,09	±	0,02
16:2 (n-6)	0,06	±	0,02	0,01	±	0,01
18:2 (n-6)	1,06	±	0,17	0,67	±	0,33
18:3 (n-6)	0,06	±	0,03	0,04	±	0,03
20:2 (n-6)	0,19	±	0,04	0,13	±	0,04
20:3 (n-6)	0,07	±	0,04	0,04	±	0,02
20:4 (n-6)	1,34	±	0,42	0,74	±	0,56
22:2 (n-6)	0,01	±	0,01	0,02	±	0,01
22:4 (n-6)	0,25	±	0,07	0,11	±	0,06
22:5 (n-6)	0,51	±	0,19	0,14	±	0,06
16:4 (n-3)	0,00	±	0,01	0,02	±	0,02
18:3 (n-3)	0,54	±	0,20	0,36	±	0,14
18:4 (n-3)	1,15	±	0,56	0,55	±	0,22
18:5 (n-3)	0,00	±	0,00	0,00	±	0,00
20:3 (n-3)	0,16	±	0,04	0,11	±	0,06
20:4 (n-3)	0,69	±	0,18	0,73	±	0,17
20:5 (n-3)	7,91	±	0,72	5,92	±	1,81
21:5 (n-3)	0,26	±	0,09	0,20	±	0,04
22:3 (n-3)	0,00	±	0,00	0,01	±	0,01
22:4 (n-3)	0,05	±	0,03	0,05	±	0,02
22:5 (n-3)	1,85	±	0,08	1,17	±	0,20
22:6 (n-3)	25,26	±	7,07	11,51	±	4,02
24:5 (n-3)	0,32	±	0,05	0,20	±	0,09
24:6 (n-3)	0,08	±	0,03	0,10	±	0,02
20:2 D5,11 (NMI)	0,14	±	0,03	0,17	±	0,04
20:2 D5,13 (NMI)	0,11	±	0,04	0,04	±	0,09
20:3 D5,11,14 (NMI)	0,02	±	0,01	0,01	±	0,02
20:4 D5,11,14,17 (NMI)	0,01	±	0,01	0,01	±	0,01
22:2 D7,13 (NMI)	0,01	±	0,01	0,00	±	0,00
22:2 D7,15 (NMI)	0,00	±	0,00	0,00	±	0,00
22:2 NMI	0,02	±	0,00	0,00	±	0,00
∑PUFA	42,64	±	6,10	23,30	±	7,58
∑PUFA(n-6)	3,55	±	0,57	1,91	±	0,99
∑PUFA(n-3)	38,26	±	5,93	20,94	±	6,53
∑NMI	0,29	±	0,05	0,24	±	0,09
∑DMA	0,16	±	0,04	0,07	±	0,05
∑Chol	4,13	±	1,84	4,07	±	2,62
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3))	14,06	±	2,68	23,54	±	6,09
∑Odd-numbered SFA	1,43	±	0,22	1,06	±	0,49
∑Branched FA	0,88	±	0,16	0,76	±	0,27
∑Odd-numbered MUFA	0,58	±	0,19	0,80	±	0,22
16:1(n-7)/16:0	0,29	±	0,11	0,61	±	0,14
∑C16/ ∑C18	0,94	±	0,10	0,85	±	0,13
∑C16 PUFA (n-1 + n-7 + n-6)	0,65	±	0,27	0,24	±	0,07
∑C16 PUFA/ ∑C18 PUFA	0,21	±	0,04	0,14	±	0,02
20:5(n-3)/22:6(n-3)	0,33	±	0,09	0,52	±	0,05
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	12,85	±	1,84	16,45	±	1,38
18:3 (n-3) + 18:4 (n-3)	1,69	±	0,76	0,91	±	0,36
16:4 (n-3) + 18:5 (n-3)	0,01	±	0,01	0,02	±	0,02
22:5 (n-3) + 22:6 (n-3)	27,12	±	7,09	12,68	±	4,15
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	6,20	±	2,45	6,79	±	1,65
MUFA (n-11)	4,61	±	1,89	6,89	±	1,72
MUFA (n-9)	17,45	±	3,19	27,62	±	6,01
MUFA (n-7)	7,87	±	1,94	14,08	±	2,35

Table A.47: FA composition of argentine.

Species	Argentine					
Tissue	Muscle			Liver		
Population	8			9		
Amount of FA (mg/100 mg wet weight)	0,91	±	0,29	4,39	±	1,02
Amount of Chol (mg/100 mg wet weight)	0,09	±	0,02	0,34	±	0,08
14:0	2,29	±	0,86	1,91	±	0,40
Iso 15:0	0,11	±	0,04	0,10	±	0,04
Antiso 15:0	0,02	±	0,01	0,00	±	0,01
15:0	0,35	±	0,08	0,31	±	0,14
Iso 16:0	0,09	±	0,05	0,16	±	0,06
16:0	18,97	±	1,30	15,47	±	2,64
Iso 17:0	0,37	±	0,12	0,76	±	0,23
Antiso 17:0	0,14	±	0,06	0,26	±	0,10
17:0	0,33	±	0,08	0,27	±	0,08
iso 18:0	0,15	±	0,02	0,29	±	0,08
iso 18:0	0,05	±	0,03	0,10	±	0,04
18:0	3,64	±	0,30	3,50	±	0,70
iso 19:0	0,03	±	0,02	0,08	±	0,05
antiso 19:0	0,04	±	0,02	0,09	±	0,02
i-20:0	0,02	±	0,01	0,10	±	0,02
20:0	0,06	±	0,02	0,07	±	0,02
21:0	0,01	±	0,01	0,07	±	0,03
22:0	0,10	±	0,03	0,06	±	0,01
24:0	0,11	±	0,08	0,04	±	0,01
4,8,12-Me 13:0	0,08	±	0,02	0,04	±	0,04
∑pristanic	0,00	±	0,00	0,00	±	0,00
∑phytanic	0,00	±	0,00	0,00	±	0,00
Forgrenet 17:1	0,12	±	0,05	0,07	±	0,04
16:1 n-10, 7Me	0,29	±	0,06	0,35	±	0,11
∑SFA	26,88	±	0,75	23,64	±	2,89
14:1 (n-7)	0,01	±	0,02	0,02	±	0,02
14:1 (n-5)	0,05	±	0,04	0,04	±	0,04
15:1 n-x	0,01	±	0,01	0,00	±	0,00
15:1 (n-5)	0,00	±	0,00	0,00	±	0,00
16:1 (n-11)	0,18	±	0,06	0,25	±	0,08
16:1 (n-9)	0,26	±	0,03	0,42	±	0,10
16:1 (n-7)	1,94	±	0,58	3,42	±	1,47
16:1 (n-5)	0,20	±	0,03	0,16	±	0,07
17:1 (n-10)	0,04	±	0,02	0,05	±	0,01
17:1 (n-8)	0,34	±	0,07	0,61	±	0,16
17:1 (n-7)	0,03	±	0,01	0,02	±	0,01
17:1 (n-6)	0,03	±	0,01	0,02	±	0,02
17:1 (n-4)	0,06	±	0,02	0,04	±	0,02
18:1 (n-11)	0,49	±	0,14	1,35	±	0,60
18:1 (n-9)	9,50	±	0,96	18,43	±	3,62
18:1 (n-7)	2,06	±	0,32	3,70	±	0,24
18:1 (n-5)	0,27	±	0,06	0,50	±	0,12
18:1 (n-4)	0,01	±	0,02	0,04	±	0,03
19:1 (n-x2)	0,11	±	0,03	0,11	±	0,04
20:1 (n-11)	0,46	±	0,22	0,47	±	0,16
20:1 (n-9)	1,62	±	0,60	1,35	±	0,71
20:1 (n-7)	0,44	±	0,22	0,45	±	0,18
20:1 (n-5)	0,21	±	0,10	0,12	±	0,07
22:1 (n-11)	1,83	±	0,94	0,88	±	0,55
22:1 (n-9)	0,88	±	0,36	0,47	±	0,24
22:1 (n-7)	0,12	±	0,04	0,10	±	0,04
24:1 (n-9)	1,21	±	0,14	1,36	±	0,17
24:1 (n-5)	0,19	±	0,13	0,10	±	0,04
∑MUFA	22,52	±	4,11	34,48	±	4,69
16:4 (n-1)	0,09	±	0,08	0,01	±	0,02
18:4 (n-1)	0,05	±	0,02	0,05	±	0,04
18:5 (n-1)	0,00	±	0,00	0,01	±	0,01
16:2 (n-4)	0,10	±	0,05	0,04	±	0,03
16:3 (n-4)	0,04	±	0,03	0,01	±	0,01
18:2 (n-4)	0,10	±	0,04	0,10	±	0,06
16:2 (n-7)	0,01	±	0,01	0,01	±	0,01
18:2 (n-7)	0,05	±	0,02	0,11	±	0,03
16:2 (n-6)	0,02	±	0,02	0,02	±	0,01
18:2 (n-6)	0,85	±	0,11	0,92	±	0,26
18:3 (n-6)	0,02	±	0,02	0,02	±	0,04
20:2 (n-6)	0,21	±	0,07	0,25	±	0,08
20:3 (n-6)	0,07	±	0,01	0,08	±	0,02
20:4 (n-6)	1,71	±	0,39	2,49	±	0,74
22:2 (n-6)	0,02	±	0,01	0,03	±	0,02
22:4 (n-6)	0,63	±	0,20	0,63	±	0,20
22:5 (n-6)	0,63	±	0,09	0,37	±	0,07
16:4 (n-3)	0,00	±	0,00	0,01	±	0,01
18:3 (n-3)	0,54	±	0,08	0,37	±	0,17
18:4 (n-3)	0,65	±	0,28	0,28	±	0,13
18:5 (n-3)	0,00	±	0,00	0,00	±	0,00
20:3 (n-3)	0,12	±	0,03	0,16	±	0,07
20:4 (n-3)	0,64	±	0,07	0,82	±	0,36
20:5 (n-3)	10,40	±	0,75	9,20	±	2,07
21:5 (n-3)	0,26	±	0,07	0,24	±	0,08
22:3 (n-3)	0,00	±	0,00	0,00	±	0,00
22:4 (n-3)	0,03	±	0,02	0,04	±	0,03
22:5 (n-3)	2,42	±	0,31	3,50	±	0,55
22:6 (n-3)	29,80	±	4,65	21,03	±	3,93
24:5 (n-3)	0,35	±	0,06	0,25	±	0,15
24:6 (n-3)	0,14	±	0,07	0,24	±	0,12
20:2 D5,11 (NMI)	0,19	±	0,04	0,29	±	0,07
20:2 D5,13 (NMI)	0,01	±	0,01	0,02	±	0,02
20:3 D5,11,14 (NMI)	0,02	±	0,03	0,01	±	0,02
20:4 D5,11,14,17 (NMI)	0,04	±	0,02	0,02	±	0,02
22:2 D7,13 (NMI)	0,04	±	0,06	0,17	±	0,16
22:2 D7,15 (NMI)	0,05	±	0,05	0,04	±	0,04
22:2 NMI	0,02	±	0,01	0,00	±	0,00
∑PUFA	49,96	±	4,21	41,29	±	6,71
∑PUFA(n-6)	4,16	±	0,61	4,81	±	0,92
∑PUFA(n-3)	45,35	±	4,34	36,14	±	6,28
∑NMI	0,36	±	0,12	0,56	±	0,23
∑DMA	0,09	±	0,05	0,10	±	0,03
∑Chol	10,62	±	1,57	7,74	±	0,96
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3))	10,89	±	0,95	19,71	±	3,28
∑Odd-numbered SFA	1,77	±	0,45	2,42	±	0,75
∑Branched FA	1,24	±	0,29	1,93	±	0,55
∑Odd-numbered MUFA	0,64	±	0,14	0,62	±	0,15
16:1(n-7)/16:0	0,10	±	0,04	0,22	±	0,07
∑C16/ ∑C18	1,19	±	0,13	0,67	±	0,07
∑C16 PUFA (n-1 + n-7 + n-6)	0,26	±	0,17	0,10	±	0,05
∑C16 PUFA/ ∑C18 PUFA	0,11	±	0,06	0,06	±	0,01
20:5(n-3)/22:6(n-3)	0,36	±	0,06	0,44	±	0,05
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	12,43	±	0,69	12,63	±	1,90
18:3 (n-3) + 18:4 (n-3)	1,19	±	0,34	0,65	±	0,28
16:4 (n-3) + 18:5 (n-3)	0,00	±	0,00	0,01	±	0,01
22:5 (n-3) + 22:6 (n-3)	32,22	±	4,44	24,53	±	3,95
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	4,32	±	1,89	2,70	±	1,45
MUFA (n-11)	2,95	±	1,18	2,94	±	1,08
MUFA (n-9)	13,47	±	1,72	22,02	±	3,81
MUFA (n-7)	4,78	±	1,16	7,81	±	1,39

Table A.48: FA composition of megrim.

Species	Megrim					
Tissue	Muscle			Liver		
Population	10			10		
Amount of FA (mg/100 mg wet weight)	1,48	±	1,68	24,66	±	9,28
Amount of Chol (mg/100 mg wet weight)	0,06	±	0,01	1,19	±	0,41
14:0	3,95	±	1,23	6,09	±	0,49
Iso 15:0	0,15	±	0,06	0,20	±	0,05
Antiso 15:0	0,02	±	0,01	0,01	±	0,02
15:0	0,36	±	0,06	0,31	±	0,08
Iso 16:0	0,05	±	0,02	0,08	±	0,02
16:0	15,52	±	2,20	12,13	±	0,87
Iso 17:0	0,21	±	0,03	0,28	±	0,05
Antiso 17:0	0,09	±	0,02	0,10	±	0,02
17:0	0,20	±	0,03	0,11	±	0,04
iso 18:0	0,11	±	0,01	0,10	±	0,02
iso 18:0	0,04	±	0,04	0,01	±	0,00
18:0	2,77	±	0,67	1,25	±	0,24
iso 19:0	0,02	±	0,03	0,04	±	0,02
antiso 19:0	0,01	±	0,01	0,01	±	0,00
i-20:0	0,06	±	0,02	0,04	±	0,00
20:0	0,08	±	0,01	0,05	±	0,01
21:0	0,03	±	0,01	0,00	±	0,01
22:0	0,08	±	0,03	0,05	±	0,02
24:0	0,12	±	0,06	0,02	±	0,00
4,8,12-Me 13:0	0,24	±	0,06	0,42	±	0,03
∑pristanic	0,00	±	0,00	0,00	±	0,00
∑phytanic	0,00	±	0,00	0,00	±	0,00
Forgrenet 17:1	0,10	±	0,03	0,11	±	0,02
16:1 n-10, 7Me	0,25	±	0,03	0,33	±	0,06
∑SFA	23,88	±	1,60	20,85	±	0,89
14:1 (n-7)	0,02	±	0,02	0,01	±	0,00
14:1 (n-5)	0,05	±	0,04	0,40	±	0,12
15:1 n-x	0,05	±	0,03	0,03	±	0,01
15:1 (n-5)	0,00	±	0,01	0,01	±	0,00
16:1 (n-11)	0,46	±	0,13	0,72	±	0,22
16:1 (n-9)	0,35	±	0,05	0,60	±	0,17
16:1 (n-7)	3,57	±	1,51	9,39	±	1,81
16:1 (n-5)	0,25	±	0,02	0,19	±	0,04
17:1 (n-10)	0,09	±	0,11	0,04	±	0,01
17:1 (n-8)	0,26	±	0,07	0,47	±	0,10
17:1 (n-7)	0,05	±	0,02	0,03	±	0,01
17:1 (n-6)	0,03	±	0,01	0,04	±	0,02
17:1 (n-4)	0,16	±	0,07	0,07	±	0,02
18:1 (n-11)	1,63	±	0,32	3,71	±	0,43
18:1 (n-9)	7,55	±	1,86	16,75	±	1,32
18:1 (n-7)	1,59	±	0,36	2,94	±	0,42
18:1 (n-5)	0,27	±	0,06	0,41	±	0,04
18:1 (n-4)	0,02	±	0,02	0,03	±	0,01
19:1 (n-x2)	0,10	±	0,03	0,16	±	0,02
20:1 (n-11)	1,08	±	0,39	1,24	±	0,22
20:1 (n-9)	5,29	±	2,21	5,76	±	0,79
20:1 (n-7)	0,12	±	0,05	0,17	±	0,07
20:1 (n-5)	0,16	±	0,09	0,03	±	0,03
22:1 (n-11)	5,25	±	2,55	4,27	±	1,42
22:1 (n-9)	0,47	±	0,15	0,75	±	0,17
22:1 (n-7)	0,06	±	0,04	0,04	±	0,01
24:1 (n-9)	1,10	±	0,43	0,49	±	0,12
24:1 (n-5)	0,21	±	0,09	0,09	±	0,03
∑MUFA	30,24	±	7,38	48,80	±	2,94
16:4 (n-1)	0,15	±	0,11	0,02	±	0,00
18:4 (n-1)	0,11	±	0,06	0,13	±	0,04
18:5 (n-1)	0,02	±	0,02	0,02	±	0,01
16:2 (n-4)	0,24	±	0,14	0,20	±	0,03
16:3 (n-4)	0,08	±	0,08	0,08	±	0,02
18:2 (n-4)	0,13	±	0,04	0,21	±	0,02
16:2 (n-7)	0,04	±	0,03	0,05	±	0,01
18:2 (n-7)	0,05	±	0,01	0,07	±	0,01
16:2 (n-6)	0,13	±	0,06	0,03	±	0,01
18:2 (n-6)	1,00	±	0,18	1,05	±	0,26
18:3 (n-6)	0,07	±	0,03	0,06	±	0,01
20:2 (n-6)	0,23	±	0,05	0,36	±	0,07
20:3 (n-6)	0,07	±	0,01	0,07	±	0,02
20:4 (n-6)	1,18	±	0,42	0,47	±	0,13
22:2 (n-6)	0,01	±	0,01	0,03	±	0,01
22:4 (n-6)	0,24	±	0,06	0,45	±	0,18
22:5 (n-6)	0,49	±	0,15	0,19	±	0,05
16:4 (n-3)	0,02	±	0,03	0,03	±	0,01
18:3 (n-3)	0,65	±	0,25	0,67	±	0,19
18:4 (n-3)	1,85	±	0,91	1,43	±	0,34
18:5 (n-3)	0,00	±	0,01	0,00	±	0,00
20:3 (n-3)	0,19	±	0,08	0,36	±	0,09
20:4 (n-3)	0,87	±	0,19	1,46	±	0,22
20:5 (n-3)	7,92	±	1,20	5,59	±	0,82
21:5 (n-3)	0,36	±	0,12	0,42	±	0,06
22:3 (n-3)	0,00	±	0,01	0,01	±	0,00
22:4 (n-3)	0,12	±	0,04	0,18	±	0,03
22:5 (n-3)	2,28	±	0,25	2,59	±	0,40
22:6 (n-3)	25,92	±	6,54	12,68	±	1,25
24:5 (n-3)	0,54	±	0,06	0,26	±	0,04
24:6 (n-3)	0,18	±	0,04	0,14	±	0,06
20:2 D5,11 (NMI)	0,13	±	0,04	0,08	±	0,01
20:2 D5,13 (NMI)	0,01	±	0,01	0,04	±	0,02
20:3 D5,11,14 (NMI)	0,06	±	0,14	0,00	±	0,00
20:4 D5,11,14,17 (NMI)	0,03	±	0,01	0,01	±	0,00
22:2 D7,13 (NMI)	0,04	±	0,04	0,01	±	0,01
22:2 D7,15 (NMI)	0,01	±	0,01	0,00	±	0,00
22:2 NMI	0,03	±	0,01	0,01	±	0,00
∑PUFA	45,15	±	5,91	29,28	±	2,99
∑PUFA(n-6)	3,42	±	0,44	2,70	±	0,64
∑PUFA(n-3)	40,91	±	5,71	25,80	±	2,56
∑NMI	0,31	±	0,12	0,23	±	0,08
∑DMA	0,31	±	0,12	0,14	±	0,03
∑Chol	6,55	±	3,15	5,30	±	2,78
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3))	9,21	±	1,97	18,47	±	1,37
∑Odd-numbered SFA	1,64	±	0,21	1,63	±	0,38
∑Branched FA	0,97	±	0,13	1,13	±	0,22
∑Odd-numbered MUFA	0,63	±	0,08	0,98	±	0,06
16:1(n-7)/16:0	0,25	±	0,14	0,77	±	0,12
∑C16/ ∑C18	1,18	±	0,18	0,82	±	0,10
∑C16 PUFA (n-1 + n-7 + n-6)	0,65	±	0,24	0,40	±	0,05
∑C16 PUFA/ ∑C18 PUFA	0,18	±	0,05	0,12	±	0,02
20:5(n-3)/22:6(n-3)	0,32	±	0,09	0,44	±	0,07
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	11,65	±	1,52	14,99	±	1,48
18:3 (n-3) + 18:4 (n-3)	2,50	±	1,15	2,10	±	0,51
16:4 (n-3) + 18:5 (n-3)	0,02	±	0,03	0,03	±	0,01
22:5 (n-3) + 22:6 (n-3)	28,20	±	6,74	15,26	±	1,45
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	11,01	±	4,88	10,78	±	2,20
MUFA (n-11)	8,42	±	3,13	9,93	±	1,71
MUFA (n-9)	14,76	±	2,98	24,36	±	1,09
MUFA (n-7)	5,63	±	1,84	12,64	±	1,96

Table A.49: FA composition of lesser sand eel

Species	Lesser sand eel			
Tissue	Muscle		Liver	
Population			4	
Amount of FA (mg/100 mg wet wei	±		18,17	± 11,39
Amount of Chol (mg/100 mg wet w	±		0,62	± 0,20
14:0	±		3,45	± 1,35
Iso 15:0	±		0,23	± 0,05
Antiso 15:0	±		0,00	± 0,00
15:0	±		0,34	± 0,02
Iso 16:0	±		0,14	± 0,02
16:0	±		14,40	± 1,09
Iso 17:0	±		0,55	± 0,19
Antiso 17:0	±		0,15	± 0,03
17:0	±		0,18	± 0,03
iso 18:0	±		0,18	± 0,13
iso 18:0	±		0,03	± 0,04
18:0	±		1,80	± 0,41
iso 19:0	±		0,01	± 0,02
antiso 19:0	±		0,00	± 0,01
i-20:0	±		0,03	± 0,02
20:0	±		0,05	± 0,01
21:0	±		0,04	± 0,04
22:0	±		0,04	± 0,02
24:0	±		0,03	± 0,04
4,8,12-Me 13:0	±		0,61	± 0,38
Σpristanic	±		0,00	± 0,00
Σphytanic	±		0,00	± 0,00
Forgrenet 17:1	±		0,26	± 0,07
16:1 n-10, 7Me	±		0,79	± 0,35
ΣSFA	±		21,66	± 0,71
14:1 (n-7)	±		0,02	± 0,02
14:1 (n-5)	±		0,10	± 0,03
15:1 n-x	±		0,02	± 0,02
15:1 (n-5)	±		0,01	± 0,00
16:1 (n-11)	±		0,18	± 0,08
16:1 (n-9)	±		0,23	± 0,07
16:1 (n-7)	±		5,59	± 0,91
16:1 (n-5)	±		0,26	± 0,06
17:1 (n-10)	±		0,05	± 0,05
17:1 (n-8)	±		0,27	± 0,06
17:1 (n-7)	±		0,03	± 0,00
17:1 (n-6)	±		0,03	± 0,01
17:1 (n-4)	±		0,12	± 0,07
18:1 (n-11)	±		1,29	± 0,40
18:1 (n-9)	±		9,22	± 3,21
18:1 (n-7)	±		1,95	± 0,65
18:1 (n-5)	±		0,50	± 0,08
18:1 (n-4)	±		0,05	± 0,04
19:1 (n-x2)	±		0,19	± 0,07
20:1 (n-11)	±		0,59	± 0,08
20:1 (n-9)	±		7,93	± 3,13
20:1 (n-7)	±		0,13	± 0,02
20:1 (n-5)	±		0,05	± 0,01
22:1 (n-11)	±		8,34	± 4,04
22:1 (n-9)	±		0,84	± 0,20
22:1 (n-7)	±		0,11	± 0,01
24:1 (n-9)	±		1,03	± 0,75
24:1 (n-7)	±		0,15	± 0,09
ΣMUFA	±		39,29	± 4,42
16:4 (n-1)	±		0,01	± 0,01
18:4 (n-1)	±		0,17	± 0,08
18:5 (n-1)	±		0,01	± 0,01
16:2 (n-4)	±		0,32	± 0,16
16:3 (n-4)	±		0,11	± 0,12
18:2 (n-4)	±		0,17	± 0,06
16:2 (n-7)	±		0,06	± 0,03
18:2 (n-7)	±		0,09	± 0,02
16:2 (n-6)	±		0,04	± 0,01
18:2 (n-6)	±		1,65	± 0,18
18:3 (n-6)	±		0,14	± 0,06
20:2 (n-6)	±		0,18	± 0,12
20:3 (n-6)	±		0,07	± 0,01
20:4 (n-6)	±		0,60	± 0,20
22:2 (n-6)	±		0,02	± 0,00
22:4 (n-6)	±		0,81	± 0,30
22:5 (n-6)	±		0,10	± 0,12
16:4 (n-3)	±		0,07	± 0,04
18:3 (n-3)	±		0,87	± 0,19
18:4 (n-3)	±		4,75	± 2,22
18:5 (n-3)	±		0,00	± 0,00
20:3 (n-3)	±		0,12	± 0,01
20:4 (n-3)	±		0,98	± 0,05
20:5 (n-3)	±		9,37	± 0,59
21:5 (n-3)	±		0,59	± 0,20
22:3 (n-3)	±		0,00	± 0,00
22:4 (n-3)	±		0,15	± 0,05
22:5 (n-3)	±		0,80	± 0,14
22:6 (n-3)	±		13,98	± 6,74
24:5 (n-3)	±		0,38	± 0,07
24:6 (n-3)	±		0,15	± 0,04
20:2 D5,11 (NMI)	±		0,07	± 0,03
20:2 D5,13 (NMI)	±		0,04	± 0,03
20:3 D5,11,14 (NMI)	±		0,06	± 0,12
20:4 D5,11,14,17 (NMI)	±		0,05	± 0,02
22:2 D7,13 (NMI)	±		0,00	± 0,00
22:2 D7,15 (NMI)	±		0,00	± 0,00
22:2 NMI	±		0,01	± 0,02
ΣPUFA	±		36,79	± 3,99
ΣPUFA(n-6)	±		3,61	± 0,65
ΣPUFA(n-3)	±		32,23	± 4,13
ΣNMI	±		0,24	± 0,17
ΣDMA	±		0,35	± 0,20
ΣChol	±		4,38	± 2,12
Terrestrial FATM (18:1 (n-9)+ 18:2 (	±		11,75	± 3,48
ΣOdd-numbered SFA	±		1,96	± 0,23
ΣBranched FA	±		2,21	± 0,72
ΣOdd-numbered MUFA	±		1,28	± 0,42
16:1(n-7)/16:0	±		0,39	± 0,05
ΣC16/ ΣC18	±		0,96	± 0,21
ΣC16 PUFA (n-1 + n-7 + n-6)	±		0,62	± 0,34
ΣC16 PUFA/ ΣC18 PUFA	±		0,07	± 0,03
20:5(n-3)/22:6(n-3)	±		0,76	± 0,26
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	±		14,98	± 1,03
18:3 (n-3) + 18:4 (n-3)	±		5,62	± 2,39
16:4 (n-3) + 18:5 (n-3)	±		0,07	± 0,03
22:5 (n-3) + 22:6 (n-3)	±		14,78	± 6,87
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	±		17,11	± 7,34
MUFA (n-11)	±		10,39	± 3,68
MUFA (n-9)	±		19,25	± 3,02
MUFA (n-7)	±		7,98	± 1,48

Table A.50: FA composition of spiny dogfish.

Species	Spiny dogfish			
Tissue	Muscle		Liver	
Population	6		6	
Amount of FA (mg/100 mg wet weight)	1,79 ± 0,75		37,73	± 6,00
Amount of Chol (mg/100 mg wet weight)	0,04 ± 0,01		0,56	± 0,26
14:0	1,32 ± 0,50		3,23	± 0,64
Iso 15:0	0,14 ± 0,03		0,18	± 0,03
Antiso 15:0	0,01 ± 0,02		0,03	± 0,03
15:0	0,25 ± 0,08		0,34	± 0,05
Iso 16:0	0,08 ± 0,01		0,07	± 0,04
16:0	16,66 ± 0,86		13,29	± 1,33
Iso 17:0	0,40 ± 0,02		0,45	± 0,04
Antiso 17:0	0,24 ± 0,05		0,11	± 0,01
17:0	0,41 ± 0,09		0,34	± 0,10
iso 18:0	0,42 ± 0,16		0,23	± 0,04
iso 18:0	0,15 ± 0,28		0,03	± 0,01
18:0	3,73 ± 0,86		2,59	± 0,38
iso 19:0	0,04 ± 0,05		0,03	± 0,02
antiso 19:0	0,06 ± 0,03		0,05	± 0,01
i-20:0	0,01 ± 0,02		0,05	± 0,01
20:0	0,08 ± 0,01		0,17	± 0,04
21:0	0,00 ± 0,00		0,03	± 0,02
22:0	0,06 ± 0,02		0,07	± 0,01
24:0	0,07 ± 0,01		0,03	± 0,01
4,8,12-Me 13:0	0,13 ± 0,20		0,11	± 0,02
Σpristanic	0,00 ± 0,00		0,00	± 0,00
Σphytanic	0,00 ± 0,00		0,00	± 0,00
Forgrenet 17:1	0,08 ± 0,03		0,12	± 0,01
16:1 n-10, 7Me	0,22 ± 0,05		0,30	± 0,04
ΣSFA	24,14 ± 0,67		21,32	± 1,41
14:1 (n-7)	0,01 ± 0,00		0,02	± 0,02
14:1 (n-5)	0,28 ± 0,10		0,04	± 0,02
15:1 n-x	0,00 ± 0,01		0,02	± 0,01
15:1 (n-5)	0,00 ± 0,00		0,00	± 0,00
16:1 (n-11)	0,29 ± 0,12		0,06	± 0,01
16:1 (n-9)	0,27 ± 0,02		0,16	± 0,02
16:1 (n-7)	2,67 ± 0,70		3,17	± 0,17
16:1 (n-5)	0,08 ± 0,05		0,19	± 0,02
17:1 (n-10)	0,06 ± 0,03		0,05	± 0,02
17:1 (n-8)	0,33 ± 0,04		0,27	± 0,05
17:1 (n-7)	0,04 ± 0,00		0,04	± 0,01
17:1 (n-6)	0,03 ± 0,01		0,02	± 0,00
17:1 (n-4)	0,10 ± 0,05		0,17	± 0,01
18:1 (n-11)	1,54 ± 0,22		1,06	± 0,22
18:1 (n-9)	12,50 ± 1,42		10,50	± 1,74
18:1 (n-7)	2,91 ± 0,31		2,07	± 0,36
18:1 (n-5)	0,36 ± 0,04		0,41	± 0,01
18:1 (n-4)	0,00 ± 0,00		0,05	± 0,03
19:1 (n-x2)	0,12 ± 0,03		0,14	± 0,01
20:1 (n-11)	2,19 ± 0,33		1,11	± 0,14
20:1 (n-9)	4,85 ± 0,63		10,73	± 1,10
20:1 (n-7)	0,57 ± 0,14		0,79	± 0,18
20:1 (n-5)	0,04 ± 0,04		0,04	± 0,03
22:1 (n-11)	2,74 ± 0,46		13,98	± 1,31
22:1 (n-9)	1,51 ± 0,27		3,91	± 0,75
22:1 (n-7)	0,05 ± 0,04		0,19	± 0,02
24:1 (n-9)	0,34 ± 0,13		1,24	± 0,13
24:1 (n-7)	0,15 ± 0,05		0,12	± 0,03
ΣMUFA	34,02 ± 2,44		50,56	± 1,16
16:4 (n-1)	0,16 ± 0,04		0,01	± 0,01
18:4 (n-1)	0,08 ± 0,04		0,16	± 0,01
18:5 (n-1)	0,07 ± 0,03		0,12	± 0,12
16:2 (n-4)	0,01 ± 0,01		0,21	± 0,03
16:3 (n-4)	0,03 ± 0,03		0,06	± 0,03
18:2 (n-4)	0,21 ± 0,07		0,31	± 0,05
16:2 (n-7)	0,16 ± 0,08		0,03	± 0,02
18:2 (n-7)	0,08 ± 0,01		0,09	± 0,01
16:2 (n-6)	0,05 ± 0,05		0,03	± 0,01
18:2 (n-6)	1,58 ± 0,18		1,45	± 0,07
18:3 (n-6)	0,08 ± 0,04		0,17	± 0,01
20:2 (n-6)	0,37 ± 0,07		0,36	± 0,09
20:3 (n-6)	0,10 ± 0,03		0,10	± 0,01
20:4 (n-6)	2,81 ± 0,65		0,61	± 0,10
22:2 (n-6)	0,02 ± 0,02		0,08	± 0,02
22:4 (n-6)	0,56 ± 0,10		0,52	± 0,07
22:5 (n-6)	0,63 ± 0,09		0,39	± 0,12
16:4 (n-3)	0,02 ± 0,01		0,06	± 0,05
18:3 (n-3)	0,67 ± 0,21		0,82	± 0,10
18:4 (n-3)	0,90 ± 0,39		2,34	± 0,77
18:5 (n-3)	0,00 ± 0,00		0,00	± 0,00
20:3 (n-3)	0,12 ± 0,04		0,14	± 0,04
20:4 (n-3)	0,58 ± 0,27		1,23	± 0,19
20:5 (n-3)	4,75 ± 1,78		4,85	± 0,86
21:5 (n-3)	0,27 ± 0,10		0,34	± 0,03
22:3 (n-3)	0,00 ± 0,00		0,01	± 0,00
22:4 (n-3)	0,05 ± 0,02		0,10	± 0,03
22:5 (n-3)	2,14 ± 0,29		1,44	± 0,22
22:6 (n-3)	24,68 ± 3,34		10,94	± 1,27
24:5 (n-3)	0,12 ± 0,10		0,26	± 0,08
24:6 (n-3)	0,06 ± 0,02		0,14	± 0,04
20:2 D5,11 (NMI)	0,13 ± 0,02		0,06	± 0,02
20:2 D5,13 (NMI)	0,02 ± 0,02		0,03	± 0,04
20:3 D5,11,14 (NMI)	0,00 ± 0,00		0,02	± 0,02
20:4 D5,11,14,17 (NMI)	0,02 ± 0,01		0,02	± 0,00
22:2 D7,13 (NMI)	0,01 ± 0,01		0,02	± 0,02
22:2 D7,15 (NMI)	0,01 ± 0,01		0,03	± 0,02
22:2 NMI	0,03 ± 0,01		0,03	± 0,00
ΣPUFA	41,35 ± 2,35		27,36	± 2,51
ΣPUFA(n-6)	6,21 ± 0,53		3,70	± 0,33
ΣPUFA(n-3)	34,35 ± 2,27		22,67	± 2,60
ΣNMI	0,22 ± 0,03		0,21	± 0,05
ΣDMA	1,13 ± 0,48		0,27	± 0,05
ΣChol	2,30 ± 1,16		1,59	± 1,03
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3)	14,75 ± 1,55		12,76	± 1,81
ΣOdd-numbered SFA	1,99 ± 0,22		2,02	± 0,19
ΣBranched FA	1,67 ± 0,16		1,47	± 0,08
ΣOdd-numbered MUFA	0,72 ± 0,09		0,75	± 0,05
16:1(n-7)/16:0	0,16 ± 0,04		0,24	± 0,03
ΣC16/ ΣC18	0,80 ± 0,05		0,78	± 0,04
ΣC16 PUFA (n-1 + n-7 + n-6)	0,43 ± 0,11		0,40	± 0,08
ΣC16 PUFA/ ΣC18 PUFA	0,13 ± 0,06		0,07	± 0,01
20:5(n-3)/22:6(n-3)	0,20 ± 0,10		0,44	± 0,05
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	7,58 ± 2,42		8,03	± 1,02
18:3 (n-3) + 18:4 (n-3)	1,56 ± 0,58		3,16	± 0,72
16:4 (n-3) + 18:5 (n-3)	0,02 ± 0,01		0,06	± 0,05
22:5 (n-3) + 22:6 (n-3)	26,82 ± 3,37		12,38	± 1,16
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	9,10 ± 1,15		28,63	± 1,67
MUFA (n-11)	6,75 ± 0,72		16,21	± 1,12
MUFA (n-9)	19,46 ± 1,87		26,54	± 1,76
MUFA (n-7)	6,40 ± 0,48		6,39	± 0,39

Table A.51: FA composition of lesser sand eel larvae

Species	Greater sand eel (larvae)		
Tissue	Whole fish		
Population	10		
Amount of FA (mg/100 mg wet weight)	11,65	±	2,14
Amount of Chol (mg/100 mg wet weight)	1,60	±	0,16
14:0	2,29	±	0,55
Iso 15:0	0,14	±	0,02
Antiso 15:0	0,03	±	0,01
15:0	0,36	±	0,06
Iso 16:0	0,01	±	0,00
16:0	15,31	±	0,65
Iso 17:0	0,57	±	0,08
Antiso 17:0	0,08	±	0,02
17:0	0,33	±	0,05
iso 18:0	0,29	±	0,01
iso 18:0	0,07	±	0,06
18:0	3,89	±	0,48
iso 19:0	0,03	±	0,00
antiso 19:0	0,02	±	0,00
i-20:0	0,03	±	0,01
20:0	0,06	±	0,01
21:0	0,02	±	0,01
22:0	0,11	±	0,01
24:0	0,14	±	0,04
4,8,12-Me 13:0	0,07	±	0,02
∑pristanic	0,00	±	0,00
∑phytanic	0,00	±	0,00
Forgrenet 17:1	0,11	±	0,01
16:1 n-10, 7Me	0,78	±	0,10
∑SFA	23,80	±	0,59
14:1 (n-7)	0,02	±	0,00
14:1 (n-5)	0,01	±	0,01
15:1 n-x	0,03	±	0,02
15:1 (n-5)	0,00	±	0,00
16:1 (n-11)	0,13	±	0,02
16:1 (n-9)	0,27	±	0,03
16:1 (n-7)	2,78	±	0,73
16:1 (n-5)	0,38	±	0,06
17:1 (n-10)	0,03	±	0,01
17:1 (n-8)	0,17	±	0,03
17:1 (n-7)	0,03	±	0,01
17:1 (n-6)	0,03	±	0,01
17:1 (n-4)	0,12	±	0,01
18:1 (n-11)	0,64	±	0,08
18:1 (n-9)	5,18	±	0,49
18:1 (n-7)	2,10	±	0,18
18:1 (n-5)	0,45	±	0,05
18:1 (n-4)	0,05	±	0,01
19:1 (n-x2)	0,22	±	0,04
20:1 (n-11)	0,43	±	0,11
20:1 (n-9)	3,49	±	1,47
20:1 (n-7)	0,11	±	0,02
20:1 (n-5)	0,03	±	0,01
22:1 (n-11)	3,12	±	1,93
22:1 (n-9)	0,34	±	0,13
22:1 (n-7)	0,14	±	0,01
24:1 (n-9)	2,04	±	0,22
24:1 (n-7)	0,09	±	0,04
∑MUFA	22,44	±	3,57
16:4 (n-1)	0,23	±	0,02
18:4 (n-1)	0,04	±	0,01
18:5 (n-1)	0,02	±	0,01
16:2 (n-4)	0,12	±	0,03
16:3 (n-4)	0,05	±	0,02
18:2 (n-4)	0,09	±	0,01
16:2 (n-7)	0,02	±	0,01
18:2 (n-7)	0,08	±	0,01
16:2 (n-6)	0,05	±	0,01
18:2 (n-6)	2,10	±	0,37
18:3 (n-6)	0,07	±	0,02
20:2 (n-6)	0,20	±	0,03
20:3 (n-6)	0,07	±	0,01
20:4 (n-6)	0,77	±	0,12
22:2 (n-6)	0,17	±	0,13
22:4 (n-6)	0,40	±	0,08
22:5 (n-6)	0,42	±	0,13
16:4 (n-3)	0,02	±	0,01
18:3 (n-3)	0,80	±	0,12
18:4 (n-3)	1,69	±	0,45
18:5 (n-3)	0,00	±	0,00
20:3 (n-3)	0,08	±	0,01
20:4 (n-3)	0,46	±	0,08
20:5 (n-3)	12,19	±	1,06
21:5 (n-3)	0,23	±	0,04
22:3 (n-3)	0,00	±	0,01
22:4 (n-3)	0,04	±	0,01
22:5 (n-3)	1,09	±	0,06
22:6 (n-3)	30,82	±	2,81
24:5 (n-3)	0,23	±	0,09
24:6 (n-3)	0,11	±	0,03
20:2 D5,11 (NMI)	0,03	±	0,03
20:2 D5,13 (NMI)	0,10	±	0,06
20:3 D5,11,14 (NMI)	0,10	±	0,01
20:4 D5,11,14,17 (NMI)	0,14	±	0,03
22:2 D7,13 (NMI)	0,02	±	0,01
22:2 D7,15 (NMI)	0,00	±	0,00
22:2 NMI	0,03	±	0,01
∑PUFA	52,67	±	3,05
∑PUFA(n-6)	4,25	±	0,32
∑PUFA(n-3)	47,76	±	3,20
∑NMI	0,42	±	0,10
∑DMA	0,62	±	0,05
∑Chol	13,95	±	1,62
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3)	8,08	±	0,71
∑Odd-numbered SFA	1,90	±	0,22
∑Branched FA	2,08	±	0,24
∑Odd-numbered MUFA	1,12	±	0,12
16:1(n-7)/16:0	0,18	±	0,05
∑C16/ ∑C18	1,10	±	0,10
∑C16 PUFA (n-1+ n-7 + n-6)	0,49	±	0,07
∑C16 PUFA/ ∑C18 PUFA	0,10	±	0,01
20:5(n-3)/22:6(n-3)	0,40	±	0,02
16:1 (n-7)+16:4(n-1)+20:5 (n-3)	15,21	±	0,99
18:3 (n-3) + 18:4 (n-3)	2,49	±	0,54
16:4 (n-3) + 18:5 (n-3)	0,02	±	0,01
22:5 (n-3) + 22:6 (n-3)	31,91	±	2,82
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	6,95	±	3,52
MUFA (n-11)	4,32	±	2,03
MUFA (n-9)	11,32	±	1,53
MUFA (n-7)	5,26	±	0,66

Table A.52: FA composition of Atlantic horse mackerel.

Species	Atlantic horse mackerel					
Tissue	Muscle			Liver		
Population	9			10		
Amount of FA (mg/100 mg wet weight)	2,44	±	1,22	9,06	±	2,46
Amount of Chol (mg/100 mg wet weight)	0,05	±	0,01	0,23	±	0,03
14:0	5,32	±	1,38	2,92	±	0,55
Iso 15:0	0,18	±	0,08	0,09	±	0,02
Antiso 15:0	0,04	±	0,02	0,02	±	0,01
15:0	0,41	±	0,08	0,19	±	0,05
Iso 16:0	0,06	±	0,03	0,07	±	0,02
16:0	16,64	±	1,32	18,31	±	2,52
Iso 17:0	0,19	±	0,03	0,21	±	0,03
Antiso 17:0	0,07	±	0,01	0,07	±	0,01
17:0	0,28	±	0,05	0,16	±	0,04
iso 18:0	0,08	±	0,01	0,07	±	0,04
iso 18:0	0,14	±	0,02	0,08	±	0,06
18:0	4,10	±	0,79	5,84	±	1,13
iso 19:0	0,05	±	0,03	0,12	±	0,08
antiso 19:0	0,02	±	0,00	0,01	±	0,01
i-20:0	0,02	±	0,01	0,01	±	0,02
20:0	0,14	±	0,03	0,10	±	0,02
21:0	0,04	±	0,01	0,06	±	0,01
22:0	0,06	±	0,01	0,05	±	0,01
24:0	0,04	±	0,01	0,01	±	0,01
4,8,12-Me 13:0	0,15	±	0,07	0,10	±	0,03
∑pristanic	0,00	±	0,00	0,00	±	0,00
∑phytanic	0,00	±	0,00	0,00	±	0,00
Forgrenet 17:1	0,04	±	0,04	0,05	±	0,02
16:1 n-10, 7Me	0,17	±	0,04	0,17	±	0,05
∑SFA	27,88	±	1,00	28,40	±	3,15
14:1 (n-7)	0,02	±	0,01	0,02	±	0,01
14:1 (n-5)	0,07	±	0,01	0,09	±	0,02
15:1 n-x	0,03	±	0,00	0,01	±	0,01
15:1 (n-5)	0,00	±	0,00	0,00	±	0,00
16:1 (n-11)	0,06	±	0,01	0,07	±	0,03
16:1 (n-9)	0,20	±	0,03	0,22	±	0,07
16:1 (n-7)	3,80	±	0,64	5,84	±	1,20
16:1 (n-5)	0,20	±	0,02	0,13	±	0,03
17:1 (n-10)	0,03	±	0,00	0,02	±	0,01
17:1 (n-8)	0,28	±	0,06	0,29	±	0,04
17:1 (n-7)	0,04	±	0,00	0,01	±	0,01
17:1 (n-6)	0,04	±	0,01	0,02	±	0,01
17:1 (n-4)	0,01	±	0,00	0,02	±	0,01
18:1 (n-11)	0,42	±	0,09	0,16	±	0,27
18:1 (n-9)	12,22	±	2,69	25,40	±	4,89
18:1 (n-7)	2,01	±	0,31	2,36	±	0,32
18:1 (n-5)	0,24	±	0,03	0,26	±	0,04
18:1 (n-4)	0,02	±	0,01	0,02	±	0,01
19:1 (n-x2)	0,07	±	0,03	0,09	±	0,04
20:1 (n-11)	0,90	±	0,34	1,15	±	0,57
20:1 (n-9)	4,91	±	1,58	2,92	±	0,93
20:1 (n-7)	0,12	±	0,04	0,06	±	0,01
20:1 (n-5)	0,07	±	0,02	0,04	±	0,01
22:1 (n-11)	7,89	±	3,13	3,73	±	1,61
22:1 (n-9)	0,45	±	0,14	0,23	±	0,07
22:1 (n-7)	0,08	±	0,03	0,06	±	0,01
24:1 (n-9)	0,93	±	0,13	0,57	±	0,10
24:1 (n-7)	0,15	±	0,03	0,07	±	0,02
∑MUFA	35,26	±	5,78	43,88	±	4,84
16:4 (n-1)	0,24	±	0,07	0,07	±	0,06
18:4 (n-1)	0,08	±	0,02	0,09	±	0,03
18:5 (n-1)	0,00	±	0,01	0,00	±	0,00
16:2 (n-4)	0,23	±	0,05	0,10	±	0,05
16:3 (n-4)	0,10	±	0,03	0,03	±	0,02
18:2 (n-4)	0,09	±	0,02	0,07	±	0,02
16:2 (n-7)	0,05	±	0,01	0,03	±	0,01
18:2 (n-7)	0,05	±	0,01	0,07	±	0,01
16:2 (n-6)	0,02	±	0,01	0,01	±	0,00
18:2 (n-6)	1,26	±	0,12	0,74	±	0,17
18:3 (n-6)	0,09	±	0,02	0,05	±	0,02
20:2 (n-6)	0,23	±	0,01	0,15	±	0,03
20:3 (n-6)	0,08	±	0,01	0,08	±	0,02
20:4 (n-6)	0,85	±	0,18	0,69	±	0,11
22:2 (n-6)	0,01	±	0,00	0,01	±	0,00
22:4 (n-6)	0,14	±	0,07	0,09	±	0,04
22:5 (n-6)	0,38	±	0,08	0,22	±	0,04
16:4 (n-3)	0,06	±	0,02	0,03	±	0,02
18:3 (n-3)	0,79	±	0,14	0,47	±	0,16
18:4 (n-3)	2,19	±	0,61	1,02	±	0,55
18:5 (n-3)	0,00	±	0,00	0,00	±	0,00
20:3 (n-3)	0,21	±	0,01	0,13	±	0,03
20:4 (n-3)	0,87	±	0,11	1,10	±	0,37
20:5 (n-3)	6,54	±	1,00	5,53	±	1,20
21:5 (n-3)	0,57	±	0,21	0,29	±	0,08
22:3 (n-3)	0,00	±	0,00	0,00	±	0,00
22:4 (n-3)	0,09	±	0,02	0,07	±	0,02
22:5 (n-3)	1,76	±	0,23	1,66	±	0,39
22:6 (n-3)	18,78	±	4,66	14,17	±	2,43
24:5 (n-3)	0,50	±	0,17	0,25	±	0,13
24:6 (n-3)	0,07	±	0,07	0,06	±	0,02
20:2 D5,11 (NMI)	0,11	±	0,02	0,16	±	0,02
20:2 D5,13 (NMI)	0,00	±	0,00	0,00	±	0,00
20:3 D5,11,14 (NMI)	0,18	±	0,13	0,05	±	0,03
20:4 D5,11,14,17 (NMI)	0,02	±	0,02	0,01	±	0,01
22:2 D7,13 (NMI)	0,01	±	0,02	0,00	±	0,01
22:2 D7,15 (NMI)	0,00	±	0,01	0,00	±	0,00
22:2 NMI	0,00	±	0,00	0,00	±	0,00
∑PUFA	36,34	±	5,97	27,28	±	4,58
∑PUFA(n-6)	3,06	±	0,25	2,04	±	0,32
∑PUFA(n-3)	32,43	±	5,79	24,77	±	4,16
∑NMI	0,32	±	0,15	0,23	±	0,04
∑DMA	0,27	±	0,10	0,03	±	0,01
∑Chol	2,63	±	1,03	2,74	±	0,76
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3)	14,27	±	2,52	26,62	±	4,63
∑Odd-numbered SFA	1,56	±	0,27	1,09	±	0,18
∑Branched FA	0,91	±	0,16	0,77	±	0,15
∑Odd-numbered MUFA	0,52	±	0,09	0,48	±	0,07
16:1(n-7)/16:0	0,23	±	0,04	0,32	±	0,08
∑C16/ ∑C18	0,91	±	0,08	0,69	±	0,12
∑C16 PUFA (n-1+ n-7 + n-6)	0,71	±	0,17	0,27	±	0,14
∑C16 PUFA/ ∑C18 PUFA	0,16	±	0,02	0,11	±	0,02
20:5(n-3)/22:6(n-3)	0,36	±	0,06	0,39	±	0,06
16:1 (n-7)+16:4(n-1)+20:5 (n-3)	10,58	±	1,18	11,44	±	0,79
18:3 (n-3) + 18:4 (n-3)	2,99	±	0,75	1,49	±	0,70
16:4 (n-3) + 18:5 (n-3)	0,06	±	0,02	0,03	±	0,02
22:5 (n-3) + 22:6 (n-3)	20,54	±	4,85	15,82	±	2,39
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	13,25	±	4,81	6,88	±	2,50
MUFA (n-11)	9,28	±	3,45	5,12	±	1,73
MUFA (n-9)	18,70	±	3,08	29,35	±	4,31
MUFA (n-7)	6,22	±	0,90	8,42	±	1,40

108

Table A.53: FA composition of Atlantic herring.

Species	Atlantic herring					
Tissue	Muscle			Liver		
Population	8			9		
Amount of FA (mg/100 mg wet weight)	4,73	±	2,88	13,37	±	4,82
Amount of Chol (mg/100 mg wet weight)	0,07	±	0,01	0,53	±	0,18
14:0	6,28	±	1,62	4,46	±	0,31
Iso 15:0	0,20	±	0,07	0,23	±	0,04
Antiso 15:0	0,06	±	0,02	0,03	±	0,01
15:0	0,38	±	0,06	0,35	±	0,08
Iso 16:0	0,06	±	0,02	0,10	±	0,01
16:0	13,28	±	1,87	11,94	±	2,39
Iso 17:0	0,22	±	0,05	0,41	±	0,02
Antiso 17:0	0,04	±	0,02	0,13	±	0,02
17:0	0,22	±	0,02	0,25	±	0,07
iso 18:0	0,08	±	0,01	0,11	±	0,04
iso 18:0	0,13	±	0,07	0,21	±	0,03
18:0	1,58	±	0,71	1,94	±	0,60
iso 19:0	0,01	±	0,00	0,00	±	0,00
antiso 19:0	0,01	±	0,00	0,01	±	0,00
i-20:0	0,02	±	0,01	0,05	±	0,01
20:0	0,19	±	0,05	0,09	±	0,02
21:0	0,03	±	0,01	0,06	±	0,02
22:0	0,10	±	0,02	0,06	±	0,01
24:0	0,05	±	0,02	0,05	±	0,02
4,8,12-Me 13:0	0,20	±	0,04	0,31	±	0,13
∑pristanic	0,00	±	0,00	0,00	±	0,00
∑phytanic	0,00	±	0,00	0,00	±	0,00
Forgrenet 17:1	0,03	±	0,01	0,03	±	0,01
16:1 n-10, 7Me	0,18	±	0,03	0,33	±	0,07
∑SFA	22,93	±	1,08	20,48	±	3,10
14:1 (n-7)	0,02	±	0,01	0,00	±	0,00
14:1 (n-5)	0,04	±	0,01	0,05	±	0,02
15:1 n-x	0,01	±	0,01	0,02	±	0,01
15:1 (n-5)	0,00	±	0,00	0,02	±	0,01
16:1 (n-11)	0,05	±	0,02	0,29	±	0,15
16:1 (n-9)	0,17	±	0,02	0,33	±	0,12
16:1 (n-7)	2,86	±	0,64	3,13	±	0,60
16:1 (n-5)	0,27	±	0,03	0,23	±	0,07
17:1 (n-10)	0,04	±	0,01	0,04	±	0,01
17:1 (n-8)	0,20	±	0,04	0,47	±	0,10
17:1 (n-7)	0,02	±	0,01	0,02	±	0,01
17:1 (n-6)	0,03	±	0,01	0,04	±	0,01
17:1 (n-4)	0,04	±	0,03	0,03	±	0,01
18:1 (n-11)	0,45	±	0,08	2,12	±	0,51
18:1 (n-9)	4,02	±	0,54	10,46	±	2,72
18:1 (n-7)	1,07	±	0,19	2,39	±	0,28
18:1 (n-5)	0,27	±	0,07	0,43	±	0,04
18:1 (n-4)	0,04	±	0,01	0,05	±	0,01
19:1 (n-x2)	0,06	±	0,00	0,14	±	0,03
20:1 (n-11)	1,07	±	0,24	2,07	±	1,15
20:1 (n-9)	8,38	±	1,91	5,05	±	1,45
20:1 (n-7)	0,12	±	0,02	0,13	±	0,04
20:1 (n-5)	0,05	±	0,01	0,07	±	0,02
22:1 (n-11)	18,63	±	4,81	4,61	±	1,80
22:1 (n-9)	0,74	±	0,15	0,38	±	0,14
22:1 (n-7)	0,13	±	0,03	0,08	±	0,02
24:1 (n-9)	0,97	±	0,15	0,88	±	0,19
24:1 (n-7)	0,14	±	0,05	0,14	±	0,05
∑MUFA	39,89	±	7,83	33,63	±	5,16
16:4 (n-1)	0,46	±	0,12	0,15	±	0,07
18:4 (n-1)	0,11	±	0,02	0,16	±	0,05
18:5 (n-1)	0,01	±	0,01	0,00	±	0,00
16:2 (n-4)	0,36	±	0,08	0,19	±	0,07
16:3 (n-4)	0,19	±	0,06	0,06	±	0,03
18:2 (n-4)	0,10	±	0,02	0,16	±	0,04
16:2 (n-7)	0,05	±	0,01	0,03	±	0,01
18:2 (n-7)	0,04	±	0,01	0,08	±	0,01
16:2 (n-6)	0,03	±	0,01	0,03	±	0,01
18:2 (n-6)	1,20	±	0,30	1,42	±	0,24
18:3 (n-6)	0,04	±	0,03	0,08	±	0,02
20:2 (n-6)	0,20	±	0,06	0,30	±	0,09
20:3 (n-6)	0,05	±	0,01	0,08	±	0,02
20:4 (n-6)	0,58	±	0,29	0,81	±	0,25
22:2 (n-6)	0,17	±	0,27	0,03	±	0,02
22:4 (n-6)	0,04	±	0,01	0,08	±	0,05
22:5 (n-6)	0,22	±	0,02	0,32	±	0,05
16:4 (n-3)	0,01	±	0,01	0,04	±	0,03
18:3 (n-3)	0,90	±	0,29	1,08	±	0,27
18:4 (n-3)	2,85	±	1,20	2,14	±	0,67
18:5 (n-3)	0,00	±	0,00	0,00	±	0,00
20:3 (n-3)	0,16	±	0,05	0,19	±	0,06
20:4 (n-3)	0,52	±	0,14	1,64	±	0,58
20:5 (n-3)	7,88	±	1,30	11,32	±	1,32
21:5 (n-3)	0,35	±	0,08	0,52	±	0,17
22:3 (n-3)	0,00	±	0,00	0,00	±	0,00
22:4 (n-3)	0,11	±	0,03	0,08	±	0,07
22:5 (n-3)	0,77	±	0,07	1,67	±	0,44
22:6 (n-3)	18,77	±	6,83	21,73	±	3,74
24:5 (n-3)	0,35	±	0,28	0,51	±	0,10
24:6 (n-3)	0,08	±	0,05	0,17	±	0,08
20:2 D5,11 (NMI)	0,04	±	0,01	0,11	±	0,02
20:2 D5,13 (NMI)	0,00	±	0,01	0,00	±	0,01
20:3 D5,11,14 (NMI)	0,05	±	0,01	0,06	±	0,01
20:4 D5,11,14,17 (NMI)	0,00	±	0,01	0,02	±	0,01
22:2 D7,13 (NMI)	0,02	±	0,01	0,02	±	0,01
22:2 D7,15 (NMI)	0,01	±	0,01	0,03	±	0,01
22:2 NMI	0,01	±	0,00	0,02	±	0,01
∑PUFA	36,60	±	7,04	45,06	±	3,43
∑PUFA(n-6)	2,52	±	0,28	3,14	±	0,30
∑PUFA(n-3)	32,74	±	6,93	41,08	±	3,25
∑NMI	0,12	±	0,02	0,25	±	0,02
∑DMA	0,08	±	0,04	0,06	±	0,02
∑Chol	2,24	±	1,83	4,17	±	1,12
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3)	6,11	±	1,04	12,95	±	2,67
∑Odd-numbered SFA	1,43	±	0,24	1,97	±	0,16
∑Branched FA	0,94	±	0,24	1,49	±	0,09
∑Odd-numbered MUFA	0,57	±	0,11	0,58	±	0,10
16:1(n-7)/16:0	0,22	±	0,07	0,26	±	0,04
∑C16/ ∑C18	1,37	±	0,26	0,73	±	0,19
∑C16 PUFA (n-1+ n-7 + n-6)	1,11	±	0,28	0,49	±	0,17
∑C16 PUFA/ ∑C18 PUFA	0,24	±	0,09	0,10	±	0,03
20:5(n-3)/22:6(n-3)	0,44	±	0,08	0,54	±	0,13
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	11,20	±	0,98	14,60	±	1,66
18:3 (n-3) + 18:4 (n-3)	3,74	±	1,48	3,22	±	0,87
16:4 (n-3) + 18:5 (n-3)	0,01	±	0,01	0,04	±	0,03
22:5 (n-3) + 22:6 (n-3)	19,54	±	6,84	23,40	±	3,63
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	27,75	±	6,84	10,04	±	3,34
MUFA (n-11)	20,21	±	4,99	9,08	±	3,02
MUFA (n-9)	14,28	±	2,42	17,09	±	3,18
MUFA (n-7)	4,36	±	0,55	5,87	±	0,68

Table A.54: FA composition of Atlantic mackerel

Species	Atlantic mackerel					
Tissue	Muscle			Liver		
Population	10			9		
Amount of FA (mg/100 mg wet weight)	9,61	±	6,92	10,05	±	4,85
Amount of Chol (mg/100 mg wet weight)	0,06	±	0,02	0,30	±	0,05
14:0	5,78	±	2,02	1,24	±	0,43
Iso 15:0	0,23	±	0,06	0,07	±	0,03
Antiso 15:0	0,06	±	0,02	0,01	±	0,01
15:0	0,47	±	0,06	0,21	±	0,07
Iso 16:0	0,05	±	0,02	0,05	±	0,02
16:0	14,50	±	2,63	14,00	±	4,21
Iso 17:0	0,24	±	0,05	0,43	±	0,14
Antiso 17:0	0,07	±	0,01	0,13	±	0,05
17:0	0,34	±	0,06	0,25	±	0,08
iso 18:0	0,14	±	0,03	0,07	±	0,03
iso 18:0	0,08	±	0,05	0,16	±	0,05
18:0	2,96	±	1,32	3,20	±	0,77
iso 19:0	0,01	±	0,01	0,01	±	0,01
antiso 19:0	0,02	±	0,01	0,03	±	0,01
i-20:0	0,03	±	0,01	0,07	±	0,02
20:0	0,17	±	0,03	0,11	±	0,03
21:0	0,06	±	0,02	0,08	±	0,03
22:0	0,07	±	0,01	0,09	±	0,03
24:0	0,02	±	0,01	0,02	±	0,01
4,8,12-Me 13:0	0,16	±	0,05	0,20	±	0,10
∑pristanic	0,00	±	0,00	0,00	±	0,00
∑phytanic	0,00	±	0,00	0,00	±	0,00
Forgrenet 17:1	0,12	±	0,05	0,11	±	0,03
16:1 n-10, 7Me	0,26	±	0,10	0,26	±	0,07
∑SFA	25,31	±	1,99	20,23	±	4,32
14:1 (n-7)	0,03	±	0,01	0,01	±	0,01
14:1 (n-5)	0,05	±	0,02	0,01	±	0,00
15:1 n-x	0,04	±	0,02	0,01	±	0,01
15:1 (n-5)	0,01	±	0,00	0,00	±	0,00
16:1 (n-11)	0,05	±	0,02	0,08	±	0,03
16:1 (n-9)	0,24	±	0,04	0,33	±	0,07
16:1 (n-7)	2,87	±	0,67	2,06	±	0,59
16:1 (n-5)	0,27	±	0,04	0,17	±	0,05
17:1 (n-10)	0,03	±	0,01	0,02	±	0,01
17:1 (n-8)	0,26	±	0,07	0,48	±	0,13
17:1 (n-7)	0,05	±	0,01	0,02	±	0,01
17:1 (n-6)	0,06	±	0,01	0,04	±	0,02
17:1 (n-4)	0,06	±	0,04	0,02	±	0,01
18:1 (n-11)	0,35	±	0,10	1,59	±	0,90
18:1 (n-9)	8,16	±	4,49	19,54	±	7,26
18:1 (n-7)	1,89	±	0,78	5,05	±	1,49
18:1 (n-5)	0,32	±	0,05	0,37	±	0,09
18:1 (n-4)	0,06	±	0,02	0,04	±	0,02
19:1 (n-x2)	0,07	±	0,02	0,10	±	0,04
20:1 (n-11)	0,64	±	0,20	1,55	±	0,79
20:1 (n-9)	5,95	±	2,31	3,44	±	0,63
20:1 (n-7)	0,16	±	0,04	0,11	±	0,04
20:1 (n-5)	0,05	±	0,01	0,11	±	0,07
22:1 (n-11)	10,50	±	5,29	4,93	±	2,37
22:1 (n-9)	0,70	±	0,20	0,82	±	0,09
22:1 (n-7)	0,10	±	0,03	0,08	±	0,02
24:1 (n-9)	0,83	±	0,23	1,07	±	0,38
24:1 (n-7)	0,10	±	0,03	0,12	±	0,04
∑MUFA	33,87	±	7,16	42,18	±	6,47
16:4 (n-1)	0,29	±	0,16	0,04	±	0,03
18:4 (n-1)	0,10	±	0,03	0,09	±	0,04
18:5 (n-1)	0,01	±	0,01	0,01	±	0,01
16:2 (n-4)	0,24	±	0,10	0,04	±	0,02
16:3 (n-4)	0,10	±	0,07	0,01	±	0,01
18:2 (n-4)	0,16	±	0,03	0,18	±	0,07
16:2 (n-7)	0,05	±	0,01	0,01	±	0,01
18:2 (n-7)	0,06	±	0,01	0,09	±	0,03
16:2 (n-6)	0,02	±	0,01	0,01	±	0,01
18:2 (n-6)	1,55	±	0,25	1,07	±	0,36
18:3 (n-6)	0,13	±	0,06	0,04	±	0,03
20:2 (n-6)	0,30	±	0,04	0,35	±	0,12
20:3 (n-6)	0,07	±	0,02	0,12	±	0,04
20:4 (n-6)	0,71	±	0,40	1,12	±	0,23
22:2 (n-6)	0,02	±	0,01	0,02	±	0,01
22:4 (n-6)	0,14	±	0,04	0,08	±	0,05
22:5 (n-6)	0,43	±	0,16	0,36	±	0,12
16:4 (n-3)	0,11	±	0,05	0,03	±	0,02
18:3 (n-3)	1,31	±	0,37	0,74	±	0,33
18:4 (n-3)	4,54	±	2,00	1,02	±	0,59
18:5 (n-3)	0,00	±	0,00	0,00	±	0,00
20:3 (n-3)	0,26	±	0,05	0,28	±	0,11
20:4 (n-3)	1,01	±	0,17	2,52	±	1,09
20:5 (n-3)	7,28	±	0,84	7,93	±	2,50
21:5 (n-3)	0,57	±	0,11	0,48	±	0,19
22:3 (n-3)	0,00	±	0,00	0,00	±	0,00
22:4 (n-3)	0,12	±	0,04	0,19	±	0,08
22:5 (n-3)	1,27	±	0,30	3,75	±	1,13
22:6 (n-3)	18,67	±	7,49	15,90	±	3,48
24:5 (n-3)	0,52	±	0,25	0,27	±	0,16
24:6 (n-3)	0,17	±	0,06	0,11	±	0,04
20:2 D5,11 (NMI)	0,08	±	0,03	0,20	±	0,10
20:2 D5,13 (NMI)	0,00	±	0,01	0,00	±	0,00
20:3 D5,11,14 (NMI)	0,22	±	0,09	0,01	±	0,01
20:4 D5,11,14,17 (NMI)	0,02	±	0,01	0,01	±	0,01
22:2 D7,13 (NMI)	0,02	±	0,02	0,00	±	0,01
22:2 D7,15 (NMI)	0,01	±	0,01	0,01	±	0,01
22:2 NMI	0,01	±	0,01	0,02	±	0,03
∑PUFA	40,20	±	6,36	36,86	±	8,46
∑PUFA(n-6)	3,37	±	0,54	3,16	±	0,71
∑PUFA(n-3)	35,81	±	6,07	33,24	±	7,67
∑NMI	0,35	±	0,08	0,23	±	0,09
∑DMA	0,28	±	0,04	0,20	±	0,03
∑Chol	1,80	±	2,18	3,74	±	2,05
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3)	11,02	±	4,21	21,35	±	6,75
∑Odd-numbered SFA	1,85	±	0,20	1,65	±	0,45
∑Branched FA	1,21	±	0,23	1,24	±	0,36
∑Odd-numbered MUFA	0,74	±	0,15	0,60	±	0,07
16:1(n-7)/16:0	0,21	±	0,07	0,15	±	0,03
∑C16/ ∑C18	0,87	±	0,16	0,51	±	0,11
∑C16 PUFA (n-1+ n-7 + n-6)	0,82	±	0,39	0,14	±	0,07
∑C16 PUFA/ ∑C18 PUFA	0,10	±	0,03	0,05	±	0,01
20:5(n-3)/22:6(n-3)	0,43	±	0,12	0,50	±	0,10
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)	10,44	±	1,07	10,03	±	2,06
18:3 (n-3) + 18:4 (n-3)	5,85	±	2,35	1,77	±	0,89
16:4 (n-3) + 18:5 (n-3)	0,11	±	0,05	0,03	±	0,02
22:5 (n-3) + 22:6 (n-3)	19,94	±	7,63	19,64	±	3,93
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)	17,15	±	7,74	9,19	±	2,88
MUFA (n-11)	11,54	±	5,50	8,15	±	3,94
MUFA (n-9)	15,87	±	3,93	25,20	±	7,11
MUFA (n-7)	5,19	±	1,07	7,46	±	1,99

Table A.55: FA composition of four bearded rockling.

Species	Four-bearded rockling				
Tissue	Muscle		Liver		
Population			2		
Amount of FA (mg/100 mg wet weight)		±	11,71	±	2,13
Amount of Chol (mg/100 mg wet weight)		±	0,29	±	0,06
14:0		±	1,61	±	0,38
Iso 15:0		±	0,22	±	0,06
Antiso 15:0		±	0,04	±	0,02
15:0		±	0,83	±	0,08
Iso 16:0		±	0,29	±	0,01
16:0		±	13,42	±	0,04
Iso 17:0		±	0,77	±	0,01
Antiso 17:0		±	0,16	±	0,17
17:0		±	0,78	±	0,04
iso 18:0		±	0,20	±	0,01
iso 18:0		±	0,11	±	0,01
18:0		±	2,82	±	0,41
iso 19:0		±	0,04	±	0,00
antiso 19:0		±	0,00	±	0,00
i-20:0		±	0,05	±	0,01
20:0		±	0,08	±	0,01
21:0		±	0,02	±	0,03
22:0		±	0,09	±	0,01
24:0		±	0,04	±	0,01
4,8,12-Me 13:0		±	0,04	±	0,01
∑pristanic		±	0,00	±	0,00
∑phytanic		±	0,00	±	0,00
Forgrenet 17:1		±	0,13	±	0,02
16:1 n-10, 7Me		±	0,20	±	0,02
∑SFA		±	21,56	±	0,12
14:1 (n-7)		±	0,03	±	0,00
14:1 (n-5)		±	0,03	±	0,01
15:1 n-x		±	0,03	±	0,00
15:1 (n-5)		±	0,01	±	0,00
16:1 (n-11)		±	0,37	±	0,46
16:1 (n-9)		±	2,97	±	3,19
16:1 (n-7)		±	2,33	±	3,22
16:1 (n-5)		±	0,25	±	0,02
17:1 (n-10)		±	0,16	±	0,05
17:1 (n-8)		±	0,93	±	0,09
17:1 (n-7)		±	0,06	±	0,00
17:1 (n-6)		±	0,07	±	0,00
17:1 (n-4)		±	0,05	±	0,01
18:1 (n-11)		±	0,37	±	0,13
18:1 (n-9)		±	11,30	±	1,11
18:1 (n-7)		±	6,22	±	0,18
18:1 (n-5)		±	0,56	±	0,02
18:1 (n-4)		±	0,08	±	0,00
19:1 (n-x2)		±	0,12	±	0,03
20:1 (n-11)		±	0,44	±	0,02
20:1 (n-9)		±	1,06	±	0,00
20:1 (n-7)		±	0,81	±	0,00
20:1 (n-5)		±	0,04	±	0,03
22:1 (n-11)		±	0,13	±	0,01
22:1 (n-9)		±	0,12	±	0,09
22:1 (n-7)		±	0,12	±	0,00
24:1 (n-9)		±	0,31	±	0,22
24:1 (n-7)		±	0,10	±	0,05
∑MUFA		±	29,07	±	1,05
16:4 (n-1)		±	0,02	±	0,02
18:4 (n-1)		±	0,06	±	0,00
18:5 (n-1)		±	0,00	±	0,00
16:2 (n-4)		±	0,15	±	0,03
16:3 (n-4)		±	0,03	±	0,03
18:2 (n-4)		±	0,01	±	0,01
16:2 (n-7)		±	0,04	±	0,04
18:2 (n-7)		±	0,16	±	0,01
16:2 (n-6)		±	0,18	±	0,15
18:2 (n-6)		±	1,19	±	0,02
18:3 (n-6)		±	0,24	±	0,01
20:2 (n-6)		±	0,62	±	0,02
20:3 (n-6)		±	0,08	±	0,00
20:4 (n-6)		±	2,48	±	0,03
22:2 (n-6)		±	0,03	±	0,00
22:4 (n-6)		±	0,47	±	0,08
22:5 (n-6)		±	0,29	±	0,00
16:4 (n-3)		±	0,02	±	0,00
18:3 (n-3)		±	0,47	±	0,01
18:4 (n-3)		±	0,75	±	0,07
18:5 (n-3)		±	0,01	±	0,01
20:3 (n-3)		±	0,30	±	0,01
20:4 (n-3)		±	0,68	±	0,01
20:5 (n-3)		±	19,37	±	0,07
21:5 (n-3)		±	0,45	±	0,06
22:3 (n-3)		±	0,01	±	0,01
22:4 (n-3)		±	0,05	±	0,01
22:5 (n-3)		±	2,25	±	0,08
22:6 (n-3)		±	18,07	±	0,43
24:5 (n-3)		±	0,16	±	0,16
24:6 (n-3)		±	0,25	±	0,03
20:2 D5,11 (NMI)		±	0,14	±	0,03
20:2 D5,13 (NMI)		±	0,01	±	0,01
20:3 D5,11,14 (NMI)		±	0,02	±	0,02
20:4 D5,11,14,17 (NMI)		±	0,01	±	0,01
22:2 D7,13 (NMI)		±	0,06	±	0,01
22:2 D7,15 (NMI)		±	0,02	±	0,00
22:2 NMI		±	0,03	±	0,02
∑PUFA		±	48,88	±	1,07
∑PUFA(n-6)		±	5,57	±	0,18
∑PUFA(n-3)		±	42,86	±	0,88
∑NMI		±	0,30	±	0,06
∑DMA		±	0,13	±	0,02
∑Chol		±	2,44	±	0,07
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3)		±	12,96	±	1,14
∑Odd-numbered SFA		±	4,02	±	0,07
∑Branched FA		±	1,83	±	0,07
∑Odd-numbered MUFA		±	0,59	±	0,04
16:1(n-7)/16:0		±	0,17	±	0,24
∑C16/ ∑C18		±	0,81	±	0,08
∑C16 PUFA (n-1 + n-7 + n-6)		±	0,43	±	0,17
∑C16 PUFA/ ∑C18 PUFA		±	0,16	±	0,06
20:5(n-3)/22:6(n-3)		±	1,07	±	0,02
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)		±	21,72	±	3,17
18:3 (n-3) + 18:4 (n-3)		±	1,22	±	0,06
16:4 (n-3) + 18:5 (n-3)		±	0,03	±	0,01
22:5 (n-3) + 22:6 (n-3)		±	20,33	±	0,52
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)		±	1,30	±	0,08
MUFA (n-11)		±	1,32	±	0,62
MUFA (n-9)		±	15,76	±	1,78
MUFA (n-7)		±	9,67	±	3,44

Table A.56: FA composition of greater fork beard.

Species	Phycis blennoides				
Tissue	Muscle		Liver		
Population			1		
Amount of FA (mg/100 mg wet weight)		±	4,49	±	
Amount of Chol (mg/100 mg wet weight)		±	0,35	±	
14:0		±	2,06	±	
Iso 15:0		±	0,27	±	
Antiso 15:0		±	0,01	±	
15:0		±	0,66	±	
Iso 16:0		±	0,26	±	
16:0		±	13,64	±	
Iso 17:0		±	0,93	±	
Antiso 17:0		±	0,39	±	
17:0		±	0,87	±	
iso 18:0		±	0,36	±	
iso 18:0		±	0,09	±	
18:0		±	4,56	±	
iso 19:0		±	0,07	±	
antiso 19:0		±	0,06	±	
i-20:0		±	0,00	±	
20:0		±	0,12	±	
21:0		±	0,03	±	
22:0		±	0,13	±	
24:0		±	0,03	±	
4,8,12-Me 13:0		±	0,08	±	
∑pristanic		±	0,00	±	
∑phytanic		±	0,00	±	
Forgrenet 17:1		±	0,05	±	
16:1 n-10, 7Me		±	0,20	±	
∑SFA		±	24,55	±	
14:1 (n-7)		±	0,00	±	
14:1 (n-5)		±	0,02	±	
15:1 n-x		±	0,00	±	
15:1 (n-5)		±	0,01	±	
16:1 (n-11)		±	0,07	±	
16:1 (n-9)		±	0,42	±	
16:1 (n-7)		±	3,80	±	
16:1 (n-5)		±	0,23	±	
17:1 (n-10)		±	0,08	±	
17:1 (n-8)		±	0,86	±	
17:1 (n-7)		±	0,05	±	
17:1 (n-6)		±	0,08	±	
17:1 (n-4)		±	0,04	±	
18:1 (n-11)		±	1,22	±	
18:1 (n-9)		±	11,10	±	
18:1 (n-7)		±	6,89	±	
18:1 (n-5)		±	0,65	±	
18:1 (n-4)		±	0,01	±	
19:1 (n-x2)		±	0,00	±	
20:1 (n-11)		±	1,85	±	
20:1 (n-9)		±	1,89	±	
20:1 (n-7)		±	1,42	±	
20:1 (n-5)		±	0,12	±	
22:1 (n-11)		±	1,13	±	
22:1 (n-9)		±	0,28	±	
22:1 (n-7)		±	0,34	±	
24:1 (n-9)		±	1,47	±	
24:1 (n-7)		±	0,14	±	
∑MUFA		±	34,18	±	
16:4 (n-1)		±	0,03	±	
18:4 (n-1)		±	0,04	±	
18:5 (n-1)		±	0,00	±	
16:2 (n-4)		±	0,08	±	
16:3 (n-4)		±	0,01	±	
18:2 (n-4)		±	0,19	±	
16:2 (n-7)		±	0,00	±	
18:2 (n-7)		±	0,09	±	
16:2 (n-6)		±	0,01	±	
18:2 (n-6)		±	1,00	±	
18:3 (n-6)		±	0,03	±	
20:2 (n-6)		±	0,79	±	
20:3 (n-6)		±	0,07	±	
20:4 (n-6)		±	4,00	±	
22:2 (n-6)		±	0,06	±	
22:4 (n-6)		±	0,81	±	
22:5 (n-6)		±	0,35	±	
16:4 (n-3)		±	0,00	±	
18:3 (n-3)		±	0,31	±	
18:4 (n-3)		±	0,27	±	
18:5 (n-3)		±	0,03	±	
20:3 (n-3)		±	0,30	±	
20:4 (n-3)		±	0,43	±	
20:5 (n-3)		±	10,79	±	
21:5 (n-3)		±	0,31	±	
22:3 (n-3)		±	0,01	±	
22:4 (n-3)		±	0,03	±	
22:5 (n-3)		±	2,60	±	
22:6 (n-3)		±	17,71	±	
24:5 (n-3)		±	0,14	±	
24:6 (n-3)		±	0,16	±	
20:2 D5,11 (NMI)		±	0,22	±	
20:2 D5,13 (NMI)		±	0,00	±	
20:3 D5,11,14 (NMI)		±	0,00	±	
20:4 D5,11,14,17 (NMI)		±	0,05	±	
22:2 D7,13 (NMI)		±	0,31	±	
22:2 D7,15 (NMI)		±	0,16	±	
22:2 NMI		±	0,08	±	
∑PUFA		±	40,65	±	
∑PUFA(n-6)		±	7,14	±	
∑PUFA(n-3)		±	33,07	±	
∑NMI		±	0,82	±	
∑DMA		±		±	
∑Chol		±	7,70	±	
Terrestrial FATM (18:1 (n-9)+ 18:2 (n-3) + 18:3 (n-3)		±	12,40	±	
∑Odd-numbered SFA		±	4,15	±	
∑Branched FA		±	2,30	±	
∑Odd-numbered MUFA		±	0,53	±	
16:1(n-7)/16:0		±	0,28	±	
∑C16/ ∑C18		±	0,68	±	
∑C16 PUFA (n-1 + n-7 + n-6)		±	0,14	±	
∑C16 PUFA/ ∑C18 PUFA		±	0,07	±	
20:5(n-3)/22:6(n-3)		±	0,61	±	
16:1 (n-7)+16:4 (n-1)+20:5 (n-3)		±	14,63	±	
18:3 (n-3) + 18:4 (n-3)		±	0,57	±	
16:4 (n-3) + 18:5 (n-3)		±	0,03	±	
22:5 (n-3) + 22:6 (n-3)		±	20,31	±	
20:1 (n-9)+22:1 (n-11)+22:1 (n-9)		±	3,30	±	
MUFA (n-11)		±	4,28	±	
MUFA (n-9)		±	15,16	±	
MUFA (n-7)		±	12,64	±	

FA compositions of results from the bachelor projects:

Table A.57: FA composition of whiting

Whiting	Muscle (n=10)	Liver (n=10)
Amount FA (% of wet weight	0,5 ± 0,1	39,8 ± 13,4
14:0	0,95 ± 0,18	5,28 ± 1,00
Iso 15:0	0,03 ± 0,01	0,25 ± 0,05
Antiso 15:0	0,00 ± 0,00	0,03 ± 0,01
15:0	0,22 ± 0,03	0,49 ± 0,11
Iso 16:0	0,01 ± 0,01	0,11 ± 0,02
16:0	17,93 ± 0,99	12,05 ± 0,69
Iso 17:0	0,11 ± 0,02	0,34 ± 0,08
Antiso 17:0	0,04 ± 0,01	0,12 ± 0,03
17:0	0,23 ± 0,02	0,23 ± 0,08
18:0	5,07 ± 0,31	2,42 ± 0,64
20:0	0,04 ± 0,01	0,08 ± 0,02
∑SFA	24,65 ± 1,08	21,42 ± 1,44
14:1 (n-7)	0,01 ± 0,00	0,03 ± 0,02
14:1 (n-5)	0,04 ± 0,02	0,05 ± 0,02
16:1 (n-11)	0,09 ± 0,02	0,24 ± 0,06
16:1 (n-9)	0,20 ± 0,02	0,45 ± 0,13
16:1 (n-7)	0,79 ± 0,14	4,05 ± 0,93
16:1 (n-5)	0,21 ± 0,03	0,22 ± 0,03
17:1 (n-8)	0,13 ± 0,02	0,32 ± 0,04
17:1 (n-4)	0,01 ± 0,01	0,02 ± 0,02
18:1 (n-11)	1,46 ± 0,37	3,71 ± 0,75
18:1 (n-9)	4,48 ± 0,45	8,06 ± 1,44
18:1 (n-7)	1,38 ± 0,15	2,02 ± 0,25
18:1 (n-5)	0,14 ± 0,03	0,26 ± 0,08
20:1 (n-11)	0,69 ± 0,08	2,63 ± 0,40
20:1 (n-9)	2,31 ± 0,37	9,81 ± 1,62
20:1 (n-7)	0,04 ± 0,03	0,21 ± 0,18
22:1 (n-11)	0,97 ± 0,27	11,10 ± 2,58
22:1 (n-9)	0,14 ± 0,02	0,78 ± 0,23
22:1 (n-7)	0,03 ± 0,01	0,07 ± 0,02
24:1 (n-9)	1,24 ± 0,19	0,77 ± 0,31
∑MUFA	14,37 ± 1,37	44,78 ± 3,34
16:4 (n-1)	0,03 ± 0,02	0,29 ± 0,13
18:4 (n-1)	0,03 ± 0,02	0,15 ± 0,04
18:5 (n-1)	0,01 ± 0,01	0,06 ± 0,03
16:2 (n-4)	0,06 ± 0,02	0,42 ± 0,11
16:3 (n-4)	0,02 ± 0,01	0,24 ± 0,11
18:2 (n-4)	0,08 ± 0,02	0,20 ± 0,03
16:2 (n-7)	0,02 ± 0,01	0,08 ± 0,04
18:2 (n-7)	0,01 ± 0,01	0,04 ± 0,01
16:2 (n-6)	0,01 ± 0,01	0,04 ± 0,02
18:2 (n-6)	0,69 ± 0,15	1,44 ± 0,22
18:3 (n-6)	0,03 ± 0,01	0,11 ± 0,04
20:2 (n-6)	0,16 ± 0,02	0,30 ± 0,07
20:3 (n-6)	0,05 ± 0,01	0,06 ± 0,01
20:4 (n-6)	1,53 ± 0,42	0,56 ± 0,34
22:4 (n-6)	0,14 ± 0,03	0,49 ± 0,29
22:5 (n-6)	0,62 ± 0,11	0,25 ± 0,07
16:4 (n-3)	0,00 ± 0,00	0,05 ± 0,02
18:3 (n-3)	0,27 ± 0,06	1,03 ± 0,20
18:4 (n-3)	0,49 ± 0,19	2,35 ± 0,84
20:3 (n-3)	0,09 ± 0,02	0,21 ± 0,03
20:4 (n-3)	0,44 ± 0,05	0,93 ± 0,11
20:5 (n-3)	9,21 ± 1,01	7,37 ± 1,55
21:5 (n-3)	0,17 ± 0,05	0,38 ± 0,15
22:5 (n-3)	1,51 ± 0,13	2,10 ± 0,49
22:6 (n-3)	44,64 ± 2,69	13,31 ± 3,39
24:5 (n-3)	0,49 ± 0,09	0,52 ± 0,15
24:6 (n-3)	0,06 ± 0,04	0,20 ± 0,06
∑PUFA	60,88 ± 1,46	33,19 ± 4,05
∑(n-6)PUFA	3,23 ± 0,54	3,25 ± 0,51
∑(n-3)PUFA	57,38 ± 1,67	28,45 ± 4,34
(n-3)/(N-6)	18,20 ± 3,00	9,00 ± 2,21
∑Chol	7,40 ± 0,67	1,29 ± 1,39

Table A.58: FA composition of silvery pout.

Silvery pout	Muscle (n=2)	Liver (n=10)
Amount FA (% of wet weight	0,8 ± 0,2	59,0 ± 7,7
14:0	2,24 ± 0,36	5,05 ± 0,27
Iso 15:0	0,11 ± 0,02	0,24 ± 0,03
Antiso 15:0	0,02 ± 0,00	0,05 ± 0,01
15:0	0,40 ± 0,01	0,35 ± 0,01
Iso 16:0	0,13 ± 0,03	0,08 ± 0,01
16:0	19,01 ± 0,17	11,07 ± 0,96
Iso 17:0	0,50 ± 0,11	0,20 ± 0,03
Antiso 17:0	0,17 ± 0,01	0,08 ± 0,02
17:0	0,34 ± 0,02	0,17 ± 0,01
18:0	4,04 ± 0,06	1,79 ± 0,28
20:0	0,11 ± 0,07	0,16 ± 0,01
∑SFA	27,08 ± 0,40	19,25 ± 1,28
14:1 (n-7)	0,01 ± 0,00	0,02 ± 0,01
14:1 (n-5)	0,02 ± 0,01	0,05 ± 0,01
16:1 (n-11)	0,28 ± 0,09	0,03 ± 0,00
16:1 (n-9)	0,30 ± 0,00	0,17 ± 0,02
16:1 (n-7)	2,34 ± 0,43	2,86 ± 0,21
16:1 (n-5)	0,19 ± 0,05	0,28 ± 0,03
17:1 (n-8)	0,43 ± 0,01	0,21 ± 0,01
17:1 (n-4)	0,02 ± 0,01	0,12 ± 0,01
18:1 (n-11)	0,61 ± 0,07	0,48 ± 0,06
18:1 (n-9)	9,66 ± 1,16	5,65 ± 1,00
18:1 (n-7)	2,23 ± 0,05	0,93 ± 0,08
18:1 (n-5)	0,28 ± 0,00	0,59 ± 0,06
20:1 (n-11)	0,55 ± 0,14	1,45 ± 0,09
20:1 (n-9)	1,61 ± 0,44	11,34 ± 0,73
20:1 (n-7)	0,48 ± 0,06	0,14 ± 0,01
22:1 (n-11)	1,55 ± 0,69	23,27 ± 2,31
22:1 (n-9)	0,72 ± 0,16	1,15 ± 0,12
22:1 (n-7)	0,12 ± 0,01	0,10 ± 0,01
24:1 (n-9)	1,62 ± 0,00	0,98 ± 0,14
∑MUFA	23,02 ± 2,85	49,83 ± 1,85
16:4 (n-1)	0,04 ± 0,03	0,28 ± 0,09
18:4 (n-1)	0,06 ± 0,00	0,08 ± 0,02
18:5 (n-1)	0,02 ± 0,00	0,02 ± 0,01
16:2 (n-4)	0,08 ± 0,00	0,31 ± 0,06
16:3 (n-4)	0,02 ± 0,00	0,17 ± 0,05
18:2 (n-4)	0,11 ± 0,00	0,10 ± 0,02
16:2 (n-7)	0,03 ± 0,00	0,05 ± 0,01
18:2 (n-7)	0,05 ± 0,00	0,06 ± 0,01
16:2 (n-6)	0,01 ± 0,00	0,02 ± 0,00
18:2 (n-6)	0,87 ± 0,19	2,23 ± 0,20
18:3 (n-6)	0,02 ± 0,00	0,10 ± 0,01
20:2 (n-6)	0,22 ± 0,00	0,33 ± 0,02
20:3 (n-6)	0,08 ± 0,03	0,03 ± 0,00
20:4 (n-6)	3,01 ± 0,55	0,28 ± 0,02
22:4 (n-6)	0,90 ± 0,29	0,13 ± 0,03
22:5 (n-6)	0,70 ± 0,07	0,12 ± 0,01
16:4 (n-3)	0,03 ± 0,01	0,07 ± 0,01
18:3 (n-3)	0,45 ± 0,05	1,44 ± 0,07
18:4 (n-3)	0,52 ± 0,02	4,92 ± 0,19
20:3 (n-3)	0,13 ± 0,03	0,23 ± 0,02
20:4 (n-3)	0,69 ± 0,07	0,83 ± 0,08
20:5 (n-3)	11,72 ± 1,88	5,62 ± 0,47
21:5 (n-3)	0,21 ± 0,03	0,42 ± 0,04
22:5 (n-3)	2,58 ± 0,01	0,88 ± 0,07
22:6 (n-3)	26,67 ± 2,09	10,91 ± 0,39
24:5 (n-3)	0,21 ± 0,07	0,71 ± 0,05
24:6 (n-3)	0,41 ± 0,27	0,23 ± 0,02
∑PUFA	49,83 ± 3,24	30,58 ± 0,73
∑(n-6)PUFA	5,81 ± 0,56	3,24 ± 0,22
∑(n-3)PUFA	43,61 ± 3,83	26,26 ± 0,72
(n-3)/(N-6)	7,57 ± 1,38	8,14 ± 0,74
∑Chol	12,82 ± 3,36	0,21 ± 0,05

Table A.59: FA composition of Norway pout.

Norway pout	Muscle (n=10)	Liver (n=10)
Amount FA (% of wet weigh	0,7 ± 0,1	70,8 ± 5,4
14:0	1,90 ± 0,21	5,77 ± 0,32
Iso 15:0	0,07 ± 0,01	0,21 ± 0,03
Antiso 15:0	0,02 ± 0,00	0,04 ± 0,01
15:0	0,25 ± 0,01	0,33 ± 0,04
Iso 16:0	0,03 ± 0,00	0,07 ± 0,01
16:0	19,08 ± 0,86	11,04 ± 0,89
Iso 17:0	0,12 ± 0,02	0,17 ± 0,02
Antiso 17:0	0,05 ± 0,01	0,08 ± 0,01
17:0	0,22 ± 0,02	0,17 ± 0,03
18:0	3,39 ± 0,22	1,90 ± 0,33
20:0	0,05 ± 0,01	0,14 ± 0,02
∑SFA	25,17 ± 0,80	19,83 ± 1,13
14:1 (n-7)	0,01 ± 0,00	0,02 ± 0,00
14:1 (n-5)	0,05 ± 0,03	0,05 ± 0,01
16:1 (n-11)	0,10 ± 0,02	0,12 ± 0,02
16:1 (n-9)	0,22 ± 0,03	0,18 ± 0,03
16:1 (n-7)	1,20 ± 0,21	4,07 ± 0,58
16:1 (n-5)	0,27 ± 0,03	0,23 ± 0,02
17:1 (n-8)	0,12 ± 0,02	0,18 ± 0,02
17:1 (n-4)	0,04 ± 0,01	0,06 ± 0,02
18:1 (n-11)	0,97 ± 0,13	1,48 ± 0,30
18:1 (n-9)	3,80 ± 0,38	4,81 ± 0,60
18:1 (n-7)	1,23 ± 0,09	1,38 ± 0,19
18:1 (n-5)	0,23 ± 0,02	0,38 ± 0,05
20:1 (n-11)	0,67 ± 0,11	1,88 ± 0,25
20:1 (n-9)	3,17 ± 0,84	12,67 ± 1,75
20:1 (n-7)	0,04 ± 0,01	0,16 ± 0,01
22:1 (n-11)	3,33 ± 1,26	16,37 ± 2,21
22:1 (n-9)	0,29 ± 0,07	0,88 ± 0,08
22:1 (n-7)	0,04 ± 0,01	0,10 ± 0,01
24:1 (n-9)	1,30 ± 0,22	0,59 ± 0,07
∑MUFA	17,08 ± 2,58	45,60 ± 2,70
16:4 (n-1)	0,12 ± 0,04	0,88 ± 0,29
18:4 (n-1)	0,07 ± 0,01	0,22 ± 0,04
18:5 (n-1)	0,05 ± 0,03	0,24 ± 0,13
16:2 (n-4)	0,14 ± 0,04	0,67 ± 0,12
16:3 (n-4)	0,07 ± 0,03	0,50 ± 0,12
18:2 (n-4)	0,12 ± 0,02	0,25 ± 0,03
16:2 (n-7)	0,05 ± 0,02	0,12 ± 0,02
18:2 (n-7)	0,03 ± 0,01	0,06 ± 0,01
16:2 (n-6)	0,01 ± 0,01	0,04 ± 0,01
18:2 (n-6)	1,09 ± 0,15	1,38 ± 0,16
18:3 (n-6)	0,05 ± 0,01	0,12 ± 0,01
20:2 (n-6)	0,17 ± 0,02	0,25 ± 0,04
20:3 (n-6)	0,05 ± 0,01	0,04 ± 0,01
20:4 (n-6)	0,82 ± 0,10	0,30 ± 0,05
22:4 (n-6)	0,15 ± 0,03	0,11 ± 0,02
22:5 (n-6)	0,48 ± 0,05	0,11 ± 0,02
16:4 (n-3)	0,02 ± 0,01	0,10 ± 0,02
18:3 (n-3)	0,47 ± 0,07	1,14 ± 0,27
18:4 (n-3)	1,46 ± 0,20	4,76 ± 1,07
20:3 (n-3)	0,10 ± 0,01	0,19 ± 0,04
20:4 (n-3)	0,55 ± 0,04	0,75 ± 0,11
20:5 (n-3)	9,97 ± 0,79	8,93 ± 1,61
21:5 (n-3)	0,40 ± 0,02	0,62 ± 0,06
22:5 (n-3)	1,60 ± 0,22	1,00 ± 0,13
22:6 (n-3)	38,53 ± 1,99	10,52 ± 1,05
24:5 (n-3)	0,76 ± 0,16	0,62 ± 0,05
24:6 (n-3)	0,13 ± 0,04	0,10 ± 0,07
∑PUFA	57,46 ± 2,01	34,01 ± 1,87
∑(n-6)PUFA	2,83 ± 0,27	2,34 ± 0,25
∑(n-3)PUFA	53,98 ± 2,01	28,73 ± 1,80
(n-3)/(N-6)	19,23 ± 1,81	12,35 ± 1,08
∑Chol	7,48 ± 0,74	0,24 ± 0,04

Table A.60: FA composition of European hake.

European hake	Muscle (n=10)	Liver (n=10)
Amount FA (% of wet weigh	0,8 ± 0,3	36,1 ± 10,8
14:0	2,95 ± 0,56	6,87 ± 0,52
Iso 15:0	0,12 ± 0,03	0,34 ± 0,05
Antiso 15:0	0,04 ± 0,01	0,09 ± 0,01
15:0	0,37 ± 0,03	0,61 ± 0,05
Iso 16:0	0,05 ± 0,01	0,12 ± 0,02
16:0	16,25 ± 1,22	14,28 ± 0,94
Iso 17:0	0,31 ± 0,07	0,33 ± 0,08
Antiso 17:0	0,10 ± 0,01	0,16 ± 0,03
17:0	0,21 ± 0,03	0,18 ± 0,02
18:0	3,47 ± 0,69	1,33 ± 0,16
20:0	0,13 ± 0,04	0,10 ± 0,03
∑SFA	23,98 ± 1,73	24,33 ± 1,34
14:1 (n-7)	0,02 ± 0,01	0,02 ± 0,01
14:1 (n-5)	0,03 ± 0,02	0,06 ± 0,01
16:1 (n-11)	0,20 ± 0,04	0,13 ± 0,03
16:1 (n-9)	0,27 ± 0,02	0,31 ± 0,04
16:1 (n-7)	2,94 ± 0,20	5,18 ± 0,53
16:1 (n-5)	0,22 ± 0,03	0,28 ± 0,03
17:1 (n-8)	0,25 ± 0,04	0,29 ± 0,04
17:1 (n-4)	0,01 ± 0,00	0,02 ± 0,01
18:1 (n-11)	1,61 ± 0,18	2,74 ± 0,74
18:1 (n-9)	7,30 ± 1,71	7,25 ± 1,76
18:1 (n-7)	1,74 ± 0,28	1,82 ± 0,26
18:1 (n-5)	0,21 ± 0,03	0,33 ± 0,05
20:1 (n-11)	2,10 ± 0,41	3,10 ± 0,57
20:1 (n-9)	7,31 ± 1,52	11,30 ± 1,38
20:1 (n-7)	0,13 ± 0,03	0,24 ± 0,03
22:1 (n-11)	8,68 ± 2,74	10,83 ± 2,49
22:1 (n-9)	0,76 ± 0,22	0,94 ± 0,19
22:1 (n-7)	0,08 ± 0,02	0,08 ± 0,02
24:1 (n-9)	1,81 ± 0,20	0,91 ± 0,17
∑MUFA	35,65 ± 6,35	45,83 ± 3,00
16:4 (n-1)	0,06 ± 0,02	0,14 ± 0,05
18:4 (n-1)	0,05 ± 0,01	0,11 ± 0,02
18:5 (n-1)	0,04 ± 0,01	0,06 ± 0,03
16:2 (n-4)	0,18 ± 0,03	0,39 ± 0,08
16:3 (n-4)	0,06 ± 0,02	0,11 ± 0,04
18:2 (n-4)	0,08 ± 0,02	0,13 ± 0,03
16:2 (n-7)	0,08 ± 0,01	0,06 ± 0,01
18:2 (n-7)	0,03 ± 0,00	0,04 ± 0,01
16:2 (n-6)	0,03 ± 0,00	0,05 ± 0,01
18:2 (n-6)	1,08 ± 0,15	1,75 ± 0,33
18:3 (n-6)	0,07 ± 0,01	0,13 ± 0,03
20:2 (n-6)	0,16 ± 0,04	0,34 ± 0,04
20:3 (n-6)	0,05 ± 0,01	0,09 ± 0,02
20:4 (n-6)	1,05 ± 0,13	0,62 ± 0,09
22:4 (n-6)	0,16 ± 0,05	0,32 ± 0,10
22:5 (n-6)	0,53 ± 0,08	0,36 ± 0,11
16:4 (n-3)	0,03 ± 0,01	0,05 ± 0,01
18:3 (n-3)	0,59 ± 0,09	1,13 ± 0,15
18:4 (n-3)	0,97 ± 0,13	1,95 ± 0,63
20:3 (n-3)	0,12 ± 0,03	0,22 ± 0,04
20:4 (n-3)	0,47 ± 0,05	0,75 ± 0,11
20:5 (n-3)	6,46 ± 0,73	4,79 ± 0,92
21:5 (n-3)	0,16 ± 0,03	0,27 ± 0,07
22:5 (n-3)	1,37 ± 0,11	1,62 ± 0,28
22:6 (n-3)	25,50 ± 4,75	13,17 ± 2,21
24:5 (n-3)	0,55 ± 0,12	0,40 ± 0,07
24:6 (n-3)	0,13 ± 0,03	0,11 ± 0,03
∑PUFA	40,08 ± 5,00	29,15 ± 3,91
∑(n-6)PUFA	3,14 ± 0,29	3,65 ± 0,52
∑(n-3)PUFA	36,35 ± 4,88	24,46 ± 3,54
(n-3)/(N-6)	11,64 ± 1,64	6,76 ± 0,89
∑Chol	4,85 ± 1,46	0,93 ± 0,49

Table A.61: FA composition of European plaice. | Table A.62: FA composition of saithe.

European plaice	Muscle (n=10)	Liver (n=10)
Amount FA (% of wet weigh	0,5 ± 0,1	8,7 ± 5,8
14:0	2,06 ± 0,19	4,53 ± 0,64
Iso 15:0	0,24 ± 0,12	0,27 ± 0,15
Antiso 15:0	0,12 ± 0,04	0,05 ± 0,03
15:0	0,78 ± 0,10	0,44 ± 0,14
Iso 16:0	0,20 ± 0,10	0,32 ± 0,16
16:0	15,68 ± 1,05	21,78 ± 2,83
Iso 17:0	0,54 ± 0,20	0,87 ± 0,48
Antiso 17:0	0,39 ± 0,17	0,63 ± 0,32
17:0	0,70 ± 0,08	0,24 ± 0,09
18:0	4,54 ± 0,32	1,82 ± 0,34
20:0	0,13 ± 0,02	0,09 ± 0,02
∑SFA	25,44 ± 0,67	30,98 ± 2,09
14:1 (n-7)	0,03 ± 0,03	0,03 ± 0,02
14:1 (n-5)	0,09 ± 0,06	0,42 ± 0,13
16:1 (n-11)	0,21 ± 0,03	0,12 ± 0,05
16:1 (n-9)	0,60 ± 0,10	0,61 ± 0,07
16:1 (n-7)	4,62 ± 0,60	17,34 ± 5,08
16:1 (n-5)	0,50 ± 0,17	0,26 ± 0,09
17:1 (n-8)	0,70 ± 0,14	0,99 ± 0,12
17:1 (n-4)	0,01 ± 0,00	0,00 ± 0,01
18:1 (n-11)	0,28 ± 0,18	0,31 ± 0,09
18:1 (n-9)	6,03 ± 1,13	17,08 ± 4,43
18:1 (n-7)	2,69 ± 0,50	4,27 ± 0,42
18:1 (n-5)	0,38 ± 0,14	0,52 ± 0,17
20:1 (n-11)	0,86 ± 0,24	0,69 ± 0,17
20:1 (n-9)	1,61 ± 0,15	2,57 ± 0,23
20:1 (n-7)	0,78 ± 0,17	1,29 ± 0,25
22:1 (n-11)	0,38 ± 0,13	0,37 ± 0,08
22:1 (n-9)	0,22 ± 0,03	0,52 ± 0,08
22:1 (n-7)	0,05 ± 0,02	0,23 ± 0,14
24:1 (n-9)	1,41 ± 0,29	0,81 ± 0,41
∑MUFA	21,46 ± 1,69	48,43 ± 8,40
16:4 (n-1)	0,08 ± 0,10	0,13 ± 0,04
18:4 (n-1)	0,05 ± 0,04	0,03 ± 0,02
18:5 (n-1)	0,02 ± 0,01	0,00 ± 0,00
16:2 (n-4)	0,12 ± 0,10	0,06 ± 0,05
16:3 (n-4)	0,07 ± 0,08	0,04 ± 0,04
18:2 (n-4)	0,17 ± 0,10	0,19 ± 0,11
16:2 (n-7)	0,07 ± 0,02	0,01 ± 0,01
18:2 (n-7)	0,04 ± 0,03	0,05 ± 0,03
16:2 (n-6)	0,03 ± 0,01	0,02 ± 0,01
18:2 (n-6)	0,46 ± 0,04	0,23 ± 0,05
18:3 (n-6)	0,02 ± 0,03	0,01 ± 0,01
20:2 (n-6)	0,29 ± 0,05	0,26 ± 0,08
20:3 (n-6)	0,12 ± 0,03	0,05 ± 0,03
20:4 (n-6)	5,84 ± 1,10	2,08 ± 0,98
22:4 (n-6)	2,03 ± 0,33	0,74 ± 0,22
22:5 (n-6)	0,80 ± 0,07	0,26 ± 0,12
16:4 (n-3)	0,06 ± 0,06	0,04 ± 0,05
18:3 (n-3)	0,13 ± 0,04	0,08 ± 0,02
18:4 (n-3)	0,17 ± 0,12	0,14 ± 0,08
20:3 (n-3)	0,09 ± 0,02	0,07 ± 0,03
20:4 (n-3)	0,26 ± 0,10	0,15 ± 0,10
20:5 (n-3)	18,45 ± 1,97	6,34 ± 2,83
21:5 (n-3)	0,34 ± 0,08	0,17 ± 0,09
22:5 (n-3)	4,80 ± 1,18	1,75 ± 0,97
22:6 (n-3)	18,14 ± 3,35	7,49 ± 3,65
24:5 (n-3)	0,16 ± 0,10	0,08 ± 0,07
24:6 (n-3)	0,19 ± 0,11	0,05 ± 0,04
∑PUFA	53,00 ± 1,81	20,52 ± 9,44
∑(n-6)PUFA	9,58 ± 1,26	3,65 ± 1,44
∑(n-3)PUFA	42,80 ± 2,07	16,35 ± 7,77
(n-3)/(N-6)	4,57 ± 0,87	4,36 ± 0,60
∑Chol	9,02 ± 0,69	7,22 ± 1,42

Saithe	Muscle (n=10)	Liver (n=10)
Amount FA (% of wet weigh	0,6 ± 0,1	70,1 ± 5,2
14:0	1,39 ± 0,35	4,33 ± 0,83
Iso 15:0	0,06 ± 0,02	0,18 ± 0,03
Antiso 15:0	0,01 ± 0,01	0,03 ± 0,01
15:0	0,26 ± 0,03	0,37 ± 0,06
Iso 16:0	0,03 ± 0,02	0,08 ± 0,01
16:0	17,75 ± 1,02	14,69 ± 1,20
Iso 17:0	0,15 ± 0,04	0,25 ± 0,07
Antiso 17:0	0,08 ± 0,03	0,11 ± 0,02
17:0	0,26 ± 0,03	0,22 ± 0,02
18:0	5,01 ± 0,42	3,18 ± 0,51
20:0	0,04 ± 0,01	0,09 ± 0,02
∑SFA	25,06 ± 0,89	23,39 ± 1,24
14:1 (n-7)	0,00 ± 0,01	0,04 ± 0,01
14:1 (n-5)	0,04 ± 0,03	0,03 ± 0,03
16:1 (n-11)	0,12 ± 0,02	0,12 ± 0,04
16:1 (n-9)	0,22 ± 0,03	0,23 ± 0,04
16:1 (n-7)	0,98 ± 0,34	4,46 ± 0,49
16:1 (n-5)	0,16 ± 0,03	0,19 ± 0,03
17:1 (n-8)	0,16 ± 0,05	0,39 ± 0,08
17:1 (n-4)	0,04 ± 0,04	0,07 ± 0,02
18:1 (n-11)	1,17 ± 0,26	1,57 ± 0,45
18:1 (n-9)	5,91 ± 1,03	15,08 ± 5,58
18:1 (n-7)	2,04 ± 0,32	3,22 ± 1,00
18:1 (n-5)	0,19 ± 0,02	0,34 ± 0,05
20:1 (n-11)	0,45 ± 0,15	1,65 ± 0,40
20:1 (n-9)	2,03 ± 0,64	7,85 ± 1,89
20:1 (n-7)	0,05 ± 0,06	0,19 ± 0,04
22:1 (n-11)	0,95 ± 0,70	8,44 ± 2,29
22:1 (n-9)	0,12 ± 0,05	0,60 ± 0,12
22:1 (n-7)	0,02 ± 0,02	0,05 ± 0,02
24:1 (n-9)	1,16 ± 0,10	0,60 ± 0,15
∑MUFA	15,81 ± 2,05	45,12 ± 3,13
16:4 (n-1)	0,04 ± 0,04	0,42 ± 0,15
18:4 (n-1)	0,05 ± 0,02	0,15 ± 0,05
18:5 (n-1)	0,01 ± 0,01	0,04 ± 0,03
16:2 (n-4)	0,07 ± 0,04	0,41 ± 0,12
16:3 (n-4)	0,02 ± 0,02	0,25 ± 0,11
18:2 (n-4)	0,11 ± 0,03	0,20 ± 0,05
16:2 (n-7)	0,04 ± 0,02	0,05 ± 0,03
18:2 (n-7)	0,02 ± 0,01	0,06 ± 0,01
16:2 (n-6)	0,03 ± 0,03	0,03 ± 0,01
18:2 (n-6)	0,90 ± 0,13	1,30 ± 0,19
18:3 (n-6)	0,03 ± 0,03	0,05 ± 0,06
20:2 (n-6)	0,19 ± 0,03	0,28 ± 0,03
20:3 (n-6)	0,08 ± 0,02	0,05 ± 0,01
20:4 (n-6)	1,64 ± 0,27	0,47 ± 0,09
22:4 (n-6)	0,13 ± 0,09	0,06 ± 0,05
22:5 (n-6)	0,57 ± 0,09	0,18 ± 0,05
16:4 (n-3)	0,01 ± 0,01	0,06 ± 0,02
18:3 (n-3)	0,37 ± 0,09	0,94 ± 0,25
18:4 (n-3)	0,71 ± 0,34	2,50 ± 1,04
20:3 (n-3)	0,13 ± 0,04	0,24 ± 0,05
20:4 (n-3)	0,61 ± 0,10	0,72 ± 0,17
20:5 (n-3)	11,50 ± 1,56	8,43 ± 0,81
21:5 (n-3)	0,24 ± 0,03	0,42 ± 0,10
22:5 (n-3)	1,48 ± 0,39	1,04 ± 0,31
22:6 (n-3)	39,70 ± 2,48	12,49 ± 1,46
24:5 (n-3)	0,27 ± 0,19	0,34 ± 0,12
24:6 (n-3)	0,06 ± 0,02	0,09 ± 0,03
∑PUFA	59,02 ± 1,71	31,28 ± 3,27
∑(n-6)PUFA	3,58 ± 0,29	2,41 ± 0,31
∑(n-3)PUFA	55,09 ± 1,79	27,28 ± 2,91
(n-3)/(N-6)	15,49 ± 1,33	11,43 ± 1,66
∑Chol	5,85 ± 0,96	0,34 ± 0,20

Appendix IV: FAME standard

Table A.63: Content of the GLC-463 FAME standard.

GLC REFERENCE STANDARDS (Continued)

CHAIN	ITEM	CODE NO.	% BY WT.	PRICE/100MG
C4:0	METHYL BUTYRATE		1.0	
C5:0	METHYL PENTANOATE		1.0	
C6:0	METHYL CAPROATE		1.0	
C7:0	METHYL HEPTANOATE		1.0	
C8:0	METHYL CAPRYLATE		2.0	
C9:0	METHYL NONANOATE		1.0	
C10:0	METHYL CAPRATE		2.0	
C11:0	METHYL UNDECANOATE		1.0	
C11:1	METHYL UNDECENOATE		1.0	
C12:0	METHYL LAURATE		4.0	
C12:1	METHYL DODECENOATE		2.0	
C13:0	METHYL TRIDECANOATE		1.0	
C13:1	METHYL TRIDECENOATE		1.0	
C14:0	METHYL MYRISTATE		4.0	
C14:1	METHYL MYRISTOLEATE		2.0	
C15:0	METHYL PENTADECANOATE		1.0	
C15:1	METHYL PENTADECENOATE		1.0	
C16:0	METHYL PALMITATE		4.0	
C16:1	METHYL PALMITOLEATE		4.0	
C16:1T	METHYL PALMITELAIDATE		1.0	
C17:0	METHYL HEPTADECANOATE		2.0	
C17:1	METHYL 10-HEPTADECENOATE		2.0	
C18:0	METHYL STEARATE		4.0	
C18:1	METHYL OLEATE		4.0	
C18:1T	METHYL ELAIDATE		1.0	
C18:1	METHYL PETROSELINATE	GLC-463	1.0	$275.00
C18:1	METHYL VACCENATE		1.0	
C18:1T	METHYL TRANSVACCENATE		1.0	
C18:2	METHYL LINOLEATE		4.0	
C18:2TT	METHYL LINOELAIDATE		2.0	
C18:3	METHYL GAMMA LINOLENATE		1.0	
C19:0	METHYL NONADECANOATE		1.0	
C19:1	METHYL 7-NONADECENOATE		1.0	
C18:3	METHYL ALPHA LINOLENATE		4.0	
C20:0	METHYL ARACHIDATE		4.0	
C20:1	METHYL 5-EICOSENOATE		2.0	
C20:1	METHYL 8-EICOSENOATE		2.0	
C20:1	METHYL 11-EICOSENOATE		2.0	
C20:2	METHYL 11-14-EICOSADIENOATE		2.0	
C20:3	METHYL HOMOGAMMA LINOLENATE		1.0	
C20:4	METHYL ARACHIDONATE		1.0	
C20:3	METHYL 11-14-17 EICOSATRIENOATE		2.0	
C22:0	METHYL BEHENATE		2.0	
C22:1	METHYL ERUCATE		4.0	
C20:5	METHYL EICOSAPENTAENOATE		2.0	
C22:2	METHYL DOCOSADIENOATE		1.0	
C22:3	METHYL DOCOSATRIENOATE		2.0	
C22:4	METHYL DOCOSATETRAENOATE		1.0	
C24:0	METHYL LIGNOCERATE		2.0	
C22:5 N3	METHYL DOCOSAPENTAENOATE		2.0	
C22:6	METHYL DOCOSAHEXAENOATE		2.0	
C24:1	METHYL NERVONATE		1.0	