Microparasites in selected populations of wild Atlantic salmon (*Salmo salar*) in Norway – Prevalence, density and diversity

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Abstract

The aim of this study was to investigate the prevalence, density and diversity of microparasites in Atlantic salmon from selected populations in Norway including and to provide an assessment of the possible spreading of microparasites between farmed- and wild salmonids. This was done by real time RT PCR screening of RNA extracted from gill tissues. The main focuses has been on SAV2 which has recently been introduced to Norway and is causing frequent outbreaks of PD in Trøndelag. The introduction of this virus makes it possible to investigate the potential transmission between wild and farmed salmon. There is reason to believe that SAV has been spread over longer distances by transport of smolt and between fish farms by currents. The high density of infected populations might cause a high infection pressure on wild salmon migrating in these areas. An increased understanding of a potential impact from the aquaculture industry on wild salmon populations can be acquired by investigating the presence of selected microparasites in wild salmon populations in areas with aquaculture. This to see if there is a connection between outbreaks of pathogenic disease and the occurrence of the causative agent in the wild populations, or if the wild salmon represents a natural reservoir. Collection of salmon from both sea and rivers enables the possible detection of difference in prevalence and the effect of these microparasites on wild populations.

SAV was not detected in any of the wild salmonids from Trøndelag and Finnmark during this study, however four Atlantic salmon from Hordaland were positive for the presence of SAV, one of them an escaped farmed salmon. Other viruses such as ISAV, SGPV and PRV that are quite prevalent in farmed salmon have also been detected with relatively high prevalences in wild salmon populations. There was a higher prevalence of both ISAV- and PRV-positive salmon were found in the sea compared to rivers indicating that transmission of these viruses happens when the salmon are migrating in the sea. SGPV was found with a higher prevalence in the rivers than in sea which makes it less likely that the transmission is from farmed salmon, and that the natural reservoir for this virus is in rivers or river mouth.

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Abbreviation

SAV	Salmonid Alphavirus
PD	Pancreas disease
ISAV	Infectious salmon anaemia virus
ISA	Infectious salmon anaemia
PMCV	Piscine myocarditis virus
CMS	Cardiomyopathy syndrome
PRV	Piscine orthoreovirus
HSMI	Heart and skeletal muscle inflammation
SGPV	Salmon gill poxvirus
PGI	Proliferative gill inflammation
Real time RT PCR	Real time reverse transcription polymerase chain reaction
RNA	Ribonucleic acid
DNA	Deoxyribonucleic acid
1SW	Salmon maturing after one year at sea
2SW	Salmon maturing after two years at sea
3+SW	Salmon maturing after three or more years at sea

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1 Introduction

1.1 Atlantic salmon (*Salmo salar*) and trout (*Salmo trutta*) biology

Atlantic salmon (*Salmo salar*) is an anadromous fish species distributed across the North Atlantic Ocean, where most of the salmon populations are performing long-distance feeding migrations. This involves long distance migrations and challenging physiological transformations that make them able to move between salt-free- and salt-rich waters. The main advantages for this type of migration are enhanced growth and increased fecundity (Jonsson, 1985). The majority of the Atlantic salmon spend 1 to 4+ years feeding at sea increasing their body mass from 15-50 grams (g) to 1-25 kilogram (kg) (Dempson and Rikardsen, 2011), before maturing and returning to their natal river to spawn. The return begins in early spring and the Atlantic salmon normally enter costal home waters and rivers several months before spawning (Klemetsen et al., 2003).

Another salmonid, the brown trout (*Salmo trutta*) is also forming both freshwater and anadromous populations. Trout occurring in rivers or lakes with free access to the sea often form anadromous populations (Klemetsen et al., 2003). Compared to the salmon the sea trout rarely migrate more than 100 km from their home river (Klemetsen et al., 2003). Sea trout may stay at sea for two or more years before returning to their natal river to spawn or they may migrate only for the summer returning to the river for overwintering. The duration of the sea sojourn is more variable for trout than for salmon (Jonsson and Jonsson, 2009a). Both Atlantic salmon and trout are spawning in the autumn and the eggs are incubated in the gravel substratum during the winter. The specific time of spawning varies among the many populations and between the two species, trout are spawning earlier than salmon. After hatching in the spring, the young salmon spend 1-8 years in the river before they become smolts at a size between 10-30 cm (Jonsson and Jonsson, 2009b) and starts migrating to the sea from early May through June. A negative aspect of the migration is an increased mortality risk caused by commercial fisheries and an increased pressure from predators and pathogens. The sea survival of the Atlantic salmon has been greatly reduced the last 20-25 years and only 1-17% of the migrating smolts will return as mature Salmon (Anon, 2018). In 2017 the number of returning wild salmon from sea was estimated to be 530 000 individuals (Anon, 2018). Both salmon and trout are iteroparous, ie. producing offspring more than once during their lifetime.

1.2 Ocean migration

The marine phase of the Atlantic salmon's life cycle is much less understood than the freshwater phase. Most of the current knowledge originates from mark/recapture and genetic studies associated with ocean fisheries and sampling surveys (Strøm, 2018). Information about the marine distribution and feeding areas of the Atlantic salmon at sea is important for understanding how the ocean environment influences feeding and growth of different salmon stocks, but also the future risks related to possible climate changes (Chittenden et al., 2013; Dempson and Rikardsen, 2011). The distribution of Atlantic salmon at sea (Fig.1) probably depends on environmental factors such as food availability, currents and water temperatures combined with genetic components that govern the population specific navigation system (Rikardsen et al., 2008).

The Norwegian salmon, from the south and middle parts of Norway probably feed in the northeast Atlantic, particularly in the Norwegian sea together with other salmon stocks from southern and central parts of Europe (Holm et al., 2003). Atlantic salmon from the north of Norway feed in Arctic areas. These areas include the eastern Barents sea, to areas around Jan Mayen Island and north to Svalbard, i.e. the Greenland Sea (Strøm et al., 2018). They spend most of their marine phase along the polar front which is probably an important feeding zone for these stocks (Chittenden et al., 2013). The occurrence of post-smolts at sea is closely associated with the North Atlantic Current along the Norwegian trench. This is believed to be a combination of strong currents favourable for transportation and concentration of food organisms in the shear zones between the water masses surrounding these currents (Haugland et al., 2006; Holm et al., 2000).

Salmon from the other side of the Atlantic, the north American salmon mainly remains in the north western Atlantic, where the Labrador Sea is considered the primary overwintering area (Ritter, 1989; Strøm, 2018). Juveniles originating in north America typically migrate and overwinters in the southern Labrador Sea feeding areas, before returning to their natal river to spawn the following spring. The ones that will return as multiple sea winter (MSW) salmon migrates to west Greenland to forage during summer and autumn before returning to the Labrador Sea for an additional winter and back to their natal river in the spring (Reddin, 2006). Intercontinental migrations of salmon between North America and Europe have also been shown. MSW salmon from southern Europe have been found on the western coast of Greenland, and American salmon originating from Canada have been found in the Norwegian sea north of

The Faroe Islands (ICES, 2017; Reddin, 2006). It is likely Atlantic salmon from most countries around the North Atlantic may be present in the area north of The Faroe Islands at some point in their lives (Hansen and Jacobsen, 2003), and that there is a change in stock complexes entering and departing these areas during the season. Higher proportions of salmon from the southern and mid parts of Europe can be found north of The Faroe Islands during early winter, and salmon from northern areas are more abundant in the late winter (Jacobsen et al., 2001). This might be explained by the fact that smolts from different areas move into the ocean at different times, smolts from southern Europe may leave their home rivers early in the spring, whereas smolt from northern parts of Europe go to sea 3-4 months later (Jacobsen et al., 2001).

Figure 1. Assumed ocean feeding areas for Atlantic salmon.

1.3 Salmon farming industry and salmon pathogens

Salmon farming has grown from being a marginal industry in the 1960s becoming one of the most important industries in Norway. In 2017 the aquaculture industry produced over 1 200 000 tons Atlantic salmon in Norway (Statistics Norway, 2017). Total loss was estimated to be 53 million salmon the same year (Hjeltnes et al., 2019). The causes for these losses are complex, but infectious disease plays an important role. The industry is facing serious problems related to control of viral diseases, skin ulcers caused by bacteria, gill diseases caused by a plethora of different pathogens, and increased production costs and losses due to lice treatments. The major viral diseases are salmonid alphavirus (SAV) causing pancreas disease (PD), piscine myocarditis virus (PMCV) causing cardiac myopathy syndrome (CMS), piscine orthoreovirus virus (PRV) associated with heart and skeletal muscle inflammation (HSMI), and infectious salmon anaemia virus (ISAV) causing ISA. The latter disease is controlled by stamping out of

infected populations. The salmon gill poxvirus (SGPV) is, together with bacteria (*Chlamydiae* species and *Candidatus* Branchiomonas cysticola) and parasites (*Paramoeba perurans*, *Paranucleospora theridion*, *Ichthyobodo* spp) believed to cause gill disease (Gunnarsson et al., 2017; Isaksen et al., 2012; Nylund et al., 2011, 2010; S. Nylund et al., 2008; Sveen et al., 2012).

Little is known about the spread of viruses and other microparasites from farmed to wild fish populations (Garseth et al., 2013b; Madhun et al., 2018). The detection of disease in wild fish and estimating disease impact on wild populations is difficult. Clinically affected fish usually disappear quickly, while asymptomatic carriers can be found.

Table 1. Average number of sites, cages, Atlantic salmon (*S. salar*) and rainbow trout (*O. mykiss*) May-September 2018 in Finnmark, Trøndelag and Hordaland. *Numbers in 1000s.

	Finnmark	Trøndelag	Hordaland
Sites	43	94	119
Cages/net pens	309	578	635
Atlantic salmon*	39289	78951	54279
Rainbow trout*	0	1184	11572

The fish farming industry is divided into two phases; juvenile (smolt) and grow-out production. The production of juveniles is in closed systems on land, and the grow-out production is in open net-pens in the sea. These open net-pens are vulnerable to escapes and most of them have no barriers to pathogen exchange within the environment. This makes it possible for potential pathogens to reach other fish farms or wild fish populations by for example local currents and boats (Johansen et al., 2011). A producer of juvenile salmon is typically serving many grow-out farm-sites that poses an additional risk of moving microparasites over a larger area. The structure of the industry is dependent on moving live fish over large distances. Fertilized eggs from broodfish stations to hatchery, smolt from smolt production sites to grow-out sites and full-grown salmon to slaughter sites. The average number of cages, Atlantic salmon and rainbow trout in Finnmark, Trøndelag and Hordaland in the summer of 2018 are listed in table 1. Atlantic salmon are produced in large dense populations and the scale of the production is well in excess of the natural production of the same species. In Norwegian aquaculture there are between 300-400 million Atlantic salmon in sea at any time. This is almost 700 times more than the total number of returning wild Atlantic salmon to the rivers. The density of susceptible

hosts is unnaturally high and will affect the dynamics of infectious diseases. An increase of hosts may cause an increase in abundance of pathogens and the rate of disease outbreaks (Fjørtoft et al., 2017; Krkošek, 2010). Most of the diseases in Norwegian salmon farming are believed to be enzootic and originate from wild fish, but today farmed fish populations are likely to represent the main reservoirs.

Diversity and density of potential microparasites normally changes over time, and the aquaculture industry may affect such changes with variations in production volume and the location of farming-sites in the fjord systems. Disease outbreaks in farms may lead to substantially increased infection pressure on wild populations in the area (Madhun et al., 2016). The wild salmon may be exposed to microparasites prevalent in the salmon farms when they are passing production sites during their migration to sea as smolts or during their return as mature spawners. Infected farmed salmon that escape will also represent a potential risk for spreading pathogens into rivers and to wild populations of salmonids. The number of escapes is decreasing from a top of 400 000-900 000 individuals per year in 2002-2006. According to The Directorate of Fisheries there was almost 160 000 farmed Atlantic salmon that escaped in year 2018.

The salmon louse, (*Lepeophtheirus salmonis)* is a major problem in the salmon farming industry. This is a naturally occurring parasite but intensive salmon farming has improved the conditions for the growth and transmission of the parasite compared with natural conditions (Torrissen et al., 2013). The salmon lice is known to spread from farmed to wild salmonids (Krkosek et al., 2012) and smolts are especially exposed during their seaward migration. Another pathogen which is believed to spread between wild- and farmed populations is the piscine orthoreovirus (PRV). PRV is found in both wild- and farmed salmon and sea trout along the entire coast of Norway. Analysis of PRV-genotypes indicate extensive transmission along the Norwegian coast probably due to substantial transportation of fish between areas over many years (Garseth et al. 2013).

Two exotic pathogens have been introduced to wild salmon populations in Norway by the salmon aquaculture. *Aeromonas salmonicida* subspecies *salmonicida*, the causative agent of classical furunculosis was introduced to Norway by rainbow trout from Denmark in 1960 and later re-introduced by salmon smolts from Scotland (Daverdin and Halvorsen, 1994). This disease spread to several farming-sites and to wild salmonids in rivers. Today this disease does not pose a problem for the aquaculture industry due to efficient vaccines, but the bacterium is

isolated sporadically from wild salmon, especially in years with high water temperatures. The ectoparasite *Gyrodactylus salaris* has been introduced to Norway several times by the import of salmonids from Sweden (Hansen et al., 2003), and later spread to different rivers and wild salmon stocks which are very susceptible. The density of juvenile salmon in infected rivers can be largely reduced due to this parasite. There have been used a lot of resources to combat *Gyrodactylus salaris,* with the goal to eradicate it where it is possible.

1.4 Salmonid alphavirus

Salmonid alphavirus (SAV) is the infectious agent causing pancreas disease (PD) in Atlantic salmon and sleeping disease (SD) in rainbow trout. This virus has been isolated from both farmed Atlantic salmon and rainbow trout in western Norway and north-west of Norway and has also been causing disease in Nordland, Troms and Finnmark. There are six subtypes of salmonid alphavirus; SAV1-6. SAV3/NSAV is the main agent for PD in salmonids in Norway (Hodneland et al., 2005). Due to the low level of genetic variance it has been suggested that SAV3 was introduced to Norwegian aquaculture once and has later been spread along the Norwegian coast (Karlsen et al., 2014a, 2006). Another subtype, SAV2 has recently been introduced to Norway. Analysis shows that the genetic identity of these strains compared to others, sequenced from Scottish farmed salmon, makes it probable that the virus was first introduced to farmed fish in Scotland before being transported to Norway with biological material (Karlsen et al., 2014a). The most important infection route for SAV is horizontal transmission. The virus can survive for extended periods in cold clean seawater and may be carried long distances with currents (Graham et al., 2007; Kristoffersen et al., 2009; Stene et al., 2014).

1.5 Aims of the study

The main goal of this study was to get an overview of the prevalence, density and diversity of microparasites that are common in farmed- and wild salmon, and in trout in selected populations of wild salmonids in Norway. Another goal was to provide an assessment of the possible spreading of microparasites between farmed- and wild salmonids. A major focus has been on SAV2, which was recently introduced to Norway and is causing frequent outbreaks of PD in Trøndelag. Another focus will be on differences in prevalence, densities, and diversity of selected microparasites (virus, bacteria and protozoans) in wild returning salmonids collected in the sea *versus* those sampled in rivers. Could single microparasites or the collected load of microparasites influence the mature salmonids (Atlantic salmon and brown trout) ability to reach the spawning ground?

2 Materials and methods

2.1 Materials

Atlantic salmon from several places in Norway were collected during the summer and autumn of 2018 from both rivers and sea/fjord-locations. The fish were caught by anglers in rivers, and in NINA's (Norwegian institute for Nature Research) and Uni Research's fish traps in fjords. A total of 701 wild Atlantic salmon in addition to 7 farmed Atlantic salmon caught in rivers and 71 sea trout (fish traps) have been examined in this study. They have been collected in Finnmark, Nord- and Sør-Trøndelag, and Hordaland (Fig. 2). All the locations are presented in table 2. The samples from Finnmark and Trøndelag were organized and brought to FDRG at the University of Bergen by the organisation SalmonCamera. The second gill-arch from salmon caught in rivers and from fish traps in Trøndelag and Finnmark was excised and preserved in 75% ethanol by instructed persons to avoid contamination and get samples of high quality. Fish from Sørfjorden in Hordaland were collected by Uni Research and gill, heart and kidney samples were collected from the fish at the laboratory of the Fish Diseases Research group at the University of Bergen. Hardangerfjord villfisklag collected breeding fish from rivers in Hordaland to the gene bank in Eidfjord, these salmon were sampled at the site directly after stripping in November. These salmonids used for breeding in Hordaland were held in closed tanks for some time before stripping.

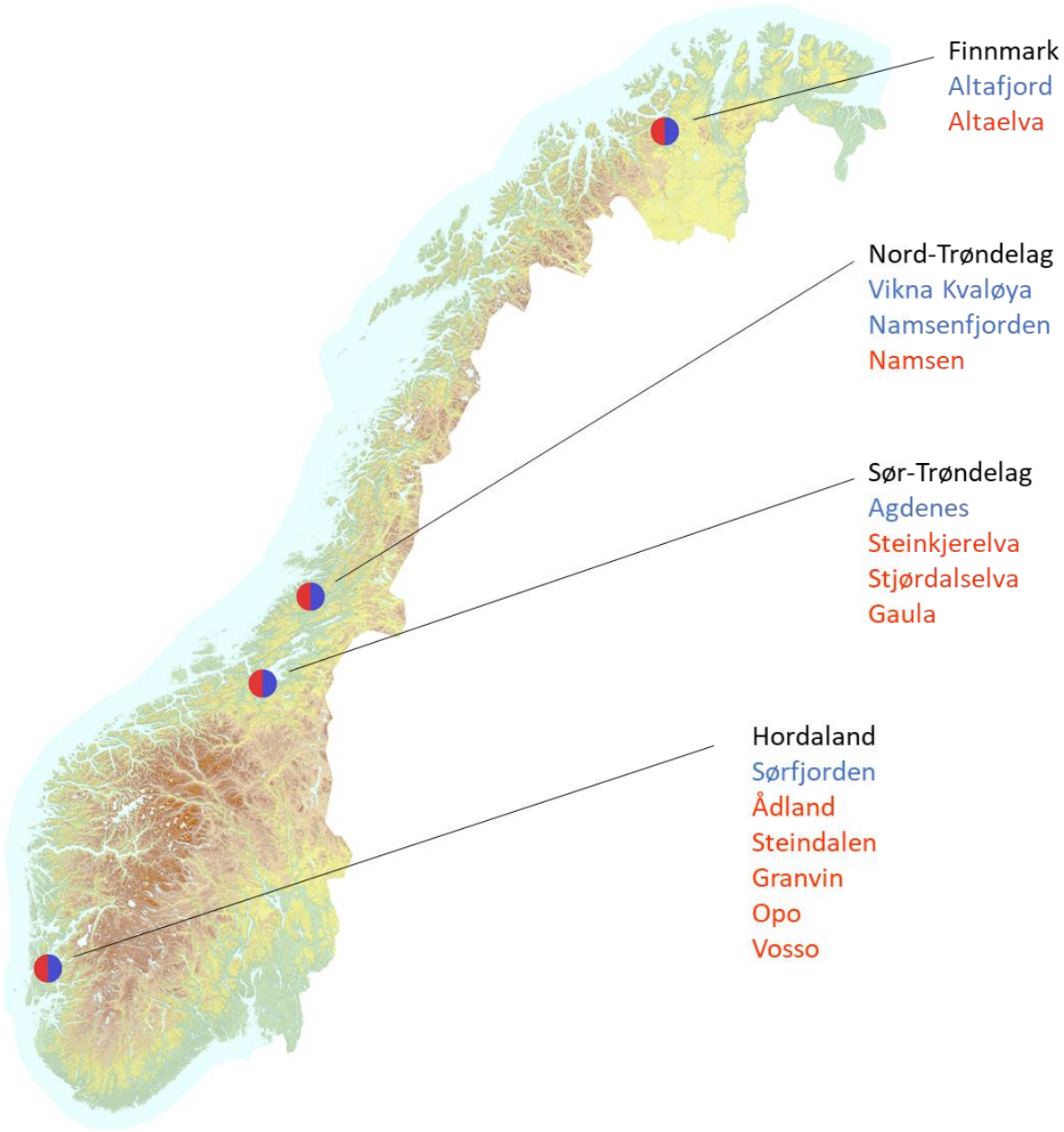

Figure 2. Map of Norway showing the four main locations were salmonids (Atlantic salmon and brown trout) have been collected. Blue and red colours indicate sea and freshwater sites respectively.

Table 2. Overview of collection sites with salinity, temperature, when the fish was capture and the number of collected Atlantic salmon (*S. salar*) and brown trout (*S. trutta*). Temperature data was not available for all sites.

County/ sampling site	Habitate	Approximate salinity	Temperature °C	Time of collection (2018)	Specie	N
Finnmark						
Altafjorden	Fjord	Salt		June-July	Salmon	81
					Trout	35
Altaelva	River	Fresh	12,0	June-August	Salmon	62
Trøndelag						
Agdenes	Fjord	Salt		June-July	Salmon	85
					Trout	14
Gaula	River	Fresh	2,0	June-August	Salmon	22
Stjørdalselva	River	Fresh	14,6	June-August	Salmon	97
Steinkjerelva	River	Fresh		June-July	Salmon	35
Vikna	Sea	Salt		June-July	Salmon	112
					Trout	8
Namsfjorden	Fjord	Salt		June-July	Salmon	113
					Trout	7
Namsen	River	Fresh	14,6	June-August	Salmon	60
Hordaland						
Sørfjorden	Fjord	Brackish		June-August	Salmon	60
Vosso	River	Fresh	16,4	October-November	Salmon	4
Opo	River	Fresh		October-November	Salmon	19
Steinsdalelva	River	Fresh		October-November	Salmon	7
					Trout	7
Granvin	River	Fresh		October-November	Salmon	27
Ådland	River	Fresh		October-November	Salmon	24

The majority of the samples were marked with an identification number and accompanied by information including weight, length, gender, species, wild or farmed etc. The weight was used to estimate the number of years the salmon had been at sea. If the weight was lacking the length (when given) was used to calculate the weight based on Norwegian Institute for Nature Research's weight table (Appendix; weight and length table).

2.1.1 Sampling sites

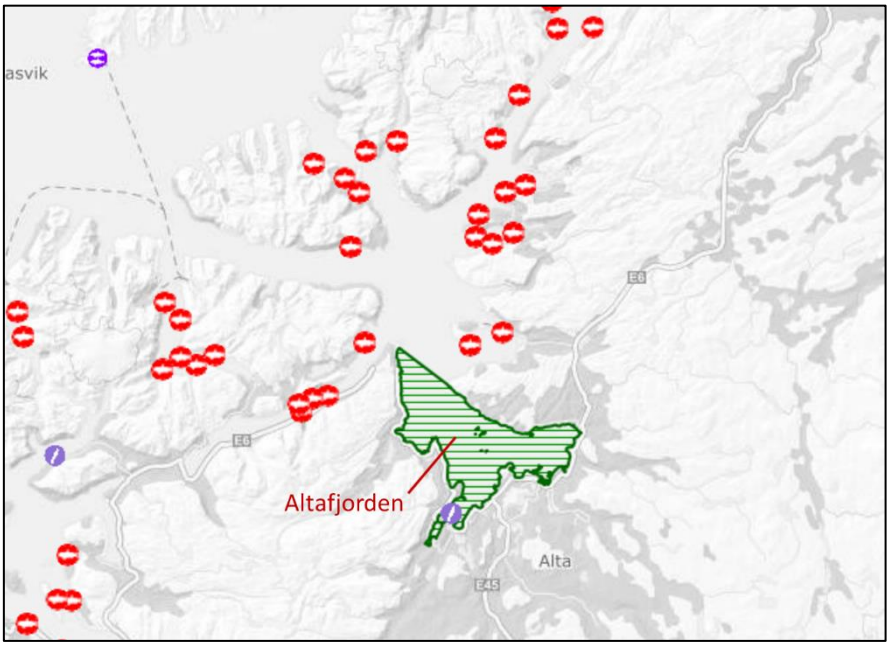

Figure 3. Overview of Altafjord and aquaculture sites producing Atlantic salmon (*S. salar*) nearby. The green shaded area indicates the part of the fjord protected as a national salmon fjord.

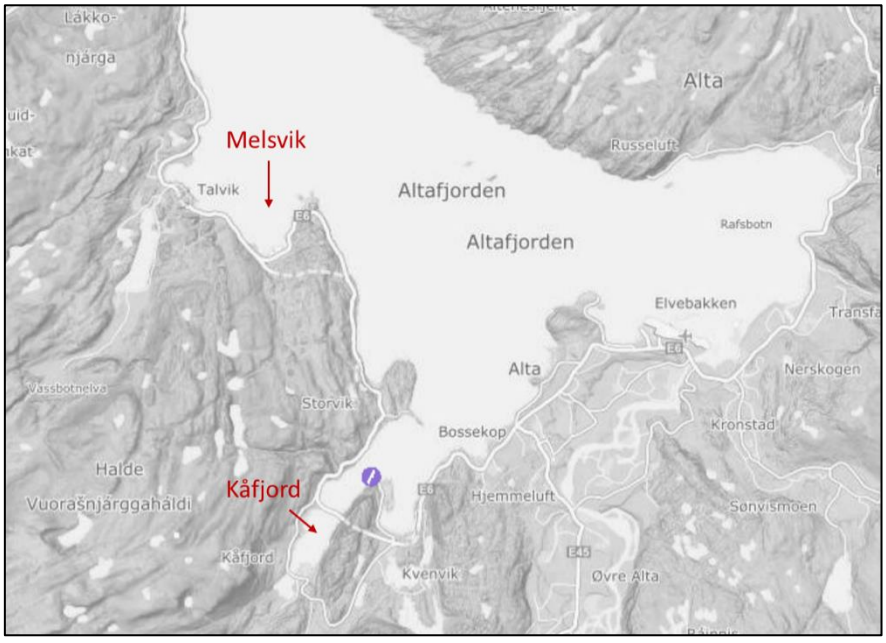

Figure 4. Location of the two fish traps in Altafjorden, at Melsvik and Kåfjord.

Altafjorden, Namsfjorden, Trondheimsfjorden and the inner fjords around Osterøy are all national fjords for protection of wild salmon in Norway. Salmon farming should not occur in these fjords. However, during migration the wild salmon will be exposed to microparasites liberated from farming sites producing Atlantic salmon in the vicinity of these fjord (Figs. 3, 5 and 6). The salmon migration through Altafjorden are mainly entering the river Alta (Fig. 3). The fish traps are located at Melsvika and Kåfjord (Fig. 4). The returning salmon in Namsfjorden are mainly entering river Namsen (Fig. 6 A), while the salmon returning to Trondheimsfjorden are entering several rivers including Orkla, Gaula, Stjørdalselva, and Steinkjerelva (byelva) (Fig. 6 B). The fish traps in Trøndelag are located at Kvaløya, Namsfjorden and Agdenes (Fig. 6 A and B). The salmon capture in Sørfjorden are mainly entering Dale river and Vosso. The fish trap in Sørfjorden are located in Trengereid.

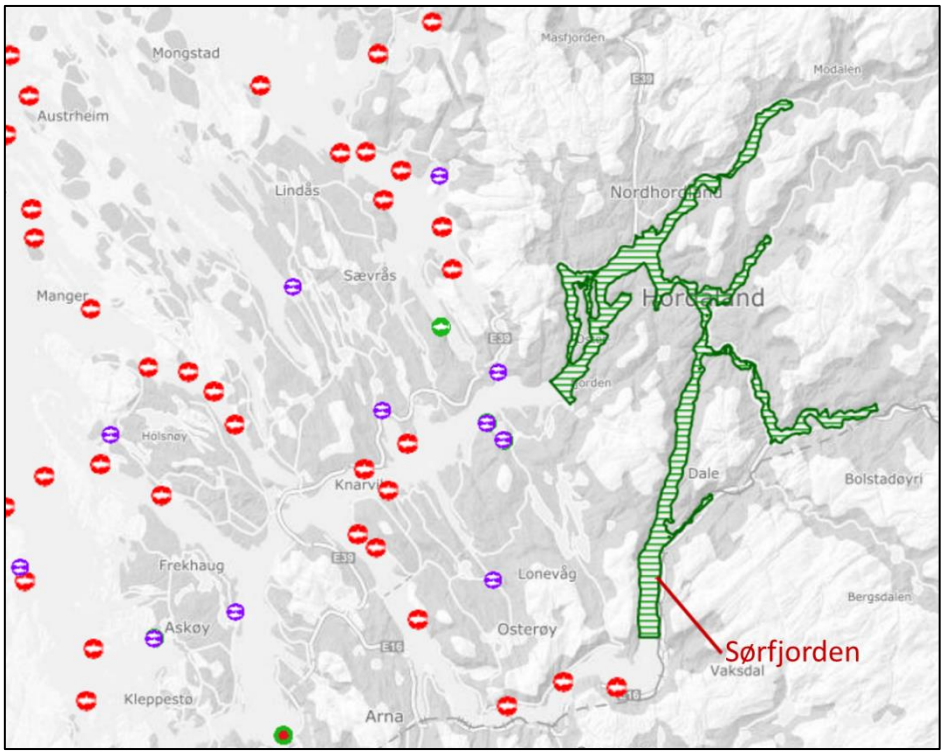

Figure 5. Sørfjorden in Hordaland and aquaculture sites producing Atlantic salmon (*S. salar*) and rainbowtrout (*O. mykiss*) nearby. The green shaded area is protected as a national salmon fjord.

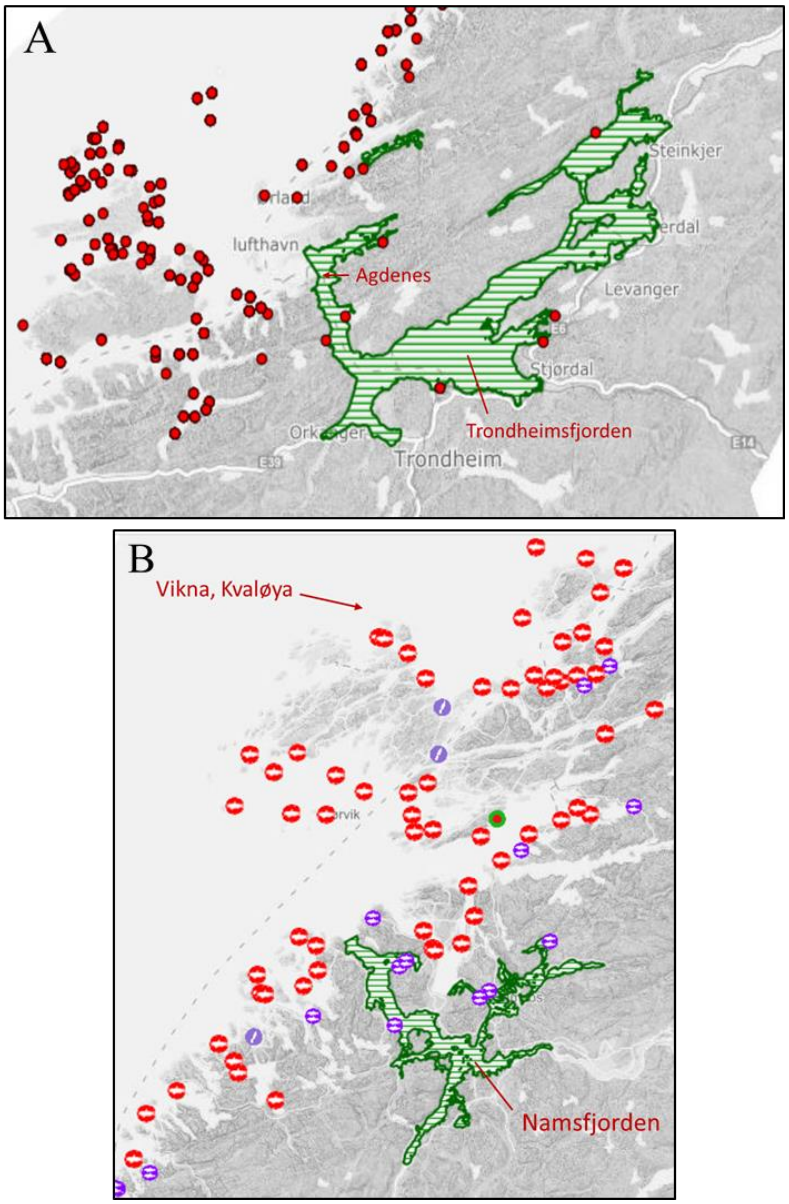

Figure 6. Overview of Namsfjorden (A) and Trondheimsfjorden (B) with aquaculture sites producing Atlantic salmon (*S. salar*) and rainbowtrout (*O. mykiss*) outside the national salmon fjord (green shaded area).

2.2 Methods

2.2.1 Sampling

After capture the fish were euthanized, weight and total length measured, and if possible, the sex determined. The second gill arch was taken from all the fish immediately after capture and stored in 75% ethanol. The samples were kept at temperatures between 4-20°C until they were sent to the FDRG-laboratory at the University of Bergen were subsamples were taken for analysis, if relevant, for sequencing and genotyping of selected microparasites. Scale samples were taken from each fish for determination of sea age and to distinguish between wild and possibly escaped farmed salmon. All salmon collected were visually inspected and if signs (structure of fin rays, signs of vaccination etc) were suggestive of escaped farmed salmon they were automatically registered as escapees.

In the laboratory a small piece, about size of a matchstick head was cut out from the sampled organs (gills, heart and kidney). The cartilage from the gill arch was removed, and a small piece from the tip off the gill arch was cut off for real time RT PCR analysis. The tip of the heart and the mid-kidney were removed before taking a smaller piece of the tissues for analyses and leaving the rest for back-up. Both compactum and spongiosum was included in the heart samples. The samples for analysing were put in a 2.0 ml tube and stored at -24 °C until further processing. Larger pieces of the organs were taken as backup samples and stored in 1.8 ml CryoTubes at -24 °C. The scalpel and tweezers were sterilized between each sample by dipping into 90 % ethanol and burned off. Each tissue was cut on a clean new petri dish. Heart is normally the best organ to determine the presence of salmonid alphavirus, but the prevalence of SAV in the gill tissues are approximately the same as heart tissues (Andersen et al., 2007; Herath et al., 2016)

2.2.2 RNA extraction

Nucleic acids and proteins can be isolated from any biological material such as living or conserved tissues, cells, virus particles. Isolation of RNA is the first step in performing many molecular techniques such as real time reverse transcription polymerase chain reaction (real time RT PCR). It is often difficult to isolate intact and high-quality RNA. RNases, enzymes that degrade RNA molecules are abundant in the environment, including on our hands and

surfaces. These enzymes are difficult to destroy, and it is therefore important to use RNase-free solutions and equipment along with cautious handling of the samples and good aseptic techniques. RNases are inhibited by strong denaturants like guanidine salts, sodium dodecylsulfate or phenol-based compounds (Johnson, 2013). Performing organic extraction methods, the sample is homogenized in a phenol-containing solution before chloroform addition, RNA extraction and phase separation by centrifugation. The sample will separate into three phases during the centrifugation; a lower organic phase containing proteins and lipids, a middle phase containing DNA, and an upper aqueous phase containing RNA. To isolate RNA the upper phase is added to isopropanol which forces the precipitation of nucleic acids in the solution and makes it possible to separate them from the rest of the solution.

1.0 ml TRI Reagent was added to the tissue samples and homogenized in "Qiagen tissue lyser II" (30/s) for 3 minutes. The samples were then incubated at room temperature for 5 minutes before adding 200 µl chloroform and mixed by shaking for 30 seconds and incubated for 5 minutes in room temperature. The samples were then centrifuged in 4 °C, 12 000 x g for 15 minutes. This step separates the mixture into three phases, where the uppermost layer is colourless and aqueous and contains RNA. 500 µl from the RNA containing layer were transferred to a new tube containing 500 µl isopropanol and mixed well by shaking for 15 seconds. Then the samples were incubated for 10 minutes before the precipitated RNA was pelleted at 4 °C, 12 000 x g for 15 minutes. The supernatant was removed, and the pellets washed twice with 1.0 ml of 75% ethanol, by vortexing it and centrifuging for 5 minutes at 4 °C and 12 000 x g. After the second wash the ethanol was removed, the pellet briefly dried for 5-10 minutes or until the alcohol had evaporated. Pellets were dissolved in 150 µl RNase-free water at 70 °C. A negative control was included for every eleventh sample prepared. The negative control followed the same protocol as the tissue sample, except that no tissue was present. The samples were frozen and stored at -24°C.

2.2.3 Real time RT PCR

The extracted RNA was later analysed by real time RT PCR for detection of RNA from specific microparasites. Real time RT PCR was performed using the AgPath-ID™ One-Step q-PCR Kit from Applied Biosystems. The one step kit makes it possible to perform both the reverse-transcriptase and the PCR-reaction in the same "tube". The real time RT PCR monitors the amplification of the target template in real time during the reaction. This makes it possible to observe the relative amount of the target template for every cycle due to a fluorescing marker.

The fluorescence signal increases proportionally with the amount of replicated cDNA and shows how many amplification-cycles it takes to reach a given threshold (in this study set to 0.1 for all assays). The results are presented graphically as an amplification curve showing how many cycles it takes to reach the threshold. The Ct-value (cycle threshold) is the intersection of these, showing the number of cycles it takes for the fluorescent signal to reach the set threshold value. A low Ct-value, few cycles before reaching the threshold, indicates a high quantity of the target-template in the sample, and a high Ct-value the opposite.

All primers and probes used in this study are listed in table 3. The "housekeeping gene" elongation factor 1 alpha (EF1A) was used as an internal control (Olsvik et al., 2005). Two controls were included for every tenth sample analysed. One sample without added template, a Negative Template Control (NTC), and one (cleaning-control) RNA-extraction control. This was included as a control to detect a potential contamination during the RNA extraction. NTC was used as a control for potential contamination of the real time q-PCR reagents.

MicroAmp® optical 96-well Reaction Plate was used and put one ice when adding mastermix and template. The reactions were run in a total volume of 12.5 µl for each well, using 10.5 µl mastermix and 2.0 µl template. For most of the assays the mastermix contained 6.25 µl 2X Q-PCR buffer, 1.0 µl (400 nM) of both forward and reverse primers, 0.22 µl probe (120 nM), 0.25 µl enzyme mix, 1.78 µl nuclease free water and 2.0 µl template. The plates were sealed with MicroAmp™ Optical Adhesive Film, centrifugated and run in the real time Q-PCR machine using the Applied Biosystems® 7500 Real-Time PCR System, and Applied Biosystems® Quantstudio 3 Real-Time PCR System. The reactions: reverse transcriptase for 10 minutes at 45 °C, denaturation and activation of the DNA polymerase for 10 minutes at 95 °C, and then 45 cycles of amplification at first 95 °C for 15 seconds then 60 °C for 45 seconds.

Some plates were prepared and frozen at -21°C over night, analysed the next day.

Table 3. Primers and probes used for detection of selected microparasites by real-time RT PCR. The efficiences of the assays are given in the respective publications.

Assay	Primer	Sequence	Reference
Infectious salmon anaemia virus (Seg.7)	Probe	CAC ATG ACC CCT CGT C	Plarre et al., 2005
	Forward	TGG GAT CAT GTG TTT CCT GCT A	
	Reverse	GAA AAT CCA TGT TCT CAG ATG CAA	
Salmonid alphavirus (NSAV)	Probe	AGCGCTGCCCAAGCGACCG	Hodneland and Endresen, 2006
	Forward	CAGTGAAATTCGATAAGAAGTGCAA	
	Reverse	TGGGAGTCGCTGGTAAAGGT	
Salmon gill poxvirus (POX MCP)	Probe	TTA TAC ACC ATC ACA TTT GTG	Nylund et. al in prep.
	Forward	CAG AGG TTT TTC ATA CGC CAG AA	
	Reverse	GAG GTC ACG GTG ATG ACA GAA C	
Piscine myocarditis virus (PMCV)	Probe	TGGTGGAGCGTTCAA	Nylund et al., 2018a
	Forward	AGGGAACAGGAGGAAGCAGAA	
	Reverse	CGTAATCCGACATCATTTTGTGA	
Infectious pancreas necrosis virus (IPNV)	Probe	TCT TGG CCC CGT TCA TT	Watanabe et al., 2006
	Forward	ACC CCA GGG TCT CCA GTC	
	Reverse	GGA TGG GAG GTC GAT CTC GTA	
Piscine reovirus (PRV M2)	Probe	CTG GCT CAA CTC TC	Nylund et al., 2018a
	Forward	CAA TCG CAA GGT CTG ATG CA	
	Reverse	GGG TTC TGT GCT GGA GAT GAG	
Candidatus Branchiomonas cycticola (Epit)	Probe	ACT TAG CGA AAG TTA AGC	Nylund et al., 2018a
	Forward	GAG TAA TAC ATC GGA ACG TGT CTA GTG	
	Reverse	CTT TCC TCT CCC AAG CTT ATG C	
Candidatus Pisciclamydia salmonis (PCh)	Probe	CAAAACTGCTAGACTAGAGT	Nylund et al., 2008
	Forward	TCA CCC CCA GGC TGC TT	
	Reverse	GAA TTC CAT TTC CCC CTC TTG	
Yersinia ruckeri (YR)	Probe	TAA TAG CAC TGA ACA TTG AC	Nylund, unpublished
	Forward	GCG AGG AGG AAG GGT TAA GTG	
	Reverse	CGG TGC TTC TTC TGC GAG TAA	
Renibacterium salmoninarum (BKD)	Probe	TGC AGA AAT GTA CTC CC	Nylund, unpublished
	Forward	CAA GGCTTG ACA TGG ATT AGA AAA	
	Reverse	CAC CTG TGA ACC AAC CAA CCC AAA A	
Paranucleospora theridion (Nuc)	Probe	TTG GCG AAG AAT GAA A	Nylund et al., 2010
	Forward	CGG ACA GGG AGC ATG GTA TAG	
	Reverse	GGT CCA GGT TGG GTC TTG AG	
Parvicapsula pseudobranchicola (Parvi)	Probe	CCG TAT TGC TGT CTT TGA	Nylund et al., 2008
	Forward	TCG TAG TCG GAT GAC AAG AAC GT	
	Reverse	AAA CAC CCC GCA CTG CAT	
Ichthyobodo spp (Costia)	Probe	TCC ACG ACT GCA AAC GAT GAC G	Isaksen et al. 2012
	Forward	ACG AAC TTA TGC GAA GGC A	
	Reverse	TGA GTA TTC ACT YCC GAT CCA T	
Paramoeba perurans (Pperu)	Probe	CTG GTT CTT TCG RGA GC	Nylund et al., 2018
	Forward	GAT AAC CGT GGT AAA TCT AGA GCT AAT A	
	Reverse	TGG CAT TGG CTT TTG AAT CT	
Elongationfactor salmon (ELA)	Probe	ATC GGT GGT ATT GGA A	Olsvik et al. 2005
	Forward	CCC CTC CAG GAC GTT TAC AAA	
	Reverse	CAC ACG GCC CAC AGG TAC A	

2.2.4 RT PCR and sequencing

RNA from selected virus (ISAV and SGPV) positive salmon was used for cDNA synthesis using the M-MLV kit (Promega, M170A and M531A). Approximately 2.0 µg of RNA and 1.0 pmol sequence-specific reverse transcription (RT) primer in a total volume of 10.0 µl was incubated at 70°C for 5 minutes and then immediately transferred to ice. RT reaction mix (1x M-MLV reaction buffer, 0.4 mM dNTPs and 100 U M-MLV) was added to each reaction to bring the final volume to 25.0 µl before the reaction was incubated at 37°C for one hour (Kloster-jensen, 2018; Nylund et al., 2019). Segment six from ISAV (HE gene) and variable 16 (V16) from SGPV were amplified by PCR using the cDNA from positive salmon gills. The PCR products were visualized using gel electrophoresis and sequenced in both directions using BigDye terminator 3.1 chemistry and the same primers as for PCR. This resulted in overlapping sequence reads covering the full length in both directions of the two targets (Kloster-jensen, 2018; Nylund et al., 2019).

2.2.5 Phylogenetic analysis

The ISA virus HE-gene sequences and the V16 sequences from SGPV were assembled with the help of Vector NTI software (InforMax, Inc.). The Vector NTI Suite software package (InforMax, Inc.) was also used for the multiple alignments of the sequences. To perform pairwise comparisons the multiple sequence alignment editor GeneDoc (Available at: www.psc.edu/biomed/genedoc) was used for manual adjustments. ISAV HE-gene sequences and SGPV V16 sequences available from Nylund et. al (2019) and Kloster-Jensen (2018) were included in the comparisons.

The phylogenetic trees based on the ISAV HE-gene and the SGPV V16 were obtained by analysis as described by Nylund et. al (2019) and Kloster-Jensen (2018). The trees were constructed using TREE-PUZZLE 5.2 (Available at: http://www.tree-puzzle.de), maximum likelihood (ML). The same evolutionary models and substitution rates as described earlier were used (Kloster-jensen, 2018; Nylund et al., 2019). Phylogenetic trees were drawn using TreeView (Page, 1996).

2.3 Prevalence

Prevalence is the proportion of the specific population found to be affected by a particular pathogen. Prevalence is the percentage of positive individuals in a population tested. It is measured by dividing the number of positive samples by the total number of samples and multiplied by 100. This method was used to give an indication of the occurrence of microparasites in tested salmonid populations.

Analysis of 27 - 30 fish will detect a prevalence of 10 % with a 95% confidence level and analysis of 55 - 60 fish will detect a prevalence of 5% (with a 95 % confidence level) in a population > 1000 individuals.

$$Prevalence\ (\%) = \frac{Number\ of\ positive\ samples}{Total\ number\ of\ samples} \times 100$$

2.4 Diversity index

Diversity index is used to describe the number of different microparasites in individual fish and populations. Range from 1 to 10.

$$Diversity\ index = \frac{number\ of\ present\ pathogens}{number\ of\ pathogens\ analysed\ for} x\ 10$$

2.5 Density

Density may give an indication of how affected, by a specific pathogen, the individual fish may be (load of microparasites). In this study density is used to give an indication of the amount of a specific RNA target (from a pathogen) that is present in a sample. Low Ct values indicate high amounts (high loads) of the specific pathogen. Even though the Ct-value is low it does not necessarily mean that the fish is clinically ill. In this study the density (load) is presented as; *D = 50 – Ct value*, for the individual fish. This density calculation is only used when the Ct values for the internal control gene is stably expressed in all tested individuals.

The recommended method for relative quantification is to use the formulae for normalized expression (NE) in individual fish and mean normalized expression (MNE) in tested populations. However, it is not possible to quantify the number of virions in individual fish

based on presence of RNA targets, but the Ct values may give an indication of carrier status or ongoing viraemia. Hence, the Ct values are used only for an indication of carrier status or ongoing viraemia.

2.6 **Statistics**

A chi-square test was used to calculate statistical significance in prevalence of some selected microparasites in sea *versus* river and between the different age-groups.

The calculation of the Chi-Square statistic:

$$\chi^2 = \sum \frac{(O - E)^2}{E}$$

O is the observed frequency and E is the expected frequency if no relationship existed between the variables.

3 Results

816 gill-samples from Atlantic salmon were analysed in this study. The salmon are mainly sorted into three different groups based on age indicating how many years they have been at sea before returning as mature salmon. The age is estimated by their weight, salmon that have been one year at sea are believed to weigh between 1 to 2.9 kilos, 2 years at sea 3 to 6.9 kilos, and 3 years at sea over 7 kilos. The Atlantic salmon included in this study are listed in table 4. Scale samples have been taken from all the fish and these be used for a more specific determination of sea age and for a more reliable separation between escaped farmed salmon and wild salmon (Unfortunately, it was not enough time to include these methods in my Master thesis).

Table 4. Average weight, length and estimated age (by weight) of the Atlantic salmon examined in this study. Salmon from the sea and fjord sampling-sites (blue letters) were captured in fish-traps, and fish from the rivers were collected by anglers. *Salmon kept in tanks for some time before sampling. 1SW = one year at sea, 2SW = two years at sea, 3+SW = three or more years at sea, Un. Age = unknown age.

County	N	weight gram	length cm	1SW	2SW	3+SW	Un.age
Finnmark							
Altafjorden	81	6534	79.3	21	22	39	0
Altaelva	62	5610	75.7	26	9	24	3
Trøndelag							
Agdenes	85	3037	64.7	51	30	2	2
Gaula	22	3866	70.2	9	6	3	4
Stjørdalselva	97	6139	81.5	7	58	28	4
Steinkjerelva	35	4985	79.3	1	33	1	0
Vikna	112	3843	72.3	43	63	6	0
Namsfjorden	121	3898	70.3	56	54	11	0
Namsen	60	6567	82.9	4	26	14	18
Hordaland							
Sørfjorden	60	5010	77.3	12	34	10	4
Vosso*	4	4239	70.2	2	1	1	0
Opo*	19	3305	75.3	8	11	0	0
Steindalselva*	7	3143	70.9	3	4	0	0
Granvin*	27	4415	80.0	5	17	5	0
Ådland*	24	2646	69.0	14	10	0	0

The majority of the wild salmon were collected in the period June- July, and a few fish were collected in August. Gill tissues were sampled from all fish and, when possible, heart and kidney tissues, were also included. The gill tissues, which were available from all specimens,

were primarily used for detection of a range of different microparasites (viruses, bacteria and protozoans). However, this tissue is not optimal for detection of some of the microparasites (ex. Piscine myocarditis virus -PMCV, *Renibacterium salmoninarum* -BKD). This means that the prevalence for some of the microparasites could be underestimated. When PMCV positive gills were detected and available the heart and kidney tissues available, these were used for confirmation of presence. Kidney tissues, when available, were used for confirmations of presence of *R. salmoninarum.*

3.1 Prevalence of microparasites

3.1.1 Virus

All gill-samples from the wild salmons included in this study were negative for presence of IPNV and ASCV.

Salmonid alphavirus

All the 816 samples were analysed for presence of salmonid alphavirus, SAV. None of the salmonids (*Salmo salar* and *Salmo trutta*) collected in Finnmark (N = 178) and Trøndelag (N = 553) were positive for presence of SAV.

Four salmon were found to be positive for SAV during screening of gill tissues from fish collected in Hordaland County (Tab. 5). One of these was a farmed salmon caught in the river Vosso, two were wild salmon collected in Granvinselva (one of them was determined to be a hybrid between wild and farmed salmon based on genetic testing), and one was a wild salmon from Steinsdalselva. The real time RT PCR Ct values were over 30 for all four indicating low amounts of target template and therefore low amounts of the virus.

The assay used to detect SAV, detects both SAV2 and SAV3. The positive samples have not been sequenced.

Table 5. Detection of salmonid alphavirus in three wild and one escaped farmed Salmon in Hordaland county. *Escaped farmed Atlantic salmon

Location	Sex	Weight	Length	Ct-value
Vosso*	Female	-	830	32.0
Steindalselva	Female	3800	820	34.7
Granvin	Male	3800	770	30.0
Granvin	Female	3500	700	32.6

Infectious salmon anaemia virus (ISAV)

All the 816 samples from salmonids in Hordaland, Trøndelag and Finnmark were analysed for the presence of infectious salmon anaemia virus (ISAV), and 76 of these samples were found to be positive, - all of them from Trøndelag and Finnmark (Tab. 6). Two locations in Trøndelag (Gaula and Steinkjerelva) were negative for presence of ISAV. The results from this study show a higher prevalence of ISAV in salmon collected in the sea (Altafjord, Agdenes, Vikna and Namsfjorden) versus the adjoining rivers (Tab. 6, Fig. 7). A chi Square test (H_0 Hypothesis: *The prevalence of ISAV in wild salmon from the sea is not different from that in the rivers*) showed a significant difference in the prevalence of ISAV in the sea *versus* the prevalence of ISAV in the adjoining rivers (Fig. 7). The salmonids collected from Hordaland County were all negative for presence of ISAV. The assay used will detect both the low-virulent and the virulent variants of the ISA virus. Because of the low number of ISAV positive fish in the rivers the chi-square test was not performed using the different year classes.

Table 6. Overview of number of salmon (gill tissues), collected in Finnmark, Trøndelag and Hordaland, that were tested for presence of ISAV. 1SW = one year at sea, 2SW = two years at sea, 3+SW = three or more years at sea, Un. Age = unknown age. Sea locations in blue letters.

County	**N**	**ISAV-Pos** N - %	1SW N - Pos	2SW N - Pos	3+SW N - Pos	Un.age-pos N - Pos
Finnmark						
Altafjorden	81	26 – 31.7	21 – 8	22 - 7	39 - 11	0 - 0
Altaelva	62	3 – 4.8	26 – 2	9 - 0	24 - 1	3 - 0
Trøndelag						
Agdenes	85	9 – 10.5	51 - 5	30 - 3	2 - 0	2 - 1
Gaula	22	0 – 0.0	9 - 0	6 - 0	3 - 0	4 - 0
Stjørdalselva	97	2 – 2.0	7 - 2	58 - 0	28 - 0	4 - 0
Steinkjerelva	35	0 – 0.0	1 - 0	33 - 0	1 - 0	0 - 0
Vikna	112	13 – 11.6	43 - 5	63 - 6	6 - 2	0 – 0
Namsfjorden	121	21 – 17.4	56 - 10	54 - 9	11 - 2	0 – 0
Namsen	60	2 – 3.3	4-0	26-1	14-1	18 - 0
Hordaland						
Sørfjorden	60	0 – 0.0	12 - 0	34 - 0	10 – 0	4 - 0
Vosso	4	0 – 0.0	2 - 0	1 – 0	1 – 0	0 – 0
Opo	19	0 – 0.0	8 – 0	11 – 0	0 – 0	0 – 0
Steindalselva	7	0 – 0.0	3 – 0	4 – 0	0 - 0	0 – 0
Granvin	27	0 – 0.0	5 – 0	17 – 0	5 – 0	0 – 0
Ådland	24	0 – 0.0	14 - 0	10 – 0	0 - 0	0 – 0

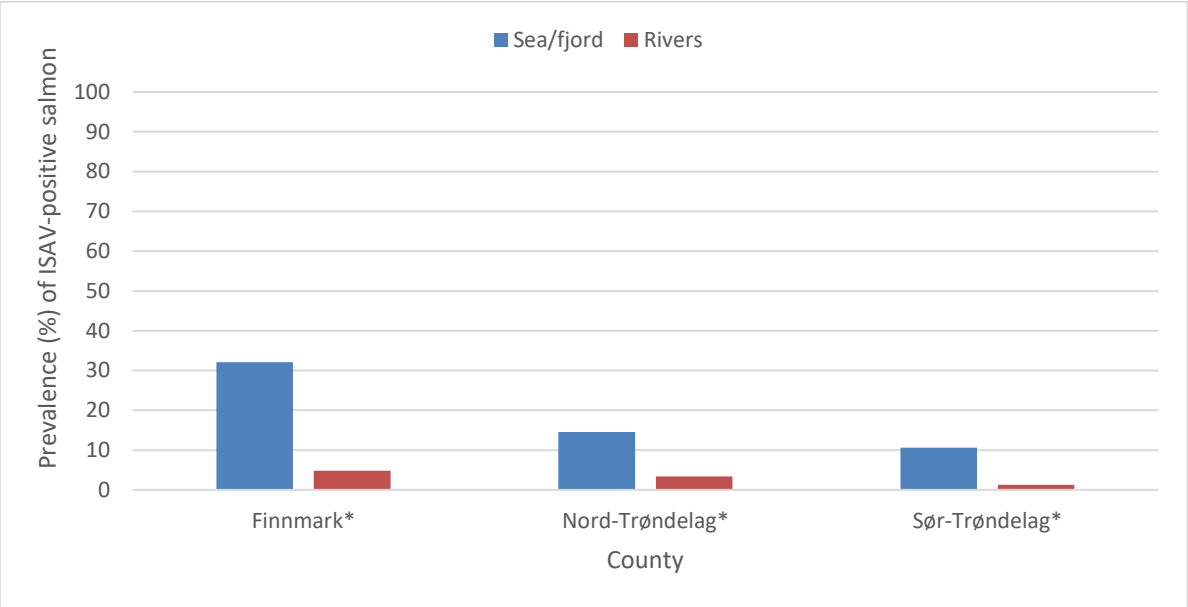

Figure 7. Prevalence of ISAV in wild Atlantic salmon (*S. salar*) from sea/fjord sites and adjoining rivers in Finnmark, Nord-Trøndelag and Sør-Trøndelag. Finnmark sea/fjord N = 81, River N = 62, Nord-Trøndelag sea N = 233 river N = 60, Sør-Trøndelag Sea N = 85 river N = 154. * = a significant difference in prevalence (Chi square, $\alpha = 0.01$).

The difference between prevalence of ISAV in sea *versus* river is significant for Finnmark, Nord-Trøndelag and Sør-Trøndelag ($\alpha = 0.01$). The number of target RNA from ISAV in wild salmon were in most positive fish low (Ct values > 30) indicating a carrier status or recent infection. However, at the sea locations, except Agdenes, Ct values below 30 were detected in a few salmon (Fig. 8). The low Ct values indicate viraemia and Ct values below 25 are found in salmon suffering from ISA. The lowest Ct values (15.9 and 19.4) were found in salmon collected in Altafjorden, and one salmon collected in Altaelva had a Ct value of 21.1. The lowest Ct values in salmon collected from Vikna and Namsfjorden were 24.5 and 23.0, respectively.

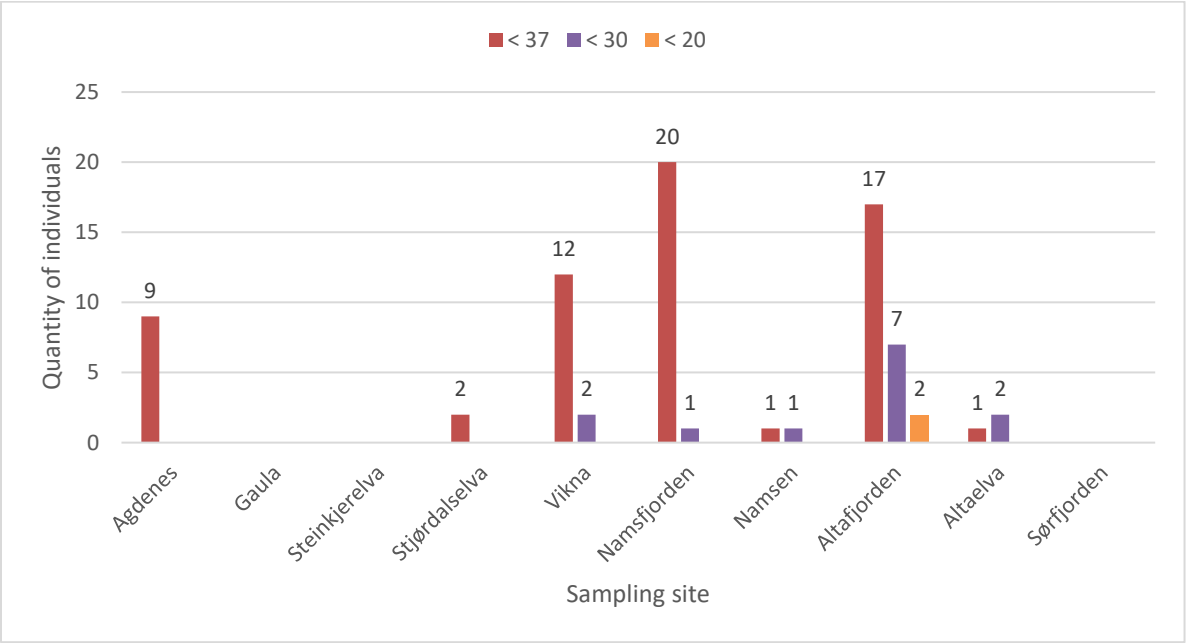

Figure 8. Grouping of ISAV positive wild Atlantic salmon (*S. salar*) with respect to the amount of target RNA based on real time RT PCR on gill tissues. The columns represent the number of individuals with Ct values in the ranges; 30-37, 20-29, and below 20

Segment six, the hemagglutinin-esterase gene, from ISAV obtained from a few salmon was sequenced and compared with ISAV sequences already published from farmed and wild salmon in the eastern North Atlantic (Nylund et al., 2019). The phylogenetic analysis showed that they were closely related to ISAV previously found in wild and farmed salmon in Norway (Fig. 9).

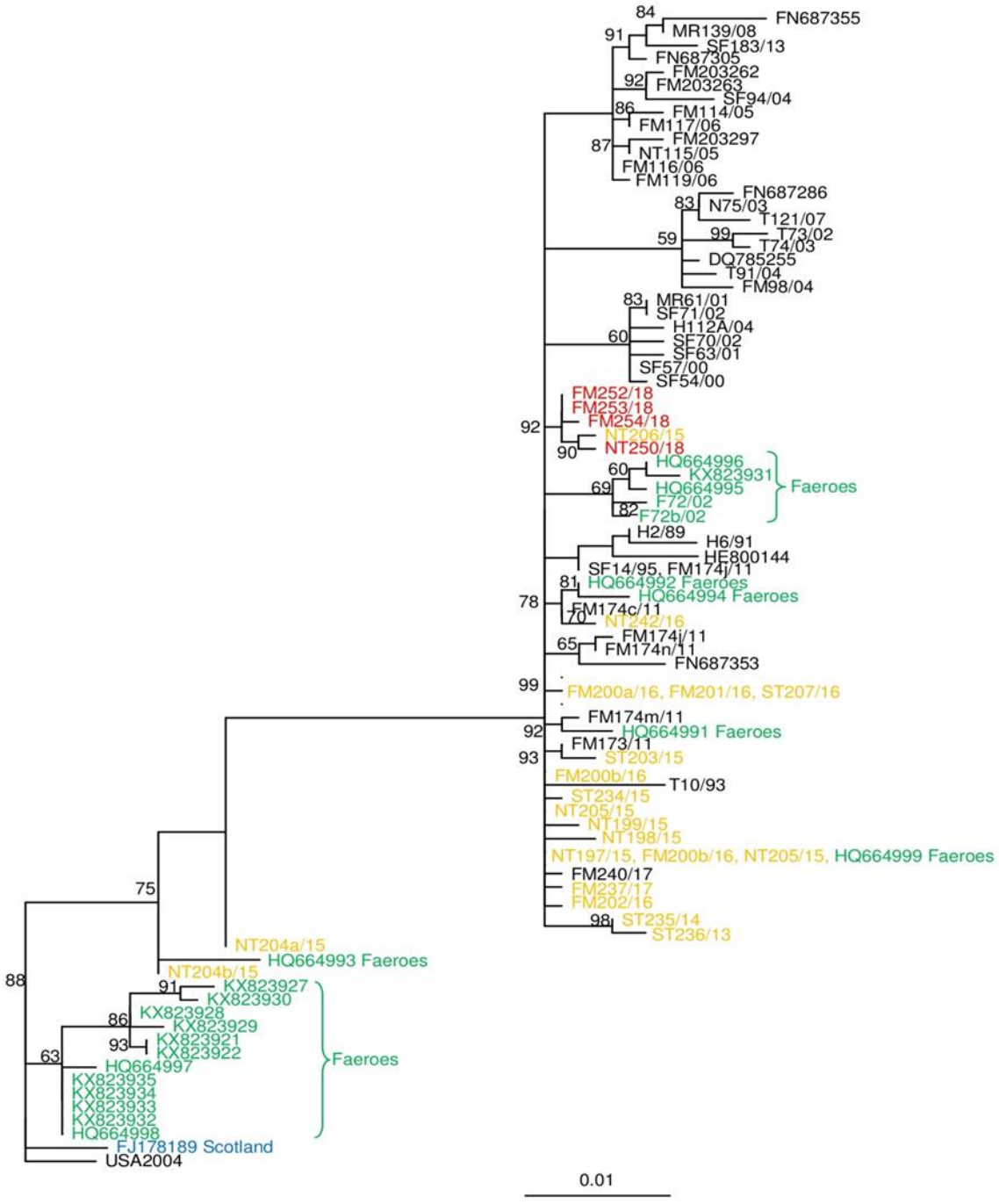

Figure 9. The phylogenetic relationship of ISAV from wild salmon collected in 2018 (red). ISAV from wild salmon collected previous years (yellow). ISAV from farmed salmon in Norway (black).

Piscine orthoreovirus

Out of the 787 samples analysed 138 were positive for PRV. PRV was detected in Atlantic salmon from all counties included in this study and in 7 of 10 examined rivers (Tab. 7). Three rivers in Hordaland were negative. The results from this study show a higher prevalence of PRV in fish collected in sea versus the adjoining rivers for all counties (Tab. 6, Fig. 10). The prevalence of PRV-positive salmon was higher in the sea than the adjoining rivers for all fish-groups sorted by age in Sør-Trøndelag and Nord-Trøndelag (Figs. 11, 12).

Table 7. Prevalence of Piscine orthoreovirus in wild Atlantic salmon (*S. salar*) from Finnmark, Trøndelag and Hordaland in 2018. * Fish held in tanks for some time before sampling. 1SW = one year at sea, 2SW = two years at sea, 3+SW = three or more years at sea, Un. Age = unknown age. Sea locations in blue letters.

County	**N**	**PRV-Pos** N - %	1SW N - Pos	2SW N - Pos	3+SW N - Pos	Un.age-pos N - Pos
Finnmark						
Altafjorden	81	5 – 6.2	21 - 3	21 - 0	39 - 2	-
Altaelva	62	1 – 1.6	26 - 0	9 - 0	24 - 1	3 - 0
Trøndelag						
Agdenes	56	25 – 44.6	27 - 12	24 - 12	3 - 1	2 - 0
Gaula	22	4 – 18.2	9 - 3	6 - 1	3 - 0	4 - 0
Stjørdalselva	97	12 – 12.4	7 - 1	58 - 7	28 - 3	4 - 1
Steinkjerelva	35	2 – 5.7	1 - 0	33 - 2	1 - 0	-
Vikna	112	55 – 49.1	43 - 23	63 - 27	6 - 5	0 – 0
Namsfjorden	121	17 – 14.0	56 - 11	54 - 5	11 - 1	0 - 0
Namsen	60	6 – 10.0	4 - 0	26 - 4	14 - 2	18 - 0
Hordaland						
Sørfjorden	60	7 – 11.6	12 - 0	34 - 3	10 - 4	4 - 0
Vosso*	4	1 – 25.0	2 - 1	1 - 0	1 - 0	-
Opo*	19	3 – 15.8	8 - 1	11 - 2	0 - 0	-
Steindalselva*	7	0 - 0	3 - 0	4 - 0	0 - 0	-
Granvin*	27	0 - 0	5 - 0	17 - 0	5 - 0	-
Ådland*	24	0 - 0	14 - 0	10 - 0	0 - 0	-

A chi square test (H_0 hypothesis: *the prevalence of PRV in wild salmon from the sea is not different from that found in salmon from rivers*) showed that there are significant differences in the prevalence of PRV in sea *versus* the prevalence of the same pathogen in the adjoining rivers for Sør-Trøndelag and Nord-Trøndelag ($\alpha = 0.01$). Performing the same test on salmon sorted by age results showed that there is significant difference in prevalence of PRV in the sea *versus*

adjoining rivers for the 2 SW-salmon from Sør-Trøndelag ($\alpha = 0.01$) but not for the other groups.

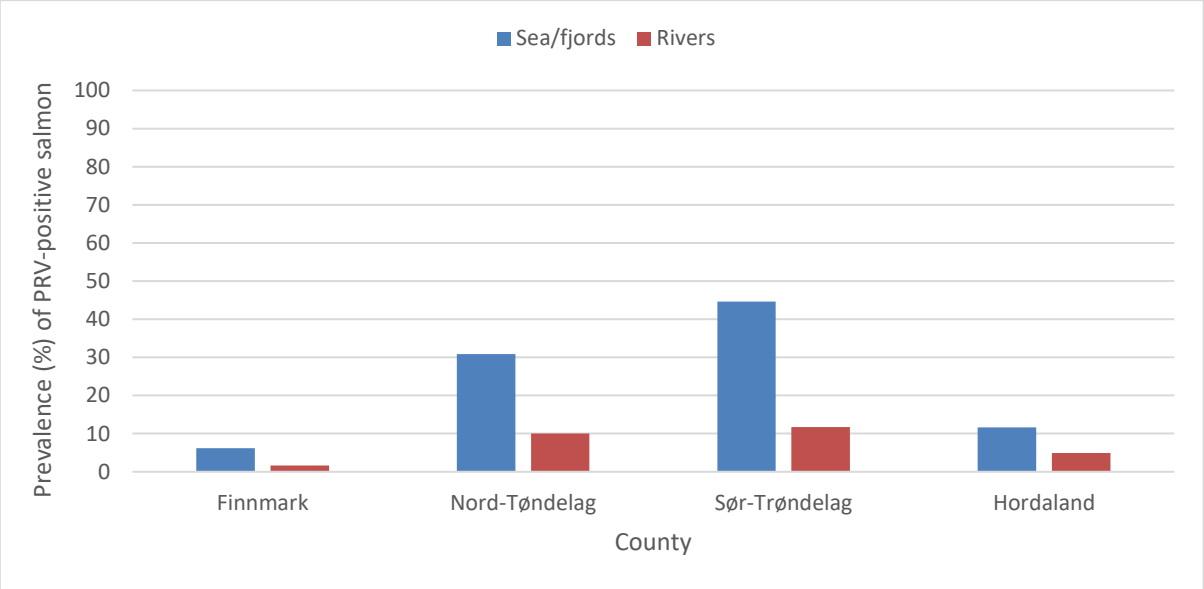

Figure 10. The prevalence of PRV in wild Atlantic salmon (*S. salar*) from sea/fjord sites and adjoining rivers in Finnmark; sea N = 81 river N = 62, Nord-Trøndelag; sea N = 233 river N = 60, Sør-Trøndelag; sea N = 56 river N = 154, Hordaland; sea N = 60 river N = 81.

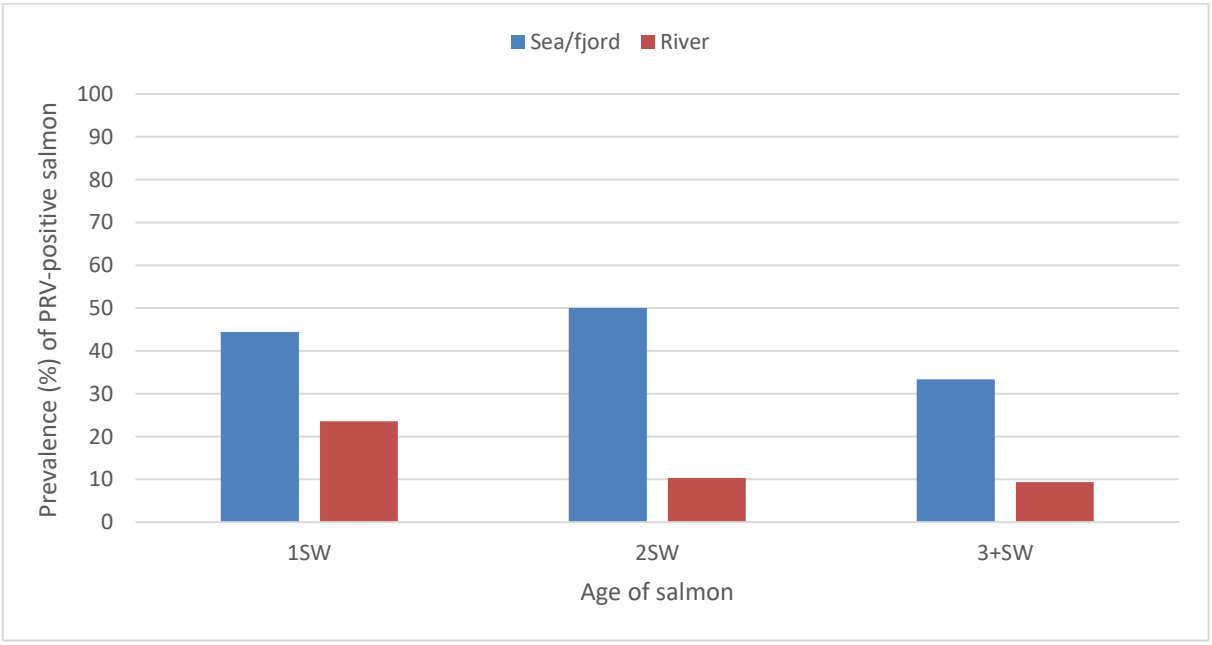

Figure 11. Prevalence of piscine orthoreovirus (PRV) in wild Atlantic salmon in sea (Agdenes) and adjoining rivers (Gaula, Stjørdalselva and Steinkjerelva) in Sør-Trøndelag by age. 1SW sea N = 27 river N = 17, 2SW sea N = 24 river N = 97, 3+SW sea N = 3 river N = 32.

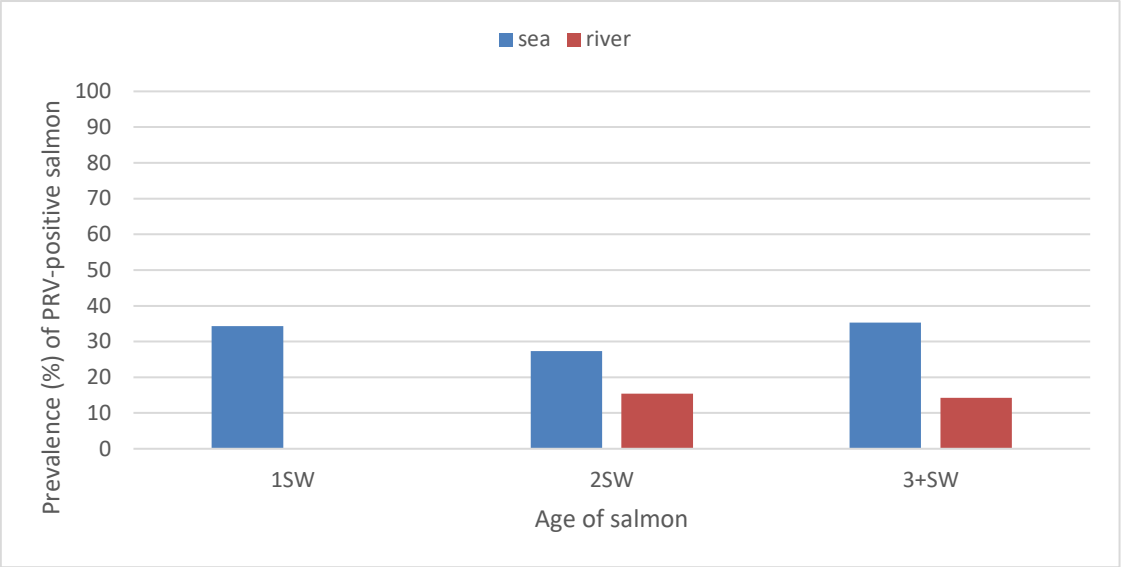

Figure 12. Prevalence of piscine orthoreovirus in wild Atlantic salmon (*S. salar*) in sea (Vikna and Namsfjorden) and adjoining river (Namsen) in Nord-Trøndelag by age. 1SW sea N = 99 river N = 4, 2SW sea N = 117 river N = 26, 3+SW sea N = 17 river N = 14.

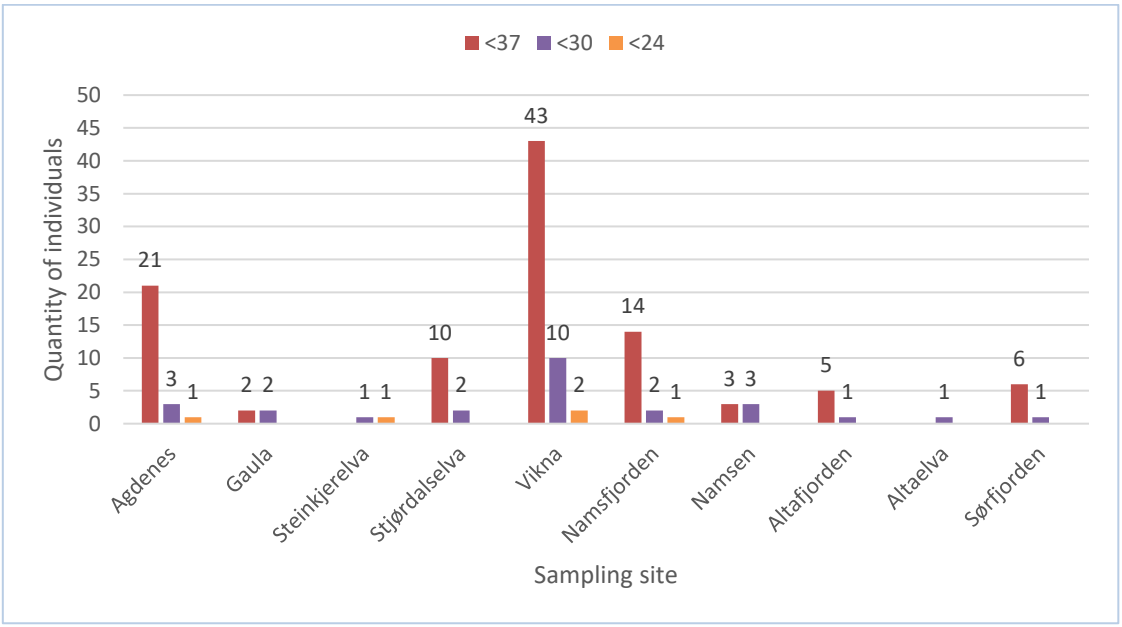

Figure 13. Grouping of PRV positive wild Atlantic salmon with respect to the amount of target RNA based on real time RT PCR of gill tissues. The columns represent the quantity of individuals with Ct values in the range 30-37, 20-30 and < 20 indicating low, middle and high viral load respectively.

In most of the PRV-positive wild salmon the amount of target RNA was found to be low (Ct values above 30) (Fig. 13) which indicates a carrier status or recent infection. Two of the sea locations stand out compared to the others, Agdenes in Sør-Trøndelag and Vikna in Nord-

Trøndelag both with a prevalence over 40 % of salmon infected with PRV (Tab. 7). Ct values below 24 are found in farmed Atlantic salmon suffering from HSMI (Løvoll et al., 2012; Wessel et al., 2012). Wild salmon with Ct values under 24 was detected at both sea and river locations: Agdenes (Ct value 17.4), Steinkjerelva (Ct value 23.3), Vikna (Ct value 19.4 and 19.8) and Namsfjorden (Ct value 22.5).

PRV was also detected in five out of the seven escaped farmed salmon capture in Vosso (Ct range 27.1-32.7).

Salmon gill poxvirus

139 of the 816 analysed samples were positive for salmonid gill poxvirus (SGPV). The virus was present in wild Atlantic salmon from all counties included in this study. Only two sampling sites were negative; Altafjorden (N = 81) and Vosso (N = 4). Seven farmed salmon caught in Vosso were also analysed for the presence of Salmonid gill poxvirus, and the virus was found in one of them (Ct value 18.3).

Salmon gill poxvirus, SGPV was detected in nine of ten rivers and at three out of five sea-locations (Tab 8. Fig. 14) indicating thatit occurs with a higher prevalence in rivers than in the sea. Sørfjorden and Vikna differ from the other sea locations with prevalences of 40.0 % and 14.3 %, respectively. SGPV was only detected in 2 out of 121 salmon from Namsfjorden and in 8 out of 60 in the adjoining river, Namsen.

Table 8. Prevalence of Salmonid gill poxvirus (SGPV) in wild Atlantic salmon (*S. salar*) in Finnmark, Trøndelag and Hordaland. 1SW = one year at sea, 2SW = two years at sea, 3+SW = three or more years at sea, Un. Age = unknown age. Sea locations in blue letters. * Fish held in tanks for some time before sampling.

County	**N**	**SGPV-Pos** N - %	1SW N - Pos	2SW N - Pos	3+SW N - Pos	Un.age-pos N - Pos
Finnmark						
Altafjorden	81	0 - 0	21 - 0	21 - 0	39 - 0	-
Altaelva	62	25 - 40.3	26 - 8	9 - 5	24 - 9	3- 3
Trøndelag						
Agdenes	85	1 – 1.2	27 - 1	24 - 0	3 - 0	-
Gaula	22	6 - 27.3	9 - 4	6 - 2	3 - 0	-
Stjørdalselva	97	10 - 10.3	7 - 0	58 - 5	28 - 5	-
Steinkjerelva	35	8 - 22.8	1 - 0	33 - 0	1 - 0	-
Vikna	112	16 - 14.3	43 - 2	63 - 12	6 - 2	-
Namsfjorden	121	2 – 1.6	56 - 0	54 - 1	11 - 1	-
Namsen	60	8 - 13.3	4 - 1	26 - 5	14 - 0	18 - 2
Hordaland						
Sørfjorden	60	24 - 40.0	12 - 6	34 - 13	10 - 4	4 - 1
Vosso*	4	0 - 0	2 - 0	1 - 0	1 – 0	-
Opo*	19	12 - 63	8 - 4	11 - 8	0 - 0	-
Steindalselva*	7	7 - 100	3 - 3	4 - 4	0 - 0	-
Granvin*	27	1 - 3.7	5 - 0	17 - 1	5 - 0	-
Ådland*	24	19 - 79.2	14 - 11	10 - 8	0 - 0	-

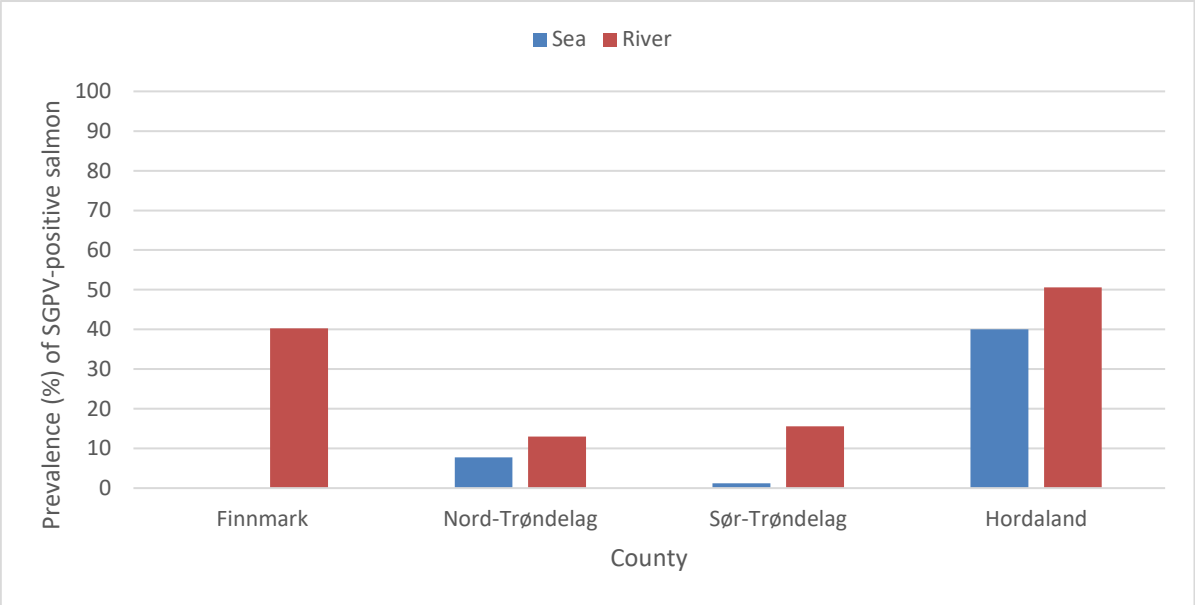

Figure 14. Prevalence of Salmonid gill poxvirus in wild Atlantic salmon (*S. salar*) in sea and rivers sorted geographically. Finnmark sea N = 81, river N = 62, Nord-Trøndelag sea N = 233, river N = 60, Sør-Trøndelag sea N = 85, river N = 154, Hordaland sea N = 60, river N = 81.

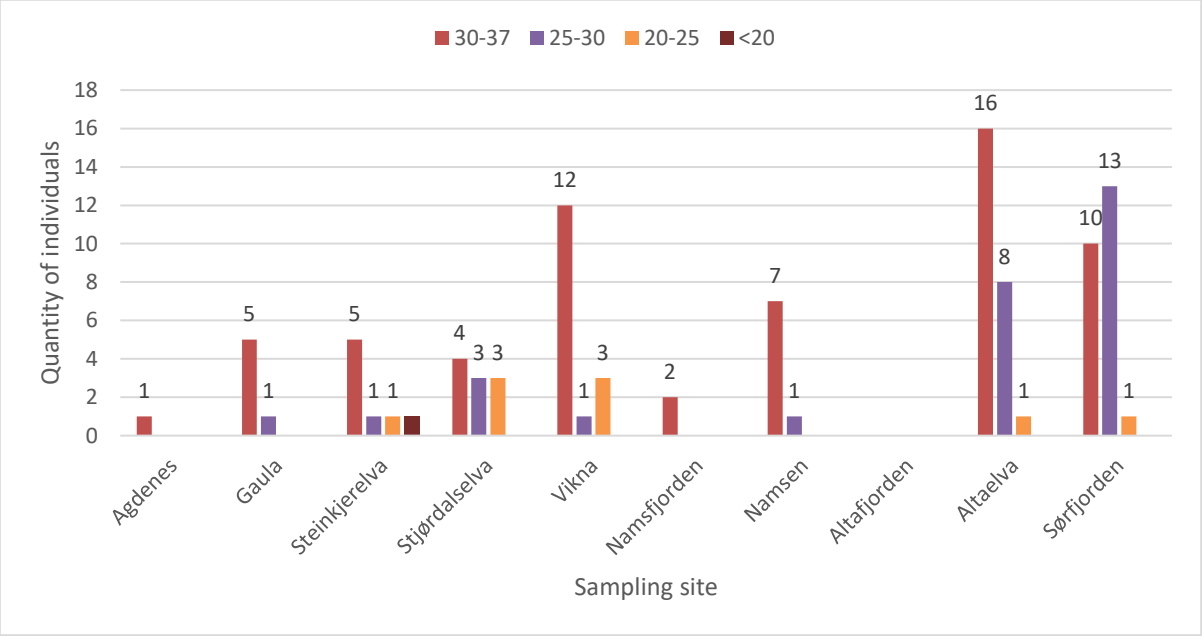

Figure 15. Grouping of SGPV positive wild Atlantic salmon (*S. salar*) with respect to the amount of target RNA based on real time RT PCR of gill tissues. The columns represent the quantity of individuals with Ct values in the ranges; 30-37, 25-30, 20-25, and <20.

Figure 15 shows the density of SGPV RNA, based on real time RT PCR Ct values, in the gill tissue samples from the positive wild salmon. The individual density of SGPV in the sea is low

compared to salmon from the adjoining rivers with some exceptions. In Nord-Trøndelag the sea location Vikna had a SGPV prevalence of 14.3 % (N = 112) and four salmon with Ct values below 30 (three below 25), compared to the adjoining river Namsen (N = 60) with a prevalence of 13.3 % and only one salmon with a Ct value below 30. Another exception is the high prevalence of SGPV positive salmon from Sørfjorden in Hordaland, a fjord with low salinity (brackish water). Gill diseases in farmed salmon are associated with Ct values below 25 (A. Nylund pers.com.).

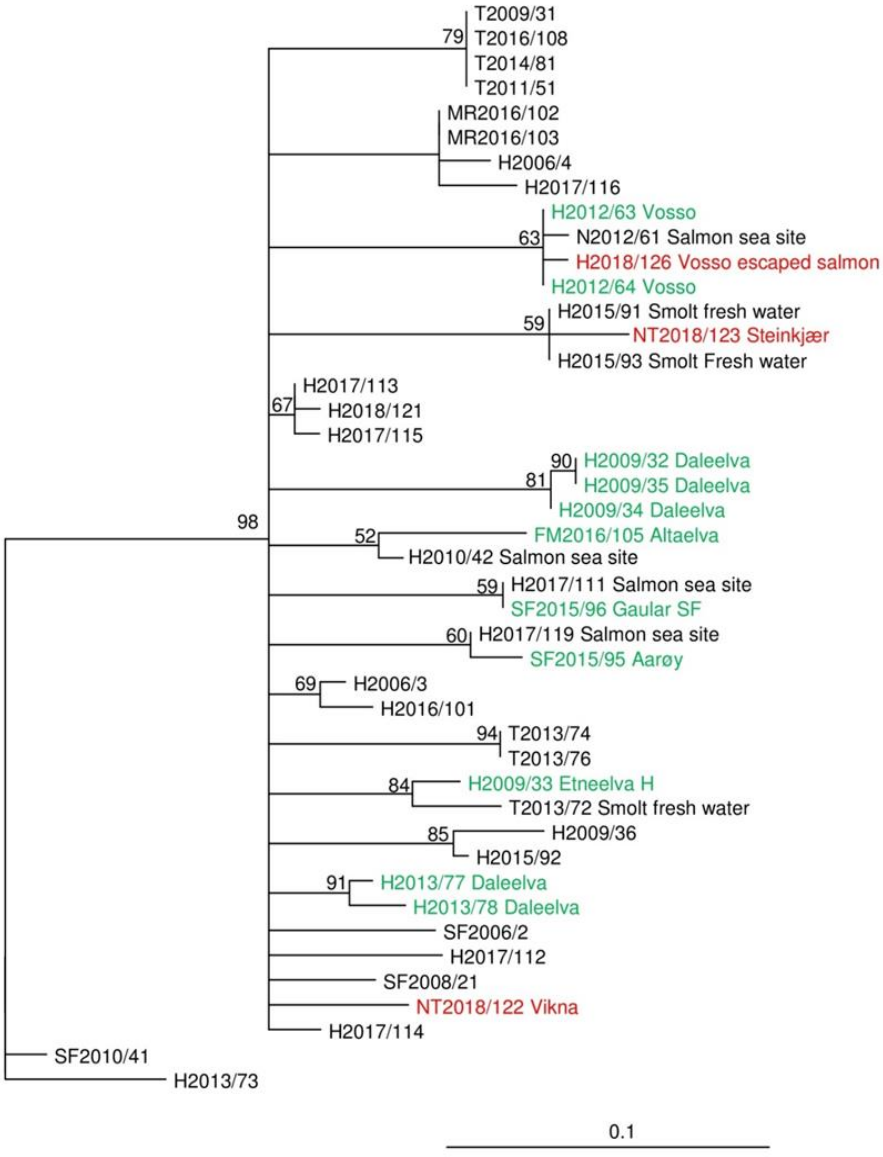

Figure 16. The phylogenetic relationship of SGPV from wild salmon in Norway compared to viruses from farmed salmon. Viruses from wild salmon included in the present study are marked with red colour, and green represent SGPV from wild salmon collected in previous years. Viruses from farmed salmon are marknad with black. H = Hordaland, SF = Sogn og Fjordane, MR = Møre og Romsdal, ST = Sør-Trøndelag, NT = Nord-Trøndelag, N = Nordland, T = Troms and FM = Finnmark.

The variable 16 (V16) from three SGPV obtained from gill tissues of salmon collected in Vosso (Hordaland) and Vikna and Steinkjerelva in Nord Trøndelag, were sequenced. A phylogenetic analysis of these viruses including sequences available from the work done by Kloster-Jensen (2018) show that the SGPV from Vosso (H2018/126) group with other viruses (H2012/63 and H2012/64) from this river and a virus (N2012/61) collected from farmed salmon in Nordland County (Fig. 16). The two viruses (NT2018/122 and NT2018/123) from Nord Trøndelag are more distantly related to each other, where NT2018/123 groups together with two viruses (H2015/91 and H2015/93) from two different smolt production sites in Hordaland County.

Piscine myocarditis virus

787 samples from Finnmark, Trøndelag and Hordaland were analysed for the presence of PMCV. The virus was detected in 10 wild salmon, where all 10 were collected in fish-traps from the sea. Six from Vikna in Trøndelag, two from Namsfjorden, and two from Sørfjorden in Hordaland. PMCV was detected from three out of the seven escaped farmed salmon collected from Vosso. The Ct values were over 30 (Ct-range 33.9 - 38.5) for all the wild salmon and under 27 (Ct-range 20.3 - 26.5) for the farmed escaped salmon.

Analysis of heart and kidney-tissues confirmed the presence of PMCV in the three escaped farmed salmon.

3.1.2 Bacteria

This study focused on four bacteria. Two of them are associated with gill disease (*Candidatus* Branhiomonas cysticola and *Candidatus* Piscichlamydia salmonis), *Yersinia ruckeri* which causes enteric redmouth disease and *Renibacterium salmoninarum* which cause bacterial kidney disease (BKD). The latter can be vertically transmitted.

Candidatus Branchiomonas cysticola

The results from this study showed that *Ca.* B. cysticola is common in wild salmon from all the included counties (Tab. 9). The prevalence of *Ca*. B. cysticola was high (over 80%) at all analysed locations (Fig. 17). The results show slightly less prevalence in freshwater compared to seawater in all counties except in Hordaland (Fig. 17). Prevalence of *Ca*. B. cysticola was 100 % for salmon held in tanks before sampling.

Table 9. Prevalence of *Candidatus* Branchiomonas cysticola in wild Atlantic salmon (*S.salar*) in Finnmark, Trøndelag and Hordaland. Sea locations marked in blue. * Fish held in tanks for some time before sampling

County	N	*C. B.* cysticola-Pos N - %
Finnmark		
Altafjorden	81	79 – 97,5
Altaelva	62	55 – 88,7
Trøndelag		
Agdenes	56	56 -100
Gaula	22	18 - 81,8
Stjørdalselva	97	81 - 83,5
Steinkjerelva	35	35 - 100
Vikna	107	107 - 100
Namsfjorden	121	115 - 95
Namsen	60	54 - 90
Hordaland		
Sørfjorden	60	59 – 98,3
Vosso*	4	4 – 100
Opo*	19	19 – 100
Steindalselva*	7	7 – 100
Granvin*	27	27-100
Ådland*	24	24 – 100

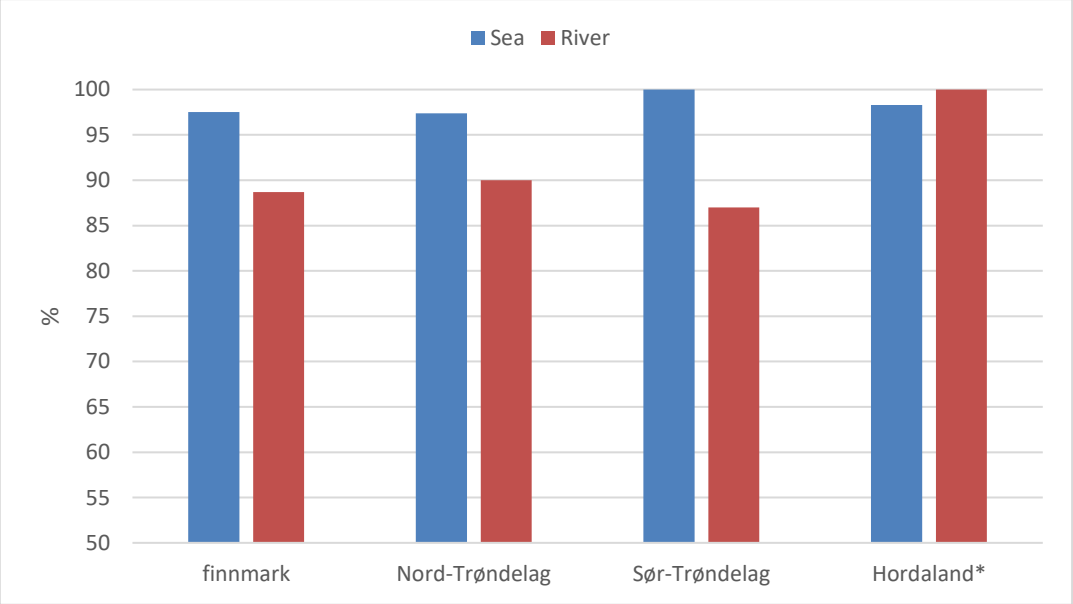

Figure 17. Prevalence of *Candidatus* Branchiomonas cysticola in sea versus the adjoining rivers in Finnmark, Nord-Trøndelag, Sør-Trøndelag and Hordaland. Finnmark sea N = 81 river N = 62, Nord-Trøndelag sea N = 228 river N = 60, Sør-Trøndelag sea N = 56 river N = 154, Hordaland sea N = 60 river N = 81. *Atlantic salmon from rivers in Hordaland were held in tanks some time before sampling.

Candidatus Piscichlamydia salmonis

Results from this study shows that *Candidatus* P. salmonis is present in wild Atlantic salmon in a large geographic area in Norway. Figure 18 shows little difference in the prevalence of *Ca*. P. salmonis in the rivers compared to the sea locations. Salmon from Gaula and the rivers in Hordaland stands out with high prevalence of *Ca*. P. salmonis although the prevalence in the salmon sampled from the rivers in Hordaland is likely due to the fish being held in tanks before sampling.

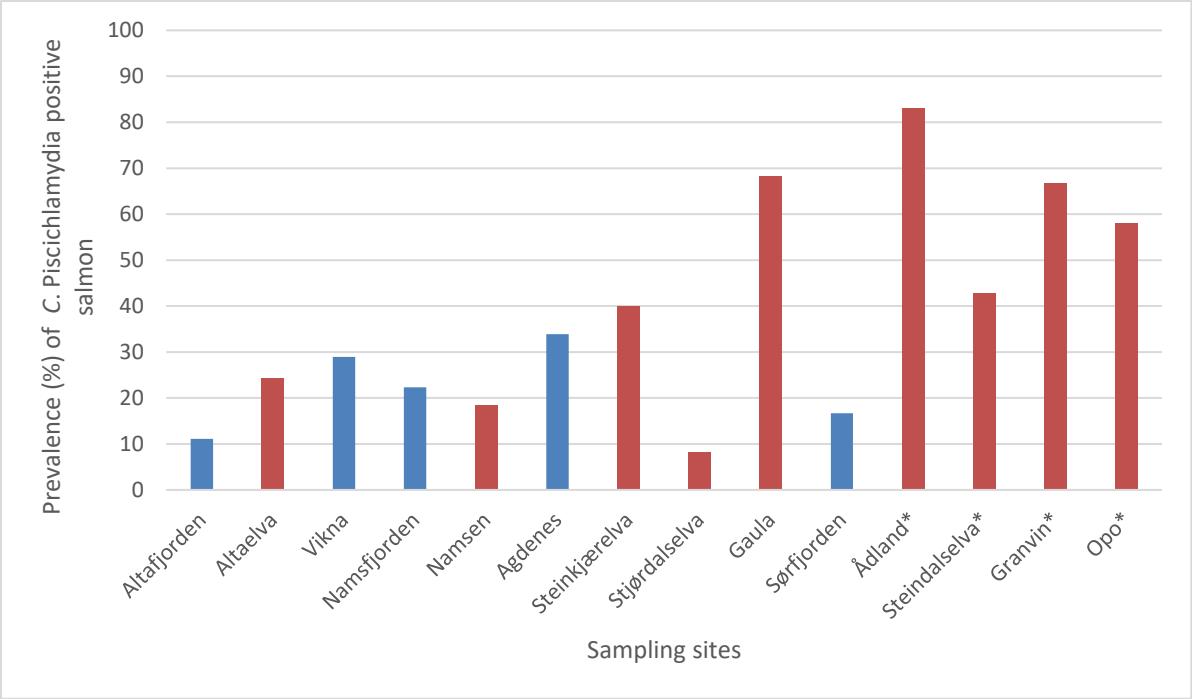

Figure 18. Prevalence of *Candidatus* Piscichlamydia in wild Atlantic salmon (*S. salar*) collected from rivers (red) and sea (blue) from Finnmark, Trøndelag and Hordaland. Altafjorden N = 81, Altaelva N = 62, Vikna N = 107, Namsfjorden N = 121, Namsen N = 60, Agdenes N = 56, Steinkjerelva N = 35, Stjørdalselva N = 97, Gaula N = 22, Ådland N = 24, Steindalselva N = 7, Granvin N = 27, Opo N = 19, Vosso N = 4. *These fish were held in tanks for some time before sampling

Yersinia ruckeri

The results from this study show that this bacterium is present in wild Atlantic salmon from both northern- and southern parts of Norway with prevalence up to 40% (Fig. 19). There is a higher prevalence in rivers than in sea. Namsen in Nord-Trøndelag and Steinkjerelva in Sør-Trøndelag stands out with prevalence over 60 %.

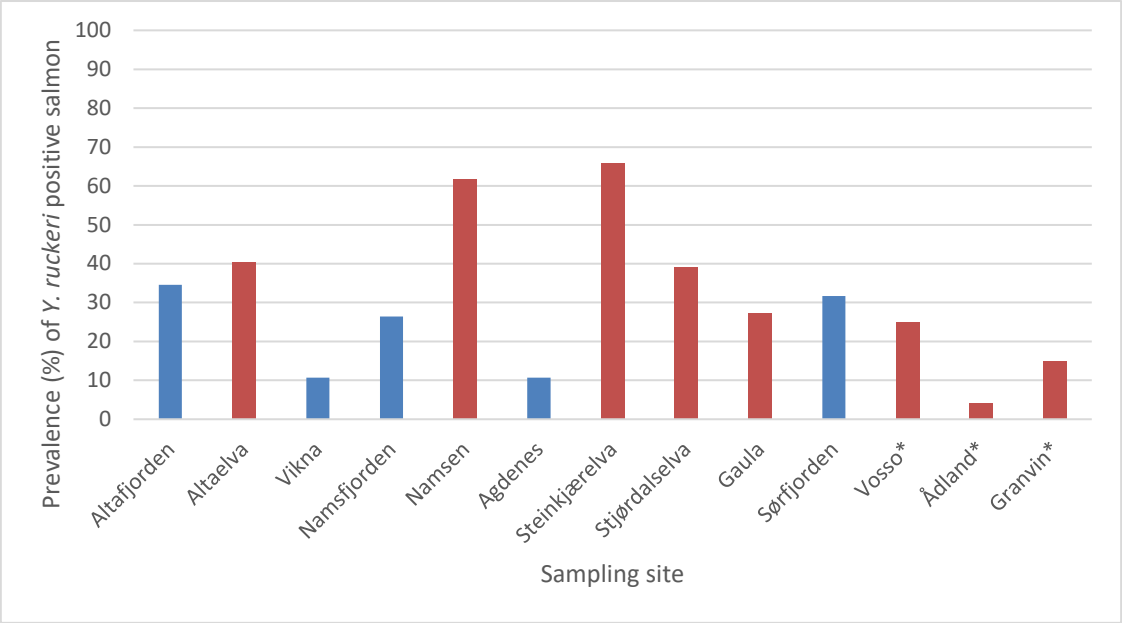

Figure 19. Prevalence of *Yersinia ruckeri* in wild Atlantic salmon (*S. salar*) collected from rivers (red) and sea (blue) from Finnmark, Trøndelag and Hordaland counties. Altafjorden N=81, Altaelva N=62, Vikna N=112, Namsfjorden N=121, Namsen N=60, Agdenes N=56, Steinkjerelva N=35, Stjørdalselva N=97, Gaula N=22, Ådland N=24, Granvin N=27. * Fish held in tanks for some time before sampling.

Renibacterium salmoninarum

780 wild Atlantic salmon from Finnmark, Trøndelag and Hordaland were analysed for *Renibacterium salmoninarum*. *R. salmoninarum* was detected in 52 of the wild salmons analysed in this study, all of them collected from sea locations. 47 from Sørfjorden (N = 60) in Hordaland, eight from Namsfjorden (N = 121) and two from Altafjorden (N = 81)

Figure 20. Prevalence of *Renibacterium salmoninarum* in wild Atlantic salmon from Trengereid in Sørfjorden, Hordaland. 1SW N = 12, 2SW N = 34, 3+SW N = 10.

Figure 20 shows the prevalence of *R. salmoninarum* from Sørfjorden in Hordaland sorted by age. This figure shows a decreasing prevalence of *R. salmoninarum* with increasing age (numbers of samples are low for 1SW and 3+SW). Three of the four salmon with unknown weight and length were positive for *R. Salmoninaum*. The amount of target RNA from *R. salmoninarum* were low in most of the positive samples with Ct values over 30 which can indicate a carrier status (Fig. 21). The lowest Ct value was 28.9, from Sørfjorden in Hordaland.

Kidney tissues from four of the *R. salmoninarum* positive fish were analysed and confirmed the presence of this bacterium.

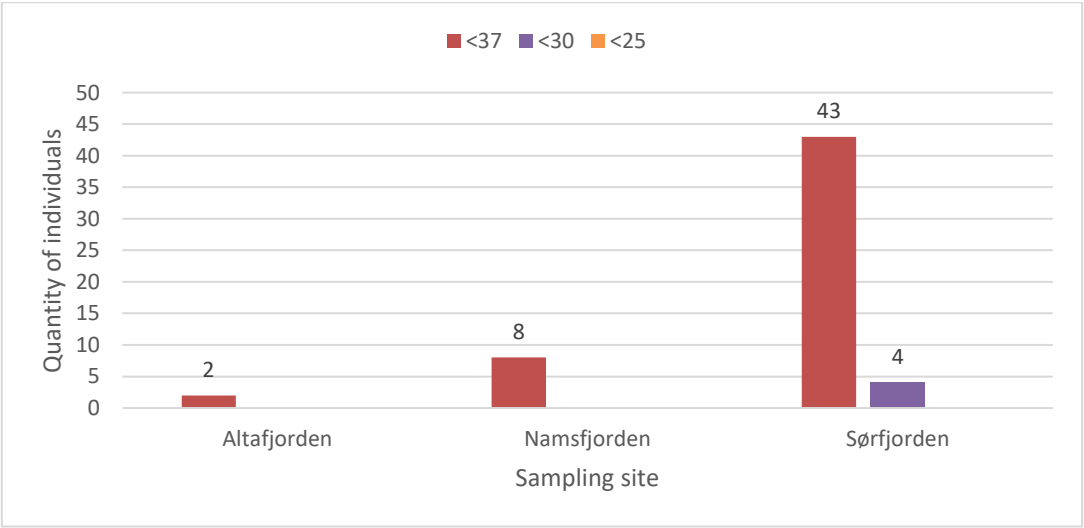

Figure 21. Grouping of *Renibacterium salmoninarum* positive wild Atlantic salmon (*S. salar*) with respect to the amount target RNA based on real time RT PCR on gill tissues. The columns represent the number of individuals with Ct values in the ranges; 30-37, 25-30 and below 25.

3.1.3 Parasites

A larger number of different parasite species have been detected in wild salmon compared to farmed salmon, but in this study the focus is on two parasites with complex life cycles (*Paranucleospora theridion* and *Parvicapsula pseudobranchicola*) and two that are transmitted directly from fish to fish (*Ichthyobodo necator* in freshwater and *Ichthyobodo salmonis* in both fresh and seawater). All 787 gill-samples were tested for the presence of *Paramoeba perurans* and were negative.

Paranucleospora theridion (Syn. *Desmozoon lepeophtheirii*)

The results from this study show that this parasite is present in wild salmon populations both in northern and southern parts of Norway (Fig. 22). Two sea locations; Vikna in Nord-Trøndelag and Sørfjorden in Hordaland stand out compared to the other locations with a prevalence over 70 %. All salmon from rivers in Hordaland had 100 % prevalence of *P. theridion*. These fish were held in tanks for some time before.

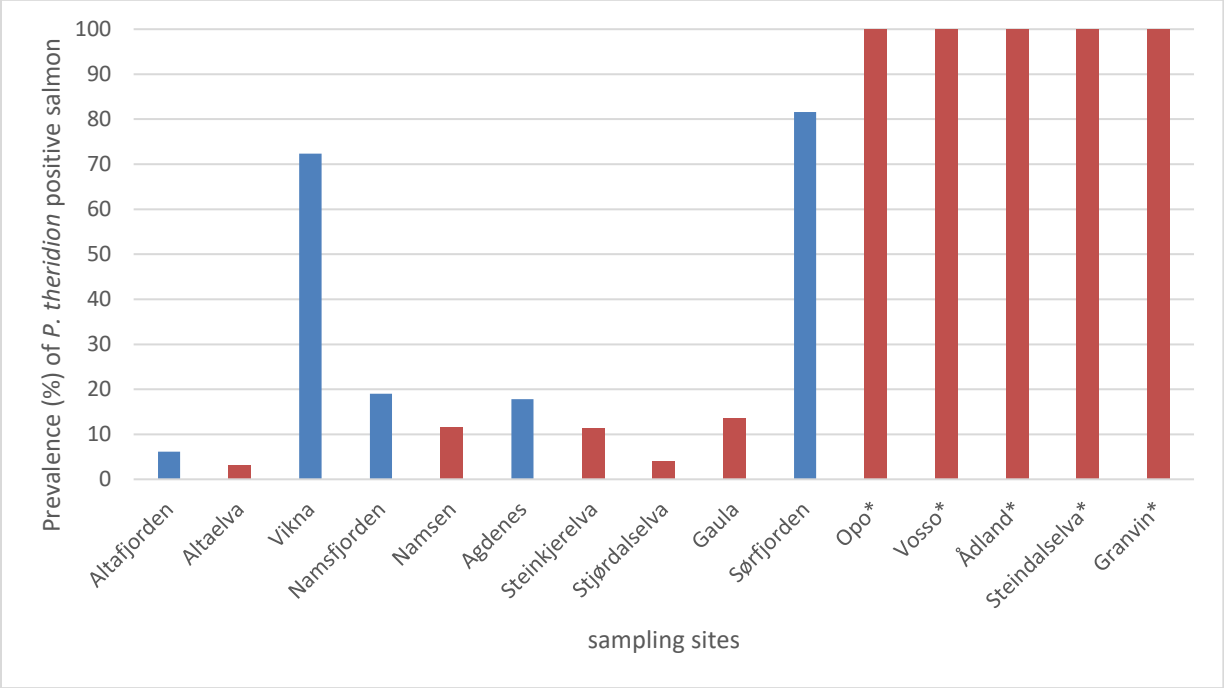

Figure 22. Prevalence of *Paranucleospora theridion* (Syn. *Desmozoon lepeoptheirii*) in wild Atlantic salmon from rivers (red) and sea (blue) in Finnmark, Trøndelag and Hordaland. Altafjorden N = 81, Altaelva N = 62, Vikna N = 112, Namsfjorden N = 121, Namsen N = 60, Agdenes N = 56, Steinkjerelva N = 35, Stjørdalselva N = 97, Gaula N = 22, Sørfjorden N = 60, Ådland N = 24, Steindalselva N = 7, Granvin N = 27, Opo N = 19, Vosso N = 4. *These fish were held in closed tanks for some time before sampling.

Parvicapsula pseudobranchicola

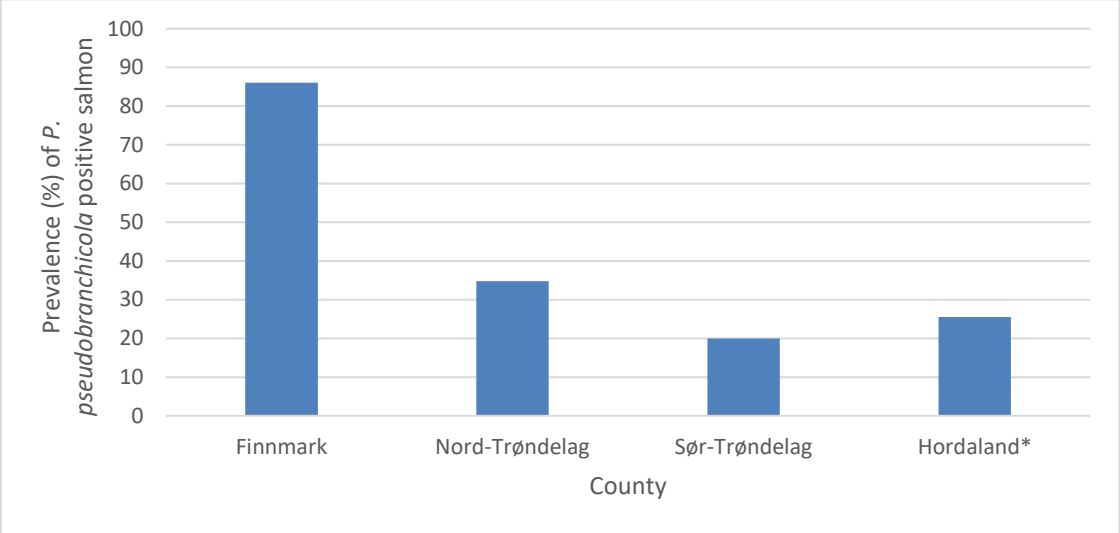

Figure 23. Prevalence of *Parvicapsula pseudobranchicola* in Finnmark, Trøndelag and Hordaland. Finnmark counties N = 143, Nord-Trøndelag N = 293, Sør-Trøndelag N = 210, Hordaland N = 141 *Fish from rivers were held in tanks for some time.

The results from this study show that there was a distinct north-south gradient in the prevalence of this parasite (Fig. 23). It is more prevalent in wild salmon in Finnmark compared to Trøndelag and Hordaland. There is no significant difference in prevalence between the different year classes of salmon from Finnmark (Altafjorden and Altaelva) (Fig. 24).

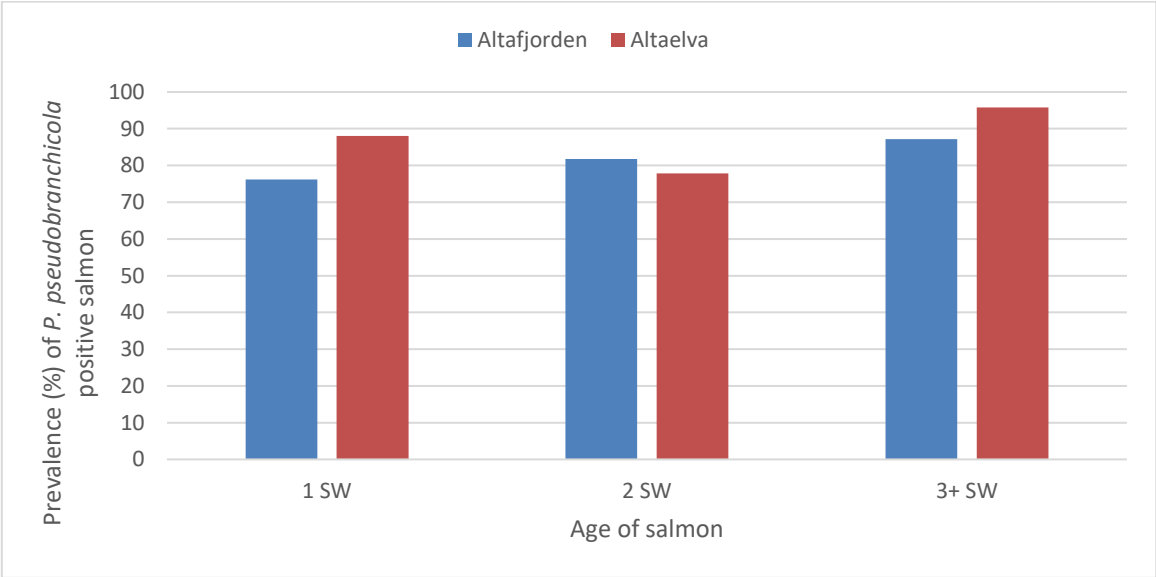

Figure 24. Prevalence of *Parvicapsula pseudobranchicola* in wild Atlantic salmon (*S. salar*) sorted by age collected from Altafjorden and Altaelva in Finnmark county. Altafjorden: 1SW N = 21, 2SW N = 22, 3+SW N = 39. Altaelva: 1SW N = 26, 2SW N = 9, 3+SW N = 39.

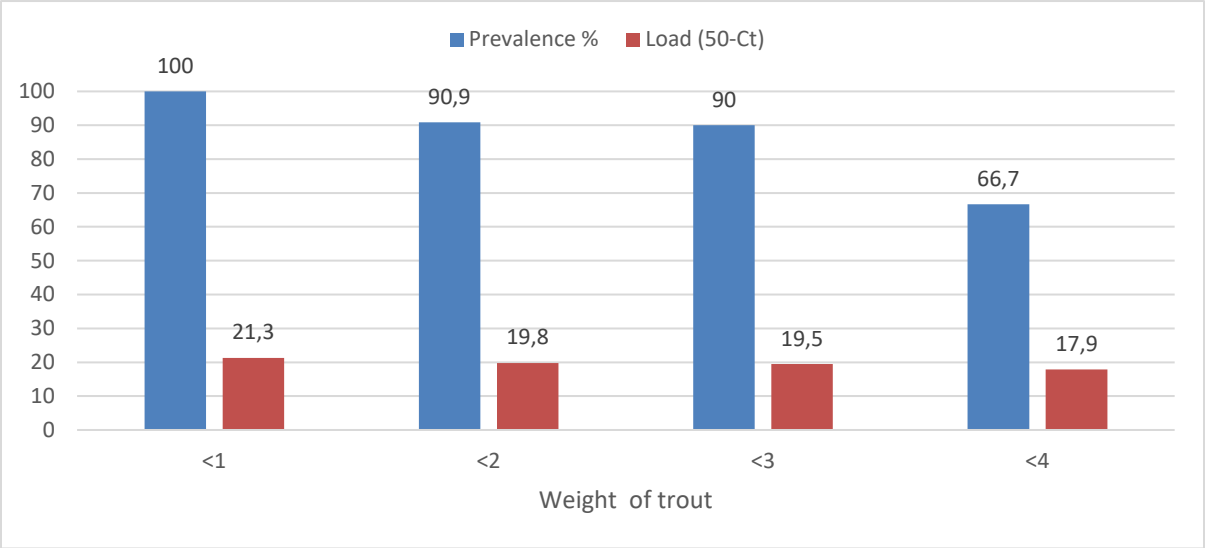

Figure 25. Load (50-Ct) and prevalence of *Parvicapsula pseudobranchicola* in trout with increasing weight collected from Altafjorden. Under one kg (<1) N = 2, between one and two kg (<2) N = 11, between two and three kg (<3) N = 10, between 3 and 4.3 kg (<4) N = 12.

The prevalence and load of *P. pseudobranchicola* from trout collected in Altafjorden (N = 35) are shown in figure 25. Both load and prevalence are decreasing with increasing weight.

Ichthyobodo spp.

Ichthyobodo spp. was detected from all the sampling sites in this study. There was no significant difference in prevalence between salmon caught in the north or the salmon caught in the south, or salmon caught in the sea versus the salmon caught in the adjoining rivers. The salmon from rivers in Hordaland that were held in closed tanks for some time before sampling represent an exception.

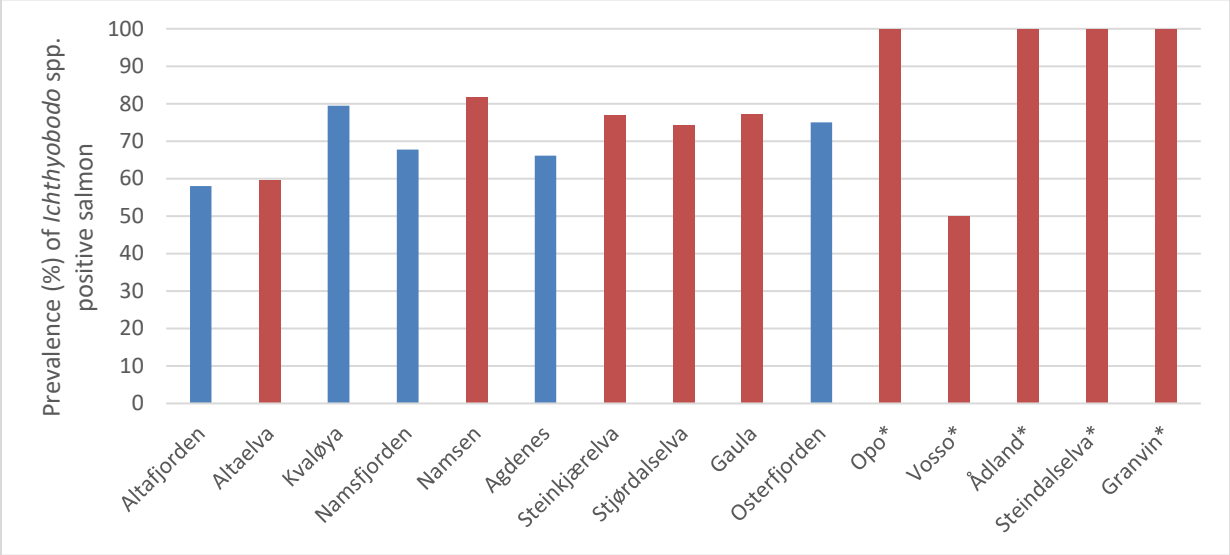

Figure 26. Prevalence of *Ichthyobodo* spp. in wild Atlantic salmon (*S. salar*) in rivers(red) and sea (blue) in Finnmark, Trøndelag and Hordaland. Altafjord N = 81, Altaelva N = 62, Kvaløya N = 112, Namsfjorden N = 121, Namsen N = 60, Agdenes N = 56, Steinkjerelva N = 35, Stjørdalselva N = 97, Gaula N = 22, Sørfjorden N = 60, Opo N = 19, Vosso N = 4, Ådland N = 24, Steindalselva N = 7, Granvins N = 27. *These fish were held in tanks for some time before sampling.

Trout (*Salmo trutta*)

Trout (*Salmo trutta*) have not been the main focus of this study, but gill tissues have been collected from some of the sites. Nine trout have been sampled from rivers in Hordaland, seven of them from Steindalselva and two from Vosso. These were held in tanks for some time before sampling. There were also some sea trout from fish traps in Finnmark, Nord-Trødelag and Sør-Trøndelag (Tab. 10).

The prevalence of trout where viruses were detected are shown in table 11, and parasites and bacteria in table 12. All samples were negative for presence of SAV, IPNV and *P. perurans*.

Table 10. Number, average weight and length of the trout (*Salmo trutta*) included in this study

	N	weight	length	Unknown
Finnmark				
Altafjorden	35	2353	69,8	-
Nord-Trøndelag				
Vikna Kvaløya	8	1975	54,4	-
Namsfjorden	7	1720	54,1	-
Sør-Trøndelag				
Agdenes	14	1223	46,3	1
Hordaland				
Steindalselva	7	1928	53,8	
Vosso	2			2

Table 11. Prevalence of virus detected in trout (*S. trutta*)

	SAV pos N-%	ISAV pos N-%	SGPV pos N-%	PRV pos N-%	ASCV pos N-%	PMCV pos N-%
Finnmark						
Altafjorden	-	2 – 5.7	-	1 – 2.8	1 – 2.8	-
Nord-Trøndelag						
Kvaløya	-	1 – 12.5	-	7 – 87.5	-	2 – 25.0
Namsfjord	-	-	-	2 – 28.6	-	-
Sør-Trøndelag						
Agdenes	-	-	1 – 7.1	1 – 7.1	-	-
Hordaland						
Steindalselva	-	-	1 – 14.3	-	-	-
Vosso	-	-	-	-	-	-

Table 12. Prevalence of bacteria and parasites detected in trout (*S. trutta*)

	Ca. B. cysticola pos N-%	*Ca*. P. salmonis pos N-%	*R. salmoninarum* pos N-%	*Y. ruckeri* pos N-%	*P. theridion* pos N-%	*P. pseudobranchicola* pos N-%	*Ichthyobodo* spp. pos N-%
Finnmark							
Altafjorden	32 – 91.4	12 – 34.3	4 – 11.4	6 – 17.1	1 – 2.8	29 – 82.8	34 – 97.1
Nord-Trøndelag							
Kvaløya	8 – 100.0	5 – 62.5	-	1 – 12.5	1 – 12.5	4 – 50.0	8 – 100.0
Namsfjorden	6 – 85.7	2 – 28.6	1 – 14.3	-	-	3 – 42.8	7 – 100.0
Sør-Trøndelag							
Agdenes	14 – 100.0	10 – 71.4	-	-	6 – 42.8	9 – 64.3	14 – 100.0
Hordaland							
Steindalselva	7 – 100.0	4 – 57.1	-	1 – 14.3	4 – 57.1	-	7 – 100.0
Vosso	-	-	-	-	-	-	-

3.2 **Diversity**

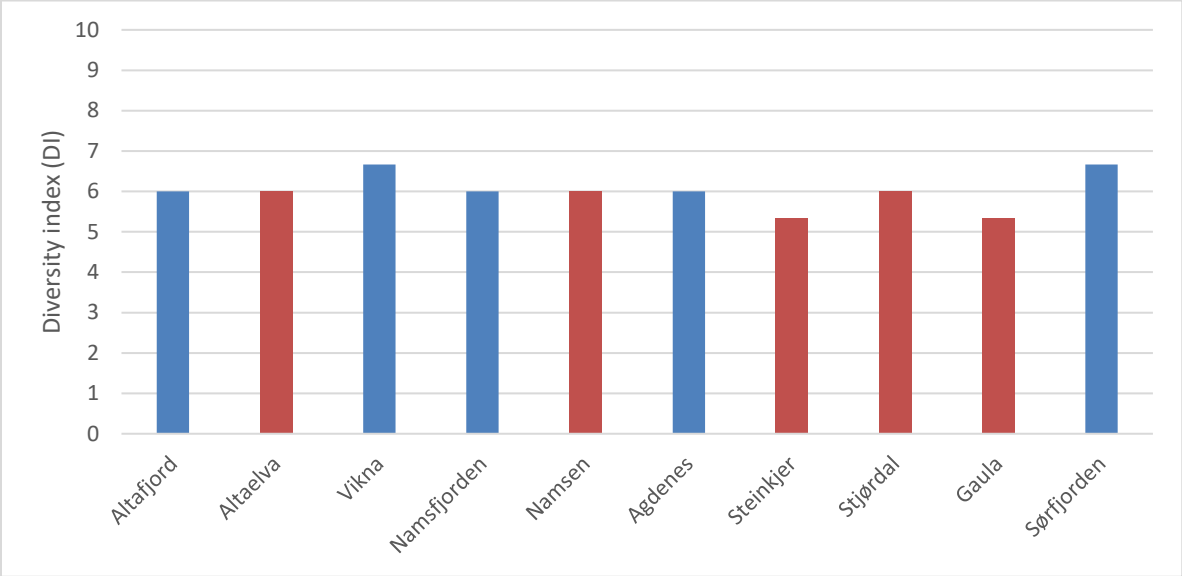

Figure 27. Diversityindex (DI) of the microparsites tested for in this study at the different collection sites. River (red) and sea/fjord (blue).

Each salmon was analysed for presence of 15 microparasites; seven viruses, four bacteria and four parasites. The results show that there was little or no difference in the total diversity of microparasites in the groups of salmon collected from the sea *versus* the salmon collected from rivers (Fig. 27). The diversity index (DI) indicating the detection of three viruses, three bacteria and three parasites (DI=6) in the salmon population at almost every location, with four exceptions; Steinkjerelva and Gaula (DI = 5.3) and Vikna and Sørfjorden (DI = 6.6). Figures 28, 29 and 30 show the salmon sorted into two groups containing individuals with either three or less microparasites and four or more. The results from Sør-Trøndelag show some higher percentage of the salmon with three or less microparasites, than four or more, at the sea location Agdenes and the river in Stjørdal. The two other sites from Sør-Trøndelag show the reverse (Fig. 28). Most of the salmon from Vikna in Nord-Trøndelag were positive for four or more microparasites, while Namsfjorden and Namsen had a lower percentage of fish detected with three or less (Fig. 29). The total load of microparasites from the two collection-sites in Finnmark was quite similar (Fig. 30). There was no significant difference in diversity between fish caught in rivers *versus* the sea.

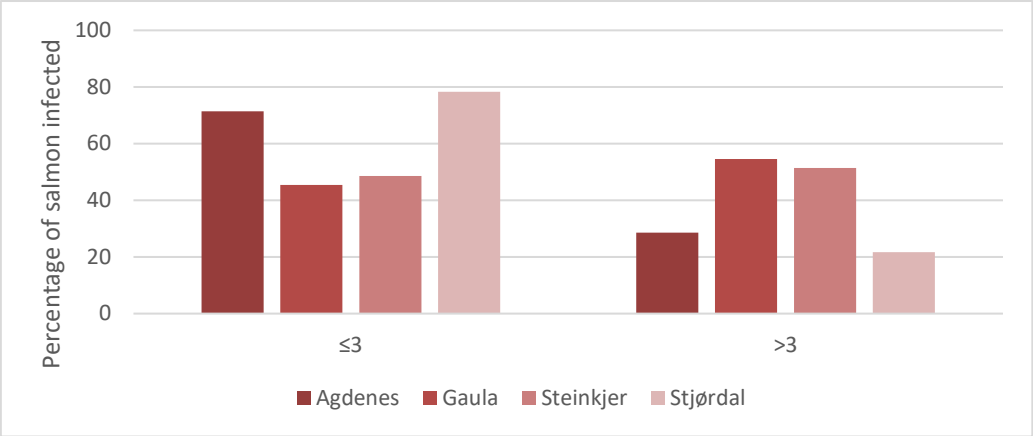

Figure 28. Percentage of wild Atlantic salmon (*S. salar*) collected from sea (Agdenes) and rivers (Gaula, Steinkjerelva and Stjørdalselva) in Sør-Trøndelag infected with three or less (≤3) or more than three (>3) microparasites.

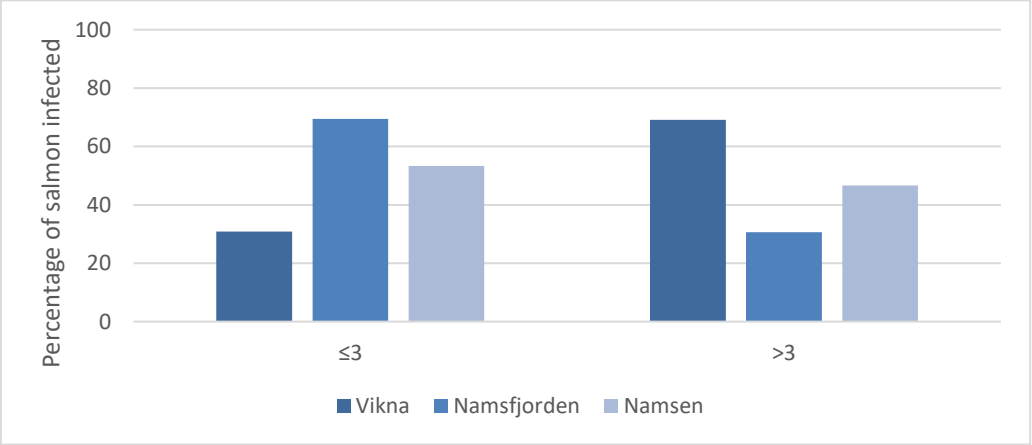

Figure 29. Percentage of wild Atlantic salmon (*S. salar*) collected from sea (Vikna and Namsfjorden) and river (Namsen) in Nord-Trøndelag infected with three or less (≤3) or more than three (>3) microparasites.

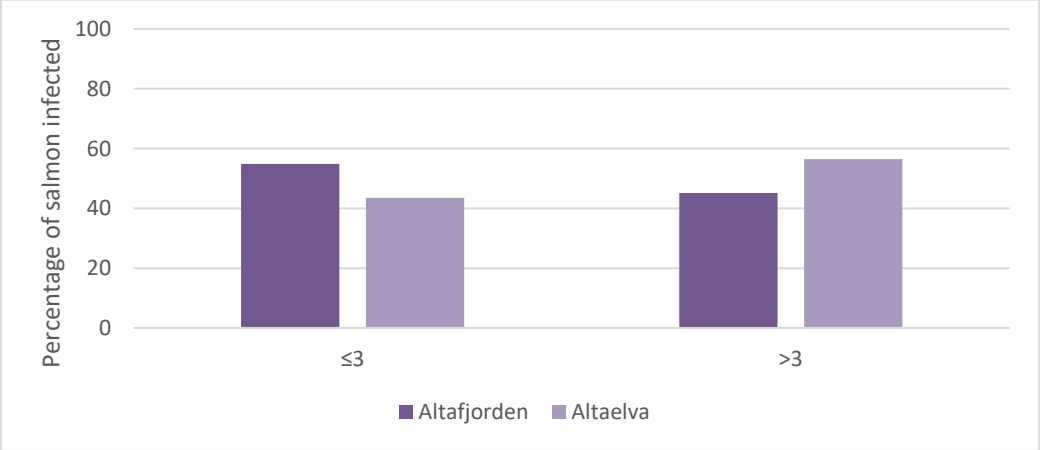

Figure 30. Percentage of wild Atlantic salmon (*S. salar*) collected from sea (Altafjorden) and river (Altaelva) in Finnmark infected with three or less (≤3) or more than three (>3) microparasites.

4 Discussion

The present study is based on real time RT PCR screening of wild salmon, from different locations along the Norwegian coast, for presence of a selection of microparasites (viruses, bacteria and protozoans). The selected microparasites are all present in farmed Atlantic salmon in Norway. The major focus is on viruses that can be transmitted directly from fish to fish and, hence, could be transmitted between farmed and wild salmon. The four bacteria included are also capable of direct transmission, but *Renibacterium salmoninarum* has not been found in farmed salmon during the last few years (Hjeltnes et al., 2019, 2018, 2017). Among the five parasites chosen *Ichthyobodo necator*, *Ichthyobodo salmonis* and *Paramoeba perurans* can be transmitted directly from fish to fish, while *Paranucleospora theridion* and *Parvicapsula pseudobranchicola* are transmitted via vectors. *I. necator* is a pure freshwater species and cannot be transmitted from farmed to wild salmon in the sea (Isaksen et al., 2010) while *I. salmonis* is present on farmed salmon in both fresh and seawater (Isaksen et al., 2011). This means that screening of wild salmon in the rivers may include both species (Isaksen et al., 2012) which makes a comparison of prevalence and densities of *Ichthyobodo* spp. on wild salmon in the sea and rivers impossible unless the screening includes two separate assays that are specific for each of these two protozoans. The assay used for detection of Ichthyobodo in this study will detect both species (Isaksen et al., 2012). Both *P. theridion* and *P. pseudobranchicola* can be found in most production areas for farmed salmon in Norway, but the former is more prevalent and associated with disease in southern Norway, while the latter is most prevalent and associated with disease in Troms and Finnmark (Hansen et al., 2015; Jørgensen et al., 2011; Nylund et al., 2018a, 2011, 2010; Sveen et al., 2012). Hence the prevalence and densities of these two parasites are expected to reflect this pattern.

4.1 Evaluation of material & methods

The salmonids included in this study have been collected from both sea-locations and rivers from several counties in Norway. The ones that are collected in the sea have been captured in fish-traps. This is considered a non-selective method as all life stages of a population may be collected including weak individuals. Salmon collected from rivers have been caught by anglers during the “salmon fishing” season. Sport-fishing may have a certain selection towards active and feeding individuals. The salmonids collected from rivers in Hordaland were used as brood stock for cultivation. They were collected by anglers during the autumn (October-November)

and held in closed tanks for some time before stripping. High prevalence of some of the microparasites might be a result of horizontal transmission in these tanks. Holding fish in tanks also include handling and stress and high prevalence here could probably be due to stressed fish swimming in contaminated water.

Escaped farmed salmon caught in fish-traps and by anglers in the rivers, have been identified based on morphological characteristics such as fin condition and signs of vaccination. Fin erosion, primerally on the dorsal and caudal fin is a well-used indicator of farmed origin salmon. Scales have been collected from all the salmonids in this study and will give a more reliable determination of age and farmed or wild origin if needed. Approximately 15 500 and 160 000 escaped farmed salmon were registered in 2017 and 2018, earlier studies from 2011 indicate that this number is probably 2-4 times higher (Skilbrei et al., 2014). Most of these fish disappear in the marine environment, but some will find their way to a river and migrate upwards with the wild salmon during the summer. The Norwegian Institute for Nature Research (NINA) and the Institute for Marine Research (IMR) investigated 175 wild salmon-stocks in Norway for genetic integrity and categorized them as green (good, no genetic impact), yellow (moderate, few genetics changes), orange (bad, moderate genetic impact) or red (severe, large genetic impact). 60 salmon populations were categorised as green, 54 as yellow, 11 as orange and 50 as red based on the results of investigation completed in 2017. The populations included in this study were categorised as red (Ådland, Opo, Granvin, Steinsdal and Vosso), yellow (Gaula, Namsen and Alta) and green (Stjørdal and Steinkjer). The incidence of escaped farmed salmon in the rivers was also estimated and indicated that there were over 10 % escaped farmed salmon in Opo, Granvin and Steindalselva, approximately 10% in Vosso and below 10 % for the remanding rivers in this study.

Farmed salmon that escape early in the production cycle can be difficult to determine as farmed due to few signs of a life in a cage, i.e. they can be very similar to the wild salmon and can be hard to identify without genetic testing. There is little reason to believe that there are any escaped salmon registered as wild salmon in this study. The Atlantic salmon from the stocks marked as red, and with a high percentage of farmed salmon in the rivers, were collected as brood stock for the stock enhancement purposes of rivers in Hardanger and were genetically tested to identify if they were farmed salmon or hybrids of farmed and wild salmon.

4.2 Viruses

4.2.1 Salmonid alphavirus (SAV)

Outbreaks of PD caused by SAV3 have been common in Western Norway for more than two decades (Hodneland et al., 2005; M. D. Jansen et al., 2010; Mona D. Jansen et al., 2010; Karlsen et al., 2006; Kristoffersen et al., 2009; Stormoen et al., 2013; Taksdal et al., 2007), and about ten year ago a new genotype of the virus, SAV2, was introduced to Norway and is now causing PD in farmed salmon in Møre og Romsdal and Trøndelag (Hjortaas et al., 2016, 2013; Karlsen et al., 2014b).There were 163 registered outbreaks of PD at aquaculture sites in Norway in 2018 (Bang Jensen et al., 2018). 63 of these caused by SAV2 in Møre og Romsdal, Sør-Trøndelag and Nord-Trøndelag (north of Hustadvika). SAV3 caused 98 outbreaks south of Hustadvika and most of them located in Hordaland and Rogaland. Figure 31 shows aquaculture sites with suspicion or detection of SAV when the majority of the wild salmonids in this study were collected in the sea (May 2018) in Hordaland (A) and Trøndelag (B). SAV was not detected in farmed salmon in Finnmark during the collection period though there have been a few outbreaks in this county (Hjeltnes et al., 2019; Jansen et al., 2017; Karlsen et al., 2006).

It is believed that SAV can transmit between farms by currents (passive horizontal transmission) (Kristoffersen et al., 2009; Stene et al., 2014), and , hence, it is possible that wild migrating salmon can be exposed to this virus in areas with high a density of fish farms with PD-outbreaks. It was not possible to detect SAV in the wild salmon collected at the sampling sites in either Trøndelag or Finnmark. There are only sporadically outbreaks of PD in Finnmark, and it was therefore little reason to believe that migrating salmon in this area should become infected. Previous testing of wild salmon from Finnmark has also been negative (Madhun et al., 2018). The situation in Trøndelag is, however, very different with high numbers of outbreaks of PD every year. Wild salmon from rivers in Trøndelag have been analysed for presence of SAV since 2013, without any detection (Nylund and Plarre, 2017, 2016, 2015, 2014, 2013), but a few escaped SAV positive farmed salmon have been found in this area: one in Namsfjorden in 2016 and three in a fish trap at Agdenes (2015 and 2017). One possible explanation for the lack of SAV positive wild salmon in Trøndelag could be that the number of returning salmon to this area is low compared to the number of farmed salmons. One farm contains more salmon than the total number of wild salmons returning to Trøndelag. The high number of farmed salmon at each locality should increase the chances for acquiring a virus passively transmitted

in sea water, and when the virus is present at such a locality the high density of farmed salmon at such a production site will make it easier for the virus to spread to non-infected salmon at the site. However, this hypothesis does not seem to be true for the situation in Hordaland County where three wild salmon were positive for presence of SAV. SAV was detected from four salmon in Hordaland County; one farmed escaped salmon and three wild salmon all with high Ct values indicating little target template and therefore low viral loads. SAV has also been detected earlier from both mature and juvenile wild salmon in rivers in western Norway (Glover et al., 2018; Nylund, 2013; Nylund et al., 2009). The main reservoir for SAV in Hordaland today is most likely farmed salmon, but it is possible that wild salmonids represent the original reservoir for SAV3, a virus that was first detected in this area (Karlsen et al., 2014a).

Lund et al. (2016) showed in an experiment that salmon which have been infected with PRV are less receptive to SAV than salmon naïve to PRV. The prevalence of PRV in wild salmon in Trøndelag was found to be 44.6 % in Sør-Trøndelag (Agdenes) and 49.1 % (Vikna) 14.0 % (Namsfjorden) in Nord-Trøndelag. The high prevalence of PRV might therefore have had an impact on the lack detection of SAV in wild salmon. However, both PRV and SAV were detected from one of the escaped farmed salmon captured in Vosso.

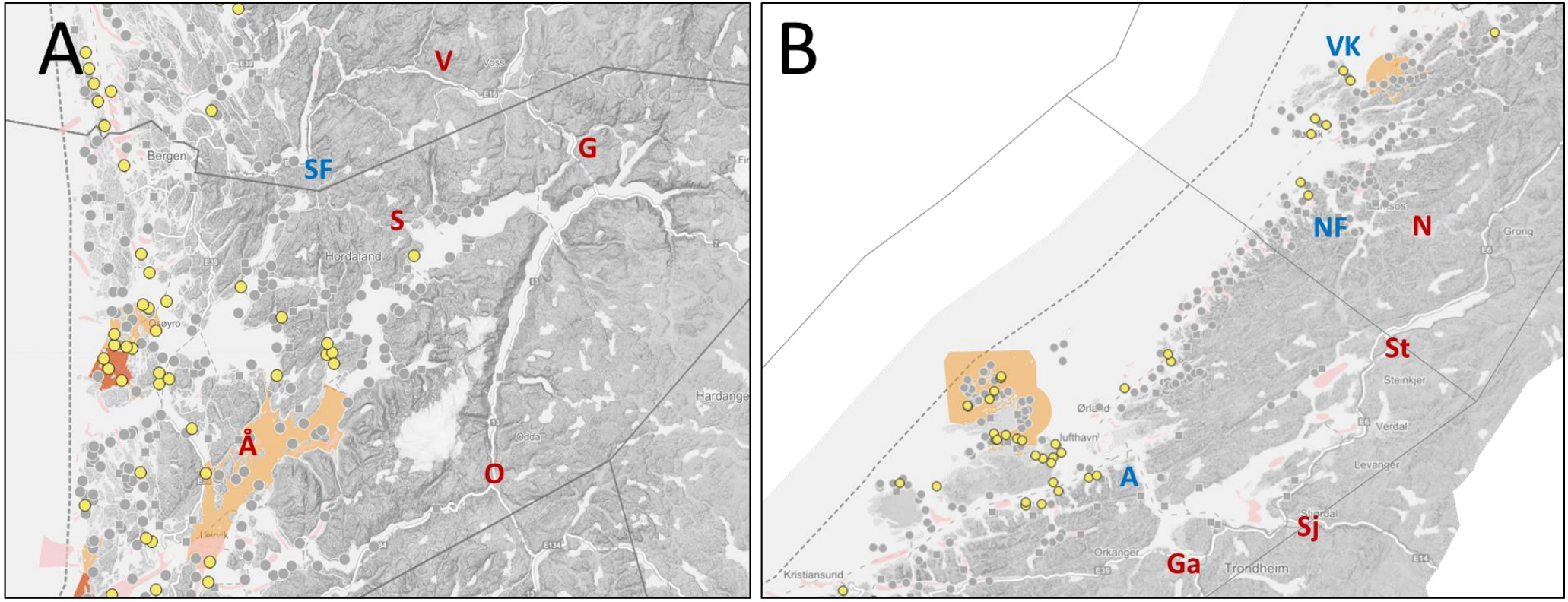

Figure 31 Overview of aquaculture sites with suspicion or detection of Salmonid alphavirus (yellow dots) during May 2018 in A: Hordaland and B: Trøndelag. The light and dark orange shaded areas are observation and control zones for ISAV. Blue letters = sea locations, red letters = rivers. SF-Sørfjorden, S-Steindalselva, V-Vosso, G-Granvin, Å-Ådlandvassdraget, VK- Vikna Kvaløya, NF- Namsfjorden, N- Namsen, St- Steinkjer, A- Agdenes, Ga- Gaula, Sj- Stjørdalselva.

4.2.2 Infectious salmon anaemia virus (ISAV)

Infectious salmon anaemia virus, ISAV occurs as low- and high virulent variants. The low-virulent ISA virus, HPR0 are common in farmed Atlantic salmon along the entire coast of Norway (Nylund et al., 2007; Plarre, 2011), and high virulent variants, HPRΔ, is causing infectious salmon anaemia (ISA). The latter, formed by a mutation in the genome segments five and six (Devold et al., 2006; Markussen et al., 2008; Plarre et al., 2012), are controlled by stamping out the infected populations and establishing control- and observation zones, (Lyngstad *et al.*, 2012; Nylund et. al 2007, 2019; Plarre *et al.*, 2012). ISAV transmits both horizontally and vertically (Vike et al., 2009). There are no systematic registration of HPR0 in farmed Atlantic salmon, the high prevalence of these variants may result in a spill over to wild Atlantic salmon.

During the last 10 years there have been approximately 10-15 outbreaks of ISA in salmon aquaculture each year (Bornø and Lie Linaker, 2015; Hjeltnes, 2013; Hjeltnes et al., 2019, 2018, 2017, 2016). In 2018 there were 13 outbreaks, five of them in Hordaland and none in Trøndelag or Finnmark. Two outbreaks occurred in Troms which is the neighbouring county to Finnmark (Fig. 32 A), and four in Finnmark in the end of 2017 (Fig. 32 B), the infected population were stamped out in the beginning of 2018. Wild salmonids are believed to represent the original natural reservoir for ISAV, but due to the growth of aquaculture and the increasing number of hosts the present main reservoir are most likely farmed salmon (Nylund et al., 2019 present study). The evolution of virulent ISAV (HPRΔ) in farmed populations could represent a potential risk for transmitting the virus to wild populations of salmon and sea trout returning to rivers. Seatrout, which can survive as carriers of ISAV HPRΔ variants, could possibly bring these viruses into rivers where there is high density of juvenile salmon.

Phylogenetic analyses of segment six sequences of low virulent HPR0 ISA viruses groups them into four major clades; CI - CIV (Nylund et al., 2019 present study). Clades, CII – CIV, seem to have evolved in farmed salmon after the beginning of salmon culture in Norway (Nylund et al., 2019). Virus found in wild salmon in Norway group into CI and CII. CI consists of viruses collected from farmed salmon at The Faroe Islands, Scotland and USA, and from wild salmon collected in the sea in Trøndelag. Members of this clade have not been detected in farmed salmon in Norway. Based on the migration routes for wild salmon from rivers in Trøndelag it is possible that positive wild salmon from Trøndelag carrying ISAV of the mid-Atlantic type (CI), could have been infected in the feeding areas around the Faeroes (Nylund et al., 2019,

present study). However, this genogroup has not been transmitted via wild salmon to farmed salmon in Norway (Nylund et al 2019, present study). CII two consists of viruses collected from both wild and farmed salmon in Norway and from farmed salmon in The Faroe Islands. The ISAV from wild salmonids collected in Trøndelag and Finnmark in 2018 are closely related to HPR0 from farmed salmon in Troms, Finnmark and The Faroe Islands. HPRΔ variants of ISAV in CII, closely related to the HPR0 ISAV from wild salmon, are also present in both Norway and the Faeroes (Nylund et. al 2019, present study). Four of the viruses from this study were sequenced, three from Finnmark and one from Nord-Trøndelag. The results showed that they grouped closely together, and that the virus from Nord-Trøndelag was quite similar to another virus from a wild salmon collected from Nord-Trøndelag in 2015.

Results from this study showed a significantly higher prevalence of ISAV at the sea locations compared to the prevalence in the rivers in both Finnmark and Trøndelag. The relatively high prevalence of ISAV at these sampling-sites cannot be directly connected to outbreaks of ISA in these areas and, as shown, the sequenced ISAV from wild salmon were of the low virulent type. One explanation could be that the HPR0 ISAV has a negative effect on the salmon decreasing their ability to reach the spawning grounds. The sampling methods, fish trap in the sea *versus* fly-fishing in the rivers, may also have affected the prevalence of ISAV in the salmon that were collected. However, if a sub-clinical infection with ISAV HPR0 affects the feeding behaviour of the salmon resulting in a reduced prevalence of fish caught by angling, it may also reduce the fitness of the salmon during spawning. This observed difference in prevalence should be addressed in future studies of the possible effect of HPR0 ISAV on salmon health.

No ISAV was detected from any of the sampling sites in Hordaland county (N = 141). Previous studies have also shown a low prevalence of ISAV in these areas (Kvamme et al., 2018; Madhun et al., 2015; Plarre et al., 2012; Shriwer, 2012).

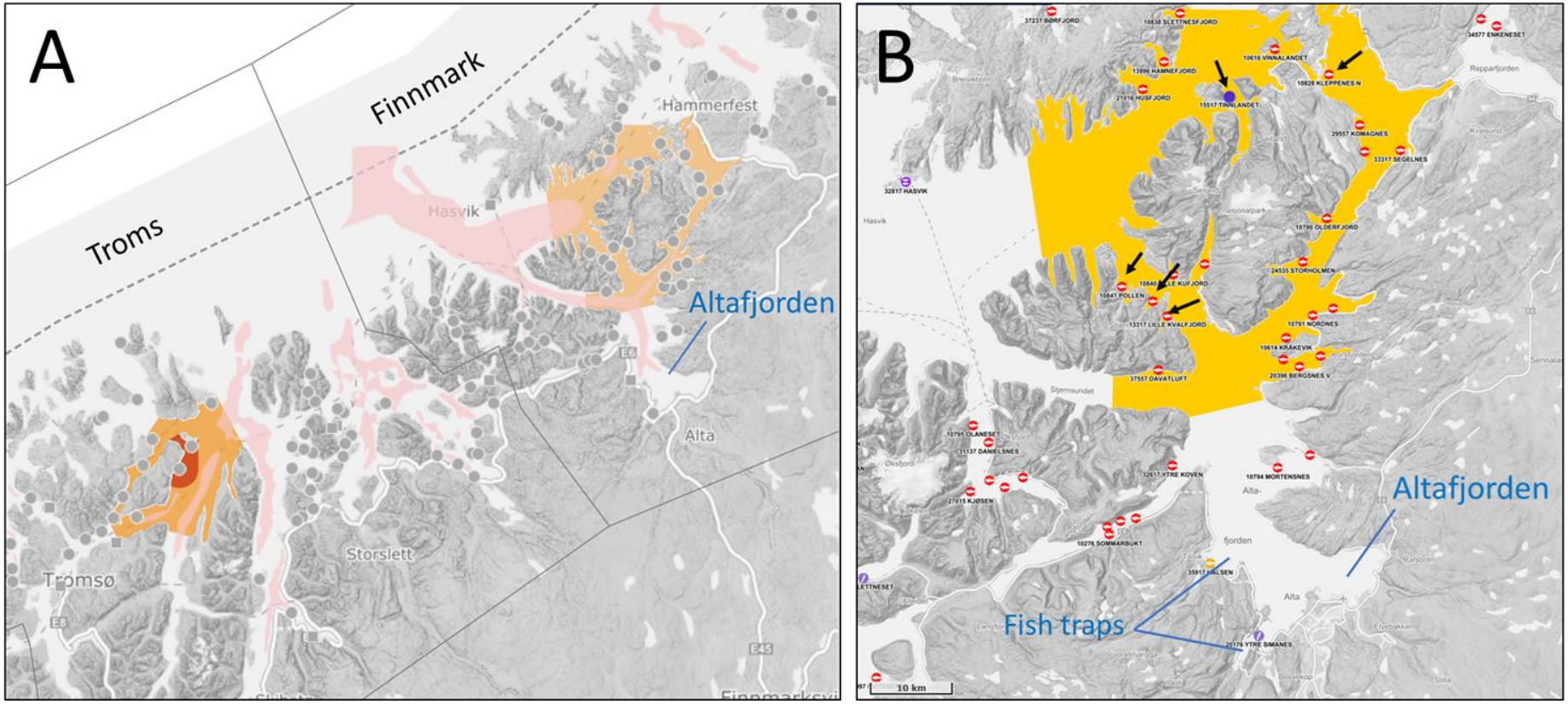

Figure 32 A: Overview of control zone (dark orange) and observation zones (orange/yellow) for ISA in Finnmark and the neighbouring county Troms, and B: overview of the farms with outbreaks of ISA close to Altafjorden in 2017, and the locations were the fish-traps are placed.

4.2.3 Piscine orthoreovirus (PRV)

Heart and skeletal muscle inflammation, HSMI, is a common and commercially important disease in Norwegian aquaculture. The disease was first described in infected salmon from Trøndelag in 1999 with severe inflammation and necrosis in heart and skeletal muscle (Kongtorp et al., 2004b, 2004a), and was later associated with several virus-like particles (Watanabe et al., 2006). Piscine orthoreovirus was in 2010 found to be the causative agent of HSMI (Palacios et al., 2010; Wessel et al., 2017).

This virus infects erythrocytes and causes inflammation in heart and skeletal muscle (Vendramin et al., 2019). It is also believed that this is an important agent of anaemia in Atlantic salmon (Takano et al., 2016; Vendramin et al., 2019). In 2018 there were registered 194 cases of HSMI; 104 reported by The Norwegian veterinary institute, and 90 by private laboratories. This total number may include some double reporting, but the total number of outbreaks is probably higher since HSMI is not notifiable disease. There is reason to believe that the majority of salmon ready for slaughter is infected with PRV (Glover et al., 2018) which probably cause a high infection pressure in the areas around fish farms. Garseth et al. (2013) studied the relationship between PRV from wild and farmed salmon populations in Norway. The results show lacking geographical pattern in the phylogenetic trees indicating extensive exchange and long-distance transportation of the virus.

PRV is a common pathogen in wild salmon and trout, but there have not been found wild salmon suffering from HSMI (Garseth et al., 2013a, 2013b, 2019; Garseth and Biering, 2018; Madhun et al., 2018, 2016; Vendramin et al., 2019). PRV was found in 138 out of the 787 salmon that were analysed for PRV in this study and detected from all counties and almost every sampling-sites, but with variable prevalence. The highest prevalence was found in salmon collected from the sea-locations in Trøndelag; 30.9 % in Nord-Trøndelag and 44.6 % in Sør-Trøndelag. The highest prevalence in adjoining rivers was found in Sør-Trøndelag (11.7 %). Statistical analyses showed a significantly higher prevalence of PRV-positive fish collected from sampling-sites at sea than salmon collected from the adjoining rivers in both Sør- and Nord-Trøndelag, and between sea- and river-collected 2 SW salmon from Sør-Trøndelag. It is known that PRV replicates in erythrocytes and in the heart and skeletal muscle of salmon, and, even if HSMI has not been described from wild salmon, it cannot be excluded that infection with PRV may reduce the fitness (swimming performance and anti-predator behaviour) of wild salmon. The number of salmon with high densities of PRV RNA was also higher in wild salmon from sea compared

to salmon from the rivers. The effect of PRV on wild salmon performance in the sea and river systems should be addressed in future studies.

4.2.4 Salmon gill poxvirus (SGPV)

Salmon gill poxvirus was first detected in farmed salmon smolt with gill disease in 2005, and has later been detected from juvenile- and grow out-sites with gill disease (A. Nylund et al., 2008; Nylund et al., 2011). SGPV transmits horizontally both in fresh- and saltwater and seems to be widely distributed in wild salmon (Wiik-Nielsen et al., 2017). An earlier study analysed both anadromous and non-anadromous salmonids from a wide geographical area in Norway and found SGPV in 25 of 26 locations with anadromous Atlantic salmon. All non-anadromous salmonids were negative and it was suggested that SGPV might be a marine virus (Garseth et al., 2018).

In this study SGPV occurred with a lower prevalence in the sea than the adjoining rivers. Salmon migrating towards the river are passing the location where the fish-traps are placed. The prevalence of SGPV was higher in the rivers both in Alta and Trøndelag than in the sea-sites in the same area. Trondheimsfjorden, Namsfjorden and Altafjorden are all national salmon fjords, and the infection pressure from farmed salmon is therefore believed to be relatively low. The results of the present study indicate that the highest infection pressure of SGPV is in the rivers or close the river mouth. This and the fact that SGPV has only been shown to replicate in Atlantic salmon, suggest that it is not a marine virus. Optimal survival and transmission of the SGPV should be higher in rivers and fresh water, where the densities of susceptible hosts are highest. However, the result from Sørfjorden (prevalence = 40.0 %) in Hordaland differ from the other results obtained from sea- and fjord locations in Trøndelag and Alta. The cause for this difference could be that Sørfjorden contains brackish water, while marine collection sites in Finnmark and Trøndelag are mainly saltwater locations (around 30 ‰). Another possibility is that the total infection pressure in sea is higher in Hordaland due to a higher density of salmon farms in this area than in Trøndelag and Finnmark.

The phylogenetic analysis of SGPV from salmon collected in Vosso (H2018/126) show that this virus grouped together with viruses collected in the same river in 2012 and from a marine site in Nordland in 2012. While SGPV from Steinkjærelva (NT201/123) grouped with two

viruses from two different smolt production sites in Hordaland. The virus from Vikna (NT2018/122) did not form a clade with other SGPV. This could indicate that rivers systems may have geographical distinct SGPV, but also that the virus is transmitted between different geographical areas. The transmission could be a result of transportation of SGPV positive smolt in connection with salmon farming, but it cannot be excluded that the virus could be transmitted between wild salmon at sea.

4.2.5 Piscine myocarditis virus (PMCV)

PMCV is found in Norwegian aquaculture along the entire coast and is the causative agent of cardiomyopathy syndrome CMS (Ferguson et al., 1990; Haugland et al., 2011; Wiik-Nielsen et al., 2012). This disease is considered an increasing problem in Norwegian aquaculture. The Norwegian Veterinary Institute registered the disease at 101 sites in 2018, and two other registered 125 outbreaks (Hjeltnes et al., 2019). There is probably some overlap in these registrations, but the disease is not notifiable, and the number of positive farming populations could be higher. A recent study found PMCV in both hearts and sexual products of broodfish and at several stages of development in their offspring indication a possible vertically pathway of transmission (Bang Jensen et al., 2019).

Garseth et. al (2012) reported the first two detection of PMCV in wild salmon. These two individuals were collected from adjacent rivers Årøy and Nausta in 2007 and 2008. Later there has also been reported both mature and juvenile wild salmon with PMCV collected from Eidfjordvassdraget (2014), Etnefjorden (2015), Daleelva (2017) and Uskedalelva (2017) (Kvamme et al., 2018). During this study, PMCV was detected from 10 wild salmon, eight from Nord-Trøndelag and two from Hordaland. It seems like PMCV occurs at low prevalence in wild salmon populations in Norway. It will be important to monitor the prevalence of this virus in wild salmon in farming-dense areas to see if the prevalence increases with the increasing number of outbreaks in the industry. This work will have to be accompanied by the development of a genotyping tool for the virus.

4.3 Bacteria and parasites

4.3.1 *Paranucleospora theridion*

P. theridion is a microsporidian parasite infecting both Atlantic salmon and salmon louse (*L. salmonis*). The lifecycle consists of one developmental stage in the salmon louse and two in Atlantic salmon (Nylund et al., 2010; Økland, 2012). Production of infective spores of this parasite is associated with the production of salmon lice in aquaculture. The infection dynamic of *P. theridion* is unclear, but transmission probably occur when waterborne spores produced in lice infects the salmon (Sveen et al., 2012). The lifecycle is temperature dependent (Sveen et al., 2012) and disease caused by *P. theridion* is associated with temperatures around 15°C over longer periods; summer and early autumn. These requirements are most often met in western Norway and presence of this parasite further north could possibly be a result of spore transmission passively through sea water. *P. theridion* has been detected in fish suffering from other diseases such as HSMI, CMS, PD and PGI, and it has been discussed if this parasite weakens the immune system and makes the salmon more susceptible to other pathogens (Gunnarsson et al., 2017; Nylund et al., 2011, 2010). *P. theridion* can also infect and multiply in wrasse, lumpfish, halibut and another fish parasite *Caligus elongatus*, but the importance of these species in the maintenance and transmission of the parasite is not known (Nylund et al. 2010; Steigen et al. 2018; A. Nylund pers.com).

P. theridion was detected from all sampling-sites, showing wide geographical distribution. Based on existing knowledge of this parasites lifecycle it is reasonable to believe that the highest prevalence should be found in areas with high densities of the salmon louse, and in southern counties due to higher temperatures. Two sampling sites stand out with a much higher prevalence than the others; Vikna in Nord-Trøndelag and Sørfjorden in Hordaland with 72.3 % and 81.6 % respectively. These are both sea-locations in areas with a high density of fish farms. These two locations differ from each other with respect to several environmental factors; Vikna is close to the coast and it is believed that the water exchange is higher in this area than in Sørfjorden which is a narrow fjord with less water exchange and low salinity. Three other sea locations Altafjorden, Namsfjorden and Agdenes had a prevalence of 6.2 %, 19.0 % and 17.8 % respectively. The low prevalence in Altafjorden might reflect the temperature dependent lifecycle of the parasite which favour higher temperatures. The fish-traps in Namsfjorden and

Agdenes are located in the protected area of the national salmon fjord, the infection pressure is probably lower here due to presence of only a few fish farms in the area.

4.3.2 *Parvicapsula pseudobranchicola*

P. pseudobranchicola is the causative agent of the disease parvicapsulosis and is common in both wild and farmed salmon in Norway, especially in the northern regions where infections in seawater farmed salmon are particularly frequent and heavy. The complete life cycle is not known, but the main host is probably a polychaete/oligochaete like other parvicapsulids (Bartholomew et al., 2006; Køie et al., 2013). In 2018 the Norwegian Veterinary Institute registered *P. pseudobranchicola* at 37 farming sites, with most outbreaks in Finnmark, and only one in Trøndelag (Hjeltnes et al., 2019). This disease is not notifiable which means that the real number probably is higher. *P. pseudobranchicola* has been detected in both wild Atlantic salmon and sea trout, also in the south-east of Norway where salmon farming does not occur, indicating that they are natural hosts (Hansen et al., 2015; Jørgensen et al., 2011).

P. pseudobranchicola was detected from all counties and sampling-sites with the highest prevalence in Finnmark (Altafjorden and Altaelva) as expected. The higher prevalence in Hordaland than Sør-Trøndelag might be a result of horizontal transmission of salmon from rivers in Hordaland held in tanks before sampling. The prevalence of *P. pseudobranchicola* showed the opposite geographical distribution compared to *P. theridion* in this study which may reflect their different dependency on temperature, or that the timing for migrations of salmon in Finnmark is not optimal for the parasite. The latter could indicate that sea trout is the main vertebrate host for the parasite.

4.3.3 *Renibacterium salmoninarum* (BKD)

Renibacterium salmoninarum is the causative agent of bacterial kidney disease (BKD) (Evelyn et al., 2011; Kent, 2011; Sanders and Fryer, 1980). BKD is not considered a problem in wild salmonid populations but might cause problems in cultivation facilities or farming sites due to a high density of hosts and ability to transmit vertically (Evelyn et al., 1986; Kristmundsson et al., 2016).

R. salmoninarum was detected from sea-locations in all counties included in this study (Finnmark, Trøndelag and Hordaland) with a prevalence of 2,5%, 5,1% and 78,3% respectively. This bacterium is common in the areas around Iceland (Kristmundsson et al., 2016). Most of the outbreaks in Norway occurs in the western parts of the country were *R. salmoninarum* is believed to be endemic in some watercourses. In 2012 *R. salmoninarum* was detected in brood fish from Voss hatchery (A. Nylund pers. com). In this case there were seven wild Atlantic salmon infected with this bacterium, and six out of them were caught in a fish-trap located in Stamnes and held together in a cage in Bolstadfjorden until they were moved to Voss hatchery. All six were marked salmon hatched at Voss. The seventh was an unmarked salmon captured by rod in Vosso (O. Kambestad pers. com). The six salmon collected from Stamnes in 2012, are like all the salmons from Sørfjorden in this study hatched at Voss from roe and milt from the genebank in Trondheim. All breeding salmon used in cultivation are tested for *R. salmoninarum*. The bacteria have in this case not transmitted vertically in the hatchery. The reason for this high prevalence is unsure but can be a result of transmission from infected salmon in the area around Iceland or that the rivers in the area are endemic. *R. salmoninarum* has previously been found occasionally in this river system and there are reasons to believe that the bacterium is endemic in the area. The high prevalence detected in this study is in any case alarming and should be further investigated.

4.3.4 Diversity

Most farmed salmon are infected with more than one microparasite, but the knowledge of how these co-infections effect the salmon performance are less understood (Downes et al., 2018; Gunnarsson et al., 2017). The results from this study showed that most of the wild Atlantic salmon analysed were infected with at least three different microparasites. There was no significant difference between the total diversity of microparasites at the different locations. Sørfjorden and Vikna had the highest diversity of microparasites (DI= 6.6). The salmon with highest number of microparasites (eight) was collected from the fish trap in Trengereid, Sørfjorden. These are also the two locations with the highest density of fish farms in the area, and this high diversity of pathogens might be a result of a higher infection pressure cannot be excluded. Vikna and Sørfjorden were also the two location with highest prevalence of P. theridion which is associated with production of salmon lice in the aquaculture.

By sorting the salmon into two groups; three or less- and more than three microparasites, some locations stand out compared to the others. Results from Finnmark showed that there were similar numbers of microparasites in the sea and in the rivers. In contrast Nord-Trøndelag there was a higher diversity of microparasites in the sea at Vikna compared to both Namsfjorden and the river Namsen. A possible outcome of co-infections might be an increased exposure to predation in the fjord or river systems. The sea location in Sør-Trøndelag, Agdenes showed the opposite results with most of the salmon infected with less than three microparasites. Two of the rivers in this area, Gaula and Steinkjer had approximately the same distribution of salmon infected with thee (or less) or more than three microparasites, whereas the third river (Stjørdal) showed a similar trend to Agdenes with a higher amount of salmon with fewer microparasites. The reason for this result might be that this river requires a higher performance of the migrating salmon and that co-infections are decreasing their performance and their ability to reach the river or migrate upstreams.

5 Conclusion and future research

- There was no SAV detected in any of the salmonids collected in Trøndelag and Finnmark. The reason for this is uncertain but future screening and analysis of wild salmon in areas with a high number of outbreaks should continue to investigate any possible transmission.
- ISAV was found with a relatively high prevalence in wild salmonids collected from Finnmark and Trøndelag. Statistical analyses showed significantly higher prevalence in sea *versus* rivers. Future studies should therefore investigate the possible effect of HPR0 ISAV on salmon health and performance.
- PRV is commonly occurring in wild salmon population. The highest prevalence was found in Atlantic salmon collected from the two sea locations in Trøndelag, this prevalence was significantly higher than found in the adjoining rivers in these areas. Future studies should be focused on the effect of PRV on wild salmon survival and performance in sea and rivers.
- SGPV occurs with a higher prevalence in salmon collected from rivers than salmon collected from sea. Phylogenetic analyses of three viruses from this study showed that SGPV from the same river-sites may group close together, but also with SGPV from smolt production- and marine sites from other counties in Norway.
- PMCV has a low prevalence in wild salmon. Future studies should investigate the prevalence of PMCV in wild populations to see if it increases with the growing number of outbreaks in the aquaculture industry.
- *Paranucleospora theridion* was found in all sampling-sites, but with a significantly higher prevalence at the two locations with the highest density of aquaculture sites in the area. The high prevalence in these areas might be a result of a high infection pressure due to the production of salmon lice in the aquaculture industry in these areas.
- *Parvicapsula pseudobranchicola* occurs in most of the wild salmon population, but with a higher prevalence in the northernmost counties.
- *Renibacterium salmoninarum* normally occurs with low prevalence in wild salmon population, but the results from this study showed a high prevalence of *R. salmoninarum* in wild salmon from Sørfjorden. All salmon collected from Sørfjorden were hatched at Voss, and therefore the high prevalence cannot be a result of vertical transmission. Further studies investigating possible reservoirs and transmission of this bacteria in wild

salmon populations in this area should be addressed to determine if it is an endemic area or if the transmission occurs around Iceland or somewhere else during feeding migration.

- *Ichthyobodo* spp., *Yersinia ruckeri*, *Candidatus* Piscichlamydia and *Candidatus* Branchiomonas cysticola are a commonly occurring microparasites in wild salmon populations.

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Appendix

5.1 Fish data

Table 13. Data on salmonids collected from Finnmark, Altafjorden.

Altafjorden	vekt	lengde	art	kjønn	dato	lokalitet
18AF1	2000	520	ss	ha	170718	Melsvik
18AF2	1800	550	ss	ha	170718	Melsvik
18AF4	8500	950	ss	hu	120718	Melsvik
18AF5	15000	1090	ss	hu	180718	Melsvik
18AF7	9500	980	ss	ha	170718	Melsvik
18AF8	2000	530	ss	ha	180718	Kåfjord
18AF13	1600	520	ss	hu	110718	Melsvik
18AF17	3000	620	ss	ha	100718	Melsvik
18AF18	12500	1030	ss	hu	110718	Kåfjord
18AF19	2500	590	ss	hu	100718	Kåfjord
18AF21	8000	900	ss	hu	100718	Melsvik
18AF25	3800	650	ss	hu	110718	Kåfjord
18AF27	2400	570	ss	ha	110718	Kåfjord
18AF28	3000	620	ss	hu	170618	Kåfjord
18AF30	8500	890	ss	hu	110718	Melsvik
18AF34	5500	790	ss	ha	110718	Melsvik
18AF35	4500	730	ss	hu	170718	Melsvik
18AF38	8000	890	ss	hu	100718	Melsvik
18AF40	7000	850	ss	ha	40718	Melsvik
18AF41	9300	950	ss	hu	30718	Melsvik
18AF42	1800	530	ss	ha	170718	Kåfjord
18AF45	2500		ss	ha	190618	Melsvik
18AF46	9000	990	ss	hu	40718	Melsvik
18AF47	7000	850	ss	hu	100718	Melsvik
18AF48	7255	860	ss	ha	100718	Melsvik
18AF49	2300	550	ss	ha	170718	Melsvik
18AF52	3000	630	ss	ha	120718	Melsvik
18AF53	5500	770	ss	hu	30718	Kåfjord
18AF55	2800	620	ss	ha	180718	Kåfjord
18AF56	9000	960	ss	hu	170718	Melsvik
18AF58	10000	960	ss	hu	100718	Kåfjord
18AF59	8400	860	ss	hu	40718	Melsvik
18AF60	2500	600	ss	ha	180718	Kåfjord
18AF61	2700	570	ss	ha	40718	Melsvik
18AF62	9500	950	ss	hu	30718	Melsvik
18AF63	8400	900	ss	ha	40718	Melsvik
18AF64	10500	930	ss	hu	280618	Melsvik

18AF65	3000	610	ss	ha	40718	Melsvik
18AF66	3000	510	ss	ha	30718	Melsvik
18AF67	7500	830	ss	hu	50718	Melsvik
18AF68	15000	1080	ss	ha	40718	Melsvik
18AF69	3500	640	ss	ha	30718	Melsvik
18AF71	7500	920	ss	hu	30718	Melsvik
18AF73	10500	970	ss	ha	100718	Kåfjord
18AF74	2500	600	ss	ha	40718	Kåfjord
18AF75	15000	1060	ss	ha	50718	Melsvik
18AF76	3500	640	ss	ha	30718	Melsvik
18AF78	8000	850	ss	hu	40718	Melsvik
18AF79	2600	570	ss	ha	40718	Melsvik
18AF81	13500	1060	ss	ha	40718	Melsvik
18AF82	7500	860	ss	hu	40718	Melsvik
18AF83	6500	800	ss	hu	30718	Melsvik
18AF84	10000	960	ss	ha	40718	Melsvik
18AF87	12200	1050	ss	ha	260618	Kåfjord
18AF88	3500	640	ss	ha	40718	Melsvik
18AF90	9400	980	ss	hu	140618	Melsvik
18AF92	13500	1120	ss	ha	30718	Melsvik
18AF93	6000	780	ss	hu	280618	Melsvik
18AF94	10500	1000	ss	hu	50718	Kåfjord
18AF95	11800	1020	ss	hu	40718	Melsvik
18AF96	5200	770	ss	ha	30718	Kåfjord
18AF97	2400	570	ss	hu	200618	Kåfjord
18AF98	5000	790	ss	hu	140618	Kåfjord
18AF100	17500	1150	ss	ha	30718	Melsvik
18AF101	8500	830	ss	hu	280618	Melsvik
18AF102	2600	560	ss	ha	40718	Melsvik
18AF103	10600	990	ss	hu	40718	Melsvik
18AF104	5000	800	ss	hu	260618	Kåfjord
18AF106	3000	580	ss	ha	200618	Kåfjord
18AF107	8000	950	ss	hu	30718	Kåfjord
18AF108	2200	570	ss	hu	190618	Kåfjord
18AF109	2500	540	ss	ha	220618	Melsvik
18AF110	10000	950	ss	hu	30718	Melsvik
18AF111	10000	900	ss	ha	30718	Melsvik
18AF112	4000	720	ss	ha	190618	Kåfjord
18AF113	6800	830	ss	hu	40718	Melsvik
18AF114	6000	820	ss	hu	140618	Melsvik
18AF115	1100	950	ss	hu	30718	Melsvik
18AF116	2500	580	ss	ha	210618	Melsvik
18AF118	7000	830	ss	hu	210618	Melsvik
18AF120	2800	660	ss	hu	140618	Kåfjord
18AF3	1500	510	st	hu	170718	Melsvik
18AF6	750	380	st	hu	100718	Melsvik

18AF9	500	490	st	hu	170718	Melsvik
18AF10	1600	510	st	ha	170718	Kafjord
18AF11	2000	560	st	hu	170718	Melsvik
18AF12	1300	470	st	hu	170618	Kåfjord
18AF14	900	410	sa	hu	100718	Melsvik
18AF15	1500	510	st	hu	170718	Melsvik
18AF16	1500	550	st	hu	110718	Kåfjord
18AF20	1800	500	st	hu	170718	Melsvik
18AF23	1800	520	st	hu	170718	Melsvik
18AF24	3700	680	st	hu	120718	Kåfjord
18AF26	2000	550	st	hu	170718	Melsvik
18AF29	1500	490	st	hu	170718	Melsvik
18AF31	3500	660	st	hu	120718	Melsvik
18AF32	2000	550	st	hu	170718	Melsvik
18AF33	1000	420	st	hu	170718	Melsvik
18AF37	3000	680	st	ha	50718	Melsvik
18AF39	2000	610	st	ha	180718	Kåfjord
18AF43	3000	630	st	ha	270618	Melsvik
18AF44	2000	560	st	ha	180718	Melsvik
18AF50	2800	590	st	hu	170718	Melsvik
18AF51	4000	690	st	ha	30718	Kåfjord
18AF57	4300	700	st	hu	40718	Melsvik
18AF72	1200	4600	st	hu	170718	Kåfjord
18AF77	3000	600	st	ha	200618	Kåfjord
18AF80	3000	650	st	hu	110618	Kåfjord
18AF85	2100	610	st	hu	140618	Kåfjord
18AF86	3000	700	st	ha	140618	Melsvik
18AF89	4500	720	st	hu	190618	Kåfjord
18AF91	1800	540	st	hu	200618	Melsvik
18AF99	2000	620	st	ha	220618	Melsvik
18AF105	3800	700	st	ha	190618	Kåfjord
18AF117	2500	540	st	hu	210618	Melsvik
18AF119	2900	680	st	hu	140618	Kåfjord
18AF70	3500	670	st	ha	110718	Kåfjord

Table 10. Data on salmon collected from Finnmark, Altaelva.

Altaelva	vekt	lengde	art	kjønn	dato	lokalitet
18AF22	5000	800	ss	hu	140718	Altaelva
18AF36	8600	940	ss	hu	140718	Altaelva
18ALT1	7000	810	ss	ha	250618	Forbyggninga
18ALT2	9500	960	ss	ha	290618	Forbyggninga
18ALT3		890	ss	ha	50618	Raipas
18ALT4	8900	990	ss	ha	10718	Elvestrand
18ALT5	1900	540	ss	ha	240618	Raipas
18ALT6	10000	990	ss	ha	20718	Forbyggninga

18ALT7	8100	930	ss	hu	300618	Raipas
18ALT8	5300	780	ss	hu	280618	killistrømmen
18ALT9	12250	1010	ss	ha	290618	Haraldholmen
18ALT10	9000	930	ss	hu	300618	Haraldholmen
18ALT21	10200	1020	ss	ha	300618	Elvestrand
18ALT22	19300	1180	ss	ha	70718	Forbyggninga
18ALT23	2000	570	ss	ha	150718	Raipas
18ALT24	1300	520	ss	ha	230718	Nedre Sten
18ALT25	8500	950	ss	u	270618	Forbyggninga
18ALT26	9000		ss	ha	90718	killistrømmen
18ALT27	10000		ss	hu	60718	Forbyggninga
18ALT28	9500	940	ss	ha	270618	Raipas
18ALT29	2000	560	ss	ha	120718	Jøraholmen
18ALT30	10000	970	ss	hu	160718	Raipas
18ALT31	3000	595	ss	ha	50618	Raipas
18ALT32	2800	630	ss		130718	Raipas
18ALT33	5900	790	ss	hu	80718	Elvestrand
18ALT34	6900		ss	hu	50618	Raipas
18ALT35	1300	515	ss	ha	220718	Langstilla
18ALT36	6900		ss	hu	230718	Vina
18ALT37	2300	610	ss	ha	80718	Elvestrand
18ALT38	11000	1000	ss	ha	140718	Sorrisniva
18ALT39	8000	890	ss	ha	260618	Raipas
18ALT40	14000	1050	ss	hu	290618	Raipas
18ALT41		500	ss	ha	230718	Jorra
18ALT42		930	ss		260718	Bollo
18ALT43						
18ALT45		600	ss		250718	Nedre Sierra
18ALT46						
18ALT47		520	ss	ha	230718	Jorra
18ALT48						
18ALT50	8600	950	ss		260718	Detsika
18ALT51	2000	590	ss	ha	220718	Langstilla
18ALT52	1800	560	ss	ha	150718	Raipas
18ALT53	2000	590	ss	ha	140718	Kista
18ALT54	2200	630	ss	ha	120718	Jorra
18ALT55	1900	600	ss	ha	130718	Raipas
18ALT56	2300	560	ss	ha	140718	Vina
18ALT57	12300	1050	ss	hu	140718	Vina
18ALT58	10000	990	ss	ha	120718	nedre Stengelsen
18ALT59	1300	530	ss	ha	150718	Raipas
18ALT60	3000	590	ss	ha	200718	Raipas
18ALT64	8000	930	ss		50818	Forbyggninga
18ALT65		580	ss		10818	langstilla
18ALT71		690	ss		290718	Sorrisniva
18ALT72		840	ss	hu	260718	nedre Sierra

18ALT73		380	ss	ha	260718	Gønges
18ALT74		625	ss	ha	80118	nedre Sierra
18ALT75		630	ss	ha	270718	langstilla
18ALT76		550	ss	HA	270718	langstilla
18ALT77		470	ss	ha	260718	øvre sierra
18ALT78		570	ss		10818	bollo
18ALT79		515	ss	ha	260718	jorra
18ALT80		618	ss	ha	260718	jorra

Table 11. Data on salmonids collected from Nord-Trøndelag, Vika

Vikna Kvaløya	vekt	lengde	art	kjønn	dato	lokalitet
2018K1	4200	710	ss	ha	80718	Vikna Kvaløya
2018K2	1800	540	ss	ha	260618	Vikna Kvaløya
2018K3	3800	710	ss	ha	170718	Vikna Kvaløya
2018K4	3600	780	ss	ha	180718	Vikna Kvaløya
2018K5	2800	640	ss	ha	160818	Vikna Kvaløya
2018K6	5400	840	ss	ha	160718	Vikna Kvaløya
2018K7	4200	710	ss	hu	90718	Vikna Kvaløya
2018K8	3400	750	ss	hu	180718	Vikna Kvaløya
2018K9	2500	640	ss	hu	260618	Vikna Kvaløya
2018K11	1500	520	ss	hu	180718	Vikna Kvaløya
2018K15	4500	790	ss	ha	150618	Vikna Kvaløya
2018K16	3800	650	ss	ha	50718	Vikna Kvaløya
2018K17	2200	640	ss	ha	180718	Vikna Kvaløya
2018K18	7200	870	ss	ha	170718	Vikna Kvaløya
2018K19	2000	610	ss	ha	160718	Vikna Kvaløya
2018K20	1900	610	ss	ha	180718	Vikna Kvaløya
2018K21	2500	620	ss	ha	260618	Vikna Kvaløya
2018K22	6100	870	ss	hu	160718	Vikna Kvaløya
2018K23	7600	890	ss	hu	160718	Vikna Kvaløya
2018K24	3500	660	ss	hu	100718	Vikna Kvaløya
2018K25	4200	750	ss	hu	180718	Vikna Kvaløya
2018K26	1600	520	ss	hu	100718	Vikna Kvaløya
2018K28	3100	640	ss	ha	170718	Vikna Kvaløya
2018K29	5100	850	ss	hu	190718	Vikna Kvaløya
2018K30	3100	660	ss	ha	160718	Vikna Kvaløya
2018K31	4800	760	ss	ha	110718	Vikna Kvaløya
2018K32	2400	640	ss	ha	170718	Vikna Kvaløya
2018K33	4800	800	ss	hu	180718	Vikna Kvaløya
2018K34	2900	700	ss	hu	160718	Vikna Kvaløya
2018K35	2700	630	ss	ha	160718	Vikna Kvaløya
2018K36	3600	730	ss		170718	Vikna Kvaløya
2018K37	3000	690	ss	ha	180718	Vikna Kvaløya
2018K38	2500	650	ss	ha	180718	Vikna Kvaløya
2018K39	5000	810	ss	ha	190718	Vikna Kvaløya

2018K40	2100	580	ss	ha	180718	Vikna Kvaløya
2018K41	5300	820	ss	ha	250718	Vikna Kvaløya
2018K42	6400	860	ss	hu	250618	Vikna Kvaløya
2018K43	6200	880	ss	ha	270718	Vikna Kvaløya
2018K44	4800	800	ss	hu	280718	Vikna Kvaløya
2018K45	6600	840	ss	hu	270718	Vikna Kvaløya
2018K46	3800	780	ss	hu	270718	Vikna Kvaløya
2018K47	5200	850	ss	ha	270718	Vikna Kvaløya
2018K48	2300	610	ss	ha	270718	Vikna Kvaløya
2018K49	6900	870	ss	hu	150618	Vikna Kvaløya
2018K50	5300	830	ss	hu	270718	Vikna Kvaløya
2018K51	2000	590	ss	ha	100718	Vikna Kvaløya
2018K52	2500	650	ss	ha	250718	Vikna Kvaløya
2018K53	4000	760	ss	hu	280718	Vikna Kvaløya
2018K54	4400	760	ss	hu	150618	Vikna Kvaløya
2018K55	2200	620	ss	hu	160718	Vikna Kvaløya
2018K56	5200	790	ss	hu	260618	Vikna Kvaløya
2018K57	4600	770	ss	hu	260618	Vikna Kvaløya
2018K58	3000	720	ss	hu	270718	Vikna Kvaløya
2018K59	6000	860	ss	hu	240718	Vikna Kvaløya
2018K60	2600	640	ss	hu	250718	Vikna Kvaløya
2018K61	2300	600	ss	ha	150618	Vikna Kvaløya
2018K62	3500	680	ss	hu	90718	Vikna Kvaløya
2018K63	6100	880	ss	ha	250718	Vikna Kvaløya
2018K65	4200	770	ss	hu	300718	Vikna Kvaløya
2018K66	2000	600	ss	ha	250718	Vikna Kvaløya
2018K68	2300	610	ss	ha	260618	Vikna Kvaløya
2018K69	2400	610	ss	ha	100718	Vikna Kvaløya
2018K70	2900	630	ss	ha	100718	Vikna Kvaløya
2018K72	2400	600	ss	ha	100818	Vikna Kvaløya
2018K73	2500	660	ss	ha	270718	Vikna Kvaløya
2018K74	5100	790	ss	hu	150618	Vikna Kvaløya
2018K75	1900	570	ss	ha	100718	Vikna Kvaløya
2018K76	3600	720	ss	hu	200718	Vikna Kvaløya
2018K77	7600	890	ss	ha	260618	Vikna Kvaløya
2018K78	4200	800	ss	hu	270718	Vikna Kvaløya
2018K79	3100	680	ss	ha	280718	Vikna Kvaløya
2018K80	2300	610	ss	hu	100718	Vikna Kvaløya
2018K81	3400	760	ss	hu	250718	Vikna Kvaløya
2018K82	2300	650	ss	ha	260718	Vikna Kvaløya
2018K83	5000	840	ss	hu	200718	Vikna Kvaløya
2018K84	2200	660	ss	ha	250718	Vikna Kvaløya
2018K85	4000	760	ss	ha	270718	Vikna Kvaløya
2018K86	8600	930	ss	hu	200718	Vikna Kvaløya
2018K87	4100	770	ss	ha	270718	Vikna Kvaløya
2018K88	2900	660	ss	ha	200718	Vikna Kvaløya

2018K89	4300	780	ss	hu	260718	Vikna Kvaløya
2018K90	4100	770	ss	hu	300718	Vikna Kvaløya
2018K91	5000	810	ss	hu	240718	Vikna Kvaløya
2018K92	6600	900	ss	hu	200718	Vikna Kvaløya
2018K93	2300	630	ss	ha	250718	Vikna Kvaløya
2018K94	3100	690	ss	hu	240718	Vikna Kvaløya
2018K95	5400	840	ss	ha	200718	Vikna Kvaløya
2018K96	2600	690	ss	hu	270718	Vikna Kvaløya
2018K97	6300	880	ss	ha	300718	Vikna Kvaløya
2018K98	3000	700	ss	ha	200718	Vikna Kvaløya
2018K99	2300	670	ss	hu	240718	Vikna Kvaløya
2018K100	2400	660	ss	ha	240718	Vikna Kvaløya
2018K101	3600	760	ss	hu	200718	Vikna Kvaløya
2018K102	3400	670	ss	hu	260718	Vikna Kvaløya
2018K103	2100	630	ss	ha	200718	Vikna Kvaløya
2018K104	4400	790	ss	hu	270718	Vikna Kvaløya
2018K105	5800	850	ss	hu	260718	Vikna Kvaløya
2018K106	3300	680	ss	ha	250718	Vikna Kvaløya
2018K107	2600	680	ss	ha	200718	Vikna Kvaløya
2018K108	2100	610	ss	ha	200718	Vikna Kvaløya
2018K109	2300	670	ss	hu	200718	Vikna Kvaløya
2018K110	1900	590	ss	ha	250718	Vikna Kvaløya
2018K111	6100	880	ss	ha	200718	Vikna Kvaløya
2018K112	2000	600	ss	ha	200718	Vikna Kvaløya
2018K113	6400	870	ss	ha	200718	Vikna Kvaløya
2018K114	7700	900	ss	hu	250718	Vikna Kvaløya
2018K115	1600	570	ss	hu	240718	Vikna Kvaløya
2018K116	4600	780	ss	ha	260718	Vikna Kvaløya
2018K117	3100	710	ss	hu	200718	Vikna Kvaløya
2018K118	4600	760	ss	hu	200718	Vikna Kvaløya
2018K119	1800	540	ss	hu	250718	Vikna Kvaløya
2018K120	8000	890	ss	hu	110718	Vikna Kvaløya
2018K10	1900	520	st	hu	100718	Vikna Kvaløya
2018K12	1800	550	st	hu	170718	Vikna Kvaløya
2018K13	2000	540	st	ha	100718	Vikna Kvaløya
2018K14	2000	540	st	ha	100718	Vikna Kvaløya
2018K27	1900	530	st	hu	100718	Vikna Kvaløya
2018K64	2500	600	st	hu	100718	Vikna Kvaløya
2018K67	1600	500	st	ha	100718	Vikna Kvaløya
2018K71	2100	570	st	hu	250618	Vikna Kvaløya

Table 12. Data on salmonids collected from Nord-Trøndelag, Namsfjorden

Namsfjorden	vekt	lengde	art	kjønn	dato	lokalitet

18NF1	2780	690	ss	hu	270618	Namsfjorden
18NF2	2860	660	ss	ha	130618	Namsfjorden
18NF3	6000	810	ss	ha	130618	Namsfjorden
18NF4	2580	620	ss	hu	260618	Namsfjorden
18NF5	3200	660	ss	ha	130618	Namsfjorden
18NF6	3120	670	ss	ha	250618	Namsfjorden
18NF7	2450	650	ss	hu	210618	Namsfjorden
18NF8	1600	540	ss	hu	130618	Namsfjorden
18NF9	3970	730	ss	hu	130618	Namsfjorden
18NF10	2300	630	ss	ha	210618	Namsfjorden
18NF11	3740	740	ss	hu	130618	Namsfjorden
18NF12	7520	890	ss	ha	230618	Namsfjorden
18NF13	8820	930	ss	ha	230618	Namsfjorden
18NF14	5680	870	ss	hu	270618	Namsfjorden
18NF15	6600	870	ss	hu	270618	Namsfjorden
18NF16	4240	730	ss	ha	270618	Namsfjorden
18NF17	1600	770	ss	ha	230618	Namsfjorden
18NF18	5750	810	ss	ha	250618	Namsfjorden
18NF19	4040	790	ss	hu	230618	Namsfjorden
18NF20	2140	560	ss	ha	250618	Namsfjorden
18NF21	6420	820	ss	hu	270618	Namsfjorden
18NF22	3860	730	ss	hu	250618	Namsfjorden
18NF23	1820	530	ss	hu	230618	Namsfjorden
18NF24	4660	770	ss	ha	250618	Namsfjorden
18NF25	1840	560	ss	hu	230618	Namsfjorden
18NF26	7320	890	ss	ha	270618	Namsfjorden
18NF27	1640	520	ss	hu	270618	Namsfjorden
18NF28	2960	640	ss	ha	270618	Namsfjorden
18NF29	7150	940	ss	hu	210618	Namsfjorden
18NF30	1700	530	ss	ha	250618	Namsfjorden
18NF31	1880	570	ss	ha	250618	Namsfjorden
18NF32	1820	550	ss	hu	270618	Namsfjorden
18NF33	3580	670	ss	ha	250618	Namsfjorden
18NF34	6360	800	ss	ha	270618	Namsfjorden
18NF35	2080	590	ss	hu	270618	Namsfjorden
18NF36	5080	810	ss	hu	270618	Namsfjorden
18NF37	8500	920	ss	ha	270618	Namsfjorden
18NF38	1720	560	ss	ha	250618	Namsfjorden
18NF39	3380	640	ss	hu	270618	Namsfjorden
18NF41	3500	730	ss	ha	210618	Namsfjorden
18NF42	6480	870	ss	hu	130618	Namsfjorden
18NF43	3640	730	ss	hu	250618	Namsfjorden
18NF44	2000	580	ss	hu	210618	Namsfjorden
18NF45	11600	1050	ss	ha	230618	Namsfjorden
18NF46	3900	760	ss	hu	210618	Namsfjorden
18NF47	5180	810	ss	ha	130618	Namsfjorden

18NF48	1800	580	ss	hu	210618	Namsfjorden
18NF49	2060	590	ss	ha	250618	Namsfjorden
18NF50	6200	890	ss	hu	270618	Namsfjorden
18NF51	5930	810	ss	hu	130618	Namsfjorden
18NF52	1320	510	ss	hu	250618	Namsfjorden
18NF53	1780	560	ss	hu	130618	Namsfjorden
18NF54	3020	630	ss	ha	270618	Namsfjorden
18NF55	2640	620	ss	ha	270618	Namsfjorden
18NF56	3180	700	ss	ha	270618	Namsfjorden
18NF57	3040	630	ss	hu	210618	Namsfjorden
18NF58	7400	890	ss	ha	210618	Namsfjorden
18NF59	2820	630	ss	ha	210618	Namsfjorden
18NF60	5800	840	ss	ha	210618	Namsfjorden
18NF61	10040	1010	ss	hu	110718	Namsfjorden
18NF62	6080	850	ss	ha	160718	Namsfjorden
18NF63	5580	840	ss	hu	110718	Namsfjorden
18NF64	4580	790	ss	hu	90718	Namsfjorden
18NF65	1700	550	ss	hu	100718	Namsfjorden
18NF66	2460	620	ss		180718	Namsfjorden
18NF67	3380	720	ss	ha	160718	Namsfjorden
18NF68	2140	590	ss		100718	Namsfjorden
18NF69	2420	620	ss	hu	100718	Namsfjorden
18NF71	5280	830	ss	ha	110718	Namsfjorden
18NF72	5300	810	ss	ha	120718	Namsfjorden
18NF73	2180	600	ss	hu	170718	Namsfjorden
18NF74	2420	620	ss	ha	180718	Namsfjorden
18NF75	3240	690	ss	hu	100718	Namsfjorden
18NF76	3020	650	ss	ha	100718	Namsfjorden
18NF77	2280	610	ss	ha	180718	Namsfjorden
18NF78	4120	720	ss	ha	20718	Namsfjorden
18NF79	2420	610	ss	ha	100718	Namsfjorden
18NF80	2480	620	ss	hu	130718	Namsfjorden
18NF81	1720	560	ss	ha	100718	Namsfjorden
18NF82	4160	770	ss	ha	110718	Namsfjorden
18NF83	1400	530	ss	ha	100718	Namsfjorden
18NF84	1280	520	ss	hu	100718	Namsfjorden
18NF86	2860	620	ss	ha	100718	Namsfjorden
18NF87	4780	770	ss	hu	110718	Namsfjorden
18NF88	1520	550	ss	ha	180718	Namsfjorden
18NF145	2580	630	ss	hu	130718	Namsfjorden
18NF146	11580	1050	ss	ha	110718	Namsfjorden
18NF147	2280	610	ss	hu	180718	Namsfjorden
18NF148	5840	840	ss		110718	Namsfjorden
18NF149	4500	790	ss	ha	90718	Namsfjorden
18NF150	1940	570	ss	hu	100718	Namsfjorden
18NF151	2620	640	ss	hu	180718	Namsfjorden

18NF152	1620	530	ss	ha	90718	Namsfjorden
18NF153	6520	790	ss	ha	90718	Namsfjorden
18NF154	2740	630	ss	ha	120718	Namsfjorden
18NF155	4860	790	ss	hu	100718	Namsfjorden
18NF156	2860	650	ss	hu	160718	Namsfjorden
18NF157	2700	640	ss	ha	100718	Namsfjorden
18NF158	4840	830	ss	hu	180718	Namsfjorden
18NF159	3980	760	ss	hu	100718	Namsfjorden
18NF160	15020	1150	ss	ha	160718	Namsfjorden
18NF161	3220	660	ss	ha	170718	Namsfjorden
18NF162	2360	610	ss	hu	100718	Namsfjorden
18NF163	6000	820	ss	hu	160718	Namsfjorden
18NF164	4000	750	ss	ha	130718	Namsfjorden
18NF165	4880	800	ss	hu	110718	Namsfjorden
18NF166	5340	820	ss	ha	170718	Namsfjorden
18NF167	2560	630	ss	hu	110718	Namsfjorden
18NF168	3000	620	ss	hu	20718	Namsfjorden
18NF169	1960	580	ss	ha	100718	Namsfjorden
18NF170	2060	580	ss	ha	90718	Namsfjorden
18NF171	2720	640	ss	ha	170718	Namsfjorden
18NF172	3920	730	ss	hu	130718	Namsfjorden
18NF173	5660	820	ss	ha	110718	Namsfjorden
18NF174	1520	510	ss	hu	20718	Namsfjorden
18NF175	1820	570	ss	ha	170718	Namsfjorden
18NF176	7480	890	ss	ha	160718	Namsfjorden
18NF177	2480	630	ss	hu	160718	Namsfjorden
18NF178	4020	720	ss	ha	120718	Namsfjorden
18NF179	2000	580	ss	ha	110718	Namsfjorden
18NF180	1280	500	ss	ha	180718	Namsfjorden
18NF40	1860	550	st	hu	270618	Namsfjorden
18NF70	1560	530	st	hu	180718	Namsfjorden
18NF85	1720	520	st	ha	100718	Namsfjorden
18NF90	2520	630	st	ha	110718	Namsfjorden
18NF95	1420	540	st	hu	110718	Namsfjorden
18NF124	1320	490	st	hu	110718	Namsfjorden
18NF137	1640	530	st	hu	110718	Namsfjorden

Table 13. Data on salmon collected from Nord-Trødelag, Namsen

Namsen	vekt	lengde	art	kjønn	dato	lokalitet
18N1	8500	900	ss	hu	150618	Holandsøya, Namsen
18N2						Namsen
18N3	4600	770	ss	ha	160618	Namsen
18N5	4200	770	ss	ha	160618	Namsen
18N6	5000		ss	ha	160618	Namsen
18N8	6200	850	ss	ha	150618	Namsen

18N10						Namsen
18N14	6300		ss	hu	150618	Namsen
18N16	8100		ss	ha	160618	Namsen
18N18	1500		ss	ha	160618	Namsen
18N21	900		ss	ha	70618	Namsen
18N22						Namsen
18N23						Namsen
18N24						Namsen
18N25						Namsen
18N26						Namsen
18N28	23000	1330	ss	ha	50618	Namsen
18N29						Namsen
18N30						Namsen
18N31						Namsen
18N32						Namsen
18N33						Namsen
18N34						Namsen
18N35						Namsen
18N36						Namsen
18N37	5100		ss	hu	80618	Namsen
18N38						Namsen
18N39	5600		ss		110618	Namsen
18N41	9700	990	ss		20618	Grong, Namsen
18N44	21100	1200	ss	ha	160618	Namsen
18N46	3100	680	ss		160618	Grong, Namsen
18N47	4000	740	ss	hu	60518	Grong, Namsen
18N48	6100	820	ss	ha	50618	Namsen
18N49	8600	920	ss	hu	160618	Grong, Namsen
18N50	3200	660	ss	ha	80718	Grong, Namsen
18N51	6700	880	ss	hu	60618	Grong, Namsen
18N54	5400	800	ss	ha	40618	Namsen
18N55	7500	920	ss		80718	Grong, Namsen
18N57	3800	740	ss	hu	80718	Grong, Namsen
18N58	5300	800	ss	ha	40618	Namsen
18N60	3800	750	ss	hu	160618	Grong, Namsen
18N81	6600	890	ss	hu	210618	Overhalla, Namsen
18N82	5400	550	ss	hu	170618	Overhalla, Namsen
18N83	6900	970	ss	hu	120818	Overhalla, Namsen
18N84	3200	690	ss	ha	130818	Overhalla, Namsen
18N85	11000	1030	ss		130818	Overhalla, Namsen
18N86	5200	830	ss	hu	130818	Overhalla, Namsen
18N87	7000	900	ss	ha	200618	Overhalla, Namsen
18N88	7700	900	ss		140818	Namsen
18N89	7200	900	ss	ha	220618	Overhalla, Namsen
18N90	14300	1140	ss	a	290618	Overhalla, Namsen
18N91	7500	880	ss	ha	210618	Overhalla, Namsen

18N92						Namsen
18N93						Namsen
18N94	6500	860	ss	ha	160818	Overhalla, Namsen
18N95	5020	820	ss	hu	120818	Overhalla, Namsen
18N96	9000	1000	ss	hu	120618	Overhalla, Namsen
18N97	3000	700	ss	hu	270618	Overhalla, Namsen
18N98	2100	610	ss	ha	160818	Nedre Vibstad, Namsen
18N99	900	480	ss	ha	130818	Overhalla, Namsen

Table 14. Data on fish collected from Sør-Trøndelag, Agdenes.

Agdenes	vekt	lengde	art	kjønn	dato	lokalitet
18A1	5000	790	ss		120618	Agdenes
18A2	7700	870	ss	hu	220618	Agdenes
18A3	2100	570	ss	hu	110618	Agdenes
18A4	1700	510	ss		110618	Agdenes
18A5	2400	600	ss	hu	220618	Agdenes
18A6	3400	680	ss	ha	160618	Agdenes
18A7	3300	680	ss	hu	220618	Agdenes
18A8	2100	570	ss		130618	Agdenes
18A9	4900	800	ss	hu	220618	Agdenes
18A10	2400	650	ss		160618	Agdenes
18A11	4000	750	ss	hu	220618	Agdenes
18A12	3400	700	ss	hu	220618	Agdenes
18A14	2100	570	ss		130618	Agdenes
18A15	1800	560	ss		110618	Agdenes
18A16	4100	780	ss	hu	230618	Agdenes
18A18	3400	720	ss	ha	230618	Agdenes
18A20	2600	630	ss		120618	Agdenes
18A21	4600	800	ss		120618	Agdenes
18A22	3000	650	ss		120618	Agdenes
18A23			ss		130618	Agdenes
18A24	2900	630	ss	hu	110618	Agdenes
18A25	1600	540	ss		210618	Agdenes
18A26	1700	540	ss	ha	110618	Agdenes
18A28	2300	590	ss	hu	210618	Agdenes
18A29	2500	660	ss	hu	210618	Agdenes
18A30	4100	750	ss	hu	220618	Agdenes
18A31	5700	830	ss		230618	Agdenes
18A32	2700	630	ss	ha	230618	Agdenes
18A33	3100	660	ss	hu	230618	Agdenes
18A34	2600	660	ss	hu	210618	Agdenes
18A35	2000	570	ss	ha	210618	Agdenes
18A36	3300	660	ss	ha	210618	Agdenes

18A37	10100	900	ss		230618	Agdenes
18A38	5100	790	ss	hu	230618	Agdenes
18A39	2200	580	ss	ha	210618	Agdenes
18A40	5400	830	ss	hu	230618	Agdenes
18A41	4300	760	ss	hu	230618	Agdenes
18A42	3000	630	ss	hu	210618	Agdenes
18A43	1100	470	ss	hu	230618	Agdenes
18A44	2800	650	ss	ha	210618	Agdenes
18A45	5400	790	ss	hu	230618	Agdenes
18A46	6300	820	ss	hu	230618	Agdenes
18A47	4800	780	ss	hu	230618	Agdenes
18A48	2500	580	ss	ha	230618	Agdenes
18A49	6300	880	ss	ha	210618	Agdenes
18A50	2700	610	ss	ha	230618	Agdenes
18A51	2200	590	ss	ha	220618	Agdenes
18A52	1600	520	ss	ha	220618	Agdenes
18A53	5900	850	ss		120618	Agdenes
18A54	4800	790	ss		120618	Agdenes
18A55			ss		160618	Agdenes
18A56	2300	600	ss	hu	220618	Agdenes
18A57	2800	650	ss	ha	220618	Agdenes
18A58	1900	580	ss	hu	220618	Agdenes
18A59	2800	680	ss		120618	Agdenes
18A62	900	460	ss	ha	140718	Agdenes
18A64	2800	670	ss	ha	20718	Agdenes
18A65	1100	510	ss	ha	40718	Agdenes
18A66	1200	510	ss	ha	300618	Agdenes
18A68	1400	540	ss	ha	60718	Agdenes
18A69	4500	760	ss	hu	150718	Agdenes
18A70	2200	600		ha	20718	Agdenes
18A71	3300	760	ss	hu	70718	Agdenes
18A72	2800	640	ss	ha	10718	Agdenes
18A73	1500	510	ss	ha	10718	Agdenes
18A74	2200	610	ss	ha	130718	Agdenes
18A75	2700	660	ss		90718	Agdenes
18A77	5400	810	ss	hu	220718	Agdenes
18A78	1000	500	ss	ha	20718	Agdenes
18A79	4000	720	ss	hu	160718	Agdenes
18A80	3300	670	ss	ha	220718	Agdenes
18A82	1100	480	ss	ha	80718	Agdenes
18A83	1300	510	ss	hu	40718	Agdenes
18A84	2600	620	ss	ha	80718	Agdenes
18A85	700	430	ss	ha	220718	Agdenes
18A86	1800	560	ss	ha	300618	Agdenes
18A87	2300	600	ss	hu	150718	Agdenes
18A89	2100	570	ss	ha	40718	Agdenes

18A90	2100	590	ss	ha	90718	Agdenes
18A92		620	ss	ha	130718	Agdenes
18A93	1800	550	ss	ha	150718	Agdenes
18A94	1900	600	ss	hu	20718	Agdenes
18A95	1700	580	ss	ha	300618	Agdenes
18A96	4000	730	ss	hu	10718	Agdenes
18A176	7300	870	ss	hu	160718	Agdenes
18A13	1000	520	st		120618	Agdenes
18A17	600	370	st		210618	Agdenes
18A19	1700	510	st		230618	Agdenes
18A27			st		230618	Agdenes
18A60	4300	800	st	hu	110618	Agdenes
18A63	1600	520	st		260618	Agdenes
18A76	1200	480	st		260618	Agdenes
18A81	400	310	st		30718	Agdenes
18A88	800	430	st		20718	Agdenes
18A91	1400	490	st		30718	Agdenes
18A104	600	360	st		150718	Agdenes
18A116	800	420	st		260618	Agdenes
18A138	800	410	st		40718	Agdenes
18A147	700	400	st		140718	Agdenes

Table 15. Data on fish collected from Sør-Trøndelag, Gaula

Gaula	vekt	lengde	art	kjønn	dato	lokalitet
18G4						
18G5	10500	1050	ss	hu		m
18G8	4200	760	ss	hu	120818	Melhus
18G10	3200	690	ss	ha	180818	Melhus
18G14	4100	720	ss	ha	240618	Melhus
18G15						
18G17	2100	580	ss	a	120818	Melhus
18G18	1600	540	ss	ha	90818	Melhus
18G19	1200	470	ss	ha	140818	Melhus
18G20	1600	560	ss	ha	260818	Melhus
18G22	2500	670	ss	ha	290818	Valdøyan
18G24	2000	580	ss	ha	40818	Melhus
18G25	1800	570	ss	ha	80818	Valdøyan
18G26	3600	740	ss	ha	80818	Melhus
18G27	2000	580	ss	ha	60818	Melhus
18G29						
18G30	8200	960	ss	ha	260818	Melhus
18G31						
18G33	2500	670	ss	ha	80818	Melhus
18G34	5000	760	ss	ha	10718	Valdøyan
18G37	6500	900	ss	ha	50818	Melhus

18G38	7000	840	ss	hu	240618	Melhus

Table 16. Data on fish collected from Sør-Trøndelag, Steinkjerelva

Steinkjerelva	vekt	lengde	art	kjønn	dato	lokalitet
18Q5	4100	780	ss	ha	160618	Steinkjær
18Q16	6995	900	ss	ha	160618	Steinkjær
18Q17	3400	725	ss	ha	150618	camping
18Q18	5400	830	ss		150618	Steinkjær
18Q19	5020	860	ss	ha	150618	Steinkjær
18Q20	6400	830	ss	ha	150618	camping
18Q31	5200	820	ss	hu	230618	Ogna
18Q32	4500	790	ss	hu	230618	Ogna
18Q34	5000	810	ss	ha		Ogna
18Q35	5600	910	ss	ha	280618	Ogna
18Q39	5600	800	ss	ha	210618	Ogna
18Q40	6200	850	ss	ha	210618	Ogna
18Q46	5000	800	ss	hu	200618	Steinkjær
18Q47	5000	800	ss	hu	160618	Steinkjær
18Q48	5200	810	ss	ha	170618	Steinkjær
18Q49	5555	820	ss	hu	190618	Steinkjær
18Q50	5200	810	ss	hu	170618	Steinkjær
18Q56	7000	880	ss	ha	150618	Steinkjær
18Q58	5200	810	ss	ha	230618	Steinkjær
18Q60	3500	600	ss	ha	150618	Steinkjær
18Q66	3100	720	ss	ha	210618	Steinkjær
18Q67	5000	800	ss	hu	250618	Steinkjær
18Q68	1710	550	ss		20718	Steinkjær
18Q69	5050	800	ss	ha	200618	Figga
18Q70	6200	820	ss	ha	200618	Steinkjær
18Q91	4140	780	ss	ha	240618	Figga
18Q93	3200	660	ss	hu	240618	Byelva
18Q94	6100	870	ss	hu	290618	Steinkjær
18Q95	5000	820	ss	ha	190618	Steinkjær
18Q96	4000		ss	ha	150618	Steinkjær
18Q97	5600		ss	hu	150618	Steinkjær
18Q99	4500		ss	ha	150618	Steinkjær
18Q100	4000		ss	hu	150618	Steinkjær
18Q103	6800	870	ss	hu	70718	Byelva
18Q112	5000	810	ss	ha	150618	Steinkjær

Table 17. Data on salmon collected from Sør-Trøndelag, Stjørdalselva.

Stjørdalselva	vekt	lengde	art	kjønn	dato	lokalitet
18S1	6000	800	ss	hu	120618	Svarthølen
18S2	8300	920	ss	ha	160618	Sone 1

18S3	6400	850	ss	hu	160618	Sone 3
18S4	8450	920	ss	hu	20618	Einang
18S5	5900	820	ss	hu	210618	sone 2
18S6						
18S7	7500	880	ss	hu	200618	sone2
18S8	6400	860	ss	hu	140618	sone3
18S9	8300	930	ss	ha	160618	sone1
18S10	4800	750	ss	hu	160618	sone3
18S11	5200	790	ss	hu	170618	smutthullet
18S12	4200	720	ss	hu	160618	sone4
18S13	7100	880	ss	hu	210618	sone2
18S14	4300	750	ss	hu	200618	sone3
18S15	4800	770	ss	ha	200618	Florholmen
18S16	9100	930	ss	hu	210618	Austkil
18S17	10000	990	ss	hu	200618	Sone1
18S18	5800	810	ss	hu	200618	Stjørdal
18S19	5200	790	ss	hu	130618	smutthullet
18S20	3500	670	ss	ha	110618	sone1
18S21	7700	920	ss	ha	10718	sone1
18S22	4900	720	ss	hu	1080618	Einang
18S23	6000	800	ss	hu	10718	sone1
18S24	6500	850	ss	hu	250618	sone 1
18S26	5800	820	ss	hu	20718	Hamilton
18S27						
18S28	3500	680	ss	hu	290618	sone 1
18S29	5200	770	ss	hu	300618	sone 3
18S30	9500	940	ss	hu	260618	sone 2
18S31	4600	760	ss	ha	250618	sone 6
18S32	4200	730	ss	hu	300618	Bjørseth
18S33	4900	770	ss	hu	250618	Stjørdal
18S34	4450	730	ss	hu	300618	Sone 1
18S35	5300	800	ss	hu	260618	Sone 2
18S36	2400	590	ss	ha	250618	Hjelseng
18S37	6300	840	ss	hu	290618	Sone 4
18S38	4400	740	ss	hu	30718	Hamilton
18S39	2100	560	ss	hu	10718	Sone 1
18S40	5560	790	ss	hu	270618	Leirfald
18S41	8800	740	ss	hu	290618	sone 3
18S42	2000	560	ss	ha	270618	sone 4
18S43	9040	950	ss	ha	260618	sone 1
18S44	6910		ss	hu	280618	sone 1
18S45	5860	830	ss	ha	250618	Iverhølen
18S46	6500	820	ss	ha	290618	sone 4
18S47	2200	600	ss	ha	270618	sone 3
18S48	8300	940	ss	hu	300618	sone 7
18S49	2000	580	ss	hu	290618	sone 1

18S50	6000	830	ss	ha	290618	sone 4
18S51	7200	880	ss	hu	290618	sone 2
18S52	5600	820	ss	ha	260618	smutthullet
18S53	5330	810	ss	hu	270618	Leirfald
18S54	4350	770	ss	hu	270618	øsfsti
18S55	5700	820	ss	ha	280618	Fornes
18S56	7300	890	ss	ha	290618	sone 3
18S57	6700	840	ss	hu	300618	sone 2
18S58	2200	590	ss	ha	290618	sone 1
18S59	8340	870	ss	ha	260618	sone 1
18S60	7000	860	ss	ha	300618	sone 6
18S61	6500	880	ss	hu	230618	sone 4
18S62						
18S63	9000	940	ss	ha	240618	sone 1
18S64	5000	760	ss	hu	300618	sone 4
18S65	6700	830	ss	ha	230618	sone 4
18S66	5370	800	ss	hu	240618	sone 1
18S67	8600	920	ss	ha	240618	sone 6
18S68	5300	770	ss	hu	240618	sone 4
18S69	1780	540	ss	ha	240618	nebbhølen
18S70	6600	860	ss	hu	230618	sone 6
18S71	8100	900	ss	hu	240618	sone 3
18S72	5000	750	ss	hu	240618	sone 3
18S73	7500	920	ss	hu	240618	Stjørdal
18S74	11800	1060	ss	ha	240618	sone 2
18S75	8500	940	ss	hu	240618	Stjørdal
18S76	6500	860	ss	hu	240618	sone 6
18S77	6900	860	ss	hu	240618	Stjørdal
18S78	4500	770	ss	ha	240618	sone 4
18S79	7200	850	ss	hu	230618	Leirfald
18S80	6700	850	ss	hu	240618	sone 4
18S81						
18S82	7550	880	ss	ha	10618	Stjørdal
18S83	4600	730	ss	hu	50618	sone 1
18S84	13900	1110	ss	ha	80618	sone 4
18S85	5900	840	ss	ha	60618	Stjørdal
18S86	8800	960	ss	hu	10618	sone 1
18S87	5500	820	ss	hu	100618	sone 3
18S88	6200	830	ss	hu	40618	sone 1
18S89	7300	890	ss	hu	90618	Leirfald
18S90	4300	710	ss	ha	80618	sone 1
18S91	5980	820	ss	ha	80618	Leirfald
18S92	6880	840	ss	hu	60618	sone 1
18S93	6200	820	ss	hu	70618	vold
18S94	7600	880	ss	ha	30618	sone 1
18S95	4700	740	ss	hu	80618	Leirfald

18S96	4600	740	ss	hu	30618	sone 4
18S97	5100	770	ss	hu	40618	sone 3
18S98	6400	850	ss	hu	80618	Stjørdal

Table 18. Data on fish collected from Hordaland, Sørfjorden (Trengereid).

Tregereid	vekt	lengde	art	kjønn	dato	lokalitet
181215T-1	5420	78	ss	ho	03.07.2018	Trengereid
181215T-2	9595	95	ss	ho	18.06.2018	Trengereid
181215T-3	4950	81	ss	ho		Trengereid
181215T-4	8960	96	ss	ho	18.06.2018	Trengereid
181215T-5	3760	75	ss		30.06.2018	Trengereid
181215T-6	7020	90	ss	ho	27.06.2018	Trengereid
181215T-7	4335	76	ss	ho	04.07.2018	Trengereid
181215T-8	8785	95	ss	ho	29.08.2018	Trengereid
181215T-9	5410	81	ss	ho	04.07.2018	Trengereid
181215T-10	8475	92	ss	ho	27.06.2018	Trengereid
181215T-11	6850	90	ss	ho	12.07.2018	Trengereid
181215T-12	2655	62	ss	hann	09.07.2018	Trengereid
181215T-13	3250	72	ss	hann	10.07.2018	Trengereid
181215T-14	2880	65	ss	hann	15.07.2018	Trengereid
181215T-15	3340	70	ss	hann	16.07.2018	Trengereid
181215T-16	10250	100	ss	ho	29.06.2018	Trengereid
181215T-17	5040	78	ss	ho	09.07.2018	Trengereid
181215T-18	6750	90	ss	ho		Trengereid
181215T-19	2330	63	ss	hann		Trengereid
181215T-20	5465	81	ss			Trengereid
181215T-21	5845	87	ss	hann	18.07.2018	Trengereid
181215T-22	2085	58	ss	hann	16.07.2018	Trengereid
181215T-23	3130	65	ss	hann	03.07.2018	Trengereid
181215T-24	1710	58	ss	hann	09.08.2018	Trengereid
181215T-25	4190	75	ss	ho	30.06.2018	Trengereid
181215T-26	3505	72	ss	hann		Trengereid
181215T-27	6125	84	ss		16.07.2018	Trengereid
181215T-28			ss			Trengereid
181215T-29	4490	75	ss	ho		Trengereid
181215T-30	4010	75	ss	hann	04.07.2018	Trengereid
181215T-31	4810	79	ss	ho	15.07.2018	Trengereid
181215T-32	3880	75	ss	ho	22.07.2018	Trengereid
181215T-33	3890	72	ss	hann	16.07.2018	Trengereid
181215T-34	3810	73	ss	ho	18.07.2018	Trengereid
181215T-35	6420	87	ss	hann	09.07.2018	Trengereid
181215T-36			ss			Trengereid
181215T-37	5860	83	ss	hann	21.07.2018	Trengereid
181215T-38	6620	85	ss	ho		Trengereid
181215T-39	5085	82	ss	hann		Trengereid

181215T-40			ss			Trengereid
181215T-41	1835	58	ss	hann	21.07.2018	Trengereid
181215T-42			ss			Trengereid
181215T-43	7435	75	ss	ho	27.06.2018	Trengereid
181215T-44	4690	78	ss	hann	28.06.2018	Trengereid
181215T-45	1305	55	ss			Trengereid
181215T-46	1750	59	ss	hann		Trengereid
181215T-47	7880	94	ss	ho	23.08.2018	Trengereid
181215T-48	2010	56	ss	hann	04.07.2018	Trengereid
181215T-49	2000	60	ss	hann	15.08.2018	Trengereid
181215T-50	1975	58	ss	hann	15.07.2018	Trengereid
181215T-51	2960	66	ss	hann	08.08.2018	Trengereid
181215T-52	8080	95	ss	ho	04.07.2018	Trengereid
181215T-53	5150	81	ss	hann	03.07.2018	Trengereid
181215T-54	4940	80	ss	ho		Trengereid
181215T-55	4200	78	ss	ho	30.06.2018	Trengereid
181215T-56	6530	85	ss	ho	04.07.2018	Trengereid
181215T-57	13055	108	ss	hann	04.07.2018	Trengereid
181215T-58	5580	81	ss	ho	29.06.2018	Trengereid
181215T-59	4995	72	ss	ho	28.06.2018	Trengereid
181215T-60	3230	75	ss	hann	18.06.2018	Trengereid

Table 19. Data on salmon collected from Hordaland, Granvinselva. These salmon were held in tanks for some time before sampling.

Granvin	vekt	lengde	art	kjønn	lokalitet
18Gr1	2300	710	ss	hann	Granvinselva
18Gr2	5900	920	ss	hann	Granvinselva
18Gr3	3800	630	ss	hann	Granvinselva
18Gr4	3800	850	ss	ho	Granvinselva
18Gr5	4700	880	ss	hann	Granvinselva
18Gr6	3800	770	ss	hann	Granvinselva
18Gr7	3000	810	ss	hann	Granvinselva
18Gr8	1700	620	ss	hann	Granvinselva
18Gr9	3000	780	ss	ho	Granvinselva
18Gr10	3100	780	ss	ho	Granvinselva
18Gr11	3400	790	ss	ho	Granvinselva
18Gr12	7000	980	ss	ho	Granvinselva
18Gr13	4600	870	ss	hann	Granvinselva
18Gr14	7100	980	ss	hann	Granvinselva
18Gr15	7600	1040	ss	ho	Granvinselva
18Gr16	3200	810	ss	ho	Granvinselva
18Gr17	5600	840	ss	ho	Granvinselva
18Gr18	3400	780	ss	hann	Granvinselva
18Gr19	4200	830	ss	ho	Granvinselva
18Gr20		880	ss (ut gentest)	ho	Granvinselva

18Gr21		730	ss (ut gentest)	ho	Granvinselva
18Gr22		700	ss (ut gentest)	ho	Granvinselva
18Gr23		640	ss (ut gentest)	hann	Granvinselva
18Gr24		650	ss (ut gentest)	hann	Granvinselva
18Gr25		1080	ss (ut gentest)	ho	Granvinselva
18Gr26		570	ss (ut gentest)	hann	Granvinselva
18Gr27		670	ss (ut gentest)	hann	Granvinselva

Table 20. Data on fish collected from Hordaland, Ådland. These salmon were held in tanks for some time before sampling.

Ådland	vekt	lengde	art	kjønn	lokalitet
18aa1	3000	720	ss	hann	Ådlandselva
18aa2	1800	650	ss	hann	Ådlandselva
18aa3	2400	670	ss	hann	Ådlandselva
18aa4	2300	700	ss	ho	Ådlandselva
18aa5	1700	610	ss	hann	Ådlandselva
18aa6	4700	820	ss	hann	Ådlandselva
18aa7	1100	540	ss	hann	Ådlandselva
18aa8	2100	630	ss	hann	Ådlandselva
18aa9	1100	540	ss	hann	Ådlandselva
18aa10	1600	570	ss	hann	Ådlandselva
18aa11	2200	720	ss	ho	Ådlandselva
18aa12	3300	800	ss	ho	Ådlandselva
18aa13	3000	760	ss	ho	Ådlandselva
18aa14	3100	800	ss	ho	Ådlandselva
18aa15	3800	820	ss	ho	Ådlandselva
18aa16	3600	800	ss	ho	Ådlandselva
18aa17	4000	810	ss	ho	Ådlandselva
18aa18	1000	540	ss	hann	Ådlandselva
18aa19	4400	820	ss (ut gentest)	hann	Ådlandselva
18aa20	1500	570	ss (ut gentest)	ho	Ådlandselva
18aa21	4500	810	ss (ut gentest)	ho	Ådlandselva
18aa22	1700	570	ss (ut gentest)	hann	Ådlandselva
18aa23		650	ss (ut gentest)	hann	Ådlandselva
18aa24		650	ss (ut gentest)	hann	Ådlandselva

Table 21. Data on salmonids collected from Steindalen. These fish were held in tanks for some time before samling

Steinsdalen	vekt	lengde	art	kjønn	lokalitet
18st1	1400	540	ss	hann	Steinsdalselva
18st2	5000	850	ss	hann	Steinsdalselva
18st3	1400	550	ss	hann	Steinsdalselva

18st4	4600	780	ss	hann	Steinsdalselva
18st5	3800	820	ss	ho	Steinsdalselva
18st13		630	ss	hann	Steinsdalselva
18st14	3200	790	ss (ut gentest)	ho	Steinsdalselva
18st6	400	370	st	ho	Steinsdalselva
18st7	600	400	st	hann	Steinsdalselva
18st8	4700	790	st	hann	Steinsdalselva
18st9		500	st	hann	Steinsdalselva
18st10		650	st	hann	Steinsdalselva
18st11		580	st	hann	Steinsdalselva
18st12	900	480	st	hann	Steinsdalselva

Table 22. Data on salmon collected from Hordaland, Opo. These fish were held in tanks for some time before sampling.

Opo	vekt	lengde	art	kjønn	lokalitet
18o1	2700	680	ss	hann	Opoelva
18o2	4800	830	ss	hann	Opoelva
18o3	3800	910	ss	ho	Opoelva
18o4	3100	790	ss	ho	Opoelva
18o5	4600	840	ss	hann	Opoelva
18o6	1500	550	ss	hann	Opoelva
18o7	3500	780	ss	ho	Opoelva
18o8	4300	820	ss	hann	Opoelva
18o9	1600	620	ss	ho	Opoelva
18o10	3700	780	ss	ho	Opoelva
18o11	2900	740	ss	ho	Opoelva
18o12	1800	620	ss (ut gentest)	hann	Opoelva
18o13	3000	770	ss (ut gentest)	ho	Opoelva
18o14	2200	650	ss (ut gentest)	hann	Opoelva
18o15	2500	700	ss (ut gentest)	hann	Opoelva
18o16	4200	810	ss (ut gentest)	hann	Opoelva
18o17	2800	750	ss (ut gentest)	ho	Opoelva
18o18	3500	750	ss (ut gentest)	hann	Opoelva
18o19	6300	910	ss (ut gentest)	hann	Opoelva

Table 23. Data on salmon collected from Hordaland, Vosso.

Vosso	vekt	lengde	art	kjønn	dato	lokalitet
18V1		530	ss	hann	41018	langhølen (bolstadelva)
18V8		790	ss	ho	311018	rongahølen (bolstadelva)
18V12		550	ss (stamfisk)	hann	11018	flage (vosso)
18V13		940	ss (stamfisk)	ho	81118	langebrua (vosso)
18V4		820	ss OD	hann	191018	hohølen (vosso)

18V5		650	ss OD	hann	241018	langebrua (vosso)
18V6		720	ss OD	ho	51118	lilandsosen (vosso)
18V7		830	ss OD	ho	21118	tokjeldo (vosso)
18V9		730	ss OD	ho	61118	hohølen (vosso)
18V10		840	ss OD	ho	251018	lilandsosen (vosso)
18V11		750	ss OD	ho	291018	hohølen (vosso)
18V2		250	st	ho	121018	vassenden (vosso)
18V3		160	st		181018	hohølen (vosso)

5.2 **Weight and lenght table**

Lengde og vekttabell for laks

cm	Slank	Middels	Kraftig
47	0,92	0,98	1,06
48	0,98	1,05	1,13
49	1,04	1,12	1,20
50	1,10	1,19	1,28
51	1,17	1,26	1,36
52	1,24	1,34	1,44
53	1,31	1,42	1,52
54	1,39	1,50	1,61
55	1,47	1,6	1,7
56	1,55	1,7	1,8
57	1,63	1,8	1,9
58	1,72	1,9	2,0
59	1,81	2,0	2,1
60	1,91	2,1	2,2
61	2,0	2,2	2,3
62	2,1	2,3	2,4
63	2,2	2,4	2,6
64	2,3	2,5	2,7
65	2,4	2,6	2,8
66	2,5	2,8	3,0
67	2,7	2,9	3,1
68	2,8	3,0	3,2
69	2,9	3,2	3,4
70	3,0	3,3	3,5
71	3,2	3,5	3,7
72	3,3	3,6	3,8
73	3,4	3,8	4,0
74	3,6	3,9	4,2
75	3,7	4,1	4,3
76	3,9	4,3	4,5
77	4,0	4,4	4,7
78	4,2	4,6	4,9
79	4,4	4,8	5,1
80	4,5	5,0	5,3
81	4,7	5,2	5,5
82	4,9	5,4	5,7
83	5,1	5,6	5,9
84	5,2	5,8	6,1
85	5,4	6,0	6,3
86	5,6	6,2	6,6
87	5,8	6,4	6,8
88	6,0	6,7	7,0
89	6,2	6,9	7,3
90	6,5	7,1	7,5
91	6,7	7,4	7,8
92	6,9	7,6	8,0
93	7,1	7,9	8,3
94	7,4	8,1	8,6
95	7,6	8,4	8,8
96	7,8	8,7	9,1
97	8,1	9,0	9,4
98	8,3	9,3	9,7
99	8,6	9,5	10,0
100	8,9	9,8	10,3
101	9,1	10,1	10,6
102	9,4	10,5	11,0
103	9,7	10,8	11,3
104	10,0	11,1	11,6
105	10,3	11,4	12,0
106	10,6	11,8	12,3
107	10,9	12,1	12,7
108	11,2	12,4	13,0
109	11,5	12,8	13,4
110	11,8	13,2	13,8
111	12,1	13,5	14,1
112	12,5	13,9	14,5
113	12,8	14,3	14,9
114	13,1	14,7	15,3
115	13,5	15,1	15,7
116	13,9	15,5	16,2
117	14,2	15,9	16,6
118	14,6	16,3	17,0
119	15,0	16,7	17,4
120	15,3	17,2	17,9
121	15,7	17,6	18,3
122	16,1	18,0	18,8
123	16,5	18,5	19,3
124	16,9	19,0	19,8
125	17,3	19,4	20,2
126	17,8	19,9	20,7
127	18,2	20,4	21,2
128	18,6	20,9	21,7
129	19,1	21,4	22,2
130	19,5	21,9	22,8

Figure 33. weight and length- table for Atlantic salmon by Norwegian Institute for Nature research, NINA. "Kraftig type" was used to calculate the weight or length of the salmon that were lacking either one of the information.