Genetic structure of a collapsed sockeye salmon stock: Atnarko River sockeye, British Columbia, Canada

by

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Declaration of Committee

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Abstract

Molecular tools have transformed management of genetically diverse species such as Pacific salmon and their mixed-stock fisheries. Here, I applied a new Single Nucleotide Polymorphisms panel to understand population structure of a collapsed sockeye salmon stock. Atnarko River sockeye is a diverse and culturally significant stock found on the Central Coast of British Columbia that collapsed in 2005, likely due to various factors that may include changes to sockeye salmon biodiversity. I found multiple genetically different populations within the stock, however not all spawner collections were genetically unique. Two highly distinct genetic clusters were generally associated with juvenile life history ecotype, although not exclusively. In-river catch predominantly assigned to the current most abundant population across all three decades of the indigenous fishery, however proportional contribution declined after collapse. My research advances understanding of Atnarko River sockeye stock collapse to inform recovery actions and has broad lessons on stewarding salmon diversity.

Keywords: sockeye salmon; genetic stock identification; population structure; collapsed stock; Atnarko River; Single Nucleotide Polymorphisms

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Introduction

Pacific salmon are a culturally and economically important group of migratory fishes that exhibit a high degree of local adaptation and metapopulation dynamics (Hilborn et al. 2003; Schtickzelle and Quinn 2007). There is an interconnected yet hierarchical nature to salmon biodiversity, where links can be found between geographic regions, ecosystems, habitats, life histories, timing, and genetic structure (Gustafson and Winans 1999; Larson et al. 2014, 2017; Hess et al. 2016; Prince et al. 2017; Thompson et al. 2020). Population and genetic diversity in salmon metapopulations can result in response diversity to environmental pressures (Hilborn et al. 2003; Braun et al. 2016). As a result of asynchronous population dynamics, salmon biodiversity offers resilience and stability to ecological systems and commercial and Indigenous fisheries (Schindler et al. 2010, 2015; Deacy et al. 2016; Nesbitt and Moore 2016). Given the importance of this biodiversity, a key challenge in salmon management is to avoid overharvest of less productive stocks in mixed-stock fisheries (Ricker 1958). Managers can either reduce harvest or increase control over fisheries to harvest of specific stocks through the application of genetic stock identification (GSI, Moore et al. 2021; Connors et al. 2022). Therefore, understanding the intricacies of salmon biodiversity and its underpinning genetics is an urgent challenge for applied science in this era of rapid global change, particularly in locations with ongoing mixed-stock fisheries.

Genetic techniques are revolutionizing the understanding of diversity within and across fish populations. Within the last fifteen years, the first socio-economically important fish genome was sequenced (Star et al. 2011), cheaper and more rapid sequencing methods have advanced (Davey and Blaxter 2010; Campbell et al. 2015), genotyping was automated (Stephens et al. 2006; Smith et al. 2007), and near instant genotyping for salmon conservation GSI challenges were developed (Baerwald et al. 2023). Single nucleotide polymorphisms (SNP) are rapidly becoming the genetic marker of choice to address many ecological and conservation questions (Gomez-Uchida et al., 2011; Shi et al., 2021; Sutherland et al., 2020) due to their improved accuracy, reproducibility, scalability, and transferability compared to previous molecular markers (Hauser et al., 2011; Morin et al., 2004). Researchers are commonly applying SNPs to challenges such as defining population structures (Sutherland et al., 2021), linking phenotypic traits to genotypes (Larson et al. 2017; Prince et al. 2017; Veale and

Russello 2017a; Thompson et al. 2020) understanding mixed-stock catch composition through GSI application (Beacham et al., 2018, 2019), and identifying hatchery origin through parental-based tagging (Beacham et al., 2019; Hasselman et al., 2017; Steele et al., 2013). SNP panels applied to GSI can incorporate regions of both putatively neutral as well as adaptive genetic variation (Ackerman et al. 2011), and can be customized to answer questions of various scales.

Sockeye salmon (*Oncorhynchus nerka*) populations can have a particularly high degree of local adaptation within and across watersheds. Fine scale adaptation has produced convergent life history traits across the species' range (Larson et al. 2019; Tigano and Russello 2022; Euclide et al. 2023), and relationships are reflected in genetic population structure. Specifically, the genetic population structure of sockeye salmon generally mirror geographic relationships across watersheds, with more similarity seen among lake-rearing populations within watersheds than between distant watersheds (Gustafson and Winans 1999; Beacham et al. 2004a, 2004b; Wood et al. 2008). However, river/sea-rearing (from here forward referred to collectively as river-type) juvenile life histories generally exhibit less spatial genetic structure (Gustafson and Winans 1999; Wood et al. 2008; Larson et al. 2019). River-type sockeye salmon are the ancestral ecotypic form of sockeye salmon and are thought to have repeatedly evolved into lake-rearing sockeye salmon after having colonized new lake habitats (lake-type; McPhee et al., 2009; Wood et al., 2008). In addition to juvenile life history ecotype, the resident life history form, known as kokanee, is also thought to have polyphyletic origin (Taylor et al. 1996; Wood et al. 2008; Beacham and Withler 2017). Lake-type sockeye salmon and kokanee can be broken down further into reproductive ecotypes with polyphyletic origins exhibiting differences in shore-spawning and stream-spawning populations within drainages (Taylor et al. 1996; Wood et al. 2008; Beacham and Withler 2017). Thus, *O. nerka* ecotypes encompass locally adaptative traits converged at spatial and hierarchical axes.

Some ecotypic differences seen among *O. nerka* populations appear to be correlated to strong parallel selection across several conserved genetic regions (Larson et al. 2017, 2019; Veale and Russello 2017a, 2017b; Tigano and Russello 2022; Euclide et al. 2023). For example, Veale & Russello (2017a) found evidence of consistent genotype-phenotype relationships among stream- and shore-spawning kokanee and lake-type sockeye salmon ecotypes within populations across their pan-Pacific range.

Although genotype-phenotype trends across some genetic regions exist (Larson et al. 2019; Tigano and Russello 2022; Euclide et al. 2023), other work has recently identified predicted genotypes in many shared regions of divergence that were not consistently associated with ecotype across watersheds (Larson et al. 2019; Euclide et al. 2023). These researchers suggest sockeye salmon ecotypes are polymorphic, and different loci across many regions are responding to each habitat's unique selective pressures (Larson et al. 2019; Euclide et al. 2023). Thus, there is continued need for studies that examine the genetic structure of *O. nerka* across different watersheds to support conservation efforts.

Sockeye salmon populations and fisheries in the Central Coast of British Columbia (BC) have struggled over the last several decades. For example, in Nuxalk Nation territory, the Atnarko sockeye salmon stock complex collapsed in 2005 and has not recovered since (Cox-Rogers 2011; Connors and Atnarko Sockeye Recovery Planning Committee 2016; Connors et al. 2019). Collapse occurred abruptly and total returns declined by approximately 90% (Figure 1, Cox-Rogers 2011; Connors and Atnarko Sockeye Recovery Planning Committee 2016; Connors et al. 2019). Targeted commercial fisheries remain closed, and relatively few Nuxalk Nation fishers still target sockeye salmon. The collapse and lack of subsequent recovery has led to economic and cultural hardship for the Nuxalk Nation, who have harvested the Atnarko River sockeye stock for millennia. Current escapement surveys indicate that spawning habitat use has contracted, further emphasizing the urgency to understand the remaining biodiversity in the Atnarko River sockeye stock.

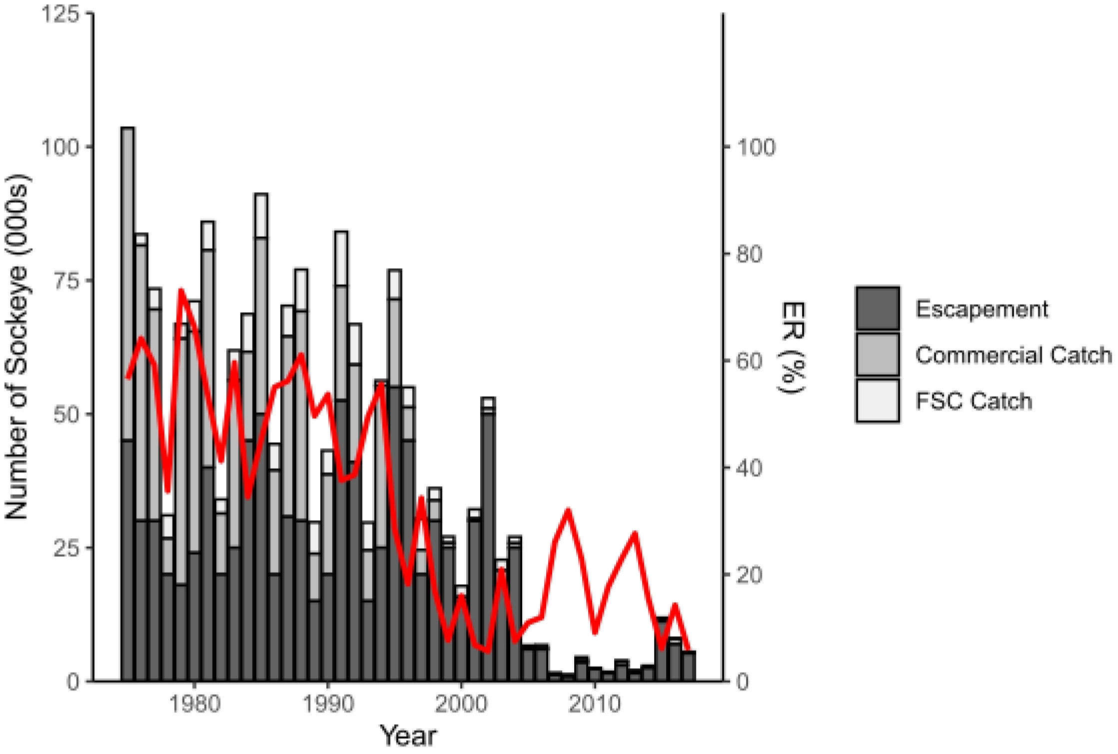


Figure 1. **Total Atnarko River sockeye escapement and harvest by commerical and Food Social and Ceremonial (FSC) fisheries from 1975 to 2017 (Cox-Rogers 2011; Connors and Atnarko Sockeye Recovery Planning Committee 2016; Connors et al. 2019). Exploitation rates (ER) shown by the red line.**

In collaboration with Fisheries and Oceans Canada (DFO), the Nuxalk Nation developed the Atnarko Sockeye salmon Recovery Plan to synthesize existing available information, identify potential contributing causes, and prioritize actions to promote recovery (Connors and Atnarko Sockeye Recovery Planning Committee 2016). Declines in marine survival from oceanic conditions (Ruggerone and Connors 2015; Malick et al. 2017) in addition to regional and local factors are suspected to have contributed to collapse (Connors and Atnarko Sockeye salmon Recovery Planning Committee 2016; Connors et al. 2019). However, the interplay between Atnarko stock collapse and stock biodiversity remains unknown. Spatial contraction from uneven perturbations across populations can significantly slow metapopulation recovery, particularly in network configurations like the lakes found in the Atnarko River watershed (Wilson et al. 2023). Thus, understanding of metapopulation structure and diversity of this culturally significant stock has been identified as a priority to inform potential recovery actions, particularly if collapse was experienced differently across spawning populations (Connors and Atnarko Sockeye salmon Recovery Planning Committee 2016). Previous molecular work suggested minimal genetic structure between two Atnarko River sockeye stock spawner populations using 10 neutral genetic markers (Nelson et al. 2003). However molecular tools have advanced, creating an opportunity to apply more refined tools in the region. Studies in this system will support recovery actions and also have relevance to the broader concepts of stock resilience and ecology of unexpected fisheries collapse (Hutchings 1996; Hutchings and Reynolds 2004; Okamoto et al. 2020; Wilson et al. 2023).

Here I aim to understand genetic population structure for Atnarko River sockeye and apply this understanding to illuminate potential shifts in stock composition through collapse. First, I apply a newly developed coastwide SNP panel designed for GSI to samples collected across spawning locations within the Atnarko River to ask- what is the contemporary genetic population structure of Atnarko River sockeye salmon? Second, I assess the accuracy of genetic baseline sample assignment in mixed-stock scenarios among Central Coast sockeye salmon collections. Finally, I use GSI on in-river mixed-stock fisheries samples collected over three decades to ask- how has Atnarko River sockeye salmon populations' catch composition changed through stock collapse? I hypothesize that each major spawning habitat across Atnarko River (e.g. Atnarko River spawners vs. spawners above each nursery lake) will be a genetically distinct population that can be used for GSI purposes. I also hypothesize that collapse was not experienced equally among populations and catch composition proportions have not remained static across the decades. Specifically, I hypothesize that there was increased relative dominance of the current largest populations, with a decrease in the other spawning populations through time. This would reflect patterns seen across recent escapement surveys. Collectively, these results can help inform ongoing recovery efforts and stewardship of this culturally significant stock.

Methods

Study system

The Central Coast of BC is a remote network of coastal fjords and channels amongst the coast mountain ranges. The region is characterized by many lakes, rivers, and streams across steep terrain with heavy rainfall. The Central Coast supports a diversity in sockeye salmon populations that vary in run-timing, spawning habitat, and juvenile rearing strategies (Connors et al. 2018). Escapement data is limited (Connors et al. 2018), however many populations are thought to be relatively small due to watershed size, with exception to Wuikinuxv Lake sockeye salmon in Rivers Inlet, where historical commercial catch has often exceeded a million sockeye salmon (Rutherford and Wood 2000). Precipitous declines in escapement were documented across many populations along the Central Coast through the 1990s (Rutherford and Wood 2000). More recently, declines in productivity have also been identified (Peterman and Dorner 2012).

Atnarko River is a 70-kilometer-long river that flows through five consecutive sockeye salmon rearing lakes on the Central Coast of BC in traditional Nuxalk Nation Territory (Figure 2). The Atnarko River joins with the Talchako River to become the Bella Coola River, which drains into the ocean in North Bentick Arm. Nuxalk Nation fishers have been harvesting Atnarko River sockeye salmon for millennia using a variety of methods prior to colonization (McIlwraith 1948). More recently, most Nuxalk fishers capture Atnarko River sockeye salmon by drift or set gillnets in the Bella Coola River. After collapse, few Nuxalk fishers specifically target sockeye salmon. The sockeye salmon that are harvested, are captured in setnets with long soak times or incidentally in chinook drift gillnets. Sockeye salmon catches are substantially lower since the collapse and peak catches have shifted later into the season over the last several decades (Cox-Rogers 2011; Connors and Atnarko Sockeye Recovery Planning Committee 2016).

Historically, adult sockeye salmon spawned throughout and between all five nursery lakes in Atnarko River (Leaney and Morris 1981; Cox-Rogers 2011). Although proportional changes across habitats are unknown, current and previous accounts of spawner observations dating back to the 1980s indicate a majority of sockeye salmon spawning concentrated in river sections between Stillwater Lake and Tenas Lake (from here referred to as Above Stillwater and Above Lonesome, Leaney and Morris 1981;

DFO 1989). Generally, it has been thought that adults spawning in Atnarko River below Stillwater Lake (from here referred to as Atnarko R) exhibit river-type life history and those above each nursery lake are predominantly lake-type sockeye salmon (Wood 2000; Cox-Rogers 2011). However, age structures from spawners directly above Lonesome Lake (Above Lonesome) indicate that some sea-rearing sockeye salmon may also spawn between the lakes (Cox-Rogers 2011). Prior to collapse river-type sockeye salmon were regularly found in other tributaries to the Bella Coola River downstream of the Atnarko River (Cox-Rogers 2011).

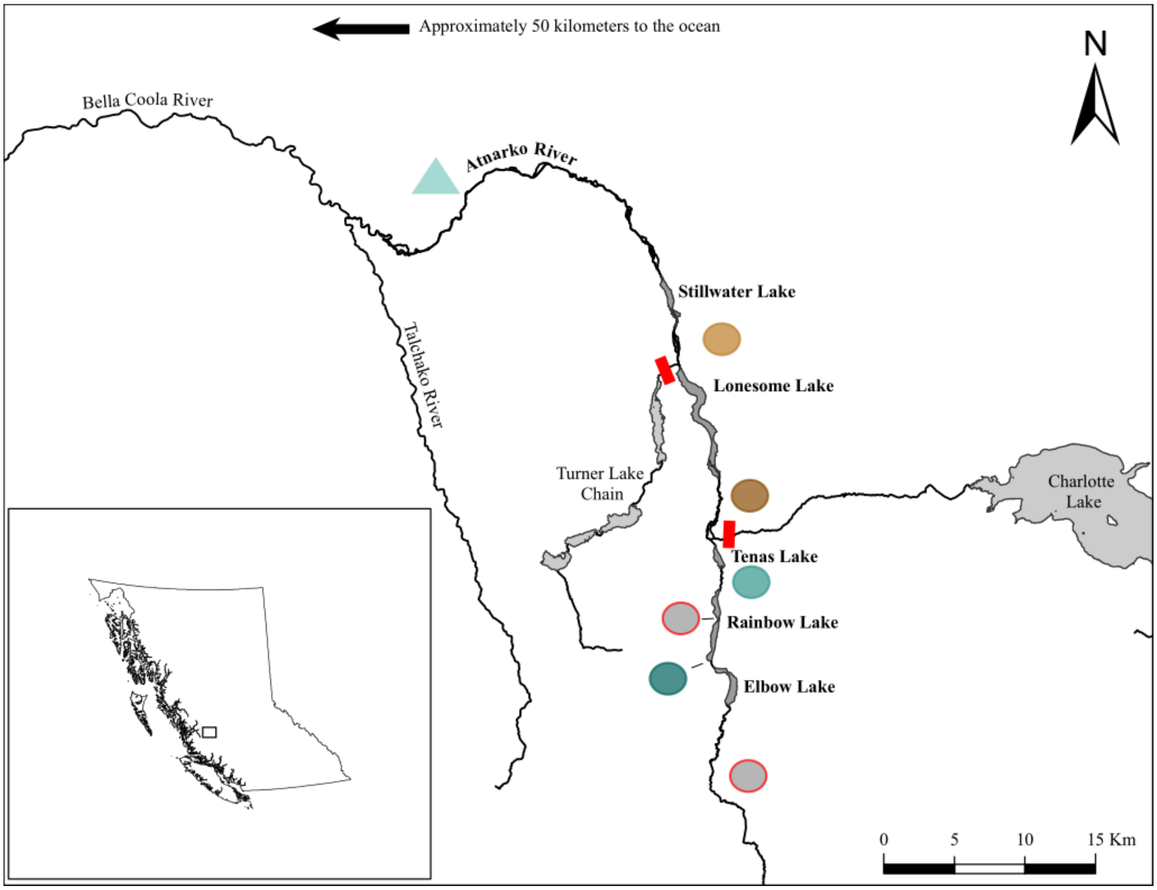


Figure 2. **Atnarko River in British Columbia, Canada. Shapes indicate the a priori hypothesized predominant juvenile life history form for each spawner sample collection site: triangles represent river-type while circles represent lake-type juvenile life history. Colours indicate a priori hypothesized genetic populations across each spawning habitat, however those in grey indicate regions where spawners have not been observed in recent years. Charlotte Lake and Turner Lake chain are not accessible to anadromous fish and marked with red. River reaches between the lakes are referenced as 'Above' the respective downstream lake.**

Baseline analysis

Sample selection

Genetic samples for each collection used in this study came from various sources, including field collections and archived tissues. I used existing genetic tissue samples archived with the DFO Molecular Genetics Lab (MGL) previously sampled for microsatellite baselines and these collections have been successfully utilized in prior publications (Beacham et al. 2005). MGL performed sample selection for baseline genotyping aimed to target a minimum of 95 individuals per watershed, and the results presented here represent a subset of larger sample selection coastwide. In cases where 95 individuals couldn't be obtained per baseline collection in a given year, samples from other years were selected and aggregated into a single collection across the spawning population. If provided with baseline sample submissions, local expertise was also considered when separating multiple habitats within a watershed, such as Kwakwa River.

In collaboration with Nuxalk Fisheries and Wildlife Lab and many other organizations, I collected additional tissue samples for baseline between 2020 and 2022 across the North and Central Coast of BC from regionally and culturally significant populations not represented in the archived collection. Here, further details on baseline additions are limited to those in Nuxalk Nation territory. I collected tissues in the fall from live and dead sockeye salmon near spawning grounds from Kimsquit River, Kimsquit Lake (shore spawners), Atnarko River between Tenas Lake and Rainbow Lake (referred to as Above Tenas from here forward), and Atnarko River between Rainbow Lake and Elbow Lake (referred to as Above Rainbow from here forward). Additional historical spawning sites in Atnarko River were inspected but no spawners were detected to collect samples from. These habitats include Rainbow Lake (shore spawners), and the Atnarko River above Elbow Lake (referred to as Above Elbow from here forward; Figure 2). It is uncertain if these spawning populations were undetected, residualized (Ricker 1938), or extirpated. Additional baseline samples for other tributaries to the Bella Coola River other than Atnarko River were collected, however they were not included due to low sample sizes (<10 individuals/collection). Nuxalk Nation and the Fisheries and Oceans Canada Salmon Enhancement Program currently operate a small-scale recovery enhancement project for the Atnarko River sockeye stock and collect spawners for broodstock from two areas: the Atnarko River and Above Lonesome. Contemporary and archived genetic samples were collected from broodstock and included in baseline samples.

In this analysis, I included all samples collected for baseline from the Atnarko River sockeye stock that could be traced to spawning habitat. I filtered additional baselines applied in downstream analyses to create a Central Coast regional set of collections from the coastwide collections in order to assess baseline performance for GSI purposes, as Pacific salmon can stray (Schtickzelle and Quinn 2007). Central Coast collections had to meet the following conditions: the collection was from a watershed within a 200 kilometer radius of Atnarko River that did not include Fraser River tributaries, and included 50 or more individuals after filtering. For the purpose of this analysis, sample size requirements were eased for the following three regionally significant locations for this study: Above Tenas, Above Rainbow, and Kimsquit R. I intentionally included two non-spawning collections, one from Long Lake collected at the Docee River Counting Fence (Long L), and one from sockeye salmon captured in Kitlope Lake. Sockeye salmon migrate up the Docee River to spawn in tributaries to Long Lake, and collections from one of the predominant spawning creeks did not meet sample size requirements after filtering. Shore spawners and river spawners are present in the Kitlope watershed, and archived tissues were collected from sockeye salmon holding in the lake. Both non-spawning collections were incorporated to include regional diversity in lieu of missing baselines for each individual spawning population.

Panel design

SNP selection for targeting in the initial panel design came from a few different published sources (Appendix A). Markers previously used for GSI were included from Columbia River Inter-Tribal Fish Commission (CRITFC) GSI panel (Hasselman et al. 2017). While markers were identified from this primary source for panel design, many came from various other sources, including but not limited to: Beacham et al. (2010), Elfstrom et al. (2006), Habicht et al.(2008), Miller et al. (2001), and C. T. Smith et al. (2005). Secondary sources of markers were selected from Veale & Russello (2017), with preferential marker selection to those identified as outliers, as well as Larson et al. (2017) selecting for high F_{ST} between targeted populations, and selection of markers identified in islands of divergence. Additional markers were designed utilizing published whole-genome re-sequencing data (Christensen et al. 2020). Specifically, these markers were selected to target loci in the vicinity of genes predicted to have potential phenotype differences, including those known to influence run-timing in other Pacific salmon species (GREB1L, Prince et al., 2017), age at maturity in Atlantic salmon (VGLL3, Ayllon et al., 2015), and the sex-determining gene located on the Y-chromosome (SdY, Larson et al., 2016; Phillips, 2013; Yano et al., 2012). Targeting SdY necessitated the addition of an SdY sequence from an Adams River male sockeye salmon into the reference genome (Personal Communication: K. Christensen). Finally, previously identified markers for species (Beacham and Wallace 2020) and other sex identification loci (Larson et al. 2016) were targeted for inclusion. Targeted marker information was provided to Scientific AgriSeq (ThermoFisher), and Targeted Genotyping by Sequencing Design Team to produce a custom AgriSeq panel of 589 primer pairs for 591 SNPs, in panel WGAG19046_DFO_SLMv01. All primer pairs, reference and alternate alleles, and genome positions of targeted SNP sites are identified in Appendix A.

Extraction and genotyping

DNA extraction protocols consisted of the following approaches applied by the MGL. For freshly extracted tissues, DNA was obtained utilizing BioSprint 96 Genomic DNA extraction kit (QIAGEN) and processed on either a BioSprint 96 (QIAGEN) or Kingfisher Flex (ThermoFisher) purification system. DNA previously extracted from MGL archives was frozen at -20 °C since being genotyped on the previous microsatellite baseline, and was predominately extracted using a Chelex-based extraction protocol (Small et al. 1998) or Wizard genomic purification kit (Promega).

The detailed procedure applied by MGL for library preparation and genotyping follows the same process as was outlined by Beacham et al. (2017) for coho salmon. In short, the process involved loading amplified DNA from 768 individuals and 589 sockeye salmon-specific amplicons per individual (Appendix A) on an Ion Torrent S5 540 chip (ThermoFisher) with an Ion Chef. Two chips are loaded consecutively with one run of the Ion Chef, then loaded onto an Ion Torrent S5 Prime sequencer. Sequencing data is aligned to the sockeye salmon genome (Christensen et al. 2020) and genotyping was conducted using the Torrent Suite Variant Caller (v5.14.1) at one or more SNP sites in each amplicon defined by a hotspot file following standard parameters. For all genotypes available, predefined SNP sites per individual were assembled to provide multi-locus genotypes that were the basic input for the genetic baseline.

Quality control and data filtering

For the coastwide panel, the MGL grouped resulting genotypes by collection location, and conservation unit for each collection as the initial reporting unit to develop the formatted baseline file for downstream use. Conservation units were based on information available described in Open Canada Data Lake-type (https://open.canada.ca/data/en/dataset/39aa4ce0-7185-448a-be87-9b69a87854a4) and River-type (https://open.canada.ca/data/en/dataset/6c8bc9b9-5f99-48fc-bd28-3c0af2ec379e) conservation unit boundaries. MGL identified and removed potentially contaminated individuals using GTScore default cut-offs, and individuals were filtered to include only those with over 250 amplicons successfully genotyped in *GTScore* (https://github.com/gjmckinney/GTscore). A single individual was removed from purported sample duplicates in pairs of individuals with 97% alleles in common and a minimum of 65% loci genotyped in common using *rubias* (Moran and Anderson 2019). Non-sockeye salmon were identified and removed both by extensive homozygosity (minimum 5% heterozygosity per individual), and by using species identification amplicons built into the panel (Beacham and Wallace 2020). I removed species identification amplicons, and all populations that were not within 200 kilometers of the Atnarko R. I filtered individuals out from the Central Coast collections if they were 80% or less successfully genotyped across all loci (Dann et al. 2009), and I removed one individual from pairs of individuals with 95% alleles in common and a minimum of 80% loci genotyped in common using *rubias* (Moran and Anderson 2019).

Separately, I filtered loci further to create two versions of the panel better suited for downstream analyses. The first panel was applied to improve the understanding of the Atnarko River sockeye stock diversity, and filtering was performed using only Atnarko River sockeye salmon collections. I created the second panel version to execute baseline performance assessment and application of GSI using Central Coast region collections. For each panel, I excluded all monomorphic loci and any loci near fixation (a minor allele frequency of <0.05 across populations). To reduce bias from allele frequency averaging, I removed loci with 80% or less successfully genotyped across all spawner samples in any one collection. Linkage disequilibrium was estimated for baseline samples by calculating pairwise r^2 values between all remaining loci using the *LDcorSV* package (Desrousseaux et al. 2012) following methods described in Hill and Robertson (1968) for each panel iteration. One locus per pair was excluded if pairwise r^2 values were >0.25 (May et al. 2020).

All filtering and analysis was performed using R version 4.2.2 (R Core Team 2022), and some pipelines, and functions were sourced from Sutherland et al. (2021; https://github.com/bensutherland/simple_pop_stats).

Population structure

I estimated pairwise F_{ST} with 95% confidence intervals (Weir and Cockerham 1984) across 1,000 bootstraps for all collections to assess genetic differentiation between collection sites using the *hierfstat* package (Goudet and Jombart 2022). In the case when F_{ST} was less than zero, I rounded the estimate to zero.

Discriminant Analysis of Principal Components (DAPC) was performed using *adegenet* (Jombart et al. 2010). This method maximizes discrimination between groups while minimizing within-group variation by performing discriminant analysis (DA) on principal components (PC, Jombart et al., 2010). I used cross-validation methods in *adegenet* (Jombart et al. 2010) to determine the number of PCs to retain in the analysis allowing for 100 replications to a maximum of 200 PCs considered (accounting for approximately 80 % of total genetic variability). I evaluated the number of PCs to retained based on the lowest root mean squared error (Jombart et al. 2010). All DA functions were retained and visualized with 95% confidence ellipses for each collection. I extracted and visually characterized allele frequencies for the top twenty contributing loci for both the first and second DA functions using ggplot2 (Jombart et al. 2010; Wickham 2016).

Using the program STRUCTURE, I performed preliminary analyses using admixture models across samples collected up to 2021 (Pritchard et al. 2000; Falush et al. 2003; Hubisz et al. 2009). I detected similar results to DAPC. Further analyses were not pursued and preliminary results are not presented here.

Baseline assessments

I evaluated baseline performance for GSI using baseline accuracy assessments and misallocation assessments described in Barclay et al. (2019). These tests estimated successful reassignment of individuals to a collection when found in a mixture, and which collections individuals assigned to when they did not successfully reassign. I performed the first set of baseline assessments to identify which spawner collections are genetically dissimilar and can be reliably distinguished from each other using this panel. In the initial baseline assessment, each collection was treated as a potential reporting unit, defined as a genetically distinct population for the purposes of GSI. After initial baseline assessments, I aggregated collections that did not meet criteria into reporting units, and repeated baseline assessments for a second round to confirm the aggregated collections met GSI criteria. Collections and reporting units were considered acceptable for mixed-stock analysis if at least 90% of the tests were within 10% of the true test mixture proportion and overall bias was within 5% of zero (Barclay et al. 2019). I determined baseline performance by comparing the estimated the proportion of tests with correct assignments to the true test mixture proportion in 90% or more of tests and overall bias (Barclay et al. 2019). I considered a reporting unit to have acceptable performance for mixed-stock analysis if at least 90% of the tests were within 10% of the true test mixture proportion and overall bias was within 5% of zero (Barclay et al. 2019).

I assessed baseline accuracy by creating test mixtures of up to 100 individuals by randomly sampling individuals from the baseline without replacement. A single mixture was created for each reporting unit composed of 1 to 100% of individuals so a full range of compositions could be examined. The remaining mixture was composed of individuals I randomly selected from other collections. The random individuals were proportionally distributed across the spawner collections. I limited test mixture sizes for each reporting unit to the maximum size of one-half of the baseline sample size to maintain accuracy in reassignment rates. Using *rubias,* I reassigned individuals in the mixtures back to the reduced baseline (Moran and Anderson 2019). *Rubias* uses a Bayesian approach using C++ coded conditional genetic stock identification models. Cross-validation and simulation are used to quantify and correct bias in estimating assignments. I analyzed each mixture using one Markov Chain Monte Carlo (MCMC) chain with 25,000 iterations, removing the first 5,000 as a burn-in period (Barclay et al. 2019). Prior parameters for each collection were set as equal. For each reporting unit, I calculated stock proportion estimates and the 90% credible interval by taking the mean and 5% and 95% quantiles of the posterior distribution from the MCMC chain. Afterwards, 100 parametric bootstrap simulations were performed to correct for bias in stock proportion estimates due to uneven populations across reporting units (Moran and Anderson 2019). Parametric bootstrap simulations correct for upward bias in mixture estimates, which can increase with increasing in variation in populations composing reporting units and decreasing genetic differentiation among reporting units (Hasselman et al. 2016; Moran and Anderson 2019).

Afterwards, I used misallocation assessments to identify which reporting units misassigned individuals were assigning to using the same process described above on new mixtures of individuals using *rubias* (Moran and Anderson 2019). In the first round of misallocation assessments, I limited test mixture sizes to one-half the size of the smallest baseline collection (10 individuals, Table 1), and replicated the process ten times for each collection using different mixtures. For each collection, I reported the mean allocation, and 5% and 95% quantiles of the posterior distribution across the 10 replicates.

I aggregated collections that did not meet criteria in baseline accuracy assessments into reporting units with the top contributing collections they misassigned to in the misallocation assessment. The baseline accuracy criteria was eased for one regionally important population (Above Stillwater). After I aggregated the Central Coast collections into reporting units, I repeated baseline assessment. In the second round of baseline assessments, I limited the misallocation test mixture sizes to one-half the size of the smallest reporting unit (20 individuals, Table 1) because removing individuals from baselines can shift allele frequencies, thus reducing baselines can effect genetic stock identification assignments (Barclay et al. 2019). Given unknown fishery proportions, I set prior parameters for each reporting unit as equal, with collection priors within each reporting unit being split equally across collections to create a flat prior distribution across all reporting units (Jasper et al. 2011). I applied code modified from the MGL's version of https://github.com/krshedd/GCL-R-Scripts.git to match laboratory outputs (https://github.com/erondeau/GCL-R-Scripts.git).

Nuxalk in-river genetic stock identification and catch composition

Mixed-stock sample selection

GSI samples were collected from Nuxalk sockeye salmon catch by a catch and sampling monitoring program led by Nuxalk Fisheries and Wildlife Lab between 1999 and 2020. I used scales originally collected to age sockeye salmon and samples were obtained from archive with the DFO Sclerochronology Lab. I selected years with thirty or more samples collected across the fishing season, and individuals if catch week could be determined from sampling data. MGL extracted DNA from a single scale per individual using a DNeasy Blood and Tissue 96 kit (QIAGEN), and followed the same genotyping methods used for baseline samples. The same quality controls and filters from baseline analysis were applied to remove misidentified species, duplicate individuals, and individuals that were not 80% or more successfully genotyped (Dann et al. 2009). MGL attempted to extract DNA from more historical samples (1976-1988), however extractions produced DNA concentrations far below target levels. Ultimately, this GSI analysis included Nuxalk sockeye salmon catch samples across three decades through stock collapse.

Catch data

Catch data obtained by NFWL were used for years between 1996 to 2022. I pooled both catch and sample data into decade bins representing periods related to collapse, 1996-2005 (representing the decade before collapse), 2006-2015 (the first decade after collapse), and 2016-2022 (the second decade after collapse). I sorted catch and sample data based on statistical fishery week, starting on Sunday through Saturday. I aggregated samples further into seasonal bins until each seasonal aggregate was composed of 15 individuals or more. The following catch bins resulted: Early, Week 28, Week 29 and Late, with Early approximately representing the month of June and the first week of July (Statistical weeks 23 to 27), and Late approximately representing the last week of July and first three weeks of August (Statistical weeks 30 to 33). Week 28 and Week 29 correspond with approximately the second and third week of July respectively. I aggregated catch data similarly, however retained the full resolution of catch weeks occurring in July. My analysis did not consider the minor sockeye salmon catch that occurs before June or after the third week of August. To represent catch through time and account for biases in catch monitoring, I averaged sockeye salmon catch across each seasonal bin and decade. Genetic samples and catch records do not distinguish targeted from incidental sockeye salmon catch, therefore I could not account for shifting fishery efforts and sample source in this analysis.

Catch composition

To reconstruct population composition of three decades of the Nuxalk in-river fishery harvests, I applied GSI referencing the reporting units created in baseline assessment in *rubias* (Moran and Anderson 2019). A flat prior was assumed across all reporting groups' parameters and Dirichlet priors for all collections within reporting units were set to one over the number of collections to create a flat prior across each reporting unit (Jasper et al. 2011). I calculated catch composition estimates and the 90% credible interval by taking the mean and 5% and 95% quantiles of the posterior distribution from a single MCMC chain for each reporting unit within each time period over 25,000 iterations, removing the first 5,000 as a burn-in period (Barclay et al. 2022). Trace plots from each reporting unit assignment proportion for each decadal and seasonal category were observed across the chain to evaluate convergence. One-hundred parametric bootstrap simulations were performed to correct for bias in stock proportion estimates when the number of collections in each reporting unit are uneven across reporting units (Moran and Anderson 2019). These parametric bootstrap simulations can correct for bias in mixture estimates associated with uneven numbers of populations within reporting units, particularly when genetic differentiation is low (Hasselman et al. 2016; Moran and Anderson 2019). I estimated catch and 90% credible intervals for each genetic reporting unit by multiplying mean catch by sample composition estimate and quantiles for each decadal and seasonal bin. To identify potential individuals from missing reference baseline populations, I visually assessed the Z-statistic as calculated by *rubias* for an approximately normal distribution (Moran and Anderson 2019; Anderson 2024). Non-normal z-scores would indicate individuals are possibly from a missing baseline population in catch samples (Anderson 2024).

Results

Baseline analysis

After I filtered samples for quality, 2,963 individuals remained in the Central Coast region sockeye salmon baseline across 29 collections (Figure B.1). Five of the 29 collections were from Atnarko watershed collections (Table 1). Average and median size across the Central Coast collections were 102 and 97 individuals respectively. The samples used represent a series of populations that exist both within larger river systems like the Wuikinuxv Lake as well as many small, isolated spawning populations. Spawning populations or collections, included those that were associated with nursery lakes, and thus are presumed to be lake-type sockeye salmon. In addition, I included three collections from locations without a known nursery lake and thus I inferred these were individuals that expressed river-type juvenile life histories.

After independent filtering, I created two modified panels out of the total 591 SNPs available, including 437 and 431 SNPs for the Atnarko River sockeye stock specifically and the GSI panel respectively (Appendix A). After filtering, I identified 77 loci and 74 loci from conserved regions of adaptation within the Atnarko River sockeye stock and GSI panels (Euclide et al. 2023).

Table 1. Reporting unit, spawner collection, a priori hypothesized predominant juvenile life history, a posteriori hypothesized juvenile life history, sample size by year, and approximate collection location for Central Coast sockeye salmon baseline samples after filtering. A priori hypothesized juvenile life histories are denoted as R if the spawning population is not associated with a nursery lake and thought to be a river-type ecotype, while L indicates if the spawning population is associated with a nursery lake. A posteriori hypothesized juvenile life history notes an updated hypothesis on the predominant juvenile life history ecotype expressed by a given spawning population from genetic analyses. Changed initial hypotheses are marked with an asterisk.

Reporting Unit[1]	Collection[1]	A priori hypothesized juvenile life history	A posteriori hypothesized juvenile life history	Year (n)	Coordinates
Above Stillwater	Above Stillwater	L	L	2020 (58), 2021 (145)	52.29713 -125.75230
Above Lonesome	Above Lonesome	L	L	2017 (40), 2018 (11), 2020 (176), 2021 (74), 2021 (83)	52.18991 -125.71142
river-type	Atnarko R	R	R	2005 (21), 2008 (32), 2020 (13), 2021 (100), 2022 (6)	52.37663 -126.09352
river type*	Above Rainbow*	L*	R*	2021 (1), 2022 (19)	52.09541 -125.71929
river-type*	Above Tenas*	L*	R*	2022 (25)	52.15010 -125.70800
river-type	Kimsquit R	R	R	2022 (32)	52.88277 -127.07722
river-type	Klinaklini R	R	R	2002 (67)	51.09258 -125.62662
Kitlope L	Kitlope L	L	L	2010 (106)	53.11453 -127.78245
Bloomfield Cr	Bloomfield Cr	L	L	2005 (106), 2021 (7), 2022 (18)	52.85660 -128.68167
Kent L	Kent L	L	L	2004 (70)	52.74182 -128.98005
Kwakwa R Lower	Kwakwa R Lower	L	L	2004 (49), 2022 (59)	52.55745 -128.70787

Reporting Unit[1]	Collection[1]	A priori hypothesized juvenile life history	A posteriori hypothesized juvenile life history	Year (n)	Coordinates
Kwakwa R Upper	Kwakwa R Upper	L	L	2004 (55), 2021 (14)	52.55571 -128.64883
Tankeeah R	Tankeeah R	L	L	2003 (65), 2004 (35)	52.29818 -128.26159
Kimsquit L shore	Kimsquit L shore	L	L	2021 (46), 2022 (42)	53.11222 -127.39611
Kadjusdis R	Kadjusdis R	L	L	2004 (2), 2021 (40), 2022 (46)	52.15238 -128.04312
Hook Nose Cr	Hook Nose Cr	L	L	2021 (22), 2022 (18)	52.12451 -127.83801
Koeye R	Koeye R	L	L	2004 (4), 2022 (93)	51.78039 -127.86247
Wuikinuxv tributaries (Owikeno Lake)	Amback Cr	L	L	2001 (23), 2002 (29), 2004 (62), 2021 (23)	51.69781 -127.04355
Wuikinuxv tributaries	Ashlulm Cr	L	L	2001 (66), 2002 (14), 2004 (15), 2021 (6)	51.68916 -126.90072
Wuikinuxv tributaries	Dallery Cr	L	L	2001 (27), 2002 (29), 2021 (4)	51.67301 -127.04353
Wuikinuxv tributaries	Genesee Cr	L	L	2002 (60), 2004 (44), 2021 (5)	51.66468 -126.66997
Wuikinuxv tributaries	Inziana R	L	L	2001 (21), 2002 (93), 2021 (6)	51.83065 -126.68201
Wuikinuxv tributaries	Marble Cr	L	L	2001 (18), 2002 (79)	51.62941 -126.68482
Wuikinuxv tributaries	Neechanz R	L	L	2002 (64), 2004 (53)	51.64728 -126.69056
Wuikinuxv tributaries	Sheemahant R	L	L	2002 (78), 2004 (25), 2021 (1)	51.74110 -126.62912
Wuikinuxv tributaries	Washwash R	L	L	2001 (44), 2002 (46), 2021 (17)	51.84430 -126.66413

Reporting Unit[1]	Collection[1]	A priori hypothesized juvenile life history	A posteriori hypothesized juvenile life history	Year (n)	Coordinates
Wanukv R	Wanukv R (Wannock R)	L	L	2002 (50)	51.67892 -127.252110
Long L	Long L	L	L	2001 (93)	51.23073 -127.33362
Long L	Smokehouse Cr	L	L	2001 (51), 2002 (20)	51.28851 -127.04763

[1] many place names applied are those listed in DFO Molecular Genetics Lab archive, and I acknowledge there is on-going work to decolonize the place names to appropriate Indigenous words and names.

Population structure

My analysis revealed little genetic divergence among three collections including the river-type Atnarko R spawners and two less abundant spawner collections with hypothesized lake-type life histories (Above Tenas and Above Rainbow, Table 2). Specifically, I found small F_{ST} values between Atnarko R and Above Tenas (F_{ST} = 0.001, 95% Confidence Interval (CI) = 0-0.002), Atnarko R and Above Rainbow (F_{ST} = 0, 95%, CI = 0-0.001), as well as Above Tenas and Above Rainbow (F_{ST} = 0, 95% CI = 0-0) in pairwise comparisons. Similarly, I found low F_{ST} values between the current two most abundant populations both hypothesized to both have lake-type life histories (Above Stillwater and Above Lonesome: F_{ST} = 0.003, 95% CI = 0.002-0.004, Table 2).

I found substantial genetic divergence among some Atnarko spawner collections. Specifically, there were high F_{ST} values in pairwise comparisons of the current most abundant population above a lake with the river-type spawning population (Above Lonesome and Atnarko R: F_{ST} = 0.073, 95% CI = 0.063-0.082), as well as when compared with the two less abundant spawner collections from above nursery lakes (Above Lonesome and Above Tenas: F_{ST} =0.077, 95% CI = 0.066-0.088; Above Lonesome and Above Rainbow: F_{ST} = 0.074, 95% CI = 0.063-0.085, Table 2). I detected high genetic divergence between the current second most abundant population above a lake and the river-type population (Above Stillwater and Atnarko R: F_{ST} = 0.075, 95% CI = 0.065-0.086). Similarly, I detected genetic differences between the current second most abundant population and the two less abundant hypothesized lake-type populations (Above Stillwater and Above Tenas: F_{ST} = 0.08, 95% CI = 0.069-0.092;

Above Stillwater and Above Rainbow: F_{ST} = 0.077, 95% CI = 0.066-0.09, Table 2) in pairwise comparisons. In other words, contrary to my predictions, the spawner collections from above less abundant nursery lakes (Above Tenas and Above Rainbow) were genetically similar to the river-type spawning population (Atnarko R), and these three spawner collections all differed from the populations from above the two more abundant populations sampled above nursery lakes (Above Stillwater and Above Lonesome).

Table 2. Pairwise F_{ST} comparisons shown by Weir-Cockerham with 95% confidence intervals between collection sites in Atnarko River watershed. River reaches are arranged in distance from ocean and significant genetic differences are noted in bold with asterisk.

	Atnarko R	Above Stillwater	Above Lonesome	Above Tenas	Above Rainbow
Atnarko R	-	**0.075* (0.065-0.086)**	**0.073* (0.063-0.082)**	0.001 (0-0.002)	0 (0-0.001)
Above Stillwater	-	-	0.003 (0.002-0.004)	**0.08* (0.069-0.092)**	**0.077* (0.066-0.09)**
Above Lonesome	-	-	-	**0.077* (0.066-0.088)**	**0.074* (0.063-0.085)**
Above Tenas	-	-	-	-	0 (0-0)
Above Rainbow	-	-	-	-	-

I produced four discriminant functions (DA) in DAPC. The corresponding eigenvalues representing the ratio of variance between groups over within groups for each DA were 984, 103, 21, and 9, respectively. The eigenvalues indicated the first two DAs reflect the most group distinction. The third and forth DA functions did not illuminate any further structure across collections, thus I retained only the first two DA functions. I retained 60 principal components (PCs) in the DAPC determined using cross-validation chosen based on the lowest reduced mean square error (0.5353). The PCs retained accounted for 40.8% of the overall genetic variation.

The first DA function from DAPC corroborates the genetic relationships that I found among collections observed in F_{ST} pairwise comparisons (Figure 3). The first DA differentiated two groups (Figure 3). The first group (Figure 3, left) consisted of the hypothesized river-type spawning population collection (Atnarko R), and the two less abundant spawning populations found above nursery lakes (Above Tenas Lake and Above Rainbow Lake). Meanwhile the second group (Figure 3, right) was composed of collections from the current two most abundant populations found above nursery lakes (Above Stillwater and Above Lonesome).

Specific loci appeared to be contributing to the patterns of genetic differentiation. Specifically, I found different top contributing loci among the first and second DAs, with exception to one loci (Larson2017_15807_28). All top contributing loci came from previously established studies (Hasselman et al., 2017; Larson et al., 2017; Veale & Russello, 2017b, Figure 4 and Figure B.2). In my analysis, allele frequencies strongly differed among the two clusters identified in the first DA axis, which separated the Atnarko R spawning population and two collections of spawners from above the less abundant nursery lakes (Above Tenas and Above Rainbow) from the current two most abundant populations above nursery lakes (Above Stillwater and Above Lonesome, Figure 3 and Figure 4). More subtle differences in allele frequencies were characterized across the second DA axis, which partially separated the current two most abundant populations found above nursery lakes (Above Stillwater and Above Lonesome, Figure B.2).

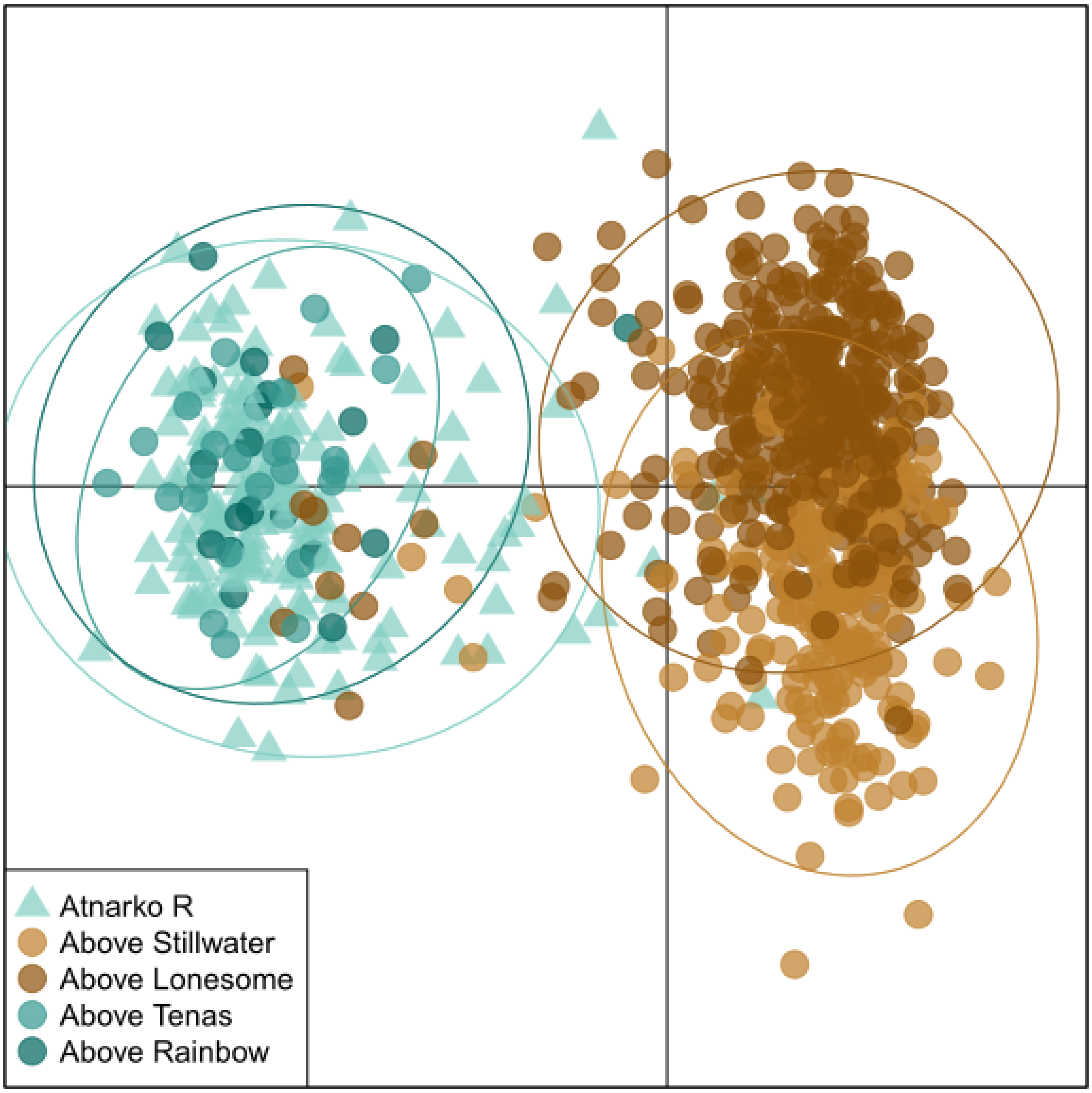


Figure 3. **Discriminant Analysis of Principal Components (DAPC) of Atnarko River sockeye stock collections using a 431 SNP panel, 95% confidence ellipses are shown. Shapes represent a priori hypothesized life histories (hypothesized river-type sockeye salmon are triangles while hypothesized lake-type sockeye salmon are circles). A posteriori hypothesized life histories are shown by color based on genetic analysis (teal represents river-type life history and brown represents lake-type life history).**

I identified three and four SNPs in the top contributing SNPs to DA1 and DA2 in conserved genomic regions of divergence identified in other sockeye salmon drainages associated with ecotype differences (Euclide et al. 2023). One SNP appeared in top contributing SNPs for both DA1 and DA2. Top contributing SNPs sourced from Larson et al. (2017) included putatively neutral and putatively adaptive outlier SNPs associated with sockeye salmon spawning ecotypes. All top contributing SNPs sourced from Veale & Russello (2017b) were outliers identified in migratory ecotype comparisons (kokanee versus anadromous sockeye salmon), with exception of one SNP (Veale2017_83545_85 in DA1), which was an outlier identified from reproductive ecotype comparisons. The remaining top contributing SNPs came from Hasselman et al. (2017) and cited works with unclear putative neutral or adaptive status.

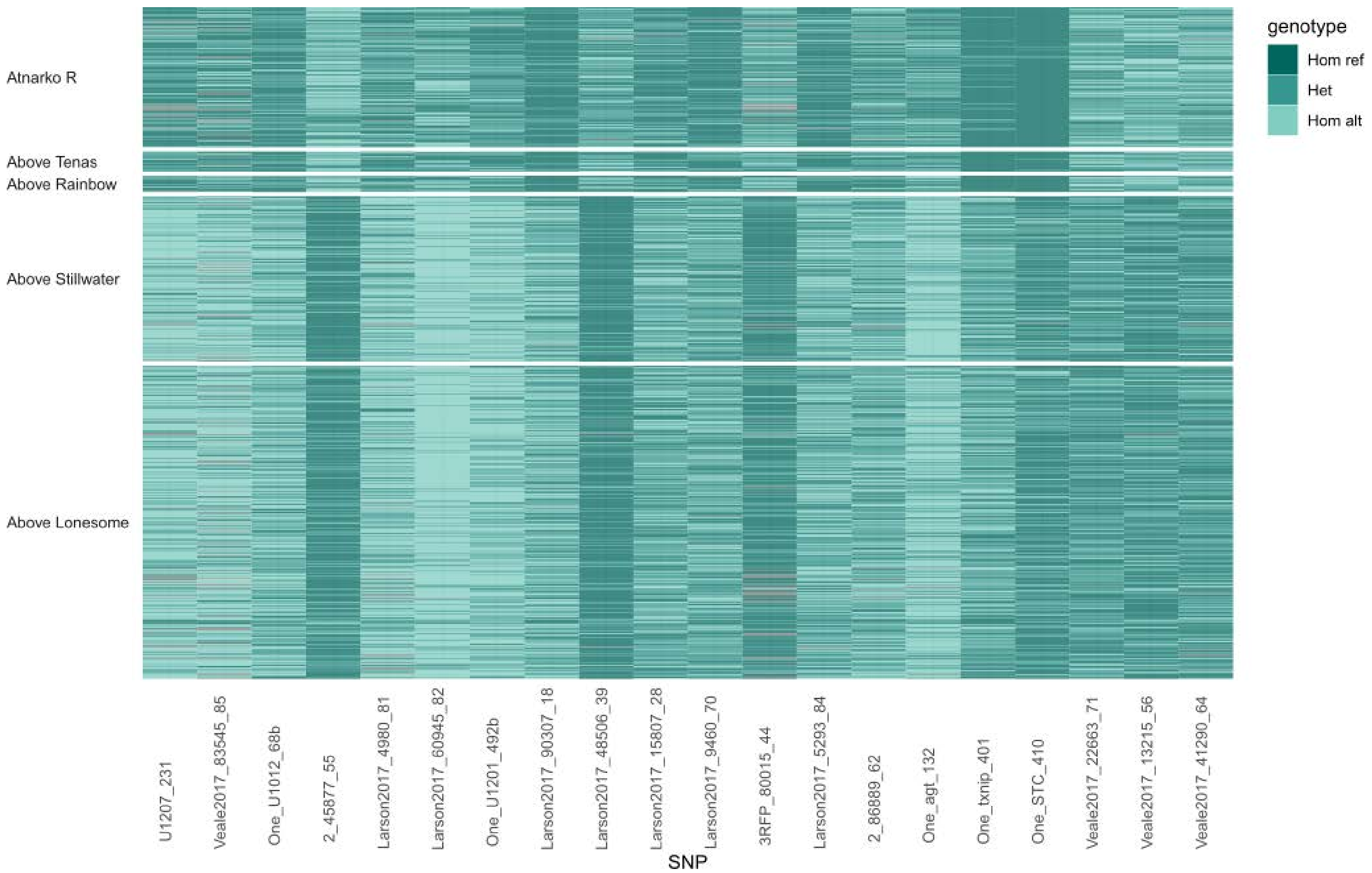


Figure 4. Characterized allele frequencies for top 20 contributing SNPs to the first DA of DAPC for the Atnarko River sockeye stock samples by collection site in decreasing contributing order. The first DA explained the largest variation seen among groups relative to within group differences, and separated the river-type spawning collection (Atnarko R) and two less abundant collections from above nursery lakes (Above Tenas and Above Rainbow) from the two dominant nursery lake population collections (Above Stillwater and Above Lonesome).

Baseline assessments

My initial baseline accuracy assessment revealed several patterns of genetic distinction and similarities across the 29 Central Coast collections (Table B.1). Population collections that met genetically distinguishable criteria from all other collections could be used as independent reporting units for GSI purposes. I found that many of the population collections hypothesized to have lake-type juvenile life history met criteria, including: Above Lonesome, Kitlope L, Bloomfield Cr, Kent L, Kwakwa R Lower, Kwakwa R Upper, Tankeeah R, Kimsquit Lake shore, Kadjusdis R, Hook Nose Cr, Koeye R, and Wanukv R. For 90% of tests using all 29 collections, the estimated proportion ranged from 1.3% to 6.1% of the true proportion and mean bias was between -2.4% and -0.6% (Table B.1). I found that the Above Stillwater collection did not meet criteria. The Above Stillwater proportional estimate was within 11.9% of the true proportion in 90% of tests with a mean bias of -5.3%, however I eased requirements for this one collection (Table B.1). I also performed all downstream analyses with Above Stillwater and Above Lonesome spawning collections combined into a single reporting unit (results can be found in Appendix C).

In my analysis, both of the current two less abundant spawner collections above nursery lakes in the Atnarko River sockeye stock (Above Rainbow and Above Tenas) were not genetically distinguishable enough from other collections in baseline accuracy assessments to be applied as individual reporting units in GSI. Sockeye salmon from above both small lakes produced proportion estimates within 10% of the true proportion in 90% of tests, however this was likely due to small sample sizes, and mean bias was over 5% from zero. Although not included in the assessment criteria, no tests observed proportional estimates falling within the 90% credible interval of the true proportion (Table B.1).

I found that the three hypothesized river-type collections (Klinaklini R, Atnarko R, and Kimsquit R) performed poorly in accuracy assessments and were too genetically similar to other collections to remain as independent reporting units for GSI. In 90% of accuracy tests, estimated proportions ranged from 13.6% to 25.4% of the true proportion in mixtures with a mean bias of 15.2%, -0.9%, and -8.1% respectively (Table B.1). Thus, apparent river-type sockeye salmon collections were not reliably distinguished by this SNP panel.

In my baseline accuracy assessments, some collections from within larger watersheds were not genetically distinguishable enough from other collections within those watersheds to be individual reporting units in a GSI application. Specifically, I found all tributaries to Wuikinuxv Lake (Amback Cr, Ashlulm Cr, Dallery Cr, Genesee Cr, Inziana R, Marble Cr, Neechanz R, Sheemahant R, and Washwash R) performed poorly, as 90% of tests estimated proportions within 25% to 41.6% of the true proportion and the mean bias ranged from -10.2% to -20.3% (Table B.1). Long L and Smokehouse Cr (a tributary to Long L) also did not meet baseline accuracy criteria, as both collections could not be distinguished from each other within the baseline assessments. Mean bias for these collections were 14.9% and 13.6%, and proportion estimates were within 31.7% and 29.5% of the true proportion in 90% of the tests (Table B.1). In other words, sockeye salmon collections were not reliably distinguishable from within the tributaries to the largest watershed of the Central Coast regional baseline (Wuikinuxv Lake), and a tributary to Long Lake could not be distinguished from the Long L (mixed tributary) samples.

I performed misallocation assessments to support grouping collections into reporting units for those collections that were not genetically distinguishable as independent reporting units for GSI purposes. I found correct assignments in composition estimates ranged from 0.1% to 98% when all 29 collections were treated as individual reporting units. Specifics can be found in Appendix B (Table B.2 and Table B.3), and I briefly summarize key results below to support how I aggregated collections into reporting units that performed poorly in the initial baseline accuracy assessment.

My initial baseline assessments were unable to distinguish among river-type collections, and all three collections with hypothesized river-type juvenile life histories predominantly assigned to Atnarko R. In my test mixtures made of Atnarko R individuals, 87.3% (90% Credible Interval (CrI) = 64.5%-98.1%) of individuals correctly reassigned to Atnarko R, while the next two top assignments included 5.3% (CrI = 2.5%-10.8%) contribution to Klinaklini R and 2.3% (CrI = 0.7%-10.9%) contribution to Kimsquit R. I found under 2.5% of Atnarko R individuals misassigned to the two most abundant populations in the Atnarko River sockeye stock (Above Lonesome and Above Stillwater).

Both Klinaklini R and Kimsquit R had high rates of misassignment to Atnarko R with estimates of 59.1% (CrI = 35.4%-81.4%) and 72.1% (CrI = 48.8%-88.4%) of Atnarko R sockeye salmon, and low rates of correct assignment rates estimated as only 5.7% (CrI = 2.5%-12.7%) and 0.3% (CrI = 0%-2.6%) correct contributions, respectively.

The current two smallest spawner collections from above nursery lakes in the Atnarko River sockeye stock could not be treated as independent reporting units and also predominantly misassigned to the Atnarko R, a collection I hypothesized to have river-type life history. Specifically, I found collections from the two less abundant spawner collections from above lakes (Above Tenas and Above Rainbow) misassigned by 80.1% (CrI = 57.9%-94.5%) and 84.1% (CrI = 61.3%-95.9%) of individuals to Atnarko R respectively.

In the initial misallocation assessment, I found the collections from within the two larger watersheds misassigned to other collections within the same watershed at high rates. All Wuikinuxv Lake tributaries (Amback Cr, Ashlulm Cr, Dallery Cr, Genesee Cr, Inziana R, Marble Cr, Neechanz R, Sheemahant R, and Washwash R) had poor correct assignments that ranged from 3.6% (CrI = 0.9%-13%) to 79.6% (CrI = 48.8%-96.1%), and individuals were predominantly misassigned to other Wuikinuxv Lake tributary collections. I also found that the Long L collection correctly assigned 60.5% (CrI = 36.4%-80%) of individuals, however 37.3% (CrI = 18.8%-59.1%) of individuals were assigned to Smokehouse Cr. In Smokehouse Cr test mixtures, 56.4% (CrI = 31.5%-74.7%) were assigned to Smokehouse Cr and 41.4% (21.6%-67.7%) assigned to Long L, the mixed Long Lake tributary collection. I found misallocation assessment supported aggregating collections from within the two larger watersheds into two respective reporting units.

I grouped baseline collections into new reporting units based on the initial baseline assessment analysis. I formed three reporting units from multiple collections for further assessments, resulting in a total of 16 reporting units (Table 1). Atnarko R, Klinaklini R, Kimsquit R, and the current two less abundant spawner collections from above nursery lakes in the Atnarko River sockeye stock (Above Tenas and Above Rainbow) were grouped together into a single reporting unit referred to as the ‘river-type’ reporting unit (Table 1). All Wuikinuxv Lake tributaries (Amback Cr, Ashlulm Cr, Dallery Cr, Genesee Cr, Inziana R, Marble Cr, Neechanz R, Sheemahant R, and Washwash R) were grouped together into a single reporting unit referred to as ‘Wuikinuxv tributaries’, and Long L and Smokehouse Cr were also grouped into the ‘Long L’ reporting unit (Table 1). All final reporting units can be found in Table 1.

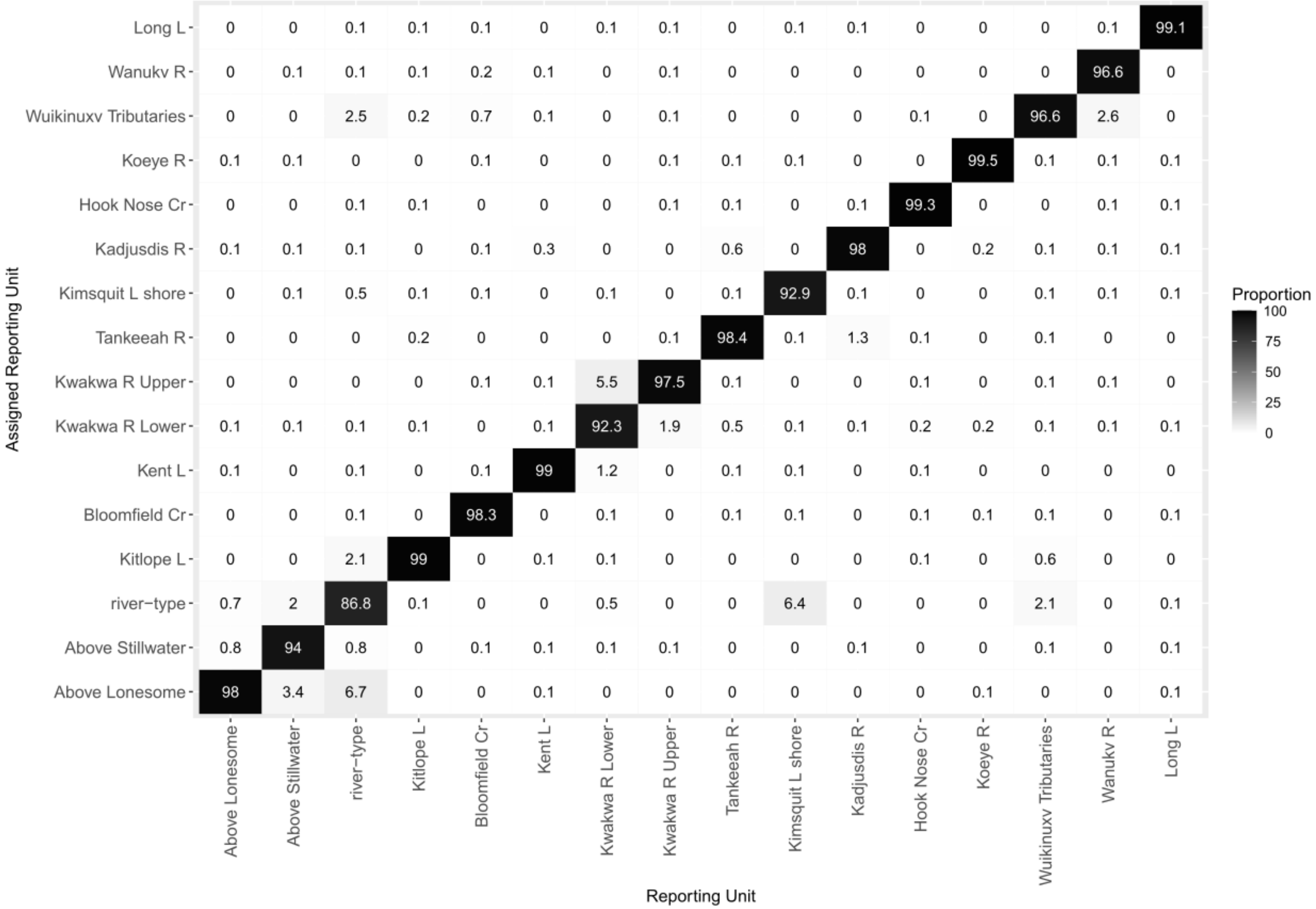
I created new test mixtures for all 16 reporting units to assess their performance, and all reporting units met criteria with exception to the current second most abundant nursery lake in the Atnarko River sockeye stock, Above Stillwater (Table 3). In test mixtures, I found the proportion estimates ranged from 0.5% to 6.6% of the true proportion in 90% of tests for groups other than Above Stillwater and mean bias was between -2.3% and 0.3% (Table 3). Above Stillwater produced estimates within 12% of the true estimate in 90% of tests with a mean bias of -3.3% (Table 3).

Table 3. Baseline accuracy assessment results from test mixtures analyzed for Central Coast regional baseline reporting units to be used for genetic stock identification (GSI). The estimated proportion within true proportion in 90% of the tests (90% within), proportion of tests within the 90% credible interval of the true proportion (within interval), mean bias across tests and maximum test mixture size (max n) is listed per reporting unit. A reporting unit is generally considered acceptable for GSI if 90% of the estimates are within 10% of the true proportion and mean bias is within 5% of zero, exceptions can be made if the management question can accommodate elevated levels of uncertainty. Test mixtures were limited to one-half of baseline samples up to a maximum of 100 individuals.

Collection	90% within	Within Interval	Mean Bias	Max n
Above Lonesome	5.6%	97.0%	-0.6%	100
Above Stillwater	12.0%	85.0%	-3.3%	100
river-type	6.6%	92.0%	-2.3%	100
Kitlope L	0.8%	100%	-0.1%	53
Bloomfield Cr	1.7%	100%	0%	65
Kent L	0.9%	100%	0%	35
Kwakwa R Lower	4.5%	100%	-0.8%	54
Kwakwa R Upper	2.3%	100%	0%	34
Tankeeah R	1.6%	98.0%	0%	50
Kimsquit L shore	2.0%	100%	0.1%	44
Kadjusdis R	1.9%	100%	0.3%	44
Hook Nose Cr	0.5%	100%	0%	20
Koeye R	0.8%	100%	-0.1%	48
Wuikinuxv tributaries	1.8%	100%	-0.3%	100
Wanukv R	1.8%	100%	0.2%	25
Long L	0.8%	100%	-0.1%	82

I identified proportional contribution to misassigned reporting units across all newly formed reporting units. I found the mean correct composition estimates ranged from 99.5% to 86.8% and can be found in Table 4 (90% credible intervals can be found in Table B.4). I summarize key results here. The top misassigned groups for the river-type reporting unit were Above Lonesome (6.7%, CrI = 1.3%-17.5%), Wuikinuxv tributaries (2.5%, CrI = 0.3%-7.3%), and Kitlope (2.1%, CrI = 0.4%-6.3%). Above Stillwater, Kimsquit Lake shore, and Wuikinuxv tributaries reporting units were all misallocated by some proportion to the river-type reporting unit, ranging from 2% to 6.4%, with all other misallocations less than 1% (Table 4).

Table 4. **Stock composition estimates (%) averaged across 10 replicates of mixtures made of 20 individuals from 16 reporting units. The cross-diagonal contains the porportion of individuals that were correctly reassigned. The 90% credible intervals can be found in Table B.4.**



Assigned Reporting Unit	Above Lonesome	Above Stillwater	river−type	Kitlope L	Bloomfield Cr	Kent L	Kwakwa R Lower	Kwakwa R Upper	Tankeeah R	Kimsquit L shore	Kadjusdis R	Hook Nose Cr	Koeye R	Wuikinuxv Tributaries	Wanukv R	Long L
Long L	0	0	0.1	0.1	0.1	0	0.1	0.1	0	0.1	0.1	0	0	0	0.1	99.1
Wanukv R	0	0.1	0.1	0.1	0.2	0.1	0	0.1	0	0	0	0	0	0	96.6	0
Wuikinuxv Tributaries	0	0	2.5	0.2	0.7	0.1	0	0.1	0	0	0	0.1	0	96.6	2.6	0
Koeye R	0.1	0.1	0	0	0.1	0	0	0.1	0.1	0.1	0	0	99.5	0.1	0.1	0.1
Hook Nose Cr	0	0	0.1	0.1	0	0	0	0.1	0.1	0	0.1	99.3	0	0	0.1	0.1
Kadjusdis R	0.1	0.1	0.1	0	0.1	0.3	0	0	0.6	0	98	0	0.2	0.1	0.1	0.1
Kimsquit L shore	0	0.1	0.5	0.1	0.1	0	0.1	0	0.1	92.9	0.1	0	0	0.1	0.1	0.1
Tankeeah R	0	0	0	0.2	0	0	0	0.1	98.4	0.1	1.3	0.1	0	0.1	0	0
Kwakwa R Upper	0	0	0	0	0.1	0.1	5.5	97.5	0.1	0	0	0.1	0	0.1	0.1	0
Kwakwa R Lower	0.1	0.1	0.1	0.1	0	0.1	92.3	1.9	0.5	0.1	0.1	0.2	0.2	0.1	0.1	0.1
Kent L	0.1	0	0.1	0	0.1	99	1.2	0	0.1	0.1	0	0.1	0	0	0	0
Bloomfield Cr	0	0	0.1	0	98.3	0	0.1	0	0.1	0.1	0	0.1	0.1	0.1	0	0.1
Kitlope L	0	0	2.1	99	0	0.1	0.1	0	0	0	0	0.1	0	0.6	0	0
river−type	0.7	2	86.8	0.1	0	0	0.5	0	0	6.4	0	0	0	2.1	0	0.1
Above Stillwater	0.8	94	0.8	0	0.1	0.1	0.1	0.1	0	0	0.1	0	0	0.1	0	0.1
Above Lonesome	98	3.4	6.7	0	0	0.1	0	0	0	0	0	0	0.1	0	0	0.1

Nuxalk in-river genetic stock identification and catch composition

I identified potential composition changes of the Atnarko River sockeye stock through the last three decades by genotyping 750 in-river Nuxalk fishery samples for GSI. Samples included eight years that spanned a period of 16 years (2003, 2005, 2006, 2008, 2009, 2010, 2018, and 2019). After I filtered samples, 457 individuals of the 750 mixed-stock samples genotyped remained. I applied sample composition to catch data to estimate catch composition. Catch data included all 16 years (Figure 5 left and Table B.5). I grouped sample and catch data into temporal strata and compared across decades and seasonal periods to identify potential changes in stock composition through the Atnarko River sockeye stock collapse via GSI.

I found that total in-river Nuxalk fishery sockeye salmon catch was lower in the decades after collapse in 2005 and peaked later in the season (Figure 5 left). Total mean catch declined from the decade before collapse (1996-2005) by over 92% in the first decade following the collapse (2006-2015), and by over 95% in the second decade after collapse. Prior to collapse, the highest catches occurred in approximately the second week of July (Week 28), compared to the last week of July (Week 30) in the decades after collapse. Before collapse (1996-2005), 50% of the mean cumulative catch occurred during the second week of July (Week 28), however 50% mean cumulative catch occurred in one week later (Week 29) in the decades following collapse (2006-2015 & 2016-2022). In addition to declines in abundance after collapse, a temporal shift occurred within Atnarko River sockeye stock catch in the most recent decade (Figure 5 left).

Catch composition

After final baseline assessments, I referenced 16 reporting units for genetic stock identification of the in-river Nuxalk fishery samples to identify potential changes in Atnarko River sockeye stock composition over collapse. Using GSI, I identified sample proportions across the season and decades. Trace plots from each reporting unit assignment proportion for each decadal and seasonal category appeared to converge across the single chain, and similar proportions of reporting unit assignments were produced in the analysis grouping Above Lonesome and Above Stillwater into a single reporting unit (Appendix C). Z-scores appeared to be approximately normal, and I detected a single individual as a potential outlier that assigned to the river-type reporting unit (Z-score = -7.9). Due to small sample sizes, I did not apply sample composition to the early season catch in the second decade after collapse (5 individuals, Table B.5). I estimated total catch and credible intervals for each genetic group by applying sample proportions and uncertainty to mean catch.

In GSI, I assigned over 90% of the Nuxalk in-river fishery catch across all decades to the current most abundant population in the Atnarko River sockeye stock (Above Lonesome, Figure 5). I found the next highest contributors to total catch samples included 5.8% to Above Stillwater (the current second most abundant population in the Atnarko River sockeye stock), 1.7% to the river-type reporting unit, as well as 1.1% and 0.4% to two nearby lake-type reporting units (Kimsquit L shore and Kitlope L). Other reporting units were assigned at various contributions of 0.1% or less.

Through the three decades of fisheries catch samples, fewer Above Lonesome sockeye salmon were caught and at lower proportions (Table 4, Figure 5, and Table B.7). I found Above Lonesome catch declined by approximately 94% and 97% in the two decades after collapse compared to catches before collapse in 2005 (Figure 5). Before collapse, over 90% of catch samples assigned to Above Lonesome sockeye salmon, while Above Lonesome sockeye salmon accounted for 75.5% catch for the first decade after collapse (2006-2015) and 72.3% in the second decade after collapse (2015-2022). Thus, the number and proportion of Above Lonesome Lake sockeye salmon caught in the fishery declined and other genetic groups made relatively higher contributions to catch after collapse.

The next highest genetic group contributing to the remaining catch across decades varied and included the current second most abundant population in the Atnarko River sockeye stock (Above Stillwater), two nearby lake-type populations (Kimsquit L shore), as well as the river-type reporting unit (Table 5). Prior to the 2005 collapse, the current second most abundant population (Above Stillwater) made up over 75% of the remaining catch, however contributions declined to 34.7% and 21.7% in the following two decades after collapse. In the first decade after collapse (2006-2015), the river-type reporting unit accounted for over 50% of the remaining catch, a 6-fold increase in relative contribution from the period before collapse, however remaining contributions declined to 21.7% in the second decade after collapse (2016-2022). Kimsquit L shore sockeye salmon contributed under 10% to remaining catch in the decades before (1996-2005) and right after collapse (2006-2015), however the population contributed the highest proportion to remaining catch post-collapse (2016-2022) consisting of 43.4% of remaining catch (Figure 5). Catch contributions to Kitlope L (a more distant lake-type population than Kimsquit L Shore) were under 10% for each decade across remaining catch contributions. Other reporting units assigned to 0.2% or lower of remaining catch across the decades (Table B.6). Thus, there were shifts in the stock composition within the in-river fishery with out-of-watershed and river-type fish apparently contributing relatively more after collapse.

Reporting units within the stock (Above Stillwater and river-type) other than the current most abundant population (Above Lonesome) tended to increase across the season in Nuxalk in-river fishery catch assignments. Few sockeye salmon assigned to other reporting units other than the current most abundant population (Above Lonesome) were captured in the second week of July (Week 28) across all decades (Figure 5 and Table B.7). Of the catch not assigned to the Above Lonesome reporting unit, the current second most abundant population (Above Stillwater) contributed the highest to remaining catch in the latter half of the fishing season across all decades, however relative proportion of Above Stillwater catch declined across the three decades during in the last half of July and August (Table 4). Catch was also assigned to the Above Stillwater reporting unit earlier in the season prior to collapse (Figure 5). The river-type reporting unit catch contributions tended to be observed in the latter half of July and August, although overall catch remained relatively low with only two instances of more than three sockeye salmon caught across seasons and decades (Table B.7). Stray populations were identified in catch, including Kimsquit L shore and Kitlope L reporting units. Kimsquit L shore sockeye salmon catch increased later in the fishing season across the decade prior to collapse (1996-2005) and second decade after collapse (2016-2022), however mean catch was never over 6 sockeye salmon at a given time period (Table B.7). Catch was assigned to Kitlope L at low proportions across all decades and seasons with exception to the early season contribution of 11.8% in the first decade after collapse (2006-2015), but all catches were under three sockeye salmon across strata (Table B.7). While some patterns of return timing were seen across reporting units other than the current most abundant population in the Atnarko River sockeye stock (Above Lonesome), I found sockeye catch assigning to alternative reporting units were sporadic and in small catch numbers despite high proportional contribution to catch in some seasonal periods across decades.

Table 5. **Estimated sample composition (with 90% credible intervals) from genetic stock composition (GSI) for sockeye salmon caught by decade and seasonal bin in Bella Coola River Nuxalk in-river fishery. Seasonal bins represent statistical weeks or combinations of statistical weeks. Early represents approximately the first week of July and the month of June whereas Late represents approximately the last week of July and first two weeks of August. Week 28 and Week 29 represent approximately the second and third week of July. Only reporting units with 1% or more sockeye salmon assigned in any temporal strata are shown. Full proportional composition can be viewed in Table B.6.**

Reporting Unit	Early	Week 28	Week 29	Late
1996-2005				
Above Lonesome	91.8% (72-100)	99.6% (95.1-100)	98.8% (94.7-100)	58.3% (46.1-70.2)
Above Stillwater	7.8% (1-25.5)	0.3% (0-4.6)	0% (0-2.8)	31.4% (20.4-43.2)
river-type	0% (0-1.8)	0% (0-0.3)	0% (0-0.3)	5.2% (1-11.1)
Kimsquit L shore	0% (0-1.8)	0% (0-0.3)	1.1% (0-3.4)	3.3% (0.7-7.7)
Kitlope L	0.1% (0-2.3)	0% (0-0.3)	0.1% (0-1.3)	1.5% (0-4.8)
2006-2015				
Above Lonesome	87.1% (70.7-99)	97.8% (86.4-100)	53.2% (35.2-71.2)	74.5% (56.7-92.1)
Above Stillwater	0% (0-4)	1.9% (0-12.6)	0% (0-2.3)	22.5% (5.3-39.9)
river-type	0% (0-1.6)	0% (0-0.8)	45.2% (27.6-63.9)	0% (0-0.8)
Kimsquit L shore	0.1% (0-1.7)	0% (0-0.9)	0% (0-1.5)	2.6% (0-8.2)
Kitlope L	11.8% (2.4-26)	0% (0-0.9)	1.3% (0-9.4)	0% (0-0.8)
2016-2022				
Above Lonesome	-	90.6% (77.1-100)	95.8% (87-100)	46.8% (29.9-64.1)
Above Stillwater	-	0% (0-3.5)	0% (0-3.4)	13% (1-27.7)
river-type	-	6.8% (0.1-18.2)	1.4% (0-7.6)	12.6% (4.7-23.2)
Kimsquit L shore	-	0% (0-1.4)	2.5% (0.3-7)	24.7% (14.2-37.2)
Kitlope L	-	2.1% (0-10.5)	0% (0-1.9)	2.5% (0-8.5)

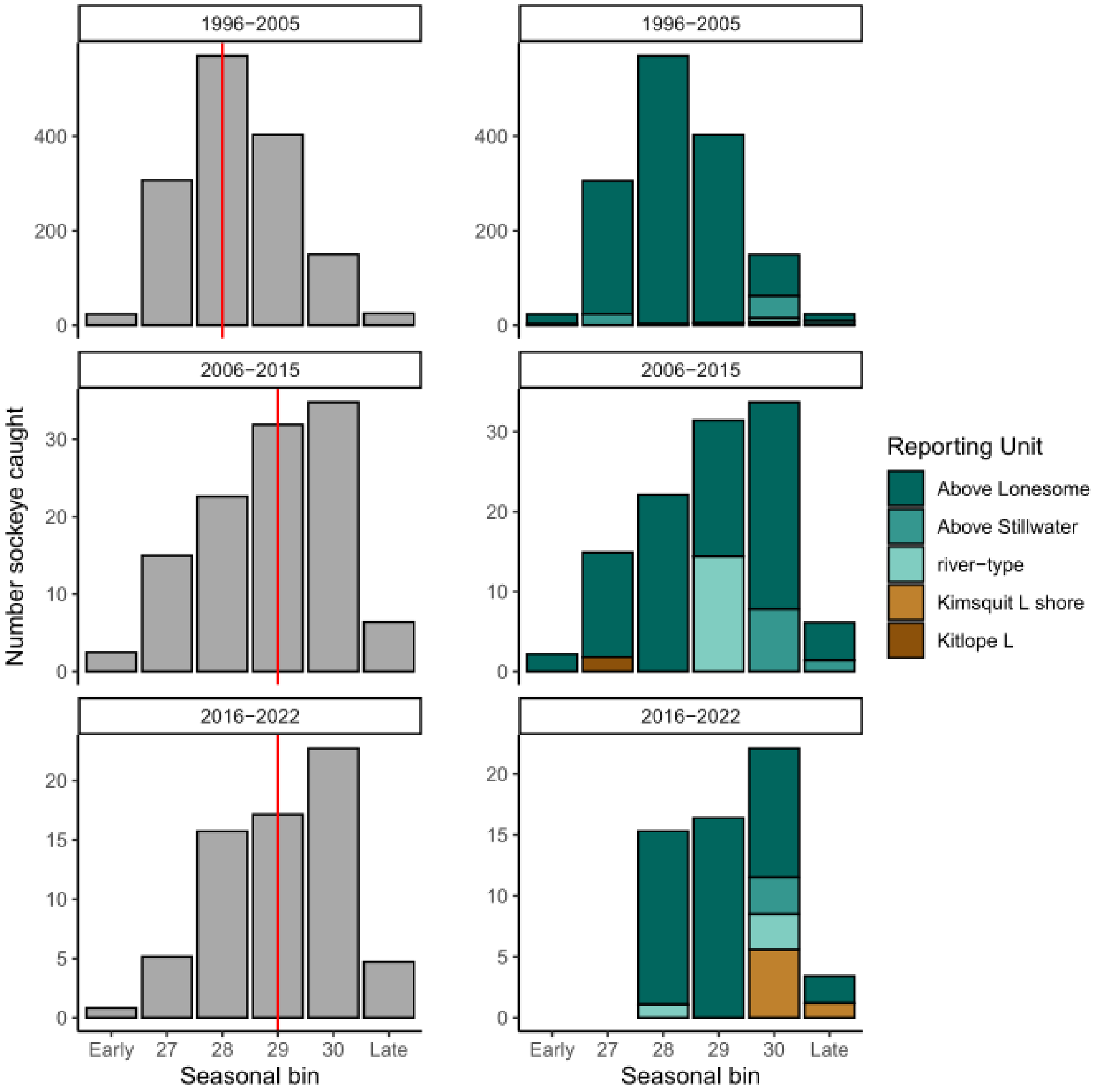


Figure 5. Mean sockeye salmon caught by decade and seasonal bin in Bella Coola River Nuxalk in-river fishery (left) and catch composition (right). Red line indicates the point at which 50% cumulative mean sockeye salmon catch occurred. Catch composition (right) was estimated by applying genetic stock identification (GSI) to catch samples collected from the fishery between 2003 and 2019. Seasonal bins represent statistical weeks or combinations of statistical weeks. Early represents approximately the first month of June whereas Late represents approximately the first three weeks of August. Week 27, 28, 29, and 30 each represent approximately the first to forth the weeks of July. Catch composition for Early or Week 27 in the second decade after collapse is not shown due to small sample sizes (n = 5). Scale of catch varies across decade and only reporting units with one or more sockeye salmon assigned in any temporal strata are shown. Full composition can be viewed in Table B.7.

Discussion

Here I developed and applied a genetic approach to illuminate population structure and composition changes across a period of years spanning the collapse of a culturally important sockeye salmon stock. Contrary to predictions, analysis revealed two strongly distinct genetic groups in the watershed, a deviation from the expected five spawner collections sampled from the Atnarko River sockeye stock. Specifically, the two spawner collections from the larger populations above lakes (Above Stillwater and Above Lonesome) were more genetically similar, and clustered away from the Atnarko R spawner collection and two less abundant spawner collections from above lakes (Above Tenas and Above Rainbow). The genetic similarities among the Atnarko R spawners and the two less abundant spawning collections from above lakes was unexpected, and challenged the long-standing assumption that these spawners occupying these habitats exhibit lake-type life-histories (Cox-Rogers 2011; Connors and Atnarko Sockeye Recovery Planning Committee 2016), and should be genetically distinct from the Atnarko R population (Gustafson and Winans 1999; Wood et al. 2008; Larson et al. 2019). I found that the current two most abundant spawner collections (Above Stillwater and Above Lonesome) were genetically distinct in the preparatory analyses for GSI applications, although this came with increased uncertainty in genetic assignments. This research provided further insight into genetic structure of other key Central Coast populations, including region-wide genetic similarities among spawning populations that were not associated with lakes. Nuxalk in-river fishery catch composition suggested collapse was not experienced equally across the identified genetic populations in the stock. Specifically, the in-river fishery primarily depended on sockeye salmon genetically assigning to the current most abundant spawning population over the last three decades. Following collapse, the non-dominant populations increased in their proportional contribution to the fishery, however they were relatively constant in mean catch across the decades. Collectively, this work highlights the key dimensions of the current genetic structure and diversity in this culturally important stock, helps clarify remaining questions to support Atnarko River sockeye stock recovery, and advances our understanding of sockeye salmon diversity across the Central Coast region.

Atnarko sockeye salmon diversity

The relationships among the Atnarko River sockeye stock collections suggest that current spawners from each major habitat are not each genetically distinct populations. Specifically, there are currently two strongly genetically distinct groups in the Atnarko River sockeye stock, as evidenced by F_{ST} pairwise comparisons, and clusters observed in DAPC. This division separates the current two most abundant populations spawning above lakes (Above Stillwater and Above Lonesome) from another group composed of the Atnarko R spawner population collection and the two less abundant spawning collections found above the lakes (Above Tenas and Above Rainbow). Strong allele frequency differences are evident across these two genetically distinct clusters. In baseline assessments, I did not detect genetic differentiation among the two less abundant spawner collections from above lakes (Above Tenas and Above Rainbow), the Atnarko R collection, and other purported river-type collections. Genetic differentiation was detected among the current two most abundant spawner collections (Above Lonesome and Above Stillwater) in baseline assessments, and more subtly in DAPC across the second discriminant analysis function. Across the second discriminant analysis function, genotype frequency differences also appear less stark among the current two most abundant populations. Misallocation analyses and DAPC suggest all genetically distinct populations within the Atnarko River sockeye stock are connected via ongoing straying or gene flow. Collectively, results suggest two separate structural dimensions to the Atnarko River sockeye stock.

The two strongly differentiated groups across DAPC and F_{ST} appear to be associated with juvenile life history differences observed across the Atnarko River sockeye stock collections. Purported phenotypes of Atnarko R and Above Lonesome collections each associate with one of the two strongly distinguished genetic groups in DAPC. Previously, it was assumed that the Atnarko R spawning population were the river-type ecotype because of the substantial distance fry would need to migrate upstream from the spawning grounds to a lake, and that the other spawning populations would be lake-type ecotypes that rely on lakes for juvenile rearing due to their proximity (Cox-Rogers 2011; Connors and Atnarko Sockeye Recovery Planning Committee 2016). Indeed, previous limnological studies in the current most abundant nursery lake (Lonesome Lake) detected juvenile *O. nerka* (Hume and Shortreed 2008). River-type sockeye salmon populations have low natal fidelity and generally demonstrate little genetic differentiation across broad spatial scales (Gustafson and Winans 1999; Wood et al. 2008; Larson et al. 2019). Therefore, I hypothesize that the two less abundant spawner collections (Above Tenas and Above Rainbow) are stray river-type sockeye salmon that are a part of a broader genetic river-type mixture.

Past genetic structure and life history expression of spawners occupying Above Tenas and Above Rainbow remain unknown. Sockeye salmon populations can show significant divergence across small geographic scales, resulting from fine scale local adaptation (Lin et al. 2008; Wood et al. 2008; Pavey et al. 2010; Gomez-Uchida et al. 2011; Larson et al. 2019). Historically, these areas may have supported genetically distinct spawning populations that produced lake-rearing offspring, and in the absence of samples pre-dating collapse, their genetic relationships to current sockeye salmon collections will remain an unknown. I hypothesize that with the broader collapse of Atnarko sockeye salmon, these initial populations were either extirpated or swamped by colonizing Atnarko R sockeye salmon. Alternatively, unfavorable marine conditions could have led to the increased expression of non-migratory sockeye salmon in these systems (Ricker 1938). A previous limnological survey indicated one of the current non-dominant nursery lakes (Rainbow Lake) may not have the appropriate physical characteristics for rearing sockeye salmon year-round due to the extensive shallow water habitat (Shortreed et al. 2001), however juvenile sockeye salmon are known to utilize various habitats across interconnected lakes under varying conditions (Walsworth et al. 2015, 2020). Finally, one, or both, of the two less abundant spawner collections (Above Rainbow and Above Tenas) may have only existed as river-type sockeye salmon. Historical genetic and ecotype expression remain uncertain for spawning populations found in these areas in the watershed.

Collectively, these analyses suggest that the current Above Stillwater and Above Lonesome spawning populations are distinct genetic populations connected with gene flow. Straying is thought to be more common when salmon populations are smaller (Berdahl et al. 2016, 2018; Westley et al. 2018). Elevated rates of immigration can erode local adaptations and homogenize genetic differences among salmon populations (Hess and Matala 2014; Peterson et al. 2014), particularly if the recipient population is small (Bett et al. 2017). Consequently, a collapse could homogenize genetically distinct populations in a watershed (Yeakel et al. 2018). Approximately 100 years ago, a flood transformed a deep and slow-moving river section surrounded by grassy meadows into Stillwater Lake (Personal Communication: R. Ratcliff). Although repeated and radiant adaptation of river-type sockeye salmon has resulted in the various populations and ecotypes of lake-type sockeye salmon (Wood et al. 2008; McPhee et al. 2009; Larson et al. 2019), cases of rapid divergence of colonizing lake-type sockeye salmon have been documented (Hendry 2001; Pavey et al. 2007; Ramstad et al. 2010). Thus genetic similarities between the current two most abundant populations and the recent origin of Stillwater Lake could also suggest this river section was recently colonized by the Above Lonesome spawning population. Previous genetic relationships and the mechanisms producing the current structure among the current two most abundant spawning populations remains uncertain, however current genetic similarities could be a consequence of the 2005 collapse.

Genotype frequencies in different loci are driving genetic differentiation among the structural dimensions of the Atnarko River sockeye stock. The majority of the top contributing SNPs were not from known conserved regions of adaptation across sockeye salmon populations (Euclide et al. 2023). However, many of the top contributing SNPs from both DA functions are located nearby or within putative coding regions, and may reflect other potential locally important genetic regions under selection specific to the heterogeneities of Atnarko River habitats (Larson et al. 2019; Tigano and Russello 2022; Euclide et al. 2023). For example, two of the top contributing SNPs from the first DA are near coding regions associated with immune function in other fish species (U1207-231 and Larson2017_9460_70), such as the leucine-rich repeat-containing protein 3-like protein (Chang et al. 2005) or 60S ribosomal protein L27 (Oh et al. 2020). Top contributing loci with strong patterns could be under direct selection, divergence through association with nearby genes experiencing strong selection (Via 2012), subject to drift through reduced recombination from genomic structures (Marques et al. 2016; Tigano and Friesen 2016; Samuk et al. 2017), or within genetic architecture under direct selection (Tigano and Russello 2022; Euclide et al. 2023). Proximity to putatively adaptive functions and varying genotype patters at different top contributing SNPs suggest that different genetic regions are important for producing local adaptations across the genetic axes within the Atnarko River sockeye stock (Euclide et al. 2023), and the mechanisms producing the observed genetic patterns could involve more than just selection on specific loci in this panel (Via 2012; Marques et al. 2016; Samuk et al. 2017; Tigano and Russello 2022; Euclide et al. 2023).

It is important to emphasize that genetic inferences about ecotype in the Atnarko River sockeye stock still have important nuances in expression of life-histories. Surprisingly, scale analyses from two recent years of spawners revealed high incidences of early saltwater migration (age-0) among the current second most abundant population, Above Stillwater (Above Stillwater: 151/183, Above Lonesome: 7/306, Atnarko R: 15/123, Personal Communication: I. Strother). In literature, the sea-rearing juvenile life history ecotype is interchangeably associated with the river-type ecotype of sockeye salmon, and together, they are scientifically understood as the ancestral straying form of sockeye salmon (Wood et al. 2008; Beacham and Withler 2017; Larson et al. 2019; Euclide et al. 2023). River-type sockeye salmon populations generally show less differentiation within drainages than lake-type sockeye salmon of the same drainage (Wood et al. 2008). This appears to be an intriguing case where a spawning population near a lake appears to predominantly express the sea-rearing life history ecotype but are strongly divergent from a nearby river-type spawning population, and genetically similar to a nearby lake-type population. Thus, it remains unclear how to classify the ecotype of the Above Stillwater spawning population, and further investigation of the local genetics and temporal expression of life histories across all spawners in the Atnarko River watershed is warranted.

There is growing evidence that indicates there is a complex genetic basis to the fine scale adaptation seen *O. nerka* across habitat moasics (Larson et al. 2019; Tigano and Russello 2022; Euclide et al. 2023). However expression of salmonid life-history traits can be a plastic and conditional response (Hazel et al. 1990; Sloat et al. 2014). Specifically, sockeye salmon fry migration from nursery lakes can be induced by low habitat quality, high rearing densities, climactic variables, and other factors, as mediated through growth (Rich et al. 2009; Walsworth et al. 2015). Expression of early saltwater migration seen in Above Stillwater sockeye salmon could indicate poor freshwater rearing conditions, or competition (Rich et al. 2009; Walsworth et al. 2015). Indeed, this work further emphasizes a current Atnarko Sockeye Recovery Plan priority to improve understanding of the Atnarko River sockeye stock's habitat quality, lake capacities, and habitat use.

Regardless of historical occupancy, the river-type populations appear to be integral in recovering historical spawning habitat within the watershed. To a certain point, higher numbers of individuals may stray if the river-type spawning populations were more abundant, establishing populations above the non-dominant lakes, or re-colonizing unoccupied historical spawning habitats. It is unclear if these small aggregates of river-type spawners within the Atnarko River sockeye stock may diverge and give rise to new genetically distinct populations within the watershed, or whether movement of individuals among spawning areas will maintain genetic similarities. In general, river-type sockeye salmon populations have higher heterozygosity compared to lake-type populations (Gustafson and Winans 1999; Beacham et al. 2004b; Larson et al. 2019), and this genetic variation may allow them to colonize new environments (Beacham et al. 2004b; Wood et al. 2008) under future climate scenarios, or build resilience to changing conditions as a cohesive mixture. Thus, river-type sockeye salmon may foster future recovery of this metapopulation, and more broadly, promote resilience in other sockeye salmon stocks struggling through climate change.

Central Coast sockeye salmon

Collections from within an iconic Central Coast watershed, Wuikinuxv Lake, also exhibited surprisingly little genetic structure across spawning populations. Similar to the Atnarko River sockeye stock, the Wuikinuxv sockeye salmon stock experienced precipitous declines and collapse in the late 1990's (Rutherford and Wood 2000). Prior to collapse, the stock supported abundant indigenous fisheries and large-scale commercial harvest, often rivaling Skeena River in catch numbers (Godfrey 1958). Initial baseline accuracy assessments, all population collections in the Wuikinuxv tributaries reporting unit performed poorly. The only genetic differentiation seen across spawning collections from the watershed was the Wanukv R, which is a later-timed lake outlet spawning population. This contrasts with studies of Alaskan sockeye salmon where even nearby tributary spawning and lake-rearing populations genetically differentiate (Lin et al. 2008; Dann et al. 2012; Ackerman et al. 2013). While historical genetic stock structure of the Wuikinuxv sockeye stock remains unknown, it is possible that the lack of contemporary genetic diversity was due to genetic homogenization during metapopulation collapse.

Kwakwa R collections showed strong genetic differentiation within a single Central Coast watershed, and demonstrates that further genetic diversity within other watershed collections may exist. Kwakwa River is a remote watershed with limited information available regarding its salmon populations. The watershed is composed of five connected lakes with sockeye salmon spawning in various feeder and outlet sections (Pers. Comm. Doug Stewart). Other than the Atnarko River watershed, I split all Central Coast collections into previous microsatellite baseline collection units. Despite accidental inclusion of recent samples collected from different spawning habitats, and the incorporation of a few mixed-stock origin samples, I detected strong differentiation in baseline assessment among the two Kwakwa R collections. I did not investigate within watershed collections outside of Atnarko R and Wuikinuxv tributaries, thus I may have overlooked structure in Kwakwa R spawning populations and other watershed collections. Regardless of the mechanisms responsible for genetic differentiation within the Kwakwa River watershed, this observation emphasizes that diverse genetic populations could remain cryptic within watersheds and potentially masked by how collections are grouped.

In the present work, I showcase broader patterns of genetic differentiation among lake-type and purported river-type populations. Across the Central Coast region, purported river-type spawning populations were genetically similar. Spawners from the Atnarko R, Kimsquit R, and Klinaklini R spawner collections are not associated with lakes and these populations were genetically indistinguishable. Genetic divergence among some river-type sockeye salmon populations has been found (Beacham et al. 2004b; Larson et al. 2019), such as within the Transboundary Rivers in Northern BC (Beacham et al. 2004b), where river-type sockeye salmon make high contributions to total returns (Eiler et al. 1992). It is unclear why some geographic regions see divergence among river-type sockeye salmon while others do not. A variety of factors could influence the potential for river-type sockeye salmon to exhibit local genetic adaptation, including geographic isolation (Wood et al. 2008), relative watershed size, habitat stability, stray rates among populations (Berdahl et al. 2016, 2018; Westley et al. 2018; Yeakel et al. 2018), as well as the size of source and receiving spawning populations (Bett et al. 2017). Although there are uncertainties in how to classify the ecotype of the second current most abundant population, these findings generally corroborate the hypothesis that many river-type spawning populations generally exhibit little population structure across broad ranges due to high straying among populations (Gustafson and Winans 1999; Beacham et al. 2004b; Wood et al. 2008).

Nuxalk in-river catch composition

Over 90% of genetic samples through the three decades assigned to the Above Lonesome reporting unit, the current most abundant population in the Atnarko River sockeye stock. In the decade after collapse, I found Above Lonesome sockeye salmon mean catch declined by nearly 95%. Although assignments to other reporting units (Above Stillwater, Atnarko R, and nearby watersheds) tended to proportionally increase in the Nuxalk in-river fishery after collapse, catch assigning to these reporting units other than the current most abundant population was sporadic and in small numbers of sockeye salmon across all decades. Fisheries dependent on homogenous metapopulations with limited response diversity can be more vulnerable to environmental change (Moore et al. 2014; Anderson et al. 2015). Indeed, collapse would most likely have been worse if the stock was entirely homogenous (e.g., only Above Lonesome sockeye salmon) as response diversity in metapopulations can provide stability to fishery yields (Hilborn et al. 2003; Schindler et al. 2010; Moore et al. 2014). However, the later and smaller catches observed in the Nuxalk in-river fishery (Connors and Atnarko Sockeye Recovery Planning Committee 2016) appear to be driven primarily by abundance of the current most abundant population.

Although overall catch assigning to reporting units other than the current most abundant population was sporadic and in small catch numbers, other genetic groups within the Atnarko River sockeye stock appear to return later in the season compared sockeye salmon assigning to the Above Lonesome reporting unit. This corroborates previous observations of later run-timing observed in sockeye salmon from the Atnarko River sockeye stock with sea-type juvenile life histories (Wood 2000). The number of sockeye salmon caught assigning to the current second most abundant population (Above Stillwater) also appeared to decrease after collapse, which is likely an effect of assignment uncertainty due to the genetic similarities seen between the current two most abundant reporting units within the stock (Above Lonesome and Above Stillwater). Further investigations are warranted to identify differences in return timing among components of the Atnarko River sockeye stock as sporadic incidence and low catch numbers of genetic groups other the current most abundant population may have produced spurious trends.

Impacts from fisheries pre-dating this analysis on Atnarko River sockeye stock components remain unknown (Connors et al. 2019). Until collapse, commercial fisheries targeting Central Coast sockeye salmon occurred for over a century. Terminal fisheries targeting enhanced Bella Coola River chum have also occurred up until 2021, and sockeye salmon have been incidentally caught in these chum fisheries. Historically, management of many Canadian salmon stocks was focused on fishery yields rather than conservation of metapopulation diversity (Walters et al. 2019), and overfishing of some populations can occur when aiming for maximum harvest (Hilborn and Walters 1992; Moore et al. 2021; Connors et al. 2022). Specifically, uneven abundance and variation in productivity among stock components can increase risk to less productive or smaller populations in mixed-stock fisheries (Connors et al. 2020; Moore et al. 2021). Hatcheries can exacerbate these factors (Moore et al. 2021), as production plans aim to increase harvest from increased productivity and abundance of select populations (Naish et al. 2007). For example, enhancement within the Skeena sockeye salmon metapopulation increased total stock size to historical abundance and sustained fisheries, but also likely facilitated continued overfishing and decreased population diversity (Walters et al. 2008; Price et al. 2021). Other dimensions of within stock diversity can also leave some components more vulnerable. Many fisheries exhibit size-selectivity, where older and larger individuals are preferentially caught due to gear or regulatory practices (Reynolds et al. 2005; Hutchings et al. 2013). For example, high rates of decline in some lakeshore spawning sockeye salmon populations have been attributed to higher fishery vulnerability due to their deeper bodies (Hamon et al. 2000; Price et al. 2019). Historical commercial fisheries may have driven stock composition changes due to uneven exploitation rates, different population-level productivity, or fishery vulnerabilities across Atnarko River sockeye stock and beyond.

Several historically documented sockeye salmon spawning populations within the Atnarko River sockeye stock, such as spawners from Rainbow Lake lakeshore or river sections above Elbow Lake, were undetected during the sampling events. Exceedingly small populations may continue to occupy these habitats and these populations could be caught in the Nuxalk in-river fishery. GSI is limited to assign individuals to the referenced baseline collections, and individuals belonging to missing and genetically distinct populations will be assigned to the reporting unit that they are most genetically similar to (Moran and Anderson 2019). Catch composition and estimated assignment uncertainty may have appeared differently with baselines included from these missing populations. Generally, lake-type sockeye salmon are more similar within watersheds rather than across (Beacham et al. 2004b; Wood et al. 2008), and larger baseline samples are most likely to contain the broadest allele frequencies (Kalinowski 2004). I hypothesize that if missing lake-type populations were present in the mixed-stock samples, individuals would assign to the current most abundant population (Above Lonesome). Alternative analyses that do not reference baseline populations could be applied to mixed-stock samples that assign to the current most abundant population. These alternative approaches could suggest presence of potentially unrepresented or extirpated populations in catch by identifying the number of genetically unique clusters of individuals (Miller et al. 2020; Qin et al. 2021). As a consequence of missing spawning population baselines, declines or loss of other populations may still be obscured within this time series.

I applied a SNP panel designed for coastwide GSI application on sockeye salmon to answer a localized question, however definitive genetic relationships among populations are best answered with SNPs specifically identified for that purpose (Candy et al. 2015; McKinney et al. 2020). This analysis may have found different or more definitive results on genetic relationships had I started with methods to identify regionally specific differentiating SNPs. Methods such as restriction site-associated DNA sequencing (RADseq, Davey and Blaxter 2010), have been used to create dense local SNP panels applied to support fisheries management via improving the separation of closely related salmon populations in GSI (McKinney et al. 2020). More recently, whole genome sequencing has been used to identify differentiating regions among fish populations (Han et al. 2020), and this approach has potential to allow for more successful identification of few and/or small regions of adaptation among populations with high gene flow (Han et al. 2020; Andersson et al. 2024). Alternatives for exploring improved differentiation using the current panel include the addition of microhaplotypes within existing SNP amplicons (McKinney et al. 2017; Hargrove et al. 2023). New tools or modifications to the existing panel could be applied locally if conservation concerns warrant efforts to definitively understand genetic differences among populations and reduce uncertainty in GSI.

There are several other caveats to this work not previously discussed. Notably, Nuxalk in-river fishery catch credible intervals were large among seasonal bins across the three decades, and larger sample sizes may have produced more precise credible intervals surrounding catch proportions by reducing sampling bias among mixed-stock samples (Moran and Anderson 2019). Additionally, temporal shifts in allele frequencies within populations can occur through time due to various processes, including homogenization (Dedrick and Baskett 2018), overharvest (Allendorf et al. 2008; Pinsky and Palumbi 2014), enhancement (Hess and Matala 2014), or collapse (Luikart et al. 1998). However, historical baseline samples are virtually nonexistent or have uncertain origins, therefore reduced uncertainty gained from improved genetic assignments may have occurred with temporally representative baseline samples. Finally, I assumed that Nuxalk in-river catch composition is representative of Atnarko River sockeye stock composition, and I did not account for the effects of potential selectivity differences among spawning populations, or ongoing commercial marine fisheries due to unknown differences across populations. Although this work has illuminated changes in composition through a period of collapse in the in-river fishery, the effects of several potentially significant factors remain unknown.

Implications for sockeye salmon management

This work has several broad lessons on stewarding salmon diversity and raises key knowledge gaps on what mechanisms are limiting the Atnarko River sockeye stock's recovery. The slowest metapopulation recoveries and highest conservation risks can occur when a disturbance is experienced unevenly across populations (Wilson et al. 2023). This is particularly true in scenarios with lower dispersal among populations, as those seen in species like sockeye salmon with high natal philopatry (Wilson et al. 2023). Historical erosion of spatial extent or population loss could be contributing to a delayed recovery in the Atnarko River sockeye stock. It is also theoretically possible that salmon populations can become trapped in a state of low abundance and low productivity after a large collapse if density dependent straying occurs (Yeakel et al. 2018). This leaves one to wonder if loss of genetic and spatial structure among the Atnarko River sockeye stock could be delaying or inhibiting recovery.

Successfully managing recovery of a metapopulation requires an understanding of local demographic processes (Wilson et al. 2023), and historical perspectives

(Bonebrake et al. 2010; Rodrigues et al. 2019). Opportunities for such perspectives are limited after populations have been lost. Ongoing efforts should continue to prioritize collecting baseline samples across the Atnarko River sockeye stock, Central Coast watersheds, and salmon populations in general. I suggest that there is a need and opportunity to integrate routine genetic sampling programs into regular escapement assessments for Pacific salmonids. This need for genetic samples is particularly high for populations not represented in genetic baselines, or among populations or regions with low sample sizes (Kalinowski 2004; Beacham et al. 2011; Hargrove et al. 2023). New genetic tools and their application to fisheries management are a key tool in the broader toolbox for managing salmon to address key root challenges, such as sustainable harvest rates. Fostering diversity in a fish stock provides long-term resilience if diversity is properly stewarded (Hilborn et al. 2003; Schindler et al. 2010; Moore et al. 2021; Connors et al. 2022).

This work also suggests that as diverse and adaptable colonizers (Wood et al. 2008; McPhee et al. 2009; Larson et al. 2019), genetic ancestral lineages of river-type sockeye salmon spawning populations may play an important role in the future, giving rise to new populations across various habitats and environmental conditions. I speculate that river-type fish may be in the process of recolonizing habitats in the Atnarko River watershed, and perhaps may play some role in maintaining fisheries in the future. Understanding the adaptation and genetic diversity of river-type sockeye salmon appears to be an important research frontier.

Conclusion

This study identifies the current genetic diversity of a collapsed sockeye salmon stock, the Atnarko River sockeye stock, as well as illuminates genetic structure across other Central Coast sockeye salmon populations. Overall, these findings showcase the complexity of fine-scale adaptation seen in sockeye salmon (Larson et al. 2019; Tigano and Russello 2022; Euclide et al. 2023). Catch composition analysis across three decades of the Nuxalk in-river fishery identified that collapse was not experienced equally across genetic components of the Atnarko River sockeye stock. This work has improved our understanding of the Atnarko River sockeye stock collapse and has clarified some of the potential mechanisms limiting recovery prospects of this culturally significant stock. Finally, this work provides a reminder of the importance in identifying layers of diversity across salmon populations prior to their degradation or loss, which will become increasingly important to inform conservation action in salmon stocks struggling through variable future climate conditions.

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Appendix A. Single nucleotide polymorphisms panel

Supplementary Data File

Description:

Table containing Single Nucleotide Polymorphisms by loci name, chromosome (Chrom), position, amplicon name, forward (FWD) primer, reverse (REV) primer, nucleotides (Nuc), orientation (O), panel, and source. Panel use indicates whether each loci was included in the Atnarko River sockeye stock population structure analysis (A) or the Central Coast regional stock identification panel (R).

Filename:

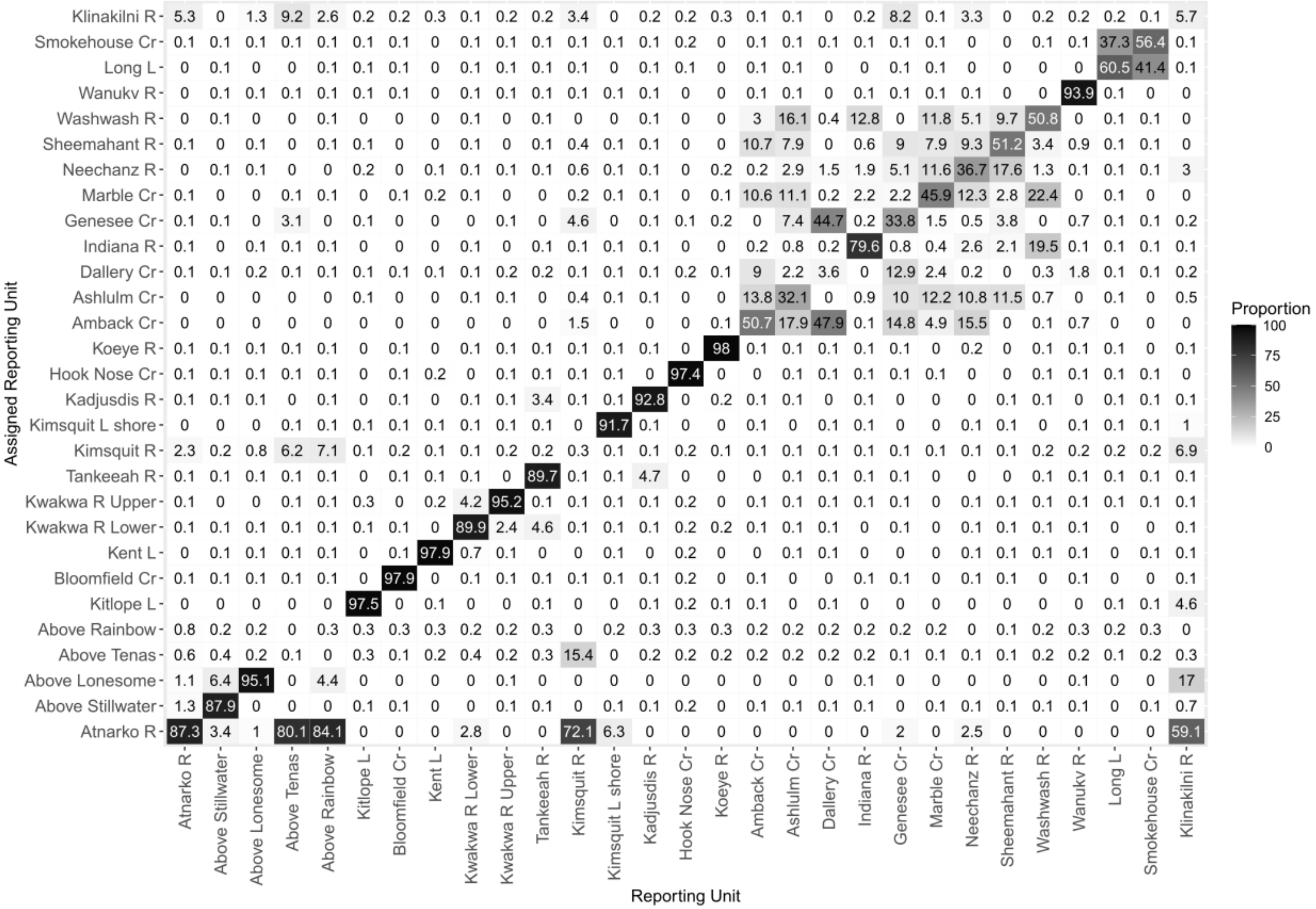
McGivney_Kate_Thesis_2024_Appendix_A.xlsx

Appendix B. Supplementary tables and figures

Table B.1. Baseline accuracy assessment results from test mixtures analyzed for Central Coast regional baseline collections. The estimated proportion within true proportion in 90% of the tests (90% within), proportion of tests within the 90% credible interval of the true proportion (within interval), mean bias across tests and maximum test mixture size (max n) is listed per collection. A collection is often considered acceptable as a reporting unit for genetic stock identification (GSI) application if 90% of the estimates are within 10% of the true proportion and mean bias is within 5% of zero. A priori hypothesized river-type juvenile life histories are noted with * and + indicates a posteriori river-type life history from genetic analyses.

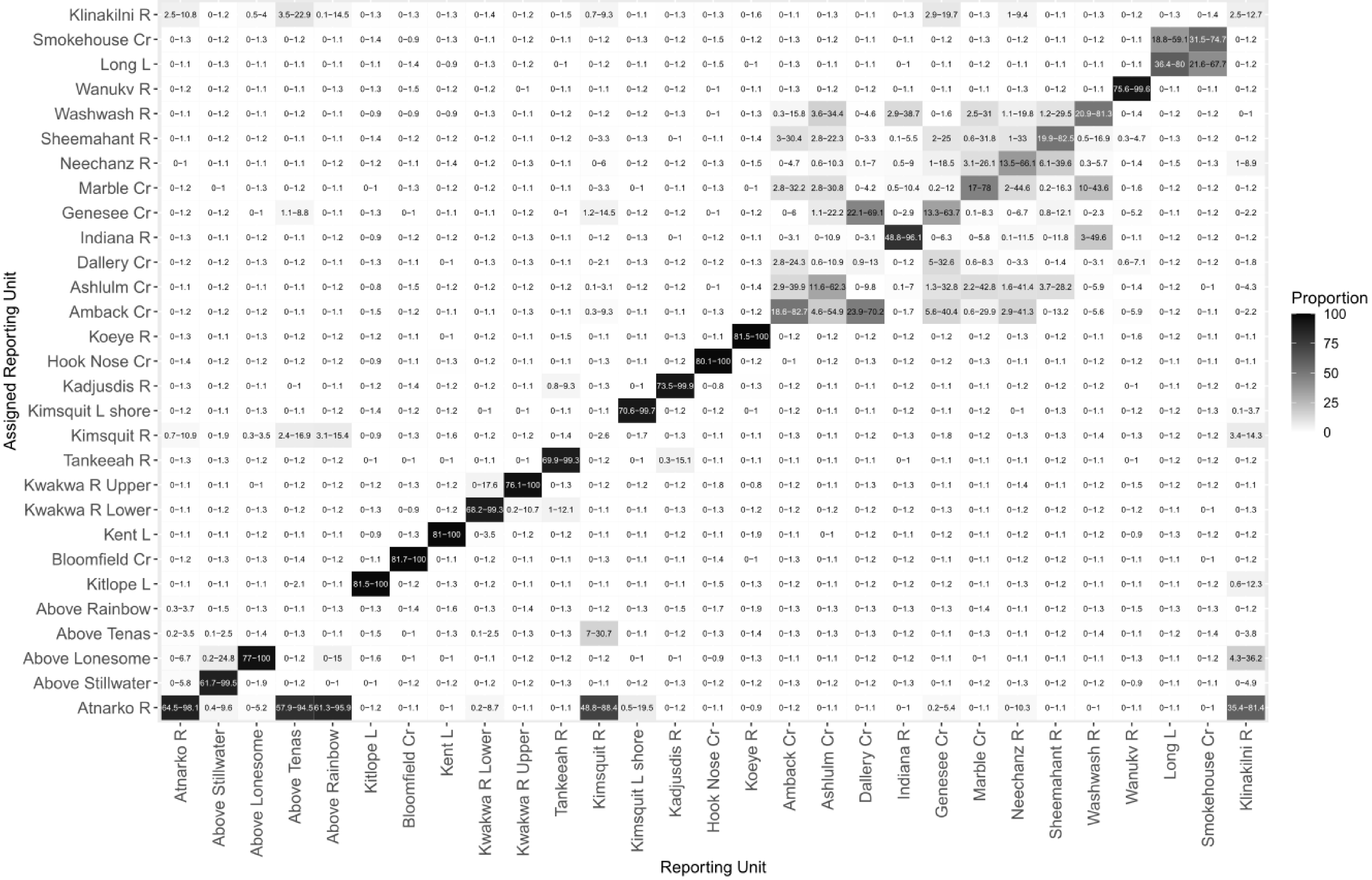
Collection	90% within	Within Interval	Mean Bias	max n
Atnarko R*+	13.6%	61.6%	-0.9%	86
Above Stillwater	11.9%	78.0%	-5.3%	100
Above Lonesome	6.1%	93.0%	-1.8%	100
Above Tenas+	9.9%	0%	-6.2%	12
Above Rainbow+	9.1%	0%	-5.5%	10
Kitlope L	2.6%	100%	-1.4%	53
Bloomfield Cr	3.8%	100%	-1.8%	65
Kent L	1.7%	100%	-1.0%	35
Kwakwa R Lower	5.6%	92.6%	-2.4%	54
Kwakwa R Upper	3.5%	100%	-1.5%	34
Tankeeah R	2.9%	100%	-1.4%	50
Kimsquit R*+	14.5%	6.2%	-8.1%	16
Kimsquit L shore	3.6%	100%	-1.0%	44
Kadjusdis R	3.3%	100%	-1.4%	44
Hook Nose Cr	1.3%	100%	-0.6%	20
Koeye R	2.4%	100%	-1.3%	48
Amback Cr	41.6%	32.4%	-17.0%	68
Ashlulm Cr	41.1%	22.0%	-20.3%	50
Dallery Cr	25.0%	13.3%	-13.6%	30
Inziana R	25.0%	38.3%	-10.2%	60
Genesee Cr	28.8%	24.1%	-12.6%	54
Marble Cr CC	37.2%	14.6%	-16.7%	48
Neechanz R	39.4%	20.7%	-18.9%	58
Sheemahant R	37.8%	28.8%	-15.4%	52
Washwash R	28.9%	26.4%	-14.0%	53
Wanukv R	2.0%	100%	-0.6%	25
Long L	31.7%	19.6%	-14.9%	46
Smokehouse Cr	29.5%	20.0%	-13.6%	35
Klinaklini R*+	25.4%	6.1%	-15.2%	33

Table B.2. **Stock composition estimates (%) averaged across 10 replicates of mixtures made of 10 individuals from each of the 29 collections assessed for baseline use in genetic stock identification (GSI). Each collection was assessed as an independent reporting unit for GSI purposes.**



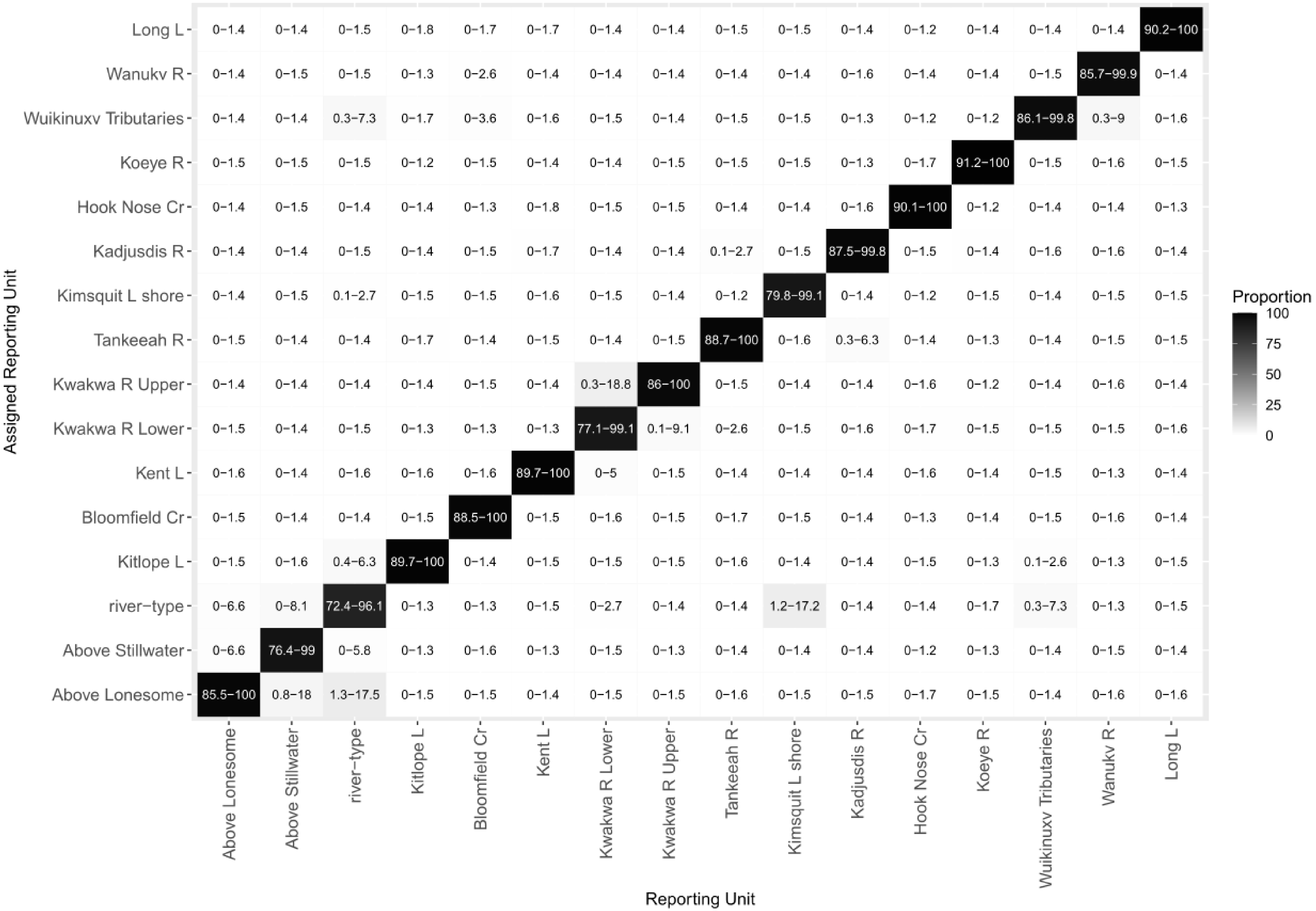
Assigned Reporting Unit	Atnarko R	Above Stillwater	Above Lonesome	Above Tenas	Above Rainbow	Kitlope L	Bloomfield Cr	Kent L	Kwakwa R Lower	Kwakwa R Upper	Tankeeah R	Kimsquit R	Kimsquit L shore	Kadjusdis R	Hook Nose Cr	Koeye R	Amback Cr	Ashlulm Cr	Dallery Cr	Indiana R	Genesee Cr	Marble Cr	Neechanz R	Sheemahant R	Washwash R	Wanukv R	Long L	Smokehouse Cr	Klinakilni R
Klinakilni R	5.3	0	1.3	9.2	2.6	0.2	0.2	0.3	0.1	0.2	0.2	3.4	0	0.2	0.2	0.3	0.1	0.1	0	0.2	8.2	0.1	3.3	0	0.2	0.2	0.2	0.1	5.7
Smokehouse Cr	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0	0.1	0.1	0.1	0.1	0.1	0.1	0	0	0.1	0.1	37.3	56.4	0.1
Long L	0	0.1	0	0	0.1	0.1	0.1	0	0.1	0.1	0.1	0.1	0	0.1	0.1	0	0.1	0.1	0	0	0.1	0.1	0	0	0	0	60.5	41.4	0.1
Wanukv R	0	0.1	0.1	0.1	0.1	0.1	0.1	0	0.1	0.1	0.1	0.1	0.1	0.1	0	0	0.1	0.1	0	0.1	0.1	0.1	0.1	0	0	93.9	0.1	0	0
Washwash R	0	0.1	0	0	0.1	0	0	0	0.1	0	0.1	0	0	0.1	0	0	3	16.1	0.4	12.8	0	11.8	5.1	9.7	50.8	0	0.1	0.1	0
Sheemahant R	0.1	0	0.1	0	0.1	0.1	0	0	0.1	0	0.1	0.4	0.1	0.1	0	0	10.7	7.9	0	0.6	9	7.9	9.3	51.2	3.4	0.9	0.1	0.1	0
Neechanz R	0	0.1	0.1	0	0	0.2	0	0.1	0.1	0.1	0.1	0.6	0.1	0.1	0	0.2	0.2	2.9	1.5	1.9	5.1	11.6	36.7	17.6	1.3	0.1	0.1	0.1	3
Marble Cr	0.1	0	0	0.1	0.1	0	0.1	0.2	0.1	0	0	0.2	0.1	0.1	0	0.1	10.6	11.1	0.2	2.2	2.2	45.9	12.3	2.8	22.4	0	0.1	0	0
Genesee Cr	0.1	0.1	0	3.1	0	0.1	0	0	0	0.1	0	4.6	0	0.1	0.1	0.2	0	7.4	44.7	0.2	33.8	1.5	0.5	3.8	0	0.7	0.1	0.1	0.2
Indiana R	0.1	0	0.1	0.1	0.1	0	0	0	0.1	0	0.1	0.1	0.1	0.1	0	0	0.2	0.8	0.2	79.6	0.8	0.4	2.6	2.1	19.5	0.1	0.1	0.1	0.1
Dallery Cr	0.1	0.1	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.2	0.1	0.1	0.1	0.2	0.1	9	2.2	3.6	0	12.9	2.4	0.2	0	0.3	1.8	0.1	0.1	0.2
Ashlulm Cr	0	0	0	0	0	0.1	0	0	0.1	0.1	0	0.4	0.1	0.1	0	0	13.8	32.1	0	0.9	10	12.2	10.8	11.5	0.7	0	0.1	0	0.5
Amback Cr	0	0	0	0	0	0	0	0	0	0	0	1.5	0	0	0	0.1	50.7	17.9	47.9	0.1	14.8	4.9	15.5	0	0.1	0.7	0	0	0
Koeye R	0.1	0.1	0.1	0.1	0.1	0	0.1	0	0.1	0.1	0.1	0.1	0.1	0.1	0	98	0.1	0.1	0.1	0.1	0.1	0	0.2	0	0.1	0.1	0.1	0	0.1
Hook Nose Cr	0.1	0.1	0.1	0.1	0.1	0	0.1	0.2	0	0.1	0.1	0.1	0.1	0	97.4	0	0	0.1	0.1	0.1	0.1	0.1	0	0	0.1	0.1	0.1	0.1	0
Kadjusdis R	0.1	0.1	0.1	0	0.1	0	0.1	0	0.1	0.1	3.4	0.1	0.1	92.8	0	0.2	0.1	0.1	0	0.1	0	0	0	0.1	0.1	0	0.1	0.1	0.1
Kimsquit L shore	0	0	0	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0	91.7	0.1	0	0	0.1	0	0.1	0.1	0	0	0.1	0.1	0	0.1	0.1	0.1	1
Kimsquit R	2.3	0.2	0.8	6.2	7.1	0.1	0.2	0.1	0.1	0.2	0.2	0.3	0.1	0.1	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.2	0.2	0.2	6.9
Tankeeah R	0.1	0.1	0.1	0.1	0.1	0	0.1	0.1	0.1	0	89.7	0.1	0.1	4.7	0	0	0	0.1	0.1	0.1	0.1	0	0	0	0.1	0.1	0.1	0.1	0.1
Kwakwa R Upper	0.1	0	0	0.1	0.1	0.3	0	0.2	4.2	95.2	0.1	0.1	0.1	0.1	0.2	0	0.1	0.1	0.1	0.1	0.1	0	0.1	0.1	0.1	0.1	0.1	0.1	0.1
Kwakwa R Lower	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0	89.9	2.4	4.6	0.1	0.1	0.1	0.2	0.2	0.1	0.1	0.1	0	0.1	0	0.1	0.1	0.1	0.1	0	0	0.1
Kent L	0	0.1	0.1	0.1	0.1	0	0.1	97.9	0.7	0.1	0	0	0.1	0	0.2	0	0	0.1	0.1	0	0	0	0.1	0.1	0.1	0.1	0	0.1	0.1
Bloomfield Cr	0.1	0.1	0.1	0.1	0.1	0	97.9	0	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0	0.1	0	0	0.1	0.1	0	0.1	0.1	0	0.1	0	0	0.1
Kitlope L	0	0	0	0	0	97.5	0	0.1	0	0	0.1	0	0	0.1	0.2	0.1	0.1	0	0.1	0	0	0	0	0	0	0	0.1	0.1	4.6
Above Rainbow	0.8	0.2	0.2	0	0.3	0.3	0.3	0.3	0.2	0.2	0.3	0	0.2	0.3	0.3	0.3	0.2	0.2	0.2	0.2	0.2	0.2	0	0.1	0.2	0.3	0.2	0.3	0
Above Tenas	0.6	0.4	0.2	0.1	0	0.3	0.1	0.2	0.4	0.2	0.3	15.4	0	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.1	0.1	0.1	0.1	0.2	0.2	0.1	0.2	0.3
Above Lonesome	1.1	6.4	95.1	0	4.4	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0.1	0	0	0	0	0	0.1	0	0	17
Above Stillwater	1.3	87.9	0	0	0	0.1	0.1	0	0	0.1	0.1	0	0.1	0.1	0.2	0	0.1	0.1	0.1	0.1	0	0.1	0.1	0.1	0.1	0.1	0	0.1	0.7
Atnarko R	87.3	3.4	1	80.1	84.1	0	0	0	2.8	0	0	72.1	6.3	0	0	0	0	0	0	0	2	0	2.5	0	0	0	0	0	59.1

Table B.3. **Stock composition 90% credible intervals estimates (%) averaged across 10 replicates of mixtures made of 10 individuals from each of the 29 collections assessed for application in genetic stock identification (GSI). Each collection was assessed as an independent reporting unit for GSI. Mean assigned proportion is indicated across a black and white scale.**



Assigned Reporting Unit	Atnarko R	Above Stillwater	Above Lonesome	Above Tenas	Above Rainbow	Kitlope L	Bloomfield Cr	Kent L	Kwakwa R Lower	Kwakwa R Upper	Tankeeah R	Kimsquit R	Kimsquit L shore	Kadjusdis R	Hook Nose Cr	Koeye R	Amback Cr	Ashlulm Cr	Dallery Cr	Indiana R	Genesee Cr	Marble Cr	Neechanz R	Sheemahant R	Washwash R	Wanukv R	Long L	Smokehouse Cr	Klinakilni R
Klinakilni R	2.5–10.8	0–1.2	0.5–4	3.5–22.9	0.1–14.5	0–1.3	0–1.3	0–1.3	0–1.4	0–1.2	0–1.5	0.7–9.3	0–1.1	0–1.3	0–1.3	0–1.6	0–1.1	0–1.3	0–1.1	0–1.3	2.9–19.7	0–1.3	1–9.4	0–1.1	0–1.3	0–1.2	0–1.3	0–1.4	2.5–12.7
Smokehouse Cr	0–1.3	0–1.2	0–1.3	0–1.2	0–1.1	0–1.4	0–0.9	0–1.3	0–1.1	0–1.2	0–1.1	0–1.2	0–1.3	0–1.2	0–1.5	0–1.2	0–1.3	0–1.2	0–1.1	0–1.1	0–1.2	0–1.3	0–1.2	0–1.1	0–1.2	0–1.1	18.8–59.1	31.5–74.7	0–1.2
Long L	0–1.1	0–1.3	0–1.1	0–1.1	0–1.1	0–1.1	0–1.4	0–0.9	0–1.3	0–1.2	0–1	0–1.2	0–1.1	0–1.2	0–1.5	0–1	0–1.3	0–1.1	0–1.1	0–1	0–1.1	0–1.2	0–1.1	0–1.1	0–1.1	0–1.1	36.4–80	21.6–67.7	0–1.2
Wanukv R	0–1.2	0–1.2	0–1.1	0–1.1	0–1.3	0–1.3	0–1.5	0–1.2	0–1.2	0–1	0–1.1	0–1.1	0–1.2	0–1.2	0–1	0–1.1	0–1.3	0–1.2	0–1.2	0–1.1	0–1.1	0–1.1	0–1.3	0–1.2	0–1.1	75.6–99.6	0–1.1	0–1.1	0–1.2
Washwash R	0–1.1	0–1.2	0–1.1	0–1.2	0–1.1	0–0.9	0–0.9	0–0.9	0–1.3	0–1.1	0–1.2	0–1.2	0–1.2	0–1.3	0–1	0–1.3	0.3–15.8	3.6–34.4	0–4.6	2.9–38.7	0–1.6	2.5–31	1.1–19.8	1.2–29.5	20.9–81.3	0–1.4	0–1.2	0–1.2	0–1
Sheemahant R	0–1.1	0–1.2	0–1.2	0–1.1	0–1.1	0–1.4	0–1.2	0–1.2	0–1.2	0–1.1	0–1.2	0–3.3	0–1.3	0–1	0–1.1	0–1.4	3–30.4	2.8–22.3	0–3.3	0.1–5.5	2–25	0.6–31.8	1–33	19.9–82.5	0.5–16.9	0.3–4.7	0–1.3	0–1.2	0–1.2
Neechanz R	0–1	0–1.1	0–1.1	0–1.1	0–1.2	0–1.2	0–1.1	0–1.4	0–1.2	0–1.3	0–1.1	0–6	0–1.2	0–1.2	0–1.3	0–1.5	0–4.7	0.6–10.3	0.1–7	0.5–9	1–18.5	3.1–26.1	13.5–66.1	6.1–39.6	0.3–5.7	0–1.4	0–1.5	0–1.3	1–8.9
Marble Cr	0–1.2	0–1	0–1.3	0–1.2	0–1.1	0–1	0–1.3	0–1.2	0–1.2	0–1.1	0–1.1	0–3.3	0–1	0–1.1	0–1.3	0–1	2.8–32.2	2.8–30.8	0–4.2	0.5–10.4	0.2–12	17–78	2–44.6	0.2–16.3	10–43.6	0–1.6	0–1.2	0–1.2	0–1.2
Genesee Cr	0–1.2	0–1.2	0–1	1.1–8.8	0–1.1	0–1.3	0–1	0–1.1	0–1.1	0–1.2	0–1	1.2–14.5	0–1.2	0–1.2	0–1	0–1.2	0–6	1.1–22.2	22.1–69.1	0–2.9	13.3–63.7	0.1–8.3	0–6.7	0.8–12.1	0–2.3	0–5.2	0–1.1	0–1.2	0–2.2
Indiana R	0–1.3	0–1.1	0–1.2	0–1.1	0–1.2	0–0.9	0–1.2	0–1.2	0–1.2	0–1.3	0–1.1	0–1.2	0–1.3	0–1	0–1.2	0–1.1	0–3.1	0–10.9	0–3.1	48.8–96.1	0–6.3	0–5.8	0.1–11.5	0–11.8	3–49.6	0–1.1	0–1.2	0–1.2	0–1.2
Dallery Cr	0–1.2	0–1.2	0–1.3	0–1.2	0–1.1	0–1.3	0–1.1	0–1	0–1.3	0–1.3	0–1.1	0–2.1	0–1.3	0–1.2	0–1.2	0–1.3	2.8–24.3	0.6–10.9	0.9–13	0–1.2	5–32.6	0.6–8.3	0–3.3	0–1.4	0–3.1	0.6–7.1	0–1.2	0–1.2	0–1.8
Ashlulm Cr	0–1.1	0–1.2	0–1.1	0–1.1	0–1.2	0–0.8	0–1.5	0–1.2	0–1.2	0–1.2	0–1.2	0.1–3.1	0–1.2	0–1.2	0–1	0–1.4	2.9–39.9	11.6–62.3	0–9.8	0.1–7	1.3–32.8	2.2–42.8	1.6–41.4	3.7–28.2	0–5.9	0–1.4	0–1.2	0–1	0–4.3
Amback Cr	0–1.2	0–1.2	0–1.2	0–1.1	0–1.1	0–1.5	0–1.2	0–1.1	0–1.1	0–1.3	0–1.1	0.3–9.3	0–1.1	0–1.1	0–1.3	0–1.2	18.6–82.7	4.6–54.9	23.9–70.2	0–1.7	5.6–40.4	0.6–29.9	2.9–41.3	0–13.2	0–5.6	0–5.9	0–1.2	0–1.1	0–2.2
Koeye R	0–1.3	0–1.1	0–1.3	0–1.2	0–1.2	0–1.2	0–1.1	0–1	0–1.2	0–1.1	0–1.5	0–1.1	0–1.1	0–1.3	0–1.1	81.5–100	0–1.2	0–1.2	0–1.2	0–1.2	0–1.2	0–1.2	0–1.3	0–1.2	0–1.1	0–1.6	0–1.2	0–1.1	0–1.1
Hook Nose Cr	0–1.4	0–1.2	0–1.2	0–1.2	0–1.2	0–0.9	0–1.1	0–1.3	0–1.2	0–1.1	0–1.1	0–1.3	0–1.1	0–1.2	80.1–100	0–1.2	0–1	0–1.2	0–1.3	0–1.2	0–1.2	0–1.3	0–1.1	0–1.1	0–1.2	0–1.2	0–1.1	0–1.1	0–1.1
Kadjusdis R	0–1.3	0–1.2	0–1.1	0–1	0–1.1	0–1.2	0–1.4	0–1.2	0–1.2	0–1.1	0.8–9.3	0–1.3	0–1	73.5–99.9	0–0.8	0–1.3	0–1.2	0–1.1	0–1.1	0–1.2	0–1.1	0–1.1	0–1.2	0–1.2	0–1.2	0–1	0–1.1	0–1.2	0–1.2
Kimsquit L shore	0–1.2	0–1.1	0–1.3	0–1.1	0–1.2	0–1.4	0–1.2	0–1.2	0–1	0–1	0–1.1	0–1.1	70.6–99.7	0–1.2	0–1.2	0–1	0–1.2	0–1.1	0–1.1	0–1.2	0–1.1	0–1.2	0–1	0–1.3	0–1.1	0–1.2	0–1.2	0–1.3	0.1–3.7
Kimsquit R	0.7–10.9	0–1.9	0.3–3.5	2.4–16.9	3.1–15.4	0–0.9	0–1.3	0–1.6	0–1.2	0–1.2	0–1.4	0–2.6	0–1.7	0–1.3	0–1.1	0–1.1	0–1.3	0–1.1	0–1.2	0–1.3	0–1.8	0–1.2	0–1.3	0–1.3	0–1.4	0–1.3	0–1.2	0–1.2	3.4–14.3
Tankeeah R	0–1.3	0–1.3	0–1.2	0–1.2	0–1.2	0–1	0–1	0–1	0–1.1	0–1	69.9–99.3	0–1.2	0–1	0.3–15.1	0–1.1	0–1.1	0–1.1	0–1.1	0–1.1	0–1	0–1.1	0–1.1	0–1.1	0–1.2	0–1.1	0–1	0–1.2	0–1.2	0–1.2
Kwakwa R Upper	0–1.1	0–1.1	0–1	0–1.2	0–1.2	0–1.2	0–1.3	0–1.2	0–17.6	76.1–100	0–1.3	0–1.2	0–1.2	0–1.2	0–1.8	0–0.8	0–1.2	0–1.1	0–1.3	0–1.3	0–1.1	0–1.1	0–1.4	0–1.1	0–1.2	0–1.5	0–1.2	0–1.2	0–1.1
Kwakwa R Lower	0–1.1	0–1.2	0–1.3	0–1.2	0–1.2	0–1.3	0–0.9	0–1.2	68.2–99.3	0.2–10.7	1–12.1	0–1.1	0–1.1	0–1.3	0–1.3	0–1.2	0–1.2	0–1.2	0–1.2	0–1.2	0–1.3	0–1.1	0–1.2	0–1.2	0–1.2	0–1.2	0–1.1	0–1	0–1.3
Kent L	0–1.1	0–1.1	0–1.2	0–1.1	0–1.1	0–0.9	0–1.3	81–100	0–3.5	0–1.2	0–1.2	0–1.1	0–1.1	0–1.2	0–1.1	0–1.9	0–1.1	0–1	0–1.2	0–1.1	0–1.2	0–1.1	0–1.2	0–1.1	0–1.2	0–0.9	0–1.3	0–1.2	0–1.2
Bloomfield Cr	0–1.2	0–1.3	0–1.3	0–1.4	0–1.2	0–1.1	81.7–100	0–1.1	0–1.2	0–1.1	0–1.1	0–1.3	0–1.1	0–1.1	0–1.4	0–1	0–1.3	0–1.1	0–1.2	0–1.2	0–1.1	0–1.1	0–1.2	0–1.2	0–1.1	0–1.1	0–1.1	0–1	0–1.2
Kitlope L	0–1.1	0–1.1	0–1.1	0–2.1	0–1.1	81.5–100	0–1.2	0–1.3	0–1.2	0–1.1	0–1.1	0–1.1	0–1.1	0–1.1	0–1.5	0–1.3	0–1.2	0–1.1	0–1.2	0–1.2	0–1.2	0–1.1	0–1.3	0–1.2	0–1.1	0–1.1	0–1.1	0–1.2	0.6–12.3
Above Rainbow	0.3–3.7	0–1.5	0–1.3	0–1.1	0–1.3	0–1.3	0–1.4	0–1.6	0–1.3	0–1.4	0–1.3	0–1.2	0–1.3	0–1.5	0–1.7	0–1.9	0–1.3	0–1.3	0–1.3	0–1.3	0–1.3	0–1.4	0–1.1	0–1.2	0–1.3	0–1.5	0–1.3	0–1.3	0–1.2
Above Tenas	0.2–3.5	0.1–2.5	0–1.4	0–1.3	0–1.1	0–1.5	0–1	0–1.3	0.1–2.5	0–1.3	0–1.3	7–30.7	0–1.1	0–1.2	0–1.3	0–1.4	0–1.3	0–1.3	0–1.3	0–1.2	0–1.1	0–1.3	0–1.1	0–1.2	0–1.4	0–1.1	0–1.2	0–1.4	0–3.8
Above Lonesome	0–6.7	0.2–24.8	77–100	0–1.2	0–15	0–1.6	0–1	0–1	0–1.1	0–1.2	0–1.2	0–1.2	0–1	0–1	0–0.9	0–1.3	0–1.1	0–1.1	0–1.2	0–1.2	0–1.1	0–1	0–1.1	0–1.1	0–1.1	0–1.3	0–1.1	0–1.2	4.3–36.2
Above Stillwater	0–5.8	61.7–99.5	0–1.9	0–1.2	0–1	0–1	0–1.2	0–1.2	0–1.2	0–1.2	0–1.3	0–1.1	0–1.2	0–1.3	0–1.2	0–1.2	0–1.3	0–1.2	0–1.2	0–1.3	0–1.1	0–1.2	0–1.3	0–1.2	0–1.2	0–0.9	0–1.1	0–1.1	0–4.9
Atnarko R	64.5–98.1	0.4–9.6	0–5.2	57.9–94.5	61.3–95.9	0–1.2	0–1.1	0–1	0.2–8.7	0–1.1	0–1.1	48.8–88.4	0.5–19.5	0–1.2	0–1.1	0–0.9	0–1.2	0–1.1	0–1.1	0–1	0.2–5.4	0–1.1	0–10.3	0–1.1	0–1	0–1.1	0–1.1	0–1	35.4–81.4

Table B.4. Stock composition 90% credible intervals estimates (%) averaged across 10 replicates of mixtures made of 20 individuals from each of the 16 reporting units used in genetic stock identification (GSI). Collections within each reporting unit can be found in Table 1. Mean assigned proportion is indicated across a black and white scale.



Assigned Reporting Unit	Above Lonesome	Above Stillwater	river−type	Kitlope L	Bloomfield Cr	Kent L	Kwakwa R Lower	Kwakwa R Upper	Tankeeah R	Kimsquit L shore	Kadjusdis R	Hook Nose Cr	Koeye R	Wuikinuxv Tributaries	Wanukv R	Long L
Long L	0−1.4	0−1.4	0−1.5	0−1.8	0−1.7	0−1.7	0−1.4	0−1.4	0−1.5	0−1.5	0−1.4	0−1.2	0−1.4	0−1.4	0−1.4	90.2−100
Wanukv R	0−1.4	0−1.5	0−1.5	0−1.3	0−2.6	0−1.4	0−1.4	0−1.4	0−1.4	0−1.4	0−1.6	0−1.4	0−1.4	0−1.5	85.7−99.9	0−1.4
Wuikinuxv Tributaries	0−1.4	0−1.4	0.3−7.3	0−1.7	0−3.6	0−1.6	0−1.5	0−1.4	0−1.5	0−1.5	0−1.3	0−1.2	0−1.2	86.1−99.8	0.3−9	0−1.6
Koeye R	0−1.5	0−1.5	0−1.5	0−1.2	0−1.5	0−1.4	0−1.4	0−1.5	0−1.5	0−1.5	0−1.3	0−1.7	91.2−100	0−1.5	0−1.6	0−1.5
Hook Nose Cr	0−1.4	0−1.5	0−1.4	0−1.4	0−1.3	0−1.8	0−1.5	0−1.5	0−1.4	0−1.4	0−1.6	90.1−100	0−1.2	0−1.4	0−1.4	0−1.3
Kadjusdis R	0−1.4	0−1.4	0−1.5	0−1.4	0−1.5	0−1.7	0−1.4	0−1.4	0.1−2.7	0−1.5	87.5−99.8	0−1.5	0−1.4	0−1.6	0−1.6	0−1.4
Kimsquit L shore	0−1.4	0−1.5	0.1−2.7	0−1.5	0−1.5	0−1.6	0−1.5	0−1.4	0−1.2	79.8−99.1	0−1.4	0−1.2	0−1.5	0−1.4	0−1.5	0−1.5
Tankeeah R	0−1.5	0−1.4	0−1.4	0−1.7	0−1.4	0−1.5	0−1.4	0−1.5	88.7−100	0−1.6	0.3−6.3	0−1.4	0−1.3	0−1.4	0−1.5	0−1.5
Kwakwa R Upper	0−1.4	0−1.4	0−1.4	0−1.4	0−1.5	0−1.4	0.3−18.8	86−100	0−1.5	0−1.4	0−1.4	0−1.6	0−1.2	0−1.4	0−1.6	0−1.4
Kwakwa R Lower	0−1.5	0−1.4	0−1.5	0−1.3	0−1.3	0−1.3	77.1−99.1	0.1−9.1	0−2.6	0−1.5	0−1.6	0−1.7	0−1.5	0−1.5	0−1.5	0−1.6
Kent L	0−1.6	0−1.4	0−1.6	0−1.6	0−1.6	89.7−100	0−5	0−1.5	0−1.4	0−1.4	0−1.4	0−1.6	0−1.4	0−1.5	0−1.3	0−1.4
Bloomfield Cr	0−1.5	0−1.4	0−1.4	0−1.5	88.5−100	0−1.5	0−1.6	0−1.5	0−1.7	0−1.5	0−1.4	0−1.3	0−1.4	0−1.5	0−1.6	0−1.4
Kitlope L	0−1.5	0−1.6	0.4−6.3	89.7−100	0−1.4	0−1.5	0−1.5	0−1.5	0−1.6	0−1.4	0−1.4	0−1.5	0−1.3	0.1−2.6	0−1.3	0−1.5
river−type	0−6.6	0−8.1	72.4−96.1	0−1.3	0−1.3	0−1.5	0−2.7	0−1.4	0−1.4	1.2−17.2	0−1.4	0−1.4	0−1.7	0.3−7.3	0−1.3	0−1.5
Above Stillwater	0−6.6	76.4−99	0−5.8	0−1.3	0−1.6	0−1.3	0−1.5	0−1.3	0−1.4	0−1.4	0−1.4	0−1.2	0−1.3	0−1.4	0−1.5	0−1.4
Above Lonesome	85.5−100	0.8−18	1.3−17.5	0−1.5	0−1.5	0−1.4	0−1.5	0−1.5	0−1.6	0−1.5	0−1.5	0−1.7	0−1.5	0−1.4	0−1.6	0−1.6

Table B.5. **Nuxalk in-river catch samples as grouped in genetic stock identification (GSI) by decade and seasonal period. Early represents approximately the month of June and the first week of July (statistical fishing weeks 23 through 27), and Late represents approximately the last week of July and the first three weeks of August (statistical fishing weeks 30 through 33). Week 28 and Week 29 are statistical fishing weeks that represent approximately the second and third week of July respectively. Early catch composition for 2016-2022 was not applied due to sample size (n = 5).**

Decade	Early	Week 28	Week 29	Late
1996-2005 (before collapse)	15	86	89	61
2006-2015 (first decade after collapse)	18	33	19	35
2016-2022 (second decade after collapse)	5	21	43	32

Table B.6. Estimated sample composition (with 90% credible intervals) for sockeye salmon caught by decade and seasonal bin in the Bella Coola River Nuxalk in-river fishery. Seasonal bins represent statistical weeks or combinations of statistical weeks. Early represents approximately the first week of July and the month of June whereas Late represents approximately the last week of July and first three weeks of August. Week 28 and Week 29 represent approximately the second and third week of July. Catch composition was not calculated for Early or Week 27 in the second decade after collapse due to small catch sample sizes (n = 5). All reporting units included in genetic stock identification (GSI) baseline are shown and sorted in highest total contribution, then ordered north to south.

Reporting Unit	Early	Week 28	Week 29	Late
1996-2005				
Above Lonesome	91.8% (72-100)	99.6% (95.1-100)	98.8% (94.7-100)	58.3% (46.1-70.2)
Above Stillwater	7.8% (1-25.5)	0.3% (0-4.6)	0% (0-2.8)	31.4% (20.4-43.2)
Kitlope L	0.1% (0-2.3)	0% (0-0.3)	0.1% (0-1.3)	1.5% (0-4.8)
Kimsquit L shore	0% (0-1.8)	0% (0-0.3)	1.1% (0-3.4)	3.3% (0.7-7.7)
river-type	0% (0-1.8)	0% (0-0.3)	0% (0-0.3)	5.2% (1-11.1)
Bloomfield Cr	0.1% (0-1.8)	0% (0-0.4)	0% (0-0.4)	0% (0-0.5)
Kwakwa R Lower	0.1% (0-2)	0% (0-0.4)	0% (0-0.3)	0% (0-0.5)
Wuikinuxv tributaries	0.1% (0-2)	0% (0-0.3)	0% (0-0.3)	0% (0-0.5)
Kent L	0% (0-1.9)	0% (0-0.4)	0% (0-0.4)	0% (0-0.5)
Kwakwa R Upper	0% (0-1.9)	0% (0-0.3)	0% (0-0.3)	0.1% (0-0.6)
Tankeeah R	0% (0-2)	0% (0-0.3)	0% (0-0.3)	0% (0-0.4)
Kadjusdis R	0% (0-1.8)	0% (0-0.3)	0% (0-0.3)	0.1% (0-0.5)
Hook Nose Cr	0% (0-1.8)	0% (0-0.3)	0% (0-0.3)	0% (0-0.5)
Koeye R	0% (0-1.8)	0% (0-0.4)	0% (0-0.3)	0% (0-0.5)
Wanukv R	0% (0-1.8)	0% (0-0.3)	0% (0-0.3)	0% (0-0.5)
Long L	0% (0-1.9)	0% (0-0.3)	0% (0-0.3)	0% (0-0.5)

Reporting Unit	Early	Week 28	Week 29	Late
2006-2015				
Above Lonesome	87.1% (70.7-99)	97.8% (86.4-100)	53.2% (35.2-71.2)	74.5% (56.7-92.1)
Above Stillwater	0% (0-4)	1.9% (0-12.6)	0% (0-2.3)	22.5% (5.3-39.9)
Kitlope L	11.8% (2.4-26)	0% (0-0.9)	1.3% (0-9.4)	0% (0-0.8)
Kimsquit L shore	0.1% (0-1.7)	0% (0-0.9)	0% (0-1.5)	2.6% (0-8.2)
river-type	0% (0-1.6)	0% (0-0.8)	45.2% (27.6-63.9)	0% (0-0.8)
Bloomfield Cr	0% (0-1.5)	0% (0-0.9)	0% (0-1.5)	0% (0-0.9)
Kwakwa R Lower	0% (0-1.6)	0.1% (0-1)	0.1% (0-1.6)	0.1% (0-0.9)
Wuikinuxv tributaries	0.3% (0-1.9)	0% (0-0.9)	0% (0-1.4)	0% (0-0.8)
Kent L	0.2% (0-1.7)	0% (0-0.9)	0% (0-1.6)	0% (0-0.8)
Kwakwa R Upper	0% (0-1.6)	0% (0-0.9)	0% (0-1.5)	0% (0-0.8)
Tankeeah R	0% (0-1.6)	0% (0-0.9)	0% (0-1.4)	0% (0-0.9)
Kadjusdis R	0% (0-1.5)	0% (0-0.9)	0% (0-1.5)	0% (0-0.8)
Hook Nose Cr	0.1% (0-1.8)	0.1% (0-0.9)	0% (0-1.4)	0% (0-0.8)
Koeye R	0% (0-1.7)	0% (0-0.9)	0.1% (0-1.5)	0% (0-0.8)
Wanukv R	0.1% (0-1.8)	0% (0-0.9)	0.1% (0-1.6)	0% (0-0.8)
Long L	0.1% (0-1.7)	0% (0-0.9)	0% (0-1.5)	0.1% (0-0.9)

Reporting Unit	Early	Week 28	Week 29	Late
2016-2022				
Above Lonesome	-	90.6% (77.1-100)	95.8% (87-100)	46.8% (29.9-64.1)
Above Stillwater	-	0% (0-3.5)	0% (0-3.4)	13% (1-27.7)
Kitlope L	-	2.1% (0-10.5)	0% (0-1.9)	2.5% (0-8.5)
Kimsquit L shore	-	0% (0-1.4)	2.5% (0.3-7)	24.7% (14.2-37.2)
river-type	-	6.8% (0.1-18.2)	1.4% (0-7.6)	12.6% (4.7-23.2)
Bloomfield Cr	-	0.3% (0-1.6)	0% (0-0.6)	0.1% (0-1)
Kwakwa R Lower	-	0% (0-1.4)	0% (0-0.7)	0% (0-0.9)
Wuikinuxv tributaries	-	0% (0-1.3)	0.2% (0-1)	0% (0-0.9)
Kent L	-	0% (0-1.4)	0.1% (0-0.7)	0.1% (0-1.1)
Kwakwa R Upper	-	0% (0-1.4)	0% (0-0.7)	0% (0-0.9)
Tankeeah R	-	0.1% (0-1.5)	0% (0-0.6)	0% (0-0.9)
Kadjusdis R	-	0% (0-1.3)	0% (0-0.6)	0.1% (0-1)
Hook Nose Cr	-	0% (0-1.4)	0% (0-0.7)	0% (0-0.9)
Koeye R	-	0.1% (0-1.5)	0% (0-0.6)	0% (0-0.8)
Wanukv R	-	0% (0-1.3)	0% (0-0.7)	0% (0-1)
Long L	-	0% (0-1.2)	0% (0-0.7)	0% (0-1)

Table B.7. Estimated catch composition (with 90% credible intervals) for sockeye salmon caught by decade and seasonal bin in the Bella Coola River Nuxalk in-river fishery. Seasonal bins represent statistical weeks or combinations of statistical weeks. Early represents approximately the first month of June whereas Late represents approximately the first three weeks of August. Week 27, 28, 29, and 30 each represent approximately the first through forth week of July. Catch composition was not calculated for Early or Week 27 due to small sample sizes (n = 5). All reporting units included in genetic stock identification (GSI) baseline are shown and sorted in highest contribution, then north to south.

Reporting Unit	Early	Week 27	Week 28	Week 29	Week 30	Late
1996-2005						
Above Lonesome	21.8 (17.1-23.7)	281.5 (220.8-306.6)	567.9 (542-570.1)	398.2 (381.8-403.1)	87.2 (68.9-104.9)	14.6 (11.5-17.6)
Above Stillwater	1.8 (0.2-6.1)	23.9 (3-78.3)	2 (0-26.2)	0 (0-11.1)	46.9 (30.5-64.5)	7.9 (5.1-10.8)
Kitlope L	0 (0-0.5)	0.4 (0-7.1)	0 (0-1.9)	0.4 (0-5.3)	2.2 (0-7.1)	0.4 (0-1.2)
Kimsquit L shore	0 (0-0.4)	0 (0-5.6)	0 (0-1.8)	4.4 (0-13.5)	5 (1-11.5)	0.8 (0.2-1.9)
River type	0 (0-0.4)	0 (0-5.5)	0 (0-1.9)	0 (0-1.2)	7.8 (1.5-16.7)	1.3 (0.3-2.8)
Bloomfield Cr	0 (0-0.4)	0.2 (0-5.5)	0 (0-2)	0 (0-1.4)	0 (0-0.7)	0 (0-0.1)
Kwakwa R Lower	0 (0-0.5)	0.3 (0-6.3)	0 (0-2)	0 (0-1.3)	0 (0-0.7)	0 (0-0.1)
Wuikinuxv tributaries	0 (0-0.5)	0.2 (0-6.2)	0 (0-2)	0 (0-1.3)	0 (0-0.7)	0 (0-0.1)
Kent L	0 (0-0.5)	0 (0-5.9)	0.1 (0-2.2)	0.1 (0-1.5)	0 (0-0.8)	0 (0-0.1)
Kwakwa R Upper	0 (0-0.4)	0 (0-5.7)	0.1 (0-1.9)	0 (0-1.3)	0.1 (0-0.8)	0 (0-0.1)
Tankeeah R	0 (0-0.5)	0.1 (0-6.1)	0 (0-1.9)	0 (0-1.4)	0 (0-0.7)	0 (0-0.1)
Kadjusdis R	0 (0-0.4)	0 (0-5.7)	0 (0-1.9)	0 (0-1.3)	0.1 (0-0.8)	0 (0-0.1)
Hook Nose Cr	0 (0-0.4)	0 (0-5.6)	0 (0-2)	0 (0-1.3)	0 (0-0.7)	0 (0-0.1)
Koeye R	0 (0-0.4)	0 (0-5.5)	0 (0-2.1)	0 (0-1.3)	0 (0-0.8)	0 (0-0.1)
Wanukv R	0 (0-0.4)	0 (0-5.6)	0 (0-1.9)	0 (0-1.3)	0.1 (0-0.8)	0 (0-0.1)
Long L	0 (0-0.4)	0 (0-5.8)	0 (0-1.9)	0 (0-1.2)	0 (0-0.7)	0 (0-0.1)

Reporting Unit	Early	Week 27	Week 28	Week 29	Week 30	Late
2006-2015						
Above Lonesome	2.2 (1.7-2.5)	13.1 (10.6-14.9)	22.1 (19.5-22.6)	17 (11.2-22.7)	25.9 (19.7-32.1)	4.7 (3.6-5.9)
Above Stillwater	0 (0-0.1)	0 (0-0.6)	0.4 (0-2.8)	0 (0-0.7)	7.8 (1.8-13.9)	1.4 (0.3-2.5)
Kitlope L	0.3 (0.1-0.6)	1.8 (0.4-3.9)	0 (0-0.2)	0.4 (0-3)	0 (0-0.3)	0 (0-0.1)
Kimsquit L shore	0 (0-0)	0 (0-0.3)	0 (0-0.2)	0 (0-0.5)	0.9 (0-2.9)	0.2 (0-0.5)
River type	0 (0-0)	0 (0-0.2)	0 (0-0.2)	14.4 (8.8-20.4)	0 (0-0.3)	0 (0-0)
Bloomfield Cr	0 (0-0)	0 (0-0.2)	0 (0-0.2)	0 (0-0.5)	0 (0-0.3)	0 (0-0.1)
Kwakwa R Lower	0 (0-0)	0 (0-0.2)	0 (0-0.2)	0 (0-0.5)	0 (0-0.3)	0 (0-0.1)
Wuikinuxv tributaries	0 (0-0)	0 (0-0.3)	0 (0-0.2)	0 (0-0.4)	0 (0-0.3)	0 (0-0.1)
Kent L	0 (0-0)	0 (0-0.3)	0 (0-0.2)	0 (0-0.5)	0 (0-0.3)	0 (0-0.1)
Kwakwa R Upper	0 (0-0)	0 (0-0.2)	0 (0-0.2)	0 (0-0.5)	0 (0-0.3)	0 (0-0.1)
Tankeeah R	0 (0-0)	0 (0-0.2)	0 (0-0.2)	0 (0-0.5)	0 (0-0.3)	0 (0-0.1)
Kadjusdis R	0 (0-0)	0 (0-0.2)	0 (0-0.2)	0 (0-0.5)	0 (0-0.3)	0 (0-0.1)
Hook Nose Cr	0 (0-0)	0 (0-0.3)	0 (0-0.2)	0 (0-0.4)	0 (0-0.3)	0 (0-0.1)
Koeye R	0 (0-0)	0 (0-0.2)	0 (0-0.2)	0 (0-0.5)	0 (0-0.3)	0 (0-0.1)
Wanukv R	0 (0-0)	0 (0-0.3)	0 (0-0.2)	0 (0-0.5)	0 (0-0.3)	0 (0-0)
Long L	0 (0-0)	0 (0-0.3)	0 (0-0.2)	0 (0-0.5)	0 (0-0.3)	0 (0-0.1)

Reporting Unit	Early	Week 27	Week 28	Week 29	Week 30	Late
2016-2022						
Above Lonesome	-	-	14.2 (12.1-15.7)	16.4 (14.9-17.1)	10.6 (6.8-14.5)	2.2 (1.4-3)
Above Stillwater	-	-	0 (0-0.6)	0 (0-0.6)	3 (0.2-6.3)	0.6 (0-1.3)
Kitlope L	-	-	0.3 (0-1.6)	0 (0-0.3)	0.6 (0-1.9)	0.1 (0-0.4)
Kimsquit L shore	-	-	0 (0-0.2)	0.4 (0-1.2)	5.6 (3.2-8.5)	1.2 (0.7-1.8)
River type	-	-	1.1 (0-2.9)	0.2 (0-1.3)	2.9 (1.1-5.3)	0.6 (0.2-1.1)
Bloomfield Cr	-	-	0 (0-0.3)	0 (0-0.1)	0 (0-0.2)	0 (0-0)
Kwakwa R Lower	-	-	0 (0-0.2)	0 (0-0.1)	0 (0-0.2)	0 (0-0)
Wuikinuxv tributaries	-	-	0 (0-0.2)	0 (0-0.2)	0 (0-0.2)	0 (0-0)
Kent L	-	-	0 (0-0.2)	0 (0-0.1)	0 (0-0.2)	0 (0-0.1)
Kwakwa R Upper	-	-	0 (0-0.2)	0 (0-0.1)	0 (0-0.2)	0 (0-0)
Tankeeah R	-	-	0 (0-0.2)	0 (0-0.1)	0 (0-0.2)	0 (0-0)
Kadjusdis R	-	-	0 (0-0.2)	0 (0-0.1)	0 (0-0.2)	0 (0-0)
Hook Nose Cr	-	-	0 (0-0.2)	0 (0-0.1)	0 (0-0.2)	0 (0-0)
Koeye R	-	-	0 (0-0.2)	0 (0-0.1)	0 (0-0.2)	0 (0-0)
Wanukv R	-	-	0 (0-0.2)	0 (0-0.1)	0 (0-0.2)	0 (0-0)
Long L	-	-	0 (0-0.2)	0 (0-0.1)	0 (0-0.2)	0 (0-0)

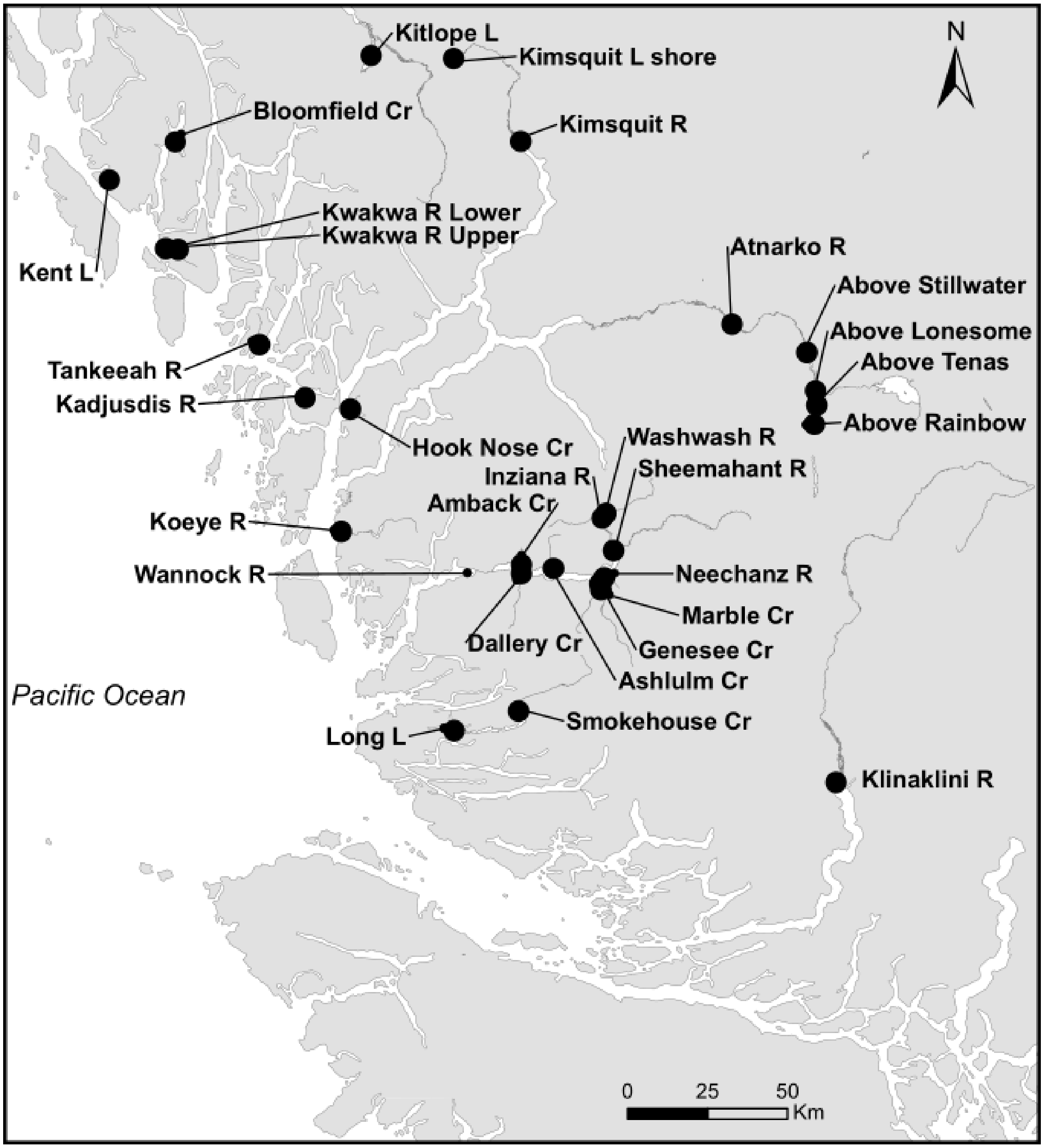


Figure B.1. Locations of Central coast collections used for Genetic Stock Identification analysis.

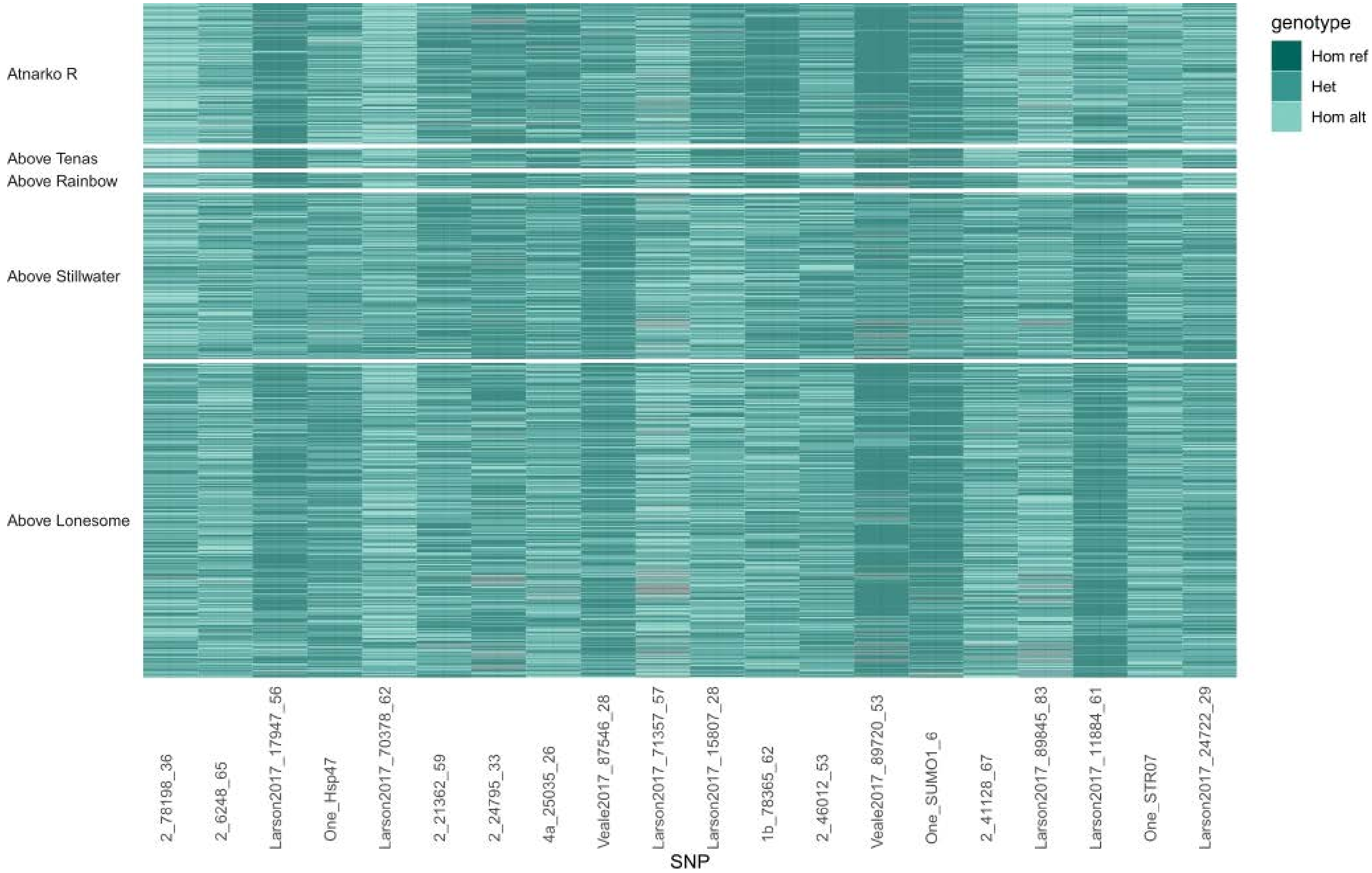


Figure B.2. **Characterized allele frequencies for the top 20 contributing SNPs to the second DA of DAPC for Atnarko River sockeye stock samples by collection site in decreasing contribution order. The second DA axis explains the second largest variation seen among groups relative to within group differences, and shows some separation between the current two most abundant populations found above nursery lakes (Above Stillwater and Above Lonesome).**

Appendix C. Baseline assessments and Nuxalk in-river catch composition with Above Stillwater and Above Lonesome as a single reporting unit

I aggregated baseline collections into new reporting units based on the initial baseline assessment results, however I also created a new reporting unit consisting of the current two most abundant lake-type populations within the Atnarko River sockeye stock (Above Stillwater and Above Lonesome). Results using the Stillwater-Lonesome reporting unit are described below.

I created test mixtures for all 15 reporting units to assess their performance. In 90% of tests for groups other than Above Stillwater, the proportion estimates ranged from 0.4% to 6.7% of the true proportion in test mixtures and mean bias was between -2.7% and 0.3% (Table B.1). When Above Lonesome and Above Stillwater collections are combined into a single reporting unit (Stillwater-Lonesome), proportional estimates were within 3.0% of the true value in 90% of tests, with a mean bias of -0.4%. Performance was reduced when the two collections were considered separate reporting units, (Table 3 and Table B.2). Specifically, Above Lonesome saw 90% of test estimates within 5.6% of the true proportion and Above Stillwater had 90% of test estimates within 12.0% (Table B.2).

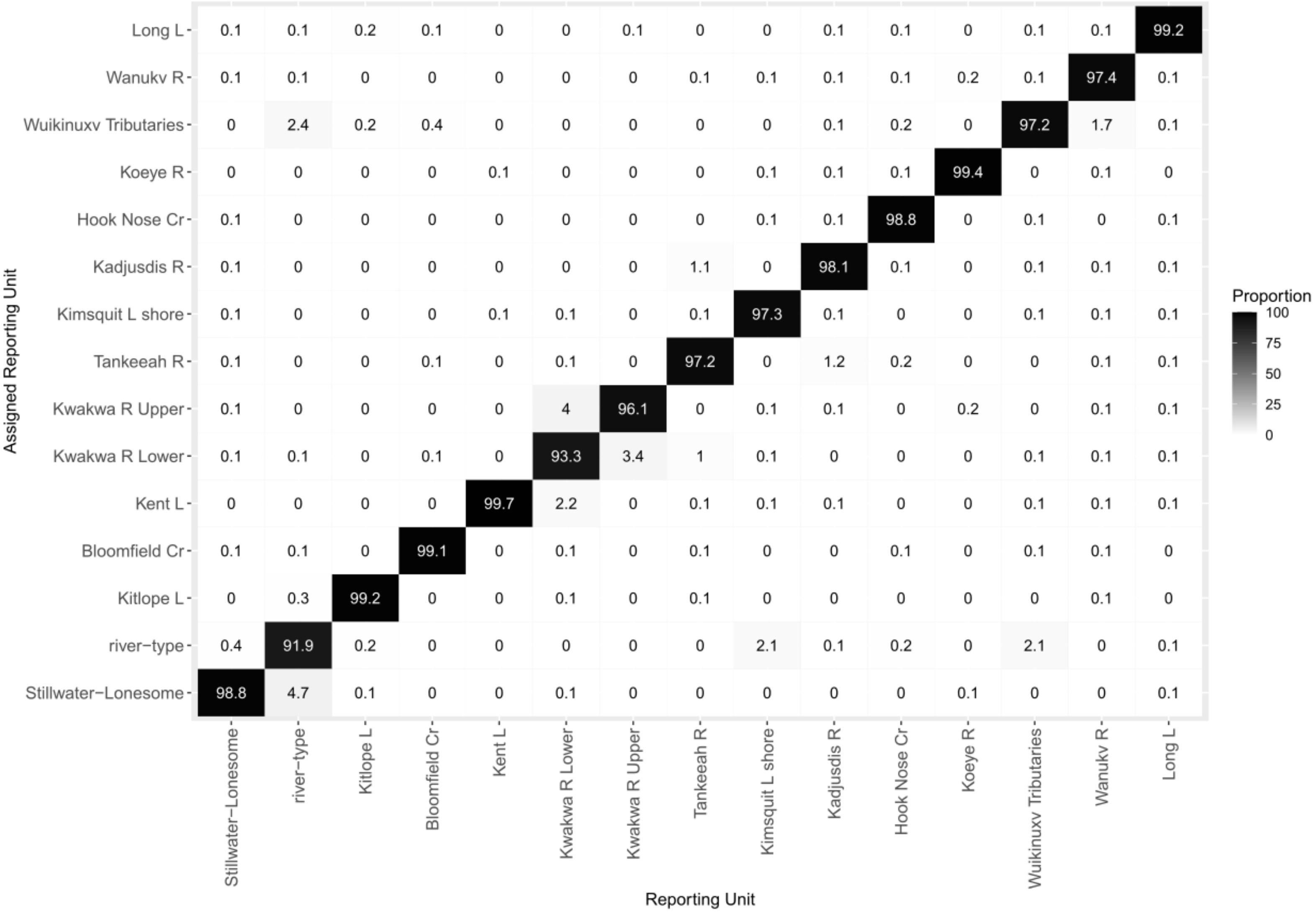
When I combined the two dominant lake-type populations in the Atnarko River sockeye stock, correct misallocation assignment proportions ranged from 91.9% to 99.6% (Table C.2). Kent L performed the best with a mean correct allocation of 99.6% (90% Credible Interval (CrI)= 90.7%-100%) while the river-type reporting unit performed the worst with a mean correct assignment of 91.9% (CrI = 77.7%-99.2%, Table C.2 and Table C.3). The top misallocated groups for the river-type were Above Lonesome (4.7%, CrI = 1.5%-15.0%), Wuikinuxv tributaries (2.5%, CrI = 0.5%-7.3%, Table C.2 and Table C.3). Kimsquit Lake shore and Wuikinuxv tributaries both misallocate 2.1% to the river-type reporting unit, and all other misallocations equate to less than 1% (Table C.2). When I grouped the two dominant lake-type populations into a single reporting unit, the Stillwater-Lonesome reporting unit correctly reassigned 98.8% (CrI = 89.4%-100%) of individuals (Table C.2 and Table C.3). Both assignment rates were slightly lower when I had kept the two collections separately, as Above Lonesome correctly reassigned 98%

(CrI = 85.5-100) of individuals and Above Stillwater correctly reassigned 94% (CrI = 76.4%-99%).

Table C.1. Baseline accuracy assessment results from test mixtures analyzed for Central Coast regional baseline reporting units to be used for genetic stock identification (GSI) with a single reporting unit formed for the current two most abundant poplations in the Atnarko River sockeye stock (Stillwater-Lonesome). The estimated proportion within true proportion in 90% of the tests (90% within), proportion of tests within the 90% credible interval of the true proportion (Within Interval), mean bias across tests and maximum test mixture size (max n) is listed per reporting unit. A reporting unit is generally considered acceptable for GSI if 90% of the estimates are within 10% of the true proportion and mean bias is within 5% of zero, exceptions can be made if the management question can accommodate elevated levels of uncertainty. Test mixtures were limited to one-half the size of baseline samples up to a maximum of 100 individuals.

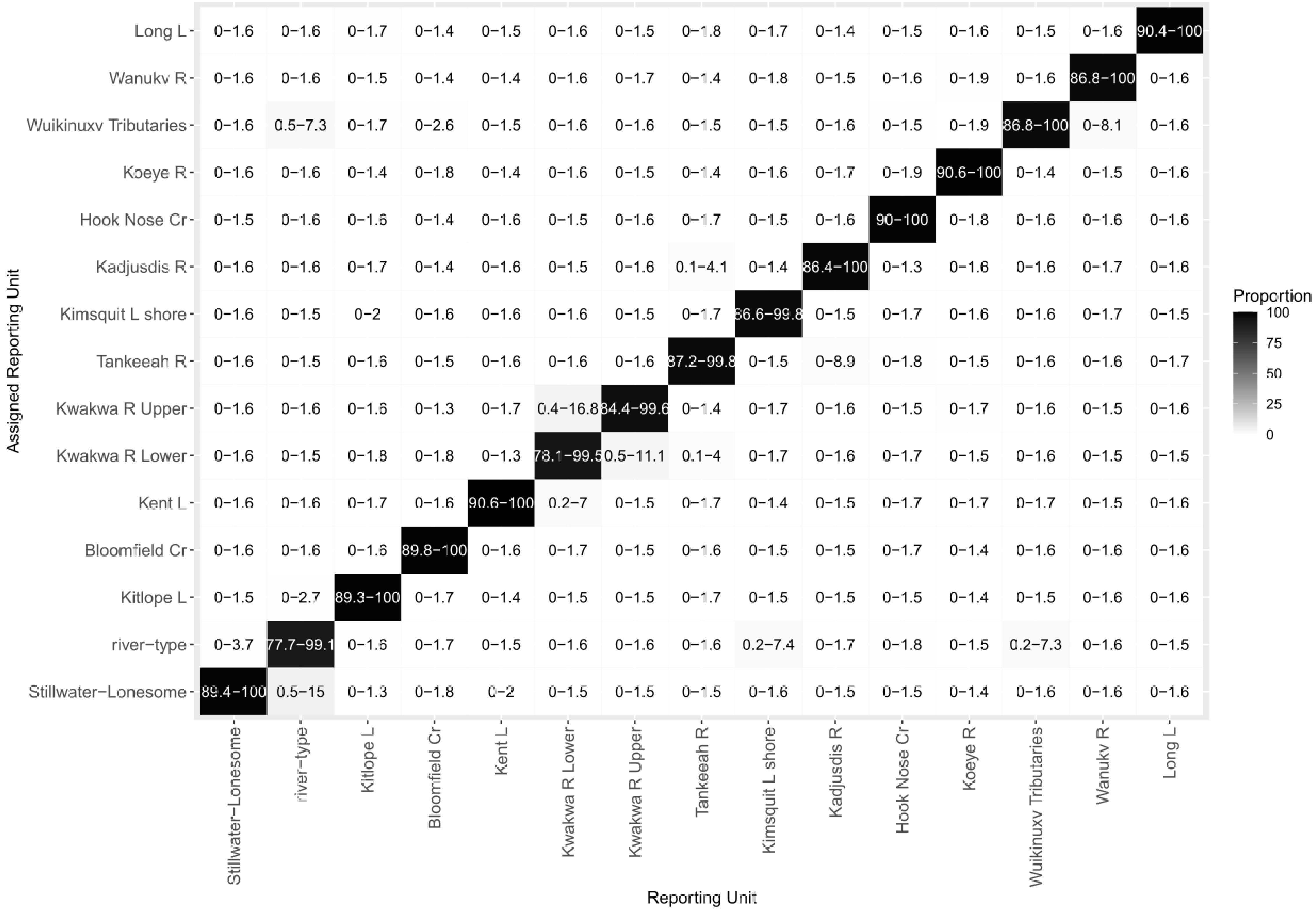
Collection	90% within	Within Interval	Mean Bias	max n
Stillwater-Lonesome	3.0%	99.0%	-0.4%	100
river-type	6.7%	94.0%	-2.7%	100
Kitlope L	0.8%	100%	0%	53
Bloomfield Cr	1.4%	100%	0%	65
Kent L	0.8%	100%	0.1%	35
Kwakwa R Lower	4.6%	96.3%	-1.2%	54
Kwakwa R Upper	2.7%	100%	0.3%	34
Tankeeah R	2.7%	100%	-0.1%	50
Kimsquit L shore	2.6%	100%	0.1%	44
Kadjusdis R	2.5%	100%	-0.2%	44
Hook Nose Cr	0.4%	100%	-0.1%	20
Koeye R	0.6%	100%	0.1%	48
Wuikinuxv tributaries	2.0%	99.0%	-0.5%	100
Wanukv R	1.6%	100%	0.2%	25
Long L	0.6%	100%	0%	82

Table C.2. **Stock composition estimates (%) averaged across 10 replicates of mixtures made of 20 individuals from the 15 reporting units (including a single reporting unit for the current two most abundant populations in Atnarko River sockeye stock aggregated as a single reporting unit, Stillwater-Lonesome).**



Assigned Reporting Unit	Stillwater−Lonesome	river−type	Kitlope L	Bloomfield Cr	Kent L	Kwakwa R Lower	Kwakwa R Upper	Tankeeah R	Kimsquit L shore	Kadjusdis R	Hook Nose Cr	Koeye R	Wuikinuxv Tributaries	Wanukv R	Long L
Long L	0.1	0.1	0.2	0.1	0	0	0.1	0	0	0.1	0.1	0	0.1	0.1	99.2
Wanukv R	0.1	0.1	0	0	0	0	0	0.1	0.1	0.1	0.1	0.2	0.1	97.4	0.1
Wuikinuxv Tributaries	0	2.4	0.2	0.4	0	0	0	0	0	0.1	0.2	0	97.2	1.7	0.1
Koeye R	0	0	0	0	0.1	0	0	0	0.1	0.1	0.1	99.4	0	0.1	0
Hook Nose Cr	0.1	0	0	0	0	0	0	0	0.1	0.1	98.8	0	0.1	0	0.1
Kadjusdis R	0.1	0	0	0	0	0	0	1.1	0	98.1	0.1	0	0.1	0.1	0.1
Kimsquit L shore	0.1	0	0	0	0.1	0.1	0	0.1	97.3	0.1	0	0	0.1	0.1	0.1
Tankeeah R	0.1	0	0	0.1	0	0.1	0	97.2	0	1.2	0.2	0	0	0.1	0.1
Kwakwa R Upper	0.1	0	0	0	0	4	96.1	0	0.1	0.1	0	0.2	0	0.1	0.1
Kwakwa R Lower	0.1	0.1	0	0.1	0	93.3	3.4	1	0.1	0	0	0	0.1	0.1	0.1
Kent L	0	0	0	0	99.7	2.2	0	0.1	0.1	0.1	0	0	0.1	0.1	0.1
Bloomfield Cr	0.1	0.1	0	99.1	0	0.1	0	0.1	0	0	0.1	0	0.1	0.1	0
Kitlope L	0	0.3	99.2	0	0	0.1	0	0.1	0	0	0	0	0	0.1	0
river−type	0.4	91.9	0.2	0	0	0	0	0	2.1	0.1	0.2	0	2.1	0	0.1
Stillwater−Lonesome	98.8	4.7	0.1	0	0	0.1	0	0	0	0	0	0.1	0	0	0.1

Table C.3. **Stock composition 90% credible intervals averaged across 10 replicates of mixtures made of 20 individuals from the 15 reporting units (including a single reporting unit for the current two most abundant populations in Atnarko River sockeye stock aggregated as a single reporting unit, Stillwater-Lonesome). Mean assigned proportion is indicated across a black and white scale.**



	Stillwater−Lonesome	river−type	Kitlope L	Bloomfield Cr	Kent L	Kwakwa R Lower	Kwakwa R Upper	Tankeeah R	Kimsquit L shore	Kadjusdis R	Hook Nose Cr	Koeye R	Wuikinuxv Tributaries	Wanukv R	Long L
Long L	0−1.6	0−1.6	0−1.7	0−1.4	0−1.5	0−1.6	0−1.5	0−1.8	0−1.7	0−1.4	0−1.5	0−1.6	0−1.5	0−1.6	90.4−100
Wanukv R	0−1.6	0−1.6	0−1.5	0−1.4	0−1.4	0−1.6	0−1.7	0−1.4	0−1.8	0−1.5	0−1.6	0−1.9	0−1.6	86.8−100	0−1.6
Wuikinuxv Tributaries	0−1.6	0.5−7.3	0−1.7	0−2.6	0−1.5	0−1.6	0−1.6	0−1.5	0−1.5	0−1.6	0−1.5	0−1.9	86.8−100	0−8.1	0−1.6
Koeye R	0−1.6	0−1.6	0−1.4	0−1.8	0−1.4	0−1.6	0−1.5	0−1.4	0−1.6	0−1.7	0−1.9	90.6−100	0−1.4	0−1.5	0−1.6
Hook Nose Cr	0−1.5	0−1.6	0−1.6	0−1.4	0−1.6	0−1.5	0−1.6	0−1.7	0−1.5	0−1.6	90−100	0−1.8	0−1.6	0−1.6	0−1.6
Kadjusdis R	0−1.6	0−1.6	0−1.7	0−1.4	0−1.6	0−1.5	0−1.6	0.1−4.1	0−1.4	86.4−100	0−1.3	0−1.6	0−1.6	0−1.7	0−1.6
Kimsquit L shore	0−1.6	0−1.5	0−2	0−1.6	0−1.6	0−1.6	0−1.5	0−1.7	86.6−99.8	0−1.5	0−1.7	0−1.6	0−1.6	0−1.7	0−1.5
Tankeeah R	0−1.6	0−1.5	0−1.6	0−1.5	0−1.6	0−1.6	0−1.6	87.2−99.8	0−1.5	0−8.9	0−1.8	0−1.5	0−1.6	0−1.6	0−1.7
Kwakwa R Upper	0−1.6	0−1.6	0−1.6	0−1.3	0−1.7	0.4−16.8	84.4−99.6	0−1.4	0−1.7	0−1.6	0−1.5	0−1.7	0−1.6	0−1.5	0−1.6
Kwakwa R Lower	0−1.6	0−1.5	0−1.8	0−1.8	0−1.3	78.1−99.5	0.5−11.1	0.1−4	0−1.7	0−1.6	0−1.7	0−1.5	0−1.6	0−1.5	0−1.5
Kent L	0−1.6	0−1.6	0−1.7	0−1.6	90.6−100	0.2−7	0−1.5	0−1.7	0−1.4	0−1.5	0−1.7	0−1.7	0−1.7	0−1.5	0−1.6
Bloomfield Cr	0−1.6	0−1.6	0−1.6	89.8−100	0−1.6	0−1.7	0−1.5	0−1.6	0−1.5	0−1.5	0−1.7	0−1.4	0−1.6	0−1.6	0−1.6
Kitlope L	0−1.5	0−2.7	89.3−100	0−1.7	0−1.4	0−1.5	0−1.5	0−1.7	0−1.5	0−1.5	0−1.5	0−1.4	0−1.5	0−1.6	0−1.6
river−type	0−3.7	77.7−99.1	0−1.6	0−1.7	0−1.5	0−1.6	0−1.6	0−1.6	0.2−7.4	0−1.7	0−1.8	0−1.5	0.2−7.3	0−1.6	0−1.5
Stillwater−Lonesome	89.4−100	0.5−15	0−1.3	0−1.8	0−2	0−1.5	0−1.5	0−1.5	0−1.6	0−1.5	0−1.5	0−1.4	0−1.6	0−1.6	0−1.6

To identify potential changes in Atnarko River sockeye stock composition over collapse, I referenced the 15 reporting units for GSI assignments on the in-river Nuxalk fishery samples after final baseline assessments. Z-scores appeared to be approximately normal, and I detected a single individual as a potential outlier that assigned to the river-type reporting unit (Z-score = -7.9). I did not apply sample composition to catch to the first two seasonal bins of catch data due to small sample sizes (5 individuals, Table B.5). I estimated total catch for each genetic group by applying sample proportions to mean catch.

Over 95% of catch across all decades was assigned to the reporting unit with the current two most abundant populations in the Atnarko River sockeye stock (Stillwater-Lonesome, Figure C.1). Next highest contributors to catch included 1.8% to the river-type reporting unit, as well as 1.2% and 0.4% to two nearby lake-type populations (Kimsquit L shore and Kitlope L). Other reporting units assigned at various contributions 0.1% or less.

Through the three decades, fewer Stillwater-Lonesome sockeye salmon were caught and at lower proportions (Figure C.1, Table C.4, and Table C.5). Stillwater-Lonesome catch declined by approximately 93% and 97% in the two decades after collapse compared to catches before collapse in 2005 (Figure C.1).

Before collapse (1999-2005), close to 98% of catch samples assigned to Stillwater-Lonesome sockeye salmon while 83.4% and 78.6% of catch samples assigned to the reporting unit in the first and second decades after collapse respectively (2006-2015 and 2015-2022,Figure C.1). Thus, genetic groups other than the current most abundant genetic group in the Atnarko River sockeye stock (Stillwater-Lonesome) made relatively higher contributions to catch after collapse.

The next highest genetic group contributing to the remaining catch across decades varied, and included a nearby lake-type population (Kimsquit L shore), as well as the river-type reporting unit (Table C.5). Prior to the 2005 collapse, the river-type reporting unit made up over 32% of the remaining catch, however contributions increased to nearly 80% in the decade immediately following collapse (2006-2015), and then decreased to 54% contribution to remaining catch in the second decade after collapse (Table C.5). Kimsquit L shore sockeye salmon contributed 36.5% to the remaining catch in the decades before (1996-2005) and only 7% in the first decade after collapse (2006-2015), however the population contributed the highest proportion to remaining catch in the second decade after collapse (2016-2022) consisting of 53.9% of the remaining catch (Figure C.1). Catch contributions to Kitlope L (a more distant lake-type population than Kimsquit L Shore) were under 15% for each decade across remaining catch contributions. Other reporting units assigned to 0.2% or lower of remaining catch across the decades (Table C.5). Thus, there were shifts in the stock composition within the in-river fishery with out-of-watershed and river-type fish apparently contributing relatively more to catch after collapse.

While Nuxalk in-river fishery catch assignments to the current most abundant reporting unit in the Atnarko River sockeye stock (Stillwater-Lonesome) tended to proportionally decrease across the season, and assignments to the river-type reporting unit tended to increase. Higher river-type reporting unit catch contributions tended to be observed in the latter half of July and August, however overall catch remained relatively low with only two instances of more than three sockeye salmon caught across seasons and decades (Table C.5). Kimsquit L shore sockeye salmon catch increased later in the fishing season across the decade prior to collapse (1996-2005) and post-collapse (2016-2022), however mean catch was never over 6 sockeye salmon at a given time period (Table B.5). Catch was assigned to Kitlope sockeye salmon at low proportions across all decades and seasons with exception to the early season contribution of 11.3% in the first decade after collapse (2006-2015), however all catches of Kitlope L were under three sockeye salmon at any given time period (Table C.5). While some patterns of return timing were seen across the non-dominant assigned reporting units, sockeye catch assigning to alternative reporting units were sporadic and in small catch numbers despite high proportional contribution to catch in some periods

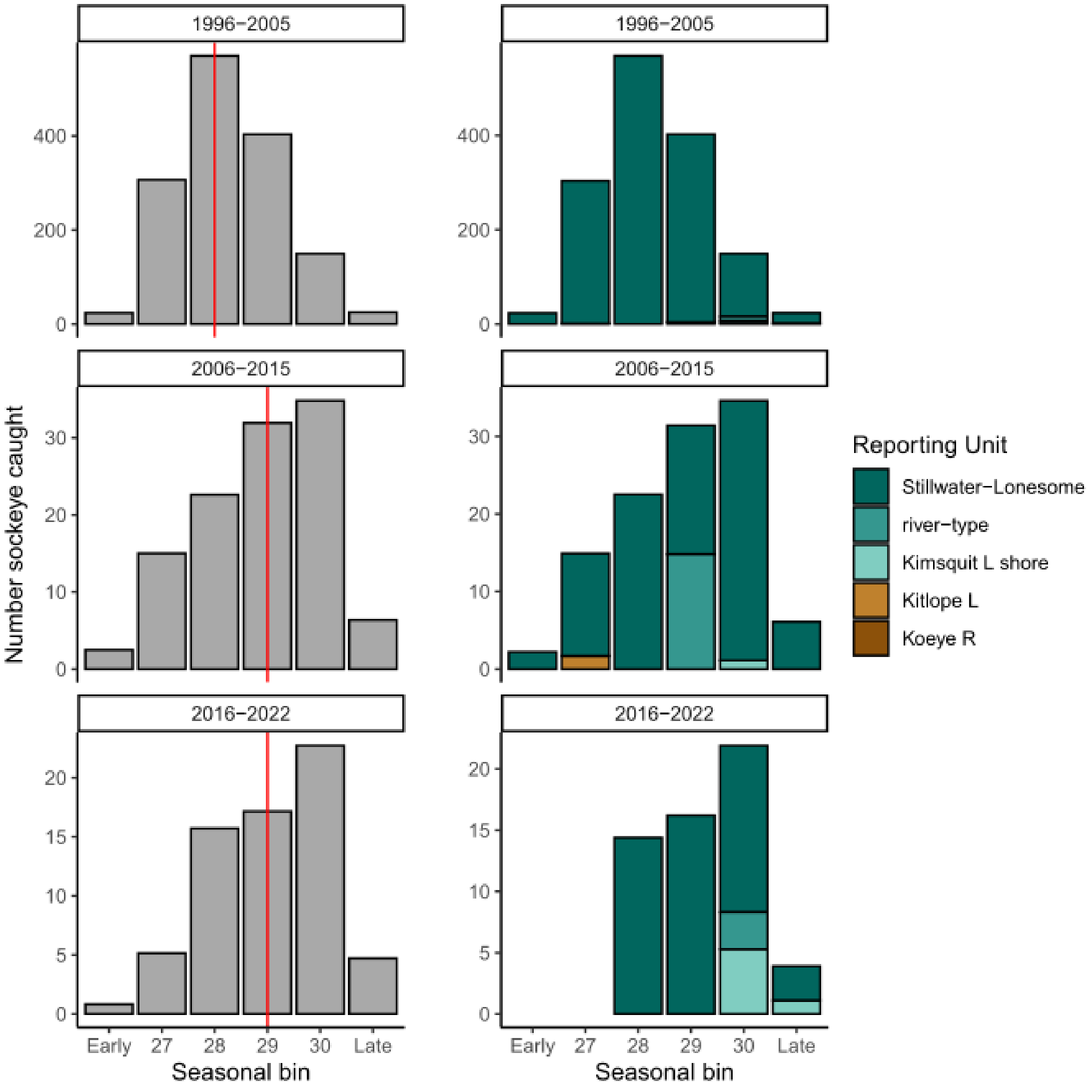


Figure C.1. **Mean sockeye salmon caught by decade and seasonal bin in the Bella Coola River Nuxalk in-river fishery (left) and catch composition (right). Red line indicates the point at which 50% cumulative mean sockeye salmon catch occurred. Catch composition (right) was estimated by applying genetic stock identification to catch samples collected from the fishery between 2003 and 2019. Seasonal bins represent statistical weeks or combinations of statistical weeks. Early represents approximately the first month of June whereas Late represents approximately the first three weeks of August. Week 27, 28, 29, and 30 each represent approximately the first to forth the weeks of July. Catch composition for Early or Week 27 are not shown due to small sample sizes (n = 5). Scale of catch varies across decade and only reporting units with one or more sockeye salmon assigned in any temporal strata are shown. Full composition estimates can be viewed in Table C.5.**

Table C.4. Estimated sample composition (with 90% credible intervals) from genetic stock composition (GSI) for sockeye salmon caught by decade and seasonal bin in the Bella Coola River Nuxalk in-river fishery. Seasonal bins represent statistical weeks or combinations of statistical weeks. Early represents approximately the first week of July and the month of June whereas Late represents approximately the last week of July and first three weeks of August. Week 28 and Week 29 represent approximately the second and third week of July. Only reporting units attributed to 1% or more of catch in any instance are only shown.

Reporting Unit	Early	Week 28	Week 29	Late
1996-2005				
Stillwater & Lonesome	98.6% (86.8-100)	99.7% (97.5-100)	98.7% (95.5-100)	89% (81.4-95.2)
Kitlope L	0% (0-2.3)	0% (0-0.4)	0.1% (0-1.3)	1.5% (0-4.7)
Kimsquit L shore	0% (0-2)	0% (0-0.4)	1.1% (0-3.4)	3.7% (1-8.1)
river-type	0% (0-2)	0% (0-0.4)	0% (0-0.3)	5.7% (1.4-11.5)
2006-2015				
Stillwater & Lonesome	88.1% (72.1-99.6)	99.6% (94.1-100)	52% (34-69.8)	96.4% (89.2-100)
Kitlope L	11.3% (1.9-25.7)	0% (0-1)	0.9% (0-9.3)	0% (0-0.9)
Kimsquit L shore	0% (0-1.6)	0% (0-0.9)	0.1% (0-1.7)	3.2% (0.4-8.8)
river-type	0% (0-1.6)	0% (0-0.9)	46.3% (28.6-64.9)	0% (0-0.9)
2016-2022				
Stillwater & Lonesome	-	91.8% (78.7-100)	94.2% (86.2-100)	59.9% (45.5-73.5)
Kitlope L	-	1.8% (0-10.2)	0.2% (0-2.7)	2.8% (0-8.9)
Kimsquit L shore	-	0% (0-1.5)	2.7% (0.4-7.3)	23.5% (13-36.1)
river-type	-	5.9% (0-17.4)	2.5% (0-8.8)	13.4% (5.5-23.8)

Table C.5. **Estimated catch composition (with 90% credible intervals) for sockeye salmon caught by decade and seasonal bin in the Bella Coola River Nuxalk in-river fishery. Seasonal bins represent statistical weeks or combinations of statistical weeks. Early represents approximately the first month of June whereas Late represents approximately the first three weeks of August. Week 27, 28, 29, and 30 each represent approximately the first to forth the weeks of July. Catch composition was not calculated for Early or Week 27 due to small sample sizes (n = 5). All reporting units included in genetic stock identification (GSI) baseline are shown and sorted in highest contribution, then north to south.**

Reporting Unit	Early	Week 27	Week 28	Week 29	Week 30	Late
1996-2005						
Stillwater-Lonesome	23.4 (20.6-23.7)	302.4 (266-306.6)	568.7 (555.9-570.1)	397.7 (384.9-403.1)	133 (121.7-142.4)	22.3 (20.4-23.8)
river-type	0 (0-0.5)	0 (0-6.2)	0 (0-2.2)	0 (0-1.4)	8.4 (2.1-17.3)	1.4 (0.4-2.9)
Kimsquit L shore	0 (0-0.5)	0 (0-6.1)	0.1 (0-2.2)	4.5 (0-13.7)	5.6 (1.5-12.1)	0.9 (0.2-2)
Kitlope L	0 (0-0.5)	0 (0-7.1)	0 (0-2.2)	0.4 (0-5.4)	2.2 (0-7.1)	0.4 (0-1.2)
Bloomfield Cr	0.1 (0-0.5)	0.9 (0-6.8)	0.2 (0-2.3)	0.2 (0-1.5)	0 (0-0.8)	0 (0-0.1)
Kwakwa R Lower	0 (0-0.5)	0.3 (0-6.7)	0 (0-2.2)	0 (0-1.4)	0 (0-0.8)	0 (0-0.1)
Wuikinuxv tributaries	0.1 (0-0.5)	0.7 (0-6.8)	0.3 (0-2.4)	0 (0-1.4)	0 (0-0.7)	0 (0-0.1)
Kent L	0 (0-0.5)	0 (0-6)	0.2 (0-2.2)	0.1 (0-1.6)	0.1 (0-0.8)	0 (0-0.1)
Kwakwa R Upper	0 (0-0.5)	0 (0-6.2)	0 (0-2)	0 (0-1.4)	0 (0-0.8)	0 (0-0.1)
Tankeeah R	0 (0-0.5)	0.4 (0-6.2)	0.3 (0-2.3)	0 (0-1.5)	0 (0-0.7)	0 (0-0.1)
Kadjusdis R	0 (0-0.5)	0.3 (0-6.5)	0.1 (0-2.2)	0 (0-1.5)	0.1 (0-0.8)	0 (0-0.1)
Hook Nose Cr	0 (0-0.5)	0.4 (0-6.7)	0.1 (0-2.2)	0.1 (0-1.6)	0 (0-0.8)	0 (0-0.1)
Koeye R	0.1 (0-0.6)	1.1 (0-7.2)	0 (0-2)	0 (0-1.4)	0 (0-0.9)	0 (0-0.1)
Wanukv R	0 (0-0.5)	0 (0-5.9)	0.1 (0-2.2)	0 (0-1.6)	0 (0-0.8)	0 (0-0.1)
Long L	0 (0-0.5)	0 (0-6)	0.1 (0-2.1)	0.1 (0-1.4)	0 (0-0.8)	0 (0-0.1)

Reporting Unit	Early	Week 27	Week 28	Week 29	Week 30	Late
2006-2015						
Stillwater-Lonesome	2.2 (1.8-2.5)	13.2 (10.8-14.9)	22.5 (21.3-22.6)	16.6 (10.8-22.3)	33.5 (31.1-34.8)	6.1 (5.7-6.4)
river-type	0 (0-0)	0 (0-0.2)	0 (0-0.2)	14.8 (9.1-20.7)	0 (0-0.3)	0 (0-0.1)
Kimsquit L shore	0 (0-0)	0 (0-0.2)	0 (0-0.2)	0 (0-0.6)	1.1 (0.1-3.1)	0.2 (0-0.6)
Kitlope L	0.3 (0-0.6)	1.7 (0.3-3.9)	0 (0-0.2)	0.3 (0-3)	0 (0-0.3)	0 (0-0.1)
Bloomfield Cr	0 (0-0)	0 (0-0.2)	0 (0-0.2)	0 (0-0.6)	0 (0-0.3)	0 (0-0.1)
Kwakwa R Lower	0 (0-0)	0 (0-0.3)	0 (0-0.2)	0 (0-0.5)	0 (0-0.3)	0 (0-0.1)
Wuikinuxv tributaries	0 (0-0)	0 (0-0.3)	0 (0-0.2)	0 (0-0.5)	0 (0-0.3)	0 (0-0.1)
Kent L	0 (0-0)	0 (0-0.3)	0 (0-0.2)	0 (0-0.5)	0 (0-0.3)	0 (0-0.1)
Kwakwa R Upper	0 (0-0)	0 (0-0.2)	0 (0-0.2)	0.1 (0-0.6)	0 (0-0.3)	0 (0-0.1)
Tankeeah R	0 (0-0)	0 (0-0.3)	0 (0-0.2)	0 (0-0.5)	0 (0-0.3)	0 (0-0.1)
Kadjusdis R	0 (0-0)	0 (0-0.3)	0 (0-0.2)	0 (0-0.5)	0 (0-0.3)	0 (0-0.1)
Hook Nose Cr	0 (0-0)	0 (0-0.3)	0 (0-0.2)	0.1 (0-0.5)	0 (0-0.3)	0 (0-0.1)
Koeye R	0 (0-0)	0 (0-0.2)	0 (0-0.2)	0 (0-0.5)	0 (0-0.3)	0 (0-0.1)
Wanukv R	0 (0-0)	0 (0-0.3)	0 (0-0.2)	0 (0-0.5)	0 (0-0.3)	0 (0-0.1)
Long L	0 (0-0.1)	0 (0-0.3)	0 (0-0.2)	0 (0-0.5)	0 (0-0.4)	0 (0-0.1)

Reporting Unit	**Early**	**Week 27**	**Week 28**	**Week 29**	**Week 30**	**Late**
2016-2022						
Stillwater-Lonesome	-	-	14.4 (12.4-15.7)	16.2 (14.8-17.1)	13.6 (10.3-16.7)	2.8 (2.1-3.5)
river-type	-	-	0.9 (0-2.7)	0.4 (0-1.5)	3 (1.2-5.4)	0.6 (0.3-1.1)
Kimsquit L shore	-	-	0 (0-0.2)	0.5 (0.1-1.3)	5.3 (3-8.2)	1.1 (0.6-1.7)
Kitlope L	-	-	0.3 (0-1.6)	0 (0-0.5)	0.6 (0-2)	0.1 (0-0.4)
Bloomfield Cr	-	-	0 (0-0.3)	0 (0-0.1)	0 (0-0.2)	0 (0-0)
Kwakwa R Lower	-	-	0 (0-0.3)	0 (0-0.1)	0 (0-0.2)	0 (0-0)
Wuikinuxv tributaries	-	-	0 (0-0.2)	0 (0-0.2)	0 (0-0.2)	0 (0-0)
Kent L	-	-	0 (0-0.3)	0 (0-0.1)	0 (0-0.2)	0 (0-0)
Kwakwa R Upper	-	-	0 (0-0.2)	0 (0-0.1)	0 (0-0.2)	0 (0-0)
Tankeeah R	-	-	0 (0-0.2)	0 (0-0.1)	0 (0-0.3)	0 (0-0.1)
Kadjusdis R	-	-	0 (0-0.2)	0 (0-0.1)	0 (0-0.2)	0 (0-0)
Hook Nose Cr	-	-	0 (0-0.2)	0 (0-0.1)	0 (0-0.2)	0 (0-0)
Koeye R	-	-	0 (0-0.2)	0 (0-0.1)	0 (0-0.2)	0 (0-0)
Wanukv R	-	-	0 (0-0.2)	0 (0-0.1)	0 (0-0.2)	0 (0-0)
Long L	-	-	0 (0-0.2)	0 (0-0.1)	0 (0-0.3)	0 (0-0.1)