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Genetic Baseline for Mixed Stock Analyses of Sockeye Salmon Harvested in Southeast Alaska for Pacific Salmon Treaty Applications, 2018

by

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Alaska Department of Fish and Game **Divisions of Sport Fish and Commercial Fisheries**

Symbols and Abbreviations

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Weights and measures (metric)

centimeter	cm
deciliter	dL
gram	g
hectare	ha
kilogram	kg
kilometer	km
liter	L
meter	m
milliliter	mL
millimeter	mm

Weights and measures (English)

cubic feet per second	ft^3/s
foot	ft
gallon	gal
inch	in
mile	mi
nautical mile	nmi
ounce	oz
pound	lb
quart	qt
yard	yd

Time and temperature

day	d
degrees Celsius	°C
degrees Fahrenheit	°F
degrees kelvin	K
hour	h
minute	min
second	s

Physics and chemistry

all atomic symbols	
alternating current	AC
ampere	A
calorie	cal
direct current	DC
hertz	Hz
horsepower	hp
hydrogen ion activity (negative log of)	pH
parts per million	ppm
parts per thousand	ppt, ‰
volts	V
watts	W

General

Alaska Administrative Code	AAC
all commonly accepted abbreviations	e.g., Mr., Mrs., AM, PM, etc.
all commonly accepted professional titles	e.g., Dr., Ph.D., R.N., etc.
at	@
compass directions:	
east	E
north	N
south	S
west	W
copyright	©
corporate suffixes:	
Company	Co.
Corporation	Corp.
Incorporated	Inc.
Limited	Ltd.
District of Columbia	D.C.
et alii (and others)	et al.
et cetera (and so forth)	etc.
exempli gratia (for example)	e.g.
Federal Information Code	FIC
id est (that is)	i.e.
latitude or longitude	lat or long
monetary symbols (U.S.)	$, ¢
months (tables and figures): first three letters	Jan,...,Dec
registered trademark	®
trademark	™
United States (adjective)	U.S.
United States of America (noun)	USA
U.S.C.	United States Code
U.S. state	use two-letter abbreviations (e.g., AK, WA)

Mathematics, statistics

all standard mathematical signs, symbols and abbreviations	
alternate hypothesis	H_A
base of natural logarithm	*e*
catch per unit effort	CPUE
coefficient of variation	CV
common test statistics	(F, t, χ^2, etc.)
confidence interval	CI
correlation coefficient (multiple)	R
correlation coefficient (simple)	r
covariance	cov
degree (angular)	°
degrees of freedom	df
expected value	*E*
greater than	>
greater than or equal to	≥
harvest per unit effort	HPUE
less than	<
less than or equal to	≤
logarithm (natural)	ln
logarithm (base 10)	log
logarithm (specify base)	$\log_2$, etc.
minute (angular)	'
not significant	NS
null hypothesis	H_O
percent	%
probability	P
probability of a type I error (rejection of the null hypothesis when true)	α
probability of a type II error (acceptance of the null hypothesis when false)	β
second (angular)	"
standard deviation	SD
standard error	SE
variance	
population	Var
sample	var

FISHERY MANUSCRIPT NO. 18-03

GENETIC BASELINE FOR MIXED STOCK ANALYSES OF SOCKEYE SALMON HARVESTED IN SOUTHEAST ALASKA FOR PACIFIC SALMON TREATY APPLICATIONS, 2018

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ABSTRACT

Sockeye salmon (*Oncorhynchus nerka*) are an important resource in Southeast Alaska (SEAK) and are harvested in subsistence, personal use, sport, and commercial fisheries. Commercial fisheries for sockeye salmon in SEAK have been prosecuted for over 100 years, with many fisheries harvesting mixed stocks composed of sockeye salmon originating from as far north as Prince William Sound and as far south as Washington State. The Alaska Department of Fish and Game uses genetic mixed stock analysis to estimate stock compositions for harvest management and to meet Pacific Salmon Treaty obligations. This report describes the methods used to develop a genetic baseline of single nucleotide polymorphism allele frequencies to be used for genetic mixed stock analysis of sockeye salmon in SEAK fisheries. This baseline includes 28,609 individuals from 345 collections representing 238 populations in up to 9 reporting groups spanning from Prince William Sound to Washington State. We used repeated 100% proof tests to measure the baseline's ability to accurately allocate mixed stock samples to reporting groups. Correct allocations in these tests ranged from 92.6% to 99.5%. The ability of this baseline to perform accurately in proof tests was due to the large amount of genetic variation found among populations both within and among the reporting groups. This baseline has been used successfully to estimate the stock composition of Pacific Salmon Treaty and domestic sockeye salmon stocks harvested in SEAK commercial fisheries.

Key words Southeast Alaska, sockeye salmon, *Oncorhynchus nerka*, mixed stock analysis, genetic baseline, single nucleotide polymorphism, SNPs, population structure, commercial fisheries

INTRODUCTION

DESCRIPTION OF SOUTHEAST ALASKA COMMERCIAL SOCKEYE SALMON FISHERIES

Sockeye salmon *Oncorhynchus nerka* are harvested in subsistence, personal use, sport, and commercial fisheries throughout Southeast Alaska (SEAK) and the Yakutat area. Commercial sockeye salmon fisheries have operated in Southeast Alaska since the late 1870s with a record harvest of 3.5 million fish in 1914 (Byerly et al. 1999). In more recent years, sockeye salmon harvests averaged 1.2 million fish (2005–2014; Conrad and Gray 2016), primarily in drift gillnet and purse seine fisheries in 19 districts (Figure 1). These fisheries harvest mixed stocks of sockeye salmon of both Alaska and non-Alaska origin, and thus the management of many of the fisheries is governed both by consideration of domestic stocks and by specific agreements between the United States and Canada in the Pacific Salmon Treaty (PST; Pacific Salmon Treaty 2008).

HISTORY OF STOCK COMPOSITION ESTIMATES IN SOUTHEAST ALASKA

Since the 1980s, the Alaska Department of Fish and Game (ADF&G) has operated intensive stock identification programs in order to effectively manage sockeye salmon stocks harvested in mixed stock fisheries and to abide by PST agreements. In the past, the majority of these stock identification programs involved scale pattern analysis, in which differences in the patterns of circuli on scales reflect average differences in fish growth history over broad geographic areas (Marshall et al. 1984). Broad-scale differences between sockeye salmon stock groups originating in Alaska and Canada have been documented in scale growth patterns during freshwater and early marine life history (Oliver et al. 1984; Bloomquist et al. 2010). However, scale pattern analysis cannot provide fine-scale resolution of individual Alaska sockeye salmon stock groupings (PSC NBTC 2005), requires a new baseline every year, and entails specialized training of staff; thus, there has been a move towards the use of genetics for stock identification.

Genetic mixed stock analysis (MSA) has been used effectively for sockeye salmon throughout their range as a tool to estimate stock compositions of mixtures of fish of unknown origin since the 1980s (Wood 1989; Seeb et al. 2000; Beacham et al. 2004a; Barclay et al. 2011; Dann et al.

2012b, among others). The earliest work used allozymes to characterize populations in SEAK and northern British Columbia for potential MSA applications (Guthrie et al. 1994). Next, microsatellite markers were used extensively for MSA in Pacific Rim-scale applications (Beacham et al. 2005). More recently, the marker of choice for MSA applications has been single nucleotide polymorphism (SNP) markers due to ease of lab-to-lab standardization, increased lab throughput, and reduced cost (Seeb et al. 2009). Pacific Rim-scale applications of MSA have been completed using 45 SNP markers at 78 populations (Habicht et al. 2010). In SEAK this small number of SNPs was used to estimate the contribution of McDonald Lake sockeye salmon to commercial net fisheries harvests in southern SEAK (Gilk-Baumer et al. 2013). However, these previous baselines were not developed specifically for management requirements in SEAK and were lacking adequate sample sizes for some populations or missing important sockeye salmon spawning aggregates from the region.

COMPONENTS OF GENETIC BASELINE FOR SOUTHEAST ALASKA

The foundation for genetic MSA of fishery samples is a genetic characterization of all the stocks that might contribute to the fishery (hereafter *baseline*). Estimating stock composition is accomplished by comparing genotypes of fish of unknown origin (i.e., fish captured in a fishery) to the baseline of population allele frequencies from these potentially contributing stocks. Such baselines are defined by 3 components: (1) populations of individuals, (2) genetic markers used to genotype fish, and (3) reporting groups aggregating populations that are genetically and/or geographically similar. For SEAK, we defined these components as follows:

1. Populations: Sockeye salmon fisheries in SEAK harvest many stocks, including stocks originating from the south (British Columbia and Pacific Northwest; Oliver et al. 1990; Bloomquist et al. 2010; Wilcock et al. 2011) and from the north (Prince William Sound; ADF&G Mark, Tag and Age Lab, http://mtalab.adfg.alaska.gov/OTO/default.aspx), thus we included collections spanning this range.

2. Genetic Markers: Single nucleotide polymorphism (SNP) markers are the markers of choice due to the availability of archived data and genotyping efficiency. We updated all collections with a standardized set of 96 markers that were used to analyze a subset of these collections in previous studies (Dann et al. 2012a; Shedd et al. 2016) to allow the possibility to distinguish among potential fine-scale stock groups.

3. Reporting Groups: Aggregating populations into reporting groups is performed before mixtures are analyzed to ensure that group identifiability meets accepted standards. Defining reporting groups is an iterative process that takes into account the following: (1) management needs (fishery management and escapement goals), (2) genetic population structure (MSA potential), (3) adequacy of representation in the baseline (number of individuals and representative value of genetic variation within groups), and (4) the expected number of fish from a reporting group in a mixture. Although this baseline has the ability to distinguish among many possible reporting groups, this report describes the reporting groups necessary to meet management needs for stocks falling under the PST in U.S. Districts 106, 108, and 111 (Figure 1). The commercial gillnet fisheries in U.S. Districts 106 and 108 harvest wild stocks of sockeye salmon bound for SEAK island and mainland lakes, as well as Canadian lakes and tributaries in the Stikine, Nass, and Skeena River drainages. The commercial gillnet fisheries in U.S. District 111 harvest wild stocks

of sockeye salmon primarily bound for several systems in the Taku River (Canada) or to Crescent and Speel lakes in Alaska.

This report describes the most comprehensive baseline to date for sockeye salmon in SEAK and was specifically designed for use in MSA of SEAK fisheries.

DEFINITIONS

To reduce confusion associated with the methods, results, and interpretation of this study, basic definitions of commonly used genetic and salmon management terms are offered here.

Bottleneck. A sharp reduction in effective population size reducing the genetic variation within a population.

District. A portion of a body of water, areas of which may be open to commercial salmon fishing. Districts are subdivided into statistical areas and used to document the spatial origin of fishery harvests. Commercial fishing districts, subdistricts, and sections in SEAK commercial fishing areas are defined in statutes listed below under *Salmon administrative area*.

F-statistics. Measures used to partition genetic diversity within and among populations in a hierarchical fashion. Common measures include: F_{IS}, the average departure of genotype frequencies from Hardy-Weinberg expectations within populations; F_{ST}, the proportion of the variation due to allele frequency differences among populations; and F_{IT}, the departure of genotype frequencies from Hardy-Weinberg expectation relative to the entire population.

Gametic Disequilibrium (or Linkage Disequilibrium). A state that exists in a population when alleles at different loci are not distributed independently of one another in the population's gamete pool. Linkage disequilibrium can occur because the loci are physically linked on the same chromosome, or because of historical events, including colonizations and population bottlenecks.

Genetic Marker. A genetic variant showing Mendelian inheritance, such as a DNA sequence that can be identified by a simple assay.

Genotype. The set of alleles for one or more loci for an individual.

Hardy-Weinberg Expectations (HWE). The genotype frequencies that would be expected from given allele frequencies, assuming random mating, no mutation (the alleles do not change), no migration or emigration (no exchange of alleles between populations), infinitely large population size, and no selective pressure for or against any traits.

Harvest. The number of salmon (sometimes derived from weight of salmon) taken from an area over a period of time.

Heterozygosity. The proportion of individuals in a population that carry different alleles (i.e., are heterozygous) at a particular marker; a measure of variability.

Lake-type. The typical anadromous form of sockeye salmon that spends 1–3 years in a nursery lake before migrating seaward (Burgner 1991).

Locus (Loci, plural). A fixed position or region on a chromosome that may contain more than one genetic marker.

Mixed Stock Analysis (MSA). A method using allele frequencies from populations and genotypes from mixture samples to estimate stock compositions of mixtures.

Polymerase Chain Reaction (PCR). A method to replicate copies of a locus across several orders of magnitude, generating millions of copies of the DNA.

Population. A randomly mating group of fish that are largely reproductively isolated from other populations.

Reporting Group. A group of populations in a genetic baseline to which portions of a mixture are allocated with mixed stock analyses; constructed based on a combination of stakeholder needs and genetic distinction.

River-type. An anadromous form of sockeye salmon that does not spend any part of its life in a nursery lake before migrating seaward (Wood et al. 2008).

Run. The total number of salmon in a stock surviving to adulthood and returning to the vicinity of the natal stream in any calendar year. A run consists of both harvested adults and the escapement to spawning grounds. With the exception of pink salmon (*O. gorbuscha*), the run is composed of several age classes of mature fish from the stock, derived from the spawning of a number of previous brood years (from 5 AAC 39.222(f)).

Salmon administrative area (Area). Geographic areas used to administer the registration of commercial salmon fishing permits (from 20AAC 05.230). Commercial salmon fishing areas designated by letter code and are defined by the following Alaska administrative code: Southeast Alaska (Area A; 5 AAC 33.100); Yakutat (Area D; 5 AAC 30.100); and Prince William Sound (Area E; 5 AAC 24.100). Districts and subdistricts within areas used to aid management are further defined by administrative code.

Salmon Stock. A locally interbreeding group of salmon that is distinguished by a distinct combination of genetic, phenotypic, life history, and habitat characteristics, or an aggregation of 2 or more interbreeding groups, which occur in the same geographic area and are managed as a unit (5 AAC 39.222(f)).

Single nucleotide polymorphism (SNP). DNA sequence variation occurring when a single nucleotide (A, T, C, or G) site differs among individuals or within an individual between paired chromosomes.

METHODS

TISSUE SAMPLING

Baseline samples were collected from spawning aggregations of sockeye salmon ranging from Prince William Sound south to Puget Sound to compile our library of tissues (Table 1; Figures 2–5). Tissues were collected by ADF&G staff and collaborators through several dedicated sockeye salmon projects: Chatham/Icy Strait Sockeye Salmon Genetic Stock Identification (State of Alaska AR 41520); PST Transboundary and Boundary Area genetic stock identification projects (Pacific Salmon Commission Northern Fund projects IHG-05-006, NF-2008-I-15A); Alaska Sustainable Salmon Fund (AKSSF) project no. 45097; Western Alaska Salmon Stock Identification Program (State of Alaska and NOAA Cooperative Agreement NA06NMF4380094); Prince William Sound Region Sockeye Salmon Genetic Structure (NFWF/Legacy Grant Project ID: 0801.11.028183); and Genetics of Copper River Sockeye (AKSSF project no. 45869). Other collections were made in collaboration with the U.S. Forest Service, National Marine Fisheries Service, Department of Fisheries and Oceans Canada, private nonprofit hatchery organizations, and nongovernmental organizations. When possible, the target sample size for each set of

spawning aggregations that might represent a population in the baseline was 95 individuals to achieve acceptable precision for estimating allele frequencies (Allendorf and Phelps 1981; Waples 1990) and to accommodate our genotyping platform.

For this baseline, we selected collections (fish collected within the same year at the same location) to represent (1) demographic distribution, (2) genetic diversity, (3) geographic coverage, and (4) among-year variation of allele frequencies within locations.

LABORATORY ANALYSIS

Assaying genotypes

We extracted genomic DNA from tissue samples using 2 methods: (1) DNeasy 96 Tissue Kit by QIAGEN (Valencia, CA) and (2) NucleoSpin 96 Tissue Kit by Macherey-Nagel (Düren, Germany). We screened 96 SNP (Figure 2) markers using Fluidigm 96.96 Dynamic Array Integrated Fluidic Circuits (IFCs), which systematically combine up to 96 assays and 96 samples into 9,216 parallel reactions. The components are pressurized into the IFC using the IFC Controller HX (Fluidigm). Each reaction is conducted in a 7.2 nL volume chamber consisting of a mixture of 20X GT Sample Loading Reagent (Fluidigm), 2X TaqMan Universal Buffer (Applied Biosystems), 5X AmpliTaq Gold DNA Polymerase (Applied Biosystems), Custom TaqMan SNP Genotyping Assay (Applied Biosystems), 2X Assay Loading Reagent (Fluidigm), 50X ROX Reference Dye (Invitrogen), and 60–400 ng/μl DNA. Thermal cycling was performed on either a Fluidigm FC1 Cycler or Eppendorf IFC Thermal Cycler as follows: 70°C for 30 min for "Hot-Mix" step, initial denaturation of 10 min at 96°C followed by 40 cycles of 96° for 15 s and 60°C for 1 min. The Dynamic Arrays were read on a Fluidigm EP1 System or BioMark System after amplification and scored using Fluidigm SNP Genotyping Analysis software.

Assays that failed to amplify on the Fluidigm system were reanalyzed on the Applied Biosystems platform. Each reaction on this platform was performed in 384-well reaction plates in a 5 μL volume consisting of 5–40 ng/μl of template DNA, 1X TaqMan Universal PCR Master Mix (Applied Biosystems), and 1X TaqMan SNP Genotyping Assay (Applied Biosystems). Thermal cycling was performed on a Dual 384-Well GeneAmp PCR System 9700 (Applied Biosystems) as follows: an initial denaturation of 10 min at 95°C followed by 50 cycles of 92°C for 1 s and annealing/extension temperature for 1 min. The plates were scanned on an Applied Biosystems Prism 7900HT Sequence Detection System after amplification and scored using Applied Biosystems' Sequence Detection Software version 2.2.

Genotypes produced on both platforms were imported and archived in the ADF&G Gene Conservation Laboratory (GCL) Oracle database, LOKI.

Laboratory quality control

We conducted quality control (QC) analyses on all collections to identify laboratory errors and to measure background discrepancy rates of the genotyping process. The QC analyses were performed as a separate event from the original genotyping, with staff duties altered to reduce the likelihood of repeated human errors. This is typically done following laboratory analysis to allow immediate action to be taken if errors are apparent. The GCL has employed 3 QC methods over the years with the details of each protocol located in Dann et al. 2012a. Briefly, these methods include (1) the *Old* method, consisting of regenotyping 8% of fish genotyped in the original project using the same DNA extraction for SNPs assayed in the original project; (2) the *39* method where genotypes for 100% of individuals genotyped for the 39 SNPs that were common to our current

and previous baselines were compared; and (3) the *New* method where 8% of project fish were re-extracted and genotyped for the same SNPs assayed in the original project. The New QC method is capable of identifying extraction, assay plate, and genotyping errors and is the best representation of the error rate of the GCL's current genotype production. All collections in this baseline were analyzed with at least one of these 3 QC methods.

For all QC methods, error rates in the original genotyping can be estimated as half the rate of discrepancies by assuming that the discrepancies among analyses were due equally to errors during the original genotyping and during quality control.

STATISTICAL ANALYSIS

Data retrieval and quality control

We retrieved genotypes from LOKI and imported them into *R*.[1] All subsequent analyses were performed in *R* unless otherwise noted.

Prior to statistical analysis, we performed 3 analyses to confirm the quality of the data used. First we identified SNP markers that were invariant in all individuals and excluded these markers from further statistical analyses. Second, we used the 80% rule (Dann et al. 2009) to exclude individuals missing genotypes for 20% or more of loci because these individuals likely had poor-quality DNA. The inclusion of individuals with poor-quality DNA might introduce genotyping errors into the baseline and reduce the accuracy of MSA. Finally, we identified individuals with identical genotypes within collections and typically removed them from further analyses. Identical genotypes can occur as a result of sampling or extracting the same individual twice, and were defined as pairs of individuals sharing the same alleles in 95% of screened loci. The sample with the most missing genotypic data from each identical pair was removed from further analyses. If both samples had the same amount of genotypic data, the first sample was removed from further analyses.

Baseline development

Hardy-Weinberg expectations

After calculating allelic frequencies for each locus, we tested observed genotype frequencies for each baseline collection for conformance to Hardy-Weinberg expectations (HWE) at each locus through Monte Carlo simulations. We used *Genepop* version 4.3 (Rousset 2008) with 10,000 burn-in steps, followed by 20 batches of 5,000 iterations/batch. We combined probabilities for each collection across loci and each locus across collections using Fisher's method (Sokal and Rohlf 1995) and examined the frequency of departures from HWE to identify collections that exhibited substantially more departures than others. We removed collections and loci from subsequent analyses if they departed significantly from HWE after correcting for multiple tests with Bonferroni's method ($\alpha = 0.05/$ no. of loci), if they departed from HWE substantially more frequently than others, or if the distribution of *p*-values across loci was indicative of nonconformance to HWE (Waples 2014). We defined *substantially more* by examining a histogram of the frequency of the number of collections in which SNPs were out of HWE. Collections that were temporally sampled were retained in the baseline to test for pooling (see *Pooling collections into populations*).

[1] *R* Development Core Team. 2017. *R*: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL http://www.R-project.org/.

Pooling collections into populations

When appropriate, we pooled collections to obtain better estimates of allele frequencies using a stepwise protocol. First, we tested for differences in allele frequencies between pairs of collections from the same geographic location using Fisher's exact test (Sokal and Rohlf 1995) of allele frequency homogeneity and based decisions on a summary across loci using Fisher's method. When tests indicated no difference between collections ($P > 0.01$), we pooled them, otherwise they were kept separately. Next, we applied the same protocol to geographically proximate collections (approximately 5 km) that were collected at similar calendar dates and might represent the same spawning aggregate. After this pooling protocol, we tested each newly pooled set of collections for conformance to HWE following the same protocol described above to ensure our pooling was appropriate. If a set of pooled collections failed to conform to HWE and the individual temporally sampled collections were too small ($n < 35$ samples, such that allele frequency estimates are not within 0.1 90% of the time), then the collection(s) was dropped from the baseline. If individual temporally sampled collections failed to conform to HWE, but conformed after being pooled, then the pooled collection was retained. After this pooling protocol, we considered these final collections (pooled or single) to be populations.

Linkage disequilibrium

Linkage disequilibrium between each pair of nuclear SNPs in each population is tested to ensure that the baseline and mixed stock analyses are based on independent, unlinked markers. The majority of this baseline has been previously tested (unpublished) and was not retested when updated with the additional populations included in this report. Original testing followed the protocol in Dann et al. (2012a) and our current study relied on the results of this original testing to determine what markers to exclude or combine.

Analysis of genetic structure

We visualized genetic relationships among populations by building a neighbor-joining tree based on pairwise F_{ST} estimates among populations. Pairwise F_{ST} estimates were calculated using the methods of Weir and Cockerham (1984) from the final set of independent markers with the package *hierfstat* (Goudet 2005). We plotted the consensus neighbor-joining tree with the package *ape* (Paradis et al. 2004).

Baseline evaluation for MSA

Defining reporting groups

The following metrics are typically used to define reporting groups by the GCL: (1) management needs; (2) 90% correct allocation in 100% proof tests for each reporting group; (3) adequacy of representation in the baseline (number of individuals and representative value of genetic variation within reporting groups); and (4) the expected proportion of fish from a reporting group potentially within a mixture (at least 5%; Habicht et al. 2012). For this report, management needs were identified through requirements of the PST for Districts 106, 108 and 111 in SEAK as briefly discussed in the *Introduction* above. Reporting groups for Transboundary stocks (those bound for systems within the Stikine and Taku drainages) that are harvested in U.S. Districts 106 and 108 include *Stikine/Taku Mainstem*, *Tahltan*, and *Other* (Tables 1 and 2). Reporting groups for Transboundary stocks harvested in U.S. District 111 include *Stikine/Taku Mainstem*, *Taku Lakes*, *Tatsamenie*, *Speel*, and *Other*. Northern Boundary stocks (those originating in the Nass and Skeena River drainages) are also harvested in U.S. Districts 106 and 108 (among other districts, but those

results will not be shown). Northern Boundary stocks harvested in U.S. Districts 106 and 108 include *Alaska*, *Nass*, *Skeena*, *All Stikine/Taku Mainstem*, and *Other*.

Self-assignment likelihood profiles

We computed a *likelihood profile* of the baseline, or the self-assignment probability for each individual within populations within reporting groups. We calculated the likelihood of each individual's genotype originating from each baseline population using leave-one-out population allele frequencies (Anderson et al. 2008). These genotype likelihoods were then rolled up to population and reporting group levels to determine the overall probability of individuals from groups being assigned back their reporting group. We visualized these probabilities as a matrix to better understand self-assignment of individuals back to their respective reporting groups and gain insight into potential misallocation in fishery mixtures.

100% proof tests

To assess the identifiability of reporting groups in mixtures, we conducted repeated 100% proof tests, sampled half of the individuals (up to a maximum of 200) without replacement from each reporting group, and analyzed them as a mixture against the reduced baseline (Dann et al. 2012a). We used the Bayesian MSA method implemented in *BAYES* (Pella and Masuda 2001) to evaluate the stock compositions of these test mixtures. The Bayesian model implemented by *BAYES* uses a Dirichlet distribution as the prior distribution for the stock proportions, and the parameters for this distribution must be specified. We defined prior parameters for each reporting group to be equal (i.e., a *flat* prior) with the prior for each reporting group subsequently divided equally among populations within that reporting group. We set the sum of all prior parameters to 1 (prior weight), which is equivalent to adding 1 fish to each mixture (Pella and Masuda 2001). We ran 1 independent Markov Chain Monte Carlo chain of 40,000 iterations and discarded the first 20,000 iterations to remove the influences of the initial start value. We used the second half of the chain to form the posterior distribution. Each proof test was repeated 10 times for each reporting group to account for variability of individuals within reporting groups due to variability within randomly drawn mixtures.

These tests provided an indication of the power of the baseline for MSA under the assumption that all the populations from a reporting group were represented in the baseline. A critical level of 90% correct allocation was used to determine if the reporting group was acceptably identifiable (Seeb et al. 2000).

RESULTS

TISSUE SAMPLING

We compiled a library of baseline tissues from 366 sockeye salmon collections taken from adult fish, totaling 29,839 samples. These collections spanned the years 1985–2014 (Table 1). The average sample size per collection was 82. Difficulties of sampling in remote locations, lack of dedicated funding to support sampling crews, challenging water conditions (i.e., brackish, swift-moving, deep), and small spawning population sizes were factors that contributed to missing population sampling goals of 95 samples per spawning aggregate (see sampling success rate under *Pooling collections into populations* below).

LABORATORY ANALYSIS

Assaying genotypes

A total of 29,839 individuals were genotyped at all 96 SNP markers (Tables 1 and 3). The number of individuals genotyped per baseline collection ranged from 3 to 252 individuals.

Laboratory quality control

All collections in this baseline underwent one of the 3 QC methods described in Dann et al. (2012a). QC for 79% of the collections in this baseline was conducted in previous unpublished baseline analyses. Those results demonstrated a low overall discrepancy rate of 0.43%. The majority of discrepancies were between heterozygotes and homozygotes and very few homozygote-homozygote discrepancies were observed (0.02%) for all QC methods.

The overall discrepancy rate for the newly genotyped collections (the New QC method) was 0.12%, with the majority of the discrepancies between heterozygotes and homozygotes. There were 8 collections that were newly genotyped but that had old data in LOKI, so we applied the 39 QC method. The overall discrepancy rate for these 8 collections was 1.8%, with the majority of the discrepancies between heterozygotes and homozygotes. Most of these conflicts came from a single collection (Kynock Creek) that had originally produced poor-quality genotypes. The current genotyping methodology at the GCL has improved the quality of these genotypes, allowing this collection to be retained in analysis. The Old QC method was applied to 12 collections because they did not have enough tissue for re-extraction. The discrepancy rate for these 12 collections was 0.05%. Again, very few homozygote-homozygote discrepancies were observed for the New (0.01%), 39 (0.12%), and Old (0.00%) QC methods.

STATISTICAL ANALYSIS

Data retrieval and quality control

All SNPs were variable for at least 1 fish screened in this analysis. No SNP markers were removed for this reason before further analyses.

A total of 393 individuals were removed from the baseline due to missing genotypes from greater than 20% of the loci (19 SNPs). The percentage of fish from a collection missing genotypes ranged from 0% to 32% (Table 1).

A duplicate check of all collections resulted in 1 set of collections, Kanalku Lake (2007, 2010, and 2013), having abnormally large numbers of duplicate genotypes. This population is thought to have undergone severe genetic bottlenecks (Steve Heinl, Fishery Biologist IV, ADF&G, Ketchikan, personal communication); therefore, alleles are nearly fixed for most SNP loci, giving it a high rate of false positives (n = 116 across all 3 collections). In the duplicate check, a single fish from a Kanalku Lake collection could share 98% of genotypes with several other fish, not only from the same year but across years as well (data not shown). For these reasons, the Kanalku Lake collections were removed from duplicate check analyses, and all fish were retained in the baseline.

After removing Kanalku Lake fish from the duplicate test, 158 fish identified in the SEAK sockeye salmon baseline collections had greater than 95% shared genotypes spread across 83 collections. The percentage of fish from a collection with duplicate genotypes ranged from 0% to 50% with an average of 3% of individuals per collection. The 2003 Brown Bear Creek collection had a total of

34 samples, of which 17 were identified as duplicate. Given the placement of these samples on extraction plates and genotyping chips, we determined these samples were duplicated in the field (2 samples were taken per fish). No fish with identical genotypes were detected in 283 of the 366 baseline collections (77%).

Baseline development

Hardy-Weinberg expectations

After adjusting for multiple tests, 1 collection (Hackett River 2009) deviated from HWE according to Fisher's summary probability over diploid loci and was removed from the baseline ($P < 0.01$; Table 1). In addition, 6 collections had a probability distribution among loci indicative of nonconformance to HWE (Waples 2014). Of these 6 collections, 3 were dropped from further analysis (Sustut River 2006, Baker River 1996, and Cedar River 1994), and 3 others were temporally collected and retained to test for pooling. Examination of F_{IS} values showed positive values for loci deviating from HWE for Hackett River, Sustut River, Baker River, and Cedar River, indicating an excess of homozygotes for each collection.

A single nuclear marker (*One_c3-98*) deviated from HWE after adjusting for multiple tests and was removed from further analysis, leaving 95 loci (Table 3). Examination of F_{IS} values showed extremely negative values for populations deviating from HWE for this locus, indicating an excess of heterozygotes.

Pooling collections into populations

Of the 29,839 samples making up 366 collections that were genotyped, the final baseline consisted of 238 populations from a total of 28,609 samples (Table 1). After pooling, the 3 temporal collections identified above (in *Hardy-Weinberg expectations*) conformed to HWE and were retained in the baseline. Fifteen populations had less than the desired minimum sample size of 35 after pooling and were removed from the baseline, as these populations did not meet our criteria for estimating allele frequencies. The goal of representing populations with at least 95 samples was met for 55% of the populations.

After pooling, no populations deviated from HWE according to Fisher's summary probability over diploid loci. However, the pooled collections for Verrett River, Mill Creek, and Takwahoni (Table 1) had probability distributions among loci indicative of nonconformance to HWE (Waples 2014) even though their overall *p*-values across loci were greater than 0.05. Each of these pooled sets of collections were split into single collections and retested for HWE conformance if the individual sample sizes were sufficient ($n > 35$). The individual samples sizes for each of the 2 collections for Verrett River were too small to retain in the baseline and were dropped from further analysis. The 2 Mill Creek collections had sufficient sample sizes and conformed to HWE so they were each retained in the baseline as separate populations. The 2011 Takwahoni collection did not conform to HWE and was dropped from the baseline; however, the 2009 Takwahoni collection conformed to HWE and had sufficient samples sizes, and thus was retained.

Linkage disequilibrium

The original testing of this baseline (data unpublished) found 2 SNP pairs were linked in more than half of all populations (*One_GPDH-201* & *One_GPDH2-187* and *MHC2_190* & *One_MHC_251*). This pattern of linkage has been documented in other regions of Alaska for these 2 markers (Dann et al. 2012a). Following the protocol set in Dann et al. (2012a) we dropped the

following markers from further analysis: *One_GPDH-201*and *One_MHC_251*. We also combined the 3 mitochondrial SNPs into a single composite locus (*One_CO1*.*One_Cytb_17*.*One_Cytb_26*), leaving a total of 91 SNP loci.

Analysis of genetic structure

The neighbor-joining tree of pairwise F_{ST} showed relationships among populations that provide insights into potential reporting groups for MSA (Figure 6). In general, genetic variation was distributed hierarchically among regions and within regions among nursery lakes. However, some population groupings were defined more by life history and habitat usage than by geographic distance. Examples included the separation of lake-type (e.g., lake-type populations in the Taku River) and river-type (e.g., mainstem populations in the Taku and Stikine rivers) sockeye salmon in the same system (Figure 6). High genetic diversity was also found in island populations (such as those near Clarence and Chatham straits; Table 1; Figures 4 and 6) when compared to populations in mainland areas (e.g., Lynn Canal and Glacier Bay populations; Table 1; Figures 4 and 6).

Baseline evaluation for MSA

Self-assignment likelihood profiles

A matrix of the overall self-assignment probability of individuals to a reporting group (likelihood profile) indicates that most groups are highly identifiable with minimal evidence of directional biases (Figure 7). Overall self-assignment probabilities of individuals back to their group averaged 0.90 and ranged from 0.73 to 0.99. The *Stikine/Taku Mainstem* group had the lowest self-assignment probability; however, the majority of the misallocation was not to a single group, but rather spread across several reporting groups.

100% proof tests

All 130 of the 100% proof tests (10 replicates for each of the 13 reporting groups tested) met our goal of 90% correct allocation (Appendices A–C). For the Northern Boundary Districts 106 and 108 groups, correct allocations in the proof tests averaged 97.4% (*Alaska*), 99.5% (*Nass*), 98.5% (*Skeena*), 98.7% (*Stikine/Taku Mainstem*), and 98.1% (*Other*) across replicates (Appendix A). The correct allocations for the Transboundary Districts 106 and 108 groups averaged 98.5% (*Stikine/Taku Mainstem*), 99.5% (*Tahltan*), and 96.5% (*Other*) across replicates (Appendix B). The correct allocations for the Transboundary District 111 groups averaged 99.2% (*Speel*), 98.3% (*Stikine/Taku Mainstem*), 99.0% (*Taku Lakes*), 99.3% (*Tatsamenie*), and 96.6% (*Other*) across replicates (Appendix C).

DISCUSSION

This report describes the most comprehensive baseline to date for sockeye salmon in SEAK and was specifically designed for use in MSA of SEAK fisheries for PST and domestic applications. We have increased the total number of populations, collection sizes, and markers compared to previous baselines in order to better characterize sockeye salmon genetic diversity and provide precise, accurate, estimates of stock composition.

GENETIC POPULATION STRUCTURE

The patterns of genetic differentiation among populations of SEAK sockeye salmon revealed by this baseline were similar to those observed in previous studies (e.g., Guthrie et al. 1994; Beacham

et al. 2005; Kondzela and Gharrett 2007; Habicht et al. 2010). In general, genetic variation was distributed among regions and within regions among nursery lakes. In addition, there were clear patterns of similarities between river-type life history types both within and among drainages. We observed high levels of divergence between lake-type populations in small island lake systems and river-type populations above obstacles to migration.

In general, river-type populations were more similar to each other both within and across drainages than to nearby lake-type populations. For example, Chilkat river-type sockeye salmon (populations 65–67; Table 1; Figure 4) clustered with Taku and Stikine river-type fish, and were more similar to these populations than to the Chilkat Lake populations (populations 68 and 69; Table 1; Figure 4) despite their proximity. This is comparable to what has been observed in other sockeye salmon populations in SEAK (Guthrie et al. 1994; Habicht et al. 2010) and across their range (Gustafson and Winans 1999; Beacham et al. 2005; Dann et al. 2012a). Wood et al. (2008) hypothesized that river-type populations tend to colonize new drainages, whereas lake-type populations evolve recurrently from these colonizations. The higher levels of migration among river-type populations leads to higher genetic variation within river-type populations compared to lake-type populations, but smaller genetic variation among river-type populations. Two exceptions to this were the Nahlin (population 119) and Hackett (population 118) rivers (Table 1; Figure 4), tributaries of the Taku River. Sockeye salmon returning to these systems have further to travel than those returning to the Taku River mainstem; they navigate through swift water canyons and elevation gains up to 3,000 feet. These factors may act as obstacles to migration, leading to higher levels of genetic distinction, as observed in the F_{ST} tree. These results are in concordance with similar patterns of genetic structure above and below obstacles observed in sockeye salmon spawning in Bristol Bay (Habicht et al. 2004).

Island populations of sockeye salmon in SEAK typically display lake-type life history traits. Lake-type sockeye salmon tend to precisely home to their natal lake, and throughout their range the natal lake tends to be the primary unit of differentiation (Grant et al. 1980; Utter et al. 1984; Wilmot and Burger 1985; Wood et al. 1994). Habicht et al. (2010) and Guthrie et al. (1994) noted similar patterns in SEAK, along with several outlier populations that clustered outside of the majority of populations in their regions. The pattern of divergence observed is reflective of many small populations separated by salt water, resulting in low migration and smaller effective population sizes more influenced by the effects of genetic drift (Hedrick 2005). This influence is most evident in the Kanalku Lake population (population 110; Table 1; Figure 4) that exhibited a severe lack of allelic richness and a high level of differentiation from all other populations in this dataset (Figure 6). These are signals of a population bottleneck and were likely triggered by the small number of sockeye salmon that are able to reach the Kanalku Lake spawning grounds and a long history of subsistence fishery exploitation (Vinzant and Heinl 2015). Other populations also exhibited large differences between neighboring populations (but nowhere near that of the Kanalku population); however, those patterns were similar to those observed in other sockeye salmon populations throughout their range (Winans et al. 1996; Varnavskaya et al. 1994; Wood 1995; Beacham 2004b; Habicht et al. 2004; Dann et al. 2013). For example, even though Redoubt Lake (population 86) and Salmon Lake (population 87) are located very near each other on Baranof Island, Salmon Lake is more similar to Ford Arm Lake (population 84) and Ford Arm Creek (population 85) than to other nearby populations (Table 1; Figures 4 and 6). In addition, the magnitude of differences observed between SEAK island populations is consistent with rates expected for populations established from a small number of individuals, due to founder effects (Nei 1987).

Analysis of genetic diversity and differentiation between populations in major river systems in SEAK may also be reflective of ancient connections between drainages in this region. Similar to Guthrie et al. (1994), this study indicated that sockeye salmon lake-type populations in the Taku and Stikine river drainages were both distinct from their respective river-type populations and showed a possible shared lineage. A conclusion of shared ancestry was also previously identified between these drainages for Chinook salmon (*O. tshawytscha*; Guthrie and Wilmot 2004). In addition, similarities were observed between populations in the Alsek River drainage and upper Copper River drainage, especially when compared to nearby Yakutat forelands populations. Genetic relationships between these populations have been documented previously in Ackerman et al. (2011) where it was hypothesized that these populations likely came in contact during the McConnell-McCauley Glaciation (Smith et al. 2001).

BASELINE PERFORMANCE

Tests of the SEAK sockeye salmon baseline for estimating mixed stock compositions demonstrated its effectiveness for producing precise, accurate estimates of stock composition for PST applications.

There is a high level of differentiation among sockeye salmon populations with this baseline. This differentiation has resulted in very few misallocations among reporting groups in either the Transboundary or Northern Boundary group testing (Appendices A–C). The *Stikine/Taku Mainstem* group has less genetic diversity among populations than alternative reporting groups, although it still met the 90% correct allocation standards. In this case, correct allocation to a population may have been lower, but misallocations went to other populations within the *Stikine/Taku Mainstem* group. This is further evidence of the effectiveness of this baseline for MSA applications.

It is important to note that baseline 100% proof tests only provide 1 measure of MSA performance and may indicate either better or worse performance than would be expected in mixtures containing multiple reporting groups. The 100% proof tests may show better performance than proof tests with multiple reporting groups because the Bayesian algorithm is informed by the composition of the mixture, where the likelihood of *BAYES* assigning a fish to the dominant reporting group increases during the analysis. On the other hand, 100% proof tests may show poorer performance than proof tests with multiple reporting groups because all misallocations are detected in 100% proof tests, but some misallocations go undetected when multiple reporting groups are present in a mixture. Fishery scenario tests could be performed in the future to provide additional insight into whether the 100% proof tests over- or underestimate correct proportions. In these tests, individuals from each reporting group would be removed from the baseline in compositions that may be expected to show up in TBR fisheries and tested against the reduced baseline. Although these tests are outside the scope of this report, these tests would provide an additional metric for understanding the power of the baseline.

This baseline is capable of providing accurate and precise estimates of stock composition estimates in SEAK fisheries for PST applications. Further testing of the baseline is likely to yield additional reporting groups suitable for MSA in multiple fisheries.

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TABLES AND FIGURES

Table 1.–Tissue collections used to describe the genetic structure of sockeye salmon spanning from Prince William Sound to Washington State, including finest-scale reporting groups, drainage or area where each tissue collection is located, collection (Col) and population (Pop) numbers, the years collected, and the numbers of individuals included in baseline analyses. Numbers of individuals include the number of samples initially genotyped for the set of 96 SNPs (Initial), removed for missing loci (Miss), removed for duplicate genotypes (Dup), and the number of individuals incorporated into the baseline (Final). Population numbers correspond to Figures 2–5.

						No. of Individuals			
Reporting Groups	Drainage/Area	Location	Col	Pop	Year Collected	Initial	Miss	Dup	Final
Alaska	Prince William Sound	Bainbridge Lake	1	1	2010	95	0	0	95
		Coghill Lake	2	2	1991	96	1	0	95
			3	2	1992	96	3	0	93
			4	2	1992	96	1	0	95
			5	2	2010	95	0	0	95
		Eshamy Creek	6	3	2008	95	0	0	95
		Eshamy Lake	7	3	1991	96	6	0	90
		Main Bay	8	4	1991	96	0	0	96
		Miners Lake	9	5	1991	96	0	0	96
			10	5	2009	95	0	0	95
	Copper River	Eyak Lake - Middle Arm	11	6	2007	95	0	0	95
		Eyak Lake - Beaches	12	7	2007	95	7	1	87
		Eyak Lake - Hatchery Creek	13	8	2010	95	0	0	95
		Mendeltna Creek	14	9	2008	95	0	1	94
			15	9	2009	94	0	0	94
		Swede Lake	16	10	2008	95	0	0	95
		Gulkana River - Fish Creek	17	11	2008	95	0	0	95
		Gulkana River - East Fork	18	12	2008	75	0	0	75
		Paxson Lake	19	13	2009	77	0	2	75
		Mentasta Lake	20	14	2008	95	0	0	95
		Tanada Creek	21	15	2005	95	0	1	94
		Tanada Lake - Outlet	22	16	2009	95	0	0	95
		Tanada Lake - Beach	23	17	2009	95	2	0	93
		Klutina River	24	18	2008	95	0	0	95
		Klutina Lake	25	19	2008	44	0	0	44
			26	19	2009	51	0	0	51
		Klutina River - Bear Hole	27	20	2008	95	1	0	94

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Table 1.–Page 2 of 13.

Reporting Groups	Drainage/Area	Location	Col	Pop	Year Collected	No. of Individuals			
						Initial	Miss	Dup	Final
Alaska (cont.)	Copper River (cont.)	Banana Lake	28	21	2008	82	2	0	80
		St. Anne Creek	29	22	2005	95	0	1	94
			30	22	2008	95	0	3	92
		Mahlo River	31	23	2008	95	0	1	94
		Tonsina Lake	32	24	2009	95	0	1	94
		Long Lake - Weir	33	25	2005	95	0	0	95
		Tebay River	34	26	2008	94	1	0	93
		Steamboat Lake	35	27	2008	95	0	0	95
		Bremner - Salmon Creek	36	28	2008	95	2	0	93
		Clear Creek	37	29	2007	95	8	0	87
		McKinley Lake	38	30	1991	95	0	0	95
			39	31	2008	95	0	0	95
		McKinley Lake - Upper	40	32	2007	95	0	0	95
		McKinley Lake - Salmon Creek	41	33	2007	95	2	0	93
		Martin Lake	42	34	2007	95	2	0	93
			43	34	2008	95	1	0	94
		Martin River Slough	44	35	2008	95	0	0	95
		Tokun Lake	45	36	2008	95	0	0	95
			46	36	2009	94	0	0	94
		Bering Lake	47	37	1991	95	0	0	95
		Kushtaka Lake	48	38	2007	95	1	0	94
			49	38	2008	95	0	0	95
	Yakutat	Mountain Stream	50	39	2007	159	0	0	159
		Situk Lake	51	40	2013	195	3	2	190
		Old Situk River	52	41	2007	163	0	0	163
		Lost/Tahwah Rivers	53	42	2003	94	1	0	93
		Ahrnklin River	54	43	2007	90	0	0	90
		Dangerous River	55	44	2009	95	0	0	95
		Akwe River	56	45	2009	95	0	0	95
		East Alsek River	57	46	2003	95	1	0	94

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Table 1.–Page 3 of 13.

Reporting Groups		Location	Col	Pop	Year Collected	No. of Individuals Initial	Miss	Dup	Final
Other	Alsek River	Datlasaka Creek	58	47	2012	95	0	0	95
		Goat Creek	59	48	2007	12	0	0	12
			60	48	2012	45	0	1	44
		Kwatini Creek	61	49	2011	65	0	0	65
		Border Slough	62	50	2007	50	0	0	50
			63	50	2008	21	0	0	21
		Border Slough	64	51	2009	32	0	0	32
			65	51	2011	39	1	0	38
		Tweedsmuir River	66	52	2007	48	0	0	48
			67	53	2009	47	0	1	46
		Vern Ritchie	68	54	2009	94	0	1	93
			69	54	2010	22	1	0	21
		Neskataheen Lake	70	55	2007	198	3	0	195
		Klukshu River	71	56	2006	95	0	0	95
			72	57	2007	95	0	1	94
		Klukshu River[1]	73	–	2008	7	0	0	0
		Kudwat Creek	74	58	2009	20	0	0	20
			75	58	2010	50	0	0	50
			76	58	2011	31	0	1	30
		Bridge River	77	59	2011	30	0	0	30
			78	59	2012	75	0	0	75
		Stinky Creek	79	60	2011	40	0	0	40
		Upper Tatshenshini River	80	61	2003	95	0	0	95
		Little Tatshenshini Lake	81	62	2001	25	0	1	24
			82	62	2003	41	0	0	41
		Blanchard River	83	63	2007	95	6	0	89
		Blanchard River[1]	84	–	2008	9	0	0	0
			85	64	2009	62	0	0	62
Alaska (cont.)	Chilkat River	Bear Flats	86	65	2007	95	0	0	95
		Mule Meadows	87	66	2003	95	0	0	95

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Table 1.–Page 4 of 13.

Reporting Groups		Location	Col	Pop	Year Collected	No. of Individuals Initial	Miss	Dup	Final
Alaska (cont.)	Chilkat River (cont.)	Mule Meadows	88	66	2007	95	0	0	95
		Mosquito Lake	89	67	2007	95	0	0	95
		Chilkat Lake	90	68	2007	95	0	0	95
			91	68	2007	95	0	0	95
			92	69	2013	190	1	0	189
	Chilkoot River	Chilkoot River	93	70	2003	164	2	3	159
		Chilkoot Lake - Bear Creek	94	71	2007	234	1	0	233
		Chilkoot Lake - Beach	95	72	2007	252	0	1	251
	Glacier Bay/Icy Strait	Vivid Lake	96	73	1993	48	0	0	48
		Seclusion Lake	97	74	2014	49	0	0	49
		Seclusion Lake - Inlet Creek	98	74	2014	68	0	0	68
		North Berg Bay Inlet	99	75	1991	54	1	0	53
			100	76	1992	100	0	0	100
		Bartlett River	101	77	2013	73	3	1	69
		Neva Lake	102	78	2008	94	0	0	94
			103	79	2009	95	0	0	95
			104	79	2013	165	1	4	160
	Outer Coast Islands	Hoktaheen Lake - Inlet	105	80	2004	50	0	3	47
		Hoktaheen Lake - Outlet	106	81	2004	50	1	0	49
		Hoktaheen Lake - Marine	107	82	2014	48	1	0	47
		Klag Bay Stream	108	83	2009	200	0	0	200
		Ford Arm Lake	109	84	2004	211	0	4	207
		Ford Arm Creek	110	85	2013	202	2	1	199
		Redoubt Lake	111	86	2013	200	0	0	200
		Salmon Lake	112	87	2007	91	0	0	91
			113	87	2008	95	1	0	94
		Benzeman Lake	114	88	1991	47	0	0	47
			115	88	1993	48	0	0	48
		Redfish Lake	116	89	1993	96	0	2	94

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Table 1.–Page 5 of 13.

Reporting Groups		Location	Col	Pop	Year Collected	No. of Individuals Initial	Miss	Dup	Final
Alaska (cont.)	Outer Coast Islands (cont.)	Falls Lake	117	90	2003	95	0	0	95
			118	90	2010	95	0	0	95
		Kutlaku Lake	119	91	2003	95	0	0	95
			120	92	2012	78	0	0	78
			121	93	2013	50	0	0	50
	Lynn Canal	Lace River	122	94	2013	68	5	0	63
		Berners Bay	123	95	2003	95	0	0	95
			124	95	2013	70	0	0	70
		Antler-Gilkey River	125	96	2013	53	0	0	53
		Windfall Lake	126	97	2003	48	0	0	48
			127	97	2007	95	0	1	94
		Steep Creek	128	98	2003	95	4	0	91
		Lake Creek - Auke Creek Weir	129	99	2013	200	0	0	200
		Lake Creek	130	99	2014	120	2	0	118
		Crescent Lake	131	100	2003	198	0	4	194
Speel	Speel Arm	Speel Lake	132	101	2003	95	0	0	95
		Snettisham - Speel Stock	133	102	2006	95	0	0	95
			134	102	2007	95	0	0	95
			135	103	2013	146	0	0	146
Alaska (cont.)	Chatham Strait	Pavlof Lake	136	104	2012	91	0	0	91
			137	104	2013	85	2	0	83
		Kook Lake - Early[1]	138	–	2010	4	0	0	0
		Kook Lake - Early	139	105	2012	84	0	0	84
			140	105	2013	64	0	0	64
		Kook Lake - Late	141	106	2007	95	1	0	94
			142	106	2010	37	0	0	37
			143	106	2012	64	0	1	63
		Sitkoh Lake	144	107	2003	95	3	0	92
			145	107	2011	139	3	0	136
			146	107	2012	124	1	0	123
		Lake Eva	147	108	2012	115	0	0	115

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Table 1.–Page 6 of 13.

Reporting Groups		Location	Col	Pop	Year Collected	No. of Individuals Initial	Miss	Dup	Final
Alaska (cont.)	Chatham Strait (cont.)	Hasselborg Lake	148	109	2012	95	0	0	95
			149	109	2013	115	0	1	114
		Kanalku Lake[2]	150	110	2007	95	0	0	95
			151	110	2010	95	1	0	94
			152	110	2013	130	0	0	130
Taku Lakes	Taku River	Kuthai Lake	153	111	2006	171	0	0	171
		King Salmon Lake	154	112	2010	151	2	0	149
			155	112	2011	65	0	0	65
		Little Trapper Lake	156	113	1990	95	1	0	94
			157	113	2006	146	3	0	143
		Little Tatsamenie Lake	158	114	2011	59	0	0	59
Tatsamenie		Tatsamenie Lake	159	115	2005	95	1	0	94
			160	115	2006	196	2	0	194
Tahltan	Stikine River	Little Tahltan Lake	161	116	1990	95	0	0	95
			162	117	2006	196	0	0	196
Stikine/Taku Mainstem	Taku River (cont.)	Hackett River	163	118	2008	56	4	0	52
		Hackett River[3]	164	–	2009	95	0	0	0
		Nahlin River	165	119	2003	50	0	0	50
			166	119	2007	34	0	0	34
			167	119	2012	95	0	0	95
		Taku River	168	120	2007	95	0	0	95
		Takwahoni/Sinwa Slough	169	121	2009	69	0	2	67
		Takwahoni/Sinwa Slough[3]	170	–	2011	41	0	0	0
		Sustahine Slough	171	122	2008	95	1	1	93
			172	122	2009	95	2	1	92
		Chunk Slough	173	123	2009	34	0	0	34
		Tuskwa/Chunk Slough	174	123	2008	95	0	0	95
		Tuskwa Slough	175	123	2008	24	0	0	24
			176	123	2008	19	1	1	17
			177	123	2009	92	0	1	91

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Table 2.–Page 7 of 13.

Reporting Groups		Location	Col	Pop	Year Collected	No. of Individuals Initial	Miss	Dup	Final
Stikine/Taku Mainstem (cont.)	Taku River (cont.)	Bear Slough	178	123	2009	95	0	0	95
		Yellow Bluff Slough	179	124	2008	34	0	0	34
			180	124	2010	31	1	0	30
			181	124	2011	17	0	0	17
		Tulsequah River	182	125	2007	15	1	0	14
			183	125	2008	53	0	0	53
			184	125	2009	95	4	2	89
		Fish Creek	185	126	2009	74	4	0	70
			186	126	2010	95	2	3	90
		Yehring Creek	187	127	2007	83	2	1	80
			188	127	2009	95	0	4	91
	Stikine River	Chutine River	189	128	2008	95	1	0	94
		Chutine Lake	190	129	2009	65	0	1	64
			191	129	2011	160	0	0	160
		Andy Smith slough	192	130	2007	10	0	0	10
			193	130	2009	18	0	0	18
		Fowler Slough	194	130	2007	11	0	0	11
			195	130	2008	8	0	0	8
			196	130	2009	8	1	0	7
		Porcupine River	197	131	2007	36	0	0	36
		Porcupine River[1]	198	–	2008	3	0	0	0
		Porcupine River[1]	199	–	2009	3	0	0	0
		Porcupine River[1]	200	–	2010	23	0	0	0
			201	131	2011	39	0	1	38
		Devil's Elbow	202	132	2007	55	0	0	55
			203	132	2008	95	2	0	93
			204	133	2009	53	0	0	53
		Scud River	205	134	2007	90	0	1	89
			206	134	2008	48	2	1	45
			207	134	2009	60	0	2	58

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Table 2.–Page 8 of 13.

Reporting Groups		Location	Col	Pop	Year Collected	No. of Individuals Initial	Miss	Dup	Final
Stikine/Taku Mainstem (cont.)	Stikine River (cont.)	Iskut River	208	135	1985	30	1	0	29
			209	135	1986	24	0	0	24
			210	135	2002	31	10	1	20
			211	135	2006	47	0	0	47
			212	135	2008	22	0	0	22
			213	135	2009	11	0	0	11
		Craigson Slough	214	136	2007	43	1	0	42
		Zappa Creek[1]	215	–	2008	7	0	0	0
		Craig River	216	137	2006	12	0	0	12
			217	137	2007	5	0	0	5
			218	137	2008	21	0	0	21
		Bronson Slough	219	138	2008	63	1	0	62
			220	138	2009	16	0	0	16
		Verrett River[3]	221	–	2010	24	0	0	0
		Verrett River[3]	222	–	2011	43	1	1	0
		Shakes Slough Creek	223	139	2006	41	0	0	41
			224	139	2007	13	0	0	13
			225	139	2009	13	0	0	13
		Christina Lake[1]	226	–	2010	14	0	0	0
		Christina Lake	227	140	2011	36	0	0	36
			228	140	2012	34	0	0	34
Alaska (cont.)	N. Clarence Strait	Petersburg Lake	229	141	2004	95	0	0	95
		Kah Sheets Lake	230	142	2003	96	0	0	96
		Mill Creek Weir - Early	231	143	2007	95	1	0	94
		Mill Creek Weir - Late	232	144	2007	95	0	0	95
		Kunk Lake	233	145	2003	96	0	0	96
		Thoms Lake	234	146	2004	95	28	1	66
			235	146	2014	27	0	0	27
		Red Bay Lake	236	147	2004	95	0	0	95
		Salmon Bay Lake	237	148	2004	95	0	0	95

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Table 2.–Page 9 of 13.

Reporting Groups		Location	Col	Pop	Year Collected	No. of Individuals Initial	Miss	Dup	Final
Alaska (cont.)	N. Clarence Strait (cont.)	Salmon Bay Lake	238	148	2007	75	0	0	75
		Shipley Lake	239	149	2003	95	0	1	94
		Sarkar Lakes	240	150	2000	45	1	0	44
			241	150	2005	50	3	0	47
		Sweetwater Lake	242	151	2003	47	0	0	47
			243	151	2007	95	0	0	95
		Luck Lake	244	152	2004	95	0	1	94
		Big Lake	245	153	2010	68	1	0	67
		Big Lake[1]	246	–	2011	25	0	2	0
			247	153	2014	95	0	1	94
		McDonald Lake	248	154	1992	96	10	0	86
			249	154	2003	140	3	5	132
			250	154	2007	95	7	0	88
			251	154	2013	70	7	0	63
	S. Clarence Strait	Karta River	252	155	1992	94	0	0	94
		McGilvery Creek	253	155	2003	96	0	0	96
			254	155	2004	95	0	0	95
			255	155	2016	190	1	2	187
		Unuk River - Gene's Lake	256	156	2007	95	0	0	95
			257	157	2008	70	0	1	69
		Helm Lake	258	158	2005	95	1	0	94
		Heckman Lake	259	159	2004	95	1	0	94
			260	159	2007	95	0	0	95
		Mahoney Creek	261	160	2003	64	0	5	59
			262	160	2007	95	0	0	95
		Kegan Lake	263	161	2004	95	0	0	95
		Fillmore Lake	264	162	2005	55	0	3	52
	W. Prince of Wales	Klawock Lk - Three Mile Cr.	265	163	2004	95	3	0	92
			266	163	2010	95	6	0	89
		Klawock Lk - Half Mile Cr.	267	164	2008	52	10	0	42

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Table 2.–Page 10 of 13.

Reporting Groups		Location	Col	Pop	Year Collected	No. of Individuals Initial	Miss	Dup	Final
Alaska (cont.)	W. Prince of Wales (cont.)	Klawock - Inlet Creek	268	164	2003	95	19	1	75
			269	164	2008	95	0	0	95
		Hetta Lake	270	165	2003	94	2	0	92
			271	165	2008	95	0	0	95
		Hetta Creek - Late	272	165	2009	95	1	0	94
		Hetta Creek - Middle	273	166	2009	95	0	0	95
		Hetta Creek - Early	274	167	2010	95	0	0	95
		Eek Creek	275	168	2004	32	1	0	31
			276	168	2007	20	0	1	19
		Klakas Lake	277	169	2004	95	0	0	95
		Essowah Lake	278	170	2004	96	1	0	95
	Southern SEAK	Hugh Smith Lake	279	171	1992	95	0	0	95
			280	171	2013	60	0	0	60
		Bushmann Creek	281	172	2004	151	0	0	151
		Cobb Creek	282	173	2007	101	2	0	99
Nass	Nass River	Kwinageese River	284	174	2001	48	0	0	48
			283	174	2012	30	2	0	28
		Bowser Lake	285	175	2001	95	1	0	94
		Bonney Creek	286	176	2001	95	0	1	94
			287	176	2012	70	0	0	70
		Brown Bear Creek[1]	288	–	1997	41	2	0	0
		Brown Bear Creek[1]	289	–	2003	34	0	17	0
		Damdochax Creek	290	177	2001	95	1	1	93
		Meziadin Lake	291	178	2001	95	0	4	91
			292	178	2006	95	0	0	95
		Hanna Creek	293	179	2006	95	0	2	93
		Tintina Creek	294	180	2006	95	0	1	94
		Gingit Creek	295	181	1997	95	1	0	94
Skeena	Skeena River	Alastair Lake	296	182	1987	34	1	0	33
			297	182	2006	86	0	1	85

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Table 2.–Page 11 of 13.

Reporting Groups		Location	Col	Pop	Year Collected	No. of Individuals Initial	Miss	Dup	Final
Skeena (cont.)	Skeena River (cont.)	Lakelelse Lake	298	183	2006	95	0	2	93
		Sustut River[3]	299	–	2006	95	0	0	0
		Sustut River	300	184	2001	81	2	0	79
		Salix Creek	301	185	1987	45	1	1	43
			302	185	1988	54	3	0	51
		Motase Lake	303	186	1987	49	0	2	47
		Slamgeesh River	304	187	2006	95	0	0	95
		Upper Babine River	305	188	2006	95	0	0	95
		Four Mile Creek	306	189	2006	85	0	0	85
		Pinkut Creek	307	190	1994	95	2	0	93
			308	190	2006	95	17	0	78
		Grizzly Creek	309	191	1987	77	0	1	76
		Pierre Creek[1]	310	–	1988	10	1	0	0
		Pierre Creek	311	192	2006	95	0	0	95
		Fulton River	312	193	2006	95	0	0	95
		Morrison River	313	194	2007	95	0	3	92
		Lower Tahlo River[1]	314	–	1988	10	0	0	0
		Lower Tahlo River	315	195	1994	85	7	0	78
		Tahlo Creek	316	196	2007	95	0	0	95
		McDonell Lake	317	197	2002	73	1	4	68
			318	197	2006	64	1	0	63
		Kitsumkalum Lake	319	198	2006	56	0	0	56
			320	199	2012	95	1	0	94
		Kitwanga River	321	200	2012	93	1	0	92
		Stephens Creek	322	201	2001	95	0	0	95
		Nangeese River[1]	323	–	2002	33	0	1	0
		Nangeese River	324	202	2006	44	2	2	40
Nass (cont.)		Kispiox River	325	203	2002	57	0	4	53
Skeena (cont.)		Swan Lake	326	204	2006	95	1	1	93
		Nanika River	327	205	1988	20	0	0	20

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Table 1.–Page 12 of 13.

Reporting Groups		Location	Col	Pop	Year Collected	No. of Individuals Initial	Miss	Dup	Final
Skeena (cont.)	Skeena River (cont.)	Nanika River	328	205	2007	95	0	1	94
Other	Fraser River	Kynock Creek	329	206	1997	95	1	0	94
		Tachie River	330	207	2001	95	1	0	94
		Stellako River	331	208	2007	94	0	0	94
		Fraser Lake	332	209	1996	85	0	0	85
		Mitchell River	333	210	2001	95	0	1	94
		Lower Horsefly River	334	211	2001	95	8	0	87
			335	211	2001	95	3	0	92
			336	211	2007	95	0	0	95
		Nahatlatch River	337	212	2002	93	1	0	92
		Cultus Lake	338	213	2002	95	3	1	91
		Chilliwack Lake	339	214	2004	95	3	2	90
		Chilko Lake	340	215	2001	96	8	1	87
		Raft River	341	216	2001	95	11	0	84
		Adams River - Late	342	217	2007	95	0	0	95
			343	217	2002	95	3	0	92
		Middle Shuswap River	344	218	2002	93	0	2	91
		Scotch River	345	219	2000	95	1	3	91
		Gates Creek	346	220	2009	95	5	0	90
		Birkenhead River	347	221	2007	95	5	0	90
		Weaver Creek	348	222	2001	95	6	0	89
		Harrison River	349	223	2007	95	0	0	95
		North Thompson River	350	224	2005	95	0	0	95
	Queen Charlotte Island	Naden River	351	225	1995	95	0	0	95
		Yakoun Lake	352	226	1993	75	5	0	70
	British Columbia	Kitimat River	353	227	2010	95	2	0	93
		Bloomfield Lake	354	228	2005	95	1	0	94
		Tankeeah River	355	229	2003	47	0	0	47
			356	230	2005	48	0	1	47
		Amback Creek	357	231	2004	95	4	0	91
		Kitlope Lake	358	232	2006	95	0	0	95

-continued-

Table 1.–Page 13 of 13.

Reporting Groups		Location	Col	Pop	Year Collected	No. of Individuals Initial	Miss	Dup	Final
Other (cont.)	Vancouver Island	Great Central Lake	359	233	2002	95	0	0	95
		Quatse River	360	234	2003	95	0	0	95
	Washington	Okanagan River	361	235	2002	95	0	0	95
		Lake Pleasant	362	236	1997	93	1	3	89
		Baker Lake[3]	363	–	1996	96	5	1	0
		Issaquah Creek	364	237	1996	95	12	1	82
		Cedar River[3]	365	–	1994	96	3	0	0
		Lake Wenatchee	366	238	1998	96	1	0	95
						29,839	393	158	28,609

[1] These collections were dropped from further analyses due to insufficient sample size.

[2] These collections did not undergo duplicate check.

[3] These collections failed to conform to Hardy-Weinberg expectations and were dropped from further analyses.

Table 2.–Reporting groups tested in this report and used for PST application by project. The finest-scale reporting groups correspond to those listed in Table 1 and used in Figures 2–6.

Fine-scale Reporting Groups	Reporting Groups Districts 106 and 108		Reporting Groups District 111
	Transboundary Rivers	Northern Boundary	TBR
Alaska	Other	Alaska	Other
Other	Other	Other	Other
Speel	Other	Other	Speel
Taku Lakes	Other	Other	Taku Lakes
Tatsamenie	Other	Other	Tatsamenie
Tahltan	Tahltan	All Stikine/Taku Mainstem	Other
Stikine/Taku Mainstem	Stikine/Taku Mainstem	All Stikine/Taku Mainstem	Stikine/Taku Mainstem
Nass	Other	Nass	Other
Skeena	Other	Skeena	Other

Table 3.–Source, observed heterozygosity (H_O), F_{IS}, and F_{ST} for the 96 single nucleotide polymorphism (SNP) markers used to analyze the population genetic structure of sockeye salmon in the Southeast Alaska region.

SNP marker	Source[1]	H_O	F_{IS}	F_{ST}
One_ACBP-79	A	0.429	0.019	0.119
One_agt-132	B	0.407	0.004	0.172
One_aldB-152	C	0.336	0.004	0.097
One_apoe-83	B	0.417	-0.008	0.188
One_c3-98[2]	B	–	–	–
One_CD9-269	B	0.334	0.008	0.092
One_cetn1-167	B	0.373	0.009	0.109
One_CFP1	D	0.330	0.007	0.164
One_cin-177	C	0.426	0.009	0.122
One_CO1[3]	A	–	–	0.280
One_ctgf-301	A	0.072	0.009	0.065
One_Cytb_17[3]	A	–	–	0.406
One_Cytb_26[3]	A	–	–	0.395
One_E2-65	A	0.231	-0.004	0.140
One_gdh-212	C	0.455	0.002	0.083
One_GHII-2165	A	0.403	0.005	0.171
One_ghsR-66	C	0.341	0.002	0.131
One_GPDH-201[4]	A	0.403	0.016	0.106
One_GPDH2-187	A	0.319	0.010	0.121
One_GPH-414	A	0.323	0.024	0.101
One_HGFA-49	A	0.291	-0.007	0.136
One_HpaI-71	A	0.308	0.007	0.147
One_HpaI-99	A	0.420	-0.001	0.171
One_hsc71-220	A	0.262	0.011	0.202
One_Hsp47	D	0.386	-0.005	0.109
One_IL8r-362	A	0.109	-0.033	0.133
One_KCT1-453	B	0.186	0.003	0.092
One_KPNA-422	A	0.336	0.010	0.109
One_LEI-87	A	0.363	0.010	0.092
One_lpp1-44	B	0.375	0.012	0.143
One_metA-253	C	0.239	0.014	0.231
One_MHC2_190	A	0.308	0.020	0.335
One_MHC2_251[4]	A	0.339	0.010	0.276
One_Mkpro-129	C	0.399	0.011	0.162
One_ODC1-196	B	0.404	0.014	0.125
One_Ots208-234	C	0.368	-0.003	0.123
One_Ots213-181	A	0.352	0.001	0.138
One_p53-534	A	0.151	0.000	0.089
One_pax7-248	C	0.158	0.007	0.120
One_PIP	D	0.420	0.001	0.152
One_Prl2	A	0.451	0.009	0.103
One_rab1a-76	B	0.162	0.013	0.173
One_RAG1-103	A	0.083	-0.010	0.068
One_RAG3-93	A	0.218	0.001	0.161

-continued-

Table 3.–Page 2 of 3.

SNP marker	Source[1]	H_O	F_{IS}	F_{ST}
One_redd1-414	C	0.364	0.012	0.144
One_RFC2-102	A	0.336	0.008	0.191
One_RFC2-285	A	0.131	0.005	0.143
One_rpo2j-261	C	0.220	0.012	0.126
One_sast-211	C	0.143	0.007	0.072
One_spf30-207	C	0.200	-0.001	0.174
One_srp09-127	C	0.201	0.010	0.173
One_ssrd-135	C	0.428	0.011	0.146
One_STC-410	A	0.285	0.014	0.194
One_STR07	A	0.407	0.006	0.179
One_SUMO1-6	C	0.164	0.012	0.089
One_sys1-230	C	0.430	0.009	0.131
One_taf12-248	C	0.133	0.013	0.228
One_Tf_ex11-750	A	0.338	-0.004	0.119
One_Tf_in3-182	A	0.097	0.012	0.154
One_tshB-92	C	0.128	0.017	0.102
One_txnip-401	C	0.100	0.010	0.089
One_U1003-75	B	0.417	0.002	0.156
One_U1004-183	B	0.400	0.003	0.159
One_U1009-91	B	0.350	0.002	0.153
One_U1010-81	B	0.126	0.009	0.114
One_U1012-68	B	0.318	0.005	0.119
One_U1013-108	B	0.205	0.005	0.130
One_U1014-74	B	0.163	0.006	0.129
One_U1016-115	B	0.410	0.012	0.174
One_U1024-197	B	0.260	-0.005	0.118
One_U1101	B	0.304	0.001	0.154
One_U1103	B	0.097	0.016	0.095
One_U1105	B	0.206	0.010	0.123
One_U1201-492	B	0.417	0.001	0.161
One_U1202-1052	B	0.240	0.013	0.137
One_U1203-175	B	0.344	0.007	0.129
One_U1204-53	B	0.342	0.012	0.117
One_U1205-57	B	0.075	0.014	0.115
One_U1206-108	B	0.231	0.012	0.122
One_U1208-67	B	0.419	0.000	0.121
One_U1209-111	B	0.115	0.007	0.102
One_U1210-173	B	0.062	0.004	0.067
One_U1212-106	B	0.414	-0.002	0.161
One_U1214-107	B	0.225	0.002	0.191

-continued-

Table 3.–Page 3 of 3.

SNP marker	Source[1]	H_O	F_{IS}	F_{ST}
One_U1216-230	B	0.421	0.008	0.156
One_U301-92	A	0.232	0.004	0.147
One_U401-224	A	0.449	-0.012	0.126
One_U404-229	A	0.219	-0.002	0.111
One_U502-167	A	0.055	-0.001	0.186
One_U503-170	A	0.160	0.046	0.178
One_U504-141	A	0.336	0.007	0.153
One_vamp5-255	C	0.238	0.011	0.090
One_vatf-214	C	0.173	0.003	0.158
One_VIM-569	A	0.260	0.012	0.090
One_ZNF-61	A	0.269	0.016	0.084
One_Zp3b-49	A	0.338	0.006	0.219
One_CO1_Cytb17_26[3]		–	0.000	0.373
Overall		0.280	0.006	0.147

Note: Weir and Cockerham (1984) estimates of F_{ST} are also provided for the set of linked loci combined as composite phenotypes. Statistics for each marker are based on the 171 populations within the baseline.

Note: Overall summary statistics are estimates from the final marker set; overall H_O is the average across loci and overall F_{IS}, and F_{ST} are estimated following Weir and Cockerham.

[1] A = Gene Conservation Laboratory of ADF&G; B = International Program for Salmon Ecological Genetics at the University of Washington; C = Hagerman Genetics Laboratory of the Columbia River Inter-Tribal Fish Commission; and D = Molecular Genetics Laboratory at the Canadian Department of Fisheries and Oceans.

[2] These SNPs were dropped due to nonconformance of HWE.

[3] These SNPs were combined into haplotypes and treated together as a single locus: *One_CO1_Cytb17_26*.

[4] These SNPs were dropped due to linkage.

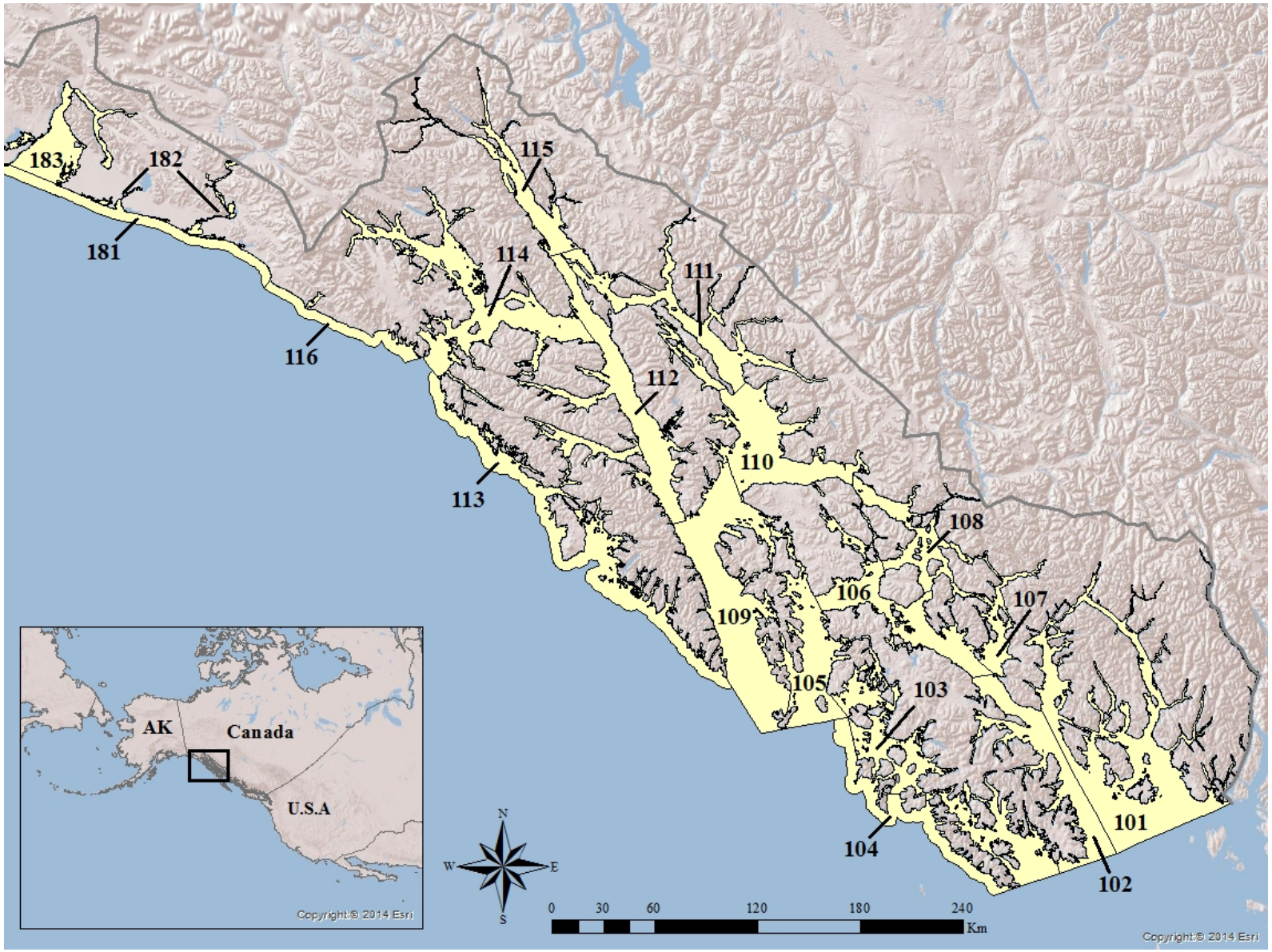

Figure 1.–Map of Southeast Alaska commercial fishing districts.

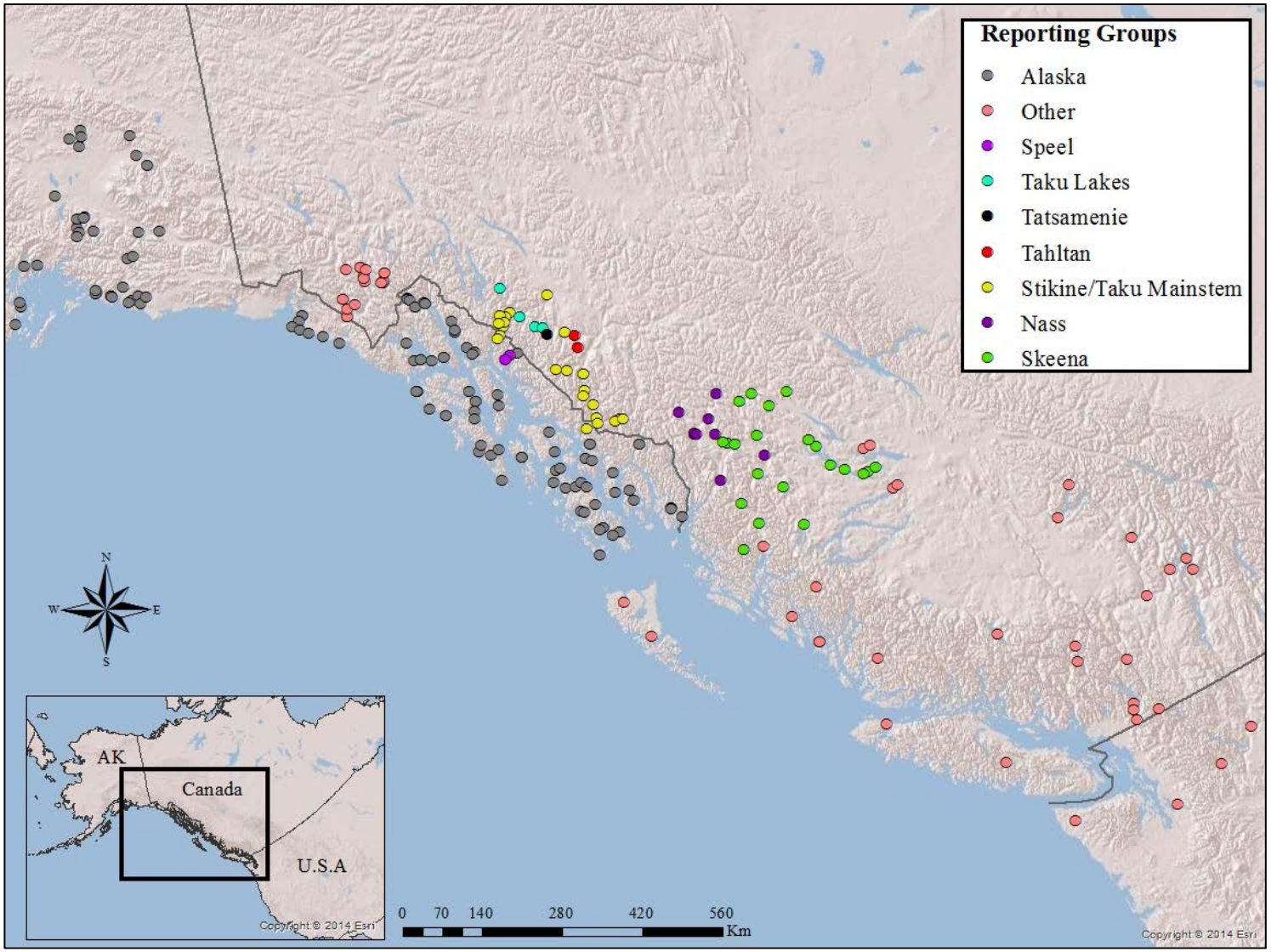

Figure 2.–Locations and fine-scale reporting group affiliations for the 238 populations represented in the sockeye salmon baseline for MSA of fish caught in Southeast Alaska fisheries. Fine-scale reporting groups included in the Northern Boundary and Transboundary groups are shown in Table 1.

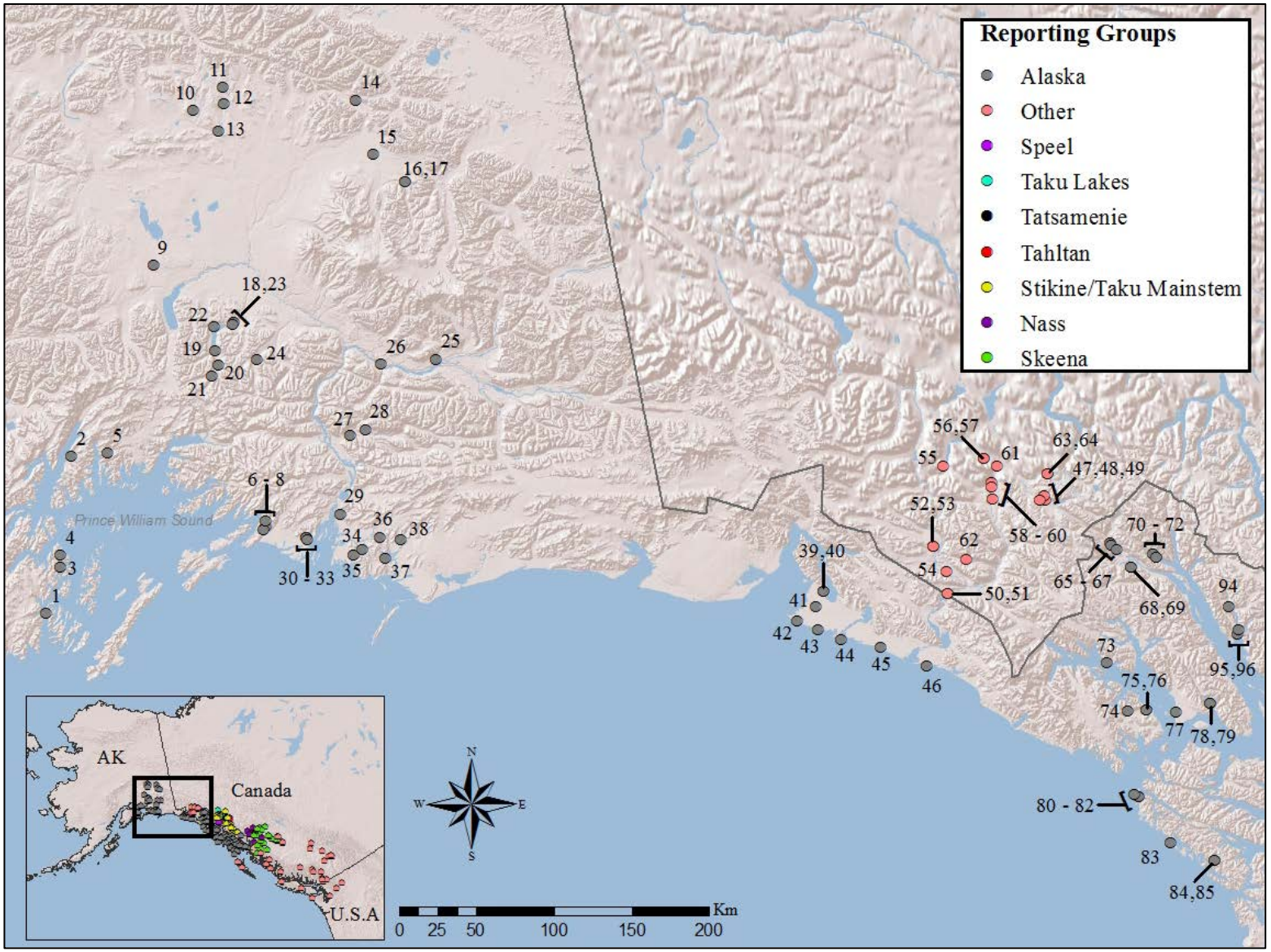

Figure 3.–Locations and fine-scale reporting group affiliations of populations spanning from Prince William Sound to northern SEAK represented in the sockeye salmon baseline for MSA. Population numbers match those in Table 1.

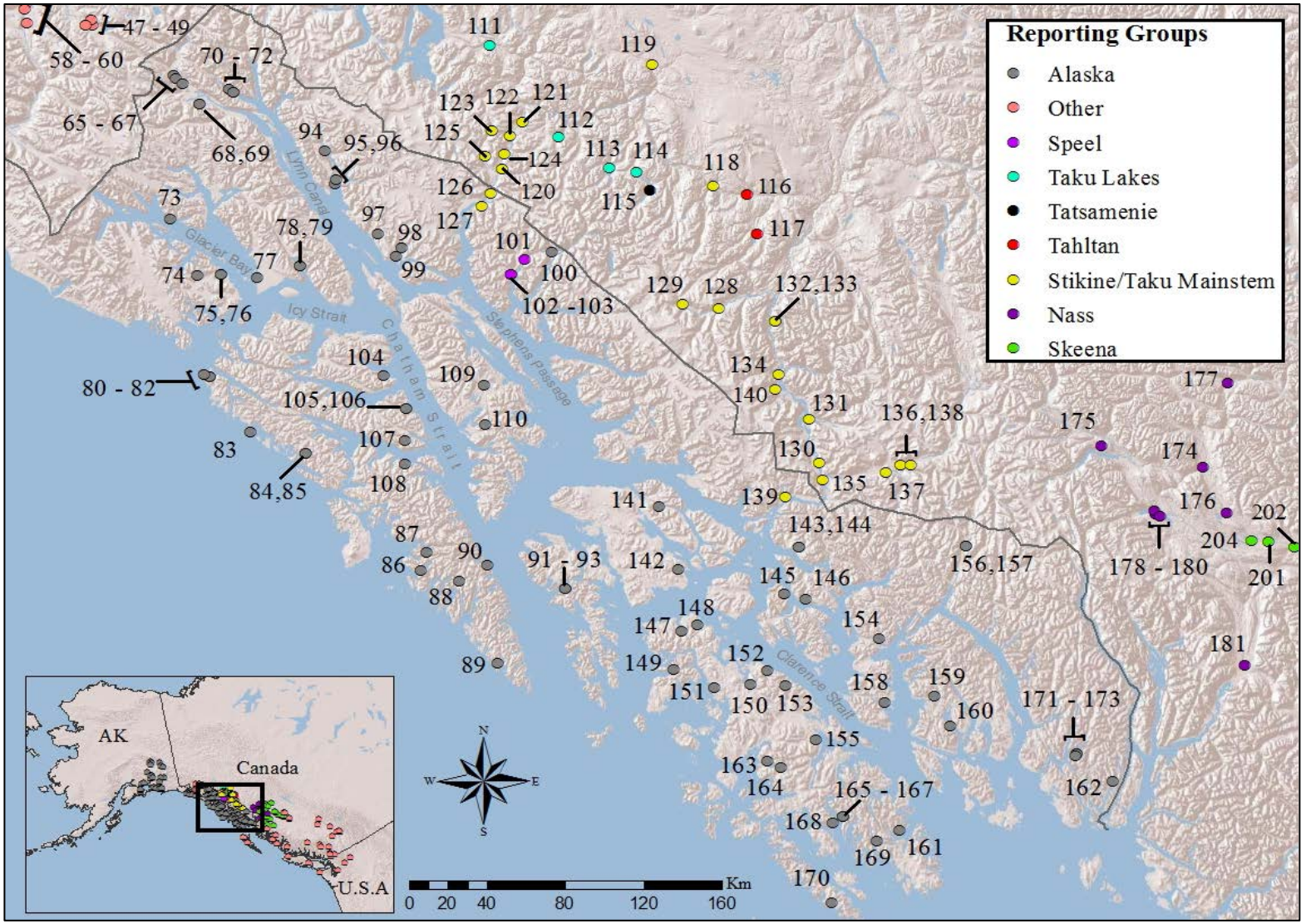

Figure 4.–Locations and fine-scale reporting group affiliations of populations in SEAK and British Columbia represented in the sockeye salmon baseline for MSA. Population numbers match those in Table 1.

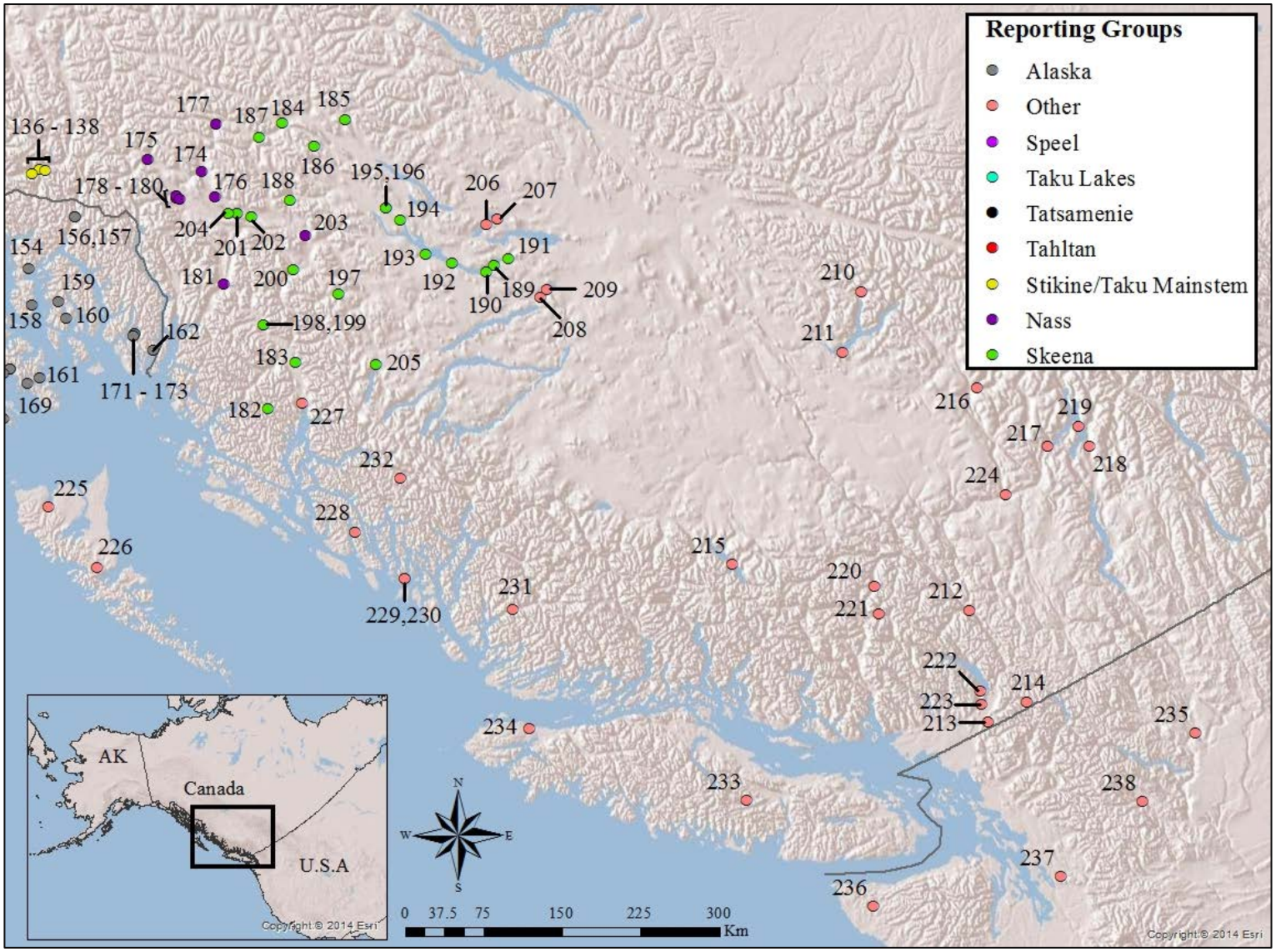

Figure 5.–Locations and fine-scale reporting group affiliations of populations in southern SEAK, British Columbia, and Washington represented in the sockeye salmon baseline for MSA. Population numbers match those in Table 1.

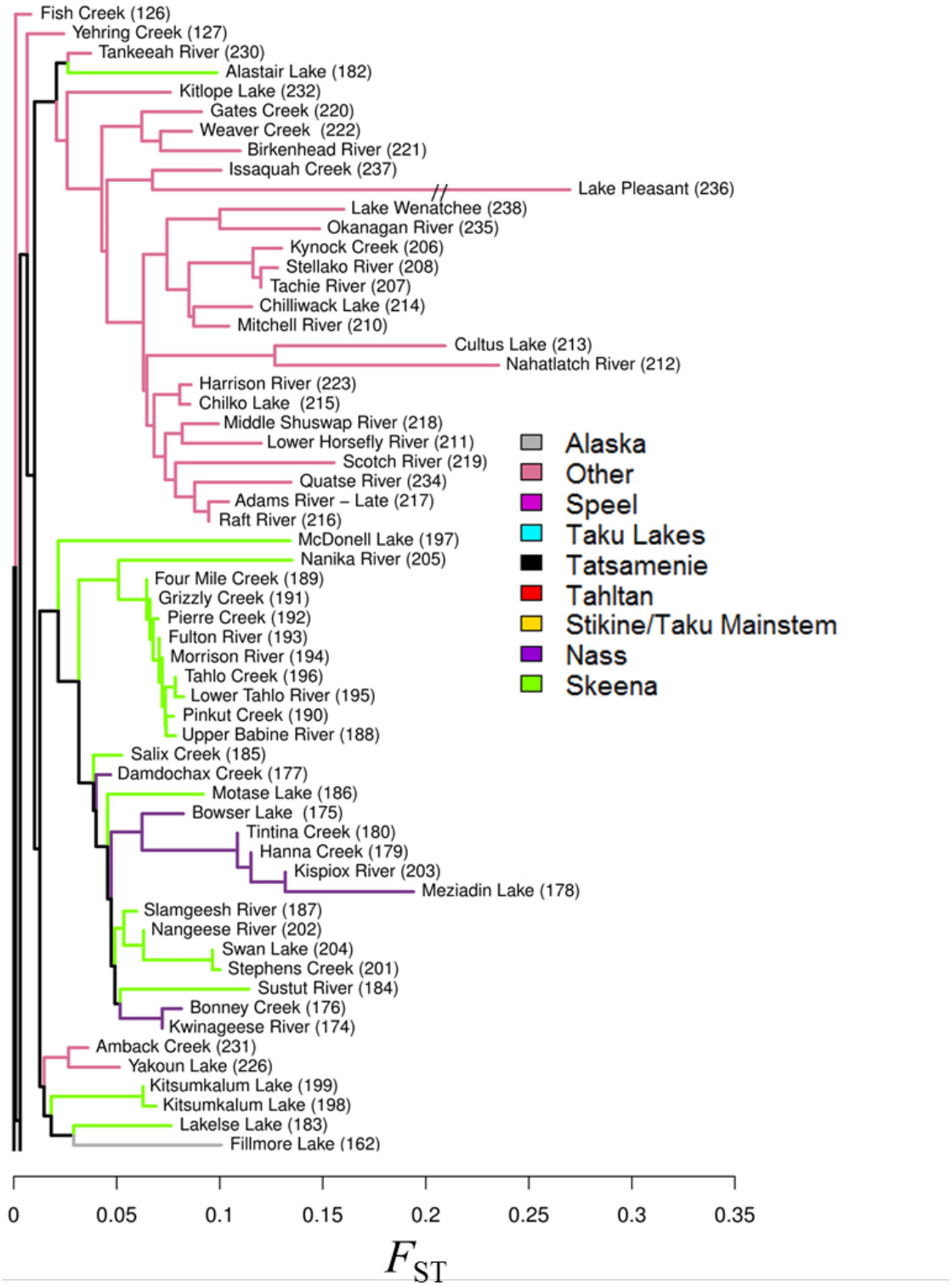

Figure 6.–Consensus neighbor-joining tree based on F_{ST} (Weir and Cockerham 1984) between 238 sockeye salmon populations sampled from spawning areas in drainages spanning from Prince William south to Washington state (see Table 1 for collection details).

Note: The branch for Kanalku Lake and Lake Pleasant have been truncated (true lengths F_{ST} ~ 0.53 and 0.42)

Note: Colors denote fine-scale reporting groups as in Figures 2–5. Numbers in parentheses correspond to unique population numbers on Table 1.

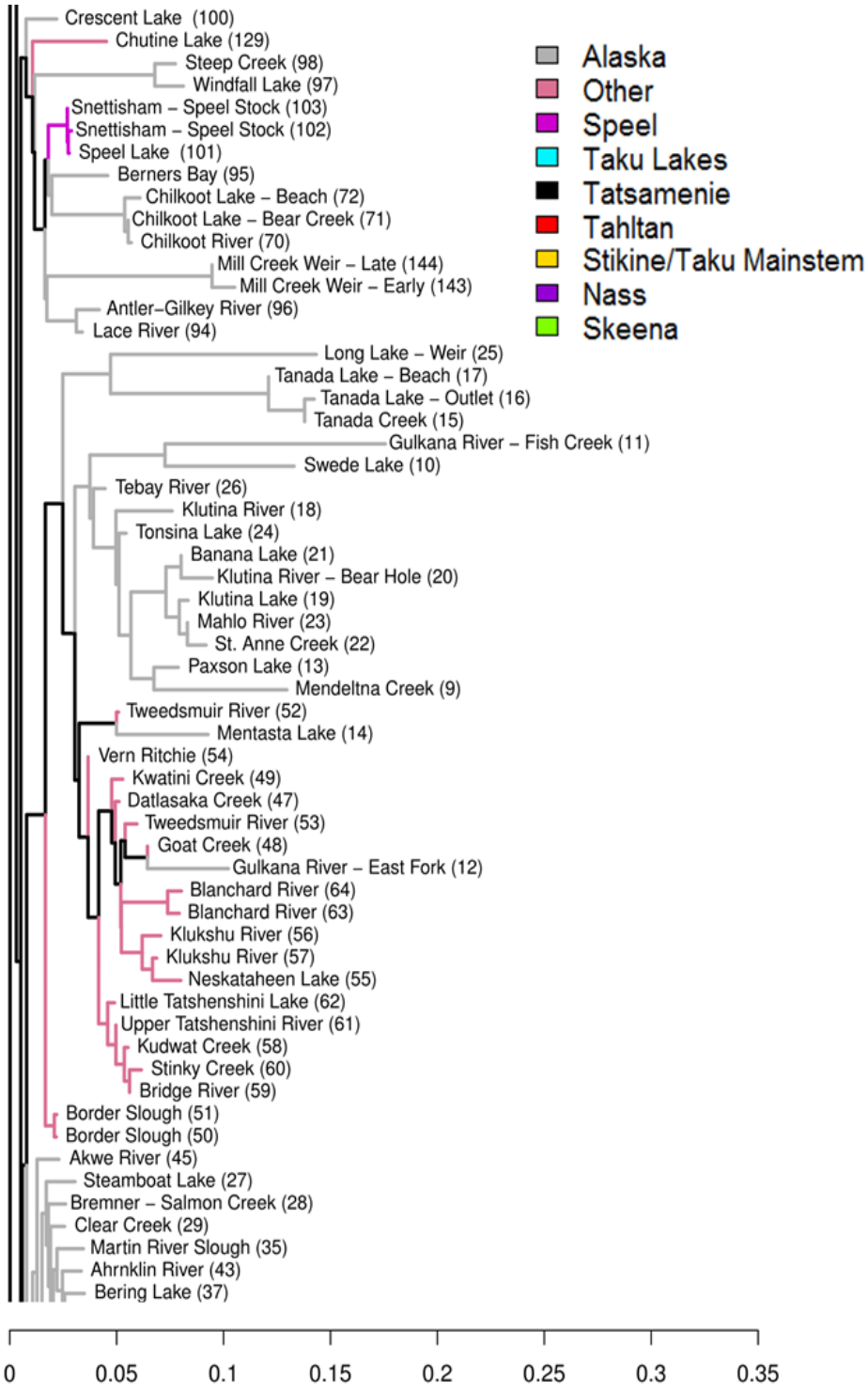

Figure 6.–Page 2 of 4.

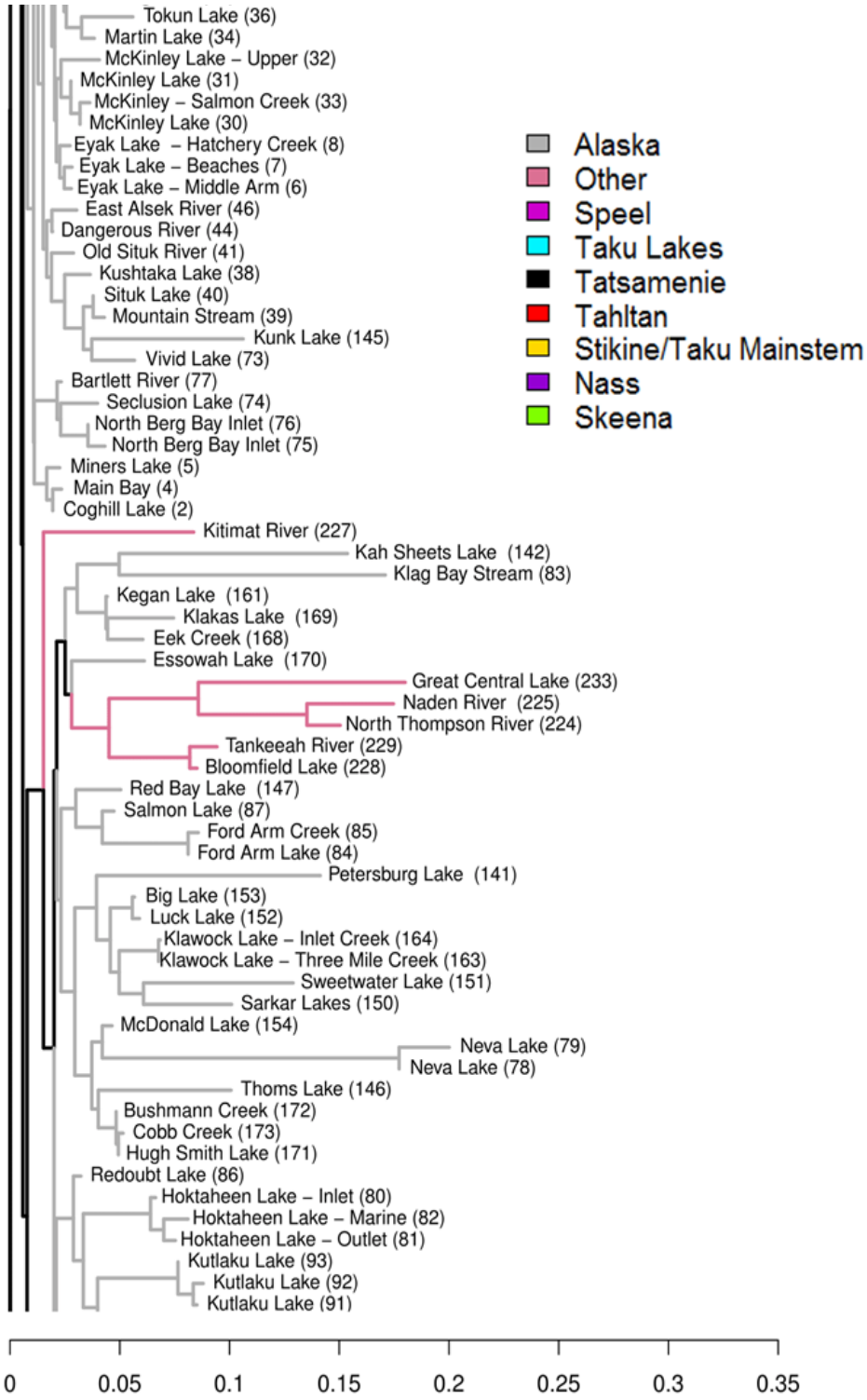

Figure 6.–Page 3 of 4.

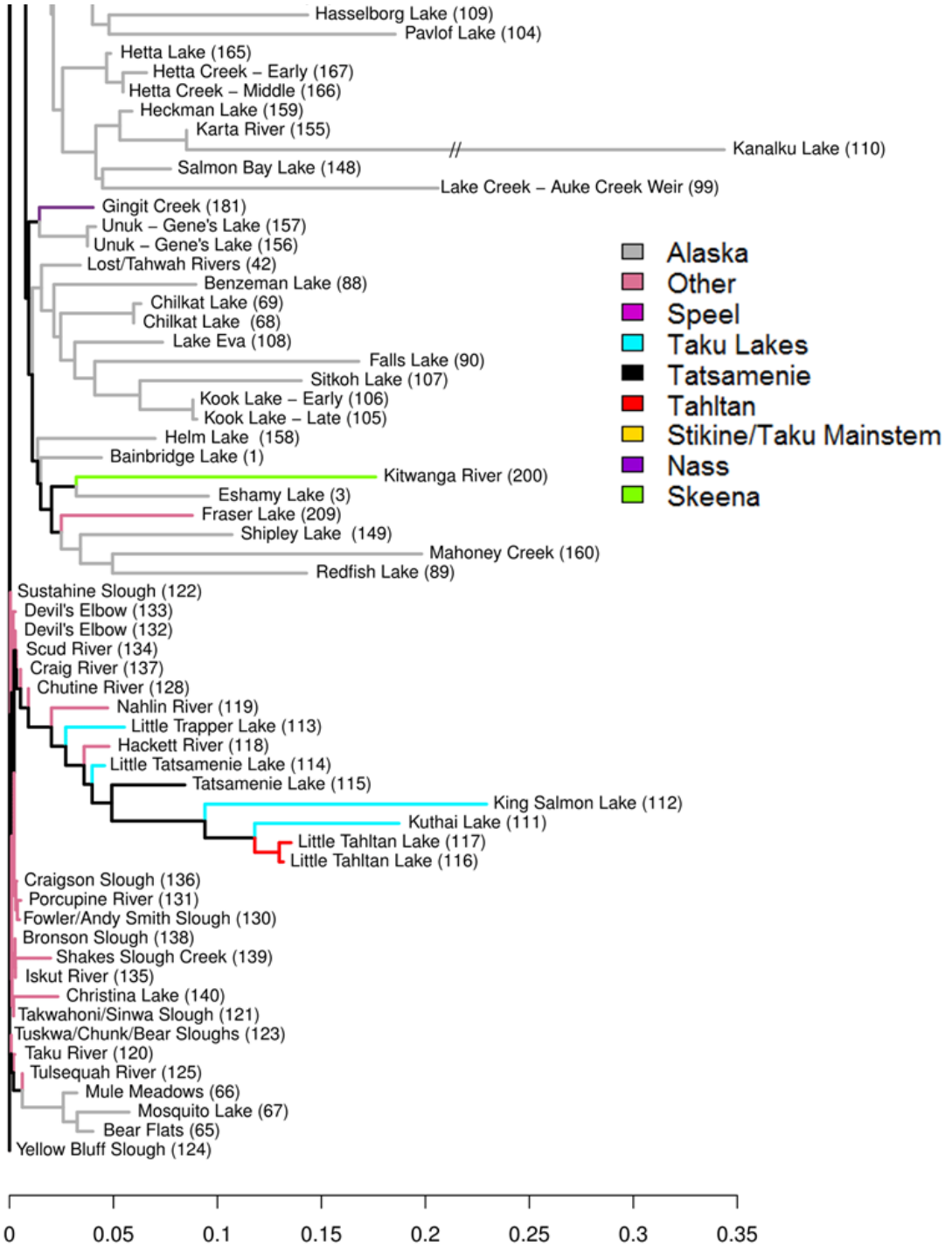

Figure 6.–Page 4 of 4.

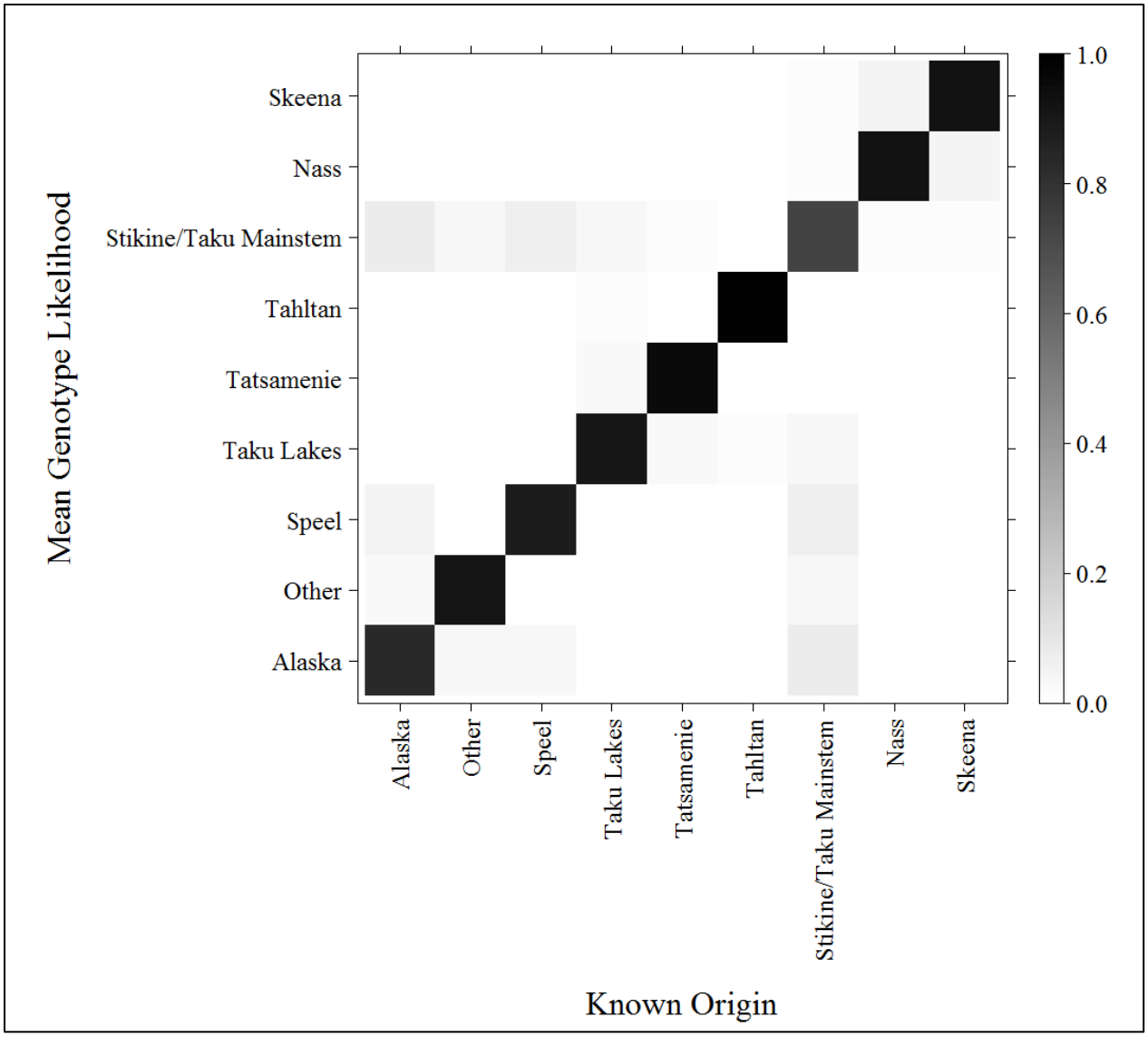

Figure 7.–Summary of mean genotype likelihood for all baseline individuals across the finest scale for each of the Northern Boundary and Transboundary reporting groups for the marker suite of 91 loci. Probabilities off the diagonal indicate uncertainty in genetic assignment and provide indications of potential misallocation.

APPENDICES

Appendix A.–Results of repeated proof tests for 5 Northern Boundary reporting groups used in Southeast Alaska Districts 106 and 108 sockeye salmon fisheries. Estimates for each replicate include the mean stock proportion, standard deviations (SD), and upper and lower bounds of the 90% credibility intervals. The proportion for each tested reporting group is in bold.

	Alaska Repeat 1				Alaska Repeat 2				Alaska Repeat 3			
Reporting Group	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Alaska	**0.982**	0.016	0.951	0.999	**0.976**	0.019	0.940	0.998	**0.980**	0.027	0.915	1.000
Nass	0.001	0.003	0.000	0.006	0.002	0.004	0.000	0.010	0.001	0.002	0.000	0.005
Skeena	0.001	0.003	0.000	0.006	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.005
All Stikine/Taku Mainstem	0.009	0.012	0.000	0.035	0.020	0.018	0.000	0.056	0.014	0.025	0.000	0.074
Other	0.007	0.009	0.000	0.026	0.001	0.003	0.000	0.006	0.004	0.007	0.000	0.020

	Alaska Repeat 4				Alaska Repeat 5				Alaska Repeat 6			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Alaska	**0.989**	0.011	0.966	1.000	**0.958**	0.029	0.908	0.999	**0.977**	0.017	0.945	0.998
Nass	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.005
Skeena	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.006	0.001	0.002	0.000	0.005
All Stikine/Taku Mainstem	0.002	0.005	0.000	0.011	0.006	0.011	0.000	0.031	0.016	0.014	0.000	0.043
Other	0.007	0.009	0.000	0.027	0.034	0.028	0.000	0.081	0.005	0.008	0.000	0.023

	Alaska Repeat 7				Alaska Repeat 8				Alaska Repeat 9			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Alaska	**0.990**	0.013	0.962	1.000	**0.961**	0.025	0.914	0.995	**0.950**	0.029	0.899	0.995
Nass	0.001	0.002	0.000	0.006	0.001	0.003	0.000	0.008	0.001	0.002	0.000	0.005
Skeena	0.001	0.002	0.000	0.005	0.003	0.005	0.000	0.013	0.001	0.003	0.000	0.006
All Stikine/Taku Mainstem	0.007	0.012	0.000	0.033	0.030	0.024	0.000	0.076	0.045	0.029	0.000	0.095
Other	0.001	0.003	0.000	0.006	0.004	0.008	0.000	0.020	0.003	0.005	0.000	0.013

	Alaska Repeat 10			
	Proportion	SD	Lower	Upper
Alaska	**0.978**	0.020	0.937	0.998
Nass	0.001	0.003	0.000	0.006
Skeena	0.001	0.002	0.000	0.006
All Stikine/Taku Mainstem	0.011	0.017	0.000	0.049
Other	0.009	0.009	0.000	0.027

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Appendix A.–Page 2 of 5.

Reporting Group	Nass Repeat 1 Proportion	SD	Lower	Upper	Nass Repeat 2 Proportion	SD	Lower	Upper	Nass Repeat 3 Proportion	SD	Lower	Upper
Alaska	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.005
Nass	**0.996**	0.005	0.986	1.000	**0.995**	0.006	0.982	1.000	**0.995**	0.005	0.984	1.000
Skeena	0.001	0.003	0.000	0.006	0.002	0.005	0.000	0.012	0.002	0.004	0.000	0.008
All Stikine/Taku Mainstem	0.001	0.003	0.000	0.006	0.001	0.002	0.000	0.005	0.001	0.003	0.000	0.006
Other	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.005

	Nass Repeat 4 Proportion	SD	Lower	Upper	Nass Repeat 5 Proportion	SD	Lower	Upper	Nass Repeat 6 Proportion	SD	Lower	Upper
Alaska	0.001	0.003	0.000	0.007	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.005
Nass	**0.995**	0.006	0.984	1.000	**0.995**	0.006	0.983	1.000	**0.994**	0.008	0.979	1.000
Skeena	0.001	0.003	0.000	0.007	0.002	0.005	0.000	0.010	0.003	0.006	0.000	0.015
All Stikine/Taku Mainstem	0.001	0.003	0.000	0.006	0.001	0.003	0.000	0.006	0.001	0.002	0.000	0.005
Other	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.005

	Nass Repeat 7 Proportion	SD	Lower	Upper	Nass Repeat 8 Proportion	SD	Lower	Upper	Nass Repeat 9 Proportion	SD	Lower	Upper
Alaska	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.005	0.001	0.003	0.000	0.007
Nass	**0.995**	0.007	0.981	1.000	**0.995**	0.006	0.983	1.000	**0.994**	0.006	0.982	1.000
Skeena	0.002	0.006	0.000	0.012	0.002	0.004	0.000	0.010	0.002	0.004	0.000	0.011
All Stikine/Taku Mainstem	0.001	0.002	0.000	0.005	0.001	0.003	0.000	0.007	0.001	0.002	0.000	0.006
Other	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.005

	Nass Repeat 10 Proportion	SD	Lower	Upper
Alaska	0.002	0.003	0.000	0.008
Nass	**0.993**	0.009	0.976	1.000
Skeena	0.004	0.007	0.000	0.018
All Stikine/Taku Mainstem	0.001	0.003	0.000	0.007
Other	0.001	0.002	0.000	0.005

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Reporting Group	Skeena Repeat 1 Proportion	SD	Lower	Upper	Skeena Repeat 2 Proportion	SD	Lower	Upper	Skeena Repeat 3 Proportion	SD	Lower	Upper
Alaska	0.002	0.003	0.000	0.008	0.001	0.002	0.000	0.006	0.002	0.004	0.000	0.010
Nass	0.021	0.012	0.006	0.043	0.001	0.003	0.000	0.007	0.006	0.006	0.000	0.017
Skeena	**0.972**	0.013	0.947	0.990	**0.991**	0.007	0.977	0.999	**0.986**	0.009	0.970	0.997
All Stikine/Taku Mainstem	0.005	0.006	0.000	0.016	0.002	0.004	0.000	0.009	0.004	0.005	0.000	0.015
Other	0.001	0.002	0.000	0.005	0.005	0.005	0.000	0.016	0.001	0.002	0.000	0.005

	Skeena Repeat 4 Proportion	SD	Lower	Upper	Skeena Repeat 5 Proportion	SD	Lower	Upper	Skeena Repeat 6 Proportion	SD	Lower	Upper
Alaska	0.001	0.003	0.000	0.006	0.001	0.003	0.000	0.006	0.004	0.005	0.000	0.014
Nass	0.001	0.003	0.000	0.007	0.002	0.004	0.000	0.010	0.001	0.002	0.000	0.006
Skeena	**0.987**	0.009	0.970	0.997	**0.995**	0.006	0.983	1.000	**0.989**	0.008	0.974	0.998
All Stikine/Taku Mainstem	0.005	0.005	0.000	0.016	0.001	0.003	0.000	0.006	0.004	0.006	0.000	0.018
Other	0.006	0.005	0.000	0.017	0.001	0.002	0.000	0.005	0.001	0.003	0.000	0.007

	Skeena Repeat 7 Proportion	SD	Lower	Upper	Skeena Repeat 8 Proportion	SD	Lower	Upper	Skeena Repeat 9 Proportion	SD	Lower	Upper
Alaska	0.001	0.003	0.000	0.007	0.003	0.006	0.000	0.015	0.001	0.002	0.000	0.006
Nass	0.007	0.006	0.000	0.019	0.004	0.006	0.000	0.016	0.003	0.005	0.000	0.014
Skeena	**0.986**	0.009	0.968	0.998	**0.978**	0.012	0.954	0.994	**0.990**	0.008	0.975	0.999
All Stikine/Taku Mainstem	0.005	0.006	0.000	0.017	0.006	0.008	0.000	0.021	0.004	0.006	0.000	0.016
Other	0.001	0.002	0.000	0.005	0.010	0.007	0.001	0.024	0.001	0.002	0.000	0.005

Reporting Group	Skeena Repeat 10 Proportion	SD	Lower	Upper
Alaska	0.001	0.002	0.000	0.005
Nass	0.011	0.011	0.000	0.032
Skeena	**0.981**	0.013	0.957	0.997
All Stikine/Taku Mainstem	0.001	0.002	0.000	0.006
Other	0.006	0.005	0.000	0.017

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Reporting Group	Stikine/Taku Mainstem Repeat 1 Proportion	SD	Lower	Upper	Stikine/Taku Mainstem Repeat 2 Proportion	SD	Lower	Upper	Stikine/Taku Mainstem Repeat 3 Proportion	SD	Lower	Upper
Alaska	0.002	0.006	0.000	0.012	0.005	0.007	0.000	0.018	0.003	0.007	0.000	0.016
Nass	0.001	0.003	0.000	0.006	0.001	0.003	0.000	0.006	0.001	0.003	0.000	0.007
Skeena	0.006	0.006	0.000	0.017	0.006	0.005	0.000	0.017	0.001	0.002	0.000	0.006
All Stikine/Taku Mainstem	**0.984**	0.010	0.966	0.996	**0.984**	0.010	0.965	0.996	**0.993**	0.009	0.976	1.000
Other	0.006	0.006	0.000	0.017	0.004	0.006	0.000	0.016	0.001	0.003	0.000	0.007

	Stikine/Taku Mainstem Repeat 4				Stikine/Taku Mainstem Repeat 5				Stikine/Taku Mainstem Repeat 6			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Alaska	0.003	0.006	0.000	0.015	0.010	0.012	0.000	0.034	0.007	0.006	0.000	0.019
Nass	0.001	0.002	0.000	0.005	0.001	0.003	0.000	0.006	0.001	0.003	0.000	0.006
Skeena	0.001	0.002	0.000	0.006	0.006	0.006	0.000	0.017	0.002	0.004	0.000	0.008
All Stikine/Taku Mainstem	**0.988**	0.009	0.971	0.998	**0.977**	0.014	0.949	0.994	**0.986**	0.009	0.969	0.997
Other	0.006	0.006	0.000	0.018	0.006	0.006	0.000	0.017	0.004	0.005	0.000	0.015

	Stikine/Taku Mainstem Repeat 7				Stikine/Taku Mainstem Repeat 8				Stikine/Taku Mainstem Repeat 9			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Alaska	0.002	0.005	0.000	0.013	0.004	0.007	0.000	0.019	0.004	0.006	0.000	0.016
Nass	0.001	0.002	0.000	0.006	0.001	0.003	0.000	0.008	0.001	0.003	0.000	0.006
Skeena	0.001	0.003	0.000	0.006	0.001	0.003	0.000	0.008	0.001	0.002	0.000	0.006
All Stikine/Taku Mainstem	**0.994**	0.007	0.980	1.000	**0.990**	0.010	0.970	1.000	**0.987**	0.010	0.968	0.998
Other	0.001	0.003	0.000	0.007	0.003	0.005	0.000	0.014	0.007	0.007	0.000	0.020

Reporting Group	Stikine/Taku Mainstem Repeat 10 Proportion	SD	Lower	Upper
Alaska	0.002	0.004	0.000	0.010
Nass	0.001	0.003	0.000	0.007
Skeena	0.007	0.006	0.000	0.020
All Stikine/Taku Mainstem	**0.986**	0.011	0.964	0.998
Other	0.003	0.008	0.000	0.020

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	Other Repeat 1				Other Repeat 2				Other Repeat 3			
Reporting Groups	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Alaska	0.002	0.005	0.000	0.012	0.005	0.007	0.000	0.020	0.006	0.007	0.000	0.021
Nass	0.005	0.006	0.000	0.016	0.001	0.002	0.000	0.006	0.001	0.003	0.000	0.006
Skeena	0.001	0.003	0.000	0.006	0.001	0.003	0.000	0.006	0.001	0.002	0.000	0.005
All Stikine/Taku Mainstem	0.008	0.009	0.000	0.027	0.002	0.003	0.000	0.008	0.009	0.010	0.000	0.028
Other	**0.984**	0.012	0.961	0.998	**0.991**	0.009	0.974	1.000	**0.982**	0.012	0.960	0.997

	Other Repeat 4				Other Repeat 5				Other Repeat 6			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Alaska	0.002	0.004	0.000	0.009	0.011	0.008	0.002	0.026	0.001	0.003	0.000	0.007
Nass	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.006
Skeena	0.001	0.002	0.000	0.005	0.001	0.003	0.000	0.006	0.001	0.002	0.000	0.005
All Stikine/Taku Mainstem	0.001	0.003	0.000	0.007	0.006	0.008	0.000	0.023	0.024	0.018	0.000	0.056
Other	**0.995**	0.006	0.983	1.000	**0.980**	0.012	0.958	0.995	**0.973**	0.019	0.940	0.999

	Other Repeat 7				Other Repeat 8				Other Repeat 9			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Alaska	0.008	0.009	0.000	0.026	0.007	0.007	0.001	0.020	0.001	0.003	0.000	0.006
Nass	0.001	0.002	0.000	0.005	0.001	0.002	0.000	0.005	0.003	0.005	0.000	0.013
Skeena	0.001	0.003	0.000	0.006	0.001	0.003	0.000	0.006	0.001	0.003	0.000	0.006
All Stikine/Taku Mainstem	0.002	0.005	0.000	0.010	0.001	0.003	0.000	0.006	0.043	0.019	0.016	0.077
Other	**0.988**	0.010	0.968	0.999	**0.989**	0.008	0.974	0.998	**0.952**	0.019	0.918	0.979

	Other Repeat 10			
Reporting groups	Proportion	SD	Lower	Upper
Alaska	0.014	0.009	0.002	0.031
Nass	0.001	0.002	0.000	0.005
Skeena	0.001	0.002	0.000	0.005
All Stikine/Taku Mainstem	0.011	0.009	0.000	0.029
Other	**0.973**	0.013	0.949	0.992

Appendix B.–Results of repeated proof tests for 3 Transboundary reporting groups used in Southeast Alaska Districts 106 and 108 sockeye salmon fisheries. Estimates for each replicate include the mean stock proportions, standard deviations (SD), and upper and lower bounds of the 90% credibility intervals. The proportion for each tested group is in bold.

	Other Repeat 1				Other Repeat 2				Other Repeat 3			
Reporting Groups	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	**0.963**	0.023	0.922	0.997	**0.952**	0.020	0.916	0.981	**0.943**	0.024	0.901	0.980
Stikine/Taku Mainstem	0.035	0.022	0.002	0.076	0.046	0.020	0.018	0.082	0.055	0.024	0.018	0.097
Tahltan	0.002	0.003	0.000	0.007	0.002	0.003	0.000	0.007	0.002	0.003	0.000	0.008

	Other Repeat 4				Other Repeat 5				Other Repeat 6			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	**0.977**	0.020	0.938	0.998	**0.964**	0.018	0.930	0.990	**0.965**	0.020	0.929	0.993
Stikine/Taku Mainstem	0.017	0.019	0.000	0.055	0.035	0.018	0.009	0.068	0.033	0.020	0.005	0.069
Tahltan	0.006	0.006	0.000	0.017	0.002	0.003	0.000	0.007	0.002	0.003	0.000	0.007

	Other Repeat 7				Other Repeat 8				Other Repeat 9			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	**0.993**	0.010	0.973	1.000	**0.960**	0.018	0.927	0.986	**0.951**	0.023	0.910	0.986
Stikine/Taku Mainstem	0.006	0.010	0.000	0.025	0.039	0.018	0.013	0.071	0.047	0.023	0.013	0.088
Tahltan	0.002	0.003	0.000	0.007	0.002	0.003	0.000	0.007	0.002	0.003	0.000	0.008

	Other Repeat 10			
	Proportion	SD	Lower	Upper
Other	**0.978**	0.021	0.937	1.000
Stikine/Taku Mainstem	0.020	0.021	0.000	0.061
Tahltan	0.002	0.003	0.000	0.007

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Reporting Groups	Stikine/Taku Mainstem Repeat 1				Stikine/Taku Mainstem Repeat 2				Stikine/Taku Mainstem Repeat 3			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.006	0.007	0.000	0.020	0.010	0.009	0.001	0.027	0.022	0.019	0.000	0.058
Stikine/Taku Mainstem	**0.993**	0.008	0.977	1.000	**0.987**	0.010	0.968	0.998	**0.972**	0.020	0.934	0.996
Tahltan	0.002	0.003	0.000	0.007	0.003	0.004	0.000	0.012	0.007	0.006	0.001	0.018

	Stikine/Taku Mainstem Repeat 4				Stikine/Taku Mainstem Repeat 5				Stikine/Taku Mainstem Repeat 6			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.007	0.007	0.000	0.020	0.013	0.009	0.003	0.031	0.007	0.007	0.000	0.020
Stikine/Taku Mainstem	**0.983**	0.010	0.964	0.995	**0.980**	0.010	0.961	0.994	**0.986**	0.009	0.969	0.997
Tahltan	0.010	0.008	0.001	0.025	0.006	0.006	0.000	0.018	0.007	0.006	0.001	0.019

	Stikine/Taku Mainstem Repeat 7				Stikine/Taku Mainstem Repeat 8				Stikine/Taku Mainstem Repeat 9			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.008	0.009	0.000	0.026	0.006	0.008	0.000	0.024	0.007	0.007	0.001	0.021
Stikine/Taku Mainstem	**0.985**	0.011	0.965	0.998	**0.987**	0.010	0.967	0.998	**0.991**	0.007	0.977	0.999
Tahltan	0.007	0.006	0.001	0.018	0.007	0.006	0.001	0.018	0.002	0.003	0.000	0.007

	Stikine/Taku Mainstem Repeat 10			
	Proportion	SD	Lower	Upper
Other	0.005	0.007	0.000	0.019
Stikine/Taku Mainstem	**0.989**	0.009	0.971	0.998
Tahltan	0.007	0.006	0.001	0.018

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	Tahltan Repeat 1				Tahltan Repeat 2				Tahltan Repeat 3			
Reporting Groups	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.002	0.004	0.000	0.010	0.002	0.004	0.000	0.010	0.002	0.004	0.000	0.010
Stikine/Taku Mainstem	0.002	0.004	0.000	0.010	0.002	0.004	0.000	0.010	0.002	0.004	0.000	0.010
Tahltan	**0.995**	0.006	0.984	1.000	**0.995**	0.006	0.984	1.000	**0.995**	0.006	0.984	1.000

	Tahltan Repeat 4				Tahltan Repeat 5				Tahltan Repeat 6			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.002	0.004	0.000	0.010	0.002	0.004	0.000	0.010	0.002	0.004	0.000	0.010
Stikine/Taku Mainstem	0.002	0.004	0.000	0.010	0.002	0.004	0.000	0.010	0.002	0.004	0.000	0.010
Tahltan	**0.995**	0.006	0.984	1.000	**0.995**	0.006	0.984	1.000	**0.995**	0.006	0.984	1.000

	Tahltan Repeat 7				Tahltan Repeat 8				Tahltan Repeat 9			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.002	0.004	0.000	0.010	0.002	0.004	0.000	0.010	0.002	0.004	0.000	0.010
Stikine/Taku Mainstem	0.002	0.004	0.000	0.010	0.002	0.004	0.000	0.010	0.002	0.004	0.000	0.010
Tahltan	**0.995**	0.006	0.984	1.000	**0.995**	0.006	0.984	1.000	**0.995**	0.006	0.984	1.000

	Tahltan Repeat 10			
	Proportion	SD	Lower	Upper
Other	0.002	0.004	0.000	0.010
Stikine/Taku Mainstem	0.002	0.004	0.000	0.010
Tahltan	**0.995**	0.006	0.984	1.000

Appendix C.–Results of repeated proof tests for 5 Transboundary reporting groups used in the Southeast Alaska District 111 sockeye salmon fishery. Estimates for each replicate include the mean stock proportion, standard deviations (SD), and upper and lower bounds of the 90% credibility intervals. The proportion for each tested group is in bold.

	Other Repeat 1				Other Repeat 2				Other Repeat 3			
Reporting Groups	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	**0.980**	0.016	0.950	1.000	**0.942**	0.027	0.896	0.984	**0.926**	0.028	0.877	0.967
Speel	0.000	0.002	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Stikine/Taku Mainstem	0.020	0.016	0.000	0.050	0.058	0.027	0.016	0.104	0.074	0.028	0.033	0.123
Taku Lakes	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000
Tatsamenie	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

	Other Repeat 4				Other Repeat 5				Other Repeat 6			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	**0.965**	0.025	0.921	1.000	**0.985**	0.013	0.960	1.000	**0.959**	0.029	0.908	1.000
Speel	0.002	0.006	0.000	0.014	0.000	0.000	0.000	0.000	0.001	0.004	0.000	0.001
Stikine/Taku Mainstem	0.033	0.024	0.000	0.076	0.015	0.013	0.000	0.039	0.041	0.029	0.000	0.090
Taku Lakes	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000
Tatsamenie	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

	Other Repeat 7				Other Repeat 8				Other Repeat 9			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	**0.973**	0.021	0.935	1.000	**0.982**	0.019	0.945	1.000	**0.961**	0.022	0.921	0.995
Speel	0.000	0.000	0.000	0.000	0.001	0.005	0.000	0.007	0.000	0.001	0.000	0.000
Stikine/Taku Mainstem	0.027	0.021	0.000	0.064	0.017	0.018	0.000	0.053	0.039	0.022	0.005	0.079
Taku Lakes	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000
Tatsamenie	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

	Other Repeat 10			
	Proportion	SD	Lower	Upper
Other	**0.990**	0.012	0.967	1.000
Speel	0.000	0.000	0.000	0.000
Stikine/Taku Mainstem	0.010	0.012	0.000	0.033
Taku Lakes	0.000	0.001	0.000	0.000
Tatsamenie	0.000	0.000	0.000	0.000

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	Speel Repeat 1				Speel Repeat 2				Speel Repeat 3			
Reporting Groups	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.004	0.005	0.000	0.014	0.004	0.005	0.000	0.014	0.004	0.005	0.000	0.014
Speel	**0.994**	0.006	0.982	1.000	**0.994**	0.006	0.981	1.000	**0.994**	0.006	0.983	1.000
Stikine/Taku Mainstem	0.002	0.004	0.000	0.008	0.002	0.004	0.000	0.011	0.001	0.003	0.000	0.007
Taku Lakes	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000
Tatsamenie	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

	Speel Repeat 4				Speel Repeat 5				Speel Repeat 6			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.004	0.005	0.000	0.014	0.004	0.005	0.000	0.014	0.004	0.005	0.000	0.014
Speel	**0.994**	0.006	0.982	1.000	**0.993**	0.007	0.980	1.000	**0.979**	0.012	0.957	0.997
Stikine/Taku Mainstem	0.002	0.003	0.000	0.008	0.002	0.005	0.000	0.012	0.016	0.011	0.000	0.037
Taku Lakes	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000
Tatsamenie	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

	Speel Repeat 7				Speel Repeat 8				Speel Repeat 9			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.004	0.005	0.000	0.013	0.005	0.005	0.000	0.016	0.004	0.005	0.000	0.014
Speel	**0.994**	0.006	0.983	1.000	**0.993**	0.007	0.978	1.000	**0.992**	0.008	0.977	1.000
Stikine/Taku Mainstem	0.002	0.004	0.000	0.008	0.002	0.005	0.000	0.013	0.003	0.006	0.000	0.016
Taku Lakes	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000
Tatsamenie	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

	Speel Repeat 10			
	Proportion	SD	Lower	Upper
Other	0.004	0.005	0.000	0.014
Speel	**0.993**	0.007	0.978	1.000
Stikine/Taku Mainstem	0.003	0.005	0.000	0.013
Taku Lakes	0.000	0.001	0.000	0.000
Tatsamenie	0.000	0.000	0.000	0.000

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Reporting Groups	Stikine/Taku Mainstem Repeat 1				Stikine/Taku Mainstem Repeat 2				Stikine/Taku Mainstem Repeat 3			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.006	0.006	0.000	0.019	0.011	0.008	0.002	0.026	0.022	0.013	0.006	0.046
Speel	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000
Stikine/Taku Mainstem	**0.984**	0.009	0.966	0.996	**0.983**	0.010	0.963	0.996	**0.976**	0.013	0.952	0.992
Taku Lakes	0.010	0.007	0.002	0.023	0.000	0.001	0.000	0.000	0.002	0.004	0.000	0.011
Tatsamenie	0.000	0.000	0.000	0.000	0.006	0.006	0.000	0.018	0.000	0.000	0.000	0.000

	Stikine/Taku Mainstem Repeat 4				Stikine/Taku Mainstem Repeat 5				Stikine/Taku Mainstem Repeat 6			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.007	0.007	0.000	0.022	0.008	0.008	0.000	0.024	0.010	0.008	0.002	0.026
Speel	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000
Stikine/Taku Mainstem	**0.988**	0.009	0.970	0.998	**0.991**	0.008	0.975	1.000	**0.981**	0.014	0.952	0.998
Taku Lakes	0.005	0.005	0.000	0.015	0.000	0.001	0.000	0.001	0.009	0.012	0.000	0.034
Tatsamenie	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000

	Stikine/Taku Mainstem Repeat 7				Stikine/Taku Mainstem Repeat 8				Stikine/Taku Mainstem Repeat 9			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.005	0.006	0.000	0.017	0.007	0.007	0.000	0.022	0.005	0.006	0.000	0.018
Speel	0.000	0.000	0.000	0.000	0.004	0.009	0.000	0.025	0.001	0.003	0.000	0.005
Stikine/Taku Mainstem	**0.985**	0.009	0.967	0.996	**0.979**	0.014	0.952	0.995	**0.993**	0.008	0.977	1.000
Taku Lakes	0.010	0.007	0.001	0.024	0.010	0.007	0.002	0.024	0.001	0.004	0.000	0.008
Tatsamenie	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

	Stikine/Taku Mainstem Repeat 10			
	Proportion	SD	Lower	Upper
Other	0.017	0.011	0.003	0.038
Speel	0.000	0.002	0.000	0.000
Stikine/Taku Mainstem	**0.974**	0.012	0.951	0.990
Taku Lakes	0.005	0.006	0.000	0.017
Tatsamenie	0.004	0.005	0.000	0.014

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Reporting Groups	Taku Lakes Repeat 1				Taku Lakes Repeat 2				Taku Lakes Repeat 3			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.004	0.005	0.000	0.013	0.005	0.005	0.000	0.016	0.005	0.005	0.000	0.015
Speel	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Stikine/Taku Mainstem	0.003	0.005	0.000	0.012	0.002	0.004	0.000	0.009	0.002	0.003	0.000	0.008
Taku Lakes	**0.993**	0.006	0.980	1.000	**0.993**	0.007	0.980	1.000	**0.994**	0.006	0.981	1.000
Tatsamenie	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

	Taku Lakes Repeat 4				Taku Lakes Repeat 5				Taku Lakes Repeat 6			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.009	0.007	0.001	0.023	0.006	0.006	0.000	0.019	0.005	0.005	0.000	0.015
Speel	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Stikine/Taku Mainstem	0.007	0.007	0.000	0.021	0.009	0.008	0.000	0.024	0.003	0.005	0.000	0.014
Taku Lakes	**0.984**	0.010	0.966	0.996	**0.985**	0.009	0.968	0.997	**0.993**	0.007	0.978	1.000
Tatsamenie	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

	Taku Lakes Repeat 7				Taku Lakes Repeat 8				Taku Lakes Repeat 9			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.010	0.007	0.001	0.023	0.005	0.005	0.000	0.016	0.004	0.004	0.000	0.013
Speel	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Stikine/Taku Mainstem	0.003	0.005	0.000	0.013	0.001	0.003	0.000	0.008	0.001	0.003	0.000	0.006
Taku Lakes	**0.988**	0.009	0.971	0.998	**0.993**	0.006	0.981	1.000	**0.995**	0.005	0.984	1.000
Tatsamenie	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000

	Taku Lakes Repeat 10			
	Proportion	SD	Lower	Upper
Other	0.010	0.007	0.002	0.024
Speel	0.000	0.000	0.000	0.000
Stikine/Taku Mainstem	0.012	0.010	0.001	0.030
Taku Lakes	**0.978**	0.012	0.956	0.994
Tatsamenie	0.000	0.000	0.000	0.000

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	Tatsamenie Repeat 1				Tatsamenie Repeat 2				Tatsamenie Repeat 3			
Reporting Groups	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.005	0.006	0.000	0.018	0.006	0.006	0.000	0.018	0.005	0.006	0.000	0.018
Speel	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000
Stikine/Taku Mainstem	0.001	0.003	0.000	0.007	0.002	0.005	0.000	0.011	0.002	0.004	0.000	0.009
Taku Lakes	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000
Tatsamenie	**0.993**	0.007	0.979	1.000	**0.992**	0.008	0.976	1.000	**0.993**	0.007	0.978	1.000

	Tatsamenie Repeat 4				Tatsamenie Repeat 5				Tatsamenie Repeat 6			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.006	0.006	0.000	0.018	0.006	0.006	0.000	0.018	0.006	0.006	0.000	0.018
Speel	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Stikine/Taku Mainstem	0.002	0.004	0.000	0.010	0.001	0.003	0.000	0.008	0.002	0.004	0.000	0.010
Taku Lakes	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000
Tatsamenie	**0.992**	0.008	0.977	1.000	**0.993**	0.007	0.979	1.000	**0.992**	0.008	0.977	1.000

	Tatsamenie Repeat 7				Tatsamenie Repeat 8				Tatsamenie Repeat 9			
	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper	Proportion	SD	Lower	Upper
Other	0.005	0.006	0.000	0.018	0.006	0.006	0.000	0.018	0.005	0.006	0.000	0.018
Speel	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
Stikine/Taku Mainstem	0.002	0.004	0.000	0.010	0.002	0.003	0.000	0.008	0.001	0.003	0.000	0.008
Taku Lakes	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.000
Tatsamenie	**0.992**	0.008	0.977	1.000	**0.993**	0.007	0.979	1.000	**0.993**	0.007	0.979	1.000

	Tatsamenie Repeat 10			
	Proportion	SD	Lower	Upper
Other	0.006	0.006	0.000	0.018
Speel	0.000	0.000	0.000	0.000
Stikine/Taku Mainstem	0.002	0.004	0.000	0.009
Taku Lakes	0.000	0.001	0.000	0.000
Tatsamenie	**0.993**	0.007	0.978	1.000