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Chum Salmon Baseline for the Western Alaska Salmon Stock Identification Program

by

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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

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TABLE OF CONTENTS

TABLE OF CONTENTS (Continued)

LIST OF TABLES

LIST OF TABLES (Continued)

LIST OF FIGURES

Figure **Page**

LIST OF APPENDICES

Appendix **Page**

ABSTRACT

Uncertainty about the magnitude, frequency, location, and timing of the nonlocal harvest of sockeye and chum salmon was the impetus for the Western Alaska Salmon Stock Identification Program. The program was designed to use genetic data in mixed stock analysis to reduce this uncertainty. A baseline of allele frequencies in spawning populations is required for use in mixed-stock analysis to estimate the stock of origin of harvested fish. This report describes the methodology used to understand the population genetic structure among chum salmon populations and to build and test a baseline for use in mixed stock analysis of chum salmon. Of the 35,921 fish from 434 collections selected to be genotyped, the final baseline was composed of 32,817 fish from 402 collections representing 310 populations. Average population sample size was 106 fish. Reporting groups were determined through a combination of stakeholder needs and identifiability using genetic information, as measured using proof tests. The final reporting groups included Asia, Kotzebue Sound, Coastal Western Alaska, Upper Yukon River, Northern District (Alaska Peninsula), Northwest District (Alaska Peninsula), South Peninsula (Alaska Peninsula), Chignik/Kodiak, and East of Kodiak.

Key words: chum salmon, *Oncorhynchus keta*, population structure, genetic baseline, mixed stock analysis, single nucleotide polymorphism, SNP

INTRODUCTION

Chum salmon *Oncorhynchus keta* support important subsistence and commercial fisheries in Western Alaska. In addition to commercial fisheries throughout the area, chum salmon are harvested in subsistence fisheries in communities in the Kuskokwim River and Bay, Yukon River, and Norton Sound (Wolfe and Spaeder 2009) and in Kotzebue Sound (Fall et al. 2007). The life history and migratory pathways of chum salmon, combined with the complex geography of Western Alaska creates the potential for harvest of nonlocal fish as they return to natal streams. While a majority of the harvest of chum salmon in Western Alaska occurs in terminal fisheries where nonlocal harvest is minimal (Linderman and Bergstrom 2009; Menard et al. 2009; Bue et al. 2009), the harvest of nonlocal fish occurs (Seeb and Crane 1999a) and can bias estimates of total run and stock productivity. The extent of this bias depends on population size; small populations are more affected by nonlocal harvest than are large populations. Uncertainty about the magnitude, frequency, location, and timing of nonlocal harvest was the impetus for the Western Alaska Salmon Stock Identification Program (WASSIP). WASSIP is a consensus-driven project with 11 signatories representing fishing, Alaska Native, and government interests who serve on the Advisory Panel (AP) and are governed by a Memorandum of Understanding. This collaboration also has a 4-member Technical Committee (TC), representing expertise in genetics, population dynamics, biometrics and salmon ecology and life history, that guides WASSIP on the use of statistical procedures to use genetic markers in mixed stock analysis (MSA), with a particular focus on reducing uncertainty in MSA estimates.

Genetic population markers have been used effectively to estimate stock compositions (specifically chum salmon) in stock mixtures of Pacific salmon. The earliest works were based on allozymes and generally covered more restricted geographic ranges. However, by the early 2000s an allozyme baseline of 356 populations from across the range had been developed for marine research and bycatch analysis (Seeb et al. 2004). More recent work is based on microsatellites and/or single nucleotide polymorphisms (SNPs) and covers broad geographic ranges (Beacham et al. 2009; Seeb et al. 2011b). Original MSA analyses of harvests in Western Alaska were accomplished with a coastwide allozyme baseline that was developed in a multi-laboratory effort (Kondzela et al. 2002; Seeb et al. 2004; Crane and Seeb 2000), but this baseline was unable to distinguish among chum salmon stocks of stakeholder interest, especially among stocks within the Coastal Western Alaska area (CWAK; Norton Sound, Lower Yukon, Lower

Kuskokwim and Bristol Bay). These baselines were replaced with ones based on newer markers, which provide greater laboratory efficiency and the potential for greater resolution. Coastwide baselines have recently been completed for microsatellites (Beacham et al. 2009) and SNPs (Seeb et al. 2011a). However, neither baseline provided the necessary resolution within CWAK.

The foundation for genetic MSA of fishery samples is the genetic characterization of all the stocks that might contribute to the fishery. This characterization is accomplished by estimating allele frequencies at specific loci within spawning populations potentially contributing to the fishery. Stocks useful for MSA are determined through a combination of the extent of genetic variation among populations and stakeholder needs (Habicht et al. 2012). Estimating stock composition is accomplished by comparing genotypes of fish of unknown origin to a baseline of allele frequencies of potentially contributing populations. Such baselines are defined by 2 components: populations of individuals and the genetic markers for which they have been genotyped. This document describes the baseline the Gene Conservation Laboratory has built for MSA of chum salmon harvests in WASSIP, in consultation with the WASSIP AP and TC. The baseline is composed of samples from populations throughout the species' range and of 96 SNPs chosen specifically for WASSIP (DeCovich et al. 2012a).

This baseline differs from the baseline previously presented to the WASSIP AP and TC (Jasper et al. 2012) in 3 primary ways: 1) the number of populations included in the baseline, 2) the set of SNPs assayed in these populations, and 3) the methods used to build the baseline. The first 2 differences were driven by the AP's request to increase the precision of stock composition estimates. We increased the number of populations, especially those from the Alaska Peninsula and south through the State of Washington, and we increased the number of SNPs from 53 to a set of 96 chosen specifically for WASSIP (DeCovich et al. 2012b). We genotyped fish in a subset of collections from our tissue archive in order to accomplish these tasks within budget. This subset was chosen in an attempt to gain the greatest representative value from our genotyping efforts for a given cost. We used information from the 53-SNP baseline analysis to exclude redundant samples. The third difference was driven primarily by the need to handle the increased numbers of potentially linked loci (Dann et al. 2012). As a byproduct of reanalyzing the baseline, we implemented novel quality control procedures for both laboratory and statistical analyses.

In this report we describe the methods used to understand the population genetic structure of chum salmon across the entire range of the species. This information was then used to build a baseline and test its usefulness for estimating the stock composition of fishery harvests in western Alaska.

An important component of constructing this baseline was the partitioning of populations into reporting groups used for MSA. The process is explained in detail in Habicht et al. (2012), but specific details pertaining to this baseline are worth mention here. The WASSIP AP provided the Gene Conservation Laboratory with groupings of populations that would be useful for estimating stock contributions in various fisheries. A final list of 9 reporting groups was accepted at the November 2011 meeting of the AP and TC (Table 1). We consider these groups as *a priori* information, and therefore mention them here instead of in the methods or results. We discuss the initially proposed groups, the final set used for WASSIP, along with the process used to determine this group in this report.

DEFINITIONS

To assist with understanding technical terms in the methods, results, and interpretation in this report, definitions of commonly used terms in genetic analyses and salmon management are listed here.

Allele. Alternative form of a given gene or DNA sequence.

Bootstrapping. Pseudorandom resampling of data with replacement to estimate the error of estimates of parameters of interest.

Credibility Interval. In Bayesian statistics, a credibility interval is a posterior probability interval. Credibility intervals differ from the confidence intervals in frequentist statistics in that they do not assume an underlying distribution (e.g., normal distribution) and are direct statements of probability: i.e., a 90% credibility interval has a 90% chance of containing the true answer.

District. Waters open to commercial salmon fishing. Commercial fishing districts, subdistricts and sections in WASSIP commercial fishing areas are defined in statutes listed below under *Salmon administrative area*.

Effective Population Size (N_e). The size of an ideal population that would be affected by genetic drift at the same rate as the actual population. This idealized population has discrete generations, an even sex ratio, constant size, random union of gametes and random survivorship of offspring (Kalinowski and Waples 2002).

Escapement (*or Spawning Abundance or Spawners*). The annual estimated size of the spawning salmon stock. The quality of escapement may be determined, not only by numbers of spawners, but also by factors such as sex ratio, age composition, temporal entry into the system, and spatial distribution with the salmon spawning habitat (from 5 AAC 39.222(f)).

F-statistics (F_{IS}, F_{ST}, F_{IT}). Measures used to hierarchically partition genetic diversity within and among populations. Common measures include: 1) F_{IS}, which is the average departure of genotype frequencies from Hardy-Weinberg expectations within a population; 2) F_{ST}, which is the proportion of the variation due to allele-frequency differences among populations; and 3) F_{IT}, which is the departure of genotype frequencies from Hardy-Weinberg expectations relative to the entire collection of populations. In this common hierarchy, the subscripts refer to comparisons between levels in the hierarchy: $_{IS}$ refers to individuals within populations, $_{ST}$ to subpopulations within the total population, and $_{IT}$ to individuals within the total population. Hierarchies and subscript notation can be extended to any level to accommodate different study designs.

Genetic Drift. Chance changes in allele frequencies that result from the sampling of gametes from generation to generation in a finite population. The magnitude of these changes is inversely related to twice effective population size ($2N_e$), because each diploid fish carries two sets of genes.

Genetic Marker (*Marker*). A known DNA sequence that can be identified by a simple assay. For the purpose of this document, a marker can be a single SNP or a combination of SNPs.

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

Hardy-Weinberg Expectations (*HWE*). Genotypic frequencies 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 of the genotypes.

Harvest. The number of salmon or weight of salmon removed from the available fish through fishing activities.

Harvest Rate. The fraction of the available fish harvested in fishing activities.

Heterozygosity. The proportion of individuals in a population that carry two different alleles at a particular marker. This statistics can be used as a measure of genetic variability in a population.

Linkage Disequilibrium. A state that exists in a population when alleles at different loci are not distributed independently of each other in a population's gamete pool, often because the loci are physically linked on the same fragment of DNA.

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

Mitochondrial DNA (*mtDNA*). Circular, maternally inherited DNA located outside the nucleus in organelles in a cell called mitochondria.

Mixed Stock Analysis (*MSA*). Method using allele frequencies from populations and genotypes from mixture samples to estimate stock compositions.

Microsatellites. DNA sequences containing short (2–5 base pairs) tandem repeats of nucleotides (e.g., GTGTGTGT).

Polymerase Chain Reaction (*PCR)*. The enzymatic amplification a single or few copies of a DNA fragment several orders of magnitude, generating millions of copies.

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 during mixed stock analyses. In this study, reporting groups were constructed based on stakeholder needs, on the extent of genetic distinction among populations, and on advice from the WASSIP Technical Committee and Advisory Panel.

Run. The number of salmon in a stock surviving to adulthood and returning to their natal streams in a calendar year. A run is composed of both harvested adult salmon and the escapement to spawning areas. A run can designate the annual return of fish in a calendar year. With the exception of pink salmon, a run is composed of several age classes because individuals from a given brood year mature at different times (from 5 AAC 39.222(f)).

Salmon Administrative Area (*Area*). Geographic areas used to administer the registration of commercial salmon fishing permits (from 20 AAC 05.230). Commercial salmon fishing areas are designated by a letter and are defined by the following Alaska administrative code: Chignik (Area L; 5 AAC 15.100); Aleutian Islands and Alaska Peninsula (Area M; 5 AAC 12.100, 5 AAC 09.100, and 5 AAC 11.101); Bristol Bay (Area T; 5 AAC 06.100); and Kuskokwim (Area W; 5 AAC 07.100). Districts and subdistricts within areas are used to aid management and are defined by administrative code.

Salmon Stock (*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

two or more interbreeding groups, which occur in the same geographic area and are managed as a unit (from 5 AAC 39.222(f)). For this report, a "stock" is a composite of all populations within reporting groups.

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

METHODS

TISSUE SAMPLING

Baseline collections

Baseline samples were collected from spawning populations of chum salmon ranging from Korea to the State of Washington (Table 2). Tissue samples were collected by ADF&G and collaborators. In some cases, only DNA extracts were available, especially for collections from Asia. Target sample size for baseline populations was 95 individuals to achieve acceptable precision for estimating allele frequencies (Allendorf and Phelps 1981; Waples 1990a) and to accommodate our SNP genotyping platform. It was evident early on that a sample size of 95 fish was not possible for some collections.

Selection of baseline collections to genotype

We selected a subset of collections to include in the WASSIP baseline to represent 1) population abundance, 2) genetic diversity, 3) geographic coverage, and 4) among-year variation of allele frequencies within populations. We attempted to find the greatest representative value by balancing maximum representation and the high cost of choosing fish from every collection with minimal representation and the low cost of choosing fish from a small subset of collections. Unlike the baseline for sockeye salmon, we chose to include populations from throughout the species' range, because past studies indicated that chum salmon from spawning areas throughout the Pacific Rim are caught in WASSIP-area fisheries (Seeb and Crane 1999a, 1999b; Seeb et al. 2004).

LABORATORY ANALYSIS

Developing and ascertaining SNPs for WASSIP

At the start of this project, ADF&G used a panel of 53 SNP markers for most chum salmon analyses. Because of the need for greater resolution among Western Alaskan stocks, we contracted the discovery of additional SNP markers for chum salmon with the International Program for Salmon Ecological Genetics (IPSEG; http://fish.washington.edu/research/seeblab) at the University of Washington. These efforts were based on cDNA sequences from two chum salmon from the Susitna and Delta rivers (Seeb et al. 2011a). This SNP development added 37 SNPs to those already available for chum salmon for use in WASSIP. Subsequent rounds of SNP development at the University of Washington were based on 16 fish from 4 populations from Western Alaska and increased the total number of SNPs to 198 (Petrou 2012). TaqMan™ assays were developed, or were available, for all 198 SNPs, including the original 53-SNP set.

We used a combination of assessments (Figure 1) to select the 96 most useful SNP markers for WASSIP (see below). These measures were performed on genotypic data collected for 188 SNP markers on 30 populations. This dataset was chosen to include populations relevant to WASSIP,

and an emphasis was placed on choosing populations from Western Alaska. We refer to this dataset as the *backbone* marker set. This process of marker selection is described in DeCovich et al. (2012b), but a brief description is given here.

We eliminated markers from further consideration if they did not conform to Hardy-Weinberg Expectations (HWE). Markers which showed significant genotypic association with each other (linkage disequilibrium) were combined into composite genotypes and tested for significant increase in information when treated together (DeCovich et al. 2012b). If there was no significant increase in information, the least useful of the associated markers was dropped from further consideration. If there was a significant increase in information the combined marker was retained, referred to hereafter as a *composite locus* and SNP markers that are not associated with any other marker are referred to as *loci*.

Scored assessments were used to determine the relative usefulness of backbone loci for MSA performance with weights set primarily to select useful markers for two objectives: 1) to increase MSA performance to distinguish among Western Alaska regions, and 2) to maintain MSA performance to distinguish among regions throughout the rest of the species' range (Figure 2). Weights were assigned to measures based on perceived benefit of the measure to achieve the objectives and the highest weights were placed on measures associated with the first objective (Figure 3). For each measure, $j\ (j = 1,2,\dots,J)$, raw values for each backbone locus, $l\ (l = 1,2,\dots,L)$, were linearly scaled into scores between 0.0 (lowest) and 1.0 (highest) using the equation:

$$S'_{l,j} = \frac{S_{l,j} - S_{min,j}}{S_{max,j} - S_{min,j}}.$$

For measure j, $S_{l,j}$ is the raw value at backbone locus l, $S_{min,j}$ is the minimal value across all backbone loci, $S_{max,j}$ is the maximal value across all backbone loci, and $S'_{l,j}$ is the scaled score for backbone locus l. Scores for each locus were summarized across measures using the following equation:

$$\bar{S}_l = \sum_{j=i}^{J} \frac{w_j S'_{l,j}}{\sum_{l=1}^{L} S'_{l,j}}.$$

Here w_j is the weight assigned to measure j, and $\bar{S}_l$ is the final score given to backbone locus l. These scores were then ranked from highest to lowest. The 96 highest ranking backbone loci were then assessed for laboratory performance. If a marker performed poorly in the laboratory, it was replaced by the next-highest ranking backbone locus. The process was repeated for each poorly performing backbone locus, until a final set of 96 backbone loci were selected.

Assaying genotypes

We extracted genomic DNA from tissue samples using a DNeasy® 96 Tissue Kit by QIAGEN® (Valencia, CA). A multiplexed preamplification PCR of 96 screened SNP markers was used to increase the concentration of template DNA. Reactions were conducted in 10 µL volumes consisting of 4 uL of genomic DNA, 5 µL of 2×Multiplex PCR Master Mix (QIAGEN) and 1 µL each (2 µM SNP unlabeled forward and reverse primers). Thermal cycling was performed on a Dual 384-Well GeneAmp® PCR system 9700 (Applied Biosystems) at 95°C for 15 min followed by 20 cycles of 95°C for 15 s, 60°C for 4 min, and a final extension at 4°C. The preamplified

DNA was then loaded into a Fluidigm® 96.96 Dynamic Array in a post-PCR laboratory at ADF&G. The Fluidigm® 96.96 Dynamic Array contains a matrix of integrated channels and valves housed in an input frame. On one side of the frame are 96 inlets to accept the sample DNA from individual fish and on the other are 96 inlets to accept the assays for 96 SNP markers. Once in the wells, the components are pressurized into the chip using the IFC Controller HX (Fluidigm).

The 96 samples and 96 assays are then systematically combined into 9,216 parallel reactions. Each reaction is a mixture of 4 µl of assay mix (1×DA Assay Loading Buffer (Fluidigm), 10×TaqMan® SNP Genotyping Assay (Applied Biosystems), and 2.5×ROX (Invitrogen)) and 5 µl of sample mix (1×TaqMan® Universal Buffer (Applied Biosystems), 0.05×AmpliTaq® Gold DNA Polymerase (Applied Biosystems), 1×GT Sample Loading Reagent (Fluidigm) and 60–400 ng/µl DNA) combined in a 7.2 nL chamber. Thermal cycling was performed with an 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° 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 failing to amplify with the Fluidigm system were reanalyzed on the Applied Biosystems platform using the preamplified DNA. 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, 1×TaqMan® Universal PCR Master Mix (Applied Biosystems), and 1×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 Gene Conservation Laboratory Oracle database, LOKI.

Laboratory quality control

We conducted a quality control analysis (QC) to identify laboratory errors and to measure the background discrepancy rate of our genotyping process. The QC analysis was a collaborative effort between ADF&G Gene Conservation Laboratory and the University of Washington IPSEG lab. The QC analyses were performed by staff not involved in the original genotyping. We applied 3 methods to the QC, depending on the type of collection and when it was genotyped. We termed these the *Original*, *Database*, and *New* QC methods. All QC DNA underwent the preamplification process as described above, unless otherwise noted.

The *Original* QC method was the method used for QC prior to beginning WASSIP. This method consisted of regenotyping 8% of the fish genotyped in the original project using the same DNA extraction for the same SNPs assayed in the original project. Discrepancy rates were calculated as the number of conflicting genotypes, divided by the total number of genotypes examined. These discrepancy rates describe the difference between original project data and QC data and are capable of identifying assay plate errors but cannot detect DNA extraction plate errors (rotations, etc.), since they were based on the same extractions. This QC method was implemented only when all tissue was exhausted during the original extraction or when the DNA was extracted off site.

The *Database* QC method compared new and old genotypes for the SNPs common to our current and previous baselines (Jasper et al. 2012). After selecting the 96 loci to analyze chum salmon (DeCovich et al. 2012b), we assayed each collection for all 96 SNPs on a single chip. Since some of these SNPs had been assayed earlier in some of the collections, we were able to compare the apparent genotypes for these SNPs in these collections. Discrepancy rates were calculated as the difference between old and new genotypes for these SNPs. These comparisons identified genotyping errors, but could not detect DNA extraction errors, since they were based on the same extractions. When a difference appeared, we used the new genotype. This provided consistency between all of the data used in our analyses. Collections requiring either the *New* or *Database* QC methods were run with the same assay plate so that the *New* QC method could identify errors in the assay plate that the *Database* method could not.

The *New* QC method is our current QC method and consists of re-extracting DNA from 8% of project fish and genotyping them for the original SNPs. These discrepancy rates measure differences between the original and QC genotypes and are capable of identifying extraction, assay plate, and genotyping errors. This QC method represents the error rate in our current genotyping procedure.

For all QC methods, error rates in the original genotyping can be estimated as half the rate of discrepancy by assuming that the discrepancies among analyses were due equally to errors during the original genotyping and to errors during quality control, and by assuming that at least one of these assays produced the correct genotype.

STATISTICAL ANALYSIS

Data retrieval and quality control

We retrieved genotypes from LOKI and imported them into *R* (R Development Core Team 2010). Subsequent analyses were performed with *R* routines unless otherwise noted. We performed 2 analyses prior to statistical analyses to confirm the quality of the data.

First, we removed from further analyses genotypes of fish that were missing a substantial number of genotypes for individual SNPs. We used an 80% rule (Dann et al. 2009) to exclude fish missing genotypes for 20% or more 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.

Second, we identified individuals with identical genotypes and removed them from further analyses. Identical genotypes can result from sampling or extracting the same fish twice. *Identical* was defined as pairs of fish with the same genotypes in 83% of SNPs (80 of the 96 backbone loci in this study). One individual from each duplicate pair was removed from further analyses.

Hardy-Weinberg expectations

After calculating allelic frequencies for each backbone locus, we tested observed genotype frequencies for each baseline collection for conformance to HWE at each marker by Monte Carlo simulation with 10,000 iterations using the *adegenet* package (Jombart 2008). We combined probabilities for each collection across backbone loci using Fisher's method (Sokal and Rohlf 1995) and removed collections that departed significantly from HWE after correcting for multiple tests with Bonferroni's method ($\alpha = 0.05$) from subsequent analyses.

Pooling collections into populations

When appropriate, we pooled collections following a step-wise protocol to obtain more accurate estimates of population allele frequencies. First, we pooled collections from the same geographic location, sampled at similar calendar dates but in different years, as suggested by Waples (1990b). We used Fisher's exact test of allele frequency homogeneity (Sokal and Rohlf 1995) and based our decisions on a summary across loci using Fisher's method. Collections that were not significantly different ($P > 0.01$) were pooled. After pooling, we treated these final collections as populations in our analyses. Finally, we tested genotypic frequencies for conformance to HWE following the same protocol described above to ensure that our pooling was appropriate and that tests for linkage disequilibrium would not result in falsely positive results due to departure from HWE.

Process for defining reporting groups

Defining reporting groups for MSA was an iterative process that took into account the following criteria: 1) sociological needs (suggested by stakeholders and fishery managers), 2) genetic population structure (MSA potential), 3) adequate 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 potentially within a mixture (Habicht et al. 2012). To evaluate potential reporting groups, we used the following metrics of these 4 factors as guidelines: 1) utility of information for fishery managers and stakeholders, 2) 90% correct allocation in tests of the baseline's ability to allocate to reporting groups, 3) 400 individuals from enough collections to adequately represent the genetic diversity in a reporting group, and 4) an expected contribution to a given mixture of at least 5% (or 20 fish) for the 400-fish mixtures proposed for WASSIP. The definition of reporting groups heavily depended on information from the *Testing reporting groups for MSA and identifying biases* section described below.

Removal of collections from the baseline

We removed collections from further analysis if they met one of the following criteria: 1) a collection did not meet our minimum desired sample size of 40 individuals after pooling, or 2) poorly documented collections that did not pool with other well-documented collections putatively sampled at the same location and time of year. In these cases, the less-documented collections were excluded.

Linkage disequilibrium

We re-evaluated the data for linkage disequilibrium between each pair of nuclear backbone loci in each population to ensure that subsequent baseline and mixed stock analyses would be based on independent markers. We used the program *Genepop* version 4.0.11 (Rousset 2008) with 100 batches of 5,000 iterations for these tests. We summarized the frequency of significant linkage disequilibrium between pairs of SNPs ($P < 0.05$) and further investigated pairs that exhibited linkage in more than half of the populations.

As done previously during locus selection (DeCovich et al. 2012b), we either removed one of the linked backbone loci or combined the pair into a composite locus for further analyses, if the pattern of linkage continued to provide information useful for MSA. We used the optimal rate of correct assignment (f_{ORCA}; Rosenberg 2005) as our measure of information. f_{ORCA} assesses the rate of correct allocation of simulated individuals to defined reporting groups based upon the markers in question. Composite loci generally have higher f_{ORCA} values than the single markers

that form them, because combinations of alleles for 2 or more composite loci can exist in more forms (9 possible) than 2 single loci (4 alleles for a pair of loci). Simple comparisons of f_{ORCA} values would always suggest combining linked pairs into composite loci. However, there is a cost associated with composite loci as estimates of frequencies for 8 phenotypically scored alleles are less precise than estimates of 1 allele frequency at each of 2 loci for a given sample size.

To account for this cost, and to ensure that we combined only SNP pairs that provided significantly more information than the single SNPs in question, we compared the difference between f_{ORCA} values of the composite locus and the single locus with the greater f_{ORCA} value in the pair ($\Delta = f_{ORCA\text{-}pair} - \max(f_{ORCA\text{-}single1}, f_{ORCA\text{-}single2})$). This difference ($\Delta$) was our test statistic, but since we did not know its underlying distribution, we conducted a sampled randomization test (Sokal and Rohlf 2005). We randomly selected 1,000 SNP pairs, calculated Δ for each pair to empirically define the test-statistic distribution, and set the 90th quantile of the distribution as a critical value (Δ_{90}). We then either combined linked backbone loci into a composite locus, if Δ was greater than this critical value, or we dropped the locus with the lower f_{ORCA} value, if Δ was less than the critical value.

This investigation of linkage disequilibrium is identical to that described in DeCovich et al. (2012b). That analysis produced the final set of 96 backbone loci used in this analysis, but it was repeated here to check for differences in associations due to the increase in populations in the full baseline.

We use the term *locus* in place of the term *backbone locus* from here on to describe the final set of loci used for analyses.

Treatment of mtDNA

The decision was made *a priori* to retain the 3 mtDNA SNP loci during the locus-selection process. These 3 markers were combined into single composite phenotypic locus, *Oke_Cr30_Cr386_ND3-69*, for the baseline. These mtDNA loci are useful for the identification of Japan-origin chum salmon, and our treatment of these loci is identical to that of Seeb et al. (2011b).

Analysis of genetic structure

Analysis of temporal variance

We examined the among-year temporal variation of allele frequencies with a hierarchical, 3-level Analysis of Variance (ANOVA). This analysis was performed on all populations with multiyear collections, but excluded all collections that were removed following the collection removal outlined above under *Pooling collections into populations*. We treated temporal samples as subpopulations, as described in Weir (1996). This method allowed the quantification of the sources of total allelic variation and permitted the calculation of the between-collection component of variance and the assessment of its magnitude relative to the between-population component of variance. This analysis was conducted using the software package *GDA* (Lewis and Zaykin 2001).

Visualization of genetic distances

We visualized pairwise F_{ST} estimates among collections from the final set of independent loci estimated with the package *hierfstat* (Goudet 2006). We constructed consensus Neighbor-

Joining trees from 1,000 bootstrapped trees by resampling loci with replacement to assess the significance of nodes in the tree across loci. We plotted the consensus tree with the *FigTree* program (Rambaut 2007). These trees provided insight into the genetic structure among populations.

Determination of reporting groups

At the March 2011 AP meeting, the AP recommended sets of reporting groups deemed useful for answering questions of stock composition for the fisheries sampled in the study. The groups were arranged hierarchically, with the finest scale (greatest number of groups) desired given first, then with alternative broad-scale groups. The fine-scale groups included: 1) Asia, 2) Kotzebue Sound, 3) Norton Bay/Shaktoolik/Unalakleet, 4) Nome/Port Clarence/Golovin/Elim, 5) Yukon River, 6) Kuskokwim River 7) Togiak/Nushagak, 8) Eastern Bristol Bay, 9) Northern District Peninsula, 10) Northwest District Peninsula, 11) South Peninsula, 12) Chignik, and 13) East of WASSIP. The broadest scale included 6 groups: 1) Asia, 2) Kotzebue Sound, 3) Arctic, Yukon, Kuskokwim (AYK), 4) Bristol Bay, 5) Alaska Peninsula/Chignik, and 6) East of WASSIP. As a starting point for testing the performance of these groups, we chose a set of 10 groups between the fine-scale and broad-scale groups, and used an iterative approach to either collapse or expand the 10 groups based on the results of the previous round of analysis (Table 3). We presented the results of these tests at the September 2011 Advisory Panel meeting.

Baseline evaluation for mixed stock analysis

We assessed the identifiability of regional reporting groups in mixtures. These tests were used to determine if the underlying genetic structure supported particular reporting groups for MSA. These tests also provided insights into potential allocation biases. The results of these tests provided key insights in interpreting the results from MSA of WASSIP mixtures.

To assess the identifiability of regional reporting groups in mixtures we conducted *100% proof tests*, in which we sampled 200 individuals without replacement from each reporting group and analyzed them as a mixture against the reduced baseline. These tests provided an indication of the power of the baseline to produce accurate MSA estimates under the assumption that all the populations from a reporting group were represented in the baseline. The AP and TC set a guideline that correct allocation for these single-reporting group tests should exceed 90% to be considered adequate (Seeb et al. 2000).

BAYES protocol

Stock compositions of these test mixtures were estimated with the program *BAYES* (Pella and Masuda 2001). The Bayesian model implemented in *BAYES* uses a Dirichlet distribution with specified parameters as the prior distribution for the stock proportions. 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 to 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 5 independent Markov Chain Monte Carlo (MCMC) chains of 40,000 iterations with different starting values and discarded the first 20,000 iterations to remove the influences of the initial start values. We defined the starting values for the first chain such that the first 1/5 of the baseline populations summed to 0.9 and the remaining populations summed to 0.1. Each chain had a different combination of 1/5 of baseline populations summing to 0.9.

We combined the second halves of these chains to form the posterior distribution and tabulated mean estimates and 90% credibility intervals from a total of 100,000 iterations. We also assessed the within- and among-chain convergence of these estimates using the Raftery-Lewis and Gelman-Rubin diagnostics, respectively. These values compare variation of estimates within a chain (Raftery and Lewis 1996) and the total variation among chains (Gelman and Rubin 1992), respectively. If the Gelman-Rubin diagnostic for any stock group estimate was greater than 1.2 and the Raftery-Lewis diagnostic suggested that each chain had not converged to stable estimates, we reanalyzed the mixture with 80,000-iteration chains following the same protocol. We repeated this procedure for each reporting group mixture. A critical level of 90% correct allocation was used to determine if the reporting group was acceptably identifiable (Seeb et al. 2000). We visualized these results as barplots using the *gplots* package (Warnes 2010).

RESULTS

TISSUE SAMPLING

Baseline collections

We compiled a library of baseline tissues and/or DNA from 64,971 chum salmon in 889 collections. We restricted the number of collections that were analyzed, based primarily on the cost and time constraints of the project, while maintaining representation from all populations that might migrate through WASSIP-area fisheries (Figure 3). Consideration was given to ensuring, to the best of our knowledge, that the collections represented the genetic diversity of Western Alaska chum salmon. We also included enough representative stocks outside the WASSIP study area to ensure these stocks would be identifiable if present in fishery samples. These collections spanned the years 1986–2010 and totaled 35,921 chum salmon from 434 collections (Table 2).

Forty-eight percent (17,540 fish) of the fish were collected at locations in the WASSIP study area, Kotzebue Sound to Chignik/Kodiak, excluding the Upper Yukon River (Figures 4 and 5).

LABORATORY ANALYSIS

Developing and ascertaining SNPs for WASSIP

Markers were assayed by the IPSEG laboratory in 80–96 fish from each of 30 collections across the species' range (see DeCovich et al. 2012b for details). Ten of these collections were from CWAK (Table 2). Of the 228 markers surveyed, 188 markers performed adequately in the laboratory and were passed on to ADF&G for further consideration.

Genotypic proportions in the 24-Mile Creek sample departed from HWE ($\alpha = 0.01$) and it was removed from the analysis. Five markers departed from HWE when tested over the 29 remaining populations ($\alpha = 0.01$; Appendix A) and were excluded from subsequent analyses. Linkage disequilibrium analyses revealed 19 pairs of loci showing significant associations ($\alpha = 0.05$) in more than 50% of the populations. These 19 pairs segregated into 15 association blocks. Two marker sets were retained as paired markers representing single loci (See *Linkage disequilibrium* below for details; Figures 6 and 7). Genotypes for these sets, *Oke_gdh1-62* & *Oke_gdh1-19,* and *Oke_pgap-92* & *Oke_pgap-11,* were renamed and used as composite phenotypes in the subsequent marker-selection analyses (Table 3; Appendix A).

The results of the scored measures were scaled and are summarized in Appendix B. This resulted in a preliminary ranking of the top 96 backbone loci. As a final step, we considered laboratory performance of the SNPs and excluded 18 of these top-ranked loci. At each step, the next highest ranked backbone locus was added to the list of backbone loci. See DeCovich et al. (2012b) for details. The resulting 96 top-ranked backbone loci were used in this study. Summary statistics for these loci are listed in Table 3. Figure 8 diagrams the reduction in the number of SNPs at each step of the process.

Assaying genotypes

We genotyped all of the fish selected from baseline samples for 96 backbone loci (Tables 2 and 3). A majority of these genotypes were produced on the Biomark platform. However, 15 SNPs in a subset of collections (31) were re-analyzed on the AB 7900 platform. The number of individuals genotyped from baseline collections ranged from 3 to 315 and averaged 76 individuals (Table 2). Thirty-one percent of the baseline was genotyped at the University of Washington as part of a study of the structure of chum salmon populations on Kodiak Island and the Alaska Peninsula (Table 2).

Quality control

Quality control demonstrated a low overall genotypic discrepancy rate of 0.6% for WASSIP chum salmon baseline collections (Table 4). The majority of discrepancies were between heterozygous and homozygous genotypes with the *Database* method producing the highest rate at 0.7%. This is likely due to comparing preamplified DNA to nonpreamplified DNA. Preamplified DNA produced higher-quality plots and is expected to produce lower error rates. The baseline for this project was based on the preamplified DNA results. The overall discrepancy rates for *Original*, *New*, and *Database* method collections were 0.4% (*Original*), 0.5% (*New*), and 0.8% (*Database*). Therefore, baseline collections of chum salmon were genotyped with a process that produced estimated error rates of 0.2% for *Original*, 0.3% for *New*, and 0.4% for *Database* QC methods and an overall rate of 0.3%, assuming that at least one of these assays produced a correct genotype and that error rates were equal between the original and QC genotyping. Sixteen collections did not fall within the 3 QC methods described above and were excluded from Table 4. These collections have been identified in Table 2.

STATISTICAL ANALYSIS

Data retrieval and quality control

All backbone loci were variable in populations in the WASSIP study area. A total of 463 fish from the WASSIP baseline collections was missing genotypes for more than 20% of the backbone loci (19 SNPs). These fish were removed from further analyses (Table 2). For baseline collections within the WASSIP area, 11 fish were removed from the Kotzebue Sound reporting group (1.4%), 198 fish from CWAK (3.0%), 100 fish from Northern District (6.9%), 13 fish from Northwest District (1.2%), 35 fish from South Peninsula (1.7%), and 255 fish from Chignik/Kodiak (5.1%).

There were 183 samples identified as duplicates in the WASSIP baseline collections. For baseline collections within the WASSIP study area, 2 duplicate individuals were removed from the Kotzebue Sound reporting group (0.3%), 18 individuals from CWAK (0.2%), 4 individuals

from Northern District (0.3%), 2 individuals from Northwest District (0.2%), 8 individuals from South Peninsula (0.4%), and 13 individuals from Chignik/Kodiak (0.3%).

Hardy-Weinberg expectation

Three baseline collections deviated from HWE ($\alpha = 0.01$) and were removed from further analyses: Namdae River 2005, Nanaimo River 2006, and Big Mission Creek–Fall 2002 (Table 2). There was no geographic pattern to the deviations from HWE. Similarly, we observed no pattern in the deviation from HWE among backbone loci.

Pooling collections into populations

The exact geographic distances between sample locations were not possible to calculate due to incomplete GPS data. However, for this analysis, every effort was made to ensure that collections pooled into populations were collected from proximate locations representing the same spawning population. Pooled collections are listed in Table 2 (pooled collections have the same *population* number).

Removal of collections from the baseline

In our pooling tests, 18 collections were too small to stand alone in the baseline and could not be pooled with others, because there was no temporal sample from the same location (Table 2). Eight temporal collections were removed because of allele-frequency heterogeneity (chi-square tests), including 7 from the Alaska Peninsula and 1 from Asia reporting groups. For the Alaska Peninsula temporal collections, poorly documented collections were excluded. In all cases, the more contemporary collections were retained because these collections were associated with latitude/longitude information collected in the field, whereas the old collections were not. In the case of the Asian discrepancy, (Amur River, Russia), neither collection had reliable metadata so the collection with the fewest individuals was removed (28 individuals after individuals were removed for missing genotypes and duplicates; Table 2). We removed 2 collections from the CWAK reporting group (Table 2). These were originally entered into the ADF&G database as Snake River, Nushagak River drainage, but were discovered to be from the same Snake River already represented from the Norton Sound area (Table 2). Also, 2 State of Washington collections were removed from the East of Kodiak reporting group due to high discrepancy rates in the QC analysis (Table 2).

Of the 36,872 fish from 433 collections selected to be genotyped, the final baseline consisted of 32,817 fish from 402 collections representing 310 populations. Average population sample size was 106 individuals (range: 41–597; Table 2; Figure 3).

Linkage disequilibrium

Three backbone locus pairs showed significant ($P < 0.05$) linkage disequilibrium in a majority of the WASSIP-area chum salmon populations. These pairs were linked in more than half of the populations (*Oke_gdh1-62* & *Oke_gdh1-191*, 82% of populations; *Oke_pgap-92* & *Oke_pgap-111*, 96% of populations; *Oke_U1021-102* & *Oke_U1022-139*, 67% of populations; Figure 6). The 90% critical value of the f_{ORCA} difference distribution (Δ_{90}) was 0.038, which was smaller than Δ for one of the linked pairs (*Oke_U1021-102* & *Oke_U1022-139*: $\Delta = 0.071$; Figure 7). Therefore, *Oke_U1021-102* & *Oke_U1022-139* were combined into a composite locus, *Oke_U1021-102_U1022-13* (Table 5).

For each of the remaining linked pairs, the backbone marker with the lowest individual f_{ORCA} value was dropped from further analyses; *Oke_gdh1-62* and *Oke_pgap-92* (Table 5). Therefore, further evaluation of this baseline proceeded with only 94 markers. The set also included the 3 mitochondrial SNPs, which were combined into a single composite locus (*Oke_Cr30_Cr386_ND3-69*). Along with the combined *Oke_U1021-102_U1022-13* locus, this resulted in a total of 91 loci in the final set. This result differs from the SNP-selection process (DeCovich et al. 2012b, Figure 8, Appendices A1 and A2), in which the linked pairs *Oke_gdh1-62* & *Oke_gdh1-191* and *Oke_pgap-92* & *Oke_pgap* had Δ values greater than $\Delta_{90,}$ and therefore were retained as composite markers.

Analysis of genetic structure

Analysis of temporal variance

We used 179 collections from 83 populations to examine temporal variance with a 4-level ANOVA. We included collections from a location in this analysis that were similar except for calendar year to avoid other sources of variation (e.g., location, seasonal differences in spawn timing, etc.). We included every temporal set of collections that was in the final set of 310 collections (Table 2). The only reporting region that did not have annually separated collections was Kotzebue Sound. The ANOVA indicated that the overall variation among years within populations was negligible ($\sigma^2_{SS} = -0.04$; Table 6) compared to the variation among populations ($\sigma^2_P = 1.28$).

Visualization of genetic distances

The Neighbor Joining tree of pairwise F_{ST} indicated that CWAK chum salmon exhibited the least diversity among populations included in the baseline (Figure 9). Eastern Bristol Bay and the more northerly populations in the Northern District were included in the same cluster. However, collections from 2 Western Alaska reporting groups formed separate clusters within the larger Western Alaska group, repor ting groups Kotzebue and Upper Yukon. In addition, the upper Kuskokwim collections clustered together. Although collections from the Northern and Southwestern districts did not cluster by district, many of the collections were on the ends of long branches indicating higher interpopulation diversity in this part of the range than in CWAK.

A similar pattern was observed among collections from the South Peninsula, Chignik, and Kodiak areas. The Sturgeon River collection (Kitoi Hatchery used Sturgeon River as the progenitor stock) was particularly divergent among Kodiak Island populations. Nunivak Island was also highly divergent.

On the eastern Pacific range, outside Western Alaska, most collections fell into geographically delineated clusters, including Susitna River, Prince William Sound, Northern Southeast Alaska, Southern Southeast Alaska, British Columbia, and Washington State. On the western Pacific range (Asia), the collections from Russia, Japan, and Korea fell into separate clusters. We observed high concordance among loci for only the Asian populations, as evidenced by 21 nodes producing the same groupings with greater than 90% bootstrap support (Figure 9).

Determination of reporting groups

We tested several scenarios of reporting groups and reported the results at the September 2011 AP meeting. The results revealed a set of 9 reporting groups supported by the results below (Table 1). The most problematic groups to distinguish were those in CWAK, including Norton

Sound, Yukon Coastal, Kuskokwim River, and Bristol Bay. In other areas, we achieved fine-scale resolution. For example, we were able to separate the Northern and Northwest Districts into separate reporting groups, and the Upper Yukon River was also included as a separate group. For the sake of completeness we provide the results of MSA performance tests for the 9 reporting groups, as well as a 12-group set with CWAK broken into the 4 subregional groups.

Baseline evaluation for mixed stock analysis

Proof tests

Correct allocations for the 12-reporting-group proof tests (CWAK divided into 4 subregional reporting groups) averaged 0.90 and ranged from 0.48 to 0.99 (Table 7; Figure 10). Nine of the 12 proof tests met our goal of 90% correct allocation. For regional reporting groups outside CWAK (Asia, Kotzebue Sound, Upper Yukon, Northern District, and Northwest District, South Peninsula, Chignik/Kodiak, and East of Kodiak), correct allocations in the proof tests averaged 98% and ranged from 96% to 99% (Tables 7–10; Figure 7). For the subregional reporting groups within CWAK (Norton Sound, Yukon Coastal, Kuskokwim, and Bristol Bay), correct allocations in the proof tests ranged from 48% to 91% and averaged 75% with misallocations to other CWAK subregional reporting groups (Tables 7 and 8; Figure 10).

Correct allocations for the 9-reporting-group proof tests averaged 0.97 and ranged from 0.83 to 0.99 (Table 8; Figure 11). Repeated proof tests demonstrated that these reporting groups met the 90% correct allocation criteria. One proof test for Chignik/Kodiak did not reach the 90% correct allocation level (correct allocation = 0.83, misallocation to South Peninsula = 0.16; Table 9). These proof tests were repeated to determine if the results were repeatable. Replicate proof tests yielded above 90% correct allocations on average for all reporting groups (Tables 9–17; Figures 12–20). Other reporting groups yielded less than 90% correct allocation, including Northern District (0.80, test 1), South Peninsula (0.80, test 1, and 0.87, test 2), and Chignik/Kodiak (0.85, test 3, and 0.78, test 10), for the 10 replicate tests.

DISCUSSION

We have described the methods used to build the chum salmon baseline for WASSIP, investigated the genetic structure among chum salmon populations throughout the Pacific Rim, and tested the performance of this baseline for use in MSA in WASSIP.

GENETIC VARIATION AMONG CHUM SALMON CONTRIBUTING TO WASSIP AREA FISHERIES

The genetic relationships among populations in this baseline (Figure 9) are concordant with those previously observed using 53 SNPs (Jasper et al. 2012; Seeb et al. 2011). Japanese and Korean chum salmon populations are most divergent from other populations, as seen previously with allozymes (Seeb and Crane 1999) and with microsatellites (Beacham et al. 2009). The clustering of Russian populations with Alaska Peninsula and Gulf of Alaska populations was anticipated by the results of previous allozyme data, which also showed an association between these regional groups (Seeb and Crane 2004). This similarity between distantly separated populations may contribute to misallocations.

Analysis of temporal variation within populations

The temporal ANOVA was performed after some temporal collections had been removed, because these collections could not be pooled with other annual collections from the same location. In most cases, the temporal collections that had been removed were the older collections. Location information for older collections is sometimes unreliable, whereas recent collections have more reliable metadata due to the use of GPS devices. The exclusion of older, often genetically heterogeneous, samples undoubtedly led to an underestimate of temporal variability in a population.

MSA PERFORMANCE

Inability to distinguish among Coastal Western Alaska reporting groups

The largest weakness of this baseline was that the updated baseline was unable to differentiate among CWAK subregional reporting groups. In the original 53-SNP baseline, we found some similarity among populations within these reporting groups (Jasper et al. 2012). Consequently, we increased the number of markers, hoping to increase the resolution of genetic differences among CWAK subregional reporting groups. We expended considerable effort to develop new markers (DeCovich et al. 2012a), selecting markers with the primary goal of distinguishing among CWAK subregional reporting groups (DeCovich et al. 2012b).

In the process of developing this new baseline, we added samples from numerous populations in the CWAK region, and these additions may have contributed to poorer, but more appropriate, MSA performance. The better population structure is represented by the baseline, the more accurately the MSA performance reflects the real world. However, increased representation of populations can also lead to poor MSA performance, especially when the geographic boundaries of reporting groups do not coincide with genetic boundaries. In these cases, adding baseline collections that are genetically intermediate between reporting groups can lead to lower MSA performance. Nevertheless, reduced performance better represents how the baseline performs with real-world mixtures in which all populations may be present.

The life history traits of chum salmon in CWAK likely underlie the challenges of distinguishing among subregional reporting groups using genetic MSA. The current understanding is that chum salmon in CWAK survived Pleistocene glaciation in a single refugium (Beringia; Seeb and Crane 1999a; McPhail and Lindsey 1970). They radiated from this refugium into CWAK drainages starting about 10,000 years ago when glaciers in the area rapidly receded (Hopkins et al. 1982). This short time, coupled with large effective population sizes due to large spawning aggregates and lower homing fidelity than in species such as sockeye salmon (Quinn 1984; Tallman and Healey 1994), resulted in reduced genetic drift. Finally, the short freshwater life histories of chum salmon may reduce among-population selection of alleles, as has been detected for some sockeye salmon markers (Gomez-Uchida et al. 2011). The common recent ancestry, low genetic drift, gene flow, and low opportunity for site-specific genetic selection makes finding adequate genetic variation for MSA among these populations challenging.

Conservative tests

Proof tests were performed with fewer fish than was the sampling goal for WASSIP mixed fisheries strata (400 individuals) and were performed with uninformative priors, making these tests conservative measures of reporting group performance in MSA. Only 200 individuals

could be used in the proof tests to avoid depopulating the baseline for reporting groups represented by fewer individuals. We anticipate using an informative prior (sequential prior based on the posterior distribution of similar mixtures) in the MSA of WASSIP mixtures to provide more accurate and precise estimates. The use of a flat prior in the proof tests is likely to have the largest negative effect on the correct assignments for reporting groups including populations with similar allele frequencies, such as the South Peninsula and Chignik/Kodiak (see below). We anticipate that an informed prior, such as the sequential prior used in MSA of fishery samples, will improve the performance of the baseline.

Effect of genetic similarity among groups on MSA performance

The effect of repeated draws of different fish for proof tests can be large. The misallocation that arises when fish are drawn from populations that are genetically similar to those of adjacent reporting regions can cause correct allocation in 100% proof tests to fall below 90%. This was observed in the original proof test for Chignik/Kodiak (Table 8; Figure 11), where the largest misallocation was to the South Peninsula reporting group. This is not surprising, because the border separating the 2 reporting groups was drawn along management district lines and because several populations are geographically close and genetically similar to one another other (Figures 3 and 4). Although the poorest independent draw yielded 80%, the average of 10 independent tests was 93% (80% to 99% range; Table 16; Figure 19). The other reporting groups that varied greatly in correct allocation among the 10 replicate tests were Northern District (80% to 99% range), and Chignik/Kodiak (78% to 98% range), but all reporting groups met the 90% correct allocation average across the 10 independent tests, the benchmark set for determining reporting group acceptability (Habicht et al. 2012).

Misallocation rates in the proof tests provide a measure of uncertainty when interpreting estimates from actual fishery samples. For example, samples from the Chignik area could contain fish from Chignik area populations that are genetically similar to those in from the South Peninsula. This could result in biased estimates with some fish from actual Chignik populations being assigned to the South Peninsula reporting group.

Baseline is adequate for WASSIP objectives

Given the reporting groups identified through the WASSIP process, we believe that the chum-salmon baseline reported here meets the goals of accurately describing the genetic structure among populations in the WASSIP area, as well as meeting our goal of 90% correct allocation in MSA applications. We are confident in the methods used to build the baseline, as well as the product of these methods, and believe that this baseline will provide accurate and precise estimates of stock composition in WASSIP fisheries.

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TABLES

Table 1.– Geographic boundaries of the successful reporting groups (left justified) and failed subregional reporting groups (indented) defined for use in mixed stock analysis of chum salmon for WASSIP.

Successful/failed reporting groups	Start point	Stop point
Asia	Western end of species range	US/Russia border
Kotzebue Sound	Point Hope	Cape Prince of Wales
Coastal Western Alaska (CWAK)	Cape Prince of Wales (excluding Upper Yukon River)	Cape Menshikof
Norton Sound	Cape Prince of Wales	Point Romanof
Yukon Coastal	Point Romanof	Summer-run populations in the Koyukuk River drainage and mainstem Yukon River up to and including the Tozitna River
Kuskokwim	Naskonat Peninsula	Cape Newenham
Bristol Bay	Cape Newenham	Cape Menshikof
Upper Yukon River	Fall-run populations in Koyukuk River drainage and all populations in Tanana River drainage	Canadian Headwaters
Northern District	Cape Menshikof	Moffit Point
Northwest District	Moffit Point	Cape Sarichef
South Peninsula	Scotch Cap	Kupreanof Point
Chignik/Kodiak	Kupreanof Point (including Kodiak Island)	Cape Douglas
East of Kodiak	Cape Douglas	Eastern end of species range

Table 2.– Background information on the collections of chum salmon used in the baseline for WASSIP, including regional and subregional reporting group, quality control (QC) notes, location, collection and population numbers, collection date, and the numbers of fish.

						No. of individuals			
Reporting Group	QC[a]	Location	Collection	Population	Date	Initial	Missing	Duplicate	Final
Asia	1	Amur River – China[b]	1		2004	30	0	0	0
		Namdae River	2	1	2005	96	6	0	90
		Namdae River[c]	3		2005	96	1	0	0
		Tokachi River	4	2	10/22/2002	80	1	1	78
		Kushiro River	5	3	10/22/1998	79	0	0	79
		Chitose River - early	6	4	10/7/2003	79	4	0	75
		Chitose River – late[b]	7		12/5/2003	80	47	0	0
		Nishibetsu River	8	5	10/22/1997	80	0	0	80
		Shibetsu River[b]	9		10/10/2003	80	46	1	0
		Abashiri River	10	6	10/19/1998	80	1	0	79
	2	Shinzunai River	11	7	10/17/2002	80	0	0	80
		Teshio River	12	8	10/23/2001	80	0	2	78
		Yurappu River - early	13	9	9/24/1997	80	0	0	80
		Yurappu River - late	14	10	11/17/1997	80	0	0	80
		Sasanai River	15	11	11/14/1990	78	1	0	77
		Shari River	16	12	10/11/2001	77	2	0	75
		Tokoro River	17	13	10/2/2005	100	31	0	69
		Tokushibetsu River	18	14	10/15/2004	80	0	0	80
		Gakko River - early	19	15	10/25/2003	80	1	1	78
		Narva[b]	20		1994	18	0	0	0
	1	Naiba	21	16	1995	99	1	0	98
	1	Tym River	22	17	1995	53	0	0	53
		Paratunka River	24	19	8/17/1998	95	0	1	94
	1	Bolshaya River	23	18	6/1/1997	96	3	0	93

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Table 2. Page 2 of 17.

Reporting Group	QC[a]	Location	Collection	Population	Date	No. of individuals			
						Initial	Missing	Duplicate	Final
		Amur River - summer run	25	20	6/1/1997	60	0	0	60
		Amur River - summer run[b]	26		7/15/2001	100	71	1	0
		Bistraya River	27	21	8/16/1998	70	2	2	66
		Hairusova River	28	22	1990	44	4	3	37
			29	22	1993	48	0	0	48
		Ozerki Hatchery	30	23	8/16/1998	95	1	1	93
		Pymta	31	24	1991	40	0	0	40
			32	24	1993	50	3	0	47
			33	24	1993	60	0	0	60
		Penzhina	34	25	1993	43	0	0	43
		Kol River	35	26	1990	79	1	0	78
			36	26	1991	46	1	0	45
		Vorovskaya	37	27	1993	101	0	0	101
		Kamchatka River	38	28	1990	50	1	0	49
		Palana River[g]	39	29	7/24/1998	95	5	0	90
		Magadan	40	30	1991	77	0	0	77
		Ossora	41	31	1990	40	2	0	38
	1		42	31	1996	49	0	0	49
		Tauy	43	32	1990	43	0	2	41
		Ola River - Hatchery	44	33	1990	79	0	1	78
		Oklan River	45	34	1993	76	1	0	75
		Anadyr River – early[b]	46		1993	32	5	0	0
		Kanchalan	47	35	1991	80	1	2	77
		Utka[b]	48		1991	40	1	0	0
		Udarnitza River	49	36	1994	44	0	0	44
					Total	3417	244	18	2852
Kotzebue Sound		Inmachuk River[d]	50	37	8/8/2005	94	2	1	91
		Kobuk River - at Kiana[d]	51	38	7/13/2004	95	0	0	95
		Kobuk - Salmon River	52	39	1991	100	1	0	99

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Table 2. Page 3 of 17.

Reporting Group	QC[a]	Location	Collection	Population	Date	No. of individuals			
						Initial	Missing	Duplicate	Final
		Kelly Lake - Noatak River	53	40	1991	95	0	0	95
		Noatak River	54	41	1991	95	3	0	92
		Selby Slough	55	42	9/21/1994	95	5	0	90
		Agiapuk River	56	43	7/25/2005	95	0	1	94
	1	American River	57	44	9/21/2005	95	9	0	86
					Total	764	11	2	742
CWAK									
Norton Sound[e]		Eldorado River	58	45	6/28/2005	95	5	1	89
		Nome River	59	46	7/15/2005	95	1	0	94
		Pilgrim River	60	47	7/13/1994	90	15	0	75
		Snake River	61	48	1993	35	2	0	33
			62	48	7/25/1995	58	1	0	57
		Snake River[f]	63		7/29/1994	24	0	0	0
		Snake River[f]	64		9/1/1996	24	0	0	0
		Solomon River	65	49	7/27/1995	65	8	0	57
			66	49	9/1/1996	5	0	0	5
		Fish River	67	50	6/26/2004	95	3	0	92
		Kwiniuk River[d,g]	68	51	6/30/2004	95	1	0	94
		Niukluk River	69	52	7/5/2004	95	2	0	93
		Tubutulik River	70	53	7/31/2009	95	2	0	93
		Shaktoolik River	71	54	7/23/2005	95	1	0	94
		Pikmiktalik River	72	55	7/2/2005	95	0	0	95
		Koyuk River	73	56	7/30/2005	46	2	1	43
		Unalakleet	74	57	1992	95	1	0	94
		Unalakleet[d,g]	75	57	6/21/2004	95	1	0	94
		Ungalik River	76	58	7/17/2005	54	2	1	51
			77	58	7/30/2010	95	2	0	93
Yukon Coastal[e]		Black River	78	59	6/11/2006	95	2	0	93
		Andreafsky River - West Fork	79	60	1993	95	10	0	85

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Table 2. Page 4 of 17.

Reporting Group	QC[a]	Location	Collection	Population	Date	No. of individuals			
						Initial	Missing	Duplicate	Final
		Andreafsky River - East Fork[d,g]	80	61	6/26/2004	95	0	1	94
		Chulinak	81	62	1989	93	0	1	92
		Beaver Creek - Anvik[b]	82		1992	15	0	0	0
	1	Otter Creek - Anvik	83	63	1993	96	35	0	61
			84	63	1993	95	0	0	95
		Yellow River - Anvik	85	64	1992	80	0	0	80
		Innoko River	86	65	1993	85	0	0	85
		Kaltag River	87	66	7/21/1992	93	1	0	92
		Nulato River	88	67	7/10/1994	95	0	0	95
		Nulato River[d,g]	89	67	7/8/2003	95	1	0	94
		Gisasa River	90	68	6/30/2004	95	0	0	95
	1	Clear Creek	91	69	2002	95	1	0	94
		Huslia River	92	70	1993	95	0	0	95
		South Fork Koyukuk River - Early	93	71	7/10/1996	93	3	0	90
		Henshaw Creek - Early	94	72	6/23/2004	95	0	1	94
		Melozitna River	95	73	6/29/2003	95	3	1	91
		Tozitna River	96	74	6/27/2003	95	3	0	92
Kuskokwim[e]		Kwethluk River	97	75	8/4/1994	48	0	0	48
			98	75	7/1/2007	95	0	0	95
		Tuluksak River	99	76	7/1/2007	93	1	0	92
		Kisaralik River	100	77	8/5/1994	95	2	0	93
		Aniak River	101	78	7/28/1992	97	4	1	92
		Salmon River[d,g]	102	79	7/5/2007	95	0	0	95
		Holokuk River	103	80	7/31/2008	95	1	2	92
			104	80	7/29/1995	11	0	0	11
		Kogrukluk River	105	81	7/9/2007	95	0	0	95
		Kasigluk River	106	82	8/5/1994	70	15	0	55
		George River	107	83	6/28/2007	95	0	0	95

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Table 2. Page 5 of 17.

Reporting Group	QC[a]	Location	Collection	Population	Date	No. of individuals			
						Initial	Missing	Duplicate	Final
		Stony River	108	84	6/27/1994	95	0	0	95
			109	84	9/25/1994	56	1	0	55
		Necons River	110	85	7/28/2007	95	0	0	95
		Tatlawiksuk River	111	86	6/29/2007	95	0	0	95
		Nunsatuk River	112	87	7/29/1994	96	4	0	92
		Takotna River	113	88	6/29/2007	95	1	0	94
	1	Big River - Fall	114	89	9/14/2008	95	1	0	94
		South Fork Kuskokwim - Fall	115	90	9/16/2008	95	0	0	95
		Windy Fork Kuskokwim - Fall	116	91	9/15/2008	95	2	0	93
		Kanektok River[d,g]	117	92	7/10/2007	95	0	1	94
	2	Goodnews River	118	93	1991	95	1	0	94
			119	93	7/22/2006	46	2	1	43
		Mekoryuk River	120	94	6/29/2006	93	14	1	78
			121	94	2006	26	0	0	26
Bristol Bay[e]		Togiak River	122	95	1993	100	8	0	92
	1		123	95	8/19/2011	93	10	0	83
		Osviak River[d,g]	124	96	8/9/2010	95	7	0	88
		Sunshine Creek	125	97	7/25/2006	47	0	0	47
		Iowithla River[d,g]	126	98	7/26/2010	95	0	0	95
		Mulchatna River	127	99	7/23/1994	95	4	0	91
	1	Kokwok River	128	100	7/22/2011	133	2	0	131
		Upper Nushagak	129	101	1992	52	0	1	51
			130	101	1993	48	0	2	46
		Stuyahok River	131	102	1992	31	0	0	31
			132	102	1993	57	2	0	55
		Klutuspak Creek	133	103	8/7/2010	75	5	0	70
		Big Creek - Naknek River	134	104	7/31/1993	70	1	0	69
		Alagnak River[d,g]	135	105	8/9/2010	95	1	2	92

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Table 2. Page 6 of 17.

Reporting Group		QC[a]	Location	Collection	Population	Date	No. of individuals			
							Initial	Missing	Duplicate	Final
			Whale Mountain Creek	136	106	7/30/1993	95	0	0	95
			Whale Mountain Creek[d,g]	137	106	8/5/2010	95	1	0	94
			Pumice Creek	138	107	7/30/2010	95	0	0	95
			Wandering Creek - Dog Salmon River	139	108	8/6/2010	50	0	0	50
						Total	6623	198	18	6344
Upper River	Yukon		Henshaw Creek – Late	140	109	9/23/1995	62	2	0	60
			South Fork Koyukuk River - Late	141	110	8/1/1996	95	2	1	92
			Jim River	142	111	8/13/2002	95	2	1	92
		1		143	111	7/26/2010	57	0	3	54
		1	17 Mile Slough (Nenana) - Fall	144	112	10/24/2010	97	7	0	90
			Tanana River Mainstem	145	113	11/10/1993	95	0	0	95
			Toklat River - Geiger Creek	146	114	10/12/1994	95	0	0	95
			Kantishna River	147	115	9/2/2001	95	0	1	94
			Chena River	148	116	8/3/1994	95	18	0	77
			Salcha River	149	117	8/18/2001	85	2	0	83
			Delta River	150	118	10/31/1994	150	0	1	149
			Bluff Cabin	151	119	1992	100	1	0	99
			Big Salt River	152	120	2001	71	2	0	69
			Chandalar River	153	121	9/19/2001	95	2	1	92
			Sheenjek River	154	122	1992	96	3	0	93
			Black River	155	123	1995	95	0	0	95
			Old Crow - Porcupine River	156	124	2007	95	0	3	92
			Fishing Branch[d]	157	125	2007	95	5	0	90
			Kluane River[d]	158	126	10/26/2001	95	8	2	85
				159	126	10/13/2007	33	4	0	29

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Table 2. Page 7 of 17.

Reporting Group	QC[a]	Location	Collection	Population	Date	No. of individuals			
						Initial	Missing	Duplicate	Final
		Pelly River	160	127	1993	84	0	0	84
		Minto Slough	161	128	1989	92	0	1	91
		Tatchun Creek	162	129	10/24/1992	93	1	0	92
		Big Creek	163	130	10/31/1995	100	0	0	100
		Teslin River	164	131	10/22/1992	94	0	2	92
		Donjek River	165	132	10/31/1994	69	3	6	60
					Total	2328	62	22	2244
Northern District		Wiggly Creek – Cinder[d]	166	133	8/4/1993	95	1	0	94
			167	133	8/13/2009	95	10	2	83
		Meshik River[d]	168	134	1992	78	0	0	78
		Plenty Bear Creek - Meshik River[d]	169	135	8/2/1993	92	2	0	90
			170	135	8/11/2009	51	3	0	48
		Braided Creek - Meshik River[d]	171	136	8/11/2009	94	0	0	94
		Three Hills River[d]	172	137	7/30/2002	50	1	0	49
		North of Cape Seniavin[d]	173	138	8/28/2001	55	10	0	45
			174	138	8/16/2009	22	0	0	22
			175	138	7/31/2010	30	0	1	29
		Right Hand Moller Bay[d]	177	139	8/16/2009	95	1	0	94
		Right Hand Moller Bay[d,h]	176		1998	95	0	0	0
		Lawrence Valley Creek[d]	178	140	8/16/2009	95	0	0	95
			179	140	1992	95	0	0	95
		Coal Valley[d]	180	141	8/27/2008	97	3	0	94
		Deer Valley[d]	181	142	8/27/2008	130	38	1	91
		Sapsuk River - Nelson Lagoon[d]	182	143	1992	80	12	0	68
			183	143	8/27/2008	95	19	0	76
					Total	1444	100	4	1245

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Table 2. Page 8 of 17.

Reporting Group	QC[a]	Location	Collection	Population	Date	No. of individuals			
						Initial	Missing	Duplicate	Final
Northwest		Moffet Creek[d]	184	144	9/5/1996	95	0	0	95
District		Joshua Green[d]	186	145	8/18/2009	95	3	0	92
		Joshua Green[d,h]	185		1994	95	1	0	0
		Frosty Creek[d]	187	146	8/30/1992	95	0	0	95
			188	146	8/20/2009	95	0	0	95
		Alligator Hole[d]	189	147	8/20/2009	95	7	0	88
			190	147	9/4/1996	95	0	0	95
		Traders Cove[d]	191	148	1992	76	0	0	76
		St. Catherine Cove[d]	192	149	1992	80	0	0	80
			193	149	8/19/2009	95	2	2	91
		Peterson Lagoon[d]	194	150	8/19/2009	95	0	0	95
			195	150	1992	86	0	0	86
					Total	1097	13	2	988
South Peninsula		Little John Lagoon[d]	196	151	1992	80	0	0	80
			197	151	8/19/2009	95	3	0	92
		Sandy Cove[d]	198	152	8/26/1996	95	2	2	91
			199	152	8/20/2009	95	0	0	95
		Russell Creek[d]	200	153	8/30/1993	93	2	0	91
			201	153	8/20/2009	95	1	0	94
		Delta Creek - Cold Bay[d]	202	154	8/29/1996	95	0	0	95
		Belkovski River[d]	203	155	6/14/1905	87	0	0	87
		Volcano Bay - Cold Bay[d]	204	156	8/15/2009	95	0	0	95
		Volcano Bay - Cold Bay[d,h]	205		1996	42	1	0	0
		Volcano Bay - Cold Bay[d,h]	206		1992	53	0	0	0
		Ruby's Lagoon - Pavlof Bay[d]	207	157	8/31/1996	95	3	0	92
		Canoe Bay[d]	208	158	1992	95	1	0	94
			209	158	8/15/2009	95	3	0	92
		Zachary Bay[d]	210	159	1992	80	3	1	76
		Foster Creek - Balboa Bay[d]	211	160	8/14/2009	95	6	0	89

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Table 2. Page 9 of 17.

Reporting Group	QC[a]	Location	Collection	Population	Date	No. of individuals			
						Initial	Missing	Duplicate	Final
			212	160	8/20/1992	95	2	0	93
		Coleman Creek[d]	213	161	9/6/1996	95	0	0	95
		Chichagof Bay[d]	214	162	8/17/2009	95	3	3	89
			215	162	8/27/1996	95	3	1	91
		Big River - Stepovak Bay[d]	216	163	8/18/1992	50	0	0	50
			217	163	8/17/2009	95	1	1	93
		Stepovak River[d]	218	164	8/17/2009	95	1	0	94
		Stepovak River[g,h]	219		1993	95	0	0	0
					Total	2100	35	8	1868
Chignik/Kodiak		Ivanof River[d]	220	165	8/23/1993	88	1	0	87
			221	165	8/14/2009	95	0	1	94
		Portage Creek[d]	222	166	8/21/1993	95	0	0	95
			223	166	8/29/2008	95	0	0	95
		North Fork Creek - Kujulik Bay[d]	224	167	8/12/2009	95	2	0	93
			225	167	8/22/1993	72	1	0	71
		North Fork Creek - Aniakchak River[d]	226	168	8/3/1993	95	1	0	94
		Main Creek - Amber Bay[d]	228	169	8/12/2009	85	0	0	85
		Main Creek - Amber Bay[g,h]	227		1993	92	2	1	0
		Northeast Creek[d]	229	170	8/23/2008	112	18	0	94
		Ocean Bay[d]	230	171	8/13/2009	79	0	1	78
		Nakililock River[d]	231	172	8/23/2008	107	12	0	95
		Chiginagak Bay River[d]	232	173	8/20/1993	70	1	0	69
			233	173	8/12/2009	92	1	1	90
		Kialagvik Creek - Wide Bay[d]	234	174	8/11/1993	90	7	0	83
			235	174	8/25/2009	95	0	1	94
		Pass Creek - Wide Bay[d]	236	175	8/24/2009	95	1	0	94
		Dry Bay River[d]	237	176	8/24/2009	71	0	0	71

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Table 2. Page 10 of 17.

Reporting Group	QC[a]	Location	Collection	Population	Date	No. of individuals			
						Initial	Missing	Duplicate	Final
		Bear Bay Creek[d]	238	177	8/19/2009	95	2	1	92
			239	177	8/11/1993	95	0	0	95
		Alagogshak River[d]	240	178	8/12/1993	95	1	0	94
		Big River - Hallo Bay[d]	242	179	9/2/2009	95	0	0	95
		Big River - Hallo Bay[d,h]	241		1993	94	2	0	0
		Karluk Lagoon[d]	243	180	8/31/2009	91	7	1	83
		Sturgeon River[d]	244	181	7/29/2008	6	0	0	6
			245	181	7/10/2009	125	22	0	103
		Big Sukhoi[d]	246	182	8/7/2009	95	0	1	94
			247	182	1992	95	0	0	95
		Deadman River[d]	248	183	8/18/2009	95	0	0	95
		Sitkinak Island[d]	249	184	8/7/2009	95	2	0	93
		NE Portage – Alitak[d]	250	185	8/18/2009	95	1	0	94
		Barling Bay Creek[d]	251	186	8/6/2009	95	2	1	92
		West Kiliuda Creek[d]	252	187	7/29/2008	4	0	0	4
			253	187	9/12/2009	87	4	0	83
		Dog Bay[d]	254	188	1992	95	0	0	95
		Coxcomb Creek[d]	255	189	8/17/2009	91	1	1	89
		Gull Cape Creek[d]	256	190	9/14/1993	95	3	0	92
			257	190	9/23/2009	95	1	0	94
		Eagle Harbor[d]	258	191	8/17/2009	95	0	1	94
		Rough Creek[d]	259	192	9/12/2009	95	18	0	77
		American River[d]	260	193	1992	95	0	0	95
		Russian River[d]	261	194	8/17/2009	95	3	0	92
			262	194	8/17/2007	95	1	1	93
		Kizhuyak River[d]	263	195	8/19/2009	95	4	1	90
			264	195	1992	88	4	0	84
		Uganik River[d]	265	196	8/20/2009	95	14	0	81
			266	196	1992	95	1	0	94

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Table 2. Page 11 of 17.

Reporting Group	QC[a]	Location	Collection	Population	Date	No. of individuals			
						Initial	Missing	Duplicate	Final
		Spiridon River – Upper[d]	267	197	8/18/2009	95	6	0	89
		Zachar River[d]	268	198	7/21/2009	67	1	0	66
		Kitoi Hatchery[d]	269	199	7/23/1993	100	1	0	99
			270	199	7/29/2009	95	0	0	95
					Total	4561	255	13	4219
East of Kodiak		McNeil River Lagoon	271	200	7/14/1994	60	1	0	59
			272	200	1996	49	0	0	49
		Chunilna River	273	201	1993	84	1	0	83
		Susitna River (Slough 11)	274	202	9/5/1996	95	1	0	94
		Talkeetna River	275	203	9/7/1995	50	0	0	50
		Spink Creek	276	204	8/27/2007	23	0	0	23
			277	204	8/30/2008	22	1	0	21
		Little Susitna River[d]	278	205	8/11/2010	95	0	0	95
		Willow Creek	279	206	8/25/2010	95	6	0	89
		Carmen Lake	280	207	8/23/2010	67	0	0	67
		Williwaw Creek	281	208	8/17/2010	67	0	0	67
	2	Beartrap Creek	282	209	8/6/2008	200	6	0	194
	2		283	209	7/28/2009	200	2	0	198
	2		284	209	7/22/2010	200	10	0	190
	2	Constantine Creek	285	210	8/22/2008	200	5	1	194
	2		286	210	8/3/2009	200	0	0	200
	2		287	210	7/30/2010	200	0	0	200
	2	Siwash Creek	288	211	8/25/2008	150	0	0	150
			289	211	8/8/2006	60	6	0	54
	2		290	211	8/19/2009	45	0	0	45
	2		291	211	8/18/2010	116	3	0	113
		Wally Noerenberg Hatchery	292	212	7/22/2002	95	1	0	94
			293	212	6/20/2006	95	0	0	95
	2		294	212	7/16/2008	100	2	0	98

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Table 2. Page 12 of 17.

Reporting Group	QC[a]	Location	Collection	Population	Date	No. of individuals			
						Initial	Missing	Duplicate	Final
	2		295	212	7/14/2009	100	2	0	98
	2	Wells River	296	213	7/25/2008	255	2	0	253
	2		297	213	8/11/2009	255	1	0	254
	2		298	213	8/6/2010	90	0	0	90
		Keta Creek	299	214	9/3/1992	95	0	0	95
		Olsen Creek	300	215	7/20/1995	95	1	0	94
		Black Bay[b]	301		1991	38	0	0	0
		Chilkat River - mainstem	302	216	2006	81	4	1	76
		Herman Creek - Chilkat River	303	217	9/19/2006	95	1	0	94
		Klehini River - Chilkat River	304	218	9/18/2006	95	2	1	92
		Wells Bridge	305	219	2006	62	16	0	46
		Sawmill Creek - Berners Bay	306	220	7/19/2006	95	0	0	95
		DIPAC Hatchery	307	221	7/27/2006	95	1	0	94
			308	221	7/27/2006	200	13	0	187
		Gastineau[b]	309		1997	42	2	0	0
		Taku River - Fall	310	222	8/30/2006	95	0	2	93
		Port Camden[b]	311		1995	35	0	0	0
		Prospect Creek	312	223	8/13/2010	95	6	0	89
		Sanborn Creek	313	224	7/27/2006	95	1	0	94
		Admiralty Creek	314	225	8/6/2010	72	8	0	64
	1	Swan Cove Creek	315	226	8/5/2010	95	2	5	88
		Long Bay	316	227	8/25/1991	66	0	1	65
			317	227	8/17/1992	95	1	0	94
		Saltery Bay	318	228	1992	48	0	0	48
		Ford Arm Lake - Fall	319	229	8/15/2006	95	0	0	95
		Sisters Lake	320	230	8/21/2006	95	7	2	86
		Hidden Falls Hatchery	321	231	8/3/2006	95	0	0	95

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Table 2. Page 13 of 17.

Reporting Group	QC[a]	Location	Collection	Population	Date	No. of individuals			
						Initial	Missing	Duplicate	Final
		Ralph's Creek	322	232	7/9/2006	95	0	0	95
		Saook Bay	323	233	7/10/2006	95	1	0	94
		Medvejie Hatchery	324	234	1997	24	0	0	24
			325	234	9/8/2009	95	0	0	95
		Nakwasina River	326	235	9/5/2006	95	2	0	93
		West Crawfish	327	236	9/8/2006	95	1	2	92
		Klahini River	328	237	1986	50	0	0	50
		Harding River	329	238	8/9/2010	45	0	0	45
		Disappearance Creek	330	239	1986	50	2	0	48
			331	239	9/25/1998	95	0	0	95
		Disappearance Creek - Fall	332	240	10/4/2007	95	9	0	86
			333	240	9/11/2010	95	14	5	76
		Karta River	334	241	7/23/2006	56	0	0	56
		Lagoon Creek - Fall	335	242	10/4/2007	95	11	6	78
			336	242	9/22/2010	95	7	0	88
		Dry Bay Creek	337	243	8/2/2006	95	1	0	94
		North Arm Creek[d]	338	244	8/4/2006	95	1	0	94
			339	244	1987	4	1	0	3
		Saginaw Creek	340	245	8/12/2010	67	25	1	41
		Sample Creek	341	246	8/13/2010	95	21	0	74
		Carroll River	342	247	8/11/2009	95	9	1	85
		Neets Bay - Summer	343	248	1997	50	0	0	50
			344	248	7/11/2006	95	0	0	95
		Neets Bay - Fall	345	249	9/30/2006	95	0	0	95
		Traitors Cove Creek	346	250	8/2/2006	95	3	1	91
		Fish Creek - Early	347	251	8/8/1988	50	1	0	49
			348	251	8/1/2006	95	13	0	82
		Fish Creek -Late	349	252	9/24/1988	50	1	0	49
		Glen Creek[b]	350		2010	43	10	0	0

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Table 2. Page 14 of 17.

Reporting Group	QC[a]	Location	Collection	Population	Date	No. of individuals			
						Initial	Missing	Duplicate	Final
		Hidden Inlet	351	253	8/13/2009	90	7	1	82
		Nakat Inlet - Summer	352	254	7/12/2006	95	0	0	95
		Stagoo	353	255	1988	50	1	0	49
		Ecstall	354	256	1988	50	0	0	50
		Kitwanga River[d]	355	257	2006	103	29	0	74
		Bag Harbor	356	258	10/18/1989	50	1	0	49
		Pallant Creek	357	259	2006	212	0	3	209
		Salmon River	358	260	1989	50	3	0	47
		Sedgewick	359	261	1989	50	0	0	50
		Surprise	360	262	10/15/1989	50	0	0	50
		Kitasoo Creek	361	263	2006	181	1	11	169
		Kitimat River	362	264	2006	108	3	1	104
		Snootli Creek	363	265	2006	199	3	6	190
		West Arm Creek	364	266	2006	188	0	2	186
		Big Qualicum River	365	267	2006	77	4	1	72
		Nanaimo River[c]	366		2006	245	6	41	0
		Goldstream River	367	268	2006	95	0	0	95
		Little Qualicum River	368	269	2006	103	3	2	98
		Mussel[b]	369		1989	31	0	0	0
		Puntledge River	370	270	2006	101	0	2	99
		Conuma River	371	271	2006	100	2	2	96
		Nahmint River	372	272	2006	102	3	4	95
		Nitinat River	373	273	2006	113	0	0	113
		Sarita River	374	274	2006	75	11	1	63
		Sooke River	375	275	2006	51	1	0	50
		Sugsaw River	376	276	2006	67	3	4	60
		Nimpkish River	377	277	2006	187	0	0	187
		Aloutte River	378	278	2006	96	1	0	95
		Inch Creek	379	279	2006	184	0	3	181

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Table 2. Page 15 of 17.

Reporting Group	QC[a]	Location	Collection	Population	Date	No. of individuals			
						Initial	Missing	Duplicate	Final
		Norrish Creek	380	280	2006	100	8	1	91
		Weaver Creek	381	281	2006	99	2	1	96
		Salmon Creek - Summer	382	282	2003	49	1	7	41
			383	282	2004	46	0	5	41
		Lower Skagit River - Fall	384	283	1998	91	0	0	91
		Skykomish River - Fall	385	284	1994	95	8	0	87
		Snoqualmie River	386	285	11/4/1996	95	11	0	84
		Upper Sauk River - Fall	387	286	1994	95	8	1	86
		Elwha River[d]	388	287	11/4/2004	95	2	0	93
		Fennel Creek[b]	389		2002	15	0	0	0
		Diru Creek - Tribal Hatchery	390	288	12/22/2002	48	2	1	45
		Mill Creek - Fall	391	289	1994	95	3	12	80
		Sherwood Creek - Fall	392	290	1994	95	2	6	87
		Sherwood Creek - Summer	393	291	1994	94	5	1	88
		Big Mission Creek	394	292	2002	11	2	0	9
		Big Mission Creek - Fall	395	292	2003	47	0	1	46
		Big Mission Creek - Fall[c]	396		2002	48	1	7	0
		Canyonfalls Creek[b]	397		2002	30	5	1	0
		Dewatto River - Fall	398	293	1998	16	1	0	15
			399	293	1998	62	3	0	59
		Dosewallips River - Summer	400	294	2000	48	4	2	42
			401	294	2003	47	0	3	44
		Hamma Hamma River	402	295	9/13/2005	95	1	0	94
		Hamma Hamma River - Summer	403	296	2001	16	0	0	16
			404	296	2001	47	1	2	44
			405	296	2003	48	0	0	48
		Hoodsport Hatchery - Fall[b]	406		1998	15	0	0	0

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Table 2. Page 16 of 17.

Reporting Group	QC[a]	Location	Collection	Population	Date	No. of individuals			
						Initial	Missing	Duplicate	Final
		Lilliwaup River - Summer	407	297	2001	48	3	0	45
		Lilliwaup River - Summer[h]	408		2002	47	1	4	0
		Lilliwaup River - Fall	409	298	2005	47	2	1	44
			410	298	2006	48	0	0	48
		Quilcene - Summer	411	299	2001	47	0	0	47
			412	299	1997	16	0	0	16
		Big Quilcene River - Summer[b]	413		1992	48	7	4	0
		Union River - summer	414	300	2000	16	1	0	15
			415	300	2003	53	1	0	52
			416	300	2004	42	0	0	42
		I-205 Seeps - Fall	417	301	2000	25	4	0	21
			418	301	2000	64	13	0	51
		Jimmy Creek - Summer	419	302	2000	46	2	0	44
			420	302	2001	49	1	0	48
		Johns Creek - Summer	421	303	1994	93	1	0	92
		Nisqually River Hatchery[d]	422	304	12/21/2004	95	1	0	94
		Hamilton Creek - Fall[i]	423		1996	38	7	0	0
		Hamilton Creek - Fall[i]	424		1997	57	9	1	0
		Kalama Creek - winter run	425	305	2003	62	4	4	54
		North Creek - Fall	426	306	1994	47	0	2	45
			427	306	1998	48	0	0	48
		Grays River - Fall	428	307	2000	48	2	0	46
			429	307	2001	47	0	0	47
		Little Creek - Fall	430	308	1994	95	0	3	92
		Satsop River	431	309	11/5/1998	95	0	0	95
		Skamokawa Creek - Fall	432	310	2000	3	0	0	3
			433	310	2001	5	2	0	3
			434	310	2002	72	2	0	70

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Table 2. Page 17 of 17.

Reporting Group	QC[a]	Location	Collection	Population	Date	No. of individuals Initial	Missing	Duplicate	Final
					Total	13587	463	183	12315
					Grand Total	35921	1381	270	32817

Note: The number of individuals initially genotyped for the set of 96 SNPs (Initial), the number removed because of missing loci (Missing) and duplication (Duplicate), and the number of fish incorporated into the baseline (Final) are included.

Note: Footnotes associated with location indicate the reason they were excluded from the baseline.

[a] Quality control notes: 1) These collections were not preamplified in the QC, and 2) The QC for these collections did not fall within the three main methods and were not included in the discrepancy calculations in Table 4.

[b] These collections have a sample size less than our desired minimum cutoff of 40 individuals.

[c] These collections failed to conform to Hardy-Weinberg expectations.

[d] These specific populations were genotyped at the University of Washington as part of a study of population structure of chum salmon from Kodiak Island and the Alaska Peninsula.

[e] These italicizaed groups are subregional reporting groups within CWAK.

[f] These collections were originally thought to be from the Nushagak Drainage, but were later discovered to be from Norton Sound, so they were removed. This population was already represented by collections from other years.

[g] These collections representing Western Alaska were part of the set of backbone populations used in the locus selection analyses detailed in DeCovich et al. (2012b).

[h] These collections lack collection metadata (collection date and GPS coordinates) and were divergent with other collections putatively collected at the same location. Removed from the baseline.

[i] These collections were removed due to high and unresolvable discrepancy rates with the quality control analysis (poor quality DNA).

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 chum salmon in the WASSIP study area.

Assay	Source[a]	H_O	F_{IS}	F_{ST}
Oke_ACOT-100	A	0.424	0.001	0.081
Oke_AhR1-78	B	0.477	-0.006	0.040
Oke_arf-319	C	0.352	-0.008	0.051
Oke_ATP5L-105	A	0.441	-0.009	0.034
Oke_azin1-90	A	0.404	-0.008	0.059
Oke_brd2-118	A	0.309	0.003	0.061
Oke_brp16-65	A	0.365	0.008	0.065
Oke_CATB-60	A	0.203	0.005	0.162
Oke_ccd16-77	A	0.415	-0.002	0.075
Oke_CD81-108	A	0.195	0.006	0.147
Oke_CD81-173	A	0.409	0.005	0.141
Oke_CKS1-94	A	0.379	0.002	0.047
Oke_CKS-389	D	0.387	0.003	0.088
Oke_Cr30[d]	A			0.200
Oke_Cr386[d]	A			0.527
Oke_ctgf-105	B	0.161	-0.005	0.047
Oke_DCXR-87	A	0.229	0.002	0.129
Oke_e2ig5-50	A	0.468	-0.013	0.046
Oke_eif4g1-43	A	0.371	-0.014	0.075
Oke_f5-71	A	0.369	-0.007	0.049
Oke_FANK1-166	A	0.311	-0.009	0.120
Oke_FBXL5-61	A	0.340	-0.003	0.105
Oke_gdh1-191	A	0.414	-0.015	0.067
Oke_gdh1-62[c]	A	0.390	-0.004	0.090
Oke_GHII-3129	B	0.220	0.007	0.146
Oke_glrx1-78	A	0.398	-0.007	0.032
Oke_GPDH-191	C	0.416	-0.007	0.068
Oke_GPH-105	B	0.464	-0.001	0.067
Oke_HP-182	B	0.330	-0.010	0.071
Oke_il-1racp-67	C	0.267	0.001	0.051
Oke_IL8r2-406	A	0.319	-0.003	0.045
Oke_KPNA2-87	B	0.180	-0.002	0.117
Oke_LAMP2-186	A	0.432	-0.006	0.107
Oke_mgll-49	A	0.460	0.002	0.065
Oke_MLRN-63	A	0.478	-0.014	0.036

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Table 3. Page 2 of 3.

Assay	Sourcea	HO	FIS	FST
Oke_Moesin-160	C	0.118	0.002	0.043
Oke_nc2b-148	A	0.405	0.011	0.084
Oke_ND3-69[d]	A			0.526
Oke_NUPR1-70	A	0.360	0.000	0.069
Oke_pgap-111	A	0.426	-0.006	0.070
Oke_*pgap*-92[c]	A	0.377	-0.006	0.076
Oke_PPA2-635	B	0.316	0.000	0.128
Oke_psmd9-57	A	0.184	0.000	0.033
Oke_rab5a-117	A	0.355	-0.001	0.133
Oke_ras1-249	B	0.423	-0.005	0.091
Oke_RFC2-618	C	0.168	-0.002	0.304
Oke_RH1op-245	C	0.163	0.001	0.123
Oke_RS27-81	A	0.297	-0.005	0.016
Oke_RSPRY1-106	A	0.250	0.001	0.108
Oke_serpin-140	C	0.440	0.002	0.072
Oke_slc1a3a-86	A	0.390	0.003	0.092
Oke_sylc-90	A	0.395	-0.001	0.059
Oke_TCP1-78	B	0.182	-0.008	0.081
Oke_Tf-278	B	0.371	-0.015	0.171
Oke_thic-84	A	0.451	-0.007	0.089
Oke_U1002-262	A	0.420	0.000	0.131
Oke_U1008-83	A	0.154	-0.015	0.097
Oke_U1010-251	A	0.294	0.020	0.137
Oke_U1012-241	A	0.460	-0.013	0.087
Oke_U1015-255	A	0.336	0.005	0.085
Oke_U1016-154	A	0.457	-0.012	0.036
Oke_U1017-52	A	0.391	-0.028	0.068
Oke_U1018-50	A	0.138	-0.002	0.114
Oke_U1021-102[b]	A	0.354	0.010	0.068
Oke_U1022-139[b]	A	0.344	-0.002	0.097
Oke_U1023-147	A	0.444	-0.001	0.098
Oke_U1024-113	A	0.160	-0.001	0.053
Oke_U1025-135	A	0.073	0.021	0.076
Oke_u200-385	C	0.463	-0.006	0.067
Oke_U2006-109	A	0.446	-0.001	0.027
Oke_U2007-190	A	0.432	-0.007	0.099

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Table 3. Page 3 of 3.

Assay	Source[a]	H_O	F_{IS}	F_{ST}
Oke_U2011-107	A	0.227	-0.012	0.095
Oke_U2015-151	A	0.162	-0.005	0.152
Oke_U2025-86	A	0.467	-0.002	0.062
Oke_U2029-79	A	0.416	0.002	0.134
Oke_U2031-37	A	0.205	0.006	0.075
Oke_U2032-74	A	0.212	-0.003	0.043
Oke_U2034-55	A	0.349	0.005	0.116
Oke_U2035-54	A	0.175	-0.003	0.126
Oke_U2037-76	A	0.143	0.006	0.038
Oke_U2041-84	A	0.426	0.007	0.030
Oke_U2043-51	A	0.208	0.001	0.083
Oke_U2048-91	A	0.451	-0.002	0.095
Oke_U2050-101	A	0.158	0.006	0.048
Oke_U2053-60	A	0.465	-0.005	0.062
Oke_U2054-58	A	0.234	-0.002	0.073
Oke_U2056-90	A	0.478	0.000	0.041
Oke_U2057-80	A	0.363	-0.009	0.102
Oke_U212-87	C	0.077	0.012	0.087
Oke_U217-172	C	0.462	-0.015	0.054
Oke_U302-195	B	0.191	-0.043	0.134
Oke_U502-241	B	0.238	-0.002	0.351
Oke_U504-228	B	0.412	-0.013	0.097
Oke_U506-110	B	0.268	0.010	0.203
Oke_U507-286	B	0.475	-0.016	0.054
Oke_U509-219	B	0.457	-0.008	0.060
Oke_U1021-102_U1022-139[b]		-	0.000	0.065
Oke_Cr30_Cr386_ND3-69[d]		-	0.000	0.437
Overall		0.331	-0.003	0.086

Note: Weir and Cockerham estimates of F_{ST} (1984) are also provided for the 2 sets of linked loci combined as composite phenotypes. Statistics for each marker are based on the 310 populations within the area.

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 (1986).

[a] A=International Program for Salmon Ecological Genetics at the University of Washington (Petrou 2012); B=Elfstrom et al. 2007; C=Smith et al. 2005a; and D=Smith et al. 2005b.

[b] These nuclear SNPs were combined into haplotypes and treated together as a single locus: "*Oke_U1021-102_U1022-139*".

[c] These SNPs were dropped due to linkage.

[d] These mitochondrial SNPs were kept for consistency with other coastwide baselines, and were combined into a haplotype *a priori*, without being subject to the same criteria as nuclear SNPs. See discussion for details. Combined locus: "*Oke_Cr30_Cr386_ND3-69*".

Table 4.–Quality control (QC) results including the number of genotypes compared, discrepancy rates and estimated error rates of the collections genotyped for the WASSIP chum salmon baseline for the 3 methods used: Original, New, and Database.

QC Method	Genotypes Compared	Discrepancy Rate			Error Rate
		Homo-homo	Homo-het	Overall	
Original	96,000	0.04%	0.35%	0.38%	0.19%
New	105,064	0.02%	0.47%	0.49%	0.25%
Database	158,844	0.13%	0.68%	0.81%	0.41%
Total	359,908	0.08%	0.53%	0.61%	0.30%

Note: See text for descriptions of methods and QC details.

Note: Discrepancy rates include the rate due to differences of alternate homozygote genotypes (Homo-homo), of homozygote and heterozygote genotypes (Homo-het) and the total discrepancy rate. Error rate assumes that differences are the result of errors that are equally likely to have occurred in the production and QC genotyping process.

Table 5.–Pairs of single nucleotide polymorphisms (SNPs) that exhibited significant ($P < 0.01$) linkage disequilibrium in 310 populations of chum salmon in the WASSIP study area, f_{ORCA} values for each locus as well as for combined loci, and decision for handling linkage for each locus pair based on the Δ_{90} of 0.0381 (see text for details).

Locus	Linkage pair	f_{ORCA}	Decision
Oke_gdh1-62	2	0.141	Drop
Oke_gdh1-191	2	0.171	Keep
Oke_gdh1-62-191	2	0.198	Drop
Oke_pgap-92	3	0.129	Drop
Oke_pgap-111	3	0.141	Keep
Oke_pgap-111-92	3	0.137	Drop
Oke_U1021-102	4	0.113	Drop
Oke_U1022-139	4	0.119	Drop
Oke_U1021-102_U1022-139	4	0.190	Combine

Table 6.–Variance components and associated *F* statistics for the ANOVA among temporal collections (P) within populations (R) nested within regional reporting groups (S).

	Between Genes within Individuals	Among Individuals within Populations	Among Temporal Collections within Populations	Among Populations within Regions	Among Regions
Variance Component	σ^2_G	σ^2_I	σ^2_{SS}	σ^2_S	σ^2_P
	30.45	-0.09	-0.04	1.61	1.28
F Statistic	F_{IT}	F_{IS}	F_{PR}	F_{RS}	F_{ST}
	0.92	0.00	0.00	0.05	0.04

Note: Variance component and *F* statistic notation follows Weir (1996): individual (I), sub-subpopulation (temporal collection in this analysis; P), subpopulation (population in this analysis; R), population (region in this analysis; S), and total (T). See text for details.

Table 7.–Estimates of stock composition, upper and lower bounds of the 90% credibility intervals, and standard deviations (SD) for mixtures of known-origin fish removed from the WASSIP baseline populations of chum salmon that comprise the Asia, Kotzebue Sound, and Norton Sound, Yukon Coastal, Kuskokwim, Bristol Bay, Upper Yukon River, Northern District, Northwest District, South Peninsula, Chignik/Kodiak, and East of Kodiak reporting groups (i.e., 100% proof tests) using the program BAYES with a flat prior.

	Asia				Kotzebue Sound				Norton Sound			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	**0.99**	0.98	1.00	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	**0.97**	0.94	0.99	0.02	0.03	0.00	0.09	0.03
Norton Sound	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01	**0.80**	0.57	0.98	0.13
Yukon Coastal	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.04	0.00	0.18	0.06
Kuskokwim	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.11	0.00	0.31	0.11
Bristol Bay	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.02	0.00	0.10	0.04
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Northern District	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00

	Yukon Coastal				Kuskokwim				Bristol Bay			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Norton Sound	0.03	0.00	0.15	0.05	0.01	0.00	0.08	0.03	0.03	0.00	0.13	0.05
Yukon Coastal	**0.91**	0.76	1.00	0.08	0.25	0.02	0.43	0.12	0.03	0.00	0.15	0.05
Kuskokwim	0.02	0.00	0.12	0.05	**0.48**	0.28	0.72	0.13	0.14	0.00	0.34	0.11
Bristol Bay	0.01	0.00	0.08	0.03	0.26	0.15	0.38	0.07	**0.79**	0.60	0.96	0.11
Upper Yukon River	0.03	0.00	0.09	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.04	0.02
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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Table 7. Page 2 of 2.

Reporting Group	Upper Yukon River				Northern District				Northwest District			
	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Norton Sound	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
Yukon Coastal	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
Kuskokwim	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
Bristol Bay	0.00	0.00	0.00	0.00	0.01	0.00	0.07	0.03	0.00	0.00	0.01	0.00
Upper Yukon River	**0.99**	0.97	1.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.00	0.00	**0.96**	0.89	0.99	0.04	0.00	0.00	0.02	0.01
Northwest District	0.00	0.00	0.00	0.00	0.01	0.00	0.06	0.02	**0.99**	0.96	1.00	0.01
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.00
Chignik/Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.01	0.00	0.00	0.00	0.00

Reporting Group	South Peninsula				Chignik/Kodiak				East of Kodiak			
	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Norton Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Yukon Coastal	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kuskokwim	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bristol Bay	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northwest District	0.00	0.00	0.03	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
South Peninsula	**0.97**	0.88	1.00	0.04	0.00	0.00	0.02	0.02	0.01	0.00	0.04	0.01
Chignik/Kodiak	0.02	0.00	0.11	0.04	**0.99**	0.96	1.00	0.02	0.01	0.00	0.04	0.01
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	**0.98**	0.95	0.99	0.01

Note: Proportions for a given mixture may not sum to 1 due to rounding error.
Note: Two hundred fish were removed from each reporting group.
Note: Correct allocations are in bold.

Table 8.– Estimates of stock composition, upper and lower bounds of the 90% credibility intervals, and standard deviations (SD) for mixtures of known-origin fish removed from the WASSIP baseline populations of chum salmon that comprise the Asia, Kotzebue Sound, and CWAK, Upper Yukon River, Northern District, Northwest District, South Peninsula, Chignik/Kodiak, and East of Kodiak reporting groups (i.e., 100% proof tests) using the program BAYES with a flat prior.

	Asia				Kotzebue Sound				CWAK			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	**0.99**	0.98	1.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	**0.98**	0.95	1.00	0.02	0.00	0.00	0.01	0.00
CWAK	0.00	0.00	0.00	0.00	0.01	0.00	0.04	0.02	**0.99**	0.97	1.00	0.01
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Northern District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

	Upper Yukon River				Northern District				Northwest District			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
Upper Yukon River	**0.99**	0.98	1.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.00	0.00	**0.99**	0.96	1.00	0.01	0.00	0.00	0.01	0.00
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	**0.99**	0.97	1.00	0.01
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.01
Chignik/Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.01	0.00	0.00	0.01	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00

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Table 8. Page 2 of 2.

	South Peninsula				Chignik/Kodiak				East of Kodiak			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00
Northwest District	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00
South Peninsula	**0.97**	0.88	1.00	0.04	0.16	0.04	0.27	0.07	0.01	0.00	0.02	0.01
Chignik/Kodiak	0.02	0.00	0.11	0.04	**0.83**	0.72	0.95	0.07	0.00	0.00	0.02	0.01
East of Kodiak	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	**0.99**	0.96	1.00	0.01

Note: Proportions for a given mixture may not sum to 1 due to rounding error.
Note: Two hundred fish were removed from each reporting group.
Note: Correct allocations are in bold.

Table 9.–Estimates of stock composition, upper and lower bounds of the 90% credibility intervals, and standard deviations (SD) for mixtures of known-origin fish removed from the WASSIP baseline populations of chum salmon that comprise the Asia reporting group (i.e., 100% proof tests) using the program BAYES with a flat prior.

	Asia Test 1				Asia Test 2				Asia Test 3			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	**0.99**	0.98	1.00	0.01	**0.99**	0.98	1.00	0.01	**0.99**	0.98	1.00	0.01
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
CWAK	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northwest District	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

	Asia Test 4				Asia Test 5				Asia Test 6			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	**0.99**	0.98	1.00	0.01	**0.99**	0.98	1.00	0.01	**0.99**	0.98	1.00	0.01
Kotzebue Sound	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00

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Table 9. Page 2 of 2.

Reporting Group	Asia Test 7				Asia Test 8				Asia Test 9			
	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	**1.00**	0.99	1.00	0.00	**1.00**	0.98	1.00	0.01	**1.00**	0.99	1.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Reporting Group	Asia Test 10			
	Proportion	Lower	Upper	SD
Asia	**0.99**	0.97	1.00	0.01
Kotzebue Sound	0.00	0.00	0.01	0.00
CWAK	0.00	0.00	0.01	0.00
Upper Yukon River	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.00	0.00
Northwest District	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.01	0.01
Chignik/Kodiak	0.00	0.00	0.01	0.00
East of Kodiak	0.00	0.00	0.00	0.00

Note: Proportions for a given mixture may not sum to 1 due to rounding error.

Note: Independent tests were repeated 10 times, with each test consisting of a different 200 individuals removed from the baseline.

Table 10.–Estimates of stock composition, upper and lower bounds of the 90% credibility intervals, and standard deviations (SD) for mixtures of known-origin fish removed from the WASSIP baseline populations of chum salmon that comprise the Kotzebue Sound reporting group (i.e., 100% proof tests) using the program BAYES with a flat prior.

	Kotzebue Sound Test 1				Kotzebue Sound Test 2				Kotzebue Sound Test 3			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.02	0.01
Kotzebue Sound	**0.91**	0.84	0.96	0.04	**0.95**	0.91	0.99	0.03	**0.99**	0.97	1.00	0.01
CWAK	0.09	0.03	0.15	0.04	0.04	0.00	0.08	0.02	0.00	0	0.01	0.01
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0	0.01	0.00
Northern District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0.00	0.00
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0	0.00	0.00

	Kotzebue Sound Test 4				Kotzebue Sound Test 5				Kotzebue Sound Test 6			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Kotzebue Sound	**0.98**	0.93	1.00	0.03	**0.99**	0.97	1.00	0.01	**0.98**	0.93	1.00	0.02
CWAK	0.02	0.00	0.07	0.02	0.00	0.00	0.02	0.01	0.02	0.00	0.06	0.02
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00

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Table 10. Page 2 of 2.

Reporting Group	Kotzebue Sound Test 7				Kotzebue Sound Test 8				Kotzebue Sound Test 9			
	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.01	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Kotzebue Sound	**0.95**	0.90	0.99	0.03	**0.98**	0.94	1.00	0.02	**0.95**	0.88	1.00	0.04
CWAK	0.04	0.00	0.09	0.03	0.01	0.00	0.06	0.02	0.04	0.00	0.11	0.04
Upper Yukon River	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Northern District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
Chignik/Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00

Reporting Group	Kotzebue Sound Test 10			
	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00
Kotzebue Sound	**0.99**	0.98	1.00	0.01
CWAK	0.00	0.00	0.02	0.01
Upper Yukon River	0.00	0.00	0.01	0.00
Northern District	0.00	0.00	0.00	0.00
Northwest District	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00

Table 11.–Estimates of stock composition, upper and lower bounds of the 90% credibility intervals, and standard deviations (SD) for mixtures of known-origin fish removed from the WASSIP baseline populations of chum salmon that comprise the CWAK reporting group (i.e., 100% proof tests) using the program BAYES with a flat prior.

	CWAK Test 1				CWAK Test 2				CWAK Test 3			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.02	0.00	0.05	0.02	0.00	0.00	0.01	0.00	0.01	0.00	0.04	0.01
CWAK	**0.98**	0.94	1.00	0.02	**0.98**	0.94	1.00	0.02	**0.98**	0.93	1.00	0.02
Upper Yukon River	0.00	0.00	0.01	0.00	0.01	0.00	0.05	0.02	0.00	0.00	0.02	0.01
Northern District	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01	0.01	0.00	0.04	0.01
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

	CWAK Test 4				CWAK Test 5				CWAK Test 6			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.03	0.01	0.01	0.00	0.04	0.02	0.01	0.00	0.04	0.01
CWAK	**0.97**	0.90	1.00	0.03	**0.98**	0.93	1.00	0.02	**0.96**	0.91	0.99	0.03
Upper Yukon River	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.06	0.02
Northern District	0.02	0.00	0.08	0.03	0.01	0.00	0.04	0.01	0.01	0.00	0.04	0.01
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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Table 11. Page 2 of 2.

Reporting Group	CWAK Test 7				CWAK Test 8				CWAK Test 9			
	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.01	0.00	0.04	0.02	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.00
CWAK	**0.95**	0.90	0.99	0.03	**0.98**	0.94	1.00	0.02	**0.97**	0.92	1.00	0.02
Upper Yukon River	0.01	0.00	0.05	0.02	0.01	0.00	0.02	0.01	0.02	0.00	0.05	0.02
Northern District	0.02	0.00	0.05	0.02	0.01	0.00	0.04	0.01	0.01	0.00	0.05	0.02
Northwest District	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Reporting Group	CWAK Test 10			
	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.01	0.01
CWAK	**0.94**	0.89	0.97	0.02
Upper Yukon River	0.03	0.00	0.06	0.02
Northern District	0.03	0.01	0.05	0.01
Northwest District	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00

Note: Proportions for a given mixture may not sum to 1 due to rounding error.

Note: Independent tests were repeated 10 times, with each test consisting of a different 200 individuals removed from the baseline.

Table 12.–Estimates of stock composition, upper and lower bounds of the 90% credibility intervals, and standard deviations (SD) for mixtures of known-origin fish removed from the WASSIP baseline populations of chum salmon that comprise the Upper Yukon River reporting group (i.e., 100% proof tests) using the program BAYES with a flat prior.

	Upper Yukon River Test 1				Upper Yukon River Test 2				Upper Yukon River Test 3			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.01	0.01	0.01	0.00	0.03	0.01	0.00	0.00	0.01	0.00
Upper Yukon River	**0.99**	0.98	1.00	0.01	**0.99**	0.97	1.00	0.01	**0.99**	0.98	1.00	0.01
Northern District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

	Upper Yukon River Test 4				Upper Yukon River Test 5				Upper Yukon River Test 6			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.00
Upper Yukon River	**0.99**	0.97	1.00	0.01	**0.99**	0.98	1.00	0.01	**0.99**	0.98	1.00	0.01
Northern District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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Table 12. Page 2 of 2.

Reporting Group	Upper Yukon River Test 7				Upper Yukon River Test 8				Upper Yukon River Test 9			
	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.01	0.01	0.00	0.00	0.02	0.01	0.00	0.00	0.02	0.01
Upper Yukon River	**0.99**	0.98	1.00	0.01	**0.99**	0.98	1.00	0.01	**0.99**	0.97	1.00	0.01
Northern District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Reporting Group	Upper Yukon River Test 10			
	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00
CWAK	0.02	0.00	0.09	0.03
Upper Yukon River	**0.98**	0.91	1.00	0.03
Northern District	0.00	0.00	0.00	0.00
Northwest District	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.00	0.00
East of Kodiak	0.00	0.00	0.00	0.00

Note: Proportions for a given mixture may not sum to 1 due to rounding error.

Note: Independent tests were repeated 10 times, with each test consisting of a different 200 individuals removed from the baseline.

Table 13.–Estimates of stock composition, upper and lower bounds of the 90% credibility intervals, and standard deviations (SD) for mixtures of known-origin fish removed from the WASSIP baseline populations of chum salmon that comprise the Northern District reporting group (i.e., 100% proof tests) using the program BAYES with a flat prior.

	Northern District Test 1				Northern District Test 2				Northern District Test 3			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
CWAK	0.18	0.10	0.26	0.05	0.01	0.00	0.02	0.01	0.07	0.00	0.16	0.05
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	**0.80**	0.71	0.88	0.05	**0.90**	0.84	0.96	0.04	**0.92**	0.83	1.00	0.06
Northwest District	0.01	0.00	0.03	0.01	0.05	0.00	0.11	0.03	0.00	0.00	0.01	0.01
South Peninsula	0.00	0.00	0.01	0.01	0.01	0.00	0.04	0.02	0.00	0.00	0.01	0.00
Chignik/Kodiak	0.00	0.00	0.02	0.01	0.02	0.00	0.06	0.02	0.00	0.00	0.01	0.00
East of Kodiak	0.01	0.00	0.02	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00

	Northern District Test 4				Northern District Test 5				Northern District Test 6			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Kotzebue Sound	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
CWAK	0.01	0.00	0.03	0.01	0.00	0.00	0.03	0.01	0.01	0.00	0.02	0.01
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	**0.98**	0.95	1.00	0.02	**0.99**	0.95	1.00	0.02	**0.97**	0.93	0.99	0.02
Northwest District	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.00	0.01	0.00	0.04	0.01
South Peninsula	0.00	0.00	0.03	0.01	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.01
Chignik/Kodiak	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.02	0.01
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.01

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Table 13. Page 2 of 2.

Reporting Group	Northern District Test 7				Northern District Test 8				Northern District Test 9			
	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
CWAK	0.00	0.00	0.01	0.01	0.03	0.00	0.14	0.05	0.01	0.00	0.02	0.01
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	**0.96**	0.92	0.99	0.02	**0.96**	0.85	1.00	0.05	**0.97**	0.92	1.00	0.02
Northwest District	0.01	0.00	0.03	0.01	0.01	0.00	0.03	0.01	0.01	0.00	0.05	0.02
South Peninsula	0.02	0.00	0.05	0.02	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01
Chignik/Kodiak	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.00	0.01	0.00	0.03	0.01
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00

Reporting Group	Northern District Test 10			
	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00
CWAK	0.01	0.00	0.08	0.03
Upper Yukon River	0.00	0.00	0.00	0.00
Northern District	**0.96**	0.89	1.00	0.04
Northwest District	0.02	0.00	0.06	0.02
South Peninsula	0.00	0.00	0.01	0.01
Chignik/Kodiak	0.00	0.00	0.02	0.01
East of Kodiak	0.00	0.00	0.01	0.00

Note: Proportions for a given mixture may not sum to 1 due to rounding error.

Note: Independent tests were repeated 10 times, with each test consisting of a different 200 individuals removed from the baseline.

Table 14.–Estimates of stock composition, upper and lower bounds of the 90% credibility intervals, and standard deviations (SD) for mixtures of known-origin fish removed from the WASSIP baseline populations of chum salmon that comprise the Northwest District reporting group (i.e., 100% proof tests) using the program BAYES with a flat prior.

	Northwest District Test 1				Northwest District Test 2				Northwest District Test 3			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.01
Northwest District	**0.98**	0.96	1.00	0.01	**0.99**	0.97	1.00	0.01	**0.99**	0.98	1.00	0.01
South Peninsula	0.01	0.00	0.02	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.00
Chignik/Kodiak	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.00
East of Kodiak	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

	Northwest District Test 4				Northwest District Test 5				Northwest District Test 6			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.01	0.01	0.00	0.00	0.02	0.01	0.01	0.00	0.03	0.01
Northwest District	**0.99**	0.97	1.00	0.01	**0.98**	0.95	1.00	0.01	**0.99**	0.96	1.00	0.01
South Peninsula	0.00	0.00	0.01	0.00	0.01	0.00	0.03	0.01	0.00	0.00	0.01	0.01
Chignik/Kodiak	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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Table 14. Page 3 of 3.

Reporting Group	Northwest District Test 7				Northwest District Test 8				Northwest District Test 9			
	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CWAK	0.01	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.01	0.00	0.03	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
Northwest District	**0.98**	0.95	1.00	0.02	**0.99**	0.97	1.00	0.01	**0.99**	0.97	1.00	0.01
South Peninsula	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.01
Chignik/Kodiak	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.00
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00

Reporting Group	Northwest District Test 10			
	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.00	0.00
Upper Yukon River	0.00	0.00	0.00	0.00
Northern District	0.01	0.00	0.03	0.01
Northwest District	**0.99**	0.96	1.00	0.02
South Peninsula	0.00	0.00	0.01	0.01
Chignik/Kodiak	0.00	0.00	0.01	0.00
East of Kodiak	0.00	0.00	0.00	0.00

Note: Proportions for a given mixture may not sum to 1 due to rounding error.
Note: Independent tests were repeated 10 times, with each test consisting of a different 200 individuals removed from the baseline.

Table 15.–Estimates of stock composition, upper and lower bounds of the 90% credibility intervals, and standard deviations (SD) for mixtures of known-origin fish removed from the WASSIP baseline populations of chum salmon that comprise the South Peninsula reporting group (i.e., 100% proof tests) using the program BAYES with a flat prior.

	South Peninsula Test 1				South Peninsula Test 2				South Peninsula Test 3			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
CWAK	0.01	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.02	0.01
Northwest District	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
South Peninsula	**0.80**	0.69	0.91	0.07	**0.87**	0.72	1.00	0.09	**0.98**	0.93	1.00	0.02
Chignik/Kodiak	0.18	0.08	0.30	0.07	0.13	0.00	0.27	0.09	0.01	0.00	0.05	0.02
East of Kodiak	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.01

	South Peninsula Test 4				South Peninsula Test 5				South Peninsula Test 6			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01	0.01	0.00	0.03	0.01
Northwest District	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
South Peninsula	**0.98**	0.91	1.00	0.03	**0.98**	0.94	1.00	0.02	**0.96**	0.85	1.00	0.05
Chignik/Kodiak	0.01	0.00	0.08	0.03	0.01	0.00	0.05	0.02	0.03	0.00	0.13	0.05
East of Kodiak	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00

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Table 15. Page 2 of 2.

Reporting Group	South Peninsula Test 7				South Peninsula Test 8				South Peninsula Test 9			
	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
CWAK	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
Northwest District	0.00	0.00	0.02	0.01	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.00
South Peninsula	**0.98**	0.94	1.00	0.02	**0.99**	0.95	1.00	0.02	**0.94**	0.85	1.00	0.05
Chignik/Kodiak	0.01	0.00	0.05	0.02	0.01	0.00	0.04	0.02	0.05	0.00	0.14	0.05
East of Kodiak	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Reporting Group	South Peninsula Test 10			
	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.01	0.00
CWAK	0.00	0.00	0.00	0.00
Upper Yukon River	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.01	0.01
Northwest District	0.00	0.00	0.00	0.00
South Peninsula	**0.94**	0.82	1.00	0.06
Chignik/Kodiak	0.06	0.00	0.17	0.06
East of Kodiak	0.00	0.00	0.01	0.00

Note: Proportions for a given mixture may not sum to 1 due to rounding error.

Note: Independent tests were repeated 10 times, with each test consisting of a different 200 individuals removed from the baseline.

Table 16.–Estimates of stock composition, upper and lower bounds of the 90% credibility intervals, and standard deviations (SD) for mixtures of known-origin fish removed from the WASSIP baseline populations of chum salmon that comprise the Chignik/Kodiak reporting group (i.e., 100% proof tests) using the program BAYES with a flat prior.

	Chignik/Kodiak Test 1				Chignik/Kodiak Test 2				Chignik/Kodiak Test 3			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.02	0.01	0.01	0.00	0.03	0.01	0.00	0.00	0.00	0.00
Upper Yukon River	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.00
Northwest District	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.02	0.00	0.07	0.02	0.02	0.00	0.14	0.05	0.15	0.00	0.29	0.09
Chignik/Kodiak	**0.97**	0.92	1.00	0.03	**0.96**	0.84	1.00	0.05	**0.85**	0.70	1.00	0.09
East of Kodiak	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

	Chignik/Kodiak Test 4				Chignik/Kodiak Test 5				Chignik/Kodiak Test 6			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.00
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.00	0.01	0.00	0.05	0.02
Northwest District	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
South Peninsula	0.05	0.00	0.23	0.08	0.05	0.00	0.22	0.08	0.00	0.00	0.03	0.01
Chignik/Kodiak	**0.94**	0.76	1.00	0.08	**0.93**	0.77	1.00	0.08	**0.98**	0.93	1.00	0.02
East of Kodiak	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.00

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Table 16. Page 2 of 2.

Reporting Group	Chignik/Kodiak Test 7				Chignik/Kodiak Test 8				Chignik/Kodiak Test 9			
	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
CWAK	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Northwest District	0.00	0.00	0.01	0.00	0.01	0.00	0.03	0.01	0.00	0.00	0.01	0.00
South Peninsula	0.08	0.02	0.15	0.04	0.01	0.00	0.06	0.02	0.03	0.00	0.11	0.04
Chignik/Kodiak	**0.91**	0.84	0.97	0.04	**0.98**	0.92	1.00	0.03	**0.96**	0.88	1.00	0.04
East of Kodiak	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01

Reporting Group	Chignik/Kodiak Test 10			
	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.00	0.00
Upper Yukon River	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.01	0.00
Northwest District	0.00	0.00	0.01	0.00
South Peninsula	0.22	0.04	0.34	0.09
Chignik/Kodiak	**0.78**	0.65	0.96	0.09
East of Kodiak	0.00	0.00	0.01	0.00

Note: Proportions for a given mixture may not sum to 1 due to rounding error.
Note: Independent tests were repeated 10 times, with each test consisting of a different 200 individuals removed from the baseline.

Table 17.–Estimates of stock composition, upper and lower bounds of the 90% credibility intervals, and standard deviations (SD) for mixtures of known-origin fish removed from the WASSIP baseline populations of chum salmon that comprise the East of Kodiak reporting group (i.e., 100% proof tests) using the program BAYES with a flat prior.

	East of Kodiak Test 1				East of Kodiak Test 2				East of Kodiak Test 3			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00
Chignik/Kodiak	0.00	0.00	0.01	0.01	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.00
East of Kodiak	**0.99**	0.97	1.00	0.01	**0.99**	0.98	1.00	0.01	**0.99**	0.98	1.00	0.01

	East of Kodiak Test 4				East of Kodiak Test 5				East of Kodiak Test 6			
Reporting Group	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
South Peninsula	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.03	0.01
Chignik/Kodiak	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.00	0.03	0.00	0.07	0.02
East of Kodiak	**0.99**	0.97	1.00	0.01	**0.99**	0.98	1.00	0.01	**0.96**	0.92	0.99	0.02

-continued-

Table 17. Page 2 of 2.

Reporting Group	East of Kodiak Test 7				East of Kodiak Test 8				East of KodiakTest 9			
	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Upper Yukon River	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.02	0.01
Northwest District	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.01	0.00
South Peninsula	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.01	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.01	0.00
East of Kodiak	**0.99**	0.98	1.00	0.01	**0.99**	0.96	1.00	0.01	**0.99**	0.97	1.00	0.01

Reporting Group	East of Kodiak Test 10			
	Proportion	Lower	Upper	SD
Asia	0.00	0.00	0.01	0.00
Kotzebue Sound	0.00	0.00	0.00	0.00
CWAK	0.00	0.00	0.00	0.00
Upper Yukon River	0.00	0.00	0.00	0.00
Northern District	0.00	0.00	0.00	0.00
Northwest District	0.00	0.00	0.00	0.00
South Peninsula	0.00	0.00	0.00	0.00
Chignik/Kodiak	0.00	0.00	0.00	0.00
East of Kodiak	**0.99**	0.98	1.00	0.01

Note: Proportions for a given mixture may not sum to 1 due to rounding error.

Note: Independent tests were repeated 10 times, with each test consisting of a different 200 individuals removed from the baseline.

FIGURES

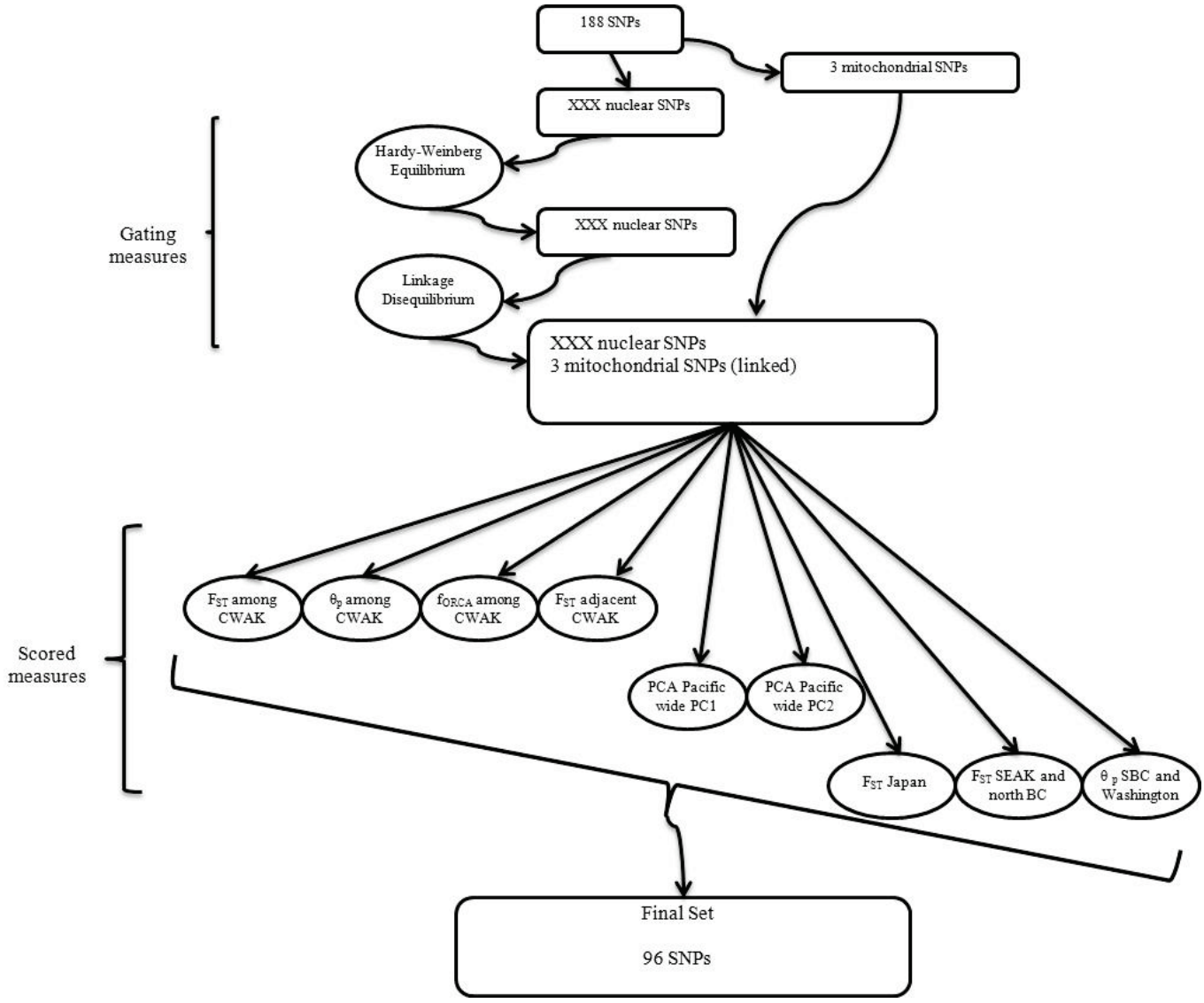

Figure 1.–Flow chart depicting the SNP selection protocol; starting with 188 SNPs at the top and ending with 96 SNPs at the end. It was decided *a priori* that the 3 mitochondrial SNPs would be retained; therefore they were not included in the measurement process. Gating measures were used to eliminate markers from further evaluation and combine linked markers. Scored measures were divided into three categories: 1) measures to distinguish among Coastal Western Alaska (CWAK) regions; 2) measures to distinguish among broad Pacific Coast regions, and 3) measures to distinguish among specific regions outside of CWAK. Weights for the scored measures are shown in Figure 2.

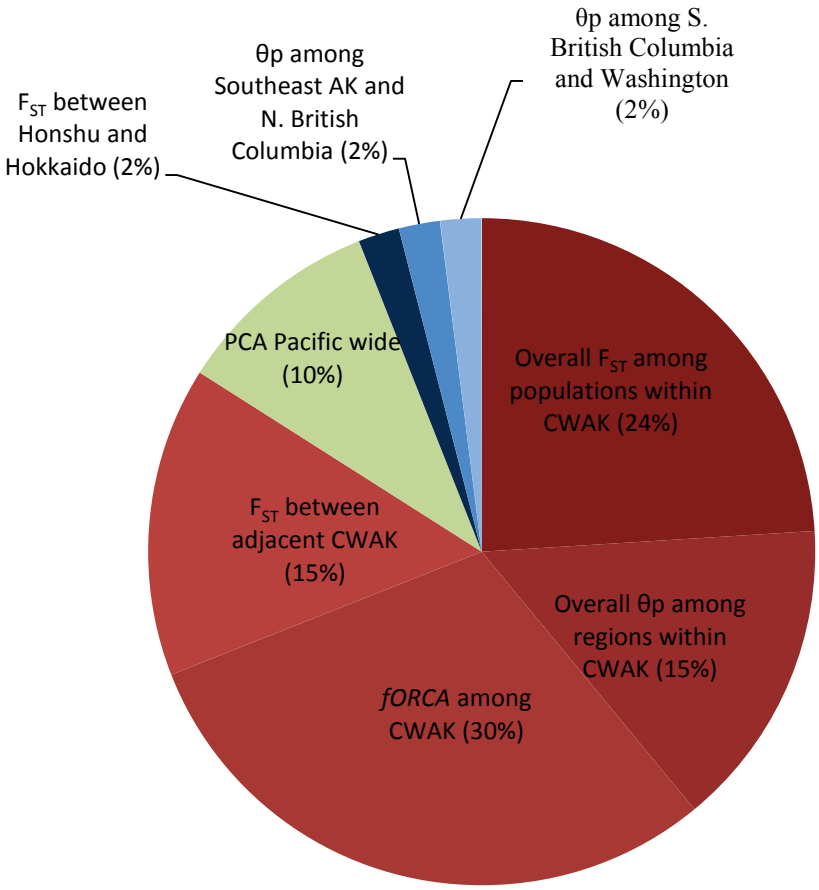

Figure 2.–Weights (in percent) given to scored measures of population structure and MSA performance.

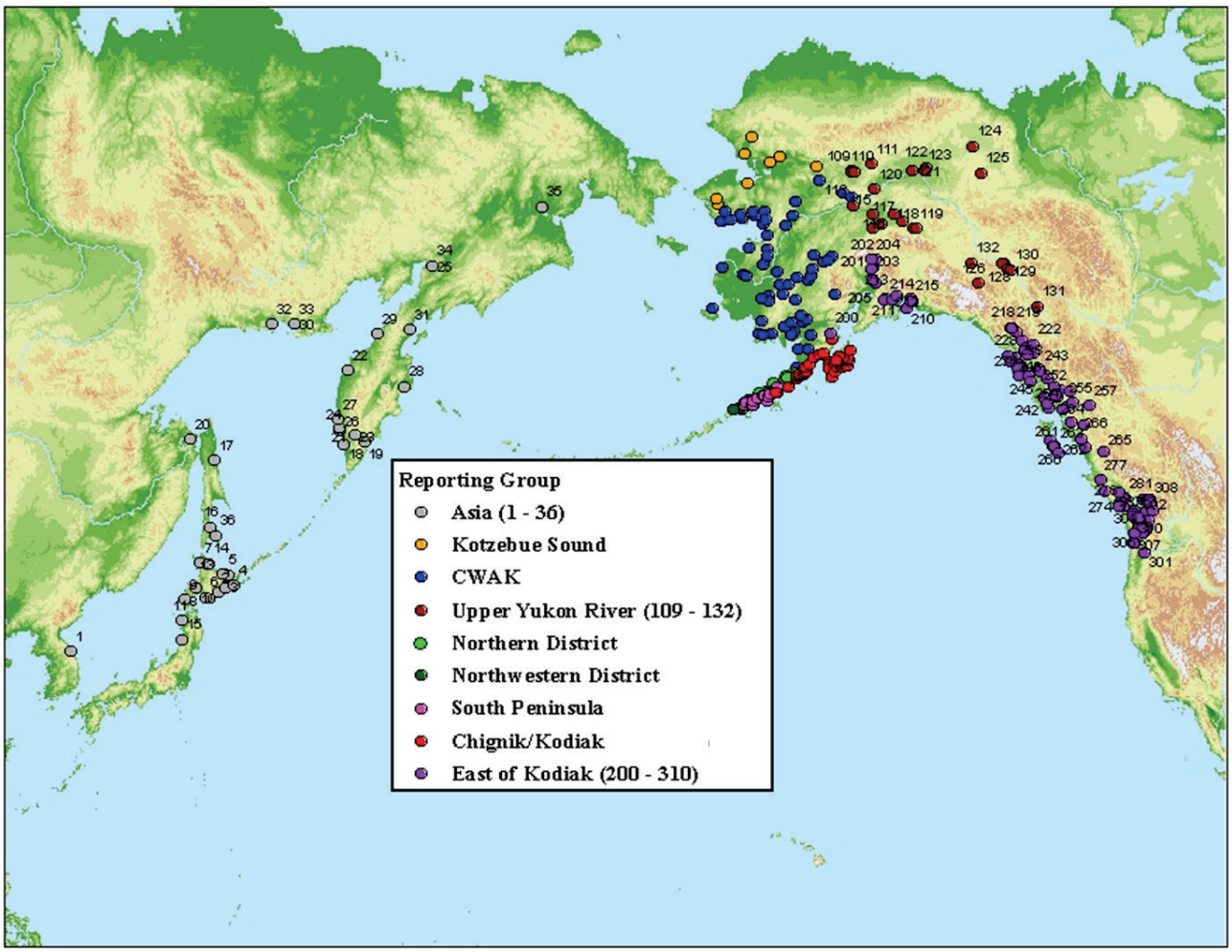

Figure 3.–The location and regional reporting group affiliation of 310 populations of chum salmon included in final baseline analyses for WASSIP. Population numbers shown for populations outside Western Alaska, Alaska Peninsula and Kodiak refer to designations in Table 2.

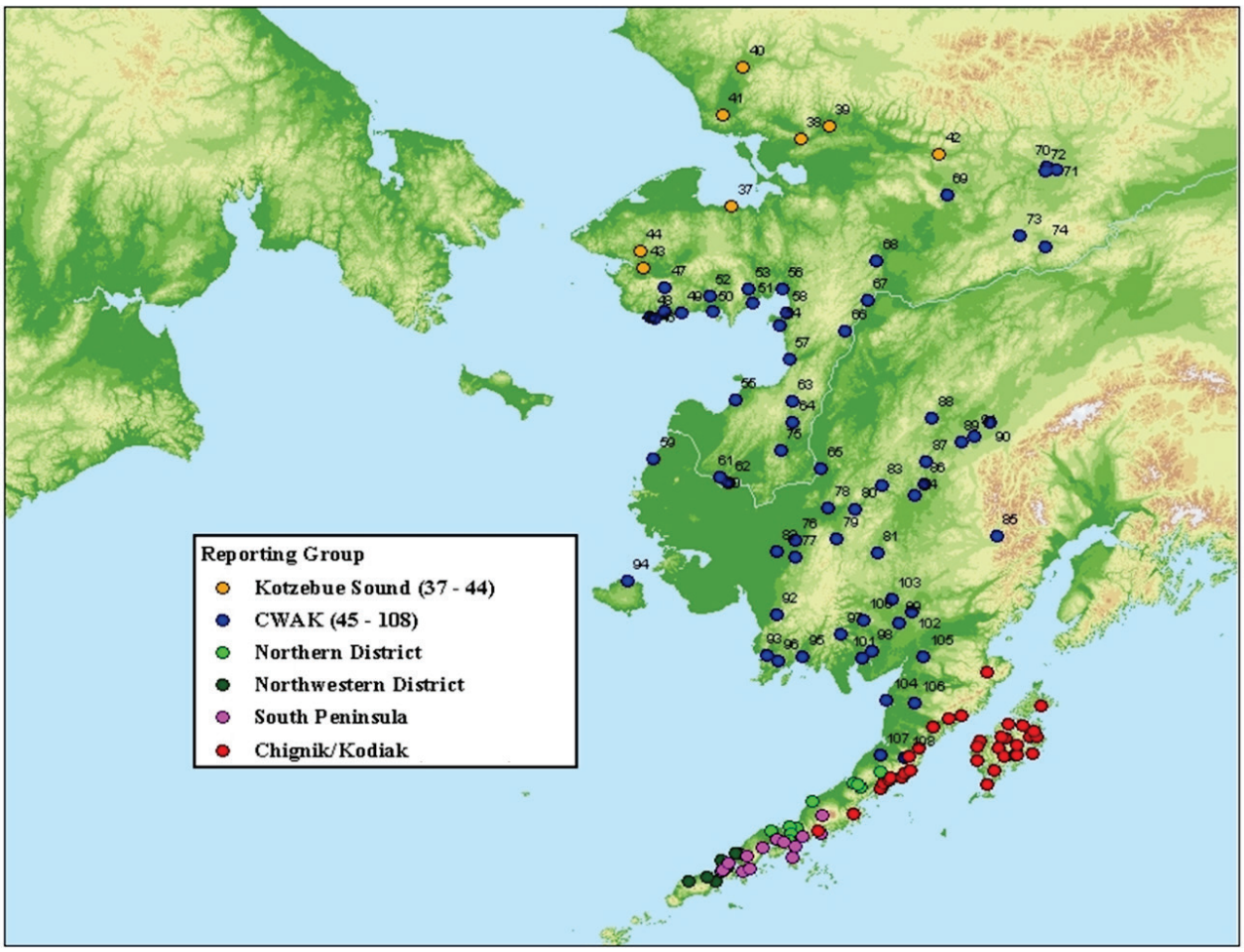

Figure 4.– The location and regional reporting group affiliation of populations of chum salmon included n final baseline analyses for WASSIP from Western Alaska, Alaska Peninsula and Kodiak. Population numbers shown for populations from Western Alaska refer to designations in Table 2.

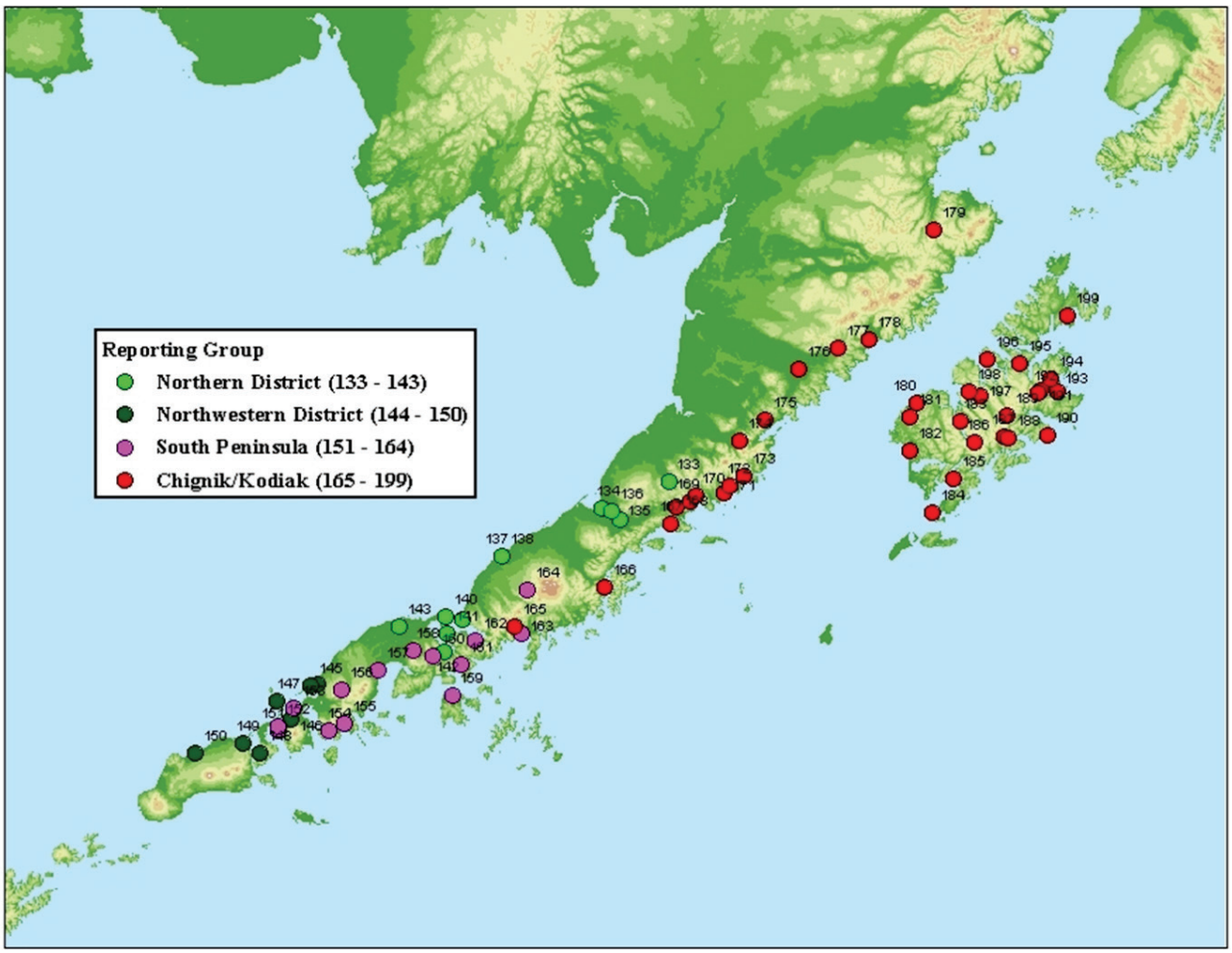

Figure 5.–The location and regional reporting group affiliation of populations of chum salmon included in final baseline analyses for WASSIP from Alaska Peninsula and Kodiak. Population numbers refer to designations in Table 2.

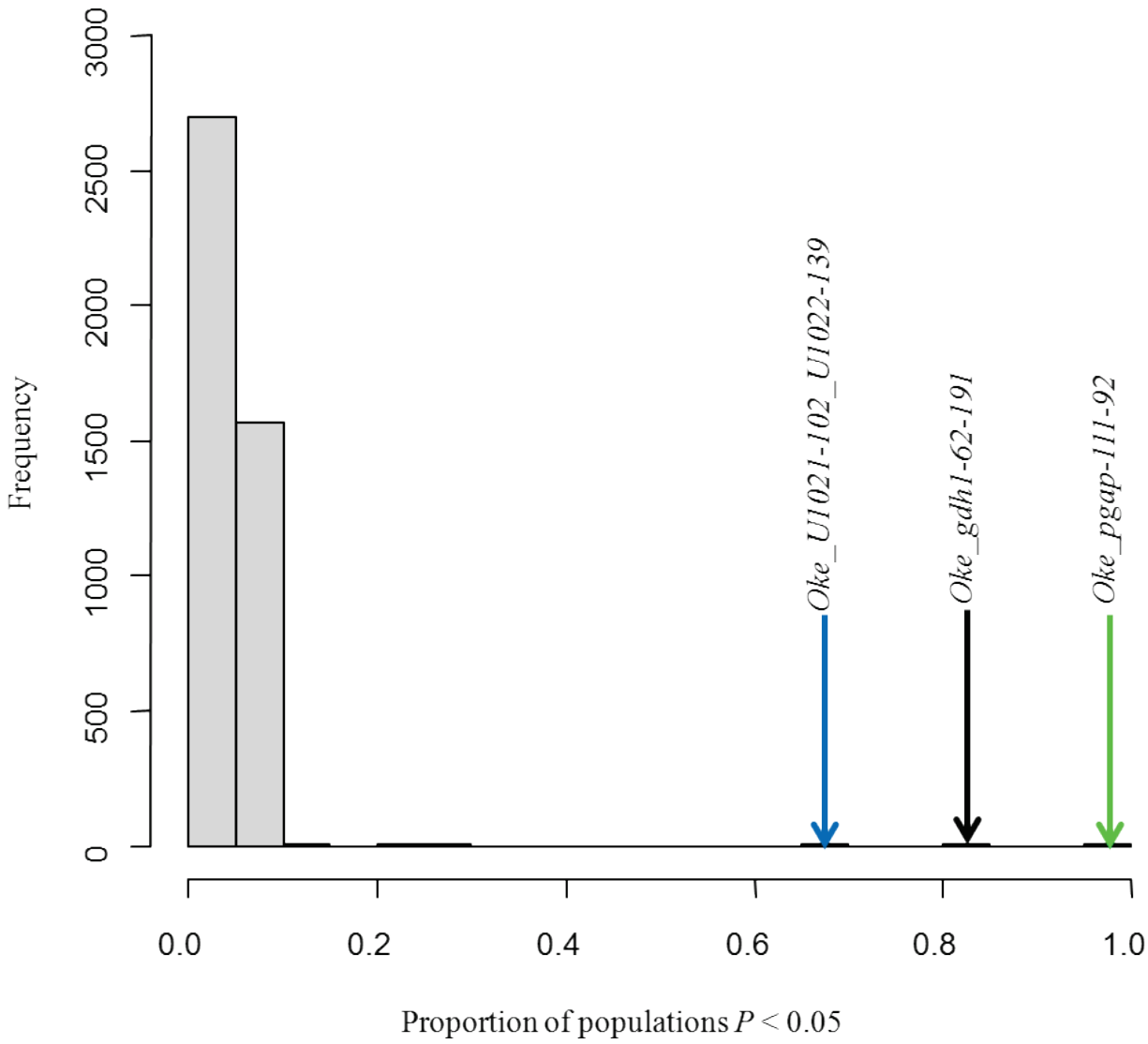

Figure 6.–Histogram of the proportion of chum salmon populations with significant ($P < 0.05$) linkage disequilibrium between the 4,278 pairs of the 93 nuclear SNPs tested in 310 WASSIP area populations.

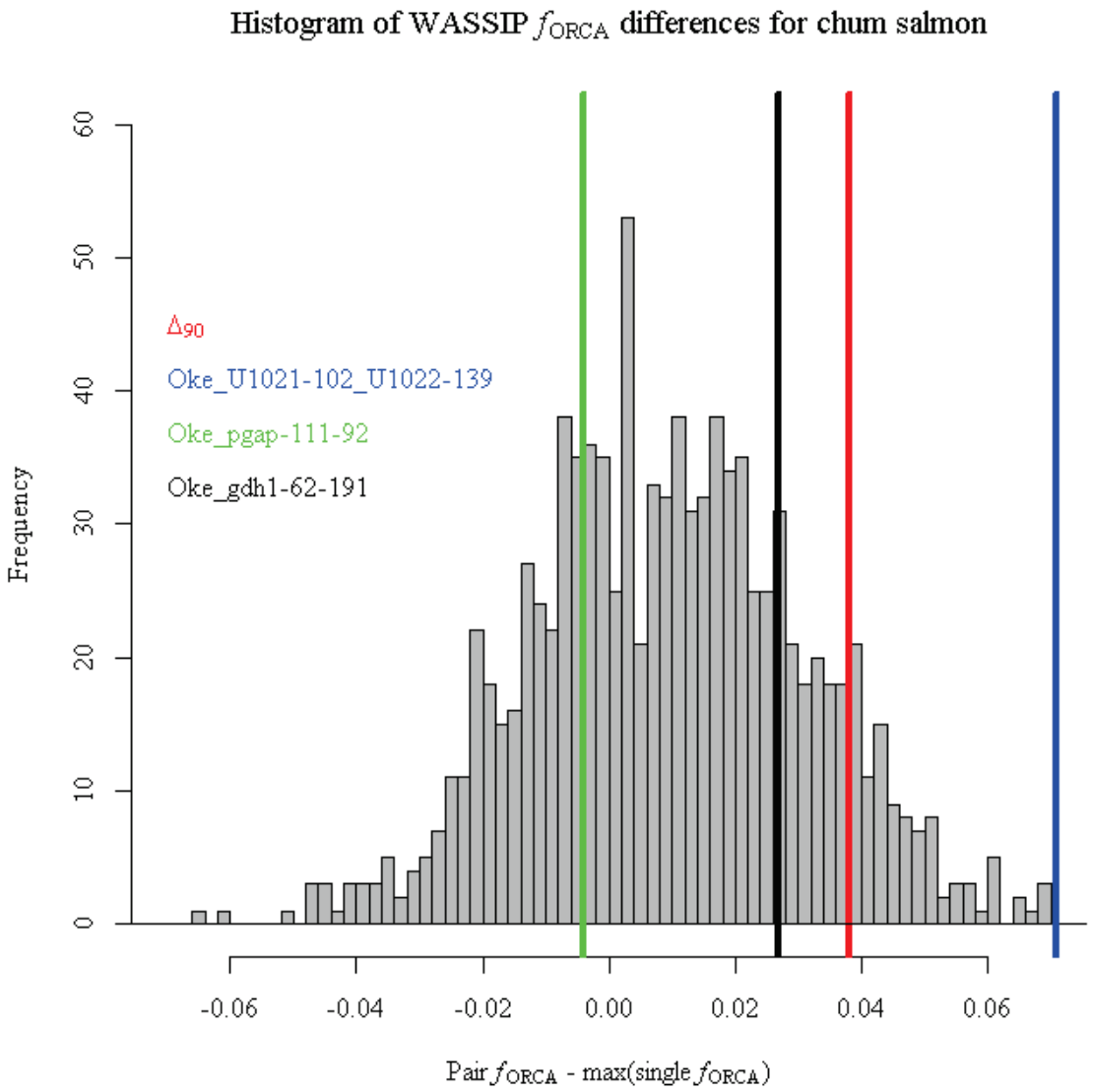

Figure 7.–The distribution of Δ for 1,000 random SNP pairs with Δ_{90} in red and the Δ values for *Oke_U1021-102_U1022-139* in blue, *Oke_pgap-111-92* in green, and *Oke*_gdh1-*62-191* in black. See text for details.

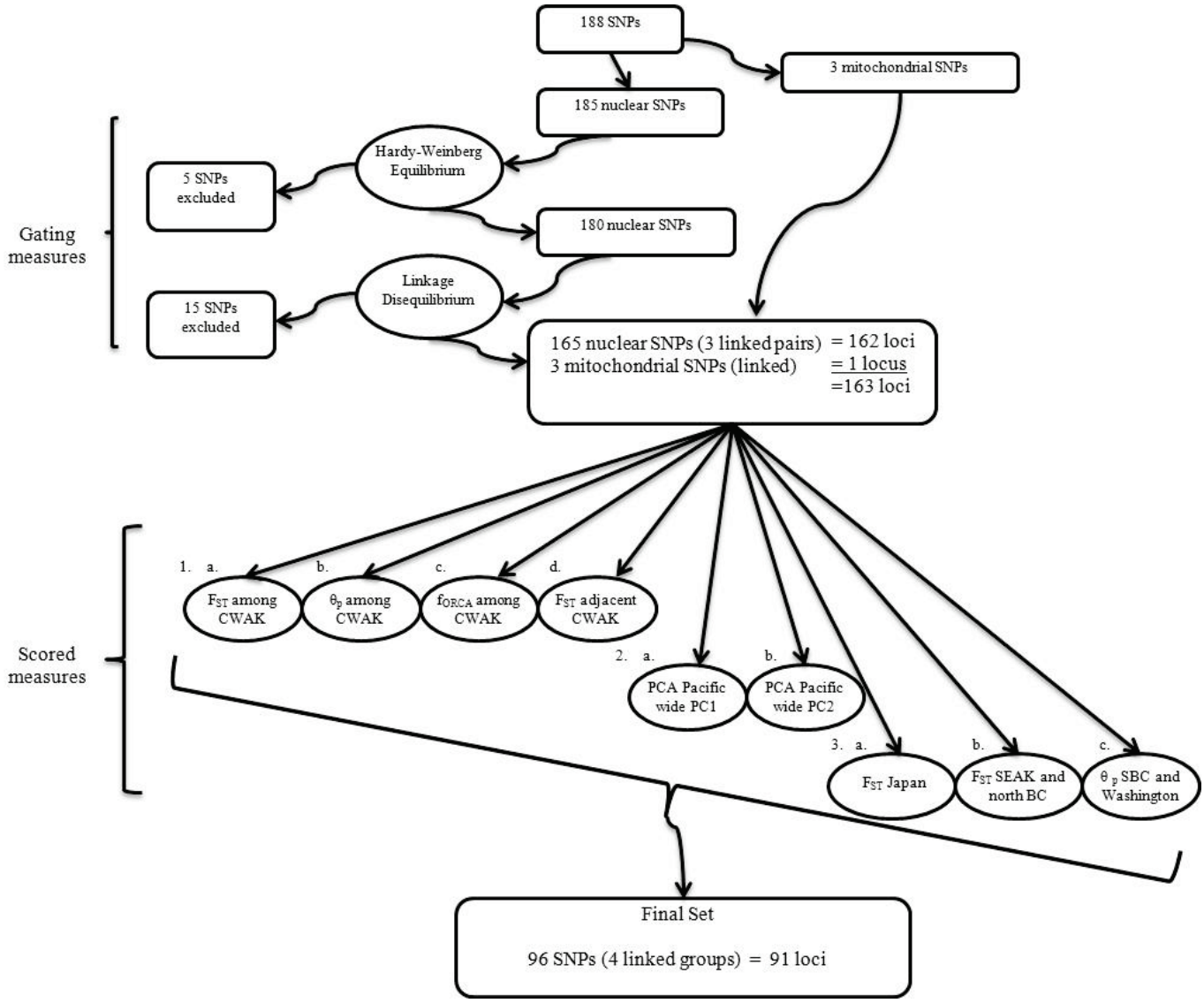

Figure 8.–Flow chart depicting the SNP selection protocol, starting with 188 SNPs at the top and ending with 91 loci at the end. Unmarked measures were used to eliminate markers from further evaluation and combine linked markers. Scored measures were divided into three categories: 1) measures to distinguish among Coastal Western Alaska (CWAK) regions, 2) measures to distinguish among broad Pacific-coast regions, and 3) measures to distinguish among specific regions outside of CWAK. Weightings for the scored measures are shown in Figure 2.

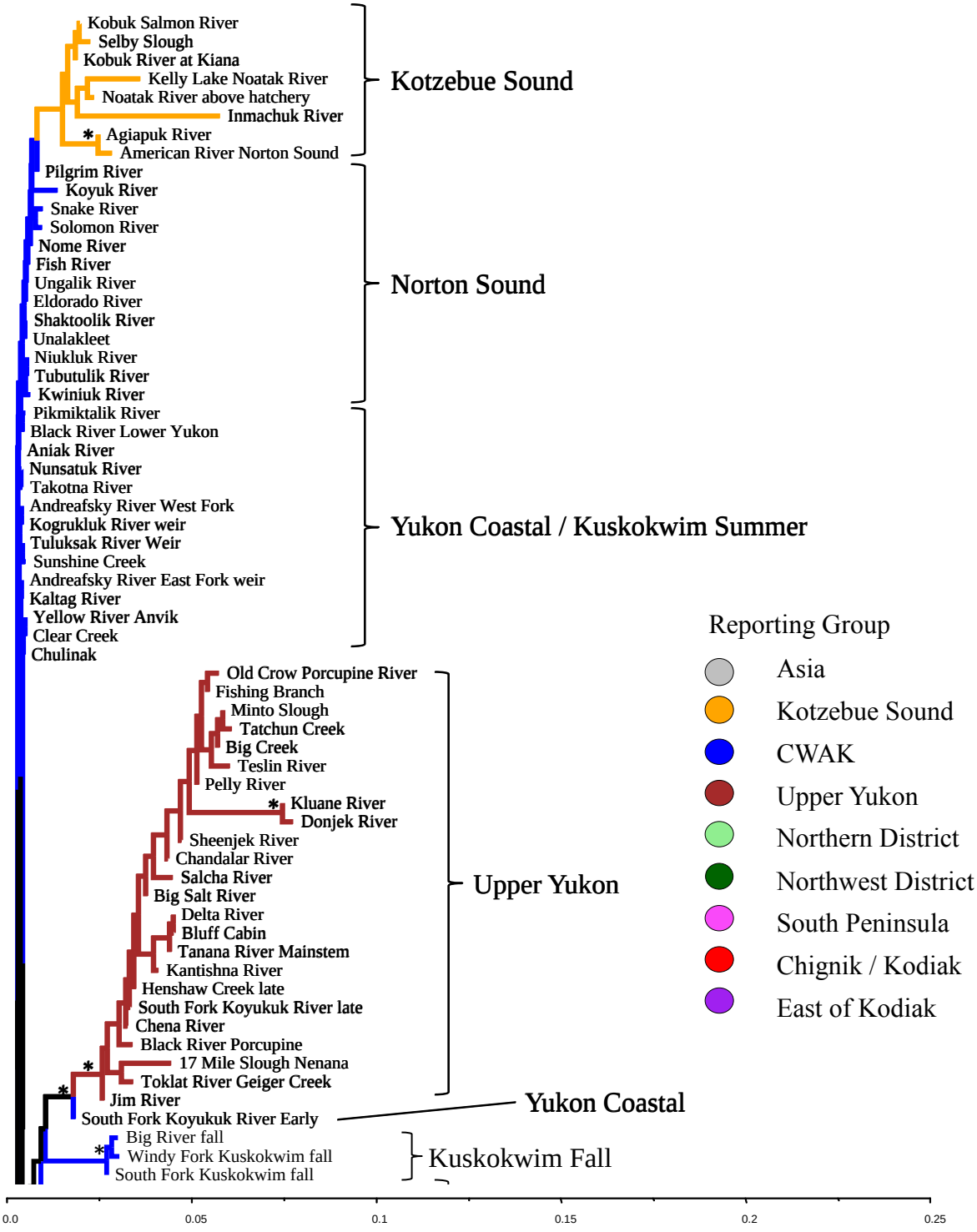

Figure 9.–Consensus neighbor-joining tree based upon pairwise F_{ST} between 310 populations of chum salmon included in the WASSIP baseline. Tree branch colors denote regional reporting group memberships, text brackets denote general population groupings and asterisks indicate nodes where bootstrap consensus > 90%.

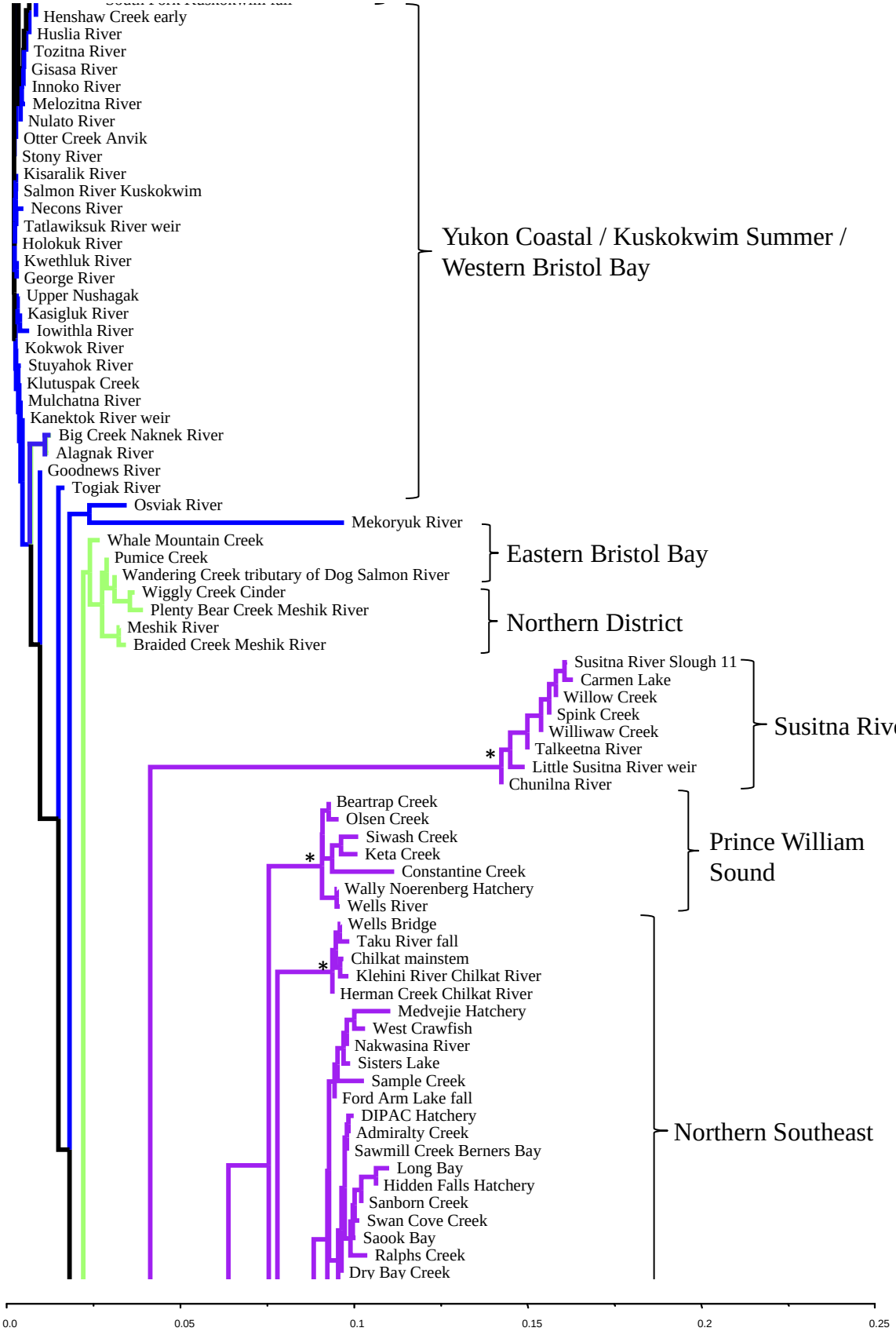

Figure 9. Page 2 of 5. Continued.

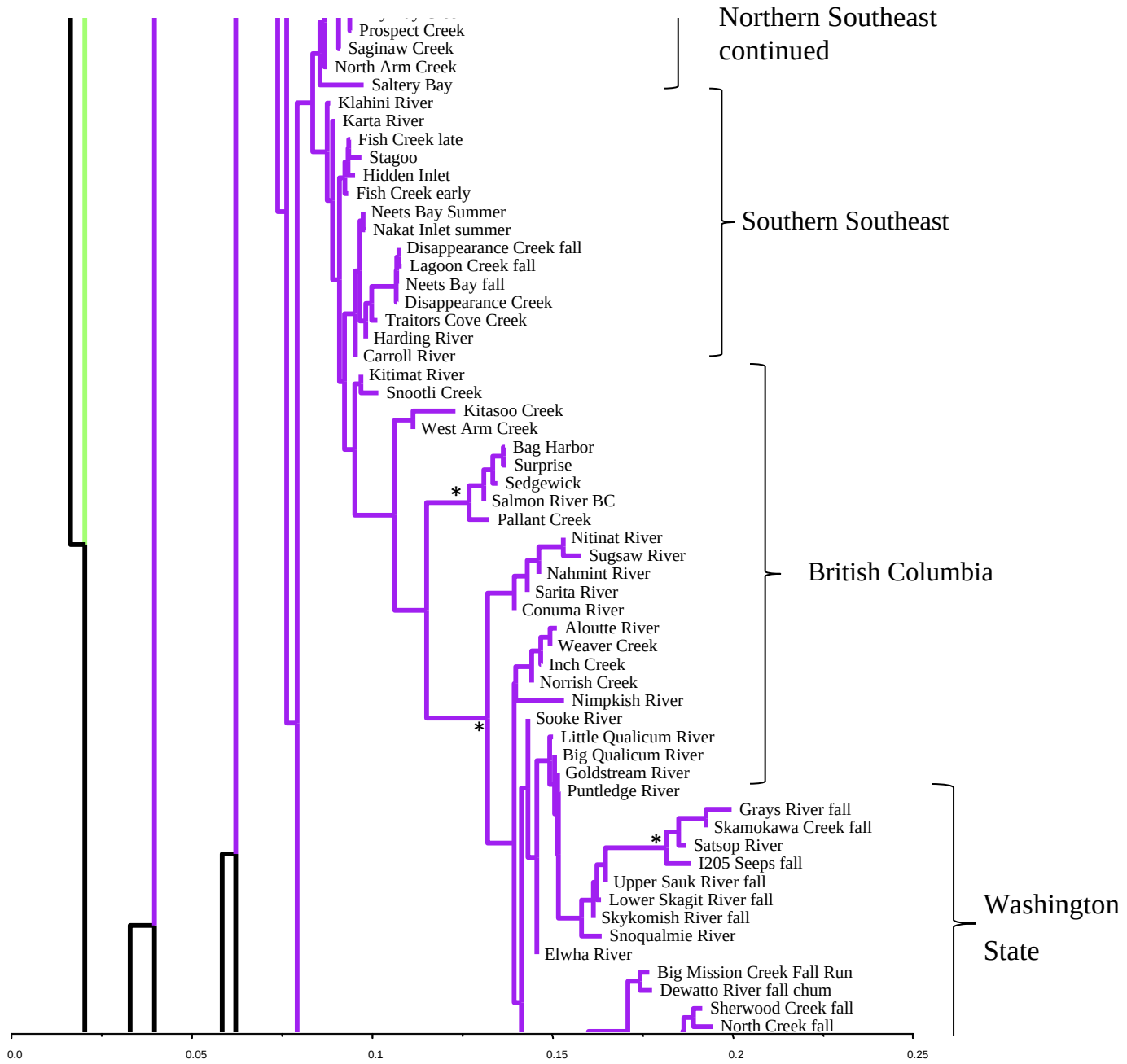

Figure 9. Page 3 of 5. Continued.

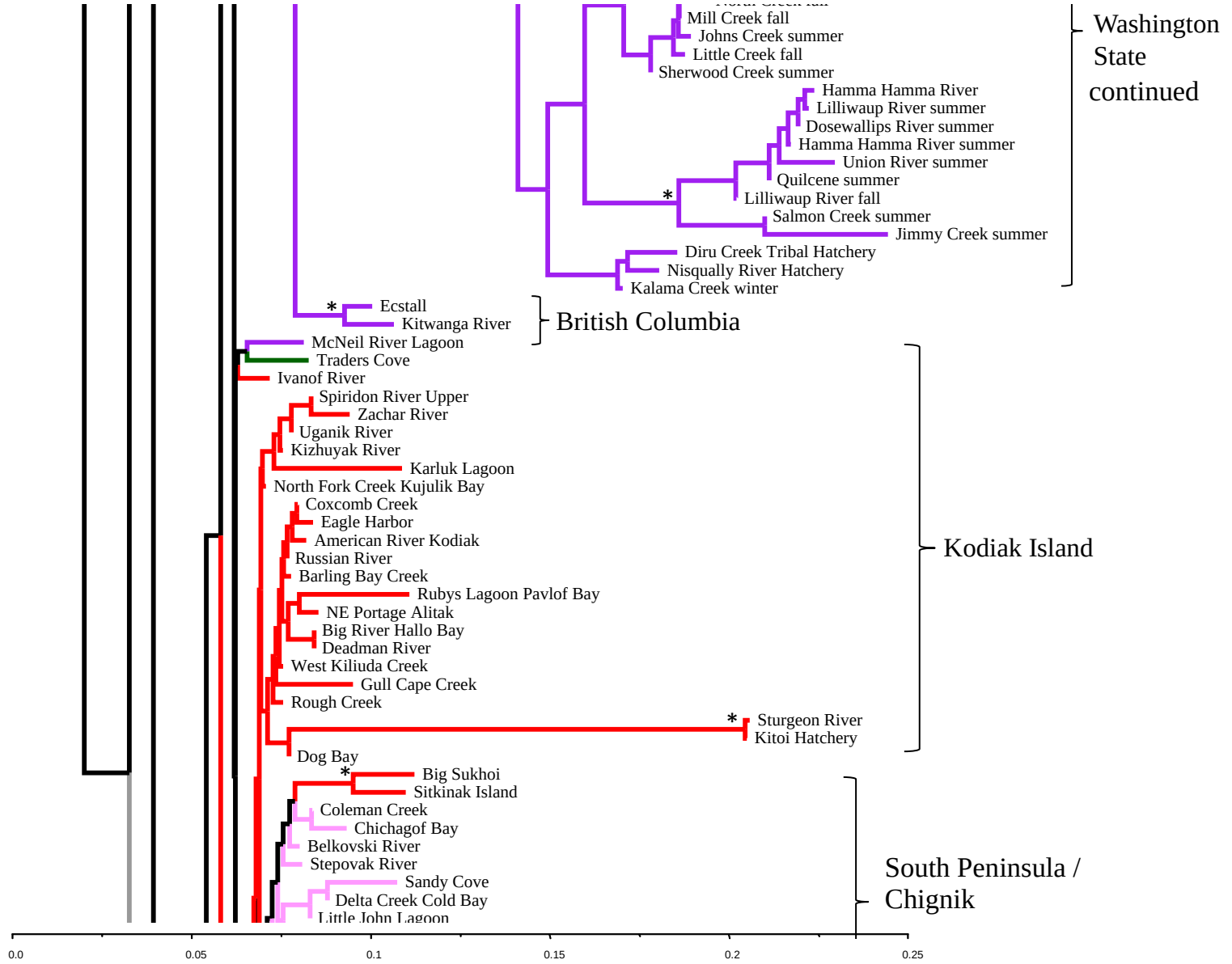

Figure 9. Page 4 of 5. Continued.

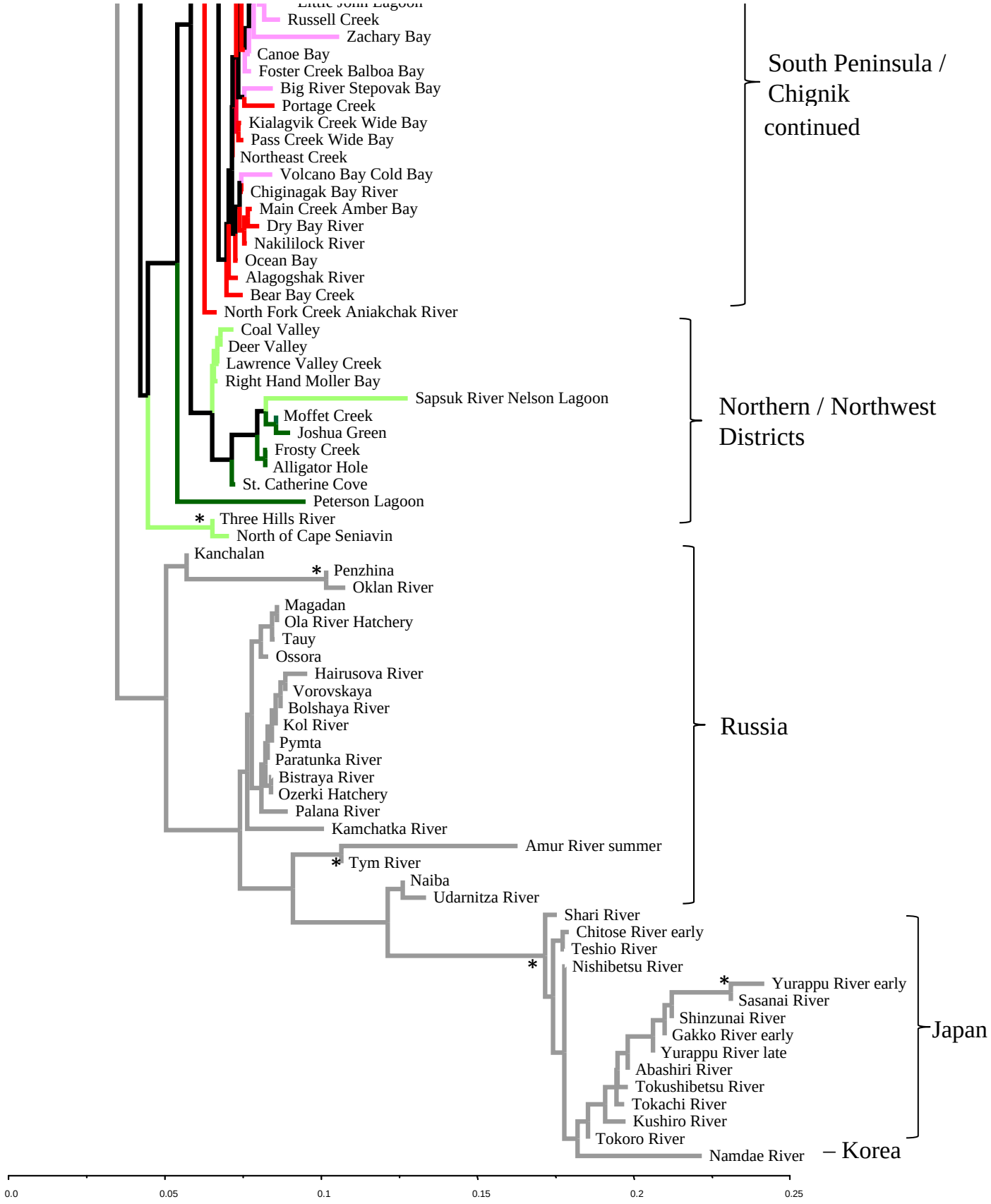

Figure 9. Page 5 of 5.

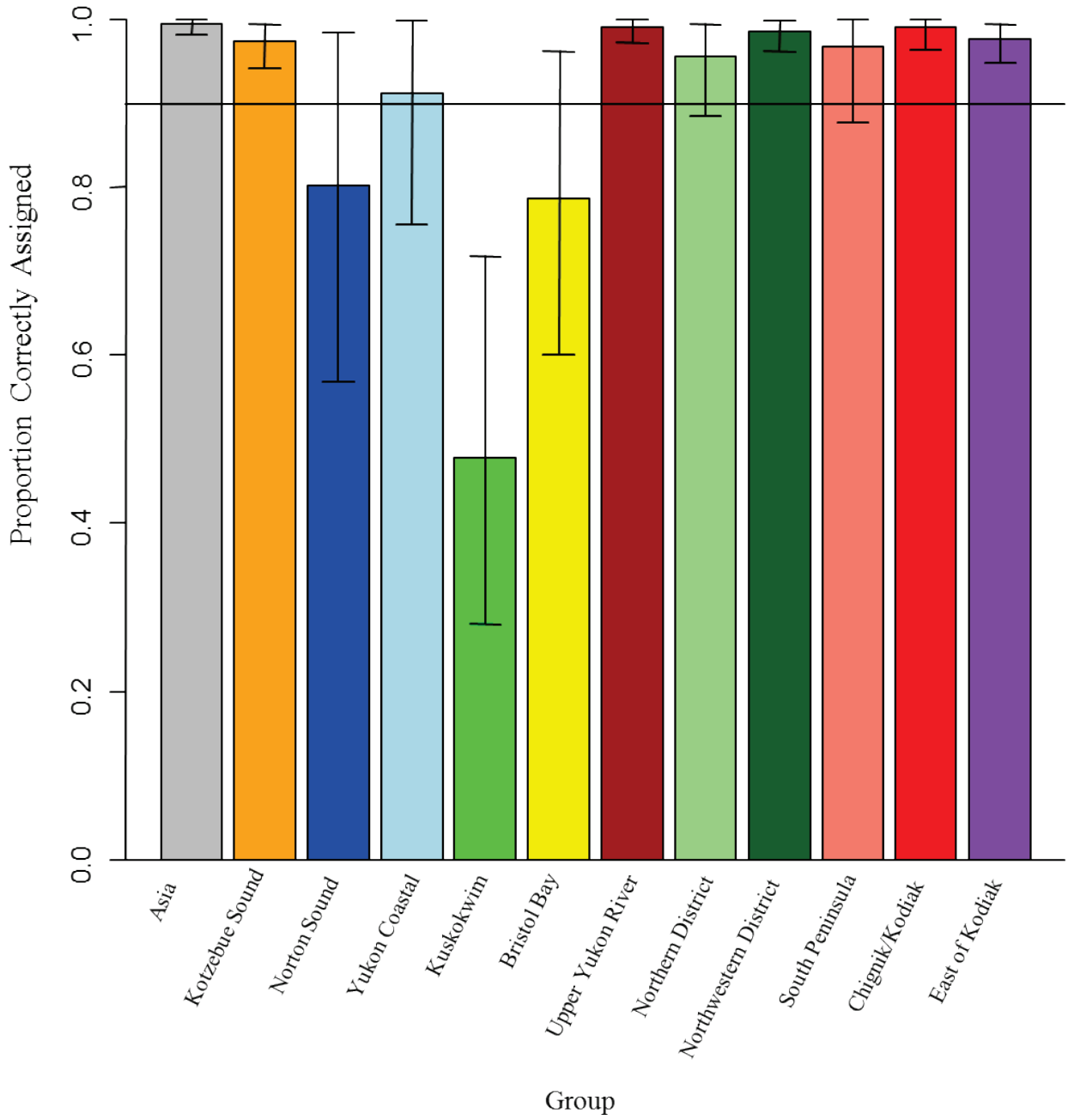

Figure 10.–Proportion of chum salmon correctly allocated back to 12 regional reporting groups of origin and 90% credibility intervals in proof tests. Proof tests are performed using sets of 200-fish mixtures of individuals removed from the baseline populations that comprise each reporting group. These mixtures are analyzed using the program BAYES with a flat prior.

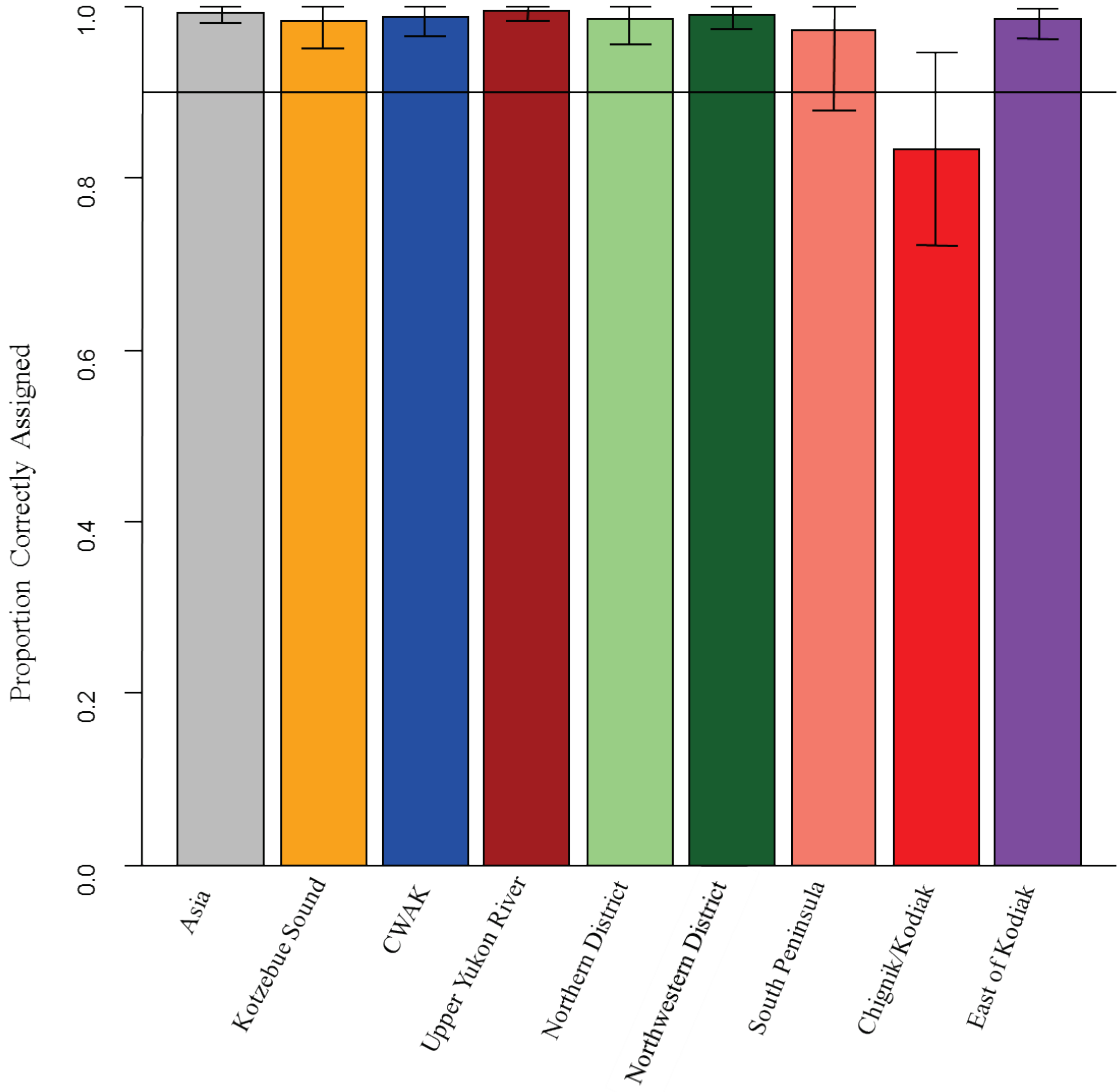

Figure 11.–Proportion of chum salmon correctly allocated back to 9 regional reporting groups of origin and 90% credibility intervals in proof tests. Proof tests are performed using sets of 200-fish mixtures of individuals removed from the baseline populations that comprise each reporting group. These mixtures are analyzed using the program BAYES with a flat prior.

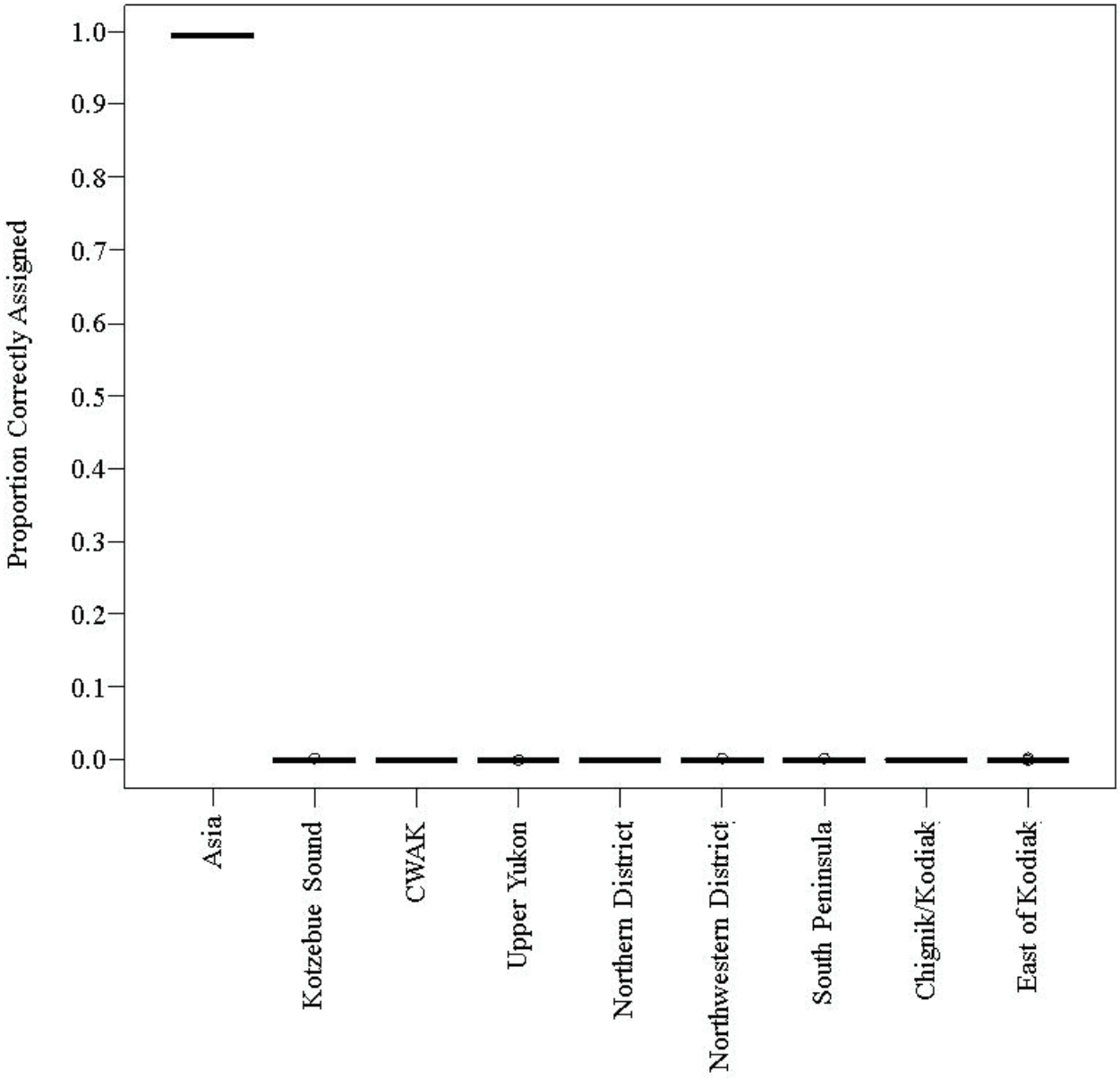

Figure 12.–Box-plot of the average proportion of chum salmon allocated to regional reporting groups for 10 repeated proof tests assembled from fish from the Asia reporting group. Proof tests are performed using independent sets of 200-fish mixtures of individuals removed from the baseline populations that comprise each reporting group. These mixtures are analyzed using the program BAYES with a flat prior.

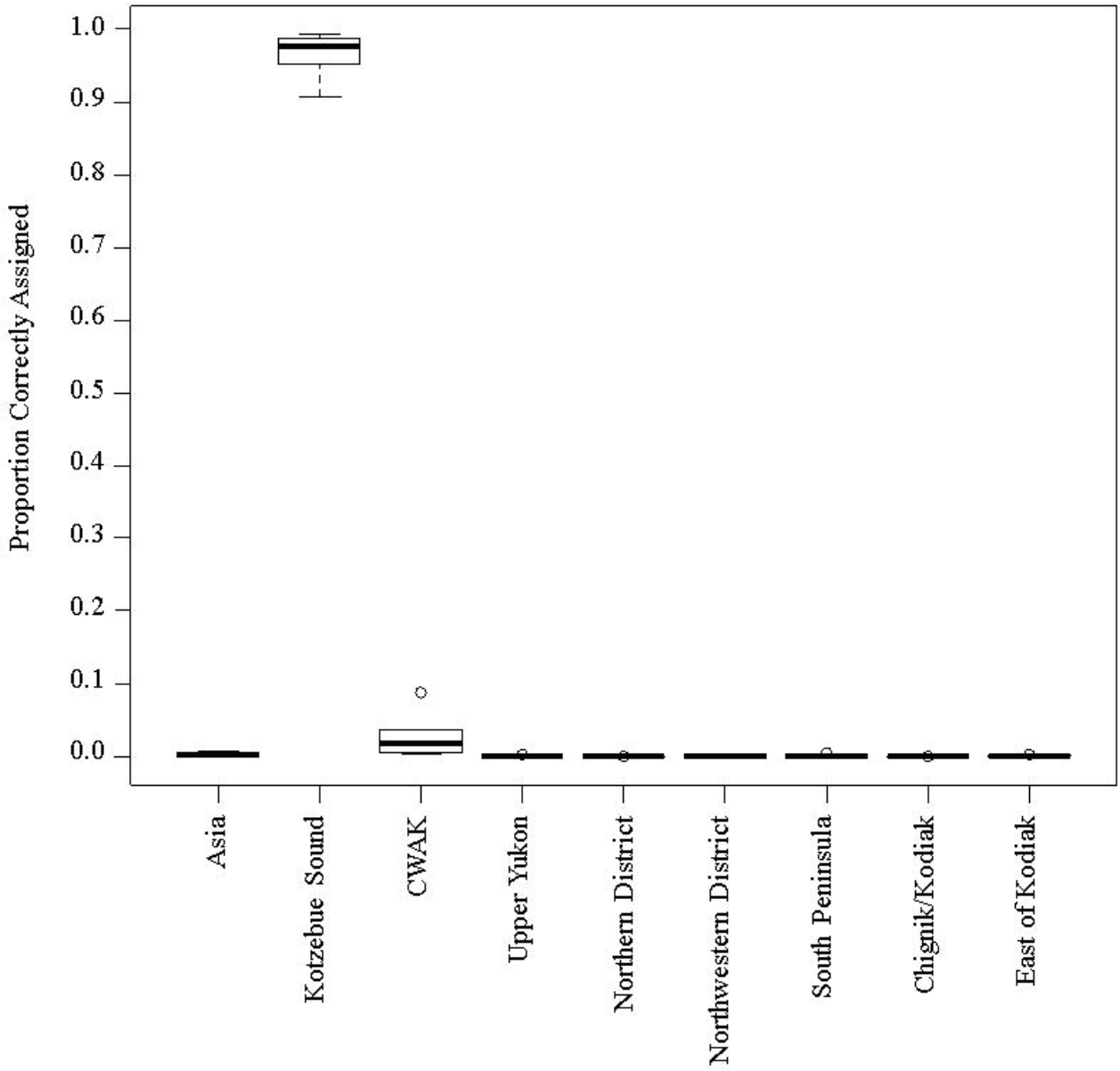

Figure 13.–Box-plot of the average proportion of chum salmon allocated to regional reporting groups for 10 repeated proof tests assembled from fish from the Kotzebue Sound reporting group. Proof tests are performed using independent sets of 200-fish mixtures of individuals removed from the baseline populations that comprise each reporting group. These mixtures are analyzed using the program BAYES with a flat prior.

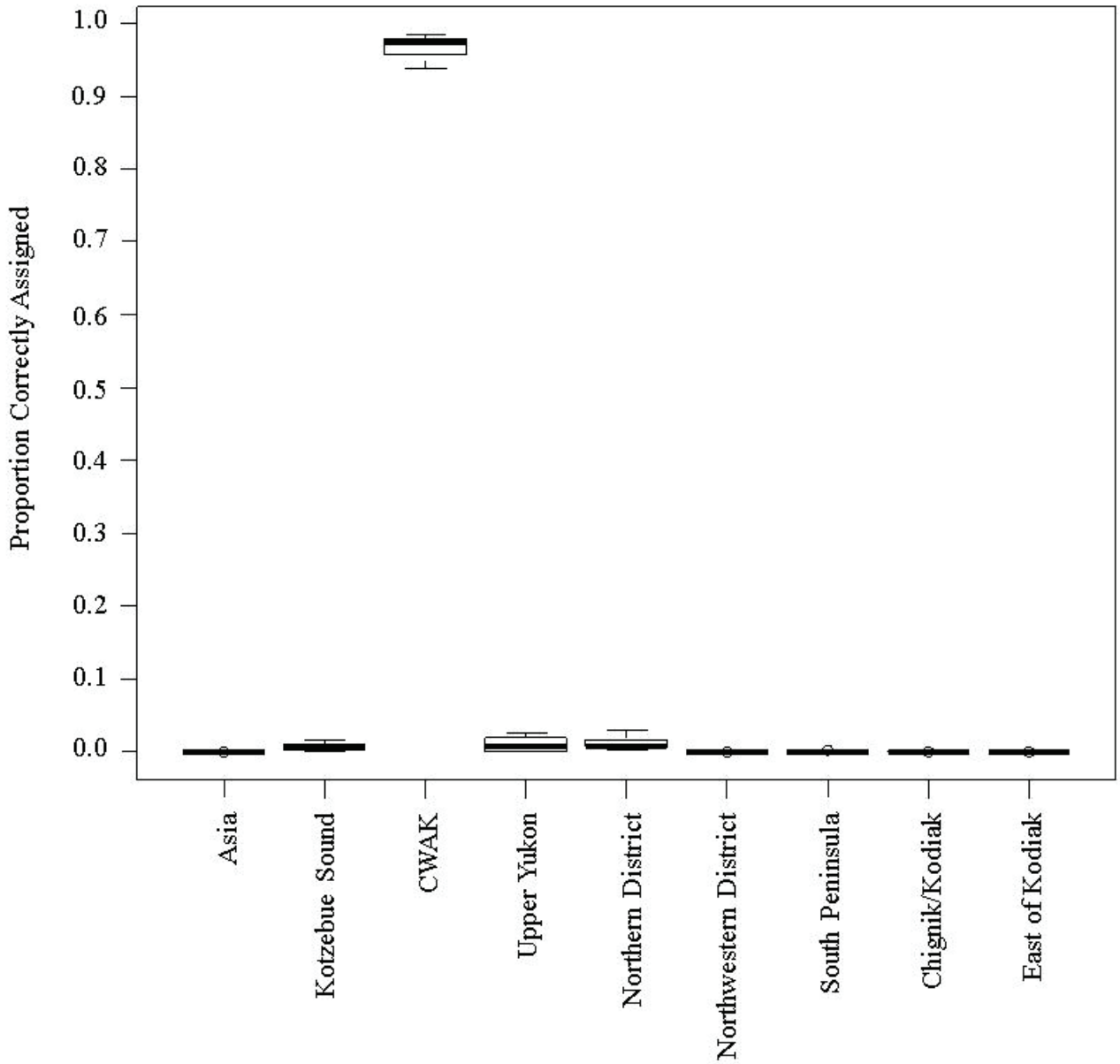

Figure 14.–Box-plot of the average proportion of chum salmon allocated to regional reporting groups for 10 repeated proof tests assembled from fish from the coastal western Alaska (CWAK) reporting group. Proof tests are performed using independent sets of 200-fish mixtures of individuals removed from the baseline populations that comprise each reporting group. These mixtures are analyzed using the program BAYES with a flat prior.

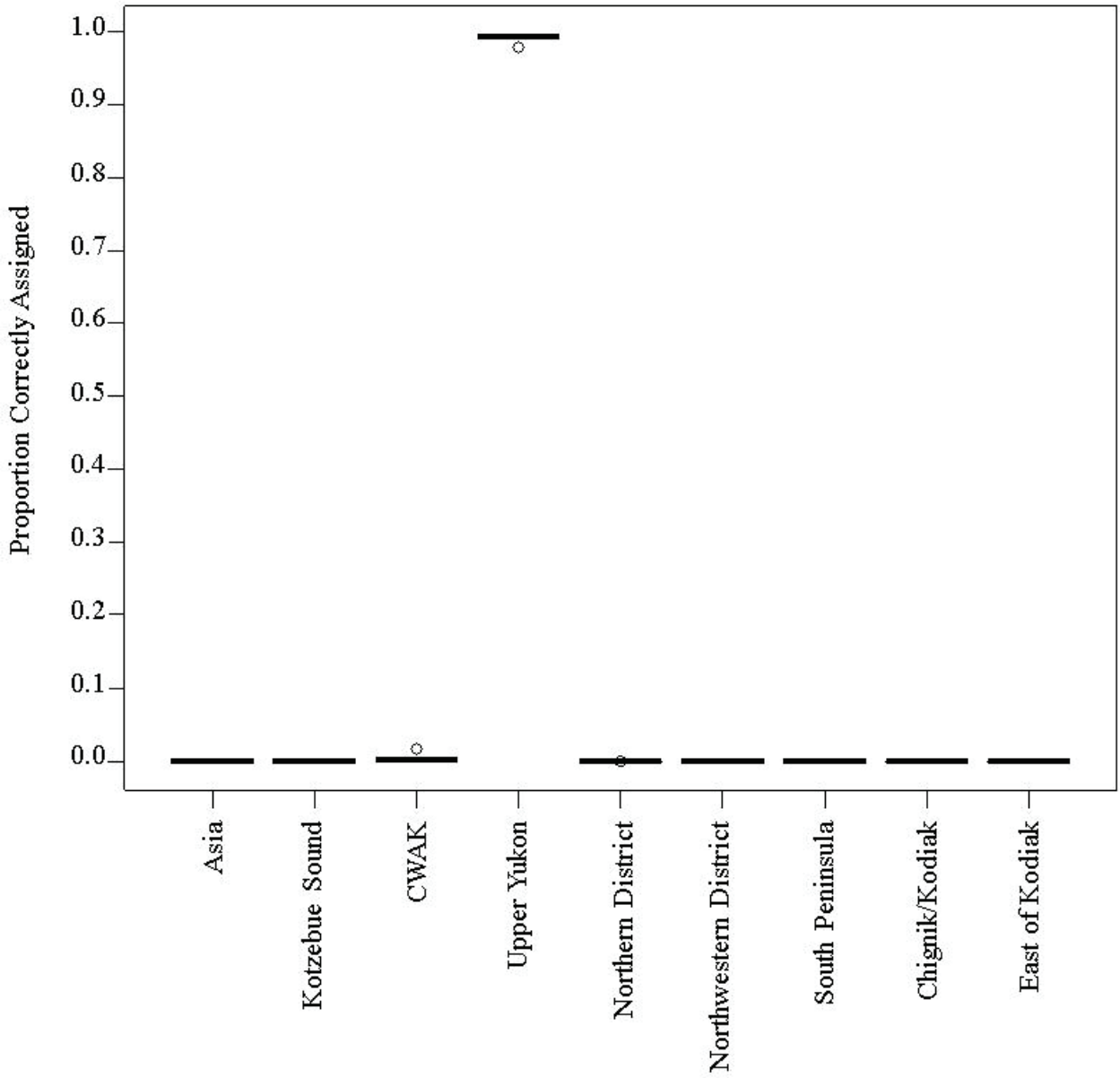

Figure 15.–Box-plot of the average proportion of chum salmon allocated to regional reporting groups for 10 repeated proof tests assembled from fish from the Upper Yukon reporting group. Proof tests are performed using independent sets of 200-fish mixtures of individuals removed from the baseline populations that comprise each reporting group. These mixtures are analyzed using the program BAYES with a flat prior.

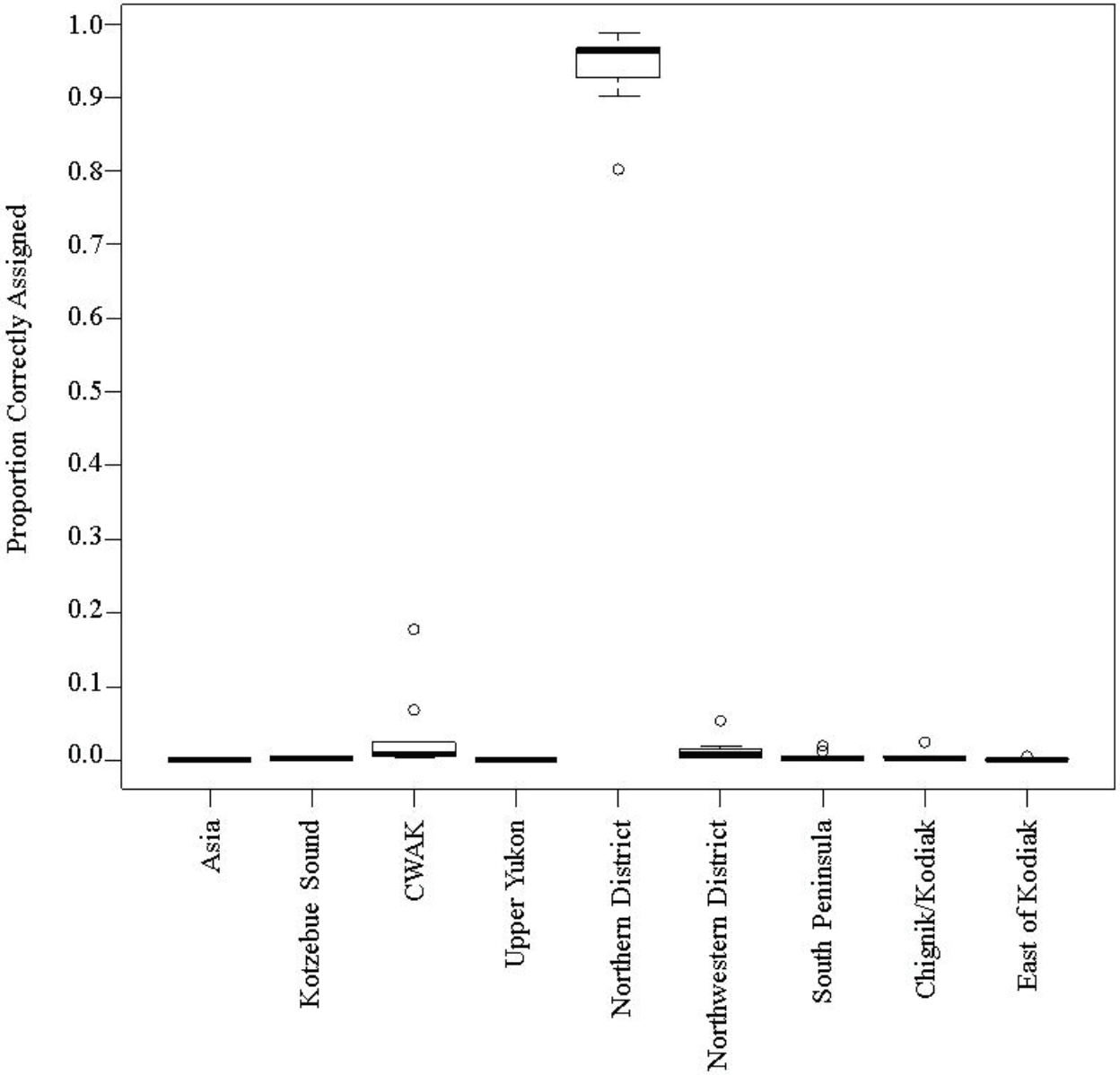

Figure 16.–Box-plot of the average proportion of chum salmon allocated to regional reporting groups for 10 repeated proof tests assembled from fish from the Northern District reporting group. Proof tests are performed using independent sets of 200-fish mixtures of individuals removed from the baseline populations that comprise each reporting group. These mixtures are analyzed using the program BAYES with a flat prior.

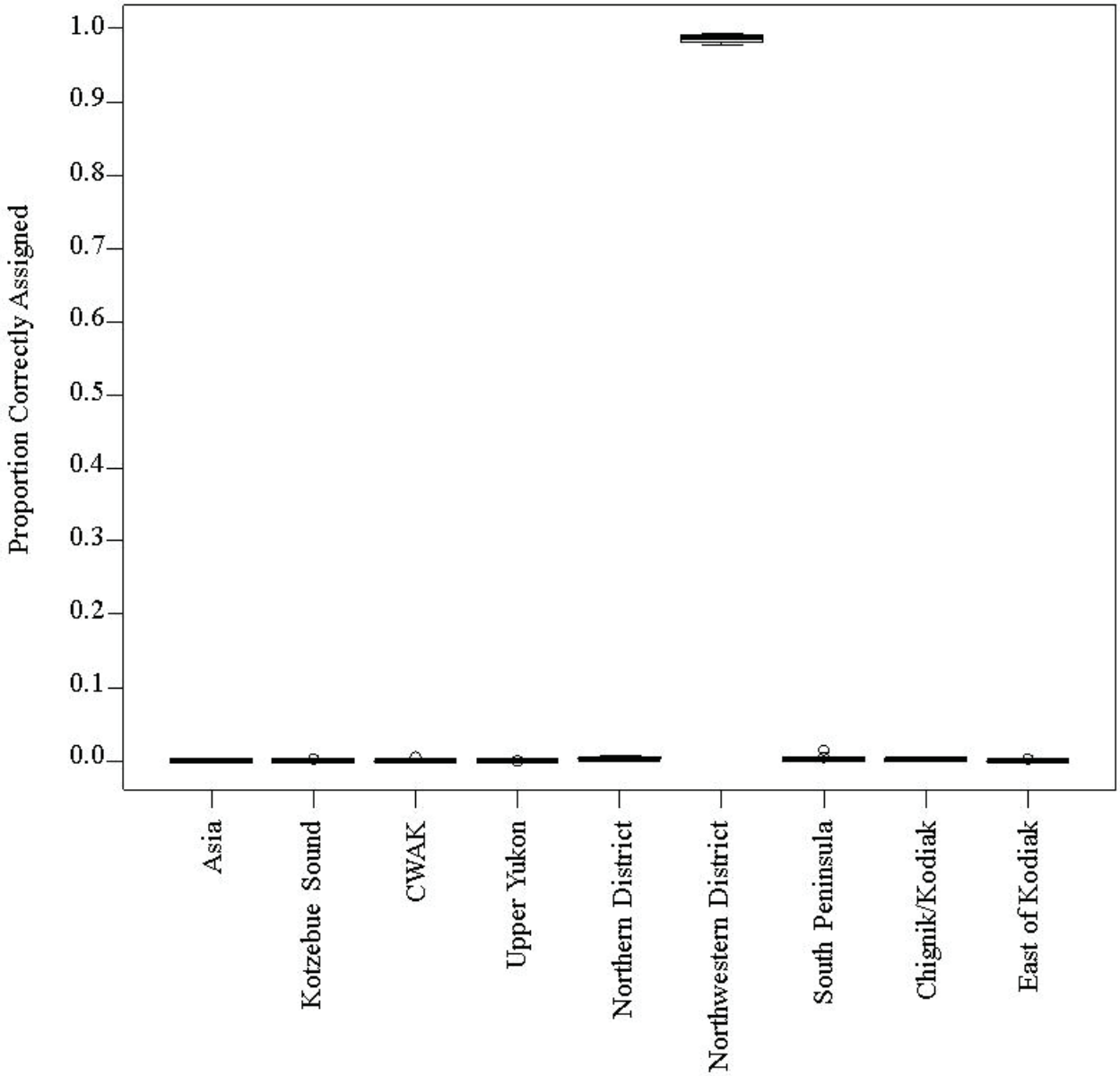

Figure 17.–Box-plot of the average proportion of chum salmon allocated to regional reporting groups for 10 repeated proof tests assembled from fish from the Northwest District reporting group. Proof tests are performed using independent sets of 200-fish mixtures of individuals removed from the baseline populations that comprise each reporting group. These mixtures are analyzed using the program BAYES with a flat prior.

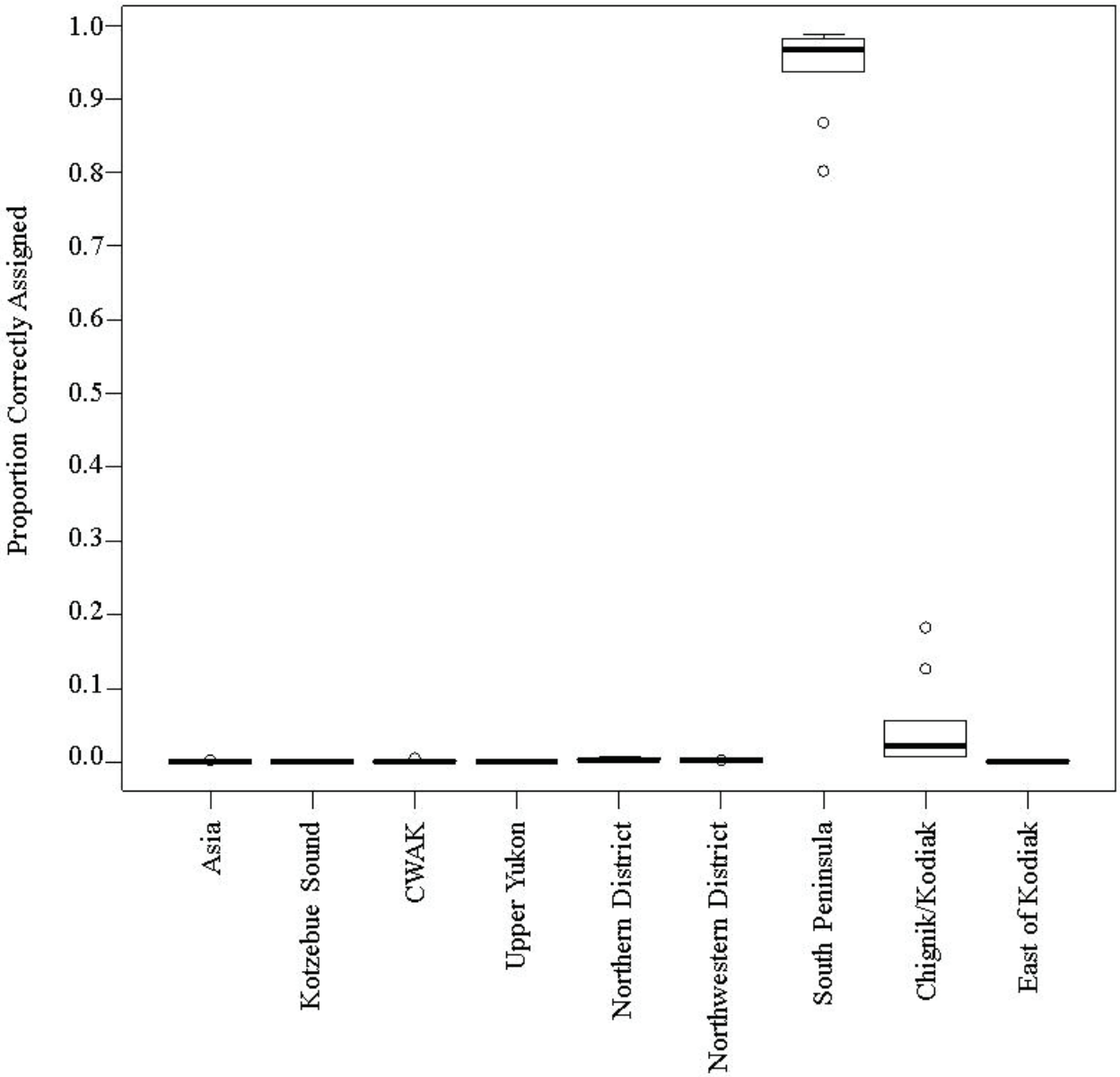

Figure 18.–Box-plot of the average proportion of chum salmon allocated to regional reporting groups for 10 repeated proof tests assembled from fish from the South Peninsula reporting group. Proof tests are performed using independent sets of 200-fish mixtures of individuals removed from the baseline populations that comprise each reporting group. These mixtures are analyzed using the program BAYES with a flat prior.

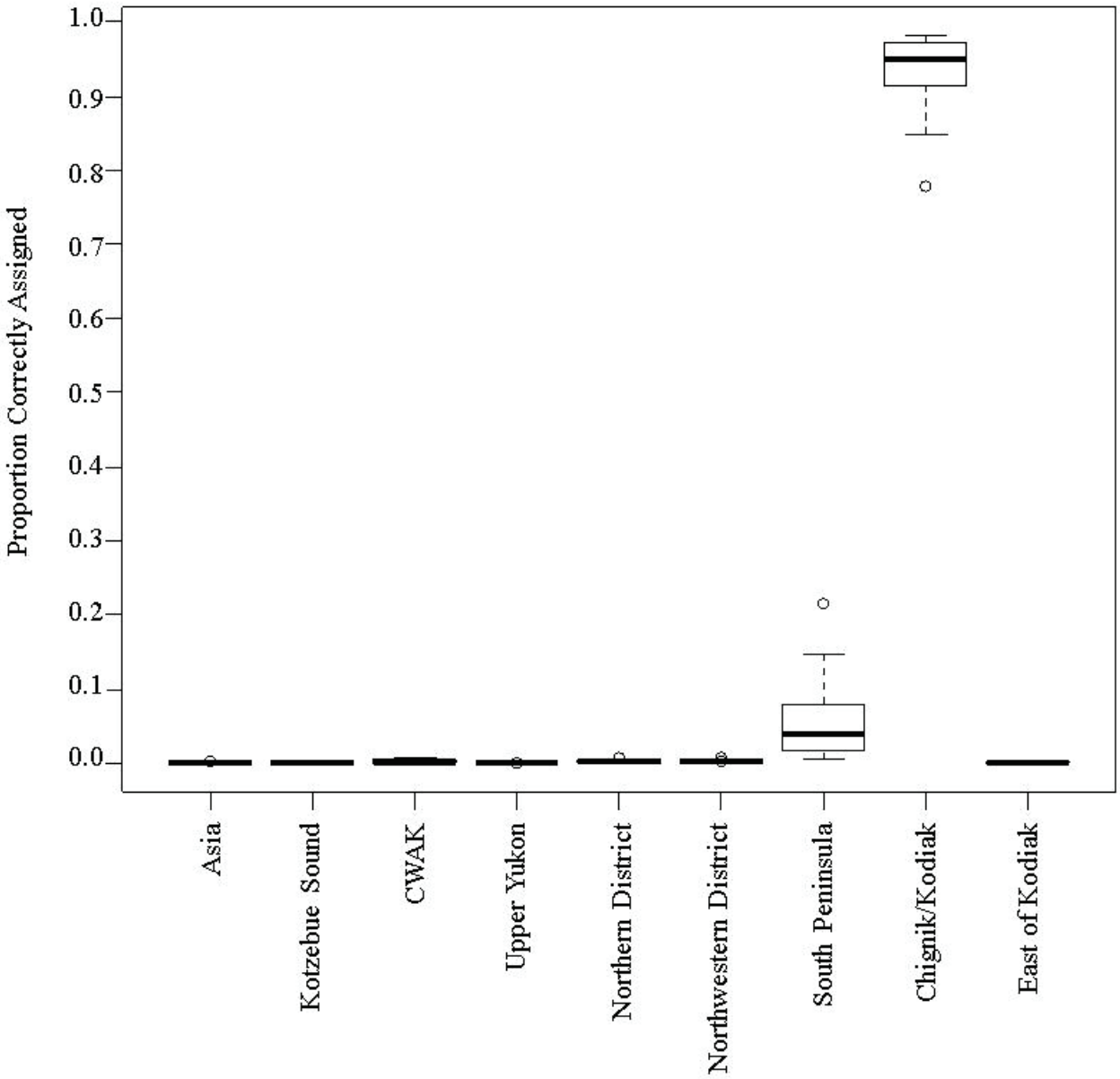

Figure 19.–Box-plot of the average proportion of chum salmon allocated to regional reporting groups for 10 repeated proof tests assembled from fish from the Chignik/Kodiak reporting group. Proof tests are performed using independent sets of 200-fish mixtures of individuals removed from the baseline populations that comprise each reporting group. These mixtures are analyzed using the program BAYES with a flat prior.

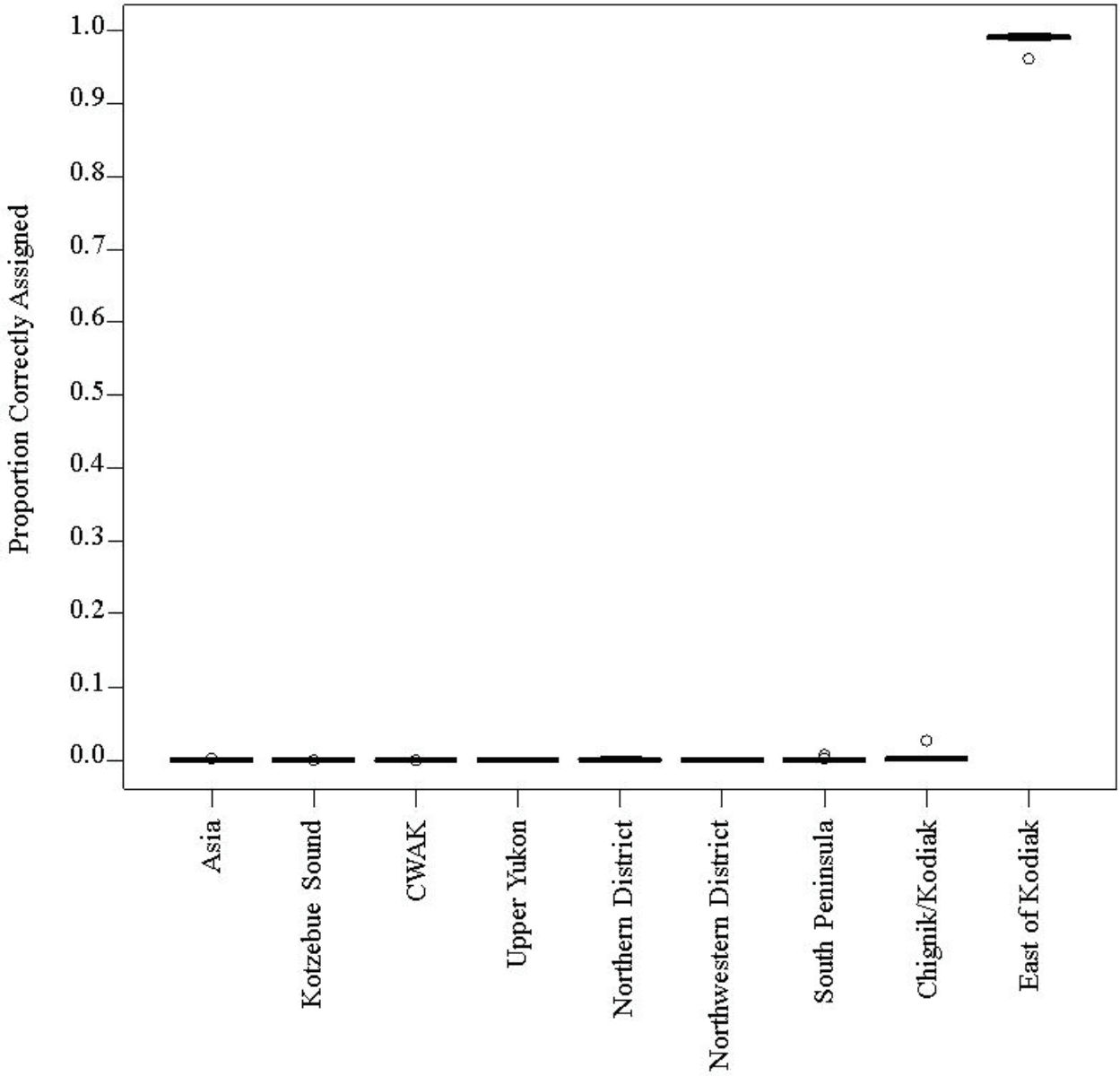

Figure 20.–Box-plot of the average proportion of chum salmon allocated to regional reporting groups for 10 repeated proof tests assembled from fish from the East of Kodiak reporting group. Proof tests are performed using independent sets of 200-fish mixtures of individuals removed from the baseline populations that comprise each reporting group. These mixtures are analyzed using the program BAYES with a flat prior.

APPENDICES

Appendix A.–Assay name, rank after locus selection process, dye used for TaqMan® assays (VIC, FAM), and forward and reverse PCR primers used for the original 188 assays screened as part of the locus selection process. Rank of N/A notes that a locus was excluded from consideration before the ranking process began. See footnotes for details.

Assay	Rank	Included in final set	VIC	FAM	Forward Primer Sequence	Reverse Primer Sequence
Oke_ACOT-100	89	X	C	G	TCAGGGACGATAAAGGGATCATCTT	GGGAGAGACACAGGTCTACCT
Oke_AhR1-278	145		T	A	GCGGACACCCTCTCACA	CCCACGGTAGTCGAAGCA
Oke_AhR1-78	73	X	G	A	AGCAGAACCAGCACCTACAG	GCTACTTGCCTTCTGCTGTTTG
Oke_APOB-60	135		C	T	CTGTGGATGGTATTCTGGATGCA	GGCACTACAAAAGAGGGAATCTCA
Oke_arf-319	59	X	T	C	TGCAGAAACTGATCATTGGTAGTGG	TCTGTTGTTACTCTGTTTCCTGCAA
Oke_ATP5L-105	93	X	C	G	GTGCACACCAATCCATTTCTGAAT	TGTTTTAAGGTGTGACTTGCTGGTA
Oke_ATP5L-248[c]	N/A		A	T	CTAGTGGATTGTGGCTTACGTCAA	GGATTCTGACTGTGGGTGTTTAACA
Oke_azin1-90	40	X	C	T	GGGAATAGTGTCATTTGGGATGCAT	GGTGAATGATATTCTGTAGTCATATTGCT TGA
Oke_brd2-118	44	X	C	T	CTCAAGCCCTCCACACTCA	GGGCCGTTTCCTGAAGCA
Oke_brp16-65	67	X	C	T	TCCACGTCACTCAGCATGATG	ACGGTCAACTTTTGGATTAGTGAAGA
Oke_CATB-60	58	X	C	T	GCTTCTATGGGTCCTACTACCGTAT	GCACTCCTCTTACACAACTCTGA
Oke_ccd16-77	1	X	A	C	TGTCTTCAGAATCCAATGCTTTCCT	GAGAAAGTTGCCGAGCTCAAG
Oke_CD123-62[b]	95		A	G	GAACAGCAGTGAATCGGTTACCT	TTGACGCTGTGTGTCTTCGA
Oke_CD81-108	101	X	G	T	CAGTATCATCATACAGCACAGATACAACA	GCCTGCTTGTTATACTGACAGTCAA
Oke_CD81-173	65	X	A	C	GATGACTGGAGTCAGCTTGCA	TTTCCTTGGCTCATCTTGCTGTA
Oke_cjo57-86	159		A	C	CAGAAGGTCTAAAGGTCCTTAACAATCA	CAGATTGAACAGTGCCCAGAGA
Oke_CKS1-70	123		G	A	GCTACCTCTATCATACCGCCAATATT	ATGTACATCTCTCCATGTGTTTTGGT
Oke_CKS1-94	98	X	G	T	TCTTCGACATGTTTAATCGAACAGAAGT	CCAGCTTTCGCTTGTCAAAACG
Oke_CKS-389	34	X	G	A	GGGCCATTCTCTGAGTTCAGT	GAGCACCGGTTGTCATGGA
Oke_CO1A1-72[b]	72		G	A	CTGTCAATGGAGGGTGATCGAAAT	CACCTAAGGTCCTGCAAGCA
Oke_CO1A1-76	136		A	T	GAGGGTGATCGAAATTGTGCTACTA	ACGACTGACATCAAGATAAATCTGCTAA TTT
Oke_col1a2-62[b]	35		G	A	GCAGGAAACCACTCTCATTCTTACT	AGACTTAGGAAATTGCACCTGCTTA
Oke_Cr30[g]	N/A	X	G	A	ACTACTCTCTGGCGGCTACA	AACCTTGGATTAGTGCTGATGTATGAG

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Assay	Rank	Included in final set	VIC	FAM	Forward Primer Sequence	Reverse Primer Sequence
Oke_Cr386[g]	N/A	X	G	-	CTTAATGTAGTAAGAACCGACCAACGA	ACTTAGGAACCAAATGCCAGGAAT
Oke_ctgf-105	102	X	G	A	TGAGTCCATGTACTACAAGAAGATGCT	TCGGTTCAAGTTAAGAGTCATTGGTT
Oke_CTR2-82	161		C	T	GCAGCAGACACACCGAAGTA	CCATTCCCATCGGCATCGT
Oke_DBLOH-79	134		C	T	GCAGATATGCCTCAGGGATGT	GACAGTCAAAGGATCAAGCTACCT
Oke_DCXR-87	20	X	A	T	GTCACCCAGAACAATAGAATGAGTCT	TCTAACACACCCACAATCTGCAAAA
Oke_DM20-548	124		G	T	CACTCCCCTCGCTTACTGATATCTA	ACGGACAGCTCATTTACATACACAA
Oke_e2ig5-50	64	X	C	T	GCACTGCTCATTCTGTCACATG	GGGAGTTCTTAGTGTGACCATAGAG
Oke_EF2-394	116		C	T	GCTTAACTGCTGTTTCTGCTATAGG	GCAGTCTCCTCCTTCTTGAAGTT
Oke_eif4ebp2-64	153		G	A	CGAAAGAAGATGGCTGCTGTGA	TGGCTTGGCTTGTAGAAACCA
Oke_eif4g1-43	63	X	G	T	GCACCCAACAGTTCATCATGTAAGT	CCACCCCCAGTAGTCAATCCT
Oke_f5-71	45	X	C	T	CTCAAATTTCCCTTTGACATCAATTCATCA	GATCCTCATGCACATCCAAACG
Oke_FANK1-166	4	X	C	T	ACTCACGTGTGGTAGAGACAGA	AGACTGAGAATCACAAGACCAACTG
Oke_FANK1-96	160		A	C	GGCTCACCTGGATGACATTATATAGG	CGTGAGTACACAACACTCTTTCAGT
Oke_FBXL5-61	22	X	G	A	TGGTGTGTAACGTCAGTGACTTAAG	CACCTCTAGAAATGACATGATCAGTGT
Oke_gdh1-191[e]	N/A	X	A	G	GTGGAGACCAAACCCAGTAGAAC	GGGTTAGAGGTCAGGGTTAGAG
Oke_gdh1-234[c,e]	N/A		C	T	CAAACCCAGTAGAACCCTGTGT	CTGGGAATGGTGATATATGTGTTCCT
Oke_gdh1-62[e]	N/A	X	C	T	CCACGTGATACAGGGAGATGTG	CACACACACTGACACGTACTGT
Oke_GHII-3129	33	X	G	A	GTCAAGCTGATACCACTCAAATCTCA	AGAATCTGACTACAGTCACTTAAAGTGATTTT
Oke_glrx1-78	86	X	C	T	CGCTCCGTCCAGTGATGTC	GGCCAAAGAGGTATTGACAAAGTAC
Oke_GNMT-100	111		C	T	GCGTCCACGCTCGTCAT	AGCGTGGACTCCATCATGTTG
Oke_GnRH-373	130		C	A	CCTGAGGAGACAAGTGCACATG	ATTGGCCATTAGGAATACAATGAATACAATATCT
Oke_GPDH-191	108	X	T	A	CCTGTACCTATAGGGCAACTTCAC	TGCCCTCTGATGGTATGATGGT
Oke_GPH-105	5	X	T	G	CAGATCAACCCTGGAAAAATATCTGATGT	TGAACAAGCAGCCCAATTCTGT
Oke_GPH-78[b]	83		G	T	GCAGCCCAATTCTGATATTTGTTTTACTAATT	TGAACAAGCAGCCCAATTCTGT
Oke_H2AX-72	143		C	T	AGGGCAACTACGCTCATAGAGTA	CGAGGACAGCAGCCATGTA

-continued-

Assay	Rank	Included in final set	VIC	FAM	Forward Primer Sequence	Reverse Primer Sequence
Oke_hmgb1-66[b]	76		G	T	GGAAACAGAATAACTACTAAGACCCTACATTATAAC	ACGCCCCCATTGGAAACC
Oke_hnRNPL-239	119		A	T	GAACGCAAGTAAGTGTTTGAAATCGA	GAAGAGAAAGACAGAAAGGGTTAGAAAACT
Oke_HP-182	42	X	A	C	CCGATGACTCCAAAGAAGTTGCT	GTCTGAATATTGTTTGAAAGAGATGGTAATGG
Oke_hsc71-199	141		G	C	CTGAAACTACCTCCCCCTAACAAG	ACAAGTCATGAGACTCAGACACAAG
Oke_HSP90BA-299	133		G	A	CACATACCAGTGTCGACCTTGA	GCACAACGATGATGAGCAGTACAT
Oke_il-1racp-67	8	X	G	A	AATTGCTCCTCCTCGCTATTTCTC	CCATCATTCAGACGACAAGGAGTAT
Oke_IL8r2-406	53	X	A	G	GGATGGACATTCACAGTCTGGTT	TTTCCAATCCCTGGCATCGT
Oke_IL8r-272[c]	N/A		T	G	AGGCTGAGGCAGTGACATG	ACCGACGCTTCTAGCAATGTAC
Oke_KPNA2-87	2	X	T	A	AGGCAGCCAGGTAAGTCAGTA	CAAAAGTAACGGTTAGGGACAGACA
Oke_lactb2-71	156		G	A	CGTCGTGAACCATGAGTGCAATA	TTCGCACAACTCTGGACGATAG
Oke_lamp2-138	114		G	A	GCATGTTACAGGACGGCAAGA	GGCTGGTATCACTGTGACATTCA
Oke_LAMP2-186	85	X	A	G	TTCTAGCCATGACCCAATGAAAGG	AACTGCTCCAAATGCTGGTTAGTA
Oke_mcfd2-86[b]	37		C	T	GGCTTGAGGGCCACATTG	GTCAAAACAAAATCTGTGCAACCCT
Oke_METK2-97	157		C	T	CCAGGACGAAGGTCAAAGTTCTT	GGCACATCCCAGAAGAGTGA
Oke_mgll-49	14	X	A	T	ACATTGTAATCTGTATTAGTCCAATGCAGAC	GGTACCACCTGCAACATCAAC
Oke_MLRN-63	103	X	G	A	CCATTTCAGCATTGCCAGATTTGAAA	GATGTCACAGACCAGTACCATGTTT
Oke_Moesin-160	100	X	T	G	TTTCAGCAAATGAAGAGAACATCAAACTG	GGGTTTCCAAACAAAGATGTCCTT
Oke_nc2b-148	17	X	A	C	CCAGCCTATTTCCTTTAGTGCATATGA	GCACCCTATTCCCTACATGGT
Oke_ND3-69[g]	N/A	X	G	A	TGGTATTGAATTTGTCGTAGAAGGCAAA	CCACGGCCTACACGTAATCATC
Oke_ndub3-58	163		C	T	GAGGCTTCAGTCGTCCTGTATC	CAGCGAAGCCCCATTTAAAGC
Oke_NHERF-123[3]	N/A		G	T	AGGAGTGAGGGCGAGAGAA	GGAACGAACTCTTCAGTAACCT
Oke_NHERF-54	155		G	A	CCCTCAATTAGCACATGAAAATCACA	CTCCTTCTTTTGCTCTCTCTCTCAA
Oke_NUPR1-70	57	X	G	T	AGACGGTGAACTCTGCTGTAGA	TCCCTTCACTGAAGCTACAGTCA
Oke_PDIA3-475	109		A	G	CCCGGTTCCTCCAGTAGTTG	CTGGTGGCCTACTACGATGTG
Oke_PDIA3-82[e]	N/A		A	C	TGCCTACGATGGACCCAGAA	ACTCAGCCCATCAGGACAAGA

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Assay	Rank	Included in final set	VIC	FAM	Forward Primer Sequence	Reverse Primer Sequence
Oke_pgap-111[f]	N/A	X	C	T	TGCAGATCTCAATTTGAACGACCTAT	AGACGACCATTATGGCTAACGTT
Oke_pgap-92[f]	N/A	X	C	G	TGCAGATCTCAATTTGAACGACCTAT	AGACGACCATTATGGCTAACGTT
Oke_pnrc2-78	144		G	A	CGTGACAGCAGGGAGATGA	CATCTCTAGGCATGCACCTTGA
Oke_PPA2-635	88	X	C	T	ACACAACTGACCATATTGACTTTCGA	TGGATAAAGATCTATATGGTGAATAAG GTCACA
Oke_psmd9-188[c]	N/A		C	T	ACTGAGGCAATATTCTGCAGGTT	GGGCTTGCGAATTAGTGATGAAATC
Oke_psmd9-57	79	X	C	T	ACTGTAGTGACTGCATTTCATATTGCT	ACCAGTTGTATTTTATTGTGCCAAATGA C
Oke_rab5a-117	104	X	C	T	GGGAATAACAGTCATTGCAGCATTT	CCATTGTTGGAAACTGGACAGC
Oke_ras1-249	62	X	T	G	GGATGACTAAGAGCGACTGTATGTG	AATTTTATGACTGCTTGAAGATTGAGT GC
Oke_RFC2-618	10	X	G	A	GACAATGTGTTAGTGTAGGCTTCACT	ACACTGGAATACTTAAGTGCACAACA
Oke_RH1op-245	6	X	C	T	TGGCCGATCTCTTCATGGTAATC	TCCAAAGACGAAATAGCCATGCA
Oke_ROA1-209	148		A	G	CAGGGTTTGATTGGTTAACTTACATTGAAT	GCTGGATCTCTCATTACCTGTAGGT
Oke_RPN1-80[b]	81		A	G	CACGCACCTTGCTAAGATAACAG	GGCTCTACCGCCAAGATAAAGTTAT
Oke_RS27-81	97	X	G	A	GCAACAAAGTGGACTATCACATTGAA	GCACCCAAGAAAGATTGATCCAGAA
Oke_RS27-94[a]	N/A		G	A	CACTTCTAGATCAATCCGCTGTTTC	GCGACTCCAGCCTTGACA
Oke_RS9-379[b]	9		A	T	GCAATCCTCCATACATTACCTGTCA	GTCTATAAGACTGCCCAGAACCAA
Oke_RSPRY1-106	7	X	A	T	GTCCTCCCTATTCTTCCACTTACCT	GCAAAGAAGCCAGACCTGAGAAA
Oke_serpin-140	41	X	A	T	TCCACAGTGAGTAATAAAGTTGCACAT	GAGCAAAGACCTAGGCCTGAAG
Oke_slc1a3a-86	61	X	C	T	TGTCTTCATCTGTGGACTCCTACA	TCACCATGACAACTCACCTAGATGA
Oke_sylc-90	28	X	A	T	TTGAGGAAACCACTGGTCTTACAAG	GCATCCTTCCTACCTTCCTTGAG
Oke_TCP1-78	90	X	A	G	CTCCAGGGCATCAGCAAATG	TGCTCATTACCACCATCTCTCTCT
Oke_TCTA-202	154		A	C	AGTTTAGCACTTACCTTGTCGGT	CAGTCTCATTGCCATCCATTTCG
Oke_TCTA-99[c]	N/A		C	G	GCTAGCACTTCATGGCAGCAT	GCCACCATCATCACGTTTAGTTCTA
Oke_Tf-278	46	X	C	A	GCCACAATTGTAATTCTAGATCCAGAGT	ACTGTACCTGGTGAGTTTTTAAAGCA
Oke_thic-84	13	X	C	T	GCTGCTGTCTTAAACCACATTCTACA	GCCTTCCTATTTGTCCTGTTCTCT
Oke_u0602-2442[c]	N/A		G	T	CAAGTATGCATGACTAGCTATGTGTATATCTT	TCTGCTATTGGTGGCCTATGTG
Oke_U1001-79[c]	N/A		A	G	GACAGTCAAAGGATCAAGCTACCT	GCAGATATGCCTCAGGGATGT

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Assay	Rank	Included in final set	VIC	FAM	Forward Primer Sequence	Reverse Primer Sequence
Oke_U1002-165[c]	N/A		C	G	GATTATTGGATCGAGAGAGTTAGAAGAGAGA	TCCTGCTGGAGCACATGTTC
Oke_txnrd1-74[b]	49		A	G	CACCCCATGTGCCTTTGGA	GACGTCCTGGCCCTTAACC
Oke_U1002-262	12	X	G	T	CCTAGACCACTCCAGACTGTTG	GCTGTGAACTCAGAATTGCTGTGTA
Oke_U1008-83	3	X	A	G	GTCACCAAACATCCTGCGAATG	ACTGTAAAACAAATACAGAAGCTCACTCA
Oke_U1010-154	139		A	G	TCCCATGGCCCTTACTCTATCAATA	GGCTTTATAAATACATTTGATTGATTGAGGTGT
Oke_U1010-251	30	X	A	G	CACCTCAATCAATCAAATGTATTTATAAAGCCA	ATCGTTGGGCCTAAACAAGGT
Oke_U1012-241	99	X	A	G	GCAGAGGTTATACCCATTTTAGATGCA	GTTGGCAGTCACGAACATTTGTTAT
Oke_U1012-60[c]	N/A		A	G	TGTACTCCTCTGCTTGGCTGTATAT	GGTAACCTGCTTGCCAACAG
Oke_U1015-255	107	X	A	G	CAGAGTGCAGAGTAATACGCATACA	ACTCTGTCATCCTCACCAAGGTAA
Oke_U1016-154	71	X	C	T	GCAGGTTGCTAAGTCATGTTACACA	ACGATAGGCACTAGGCAACATAAAG
Oke_U1017-52	84	X	C	T	TGGCAATGGGATGTCAAGTTATGA	CCAAGGAGTCCATGGTAATAAGCAA
Oke_U1018-50	50	X	C	T	TCCAGGTTGCTGACAATGTAAAAGT	TGTGTTGCACAATATCCACTACTTTGA
Oke_U1019-218	70		C	T	GCAGTCACACATTTTCTTCATCACA	TTCCTACAGAGGCAGATGCTAGT
Oke_U1020-75[b]	146		C	G	GCCAATCGCGGAAGTCTCA	GTTCACAAACGGCACAACAGTAC
Oke_U1021-102[d]	N/A	X	G	T	TCGAGGATTTGAGGATTAGGCTACT	AGCAAAATCACTAAGTCTCTCGTGTT
Oke_U1022-114[c]	N/A		A	G	GGAGTACTGCAATTGTCGCTTTTTAA	CAGTCCACCACGTGTTTGTG
Oke_U1022-139[d]	N/A	X	A	G	AACATTAAAACTGTGGTTTTGACCTCTTG	CAGTCCACCACGTGTTTGTG
Oke_U1023-147	26	X	A	C	TCTTAAAATGGAGAGAGCGATTAATGAAGG	GGCTTCAGTTGACCATGTACTCATA
Oke_U1024-113	54	X	A	G	CATGCTGGTGAATTATTGGACAATGT	CTGCTACATATGAAACTAGAGAACACACT
Oke_U1025-135	91	X	G	T	GGCTAGGGTTCTATTTGGACCAT	CAGTAGTGTTCTGTCCTGTAGTTCAA
Oke_U1027-89[b]	21		A	G	GCTCTGAAAAATATCTGACGTGATTGG	ATCTAGGGTCAGCCATCAGGAA
Oke_U1028-100[b]	29		A	C	CCTACTATTTCAGAGGCTTGACACA	CCCTCCAAGTCCCCAGTCA
Oke_U1031-132[b]	78		C	T	ACTAGAGCAGGCTTTTCTGTTTAGC	CGGTTATGCCTTAAATCTTTACCCATAAATAAAA
Oke_U2001-629[b]	75		C	T	CCCCACTCCTTCTACTCATCCAT	TTAGTACAAATGAACGAGGGTTGGAA

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Assay	Rank	Included in final set	VIC	FAM	Forward Primer Sequence	Reverse Primer Sequence
Oke_U2002-200	125		A	C	CCAGTGTTGTAGAAAACATGTGCTCTA	GCGCTTACGCTTCAATTTGCA
Oke_U2003-142	129		C	T	CTCCTCACTAACAGTAGCTGCAATT	CCTTGAAAGTGAGATATCTGTAGTTCGT
Oke_u200-385	52	X	G	T	CCCATAATTTTGCAACCCTAGTCACA	CCTTTCCCCATATCCTGTCACTTTT
Oke_U2005-62	150		A	G	GTACAGCAGAGACTAAAGCTATACAACA	GAGGTCAAGGCTTCAACATCAC
Oke_U1103-150[a]	N/A		C	A	ACCTCTCGACTTATTCCAAATTTTGTTACA	GGTATTGTGTGTAGTGGTTAAAGGG
Oke_u1-519	131		A	T	AGGTTTGTATGCGGCTGCTT	CAACTCAGCACAAGAACTGTTCAC
Oke_U2006-109	43	X	G	T	CCAACACCACTTTCCATTAATAAGCA	GCACACCCTAATTGACAAACAAACC
Oke_U2007-190	47	X	C	G	ACAGGCTGTGATGAGTTAACAATGTAAA	CATGTCGTCTACTTTGATGCCAATT
Oke_U2010-94	120		C	T	CCGCAGACAGTGGTCAATACT	GCCCTTCTCTTTCTCCATACTTTTCT
Oke_U2011-107	36	X	G	T	CCGTTTCTGTCAGACTCTGGTAAA	CTGGAGTGACTCAGGATCATAGC
Oke_U2015-151	25	X	C	T	GCATTTTATCCTCAAACTTTTCAACTGACA	ACGAATCCACCTAAAATCCACCAAA
Oke_U2016-118	110		C	T	ACGTGTCCTGTTCAAATTAGCAGTA	GAGGTGCATGCTTTTGTTCCA
Oke_U2017-87[b]	15		A	C	CAGGAGCCATTGGAAGAGTAGAG	CCATGATTTGAAAAGAGCTGAACCAT
Oke_U2019-112	149		A	C	GAATTTGACTGCCTGGCGAAAG	CGTACTGCTGATCCCAAATGATTTT
Oke_u202-131	113		C	T	GCTCTGGTCCAGGTCGTT	ACGTTCTTCGCCTCATGTTACATTA
Oke_u202-131	113		A	C	GCTATGACACTGCACTTTTGACTTT	GCAATTAGCTGCTAAGCACTAGCT
Oke_U2021-86	115		A	C	TGTGGCTCCAGCCAAAGTT	GCATCCTCAGTTCCAGCATAATGAT
Oke_U2022-101[b]	105		G	C	TGTCCTAATGACAGGCCTTGC	GTCACTGCAGCCTAACGTTATATTG
Oke_U2023-99	147		C	T	CACTATTTTGACAAGTGTTAAGATCATTTTGTGT	TGTGATCAACAGTTTTACACTCAATGGA
Oke_U2024-93	112		C	T	CGTCTTTCCAATACCACAGAGATACA	GAAGTGTTGACCTCTGCTCCTT
Oke_U2025-86	32	X	A	G	AAATCCCCATGGAGAAACACAATGA	ATTGTCCTTCCGCAGTGGT
Oke_U2026-64	132		G	T	CTTCCCACGTCTTTTCTGTCTCA	GCCTCTCACGTTACACTGTCATTTT
Oke_U2029-79	31	X	C	T	GGTTTGATTTCGTCGCGATTTGA	AAATCCCAGGGAGCGAAAGTC
Oke_U2031-37	16	X	A	T	CACACTTTCAATCAAATGTTGTGCAG	CGTTTGAGACGCCCTTCACT
Oke_U2032-74	69	X	G	A	GCTATTCCAATGTAAATCCTGTACTGTGT	AACCCTATCTGCTCATTGGTCATG
Oke_U2038-32[a]	N/A		C	T	CGACTTCCTGGCGTCATCTTC	GGGTACTTTCATACAGTACAGCTCT
Oke_U2040-77[a]	N/A		A	C	GGGCTAGAATTCTACTTGGTGACA	CCTTCCACAGTCTCATTTTGCTCTT

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Assay	Rank	Included in final set	VIC	FAM	Forward Primer Sequence	Reverse Primer Sequence
Oke_U2041-84	51	X	G	T	CCAGACCATGTGCTTGTTTGTCATA	GTGAATATTTTGGCAAGCCTGTACA
Oke_U2042-61	138		C	T	GCAATGCACATCTGAAATCTGCTAT	ACTCATTTTCAGATGTTCTTCCTTTGTCT
Oke_U2043-51	80	X	G	A	CACAAACCTACTACAGACAGCAGTT	GCCAGCTTTGTAGTCTTGTGGAAA
Oke_U2045-43	127		G	A	GACCCCGGGTCACCAC	CCAGGTGTGGCAGTGGAT
Oke_U2047-49	126		G	A	TTAGCTAGTATGTTAGCGTAGCACTT	TGCTGAATTTGAGGAACTAAACGTTAGT
Oke_U2033-122[b]	106		G	T	ACGCCCTTCCCCGATTC	GGCCTGGGTATGACTCAACATG
Oke_U2034-55	96	X	C	T	GGGAAGAAAAGCCTACCATAAACAG	CCCAGAGCGAATGCCAACA
Oke_U2035-54	82	X	G	A	CGCCAATAACGCTCCAACAAC	CTTCACACCCTGAGAACTGGTTTTA
Oke_U2037-76	60	X	C	G	CATATCAGGTGTGTCTCAACAGTCT	GGCATTCACTACATCACATGACCTT
Oke_U2048-91	87	X	A	C	AGTTGGGTCTTAAAGATGATCATTTGCT	GGACTCTTGACGGCCATCTTA
Oke_U2049-99	140		C	T	CATTGTAGCAGAGGGTCAACGATAT	ACACACGGCATTGCAAACTC
Oke_U2050-101	74	X	C	T	CTCTGAGTGTCACAATCACATATCGT	GTGTAAACGCATTCGAAGTCCTTT
Oke_U2052-56	122		C	T	GTGCCATGTTAGCCAAAAAGTTTCA	TCCATGTTAGCAGCGAACGTT
Oke_U2053-60	56	X	C	T	TCTGCTTTTGTCGTCTCACCAA	CACACGAGGGTGGACTTAGTT
Oke_U2054-58	77	X	C	T	CGTCTCATTCAGCTCTTTGATGTC	TTGGTTCAAGATGACACTGGTGT
Oke_U2056-90	55	X	G	T	CCATCACGTCACCATTACACTGT	GACATTAGCTGGCAGTCTGATCA
Oke_U2057-80	11	X	A	G	GCAGTTGTCATGGCAGTAAGG	GCCCCTCGTTCATTTTCAGATG
Oke_U212-87	18	X	C	A	TTGATTCATACTCAAGGTGAGCAGATT	GCTGGTGGCCCTTGTGA
Oke_u216-222	128		G	A	CGCAATATTAAGTGCGTCATACTTGT	CCCAGATGTTATTGTTTAAACTAGAGAA TGC
Oke_u217-172	94	X	T	C	GGATGGAAGAAGTTAGTTGTGTCAGA	CAAGTGGCAAAGTTTAAGAGTATAAAA ACCTAA
Oke_U302-195	19	X	C	A	GACCCTCAGCTATTTTAAGAACCTCAA	ACCTACCTCCTGCCAAGTTTTAAAC
Oke_U401-143	142		T	A	GCACTGGAAAGCACTCATCCTT	GCAGTCAGACACCATGCAAAA
Oke_U401-220[c]	N/A		G	A	TGACTGCATTCACTACTGACAAAGT	TGCAGCAAATGCTTGAGACTTACT
Oke_U502-241	68	X	G	A	ATGATCATTACACAGATGCACCTTGT	GCCAATTACACACTCACTCACAACT
Oke_U507-87[c]	N/A		G	T	GAAGACTGGACACACACGATATGT	GGCTGAGGCCATTCTATTCCC
Oke_U509-219	92	X	C	T	GCACCCCACCTGGCTT	TCACTCACTCTGCGTCTCTCT
Oke_U510-204	137		G	T	GCTCCCTGGACGGGTATATATG	CATCCGCCAATACTTCCTCGTA

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Assay	Rank	Included in final set	VIC	FAM	Forward Primer Sequence	Reverse Primer Sequence
Oke_U511-271	151		T	A	GACACAACGTTTTGGGACATTCAG	CGATGAGAAGGTGTCCACATACTTT
Oke_U514-150	152		C	T	GCATCATTAGTAAGGCGTCATTGG	GGCCAAGGATTATAGAGACAACACT
Oke_UBA3-245[c]	N/A		C	T	GAGAGGTGATAAGACAATGAGAAGTGTTA	GCGTTGAGTATGTCAGAATGCTACA
Oke_uqcrfs-69	158		C	G	CGCTGCTCTCCTGAGAAGATTTC	GCAGTCCGATTCGCTCACA
Oke_U503-272	118		C	T	GCAGAGAGAGGTCTGAATGAAACAG	CACGTCCTTTATCTTGCCTCTGTAT
Oke_U504-228	39	X	A	G	CTTAACTCAGTCACACCAACTCACT	GTGAGTTACAATGAGCTGCATGAG
Oke_U505-112	121		T	G	GAATACAGCATTGTGGGTAA	CTCAGTTGGTGCAGTAGGA
Oke_U506-110	27	X	C	T	CGTGGTTGGTTTCATTGACTCTCA	CGTTTCTCAAGATGTTCCTCTCCAA
Oke_U507-286	66	X	T	G	TGGTCATAGCTTGCACTGTACAAA	CCTAACTGTTCTTGCCCATATAGTGAA
Oke_XBP1-82[a]	N/A		C	T	TCTGCTCCGGAGTCTTCTGTAT	AAGGAGAGTGTTTAACAAAATTATACA GGATGT
Oke_zn593-152	117		A	C	GTTTTGAAAAGTTATTTCTCGCGTAGATTAA GA	AACTAGCTAGTTATCTAGTAGTAGCTAA ATTAGCT

[a] These SNPs were dropped because they were not in Hardy-Weinberg Equilibrium.

[b] These SNPs were dropped due to poor laboratory performance.

[c] These SNPs were dropped due to linkage.

[d] These SNPs were combined into a phenotypic locus, which is used in all WASSIP analyses. See discussion for details. Combined locus: "Oke_U1021-102-139".

[e] These SNPs were combined into a phenotypic locus, Oke_gdh1-191-234, in preliminary investigations of linkage. However, Oke_gdh1-191 was retained and Oke_gdh1-234 dropped after the linkage was not shown to be useful in proof tests using the complete baseline. See discussion for details.

[f] These SNPs were combined into a phenotypic locus, Oke_pgap-111-92, in preliminary investigations of linkage. However, Oke_pgap-111 was retained and Oke_pgap-92 dropped after the linkage was not shown to be useful in proof tests using the complete baseline. See discussion for details.

[g] These mitochondrial SNPs were kept for consistency with other coastwide baselines, and were combined into a haplotype a priori, without being subject to the same criteria as nuclear SNPs. See text for details. Combined locus: "Oke_Cr30_Cr386_ND3-69".

Appendix B.–Assay name, and scaled, scored measure values from tests outlined in Figure 1.

	Scored Measures								
Assay	1.a	1.b.i	1.b.ii	1.b.iii	2.a.i	2.a.ii	3.a	3.b	3.c
Oke_ACOT-100	0.0574	0.3294	0.5802	0.1114	0.2857	0.0667	0.0199	0.0696	0.5538
Oke_AhR1-278	0.0457	0.3211	0.1728	0.1341	0.1071	0.0222	0.0121	0.0273	0.2051
Oke_AhR1-78	0.1675	0.0387	0.4753	0.1675	0.0357	0.0889	0.4389	0.0307	0.1924
Oke_APOB-60	0.0271	0.3654	0.2469	0.0406	0.1071	0.3556	0.2425	0.2108	0.2330
Oke_arf-319	0.1430	0.5707	0.3395	0.1241	0.1429	0.0444	0.2729	0.4250	0.2198
Oke_ATP5L-105	0.0459	0.2816	0.8333	0.0717	0.1071	0.0667	0.0990	0.0410	0.1649
Oke_azin1-90	0.1360	0.4573	0.7469	0.1112	0.0357	0.0444	0.3625	0.2700	0.4214
Oke_brd2-118	0.1790	0.5418	0.6358	0.0961	0.0714	0.1333	0.0111	0.0346	0.2510
Oke_brp16-65	0.0588	0.1841	0.9444	0.0826	0.2143	0.1333	0.0666	0.0267	0.2739
Oke_CATB-60	0.0476	0.3947	0.6296	0.1394	0.5714	0.1556	0.0844	0.0297	0.2482
Oke_ccd16-77	1.0000	0.3224	0.7593	0.2006	0.1071	0.1111	0.9601	0.0414	0.4675
Oke_CD123-62	0.0707	0.3543	0.5062	0.0942	0.4286	0.0222	0.0044	0.0417	0.4297
Oke_CD81-108	0.0488	0.4185	0.4136	0.0960	0.5000	0.0889	0.0666	0.0631	0.2043
Oke_CD81-173	0.1213	0.2569	0.4012	0.1910	0.4643	0.0222	0.1175	0.0399	0.2074
Oke_cjo57-86	0.0190	0.2687	0.2037	0.0624	0.0357	0.0889	0.0025	0.0457	0.2407
Oke_CKS1-70	0.0557	0.2411	0.4383	0.0591	0.3571	0.0889	0.0000	0.0905	0.1790
Oke_CKS1-94	0.0580	0.2583	0.7284	0.0669	0.1786	0.0889	0.0075	0.0588	0.1824
Oke_CKS-389	0.1310	0.3652	0.6790	0.1617	0.0714	0.1111	1.0000	0.0294	0.3436
Oke_CO1A1-72	0.2539	0.0220	0.3889	0.0730	0.3571	0.0889	0.0011	0.0299	0.2219
Oke_CO1A1-76	0.0326	0.2879	0.5247	0.0442	0.1429	0.0000	0.0656	0.0406	0.1872
Oke_col1a2-62	0.2228	0.1547	0.6728	0.0403	0.5714	0.0222	0.2906	0.5050	0.2878
Oke_ctgf-105	0.1435	0.4494	0.2407	0.0731	0.2857	0.0444	0.0994	0.0273	0.2536
Oke_CTR2-82	0.0227	0.2933	0.0185	0.0715	0.0357	0.2444	0.1424	0.0332	0.2057
Oke_DBLOH-79	0.0855	0.1298	0.1481	0.0777	0.4286	0.1778	0.2183	0.0374	0.2404

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Assay	Scored Measures								
	1.a	1.b.i	1.b.ii	1.b.iii	2.a.i	2.a.ii	3.a	3.b	3.c
Oke_DCXR-87	0.0823	0.4332	0.9259	0.1963	0.4643	0.0667	0.0994	0.3286	0.3178
Oke_DM20-548	0.1111	0.5472	0.0494	0.0401	0.1786	0.1556	0.3110	0.1131	0.2796
Oke_e2ig5-50	0.0751	0.4060	0.7778	0.0889	0.0000	0.2444	0.0796	0.0499	0.2021
Oke_EF2-394	0.0454	0.3090	0.2284	0.1847	0.1071	0.2000	0.0457	0.0754	0.2139
Oke_eif4ebp2-64	0.0758	0.2854	0.0123	0.0364	0.1786	0.1778	0.0315	0.1413	0.3497
Oke_eif4g1-43	0.0841	0.4037	0.9198	0.0755	0.0357	0.0667	0.0034	0.0304	0.1932
Oke_f5-71	0.2455	0.2388	0.5123	0.1398	0.0357	0.0889	0.1468	0.0311	0.3283
Oke_FANK1-166	0.3360	0.9959	0.9753	0.1422	0.6429	0.1778	0.4548	0.1399	0.1925
Oke_FANK1-96	0.0187	0.2363	0.0370	0.0457	0.3214	0.0000	0.7045	0.0301	0.1993
Oke_FBXL5-61	0.2058	0.4710	0.7531	0.0853	0.4286	0.0667	0.2595	0.2530	0.1541
Oke_gdh1-191-234	0.0630	0.3173	0.9630	0.1517	0.2857	0.4222	0.0489	0.4724	0.3248
Oke_GHII-3129	0.2212	0.4253	0.3704	0.1562	0.1786	0.3778	0.0590	0.1264	0.2143
Oke_glrx1-78	0.0920	0.2562	0.5432	0.1687	0.0000	0.1111	0.0433	0.0368	0.3632
Oke_GNMT-100	0.0592	0.3775	0.4877	0.0760	0.2143	0.0667	0.0164	0.0364	0.2187
Oke_GnRH-373	0.0607	0.2379	0.3519	0.0391	0.2143	0.2000	0.0817	0.1532	0.2205
Oke_GPDH-191	0.0751	0.3088	0.3210	0.1164	0.0357	0.2222	0.4166	0.0444	0.2763
Oke_GPH-105	0.2587	0.5446	0.8642	0.4529	0.2500	0.0222	0.4713	0.0304	0.3567
Oke_GPH-78	0.1246	0.0877	0.2346	0.2882	0.1429	0.1111	0.0523	0.0321	0.2809
Oke_H2AX-72	0.0111	0.2976	0.2901	0.0233	0.1071	0.0444	0.9936	0.2693	0.2391
Oke_hmgb1-66	0.0854	0.4424	0.5556	0.1630	0.0714	0.0222	0.1533	0.0457	0.1552
Oke_hnRNPL-239	0.0526	0.2448	0.3765	0.1431	0.1071	0.1111	0.0013	0.0635	0.2043
Oke_HP-182	0.0581	0.4004	0.8889	0.2042	0.0357	0.0889	0.0083	0.2536	0.1929
Oke_hsc71-199	0.0300	0.2817	0.3827	0.0733	0.0714	0.1333	0.0335	0.0305	0.2232
Oke_HSP90BA-299	0.1194	0.2607	0.1049	0.1393	0.0714	0.0222	0.0013	0.0273	0.2059

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Assay	Scored Measures								
	1.a	1.b.i	1.b.ii	1.b.iii	2.a.i	2.a.ii	3.a	3.b	3.c
Oke_il-1racp-67	0.2146	0.3006	0.7654	0.5868	0.3214	0.0667	0.0335	0.0531	0.2158
Oke_IL8r2-406	0.1629	0.2881	0.8272	0.0425	0.0714	0.2222	0.0689	0.0368	0.2016
Oke_KPNA2-87	0.8135	0.5792	0.5679	0.4080	0.1786	0.1556	0.0461	1.0000	0.2002
Oke_lactb2-71	0.0446	0.3361	0.1605	0.0491	0.0714	0.0222	0.0220	0.1200	0.3136
Oke_lamp2-138	0.0276	0.3575	0.5185	0.0959	0.0357	0.2444	0.0124	0.0269	0.2197
Oke_LAMP2-186	0.0493	0.2272	0.8457	0.0606	0.0000	0.2889	0.0124	0.0821	0.4173
Oke_mcfd2-86	0.1271	0.4873	0.9074	0.0562	0.4643	0.0000	0.0300	0.0253	0.4495
Oke_METK2-97	0.0224	0.2570	0.2099	0.0380	0.1786	0.0444	0.1548	0.1819	0.2130
Oke_mgll-49	0.2706	0.5189	0.6481	0.1920	0.0714	0.1333	0.0315	0.1802	0.4702
Oke_MLRN-63	0.0679	0.2791	0.5617	0.0781	0.1071	0.0222	0.5309	0.0955	0.2055
Oke_Moesin-160	0.0654	0.2517	0.6420	0.0911	0.0357	0.1111	0.0335	0.0884	0.4326
Oke_Cr30_Cr386_ND3-694	0.0871	0.4161	0.0802	0.0839	1.0000	1.0000	0.3010	0.0635	0.2043
Oke_nc2b-148	0.1780	0.4464	0.8827	0.2077	0.2500	0.1556	0.0205	0.0264	0.2597
Oke_ndub3-58	0.0333	0.2663	0.1235	0.0379	0.1071	0.0222	0.0036	0.1758	0.2028
Oke_NHERF-54	0.0467	0.2865	0.0000	0.0698	0.0714	0.1778	0.3082	0.0700	0.4357
Oke_NUPR1-70	0.0783	0.2143	0.9568	0.0386	0.0357	0.3111	0.2391	0.2188	0.1983
Oke_PDIA3-475	0.0453	0.3159	0.4691	0.0563	0.0357	0.2000	0.1039	0.6796	0.2018
Oke_pgap-111-92	0.0723	0.2923	0.9136	0.0885	0.5714	0.3333	0.0811	0.0000	0.2254
Oke_pnrc2-78	0.0888	0.1901	0.0247	0.1082	0.1786	0.1333	0.0929	0.2213	0.1967
Oke_PPA2-635	0.0738	0.3094	0.5926	0.0366	0.4286	0.0444	0.7409	0.0377	0.1550
Oke_psmd9-57	0.0778	0.1953	0.7222	0.0954	0.0714	0.0889	0.2217	0.3691	0.1974
Oke_rab5a-117	0.0436	0.3379	0.4506	0.0902	0.5714	0.0444	0.1942	0.0306	0.1487
Oke_ras1-249	0.1115	0.3507	0.7716	0.0368	0.2857	0.1778	0.0099	0.0892	0.1979
Oke_RFC2-618	0.1751	0.4628	0.8765	0.2420	0.6429	0.1556	0.0335	0.0646	0.2093

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Assay	Scored Measures								
	1.a	1.b.i	1.b.ii	1.b.iii	2.a.i	2.a.ii	3.a	3.b	3.c
Oke_RH1op-245	0.3183	0.8951	0.5309	0.3724	0.2500	0.2222	0.0335	0.1446	0.2113
Oke_ROA1-209	0.0114	0.3085	0.1790	0.0460	0.3214	0.2667	0.0922	0.0263	0.1848
Oke_RPN1-80	0.0553	0.1979	0.6852	0.1031	0.1071	0.3556	0.1441	0.1103	0.2228
Oke_RS27-81	0.0320	0.2833	0.6111	0.1598	0.1429	0.0000	0.1273	0.1147	0.2109
Oke_RS9-379	0.5937	0.6645	0.3148	0.0388	0.2143	0.3778	0.0304	0.0740	0.1425
Oke_RSPRY1-106	0.2853	0.6926	0.7840	0.3032	0.2500	0.1778	0.1110	0.3041	0.7407
Oke_serpin-140	0.1132	0.4155	0.6543	0.1618	0.1786	0.1778	0.3086	0.0926	0.3065
Oke_slc1a3a-86	0.0810	0.3185	0.7037	0.1324	0.2143	0.0667	0.0213	0.3282	0.2138
Oke_sylc-90	0.1936	0.6300	0.8210	0.0769	0.1786	0.0444	0.0516	0.0299	0.2140
Oke_TCP1-78	0.0540	0.2817	0.7099	0.0357	0.2857	0.2667	0.0079	0.1276	0.2477
Oke_TCTA-202	0.0000	0.2910	0.2531	0.0330	0.0357	0.1111	0.0218	0.5906	0.3207
Oke_Tf-278	0.1218	0.4304	0.6605	0.1137	0.1786	0.3556	0.0245	0.0805	0.2508
Oke_thic-84	0.1839	0.7571	0.8148	0.0862	0.3214	0.0667	0.6559	0.6753	0.1357
Oke_txnrd1-74	0.1129	0.3721	0.6173	0.1832	0.1071	0.2222	0.0275	0.1275	0.2730
Oke_U1002-262	0.1965	0.7675	0.9383	0.1253	0.3571	0.1556	0.1407	0.0482	0.0000
Oke_U1008-83	0.7063	1.0000	0.9938	0.1585	0.2500	0.2667	0.0335	0.0553	0.2232
Oke_U1010-154	0.0441	0.2887	0.1111	0.0888	0.3214	0.3333	0.0317	0.0635	0.2043
Oke_U1010-251	0.1580	0.3968	0.9321	0.0588	0.1429	0.2222	0.0747	0.0407	0.6786
Oke_U1015-255	0.1924	0.7097	0.0926	0.0961	0.1071	0.1111	0.1306	0.1241	0.5305
Oke_U1016-154	0.1016	0.3570	0.6667	0.0773	0.0357	0.1333	0.0090	0.0601	0.1857
Oke_U1017-52	0.0781	0.3539	0.7160	0.1882	0.3571	0.0444	0.0474	0.1760	0.1689
Oke_U1018-50	0.1539	0.5187	0.5000	0.0318	0.2143	0.1778	0.0185	0.0393	0.2210
Oke_U1019-218	0.1043	0.2720	0.0617	0.0531	0.2500	0.0444	0.0339	0.0655	0.2257
Oke_U1020-75	0.0234	0.2814	0.7963	0.0691	0.1071	0.0222	0.0339	0.3277	0.3000

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Assay	Scored Measures								
	1.a	1.b.i	1.b.ii	1.b.iii	2.a.i	2.a.ii	3.a	3.b	3.c
Oke_U1012-241	0.0689	0.3430	0.2778	0.1831	0.0714	0.1333	0.0121	0.0539	0.3567
Oke_U1023-147	0.2900	0.9239	0.0679	0.1240	0.4643	0.0444	0.2330	0.0270	0.1330
Oke_U1024-113	0.0942	0.3149	0.5864	0.2240	0.1429	0.1111	0.0172	0.2094	0.2030
Oke_U1025-135	0.0979	0.3304	0.3642	0.1596	0.1071	0.2222	0.0059	0.0635	0.2043
Oke_U1027-89	0.3172	0.6341	0.3086	0.0848	0.3929	0.1111	0.0341	0.2750	0.2914
Oke_U1028-100	0.1679	0.3537	0.9691	0.1342	0.0714	0.0667	0.1189	0.0274	0.1547
Oke_U1021-102-139	0.0422	0.2912	0.9877	0.0951	0.7857	0.4667	0.3113	0.0741	0.3276
Oke_U1031-132	0.0664	0.3438	0.5988	0.1580	0.0357	0.1111	0.0326	0.2608	0.2706
Oke_u1-519	0.0364	0.3416	0.0741	0.0759	0.2500	0.3333	0.4837	0.2819	0.1693
Oke_U2001-629	0.1118	0.5249	0.4815	0.0626	0.0000	0.3556	0.0295	0.0591	0.5532
Oke_U2002-200	0.0897	0.1493	0.1975	0.0762	0.3929	0.0667	0.4690	0.0332	0.4303
Oke_U2003-142	0.0805	0.4180	0.1296	0.0886	0.2857	0.0889	0.0343	0.0520	0.2544
Oke_u200-385	0.2165	0.0000	0.6235	0.1137	0.3929	0.0889	0.1219	0.0423	0.2641
Oke_U2005-62	0.0216	0.2504	0.1914	0.0741	0.0357	0.2222	0.0000	0.3450	0.1865
Oke_U2006-109	0.1048	0.4788	0.8086	0.0467	0.1429	0.0667	0.9972	0.1822	0.2207
Oke_U2007-190	0.0575	0.3737	0.9506	0.0433	0.2500	0.2889	0.5159	0.0764	0.4238
Oke_U2010-94	0.1204	0.1702	0.2963	0.0598	0.2500	0.1556	0.0021	0.0867	0.2631
Oke_U2011-107	0.1400	0.5935	0.7901	0.0855	0.3214	0.0222	0.1476	0.0668	0.1917
Oke_U2015-151	0.3144	0.5715	0.2593	0.1030	0.5357	0.0889	0.0335	0.0441	0.2336
Oke_U2016-118	0.0761	0.4974	0.2160	0.0762	0.3571	0.0222	0.3064	0.0744	0.5866
Oke_U2017-87	0.1804	0.6579	0.9815	0.1484	0.2500	0.0222	0.0335	0.0273	0.1855
Oke_U2019-112	0.0192	0.2897	0.2654	0.0429	0.3214	0.0222	0.1225	0.0360	0.3695
Oke_u202-131	0.0055	0.3281	0.0309	0.0348	0.2143	0.2222	0.3411	0.0271	0.2038
Oke_u202-131	0.1214	0.4778	0.1173	0.0533	0.2143	0.2222	0.2600	0.0635	0.2043

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Assay	Scored Measures								
	1.a	1.b.i	1.b.ii	1.b.iii	2.a.i	2.a.ii	3.a	3.b	3.c
Oke_U2021-86	0.1181	0.5071	0.0988	0.0921	0.1071	0.0444	0.1661	0.0652	0.5398
Oke_U2022-101	0.0837	0.4021	0.4198	0.0896	0.2500	0.0222	0.0335	0.0669	0.2213
Oke_U2023-99	0.0238	0.2900	0.1543	0.0681	0.5357	0.0667	0.0335	0.0393	0.1979
Oke_U2024-93	0.0876	0.2239	0.2840	0.1064	0.1429	0.1556	0.3680	0.0422	0.5827
Oke_U2025-86	0.1318	0.3850	0.4568	0.3464	0.0357	0.0667	0.4312	0.0271	0.3043
Oke_U2026-64	0.1156	0.2972	0.0432	0.0568	0.3929	0.0000	0.2021	0.0634	0.7902
Oke_U2029-79	0.1379	0.5032	0.5370	0.1830	0.0714	0.2444	0.5102	0.0370	0.9166
Oke_U2031-37	0.2681	0.5468	0.2716	0.3078	0.2143	0.2000	0.0532	0.0775	0.2208
Oke_U2032-74	0.1675	0.5495	0.4444	0.0732	0.0000	0.1556	0.0147	0.0450	0.2170
Oke_U2033-122	0.0525	0.2828	0.5741	0.0504	0.1786	0.1111	0.0275	0.4354	0.2156
Oke_U2034-55	0.0752	0.2844	0.3272	0.1398	0.2500	0.2222	0.3159	0.0533	0.2106
Oke_U2035-54	0.0271	0.3524	0.7407	0.0716	0.1429	0.0444	0.0116	0.8043	0.3106
Oke_U2037-76	0.1643	0.3762	0.6914	0.0293	0.2857	0.0222	0.0339	0.1121	0.2126
Oke_U2041-84	0.1184	0.4204	0.9012	0.0925	0.1071	0.0444	0.0280	0.0271	0.1996
Oke_U2042-61	0.0282	0.2759	0.0556	0.1134	0.5000	0.1778	0.0334	0.2957	0.3332
Oke_U2043-51	0.0699	0.3063	0.8580	0.0508	0.1429	0.0667	0.0921	0.0386	0.2182
Oke_U2045-43	0.0781	0.1079	0.3333	0.0679	0.3214	0.0889	0.1742	0.0489	0.5615
Oke_U2047-49	0.0517	0.3310	0.3025	0.0511	0.4286	0.0222	0.3364	0.0885	0.1972
Oke_U2048-91	0.1185	0.3280	0.4938	0.1194	0.0714	0.0000	0.0506	0.1286	0.6156
Oke_U2049-99	0.0445	0.2401	0.1358	0.1111	0.1786	0.2889	0.0435	0.0922	0.3078
Oke_U2050-101	0.1235	0.5504	0.4074	0.0865	0.1786	0.0444	0.0335	0.4249	0.2760
Oke_U2052-56	0.0500	0.2787	0.3457	0.0439	0.2143	0.2000	0.2585	0.2368	0.5074
Oke_U2053-60	0.1422	0.5055	0.7346	0.0591	0.2143	0.0000	0.0021	0.0307	0.2203

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Assay	Scored Measures								
	1.a	1.b.i	1.b.ii	1.b.iii	2.a.i	2.a.ii	3.a	3.b	3.c
Oke_U2054-58	0.0485	0.4004	0.8025	0.0761	0.3214	0.0222	0.0153	0.0830	0.1978
Oke_U2056-90	0.0831	0.4367	0.8704	0.0587	0.1429	0.1111	0.3691	0.0511	0.2184
Oke_U2057-80	0.3143	0.5460	0.8951	0.0329	0.4286	0.1333	0.0439	0.1017	0.2228
Oke_U212-87	0.1857	0.5224	0.8519	0.1770	0.1429	0.1778	0.0555	0.1887	0.2226
Oke_u216-222	0.0981	0.4313	0.1852	0.0680	0.2500	0.0222	0.0335	0.0428	0.2142
Oke_u217-172	0.0250	0.3265	0.6975	0.1142	0.0357	0.2222	0.0764	0.0681	0.1826
Oke_U302-195	0.1963	0.5079	1.0000	0.0476	0.4643	0.0667	0.1299	0.0526	0.1690
Oke_U401-143	0.0356	0.3126	0.4259	0.0367	0.0357	0.1556	0.0220	0.0289	0.2449
Oke_U502-241	0.0586	0.2436	0.1667	0.1108	0.6786	0.2667	0.4483	0.9749	1.0000
Oke_U503-272	0.0589	0.4119	0.2222	0.1279	0.1429	0.1333	0.1654	0.0639	0.2059
Oke_U504-228	0.1132	0.5651	0.8395	0.0788	0.3571	0.0222	0.0144	0.2372	0.1268
Oke_U505-112	0.0122	0.2956	0.6049	0.0717	0.1429	0.1556	0.0025	0.0296	0.2064
Oke_U506-110	0.2871	0.4464	0.4321	0.0688	0.0357	0.2222	0.0335	0.6895	0.5095
Oke_U507-286	0.1074	0.3362	0.5494	0.1152	0.0357	0.2222	0.4071	0.0503	0.3795
Oke_U509-219	0.0913	0.3271	0.4630	0.0697	0.1786	0.1111	0.6675	0.0390	0.3469
Oke_U510-204	0.1057	0.5114	0.1420	0.0465	0.0357	0.0000	0.0552	0.1284	0.2463
Oke_U511-271	0.0106	0.3235	0.3951	0.0349	0.0357	0.1111	0.0335	0.0436	0.1724
Oke_U514-150	0.0517	0.3232	0.0062	0.0840	0.1786	0.0889	0.0331	0.2469	0.2578
Oke_uqcrfs-69	0.0526	0.3389	0.0864	0.0526	0.0000	0.1778	0.0124	0.0635	0.2043
Oke_zn593-152	0.0659	0.3813	0.3580	0.0733	0.2143	0.0889	0.0497	0.0722	0.2492
Sum of scores	19.7775	61.5583	81.5000	17.6069	35.6429	22.2444	25.2256	21.8533	45.5419