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New Genetic Baseline for Upper Cook Inlet Chinook Salmon Allows for the Identification of More Stocks in Mixed Stock Fisheries: 413 Loci and 67 Populations

by

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

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Weights and measures (metric)

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

Weights and measures (English)

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

Time and temperature

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

Physics and chemistry

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

General

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

Mathematics, statistics

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

FISHERY MANUSCRIPT SERIES NO. 19-06

NEW GENETIC BASELINE FOR UPPER COOK INLET CHINOOK SALMON ALLOWS FOR THE IDENTIFICATION OF MORE STOCKS IN MIXED STOCK FISHERIES: 413 LOCI AND 67 POPULATIONS

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ABSTRACT

This report describes an updated genetic baseline for Upper Cook Inlet Chinook salmon that allows for the identification of more stocks in mixed stock fisheries than previously possible. Chinook salmon are harvested in commercial, sport, subsistence, and personal use fisheries in Upper Cook Inlet, Alaska. Harvests often occur in areas where stocks intermingle, highlighting the need for understanding stock of origin in fishery catches to improve fishery management. Mixed stock analysis (MSA) has been used to estimate the stock composition of harvests in Cook Inlet since 2013. However, MSA applications have been limited by inadequate genetic structure, making northern Cook Inlet stocks of management and fishery importance difficult to distinguish: west Cook Inlet, Yentna River, and western Susitna stocks were indistinguishable; and eastern Susitna River and Matanuska River stocks were indistinguishable. Here we use cutting-edge genotyping by sequencing techniques to produce a baseline containing 67 Chinook salmon populations and 413 genetic markers and examine the baseline for population structure and test for potential reporting groups (stocks) using new baseline evaluation methods. Tests of potential reporting groups revealed 10 groups with adequate genetic divergence to meet the criteria for reporting groups. The 10 groups identified were (1) *West*, (2) *Susitna*, (3) *Deshka*, (4) *Yentna*, (5) *Knik-Turnagain*, (6) *Kenai Mainstem*, (7) *Kenai Tributary*, (8) *Kasilof Mainstem*, (9) *Kasilof Tributary*, and (10) *South Kenai Pen*. The data presented in this report will allow for more accurate, precise and finer-scale reporting group estimates for MSA studies in Cook Inlet and improved fisheries management.

Key words: Chinook salmon, Cook Inlet, *Oncorhynchus tshawytscha*, single nucleotide polymorphism, SNP, genotyping by sequencing, GT-seq, mixed stock analysis, MSA, *rubias*, genetic baseline

INTRODUCTION

BACKGROUND

Chinook salmon *Oncorhynchus tshawytscha* are harvested in subsistence, personal use, sport, and commercial fisheries throughout Cook Inlet in both State of Alaska and Federal Exclusive Economic Zone waters. Sport fishing occurs in both salt and fresh water, where an average of 46,388 Chinook salmon were harvested annually over a 20-year period.[1] Commercial harvests occur in the Northern District set gillnet Chinook salmon fishery, and as a nontargeted species in Northern, Central, and Lower districts set gillnet and drift gillnet fisheries, averaging 13,302 fish annually (1997–2016; Hollowell et al. 2017; Shields and Frothingham 2018). Additionally, annual harvests average roughly 1,300 fish for subsistence use and 1,000 fish for personal use (1997–2015; Fall et al. 2018). The marine fisheries harvest stocks of Chinook salmon originating from a variety of tributaries in Cook Inlet and from other areas. However, until recently, understanding of the stock composition of these mixed stock fisheries within Cook Inlet has been limited to tagging studies that identified a small number of stocks (McKinley 1999; Begich 2007).

Decreased returns of Chinook salmon in the region and throughout Alaska have prompted statewide concern about the health of Chinook salmon stocks (ADF&G Chinook Salmon Research Team 2013). To address these concerns, the Chinook Salmon Research Initiative (CSRI) implemented stock assessment programs targeting 12 indicator stocks from around the state, including the Kenai and Susitna rivers. One of the major knowledge gaps identified by the CSRI was stock of origin in fishery catches. In Cook Inlet, Chinook salmon population declines resulted in a fishery disaster declaration by the United States Secretary of Commerce based on very low returns in 2010, 2011, and 2012, the cause of which was poorly understood. Funding

[1] Alaska Sport Fishing Survey database [Internet]. 1996–2017. Anchorage, AK: Alaska Department of Fish and Game, Division of Sport Fish (accessed November 2018). Available from: http://www.adfg.alaska.gov/sf/sportfishingsurvey/.

for disaster research was made available through the Pacific States Marine Fisheries Commission and was directed, in part, at improving management of Chinook salmon in Cook Inlet by developing genomic resources capable of addressing new questions. Stock-specific harvest information allows for estimating exploitation and productivity of single stocks, thereby supporting sustainable fisheries management by the Alaska Department of Fish and Game (ADF&G). Genomic information can be used to estimate stock-specific harvest by conducting mixed stock analysis (MSA).

Genetic baselines are the cornerstone for successful MSA using genetic markers (e.g., Crane et al. 2000; Seeb et al. 2000; Beacham et al. 2009; Habicht et al. 2010). These genetic baselines illuminate population structure and guide the delineation of reporting groups (stocks) for MSA. ADF&G has collected baseline samples from throughout Cook Inlet rivers for over 28 years and has used genetic mixed stock analysis to estimate the stock composition of Chinook salmon harvested in Cook Inlet fisheries since 2013. However, to date, resolution among stocks has been poor, especially for stocks in northern and western Cook Inlet (Barclay and Habicht 2015).

Since 2005, several large investments were made to gain a greater ability to distinguish individual stocks and stock groups from mixed stock fishery harvests. Early studies were limited to Kenai and Kasilof rivers (Adams et al. 1994; Begich et al. 2010; Rogers Olive et al. 2013), and broadscale analyses with a few Cook Inlet populations (Crane et al. 1996; Teel et al. 1999; Templin et al. 2011). Directed efforts were made to increase the number of populations and the number of genetic markers in the Cook Inlet baseline, and the baseline has been updated 4 times to incorporate the latest information inclusive of this study (Table 1). This report provides results for an order of magnitude increase in the number of genetic markers made possible by new, cost-effective, laboratory techniques.

Barclay et al. (2012) provided the first comprehensive look at Chinook salmon population structure in Cook Inlet but did not test performance of reporting groups. That study, using a baseline of 30 populations, found 2 regional genetic groups: a northern region with little divergence (west Cook Inlet, Yentna River, Susitna River, Knik Arm, and Turnagain Arm populations); and a southern region with higher divergence (Kenai River, Kasilof River, and southern Kenai Peninsula populations). This population structure foreshadowed the challenges of distinguishing among reporting groups in western and northern Cook Inlet, and corroborated findings from previous studies showing high divergences among southern region populations (Begich et al. 2010; Templin et al. 2011; Rogers Olive et al. 2013). At the time, many areas of northern Cook Inlet were underrepresented in the baseline, precluding a robust test of MSA performance.

In 2013, samples from 13 northern Cook Inlet populations were added to the baseline, and baseline evaluation tests were performed to evaluate reporting groups for analyzing Upper Subdistrict (also known as Eastside Set Gillnet; ESSN) commercial harvests (Eskelin et al. 2013). The tests revealed that the baseline had sufficient variation among populations to identify 4 groups: 1) *Kenai River mainstem*, 2) *Kenai River tributary*, 3) *Kasilof River mainstem*, and 4) *other Cook Inlet* populations. The updated baseline was then used to analyze ESSN harvests from 2010, 2011, and 2013, marking the first MSA of Chinook salmon fishery harvests in Cook Inlet.

Additional baseline sampling occurred in 2013 and 2014 as part of the Susitna-Watana Hydroelectric project (Study 9.14 *Genetic Baseline Study for Selected Fish Species*, AEA 2012). In 2015, the baseline was updated with 25 additional northern Cook Inlet populations for a total of 55 populations and 39 single nucleotide polymorphism (SNP) markers (Barclay and Habicht 2015). The baseline was tested with emphasis on splitting out reporting groups in northern Cook Inlet. For these tests, 5 reporting groups were selected based on an assessment of population structure and management needs for fisheries in Central and Northern Cook Inlet: (1) *NorthWestCI* (populations from streams draining into western Upper Cook Inlet, Yentna River, and western Susitna River); (2) *MatSu* (Eastern Susitna River and Matanuska River populations); (3) *KnikTurnagain* (populations from Knik and Turnagain arms); (4) *KenaiKasilof* (populations from the Kenai and Kasilof rivers); and (5) *SKenaiPen* (populations from Kenai Peninsula streams, south of the Kasilof River). The results from these tests indicated that the *KenaiKasilof* and *SKenaiPen* reporting groups performed well and *NorthWestCI*, *MatSu*, and *KnikTurnagain* reporting groups performed adequately for MSA. However, the challenges discriminating among northern Cook Inlet populations persisted. Despite its limitations, due to management needs, the Barclay and Habicht (2015) baseline has been used for the MSA of ESSN commercial (Eskelin and Barclay 2015, 2016, 2017, 2018), Northern District commercial, and Tyonek subsistence fisheries (St. Saviour et al. 2019). This baseline was also combined with the Templin et al. (2011) baseline for the MSA of Cook Inlet marine sport fishery harvests (Barclay et al. 2016).

Developing marker sets that are specifically designed to distinguish among reporting groups and increasing the number of markers screened in baselines have both increased resolution for MSA applications (e.g., Larson et al. 2014a; McKinney et al. 2019). Fortunately, new techniques have been developed for both assessing marker utility in MSA (Larson et al. 2014b) and for screening large numbers of markers cost effectively (Genotyping-in-Thousands by sequencing [GT-seq]; Campbell et al. 2015). In addition, a GT-seq marker panel for Chinook salmon is already available, although it was designed for distinguishing among Pacific Northwest populations (Janowitz-Koch et al. 2019).

In 2017, 2 projects contributed funding to identify markers, develop marker panels, and screen markers in collections of Chinook salmon from Cook Inlet. The first project was funded through the Pacific States Marine Fisheries Commission using Cook Inlet disaster relief funding. This project was a collaborative project between the University of Washington (UW) and ADF&G. The primary objective of this project was to increase MSA resolution of Chinook salmon reporting groups in Cook Inlet through the development of a high-resolution baseline consisting of hundreds of genetic markers in a subset of key populations. This project leveraged cutting-edge techniques developed at UW (Larson et al. 2014a) to assess thousands of SNPs for distinguishing among west Cook Inlet and Yentna River stocks (Dann et al. 2018). Selected markers were used to develop a GT-seq panel (McKinney et al. 2019). In this project, both this new UW panel and the panel developed by the Columbia River Inter-Tribal Fish Commission (CRITFC) were used to screen a subset of key populations. The second project was funded by the Alaska Sustainable Salmon Fund (project number 44908) and was used to screen these 2 marker panels on additional Cook Inlet populations to fill out the baseline.

This report describes the development and MSA performance of a high-resolution baseline using new genotyping techniques and MSA reporting group evaluation methods. This study was designed to provide fishery managers with a better understanding of harvest composition patterns

through space and time for improved stock-specific management of fisheries in Cook Inlet. Definitions of commonly used genetic terms are provided in Appendix A to better understand the methods, results, and interpretation of this study.

OBJECTIVES

The goal of this study was to develop a high-resolution genetic baseline for Cook Inlet Chinook salmon that provides finer-scale reporting group resolution than currently available to support sustainable fisheries management. Project tasks included the following:

1. Genotype Cook Inlet Chinook salmon populations for 656 SNP markers.
2. Conduct baseline development analyses.
3. Analyze the baseline for population structure.
4. Conduct baseline evaluation tests to describe new limits of resolution for MSA reporting groups.

METHODS

TISSUE SAMPLING

Tissue samples suitable for genetic analyses (hereafter, *genetic samples*) were collected and subsequently frozen (heart, muscle, liver, and eye; samples collected prior to 2003) or preserved in 95% reagent alcohol (axillary process or fin). Frozen tissues were placed into individual vials, and ethanol-preserved samples were placed collectively into 125–500 ml containers, with 1 or more containers for each collection site for each year.

Baseline genetic samples were collected from spawning aggregates of Chinook salmon by ADF&G personnel using weirs, gillnets, beach seines, or hook-and-line gear (Table 2; Figure 1). Target sample size for each baseline aggregate was 95 individuals across all years to achieve acceptable precision to estimate allele frequency (Allendorf and Phelps 1981; Waples 1990a).

Baseline samples were selected for analysis to maximize the number of individuals per location and the total number of samples selected was kept close to 8,000 to stay within budget. When available, samples from locations with archived DNA were selected to reduce analysis costs. Because DNA is archived on 96-well plates, and laboratory analysis is most efficiently conducted on full plates, some individuals from nontargeted locations were genotyped but not included in the statistical analysis.

LABORATORY ANALYSIS

Genotyping

Genomic DNA was extracted from tissue samples using either the DNeasy 96 Blood and Tissue Kit (QIAGEN) or the NucleoSpin 96 Tissue Kit (Macherey-Nagel).

Samples were sequenced for 588 amplicons that were partitioned into 2 panels hereafter referred to as the UW (289 amplicons) and CRITFC (299 amplicons) panels. Of the 289 UW amplicons, 230 contained 1 SNP locus and 59 contained 2–4 SNP loci (366 SNPs total; Appendix B; Dann et al. 2018; McKinney et al. 2019). All 299 CRITFC amplicons contained 1 SNP locus (Janowitz-Koch et al. 2019). For each panel, sequencing followed the GT-seq methods described in Campbell et al. (2015) other than deviations as follows: during PCR2, the volume was

increased to use 2 µL of 10 µM well-specific i5 tag primers per well bringing the final reaction volume to 11 µL; and during the purification step with magnetic beads, the final elution volume was increased to 17 µL and no additional TE (pH 8.0) with 1% TWEEN 20 was added. The quantification by qPCR was completed using triplicate dilutions of 1:1000, 1:5000, and 1:10000. Four microliters of each dilution was used as template in 10 µL reaction using 6 µL Kapa Library Quantification Kit - Illumina/ROX Low (Kapa Biosystems). The qPCRs were performed in 384-well plates on a QuantStudio 12K Flex Real-Time PCR System (Life Technologies). Final dilutions of each plate library were normalized to 4 nM. The final pooled library went through an additional purification step via magnetic beads. This involved adding 46.4 µL of Agencourt AMPure XP magnetic beads to 58 µL of pooled library in a 1.5 mL tube. After the tube incubated at room temperature for 7 minutes, it was placed in a magnetic stand for 5 minutes. The supernatant was discarded. A double wash of 80% ethanol (ETOH) was performed, each for 30 seconds. The tube incubated at room temperature for 5 minutes to dry off any residual ETOH. The elution was performed with 30 µL of 1X Low-EDTA TE (pH 8.0) incubated for 5 minutes before final transfer to a new 1.5 mL tube. The elution product was quantified for DNA yield via the manufacturer's direction for the Qubit 3.0 (Thermo Fisher Scientific). The final pooled library was sequenced at a final concentration of 3.5 pM on an Illumina NextSeq 500 with single end read flow cells using 150 cycles.

Locus genotypes (single SNPs or microhaplotypes) for each sample were called using the GTscore software (https://github.com/gjmckinney/GTscore) with 1 modification (likelihood threshold *p*-value < 0.001; McKinney et al. 2019). Single SNPs not conforming to expected allelic ratios (e.g., polyploid or off-target amplification) were removed before allele calls were assigned. Alleles from multiple SNPs known to be linked (i.e., on the same amplicon), were combined to form microhaplotype loci (Table 3; Appendix B). Combining linked SNPs into microhaplotypes has been shown to increase the accuracy of MSAs (McKinney et al. 2017; Baetscher et al. 2018). Genotypes were imported and archived in the Gene Conservation Laboratory Oracle database, LOKI. From this point forward, each single SNP or microhaplotype was referred to as a locus.

Fluidigm SNP Genotyping Technology was employed to reproduce genotypes for 42 SNP loci for the quality control (QC) analysis of newly extracted baseline samples (Appendix B). These samples were genotyped using Fluidigm 192.24 Dynamic Array Integrated Fluidic Circuits (IFCs), which systematically combine up to 24 assays and 192 samples into 4,608 parallel reactions. The components were pressurized into the IFC using the IFC Controller RX (Fluidigm). Each reaction was conducted in a 9 nL volume chamber consisting of a mixture of 20X Fast GT Sample Loading Reagent (Fluidigm), 2X TaqMan GTXpress Master Mix (Applied Biosystems), Custom TaqMan SNP Genotyping Assay (Applied Biosystems), 2X Assay Loading Reagent (Fluidigm), 50X ROX Reference Dye (Invitrogen), and 60–400 ng/µL DNA. Thermal cycling was performed on a Fluidigm FC1 Cycler using a Fast-PCR protocol as follows: an initial "Hot-Start" denaturation of 95ºC for 2 min followed by 40 cycles of denaturation at 95ºC for 2 s and annealing at 60ºC for 20 s, with a final "Cool-Down" at 25ºC for 10 s. The Dynamic Array IFCs were read on a BioMark or EP1 System (Fluidigm) after amplification and scored using Fluidigm SNP Genotyping Analysis software.

Laboratory Failure Rates and Quality Control

QC analyses were conducted to identify laboratory errors and to measure the background discrepancy rate of the genotyping process. Separate QC methods were used for samples that had

previously been genotyped using TaqMan SNP assays and samples that had never been genotyped.

The QC protocol for previously genotyped samples consisted of comparing old TaqMan SNP genotypes (old genotypes) in the database with the new GT-seq genotypes (new genotypes) for the same SNP markers and individuals. Inconsistencies between the old and new genotypes were checked for laboratory errors, laboratory errors were corrected, and the old genotypes were replaced with the new genotypes.

The QC protocol for samples that had not been previously genotyped consisted of re-extracting 8% of project fish and genotyping them for 42 SNP loci included in the original GT-seq project following the Fluidigm genotyping protocol above (Appendix B). Laboratory errors found during the QC process were corrected, and genotypes were corrected in the database. Inconsistencies not attributable to laboratory error were recorded, but original genotype scores were retained in the database.

For all genotyped samples, the overall failure rate was calculated by dividing the number of failed single-locus genotypes by the number of assayed single-locus genotypes. Discrepancy rates were calculated for the newly genotyped samples as the number of conflicting genotypes divided by the total number of genotypes compared. Assuming that the discrepancies were due equally to errors during both genotyping events (GT-seq and Fluidigm) and that these analyses are unbiased, the error rate in the GT-seq genotyping was estimated as half the overall rate of discrepancies. This QC method is the best representation of the error rate of the Gene Conservation Laboratory's current genotype production.

STATISTICAL ANALYSIS

Data Retrieval and Quality Control

Genotypes were retrieved from LOKI and imported into *R* (R Core Team 2019) with the *RJDBC* package.[2] All subsequent analyses were performed in *R*, unless otherwise noted.

Prior to statistical analysis, 4 analyses were performed to confirm the quality of the data. First, loci were identified that had only 1 allele in all baseline individuals, or that had an alternate allele occurring in fewer than 1% of all genotypes for the given locus. These loci were considered invariant and they were excluded from further statistical analyses.

Second, loci were identified that had 100% failure rates for at least 1 location. These loci were excluded from further analysis.

Third, individuals were identified that were missing substantial genotypic data because they likely had poor quality DNA. The 80% rule (missing data at 20% or more of loci; Dann et al. 2009) was used to identify individuals missing substantial genotypic data. These individuals were removed from further analyses. The inclusion of individuals with poor quality DNA might introduce genotyping errors into the baseline and reduce the accuracies of MSA.

The fourth QC analysis identified individuals with duplicate genotypes and removed them from further analyses. Duplicate genotypes can occur as a result of sampling or extracting the same

[2] Urbanek, S. RJDBC: Provides access to databases through the JDBC interface. Available from https://cran.r-project.org/web/packages/RJDBC/index.html (accessed December 2019).

individual twice and were defined as pairs of individuals sharing the same alleles in 99% of screened loci with genotypic data. The sample with the most missing genotypic data from each duplicate pair was removed from further analyses. If both samples had the same amount of genotypic data, the first sample was removed from further analyses.

Baseline Development

Each SNP locus within each collection was tested for conformance to Hardy-Weinberg expectations (HWE) using the program *Genepop* version 4.1.4 (Rousset 2008). Probabilities were combined for each collection across loci and for each locus across collections using Fisher's method (Sokal and Rohlf 1995). Collections and loci that violated HWE after adjusting the significance level (α) to correct for multiple comparisons using Bonferroni's method (Rice 1989; $\alpha = 0.05 / \#$ of collections or loci) were removed from subsequent analyses. Collections violating HWE were removed because the conditional genetic stock identification model assumes Hardy-Weinberg equilibrium (Moran and Anderson 2019). SNP loci violating HWE were removed at this stage because they can cause significant summary results in exact tests of allele frequency homogeneity and, thereby, influence how collections are pooled into populations (see next paragraph).

When appropriate, some collections were pooled to obtain better estimates of allele frequencies. Collections from the same geographic location, sampled at similar calendar dates but in different years, were pooled as suggested by Waples (1990a). Additionally, if a pair of collections sampled at different, but proximate, locations on similar calendar dates had insufficient samples (<50) and might represent the same population, they were tested for differences in allele frequencies to determine if they could be pooled. Fisher's exact test of allele frequency homogeneity (Sokal and Rohlf 1995) was used to test for pooling, and pooling decisions were based on a summary across loci using Fisher's method (Fisher 1925). When these tests indicated no difference between collections ($P > 0.01$), they were pooled. After this pooling protocol, any collection with roughly 50 samples or more was retained for subsequent analysis. Though not meeting the sample goal of 95, sample sizes close to 50 are adequate to use in mixture analysis (Wood et al. 1987; Waples 1990b) and to estimate allele frequencies given the heterozygosities observed at the loci assayed (Table 4; Gregorius 1980). Finally, populations were tested for conformance to HWE following the same protocol described above to ensure that the pooling was appropriate, and that tests for linkage disequilibrium would not result in false positive results due to departure from HWE. Populations that conformed to HWE were used in subsequent analyses.

When testing populations for conformance to HWE, probabilities were combined for each SNP locus across populations using Fisher's method (Fisher 1925), and frequencies of departures from HWE were examined to identify loci that exhibited substantially more departures than others. Loci were removed if they had significant departures from HWE across populations after adjusting the significance level (α) to correct for multiple comparisons using Bonferroni's method ($\alpha = 0.05 / \#$ loci). These loci were removed because the conditional genetic stock identification model assumes Hardy-Weinberg equilibrium (Moran and Anderson 2019).

Linkage disequilibrium tests were performed between each pair of loci (SNP and microhaplotype) in each population to ensure that subsequent analyses would be based on independent markers. The tests were performed using the program *Genepop* version 4.1.4 (Rousset 2008) with 100 batches of 5,000 iterations. The frequency of significant linkage

disequilibrium between pairs of loci ($P < 0.05$) was summarized. Pairs were considered linked if they exhibited linkage in more than half of all populations. F_{ST} (Weir and Cockerham 1984) was then calculated for each locus using the *R* package *hierfstat*.[3] When locus pairs were found to be linked, the locus with the lowest F_{ST} value of each linked pair was removed from further analysis.

Analysis of Genetic Structure

Temporal variation of allele frequencies was examined with a hierarchical, 3-level analysis of variance (ANOVA). The temporal samples were treated as subpopulations based on the method described in Weir (1996). This method allowed the quantification of the sources of total allelic variation and permitted the calculation of the among-years component of variance and the assessment of its magnitude relative to the among-population component of variance. This analysis was conducted using the software program *GDA*.[4] For this test, only temporal collections with greater than 50 samples were used to maximize power and retain relatively balanced sample sizes (Ryman et al. 2006).

To visualize genetic distances among populations, pairwise F_{ST} (Weir and Cockerham 1984) estimates were calculated from the final set of independent markers with the *R* package *hierfstat*.[3] Using the pairwise F_{ST} estimates, 1,000 bootstrapped neighbor-joining (NJ) trees were constructed by resampling loci with replacement to assess the stability of tree nodes. The consensus tree was then plotted with the *APE* package (Paradis et al. 2004). These trees provided insight into the variability of the genetic structure of the collections and assisted in the selection of reporting groups used in baseline evaluation tests for MSA.

Baseline Evaluation for Mixed Stock Analysis

Baseline Evaluation Tests

Baseline evaluation tests were performed to assess the identifiability of reporting groups in mixtures of fish. Test mixtures of 190 individuals were constructed by randomly sampling from the baseline without replacement predetermined mixture compositions. These mixtures were analyzed against the reduced baseline (full baseline minus the 190 individuals removed for the test mixture). To explore a range of stock compositions, up to 100 test mixtures were constructed for each reporting group with compositions varying from 1% to 100% of that group, and the composition randomly split among the remaining groups. Because the removal of individuals from the baseline can reduce the accuracy of population allele frequency estimates and, consequently, the identifiability of reporting groups for MSA, test mixture compositions were limited to remove no more than half of the total number of fish in a reporting group. Therefore, the range of test mixture compositions was reduced for reporting groups represented by fewer than 380 fish. For example, if a reporting group was represented by 300 fish, the largest stock composition tested for that reporting group was 79% (150 fish). For reporting groups containing fewer than 450 fish and populations with fewer than 50 fish, random samples were selected in proportion to the number of fish in each population to avoid random sample sizes exceeding the total number of fish in a population.

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[3] Goudet, J., and T. Jombart. 2015. hierfstat: Estimation and tests of hierarchical F-statistics. R package version 0.04-22. Available from https://CRAN.R-project.org/package=hierfstat (Acessed December 2019).

[4] Lewis, P. O., and D. Zaykin. 2001. Genetic data analysis: computer program for the analysis of allelic data. Version 1.0. Available from http://lewis.eeb.uconn.edu/lewishome/software.html (Accessed March 10, 2009; site currently discontinued).

The stock composition of the test mixtures was estimated using the *R* package *rubias* (Moran and Anderson 2019). The *rubias* package is a Bayesian approach to the conditional genetic stock identification model based upon computationally efficient C code implemented in *R*. It uses cross-validation and simulation to quantify and correct for biases in reporting group estimates. Each mixture was analyzed for 1 Markov Chain Monte Carlo chain with 25,000 iterations and the first 5,000 iterations were discarded to remove the influence of starting values. The prior parameters for each reporting group were defined to be equal (i.e., a flat prior). Within each reporting group, the population prior parameters were divided equally among the populations within that reporting group. Stock proportion estimates and the 90% credibility intervals for each test mixture were calculated by taking the mean and 5% and 95% quantiles of the posterior distribution from the single chain output. After the Markov Chain Monte Carlo analysis, 100 parametric bootstrap simulations were performed to correct for biases in the stock proportion estimates.

The performance of each reporting group was assessed by calculating the proportion of tests with correct allocations within 10% of the true test mixture proportion and overall bias among tests. As a guideline, we considered a reporting group's performance to be adequate for MSA if at least 90% of tests were within 10% of the true test mixture proportion and overall bias did not exceed ±5%. However, deviation from this guideline is permitted if there is a willingness to accept higher levels of MSA uncertainty in order to include specific reporting groups to support improved information to meet a management need. These tests provided an indication of the power of the baseline for MSA when all populations from a reporting group were assumed to be represented in the baseline.

To assess reporting group performance using reduced sets of loci, baseline evaluation tests were performed for 3 datasets. The first round of tests used the full baseline dataset (UW and CRITFC panels), the second round of tests used the UW panel dataset, and third round of tests used the CRITFC panel dataset.

Misallocation Assessment

To understand the direction of bias among reporting groups when estimating stock proportions, additional mixtures were created by randomly sampling without replacement 150 fish from a single reporting group in the baseline and then rebuilding the baseline without the sampled fish. Stock compositions for these mixtures were estimated following the *rubias* protocol describe above. This was repeated 10 times for each reporting group using different mixtures and baselines to account for variation among populations within reporting groups. Mean allocations were summarized for each reporting group by averaging allocations across the 10 sample repeats.

RESULTS

TISSUE SAMPLING

A total of 15,545 genetic samples were collected from spawning populations of Chinook salmon throughout Cook Inlet (Table 2). These samples were collected at 88 locations throughout Cook Inlet drainages. Target sample sizes of 95 fish were met at 53 locations.

LABORATORY ANALYSIS

Genotyping

A total of 8,024 fish collected over spawning areas, fish wheels, and weirs were selected for analysis and sequenced for the UW and CRITFC panels (Table 1; Appendix B). Of the 289 amplicons in the UW panel, 19 were removed before assigning allele calls due to allelic ratios not conforming to expectations. Of the 299 amplicons in the CRITFC panel, 11 were removed before assigning allele calls due to allelic ratios not conforming to expectations, and an amplicon associated with sex identification (*Ots_SEXY3-1*) was also removed because of uncertainty in its ability to accurately determine sex in Chinook salmon. After removing amplicons, 270 UW and 287 CRITFC amplicons remained (557 total amplicons) and were assigned allele calls. Within the UW panel, 136 SNPs within 59 amplicons were combined in such a way as to create 59 microhaplotype loci. No SNPs were combined in the CRITFC panel. After genotyping, 557 loci were imported into LOKI.

Laboratory Failure Rates and Quality Control

For all samples selected for analysis, the overall failure rate for genotypes at the 557 loci was 2.41%. For previously genotyped samples, no inconsistencies were found that were attributable to laboratory errors. A total of 568 fish selected for analysis did not have pre-existing genotypes. The overall discrepancy rate for these samples was 0.15%; therefore, the overall estimated error rate was 0.08%.

STATISTICAL ANALYSIS

Data Retrieval and Quality Control

For all baseline collections, 35 loci had only 1 allele among all individuals, and 57 loci had minor alleles that present in fewer than 1% of individuals (Appendix B). These 92 loci were considered invariant and removed. Four of these removed loci contained microhaplotypes, whereas the remaining 88 contained single SNPs. Additionally, 13 loci had 100% failure rates for at least 1 location and were also removed. After removing invariant and failed loci, 452 loci remained for further analysis: 397 with single SNPs, and 55 with multiple SNPs that were combined into microhaplotypes. Using the 80% rule for sufficiently complete genotypes, 87 individuals were removed from the baseline collections. Based on the criterion for detecting duplicate individuals, 14 individuals were removed from baseline collections as duplicate individuals.

Baseline Development

Over the 397 SNPs (single-SNP loci) and 156 collections, 606 of 61,932 tests deviated significantly from HWE ($P < 0.01$) without adjusting for multiple comparisons. These were spread over 199 loci and 132 collections. After adjusting for multiple comparisons, 1 collection (Ship Creek 2009), and 13 loci were out of HWE.

Gene Conservation Laboratory records showed that the Ship Creek samples had their DNA extracted into 4 plates (plate IDs 8256, 8257, 8258, and 8259) and all but one plate (8259) included DNA from Deception Creek fish. Separate HWE tests were performed on the fish from each of the extraction plates to determine if individuals from 1 or more plates could be the cause of the deviation from HWE. The tests revealed that 1 extraction plate (8258) deviated from

HWE, and the individuals (60 fish) from that plate were dropped from the analysis. Pairwise Fisher's exact tests of allele frequency homogeneity (see pooling methods) were performed for the 3 remaining plates. The overall *p*-values for the tests, including plate 8256, were less than 0.01, indicating differences in allele frequencies; the test for plates 8257 and 8259 had *p*-values greater than 0.01 indicating no difference in allele frequencies. The 48 fish from plate 8256 were dropped from further analysis and the 172 fish from plates 8257 and 8259 were retained for further analysis. After removal of some Ship Creek individuals, 568 of 61,932 tests deviated significantly from HWE ($P < 0.01$) without adjusting for multiple comparisons. These were spread over 180 loci and 132 collections. After adjusting for multiple comparisons, all collections conformed to HWE expectations, and 9 loci did not conform to HWE expectations and were removed from further analyses.

A total of 67 populations were retained after dropping collections with insufficient sample sizes (7 collections) and pooling collections (pooled collections and collections taken at different sites are referred to as *populations*; Table 2). One population was identified after pooling proximate collections from different sampling locations (Happy River). Despite their lower sample sizes, Deep Creek (41 fish) and Happy River (45 fish) were retained in order to represent those populations in the baseline. Over the remaining 388 single-SNP loci and 67 populations, 183 of 25,996 tests did not conform to HWE ($P < 0.01$) before adjusting for multiple comparisons. These were spread over 135 loci, and no loci were out of HWE in more than 8 of the 67 populations. No population was out of HWE at more than 9 of 388 loci. After adjusting for multiple comparisons, all populations conformed to HWE and 5 loci did not conform to HWE. Those 5 loci (SNP) were dropped from further analysis, leaving a total of 438 loci (383 SNP and 55 microhaplotype loci).

In the tests for linkage disequilibrium, 26 of 95,703 locus pairs showed significant linkage ($P < 0.05$) in greater than 50% of populations. Most linkage occurred between 2 loci (23 pairs); however, 3 loci showed pairwise linkage and formed a group of 3 linked locus pairs. A total of 25 loci with the lowest F_{ST} of each linked pair were identified and removed from further analysis. After removing these loci, a final set of 413 loci remained for the analysis of genetic structure and baseline evaluation tests for MSA (Table 3).

Analysis of Genetic Structure

A total of 9 populations had temporal samples collected from 50 or more fish and were included in the analysis of temporal variation of allele frequencies (Table 2). Temporal samples ranged from 1 to 4 years apart for 7 populations and 20 to 23 years apart for 2 populations. The 3-level ANOVA indicated that the ratio of variation among temporal collections to the variation among populations was 1.6%.

Overall F_{ST} was 0.036 (Table 3), and pairwise F_{ST} varied from 0.00 to 0.10 (Appendix C). The NJ tree shows that populations generally cluster by drainage and coastal proximity (Figure 2). Within drainages, the most genetically divergent populations were generally those farthest upstream. The least genetically divergent populations were concentrated in the most northwestern portion of Cook Inlet. These included populations from the west side of Cook Inlet, Yentna and Susitna river drainages, and Knik and Turnagain arms.

Ten reporting groups (italics) were identified to test for MSA performance (Table 2; Figure 1):

(1) *West* (West side populations from Straight Creek north to the Susitna River and Alexander Creek)
(2) *Susitna* (Susitna River mainstem populations excluding Deshka River)
(3) *Deshka* (Deshka River population)
(4) *Yentna* (Yentna River populations)
(5) *Knik-Turnagain* (Knik Arm, Turnagain Arm, and Little Susitna River populations)
(6) *Kenai Tributary* (Kenai River tributary populations)
(7) *Kenai Mainstem* (Kenai River mainstem populations)
(8) *Kasilof Tributary* (Crooked Creek population)
(9) *Kasilof Mainstem* (Kasilof mainstem populations)
(10) *South Kenai Pen.* (Southern Kenai peninsula populations from the Ninilchik River south to Anchor River)

Baseline populations formed 3 major clusters on the tree (Figure 2). The first cluster, at the bottom of the tree, included *West*, *Yentna*, *Deshka*, and *Susitna* populations. In this cluster, populations generally clustered with other populations from the same reporting group or with geographically proximate populations. This cluster included all baseline populations west of the Susitna River mainstem.

The second and most distinct cluster, in the middle of the tree, included populations from *Kenai Tributary*, *Kenai Mainstem*, *Kasilof Tributary*, *Kasilof Mainstem*, *Knik-Turnagain*, and *South Kenai Pen.* reporting groups. Within this cluster, there appears to be an affinity among lower and middle Kenai River mainstem and Kasilof River mainstem populations, and among populations from the *South Kenai Pen.* reporting group, Crooked Creek, and Slikok Creek. Populations from Knik Arm (excluding Moose and Granite creeks) and Turnagain Arm form their own subcluster. In general, populations from the *Kenai Tributary* and *Kenai Mainstem* groups were more genetically distinct with increasing river distance from Cook Inlet. Among populations from the *South Kenai Pen.* reporting group, genetic distinction generally increased from northern to southern populations.

The third cluster, at the top of the tree, only included populations from the *Susitna* reporting group. In this cluster, eastern Susitna River (below the Talkeetna River) and Chunilna Creek formed a subcluster, and Talkeetna River and upper Susitna River populations formed another subcluster. Genetic distinction among Talkeetna River populations generally increased with distance from Cook Inlet. However, the opposite was true for the remaining populations in this cluster, where genetic distinction generally decreased with distance from Cook Inlet.

On an inletwide scale, there appears to be an affinity among northern populations and among southern populations (i.e., *West*, *Susitna*, *Yentna, Deshka,* and *Knik-Turnagain* are more basal, whereas *Kenai Tributary*, *Kenai Mainstem*, *Kasilof Tributary*, *Kasilof Mainstem*, and *South Kenai Pen.* share a cluster). Several populations appeared to be more genetically distinct (on longer branches): Russian River, Grant Creek, Deshka River, and Nikolai Creek. All but 10 of 65 nodes were well supported (50% of bootstrap trees). The 10 nodes that were not well supported occurred before populations in the *Susitna*, *Yentna*, *Deshka*, and *West* reporting groups.

Baseline Evaluation for Mixed Stock Analysis

Baseline Evaluation Tests

Baseline evaluation test mixtures were constructed with proportions ranged from 1% to 100% for *Susitna*, *Yentna*, *Knik-Turnagain*, *Kenai Tributary,* and *South Kenai Pen.* (100 mixtures each) reporting groups, and from 1% to 80% for *Deshka*, *Kasilof Tributary*, and *Kasilof Mainstem* (80 mixtures each) reporting groups. Samples for the *South Kenai Pen.* test mixtures were selected in proportion to the number of fish in each population due to the lower overall sample size (<450 fish) of the reporting group and low sample size of the Deep Creek population (41 fish).

In the baseline evaluation tests using the combined UW and CRITFC panels, all reporting groups performed adequately for MSA (Table 4; Figure 3). Correct allocation estimates among reporting groups ranged from within 2.0–7.3% (mean: 3.9%) of the true value 90% of the time and, in general, were negatively biased. Overall bias among reporting groups ranged from –1.9% to 0.1% (mean: –0.6%).

In the baseline evaluation tests using the UW panel, all reporting groups performed adequately for MSA (Table 4; Figure 4). Correct allocation estimates among reporting groups ranged from within 3.1–10.3% (mean: 5.2%) of the true value 90% of the time and, in general, were negatively biased. Overall bias among reporting groups ranged from –2.4% to 0.7% (mean: –0.8%).

In the baseline evaluation tests using the CRITFC panel, all but 2 reporting groups (*West* and *Yentna*) performed adequately for MSA (Table 4; Figure 5). Correct allocation estimates among reporting groups ranged from within 3.1–8.4% (mean: 5.0%) of the true value 90% of the time for all reporting groups except *West*, where estimates were within 10.6% of the true value 90% of the time, and *Yentna*, where estimates were within 11.1% of the true value 90% of the time. Overall bias among reporting groups ranged from –3.7% to 0.1% (mean: –0.9%).

Misallocation Assessment

In the misallocation assessment analysis, correct allocation means all 100 mixtures ranged from 82.3% to 100.0% (Appendix D). Average mean correct allocation among repeats for each reporting group ranged from 94.0% to 99.0% (Figure 6). The *West* reporting group had the lowest average mean correct allocation (94%) and misallocated to *Yentna* (2.9%), *Knik-Turnagain* (1.1%), *Susitna* (1.0%), and *Deshka* (0.9%) reporting groups. The *Yentna* reporting group had an average mean correct allocation of 94.4% and misallocated to *West* (3.5%), *Susitna* (2.0%), and *Deshka* (0.1%) reporting groups. The *Kasilof Mainstem* reporting group had an average mean correct allocation of 95.6% and misallocated to *Kenai Mainstem* (2.3%), *Kasilof Tributary* (2.0%), and *Kenai Tributary* (0.1%) reporting groups. The *Knik-Turnagain* reporting group had an average mean correct allocation of 95.7% and misallocated to *Susitna* (3.2%), *West* (0.6%), *Yentna* (0.2%), and *Deshka* (0.1%) reporting groups. The *Kenai Tributary* reporting group had an average mean correct allocation of 97.8% and misallocated to *Kasilof Tributary* (1.7%) and *Kenai Mainstem* (0.5%) reporting groups. Average correct allocations for *Susitna*, *Deshka*, *Kenai Mainstem*, *Kasilof Tributary*, and *S. Kenai Pen.* reporting groups ranged from 98.4% to 99.0%, and misallocations to individual reporting groups never exceeded 0.9%.

DISCUSSION

COMPARISON TO PREVIOUS FINDINGS OF POPULATION STRUCTURE

Variation Among Populations

This study provides a major update to the 2015 baseline (Barclay and Habicht 2015) by adding collections for 11 new northern Cook Inlet populations and screening for an order of magnitude more genetic markers. We found concordant patterns of genetic variation among populations included in both baselines: (1) populations from the same drainage tended to cluster tighter in the NJ consensus tree; (2) the most genetically divergent populations were generally the furthest upstream from Cook Inlet or more southerly within Cook Inlet; (3) West Cook Inlet and Yentna River populations showed genetic similarity to each other and the lowest population from the Susitna River, Sucker Creek; and (4) Lewis and Deshka rivers clustered beyond a significant node (Figure 2).

Ten of the 11 new populations grouped with proximate populations within geographic areas: (1) a new west side population, Nikolai Creek, grouped with Chuitna River (population numbers 2 and 3; Table 2; Figure 2); (2) populations from the Chulitna River (Honolulu and Pass creeks) both grouped with other Chulitna populations (pop. numbers 11–18); (3) upper Susitna mainstem population, Cheechako Creek, was most similar to Portage Creek (pop. numbers 8 and 9); (4) Upper Talkeetna – no name #2 grouped with the other Talkeetna populations (pop. numbers 19–23); (5) Sheep Creek and North Fork Kashwitna River grouped with other lower Susitna River mainstem populations and Chunilna Creek (pop. numbers 24–30); (6) Granite Creek was similar to the existing population from Matanuska River (Moose Creek; pop. numbers 40 and 41); and (7) Eagle River and Bird Creek grouped with other *Knik-Turnagain* populations (excluding Matanuska River populations; pop. numbers 39 and 42–48). Happy River was the only new population that did not group with proximate populations. Happy River, located in the Skwentna River (*Yentna*), grouped with Chulitna River (*Susitna*) populations and the Coal Creek population (*West*; pop. numbers 4, 33, and 11–16).

With the addition of Cheechako Creek, Sheep Creek, and Kashwitna River populations, eastern Susitna River populations (pop. numbers 8, 9, and 19–30; Table 2; Figure 2) formed 2 distinct clusters: (1) populations from the upper Susitna and Talkeetna rivers (pop. numbers 8, 9 and 19–23), and (2) lower Susitna River populations (below the Talkeetna River confluence; pop. numbers 24–30). In the upper Susitna and Talkeetna river cluster, populations were generally more divergent upstream and less divergent downstream, which has been a pattern observed in the Chulitna River and elsewhere in Cook Inlet (Barclay and Habicht 2015). However, in the lower Susitna cluster (pop. numbers 24–30), we observed the opposite pattern of genetic diversity, where lower mainstem populations were more divergent than mainstem populations farther up in the drainage. This pattern cannot be explained by swimming distances from Cook Inlet as some less divergent populations (e.g., Sheep Creek) have to swim farther than more divergent populations (e.g., Deception Creek). This pattern may be due to genetic isolation by distance; if proximate populations within the Susitna River are more genetically similar, then one would anticipate populations in the upper section of the lower Susitna River to be similar to populations in lower sections of the Talkeetna, upper Susitna, and Chulitna rivers. This was the pattern observed.

In previous baselines (Barclay et al. 2012; Barclay and Habicht 2015), Moose Creek was the only representative population from the Matanuska River drainage and showed genetic similarity to eastern Susitna River populations. Barclay et al. (2012) hypothesized that this genetic relationship could have been caused by Susitna River fish recolonizing Moose Creek after it was nearly extirpated by coal mining. In this study, we added Granite Creek and observed that it was most similar to the existing population from Moose Creek, and although they cluster on their own branch, these 2 populations are also similar to Susitna River populations. This new evidence suggests that either the Moose Creek population survived the coal mining or was recolonized by other Matanuska River Chinook salmon. The addition of Kings River to the baseline would improve our understanding of population structure in the Matanuska River.

Some genetic similarities observed in the 2015 baseline decreased in the new baseline. Previously, Juneau Creek was the Kenai River tributary most similar to the upper Kenai River mainstem populations and had to be included with the mainstem populations in reporting groups to avoid misallocation of the *Kenai River tributaries* reporting group to *Kenai River mainstem* reporting group during MSA (Eskelin et al. 2013; Eskelin and Barclay 2015, 2016, 2017, 2018). In the current baseline, misallocation between these populations decreased, allowing Juneau Creek to be grouped with *Kenai River tributaries* populations. Decreases in genetic similarities were also observed between 2 sets of collections that were pooled in the 2015 baseline to represent Willow Creek and Kasilof River mainstem populations; collections from Willow and Deception creeks were pooled to represent Willow Creek and the middle and lower Kasilof River collections were pooled to represent the Kasilof River mainstem (Table 2). When these sets of collections were tested for homogeneity of allele frequencies with the current baseline, test results were significant ($P < 0.01$), indicating that their allele frequencies differed; the collections were kept as separate baseline populations. These decreases in genetic similarities can be attributed to the increased power of the current baseline to discriminate among populations.

Variation Within Populations

In the analysis of temporal variation of allele frequencies, the ratio of the variation among temporal collections to variation among populations was lower (1.6%) than what was found in Barclay and Habicht (2015; 5.3%). To account for this difference, the analysis of temporal variation was repeated using the 22 temporal collections in this study and 34 overlapping loci between the 2 baselines (results not shown). With the reduced set of loci, the ratio of variation among temporal collections to variation among populations was very similar (1.7%) to the most recent analysis, ruling out the possibility that the differences in temporal variation are due to the loci used in the analyses. All temporal collections (105 collections) were used in the 2015 analysis, regardless of their sample size. Consequently, many collections had samples sizes of fewer than 50 fish and the range of collection years for populations was greater than in the current analysis. The higher temporal variation observed in the 2015 analysis may be due to the reduced accuracy of allele frequency estimates for collections with small sample sizes, differences in allele frequencies between collections sampled many years apart (i.e., genetic drift), or both. On the other hand, the higher temporal variation observed in the 2015 analysis could be due to the variation among a greater number of populations; 41 populations were included in the 2015 analysis and 9 were included in the current analysis. If the higher temporal variation was due to the number of years between collections, older collections may need to be replaced by more contemporary collections in future baseline updates to reflect current population allele frequencies.

DELINEATION AND PERFORMANCE OF REPORTING GROUPS

Delineating reporting groups for MSA is dictated by the fishery management question at hand, the expected composition of the mixture, the genetic structure of the underlying populations, and the availability of sufficient baseline samples to represent groups of populations (Pella and Milner 1987; Koljonen et al. 2005; Habicht et al. 2012). This report only incorporates population structure and geographic distribution in delineating reporting groups that might perform well in MSA applications within marine waters of Cook Inlet. These population structure results can be used to address fishery management questions with genetic analyses. Baseline evaluation test results and the underlying population structure identified in this report can be used to provide insights into alternative reporting groups that might perform well and help answer stakeholder questions. Alternate reporting groups will need to be tested on a case-by-case basis, depending on study objectives and the potential composition of the mixed stock sample being analyzed (e.g., within rivers).

The consistency of baseline evaluation test performance with differing stock compositions was likely due to the genetic similarities among populations within reporting groups and depth of genetic structure among the reporting groups (Table 4; Figures 3–5). For example, correct allocations for the *Susitna*, *Deshka*, *Knik-Turnagain, Kenai Tributary*, *Kenai Mainstem*, *Kasilof Tributary*, *Kasilof Mainstem*, and *South Kenai Pen.* reporting groups were generally closer to the true proportions compared to correct allocations for the *West* and *Yentna* reporting groups. Within the well-performing reporting groups, populations tended to cluster closely with geographically proximate populations and were at the end of longer branches on the NJ consensus tree (Figure 2). The *West* and *Yentna* reporting groups, on the other hand, had comparatively shallow population structure (i.e., on shorter branches) and some populations clustered closely with populations outside of their reporting group.

There may be other fine-scale reporting groups that will perform well, especially for questions where the baseline can be restricted to a defined geographic area, the composition is not expected to be complex, or both. For example, a reporting group consisting of a single or combination of populations from the Chulitna River might perform well on a mixed-stock sample of migrating fish collected in the lower Susitna River. Alternatively, the combination of populations from the eastern Susitna River or Talkeetna River might perform well as reporting groups for a similar mixture. Within the Kenai River, reporting groups consisting of combinations of populations from upper-tributary versus lower-tributary spawners or upper-mainstem versus lower-mainstem spawners might perform well on a mixed -stock sample of migrating fish collected in the lower Kenai River or in fisheries in salt water near the mouth of the Kenai River.

At the other extreme, this baseline and the 10 reporting groups would not be appropriate for fishery mixtures captured in Lower Cook Inlet. Lower Cook Inlet fishery mixtures are known to include fish from outside of Cook Inlet populations (Barclay et al. 2016). Therefore, baselines used to analyze fisheries in lower Cook Inlet or outside of Cook Inlet should include Chinook salmon stocks from a broader geographic range and should include broader reporting groups within Cook Inlet.

When comparing the baseline evaluation test results for different locus panels, reporting groups performed best when both panels were used, but if only 1 panel was used, the UW panel performed better than the CRITFC panel (Table 4; Figures 3–5). The better performance of both panels over the single panels is consistent with previous studies that generally find that more loci

provide improved MSA performance (e.g., McKinney et al. 2019). The better performance of the UW panel was anticipated, since this panel was designed to distinguish among northern and western Cook Inlet populations (Dann et al. 2018). The UW panel generally produced more precise (lower root mean square error) and accurate (lower bias) results than the CRITFC panel; all reporting groups met the criteria for acceptable MSA performance with the UW panel, but the *West* and *Yentna* reporting groups did not meet the criteria with the CRITFC panel. It is interesting to note that the average F_{ST} values were similar between the 2 panels (Table 3), so one variable that might be influencing MSA performance is the difference in the number of loci between the 2 panels (UW panel has 218 loci; CRITFC panel has 195 loci).

APPLICATION TO CHINOOK SALMON RESEARCH

Chinook salmon spawning within the Kenai and Susitna river drainages of Cook Inlet include 2 of 12 stocks intensively studied under the CSRI to provide statewide indices of productivity and abundance trends across the many river systems in Alaska. The CSRI identified several projects as beneficial to increasing knowledge of the Susitna and Kenai river stocks, including comprehensive estimation of stock-specific marine harvest of Chinook salmon in Cook Inlet fisheries and estimation of inriver run size of the Susitna River stock. This current baseline with enhanced marker capabilities can be used in a broad array of applications to help address gaps in current stock assessment and improve fisheries management, and include the following:

1. ***Finer scale estimates of stock-specific marine harvest of Chinook salmon in Cook Inlet fisheries.*** This new baseline can be used to comprehensively estimate stock-specific marine harvest of Chinook salmon in Cook Inlet fisheries using genetic MSA at a finer scale than was previously possible. This project is needed to estimate contributions of relevant indicator stocks in mixed stock harvests in Cook Inlet. A comprehensive estimate of marine harvests would involve sampling harvests from commercial set and drift gillnet fisheries in the Central and Northern Districts of Upper Cook Inlet and the Tyonek subsistence fishery to obtain genetic tissues for MSA.
2. ***Susitna River mainstem abundance and total run.*** With this baseline, the Deshka River stock is now highly identifiable in mixed stock samples making it possible to estimate inriver abundance of the Susitna River mainstem stock using genetic mark–recapture methods (Hamazaki and DeCovich 2014). This project would involve operation of fish wheels in the lower Susitna River to sample Chinook salmon for age-sex-size information and genetic tissues for identification of Deshka River, Susitna River mainstem above the Deshka River, and Yentna River stocks. Mark–recapture estimates of abundance can be calculated from genetic stock composition estimates at the lower-river fish wheels and counts of fish passing through the Deshka River weir. Resultant estimates can be combined with stock-specific marine fishery harvests (described above) to estimate the total Susitna River mainstem run.
3. ***Kenai River abundance and total run.*** Inriver Chinook salmon abundance can be estimated for the Kenai River using genetic mark–recapture methods because the Russian River stock is highly identifiable, counted, and contributes adequately to the Kenai River run. Similar to the methods described for the Susitna River, this program would involve genetic samples from drift gillnets associated with the sonar project in the lower river and counts from the existing Russian River weir site. Mark–recapture estimates of abundance can be calculated from genetic sampling at the lower-river sonar combined with counts of

fish passing through the Russian River weir site. Total run can be estimated for the Kenai River by combining fishery harvest and inriver abundance estimates.

4. ***Retrospective run reconstruction for Kenai River.*** Total run can be reconstructed retrospectively for the Kenai River using archived genetic tissue samples from marine harvests in Cook Inlet and drift gillnets associated with the sonar project in the lower river. This would involve regenotyping archived samples using the baseline genetic markers.
5. ***Hatchery contributions to fishery harvests.*** Hatchery fish can be identified in fishery harvests using parentage-based tagging techniques (Anderson and Garza 2006). The large increase in numbers of genetic markers available for analyses within Cook Inlet enable such pedigree-based analyses. These analyses would involve collecting samples from fishery harvests and hatchery broodstock from potential brood years contributing to the fishery and genotyping them. Genotypes from the broodstock samples (parents) could then be used to identify hatchery fish in a harvest sample by assigning hatchery fish to their parents.
6. ***Spawner abundance.*** Spawner abundance can be estimated using transgenerational (Rawding et al. 2014) or close-kin (Bravington et al. 2016) mark–recapture techniques. Transgenerational mark–recapture would involve collecting samples inriver from spawning fish and outmigrating juveniles the following spring and genotyping them. Parentage analysis would then be conducted to determine parent–offspring relationships among the genotyped samples. Spawner abundance can then be estimated using the number of sampled spawners assigned to juveniles as parents and the number of juveniles and spawners genotyped. Another approach is to use close-kin mark–recapture techniques that only require genotypes from juveniles to identify full- and half-sibling relationships in the sample. The number of sibling groups (families) in the sample could then be used to estimate spawner abundance.

Although the updated baseline described here has increased potential to address questions of interest about fisheries management in Cook Inlet, there are trade-offs between capabilities and costs. For large projects (≥1,200 fish), the cost of assessing 300–400 markers using GT-seq methods is similar to the per-fish cost of screening just 96 markers using Fluidigm methods. Because of this, GT-seq may be cost prohibitive for smaller projects, too slow for in-season analysis, and may not be necessary for projects where lower resolution is adequate. When designing genetic studies, researchers and managers must consider several factors, including which reporting groups are of interest, what level of precision is required, what fishing area and time strata need to be analyzed, how many samples are likely to be collected, how quickly results are needed, and potential budgetary limitations. These considerations will inform the choice of baseline for answering questions important to fisheries management.

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REFERENCES CITED

Adams, N. S., W. J. Spearman, C. V. Burger, K. P. Currens, C. B. Schreck, and H. W. Li. 1994. Variation in mitochiondrial DNA and allozymes discriminates early and late forms of Chinook salmon (*Onchohynchus tshawytscha*) in the Kenai and Kasilof Rivers, Alaska. Canadian Journal of Fisheries and Aquatic Science 51(S1):172–181.

ADF&G Chinook Salmon Research Team. 2013. Chinook salmon stock assessment and research plan, 2013. Alaska Department of Fish and Game, Special Publication No. 13-01, Anchorage.

AEA (Alaska Energy Authority). 2012. Revised study plan: Susitna-Watana hydroelectric project (FERC No. 14241. Prepared for the Federal Energy Regulatory Commission by the Alaska Energy Authority, Anchorage, AK.

Allendorf, F. W., and S. R. Phelps. 1981. Use of allelic frequencies to describe population structure. Canadian Journal of Fisheries and Aquatic Sciences 38(12):1507–1514.

Anderson, E. C., and J. C. Garza. 2006. The power of single-nucleotide polymorphisms for large-scale parentage inference. Genetics 172(4):2567–2582.

Baetscher, D. S., A. J. Clemento, T. C. Ng, E. C. Anderson, and J. C. Garza. 2018. Microhaplotypes provide increased power from short-read DNA sequences for relationship inference. Molecular Ecology Resources 18(2):296–305.

Barclay, A. W., B. J. Failor, and C. Habicht. 2016. Report to the Alaska Board of Fisheries: Progress report on genetic and coded wire tag mixed stock analysis of Chinook salmon harvested in Cook Inlet marine sport fishery, 2014–2016. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report 5J16-09, Anchorage.

Barclay, A. W., and C. Habicht. 2012. Genetic baseline for Upper Cook Inlet sockeye salmon: 96 SNPs and 10,000 fish. Alaska Department of Fish and Game, Fishery Manuscript Series No. 12-06, Anchorage.

Barclay, A. W., and C. Habicht. 2015. Genetic baseline for Upper Cook Inlet Chinook salmon: 42 SNPs and 7,917 fish. Alaska Department of Fish and Game, Fishery Manuscript Series No. 15-01, Anchorage.

Barclay, A. W., C. Habicht, R. A. Merizon, and R. J. Yanusz. 2012. Genetic baseline for Upper Cook Inlet Chinook salmon: 46 SNPs and 5,279 fish. Alaska Department of Fish and Game, Fishery Manuscript Series No. 12-02, Anchorage.

Beacham, T. D., J. R. Candy, C. Wallace, S. Urawa, S. Sato, N. V Varnavskaya, K. D. Le, and M. Wetklo. 2009. Microsatellite stock identification of chum salmon on a Pacific Rim basis. North American Journal of Fisheries Management 29(6):1757-1776.

Begich, R. N. 2007. Contributions of coded wire tagged Chinook salmon stocks to the early-run marine sport fishery in Cook Inlet, 1999 through 2001. Alaska Department of Fish and Game, Fishery Data Series No. 07-54, Anchorage.

Begich, R. N., W. D. Templin, A. W. Barclay, and L. W. Seeb. 2010. Development of microsatellite genetic markers for Kenai River Chinook salmon. Alaska Department of Fish and Game, Fishery Data Series No. 10-38, Anchorage.

Bravington, M. V., H. J. Skaug, and E. C. Anderson. 2016. Close-kin mark-recapture. Statistical Science 31(2):259–274.

Campbell, N. R., S. A. Harmon, and S. R. Narum. 2015. Genotyping-in-thousands by sequencing (GT-seq): A cost effective SNP genotyping method based on custom amplicon sequencing. Molecular Ecology Resources 15(4):855–867.

Crane, P. A., W. D. Templin, D. M. Eggers, and L. W. Seeb. 2000. Genetic stock identification of Southeast Alaska chinook salmon fishery catches. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report 5J00-01, Anchorage.

Crane, P. A., W. D. Templin, and L. W. Seeb. 1996. Genetic stock identification of Alaska Chinook salmon. Alaska Department of Fish and Game, Division of Commercial Fisheries Management and Development, Regional Information Report 5J96-17, Juneau.

REFERENCES CITED (Continued)

Dann, T. H., C. Habicht, J. R. Jasper, H. A. Hoyt, A. W. Barclay, W. D. Templin, T. T. Baker, F. W. West, and L. F. Fair. 2009. Genetic stock composition of the commercial harvest of sockeye salmon in Bristol Bay, Alaska, 2006–2008. Alaska Department of Fish and Game, Fishery Manuscript Series No. 09-06, Anchorage.

Dann, T. H., C. Habicht, W. D. Templin, L. W. Seeb, G. McKinney, and J. E. Seeb. 2018. Identification of genetic markers useful for mixed stock analysis of Chinook salmon in Cook Inlet, Alaska. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report 5J18-04, Anchorage.

Eskelin, A., and A. W. Barclay. 2016. Mixed stock analysis and age, sex, and length composition of Chinook salmon in Upper Cook Inlet, Alaska, 2015. Alaska Department of Fish and Game, Fishery Data Series No. 16-16, Anchorage.

Eskelin, A., and A. W. Barclay. 2017. Eastside set gillnet chinook salmon harvest composition study in Upper Cook Inlet, Alaska, 2016, including large fish harvest for 2015 and 2016. Alaska Department of Fish and Game, Fishery Data Series No. 17-50, Anchorage.

Eskelin, A., and A. W. Barclay. 2018. Eastside set gillnet Chinook salmon harvest composition in Upper Cook Inlet, Alaska, 2017. Alaska Department of Fish and Game, Fishery Data Series No. 18-30, Anchorage.

Eskelin, T., and A. W. Barclay. 2015. Mixed stock analysis and age, sex, and length composition of Chinook salmon in Upper Cook Inlet, Alaska, 2014. Alaska Department of Fish and Game, Fishery Data Series No. 15-19, Anchorage.

Eskelin, T., A. W. Barclay, and A. Antonovich. 2013. Mixed stock analysis and age, sex, and length composition of Chinook salmon in Upper Cook Inlet, Alaska, 2010–2013. Alaska Department of Fish and Game, Fishery Data Series No. 13-63, Anchorage.

Fall, J. A., A. Godduhn, G. Halas, L. Hutchinson-Scarbrough, B. Jones, E. Mikow, L. A. Sill, A. Trainor, A. Wiita, and T. Lemons. 2018. Alaska subsistence and personal use salmon fisheries 2015 annual report. Alaska Department of Fish and Game, Division of Subsistence, Technical Paper No. 440, Anchorage.

Fisher, R. A. 1925. Statistical methods for research workers. Oliver and Boyd, Edinburgh, Scotland.

Gregorius, H. R. 1980. The probability of losing an allele when diploid genotypes are sampled. Biometrics 36(4):643–652.

Habicht, C., L. W. Seeb, K. W. Myers, E. V Farley, and J. E. Seeb. 2010. Summer–fall distribution of stocks of immature sockeye salmon in the Bering Sea as revealed by single-nucleotide polymorphisms. Transactions of the American Fisheries Society 139(4):1171–1191.

Habicht, C., W. D. Templin, N. A. DeCovich, and J. R. Jasper. 2012. Western Alaska salmon stock identification program technical document 15: Chum salmon reporting group evaluations using simulated fishery mixtures. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report 5J12-22, Anchorage.

Hamazaki, T., and N. DeCovich. 2014. Application of the genetic mark–recapture technique for run size estimation of Yukon River Chinook salmon. North American Journal of Fisheries Management 34(2):276–286.

Hollowell, G., E. O. Otis, and E. Ford. 2017. 2016 Lower Cook Inlet area finfish management report. Alaska Department of Fish and Game, Fishery Management Report No. 17-26, Anchorage.

Janowitz-Koch, I., C. Rabe, R. Kinzer, D. Nelson, M. A. Hess, and S. R. Narum. 2019. Long-term evaluation of fitness and demographic effects of a Chinook Salmon supplementation program. Evolutionary Applications 12(3):456–469.

Koljonen, M-L., J. J. Pella, and M. Masuda. 2005. Classical individual assignments versus mixture modeling to estimate stock proportions in Atlantic salmon (*Salmo salar*) catches from DNA microsatellite data. Canadian Journal of Fisheries and Aquatic Sciences 62(9):2143–2158.

REFERENCES CITED (Continued)

Larson, W. A., J. E. Seeb, C. E. Pascal, W. D. Templin, and L. W. Seeb. 2014a. Single-nucleotide polymorphisms (SNPs) identified through genotyping-by-sequencing improve genetic stock identification of Chinook salmon (*Oncorhynchus tshawytscha*) from western Alaska. Canadian Journal of Fisheries and Aquatic Sciences 71(5):698–708.

Larson, W. A., L. W. Seeb, M. V. Everett, R. K. Waples, W. D. Templin, and J. E. Seeb. 2014b. Genotyping by sequencing resolves shallow population structure to inform conservation of Chinook salmon (*Oncorhynchus tshawytscha*). Evolutionary Applications 7(3):355–369.

McKinley, T. R. 1999. Contributions of coded wire tagged Chinook salmon to the recreational fishery in Central Cook Inlet, Alaska, 1996. Alaska Department of Fish and Game, Fishery Data Series No. 99-2, Anchorage.

McKinney, G. J., C. E. Pascal, W. D. Templin, S. E. Gilk-Baumer, T. H. Dann, L. W. Seeb, and J. E. Seeb. 2019. Dense SNP panels resolve closely related Chinook salmon populations. Canadian Journal of Fisheries and Aquatic Sciences doi.org/10.1139/cjfas-2019-0067.

McKinney, G. J., J. E. Seeb, and L. W. Seeb. 2017. Managing mixed-stock fisheries: genotyping multi-SNP haplotypes increases power for genetic stock identification. Canadian Journal of Fisheries and Aquatic Sciences 74(4):429–434.

Moran, B. M., and E. C. Anderson. 2019. Bayesian inference from the conditional genetic stock identification model. Canadian Journal of Fisheries and Aquatic Sciences 76(4):551–560.

Paradis, E., J. Claude, and K. Strimmer. 2004. APE: Analyses of phylogenetics and evolution in R language. Bioinformatics 20(2):289–290.

Pella, J. J., and G. B. Milner. 1987. Use of genetic marks in stock composition analysis. Pages 247–276 [*In*] N. Ryman and F. Utter, editors. Population genetics and fishery management. The Blackburn Press, Caldwell, New Jersey.

R Core Team. 2019. R: A language and environment for statistical computing. Vienna, Austria.

Rawding, D. J., C. S. Sharpe, and S. M. Blankenship. 2014. Genetic-based estimates of adult Chinook salmon spawner abundance from carcass surveys and juvenile out-migrant traps. Transactions of the American Fisheries Society 143(1):55–67.

Rice, W. R. 1989. Analyzing tables of statistical test. Evolution 43(1):223–225.

Ricker, W. E. 1958. Maximum sustained yields from fluctuating environments and mixed stocks. Journal of the Fisheries Research Board of Canada 15(5):991–1006.

Rogers Olive, S. D., A. W. Barclay, T. R. McKinley, and W. D. Templin. 2013. Genetic baseline of Kenai River Chinook salmon for mixed stock analyses, 2013. Alaska Department of Fish and Game, Fishery Manuscript Series No. 13-12, Anchorage.

Rousset, F. 2008. GENEPOP'007: A complete re-implementation of the GENEPOP software for Windows and Linux. Molecular Ecology Resources 8(1):103–106.

Ryman, N., S. Palm, C. André, G. R. Carvalho, T. G. Dahlgren, P. E. Jorde, L. Laikre, L. C. Larsson, A. Palmé, and D. E. Ruzzante. 2006. Power for detecting genetic divergence: Differences between statistical methods and marker loci. Molecular Ecology 15(8):2031–2045.

St. Saviour, A., A. W. Barclay, and N. Logelin. 2019. Northern Cook Inlet Chinook salmon marine harvest stock composition, 2014–2015. Alaska Department of Fish and Game, Fishery Data Series No. 19-03, Anchorage.

Seeb, L. W., C. Habicht, W. D. Templin, K. E. Tarbox, R. Z. Davis, L. K. Brannian, and J. E. Seeb. 2000. Genetic diversity of sockeye salmon of Cook Inlet, Alaska, and its application to management of populations affected by the *Exxon Valdez* oil spill. Transactions of the American Fisheries Society 129(6):1223–1249.

Shields, P., and A. Frothingham. 2018. Upper Cook Inlet commercial fisheries annual management report, 2017. Alaska Department of Fish and Game, Fishery Management Report No. 18-10, Anchorage.

REFERENCES CITED (Continued)

Sokal, R. R., and F. J. Rohlf. 1995. Biometry: The principles and practice of statistics in biological research. 3rd edition. New York: W. H. Freeman.

Teel, D. J., P. A. Crane, C. M. I. Guthrie, A. R. Marshall, D. M. Van Doornik, W. D. Templin, N. V. Varnavskaya, and L. W. Seeb. 1999. Comprehensive allozyme database discriminates chinook salmon around the Pacific Rim. (NPAFC document 440). Alaska Department of Alaska Department of Fish and Game, Division of Commercial Fisheries, 333 Raspberry Road, Anchorage, AK 99518.

Templin, W. D., J. E. Seeb, J. R. Jasper, A. W. Barclay, and L. W. Seeb. 2011. Genetic differentiation of Alaska Chinook salmon: The missing link for migratory studies. Molecular Ecology Resources 11(S1):226–264.

Waples, R. S. 1990a. Conservation genetics of pacific salmon. III. Estimating effective population size. Journal of Heredity 81(4):277–289.

Waples, R. S. 1990b. Temporal changes of allele frequency in Pacific salmon: Implications for mixed-stock fishery analysis. Canadian Journal of Fisheries and Aquatic Sciences 47(5):968–976.

Weir, B. 1996. Genetic data analysis. 2nd edition. Sinauer Associates, Inc. Sunderland, MA.

Weir, B. S., and C. C. Cockerham. 1984. Estimating F-statistics for the analysis of population structure. Evolution 38(6):1358–1370.

Wood, C. C., S. Mckinnell, T. J. Mulligan, and D. A. Fournier. 1987. Stock identification with the maximum-likelihood mixture model: sensitivity analysis and application to complex problems. Canadian Journal of Fisheries and Aquatic Sciences 44(4):866–881.

TABLES AND FIGURES

Table 1.–Cook Inlet Chinook salmon genetic baseline update information including year of update, report reference, numbers of populations and loci in the baseline, and names and descriptions of reporting groups identified in each update.

Year	Reference[a]	No. Pops	No. Loci	MSA Reporting Groups	
				Name	Description
2012	1	30	38	– [b]	– [b]
2013	2	43	39	*Kenai River tributaries*	Kenai River tributary populations (excluding Juneau Creek)
				Kenai River mainstem	Kenai River mainstem and Juneau Creek populations
				Kasilof River mainstem	Kasilof River mainstem populations
				Cook Inlet other	All other Cook Inlet populations
2015	3	55	39	*NorthWestCI*	Western Upper cook Inlet, Yentna River, and western Susitna River populations
				MatSu	Matanuska and eastern Susitna river populations
				KnikTurnagain	Knik Arm and Turnagain Arm populations
				KenaiKasilof	Kenai and Kasilof river populations
				SKenaiPen	Kenai Peninsula populations south of the Kasilof River
2019	4	67	413	*West*	Western Upper Cook Inlet and Alexander Creek populations
				Susitna	Susitna River populations
				Deshka	Deshka River population
				Yentna	Yentna River populations
				Knik-Turnagain	Knik Arm, Turnagain Arm, and Little Susitna River populations
				Kenai Tributary	Kenai River tributary populations
				Kenai Mainstem	Kenai River mainstem populations
				Kasilof Tributary	Kasilof River tributary populations
				Kasilof Mainstem	Kasilof River mainstem populations
				South Kenai Pen.	Kenai Peninsula populations south of the Kasilof River

[a] 1 = Barclay and Habicht (2012); 2 = Eskelin et al. (2013); 3 = Barclay and Habicht (2015); 4 = this report.

[b] No reporting groups were tested for the 2012 baseline.

Table 2.–Tissue collections of Chinook salmon throughout Upper Cook Inlet, including the population number associated with Figure 1, reporting group affiliation, years collected, and numbers of samples collected (N_c), genotyped (N_g), and included in the baseline (N_b).

Pop. No.[a,b]	Reporting Group[c]	Location	Collection Year	N_c	N_g	N_b
—	*West*	Crescent River[d]	2010	3	3	0
—			2012	1	0	0
1		Straight Creek	2010	105	95	93
2		Nikolai Creek[d]	2012	33	33	33
2			2013[e]	48	48	48
—		Chuitna River	2008	20	0	0
3			2009	122	95	92
4		Coal Creek	2009	42	42	42
4			2010	35	35	34
4			2011	43	43	43
5		Theodore River	2010	34	34	34
5			2011	55	55	55
5			2012	104	30	30
—			2013	47	0	0
—			2014	45	0	0
6		Lewis River	2011	47	47	47
6			2012	42	42	42
6			2014	7	7	7
—		Wolverine Creek[d]	2011	1	0	0
7		Sucker Creek	2011[f]	91	91	91
7			2012[f]	53	53	53
—		Alexander Creek	2014	56	0	0
—			2015	100	0	0
—			2016	100	0	0
—	*Susitna*	Kosina Creek[d]	2012	10	0	0
—			2013	3	1	0
—		Fog Creek[d]	2014	12	0	0
—		Devil Creek[d]	2014	2	0	0
—		Chinook Creek[d]	2014	7	0	0
8		Cheechako Creek[d]	2014	57	57	57
9		Portage Creek	2009	15	15	15
9			2010	10	10	10
9			2011	116	116	114
—			2012	1	0	0
9			2013	25	25	25

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Pop. No.[a,b]	Reporting Group[c]	Location	Collection Year	N_c	N_g	N_b
—	*Susitna (cont.)*	Indian River	2012	1	0	0
10			2013	81	81	78
10			2014	20	20	20
—		4th of July Creek[d]	2014	25	0	0
—		Chulitna River - East Fork	2009	5	0	0
—			2010	2	0	0
—			2011	6	0	0
11			2013	64	64	64
11			2014	33	33	33
12		Chulitna River - Middle Fork	2009[f]	72	72	72
12			2010[f]	104	97	97
12			2013[f]	61	60	60
13		Honolulu Creek	2013	31	31	31
13			2014	75	75	75
14		Pass Creek	2013	33	33	33
14			2014	71	71	71
15		Byers Creek	2013[f]	55	55	55
15			2014[f]	54	54	54
16		Spink Creek[d]	2013	56	56	56
16			2014	18	18	18
17		Bunco Creek	2013	103	103	103
—		Bunco Lake[d]	2013	3	0	0
18		Troublesome Creek	2013	71	71	71
18			2014	48	48	48
19		Talkeetna River - No Name #1[d]	2013	71	71	71
19			2014	13	13	13
20		Talkeetna River - No Name #2[d]	2013	25	25	25
20			2014	28	28	28
—		Prairie Creek	1995	52	0	0
21			2008	117	114	110
21			2013	32	32	32
22		Iron Creek - East Fork	2013	57	57	56
22			2014	46	46	46
23		Disappointment Creek	2013[f]	64	64	64
23			2014[f]	69	69	69
24		Chunilna Creek - Clear Creek	2009	50	50	49
24			2012	79	52	52
24			2013	5	5	3

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Pop. No.[a,b]	Reporting Group[c]	Location	Collection Year	N_c	N_g	N_b
—	*Susitna (cont.)*	Montana Creek	2008	33	0	0
25			2009	155	92	90
25			2010	30	30	30
—			2013	213	0	0
—			2014	227	0	0
—			2015	111	0	0
—		Goose Creek[d]	2014	17	0	0
26		Sheep Creek[d]	2013	29	24	24
26			2014	36	36	36
27		Kashwitna River - North Fork[d]	2013	12	12	12
27			2014	50	50	50
28		Little Willow Creek	2013	55	55	55
28			2014	49	49	49
29		Willow Creek[d]	2005	74	74	70
—		Deception Creek	1991	152	0	0
—			1997	15	0	0
30			2009	122	100	100
—			2012	49	0	0
—			2013	245	0	0
—			2014	169	0	0
—			2015	44	0	0
—			2016	90	0	0
—			2017	165	0	0
—			2018	63	0	0
31	*Deshka*	Deshka River	1995[f]	51	51	51
31			2005[f]	200	105	104
31			2012[f]	52	52	52
31			2015[e,f]	120	95	95
—	*Yentna*	Clearwater Creek[d]	2012	26	0	0
—		Nakochna River[d]	2014	22	0	0
32		Red Creek	2012	29	29	29
32			2013	82	82	82
33		Happy River[d]	2012	18	18	18
33		Red Salmon Creek[d]	2012	12	12	12
33			2014	15	15	15

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Pop. No.[a,b]	Reporting Group[c]	Location	Collection Year	N_c	N_g	N_b
34	*Yentna (cont.)*	Hayes River[d]	2012	5	5	5
34			2013	45	45	45
34			2014	24	24	24
35		Canyon Creek[d]	2012	31	31	30
35			2013	61	61	61
—		Talachulitna River	1995	58	0	0
36			2008	74	74	74
36			2010	48	48	46
—		Lake Creek[d]	2008	1	0	0
37		Sunflower Creek	2009	53	53	49
37			2011	74	74	74
38		Peters Creek	2009	27	27	27
38			2010	6	6	6
38			2011	37	37	37
38			2012	40	40	40
39	*Knik-Turnagain*	Little Susitna River	2009	3	3	3
39			2010	122	122	122
40		Granite Creek[d]	2013	15	14	14
40			2014	36	36	36
40			2015 [e,f]	33	33	33
—		Kings River[d]	2013	4	0	0
41		Moose Creek	1995	20	20	20
—			2008	33	0	0
41			2009	22	22	20
41			2012	80	80	80
42		Eagle River[d]	2009	7	6	6
42			2011	4	4	4
42			2012	68	68	68
—			2014	4	0	0
—			2015	5	0	0
43		Ship Creek	2009	311	280	172
—			2012	297	0	0
—			2013	52	0	0
—			2014	137	0	0
—			2015	120	0	0
—			2016	131	0	0
—			2017	138	0	0
—			2018	127	0	0

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Pop. No.[a,b]	Reporting Group[c]	Location	Collection Year	N_c	N_g	N_b
—	*Knik-Turnagain*	Campbell Creek	2010	3	0	0
44	*(cont.)*		2011	33	21	21
44			2012	75	75	75
—		Rabbit Creek[d]	2011	8	7	0
45		Bird Creek	2009	2	2	2
45			2011	35	32	32
—			2012	5	0	0
—			2014	18	0	0
45			2015[e]	50	50	49
—		Carmen River[d]	2003	5	5	0
46			2011	19	19	19
46			2012	31	31	31
46			2013[e]	24	24	24
—		Granite Creek[d]	2011	1	0	0
—		Canyon Creek[d]	2013	22	0	0
—		Sixmile Creek[d]	2014	3	0	0
47		Resurrection Creek	2010	24	24	24
47			2011	61	61	61
47			2012	13	13	13
48		Chickaloon River	2008	2	2	2
—			2009	1	1	0
48			2010	65	65	64
48			2011	63	8	8
49	*Kenai Mainstem*	Upper Kenai River Mainstem	2009	200	95	92
50		Middle Kenai River Mainstem	2003[f]	87	87	80
50			2004	39	39	39
50			2006[f]	183	183	180
51		Lower Kenai River Mainstem	2010	37	37	36
51			2011	90	89	89
52	*Kenai Tributary*	Grant Creek[d]	2011	23	23	23
52			2012	36	32	32
52			2013[e]	33	33	32
53		Quartz Creek	2006	35	34	32
53			2008	34	34	34
—			2009	41	0	0
53			2010	4	4	4
53			2011	13	13	12

-continued-

Table 2.–Page 6 of 7.

Pop. No.[a,b]	Reporting Group[c]	Location	Collection Year	N_c	N_g	N_b
—	*Kenai Tributary*	Daves Creek[d]	2007	8	8	0
—	*(cont.)*		2008	5	5	0
54		Crescent Creek	2006	165	165	165
55		Juneau Creek	2005	32	32	29
55			2006	91	64	64
55			2007	24	24	23
56		Russian River	2005	24	24	24
56			2006	16	16	16
56			2007[f]	84	83	82
56			2008[f]	91	91	89
57		Benjamin Creek	2005	56	56	54
—			2006	150	0	0
58		Killey River	2005[f]	68	68	65
58			2006[f]	198	103	102
59		Funny River	2005	37	37	35
59			2006	183	95	93
60		Slikok Creek	2004	48	48	24
—			2005	100	0	0
60			2008	58	57	57
—	*Kasilof Mainstem*	Kasilof River Mainstem[d]	2009	8	0	0
61		Middle Kasilof River Mainstem	2005	273	190	190
62		Lower Kasilof River Mainstem	2005	144	132	132
63	*Kasilof Tributary*	Crooked Creek	1992[f]	95	95	94
63			2005[f]	212	117	116
—			2009	184	0	0
—			2011	200	0	0
—			2013	200	0	0
63			2015[e,f]	200	95	95
—			2016	205	0	0
—	*South Kenai Pen.*	Ninilchik River	2006	190	0	0
—			2009	93	0	0
64			2010	50	50	49
—			2011	49	0	0
—			2012	34	0	0
—			2013	22	0	0
—			2014	216	0	0
64			2015[e]	207	95	95
—			2016	308	0	0
—			2017	152	0	0
—			2018	454	0	0

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Table 2.–Page 7 of 7.

Pop. No.[a,b]	Reporting Group[c]	Location	Collection Year	N_c	N_g	N_b
—	*South Kenai Pen.*	Deep Creek	2009	100	0	0
65	*(cont.)*		2010	99	41	41
—			2011	50	0	0
66		Stariski Creek	2011	57	56	56
66			2012	50	50	50
67		Anchor River	2006	200	95	95
—			2009	10	0	0
67			2010	50	50	50
—			2011	50	0	0
—			2012	50	0	0
			Total	15,545	8,024	7,787

[a] Unique population numbers represent all the analyzed collections that contribute to a single population and correspond to population numbers on Figure 1.

[b] Em dashes indicate collections that were not included in the baseline.

[c] Baseline evaluation tests for MSA were performed on the 10 reporting groups.

[d] The target sample size of 95 fish was not met at these locations.

[e] Collections that did not have archived DNA prior to this study.

[f] These temporal samples were used in the analysis of temporal variation of allele frequencies.

Table 3.–Panel, locus name, number of alleles, observed heterozygosity (H_o), and F_{ST} for 413 loci used to analyze the population genetic structure of Upper Cook Inlet Chinook salmon.

Panel	Locus Name	No. Alleles[a]	H_o	F_{ST}	Panel	Locus Name	No. Alleles[a]	H_o	F_{ST}
CRITFC	*Ots_100884-287*	2	0.346	0.029	CRITFC	*Ots_110064-383*	2	0.294	0.025
CRITFC	*Ots_101554-407*	2	0.260	0.025	CRITFC	*Ots_110201-363*	2	0.427	0.027
CRITFC	*Ots_102414-395*	2	0.504	0.012	CRITFC	*Ots_110381-164*	2	0.476	0.048
CRITFC	*Ots_102801-308*	2	0.050	0.019	CRITFC	*Ots_110551-64*	2	0.393	0.024
CRITFC	*Ots_102867-609*	2	0.413	0.024	CRITFC	*Ots_110689-218*	2	0.377	0.026
CRITFC	*Ots_103041-52*	2	0.288	0.046	CRITFC	*Ots_111084b-619*	2	0.230	0.021
CRITFC	*Ots_103122-180*	2	0.051	0.093	CRITFC	*Ots_112208-722*	2	0.046	0.066
CRITFC	*Ots_104048-194*	2	0.173	0.090	CRITFC	*Ots_112301-43*	2	0.057	0.026
CRITFC	*Ots_104063-132*	2	0.468	0.051	CRITFC	*Ots_112419-131*	2	0.042	0.048
CRITFC	*Ots_105105-613*	2	0.144	0.020	CRITFC	*Ots_112820-284*	2	0.341	0.026
CRITFC	*Ots_105132-200*	2	0.407	0.054	CRITFC	*Ots_112876-371*	2	0.428	0.067
CRITFC	*Ots_105385-421*	2	0.478	0.031	CRITFC	*Ots_113242-216*	2	0.341	0.021
CRITFC	*Ots_105407-117*	2	0.138	0.040	CRITFC	*Ots_113457-40R*	2	0.417	0.020
CRITFC	*Ots_105897-124*	2	0.053	0.019	CRITFC	*Ots_115987-325*	2	0.186	0.023
CRITFC	*Ots_106419b-618*	2	0.092	0.049	CRITFC	*Ots_117432-409*	2	0.481	0.020
CRITFC	*Ots_106499-70*	2	0.410	0.031	CRITFC	*Ots_118175-479*	2	0.227	0.029
CRITFC	*Ots_106747-239*	2	0.488	0.019	CRITFC	*Ots_118205-61*	2	0.351	0.014
CRITFC	*Ots_107074-284*	2	0.381	0.020	CRITFC	*Ots_118938-325*	2	0.265	0.073
CRITFC	*Ots_107806-821*	2	0.466	0.014	CRITFC	*Ots_120950-417*	2	0.437	0.033
CRITFC	*Ots_108007-208*	2	0.018	0.044	CRITFC	*Ots_123048-521*	2	0.328	0.039
CRITFC	*Ots_108390-329*	2	0.180	0.040	CRITFC	*Ots_123921-111*	2	0.315	0.031
CRITFC	*Ots_108735-302*	2	0.193	0.017	CRITFC	*Ots_127236-62*	2	0.257	0.024
CRITFC	*Ots_108820-336*	2	0.455	0.046	CRITFC	*Ots_127760-569*	2	0.436	0.032
CRITFC	*Ots_109525-816*	2	0.078	0.118	CRITFC	*Ots_128302-57*	2	0.436	0.077
CRITFC	*Ots_109693-392*	2	0.264	0.024	CRITFC	*Ots_128693-461*	2	0.398	0.010

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Table 3.–Page 2 of 8.

Panel	Locus Name	No. Alleles[a]	H_o	F_{ST}	Panel	Locus Name	No. Alleles[a]	H_o	F_{ST}
CRITFC	*Ots_128757-61R*	2	0.071	0.022	CRITFC	*Ots_crRAD24807-74*	2	0.400	0.026
CRITFC	*Ots_129144-472*	2	0.028	0.024	CRITFC	*Ots_crRAD25367-50*	2	0.372	0.023
CRITFC	*Ots_130720-99*	2	0.463	0.038	CRITFC	*Ots_crRAD255-59*	2	0.296	0.018
CRITFC	*Ots_131460-584*	2	0.107	0.027	CRITFC	*Ots_crRAD26165-69*	2	0.195	0.018
CRITFC	*Ots_131906-141*	2	0.417	0.038	CRITFC	*Ots_crRAD27515-69*	2	0.067	0.037
CRITFC	*Ots_94857-232R*	2	0.440	0.060	CRITFC	*Ots_crRAD2806-42*	2	0.434	0.026
CRITFC	*Ots_94903-99R*	2	0.321	0.063	CRITFC	*Ots_crRAD28677-65*	2	0.426	0.049
CRITFC	*Ots_95442b-204*	2	0.342	0.022	CRITFC	*Ots_crRAD34397-33*	2	0.214	0.037
CRITFC	*Ots_96222-525*	2	0.263	0.004	CRITFC	*Ots_crRAD35313-66*	2	0.494	0.042
CRITFC	*Ots_96500-180*	2	0.435	0.032	CRITFC	*Ots_crRAD36072-29*	2	0.089	0.039
CRITFC	*Ots_96899-357R*	2	0.306	0.024	CRITFC	*Ots_crRAD36152-44*	2	0.032	0.105
CRITFC	*Ots_97660-56*	2	0.048	0.035	CRITFC	*Ots_crRAD42058-48*	2	0.257	0.057
CRITFC	*Ots_99550-204*	2	0.120	0.023	CRITFC	*Ots_crRAD44588-67*	2	0.036	0.023
CRITFC	*Ots_afmid-196*	2	0.066	0.016	CRITFC	*Ots_crRAD47297-55*	2	0.397	0.040
CRITFC	*Ots_AldoB4-183*	2	0.222	0.020	CRITFC	*Ots_crRAD55400-59*	2	0.410	0.036
CRITFC	*Ots_AsnRS-60*	2	0.373	0.036	CRITFC	*Ots_crRAD57376-68*	2	0.435	0.039
CRITFC	*Ots_brp16-64*	2	0.386	0.022	CRITFC	*Ots_crRAD57520-66*	2	0.349	0.021
CRITFC	*Ots_CCR7*	2	0.027	0.064	CRITFC	*Ots_crRAD57537-24*	2	0.433	0.033
CRITFC	*Ots_CD59-2*	2	0.491	0.024	CRITFC	*Ots_crRAD57687-34*	2	0.489	0.031
CRITFC	*Ots_CD63*	2	0.119	0.141	CRITFC	*Ots_crRAD60620-51*	2	0.088	0.028
CRITFC	*Ots_cgo24-22*	2	0.470	0.029	CRITFC	*Ots_crRAD69327-53*	2	0.086	0.026
CRITFC	*Ots_CirpA*	2	0.467	0.038	CRITFC	*Ots_crRAD73823-60*	2	0.335	0.020
CRITFC	*Ots_cox1-241*	2	0.092	0.104	CRITFC	*Ots_crRAD75581-70*	2	0.442	0.036
CRITFC	*Ots_crRAD11620-55*	2	0.075	0.018	CRITFC	*Ots_crRAD9615-69*	2	0.030	0.008
CRITFC	*Ots_crRAD12037-39*	2	0.479	0.038	CRITFC	*Ots_DESMIN19-SNP1*	2	0.459	0.014
CRITFC	*Ots_crRAD16540-50*	2	0.141	0.031	CRITFC	*Ots_E2-275*	2	0.305	0.024
CRITFC	*Ots_crRAD20262-46*	2	0.353	0.016	CRITFC	*Ots_EP-529*	2	0.152	0.115
CRITFC	*Ots_crRAD20376-66*	2	0.425	0.031	CRITFC	*Ots_Est1363*	2	0.202	0.081
CRITFC	*Ots_crRAD21115-24*	2	0.026	0.069	CRITFC	*Ots_Est740*	2	0.160	0.017

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Table 3.–Page 3 of 8.

Panel	Locus Name	No. Alleles[a]	H_o	F_{ST}	Panel	Locus Name	No. Alleles[a]	H_o	F_{ST}
CRITFC	*Ots_ETIF1A*	2	0.490	0.017	CRITFC	*Ots_nkef-192*	2	0.270	0.043
CRITFC	*Ots_FARSLA-220*	2	0.363	0.016	CRITFC	*Ots_NOD1*	2	0.466	0.052
CRITFC	*Ots_FGF6A*	2	0.436	0.033	CRITFC	*Ots_nramp-321*	2	0.036	0.022
CRITFC	*Ots_GDH-81x*	2	0.074	0.038	CRITFC	*Ots_ntl-255*	2	0.457	0.016
CRITFC	*Ots_GPDH-338*	2	0.078	0.022	CRITFC	*Ots_Ostm1*	2	0.377	0.075
CRITFC	*Ots_GPH-318*	2	0.123	0.028	CRITFC	*Ots_P450*	2	0.282	0.024
CRITFC	*Ots_GST-207*	2	0.060	0.033	CRITFC	*Ots_P450-288*	2	0.312	0.088
CRITFC	*Ots_GTH2B-550*	2	0.471	0.020	CRITFC	*Ots_P53*	2	0.443	0.018
CRITFC	*Ots_HFABP-34*	2	0.206	0.022	CRITFC	*Ots_parp3-286*	2	0.369	0.042
CRITFC	*Ots_hnRNPL-533*	2	0.315	0.020	CRITFC	*Ots_PEMT*	2	0.257	0.040
CRITFC	*Ots_hsc71-3'-488*	2	0.460	0.030	CRITFC	*Ots_PGK-54*	2	0.030	0.014
CRITFC	*Ots_hsc71-5'-453*	2	0.033	0.076	CRITFC	*Ots_pigh-105*	2	0.419	0.049
CRITFC	*Ots_hsp27b-150*	2	0.119	0.116	CRITFC	*Ots_pop5-96*	2	0.084	0.004
CRITFC	*Ots_Hsp90a*	2	0.421	0.019	CRITFC	*Ots_ppie-245*	2	0.469	0.027
CRITFC	*Ots_HSP90B-100*	2	0.228	0.024	CRITFC	*Ots_Prl2*	2	0.478	0.038
CRITFC	*Ots_IGF-I.1-76*	2	0.459	0.098	CRITFC	*Ots_RAD1104-38*	2	0.275	0.056
CRITFC	*Ots_Ikaros-250*	2	0.120	0.024	CRITFC	*Ots_RAD1832-39*	2	0.346	0.092
CRITFC	*Ots_IL11*	2	0.242	0.014	CRITFC	*Ots_RAD3513-49*	2	0.476	0.037
CRITFC	*Ots_IsoT*	2	0.363	0.037	CRITFC	*Ots_RAD4543-52*	2	0.399	0.030
CRITFC	*Ots_LEI-292*	2	0.031	0.052	CRITFC	*Ots_RAD7936-50*	2	0.372	0.023
CRITFC	*Ots_LWSop-638*	2	0.059	0.014	CRITFC	*Ots_RAG3*	2	0.294	0.043
CRITFC	*Ots_mapK-3'-309*	2	0.067	0.025	CRITFC	*Ots_redd1-187*	2	0.439	0.063
CRITFC	*Ots_mapKpr-151*	2	0.382	0.036	CRITFC	*Ots_S7-1*	2	0.173	0.018
CRITFC	*Ots_MHC1*	2	0.432	0.026	CRITFC	*Ots_SClkF2R2-135*	2	0.371	0.068
CRITFC	*Ots_MHC2*	2	0.026	0.023	CRITFC	*Ots_SERPC1-209*	2	0.190	0.038
CRITFC	*Ots_mybp-85*	2	0.166	0.035	CRITFC	*Ots_SL*	2	0.476	0.062
CRITFC	*Ots_myo1a-384*	2	0.141	0.028	CRITFC	*Ots_SWS1op-182*	2	0.459	0.010
CRITFC	*Ots_myoD-364*	2	0.173	0.020	CRITFC	*Ots_TAPBP*	2	0.325	0.029
CRITFC	*Ots_nelfd-163*	2	0.230	0.031	CRITFC	*Ots_TCTA-58*	2	0.164	0.024

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Table 3.–Page 4 of 8.

Panel	Locus Name	No. Alleles[a]	H_o	F_{ST}	Panel	Locus Name	No. Alleles[a]	H_o	F_{ST}
CRITFC	*Ots_TF1-SNP1*	2	0.036	0.028	UW	*Ots_102420-494*	2	0.202	0.092
CRITFC	*Ots_TGFB*	2	0.495	0.012	UW	*Ots_il13Ra2B-37*	2	0.036	0.023
CRITFC	*Ots_Thio*	2	0.458	0.022	UW	*Ots_ins-115*	2	0.037	0.012
CRITFC	*Ots_TLR3*	2	0.459	0.014	UW	*Ots_RAD10400*	2	0.486	0.026
CRITFC	*Ots_tpx2-125*	2	0.178	0.038	UW	*Ots_RAD10412*	2	0.144	0.015
CRITFC	*Ots_txnip-321*	2	0.020	0.100	UW	*Ots_RAD10515*	2	0.476	0.049
CRITFC	*Ots_u07-07.161*	2	0.481	0.033	UW	*Ots_RAD10583*	2	0.252	0.018
CRITFC	*Ots_u07-17.135*	2	0.071	0.014	UW	*Ots_RAD1072*	2	0.351	0.030
CRITFC	*Ots_u07-25.325*	2	0.159	0.026	UW	*Ots_RAD10807*	2	0.444	0.022
CRITFC	*Ots_u07-49.290*	2	0.351	0.028	UW	*Ots_RAD11425*	2	0.279	0.054
CRITFC	*Ots_u07-53.133*	2	0.369	0.030	UW	*Ots_RAD1149*	2	0.152	0.019
CRITFC	*Ots_u07-57.120*	2	0.382	0.036	UW	*Ots_RAD11821*	2	0.403	0.064
CRITFC	*Ots_u1002-75*	2	0.150	0.032	UW	*Ots_RAD11839*	2	0.341	0.025
CRITFC	*Ots_u1004-117*	2	0.099	0.027	UW	*Ots_RAD12182*	2	0.321	0.063
CRITFC	*Ots_u1006-171*	2	0.121	0.040	UW	*Ots_RAD1282*	2	0.283	0.045
CRITFC	*Ots_u1007-124*	2	0.336	0.014	UW	*Ots_RAD1372*	2	0.113	0.017
CRITFC	*Ots_u211-85*	2	0.244	0.029	UW	*Ots_RAD14482*	2	0.038	0.008
CRITFC	*Ots_U212-158*	2	0.038	0.014	UW	*Ots_RAD14528*	2	0.050	0.030
CRITFC	*Ots_U2362-227*	2	0.215	0.019	UW	*Ots_RAD14650*	2	0.396	0.038
CRITFC	*Ots_U2362-330*	2	0.287	0.016	UW	*Ots_RAD14852*	2	0.030	0.010
CRITFC	*Ots_U2446-123*	2	0.469	0.022	UW	*Ots_RAD1510*	2	0.148	0.034
CRITFC	*Ots_U2567-104*	2	0.351	0.062	UW	*Ots_RAD15440*	2	0.399	0.056
CRITFC	*Ots_u4-92*	2	0.235	0.020	UW	*Ots_RAD161*	2	0.276	0.030
CRITFC	*Ots_U5049-250*	2	0.198	0.042	UW	*Ots_RAD16976*	2	0.257	0.016
CRITFC	*Ots_u6-75*	2	0.088	0.041	UW	*Ots_RAD17721*	2	0.045	0.037
CRITFC	*Ots_unk526*	2	0.251	0.074	UW	*Ots_RAD17873*	2	0.328	0.038
CRITFC	*Ots_zn593-346*	2	0.213	0.055	UW	*Ots_RAD2068*	2	0.038	0.064
CRITFC	*Ots_Zp3b-215*	2	0.068	0.052	UW	*Ots_RAD2102*	2	0.472	0.037
CRITFC	*Ots_ZR-575*	2	0.093	0.034	UW	*Ots_RAD21143*	2	0.369	0.104

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Table 3.–Page 5 of 8.

Panel	Locus Name	No. Alleles[a]	H_o	F_{ST}	Panel	Locus Name	No. Alleles[a]	H_o	F_{ST}
UW	*Ots_RAD2150*	2	0.494	0.009	UW	*Ots_RAD5426-36*	2	0.473	0.028
UW	*Ots_RAD21978*	2	0.209	0.054	UW	*Ots_RAD5429*	2	0.461	0.026
UW	*Ots_RAD2207*	2	0.127	0.010	UW	*Ots_RAD5848*	2	0.110	0.019
UW	*Ots_RAD22318*	2	0.148	0.037	UW	*Ots_RAD6097*	2	0.223	0.023
UW	*Ots_RAD2234*	2	0.274	0.030	UW	*Ots_RAD6121*	2	0.359	0.048
UW	*Ots_RAD2357*	2	0.488	0.031	UW	*Ots_RAD6618-57*	2	0.481	0.025
UW	*Ots_RAD2442*	2	0.358	0.015	UW	*Ots_RAD6688*	2	0.316	0.033
UW	*Ots_RAD249*	2	0.485	0.034	UW	*Ots_RAD6755*	2	0.217	0.020
UW	*Ots_RAD2677*	2	0.250	0.028	UW	*Ots_RAD679*	2	0.406	0.017
UW	*Ots_RAD2683*	2	0.473	0.041	UW	*Ots_RAD7145*	2	0.476	0.015
UW	*Ots_RAD2856*	2	0.276	0.018	UW	*Ots_RAD7165*	2	0.312	0.062
UW	*Ots_RAD3092*	2	0.397	0.038	UW	*Ots_RAD7695*	2	0.339	0.085
UW	*Ots_RAD3123*	2	0.169	0.044	UW	*Ots_RAD8200-45*	2	0.459	0.038
UW	*Ots_RAD3386*	2	0.439	0.022	UW	*Ots_RAD8354*	2	0.389	0.038
UW	*Ots_RAD3391*	2	0.450	0.092	UW	*Ots_RAD856*	2	0.344	0.022
UW	*Ots_RAD3470*	2	0.446	0.042	UW	*Ots_RAD8560*	2	0.376	0.025
UW	*Ots_RAD3635*	2	0.358	0.042	UW	*Ots_RAD9039*	2	0.352	0.047
UW	*Ots_RAD3703*	2	0.133	0.197	UW	*Ots_RAD9536*	2	0.470	0.023
UW	*Ots_RAD3737*	2	0.460	0.033	UW	*Ots_RAD9704*	2	0.322	0.031
UW	*Ots_RAD3766*	2	0.246	0.043	UW	*Ots_RAD9970*	2	0.414	0.038
UW	*Ots_RAD3858*	2	0.209	0.019	UW	*Ots_Tf-3545*	2	0.234	0.034
UW	*Ots_RAD3925*	2	0.466	0.034	UW	*Ots_uwRAD100237-35*	2	0.462	0.038
UW	*Ots_RAD4043*	2	0.410	0.020	UW	*Ots_uwRAD10049-30*	2	0.419	0.039
UW	*Ots_RAD4185*	2	0.455	0.042	UW	*Ots_uwRAD103380*	4	0.458	0.026
UW	*Ots_RAD4369-50*	2	0.490	0.024	UW	*Ots_uwRAD103394*	8	0.604	0.023
UW	*Ots_RAD4438*	2	0.376	0.047	UW	*Ots_uwRAD10481*	8	0.476	0.038
UW	*Ots_RAD4778*	2	0.484	0.031	UW	*Ots_uwRAD105150*	4	0.577	0.053
UW	*Ots_RAD4999*	2	0.386	0.035	UW	*Ots_uwRAD108943-82*	2	0.144	0.020
UW	*Ots_RAD5189*	2	0.081	0.025	UW	*Ots_uwRAD109411-88*	2	0.188	0.028

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Panel	Locus Name	No. Alleles[a]	H_o	F_{ST}	Panel	Locus Name	No. Alleles[a]	H_o	F_{ST}
UW	*Ots_uwRAD111430-75*	2	0.414	0.015	UW	*Ots_uwRAD26757-40*	2	0.319	0.030
UW	*Ots_uwRAD112461-53*	2	0.460	0.066	UW	*Ots_uwRAD27324-86*	2	0.499	0.030
UW	*Ots_uwRAD13171*	8	0.026	0.039	UW	*Ots_uwRAD28238*	16	1.000	0.048
UW	*Ots_uwRAD13435-36*	2	0.024	0.021	UW	*Ots_uwRAD28544-83*	2	0.069	0.021
UW	*Ots_uwRAD13711-36*	2	0.429	0.027	UW	*Ots_uwRAD2868*	4	0.492	0.031
UW	*Ots_uwRAD15287-93*	2	0.362	0.034	UW	*Ots_uwRAD29121-80*	2	0.477	0.042
UW	*Ots_uwRAD15416-20*	2	0.377	0.036	UW	*Ots_uwRAD30047-22*	2	0.391	0.034
UW	*Ots_uwRAD15859-82*	2	0.206	0.019	UW	*Ots_uwRAD30345-79*	2	0.250	0.019
UW	*Ots_uwRAD16441-51*	2	0.489	0.027	UW	*Ots_uwRAD30562*	4	0.688	0.029
UW	*Ots_uwRAD16523*	4	0.295	0.021	UW	*Ots_uwRAD30759-70*	2	0.336	0.056
UW	*Ots_uwRAD17027-82*	2	0.384	0.024	UW	*Ots_uwRAD31577-39*	2	0.433	0.030
UW	*Ots_uwRAD18602*	16	1.000	0.018	UW	*Ots_uwRAD32074-29*	2	0.365	0.058
UW	*Ots_uwRAD19423*	4	0.533	0.037	UW	*Ots_uwRAD32279*	4	0.328	0.024
UW	*Ots_uwRAD19707-58*	2	0.475	0.037	UW	*Ots_uwRAD33013-41*	2	0.225	0.028
UW	*Ots_uwRAD20110*	4	0.418	0.036	UW	*Ots_uwRAD33876*	4	0.457	0.040
UW	*Ots_uwRAD20343-73*	2	0.318	0.039	UW	*Ots_uwRAD35239*	4	0.498	0.082
UW	*Ots_uwRAD20459-73*	2	0.427	0.015	UW	*Ots_uwRAD35949*	8	0.578	0.026
UW	*Ots_uwRAD20487-34*	2	0.350	0.054	UW	*Ots_uwRAD36202-84*	2	0.250	0.022
UW	*Ots_uwRAD20587-70*	2	0.440	0.108	UW	*Ots_uwRAD36916-34*	2	0.350	0.027
UW	*Ots_uwRAD22283-81*	2	0.228	0.044	UW	*Ots_uwRAD37035*	4	0.393	0.051
UW	*Ots_uwRAD22426-70*	2	0.266	0.011	UW	*Ots_uwRAD37661-63*	2	0.366	0.032
UW	*Ots_uwRAD23565-85*	2	0.428	0.046	UW	*Ots_uwRAD37744*	4	0.471	0.078
UW	*Ots_uwRAD23604-72*	2	0.202	0.034	UW	*Ots_uwRAD38104*	4	0.449	0.026
UW	*Ots_uwRAD23793-37*	2	0.431	0.010	UW	*Ots_uwRAD3830*	4	0.292	0.016
UW	*Ots_uwRAD25234-50*	2	0.485	0.028	UW	*Ots_uwRAD38331-60*	2	0.451	0.034
UW	*Ots_uwRAD25273-29*	2	0.239	0.031	UW	*Ots_uwRAD38337-23*	2	0.385	0.042
UW	*Ots_uwRAD25876-38*	2	0.336	0.023	UW	*Ots_uwRAD3884-24*	2	0.251	0.019
UW	*Ots_uwRAD26189-22*	2	0.292	0.045	UW	*Ots_uwRAD392*	8	0.287	0.035
UW	*Ots_uwRAD26644*	4	0.294	0.013	UW	*Ots_uwRAD4000*	4	0.425	0.047

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Panel	Locus Name	No. Alleles[a]	H_o	F_{ST}	Panel	Locus Name	No. Alleles[a]	H_o	F_{ST}
UW	*Ots_uwRAD40086*	8	0.439	0.043	UW	Ots_uwRAD63065	4	0.556	0.028
UW	*Ots_uwRAD40163*	4	0.499	0.084	UW	*Ots_uwRAD63105*	4	0.236	0.029
UW	*Ots_uwRAD40588*	8	0.271	0.083	UW	*Ots_uwRAD64082-59*	2	0.375	0.053
UW	*Ots_uwRAD418*	4	0.269	0.022	UW	*Ots_uwRAD64288-27*	2	0.348	0.062
UW	*Ots_uwRAD42562-83*	2	0.187	0.047	UW	*Ots_uwRAD64291*	4	0.409	0.044
UW	*Ots_uwRAD42851-34*	2	0.289	0.008	UW	*Ots_uwRAD65000-38*	2	0.449	0.024
UW	*Ots_uwRAD42864*	4	0.205	0.043	UW	*Ots_uwRAD66360-86*	2	0.473	0.050
UW	*Ots_uwRAD43082*	4	0.098	0.025	UW	*Ots_uwRAD66433-66*	2	0.399	0.033
UW	*Ots_uwRAD44834-35*	2	0.283	0.037	UW	*Ots_uwRAD66791-35*	2	0.401	0.014
UW	*Ots_uwRAD47191-85*	2	0.404	0.036	UW	*Ots_uwRAD66848-87*	2	0.320	0.008
UW	*Ots_uwRAD48032*	4	0.356	0.022	UW	*Ots_uwRAD68831-89*	2	0.300	0.084
UW	*Ots_uwRAD48649*	4	0.337	0.015	UW	*Ots_uwRAD69027-28*	2	0.453	0.046
UW	*Ots_uwRAD48855*	4	0.241	0.023	UW	*Ots_uwRAD70063-84*	2	0.449	0.041
UW	*Ots_uwRAD50458-55*	2	0.182	0.037	UW	*Ots_uwRAD71514-85*	2	0.438	0.035
UW	*Ots_uwRAD52242-86*	2	0.220	0.028	UW	*Ots_uwRAD72961*	4	0.271	0.019
UW	*Ots_uwRAD54614-39*	2	0.301	0.109	UW	*Ots_uwRAD73097-70*	2	0.254	0.026
UW	*Ots_uwRAD54653-62*	2	0.204	0.016	UW	*Ots_uwRAD73366-86*	2	0.036	0.072
UW	*Ots_uwRAD55425-75*	2	0.247	0.034	UW	*Ots_uwRAD73402-56*	2	0.479	0.026
UW	*Ots_uwRAD55538*	4	0.165	0.066	UW	*Ots_uwRAD73604-77*	2	0.309	0.035
UW	*Ots_uwRAD55571-60*	2	0.390	0.031	UW	*Ots_uwRAD73786*	16	1.000	0.038
UW	*Ots_uwRAD5667*	4	0.453	0.045	UW	*Ots_uwRAD74404-68*	2	0.495	0.028
UW	*Ots_uwRAD57006-22*	2	0.412	0.048	UW	*Ots_uwRAD74511-75*	2	0.285	0.073
UW	*Ots_uwRAD57654-68*	2	0.061	0.027	UW	*Ots_uwRAD74833*	8	0.483	0.041
UW	*Ots_uwRAD57669-42*	2	0.473	0.035	UW	*Ots_uwRAD75069-22*	2	0.243	0.040
UW	*Ots_uwRAD59572-55*	2	0.362	0.028	UW	*Ots_uwRAD75627-78*	2	0.291	0.035
UW	*Ots_uwRAD59667*	4	0.272	0.042	UW	*Ots_uwRAD75885-40*	2	0.399	0.019
UW	*Ots_uwRAD59888-48*	2	0.408	0.034	UW	*Ots_uwRAD77831-61*	2	0.457	0.027
UW	*Ots_uwRAD60132-39*	2	0.450	0.050	UW	*Ots_uwRAD80431-68*	2	0.467	0.022
UW	*Ots_uwRAD61345-53*	2	0.163	0.016	UW	*Ots_uwRAD80510*	8	0.469	0.026

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Panel	Locus Name	No. Alleles[a]	H_o	F_{ST}
UW	*Ots_uwRAD81084*	4	0.142	0.048
UW	*Ots_uwRAD81543-79*	2	0.199	0.012
UW	*Ots_uwRAD82047*	4	0.232	0.047
UW	*Ots_uwRAD82247*	4	0.160	0.026
UW	*Ots_uwRAD83004-24*	2	0.487	0.028
UW	*Ots_uwRAD83732*	8	0.490	0.027
UW	*Ots_uwRAD84318-70*	2	0.410	0.040
UW	*Ots_uwRAD86211-43*	2	0.237	0.066
UW	*Ots_uwRAD8662*	4	0.311	0.022
UW	*Ots_uwRAD88897-35*	2	0.456	0.014
UW	*Ots_uwRAD92666-82*	2	0.298	0.039
UW	*Ots_uwRAD92901-83*	2	0.259	0.033
UW	*Ots_uwRAD93789*	4	0.611	0.023
UW	*Ots_uwRAD9688*	4	0.325	0.040
UW	*Ots_uwRAD98255*	4	0.320	0.029
CRITFC	*Sum/Average*	390	0.275	0.036
UW	*Sum/Average*	612	0.347	0.036
Both	*Sum/Average*	1002	0.313	0.036

Note: These summary statistics are based upon the 67 populations within Upper Cook Inlet detailed in Table 2.

[a] Loci with more than 2 alleles are microhaplotype loci produced by combining either 2 (4alleles), 3 (8 alleles), or 4 (16 alleles) SNPs within the same amplicon.

Table 4.–Baseline evaluation test correct allocation (%) summary results calculated using the *R* package *rubias* for 10 reporting groups, including the number of test mixtures (N), range of compositions tested (Range), root mean square error (RMSE), the maximum percentage points from the true proportion where 90% of point estimates occurred (Within), mean bias (Bias), and the proportion of 90% credibility intervals containing the true proportion (PCI) for each reporting group.

Panel	# Loci	Reporting group	N	Range	RMSE	Within	Bias	PCI
UW & CRITFC	413	*West*	100	1–100%	4.5	7.1	–0.3	83.0
		Susitna	100	1–100%	2.2	3.5	–0.2	97.0
		Deshka	80	1–80%	1.4	2.1	0.1	100.0
		Yentna	100	1–100%	4.8	7.3	–1.9	80.0
		Knik-Turnagain	100	1–100%	3.1	5.1	–1.2	93.0
		Kenai Tributary	100	1–100%	1.9	2.8	–0.9	99.0
		Kenai Mainstem	100	1–100%	2.0	2.0	–0.2	97.0
		Kasilof Tributary	80	1–80%	2.1	3.4	0.1	100.0
		Kasilof Mainstem	80	1–80%	1.9	3.5	–0.9	97.5
		South Kenai Pen.	100	1–100%	1.5	2.4	–0.3	100.0
UW	218	*West*	100	1–100%	6.7	10.3	–1.6	71.0
		Susitna	100	1–100%	3.8	6.3	–0.2	89.0
		Deshka	80	1–80%	2.1	3.4	–0.2	100.0
		Yentna	100	1–100%	5.2	8.8	–2.4	79.0
		Knik-Turnagain	100	1–100%	3.4	5.4	–0.8	92.0
		Kenai Tributary	100	1–100%	2.1	3.3	–1.1	98.0
		Kenai Mainstem	100	1–100%	2.3	3.2	–0.3	97.0
		Kasilof Tributary	80	1–80%	2.8	4.0	0.7	96.3
		Kasilof Mainstem	80	1–80%	2.9	4.8	–1.8	93.8
		South Kenai Pen.	100	1–100%	1.7	3.1	–0.2	100.0
CRITFC	195	*West*	100	1–100%	7.0	10.6	0.0	81.0
		Susitna	100	1–100%	4.9	8.1	–1.0	76.0
		Deshka	80	1–80%	2.4	3.7	–0.5	97.5
		Yentna	100	1–100%	7.2	11.1	–3.7	69.0
		Knik-Turnagain	100	1–100%	4.9	8.4	–1.6	80.0
		Kenai Tributary	100	1–100%	2.7	4.3	–1.1	95.0
		Kenai Mainstem	100	1–100%	2.1	3.1	0.1	97.0
		Kasilof Tributary	80	1–80%	3.4	5.1	0.1	97.5
		Kasilof Mainstem	80	1–80%	2.2	3.6	–1.1	98.8
		South Kenai Pen.	100	1–100%	2.0	3.3	–0.6	100.0

Note: Baseline evaluation tests were performed with 190 fish test mixtures analyzed using the combined University of Washington (UW) and Columbia River Inter-Tribal Fish Commission (CRITFC) GT-seq panels and each panel separately.

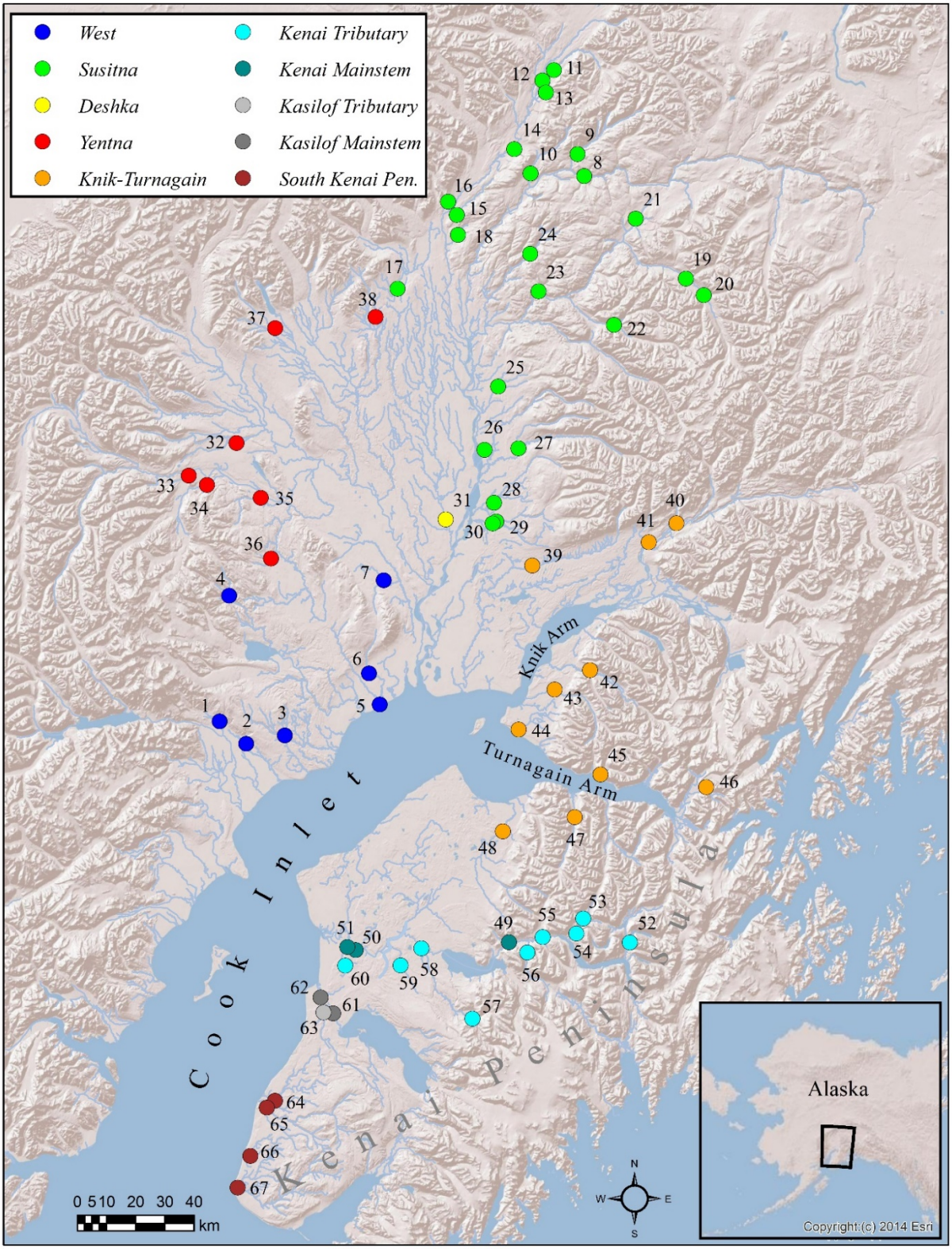

Figure 1.–Sampling locations for populations of Chinook salmon originating in Cook Inlet, Alaska, 1992–2015.

Note: Numbers correspond to population numbers in Table 2 and Figure 2. Circle colors correspond to the 10 Cook Inlet reporting groups used in the baseline evaluation tests.

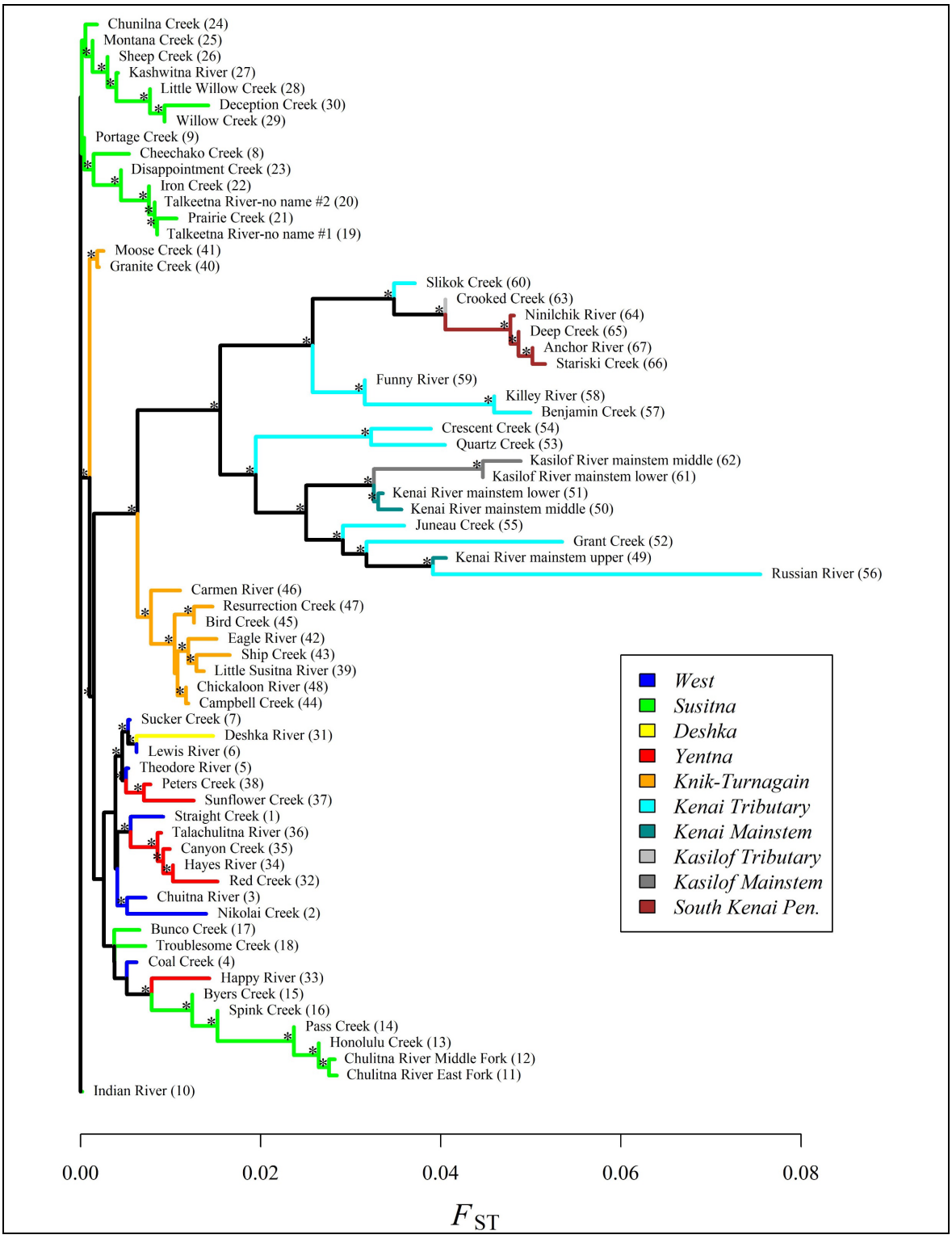

Figure 2.–Consensus neighbor-joining (NJ) tree based on pairwise F_{ST} between Chinook salmon populations sampled from spawning areas in drainages of Cook Inlet, Alaska (see Table 2 for collection details).

Note: Colors denote groups as in Figures 1, 3, 4, and 5. Numbers in parentheses correspond to unique population numbers on Table 2. Bootstrap consensus nodes occurring in >50% of trees are marked with an asterisk.

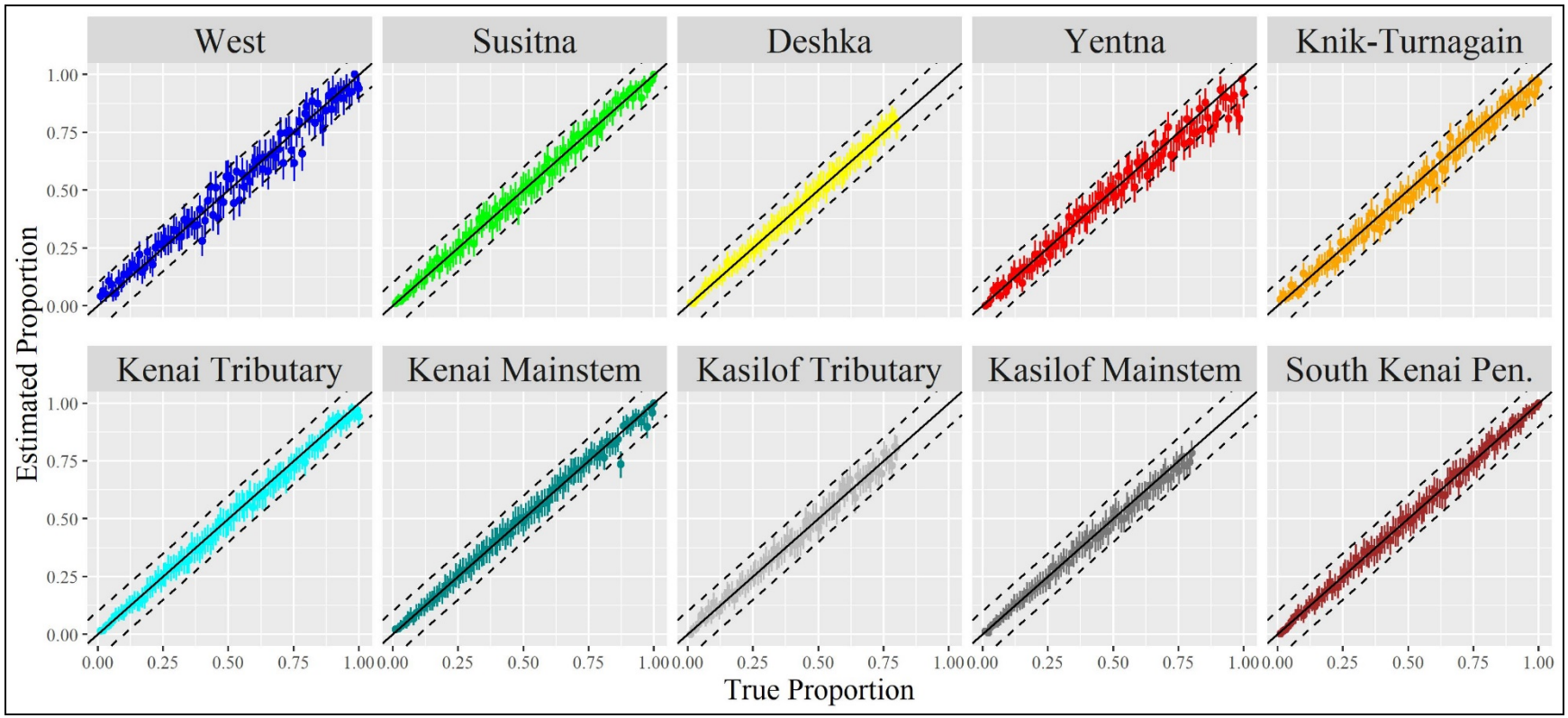

Figure 3.–Results of baseline evaluation test mixtures analyzed using the University of Washington and Columbia River Inter-Tribal Fish Commission locus panels (413 loci).

Note: Baseline evaluation tests were conducted using the *R* package *rubias* (Moran and Anderson 2019). Each test mixture contained 190 fish with true proportions ranging from 1% to 100% for each of the 10 reporting groups (Table 2). The points represent the mean correct allocation (y-axis) for each scenario (x-axis) with 90% credibility intervals for each point. The solid diagonal line indicates where the estimated proportion equals the true proportion. A reporting group is considered sufficiently identifiable for mixed stock analysis if 90% of point estimates are within ±0.10 of the true proportion (dotted lines). See Table 4 for baseline evaluation test summary statistics. Baseline evaluation tests were not performed for scenarios where *Deshka*, *Kasilof Tributary*, and *Kasilof Mainstem* comprised over 80% of the mixture sample to avoid removing more than 50% of baseline samples from those groups (see baseline evaluation test methods in text).

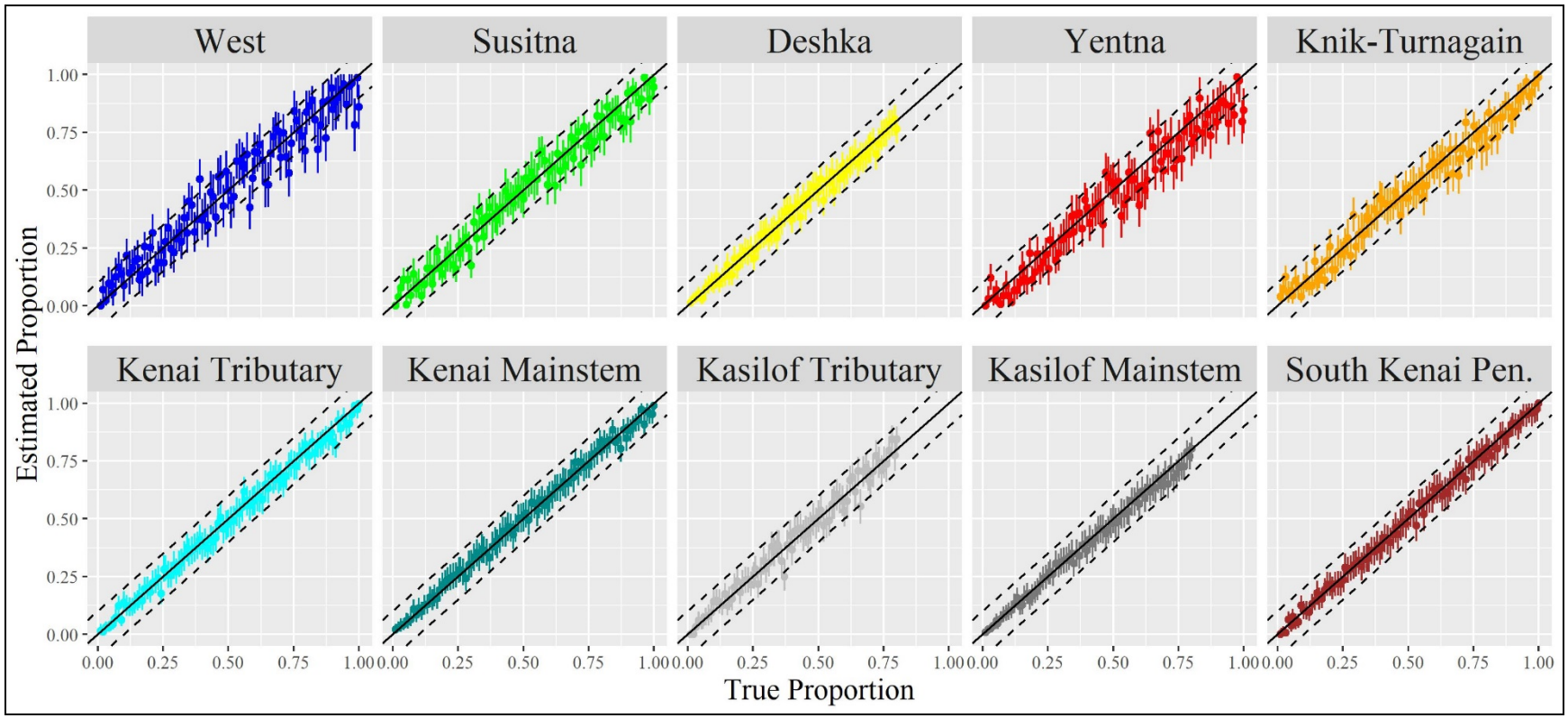

Figure 4.–Results of baseline evaluation test mixtures analyzed using the final set of loci from the Columbia River Inter-Tribal Fish Commission locus panel (195 loci).

Note: Baseline evaluation tests were conducted using the *R* package *rubias* (Moran and Anderson 2019). Each test mixture contained 190 fish with true proportions ranging from 1% to 100% for each of the 10 reporting groups (Table 2). The points represent the mean correct allocation (y-axis) for each scenario (x-axis) with 90% credibility intervals for each point. The solid diagonal line indicates where the estimated proportion equals the true proportion. A reporting group is considered sufficiently identifiable for mixed stock analysis if 90% of point estimates are within ±0.10 of the true proportion (dotted lines). See Table 4 for baseline evaluation test summary statistics. Baseline evaluation tests were not performed for scenarios where *Deshka*, *Kasilof Tributary*, and *Kasilof Mainstem* comprised over 80% of the mixture sample to avoid removing more than 50% of baseline samples from those groups (see baseline evaluation test methods in text).

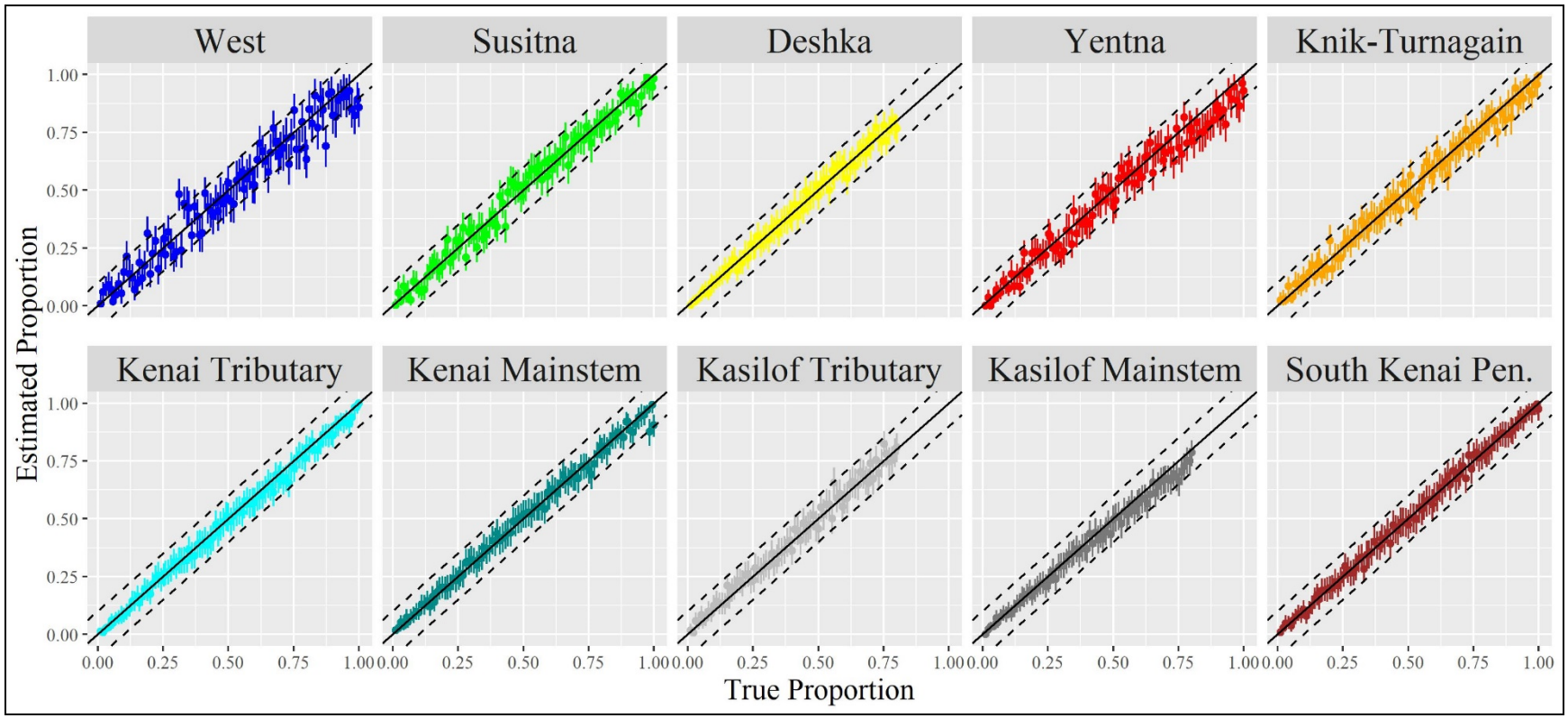

Figure 5.–Results of baseline evaluation test mixtures analyzed using the final set of loci from the University of Washington locus panel (218 loci).

Note: Baseline evaluation tests were conducted using the *R* package *rubias* (Moran and Anderson 2019). Each test mixture contained 190 fish with true proportions ranging from 1% to 100% for each of the 10 reporting groups (Table 2). The points represent the mean correct allocation (y-axis) for each scenario (x-axis) with 90% credibility intervals for each point. The solid diagonal line indicates where the estimated proportion equals the true proportion. A reporting group is considered sufficiently identifiable for mixed stock analysis if 90% of point estimates are within ±0.10 of the true proportion (dotted lines). See Table 4 for baseline evaluation test summary statistics. Baseline evaluation tests were not performed for scenarios where *Deshka*, *Kasilof Tributary*, and *Kasilof Mainstem* comprised over 80% of the mixture sample to avoid removing more than 50% of baseline samples from those groups (see baseline evaluation test methods in text).

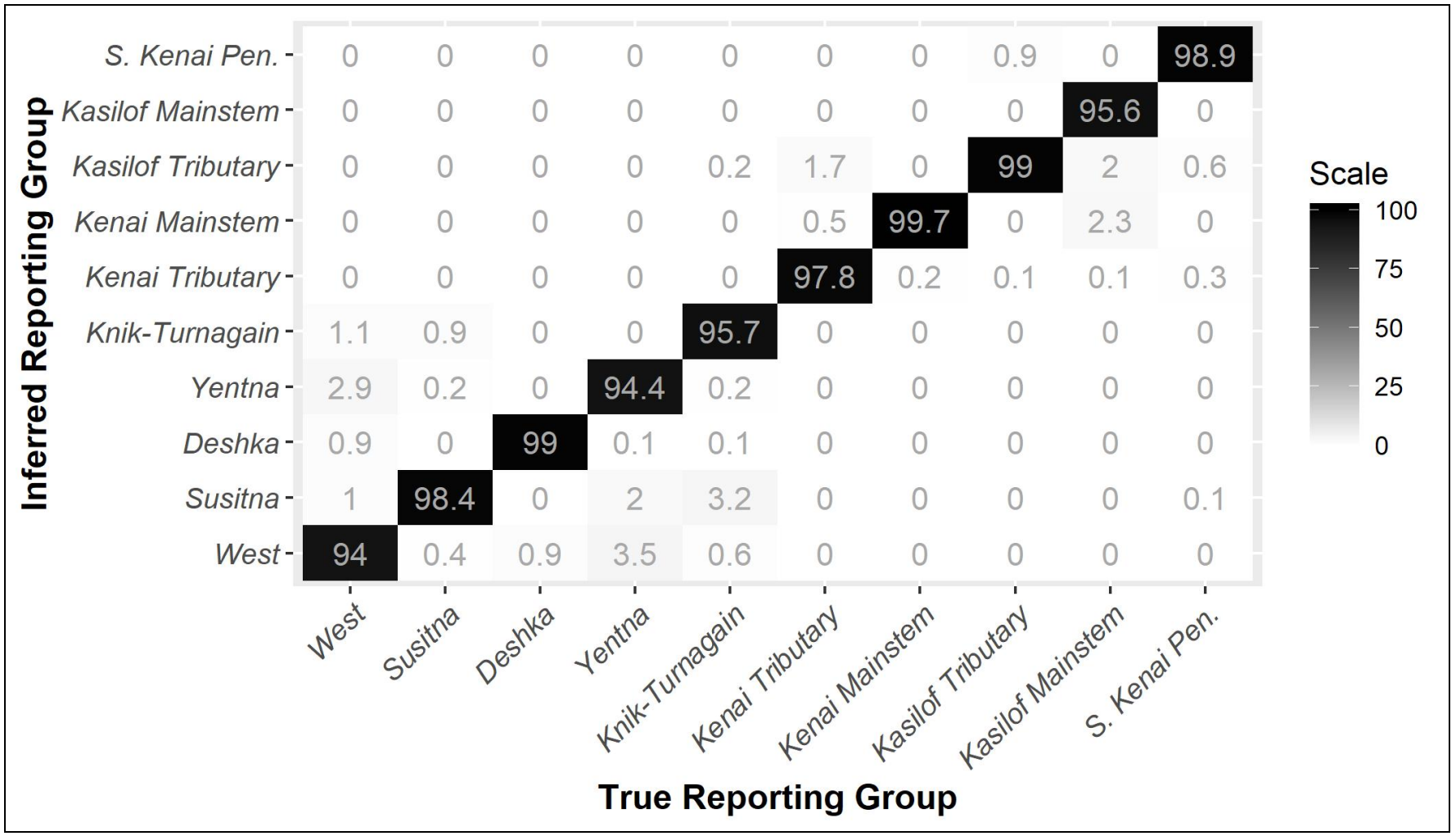

Figure 6.–Heatmap of average stock composition estimates (%) for 10 replicate mixtures of the 10 reporting groups identified in the genetic structure analysis. Stock composition estimates off the diagonal indicate the potential for misallocation among reporting groups.

Note: Each replicate was a sample of 150 individuals from a single reporting group removed from the genetic baseline. Estimates for each replicate can be found in Appendix D1.

APPENDICES

Appendix A.–Definitions of commonly used terms in this report.

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

Amplicon. A DNA sequence targeted for amplification.

Bootstrapping. A method of resampling data with replacement to assess the variation of parameters of interest.

F_{ST}. Fixation index is an estimate of the proportion of the variation at a locus attributable to divergence among populations.

Gene flow. The introduction of genes to a population, through migration and mating from another population of the same species, thereby altering the allele frequencies of the population.

Genetic drift. The change in allele frequencies in a population through time due to random sampling at each generation. The effect of genetic drift increases with smaller population size and shorter number of generations.

Genetic marker. A known DNA sequence that can be identified by a simple assay.

Genotype. The pair of alleles for one site at a locus (SNP) or a set of phased alleles for multiple sites within a locus (microhaplotype).

Genotyping-in-Thousands by sequencing (*GT-seq*). A genotyping method that uses next-generation sequencing of multiplexed PCR products to generate genotypes from panels of hundreds of targeted SNPs for thousands of individual fish (Campbell et al. 2015).

Linkage disequilibrium. A state that exists in a population when alleles at different loci are not distributed independently in the population's gamete pool, sometimes because the loci are physically linked.

Microhaplotype. Two or more closely linked SNPs within an amplicon associated in multiple phased, allelic combinations.

Hardy-Weinberg expectations (*HWE*). Genotype frequencies expected from a given set of allele frequencies for a locus. Fit to HWE genotypic proportions assumes random mating, no mutation (the alleles remain unchanged), no migration or emigration (no exchange of alleles between populations), infinitely large population size, and no selective pressure for or against the alleles.

Heterozygosity. The proportion of individuals in a population that have 2 different allele forms (are heterozygous) at a particular marker. Average heterozygosity can be used as measure of variability in a sample.

Locus (plural, loci). A region on a chromosome containing one or more SNPs. When more than one SNP are present, they are combined in phase to form a microhaplotypes.

Linked markers. Genetic markers showing linkage disequilibrium, or physical linkage on a chromosome.

Microsatellite. A locus made up of short repeated sequences of DNA. The number of repeats determines the allele size.

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

Polymerase Chain Reaction (*PCR*). A method to amplify DNA sequences, which can be used to generate millions of copies of the target DNA.

Phase (allelic). Whether alleles within a locus are on the same chromosome or on different chromosomes.

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Population. A locally interbreeding group of spawning individuals that do not interbreed with individuals in other spawning aggregations, and that may be uniquely adapted to a particular spawning habitat. This produces isolation among populations and may lead to the appearance of unique attributes (Ricker 1958) that result in different productivity rates (Pearcy 1992; NRC 1996). This population definition is analogous to 'spawning aggregations' described by Baker et al. (1996) and 'demes' described by the NRC (1996).

Reporting group. A group of populations in a genetic baseline to which portions of a mixture are allocated during mixed stock analysis.

Single nucleotide polymorphism (*SNP*). DNA nucleotide variation (A, T, C, or G) at a single nucleotide site. SNPs can differ among individuals or within an individual between homologous nucleotide sites on paired chromosomes.

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

Appendix B.–Panel, amplicon/locus name, number of SNPs on the amplicon/locus identified by Dann et al. (2018) and McKinney et al. (2019) for the UW panel, and by Janowitz-Koch et al. (2019) for the CRITFC panel, and reason for not including loci on amplicons from final baseline dataset.

Panel	Amplicon/Locus Name	No. SNPs	Reason for removing
CRITFC	*Ots_100884-287*	1	
CRITFC	*Ots_101119-381*	1	Invariant
CRITFC	*Ots_101554-407*	1	
CRITFC	*Ots_101704-143*	1	Invariant
CRITFC	*Ots_101770-82*	1	Invariant
CRITFC	*Ots_102213-210*	1	Invariant
CRITFC	*Ots_102414-395*	1	
CRITFC	*Ots_102457-132*	1	Out of Hardy-Weinberg equilibrium
CRITFC	*Ots_102801-308*	1	
CRITFC	*Ots_102867-609*	1	
CRITFC	*Ots_103041-52*	1	
CRITFC	*Ots_103122-180*	1	
CRITFC	*Ots_104048-194*	1	
CRITFC	*Ots_104063-132*	1	
CRITFC	*Ots_104415-88*	1	Out of Hardy-Weinberg equilibrium
CRITFC	*Ots_105105-613*	1	
CRITFC	*Ots_105132-200*	1	
CRITFC	*Ots_105385-421*	1	
CRITFC	*Ots_105401-325*	1	Invariant
CRITFC	*Ots_105407-117*	1	
CRITFC	*Ots_105897-124*	1	
CRITFC	*Ots_106313-729*	1	Invariant
CRITFC	*Ots_106419b-618*	1	
CRITFC	*Ots_106499-70*	1	
CRITFC	*Ots_106747-239*	1	
CRITFC	*Ots_107074-284*	1	
CRITFC	*Ots_107285-93*	1	Invariant
CRITFC	*Ots_107607-315*	1	Invariant
CRITFC	*Ots_107806-821*	1	
CRITFC	*Ots_108007-208*	1	
CRITFC	*Ots_108390-329*	1	
CRITFC	*Ots_108735-302*	1	
CRITFC	*Ots_108820-336*	1	
CRITFC	*Ots_109525-816*	1	
CRITFC	*Ots_109693-392*	1	
CRITFC	*Ots_110064-383*	1	
CRITFC	*Ots_110201-363*	1	

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Panel	Amplicon/Locus Name	No. SNPs	Reason for removing
CRITFC	*Ots_110381-164*	1	
CRITFC	*Ots_110495-380*	1	Allelic ratios did not conform to the expected
CRITFC	*Ots_110551-64*	1	
CRITFC	*Ots_110689-218*	1	
CRITFC	*Ots_111084b-619*	1	
CRITFC	*Ots_111312-435*	1	Linked with other another locus
CRITFC	*Ots_111681-657*	1	Invariant
CRITFC	*Ots_112208-722*	1	
CRITFC	*Ots_112301-43*	1	
CRITFC	*Ots_112419-131*	1	
CRITFC	*Ots_112820-284*	1	
CRITFC	*Ots_112876-371*	1	
CRITFC	*Ots_113242-216*	1	
CRITFC	*Ots_113457-40R*	1	
CRITFC	*Ots_115987-325*	1	
CRITFC	*Ots_117242-136*	1	Invariant
CRITFC	*Ots_117259-271*	1	Invariant
CRITFC	*Ots_117370-471*	1	Invariant
CRITFC	*Ots_117432-409*	1	
CRITFC	*Ots_118175-479*	1	
CRITFC	*Ots_118205-61*	1	
CRITFC	*Ots_118938-325*	1	
CRITFC	*Ots_120950-417*	1	
CRITFC	*Ots_122414-56*	1	Invariant
CRITFC	*Ots_123048-521*	1	
CRITFC	*Ots_123921-111*	1	
CRITFC	*Ots_124774-477*	1	Invariant
CRITFC	*Ots_126619-400*	1	Allelic ratios did not conform to the expected
CRITFC	*Ots_127236-62*	1	
CRITFC	*Ots_127760-569*	1	
CRITFC	*Ots_128302-57*	1	
CRITFC	*Ots_128693-461*	1	
CRITFC	*Ots_128757-61R*	1	
CRITFC	*Ots_129144-472*	1	
CRITFC	*Ots_129170-683*	1	Missing data for at least 1 location
CRITFC	*Ots_129458-451*	1	Invariant
CRITFC	*Ots_129870-55*	1	Invariant
CRITFC	*Ots_130720-99*	1	

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Panel	Amplicon/Locus Name	No. SNPs	Reason for removing
CRITFC	*Ots_131460-584*	1	
CRITFC	*Ots_131802-393*	1	Invariant
CRITFC	*Ots_131906-141*	1	
CRITFC	*Ots_94857-232R*	1	
CRITFC	*Ots_94903-99R*	1	
CRITFC	*Ots_95442b-204*	1	
CRITFC	*Ots_96222-525*	1	
CRITFC	*Ots_96500-180*	1	
CRITFC	*Ots_96899-357R*	1	
CRITFC	*Ots_97077-179R*	1	Invariant
CRITFC	*Ots_97660-56*	1	
CRITFC	*Ots_98409-850*	1	Invariant
CRITFC	*Ots_98683-796*	1	Invariant
CRITFC	*Ots_99550-204*	1	
CRITFC	*Ots_afmid-196*	1	
CRITFC	*Ots_AldB1-122*	1	Linked with other another locus
CRITFC	*Ots_aldb-177M*	1	Invariant
CRITFC	*Ots_ALDBINT1-SNP1*	1	Invariant
CRITFC	*Ots_AldoB4-183*	1	
CRITFC	*Ots_ARNT*	1	Allelic ratios did not conform to the expected
CRITFC	*Ots_arp-436*	1	Invariant
CRITFC	Ots_AsnRS-60[a]	1	
CRITFC	*Ots_aspat-196*	1	Invariant
CRITFC	*Ots_BMP2-SNP1*	1	Invariant
CRITFC	*Ots_brp16-64*	1	
CRITFC	*Ots_Cath_D141*	1	Invariant
CRITFC	*Ots_CCR7*	1	
CRITFC	*Ots_CD59-2*	1	
CRITFC	*Ots_CD63*	1	
CRITFC	*Ots_cgo24-22*	1	
CRITFC	*Ots_Chin30up-211*	1	Invariant
CRITFC	*Ots_CirpA*	1	
CRITFC	*Ots_cox1-241*	1	
CRITFC	*Ots_CRB211*	1	Invariant
CRITFC	*Ots_crRAD10447-25*	1	Invariant
CRITFC	*Ots_crRAD11620-55*	1	
CRITFC	*Ots_crRAD12037-39*	1	
CRITFC	*Ots_crRAD12711-37*	1	Invariant

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Panel	Amplicon/Locus Name	No. SNPs	Reason for removing
CRITFC	*Ots_crRAD13725-51*	1	Invariant
CRITFC	*Ots_crRAD16540-50*	1	
CRITFC	*Ots_crRAD17527-58*	1	Missing data for at least 1 location
CRITFC	*Ots_crRAD18289-33*	1	Invariant
CRITFC	*Ots_crRAD18492-65*	1	Invariant
CRITFC	*Ots_crRAD18937-60*	1	Invariant
CRITFC	*Ots_crRAD20262-46*	1	
CRITFC	*Ots_crRAD20376-66*	1	
CRITFC	*Ots_crRAD20887-70*	1	Invariant
CRITFC	*Ots_crRAD21115-24*	1	
CRITFC	*Ots_crRAD22960-32*	1	Linked with other another locus
CRITFC	*Ots_crRAD23631-48*	1	Invariant
CRITFC	*Ots_crRAD24807-74*	1	
CRITFC	*Ots_crRAD25367-50*	1	
CRITFC	*Ots_crRAD255-59*	1	
CRITFC	*Ots_crRAD26081-28*	1	Invariant
CRITFC	*Ots_crRAD26165-69*	1	
CRITFC	*Ots_crRAD26541-47*	1	Allelic ratios did not conform to the expected
CRITFC	*Ots_crRAD27164-55*	1	Invariant
CRITFC	*Ots_crRAD27515-69*	1	
CRITFC	*Ots_crRAD2806-42*	1	
CRITFC	*Ots_crRAD28677-65*	1	
CRITFC	*Ots_crRAD292-21*	1	Invariant
CRITFC	*Ots_crRAD30341-48*	1	Allelic ratios did not conform to the expected
CRITFC	*Ots_crRAD33054-62*	1	Out of Hardy-Weinberg equilibrium
CRITFC	*Ots_crRAD33491-71*	1	Invariant
CRITFC	*Ots_crRAD34397-33*	1	
CRITFC	*Ots_crRAD35313-66*	1	
CRITFC	*Ots_crRAD36072-29*	1	
CRITFC	*Ots_crRAD36152-44*	1	
CRITFC	*Ots_crRAD3758-51*	1	Allelic ratios did not conform to the expected
CRITFC	*Ots_crRAD38095-29*	1	Invariant
CRITFC	*Ots_crRAD38746-36*	1	Invariant
CRITFC	*Ots_crRAD42058-48*	1	
CRITFC	*Ots_crRAD44588-67*	1	
CRITFC	*Ots_crRAD46081-56*	1	Invariant
CRITFC	*Ots_crRAD46751-42*	1	Invariant
CRITFC	*Ots_crRAD47297-55*	1	

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Panel	Amplicon/Locus Name	No. SNPs	Reason for removing
CRITFC	*Ots_crRAD48459-74*	1	Allelic ratios did not conform to the expected
CRITFC	*Ots_crRAD5061-27*	1	Linked with other another locus
CRITFC	*Ots_crRAD55400-59*	1	
CRITFC	*Ots_crRAD55475-26*	1	Invariant
CRITFC	*Ots_crRAD57376-68*	1	
CRITFC	*Ots_crRAD57520-66*	1	
CRITFC	*Ots_crRAD57537-24*	1	
CRITFC	*Ots_crRAD57687-34*	1	
CRITFC	*Ots_crRAD60614-46*	1	Invariant
CRITFC	*Ots_crRAD60620-51*	1	
CRITFC	*Ots_crRAD61523-71*	1	Out of Hardy-Weinberg equilibrium
CRITFC	*Ots_crRAD66330-60*	1	Invariant
CRITFC	*Ots_crRAD69327-53*	1	
CRITFC	*Ots_crRAD73823-60*	1	
CRITFC	*Ots_crRAD74766-28*	1	Invariant
CRITFC	*Ots_crRAD75581-70*	1	
CRITFC	*Ots_crRAD76512-28*	1	Out of Hardy-Weinberg equilibrium
CRITFC	*Ots_crRAD78968-46*	1	Invariant
CRITFC	*Ots_crRAD92420-25*	1	Invariant
CRITFC	*Ots_crRAD9615-69*	1	
CRITFC	*Ots_DDX5-171*	1	Invariant
CRITFC	*Ots_DESMIN19-SNP1*	1	
CRITFC	*Ots_E2-275*[a]	1	
CRITFC	*Ots_EndoRB1-486*	1	Invariant
CRITFC	*Ots_EP-529*	1	
CRITFC	*Ots_Est1363*	1	
CRITFC	*Ots_Est740*	1	
CRITFC	*Ots_ETIF1A*[a]	1	
CRITFC	*Ots_FARSLA-220*[a]	1	
CRITFC	*Ots_FGF6A*	1	
CRITFC	*Ots_FGF6B*[a]	1	Linked with other another locus
CRITFC	*Ots_GCSH*	1	Invariant
CRITFC	*Ots_GDH-81x*	1	
CRITFC	*Ots_GH2*[a]	1	Allelic ratios did not conform to the expected
CRITFC	*Ots_GnRH-271*	1	Invariant
CRITFC	*Ots_GPDH-338*[a]	1	
CRITFC	*Ots_GPH-318*[a]	1	
CRITFC	*Ots_GST-207*[a]	1	

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Panel	Amplicon/Locus Name	No. SNPs	Reason for removing
CRITFC	*Ots_GST-375*	1	Invariant
CRITFC	*Ots_GTH2B-550*[a]	1	
CRITFC	*Ots_HFABP-34*	1	
CRITFC	*Ots_HMGB1-73*	1	Invariant
CRITFC	*Ots_hnRNPL-533*[a]	1	
CRITFC	*Ots_hsc71-3'-488*	1	
CRITFC	*Ots_hsc71-5'-453*	1	
CRITFC	*Ots_hsp27b-150*	1	
CRITFC	*Ots_Hsp90a*	1	
CRITFC	*Ots_HSP90B-100*[a]	1	
CRITFC	*Ots_IGF-I.1-76*[a]	1	
CRITFC	*Ots_Ikaros-250*[a]	1	
CRITFC	*Ots_IL11*	1	
CRITFC	*Ots_IL8R_C8*	1	Allelic ratios did not conform to the expected
CRITFC	*Ots_IsoT*	1	
CRITFC	*Ots_LEI-292*[a]	1	
CRITFC	*Ots_LWSop-638*[a]	1	
CRITFC	*Ots_mapK-3'-309*	1	
CRITFC	*Ots_mapKpr-151*	1	
CRITFC	*Ots_MetA*	1	Invariant
CRITFC	*Ots_MHC1*	1	
CRITFC	*Ots_MHC2*	1	
CRITFC	*Ots_MTA-SNP1*	1	Invariant
CRITFC	*Ots_mybp-85*	1	
CRITFC	*Ots_Myc-366*	1	Invariant
CRITFC	*Ots_myo1a-384*	1	
CRITFC	*Ots_myoD-364*	1	
CRITFC	*Ots_NAML12-SNP1*	1	Linked with other another locus
CRITFC	*Ots_nelfd-163*	1	
CRITFC	*Ots_NFYB-147*	1	Invariant
CRITFC	*Ots_nkef-192*	1	
CRITFC	*Ots_NOD1*[a]	1	
CRITFC	*Ots_nramp-321*	1	
CRITFC	*Ots_ntl-255*	1	
CRITFC	*Ots_Ostm1*	1	
CRITFC	*Ots_Ots311-101x*	1	Invariant
CRITFC	*Ots_P450-288*	1	
CRITFC	*Ots_P450*[a]	1	

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Panel	Amplicon/Locus Name	No. SNPs	Reason for removing
CRITFC	*Ots_P53*[a]	1	
CRITFC	*Ots_parp3-286*	1	
CRITFC	*Ots_PEMT*	1	
CRITFC	*Ots_PGK-54*[a]	1	
CRITFC	*Ots_pigh-105*	1	
CRITFC	*Ots_pop5-96*	1	
CRITFC	*Ots_ppie-245*	1	
CRITFC	*Ots_Prl2*[a]	1	
CRITFC	*Ots_RAD1104-38*	1	
CRITFC	*Ots_RAD1832-39*	1	
CRITFC	*Ots_RAD3513-49*	1	
CRITFC	*Ots_RAD4543-52*	1	
CRITFC	*Ots_RAD7936-50*	1	
CRITFC	*Ots_RAD9480-51*	1	Linked with other another locus
CRITFC	*Ots_RAG3*[a]	1	
CRITFC	*Ots_RAS1*	1	Invariant
CRITFC	*Ots_redd1-187*	1	
CRITFC	*Ots_RFC2-558*	1	Invariant
CRITFC	*Ots_S7-1*[a]	1	
CRITFC	*Ots_SClkF2R2-135*[a]	1	
CRITFC	*Ots_sept9-78*	1	Allelic ratios did not conform to the expected
CRITFC	*Ots_SERPC1-209*[a]	1	
CRITFC	*Ots_SEXY3-1*	1	Sex determination may not be accurate
CRITFC	*Ots_Sl*[a]	1	
CRITFC	*Ots_slc7a2-71*	1	Invariant
CRITFC	*Ots_stk6-516*	1	Invariant
CRITFC	*Ots_SWS1op-182*[a]	1	
CRITFC	*Ots_TAPBP*[a]	1	
CRITFC	*Ots_TCTA-58*	1	
CRITFC	*Ots_TF1-SNP1*	1	
CRITFC	*Ots_TGFB*	1	
CRITFC	*Ots_Thio*	1	
CRITFC	*Ots_TLR3*	1	
CRITFC	*Ots_TNF*	1	Invariant
CRITFC	*Ots_Tnsf*[a]	1	Linked with other another locus
CRITFC	*Ots_tpx2-125*	1	
CRITFC	*Ots_trnau1ap-86*	1	Invariant
CRITFC	*Ots_txnip-321*	1	

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Panel	Amplicon/Locus Name	No. SNPs	Reason for removing
CRITFC	*Ots_u07-07.161*	1	
CRITFC	*Ots_u07-17.135*	1	
CRITFC	*Ots_u07-17.373*	1	Invariant
CRITFC	*Ots_u07-18.378*	1	Invariant
CRITFC	*Ots_u07-19.260*	1	Invariant
CRITFC	*Ots_u07-20.332*	1	Invariant
CRITFC	*Ots_u07-25.325*	1	
CRITFC	*Ots_u07-49.290*	1	
CRITFC	*Ots_u07-53.133*	1	
CRITFC	*Ots_u07-57.120*	1	
CRITFC	*Ots_u07-64.221*	1	Invariant
CRITFC	*Ots_u1002-75*	1	
CRITFC	*Ots_u1004-117*	1	
CRITFC	*Ots_u1006-171*	1	
CRITFC	*Ots_u1007-124*	1	
CRITFC	*Ots_u1008-108*	1	Invariant
CRITFC	*Ots_u202-161*[a]	1	Allelic ratios did not conform to the expected
CRITFC	*Ots_u211-85*[a]	1	
CRITFC	*Ots_U212-158*[a]	1	
CRITFC	*Ots_U2305-63*	1	Out of Hardy-Weinberg equilibrium
CRITFC	*Ots_U2362-227*	1	
CRITFC	*Ots_U2362-330*	1	
CRITFC	*Ots_U2446-123*	1	
CRITFC	*Ots_U2567-104*	1	
CRITFC	*Ots_u4-92*	1	
CRITFC	*Ots_U5049-250*	1	
CRITFC	*Ots_U5121-34*	1	Out of Hardy-Weinberg equilibrium
CRITFC	*Ots_u6-75*[a]	1	
CRITFC	*Ots_unk526*[a]	1	
CRITFC	*Ots_USMG5-67*	1	Invariant
CRITFC	*Ots_vatf-251*	1	Invariant
CRITFC	*Ots_zn593-346*	1	
CRITFC	*Ots_Zp3b-215*[a]	1	
CRITFC	*Ots_ZR-575*	1	
UW	*Ots_102420-494*[a]	1	
UW	*Ots_104569-86*	1	Missing data for at least 1 location
UW	*Ots_arf-188*	1	Invariant
UW	*Ots_E9BAC*	1	Invariant

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Panel	Amplicon/Locus Name	No. SNPs	Reason for removing
UW	*Ots_HGFA-446*	1	Invariant
UW	*Ots_hsp47-339*	1	Invariant
UW	*Ots_HSP90B-385*[a]	1	Invariant
UW	*Ots_hsp90BA-252*[a]	1	Linked with other another locus
UW	*Ots_il13Ra2B-37*[a]	1	
UW	*Ots_il-1racp-166*[a]	1	Out of Hardy-Weinberg equilibrium
UW	*Ots_ins-115*[a]	1	
UW	*Ots_PSMB1-197*	1	Invariant
UW	*Ots_RAD10099*	1	Missing data for at least 1 location
UW	*Ots_RAD10400*	1	
UW	*Ots_RAD10412*	1	
UW	*Ots_RAD10515*	1	
UW	*Ots_RAD10583*	1	
UW	*Ots_RAD1072*	1	
UW	*Ots_RAD10807*	1	
UW	*Ots_RAD11425*	1	
UW	*Ots_RAD11441*	1	Invariant
UW	*Ots_RAD1149*	1	
UW	*Ots_RAD11821*	1	
UW	*Ots_RAD11839*	1	
UW	*Ots_RAD12182*	1	
UW	*Ots_RAD1282*	1	
UW	*Ots_RAD1372*	1	
UW	*Ots_RAD14482*	1	
UW	*Ots_RAD14528*	1	
UW	*Ots_RAD14650*	1	
UW	*Ots_RAD14852*	1	
UW	*Ots_RAD1507*	1	Missing data for at least 1 location
UW	*Ots_RAD1510*	1	
UW	*Ots_RAD15440*	1	
UW	*Ots_RAD161*	1	
UW	*Ots_RAD16976*	1	
UW	*Ots_RAD17721*	1	
UW	*Ots_RAD17873*	1	
UW	*Ots_RAD18973*	1	Invariant
UW	*Ots_RAD2068*	1	
UW	*Ots_RAD2102*	1	
UW	*Ots_RAD21143*	1	

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Panel	Amplicon/Locus Name	No. SNPs	Reason for removing
UW	*Ots_RAD2150*	1	
UW	*Ots_RAD21978*	1	
UW	*Ots_RAD2207*	1	
UW	*Ots_RAD22318*	1	
UW	*Ots_RAD2234*	1	
UW	*Ots_RAD2357*	1	
UW	*Ots_RAD2442*	1	
UW	*Ots_RAD249*	1	
UW	*Ots_RAD2598*	1	Out of Hardy-Weinberg equilibrium
UW	*Ots_RAD2677*	1	
UW	*Ots_RAD2683*	1	
UW	*Ots_RAD2856*	1	
UW	*Ots_RAD3092*	1	
UW	*Ots_RAD3123*	1	
UW	*Ots_RAD3386*	1	
UW	*Ots_RAD3391*	1	
UW	*Ots_RAD3425*	1	Invariant
UW	*Ots_RAD3470*	1	
UW	*Ots_RAD3635*	1	
UW	*Ots_RAD3703*	1	
UW	*Ots_RAD3737*	1	
UW	*Ots_RAD3752*	1	Missing data for at least 1 location
UW	*Ots_RAD3766*	1	
UW	*Ots_RAD3858*	1	
UW	*Ots_RAD3925*	1	
UW	*Ots_RAD4043*	1	
UW	*Ots_RAD4185*	1	
UW	*Ots_RAD4369-50*	1	
UW	*Ots_RAD4438*	1	
UW	*Ots_RAD4778*	1	
UW	*Ots_RAD4999*	1	
UW	*Ots_RAD5189*	1	
UW	*Ots_RAD5426-36*	1	
UW	*Ots_RAD5429*	1	
UW	*Ots_RAD5848*	1	
UW	*Ots_RAD6097*	1	
UW	*Ots_RAD6121*	1	
UW	*Ots_RAD6184*	1	Out of Hardy-Weinberg equilibrium

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Panel	Amplicon/Locus Name	No. SNPs	Reason for removing
UW	*Ots_RAD6618-57*	1	
UW	*Ots_RAD6688*	1	
UW	*Ots_RAD6755*	1	
UW	*Ots_RAD679*	1	
UW	*Ots_RAD7145*	1	
UW	*Ots_RAD7165*	1	
UW	*Ots_RAD7695*	1	
UW	*Ots_RAD8200-45*	1	
UW	*Ots_RAD8354*	1	
UW	*Ots_RAD856*	1	
UW	*Ots_RAD8560*	1	
UW	*Ots_RAD9039*	1	
UW	*Ots_RAD9536*	1	
UW	*Ots_RAD9704*	1	
UW	*Ots_RAD9756*	1	Missing data for at least 1 location
UW	*Ots_RAD995*	1	Missing data for at least 1 location
UW	*Ots_RAD9970*	1	
UW	*Ots_Tf-3545*[a]	1	
UW	*Ots_uwRAD100237*	1	
UW	*Ots_uwRAD10049*	1	
UW	*Ots_uwRAD101818*	1	Invariant
UW	*Ots_uwRAD103380*	2	
UW	*Ots_uwRAD103394*	3	
UW	*Ots_uwRAD10481*	3	
UW	*Ots_uwRAD105150*	2	
UW	*Ots_uwRAD108943*	1	
UW	*Ots_uwRAD109411*	1	
UW	*Ots_uwRAD111430*	1	
UW	*Ots_uwRAD112461*	1	
UW	*Ots_uwRAD12524*	1	Out of Hardy-Weinberg equilibrium
UW	*Ots_uwRAD12688*	1	Linked with other another locus
UW	*Ots_uwRAD13045*	3	Missing data for at least 1 location
UW	*Ots_uwRAD13171*	3	
UW	*Ots_uwRAD13435*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD13435*	1	
UW	*Ots_uwRAD13711*	1	
UW	*Ots_uwRAD13755*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD14092*	1	Allelic ratios did not conform to the expected

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Panel	Amplicon/Locus Name	No. SNPs	Reason for removing
UW	*Ots_uwRAD15287*	1	
UW	*Ots_uwRAD15416*	1	
UW	*Ots_uwRAD15859*	1	
UW	*Ots_uwRAD16441*	1	
UW	*Ots_uwRAD16502*	1	Linked with other another locus
UW	*Ots_uwRAD16523*	2	
UW	*Ots_uwRAD16625*	1	Linked with other another locus
UW	*Ots_uwRAD17027*	1	
UW	*Ots_uwRAD17420*	2	Missing data for at least 1 location
UW	*Ots_uwRAD18602*	4	
UW	*Ots_uwRAD19139*	1	Invariant
UW	*Ots_uwRAD19423*	2	
UW	*Ots_uwRAD19707*	1	
UW	*Ots_uwRAD20110*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD20110*	2	
UW	*Ots_uwRAD20292*	1	Missing data for at least 1 location
UW	*Ots_uwRAD20343*	1	
UW	*Ots_uwRAD20459*	1	
UW	*Ots_uwRAD20487*	1	
UW	*Ots_uwRAD20587*	1	
UW	*Ots_uwRAD21392*	1	Linked with other another locus
UW	*Ots_uwRAD21678*	1	Missing data for at least 1 location
UW	*Ots_uwRAD22283*	1	
UW	*Ots_uwRAD22426*	1	
UW	*Ots_uwRAD23565*	1	
UW	*Ots_uwRAD23604*	1	
UW	*Ots_uwRAD23793*	1	
UW	*Ots_uwRAD24458*	2	Linked with other another locus
UW	*Ots_uwRAD25055*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD25055*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD25234*	1	
UW	*Ots_uwRAD25273*	1	
UW	*Ots_uwRAD25876*	1	
UW	*Ots_uwRAD26189*	1	
UW	*Ots_uwRAD26644*	2	
UW	*Ots_uwRAD26657*	1	Invariant
UW	*Ots_uwRAD26757*	1	
UW	*Ots_uwRAD27324*	1	

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Panel	Amplicon/Locus Name	No. SNPs	Reason for removing
UW	*Ots_uwRAD28238*	4	
UW	*Ots_uwRAD28544*	1	
UW	*Ots_uwRAD2868*	2	
UW	*Ots_uwRAD29121*	1	
UW	*Ots_uwRAD29769*	1	Linked with other another locus
UW	*Ots_uwRAD30047*	1	
UW	*Ots_uwRAD30345*	1	
UW	*Ots_uwRAD30562*	2	
UW	*Ots_uwRAD30759*	1	
UW	*Ots_uwRAD31577*	1	
UW	*Ots_uwRAD31796*	1	Linked with other another locus
UW	*Ots_uwRAD32074*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD32074*	1	
UW	*Ots_uwRAD32279*	2	
UW	*Ots_uwRAD32287*	1	Invariant
UW	*Ots_uwRAD32287*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD33013*	1	
UW	*Ots_uwRAD33876*	2	
UW	*Ots_uwRAD34802*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD35239*	2	
UW	*Ots_uwRAD35949*	3	
UW	*Ots_uwRAD36202*	1	
UW	*Ots_uwRAD36916*	1	
UW	*Ots_uwRAD37035*	2	
UW	*Ots_uwRAD37275*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD37661*	1	
UW	*Ots_uwRAD37744*	2	
UW	*Ots_uwRAD38104*	2	
UW	*Ots_uwRAD3830*	2	
UW	*Ots_uwRAD38331*	1	
UW	*Ots_uwRAD38337*	1	
UW	*Ots_uwRAD3884*	1	
UW	*Ots_uwRAD392*	3	
UW	*Ots_uwRAD4000*	2	
UW	*Ots_uwRAD40086*	3	
UW	*Ots_uwRAD40163*	2	
UW	*Ots_uwRAD40477*	1	Linked with other another locus
UW	*Ots_uwRAD40588*	3	

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Panel	Amplicon/Locus Name	No. SNPs	Reason for removing
UW	*Ots_uwRAD418*	2	
UW	*Ots_uwRAD42562*	1	
UW	*Ots_uwRAD42851*	1	
UW	*Ots_uwRAD42864*	2	
UW	*Ots_uwRAD43082*	2	
UW	*Ots_uwRAD43086*	1	Invariant
UW	*Ots_uwRAD44834*	1	
UW	*Ots_uwRAD44889*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD44889*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD44889*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD44889*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD4502*	3	Invariant
UW	*Ots_uwRAD45063*	1	Linked with other another locus
UW	*Ots_uwRAD46842*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD47191*	1	
UW	*Ots_uwRAD48032*	2	
UW	*Ots_uwRAD48649*	2	
UW	*Ots_uwRAD48855*	2	
UW	*Ots_uwRAD50458*	1	
UW	*Ots_uwRAD51032*	2	Linked with other another locus
UW	*Ots_uwRAD52242*	1	
UW	*Ots_uwRAD53050*	1	Linked with other another locus
UW	*Ots_uwRAD53513*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD54614*	1	
UW	*Ots_uwRAD54653*	1	
UW	*Ots_uwRAD55425*	1	
UW	*Ots_uwRAD55538*	2	
UW	*Ots_uwRAD55571*	1	
UW	*Ots_uwRAD5667*	2	
UW	*Ots_uwRAD57006*	1	
UW	*Ots_uwRAD57654*	1	
UW	*Ots_uwRAD57669*	1	
UW	*Ots_uwRAD59572*	1	
UW	*Ots_uwRAD59667*	2	
UW	*Ots_uwRAD59888*	1	
UW	*Ots_uwRAD60124*	1	Out of Hardy-Weinberg equilibrium
UW	*Ots_uwRAD60132*	1	
UW	*Ots_uwRAD60285*	1	Allelic ratios did not conform to the expected

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Appendix B.–Page 15 of 16.

Panel	Amplicon/Locus Name	No. SNPs	Reason for removing
UW	*Ots_uwRAD60332*	1	Linked with other another locus
UW	*Ots_uwRAD61345*	1	
UW	*Ots_uwRAD62017*	1	Out of Hardy-Weinberg equilibrium
UW	*Ots_uwRAD63065*	2	
UW	*Ots_uwRAD63105*	2	
UW	*Ots_uwRAD64082*	1	
UW	*Ots_uwRAD64288*	1	
UW	*Ots_uwRAD64291*	2	
UW	*Ots_uwRAD65000*	1	
UW	*Ots_uwRAD65466*	2	Missing data for at least 1 location
UW	*Ots_uwRAD66360*	1	
UW	*Ots_uwRAD66433*	1	
UW	*Ots_uwRAD66791*	1	
UW	*Ots_uwRAD66848*	1	
UW	*Ots_uwRAD68831*	1	
UW	*Ots_uwRAD69027*	1	
UW	*Ots_uwRAD70063*	1	
UW	*Ots_uwRAD71514*	1	
UW	*Ots_uwRAD72961*	2	
UW	*Ots_uwRAD73097*	1	
UW	*Ots_uwRAD73140*	2	Linked with other another locus
UW	*Ots_uwRAD73366*	1	
UW	*Ots_uwRAD73402*	1	
UW	*Ots_uwRAD73604*	1	
UW	*Ots_uwRAD73786*	4	
UW	*Ots_uwRAD74404*	1	
UW	*Ots_uwRAD74511*	1	
UW	*Ots_uwRAD74833*	3	
UW	*Ots_uwRAD75069*	1	
UW	*Ots_uwRAD75627*	1	
UW	*Ots_uwRAD75885*	1	
UW	*Ots_uwRAD76197*	1	Out of Hardy-Weinberg equilibrium
UW	*Ots_uwRAD7776*	1	Linked with other another locus
UW	*Ots_uwRAD77831*	1	
UW	*Ots_uwRAD80431*	1	
UW	*Ots_uwRAD80510*	3	
UW	*Ots_uwRAD81084*	2	
UW	*Ots_uwRAD81543*	1	

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Panel	Amplicon/Locus Name	No. SNPs	Reason for removing
UW	*Ots_uwRAD81927*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD82047*	2	
UW	*Ots_uwRAD82247*	2	
UW	*Ots_uwRAD82889*	2	Linked with other another locus
UW	*Ots_uwRAD83004*	1	
UW	*Ots_uwRAD83732*	3	
UW	*Ots_uwRAD84318*	1	
UW	*Ots_uwRAD84598*	1	Allelic ratios did not conform to the expected
UW	*Ots_uwRAD86211*	1	
UW	*Ots_uwRAD8662*	2	
UW	*Ots_uwRAD8834*	2	Linked with other another locus
UW	*Ots_uwRAD88897*	1	
UW	*Ots_uwRAD92666*	1	
UW	*Ots_uwRAD92901*	1	
UW	*Ots_uwRAD93170*	1	Invariant
UW	*Ots_uwRAD93789*	2	
UW	*Ots_uwRAD9688*	2	
UW	*Ots_uwRAD98255*	2	
UW	*Ots_ZNF330-181*	1	Invariant
CRITFC	Total	299	
UW	Total	366	
Both	Total	665	

[a] The SNPs on these amplicons were used in the quality control analysis of newly extracted DNA.

Note: Loci with allelic ratios not conforming to the expected ratios were removed prior to the baseline analysis. Loci with more than 2 alleles are microhaplotypes produced by combining either 2 (4 alleles), 3 (8 alleles), or 4 (16 alleles) SNPs within the same amplicon.

Appendix C.–Pairwise F_{ST} (Weir and Cockerham 1984) between Chinook salmon populations sampled from spawning areas in drainages of Cook Inlet, Alaska.

Pop. No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
1	0.00																						
2	0.01	0.00																					
3	0.01	0.01	0.00																				
4	0.01	0.02	0.01	0.00																			
5	0.01	0.01	0.00	0.01	0.00																		
6	0.01	0.01	0.00	0.01	0.00	0.00																	
7	0.01	0.01	0.01	0.01	0.00	0.00	0.00																
8	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.00															
9	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00														
10	0.01	0.01	0.01	0.01	0.01	0.00	0.01	0.01	0.00	0.00													
11	0.04	0.04	0.03	0.02	0.03	0.03	0.03	0.03	0.03	0.03	0.00												
12	0.04	0.04	0.03	0.02	0.03	0.03	0.03	0.03	0.03	0.02	0.00	0.00											
13	0.03	0.04	0.03	0.02	0.03	0.03	0.03	0.02	0.02	0.02	0.00	0.00	0.00										
14	0.03	0.04	0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.00	0.00	0.00	0.00									
15	0.02	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00								
16	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.00							
17	0.01	0.02	0.01	0.01	0.01	0.00	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.01	0.01	0.01	0.00						
18	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.01	0.01	0.01	0.01	0.00					
19	0.02	0.02	0.02	0.02	0.01	0.02	0.01	0.01	0.01	0.01	0.04	0.04	0.04	0.03	0.02	0.02	0.02	0.02	0.00				
20	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.04	0.04	0.03	0.03	0.02	0.02	0.02	0.02	0.00	0.00			
21	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.04	0.04	0.04	0.03	0.02	0.02	0.02	0.02	0.00	0.00	0.00		
22	0.02	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.04	0.03	0.03	0.03	0.02	0.02	0.01	0.01	0.00	0.00	0.00	0.00	
23	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.04	0.03	0.03	0.03	0.02	0.02	0.01	0.01	0.00	0.00	0.00	0.00	0.00

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Pop. No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
24	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.03	0.03	0.03	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00
25	0.01	0.01	0.01	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.03	0.03	0.03	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00
26	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.03	0.03	0.03	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
27	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.03	0.03	0.03	0.03	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
28	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.04	0.04	0.03	0.03	0.02	0.02	0.01	0.01	0.02	0.02	0.02	0.02	0.01
29	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.02	0.01	0.01	0.04	0.04	0.03	0.03	0.02	0.02	0.01	0.01	0.02	0.02	0.02	0.02	0.01
30	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.02	0.04	0.04	0.04	0.04	0.02	0.02	0.02	0.02	0.02	0.02	0.03	0.02	0.02
31	0.02	0.02	0.01	0.02	0.01	0.01	0.01	0.02	0.01	0.01	0.04	0.05	0.04	0.04	0.02	0.02	0.02	0.02	0.03	0.02	0.03	0.02	0.02
32	0.01	0.02	0.02	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.04	0.04	0.04	0.03	0.02	0.02	0.02	0.02	0.03	0.02	0.03	0.02	0.02
33	0.02	0.03	0.02	0.01	0.02	0.02	0.02	0.02	0.01	0.01	0.02	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.02	0.02	0.03	0.02	0.02
34	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.03	0.03	0.02	0.02	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.02
35	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.02	0.01	0.01	0.03	0.03	0.03	0.02	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.02
36	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.03	0.03	0.03	0.02	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.02
37	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.02	0.01	0.01	0.04	0.04	0.04	0.03	0.02	0.02	0.01	0.01	0.02	0.02	0.03	0.02	0.02
38	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.02	0.01	0.01	0.03	0.03	0.03	0.03	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.01
39	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.04	0.04	0.04	0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.03	0.02	0.02
40	0.01	0.01	0.01	0.01	0.01	0.00	0.01	0.01	0.00	0.00	0.03	0.03	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
41	0.01	0.02	0.01	0.01	0.01	0.00	0.00	0.01	0.00	0.00	0.03	0.03	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
42	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.04	0.04	0.04	0.04	0.02	0.02	0.02	0.02	0.03	0.03	0.03	0.03	0.02
43	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.04	0.04	0.04	0.04	0.03	0.02	0.02	0.02	0.03	0.03	0.03	0.02	0.02
44	0.02	0.02	0.01	0.02	0.01	0.01	0.01	0.02	0.01	0.01	0.04	0.04	0.04	0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
45	0.02	0.02	0.01	0.02	0.01	0.01	0.01	0.02	0.01	0.01	0.04	0.04	0.04	0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.01
46	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.02	0.01	0.01	0.04	0.04	0.03	0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.01

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Pop. No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
47	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.04	0.04	0.04	0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.03	0.02	0.02
48	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.02	0.01	0.01	0.04	0.04	0.04	0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
49	0.05	0.05	0.04	0.04	0.04	0.04	0.04	0.05	0.04	0.04	0.07	0.07	0.07	0.06	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.04
50	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.06	0.06	0.06	0.06	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
51	0.04	0.04	0.03	0.04	0.03	0.03	0.04	0.04	0.03	0.03	0.06	0.06	0.06	0.05	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
52	0.06	0.06	0.05	0.06	0.05	0.05	0.06	0.06	0.05	0.05	0.08	0.08	0.08	0.07	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.05
53	0.05	0.05	0.04	0.04	0.04	0.04	0.04	0.05	0.04	0.04	0.07	0.07	0.07	0.06	0.05	0.05	0.04	0.05	0.05	0.05	0.05	0.05	0.04
54	0.04	0.05	0.04	0.05	0.04	0.04	0.04	0.04	0.04	0.04	0.07	0.07	0.07	0.06	0.05	0.05	0.04	0.05	0.05	0.05	0.05	0.04	0.04
55	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.07	0.07	0.06	0.06	0.05	0.05	0.04	0.04	0.04	0.04	0.04	0.04	0.04
56	0.08	0.08	0.08	0.08	0.08	0.08	0.08	0.08	0.08	0.07	0.10	0.10	0.10	0.09	0.08	0.08	0.08	0.08	0.08	0.08	0.08	0.08	0.08
57	0.06	0.06	0.05	0.05	0.05	0.05	0.05	0.06	0.05	0.05	0.08	0.08	0.07	0.07	0.06	0.06	0.05	0.05	0.06	0.06	0.06	0.06	0.05
58	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.07	0.07	0.07	0.07	0.05	0.05	0.05	0.05	0.05	0.05	0.06	0.05	0.05
59	0.04	0.04	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.06	0.06	0.06	0.05	0.04	0.04	0.03	0.03	0.04	0.04	0.04	0.04	0.03
60	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.07	0.07	0.07	0.06	0.05	0.05	0.04	0.04	0.04	0.05	0.05	0.04	0.04
61	0.05	0.05	0.04	0.05	0.04	0.04	0.05	0.05	0.04	0.04	0.07	0.07	0.07	0.06	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05
62	0.05	0.06	0.05	0.05	0.05	0.05	0.05	0.06	0.05	0.05	0.08	0.07	0.07	0.07	0.06	0.06	0.05	0.06	0.06	0.05	0.06	0.05	0.05
63	0.05	0.04	0.04	0.04	0.04	0.04	0.04	0.05	0.04	0.04	0.07	0.07	0.07	0.06	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.04
64	0.06	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.08	0.08	0.08	0.07	0.06	0.06	0.06	0.05	0.06	0.06	0.06	0.05	0.05
65	0.06	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.08	0.08	0.08	0.07	0.06	0.06	0.05	0.05	0.06	0.06	0.06	0.05	0.05
66	0.06	0.06	0.05	0.06	0.05	0.05	0.05	0.06	0.05	0.05	0.08	0.08	0.08	0.07	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.05
67	0.06	0.05	0.05	0.05	0.05	0.05	0.05	0.06	0.05	0.05	0.08	0.08	0.08	0.07	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.05

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Pop. No.	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
24	0.00																						
25	0.00	0.00																					
26	0.00	0.00	0.00																				
27	0.00	0.00	0.00	0.00																			
28	0.01	0.01	0.00	0.00	0.00																		
29	0.01	0.01	0.00	0.00	0.00	0.00																	
30	0.02	0.01	0.01	0.01	0.00	0.00	0.00																
31	0.02	0.01	0.02	0.02	0.02	0.02	0.03	0.00															
32	0.02	0.02	0.02	0.02	0.02	0.02	0.03	0.02	0.00														
33	0.02	0.02	0.02	0.02	0.02	0.02	0.03	0.03	0.01	0.00													
34	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.00	0.01	0.00												
35	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.01	0.01	0.00	0.00											
36	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.00	0.01	0.00	0.00	0.00										
37	0.01	0.01	0.01	0.02	0.02	0.02	0.03	0.02	0.02	0.02	0.02	0.01	0.01	0.00									
38	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.01	0.01	0.02	0.01	0.01	0.01	0.01	0.00								
39	0.02	0.01	0.02	0.02	0.02	0.02	0.03	0.02	0.03	0.03	0.02	0.02	0.02	0.02	0.02	0.00							
40	0.00	0.00	0.00	0.01	0.01	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.02	0.00						
41	0.01	0.00	0.00	0.01	0.01	0.01	0.02	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.00					
42	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.03	0.03	0.02	0.02	0.02	0.03	0.02	0.00	0.02	0.02	0.00				
43	0.02	0.02	0.02	0.02	0.02	0.02	0.03	0.03	0.03	0.03	0.02	0.02	0.02	0.03	0.02	0.00	0.02	0.02	0.01	0.00			
44	0.02	0.01	0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.03	0.02	0.02	0.02	0.02	0.02	0.00	0.01	0.01	0.01	0.01	0.00		
45	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.03	0.03	0.02	0.02	0.02	0.02	0.02	0.00	0.01	0.01	0.01	0.01	0.00	0.00	
46	0.01	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00

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Pop. No.	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
47	0.02	0.02	0.02	0.02	0.02	0.02	0.03	0.02	0.03	0.03	0.02	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.01
48	0.02	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.02	0.03	0.02	0.02	0.02	0.02	0.02	0.00	0.01	0.01	0.01	0.01	0.00	0.00	0.01
49	0.04	0.04	0.04	0.04	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
50	0.04	0.04	0.04	0.04	0.04	0.04	0.05	0.05	0.05	0.05	0.04	0.04	0.04	0.05	0.04	0.04	0.04	0.04	0.04	0.04	0.03	0.03	0.04
51	0.04	0.03	0.03	0.03	0.04	0.04	0.05	0.04	0.04	0.04	0.04	0.04	0.04	0.05	0.04	0.04	0.03	0.03	0.04	0.04	0.03	0.03	0.04
52	0.06	0.05	0.06	0.05	0.06	0.06	0.07	0.06	0.07	0.07	0.06	0.06	0.06	0.06	0.06	0.05	0.05	0.05	0.06	0.06	0.05	0.05	0.06
53	0.04	0.04	0.04	0.04	0.05	0.04	0.05	0.05	0.05	0.05	0.05	0.05	0.04	0.05	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
54	0.04	0.04	0.04	0.04	0.05	0.04	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.04	0.04	0.04	0.04	0.04	0.04	0.03	0.03	0.04
55	0.04	0.04	0.04	0.04	0.04	0.04	0.05	0.05	0.05	0.05	0.04	0.04	0.04	0.05	0.04	0.04	0.04	0.04	0.04	0.04	0.03	0.03	0.04
56	0.08	0.08	0.08	0.08	0.08	0.08	0.09	0.08	0.09	0.09	0.08	0.08	0.08	0.09	0.08	0.08	0.07	0.08	0.08	0.08	0.08	0.08	0.08
57	0.05	0.05	0.05	0.05	0.05	0.06	0.07	0.06	0.06	0.06	0.06	0.06	0.05	0.06	0.06	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05
58	0.05	0.05	0.05	0.05	0.05	0.05	0.06	0.05	0.06	0.06	0.05	0.05	0.05	0.06	0.05	0.05	0.05	0.05	0.04	0.05	0.04	0.04	0.04
59	0.03	0.03	0.03	0.03	0.03	0.03	0.04	0.04	0.04	0.04	0.04	0.04	0.03	0.04	0.03	0.03	0.03	0.03	0.03	0.03	0.02	0.02	0.03
60	0.04	0.04	0.04	0.04	0.04	0.04	0.05	0.05	0.05	0.05	0.05	0.05	0.04	0.05	0.04	0.04	0.04	0.04	0.04	0.04	0.03	0.03	0.04
61	0.05	0.04	0.04	0.04	0.05	0.05	0.06	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.04	0.04	0.04	0.04	0.05	0.04	0.04	0.04
62	0.05	0.05	0.05	0.05	0.05	0.05	0.06	0.06	0.06	0.06	0.06	0.06	0.05	0.06	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05
63	0.04	0.04	0.04	0.04	0.04	0.04	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.04	0.04	0.04	0.04	0.04	0.03	0.03	0.04
64	0.05	0.05	0.05	0.05	0.05	0.05	0.06	0.06	0.06	0.06	0.06	0.06	0.05	0.06	0.05	0.05	0.05	0.05	0.05	0.05	0.04	0.04	0.05
65	0.05	0.05	0.05	0.05	0.05	0.05	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.05	0.05	0.05	0.05	0.05	0.05	0.04	0.04	0.05
66	0.06	0.05	0.05	0.05	0.05	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05
67	0.05	0.05	0.05	0.05	0.05	0.05	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.04	0.05

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Pop. No.	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67
47	0.00																				
48	0.01	0.00																			
49	0.04	0.04	0.00																		
50	0.04	0.03	0.02	0.00																	
51	0.04	0.03	0.02	0.00	0.00																
52	0.06	0.05	0.03	0.04	0.04	0.00															
53	0.04	0.04	0.05	0.04	0.04	0.06	0.00														
54	0.04	0.03	0.04	0.04	0.04	0.05	0.01	0.00													
55	0.04	0.03	0.01	0.02	0.02	0.03	0.03	0.03	0.00												
56	0.08	0.07	0.04	0.05	0.06	0.06	0.08	0.07	0.05	0.00											
57	0.05	0.05	0.05	0.05	0.05	0.07	0.06	0.06	0.05	0.09	0.00										
58	0.04	0.04	0.05	0.05	0.04	0.07	0.06	0.06	0.05	0.09	0.00	0.00									
59	0.03	0.02	0.04	0.03	0.03	0.05	0.05	0.04	0.03	0.07	0.02	0.01	0.00								
60	0.03	0.03	0.04	0.04	0.04	0.06	0.05	0.05	0.04	0.08	0.04	0.03	0.01	0.00							
61	0.05	0.04	0.03	0.01	0.01	0.05	0.05	0.04	0.03	0.07	0.05	0.05	0.03	0.04	0.00						
62	0.05	0.05	0.04	0.02	0.02	0.06	0.05	0.05	0.04	0.07	0.06	0.05	0.04	0.05	0.00	0.00					
63	0.04	0.04	0.05	0.04	0.04	0.06	0.05	0.05	0.04	0.08	0.04	0.04	0.01	0.01	0.04	0.05	0.00				
64	0.05	0.05	0.05	0.04	0.04	0.06	0.06	0.06	0.05	0.09	0.06	0.05	0.02	0.02	0.05	0.06	0.01	0.00			
65	0.05	0.04	0.05	0.05	0.05	0.07	0.06	0.06	0.05	0.09	0.06	0.05	0.02	0.02	0.05	0.06	0.01	0.00	0.00		
66	0.05	0.05	0.05	0.05	0.05	0.07	0.06	0.06	0.05	0.09	0.07	0.06	0.03	0.02	0.05	0.06	0.01	0.00	0.00	0.00	
67	0.05	0.05	0.05	0.05	0.05	0.07	0.06	0.06	0.05	0.08	0.06	0.06	0.03	0.02	0.05	0.06	0.01	0.00	0.00	0.00	0.00

Note: Population numbers correspond to population numbers on Table 2 and Figures 1 and 2.

Appendix D.–Estimates of stock composition (%) for 10 replicates of mixtures for each of 10 reporting groups using the University of Washington and Columbia River Inter-Tribal Fish Commission locus panels (413 loci). Each replicate was a sample of 150 individuals from a single reporting group removed from the genetic baseline. Estimates for each replicate describe the posterior distributions by the mean, 90% credibility interval (CI), and standard deviation (SD).

		90% CI				90% CI		
Reporting Group	Mean	5%	95%	SD	Mean	5%	95%	SD
	West Replicate 1				*West* Replicate 2			
West	82.3	74.3	89.6	4.7	89.6	81.9	97.0	4.6
Susitna	5.3	1.2	10.0	2.8	3.0	0.0	7.5	2.5
Deshka	2.8	0.0	6.6	2.1	2.1	0.0	6.2	2.3
Yentna	9.7	4.3	15.5	3.5	5.3	0.2	11.0	3.4
Knik-Turnagain	0.0	0.0	2.9	1.3	0.0	0.0	0.9	0.5
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.2	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	West Replicate 3				*West* Replicate 4			
West	90.7	83.4	97.4	4.2	93.4	86.6	99.9	4.1
Susitna	0.2	0.0	4.2	2.2	0.4	0.0	4.4	2.1
Deshka	1.0	0.0	4.3	1.8	1.8	0.0	5.3	2.0
Yentna	5.9	1.8	10.9	2.8	4.4	0.0	9.9	3.1
Knik-Turnagain	2.1	0.0	7.2	2.7	0.0	0.0	1.5	0.7
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.2	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	West Replicate 5				*West* Replicate 6			
West	95.3	89.0	100.0	3.6	95.4	88.4	100.0	3.9
Susitna	1.5	0.0	5.8	2.4	0.0	0.0	4.2	2.1
Deshka	0.0	0.0	2.0	1.0	1.3	0.0	5.0	2.0
Yentna	0.0	0.0	3.0	1.4	0.0	0.0	5.1	2.2
Knik-Turnagain	3.1	0.0	7.3	2.3	3.3	0.4	6.9	2.0
Kenai Tributary	0.1	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.4	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	West Replicate 7				*West* Replicate 8			
West	99.3	91.8	100.0	4.2	96.6	90.4	100.0	3.7
Susitna	0.0	0.0	0.7	0.5	0.0	0.0	2.0	1.0
Deshka	0.3	0.0	4.1	2.1	0.1	0.0	3.3	1.7
Yentna	0.0	0.0	6.0	3.5	3.3	0.0	8.5	3.1
Knik-Turnagain	0.4	0.0	4.0	1.9	0.0	0.0	2.0	0.9
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.4	0.3	0.0	0.0	0.3	0.2
	West Replicate 9				*West* Replicate 10			
West	99.9	96.5	100.0	1.7	98.1	91.2	100.0	3.7
Susitna	0.0	0.0	2.7	1.2	0.0	0.0	4.3	2.2
Deshka	0.0	0.0	0.9	0.5	0.0	0.0	2.6	1.4
Yentna	0.0	0.0	1.6	0.8	0.0	0.0	4.7	2.1
Knik-Turnagain	0.0	0.0	1.0	0.5	1.9	0.0	6.2	2.2
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.4	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Susitna Replicate 1				*Susitna* Replicate 2			
West	0.0	0.0	0.5	0.4	0.0	0.0	3.2	1.4
Susitna	99.8	97.9	100.0	1.0	99.6	96.4	100.0	1.7
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.2	0.2
Yentna	0.1	0.0	1.4	0.6	0.3	0.0	2.1	0.9
Knik-Turnagain	0.0	0.0	0.8	0.5	0.0	0.0	1.1	0.6
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.2	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.3	0.0	0.0	0.2	0.2

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	Susitna Replicate 3				*Susitna* Replicate 4			
West	0.7	0.0	3.3	1.2	3.1	0.7	6.2	1.8
Susitna	99.2	96.2	100.0	1.5	96.6	93.0	99.6	2.0
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.2	0.0	3.0	1.3
Knik-Turnagain	0.0	0.0	1.6	0.8	0.0	0.0	0.8	0.4
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Susitna Replicate 5				*Susitna* Replicate 6			
West	0.0	0.0	3.0	1.4	0.0	0.0	1.3	0.7
Susitna	99.9	96.5	100.0	1.7	100.0	98.1	100.0	1.0
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.3	0.0	0.0	0.5	0.2
Knik-Turnagain	0.0	0.0	1.6	0.9	0.0	0.0	0.6	0.4
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Susitna Replicate 7				*Susitna* Replicate 8			
West	0.0	0.0	0.6	0.4	0.0	0.0	0.5	0.3
Susitna	95.1	89.8	99.1	2.9	99.8	97.5	100.0	1.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	1.5	0.0	4.3	1.5	0.1	0.0	1.6	0.8
Knik-Turnagain	3.4	0.0	8.6	2.8	0.0	0.0	1.4	0.7
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	Susitna Replicate 9				*Susitna* Replicate 10			
West	0.1	0.0	2.4	1.2	0.0	0.0	3.0	1.4
Susitna	96.8	92.5	100.0	2.4	97.2	93.3	100.0	2.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	1.3	0.6	0.0	0.0	1.2	0.6
Knik-Turnagain	3.1	0.4	7.5	2.3	2.8	0.3	6.2	1.8
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.3
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Deshka Replicate 1				*Deshka* Replicate 2			
West	0.0	0.0	0.4	0.3	1.9	0.0	4.7	1.5
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	99.8	98.2	100.0	0.8	98.1	95.2	100.0	1.6
Yentna	0.0	0.0	0.4	0.2	0.0	0.0	0.4	0.3
Knik-Turnagain	0.2	0.0	1.2	0.5	0.0	0.0	0.6	0.3
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.2	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Deshka Replicate 3				*Deshka* Replicate 4			
West	0.0	0.0	0.8	0.4	0.0	0.0	1.9	0.9
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.4	0.3
Deshka	100.0	98.4	100.0	0.8	99.9	97.7	100.0	1.1
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.4	0.3
Knik-Turnagain	0.0	0.0	0.5	0.3	0.0	0.0	0.7	0.3
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	Deshka Replicate 5				*Deshka* Replicate 6			
West	2.4	0.5	5.3	1.6	2.3	0.0	5.8	1.9
Susitna	0.0	0.0	0.4	0.2	0.0	0.0	0.3	0.2
Deshka	97.5	94.3	99.7	1.7	97.6	93.9	100.0	2.0
Yentna	0.0	0.0	0.3	0.3	0.0	0.0	0.4	0.3
Knik-Turnagain	0.0	0.0	0.9	0.5	0.0	0.0	0.6	0.3
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Deshka Replicate 7				*Deshka* Replicate 8			
West	0.0	0.0	2.2	1.2	0.0	0.0	0.8	0.4
Susitna	0.0	0.0	0.4	0.2	0.0	0.0	0.3	0.2
Deshka	99.9	97.5	100.0	1.3	99.9	98.5	100.0	0.7
Yentna	0.0	0.0	1.1	0.5	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.5	0.4	0.0	0.0	0.6	0.3
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.3
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.2	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Deshka Replicate 9				*Deshka* Replicate 10			
West	2.4	0.0	6.2	2.1	0.0	0.0	1.9	0.9
Susitna	0.0	0.0	0.4	0.3	0.0	0.0	0.3	0.2
Deshka	97.6	93.8	100.0	2.1	99.9	97.8	100.0	1.1
Yentna	0.0	0.0	0.5	0.3	0.0	0.0	0.6	0.4
Knik-Turnagain	0.0	0.0	0.7	0.4	0.0	0.0	0.7	0.4
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.2	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.4	0.2	0.0	0.0	0.3	0.2

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	Yentna Replicate 1				*Yentna* Replicate 2			
West	0.0	0.0	5.9	3.4	5.2	0.0	11.7	3.8
Susitna	1.7	0.0	6.5	2.6	0.0	0.0	1.4	0.8
Deshka	0.0	0.0	0.4	0.3	0.0	0.0	0.3	0.2
Yentna	98.3	91.8	100.0	3.7	94.8	87.9	100.0	3.9
Knik-Turnagain	0.0	0.0	3.2	1.5	0.0	0.0	0.9	0.5
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Yentna Replicate 3				*Yentna* Replicate 4			
West	0.0	0.0	5.7	3.3	3.6	0.0	11.1	4.4
Susitna	0.0	0.0	3.6	1.8	0.8	0.0	4.2	1.8
Deshka	0.3	0.0	1.5	0.6	0.0	0.0	0.3	0.2
Yentna	99.7	94.0	100.0	3.4	95.1	87.5	100.0	4.4
Knik-Turnagain	0.0	0.0	0.6	0.4	0.4	0.0	2.8	1.2
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Yentna Replicate 5				*Yentna* Replicate 6			
West	0.0	0.0	4.9	2.8	1.0	0.0	7.7	4.0
Susitna	1.3	0.0	4.6	1.8	0.0	0.0	2.5	1.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.6	0.3
Yentna	98.7	92.8	100.0	3.2	98.9	92.3	100.0	4.0
Knik-Turnagain	0.0	0.0	0.7	0.4	0.0	0.0	1.6	0.8
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.3	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.2	0.2	0.0	0.0	0.4	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.3	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	Yentna Replicate 7				*Yentna* Replicate 8			
West	9.1	2.4	16.4	4.3	11.9	5.4	19.0	4.1
Susitna	0.0	0.0	3.2	1.6	0.0	0.0	3.5	1.8
Deshka	0.0	0.0	1.3	0.6	0.0	0.0	0.3	0.2
Yentna	90.8	83.5	97.5	4.3	88.1	80.9	94.5	4.2
Knik-Turnagain	0.0	0.0	2.3	1.1	0.0	0.0	0.6	0.3
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.4	0.2
South Kenai Pen.	0.0	0.0	0.2	0.2	0.0	0.0	0.3	0.2
	Yentna Replicate 9				*Yentna* Replicate 10			
West	0.0	0.0	5.7	3.3	4.0	0.0	10.1	3.5
Susitna	4.5	0.5	9.2	2.7	11.8	6.5	17.6	3.4
Deshka	0.2	0.0	1.5	0.6	0.0	0.0	0.4	0.3
Yentna	95.3	88.8	100.0	3.7	84.1	76.6	91.2	4.4
Knik-Turnagain	0.0	0.0	1.9	0.9	0.0	0.0	0.7	0.4
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.4	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.2	0.2
	Knik-Turnagain Replicate 1				*Knik-Turnagain* Replicate 2			
West	0.0	0.0	2.6	1.2	1.0	0.0	4.2	1.6
Susitna	0.8	0.0	5.4	2.7	11.1	5.8	17.1	3.5
Deshka	0.3	0.0	1.7	0.7	0.0	0.0	1.1	0.5
Yentna	0.6	0.0	2.3	0.8	0.0	0.0	0.4	0.3
Knik-Turnagain	97.9	92.9	100.0	2.9	87.9	81.7	93.2	3.5
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.4	0.0	1.9	0.7	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.8	0.4	0.0	0.0	0.2	0.2

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	Knik-Turnagain Replicate 3				*Knik-Turnagain* Replicate 4			
West	0.0	0.0	1.2	0.6	0.0	0.0	1.6	0.8
Susitna	11.0	5.7	16.7	3.4	0.3	0.0	4.2	2.2
Deshka	0.2	0.0	1.7	0.7	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.9	0.4
Knik-Turnagain	88.8	82.9	94.2	3.4	99.7	95.5	100.0	2.3
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Knik-Turnagain Replicate 5				*Knik-Turnagain* Replicate 6			
West	0.0	0.0	0.4	0.2	0.0	0.0	0.8	0.5
Susitna	0.6	0.0	4.2	2.0	0.0	0.0	0.7	0.5
Deshka	0.0	0.0	0.2	0.2	0.4	0.0	1.8	0.7
Yentna	0.0	0.0	0.4	0.3	0.9	0.1	2.4	0.7
Knik-Turnagain	99.4	95.7	100.0	2.0	97.5	94.5	99.5	1.5
Kenai Tributary	0.0	0.0	0.3	0.2	0.5	0.0	1.8	0.7
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.4	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.7	0.0	2.4	0.9
Kasilof Mainstem	0.0	0.0	0.4	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.6	0.3
	Knik-Turnagain Replicate 7				*Knik-Turnagain* Replicate 8			
West	0.0	0.0	1.0	0.5	0.5	0.0	3.0	1.3
Susitna	5.1	1.2	10.0	2.7	0.0	0.0	4.8	2.5
Deshka	0.2	0.0	1.8	0.8	0.0	0.0	0.6	0.3
Yentna	0.0	0.0	0.3	0.2	0.2	0.0	1.6	0.6
Knik-Turnagain	93.9	88.6	98.3	2.9	99.2	94.2	100.0	2.7
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.6	0.0	1.9	0.7	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.1	0.0	0.7	0.3	0.0	0.0	0.3	0.2

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	Knik-Turnagain Replicate 9				*Knik-Turnagain* Replicate 10			
West	4.1	1.2	8.0	2.1	0.0	0.0	2.5	1.3
Susitna	2.8	0.0	8.0	3.0	0.0	0.0	0.5	0.4
Deshka	0.0	0.0	1.0	0.5	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.3	0.0	1.7	0.7
Knik-Turnagain	93.0	87.2	98.2	3.5	99.7	96.8	100.0	1.6
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.4	0.2
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.5	0.3
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Kenai Tributary Replicate 1				*Kenai Tributary* Replicate 2			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.2	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.5	0.3	0.0	0.0	0.5	0.3
Kenai Tributary	96.8	92.7	100.0	2.3	100.0	97.3	100.0	1.4
Kenai Mainstem	1.2	0.0	3.5	1.2	0.0	0.0	1.5	0.7
Kasilof Tributary	1.9	0.0	5.5	1.9	0.0	0.0	2.1	1.2
Kasilof Mainstem	0.0	0.0	0.4	0.3	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Kenai Tributary Replicate 3				*Kenai Tributary* Replicate 4			
West	0.0	0.0	0.2	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.6	0.3	0.1	0.0	0.9	0.4
Kenai Tributary	98.7	95.1	100.0	2.0	98.4	95.2	100.0	1.7
Kenai Mainstem	0.0	0.0	0.4	0.3	0.0	0.0	0.8	0.4
Kasilof Tributary	1.2	0.0	4.7	1.9	1.5	0.0	4.3	1.5
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	Kenai Tributary Replicate 5				*Kenai Tributary* Replicate 6			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.2	0.2
Knik-Turnagain	0.0	0.0	0.7	0.3	0.0	0.0	0.6	0.3
Kenai Tributary	96.9	92.9	100.0	2.3	99.9	96.9	100.0	1.7
Kenai Mainstem	1.9	0.1	4.5	1.4	0.0	0.0	0.4	0.3
Kasilof Tributary	1.2	0.0	4.4	1.7	0.1	0.0	3.0	1.6
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Kenai Tributary Replicate 7				*Kenai Tributary* Replicate 8			
West	0.0	0.0	0.2	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.2	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.4	0.3	0.0	0.0	0.5	0.3
Kenai Tributary	98.5	95.0	100.0	1.9	99.9	96.8	100.0	1.8
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	1.5	0.0	4.8	1.8	0.0	0.0	3.1	1.7
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Kenai Tributary Replicate 9				*Kenai Tributary* Replicate 10			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.6	0.3	0.0	0.0	0.5	0.3
Kenai Tributary	92.3	87.5	96.2	2.6	96.3	92.1	100.0	2.4
Kenai Mainstem	1.1	0.0	3.5	1.3	0.4	0.0	2.2	1.0
Kasilof Tributary	6.6	3.2	10.7	2.3	3.3	0.2	7.0	2.1
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	Kenai Mainstem Replicate 1				*Kenai Mainstem* Replicate 2			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.4	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.5	0.3	0.0	0.0	0.6	0.3
Kenai Tributary	0.9	0.0	4.0	1.7	0.0	0.0	1.7	0.9
Kenai Mainstem	99.1	95.7	100.0	1.9	99.9	97.9	100.0	1.1
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.4	0.3	0.0	0.0	0.4	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Kenai Mainstem Replicate 3				*Kenai Mainstem* Replicate 4			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.6	0.3	0.0	0.0	0.5	0.3
Kenai Tributary	1.0	0.0	3.2	1.2	0.0	0.0	0.7	0.4
Kenai Mainstem	98.7	96.1	100.0	1.5	99.9	98.5	100.0	0.7
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.3	0.0	1.3	0.5	0.0	0.0	0.4	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Kenai Mainstem Replicate 5				*Kenai Mainstem* Replicate 6			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.2	0.2
Deshka	0.0	0.0	0.2	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.2	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.5	0.3	0.0	0.0	0.5	0.3
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	2.9	1.6
Kenai Mainstem	100.0	98.7	100.0	0.6	100.0	97.0	100.0	1.7
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.2	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	Kenai Mainstem Replicate 7				*Kenai Mainstem* Replicate 8			
West	0.0	0.0	0.4	0.2	0.0	0.0	0.4	0.2
Susitna	0.0	0.0	0.2	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.4	0.2
Knik-Turnagain	0.0	0.0	0.5	0.3	0.0	0.0	0.5	0.3
Kenai Tributary	0.0	0.0	1.3	0.7	0.0	0.0	1.7	0.9
Kenai Mainstem	99.8	97.8	100.0	1.0	99.9	97.9	100.0	1.1
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.2	0.0	1.1	0.5	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Kenai Mainstem Replicate 9				*Kenai Mainstem* Replicate 10			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.5	0.3	0.0	0.0	0.5	0.3
Kenai Tributary	0.0	0.0	3.4	1.7	0.0	0.0	0.5	0.3
Kenai Mainstem	99.9	96.3	100.0	1.8	99.9	98.5	100.0	0.7
Kasilof Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Mainstem	0.0	0.0	0.4	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Kasilof Tributary Replicate 1				*Kasilof Tributary* Replicate 2			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.4	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.5	0.3	0.0	0.0	0.5	0.3
Kenai Tributary	0.0	0.0	0.6	0.4	0.4	0.0	2.8	1.2
Kenai Mainstem	0.0	0.0	0.4	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	99.9	96.7	100.0	1.7	99.6	95.6	100.0	2.3
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	3.1	1.6	0.0	0.0	3.2	1.8

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	Kasilof Tributary Replicate 3				*Kasilof Tributary* Replicate 4			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.5	0.3	0.0	0.0	0.5	0.3
Kenai Tributary	0.3	0.0	2.5	1.1	0.0	0.0	0.4	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	99.7	96.7	100.0	1.5	97.5	93.4	100.0	2.3
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	0.0	0.0	2.0	0.9	2.5	0.0	6.6	2.3
	Kasilof Tributary Replicate 5				*Kasilof Tributary* Replicate 6			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.5	0.3	0.0	0.0	0.6	0.3
Kenai Tributary	0.1	0.0	2.1	1.0	0.0	0.0	0.4	0.3
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.4	0.2
Kasilof Tributary	99.9	95.4	100.0	2.5	99.9	95.5	100.0	2.5
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.4	0.3
South Kenai Pen.	0.0	0.0	4.1	2.2	0.0	0.0	4.2	2.4
	Kasilof Tributary Replicate 7				*Kasilof Tributary* Replicate 8			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.6	0.3	0.0	0.0	0.6	0.3
Kenai Tributary	0.0	0.0	0.8	0.5	0.0	0.0	0.4	0.3
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	97.9	93.4	100.0	2.5	100.0	95.9	100.0	2.1
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.2	0.2
South Kenai Pen.	2.0	0.0	6.3	2.4	0.0	0.0	3.9	2.0

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	Kasilof Tributary Replicate 9				*Kasilof Tributary* Replicate 10			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.2	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.5	0.3	0.0	0.0	0.5	0.3
Kenai Tributary	0.6	0.0	2.5	1.0	0.0	0.0	1.7	0.8
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	95.2	90.2	99.7	2.9	99.9	95.6	100.0	2.4
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	4.1	0.1	8.9	2.7	0.0	0.0	3.9	2.1
	Kasilof Mainstem Replicate 1				*Kasilof Mainstem* Replicate 2			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.4	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.5	0.3	0.0	0.0	0.5	0.3
Kenai Tributary	0.0	0.0	0.3	0.2	0.1	0.0	0.8	0.4
Kenai Mainstem	3.6	0.4	7.5	2.2	2.7	0.0	6.4	2.1
Kasilof Tributary	1.9	0.1	4.4	1.3	3.0	0.8	5.9	1.6
Kasilof Mainstem	94.5	89.9	98.2	2.5	94.2	89.7	98.1	2.6
South Kenai Pen.	0.0	0.0	0.2	0.2	0.0	0.0	0.3	0.2
	Kasilof Mainstem Replicate 3				*Kasilof Mainstem* Replicate 4			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.4	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.2	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.5	0.3	0.0	0.0	0.5	0.3
Kenai Tributary	0.0	0.0	0.2	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	2.6	0.0	5.8	1.8	6.1	2.5	10.3	2.4
Kasilof Tributary	1.8	0.0	4.2	1.3	1.7	0.0	4.3	1.4
Kasilof Mainstem	95.6	91.6	99.2	2.3	92.1	87.4	96.4	2.7
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	Kasilof Mainstem Replicate 5				*Kasilof Mainstem* Replicate 6			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.1	0.0	0.6	0.3	0.0	0.0	0.6	0.3
Kenai Tributary	0.1	0.0	0.9	0.4	0.2	0.0	1.0	0.4
Kenai Mainstem	0.0	0.0	0.7	0.4	0.0	0.0	3.2	1.7
Kasilof Tributary	2.2	0.2	5.0	1.5	0.9	0.0	3.3	1.3
Kasilof Mainstem	97.6	94.7	99.9	1.6	98.9	95.0	100.0	2.2
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Kasilof Mainstem Replicate 7				*Kasilof Mainstem* Replicate 8			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.2	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.4	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.5	0.3	0.0	0.0	0.6	0.3
Kenai Tributary	0.1	0.0	0.7	0.4	0.1	0.0	0.6	0.3
Kenai Mainstem	2.5	0.0	5.9	1.9	0.0	0.0	1.0	0.5
Kasilof Tributary	2.6	0.6	5.2	1.4	2.4	0.4	5.1	1.5
Kasilof Mainstem	94.7	90.5	98.2	2.4	97.4	94.4	99.7	1.6
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Kasilof Mainstem Replicate 9				*Kasilof Mainstem* Replicate 10			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.4	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.5	0.3	0.0	0.0	0.5	0.3
Kenai Tributary	0.1	0.0	0.9	0.4	0.2	0.0	1.0	0.4
Kenai Mainstem	3.1	0.2	6.6	2.0	2.4	0.0	6.0	1.9
Kasilof Tributary	1.8	0.0	4.3	1.3	1.5	0.0	4.0	1.3
Kasilof Mainstem	95.0	90.5	98.5	2.4	95.9	91.4	99.4	2.4
South Kenai Pen.	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	South Kenai Pen. Replicate 1				*South Kenai Pen.* Replicate 2			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.2	0.0	1.2	0.5	0.1	0.0	0.9	0.4
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.1	0.0	0.7	0.3	0.1	0.0	0.8	0.3
Kenai Tributary	0.6	0.0	1.8	0.6	0.6	0.1	1.9	0.6
Kenai Mainstem	0.0	0.0	0.2	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	1.6	0.0	6.2	2.5	0.0	0.0	4.3	2.3
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.4	0.2
South Kenai Pen.	97.6	92.7	100.0	2.7	99.1	94.8	100.0	2.4
	South Kenai Pen. Replicate 3				*South Kenai Pen.* Replicate 4			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.2	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.5	0.3	0.0	0.0	0.5	0.3
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.0	0.0	2.9	1.4	0.0	0.0	3.3	1.7
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	100.0	97.0	100.0	1.5	100.0	96.5	100.0	1.8
	South Kenai Pen. Replicate 5				*South Kenai Pen.* Replicate 6			
West	0.0	0.0	0.2	0.2	0.0	0.0	0.3	0.2
Susitna	0.1	0.0	1.0	0.4	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.2	0.2
Yentna	0.0	0.0	0.4	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.7	0.4	0.0	0.0	0.6	0.3
Kenai Tributary	0.7	0.2	2.1	0.7	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.7	0.0	4.8	2.4	0.0	0.0	1.6	0.8
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	98.4	94.1	100.0	2.5	100.0	98.1	100.0	0.9

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	South Kenai Pen. Replicate 7				*South Kenai Pen.* Replicate 8			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.2	0.0	1.1	0.4	0.1	0.0	1.1	0.5
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.1	0.0	0.7	0.4	0.0	0.0	0.7	0.4
Kenai Tributary	0.6	0.1	1.9	0.6	0.5	0.0	1.8	0.6
Kenai Mainstem	0.0	0.0	0.4	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.1	0.0	3.7	1.9	3.3	0.0	7.8	2.5
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	99.0	95.1	100.0	2.1	96.1	91.5	99.9	2.6
	South Kenai Pen. Replicate 9				*South Kenai Pen.* Replicate 10			
West	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Susitna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Knik-Turnagain	0.0	0.0	0.5	0.3	0.0	0.0	0.5	0.3
Kenai Tributary	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kenai Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof Tributary	0.7	0.0	4.9	2.4	0.0	0.0	2.9	1.3
Kasilof Mainstem	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
South Kenai Pen.	99.3	94.9	100.0	2.5	100.0	97.0	100.0	1.4