Genetic Baseline for Cook Inlet Coho Salmon and Evaluations for Mixed Stock Analysis

by

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and

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Symbols and Abbreviations

The following symbols and abbreviations, and others approved for the Système International d'Unités (SI), are used without definition in the following reports by the Divisions of Sport Fish and of Commercial Fisheries: Fishery Manuscripts, Fishery Data Series Reports, Fishery Management Reports, and Special Publications. All others, including deviations from definitions listed below, are noted in the text at first mention, as well as in the titles or footnotes of tables, and in figure or figure captions.

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

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GENETIC BASELINE FOR COOK INLET COHO SALMON AND EVALUATIONS FOR MIXED STOCK ANALYSIS

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ABSTRACT

This report describes the updated genetic baseline for Cook Inlet coho salmon and includes new evaluations for mixed stock analysis (MSA) in Cook Inlet. Coho salmon are harvested in commercial fisheries in Upper Cook Inlet, Alaska, with an average annual harvest of 180,005 fish (2008–2017). Harvests often occur in areas where stocks intermingle, so the exploitation and productivity of individual stocks are not well known. This lack of knowledge hinders fishery management based on the sustained yield principle. Genetic analysis, using single nucleotide polymorphism (SNP) technology, can discriminate among discrete fish stocks in fishery samples when adequate stock structure exists. Here, we update a previously reported baseline of 84 populations using 86 SNP markers with an additional 10 populations and a set of 82 SNP markers included in the previous baseline to determine population structure and test potential reporting groups for MSA. Testing of potential reporting groups revealed 11 groups with adequate genetic divergence to meet the criteria for reporting groups. The data presented in this report will allow for additional baseline evaluation tests tailored for specific MSA study objectives pertinent to Cook Inlet mixed stock fisheries in the future.

Key words: coho salmon, Cook Inlet, *Oncorhynchus kisutch*, single nucleotide polymorphism, SNP, mixed stock analysis, MSA, baseline

INTRODUCTION

BACKGROUND

Populations of coho salmon *Oncorhynchus kisutch* support important fisheries in the Upper Cook Inlet management area (UCI; Figure 1). Annual total harvest of coho salmon in the UCI commercial fishery averaged 180,005 fish between 2008 and 2017 (Shields and Frothingham 2018). Most harvests occur during homeward migration in the open ocean or in the lower reaches of river drainages—areas where stocks are mixed. Without stock-specific harvest and escapement information, the exploitation and productivity of any single stock cannot be estimated, limiting management for sustained yield by the Alaska Department of Fish and Game (ADF&G) under the Policy for the Management of Sustainable Salmon Fisheries (5 AAC 39.222).

Mixed stock analysis using genetic markers (MSA) has been widely applied in the Pacific Northwest to apportion coho salmon sampled from mixtures of fish harvested during the migratory portion of their life cycle to regional stock groupings. This method requires the genetic characterization of populations contributing to the mixture (baseline) as well as the fishery samples (Pella and Milner 1987). MSA has been used to estimate the migration patterns of juvenile coho salmon in marine waters off the coasts of Washington and Oregon (e.g., Teel et al. 2003; Van Doornik et al. 2007), and to estimate the stock contributions to fishery catches in the coastal waters of British Columbia and the Fraser River (e.g., Small et al. 1998; Beacham et al. 2012). In Alaska, MSA has been used for inriver applications to estimate the stock composition of test fishery catches in the Kuskokwim (Crane et al. 2007) and Yukon (Flannery and Loges 2016) rivers and in marine waters to estimate the compositions of the offshore test fishery catches and commercial fishery harvests in Cook Inlet (Barclay et al. 2017a).

The genetic diversity of coho salmon has been described for both fine- and broadscale geographic areas (e.g., Small et al. 1998; Olsen et al. 2003; Ford et al. 2004; Bucklin et al. 2007; Johnson and Banks 2008; Beacham et al. 2011, Barclay et al. 2017b). Olsen et al. (2003) was the first to evaluate the genetic diversity patterns in coho salmon in Alaska, including 6 Kenai River and 2 west Cook Inlet populations. This dataset demonstrated significant genetic diversity among coho salmon populations, but weak regional structuring of populations statewide. Olsen et al. (2003) concluded that the diversifying influence of genetic drift was stronger than the homogenizing influence of gene flow in coho salmon in Alaska. These results suggested the possibility of distinguishing among coho salmon stocks within Cook Inlet, but given the lack of overall regional structure,

relatively intensive baseline sampling would be required to represent the full genetic diversity of coho salmon within Cook Inlet.

The most comprehensive analysis of Cook Inlet coho salmon population structure was reported in Barclay et al. (2017b). They examined 84 populations for 86 single nucleotide polymorphism (SNP) markers and tested for potential MSA reporting groups (stocks) for analyzing test fishery catches and commercial fishery in Cook Inlet. The baseline was augmented with genetic samples from fish captured in fish wheels, radiotagged, and successfully tracked to specific spawning sites, where access to ground sampling was limited. Population structure indicated that populations generally cluster by drainage, with the most genetically distinct populations in the more southerly drainages and in the upper reaches of the larger drainages. Testing of potential reporting groups revealed 7 groups with adequate genetic divergence to meet the criteria for reporting groups: 1) *Southwest CI*; 2) *Northwest CI/Yentna*; 3) *Susitna*; 4) *Knik*; 5) *Turnagain/Northeast CI*; 6) *Kenai/Kasilof*; and 7) *Southeast CI*. Barclay et al. (2017b) concluded that, due to the sparse representation of collections in the baseline for the Yentna River drainage, additional representation within this drainage would be prudent before using it as its own reporting group in MSA. This baseline was used to analyze the Cook Inlet offshore test fish catches and commercial fishery harvests from 2013 to 2016 (Barclay et al. 2017a).

In the fall of 2015, the Matanuska-Susitna Borough funded a new baseline study (this study) to increase the representation of fine-scale stocks of management interest. The study identified 3 gaps in the Barclay et al. (2017b) baseline that needed to be filled before MSA could be conducted within the Susitna River Drainage or with finer-scale reporting groups within Upper Cook Inlet. These gaps were: 1) inadequate representation of Yentna River tributaries (e.g., Upper Yentna River tributaries, Lake Creek, Kahiltna River, and Yentna River mainstem tributaries); 2) inadequate representation of Knik River above Jim Creek; and 3) inadequate representation of tributaries with weirs (Deshka River and Jim Creek).

Here we report an update to the Barclay et al. (2017b) baseline with additional samples collected from the Yentna River, Deshka River, Knik River, and Jim Creek in 2016 and 2017 and test the baseline for finer-scale reporting groups for MSA in Upper Cook Inlet. Sufficient ground samples were available for all baseline populations; therefore, radiotagged fish were not included in this report.

DEFINITIONS

Definitions of commonly used genetic terms are provided here to better understand the methods, results, and interpretation of this study.

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

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.

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.

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 set of alleles for 1 or more loci for a fish.

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 fixed position or region on a chromosome.

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.

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. Reporting groups are synonymous with *stock* in mixed stock analysis applications.

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)).

METHODS

TISSUE SAMPLING

Baseline

Tissue samples suitable for genetic analyses (genetic samples) were collected and preserved in 95% ethanol (axillary process or fin; Table 1). Tissues were either placed into individual 2 ml vials or collectively into 125–500 ml containers, with 1 or more containers for each collection site in each year. Collection information including location name, latitude, longitude, and collection year were recorded for each sample.

Most baseline genetic samples were collected from spawning aggregates of coho salmon by ADF&G and U.S. Fish and Wildlife Service (USFWS) personnel using fish wheels, weirs, gillnets, beach seines, or hook-and-line gear. A few baseline genetic samples were collected opportunistically by other agencies and organizations, including LGL Alaska Research Associates Inc., Cook Inlet Aquaculture Association, Redoubt Mountain Lodge, and the National Park Service. Target sample size for each baseline aggregate was 95 individuals across all years to achieve acceptable precision of allele frequency estimates (Waples 1990; Kalinowski 2004).

LABORATORY ANALYSIS

Assaying Genotypes

Genomic DNA was extracted from tissue samples using either the DNeasy 96 Blood and Tissue Kit by QIAGEN or the NucleoSpin 96 Tissue Kit by Macherey-Nagel. Samples collected prior to 2015 were genotyped for 96 loci (Barclay et al. 2017b; Table 2). Samples collected from 2015 to 2017 were genotyped for 95 loci because 1 locus (*Oki_IGF-I.1-163*) was excluded due to high genotyping failure rates when analyzing earlier baseline samples (Table 2). The following methods, using 4 genotyping platforms, were used for acquiring the SNP genotypes for this project over a 5-year period.

Life Technologies OpenArray Technology was used in the initial study on 64 of the markers. A 2.5 µL sample of unnormalized DNA was loaded into an OpenArray 384-well Sample Plate. After drying the plates overnight, a reaction mix containing 2.5 µL Type I molecular grade water and 2.5 µL of 2X TaqMan OpenArray Genotyping Master Mix was added to each of the wells. The OpenArray 384-well Sample Plate was sealed and briefly centrifuged. Samples were transferred to the OpenArray Plates with the QuantStudio OpenArray AccuFill System leaving 1 cell without any template for a no-template control. Real-time polymerase chain reaction (PCR) data was collected using the QuantStudio 12K Flex Instrument following the standard Life Technologies protocol. Data scoring was performed using TaqMan Genotyper Software (Life Technologies).

Fluidigm SNP Genotyping Technology was employed for the rest of the study and included use of 96.96 and 192.24 Dynamic Array Integrated Fluidic Circuits (IFCs). The components were pressurized using the IFC Controllers HX and RX (Fluidigm) and reactions were conducted in 7.2 nL or 9.0 nL volume chambers, respectively. The first set of 96.96 IFC runs contained a mixture of 20X GT Sample Loading Reagent (Fluidigm), 2X TaqMan Universal Buffer (Applied Biosystems), 5X AmpliTaq Gold DNA Polymerase (Applied Biosystems), Custom TaqMan SNP Genotyping Assay (Applied Biosystems), 2X Assay Loading Reagent (Fluidigm), 50X ROX Reference Dye (Invitrogen), and 60–400 ng/µL DNA. One cell was not loaded with any DNA to serve as the no-template control. Thermal cycling was performed with an Eppendorf IFC Thermal

Cycler as follows: 70°C for 30 min for a "Hot-Mix" step, initial denaturation of 10 min at 96°C followed by 40 cycles of 96° for 15 s and 60° for 1 min. The updated methods for the 96.96 IFCs were run on the rest of the samples and consisted 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 96.96 IFC required a "Thermal-Mix" step of 70ºC for 30 min and 25ºC for 10 min prior to PCR. All IFCs were read on a Biomark or EP1 System (Fluidigm) after amplification and scored using Fluidigm SNP Genotyping Analysis software.

Assays that failed to amplify with either the Fluidigm or OpenArray methods were reanalyzed on 1 of 2 platforms, either the Applied Biosystems Prism 7900HT Sequence Detection System (prior to August 2014) or Life Technologies QuantStudio 12K Flex Real-Time PCR System (after August 2014). The samples that were reanalyzed on the Applied Biosystems Prism 7900HT Sequence Detection System were genotyped in 384-well reaction plates in a 5 µL volume consisting of 6–40 ng/µL of DNA, 2X TaqMan Universal PCR Master Mix (Applied Biosystems), and Custom TaqMan SNP Genotyping Assay (Applied Biosystems). One cell was not loaded with any DNA to serve as the no-template control. Thermal cycling was performed on a Dual 384-Well GeneAmp PCR System 9700 (Applied Biosystems) as follows: an initial denaturation of 10 min at 95°C followed by 50 cycles of 92°C for 1 s and annealing/extension temperature for 1 min. The plates were scanned on the Applied Biosystems Prism 7900HT Sequence Detection System after amplification and scored using Applied Biosystems Sequence Detection Software version 2.2.

For the samples reanalyzed on the QuantStudio 12K Flex Real-Time PCR System (Life Technologies), each reaction was performed in 384-well plates in a 5 µL volume consisting of 6–40 ng/µL of DNA, 2X TaqMan GTXpress Master Mix (Applied Biosystems), and Custom TaqMan SNP Genotyping Assay (Applied Biosystems). One cell was not loaded with any DNA to serve as the no-template control. Thermal cycling was performed on a Dual 384-Well GeneAmp PCR System 9700 (Applied Biosystems) as follows: an initial "Hot-Start" denaturation of 95°C for 10 min followed by 40 cycles of denaturation at 92°C for 1 s and annealing at 60°C for 1 min, with a final "Cool-Down" hold at 10°C. The plates were scanned on the system after amplification and scored using the Life Technologies QuantStudio 12K Flex Software.

Regardless of method, a genotype for a given locus and DNA sample was considered a failure if the sample appeared as an outlier to the heterozygous or homozygous clusters. Failures could be due to low-quantity or low-quality DNA or to sample contamination. Genotypes produced on all platforms were imported and archived in the Gene Conservation Laboratory (GCL) Oracle database, LOKI.

Laboratory Failure Rates and Quality Control

Quality control (QC) analyses were conducted to identify laboratory errors and to measure the background discrepancy rate of the genotyping process. These analyses were performed as a separate genotyping event from the original genotyping, with staff duties altered to reduce the likelihood of repeated human errors. The QC protocol consisted of re-extracting 8% of project fish and genotyping them for the same SNPs assayed in the original project. Laboratory errors (e.g.,

extraction errors, assay plate mishandling) 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. Discrepancy rates were calculated as the number of conflicting genotypes divided by the total number of genotypes compared. These rates describe the difference between original project data and QC data for all SNPs and provide a measure of genotyping error rate. The overall failure rate was calculated by dividing the number of failed single-locus genotypes by the number of assayed single-locus genotypes. Assuming that the discrepancies among analyses were due equally to errors during original genotyping and during QC genotyping and that these analyses are unbiased, the error rate in the original genotyping was estimated as half the overall rate of discrepancies. This QC method is the best representation of the error rate of the GCL's current genotype production.

STATISTICAL ANALYSIS

Data Retrieval and Quality Control

We retrieved genotypes from LOKI and imported them into R[1] with the *RJDBC* package.[2] All subsequent analyses were performed in *R*, unless otherwise noted.

Prior to statistical analysis, we performed 3 analyses to confirm the quality of the data. First, we identified SNP markers that were fixed for 1 allele (i.e., only 1 allele present) in all baseline individuals, or that had an alternate allele occurring in fewer than 1% of fish in the baseline for the given marker. We considered these markers invariant and excluded them from further statistical analyses. Second, we identified individuals that were missing substantial genotypic data because they likely had poor quality DNA. We used the 80% rule (missing data at 20% or more of loci; Dann et al. 2009) to identify individuals missing substantial genotypic data. We removed these individuals 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 final QC analysis identified individuals with duplicate genotypes and removed them from further analyses. Duplicate pairs can occur as a result of sampling or extracting the same individual twice and were defined as pairs of individuals sharing the same alleles in 100% 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

Hardy-Weinberg expectations

For each locus within each collection, we tested for conformance to Hardy-Weinberg expectations (HWE) using the program *Genepop* version 4.1.4 (Rousset 2008). We combined probabilities for each collection across loci and for each locus across collections using Fisher's method (Sokal and Rohlf 1995) and removed collections and loci that violated HWE from subsequent analyses after

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correcting for multiple tests with Bonferroni's method (Rice 1989; α = 0.05 / # of collections or loci).

Pooling collections into populations

When appropriate, we pooled some collections to obtain better estimates of allele frequencies following a stepwise protocol. First, we pooled collections from the same geographic location, sampled at similar calendar dates but in different years, as suggested by Waples (1990). We then tested for differences in allele frequencies between pairs of collections that might represent single populations. These pairs of collections were selected if they were sampled on similar calendar dates, and at locations separated by apparently contiguous spawning areas, and therefore, where gene flow between locations was likely. We used Fisher's exact test (Sokal and Rohlf 1995) of allele frequency homogeneity and based our decisions on a summary across loci using Fisher's method. When these tests indicated no difference between collections ($P > 0.01$), we pooled them. 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 estimate allele frequencies given the heterozygosities observed at the loci assayed (Table 2; Gregorius 1980) and to use in mixture analysis (Wood et al. 1987; Waples 1990). Finally, we tested populations for conformance to HWE following the same protocol described above to ensure that our pooling was appropriate, and that tests for linkage disequilibrium would not result in falsely positive results due to departure from HWE. Populations that conformed to HWE were used in subsequent analyses.

Removal of loci from the baseline

When testing populations for conformance to HWE we combined probabilities for each locus across populations using Fisher's method (Sokal and Rolf 1995) and examined the frequency of departures from HWE to identify loci that exhibited substantially more departures than others. We removed loci with significant departures from HWE across populations after correcting for multiple tests with Bonferroni's method ($α = 0.05$ / # loci).

Removal of collections from the baseline

We removed some collections from further analysis for other reasons as per other GCL regional baselines. Collections that did not pool with other collections from the same location were removed because they either lacked reliable collection data to discern their exact sample date and location or they were juvenile collections and we had adult collections with sufficient sample size from the same location. Juvenile collections were selected for removal instead of adult collections because they more likely contain a high proportion of related individuals with similar genotypes and therefore do not have representative baseline allele frequencies for the population.

Linkage disequilibrium

We tested for linkage disequilibrium between each pair of nuclear markers in each population to ensure that subsequent analyses would be based on independent markers. We used the program *Genepop* version 4.1.4 (Rousset 2008) with 100 batches of 5,000 iterations for these tests and summarized the frequency of significant linkage disequilibrium between pairs of SNPs ($P < 0.05$). We considered pairs to be linked if they exhibited linkage in more than half of all populations. When SNP pairs were found to be linked, we either removed 1 locus of the linked pair or combined the genotypes of the pair into a composite, haploid marker for further analyses if the pattern of

linkage provided information useful for MSA. We followed the methods in Barclay and Habicht (2012) for assessing whether the single or the haploid marker was more informative for MSA.

Analysis of Genetic Structure

Interannual variation

We examined the temporal variation (among years) of allele frequencies with a hierarchical, 3-level analysis of variance (ANOVA). We treated the temporal samples 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 package GDA.[3] For this test, only temporal collections with at least 50 samples were used to maximize power and retain relatively balanced sample sizes (Ryman et al. 2006).

Visualization of genetic distances

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 package *hierfstat*.[4] 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. We plotted the consensus tree with the package *APE* (Paradis et al. 2004). These trees provided insight into the variability of the population genetic structure among loci and assisted in the selection of reporting groups used in baseline evaluation tests for MSA.

Baseline Evaluation for Mixed Stock Analysis

We used the results from the NJ consensus tree and the geographic distribution of populations to delineate reporting groups that might perform adequately for MSA within Cook Inlet. We assessed the accuracy and precision for MSA of these reporting groups using 100% proof tests. Methods for these tests followed those used by Habicht et al. (2012).

Proof tests

For 100% proof tests, mixtures were created by randomly sampling 200 fish from a single reporting group in the baseline and then rebuilding the baseline without the sampled fish (for *Kasilof*, only 100 fish were sampled for mixtures to allow adequate baseline sample size of $N > 200$ (Templin et al. 2011). These tests provide a measure of the potential accuracy and precision possible for designated reporting groups, as well as a means to understand the direction of bias when estimating stock proportions.

The stock composition of the proof test mixtures was estimated using the software package BAYES (Pella and Masuda 2001). BAYES employs a Bayesian algorithm to estimate the most probable contribution of the baseline populations to explain the combination of genotypes in the mixture sample. We followed the same BAYES protocol as reported in Barclay and Habicht (2015). We ran 1 Markov Chain Monte Carlo chain with 40,000 iterations and discarded the first

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

[4]   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.

20,000 iterations for each proof test to form the posterior distribution. 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 proof test mixture were calculated by taking the mean and 5% and 95% quantiles of the posterior distribution from the single chain output.

Proof tests were repeated 10 times for each reporting group using different mixtures and baselines. These tests provided an indication of the power of the baseline for MSA, assuming all populations were represented in the baseline.

When the correct allocation means for repeated tests for a given reporting group averaged less than 90%, we considered this reporting group a failure and not appropriate for MSA. For failed reporting groups, we identified the reporting group that the failed group most commonly misallocated to in these tests. We then created a new reporting group by combining the failed reporting group with the reporting group it most commonly misallocated to. We then performed a 100% proof test to determine if this new reporting group was appropriate for MSA.

RESULTS

TISSUE SAMPLING

Baseline

A total of 15,107 genetic samples were collected from spawning populations of coho salmon throughout Cook Inlet (Table 1). These samples were collected at 128 locations throughout Cook Inlet drainages. Target sample size of 95 fish was met at 68 locations.

LABORATORY ANALYSIS

Assaying Genotypes

A total of 10,586 fish collected from spawning areas and weirs were selected for analysis and assayed for 95 SNP markers (Table 1). Baseline samples not included in the analysis were from locations with a total sample size fewer than 47 individuals, or locations where a subset of fish were chosen for analysis.

Laboratory Failure Rates and Quality Control

The overall failure rate for genotypes of all samples selected for analysis at the 95 SNP markers was 0.79%. A subset of 137 baseline collections (81% of selected baseline collections) were included in the QC analysis. The overall discrepancy rate was 0.28%; therefore, the overall estimated error rate was 0.14%.

STATISTICAL ANALYSIS

Data Retrieval and Quality Control

For all baseline collections, no SNPs were fixed for 1 allele, and 13 SNPs had alternate alleles that occurred in fewer than 1% of fish (Table 2). These 13 markers were considered invariant and removed; the remaining 82 SNPs were kept for subsequent analyses. Using the 80% rule for sufficiently complete genotypes, 186 individuals were removed from the baseline collections.

Based on the criterion for detecting duplicate individuals, 30 individuals were removed from baseline collections as duplicate individuals.

Baseline Development

Hardy-Weinberg expectations within collections

Over the remaining 82 SNPs (Table 2) and 168 collections (Table 1), 114 of 13,776 tests deviated significantly from HWE ($P < 0.01$) without adjusting for multiple tests. These were spread over 60 SNPs, and no SNPs were out of HWE in more than 6 collections. No collections departed HWE at more than 8 SNPs. After adjusting for multiple tests, all collections conformed to HWE.

Pooling collections into populations and Hardy-Weinberg expectations within populations

A total of 94 populations were identified after dropping collections for insufficient sample size and pooling collections (pooled and nonpooled collections are referred to as *populations*; Table 1). Collections pooled from different sampling sites included collections from the Chuitna River, West Fork Yentna River, Kichatna River, Peters Creek, and the Chickaloon River drainages. Over all variant SNPs and populations, 86 of 7,708 tests did not conform to HWE ($P < 0.01$) without adjusting for multiple tests. These were spread over 47 SNPs, and no SNPs were out of HWE in more than 5 of the 94 populations. No population was out of HWE at more than 5 of 82 SNPs. After adjusting for multiple tests, all populations conformed to HWE.

Removal of loci from the baseline

After combining the HWE *p*-values across populations and adjusting for multiple tests, all 82 SNPs conformed to HWE; therefore, no additional loci were removed from the baseline.

Removal of collections from the baseline

A total of 18 collections were dropped from further analysis: 3 juvenile collections and 15 adult collections. Two juvenile collections were dropped because sufficient adult samples were collected from the same location. One juvenile collection was dropped because it had insufficient samples and could not be pooled with another collection. Adult collections were dropped for several reasons: 1) they had insufficient samples size and could not be pooled with another collection (10 collections); 2) the sampling location was not certain (2 collections); 3) they were collected at a weir and include more than 1 population (2 collections); or 4) they did not conform to HWE (1 collection).

Linkage disequilibrium

No SNP pairs showed significant linkage ($P < 0.05$) in greater than 50% of populations. Therefore, no SNPs were considered linked and no further linkage disequilibrium analyses were performed.

Analysis of Genetic Structure

Temporal variation

A total of 11 populations had collections of 50 or more fish from multiple years and were included in the analysis of temporal variation of allele frequencies. Within populations, 7 pairs of collections were 1 year apart (Question, Canyon, McRoberts, and Gruska creeks; and Deshka, Talachulitna, and Little Susitna rivers), 1 pair was 4 years apart (Fish Creek), 1 pair was 7 years apart (Jim Creek), and 2 pairs were 15 years apart (Crescent River and Skilak Lake outlet; Table 1). The

3-level ANOVA indicated that the ratio of variation among temporal collections to the variation among populations was 8.6%.

Visualization of genetic distances

Overall F_{ST} was 0.05 (Table 2), and pairwise F_{ST} varied from 0.00 to 0.17 (Appendix A1). 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 furthest upstream and those from the most southern portion of Cook Inlet. The least genetically divergent populations were concentrated in the most northwestern portion of Cook Inlet. These included those from the Chuitna River and northwest, including other coastal populations and populations from the Susitna and Yentna river drainages.

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

1) *Southwest CI* (West side populations south of Little Jack Creek)
2) *Northwest CI* (West side populations from Little Jack Creek north to the Susitna River and Alexander Creek)
3) *Susitna* (Susitna River mainstem tributary populations, excluding Deshka River)
4) *Deshka* (Deshka River population)
5) *Yentna* (Yentna River populations)
6) *Knik* (Knik Arm, Little Susitna River, and Campbell Creek populations)
7) *Jim* (Jim Creek populations)
8) *Turnagain/Northeast CI* (Turnagain Arm and northeast Cook Inlet populations)
9) *Kenai* (Kenai River populations)
10) *Kasilof* (Kasilof River populations)
11) *Southeast CI* (Kenai Peninsula populations south of the Kasilof River)

Populations from the *Kenai* and *Kasilof* reporting groups and *Southwest CI* and *Southeast CI* reporting groups formed the 2 most distinct clusters on the tree (Figure 2). In general, populations in the *Kenai* and *Kasilof* cluster were more genetically distinct with increasing river distance from Cook Inlet. Within this group, all Kasilof River populations formed a single cluster. Among populations from the *Southwest CI* and *Southeast CI* cluster, genetic distinction generally increased from northern to southern populations. On an inlet-wide scale, there appears to be affinity among northern populations and among southern populations (i.e., *Susitna*, *Northwest CI*, and *Yentna* are more basal, whereas *Southeast CI* and *Southwest CI* share a cluster).

Several populations appeared to be more genetically distinct than most: Russian River, East Fork Moose River, Chester Creek, Sixmile Creek, and Fox River. Of the 30 well-supported nodes (50% of bootstrap trees), none occurred in the *Northwest CI* or *Susitna* reporting groups, 9 occurred within the *Kenai* reporting group, 3 occurred within the *Kasilof* reporting group, 6 occurred within the *Knik* reporting group, 3 occurred in the *Yentna* reporting group, 3 occurred in the *Turnagain/Northeast CI* reporting group, 3 occurred in the *Southwest CI* reporting group, and the *Southeast CI* and *Jim* reporting groups had 1 each. The remaining well-supported node occurred before a *Southeast CI* population (Port Graham) and 5 *Southwest CI* populations (Kamishak River, Douglas Reef River, Douglas River, McNeil River, and Little Kamishak River).

Baseline Evaluation for Mixed Stock Analysis

Proof tests

Correct allocation means for all 110 repeated proof tests ranged from 82.6% to 99.5% (Figure 3; Appendix B1). The *Southeast CI*, *Southwest CI*, *Kenai,* and *Jim* reporting groups had the highest correct allocation means (>96%) and the least variation among repeats. *Kasilof* had the next highest correct allocation means with repeats ranging from 94.3% to 98.6%, followed by *Turnagain/Northeast CI* with correct allocations means ranging from 93.2% to 98.0%. The *Deshka* and *Knik* reporting groups had relatively high correct allocation means that varied less than 7.0% among repeats (ranging from 92.0% to 99.0% for the *Deshka* group and from 91.4% to 97.8% for the *Knik* group). The *Yentna* reporting group had relatively high correct allocations with little variation in 6 of the 10 repeats (ranging from 95.9% to 97.2%) and correct allocations in 3 of 10 repeats ranging from 90.4% to 94.1%; however, the correct allocation for 1 repeat dropped considerably (86.7%). *Northwest CI* and *Susitna* reporting groups had the most variable results, with correct allocation means ranging from 84.1% to 97.1% for the *Northwest CI* group and from 82.6% to 95.9% for the *Susitna* group.

Correct allocation means among repeats averaged greater than 90% for each reporting group (Table 3).

DISCUSSION

This study expands and updates a previously reported baseline of coho salmon in UCI (Barclay et al. 2017b) to fill gaps and allow for MSA within the Susitna River drainage and finer-scale reporting groups in Upper Cook Inlet. Three gaps were identified in the Barclay et al. (2017b) study: 1) inadequate representation of Yentna River tributaries (e.g., Upper Yentna River tributaries, Lake Creek, Kahiltna River, and Yentna River mainstem tributaries); 2) inadequate representation of Knik River above Jim Creek; and 3) inadequate representation of tributaries with weirs (Deshka River and Jim Creek).

EXPANDED BASELINE

Adequate representation of populations is a prerequisite for applying genetic data to MSA applications (Utter and Ryman 1993). Population structure, both within and among reporting groups, determines how many populations are required to adequately represent reporting groups. Lower representation of populations in the baseline is needed when the structure is organized by groups of genetically similar populations and when those groups align with the reporting groups of interest. Conversely, higher representation of populations is needed when the reporting groups contain populations that are genetically divergent from one another.

This study added 8 new populations from the Yentna River to the 3 in the previous baseline (Barclay et al. 2017b). The Yentna River was previously represented by Canyon Creek, Talachulitna River, and Hayes River, all of which are Skwentna River tributaries. The new populations include West Fork Yentna River (Upper Yentna), Red and Clearwater creeks and Kichatna River (Yentna River mainstem), Red Salmon Creek (Skwentna River), Camp and Sunflower Creeks (Lake Creek), and Peters Creek (Kahiltna River). The inclusion of these new populations improves our understanding of population structure and increases the diversity of Yentna River baseline populations and the identifiability of the Yentna River as an MSA reporting group.

This study adds genetic data from 2 new populations from the Knik River: McRoberts Creek, a Jim Creek tributary; and Hunter Creek, a Knik River tributary above Jim Creek. The Knik River drainage was represented in the previous baseline by 117 Jim Creek samples collected above McRoberts Creek (Barclay et al. 2017b). Jim Creek was not tested as an MSA reporting group in the previous baseline, because there were not enough samples to create mixtures for baseline evaluation tests and it was uncertain if the samples represented the entire Jim Creek drainage. In addition, no samples had been analyzed from coho salmon spawning in the Knik River drainage above Jim Creek; therefore, it was unknown if Jim Creek fish could be distinguished from other Knik River fish in MSA. The Knik River populations added by this study improve our understanding of population structure within the Knik River drainage and allow for baseline evaluation tests of Jim Creek as a potential MSA reporting group.

This study adds 2 new baseline collections from the Deshka River weir to replace the radiotagged collection used to represent Deshka River in the previous baseline. The original baseline collection for the Deshka River was collected at the Deshka River weir in 2013. Results from initial Hardy-Weinberg equilibrium tests suggested the collection contained fish from more than 1 population and, therefore, could not be considered a single baseline population. However, QC analyses observed a relatively high genotyping error rate for these samples, indicating poor quality DNA samples, which can produce erroneous genotypes and Hardy-Weinberg test results. Genetic tissues samples from 59 radiotagged coho salmon with final locations throughout the Deshka River were used to augment the previous baseline, and tests for Hardy-Weinberg equilibrium indicated that those samples represented a single population. This study replaces the radiotagged baseline samples with 380 samples collected at the weir in 2015 and 2016. The larger sample size of these new collections provides for more accurate estimates of allele frequencies and allows for testing of Deshka River as a potential reporting group for MSA.

Although the primary focus of this study was to improve baseline representation in the Yentna, Deshka, and Knik rivers, this study also added additional samples to 2 populations included in the previous baseline (Alexander and Williwaw creeks) and new samples to a previously unrepresented population in Knik Arm (Sixmile Creek). These additional samples provided for more accurate estimates of allele frequencies for Alexander and Williwaw creek and increased baseline representation of Knik Arm populations, thus improving the accuracy of the baseline for MSA applications.

COMPARISON TO PREVIOUS BASELINE

Among Population Variation

The patterns of variation revealed in this study are consistent with those revealed in Barclay et al. (2017b). In both studies, populations from the same drainage tended to cluster together in the NJ consensus tree, and bootstrap support for nodes grouping populations by drainage were often fewer than 50%. Additionally, the most genetically divergent populations within rivers were generally those furthest upstream or most southerly within Cook Inlet, and least genetically divergent populations were from northwest Cook Inlet populations in both studies. However, with the addition of new populations from northwest Cook Inlet in this study, some new patterns of variation have been revealed.

The Yentna River was previously represented by 3 populations, all of which were in the Skwentna River and clustered together in the NJ consensus tree with northwest Cook Inlet population McArthur River (Barclay et al. 2017b). The addition of Yentna River populations from above and

below the Skwentna River reveals 2 groups of Yentna River populations: western (populations within and above the Skwentna River) and eastern (populations from Lake Creek and the Kahiltna River) Yentna River (Figures 1 and 2). Variation among populations within the western group was lower than in the eastern group, and western Yentna populations show an affinity to *Northwestern CI* populations, whereas the eastern Yentna populations show an affinity to *Susitna* populations from the Chulitna River (population numbers 24–27). These patterns of variation suggest that western and eastern Yentna River populations originated from different colonization events.

The Knik River was previously represented by samples collected from Jim Creek above McRoberts Creek. Although all 3 Knik populations cluster beyond a significant node, Jim and McRoberts creeks (Jim Creek drainage) are more genetically similar to each other and are genetically distinct from Hunter Creek (i.e., they cluster at the end of a long, and supported, branch). This finding is important because one of the goals of this study was to determine whether Jim Creek drainage coho salmon could be genetically distinguished from coho salmon spawning farther up the Knik River drainage and test Jim Creek as a reporting group for MSA. Distinguishing Jim Creek fish in a mixed stock sample will increase our understanding of the exploitation rate of this stock and, with escapement estimates from the Jim Creek weir, provide managers with the ability to reconstruct total annual run sizes.

Interannual Variation

In the analysis of temporal variation of allele frequencies, the ratio of the variation among years to variation among populations was 8.6%, whereas the previous baseline the ratio was 12.5% (Barclay et al. 2017b). This decrease in the estimate in proportion of interannual variation is due to a difference in the collections included in each baseline. This study added temporal collections from the Deshka River, Jim Creek, and McRoberts Creek, and excluded the Indian River collection from 2014 because pooling test results indicated significant allele frequency differences with the 2013 collection. Additionally, Chuitna River and Wilson Creek collections (Chuitna River) were used in the analysis of temporal variation in the previous report; however, the exact sampling location of these collections is uncertain, and they were not considered the same sampling location in this study, so they were not included in the current estimate of temporal variation. Although the estimate of temporal variation observed in this study is lower than the previous baseline, it is still relatively high compared to other species of salmon in Cook Inlet (sockeye salmon *O. nerka*, 1.6%, Barclay and Habicht 2012; Chinook salmon *O. tshawytscha*, 5.3%, Barclay and Habicht 2015).

The proportion of variation accounted for among years relative to the variation among populations was lower in Cook Inlet than anywhere else in the coho salmon species range. Values reported for coho salmon in the southern portion of its range varied from 21% to over 40% in Oregon (Van Doornik et al. 2002; Ford et al. 2004), and in the northern range were 14% in the Kuskokwim River (Crane et al. 2007). Highly unimodal age-at-maturity distributions for coho salmon may explain why temporal (interannual) variation accounts for so much of the among-collection variation compared to other Pacific salmon species, especially in the southern portions of the species range (Waples 1990). Regional variation in age-at-maturity distributions may partially explain why temporal variation is not as pronounced in Cook Inlet (and Kuskokwim River) populations. In Alaska, coho salmon primarily spawn at age 2.1, but at least in Cook Inlet, the age-at-maturity is less unimodally distributed. From 2009 to 2011, age-2.1 fish made up only 77–85% of the Cook Inlet commercial harvest (Tobias and Willette 2012a, 2012b; Tobias et al. 2013).

EVALUATION FOR MSA

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). In this report, we only incorporated the 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 management concerns with genetic analyses. Proof 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 to 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 proof tests using the reporting groups we tested show promise for using MSA for coho salmon to resolve management questions in Cook Inlet fisheries (Figure 3; Appendix B1). The consistency in performance of the proof tests across replicates indicates genetic similarities among populations within the reporting group, as each replicate consists of a random set of individuals within the reporting group. For example, *Southwest CI, Jim*, *Kenai*, *Kasilof*, and *Southeast CI* all allocated above 94% in every proof test replicate. Many of the populations within these reporting groups clustered together above a significant node in the NJ consensus tree (Figure 2). The *Northwest CI*, *Yentna*, and *Susitna* reporting groups, on the other hand, showed higher variation among replicates (82.6–97.2%, Figure 3). The populations within these clusters had comparatively shallow population structure, with few populations joined by significant nodes in the NJ tree (pairwise $F_{ST} < 0.06$ between all population pairs; Appendix A1; Figure 2). The proof tests used here may be optimistic because mixture samples constructed for these tests were made up of populations from single reporting groups. Proof tests performed using mixtures composed of a single reporting group often produce more optimistic results due to the way the Bayesian algorithm is informed by the composition of the mixture. For example, if the majority of fish in a sample come from a single reporting group, the likelihood of BAYES assigning a fish to that reporting group increases. Future tests exploring a wide range of stock compositions for each reporting group would better evaluate the baseline for MSA.

There may be other fine-scale reporting groups that will perform well, especially for questions where the baseline can be restricted and/or the composition is not expected to be complex. For example, a reporting group consisting of a single or combination of populations from the Chulitna River (population numbers 24–27) might perform well on a mixed stock sample of migrating fish collected in the lower Susitna River (Table 1; Figures 1 and 2). Within the Kenai River, reporting groups consisting of single or combinations of populations from tributary versus 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 may not be appropriate for fishery mixtures captured in Lower Cook Inlet. Lower Cook Inlet fishery mixtures may include fish from outside of Cook Inlet populations (e.g., Barclay et al. 2016, Chinook salmon). Therefore, baselines used to analyze fisheries outside of Cook Inlet should include coho salmon stocks from outside of Cook Inlet.

The increased resolution of this baseline will allow for finer-scale MSA estimates of coho salmon harvests in Cook Inlet, thereby improving our knowledge of exploitation and productivity of coho salmon stocks and the ability to manage Cook Inlet coho salmon on a stock-specific basis.

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REFERENCES CITED

Baker, T. T., A. C. Wertheimer, R. D. Burkett, R. Dunlap, D. M. Eggers, E. I. Fritts, A. J. Gharrett, R. A. Holmes, and R. L. Wilmot. 1996. Status of Pacific salmon and steelhead escapements in southern Alaska. Fisheries 21(10):6–18.

Barclay, A. W., C. Habicht, W. Gist, and T. M. Willette. 2017a. Genetic stock identification of Upper Cook Inlet coho salmon harvest, 2013-2015. Alaska Department of Fish and Game, Fishery Manuscript Series No. 17-04, Anchorage.

Barclay, A. W., P. A. Crane, D. B. Young, H. A. Hoyt, and C. Habicht. 2017b. Current status of genetic studies of coho salmon from Southcentral Alaska and evaluations for mixed-stock analysis in Cook Inlet. Alaska Department of Fish and Game, Fishery Manuscript Series No. 17-01, Anchorage.

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. 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., 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.

Beacham, T. D., J. R. Candy, C. Wallace, M. Wetklo, L. Deng, and C. MacConnachie. 2012. Microsatellite mixed-stock identification of coho salmon in British Columbia. Marine and Coastal Fisheries 4(1):85–100.

Beacham, T. D., M. Wetklo, L. Deng, and C. MacConnachie. 2011. Coho salmon population structure in North America determined from microsatellites. Transactions of the American Fisheries Society 140:253–270.

Bucklin, K. A., M. A. Banks, and D. Hedgecock. 2007. Assessing genetic diversity of protected coho salmon (Oncorhynchus kisutch) populations in California. Canadian Journal of Fisheries and Aquatic Sciences 64:30–42.

Campbell, N. R., and S. R. Narum. 2011. Development of 54 novel single-nucleotide polymorphism (SNP) assays for sockeye and coho salmon and assessment of available SNPs to differentiate stocks in the Columbia. Molecular Ecology Resources 11(S1):20–30.

Crane, P. A., D. Molyneaux, C. Lewis, and J. Wenberg. 2007. Genetic variation among coho salmon populations from the Kuskokwim Region and application to stock-specific harvest estimation. U.S. Fish and Wildlife Service, Alaska Fisheries Technical Report 96, Anchorage.

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.

Flannery, B., and R. Loges. 2016. Yukon River coho salmon microsatellite baseline. Final Report for Fisheries Resource Monitoring Program Study 14-206, U. S. Fish and Wildlife Service, Conservation Genetics Lab, Anchorage.

Ford, M. J., D. Teel, D. M. Van Doornik, D. Kuligowski, and P. W. Lawson. 2004. Genetic population structure of central Oregon Coast coho salmon (*Oncorhynchus kisutch*). Conservation Genetics 5(6):797–812.

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

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.

REFERENCES CITED (Continued)

Johnson, M. A., and M. A. Banks. 2008. Genetic structure, migration, and patterns of allelic richness among coho salmon (Oncorhynchus kisutch) populations of the Oregon coast. Canadian Journal of Fisheries and Aquatic Sciences 65:1274–1285.

Kalinowski, S. T. 2004. Genetic polymorphism and mixed-stock fisheries analysis. Canadian Journal of Fisheries and Aquatic Sciences 61:1075–1082.

Koljonen, M., 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 62:2143–2158.

NRC (National Research Council). 1996. Upstream: salmon and society in the Pacific Northwest. Committee on the Protection and Management of Pacific Northwest Salmonids. National Academy Press, Washington D. C.

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

Olsen, J. B., S. J. Miller, W. J. Spearman, and J. K. Wenburg. 2003. Patterns of intra- and inter-population genetic diversity in Alaskan coho slamon: Implications for conservation. Conservation Genetics 4:557–569.

Pearcy, W. G. 1992. Ocean ecology of north Pacific salmonids. University of Washington Press, Seattle.

Pella, J., and M. Masuda. 2001. Bayesian methods for analysis of stock mixtures from genetic characters. Fishery Bulletin 99:151–167.

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, WASHU-B-87-001 C2.

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

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.

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 15:203–2045.

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.

Small, M. P., R. E. Withler, and T. D. Beacham. 1998. Population structure and stock identification of British Columbia coho salmon, *Oncorhynchus kisutch*, based on microsatellite DNA variation. Fisheries Bulletin 96:843–858.

Smith, C. T., L. Park, D. Vandoornik, L. W. Seeb, and J. E. Seeb. 2006. Characterization of 19 single nucleotide polymorphism markers for coho salmon. Molecular Ecology Notes 6(3):715–720.

Sokal, R. R., and F. J. Rohlf. 1995. Biometry. 3rd edition. Freeman, San Francisco.

Starks, H. A., A. J. Clemento, and J. C. Garza. 2015. Discovery and characterization of single nucleotide polymorphisms in coho salmon, *Oncorhynchus kisutch*. Molecular Ecology Resources 16(1):277–287. doi: 10.1111/1755-0998.12430

Teel, D. J., D. M. Vandoornik, D. R. Kuligowski, and W. S. Grant. 2003. Genetic analysis of juvenile coho salmon (Oncorhynchus kisutch) off Orgeon and Washington reveals few Columbia River wild fish. Fishery Bulletin 101(3):640–652.

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):226–246.

REFERENCES CITED (Continued)

Tobias, T. M., W. M. Gist, and T. M. Willette. 2013. Abundance, age, sex, and size of Chinook, sockeye, coho, and chum salmon returning to Upper Cook Inlet, Alaska, 2011. Alaska Department of Fish and Game, Fishery Data Series No. 13-49, Anchorage.

Tobias, T. M., and T. M. Willette. 2012a. Abundance, age, sex, and size of Chinook, sockeye, coho, and chum salmon returning to Upper Cook Inlet, Alaska, 2009. Alaska Department of Fish and Game, Fishery Data Series No. 12-11, Anchorage.

Tobias, T. M., and T. M. Willette. 2012b. Abundance, age, sex, and size of Chinook, sockeye, coho, and chum salmon returning to Upper Cook Inlet, Alaska, 2010. Alaska Department of Fish and Game, Fishery Data Series No. 12-14, Anchorage.

Utter, F., and N. Ryman. 1993. Genetic markers and mixed stock fisheries. Fisheries 18(8):11–21.

Van Doornik, D. M., M. J. Ford, and D. J. Teel. 2002. Patterns of temporal genetic variation in coho salmon: Estimates of the effective proportion of 2-year-olds in natural and hatchery populations. Transactions of the American Fisheries Society 131:1007–1019.

Van Doornik, D. M., D. J. Teel, D. R. Kuligowski, C. A. Morgan, and E. Casillas. 2007. Genetic analyses provide insight into the early ocean stock distribution and survival of juvenile coho salmon off the coasts of Washinton and Oregon. North American Journal of Fisheries Management 27(1):220–237.

Waples, R. S. 1990. Temporal changes of allele frequency in Pacific salmon: implications of 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 38:1358–1370.

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):886–881.

TABLES AND FIGURES

Table 1.–Tissue collections of coho salmon throughout Upper Cook Inlet, including the years collected, number of samples collected (N_c), the number of individuals genotyped (N_g), the number of individuals analyzed from each collection included in the baseline (N_b), and source of the collection.

Pop. No.	Reporting Group	Location	Collection Year	N_c	N_g	N_b	Source[a]
	Southwest						
1		Douglas River	2013	106	95	92	A
—[b]			2014[c]	150	0	0	A
2		Douglas Reef River	2013	113	95	94	A
—[b]			2014	128	0	0	A
3		Kamishak River	2013	110	95	92	A
—[b]			2014	106	0	0	A
4		Little Kamishak River	2013	96	95	90	A
—[b]			2014[c]	175	150	0	A
5		McNeil River	2013	41	41	41	A
5			2014	12	12	12	A
—[b]			2014[c]	171	100	0	A
—[b]		Sunday Creek	2012[c]	7	0	0	A
—[b]		Brown's Peak Creek	2013	9	0	0	A
—[b]			2014	4	0	0	A
6		Knoll's Head Creek	2014[c]	200	150	150	A
—[b]		Fitz Creek	2013	3	0	0	A
7		Silver Salmon Creek	2013	160	95	93	B
8		Tuxedni River	2012	86	81	81	C
9		Crescent River	1998	99	95	93	D
—[b]			2012	1	0	0	C
9			2013	227	95	91	E
10		Harriet Creek	2012	1	1	1	C
10			2014	63	63	63	A
	Northwest						
—[b]		Packers Creek	2013	4	4	0	A
—[b]			2014	37	36	0	A
11		Little Jack Creek	2013	104	95	95	A
12		Montana Bill Creek	2012	101	95	95	C
—[b]		Big River	2009	19	0	0	C
13		Kustatan River	2013	119	95	95	A
14		McArthur River (unnamed stream)	2014	100	95	95	A

-continued-

Table 1.–Page 2 of 7.

Pop. No.	Reporting Group	Location	Collection Year	N_c	N_g	N_b	Source[a]
	Northwest						
15		Farro Creek	2013	17	17	17	A
15			2014	111	78	78	A
—[b]		Straight Creek	2014	15	0	0	A
16		Chuitna River	1992	54	54	53	D
16		Wilson Creek	2010[c]	223	95	94	C
—[b]		Middle Creek	2008[c]	40	0	0	C
—[b]		Lone Creek	2008[c]	70	0	0	C
17		Coal Creek	2013	41	41	39	A
17			2014	46	46	46	A
18		Theodore River	2012	19	19	17	C
18			2013	60	60	60	F
19		Lewis River	2013	57	57	56	F
20		Alexander Creek[d]	2014	101	95	92	F
20			2015	100	48	47	F
	Susitna						
21		Portage Creek	2014	63	61	59	A
22		Indian River	2013	105	95	94	G
22			2014	52	50	0	A
—[b]		Lane Creek	2014	10	0	0	A
23		Whiskers Creek	2013	79	79	79	G
—[b]			2014	2	2	1	A
—[b]		Whiskers Slough	2013[c]	41	41	0	G
—[b]		Honolulu Creek	2013	4	0	0	G
24		Spink Creek	2008	38	33	32	C
24			2014	62	62	62	A
25		Byers Creek	2014	57	56	55	A
26		Bunco Creek	2013	9	9	9	G
26			2014	56	56	55	A
—[b]		Swan Lake	2009	20	0	0	C
27		Troublesome Creek	2013	92	90	88	G
—[b]			2014	15	0	0	A
28		Prairie Creek	2014	53	53	51	A
—[b]		Iron Creek	2013	28	28	0	G
—[b]			2014	12	12	0	A
29		Sheep River	2013	115	95	95	G

-continued-

Table 1.–Page 3 of 7.

Pop. No.	Reporting Group	Location	Collection Year	N_c	N_g	N_b	Source[a]
	Susitna (cont.)						
30		Larson Lake outlet	2011	84	84	84	C
30			2014	48	48	48	A
31		Chunilna Creek	2013	66	66	64	G
31			2014	70	30	30	A
—[b]		Fish Creek (Chunilna Creek drainage)	2013	1	0	0	G
32			2014	65	65	65	A
—[b]		Birch Creek	2014	2	0	0	A
—[b]		Answer Creek	2013	7	7	0	A
33		Question Creek	2013	77	77	76	A
33			2014	76	57	50	A
—[b]		Rabideux Creek	2014	1	0	0	A
34		Montana Creek	2013	200	87	87	F
35		Sheep Creek	2014	47	47	47	A
—[b]		Kashwitna River	2014	24	0	0	A
—[b]		Willow Creek	2014	27	27	0	A
	Deshka						
—[b]		Deshka River	2013	100	95	0	F
36			2015	300	190	190	F
36			2016	300	190	190	F
	Yentna						
37		West Fork Yentna River - no name A	2017	73	73	68	H
37		West Fork Yentna River - no name B	2017	105	95	92	H
38		Clearwater Creek	2017	81	81	80	H
39		Kichatna River	2017	107	94	91	H
39		Nakochna River (upper)	2017	36	33	33	H
39		Nakochna River (lower)	2014	8	8	8	A
39			2015	3	3	3	H
39			2016	6	6	6	H
39			2017	11	11	44	H
40		Red Creek	2014	26	26	26	A
40			2015	46	44	44	H
40			2017	62	30	29	H
41		Red Salmon Creek	2017	89	88	79	H

-continued-

Table 1.–Page 4 of 7.

Pop. No.	Reporting Group	Location	Collection Year	N_c	N_g	N_b	Source[a]
	Yentna (cont.)						
42		Hayes River	2014	87	84	84	A
43		Canyon Creek	2013	55	55	55	A
43			2014	105	50	50	A
44		Talachulitna River	2013	74	73	72	A
44			2014	50	50	50	A
45		Sunflower Creek	2014	8	8	8	A
45			2015	3	3	3	H
45			2016	9	9	9	H
45			2017	37	37	36	H
46		Camp Creek	2016	51	51	50	H
46			2017	53	50	47	H
47		Martin Creek	2013	36	35	35	A
47			2016	4	4	4	H
47		Peters Creek	2017	108	95	93	H
	Knik						
48		Little Susitna River	2013	97	95	94	F
48			2014	100	50	50	F
49		Fish Creek	2009	203	95	93	C
49			2013	94	94	92	F
—[b]			2014	100	0	0	F
50		Cottonwood Creek	2014	94	76	73	A
51		Wasilla Creek	2013	9	9	9	A
51			2014	91	91	91	A
52		Rabbit Slough	2011	95	95	95	C
—[b]		Matanuska River	2008	135	0	0	D
53			2009	194	95	94	D
—[b]			2014	3	0	0	A
54		Eska Creek	2013	61	61	59	A
54			2014	65	35	35	A
55		Hunter Creek	2016	9	9	9	H
55			2017	96	96	92	H
	Jim						
56		Jim Creek (upper)	2009	68	68	68	A
—[b]			2011	7	0	0	C
56			2014	140	50	49	A
56			2016	106	101	101	H

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Table 1.–Page 5 of 7.

Pop. No.	Reporting Group	Location	Collection Year	N_c	N_g	N_b	Source[a]
	Jim (cont.)						
—[b]		Jim Creek (weir)	2016	123	95	0	H
—[b]			2017	100	100	0	H
57		McRoberts Creek	2016	71	71	69	H
57			2017	108	108	107	H
	Knik						
—[b]		Eagle River	2014	24	24	0	J
—[b]			2015	11	11	0	J
—[b]		Sixmile Creek	2009	46	46	0	C
—[b]			2014	43	43	0	J
58			2015	125	95	93	J
—[b]		Ship Creek	1991	11	0	0	C
59			2012	400	95	93	C
—[b]			2013	200	0	0	F
—[b]			2014	189	0	0	F
60		Chester Creek	2011	54	54	53	C
60			2013	2	2	2	A
60			2014	24	24	22	A
—[b]		Campbell Creek[e]	1995	5	0	0	C
61			2009	125	95	94	C
—[b]			2010	9	0	0	C
	Turnagain/Northeast						
62		Rabbit Creek	2011	54	54	53	C
62			2013	2	2	2	C
62			2014	7	7	7	A
—[b]		California Creek	2014	9	0	0	A
63		Placer Creek	2014	75	73	71	A
64		Williwaw Creek	2013	22	22	22	A
64			2014	50	50	49	A
64			2017	35	33	30	F
—[b]		Portage Creek	2013	5	0	0	A
—[b]			2014	17	0	0	A
65		Explorer Creek	2013	95	95	91	A
65			2014	69	50	48	A
—[b]		Placer River	2014	6	0	0	A
—[b]		Ingram Creek	2013	7	7	0	A
—[b]			2014	6	6	0	A
66		East Fork Sixmile Creek	2014[c]	100	90	90	A
67		Resurrection Creek	2010	96	95	93	C

-continued-

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Table 1.–Page 6 of 7.

Pop. No.	Reporting Group	Location	Collection Year	N_c	N_g	N_b	Source[a]
	Turnagain/Northeast (cont.)						
68		Chickaloon River	2010	82	82	80	C
68		Mystery Creek	2010	22	22	20	C
69		Sucker Creek	1997	94	94	91	D
70		Gruska Creek	2013	53	53	53	A
70			2014	55	50	50	A
71		Bishop Creek	2014	62	62	57	A
	Kenai						
72		Trail Creek	2006	134	108	108	D
—[b]		Moose Creek	1993[c]	150	0	0	C
73		Grant Creek	2013	100	95	95	H
74		South Fork Snow River	1998	73	73	71	D
74			2002	50	24	24	D
75		Summit Creek	2002	50	50	50	D
75		Quartz Creek	1998	75	74	73	D
76		Tern Lake	2002	96	95	95	D
—[b]		Kenai Lake outlet	1999	56	0	0	D
—[b]			2002	57	0	0	D
77			2014	117	95	95	A
—[b]		Russian River	2002	31	0	0	D
78			2013	101	95	93	A
78			2014	100	50	47	A
79		Skilak River	2003	100	95	94	D
80		Skilak Lake outlet	1999	80	80	78	D
—[b]			2002	50	0	0	D
80			2014	95	95	95	A
81		Killey River	2000	68	70	67	D
81			2002	49	25	25	D
82		East Fork Moose River	2002	100	94	93	D
83		Funny River	2006	150	92	92	D
—[b]		Soldotna Creek	2013	8	0	0	A
84		Slikok Creek	2008	67	66	65	D
—[b]		Beaver Creek	2013	12	0	0	A
	Kasilof						
85		Glacier Creek	2009	68	65	65	D
86		Indian Creek	2009	55	55	55	D
87		Nikolai Creek	2009	92	92	88	D
88		Tustumena Lake outlet	2009	100	95	90	D

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Table 1.–Page 7 of 7.

Pop. No.	Reporting Group	Location	Collection Year	N_c	N_g	N_b	Source[a]
	Southeast						
89		Ninilchik River	2013	108	95	94	A
—[b]			2014	100	0	0	A
90		Deep Creek	2013	101	95	89	A
—[b]			2014	100	0	0	A
91		Stariski Creek	2013	61	61	53	A
91			2014	100	34	34	A
92		Anchor River	2006	164	55	55	C
92			2009	40	40	40	C
93		Fox River	2013	117	117	109	A
—[b]			2014	111	0	0	A
94		Port Graham River	2014	114	95	95	A
Sample total				15,107	10,586	9,553	

Note: Unique population numbers represent all the analyzed collections that contribute to a single population and correspond to population numbers on Figure 1. Proof tests for MSA were performed on the 11 reporting groups.

[a] A = Initial baseline project, B = National Park Service, C = ADF&G archives, D = US Fish and Wildlife Service archives, E = Redoubt Mountain Lodge, F = ADF&G = Division of Sport Fish, G = Alaska Energy Authority, H = this project, I = Cook Inlet Aquaculture Association, J = Joint Base Elmendorf–Richardson Air Force Base (JBER) Fish and Wildlife.

[b] This collection was not used in the baseline.

[c] Juvenile collection.

[d] Alexander Creek is genetically more similar to northwest Cook Inlet populations than Susitna River populations, so it was included in the *Northwest CI* reporting group.

[e] Campbell Creek is genetically similar to Ship Creek stock, so it was grouped with Knik Arm populations.

Table 2.–Source information for 96 single nucleotide polymorphisms (SNPs) and observed heterozygosity (H$_o$) and F_{ST} for the 95 SNPs used to analyze the population genetic structure of Cook Inlet coho salmon. These summary statistics are based upon the 94 populations detailed in Table 1.

Assay Name	Source [a]	H$_o$	F_{ST}[b]
Oki_arf-115	A	0.03	0.07
Oki_arp-105	B	0.45	0.05
Oki_aspAT-273	B	0.42	0.11
Oki_bcAKal-274	B	0.27	0.07
Oki_Car-353	C	0.12	0.02
Oki_carban-140	B	0.42	0.06
Oki_Cr-209[c, d]	A	-	0.04
Oki_E2-87	A	0.18	0.04
Oki_eif4ebp2-58	A	0.02	0.05
Oki_gdh-189	B	0.41	0.06
Oki_gh-183	B	0.30	0.04
Oki_GPDH-146	A	0.07	0.04
Oki_GPDH-188	A	0.07	0.05
Oki_HGFA-311	A	0.40	0.04
Oki_hsf1b-85	B	0.11	0.03
Oki_IGF-I.1-163[e]	A	-	-
Oki_il1rac-169[d]	C	0.01	0.08
Oki_il-1racp-176	A	0.08	0.03
Oki_ins-167	A	0.36	0.04
Oki_ins-323	A	0.02	0.03
Oki_LWSop-554	A	0.14	0.15
Oki_metA-220[d]	B	0.00	0.02
Oki_nips-159	B	0.42	0.04
Oki_p53-20	B	0.21	0.07
Oki_parp3-19	B	0.29	0.09
Oki_pigh-33	B	0.16	0.03
Oki_pop5-265	B	0.30	0.06
Oki_rpo2j-235	B	0.46	0.06
Oki_SClkF2R2-120	A	0.29	0.06
Oki_SECC22-67	B	0.33	0.03
Oki_serpin-328	A	0.23	0.05
Oki_spf30-119[d]	B	0.00	0.00
Oki_srp09-107	B	0.08	0.03

-continued-

Table 2.–Page 2 of 3.

Assay Name	Source [a]	H_o	F_{ST}[b]
Oki_SWS1op-38	A	0.30	0.04
Oki_sys1-141	B	0.13	0.08
Oki_taf12-40[d]	B	0.00	0.02
Oki_TniUPP-230	C	0.48	0.05
Oki_txnip-35[d]	B	0.01	0.02
Oki_U202-136	C	0.24	0.06
Oki_U216-151[d]	C	0.00	0.01
Oki_u6-257	A	0.46	0.06
Oki_vatf-363	B	0.37	0.06
Oki100974-29[d]	D	0.00	0.01
Oki101119-1006	D	0.16	0.05
Oki101419-103	D	0.46	0.05
Oki101554-35[d]	D	0.00	0.01
Oki101770-525	D	0.40	0.03
Oki102213-604	D	0.30	0.04
Oki102414-499	D	0.43	0.05
Oki102801-511	D	0.08	0.03
Oki103271-161	D	0.08	0.06
Oki103577-70	D	0.48	0.04
Oki103713-182	D	0.44	0.04
Oki104515-99	D	0.38	0.05
Oki104519-45	D	0.47	0.04
Oki104569-261[d]	D	0.00	0.00
Oki105105-245	D	0.35	0.09
Oki105115-49	D	0.19	0.07
Oki105132-169	D	0.41	0.06
Oki105235-460	D	0.41	0.07
Oki105385-521	D	0.07	0.03
Oki105407-161	D	0.47	0.04
Oki105897-298	D	0.06	0.03
Oki106172-60	D	0.45	0.06
Oki106313-353	D	0.38	0.02
Oki106419-292	D	0.28	0.04
Oki106479-278	D	0.17	0.05
Oki107336-45	D	0.27	0.03

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Table 2.–Page 3 of 3.

Assay Name	Source [a]	H_o	F_{ST}[b]
Oki107607-213	D	0.26	0.09
Oki107974-46	D	0.45	0.04
Oki108505-331[d]	D	0.00	0.00
Oki109651-152	D	0.46	0.05
Oki109874-122	D	0.12	0.04
Oki109894-418	D	0.08	0.12
Oki110078-191	D	0.28	0.04
Oki110689-43[d]	D	0.00	0.02
Oki111681-407	D	0.05	0.02
Oki113457-324	D	0.41	0.03
Oki114448-101	D	0.22	0.03
Oki114587-309	D	0.33	0.04
Oki116362-411	D	0.21	0.06
Oki116865-244	D	0.47	0.03
Oki117043-374	D	0.37	0.11
Oki117144-64	D	0.37	0.06
Oki117286-291[d]	D	0.00	0.01
Oki117742-259	D	0.40	0.04
Oki117815-369	D	0.35	0.04
Oki118152-314	D	0.14	0.03
Oki118175-264	D	0.41	0.04
Oki118654-330	D	0.44	0.07
Oki94903-192	D	0.36	0.03
Oki95318-100	D	0.42	0.09
Oki96127-66	D	0.43	0.05
Oki96158-278	D	0.39	0.04
Oki96376-63	D	0.34	0.04
Oki97954-228	D	0.26	0.04
Average/Overall[f]		0.29	0.05

[a]   A = Smith et al. 2006; B = Campbell and Narum 2011; C = Matt Smith, unpublished, University of Washington, e-mail matt_smith@fws.gov; D = Starks et al. 2015.
[b]   Weir and Cockerham (1984).
[c]   Mitochondrial SNP marker.
[d]   These were removed from further analysis because they were invariant.
[e]   This SNP marker was not genotyped for samples collected after 2014 due to high genotyping failure rates in earlier analyses.
[f]   Overall statistics are based on the 82 variant SNPs used in the proof tests for mixed stock analysis.

Table 3.–Estimates of average stock composition (%) for 10 replicates of 100% proof tests of the 11 reporting groups identified in the genetic structure analysis. Each replicate was a sample of 100 or 200 individuals removed from the genetic baseline. Bold numbers indicate correct allocations.

Allocated to:	Southwest CI	Northwest CI	Susitna	Deshka	Yentna	Knik	Jim	Turnagain/ Northeast CI	Kenai	Kasilof	Southeast CI
							Test Group				
Southwest CI	**98.1**	0.4	0.1	0.1	0.1	0.1	0.1	0.2	0.1	0.6	0.3
Northwest CI	0.4	**90.9**	1.6	0.7	0.9	0.8	0.1	0.7	0.1	0.1	0.1
Susitna	0.2	3.3	**91.1**	1.2	1.9	0.6	0.1	0.8	0.1	0.2	0.1
Deshka	0.1	0.8	1.9	**95.7**	0.7	0.3	0.1	0.2	0.1	0.1	0.1
Yentna	0.1	2.8	3.4	1.7	**94.4**	0.4	0.1	0.4	0.1	0.2	0.1
Knik	0.1	0.8	0.6	0.2	0.3	**94.9**	0.1	0.9	0.1	0.1	0.2
Jim	0.1	0.1	0.2	0.1	0.1	2.1	**99.2**	0.3	0.1	0.1	0.1
Turnagain/ Northeast CI	0.2	0.7	0.4	0.2	1.2	0.4	0.1	**96.2**	0.1	0.3	0.3
Kenai	0.2	0.1	0.1	0.1	0.1	0.1	0.0	0.1	**99.2**	0.1	0.1
Kasilof	0.1	0.1	0.5	0.1	0.1	0.1	0.0	0.1	0.1	**97.5**	0.1
Southeast CI	0.4	0.1	0.1	0.1	0.2	0.1	0.0	0.1	0.1	0.7	**98.4**

Note: Stock composition estimates may not sum to 1 due to rounding error.
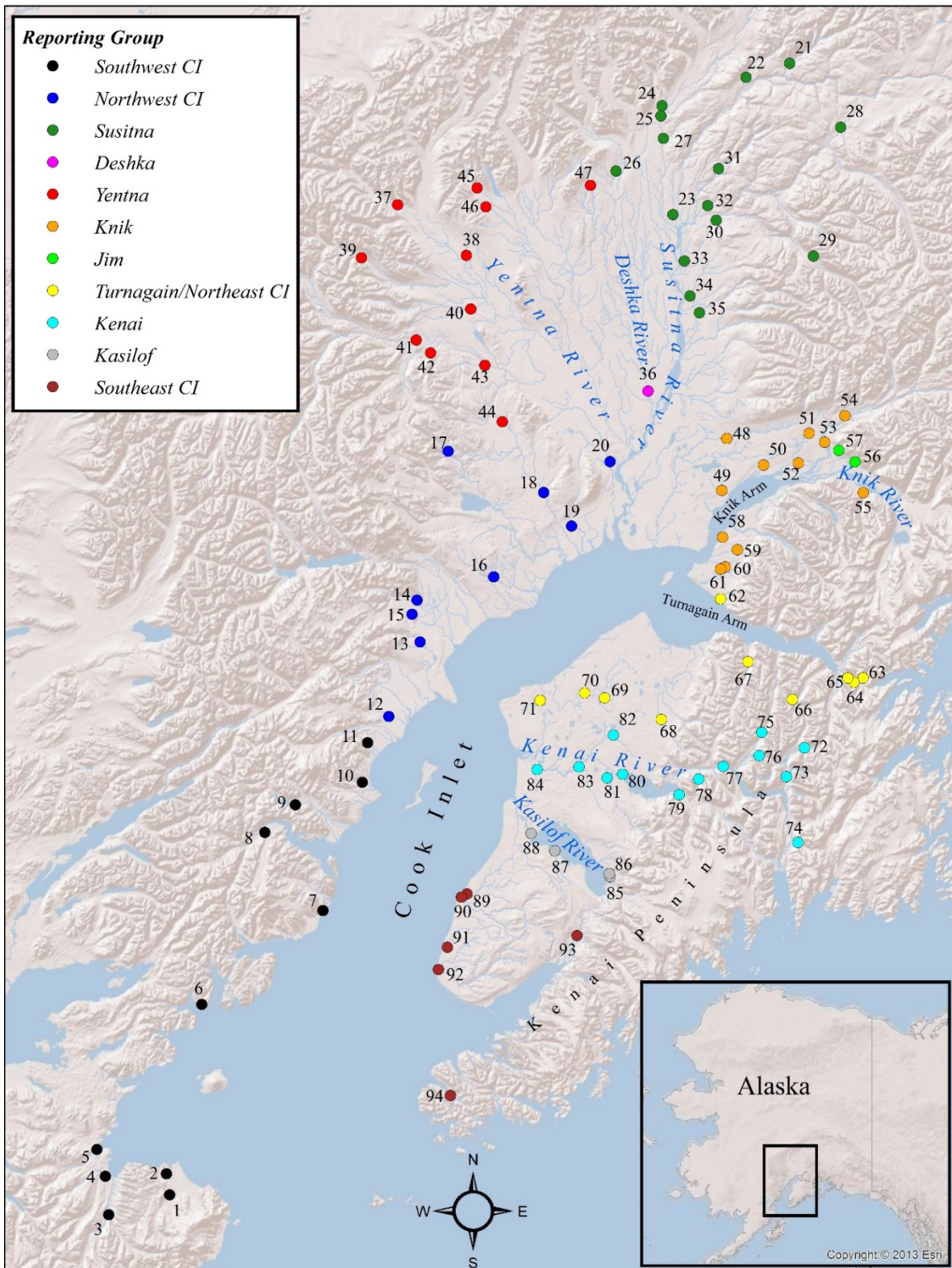
Figure 1.–Sampling locations for coho salmon originating in Cook Inlet, Alaska, 1991–2017. Numbers correspond to population numbers on Table 1.

Note: Colored circles correspond to the 11 Cook Inlet reporting groups used in the mixed stock analysis proof tests.
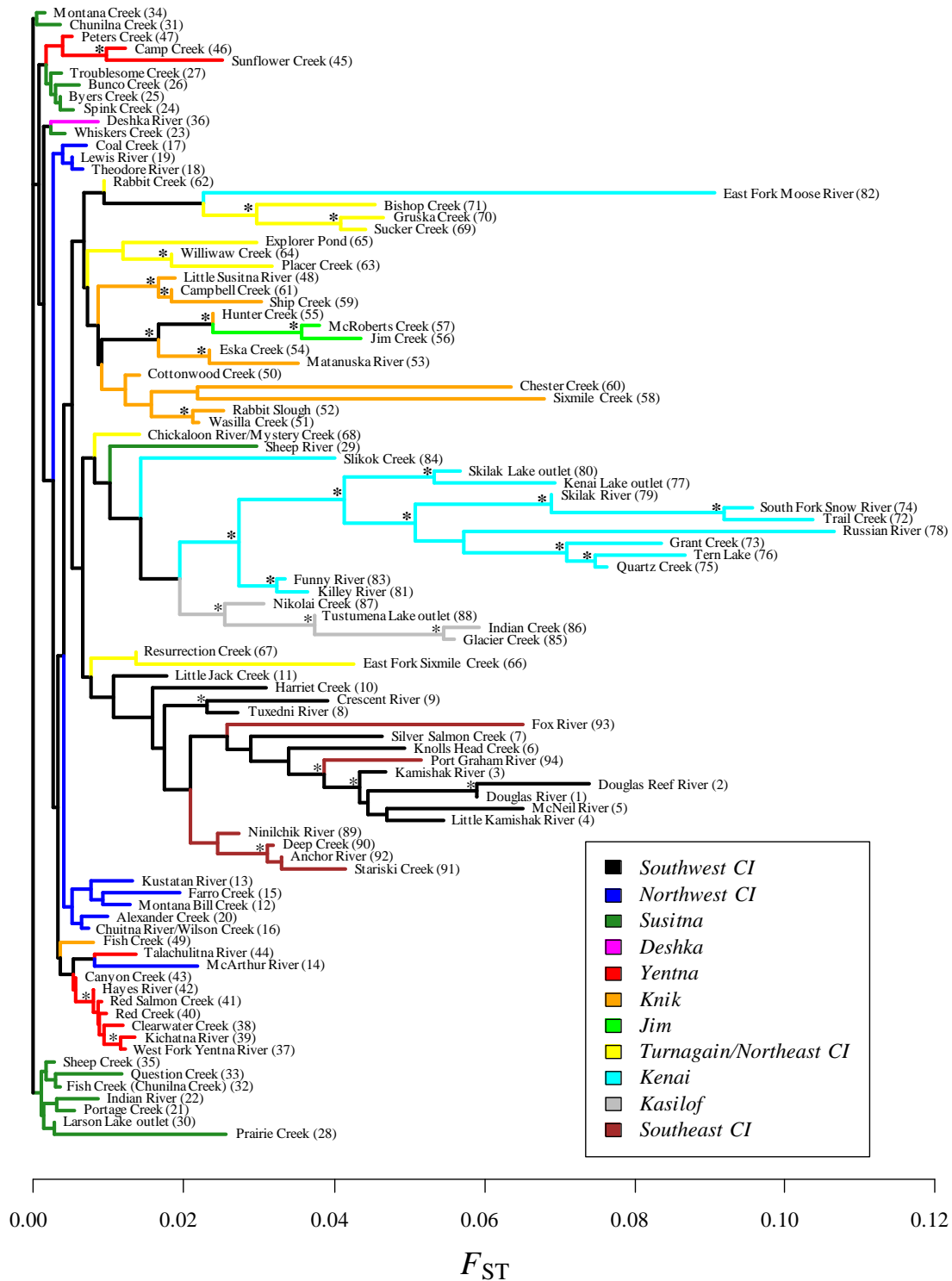
Figure 2.–Consensus neighbor-joining tree based on F_{ST} between coho salmon populations sampled from spawning areas in drainages of Cook Inlet, Alaska (see Table 1 for collection details).

Source: Appendix A1.

Note: Colors denote reporting groups as in Figure 1. Numbers in parentheses correspond to unique population numbers on Table 1 and Figure 1. Bootstrap consensus nodes occurring in >50% of trees are marked with an asterisk.
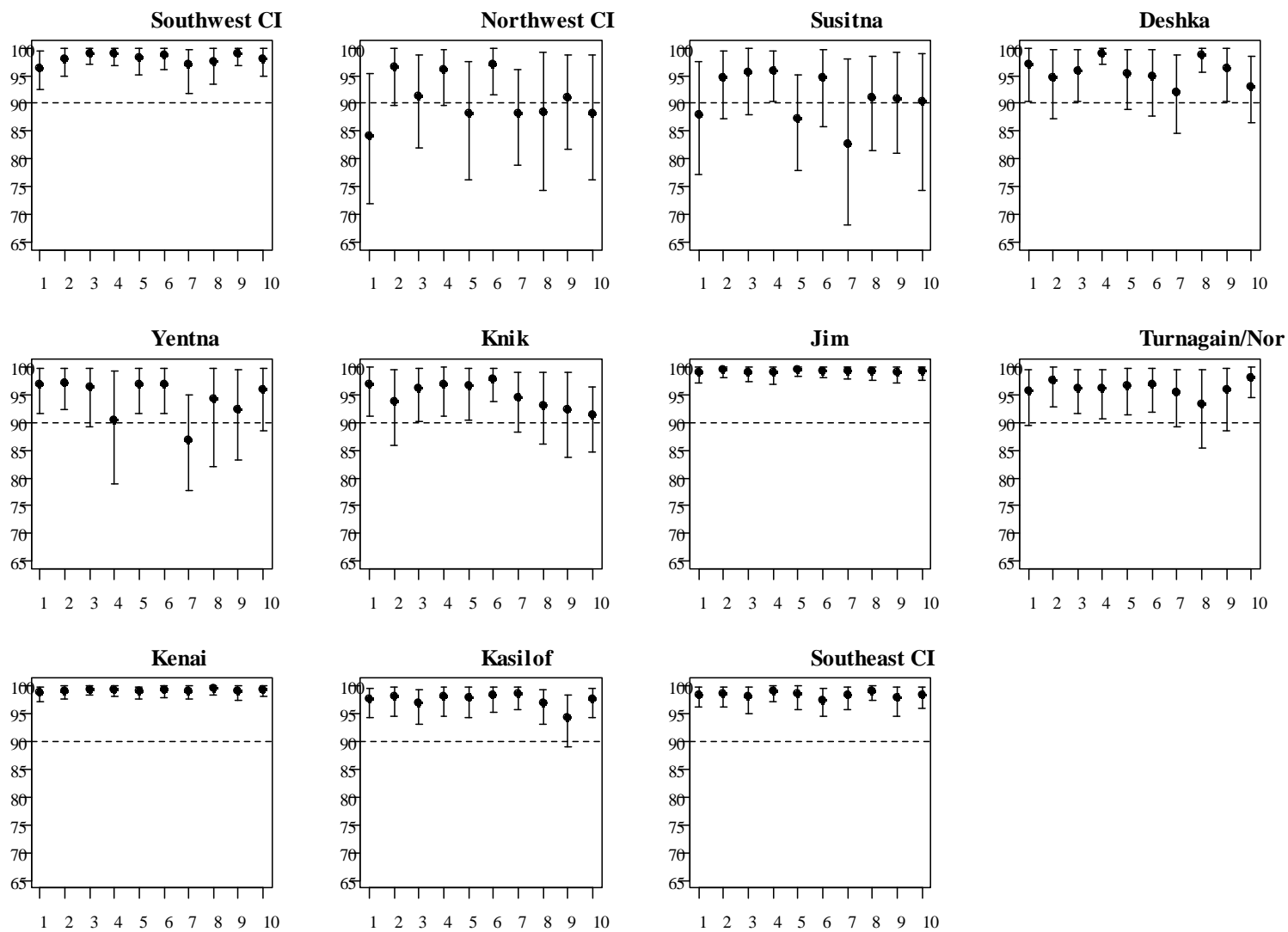
Figure 3.–Results of repeated proof testing for 11 reporting groups. The points represent the correct allocation mean from each replicate with 90% credibility intervals for each point.

APPENDIX A

Appendix A1.–Pairwise F_{ST} (Weir and Cockerham 1984) between coho salmon populations sampled from spawning areas in drainages of Cook Inlet, Alaska. Population numbers correspond to population numbers on Table 1.

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	0.02	0.03	0.00																				
4	0.02	0.04	0.01	0.00																			
5	0.04	0.05	0.03	0.03	0.00																		
6	0.04	0.05	0.03	0.04	0.05	0.00																	
7	0.04	0.06	0.03	0.04	0.04	0.05	0.00																
8	0.04	0.05	0.03	0.04	0.05	0.03	0.04	0.00															
9	0.06	0.07	0.05	0.05	0.07	0.05	0.05	0.02	0.00														
10	0.05	0.07	0.04	0.04	0.06	0.05	0.05	0.03	0.04	0.00													
11	0.06	0.08	0.05	0.06	0.07	0.05	0.05	0.02	0.03	0.03	0.00												
12	0.06	0.08	0.05	0.06	0.07	0.05	0.04	0.02	0.04	0.03	0.01	0.00											
13	0.07	0.08	0.05	0.07	0.08	0.06	0.05	0.03	0.04	0.04	0.02	0.01	0.00										
14	0.08	0.09	0.07	0.08	0.09	0.06	0.06	0.04	0.06	0.04	0.04	0.03	0.02	0.00									
15	0.06	0.07	0.05	0.06	0.06	0.05	0.04	0.03	0.04	0.03	0.02	0.01	0.02	0.03	0.00								
16	0.06	0.08	0.05	0.06	0.06	0.05	0.05	0.03	0.04	0.03	0.01	0.01	0.01	0.03	0.01	0.00							
17	0.06	0.08	0.05	0.05	0.07	0.05	0.05	0.03	0.05	0.03	0.02	0.02	0.02	0.02	0.02	0.01	0.00						
18	0.06	0.08	0.05	0.06	0.07	0.05	0.05	0.02	0.04	0.04	0.01	0.02	0.01	0.02	0.02	0.01	0.01	0.00					
19	0.06	0.08	0.05	0.05	0.06	0.05	0.05	0.03	0.04	0.03	0.02	0.01	0.01	0.02	0.02	0.00	0.00	0.00	0.00				
20	0.07	0.08	0.06	0.06	0.08	0.06	0.05	0.03	0.04	0.03	0.02	0.01	0.01	0.03	0.02	0.00	0.01	0.01	0.01	0.00			
21	0.07	0.08	0.05	0.06	0.07	0.05	0.05	0.03	0.05	0.03	0.02	0.02	0.02	0.03	0.03	0.01	0.01	0.01	0.01	0.02	0.00		
22	0.07	0.08	0.06	0.06	0.08	0.06	0.06	0.04	0.05	0.04	0.03	0.02	0.02	0.03	0.03	0.01	0.02	0.02	0.01	0.02	0.01	0.00	
23	0.07	0.08	0.06	0.06	0.08	0.06	0.06	0.03	0.05	0.03	0.02	0.02	0.02	0.02	0.03	0.01	0.01	0.01	0.01	0.01	0.01	0.01	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	0.06	0.08	0.06	0.07	0.08	0.06	0.06	0.04	0.05	0.04	0.03	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.01	0.02	0.01	0.01	0.01
25	0.06	0.07	0.05	0.05	0.07	0.05	0.05	0.02	0.04	0.03	0.02	0.01	0.02	0.02	0.02	0.01	0.01	0.01	0.00	0.02	0.01	0.01	0.00
26	0.07	0.09	0.06	0.07	0.08	0.06	0.05	0.03	0.05	0.03	0.02	0.01	0.01	0.02	0.02	0.01	0.02	0.01	0.01	0.02	0.01	0.01	0.01
27	0.07	0.09	0.06	0.08	0.09	0.06	0.06	0.04	0.05	0.04	0.02	0.01	0.01	0.03	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
28	0.08	0.10	0.07	0.08	0.09	0.07	0.08	0.05	0.06	0.04	0.04	0.04	0.04	0.05	0.04	0.03	0.04	0.04	0.03	0.03	0.03	0.03	0.03
29	0.06	0.08	0.05	0.06	0.07	0.05	0.05	0.04	0.06	0.04	0.04	0.03	0.04	0.06	0.04	0.03	0.03	0.04	0.03	0.02	0.02	0.03	0.03
30	0.06	0.07	0.05	0.06	0.07	0.05	0.05	0.03	0.04	0.03	0.02	0.02	0.01	0.03	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
31	0.07	0.08	0.06	0.06	0.08	0.06	0.06	0.04	0.05	0.04	0.02	0.02	0.02	0.03	0.03	0.01	0.01	0.01	0.01	0.02	0.01	0.01	0.01
32	0.06	0.08	0.05	0.06	0.08	0.06	0.05	0.03	0.04	0.03	0.02	0.02	0.02	0.02	0.03	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
33	0.07	0.09	0.06	0.07	0.09	0.07	0.07	0.05	0.05	0.04	0.02	0.02	0.02	0.04	0.04	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
34	0.06	0.08	0.05	0.06	0.08	0.06	0.05	0.03	0.04	0.03	0.01	0.01	0.02	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
35	0.06	0.08	0.05	0.06	0.07	0.05	0.05	0.03	0.04	0.04	0.02	0.01	0.01	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
36	0.07	0.09	0.06	0.07	0.08	0.06	0.06	0.04	0.05	0.04	0.02	0.02	0.02	0.02	0.03	0.02	0.01	0.01	0.01	0.02	0.02	0.02	0.01
37	0.07	0.08	0.06	0.07	0.07	0.06	0.05	0.03	0.05	0.04	0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.01	0.02	0.02	0.02	0.02
38	0.07	0.08	0.06	0.06	0.08	0.06	0.04	0.03	0.05	0.03	0.03	0.02	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.02	0.02	0.02	0.02
39	0.07	0.08	0.06	0.07	0.07	0.06	0.05	0.03	0.05	0.04	0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.02	0.02	0.02	0.02
40	0.07	0.08	0.06	0.06	0.07	0.06	0.05	0.03	0.05	0.03	0.02	0.01	0.01	0.02	0.02	0.01	0.02	0.01	0.01	0.02	0.02	0.02	0.02
41	0.07	0.08	0.05	0.06	0.07	0.05	0.04	0.02	0.04	0.03	0.02	0.01	0.02	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.02	0.02	0.01
42	0.06	0.08	0.05	0.06	0.07	0.06	0.05	0.03	0.05	0.04	0.02	0.01	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.02	0.02	0.01
43	0.06	0.08	0.05	0.06	0.08	0.05	0.05	0.03	0.04	0.03	0.02	0.01	0.01	0.02	0.02	0.01	0.01	0.01	0.00	0.01	0.01	0.01	0.01
44	0.08	0.10	0.08	0.09	0.09	0.07	0.07	0.04	0.06	0.04	0.02	0.02	0.02	0.02	0.02	0.01	0.02	0.01	0.01	0.02	0.02	0.02	0.02
45	0.07	0.09	0.07	0.08	0.09	0.07	0.06	0.05	0.06	0.04	0.04	0.03	0.03	0.05	0.04	0.03	0.03	0.03	0.03	0.03	0.03	0.04	0.03
46	0.07	0.09	0.06	0.07	0.08	0.07	0.06	0.03	0.04	0.04	0.03	0.02	0.02	0.03	0.03	0.02	0.01	0.01	0.01	0.02	0.02	0.02	0.02

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	0.06	0.07	0.06	0.06	0.07	0.05	0.05	0.03	0.05	0.04	0.02	0.01	0.01	0.03	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
48	0.06	0.07	0.05	0.05	0.07	0.06	0.05	0.04	0.04	0.04	0.03	0.03	0.03	0.04	0.03	0.02	0.02	0.02	0.02	0.03	0.02	0.02	0.02
49	0.07	0.08	0.05	0.06	0.07	0.06	0.05	0.03	0.04	0.03	0.02	0.01	0.01	0.02	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.02	0.01
50	0.06	0.07	0.05	0.06	0.06	0.06	0.05	0.03	0.05	0.04	0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.01	0.02	0.02	0.02	0.02
51	0.06	0.08	0.06	0.07	0.07	0.06	0.06	0.04	0.05	0.05	0.03	0.03	0.03	0.04	0.04	0.02	0.02	0.02	0.02	0.03	0.02	0.03	0.02
52	0.06	0.08	0.06	0.07	0.07	0.06	0.05	0.04	0.06	0.05	0.04	0.03	0.03	0.03	0.04	0.03	0.02	0.02	0.02	0.03	0.03	0.03	0.03
53	0.08	0.09	0.06	0.07	0.08	0.08	0.07	0.04	0.06	0.06	0.04	0.04	0.05	0.05	0.04	0.03	0.04	0.03	0.03	0.04	0.05	0.04	0.04
54	0.06	0.08	0.05	0.06	0.06	0.05	0.06	0.03	0.05	0.04	0.03	0.02	0.03	0.03	0.03	0.02	0.02	0.02	0.02	0.03	0.02	0.03	0.02
55	0.07	0.09	0.06	0.06	0.07	0.06	0.05	0.03	0.05	0.04	0.03	0.02	0.03	0.03	0.03	0.02	0.02	0.02	0.01	0.03	0.03	0.03	0.03
56	0.10	0.12	0.08	0.09	0.09	0.08	0.07	0.05	0.07	0.08	0.06	0.05	0.06	0.05	0.06	0.05	0.04	0.04	0.04	0.05	0.05	0.05	0.05
57	0.09	0.12	0.08	0.09	0.09	0.08	0.07	0.05	0.07	0.06	0.05	0.04	0.05	0.05	0.05	0.04	0.04	0.04	0.03	0.05	0.04	0.05	0.04
58	0.12	0.14	0.11	0.12	0.11	0.11	0.10	0.10	0.10	0.10	0.09	0.07	0.08	0.07	0.07	0.06	0.07	0.06	0.05	0.08	0.07	0.08	0.07
59	0.06	0.07	0.05	0.06	0.07	0.06	0.06	0.05	0.06	0.04	0.04	0.03	0.03	0.05	0.04	0.03	0.03	0.03	0.03	0.04	0.04	0.03	0.04
60	0.11	0.13	0.11	0.11	0.11	0.11	0.11	0.08	0.09	0.10	0.08	0.07	0.07	0.07	0.07	0.06	0.06	0.06	0.05	0.08	0.07	0.07	0.07
61	0.05	0.07	0.04	0.05	0.06	0.05	0.05	0.03	0.05	0.04	0.03	0.02	0.02	0.04	0.03	0.02	0.02	0.02	0.01	0.03	0.02	0.02	0.02
62	0.05	0.07	0.04	0.05	0.06	0.05	0.04	0.03	0.04	0.03	0.02	0.01	0.01	0.02	0.02	0.01	0.01	0.01	0.01	0.02	0.01	0.01	0.01
63	0.08	0.09	0.07	0.08	0.09	0.07	0.07	0.05	0.06	0.06	0.05	0.03	0.03	0.05	0.04	0.03	0.04	0.04	0.03	0.04	0.04	0.04	0.04
64	0.07	0.09	0.05	0.06	0.08	0.06	0.06	0.04	0.05	0.04	0.03	0.02	0.02	0.03	0.03	0.01	0.02	0.02	0.01	0.02	0.02	0.02	0.02
65	0.07	0.09	0.06	0.07	0.09	0.07	0.07	0.05	0.06	0.05	0.04	0.03	0.03	0.05	0.04	0.03	0.03	0.03	0.03	0.04	0.04	0.04	0.03
66	0.08	0.10	0.07	0.08	0.10	0.08	0.06	0.05	0.05	0.05	0.05	0.04	0.04	0.05	0.06	0.05	0.04	0.04	0.04	0.04	0.05	0.05	0.05
67	0.05	0.07	0.04	0.05	0.06	0.05	0.04	0.03	0.04	0.03	0.02	0.01	0.01	0.02	0.02	0.01	0.01	0.01	0.01	0.02	0.01	0.02	0.01
68	0.06	0.07	0.05	0.05	0.06	0.05	0.05	0.03	0.04	0.03	0.02	0.02	0.02	0.03	0.03	0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.02
69	0.07	0.08	0.07	0.07	0.08	0.06	0.07	0.05	0.06	0.06	0.05	0.05	0.06	0.06	0.05	0.04	0.04	0.04	0.03	0.04	0.05	0.06	0.04

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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
70	0.08	0.09	0.08	0.08	0.09	0.06	0.08	0.06	0.07	0.06	0.06	0.05	0.06	0.06	0.05	0.04	0.04	0.05	0.04	0.05	0.05	0.06	0.05
71	0.09	0.10	0.07	0.08	0.08	0.07	0.08	0.06	0.07	0.06	0.06	0.05	0.06	0.06	0.06	0.04	0.04	0.04	0.03	0.05	0.04	0.06	0.05
72	0.11	0.14	0.10	0.11	0.11	0.10	0.13	0.11	0.12	0.10	0.11	0.11	0.11	0.12	0.11	0.10	0.11	0.11	0.11	0.11	0.12	0.12	0.11
73	0.08	0.10	0.07	0.08	0.09	0.08	0.09	0.07	0.08	0.09	0.08	0.10	0.09	0.10	0.10	0.09	0.09	0.08	0.09	0.09	0.09	0.10	0.09
74	0.11	0.13	0.10	0.11	0.11	0.09	0.13	0.10	0.11	0.10	0.10	0.10	0.10	0.11	0.10	0.09	0.10	0.10	0.10	0.11	0.11	0.12	0.10
75	0.08	0.10	0.07	0.08	0.08	0.07	0.09	0.08	0.09	0.08	0.08	0.09	0.09	0.09	0.08	0.08	0.08	0.07	0.08	0.09	0.09	0.10	0.09
76	0.09	0.12	0.08	0.09	0.10	0.08	0.10	0.09	0.09	0.09	0.09	0.09	0.09	0.10	0.10	0.09	0.09	0.08	0.10	0.09	0.10	0.11	0.10
77	0.08	0.10	0.07	0.09	0.09	0.06	0.08	0.08	0.09	0.08	0.06	0.07	0.08	0.10	0.08	0.07	0.08	0.07	0.07	0.07	0.08	0.09	0.08
78	0.12	0.16	0.11	0.12	0.14	0.09	0.12	0.10	0.11	0.11	0.11	0.12	0.11	0.13	0.12	0.11	0.11	0.10	0.11	0.12	0.12	0.14	0.12
79	0.09	0.12	0.08	0.09	0.09	0.08	0.09	0.07	0.08	0.07	0.06	0.07	0.07	0.09	0.07	0.06	0.08	0.07	0.07	0.07	0.08	0.09	0.07
80	0.08	0.10	0.07	0.08	0.09	0.06	0.07	0.07	0.08	0.07	0.05	0.06	0.06	0.08	0.06	0.05	0.06	0.06	0.06	0.06	0.07	0.08	0.06
81	0.06	0.08	0.05	0.06	0.06	0.06	0.05	0.05	0.06	0.04	0.04	0.04	0.04	0.07	0.04	0.03	0.04	0.04	0.04	0.04	0.04	0.05	0.04
82	0.12	0.15	0.11	0.12	0.12	0.10	0.11	0.10	0.09	0.11	0.10	0.10	0.10	0.11	0.10	0.09	0.10	0.09	0.09	0.09	0.10	0.11	0.11
83	0.06	0.09	0.06	0.06	0.07	0.06	0.06	0.05	0.05	0.05	0.04	0.04	0.04	0.06	0.04	0.02	0.03	0.03	0.03	0.03	0.04	0.04	0.03
84	0.08	0.11	0.07	0.09	0.10	0.08	0.06	0.06	0.07	0.06	0.04	0.04	0.04	0.06	0.04	0.04	0.05	0.04	0.04	0.03	0.05	0.05	0.04
85	0.08	0.10	0.07	0.07	0.10	0.06	0.08	0.06	0.08	0.07	0.06	0.06	0.06	0.08	0.06	0.05	0.05	0.05	0.05	0.06	0.07	0.08	0.06
86	0.08	0.10	0.07	0.08	0.10	0.06	0.08	0.06	0.08	0.07	0.07	0.06	0.06	0.08	0.06	0.06	0.06	0.06	0.06	0.06	0.07	0.08	0.06
87	0.05	0.07	0.04	0.05	0.06	0.04	0.05	0.04	0.05	0.05	0.04	0.03	0.04	0.06	0.04	0.02	0.03	0.03	0.03	0.03	0.04	0.04	0.03
88	0.06	0.08	0.05	0.06	0.07	0.05	0.05	0.04	0.06	0.05	0.04	0.04	0.04	0.06	0.04	0.03	0.04	0.04	0.04	0.04	0.04	0.05	0.04
89	0.04	0.06	0.03	0.04	0.05	0.04	0.04	0.03	0.03	0.03	0.03	0.03	0.04	0.05	0.03	0.03	0.02	0.03	0.03	0.03	0.02	0.03	0.03
90	0.03	0.06	0.02	0.03	0.04	0.04	0.04	0.03	0.04	0.03	0.03	0.04	0.04	0.05	0.04	0.03	0.03	0.03	0.03	0.04	0.03	0.04	0.04
91	0.03	0.05	0.02	0.03	0.04	0.04	0.03	0.03	0.04	0.04	0.04	0.04	0.05	0.06	0.04	0.04	0.04	0.05	0.04	0.05	0.05	0.06	0.05
92	0.03	0.06	0.02	0.03	0.04	0.04	0.04	0.03	0.03	0.03	0.03	0.03	0.04	0.05	0.04	0.03	0.03	0.03	0.03	0.03	0.04	0.04	0.04
93	0.06	0.08	0.05	0.06	0.08	0.06	0.06	0.05	0.07	0.05	0.06	0.06	0.08	0.08	0.07	0.07	0.06	0.07	0.06	0.06	0.08	0.08	0.06
94	0.03	0.04	0.02	0.03	0.04	0.03	0.03	0.03	0.05	0.05	0.05	0.06	0.06	0.07	0.06	0.06	0.05	0.05	0.05	0.06	0.06	0.07	0.06

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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	0.01	0.00	0.00																				
27	0.00	0.00	0.01	0.00																			
28	0.03	0.02	0.03	0.03	0.00																		
29	0.03	0.03	0.04	0.03	0.04	0.00																	
30	0.01	0.00	0.01	0.00	0.02	0.03	0.00																
31	0.01	0.00	0.01	0.01	0.03	0.03	0.01	0.00															
32	0.01	0.01	0.01	0.01	0.03	0.03	0.00	0.01	0.00														
33	0.02	0.02	0.02	0.02	0.04	0.03	0.01	0.01	0.01	0.00													
34	0.01	0.01	0.01	0.00	0.03	0.03	0.00	0.00	0.01	0.01	0.00												
35	0.01	0.01	0.01	0.01	0.02	0.03	0.01	0.01	0.00	0.01	0.00	0.00											
36	0.01	0.01	0.01	0.02	0.03	0.04	0.01	0.01	0.01	0.02	0.01	0.01	0.00										
37	0.01	0.01	0.01	0.01	0.04	0.04	0.02	0.01	0.02	0.03	0.02	0.02	0.02	0.00									
38	0.01	0.01	0.01	0.02	0.04	0.04	0.01	0.01	0.01	0.03	0.02	0.01	0.01	0.01	0.00								
39	0.02	0.01	0.02	0.01	0.04	0.04	0.01	0.02	0.02	0.03	0.02	0.02	0.02	0.00	0.01	0.00							
40	0.01	0.01	0.01	0.01	0.04	0.04	0.01	0.01	0.01	0.02	0.01	0.01	0.01	0.00	0.00	0.01	0.00						
41	0.01	0.01	0.01	0.01	0.03	0.04	0.01	0.01	0.01	0.03	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00					
42	0.01	0.01	0.01	0.01	0.03	0.04	0.01	0.01	0.01	0.02	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00				
43	0.01	0.00	0.01	0.01	0.03	0.03	0.01	0.01	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.00			
44	0.01	0.01	0.01	0.01	0.04	0.05	0.02	0.02	0.03	0.03	0.01	0.02	0.02	0.01	0.02	0.02	0.01	0.01	0.01	0.01	0.00		
45	0.03	0.02	0.03	0.02	0.06	0.06	0.03	0.03	0.03	0.04	0.02	0.03	0.03	0.03	0.03	0.02	0.02	0.03	0.02	0.02	0.03	0.00	
46	0.02	0.01	0.02	0.01	0.04	0.04	0.01	0.01	0.02	0.02	0.01	0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.01	0.02	0.02	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	0.01	0.01	0.01	0.00	0.03	0.03	0.01	0.01	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.01	0.02	0.01
48	0.02	0.02	0.02	0.02	0.04	0.04	0.02	0.02	0.02	0.03	0.02	0.02	0.02	0.03	0.02	0.03	0.03	0.03	0.02	0.02	0.03	0.04	0.03
49	0.01	0.01	0.01	0.01	0.04	0.04	0.01	0.01	0.01	0.02	0.01	0.01	0.01	0.02	0.01	0.02	0.01	0.01	0.01	0.01	0.01	0.03	0.02
50	0.01	0.01	0.02	0.02	0.05	0.04	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	0.02	0.03	0.02
51	0.03	0.02	0.04	0.02	0.05	0.04	0.02	0.02	0.03	0.03	0.02	0.02	0.03	0.03	0.03	0.03	0.02	0.02	0.02	0.02	0.03	0.05	0.04
52	0.03	0.03	0.04	0.03	0.05	0.04	0.03	0.03	0.04	0.04	0.03	0.02	0.03	0.03	0.03	0.03	0.02	0.02	0.03	0.02	0.03	0.05	0.04
53	0.04	0.03	0.04	0.04	0.06	0.06	0.04	0.04	0.05	0.06	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.03	0.04	0.03	0.03	0.07	0.05
54	0.03	0.02	0.02	0.02	0.05	0.04	0.02	0.02	0.03	0.03	0.03	0.02	0.03	0.02	0.02	0.03	0.02	0.02	0.02	0.02	0.02	0.05	0.03
55	0.02	0.02	0.02	0.02	0.05	0.05	0.02	0.02	0.02	0.04	0.03	0.02	0.03	0.02	0.02	0.03	0.02	0.02	0.02	0.02	0.03	0.04	0.03
56	0.05	0.04	0.05	0.04	0.08	0.07	0.05	0.05	0.05	0.06	0.05	0.04	0.05	0.04	0.05	0.05	0.05	0.04	0.04	0.04	0.05	0.07	0.05
57	0.04	0.03	0.04	0.04	0.06	0.07	0.04	0.04	0.04	0.05	0.04	0.04	0.05	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.06	0.05
58	0.07	0.07	0.08	0.07	0.10	0.09	0.07	0.08	0.07	0.08	0.07	0.06	0.07	0.07	0.07	0.07	0.07	0.07	0.06	0.07	0.07	0.10	0.08
59	0.03	0.03	0.03	0.03	0.05	0.05	0.03	0.03	0.04	0.04	0.03	0.03	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.03	0.04	0.05	0.04
60	0.07	0.06	0.07	0.07	0.10	0.08	0.07	0.06	0.08	0.08	0.07	0.06	0.07	0.06	0.07	0.06	0.06	0.06	0.06	0.06	0.06	0.09	0.07
61	0.02	0.01	0.02	0.02	0.04	0.03	0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.03	0.02	0.03	0.02	0.02	0.02	0.02	0.03	0.03	0.03
62	0.01	0.01	0.01	0.01	0.03	0.03	0.01	0.01	0.01	0.02	0.01	0.01	0.02	0.02	0.02	0.02	0.01	0.01	0.01	0.01	0.02	0.03	0.02
63	0.03	0.03	0.03	0.03	0.06	0.05	0.03	0.04	0.04	0.04	0.04	0.04	0.04	0.03	0.04	0.04	0.03	0.03	0.03	0.03	0.04	0.05	0.05
64	0.02	0.02	0.02	0.01	0.04	0.03	0.02	0.02	0.02	0.02	0.02	0.01	0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.04	0.03
65	0.03	0.03	0.03	0.03	0.05	0.06	0.03	0.03	0.04	0.05	0.03	0.04	0.04	0.03	0.04	0.03	0.03	0.03	0.03	0.03	0.03	0.04	0.04
66	0.06	0.05	0.04	0.05	0.07	0.06	0.04	0.05	0.05	0.05	0.04	0.04	0.04	0.06	0.05	0.05	0.05	0.04	0.05	0.04	0.05	0.05	0.04
67	0.02	0.01	0.01	0.01	0.04	0.03	0.01	0.01	0.01	0.02	0.01	0.01	0.02	0.02	0.01	0.02	0.02	0.01	0.01	0.01	0.02	0.03	0.02
68	0.02	0.01	0.02	0.02	0.04	0.03	0.01	0.01	0.01	0.02	0.01	0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.03	0.04	0.02
69	0.05	0.04	0.06	0.05	0.06	0.06	0.04	0.05	0.05	0.06	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.04	0.05	0.04	0.05	0.07	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
70	0.05	0.04	0.06	0.05	0.06	0.06	0.05	0.05	0.05	0.06	0.05	0.05	0.05	0.06	0.05	0.06	0.06	0.05	0.05	0.05	0.05	0.07	0.06
71	0.05	0.04	0.06	0.04	0.06	0.07	0.04	0.04	0.04	0.05	0.05	0.04	0.04	0.05	0.04	0.05	0.05	0.05	0.05	0.05	0.06	0.07	0.05
72	0.11	0.11	0.12	0.11	0.13	0.14	0.11	0.11	0.12	0.13	0.11	0.11	0.12	0.11	0.12	0.12	0.11	0.11	0.11	0.11	0.11	0.11	0.11
73	0.09	0.09	0.10	0.10	0.11	0.11	0.09	0.10	0.09	0.10	0.09	0.09	0.09	0.09	0.09	0.10	0.09	0.09	0.09	0.09	0.10	0.10	0.09
74	0.10	0.10	0.11	0.10	0.12	0.14	0.10	0.10	0.11	0.12	0.10	0.11	0.11	0.10	0.11	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10
75	0.09	0.09	0.10	0.09	0.10	0.11	0.08	0.09	0.09	0.10	0.09	0.08	0.09	0.09	0.09	0.09	0.08	0.08	0.08	0.08	0.09	0.10	0.08
76	0.10	0.10	0.10	0.10	0.11	0.11	0.10	0.10	0.10	0.11	0.10	0.09	0.10	0.10	0.10	0.11	0.10	0.10	0.10	0.09	0.10	0.10	0.10
77	0.09	0.08	0.09	0.08	0.09	0.09	0.08	0.08	0.09	0.09	0.08	0.08	0.08	0.09	0.09	0.09	0.08	0.08	0.08	0.07	0.08	0.10	0.08
78	0.12	0.12	0.13	0.12	0.15	0.14	0.11	0.12	0.12	0.13	0.12	0.12	0.11	0.12	0.12	0.13	0.11	0.12	0.12	0.11	0.12	0.13	0.11
79	0.08	0.07	0.08	0.08	0.09	0.10	0.08	0.07	0.09	0.09	0.07	0.08	0.09	0.07	0.08	0.08	0.07	0.07	0.07	0.07	0.07	0.07	0.06
80	0.07	0.06	0.08	0.06	0.08	0.07	0.06	0.06	0.07	0.07	0.07	0.06	0.07	0.07	0.07	0.07	0.07	0.07	0.06	0.06	0.07	0.08	0.07
81	0.05	0.04	0.05	0.05	0.05	0.04	0.03	0.04	0.04	0.05	0.04	0.04	0.05	0.05	0.05	0.05	0.05	0.05	0.04	0.04	0.06	0.06	0.04
82	0.10	0.09	0.11	0.10	0.11	0.12	0.09	0.10	0.10	0.11	0.10	0.09	0.11	0.10	0.10	0.10	0.10	0.10	0.09	0.10	0.10	0.12	0.10
83	0.04	0.04	0.05	0.04	0.05	0.04	0.03	0.04	0.04	0.04	0.03	0.03	0.04	0.05	0.05	0.05	0.04	0.04	0.04	0.04	0.05	0.06	0.04
84	0.04	0.04	0.04	0.04	0.07	0.05	0.04	0.05	0.05	0.06	0.04	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.04	0.04	0.06	0.05
85	0.06	0.05	0.06	0.07	0.09	0.07	0.05	0.06	0.06	0.07	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.05	0.07	0.06	0.06
86	0.07	0.06	0.07	0.07	0.10	0.08	0.06	0.06	0.07	0.08	0.07	0.06	0.07	0.07	0.06	0.07	0.06	0.06	0.06	0.06	0.08	0.07	0.07
87	0.04	0.03	0.04	0.03	0.06	0.04	0.03	0.03	0.03	0.04	0.03	0.03	0.04	0.04	0.04	0.04	0.04	0.03	0.03	0.03	0.05	0.05	0.04
88	0.05	0.03	0.05	0.05	0.07	0.05	0.04	0.04	0.04	0.05	0.04	0.04	0.05	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.05	0.06	0.04
89	0.03	0.02	0.03	0.03	0.04	0.03	0.02	0.03	0.02	0.03	0.02	0.02	0.04	0.04	0.04	0.04	0.04	0.03	0.03	0.03	0.04	0.05	0.03
90	0.04	0.03	0.04	0.04	0.05	0.03	0.03	0.04	0.03	0.04	0.03	0.03	0.04	0.04	0.04	0.05	0.04	0.04	0.04	0.04	0.05	0.06	0.04
91	0.05	0.04	0.05	0.05	0.07	0.05	0.04	0.05	0.04	0.05	0.04	0.04	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.04	0.07	0.07	0.06
92	0.04	0.03	0.04	0.04	0.05	0.04	0.03	0.04	0.03	0.04	0.03	0.03	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.05	0.05	0.04
93	0.07	0.06	0.07	0.07	0.08	0.07	0.07	0.08	0.07	0.08	0.06	0.06	0.08	0.07	0.08	0.07	0.07	0.07	0.07	0.06	0.08	0.09	0.07
94	0.07	0.06	0.07	0.07	0.08	0.06	0.06	0.06	0.06	0.07	0.06	0.05	0.06	0.07	0.06	0.07	0.06	0.06	0.06	0.06	0.08	0.07	0.06

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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	68	69
47	0.00																						
48	0.02	0.00																					
49	0.01	0.02	0.00																				
50	0.02	0.02	0.01	0.00																			
51	0.02	0.02	0.02	0.02	0.00																		
52	0.03	0.03	0.02	0.01	0.01	0.00																	
53	0.04	0.04	0.04	0.03	0.03	0.04	0.00																
54	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.00															
55	0.02	0.02	0.03	0.02	0.03	0.03	0.03	0.01	0.00														
56	0.04	0.04	0.05	0.05	0.04	0.05	0.03	0.02	0.01	0.00													
57	0.04	0.04	0.04	0.04	0.04	0.05	0.04	0.02	0.01	0.01	0.00												
58	0.07	0.07	0.06	0.06	0.06	0.07	0.09	0.08	0.07	0.08	0.08	0.00											
59	0.03	0.01	0.03	0.03	0.03	0.03	0.05	0.03	0.03	0.06	0.05	0.09	0.00										
60	0.07	0.07	0.06	0.05	0.05	0.05	0.06	0.06	0.06	0.09	0.09	0.09	0.08	0.00									
61	0.02	0.00	0.02	0.01	0.01	0.02	0.03	0.02	0.02	0.04	0.04	0.06	0.01	0.06	0.00								
62	0.01	0.02	0.01	0.01	0.01	0.02	0.03	0.01	0.02	0.04	0.03	0.07	0.02	0.05	0.01	0.00							
63	0.03	0.04	0.03	0.03	0.04	0.04	0.06	0.03	0.03	0.05	0.05	0.09	0.05	0.08	0.03	0.03	0.00						
64	0.02	0.03	0.02	0.02	0.03	0.03	0.04	0.02	0.02	0.04	0.04	0.07	0.04	0.07	0.02	0.01	0.01	0.00					
65	0.03	0.03	0.04	0.03	0.04	0.04	0.04	0.03	0.03	0.06	0.05	0.09	0.04	0.07	0.03	0.03	0.04	0.02	0.00				
66	0.05	0.05	0.04	0.05	0.07	0.07	0.07	0.06	0.05	0.08	0.07	0.11	0.07	0.10	0.05	0.04	0.07	0.05	0.06	0.00			
67	0.01	0.01	0.01	0.01	0.02	0.02	0.03	0.02	0.02	0.04	0.03	0.06	0.03	0.06	0.01	0.01	0.03	0.02	0.03	0.03	0.00		
68	0.02	0.02	0.02	0.02	0.02	0.03	0.04	0.02	0.03	0.05	0.04	0.09	0.04	0.07	0.02	0.01	0.03	0.02	0.04	0.05	0.01	0.00	
69	0.05	0.05	0.04	0.05	0.04	0.05	0.06	0.04	0.06	0.08	0.08	0.11	0.06	0.07	0.05	0.04	0.06	0.05	0.07	0.08	0.04	0.05	0.00

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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	68	69
70	0.05	0.05	0.04	0.05	0.04	0.06	0.06	0.04	0.06	0.08	0.07	0.11	0.06	0.07	0.05	0.04	0.07	0.05	0.06	0.08	0.04	0.06	0.01
71	0.04	0.05	0.03	0.05	0.05	0.06	0.07	0.05	0.06	0.08	0.06	0.10	0.07	0.10	0.05	0.04	0.07	0.05	0.07	0.08	0.04	0.05	0.03
72	0.11	0.10	0.11	0.10	0.12	0.12	0.11	0.10	0.09	0.11	0.10	0.16	0.10	0.17	0.10	0.10	0.12	0.10	0.09	0.12	0.10	0.10	0.15
73	0.08	0.08	0.09	0.08	0.09	0.10	0.10	0.08	0.08	0.09	0.09	0.15	0.10	0.17	0.09	0.09	0.11	0.09	0.09	0.10	0.08	0.08	0.12
74	0.10	0.09	0.10	0.09	0.11	0.12	0.10	0.09	0.08	0.10	0.09	0.15	0.10	0.16	0.09	0.09	0.11	0.09	0.08	0.12	0.10	0.09	0.13
75	0.08	0.07	0.08	0.07	0.09	0.09	0.09	0.07	0.07	0.09	0.08	0.13	0.08	0.15	0.07	0.07	0.10	0.08	0.08	0.09	0.07	0.07	0.12
76	0.09	0.08	0.10	0.09	0.10	0.10	0.10	0.08	0.08	0.10	0.09	0.14	0.09	0.16	0.08	0.08	0.10	0.09	0.08	0.10	0.08	0.08	0.13
77	0.07	0.07	0.08	0.08	0.07	0.08	0.08	0.06	0.07	0.10	0.09	0.14	0.07	0.15	0.07	0.07	0.08	0.06	0.07	0.09	0.06	0.06	0.09
78	0.11	0.11	0.11	0.11	0.11	0.12	0.12	0.10	0.09	0.12	0.11	0.17	0.11	0.17	0.11	0.09	0.13	0.12	0.10	0.11	0.10	0.10	0.13
79	0.07	0.07	0.08	0.07	0.08	0.09	0.08	0.07	0.06	0.08	0.07	0.13	0.07	0.13	0.07	0.07	0.09	0.06	0.07	0.09	0.07	0.06	0.10
80	0.06	0.05	0.07	0.06	0.06	0.07	0.06	0.05	0.06	0.08	0.07	0.11	0.06	0.12	0.05	0.05	0.07	0.06	0.06	0.08	0.05	0.05	0.08
81	0.04	0.03	0.04	0.04	0.04	0.05	0.06	0.04	0.04	0.08	0.07	0.09	0.04	0.09	0.03	0.03	0.05	0.04	0.05	0.06	0.03	0.03	0.07
82	0.10	0.10	0.09	0.09	0.09	0.10	0.10	0.09	0.09	0.12	0.11	0.15	0.11	0.11	0.10	0.07	0.11	0.09	0.09	0.12	0.09	0.08	0.09
83	0.04	0.03	0.04	0.04	0.04	0.05	0.05	0.04	0.04	0.07	0.06	0.08	0.05	0.09	0.03	0.03	0.04	0.03	0.04	0.06	0.03	0.02	0.07
84	0.04	0.05	0.04	0.05	0.06	0.06	0.07	0.05	0.06	0.08	0.08	0.10	0.07	0.12	0.04	0.04	0.05	0.04	0.05	0.06	0.04	0.03	0.09
85	0.06	0.06	0.06	0.06	0.07	0.07	0.08	0.06	0.06	0.09	0.09	0.12	0.06	0.10	0.05	0.05	0.08	0.07	0.07	0.08	0.05	0.06	0.08
86	0.06	0.06	0.06	0.06	0.07	0.07	0.08	0.06	0.07	0.10	0.09	0.12	0.07	0.11	0.05	0.06	0.08	0.07	0.07	0.09	0.06	0.06	0.07
87	0.03	0.04	0.03	0.04	0.04	0.04	0.05	0.03	0.04	0.07	0.06	0.09	0.05	0.08	0.03	0.03	0.04	0.03	0.05	0.06	0.03	0.03	0.05
88	0.04	0.04	0.05	0.04	0.04	0.04	0.05	0.03	0.05	0.07	0.07	0.09	0.05	0.08	0.04	0.04	0.06	0.05	0.05	0.07	0.03	0.03	0.06
89	0.03	0.03	0.03	0.04	0.04	0.04	0.05	0.03	0.04	0.06	0.06	0.09	0.04	0.09	0.03	0.03	0.06	0.04	0.05	0.06	0.02	0.03	0.05
90	0.04	0.04	0.04	0.04	0.05	0.05	0.05	0.03	0.04	0.06	0.05	0.08	0.05	0.09	0.03	0.03	0.06	0.04	0.05	0.06	0.03	0.03	0.06
91	0.05	0.04	0.05	0.05	0.06	0.06	0.06	0.05	0.05	0.07	0.07	0.09	0.06	0.10	0.04	0.04	0.06	0.05	0.06	0.07	0.04	0.04	0.06
92	0.03	0.03	0.03	0.04	0.05	0.05	0.05	0.04	0.04	0.06	0.06	0.08	0.04	0.09	0.03	0.03	0.06	0.04	0.05	0.05	0.03	0.03	0.05
93	0.06	0.08	0.07	0.07	0.09	0.08	0.09	0.08	0.08	0.10	0.10	0.12	0.09	0.14	0.08	0.07	0.10	0.07	0.08	0.08	0.06	0.07	0.09
94	0.06	0.06	0.06	0.06	0.06	0.06	0.07	0.06	0.05	0.08	0.08	0.11	0.06	0.11	0.05	0.05	0.07	0.06	0.07	0.07	0.04	0.06	0.06

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Pop. No.	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94
70	0.00																								
71	0.03	0.00																							
72	0.13	0.14	0.00																						
73	0.13	0.11	0.07	0.00																					
74	0.12	0.12	0.02	0.06	0.00																				
75	0.11	0.10	0.05	0.02	0.04	0.00																			
76	0.13	0.11	0.05	0.02	0.05	0.01	0.00																		
77	0.09	0.10	0.09	0.08	0.08	0.06	0.07	0.00																	
78	0.13	0.13	0.11	0.07	0.10	0.07	0.08	0.08	0.00																
79	0.09	0.10	0.03	0.06	0.03	0.05	0.05	0.05	0.09	0.00															
80	0.08	0.08	0.10	0.06	0.08	0.05	0.06	0.02	0.07	0.05	0.00														
81	0.06	0.07	0.09	0.08	0.08	0.06	0.07	0.04	0.09	0.05	0.03	0.00													
82	0.09	0.09	0.15	0.14	0.14	0.13	0.14	0.13	0.13	0.11	0.12	0.09	0.00												
83	0.06	0.06	0.09	0.08	0.09	0.06	0.07	0.05	0.09	0.05	0.04	0.01	0.09	0.00											
84	0.09	0.09	0.11	0.11	0.12	0.10	0.10	0.07	0.13	0.08	0.07	0.04	0.12	0.03	0.00										
85	0.08	0.09	0.12	0.11	0.12	0.10	0.11	0.07	0.10	0.08	0.07	0.06	0.12	0.06	0.08	0.00									
86	0.08	0.08	0.12	0.11	0.11	0.09	0.10	0.07	0.10	0.08	0.07	0.06	0.12	0.06	0.07	0.01	0.00								
87	0.05	0.05	0.10	0.08	0.09	0.07	0.08	0.05	0.10	0.06	0.05	0.04	0.09	0.03	0.05	0.03	0.03	0.00							
88	0.07	0.07	0.11	0.09	0.10	0.08	0.09	0.05	0.10	0.06	0.04	0.03	0.11	0.04	0.05	0.02	0.02	0.02	0.00						
89	0.06	0.06	0.11	0.07	0.10	0.07	0.09	0.07	0.11	0.08	0.06	0.04	0.10	0.04	0.06	0.06	0.07	0.03	0.04	0.00					
90	0.06	0.06	0.10	0.07	0.09	0.06	0.08	0.06	0.10	0.07	0.05	0.04	0.10	0.04	0.05	0.06	0.06	0.03	0.03	0.01	0.00				
91	0.06	0.06	0.11	0.07	0.10	0.07	0.08	0.07	0.11	0.08	0.06	0.04	0.11	0.05	0.07	0.06	0.06	0.04	0.04	0.02	0.01	0.00			
92	0.06	0.06	0.10	0.06	0.09	0.06	0.07	0.06	0.10	0.07	0.05	0.03	0.10	0.03	0.05	0.06	0.06	0.03	0.04	0.01	0.00	0.01	0.00		
93	0.09	0.09	0.12	0.11	0.13	0.11	0.11	0.10	0.14	0.10	0.09	0.08	0.13	0.08	0.08	0.10	0.11	0.06	0.08	0.06	0.05	0.06	0.05	0.00	
94	0.07	0.08	0.11	0.08	0.11	0.08	0.09	0.06	0.09	0.09	0.06	0.05	0.11	0.06	0.08	0.07	0.07	0.04	0.05	0.03	0.03	0.03	0.03	0.05	0.00

APPENDIX B

Appendix B1.–Estimates of stock composition (%) for 10 replicates of 100% proof tests for each of 11 reporting groups included as part of the Cook Inlet coho salmon genetic baseline with 82 loci. Each replicate was a sample of 100 or 200 individuals removed from the genetic baseline. Estimates for each replicate describe the posterior distributions by the mean, 90% credibility interval (CI), and standard deviation (SD).

Reporting Group	Mean	90% CI		SD	Mean	90% CI		SD
		5%	95%			5%	95%	
	Southwest CI Replicate 1				*Southwest CI* Replicate 2			
Southwest CI	96.3	92.4	99.4	2.2	98.0	94.9	99.8	1.6
Northwest CI	1.9	0.0	5.7	2.0	0.2	0.0	1.3	0.6
Susitna	0.4	0.0	2.2	0.9	0.1	0.0	0.5	0.3
Deshka	0.2	0.0	1.1	0.5	0.1	0.0	0.3	0.2
Yentna	0.3	0.0	2.1	0.8	0.1	0.0	0.9	0.4
Knik	0.1	0.0	0.6	0.3	0.1	0.0	0.6	0.3
Jim	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Turnagain/Northeast CI	0.1	0.0	0.8	0.4	0.1	0.0	0.7	0.4
Kenai	0.2	0.0	0.9	0.4	0.6	0.0	2.1	0.7
Kasilof	0.1	0.0	0.5	0.3	0.1	0.0	0.3	0.2
Southeast CI	0.3	0.0	1.8	0.7	0.6	0.0	2.8	1.0
	Southwest CI Replicate 3				*Southwest CI* Replicate 4			
Southwest CI	99.0	97.0	100.0	1.0	98.9	96.8	100.0	1.1
Northwest CI	0.2	0.0	1.0	0.5	0.1	0.0	0.7	0.4
Susitna	0.1	0.0	0.4	0.2	0.2	0.0	1.4	0.6
Deshka	0.1	0.0	0.6	0.3	0.1	0.0	0.4	0.2
Yentna	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.3
Knik	0.1	0.0	0.6	0.3	0.1	0.0	0.6	0.3
Jim	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Turnagain/Northeast CI	0.1	0.0	0.8	0.4	0.2	0.0	1.0	0.4
Kenai	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.2
Kasilof	0.1	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Southeast CI	0.2	0.0	1.0	0.5	0.2	0.0	1.0	0.5
	Southwest CI Replicate 5				*Southwest CI* Replicate 6			
Southwest CI	98.3	95.2	99.9	1.6	98.7	96.1	99.9	1.3
Northwest CI	0.1	0.0	0.6	0.3	0.3	0.0	1.8	0.7
Susitna	0.1	0.0	0.6	0.3	0.1	0.0	0.8	0.4
Deshka	0.1	0.0	0.4	0.2	0.1	0.0	0.5	0.3
Yentna	0.1	0.0	0.5	0.3	0.1	0.0	0.6	0.3
Knik	0.1	0.0	0.5	0.3	0.1	0.0	0.4	0.3
Jim	0.0	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Turnagain/Northeast CI	0.2	0.0	1.6	0.8	0.1	0.0	0.8	0.4
Kenai	0.1	0.0	0.9	0.4	0.1	0.0	0.4	0.2
Kasilof	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Southeast CI	0.8	0.0	3.1	1.1	0.3	0.0	2.0	0.8

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| Reporting Group | 90% CI | | | | | 90% CI | | | |
	Mean	5%	95%	SD	Mean	5%	95%	SD
	Southwest CI Replicate 7					*Southwest CI* Replicate 8			
Southwest CI	97.0	91.8	99.8	2.6	97.5	93.5	99.8	2.1
Northwest CI	0.5	0.0	3.3	1.2	0.1	0.0	0.8	0.4
Susitna	0.3	0.0	2.0	0.9	0.1	0.0	0.4	0.2
Deshka	0.1	0.0	0.6	0.3	0.1	0.0	0.4	0.2
Yentna	0.1	0.0	0.7	0.4	0.1	0.0	0.6	0.3
Knik	0.1	0.0	0.7	0.4	0.1	0.0	0.4	0.2
Jim	0.1	0.0	0.6	0.3	0.1	0.0	0.5	0.2
Turnagain/Northeast CI	1.0	0.0	4.8	1.7	0.1	0.0	0.4	0.2
Kenai	0.4	0.0	1.6	0.6	0.4	0.0	1.6	0.6
Kasilof	0.1	0.0	0.4	0.2	0.1	0.0	0.8	0.4
Southeast CI	0.3	0.0	2.1	0.8	1.3	0.0	5.1	1.8
	Southwest CI Replicate 9					*Southwest CI* Replicate 10			
Southwest CI	98.9	96.8	100.0	1.1	98.1	95.0	99.9	1.6
Northwest CI	0.2	0.0	1.4	0.6	0.5	0.0	2.6	1.0
Susitna	0.1	0.0	0.6	0.4	0.3	0.0	1.6	0.6
Deshka	0.1	0.0	0.4	0.2	0.1	0.0	0.5	0.3
Yentna	0.1	0.0	0.9	0.4	0.3	0.0	1.8	0.7
Knik	0.1	0.0	0.7	0.3	0.1	0.0	0.6	0.3
Jim	0.0	0.0	0.3	0.1	0.1	0.0	0.3	0.2
Turnagain/Northeast CI	0.1	0.0	0.5	0.2	0.1	0.0	0.9	0.4
Kenai	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Kasilof	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.2
Southeast CI	0.2	0.0	1.0	0.5	0.3	0.0	2.0	0.8
	Northwest CI Replicate 1					*Northwest CI* Replicate 2			
Southwest CI	0.2	0.0	1.0	0.8	0.2	0.0	1.0	0.6
Northwest CI	84.1	71.9	95.4	7.0	96.5	89.7	99.9	3.4
Susitna	12.0	0.1	23.6	6.8	0.5	0.0	3.0	1.2
Deshka	1.5	0.0	7.0	2.5	0.9	0.0	4.9	1.8
Yentna	0.7	0.0	4.4	1.9	1.1	0.0	6.5	2.4
Knik	0.3	0.0	2.0	0.9	0.3	0.0	1.5	0.9
Jim	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Turnagain/Northeast CI	0.9	0.0	4.0	1.5	0.2	0.0	1.1	0.8
Kenai	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Kasilof	0.1	0.0	0.4	0.2	0.1	0.0	0.8	0.4
Southeast CI	0.1	0.0	0.8	0.4	0.1	0.0	0.6	0.3

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	Northwest CI Replicate 3				*Northwest CI* Replicate 4			
Southwest CI	0.3	0.0	1.9	0.8	0.3	0.0	1.4	1.0
Northwest CI	91.4	82.0	98.7	5.1	96.0	89.7	99.8	3.3
Susitna	2.3	0.0	9.7	3.5	1.0	0.0	5.4	2.0
Deshka	2.0	0.0	6.8	2.4	0.8	0.0	4.2	1.5
Yentna	3.4	0.0	11.6	4.1	0.8	0.0	4.6	1.7
Knik	0.2	0.0	1.1	0.6	0.3	0.0	1.7	0.8
Jim	0.1	0.0	0.5	0.3	0.1	0.0	0.5	0.3
Turnagain/Northeast CI	0.2	0.0	1.0	0.5	0.6	0.0	3.0	1.1
Kenai	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.2
Kasilof	0.1	0.0	0.4	0.2	0.1	0.0	0.7	0.3
Southeast CI	0.1	0.0	0.5	0.3	0.1	0.0	0.4	0.2
	Northwest CI Replicate 5				*Northwest CI* Replicate 6			
Southwest CI	0.1	0.0	0.7	0.4	0.2	0.0	1.4	0.6
Northwest CI	88.2	76.3	97.5	6.5	97.1	91.5	99.8	2.7
Susitna	0.6	0.0	3.6	1.4	0.7	0.0	4.6	1.8
Deshka	1.0	0.0	4.4	1.6	0.4	0.0	2.2	1.0
Yentna	3.4	0.0	10.5	3.6	0.4	0.0	2.4	1.3
Knik	5.8	0.0	17.2	6.2	0.3	0.0	1.9	0.8
Jim	0.1	0.0	0.5	0.3	0.1	0.0	0.4	0.2
Turnagain/Northeast CI	0.5	0.0	2.8	1.2	0.5	0.0	2.3	0.9
Kenai	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Kasilof	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.3
Southeast CI	0.1	0.0	0.7	0.4	0.1	0.0	0.6	0.3
	Northwest CI Replicate 7				*Northwest CI* Replicate 8			
Southwest CI	0.2	0.0	1.6	0.7	1.9	0.0	9.6	3.4
Northwest CI	88.1	78.8	96.1	5.2	88.5	74.3	99.1	7.7
Susitna	6.9	0.0	16.0	5.1	2.3	0.0	10.0	3.5
Deshka	0.3	0.0	2.0	0.9	0.3	0.0	1.7	0.8
Yentna	2.6	0.0	10.3	3.6	5.7	0.0	17.0	5.9
Knik	0.4	0.0	2.0	1.3	0.3	0.0	1.4	1.0
Jim	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Turnagain/Northeast CI	1.1	0.0	3.3	1.3	0.6	0.0	2.9	1.3
Kenai	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.2
Kasilof	0.2	0.0	0.9	0.5	0.1	0.0	0.3	0.2
Southeast CI	0.1	0.0	0.8	0.4	0.2	0.0	1.5	0.7

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Reporting Group	Mean	90% CI 5%	95%	SD	Mean	90% CI 5%	95%	SD
		Northwest CI Replicate 9				*Northwest CI* Replicate 10		
Southwest CI	0.1	0.0	0.9	0.4	0.5	0.0	2.8	1.1
Northwest CI	91.1	81.8	98.8	5.2	88.2	76.1	98.8	7.0
Susitna	4.7	0.0	13.6	4.7	2.0	0.0	9.1	3.2
Deshka	0.2	0.0	1.5	0.7	0.2	0.0	1.1	0.5
Yentna	1.9	0.0	9.1	3.2	7.9	0.0	20.2	6.9
Knik	0.2	0.0	1.0	0.7	0.2	0.0	1.2	0.6
Jim	0.1	0.0	0.3	0.2	0.1	0.0	0.4	0.2
Turnagain/Northeast CI	1.3	0.0	7.5	2.6	0.6	0.0	2.6	1.0
Kenai	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Kasilof	0.1	0.0	0.8	0.4	0.1	0.0	0.5	0.3
Southeast CI	0.1	0.0	0.5	0.3	0.1	0.0	0.7	0.4
		Susitna Replicate 1				*Susitna* Replicate 2		
Southwest CI	0.1	0.0	0.6	0.4	0.1	0.0	0.5	0.3
Northwest CI	0.9	0.0	5.7	2.2	2.2	0.0	8.2	3.0
Susitna	87.9	77.2	97.5	6.2	94.7	87.3	99.4	3.9
Deshka	0.8	0.0	4.5	1.6	0.2	0.0	1.4	0.7
Yentna	7.9	0.0	18.2	5.9	0.8	0.0	4.5	1.8
Knik	1.6	0.2	4.9	1.6	1.0	0.0	3.2	1.1
Jim	0.1	0.0	0.8	0.4	0.1	0.0	0.9	0.5
Turnagain/Northeast CI	0.2	0.0	1.4	0.7	0.5	0.0	3.4	1.3
Kenai	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.2
Kasilof	0.1	0.0	0.6	0.4	0.2	0.0	1.1	0.6
Southeast CI	0.1	0.0	0.8	0.4	0.1	0.0	0.7	0.4
		Susitna Replicate 3				*Susitna* Replicate 4		
Southwest CI	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Northwest CI	0.6	0.0	3.7	1.6	0.4	0.0	2.2	0.9
Susitna	95.6	87.9	99.8	3.9	95.9	90.3	99.4	2.9
Deshka	1.7	0.0	7.8	2.7	1.0	0.0	5.2	1.9
Yentna	0.9	0.0	5.0	2.1	0.4	0.0	2.8	1.2
Knik	0.6	0.0	3.2	1.2	0.8	0.0	2.5	0.9
Jim	0.1	0.0	0.6	0.3	0.8	0.0	2.9	1.0
Turnagain/Northeast CI	0.2	0.0	0.9	0.6	0.3	0.0	1.9	0.9
Kenai	0.1	0.0	0.3	0.2	0.1	0.0	0.4	0.2
Kasilof	0.1	0.0	0.7	0.3	0.1	0.0	0.8	0.5
Southeast CI	0.1	0.0	0.8	0.4	0.1	0.0	0.5	0.3

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| Reporting Group | 90% CI | | | | | 90% CI | | |
	Mean	5%	95%	SD	Mean	5%	95%	SD
	Susitna Replicate 5					*Susitna* Replicate 6		
Southwest CI	0.1	0.0	0.8	0.4	0.1	0.0	0.9	0.5
Northwest CI	1.7	0.0	8.6	3.1	1.4	0.0	6.4	2.5
Susitna	87.3	77.8	95.2	5.3	94.6	85.7	99.7	4.5
Deshka	7.4	1.5	13.7	3.7	2.0	0.0	7.4	2.6
Yentna	0.9	0.0	5.2	1.9	1.1	0.0	7.3	2.7
Knik	0.3	0.0	2.1	0.8	0.2	0.0	1.0	0.7
Jim	0.1	0.0	0.5	0.3	0.1	0.0	0.3	0.2
Turnagain/Northeast CI	0.5	0.0	3.0	1.4	0.2	0.0	1.3	0.6
Kenai	0.1	0.0	0.4	0.3	0.1	0.0	0.3	0.2
Kasilof	1.5	0.0	5.2	1.9	0.1	0.0	0.4	0.2
Southeast CI	0.2	0.0	1.4	0.7	0.2	0.0	1.1	0.5
	Susitna Replicate 7					*Susitna* Replicate 8		
Southwest CI	0.1	0.0	0.6	0.5	0.1	0.0	0.6	0.4
Northwest CI	2.6	0.0	11.7	4.2	4.5	0.0	13.6	4.8
Susitna	82.6	68.2	98.0	9.0	91.0	81.6	98.4	5.2
Deshka	0.9	0.0	4.6	1.7	0.7	0.0	4.1	1.5
Yentna	12.6	0.0	27.8	9.6	0.4	0.0	2.3	1.2
Knik	0.3	0.0	1.5	0.7	0.3	0.0	1.8	0.8
Jim	0.1	0.0	0.5	0.3	0.1	0.0	0.6	0.3
Turnagain/Northeast CI	0.5	0.0	3.5	1.4	0.4	0.0	2.3	1.1
Kenai	0.1	0.0	0.3	0.2	0.2	0.0	1.0	0.5
Kasilof	0.1	0.0	0.6	0.3	2.2	0.0	6.6	2.3
Southeast CI	0.2	0.0	1.1	0.5	0.1	0.0	0.5	0.3
	Susitna Replicate 9					*Susitna* Replicate 10		
Southwest CI	0.2	0.0	1.3	0.6	0.1	0.0	0.4	0.2
Northwest CI	0.7	0.0	4.6	1.8	0.5	0.0	3.1	1.4
Susitna	90.9	81.0	99.3	5.7	90.3	74.4	98.9	7.4
Deshka	0.3	0.0	2.1	0.9	4.0	0.0	10.2	3.4
Yentna	6.1	0.0	14.6	5.1	3.3	0.0	18.0	6.1
Knik	0.3	0.0	1.8	0.8	0.9	0.0	2.9	1.1
Jim	0.1	0.0	0.5	0.3	0.1	0.0	0.5	0.3
Turnagain/Northeast CI	1.0	0.0	4.5	1.8	0.7	0.0	3.9	1.5
Kenai	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Kasilof	0.2	0.0	1.1	0.5	0.1	0.0	0.4	0.3
Southeast CI	0.1	0.0	0.6	0.3	0.1	0.0	0.3	0.2

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Reporting Group	Mean	90% CI		SD	Mean	90% CI		SD
		5%	95%			5%	95%	
	Deshka Replicate 1				*Deshka* Replicate 2			
Southwest CI	0.1	0.0	0.3	0.2	0.1	0.0	0.4	0.2
Northwest CI	0.2	0.0	1.4	0.7	0.5	0.0	2.9	1.1
Susitna	1.3	0.0	8.2	2.9	2.8	0.0	10.2	3.6
Deshka	97.1	90.4	99.9	3.2	94.6	87.2	99.6	3.9
Yentna	0.2	0.0	1.3	0.6	1.3	0.0	6.4	2.4
Knik	0.2	0.0	1.4	0.6	0.2	0.0	1.5	0.6
Jim	0.1	0.0	0.3	0.2	0.1	0.0	0.4	0.2
Turnagain/Northeast CI	0.6	0.0	3.5	1.3	0.2	0.0	1.1	0.5
Kenai	0.1	0.0	0.8	0.4	0.1	0.0	0.6	0.3
Kasilof	0.1	0.0	0.4	0.2	0.1	0.0	0.5	0.3
Southeast CI	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
	Deshka Replicate 3				*Deshka* Replicate 4			
Southwest CI	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Northwest CI	0.6	0.0	3.3	1.2	0.2	0.0	1.0	0.5
Susitna	0.8	0.0	5.1	1.8	0.1	0.0	0.9	0.5
Deshka	95.8	90.3	99.7	3.0	99.0	97.0	100.0	1.0
Yentna	1.9	0.0	6.6	2.4	0.1	0.0	0.9	0.4
Knik	0.5	0.0	2.8	1.0	0.1	0.0	0.6	0.3
Jim	0.1	0.0	0.6	0.3	0.1	0.0	0.4	0.2
Turnagain/Northeast CI	0.1	0.0	0.5	0.3	0.1	0.0	0.6	0.3
Kenai	0.1	0.0	0.4	0.2	0.1	0.0	0.5	0.3
Kasilof	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Southeast CI	0.1	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Deshka Replicate 5				*Deshka* Replicate 6			
Southwest CI	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Northwest CI	1.2	0.0	5.9	2.1	0.2	0.0	1.4	0.7
Susitna	0.7	0.0	4.5	1.9	3.3	0.0	11.1	3.9
Deshka	95.3	89.0	99.7	3.4	94.9	87.6	99.7	3.9
Yentna	2.0	0.0	8.4	3.0	0.8	0.0	4.8	1.8
Knik	0.3	0.0	1.9	0.8	0.1	0.0	0.9	0.4
Jim	0.1	0.0	0.4	0.2	0.1	0.0	0.5	0.3
Turnagain/Northeast CI	0.1	0.0	0.7	0.4	0.2	0.0	1.3	0.6
Kenai	0.1	0.0	0.5	0.2	0.1	0.0	0.3	0.2
Kasilof	0.1	0.0	0.8	0.4	0.1	0.0	0.6	0.3
Southeast CI	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2

Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
	Deshka Replicate 7				*Deshka* Replicate 8			
Southwest CI	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Northwest CI	1.8	0.0	7.6	2.7	0.2	0.0	1.0	0.5
Susitna	1.1	0.0	6.6	2.3	0.3	0.0	2.0	0.9
Deshka	92.1	84.6	98.7	4.2	98.6	95.6	99.9	1.5
Yentna	4.3	0.0	12.6	4.4	0.3	0.0	1.7	0.8
Knik	0.2	0.0	1.1	0.5	0.1	0.0	0.9	0.4
Jim	0.1	0.0	0.3	0.2	0.1	0.0	0.6	0.3
Turnagain/Northeast CI	0.3	0.0	1.8	0.8	0.1	0.0	0.7	0.4
Kenai	0.1	0.0	0.3	0.2	0.1	0.0	0.5	0.3
Kasilof	0.1	0.0	0.5	0.3	0.1	0.0	0.4	0.2
Southeast CI	0.1	0.0	0.3	0.2	0.0	0.0	0.3	0.2
	Deshka Replicate 9				*Deshka* Replicate 10			
Southwest CI	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Northwest CI	0.5	0.0	3.2	1.3	1.2	0.0	6.3	2.3
Susitna	0.9	0.0	5.8	2.1	0.7	0.0	4.4	1.7
Deshka	96.3	90.4	99.8	3.0	92.9	86.6	98.5	3.6
Yentna	1.4	0.0	6.1	2.2	4.5	0.0	10.7	3.5
Knik	0.1	0.0	0.8	0.5	0.1	0.0	0.7	0.4
Jim	0.1	0.0	0.3	0.2	0.1	0.0	0.4	0.2
Turnagain/Northeast CI	0.3	0.0	2.1	0.9	0.1	0.0	0.7	0.5
Kenai	0.2	0.0	0.9	0.4	0.1	0.0	0.8	0.3
Kasilof	0.1	0.0	0.4	0.3	0.1	0.0	0.7	0.4
Southeast CI	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
	Yentna Replicate 1				*Yentna* Replicate 2			
Southwest CI	0.1	0.0	0.6	0.4	0.2	0.0	1.6	0.6
Northwest CI	0.3	0.0	1.7	0.8	0.3	0.0	2.0	1.0
Susitna	0.8	0.0	4.5	1.7	0.9	0.0	4.3	1.7
Deshka	0.8	0.0	4.4	1.6	0.4	0.0	2.6	1.1
Yentna	97.0	91.7	99.8	2.7	97.2	92.4	99.8	2.4
Knik	0.3	0.0	2.0	0.8	0.2	0.0	1.4	0.7
Jim	0.1	0.0	0.4	0.2	0.1	0.0	0.5	0.3
Turnagain/Northeast CI	0.2	0.0	1.3	0.6	0.1	0.0	0.7	0.5
Kenai	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Kasilof	0.2	0.0	1.2	0.5	0.1	0.0	0.4	0.2
Southeast CI	0.2	0.0	1.2	0.5	0.4	0.0	2.0	0.7

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| Reporting Group | 90% CI | | | | | 90% CI | | |
	Mean	5%	95%	SD	Mean	5%	95%	SD
	Yentna Replicate 3					*Yentna* Replicate 4		
Southwest CI	0.1	0.0	0.5	0.4	0.1	0.0	0.5	0.3
Northwest CI	0.8	0.0	4.8	1.9	0.4	0.0	2.2	1.0
Susitna	1.3	0.0	7.3	2.6	7.7	0.0	19.2	6.6
Deshka	0.7	0.0	4.0	1.4	0.3	0.0	1.8	0.8
Yentna	96.3	89.3	99.9	3.5	90.4	79.0	99.4	6.5
Knik	0.2	0.0	1.2	0.6	0.1	0.0	0.7	0.5
Jim	0.1	0.0	0.4	0.2	0.1	0.0	0.6	0.3
Turnagain/Northeast CI	0.1	0.0	0.8	0.4	0.1	0.0	0.7	0.5
Kenai	0.2	0.0	1.1	0.5	0.1	0.0	0.7	0.3
Kasilof	0.1	0.0	0.5	0.3	0.1	0.0	0.3	0.2
Southeast CI	0.1	0.0	0.9	0.4	0.6	0.0	3.2	1.1
	Yentna Replicate 5					*Yentna* Replicate 6		
Southwest CI	0.1	0.0	0.6	0.3	0.1	0.0	0.9	0.4
Northwest CI	0.5	0.0	3.4	1.5	0.6	0.0	3.4	1.3
Susitna	0.9	0.0	4.2	1.8	0.8	0.0	4.8	1.7
Deshka	0.2	0.0	1.3	0.6	0.6	0.0	3.4	1.3
Yentna	96.8	91.5	99.8	2.7	96.9	91.6	99.8	2.7
Knik	0.1	0.0	0.8	0.5	0.1	0.0	0.5	0.3
Jim	0.1	0.0	0.5	0.3	0.1	0.0	0.3	0.2
Turnagain/Northeast CI	0.4	0.0	2.5	1.1	0.3	0.0	1.8	0.8
Kenai	0.1	0.0	0.3	0.2	0.2	0.0	1.1	0.4
Kasilof	0.1	0.0	0.6	0.3	0.2	0.0	1.2	0.5
Southeast CI	0.6	0.0	2.7	1.0	0.1	0.0	0.6	0.3
	Yentna Replicate 7					*Yentna* Replicate 8		
Southwest CI	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.2
Northwest CI	2.6	0.0	10.2	3.6	0.8	0.0	4.9	1.9
Susitna	0.5	0.0	3.3	1.5	3.2	0.0	14.4	5.0
Deshka	1.0	0.0	5.0	1.8	0.3	0.0	1.9	0.8
Yentna	86.7	77.8	95.0	5.2	94.1	82.1	99.8	5.8
Knik	0.2	0.0	1.3	0.7	0.9	0.0	5.7	2.1
Jim	0.1	0.0	0.4	0.2	0.1	0.0	0.7	0.3
Turnagain/Northeast CI	8.5	0.0	15.8	4.5	0.2	0.0	0.9	0.5
Kenai	0.1	0.0	0.8	0.4	0.2	0.0	1.1	0.5
Kasilof	0.1	0.0	0.6	0.3	0.1	0.0	0.6	0.3
Southeast CI	0.1	0.0	0.6	0.3	0.1	0.0	0.4	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 9				*Yentna* Replicate 10		
Southwest CI	0.1	0.0	0.3	0.2	0.1	0.0	0.7	0.4
Northwest CI	0.9	0.0	5.9	2.2	1.4	0.0	7.3	2.6
Susitna	2.9	0.0	11.6	4.1	0.5	0.0	3.0	1.4
Deshka	2.5	0.0	9.1	3.2	0.2	0.0	1.3	0.7
Yentna	92.3	83.1	99.5	5.1	95.9	88.5	99.8	3.6
Knik	0.3	0.0	1.6	0.7	0.4	0.0	2.3	1.0
Jim	0.1	0.0	0.5	0.3	0.1	0.0	0.3	0.2
Turnagain/Northeast CI	0.7	0.0	4.4	1.6	0.9	0.0	4.8	1.8
Kenai	0.1	0.0	0.5	0.3	0.2	0.0	1.0	0.5
Kasilof	0.1	0.0	0.4	0.2	0.3	0.0	1.7	0.7
Southeast CI	0.1	0.0	0.5	0.3	0.1	0.0	0.8	0.4
		Knik Replicate 1				*Knik* Replicate 2		
Southwest CI	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.2
Northwest CI	0.3	0.0	1.7	0.8	1.4	0.0	5.4	2.0
Susitna	0.2	0.0	1.0	0.5	0.4	0.0	2.8	1.1
Deshka	0.1	0.0	0.8	0.4	0.2	0.0	1.2	0.6
Yentna	0.1	0.0	0.6	0.4	0.3	0.0	1.8	0.8
Knik	97.0	91.1	99.9	2.9	93.7	86.0	99.6	4.3
Jim	1.4	0.0	6.0	2.1	3.6	0.0	9.8	3.4
Turnagain/Northeast CI	0.6	0.0	3.4	1.3	0.2	0.0	0.9	0.6
Kenai	0.1	0.0	0.3	0.2	0.1	0.0	0.4	0.2
Kasilof	0.2	0.0	1.0	0.4	0.1	0.0	0.4	0.2
Southeast CI	0.1	0.0	0.3	0.2	0.1	0.0	0.4	0.2
		Knik Replicate 3				*Knik* Replicate 4		
Southwest CI	0.1	0.0	0.5	0.3	0.1	0.0	0.4	0.2
Northwest CI	0.8	0.0	4.5	1.6	0.7	0.0	4.0	1.7
Susitna	0.5	0.0	3.2	1.2	0.6	0.0	3.3	1.2
Deshka	0.4	0.0	2.5	1.0	0.3	0.0	2.1	0.9
Yentna	0.5	0.0	3.0	1.1	0.3	0.0	2.1	0.9
Knik	96.1	90.1	99.8	3.1	96.9	91.2	99.9	2.9
Jim	1.0	0.0	4.3	1.5	0.2	0.0	1.5	0.6
Turnagain/Northeast CI	0.2	0.0	1.3	0.7	0.6	0.0	4.0	1.6
Kenai	0.0	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Kasilof	0.1	0.0	0.3	0.2	0.1	0.0	0.4	0.3
Southeast CI	0.3	0.0	1.8	0.7	0.1	0.0	0.4	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 Replicate 5				*Knik* Replicate 6		
Southwest CI	0.2	0.0	1.1	0.7	0.2	0.0	1.3	0.6
Northwest CI	0.7	0.0	4.5	1.7	0.3	0.0	1.8	0.9
Susitna	0.3	0.0	1.7	0.9	0.3	0.0	2.1	0.9
Deshka	0.3	0.0	1.7	0.7	0.2	0.0	1.4	0.6
Yentna	0.2	0.0	1.0	0.6	0.2	0.0	1.3	0.6
Knik	96.6	90.4	99.9	3.1	97.7	93.8	99.9	2.0
Jim	0.3	0.0	1.6	0.7	0.4	0.0	2.1	0.8
Turnagain/Northeast CI	1.2	0.0	6.1	2.2	0.2	0.0	1.5	0.8
Kenai	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.3
Kasilof	0.1	0.0	0.4	0.2	0.2	0.0	1.3	0.5
Southeast CI	0.2	0.0	1.0	0.4	0.1	0.0	0.3	0.2
		Knik Replicate 7				*Knik* Replicate 8		
Southwest CI	0.1	0.0	0.8	0.3	0.1	0.0	0.8	0.3
Northwest CI	0.3	0.0	1.6	0.7	0.4	0.0	2.6	1.2
Susitna	0.9	0.0	4.9	1.8	0.6	0.0	3.4	1.2
Deshka	0.5	0.0	3.2	1.2	0.2	0.0	1.5	0.7
Yentna	1.2	0.0	5.0	1.8	0.2	0.0	1.1	0.6
Knik	94.4	88.3	99.0	3.3	93.1	86.0	99.1	4.0
Jim	2.0	0.0	5.5	1.8	4.5	0.0	10.0	3.2
Turnagain/Northeast CI	0.3	0.0	1.7	1.0	0.4	0.0	2.5	1.2
Kenai	0.1	0.0	0.3	0.2	0.1	0.0	0.4	0.2
Kasilof	0.1	0.0	0.4	0.2	0.2	0.0	1.0	0.4
Southeast CI	0.1	0.0	0.8	0.4	0.2	0.0	1.0	0.4
		Knik Replicate 9				*Knik* Replicate 10		
Southwest CI	0.1	0.0	0.4	0.3	0.1	0.0	0.5	0.3
Northwest CI	3.2	0.0	10.5	3.8	0.5	0.0	3.0	1.3
Susitna	0.3	0.0	2.0	0.8	1.4	0.0	6.2	2.2
Deshka	0.3	0.0	1.7	0.7	0.6	0.0	3.0	1.1
Yentna	0.6	0.0	3.4	1.3	0.7	0.0	4.1	1.5
Knik	92.4	83.7	99.0	4.7	91.4	84.8	96.5	3.6
Jim	2.6	0.0	6.6	2.2	4.6	1.8	8.0	1.9
Turnagain/Northeast CI	0.2	0.0	1.4	0.8	0.4	0.0	2.2	1.2
Kenai	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.2
Kasilof	0.1	0.0	0.8	0.4	0.1	0.0	0.4	0.2
Southeast CI	0.1	0.0	0.8	0.4	0.3	0.0	1.6	0.7

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Reporting Group	Mean	90% CI 5%	90% CI 95%	SD	Mean	90% CI 5%	90% CI 95%	SD
		Jim Replicate 1				*Jim* Replicate 2		
Southwest CI	0.1	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Northwest CI	0.2	0.0	0.9	0.4	0.1	0.0	0.4	0.2
Susitna	0.1	0.0	0.5	0.2	0.1	0.0	0.5	0.3
Deshka	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Yentna	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Knik	0.2	0.0	1.6	0.7	0.1	0.0	0.5	0.3
Jim	99.1	97.2	100.0	1.0	99.4	98.1	100.0	0.7
Turnagain/Northeast CI	0.1	0.0	0.5	0.3	0.1	0.0	0.4	0.2
Kenai	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof	0.1	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Southeast CI	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.1
		Jim Replicate 3				*Jim* Replicate 4		
Southwest CI	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Northwest CI	0.2	0.0	1.2	0.5	0.3	0.0	1.6	0.6
Susitna	0.1	0.0	0.9	0.4	0.1	0.0	0.7	0.4
Deshka	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Yentna	0.1	0.0	0.5	0.3	0.1	0.0	0.5	0.2
Knik	0.1	0.0	0.8	0.4	0.2	0.0	1.2	0.6
Jim	99.1	97.2	100.0	0.9	99.0	96.9	100.0	1.0
Turnagain/Northeast CI	0.1	0.0	0.5	0.3	0.1	0.0	0.5	0.3
Kenai	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.1
Kasilof	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Southeast CI	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
		Jim Replicate 5				*Jim* Replicate 6		
Southwest CI	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Northwest CI	0.1	0.0	0.3	0.2	0.1	0.0	0.5	0.3
Susitna	0.1	0.0	0.3	0.2	0.1	0.0	0.4	0.2
Deshka	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Yentna	0.1	0.0	0.3	0.2	0.1	0.0	0.4	0.3
Knik	0.1	0.0	0.6	0.4	0.1	0.0	0.6	0.3
Jim	99.4	98.2	100.0	0.6	99.4	98.0	100.0	0.7
Turnagain/Northeast CI	0.1	0.0	0.3	0.2	0.1	0.0	0.4	0.2
Kenai	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Southeast CI	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
		Jim Replicate 7				*Jim* Replicate 8		
Southwest CI	0.0	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Northwest CI	0.1	0.0	0.5	0.3	0.2	0.0	0.9	0.4
Susitna	0.1	0.0	0.4	0.2	0.1	0.0	0.6	0.3
Deshka	0.1	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Yentna	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.2
Knik	0.1	0.0	0.7	0.4	0.1	0.0	0.8	0.4
Jim	99.3	97.9	100.0	0.7	99.2	97.6	100.0	0.8
Turnagain/Northeast CI	0.1	0.0	0.4	0.2	0.1	0.0	0.5	0.3
Kenai	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Southeast CI	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
		Jim Replicate 9				*Jim* Replicate 10		
Southwest CI	0.1	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Northwest CI	0.3	0.0	1.6	0.6	0.1	0.0	0.8	0.4
Susitna	0.1	0.0	0.8	0.4	0.1	0.0	0.8	0.4
Deshka	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Yentna	0.1	0.0	0.4	0.2	0.1	0.0	0.5	0.3
Knik	0.1	0.0	0.6	0.3	0.1	0.0	0.6	0.4
Jim	99.1	97.2	100.0	0.9	99.2	97.6	100.0	0.8
Turnagain/Northeast CI	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.2
Kenai	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Kasilof	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Southeast CI	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
		Turnagain/Northeast CI Replicate 1				*Turnagain/Northeast CI* Replicate 2		
Southwest CI	0.3	0.0	1.6	0.6	0.1	0.0	0.4	0.2
Northwest CI	0.4	0.0	2.3	1.0	0.2	0.0	1.5	0.8
Susitna	0.3	0.0	1.8	0.8	0.7	0.0	3.4	1.3
Deshka	0.4	0.0	2.4	0.9	0.2	0.0	1.0	0.5
Yentna	0.4	0.0	2.8	1.1	0.3	0.0	1.9	0.9
Knik	1.9	0.0	7.4	2.7	0.7	0.0	4.4	1.6
Jim	0.2	0.0	1.0	0.4	0.1	0.0	0.4	0.2
Turnagain/Northeast CI	95.7	89.5	99.6	3.2	97.5	92.7	99.9	2.4
Kenai	0.1	0.0	0.5	0.3	0.1	0.0	0.3	0.2
Kasilof	0.1	0.0	0.5	0.3	0.1	0.0	0.4	0.2
Southeast CI	0.2	0.0	1.5	0.6	0.1	0.0	0.6	0.3

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Reporting Group	Mean	90% CI		SD	Mean	90% CI		SD
		5%	95%			5%	95%	
	Turnagain/Northeast CI				*Turnagain/Northeast CI*			
	Replicate 3				Replicate 4			
Southwest CI	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.3
Northwest CI	0.4	0.0	2.7	1.1	0.4	0.0	2.4	1.0
Susitna	0.4	0.0	2.6	1.0	1.1	0.0	6.3	2.2
Deshka	0.1	0.0	0.8	0.4	0.1	0.0	0.8	0.4
Yentna	0.2	0.0	1.2	0.5	0.4	0.0	2.5	1.0
Knik	1.9	0.0	5.3	1.8	0.3	0.0	1.5	0.9
Jim	0.5	0.0	2.0	0.7	1.1	0.0	3.1	1.0
Turnagain/Northeast CI	96.2	91.5	99.5	2.5	96.2	90.6	99.5	2.8
Kenai	0.1	0.0	0.8	0.4	0.1	0.0	0.3	0.2
Kasilof	0.1	0.0	0.4	0.2	0.2	0.0	1.0	0.4
Southeast CI	0.1	0.0	0.6	0.3	0.1	0.0	0.8	0.4
	Turnagain/Northeast CI				*Turnagain/Northeast CI*			
	Replicate 5				Replicate 6			
Southwest CI	0.2	0.0	1.0	0.4	0.7	0.0	2.7	0.9
Northwest CI	0.2	0.0	1.3	0.6	0.7	0.0	4.2	1.5
Susitna	0.5	0.0	2.7	1.1	0.5	0.0	2.8	1.1
Deshka	0.3	0.0	1.8	0.8	0.1	0.0	0.8	0.4
Yentna	0.5	0.0	3.0	1.2	0.4	0.0	2.6	1.1
Knik	1.5	0.0	5.5	1.9	0.2	0.0	1.1	0.6
Jim	0.1	0.0	0.7	0.3	0.1	0.0	0.6	0.3
Turnagain/Northeast CI	96.5	91.4	99.8	2.7	96.9	91.9	99.8	2.5
Kenai	0.1	0.0	0.4	0.2	0.1	0.0	0.7	0.4
Kasilof	0.1	0.0	0.5	0.3	0.1	0.0	0.4	0.2
Southeast CI	0.1	0.0	0.4	0.2	0.1	0.0	0.8	0.4
	Turnagain/Northeast CI				*Turnagain/Northeast CI*			
	Replicate 7				Replicate 8			
Southwest CI	0.1	0.0	0.4	0.2	0.2	0.0	1.1	0.6
Northwest CI	1.0	0.0	4.4	1.6	2.9	0.0	9.5	3.4
Susitna	0.8	0.0	4.0	1.5	0.8	0.0	5.1	2.0
Deshka	0.2	0.0	1.1	0.5	0.2	0.0	1.2	0.6
Yentna	0.1	0.0	0.8	0.4	1.7	0.0	8.5	2.9
Knik	1.3	0.0	5.6	2.4	0.6	0.0	3.6	1.4
Jim	0.7	0.0	2.7	1.0	0.2	0.0	1.1	0.5
Turnagain/Northeast CI	95.4	89.1	99.4	3.3	93.2	85.4	99.4	4.4
Kenai	0.1	0.0	0.4	0.2	0.1	0.0	0.8	0.4
Kasilof	0.2	0.0	1.2	0.5	0.1	0.0	0.7	0.4
Southeast CI	0.1	0.0	0.7	0.3	0.1	0.0	0.5	0.3

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Reporting Group	Mean	90% CI		SD	Mean	90% CI		SD
		5%	95%			5%	95%	
	Turnagain/Northeast CI Replicate 9				*Turnagain/Northeast CI* Replicate 10			
Southwest CI	0.1	0.0	0.7	0.4	0.1	0.0	0.8	0.4
Northwest CI	0.5	0.0	2.7	1.1	0.2	0.0	1.1	0.6
Susitna	2.3	0.0	9.5	3.3	0.3	0.0	2.0	0.9
Deshka	0.2	0.0	1.0	0.5	0.1	0.0	0.7	0.4
Yentna	0.2	0.0	1.1	0.6	0.1	0.0	0.7	0.4
Knik	0.5	0.0	2.9	1.1	0.3	0.0	1.7	0.8
Jim	0.1	0.0	0.5	0.2	0.4	0.0	1.7	0.6
Turnagain/Northeast CI	95.9	88.6	99.8	3.6	98.0	94.5	99.9	1.8
Kenai	0.1	0.0	0.6	0.3	0.1	0.0	0.6	0.4
Kasilof	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Southeast CI	0.2	0.0	1.5	0.7	0.3	0.0	1.7	0.7
	Kenai Replicate 1				*Kenai* Replicate 2			
Southwest CI	0.3	0.0	1.2	0.5	0.0	0.0	0.3	0.2
Northwest CI	0.3	0.0	1.3	0.5	0.1	0.0	0.5	0.3
Susitna	0.1	0.0	0.3	0.2	0.1	0.0	0.5	0.3
Deshka	0.1	0.0	0.3	0.2	0.1	0.0	0.6	0.3
Yentna	0.1	0.0	0.4	0.2	0.1	0.0	0.5	0.2
Knik	0.1	0.0	0.7	0.3	0.1	0.0	0.6	0.3
Jim	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Turnagain/Northeast CI	0.1	0.0	0.4	0.2	0.2	0.0	1.0	0.4
Kenai	98.9	97.3	99.8	0.8	99.2	97.6	100.0	0.8
Kasilof	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.2
Southeast CI	0.1	0.0	0.5	0.3	0.0	0.0	0.3	0.2
	Kenai Replicate 3				*Kenai* Replicate 4			
Southwest CI	0.0	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Northwest CI	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Susitna	0.1	0.0	0.3	0.2	0.1	0.0	0.4	0.2
Deshka	0.0	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Yentna	0.0	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Knik	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.2
Jim	0.0	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Turnagain/Northeast CI	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Kenai	99.5	98.3	100.0	0.6	99.4	98.2	100.0	0.6
Kasilof	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Southeast CI	0.0	0.0	0.3	0.2	0.1	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 Replicate 5				*Kenai* Replicate 6		
Southwest CI	0.3	0.0	1.2	0.4	0.1	0.0	0.3	0.2
Northwest CI	0.2	0.0	1.1	0.4	0.1	0.0	0.4	0.2
Susitna	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Deshka	0.0	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Yentna	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Knik	0.1	0.0	0.4	0.2	0.2	0.0	0.9	0.4
Jim	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.1
Turnagain/Northeast CI	0.1	0.0	0.3	0.2	0.1	0.0	0.4	0.3
Kenai	99.0	97.6	99.9	0.7	99.3	97.9	100.0	0.7
Kasilof	0.1	0.0	0.3	0.2	0.1	0.0	0.4	0.2
Southeast CI	0.1	0.0	0.6	0.3	0.1	0.0	0.3	0.2
		Kenai Replicate 7				*Kenai* Replicate 8		
Southwest CI	0.0	0.0	0.3	0.2	0.0	0.0	0.3	0.2
Northwest CI	0.1	0.0	0.4	0.2	0.0	0.0	0.3	0.2
Susitna	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Deshka	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Yentna	0.1	0.0	0.7	0.3	0.0	0.0	0.3	0.2
Knik	0.2	0.0	0.9	0.4	0.1	0.0	0.3	0.2
Jim	0.1	0.0	0.7	0.3	0.0	0.0	0.3	0.2
Turnagain/Northeast CI	0.1	0.0	0.5	0.3	0.1	0.0	0.3	0.2
Kenai	99.2	97.7	100.0	0.8	99.5	98.4	100.0	0.5
Kasilof	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Southeast CI	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
		Kenai Replicate 9				*Kenai* Replicate 10		
Southwest CI	0.1	0.0	0.3	0.2	0.1	0.0	0.3	0.2
Northwest CI	0.1	0.0	0.8	0.4	0.1	0.0	0.3	0.2
Susitna	0.1	0.0	0.6	0.3	0.1	0.0	0.5	0.2
Deshka	0.1	0.0	0.5	0.3	0.0	0.0	0.3	0.2
Yentna	0.1	0.0	0.5	0.3	0.1	0.0	0.3	0.2
Knik	0.1	0.0	0.7	0.3	0.1	0.0	0.3	0.2
Jim	0.0	0.0	0.3	0.1	0.1	0.0	0.3	0.2
Turnagain/Northeast CI	0.2	0.0	1.1	0.5	0.1	0.0	0.4	0.2
Kenai	99.1	97.3	100.0	0.9	99.4	98.2	100.0	0.6
Kasilof	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Southeast CI	0.1	0.0	0.3	0.2	0.1	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 Replicate 1				*Kasilof* Replicate 2		
Southwest CI	0.9	0.0	3.1	1.1	0.1	0.0	0.8	0.4
Northwest CI	0.1	0.0	0.7	0.4	0.1	0.0	0.7	0.4
Susitna	0.1	0.0	0.8	0.5	0.1	0.0	0.8	0.4
Deshka	0.1	0.0	0.6	0.3	0.1	0.0	0.6	0.3
Yentna	0.1	0.0	0.7	0.4	0.1	0.0	0.6	0.3
Knik	0.1	0.0	0.9	0.5	0.1	0.0	0.7	0.4
Jim	0.1	0.0	0.5	0.3	0.1	0.0	0.5	0.3
Turnagain/Northeast CI	0.1	0.0	0.8	0.4	0.6	0.0	3.5	1.3
Kenai	0.1	0.0	0.6	0.3	0.1	0.0	0.7	0.4
Kasilof	97.6	94.3	99.6	1.7	98.2	94.6	99.9	1.8
Southeast CI	0.4	0.0	2.5	1.0	0.2	0.0	1.5	0.7
		Kasilof Replicate 3				*Kasilof* Replicate 4		
Southwest CI	1.3	0.0	4.5	1.6	0.1	0.0	0.9	0.4
Northwest CI	0.1	0.0	0.6	0.3	0.1	0.0	0.9	0.5
Susitna	0.1	0.0	0.6	0.3	0.2	0.0	1.3	0.6
Deshka	0.1	0.0	0.5	0.3	0.2	0.0	1.2	0.6
Yentna	0.1	0.0	0.6	0.3	0.2	0.0	1.3	0.6
Knik	0.1	0.0	0.6	0.4	0.1	0.0	0.7	0.4
Jim	0.1	0.0	0.6	0.3	0.1	0.0	0.6	0.3
Turnagain/Northeast CI	0.1	0.0	0.8	0.4	0.5	0.0	3.1	1.1
Kenai	0.1	0.0	0.6	0.3	0.1	0.0	0.8	0.4
Kasilof	96.9	93.1	99.4	2.0	98.1	94.5	99.9	1.8
Southeast CI	1.0	0.0	4.3	1.5	0.1	0.0	0.8	0.4
		Kasilof Replicate 5				*Kasilof* Replicate 6		
Southwest CI	0.2	0.0	1.0	0.5	0.1	0.0	0.8	0.4
Northwest CI	0.2	0.0	1.3	0.7	0.1	0.0	0.7	0.4
Susitna	0.2	0.0	1.1	0.6	0.3	0.0	1.5	0.8
Deshka	0.2	0.0	1.1	0.6	0.2	0.0	1.1	0.5
Yentna	0.5	0.0	2.9	1.1	0.1	0.0	0.6	0.4
Knik	0.2	0.0	1.0	0.5	0.1	0.0	0.6	0.3
Jim	0.1	0.0	0.6	0.3	0.1	0.0	0.5	0.3
Turnagain/Northeast CI	0.2	0.0	0.9	0.5	0.3	0.0	1.9	0.8
Kenai	0.1	0.0	0.6	0.4	0.1	0.0	0.5	0.3
Kasilof	98.0	94.4	99.9	1.8	98.4	95.3	99.9	1.6
Southeast CI	0.2	0.0	1.0	0.5	0.2	0.0	1.1	0.5

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Reporting Group	Mean	90% CI		SD	Mean	90% CI		SD
		5%	95%			5%	95%	
	Kasilof Replicate 7				*Kasilof* Replicate 8			
Southwest CI	0.2	0.0	1.4	0.6	0.8	0.0	3.0	1.1
Northwest CI	0.1	0.0	0.6	0.3	0.1	0.0	0.8	0.4
Susitna	0.1	0.0	0.8	0.4	0.2	0.0	1.0	0.5
Deshka	0.1	0.0	0.6	0.3	0.2	0.0	1.3	0.6
Yentna	0.1	0.0	0.6	0.3	0.1	0.0	0.7	0.4
Knik	0.1	0.0	0.6	0.3	0.1	0.0	0.8	0.4
Jim	0.1	0.0	0.6	0.3	0.1	0.0	0.5	0.3
Turnagain/Northeast CI	0.1	0.0	0.9	0.5	0.2	0.0	1.0	0.5
Kenai	0.1	0.0	0.6	0.3	0.1	0.0	0.6	0.3
Kasilof	98.6	95.7	99.9	1.4	97.0	93.1	99.5	2.0
Southeast CI	0.3	0.0	1.9	0.8	1.1	0.0	4.5	1.6
	Kasilof Replicate 9				*Kasilof* Replicate 10			
Southwest CI	1.5	0.0	5.1	1.8	0.9	0.0	3.1	1.1
Northwest CI	0.2	0.0	1.1	0.6	0.1	0.0	0.7	0.4
Susitna	0.3	0.0	1.9	0.9	0.1	0.0	0.8	0.4
Deshka	0.1	0.0	0.7	0.4	0.2	0.0	1.1	0.5
Yentna	0.4	0.0	2.4	1.0	0.1	0.0	0.6	0.3
Knik	0.1	0.0	0.8	0.4	0.1	0.0	0.7	0.4
Jim	0.1	0.0	0.5	0.3	0.1	0.0	0.5	0.3
Turnagain/Northeast CI	0.3	0.0	1.7	0.8	0.2	0.0	1.1	0.6
Kenai	0.1	0.0	0.6	0.4	0.1	0.0	0.7	0.4
Kasilof	94.4	89.0	98.3	2.8	97.6	94.4	99.6	1.7
Southeast CI	2.5	0.0	7.8	2.8	0.4	0.0	2.2	0.9
	Southeast CI Replicate 1				*Southeast CI* Replicate 2			
Southwest CI	0.1	0.0	0.9	0.4	0.2	0.0	1.2	0.6
Northwest CI	0.1	0.0	0.4	0.2	0.1	0.0	0.5	0.3
Susitna	0.1	0.0	0.6	0.3	0.1	0.0	0.9	0.4
Deshka	0.1	0.0	0.6	0.3	0.1	0.0	0.5	0.2
Yentna	0.1	0.0	0.4	0.2	0.3	0.0	1.9	0.7
Knik	0.2	0.0	1.3	0.5	0.2	0.0	1.5	0.6
Jim	0.1	0.0	0.6	0.3	0.0	0.0	0.3	0.2
Turnagain/Northeast CI	0.6	0.0	2.4	0.9	0.1	0.0	0.7	0.4
Kenai	0.1	0.0	0.4	0.2	0.1	0.0	0.3	0.2
Kasilof	0.1	0.0	0.4	0.2	0.1	0.0	0.4	0.2
Southeast CI	98.5	96.2	99.9	1.2	98.6	96.2	99.9	1.2

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Reporting Group	90% CI					90% CI			
	Mean	5%	95%	SD		Mean	5%	95%	SD
	Southeast CI Replicate 3					*Southeast CI* Replicate 4			
Southwest CI	0.5	0.0	2.6	1.1		0.2	0.0	1.3	0.6
Northwest CI	0.1	0.0	0.5	0.3		0.1	0.0	0.4	0.2
Susitna	0.1	0.0	0.9	0.4		0.1	0.0	0.5	0.3
Deshka	0.1	0.0	0.4	0.2		0.1	0.0	0.4	0.2
Yentna	0.1	0.0	0.4	0.2		0.1	0.0	0.5	0.3
Knik	0.3	0.0	1.8	0.7		0.1	0.0	0.4	0.2
Jim	0.1	0.0	0.6	0.3		0.1	0.0	0.3	0.2
Turnagain/Northeast CI	0.5	0.0	2.3	0.8		0.1	0.0	0.3	0.2
Kenai	0.1	0.0	0.3	0.2		0.1	0.0	0.3	0.2
Kasilof	0.1	0.0	0.5	0.2		0.2	0.0	1.2	0.5
Southeast CI	98.1	95.1	99.8	1.6		99.1	97.1	100.0	1.0
	Southeast CI Replicate 5					*Southeast CI* Replicate 6			
Southwest CI	0.6	0.0	3.1	1.3		0.3	0.0	1.8	0.7
Northwest CI	0.1	0.0	0.4	0.2		0.2	0.0	1.0	0.4
Susitna	0.1	0.0	0.5	0.3		0.3	0.0	1.5	0.6
Deshka	0.1	0.0	0.6	0.3		0.1	0.0	0.4	0.2
Yentna	0.1	0.0	0.4	0.2		0.2	0.0	1.2	0.5
Knik	0.1	0.0	0.5	0.3		0.7	0.0	2.7	1.0
Jim	0.1	0.0	0.3	0.2		0.1	0.0	0.3	0.2
Turnagain/Northeast CI	0.1	0.0	0.5	0.3		0.6	0.0	2.8	1.0
Kenai	0.1	0.0	0.3	0.2		0.1	0.0	0.3	0.2
Kasilof	0.1	0.0	0.7	0.4		0.1	0.0	0.7	0.3
Southeast CI	98.7	95.9	100.0	1.5		97.5	94.5	99.6	1.6
	Southeast CI Replicate 7					*Southeast CI* Replicate 8			
Southwest CI	0.3	0.0	1.9	0.9		0.2	0.0	1.0	0.5
Northwest CI	0.1	0.0	0.8	0.4		0.1	0.0	0.6	0.3
Susitna	0.2	0.0	1.1	0.5		0.1	0.0	0.5	0.3
Deshka	0.2	0.0	1.2	0.5		0.1	0.0	0.5	0.3
Yentna	0.2	0.0	1.0	0.5		0.1	0.0	0.7	0.3
Knik	0.2	0.0	1.1	0.5		0.1	0.0	0.7	0.3
Jim	0.1	0.0	0.3	0.2		0.0	0.0	0.3	0.2
Turnagain/Northeast CI	0.1	0.0	0.8	0.4		0.1	0.0	0.4	0.2
Kenai	0.1	0.0	0.3	0.2		0.0	0.0	0.3	0.2
Kasilof	0.1	0.0	0.4	0.2		0.1	0.0	0.3	0.2
Southeast CI	98.5	95.7	99.9	1.4		99.1	97.4	100.0	0.9

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Reporting Group	Mean	90% CI 5%	95%	SD		Mean	90% CI 5%	95%	SD
	Southeast CI Replicate 9					*Southeast CI* Replicate 10			
Southwest CI	0.4	0.0	2.3	1.1		0.2	0.0	1.0	0.5
Northwest CI	0.1	0.0	0.5	0.3		0.1	0.0	0.6	0.3
Susitna	0.1	0.0	0.9	0.4		0.1	0.0	0.8	0.4
Deshka	0.1	0.0	0.4	0.2		0.1	0.0	0.3	0.2
Yentna	0.1	0.0	0.5	0.3		0.1	0.0	0.6	0.3
Knik	0.3	0.0	1.5	0.6		0.2	0.0	1.3	0.5
Jim	0.1	0.0	0.6	0.3		0.1	0.0	0.6	0.3
Turnagain/Northeast CI	0.8	0.0	3.1	1.1		0.5	0.0	2.3	0.8
Kenai	0.1	0.0	0.3	0.2		0.1	0.0	0.3	0.2
Kasilof	0.1	0.0	0.7	0.3		0.1	0.0	0.4	0.2
Southeast CI	97.9	94.7	99.8	1.7		98.5	96.1	99.9	1.2