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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

by

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November 2016

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

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Weights and measures (metric)	
centimeter	cm
deciliter	dL
gram	g
hectare	ha
kilogram	kg
kilometer	km
liter	L
meter	m
milliliter	mL
millimeter	mm

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

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

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

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

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

REGIONAL INFORMATION REPORT 5J16-09

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

by

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ABSTRACT

Chinook salmon *Oncorhynchus tshawytscha* stocks support important fisheries in Cook Inlet, Alaska. Many Chinook salmon stocks in Alaska have been in decline since 2007. Stock-specific harvest of Chinook salmon in the Cook Inlet marine sport fishery was identified as one of many information gaps hindering an understanding of the reasons for these declines. Here we report genetic baseline evaluation tests for mixed stock analysis (MSA) and select mixed stock analysis results using genetic and coded wire tag data (gcMSA) from Chinook salmon harvested in the Cook Inlet marine sport fishery from 2014 to 2016. Results of the baseline tests indicated adequate genetic variation to distinguish among 4 reporting groups of interest to management (*Outside CI*, *West/Susitna*, *CI Other*, and *Kenai*). The gcMSA results were obtained from 2,574 Chinook salmon sampled from the Cook Inlet marine sport fishery. This is a progress report to provide information to the Alaska Board of Fisheries on results to date for a research project that is scheduled to end in 2017. At the time of this report, adequate samples were available to report stock composition estimates for the Central Cook Inlet early period (April 1–June 24) for all 3 years and Lower Cook Inlet summer (April 1–August 30) and winter (January 1–March 31 and October 1–December 31) periods for 2014 and 2015 only. The *Outside CI* reporting group dominated all mixtures. The proportion of Cook Inlet Chinook salmon stocks was highest in Central Cook Inlet early period, with estimated contributions of 24.7%, 19.5%, and 10.1% in 2014, 2015, and 2016, respectively. Estimated contributions of the *Outside CI* reporting group in Lower Cook Inlet harvest samples was 97.9% and 99.0% in the summer period for 2014 and 2015, respectively and 99.8% in the winter period for both 2014 and 2015.

Key words: Chinook salmon, Cook Inlet, *Oncorhynchus tshawytscha*, single nucleotide polymorphism, SNP, mixed stock analysis, MSA, coded wire tag, CWT

INTRODUCTION

Chinook salmon *Oncorhynchus tshawytscha* stocks support important subsistence, personal use, sport, and commercial fisheries in Cook Inlet, Alaska. Annual harvests average roughly 1,300 fish for subsistence use and 1,100 fish for personal use (1996–2013; Fall et al. 2015). Sport fishing for Chinook salmon occurs in both salt and fresh waters of Cook Inlet, where an estimated 49,621 fish are harvested annually (2001–2015; Kathrin Sundet, Alaska Department of Fish and Game, pers. comm.). Commercial harvests occur in the Northern District set gillnet Chinook salmon fishery, and as a nontargeted species in Northern, Central, and Lower districts set gillnet and drift gillnet fisheries, averaging 13,529 fish annually (1996–2015; Shields and Dupuis 2016; Hollowell et al. 2016).

Productivity of some major stocks within Cook Inlet has declined in concert with stocks statewide, since 2007 (ADF&G 2013). A research plan was developed in 2013 to identify information needed to understand declines of Chinook salmon across Alaska. The plan focused on 12 indicator stocks including the 2 largest producers of Chinook salmon within Cook Inlet: the Susitna and Kenai rivers (ADF&G 2013). In this plan, the lack of stock-specific harvest estimates of Chinook salmon in marine waters of Cook Inlet was identified as an information gap. Several projects were recommended to fill this gap, including a project to estimate the stock-specific harvest of Chinook salmon in the Cook Inlet marine sport fishery.

The Cook Inlet marine sport fishery occurs in the Lower Cook Inlet Management Area (LCIMA; Kerkvliet et al. 2013). The LCIMA includes marine waters bounded by the west side of the Kenai Peninsula south of the Kasilof River drainage to Gore Point, and the west side of Cook Inlet from the south end of Chisik Island to Cape Douglas (Figure 1). Fishing occurs year round, mainly from boats trolling within 3 miles of shore and harvests average 14,257 Chinook salmon annually (2013–2015; Kerkvliet et al. *In prep*). For management purposes, the LCIMA marine sport fishery is divided into 2 geographic areas and those geographic areas are further divided into 2 temporal periods each. Geographic areas include Lower Cook Inlet (LCI) and Central

Cook Inlet (CCI) areas each with separate management strategies (Kerkvliet et al. 2013). The LCI area is located south of the latitude of Bluff Point (lat 59°40.0′N) and includes Kachemak Bay, and the CCI area is located north of Bluff Point. These areas are primarily accessed by sport anglers through the Homer small boat harbor and tractor launches at the Anchor Point and Deep Creek marine access areas. These 2 geographic areas are each divided into 2 temporal periods: CCI has Early (4/1–6/24) and Late (6/25–9/30) periods, while LCI has Summer (4/1–9/30) and Winter (1/1–3/31 and 10/1–12/31) periods.

The marine sport fishery in Cook Inlet became popular in the late 1980s and early 1990s, and harvests of Chinook salmon in the fishery increased with the growth of the guided sport fishing and tourism industries (McKinley 1999; Begich 2007). As the harvest of Chinook salmon in the fishery increased, so did management concerns regarding which stocks were being harvested. To address the question of which stocks are harvested in the marine sport fishery, earlier studies used coded wire tags (CWT) to estimate the harvest of select Cook Inlet Chinook salmon stocks (McKinley 1999; Begich 2007). These studies relied on recoveries of adult Chinook salmon that were tagged as juveniles from select wild and hatchery stocks. This method increased the knowledge of harvest rates of Cook Inlet Chinook salmon stocks present in the harvest; however, because relatively few stocks were tagged, the majority of the harvest was still of unknown origin.

Genetic mixed stock analysis (MSA) has been used in Cook Inlet to estimate the stock composition of sockeye salmon in the commercial fishery since the 1990s (Seeb et al. 2000; Habicht et al. 2007; Barclay et al. 2010a, 2010b, 2013, 2014). With the development of comprehensive genetic baselines for Upper Cook Inlet Chinook salmon (Barclay et al. 2012; Barclay and Habicht 2015), this method has more recently been used to estimate the stock composition of Chinook salmon harvested in the Upper Subdistrict set gillnet fishery (Eskelin et al 2013; Eskelin and Barclay 2015, 2016). These analyses estimated stock-specific commercial fishery harvests in Upper Cook Inlet during periods when fish are returning to Cook Inlet streams to spawn. These harvests are believed to be 100% Cook Inlet fish; therefore, the genetic baselines used to discriminate stocks in Upper Cook Inlet fishery harvests only contain Cook Inlet populations.

Conducting MSA on the Cook Inlet marine sport fishery harvest of Chinook salmon, where stocks from outside Cook Inlet are known to be present (McKinley 1999; Begich 2007) requires the use of a baseline containing populations from a much wider geographic range. Such a coastwide baseline was developed in 2011, which included 172 Chinook salmon populations from throughout the North Pacific analyzed for 43 single nucleotide polymorphism (SNP) markers (Templin et al. 2011). The population structure observed in this baseline reflected the rich diversity among populations of Chinook salmon across the Pacific Rim stemming from colonization from glacial refugia (Beringia vs. Cascadia) and life history (stream- vs. ocean-type), among other factors. However, this baseline was developed for broad-scale MSA of fishery harvests on the high seas and only contained 16 Chinook salmon populations from Cook Inlet. The most recent Cook Inlet baseline contains 55 Chinook salmon populations from throughout Cook Inlet analyzed for a set of 42 SNP markers included in the Templin et al. (2011) baseline (Barclay and Habicht 2015). The overlap in the marker sets between these baselines allows them to be merged to form a coastwide baseline with a comprehensive set of populations from within Cook Inlet.

Here we report genetic baseline evaluation tests for MSA and a subset of gcMSA results from Chinook salmon harvested in the Cook Inlet marine sport fishery in 2014–2016. This baseline combines the populations from outside of Cook Inlet from Templin et al. (2011) and the 55 Cook Inlet populations reported in Barclay and Habicht (2015) analyzed for 42 SNP markers common to both, hereafter referred to as the Cook Inlet coastwide baseline. We conduct gcMSA on harvests from the marine sport fishery in LCIMA for Chinook salmon from periods analyzed to date from 2014 to 2016.

This is a progress report on results to date for a project that is scheduled to end in 2017. This report is being released to provide the Alaska Board of Fisheries with information that might be useful for their regulatory proposal deliberations at the Lower Cook Inlet meeting scheduled for November/December, 2016. As such, some of the 2016 strata have not been analyzed and extrapolation from stock proportions to stock-specific harvest numbers have not been calculated for any strata. The final report for this project is scheduled to be completed by fall of 2017.

OBJECTIVES

1. Evaluate the Cook Inlet Chinook salmon coastwide baseline for MSA.
2. Sample the Cook Inlet Chinook salmon marine sport fishery, 2014–2016.
3. Determine location of origin for fish containing CWTs.
4. Analyze a subset of Chinook salmon fishery samples for 42 SNP markers.
5. Using both genetic and CWT information, estimate the stock composition of Chinook salmon harvested in the Cook Inlet marine sport fishery for both temporal strata in the LCI area for the 2014 and 2015 seasons and the *Early* stratum in the CCI area for each of the 2014–2016 seasons.

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.

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

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.

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.

Mixed stock analysis (*MSA*). A method using allele frequencies from baseline populations and genotypes from mixture samples to estimate stock compositions of mixtures. gcMSA is a method that combines MSA methods using genetic data and origin information from coded wire tags.

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; National Research Council 1996). This population definition is analogous to *spawning aggregations* described by Baker et al. (1996) and *demes* described by the National Research Council (1996).

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

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

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

METHODS

HARVEST SAMPLING

Field Sampling

Sampling of sport fish harvests at the Homer small boat harbor and tractor launches at the Anchor Point and Deep Creek marine access areas collected representative samples of the harvest in LCIMA (Figure 1). Sport anglers returning to these ports were surveyed for effort and catch information, and biological and genetic samples were collected.

Four technicians were assigned to the project, working 7.5 hours each scheduled work day, 5 days per week. Technicians were generally stationed in each port from early May to late August, which encompassed the majority of the marine sport fishing season. Sampling was scheduled during periods each day to maximize the number of anglers encountered, and salmon were examined and sampled—in the case of the Homer small boat harbor—to distribute sampling effort throughout the area. Interested anglers were provided kits to collect genetic, biological, and effort information during the winter fishery. Additional biological and genetic samples were collected by project staff and volunteers at Chinook salmon fishing derbies scheduled during the winter fishery months.

Genetic Tissues

Genetic tissue samples were collected from harvests of Chinook salmon in the marine sport fishery in 2014, 2015, and 2016. In each year, a sample of axillary process, fin, or muscle tissue was removed from each fish. Tissue samples were preserved for DNA analysis using 2 methods. In 2014 and 2015, tissues were placed in individually labeled 2 mL plastic vials and preserved in 95% ethanol. In 2016, tissues were placed and stapled onto numbered Whatman® (GE Healthcare Life Sciences) paper cards. Samples were placed into numbered grid locations on cards that were then placed in an airtight case with desiccant beads to preserve samples. Vial numbers and/or Whatman paper card and grid numbers were recorded on data sheets. Genetic tissues were sent to the Alaska Department of Fish and Game (ADF&G) Gene Conservation Laboratory for long-term storage and genetic analysis.

Coded Wire Tags

All Chinook salmon encountered were checked for the presence/absence of an adipose fin. Fish missing an adipose fin may have a CWT in their head. With permission of the angler, heads of all adipose finclipped fish` were collected and frozen. All collected heads were sent to the ADF&G Mark, Tag, and Age Laboratory in Juneau for CWT extraction and decoding to determine release location.

Subsampling for Genetic/Coded Wire Tag Mixed Stock Analysis

Samples were stratified geographically and temporally into 4 strata: (1) Central Cook Inlet April 1 to June 24 (CCI Early); (2) Central Cook Inlet June 25 to September 30 (CCI Late); (3) Lower Cook Inlet April 1 to September 30 (LCI Summer); and (4) Lower Cook Inlet January 1 to March 31 and October 1 to December 31 (LCI Winter). Samples were assigned an origin variable denoting whether the stock origin of the fish was known (through CWT recovery) or unknown (all other genetic samples).

Genetic Tissues

A systematic random sample of the unknown samples (target 300 fish) was identified and stratified by user group (private or charter fishermen) using SAS software (Copyright © 2011, SAS Institute Inc., Cary, NC, USA). Proportions of harvest by user groups were determined through final Statewide Harvest Survey estimates when available. When final Statewide Harvest Survey estimates were not available for a specific year or stratum, the average harvest by user group of the preceding 3 years was used as a proxy. The number of samples selected for genetic analysis varied across strata from year to year depending on the samples available for analysis among strata. For example, if fewer tissue samples were collected for a stratum than were budgeted to be processed, additional unknown samples were subsampled in proportion to harvest to increase the sample size of the remaining strata.

Known-Origin Samples

A systematic random sample of the known-origin samples that matched the proportion of samples selected for the genetic analysis was identified using SAS software. For example, if 60% of the unknown samples within a stratum (spatial, temporal, and user group) were selected for genetic analysis, then 60% of the known-origin fish would also be selected for gcMSA.

LABORATORY ANALYSIS

Assaying Genotypes

We extracted genomic DNA from tissue samples using a NucleoSpin® 96 Tissue Kit by Macherey-Nagel (Düren, Germany). DNA was screened for 42 SNP markers for all 3 years; however, to ensure that DNA concentrations were high enough with the dry sampling method used to preserve samples in 2016, a preamplification step was added before screening the DNA.

DNA from the 2014 and 2015 samples was genotyped using Fluidigm® 192.24 Dynamic Array™ Integrated Fluidic Circuits (IFCs), which systematically combine up to 24 assays and 192 samples into 4,608 parallel reactions. The components were pressurized into the IFC using the IFC Controller RX (Fluidigm). Each reaction was conducted in a 9 nL volume chamber consisting of a mixture of 20X Fast GT Sample Loading Reagent (Fluidigm), 2X TaqMan® GTXpress™ Master Mix (Applied Biosystems™), Custom TaqMan® SNP Genotyping Assay (Applied Biosystems), 2X Assay Loading Reagent (Fluidigm), 50X ROX Reference Dye (Invitrogen™), and 60–400 ng/µl DNA. Thermal cycling was performed on a Fluidigm FC1™ Cycler using a Fast PCR protocol as follows: an initial "Hot-Start" denaturation of 95ºC for 2 min followed by 40 cycles of denaturation at 95ºC for 2 s and annealing at 60ºC for 20 sec, with a final "Cool-Down" at 25ºC for 10 sec. The Dynamic Array IFCs were read on a Biomark™ or EP1™ System (Fluidigm) after amplification and genotyped using Fluidigm SNP Genotyping Analysis software.

The concentration of template DNA from the 2016 samples was increased using a multiplexed preamplification PCR of 42 screened SNP markers. Reactions were conducted in 10 µL volumes consisting of 4 uL of genomic DNA, 5 µL of 2X Multiplex PCR Master Mix (QIAGEN) and 1 µL each (2 µM SNP unlabeled forward and reverse primers). Thermal cycling was performed on a Dual 384-Well GeneAmp® PCR system 9700 (Applied Biosystems) at 95°C hold for 15 min followed by 20 cycles of 95°C for 15 s, 60°C for 4 min, and a final extension hold at 4°C.

We screened 158 of 350 preamplified DNA from the 2016 samples using the same methods as described for the 2014 and 2015 samples. The remaining 192 preamplified DNA samples were screened for 42 SNP markers using similar methods; however, Fluidigm® 96.96 Dynamic Array IFCs were used instead of Dynamic Array 192.24 IFCs.

Assays that failed to amplify on the Fluidigm system were reanalyzed with 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). 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 genotyped using the Life Technologies QuantStudio 12K Flex Software.

Genotypes were imported and archived in the Gene Conservation Laboratory's Oracle database, LOKI.

Laboratory Failure Rates and Quality Control

Overall failure rate was calculated by dividing the number of failed single-locus genotypes by the number of assayed single-locus genotypes. An individual genotype was considered a failure when a locus for a fish could not be satisfactorily genotyped.

Quality control (QC) measures were used to identify laboratory errors and to determine the reproducibility of genotypes. In this process, 8 of every 96 fish (1 row per 96-well plate) were reanalyzed for all markers by staff not involved with the original analysis. Laboratory errors found during the QC process were corrected, and genotypes were corrected in the database. Inconsistencies not attributable to laboratory error were recorded, but original genotype scores were retained in the database.

STATISTICAL ANALYSIS

Data Retrieval and Quality Control

We retrieved genotypes from LOKI and imported them into *R*[1] with the *RJDBC* package (Urbanek 2014). All subsequent analyses were performed in *R*, unless otherwise noted.

Prior to statistical analysis, we performed 2 analyses to confirm the quality of the data. First, 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 and reduce the accuracy of MSA.

The final QC analysis identified individuals with duplicate genotypes and removed them from further analyses. Duplicate genotypes can occur as a result of sampling or extracting the same individual twice and were defined as pairs of individuals sharing the same alleles in 95% of screened loci. The sample with the most missing genotypic data from each 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 Evaluation for Mixed Stock Analysis

Four reporting groups that were of interest to management, would likely perform adequately for MSA, and would provide estimates of Kenai and Susitna river stocks were identified at the beginning of the study (Table 1; Figures 2 and 3). These groups are:

1) *Outside CI* (Populations outside of Cook Inlet)
2) *West/Susitna* (Western Cook Inlet, Yentna River, and Susitna River populations)
3) *CI Other* (Cook Inlet populations from Turnagain Arm, Knik Arm, Kasilof River, and southern coastal Kenai Peninsula)
4) *Kenai* (Kenai River populations)

We assessed the accuracy and precision for MSA using these reporting groups with 100% proof tests generally following methods used by Barclay and Habicht (2015). In the 100% proof tests, mixtures were created by randomly sampling 400 fish from the baseline for a single reporting group, rebuilding the baseline without the sampled fish, and conducting MSA to evaluate how well the mixture allocated back to its group of origin. 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 ran 1 Markov Chain Monte Carlo chain with 40,000 iterations and discarded the first 20,000 iterations to remove the influence of starting values. The prior parameters for each reporting group were defined to be equal (i.e., a *flat* prior). Within each reporting group, the

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[1] *R* Development Core Team. 2016. *R*: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. http://www.R-project.org/.

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. Mean bias, root mean square error (RMSE), and mean 90% credibility intervals width were calculated for all proof tests to compare the predictive power of the baseline for each reporting group in terms of precision and accuracy. Mean bias indicates if there is a directional bias in the mean point estimate of the posterior (i.e., accuracy of the mean), RMSE shows the variability in the central tendency of the mean between replicates (i.e., precision of the posterior between replicates), and mean 90% credibility intervals width shows variation within the posterior for each replicate (i.e., precision of posterior within replicates).

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

Mixed Stock Analysis

We combined data from 2 sources to estimate the stock compositions of the harvest samples. The first source was genetic data from the fish of unknown origin and the second was known-origin data derived from coded-wire-tagged fish. To incorporate the stock compositions of CWT samples of known origin with stock compositions of genetic samples of unknown origin into a combined gcMSA, mixtures of sample size n were partitioned into known (k) and unknown (u) components and a separate Bayesian analysis was done on each component.

Analysis using genetic data: We estimated the stock composition of the genetic samples selected for MSA using the same BAYES protocol as was used for the proof tests, except that we ran 4 Markov Chain Monte Carlo chains of 40,000 iterations each. We formed the BAYES posterior distribution for each mixture from the last 20,000 iterations of each chain for a total length of 80,000 iterations. We assessed the among-chain convergence of these estimates in BAYES using the Gelman-Rubin shrink factor, which compares the variation of estimates within a chain to the total variation among chains (Gelman and Rubin 1992). If a shrink factor for any stock group estimate was greater than 1.2, we reanalyzed the mixture with 80,000-iteration chains following the same protocol.

Analysis incorporating CWT data: We incorporated uncertainty around proportions of known individuals in the mixture. To allow for uncertainty in the known component r, we placed a uniform distribution on it resulting in the following posterior:

$$r|n,k \sim \text{Beta}(k+1, n-k+1).$$

The known component is then partitioned into 4 stocks, where k_i is the count of known fish from stock i. To allow for uncertainty in the known stock composition $\mathbf{P}_K$, we place a unit Dirichlet distribution on them, resulting in the following posterior distribution:

$$\mathbf{P}_K|k \sim \text{Dirchlet}\left(k_1+\frac{1}{4}, \dots, k_4+\frac{1}{4}\right).$$

The posterior distributions from the known CWT and unknown genetic components were then combined by the following equation to estimate the proportion of each stock (p_i) in the mixture:

$$p_i = rp_{K,i} + (1-r)p_{U,i},$$

where r is the known proportion of the mixture, $p_{K,i}$ is stock i's composition in the known portion of the mixture, and $p_{U,i}$ is stock i's composition in the unknown portion of the mixture. Stock proportion estimates and 90% credibility intervals for each mixture were calculated by taking the mean and 5% and 95% quantiles of the combined posterior distribution.

RESULTS

HARVEST SAMPLING

Field Sampling

Genetic tissue and head samples were collected from 8,551 Chinook salmon harvested in the Cook Inlet marine sport fishery CCI Early (2014–2016; n=1,446), CCI Late (2014–2015; n=65), LCI Summer (2014–2015; n=5,614), and LCI Winter (2014–2015; n=1,426) strata (Table 2; Appendix A1).

Anglers were generally willing to participate in the project, allowing staff to collect biological data, genetic tissue samples, and effort data. Participation was widespread and anglers were very encouraging of this project gathering more information on the fishery.

Genetic Tissues

A total of 7,304 genetic samples were collected in 2014, 2015, and 2016, at docks, during derbies, and through participation in voluntary catch sampling in the winter months (Table 2; Appendix A1). These samples were partitioned each year into separate collections depending on where they were sampled (Homer, Anchor Point, or Deep Creek) for a total of 9 collections.

Known-Origin Samples

A total of 1,247 heads were collected from fish missing their adipose fin (Table 2; Appendix A1). Of the heads that were processed, approximately 38% contained CWTs and their origin was determined. The majority of these known-origin fish came from British Columbia, Washington, and Oregon (Table 3). Known-origin fish identified as originating from Alaska were all from outside of Cook Inlet.

Subsampling for Genetic/Coded Wire Tag Mixed Stock Analysis

A total of 2,483 fish selected for genetic analysis and 135 CWT fish of known origin were selected for gcMSA (Table 2). These samples include those from CCI Early (2014–2016), LCI Summer (2014–2015), and LCI Winter (2014–2015) strata. No samples were selected from the CCI Late stratum in 2014 and 2015 due to insufficient sample sizes for gcMSA. Samples from the 2016 CCI Late, LCI Summer and LCI Winter strata have not yet been selected or analyzed as sample and data collection is still underway. Data collection from the LCI Winter stratum will be completed December 31, 2016.

LABORATORY ANALYSIS

Assaying Genotypes

A total of 2,483 fish from the 2014–2016 sport harvest samples were selected for analysis and assayed for 42 SNP markers (Tables 2 and 4).

Laboratory Failure Rates and Quality Control

Genotyping failure rates among the 9 collections ranged from 0.55% to 3.02%. Discrepancy rates between original and QC analyses were uniformly low and ranged from 0.00% to 1.74%. Assuming equal error rates in the original and the QC analyses, estimated error rates in the samples is half of the discrepancy rate (0.00–0.87%).

STATISTICAL ANALYSIS

Data Retrieval and Quality Control

Twenty-nine of the assayed harvest individuals (1.14%) were removed from further analyses, based upon the 80% rule. No sport harvest tissue samples were identified as duplicates.

Baseline Evaluation for Mixed Stock Analysis

The average correct allocation for all 10 repeated proof tests for each of the 4 reporting groups ranged from 86.6% to 98.7% (Table 5; Appendix B1; Figure 4). The *Outside CI* and *Kenai* reporting groups had the highest correct allocations across all repeated tests averaging 98.7% (RMSE = 1.4%; 90% credibility interval width = 3.0%) and 96.8% (RMSE = 3.5%; 90% credibility interval width = 8.2%) for each group, respectively. The *West/Susitna* and *CI Other* allocations had more variation with correct allocations averaging 92.9% (RMSE = 8.7%; 90% credibility interval width = 21.4%) and 86.6% (RMSE = 14.1%; 90% credibility interval width = 17.6%) for each group, respectively. *West/Susitna* fish misallocated primarily to the *CI Other* reporting group (6.1%), whereas *CI Other* fish misallocated primarily to both *West/Susitna* (7.4%) and *Kenai* (5.7%). *Outside CI* fish misallocated at less than 1% to the other reporting groups and the other reporting groups misallocated to *Outside CI* at less than 1%.

Mixed Stock Analysis

A total of 2,483 genetic samples and 135 known-origin CWT samples were subsampled from the 2014–2016 collections to create 7 mixtures for which stock composition was estimated (Table 2). Mixture sample sizes ranged from 304 to 418 fish, with CWT samples comprising 3.1–7.7% of the mixtures. All reporting groups had shrink factors less than 1.2 for each mixture, indicating convergence among chains. Stock composition estimates including the known-origin CWT samples differed by less than 1% from the original BAYES estimates (data not shown).

Lower Cook Inlet Marine Sport Fishery

The *Outside CI* reporting group was the dominant reporting group in the LCI Summer and Winter harvest mixtures in 2014 and 2015 (Tables 6 and 7; Figures 5 and 6). The *Outside CI* group contributed 97.9% to the 2014 Summer mixture, and 99.0% to the 2015 Summer mixture. Allocations to the other reporting groups in 2014 were *CI Other* (1.5%), *West/Susitna* (0.1%), and *Kenai* (0.5%). The lower end of credibility intervals for *West/Susitna* and *Kenai* reporting groups included 0.0% and for *CI Other* the lower level was 0.4%. Allocations to the other reporting groups in 2015 were *CI Other* (0.2%), *West/Susitna* (0.7%), and *Kenai* (0.1%). The lower end of credibility intervals for all of these reporting groups included 0.0%.

The *Outside CI* group contributed 99.8% to the 2014 Winter mixture and 99.8% to the 2015 Winter mixture. Allocations to Cook Inlet reporting groups were all less than 0.1%. Credibility intervals around these estimates were narrow and ranged from 99.2% to 100% for the *Outside CI* group and 0.0% to 0.4% for each of the Cook Inlet groups between 2014 and 2015.

Central Cook Inlet Marine Sport Fishery

The combined contribution of Cook Inlet reporting groups in the CCI Early mixture was higher than in the LCI fishery mixtures. However, *Outside CI* was still the dominant reporting group, contributing between 75.3% and 89.9% to the mixtures in all years of the study (Tables 6–8; Figures 5–7). The combined contribution of Cook Inlet stocks in the Early fishing period dropped from 24.7% in 2014 to 10.1% in 2016. In all 3 years of the study, *West/Susitna* and *CI Other* comprised the largest portion of the CCI Early harvest—*West/Susitna* contributing 13.8% in 2014, 6.4% in 2015, and 4.2% in 2016, and *CI Other* contributing 10.4% in 2014, 12.7% in 2015, and 4.2% in 2016. *Kenai* had the lowest contributions in the harvest, contributing less than 1% in 2014 and 2015 and 1.7% in 2016; credibility intervals for *Kenai* included 0.0% in all 3 years.

DISCUSSION

This report includes baseline evaluation test results for a combined Cook Inlet and coastwide baseline and the gcMSA of harvest samples collected from the Cook Inlet marine sport fishery. In these analyses, the baseline was built from genetic data from previously reported Chinook salmon baselines (Templin et al. 2011; Barclay and Habicht 2015) combined to represent all populations expected to be potentially present in LCIMA fisheries. Mixed stock analysis of harvest samples included both genetic and coded wire tag data. Analyses were performed on harvest samples collected from the Cook Inlet marine sport harvest in the LCI fishery (Summer and Winter) in 2014 and 2015 and the CCI fishery (Early) from 2014 through 2016. These results represent the first mixed stock analysis using genetic information of Chinook salmon captured in the Cook Inlet marine sport fishery and a new baseline for use in mixed stock analyses in Cook Inlet where Chinook salmon stocks from outside Cook Inlet may be present.

MANAGEMENT IMPLICATIONS

Knowledge of stock composition of the harvest reinforces that regulations established for the sport fisheries provided a measure of protection to local stocks during surveyed years. This project provides fisheries managers with a snapshot regarding stock composition of the harvest in the CCI and LCI marine sport Chinook salmon fisheries, but estimates should be used with caution in developing management strategies because of potential shifts in harvest patterns and changes to relative productivity of local and nonlocal stocks (see MAKING INFERENCES OUTSIDE THE STUDY YEARS below).

REPRESENTATIVENESS OF HARVEST SAMPLES

Samples collected in this study likely represented unbiased samples of the harvest for each stratum despite some deviations from random sampling. Boats were equally likely to be sampled regardless of where fishing took place. Fish were sampled regardless of the location of harvest, and all fish on a vessel were sampled. Finally, sampling was conducted 7 days per week, sampling effort was distributed widely over the LCIMA during the summer months, and increased sampling effort was applied during periods of relatively high sport angling effort during winter months. These measures likely yielded unbiased samples of true harvests.

However, sampling of the Chinook salmon harvest in the Cook Inlet marine sport fishery presented some unique challenges. Ideally, samples would be collected proportional to the total harvest over time. Realistically, the numbers of fish available to the sampler might not have been proportional to the harvest in some instances because some landing sites were not sampled, fish were processed and carcasses disposed of at sea or in the harbor, or fish were kept on the boat and taken home to be processed later. Additionally, there was a maximum capacity that the sampler could work on days of very high harvest. This saturation effect could have resulted in undersampling of peak harvest days and subsequent underrepresentation of these days in gcMSA.

The Homer harbor and associated facilities cover a large area that makes distributing sampling effort in a representative manner difficult. Samplers moved between the public fish cleaning stations, boats cleaning fish on deck, the boat ramp, the fish cleaning table near the salmon enhancement lagoon, and numerous charter cleaning facilities in an effort to sample harvests from throughout the day's landings. Ideally, due to the high volume of charter-caught fish, approximately 4 or 5 charter boats would be randomly selected from a list of all known charter vessels for each sampling day; however, the reality of sampling in the dynamic atmosphere of a harbor makes this problematic. Upon arriving at the dock, the sampler may find any of the following scenarios: none of the vessels have gone out that day, some vessels have already returned and processed all or a portion of their catch, some vessels decided not to target Chinook salmon that day, or all vessels return at once. Samplers must systematically move between processing locations to obtain samples and some fish may not get sampled. Additionally, sampling must be distributed between private- and charter-caught fish throughout the shift to spread samples over time and avoid selecting for early- or late-returning boats.

Preseason annual limit restrictions implemented in 2014 and 2015 impacted the ability of samplers to collect data and genetic samples primarily from the CCI Late stratum. Anglers expressed concerns about participating in the CCI Late fishery during those 2 seasons, opting instead to take advantage of the apparently plentiful feeder Chinook salmon fishery occurring south of Bluff Point (lat 54°40.0′N; LCI Summer).

Nearly all harvest during sampling hours was easily intercepted at the Anchor Point and Deep Creek tractor launches. Anglers were funneled through the launch facility giving the samplers time to speak with vessel operators and either sample harvested fish on the spot, or follow anglers to processing facilities to sample the fish. An unknown amount of harvest was unobserved when technicians had to leave the launch site to sample fish but that harvest and effort would not be expected to vary greatly from the observed portion of the harvest.

There was no concentration of sport fishing effort during the LCI Winter fishery so assigning a port sampler to the area during that time period was impractical. Two winter Chinook salmon derbies presented concentrations of effort and were sampled by the project biologist and available staff during all 3 years. Additionally, interested anglers were either provided sampling kits to sample their harvest or provided contact information so that project staff could sample Chinook salmon when they returned to port, which proved moderately successful.

Taking all this information into consideration, we believe that the samples adequately represent each stratum of the sport fishery harvest resulting in unbiased stock composition estimates of the catch.

CODED WIRE TAG DATA

Coded wire tag data are a useful addition to this work when taken in appropriate context. It should be noted that in recent years, a portion of Cook Inlet hatchery fish have been adipose-clipped and thermally marked, but not coded-wire-tagged, so recovery and analysis of heads from these fish would not provide specific release location (Appendix C1). While it appears as though Cook Inlet hatchery fish are not included in the heads sampled for CWT analysis due to the above (Table 3), they likely make up some proportion of the "No Tags" (i.e., the heads having no valid CWTs). Beginning in the 2015 CCI Early and LCI Summer fisheries, otoliths were collected from heads submitted to the ADF&G Mark, Tag, and Age Laboratory. Since all Cook Inlet hatchery fish are thermally marked, otoliths could potentially be used to provide additional information on the harvest of Cook Inlet hatchery fish in the Cook Inlet marine sport fishery should the resources become available. While data from thermal mark analysis would not provide stock-specific information on Cook Inlet hatchery fish, it could provide information as to whether heads in the "No Tag" category are of Cook Inlet origin. Coded wire tagging of Cook Inlet hatchery fish resumed in 2015 and ADF&G expects to begin to see those fish harvested in the Cook Inlet marine sport fishery in 2017.

BASELINE EVALUATION TESTS

A key objective of this project was to estimate harvest for indicator stocks identified by the Chinook Salmon Research Initiative (ADF&G 2013). Data available when this project was proposed (Barclay et al. 2012) indicated that one of the indicator stocks (Kenai River) was genetically distinct enough to represent a reporting group for MSA applications. However, these data also indicated that the other indicator stock in Cook Inlet (Susitna River) was genetically too similar to other western Cook Inlet stocks to be estimated separately in MSA, leading to the broader reporting group (*West/Susitna*). These initial tests also indicated that misallocation occurred between this broader reporting group and *CI Other* reporting group. At the time, both of these reporting groups were missing baseline populations and we anticipated improved MSA performance once the baseline was augmented. During the period of this project, the baseline for these areas was augmented in other studies (Barclay and Habicht 2015). This new augmented baseline was used for the MSA analyses and misallocations between *West/Susitna* and *CI Other* persist, but both *Kenai* and *Outside CI* continued to perform well (Table 5). Although our standard criteria for defining reporting groups is greater than 90% correct allocation in 100% proof tests, we decided to retain all 4 reporting groups despite the subpar performance of the *CI Other* (86.6%) because of the value of this reporting group to meeting key objectives of the Chinook Salmon Research Initiative.

The biases in misallocations observed in the baseline evaluation tests provide valuable information when interpreting results from this study (Table 5). Estimates for *Kenai* and *Outside CI* contain low bias, while estimates for the *West/Susitna* and *CI Other* suggest they may be trading misallocations with each other. These differences in MSA performance among these reporting groups is captured in the increased credibility intervals observed for *West/Susitna* and *CI Other* reporting group estimates compared with *Kenai* and *Outside CI* reporting group estimates (Tables 6–8).

FUTURE EXAMINATION OF STOCKS IN "*OUTSIDE COOK INLET*" REPORTING GROUP

This study was designed to focus on the indicator stocks identified in the research plan developed to understand declines of Chinook salmon in Alaska (ADF&G 2013). Of these indicator stocks, the stocks thought most likely to occur at adequate proportions in samples from the Cook Inlet marine sport harvest were the Susitna River and Kenai River stocks. As a result, the reporting groups defined for this project aimed at obtaining information for these 2 stocks. The genetic stock structure for Chinook salmon allowed for Kenai River to stand alone as a reporting group, but Susitna River had to be combined with western Cook Inlet populations due to genetic similarity between populations from these areas. The other 2 reporting groups were included to absorb fish originating from other baseline stocks (*CI Other* and *Outside CI*).

Data from this study show that the vast majority of fish harvested in Cook Inlet marine sport fishery originate from outside Cook Inlet. Given this result, it may be reasonable to re-examine the mixtures using additional reporting groups that split *Outside CI* reporting group into finer-scale reporting groups. Defining appropriate finer-scale reporting groups requires (1) determining objectives for finer-scale reporting groups, (2) examining population structure to determine potential finer-scale reporting groups, and (3) identifying finer-scale reporting groups that are likely to receive significant allocations (Habicht et al. 2012).

Determining objectives for finer-scale reporting groups would require staff to consider what information would be useful for managing the fisheries throughout the state. For example, would it be useful to estimate proportions for other indicator stocks or for reporting groups of stocks that spawn outside the state?

The next step would be to determine if population structure is adequate to allow MSA to distinguish among the stocks of interest. Templin et al. (2011) provides a detailed analysis of potential reporting groups that are outside of Cook Inlet. Additional tests could be conducted with the data used in this study to test reporting groups not tested in Templin et al. (2011).

Finally, identifying fine-scale reporting groups that are likely to receive significant allocations would be the last step. Reporting groups that account for less than 5% of the mixture are likely to get allocations with credibility intervals that include 0.0, which are difficult to interpret. Determining which reporting groups are likely to receive significant (>5%) allocations may be a benefit of the results from an ongoing MSA analysis of Chinook salmon captured in the commercial and sport fisheries in the Kodiak Management Area (Foster and Dann 2015). In this study, the following reporting groups will be used: *Russia, Eastern Bering Sea, North Alaska Peninsula, Chignik, Kodiak, Cook Inlet, Copper, Southeast Alaska/Northeast Gulf of Alaska, British Columbia,* and *West Coast US*. Allocations to these reporting groups may provide information to determine appropriate fine-scale reporting groups for the Cook Inlet study. Results from the Kodiak Management Area studies will be released in preparation for the Kodiak Board of Fisheries Meeting scheduled for January, 2017.

MAKING INFERENCES OUTSIDE THE STUDY YEARS

Like most other scientific studies, these analyses represent environmental and fishery conditions during a specific period of time. Nonetheless, these studies are conducted so that future scientific and regulatory activities may be better informed. We expect that these results will be cited in the future as the most comprehensive data set available to examine stock composition of Chinook salmon captured in the Cook Inlet marine sport fishery. However, while this 3-year data set provides some measure of interannual variability in stock composition, some caution must be exercised when extrapolating the results to years not analyzed because changes in relative abundance among reporting groups, prosecution of fisheries, or migratory behavior due to ocean conditions might affect the distribution of stock-specific harvests among fisheries.

Additional samples will be collected in 2017 under a new project funded by the Pacific States Marine Fishery Commission, adding an additional year of data to the data set reported here; a report on the analysis of these samples is scheduled for release in fall of 2018.

Relative abundance among reporting groups: Alaska stocks and west coast salmon stocks are known to have inverse production regimes: when one is high, the other is low (Hare et al. 1999). During the 3 years of this study, the production regime resulted in high productivity for southern stocks (southern British Columbia [BC] and West Coast US) and low productivity for northern stocks (Alaska and northern BC stocks; Chinook Technical Committee 2016). Extrapolation of this study's findings to years with the opposite production regime would likely be inaccurate. Further examination of the stock composition of fish allocated to stocks outside Cook Inlet may provide additional insights into the effects of these differences in productivity.

Prosecution of fisheries: Data collection occurred as harvest increased in the LCI Summer and Winter fisheries. The increase was primarily attributed to the following: (1) shifts in effort and harvest from the CCI Early fishery to the LCI Summer fishery resulting from emergency orders restricting CCI fisheries, (2) strong success harvesting feeder Chinook salmon in the LCI Summer and Winter fisheries, (3) improved returns of stocked Chinook salmon to Kachemak Bay terminal fisheries in 2014 and 2015, and (4) favorable weather conditions throughout the year. In 2016, feeder Chinook salmon fishing success that began in 2015 continued.

A longer time series of data collection may provide insights into the effects of these temporal variables.

MAKING INFERENCES ABOUT PRESENCE OF STOCKS IN LOWER COOK INLET

This project was designed to estimate the stock composition of Chinook salmon harvested in the Cook Inlet marine sport fishery, and these estimates may not represent the stocks present in the LCIMA. Fishing effort in this fishery is not random through time and space. Anglers are more likely to fish when and where fish are biting and closer to access points. In addition, stock-specific fish behavior may affect which stocks are vulnerable to hook-and-line fishing. For example, stream-type Chinook salmon are known to feed more offshore during ocean residence, whereas ocean-type Chinook salmon are known to feed more nearshore (Groot and Margolis 1991). Populations from northern latitudes (Alaska) are almost exclusively stream-type Chinook salmon, whereas southern populations (southern BC to California) are a mix of stream- and ocean-type salmon. Maturing fish destined for Cook Inlet tributaries (stream-type) may be traversing the LCIMA on their homeward migration and not feeding as actively as ocean-type feeder Chinook salmon from southern populations.

EXTRAPOLATING STOCK PROPORTIONS TO STOCK-SPECIFIC HARVEST NUMBERS

The final report for this project will extrapolate from stock composition proportions to stock-specific harvests in the LCIMA for 2014 to 2016. At the time of this report, harvest data for all strata were not available.

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TABLES AND FIGURES

Table 1.–Genetic baseline tissue collections of Chinook salmon collected throughout their coastal range, including reporting group used for mixed stock analysis, years sampled, and number of samples analyzed from each collection included in the baseline (n). Population numbers correspond to baseline sampling sites on Figure 3.

Pop. No.	Reporting Group	Geographic Region	Location[a]	Sample Year(s)	n
1	*Outside CI*	Russia	Bistraya River	1998	94
2			Bolshaya River	1998, 2002	76
3			Kamchatka River late	1997, 1998	115
4			Pakhatcha River	2002	50
5		Western Alaska	Pilgrim River	2005, 2006	72
6			Unalakleet River	2005	82
7			Golsovia River	2005, 2006	112
8			Andreafsky River	2002, 2003	233
9			Anvik River	2002	51
10			Gisasa River	2001	99
11			Tozitna River	2002, 2003	355
12			Henshaw Creek	2001	145
13			South Fork Koyukuk River	2003	51
14			Kantishna River	2005	187
15			Chena River	2001	181
16			Salcha River	2005	188
17			Beaver Creek	1997	91
18			Chandalar River	2002, 2003, 2004	168
19			Sheenjek River	2002, 2004, 2006	47
20			Chandindu River	2000, 2001, 2003	237
21			Klondike River	1995, 2001, 2003	74
22			Stewart River	1997	98
23			Mayo River	1992, 1997, 2003	122
24			Blind River	2003	134
25			Pelly River	1996, 1997	116
26			Little Salmon River	1987, 1997	86
27			Big Salmon River	1987, 1997	106
28			Tatchun Creek	1987, 1997, 2002, 2003	163
29			Nordenskiold River	2003	55
30			Nisutlin River	1987, 1997	55
31			Takhini River	1997, 2002, 2003	160
32			Whitehorse Hatchery	1985, 1987, 1997	218
33			Goodnews River	1993, 2005, 2006	367
34			Arolik River	2005	148
35			Kanektok River	1992, 1993, 2005	243

-continued-

Table 1.–Page 2 of 6.

Pop. No.	Reporting Group	Geographic Region	Location[a]	Sample Year(s)	n
36	*Outside CI*	Western Alaska	Eek River	2002, 2005	171
37			Kwethluk River	2001	94
38			Kisaralik River	2001, 2005	191
39			Tuluksak River	1993, 1994, 2005	195
40			Aniak River	2002, 2006	251
41			George River	2002, 2005	191
42			Kogrukluk River	1992, 1993, 2005	149
43			Stony River	1994	94
44			Cheeneetnuk River	2002, 2006	115
45			Gagaryah River	2006	190
46			Takotna River	1994, 2005	170
47			Tatlawiksuk River	2002, 2005	190
48			Salmon River - Pitka Fork	1995	96
49			Togiak River	1993, 1994	154
50			Nushagak River	1992, 1993	57
51			Mulchatna River	1994	97
52			Stuyahok River	1993, 1994	87
53			Naknek River	1995, 2004	110
54			Big Creek	2004	66
55			King Salmon River	2006	131
56			Meshik River	2006	42
57			Milky River	2006	66
58			Nelson River	2006	94
59			Black Hills Creek	2006	51
60			Steelhead Creek	2006	93
61		Kodiak	Chignik River	1995, 2006	75
62			Ayakulik River	1993, 2006	135
63			Karluk River	1993, 2006	139
64	*West/Susitna*	West Side Cook Inlet	Straight Creek	2010	95
65			Chuitna River	2008, 2009	134
66			Coal Creek	2009, 2010, 2011	118
67			Theodore River	2010, 2011, 2012	191
68			Lewis River	2011, 2012	87
69		Yentna River	Red Creek	2012, 2013	111
70			Hayes River	2012, 2013	50
71			Canyon Creek	2012, 2013	91
72			Talachulitna River	1995, 2008, 2010	178
73			Sunflower Creek	2009, 2011	123
74			Peters Creek	2009, 2010, 2011, 2012	107

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Table 1.–Page 3 of 6.

Pop. No.	Reporting Group	Geographic Region	Location[a]	Sample Year(s)	n
75	*West/Susitna*	Susitna River	Portage Creek	2009, 2010, 2011, 2013	162
76			Indian River	2013	79
77			Chulitna River middle fork	2009, 2010	169
78			Chulitna River east fork	2009, 2010, 2011, 2013	77
79			Byers Creek	2013	55
80			Spink Creek	2013	56
81			Troublesome Creek	2013	71
82			Bunco Creek	2013	99
83			unnamed Talkeetna trib.	2013	69
84			Prairie Creek	1995, 2008	162
85			Iron Creek	2013	57
86			Disappointment Creek	2013	64
87			Chunilna Creek	2009, 2012	80
88			Montana Creek	2008, 2009, 2010	213
89			Little Willow Creek	2013	54
90			Willow Creek	2005, 2009	170
91			Deshka River	1995, 2012, 2005	303
92			Sucker Creek	2011, 2012	144
93	*CI Other*	Knik Arm	Little Susitna River	2009, 2010	124
94			Moose Creek	1995, 2008, 2009, 2012	149
95			Eagle River	2009, 2011, 2012	77
96			Ship Creek	2009	268
97		Turnagain Arm	Campbell Creek	2010, 2011, 2012	110
98			Carmen River	2011, 2012	50
99			Resurrection Creek	2010, 2011, 2012	97
100			Chickaloon River	2008, 2010, 2011	128
101	*Kenai*	Kenai River	Grant Creek	2011, 2012	55
102			Quartz Creek	2006, 2007,2008, 2009, 2010, 2011	131
103			Crescent Creek	2006	163
104			Juneau Creek	2005, 2006, 2007	142
105			Russian River	2005, 2006, 2007, 2008	214
106			Kenai Upper Mainstem	2009	191
107			Benjamin Creek	2005, 2006	204
108			Killey River	2005, 2006	255
109			Funny River	2005, 2006	219

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Table 1.–Page 4 of 6.

Pop. No.	Reporting Group	Geographic Region	Location[a]	Sample Year(s)	n
110	*Kenai*	Kenai River	Kenai Middle Mainstem	2003, 2004, 2006	299
111			Kenai Lower Mainstem	2010, 2011	126
112			Slikok Creek	2004, 2005, 2008	137
113	*CI Other*	Kasilof River	Kasilof River mainstem	2005	316
114			Crooked Creek	2005, 2011	306
115		Coastal Kenai Peninsula	Ninilchik River	2006, 2010	209
116			Deep Creek	2009, 2010	196
117			Stariski Creek	2011, 2012	99
118			Anchor River	2006, 2010	250
119	*Outside CI*	Copper River	Indian River	2004, 2005	50
120			Bone Creek	2004, 2005	78
121			E. Fork Chistochina River	2004	132
122			Otter Creek	2005	128
123			Sinona Creek	2004, 2005	156
124			Gulkana River	2004	210
125			Mendeltna Creek	2004	132
126			Kiana Creek	2004	75
127			Manker Creek	2004, 2005	62
128			Tonsina River	2004, 2006	96
129			Tebay River	2004, 2005, 2006	68
130		Northeast Gulf of Alaska	Situk River	1988, 1990, 1991,	127
131			Big Boulder Creek	1992, 1993, 1995,	171
132			Tahini River	1992, 2004	168
133			Tahini River - Pullen Creek Hatchery	2005	78
134			Kelsall River	2004	153
135		Southeast Alaska	King Salmon River	1989, 1990, 1993	142
136			King Creek	2003	172
137			Chickamin River	1990, 2003	134
138			Chickamin River - Little Port Walter	1993, 2005	217
139			Chickamin River - Whitman Lake	1992, 1998, 2005	378
140			Humpy Creek	2003	123
141			Butler Creek	2004	190
142			Clear Creek	1989, 2003, 2004	194
143			Cripple Creek	1988, 2003	142
144			Genes Creek	1989, 2003, 2004	93

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Table 1.–Page 5 of 6.

Pop. No.	Reporting Group	Geographic Region	Location[a]	Sample Year(s)	n
145	*Outside CI*	Southeast Alaska	Kerr Creek	2003, 2004	151
146			Unuk River - Little Port Walter	2005	149
147			Unuk River - Deer Mountain Hatchery	1992, 1994	147
148			Keta River	1989, 2003	144
149			Blossom River	2004	189
150			Andrews Creek	1989, 2004	151
151			Crystal Lake Hatchery	1992, 1994, 2005	396
152			Medvejie Hatchery	1998, 2005	273
153			Hidden Falls Hatchery	1994, 1998	154
154			Macaulay Hatchery	2005	135
155			Klukshu River	1989, 1990	170
156			Kowatua River	1989, 1990	135
157			Little Tatsemenie River	1989, 1990, 2005	230
158			Upper Nahlin River	1989, 1990	130
159			Nakina River	1989, 1990	132
160			Dudidontu River	2005	85
161			Tahltan River	1989	95
162		British Columbia	Kateen River	2005	94
163			Damdochax Creek	1996	65
164			Kincolith Creek	1996	109
165			Kwinageese Creek	1996	62
166			Oweegee Creek	1996	80
167			Bulkley River	1999	91
168			Sustut River	2001	130
169			Ecstall River	2001, 2002	86
170			Lower Kalum River	2001	142
171			Lower Atnarko River	1996	143
172			Kitimat River	1997	140
173			Wannock River	1996	144
174			Klinaklini River	1997	83
175			Porteau Cove	2003	154
176			Conuma River	1997, 1998	108
177			Marble Creek	1996, 1999, 2000	144
178			Nitinat River	1996	99
179			Robertson Creek	1996, 2003	103
180			Sarita River	1997, 2001	155
181			Big Qualicum River	1996	141

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Table 1.–Page 6 of 6.

Pop. No.	Reporting Group	Geographic Region	Location[a]	Sample Year(s)	n
182	*Outside CI*	British Columbia	Nanaimo River	2002	78
183			Quinsam River	1996	119
184			Morkill River (Su)	2001	153
185			Salmon River (Su)	1997	92
186			Torpy River (Su)	2001	85
187			Chilko River (Su)	1995, 1996, 1999, 2002	242
188			Nechako River (Su)	1996	115
189			Quesnel River (Su)	1996	144
190			Stuart River (Su)	1996	161
191			Clearwater River (Su)	1997	147
192			Louis River (Sp)	2001	178
193			Lower Adams River (Fa)	1996	44
194			Lower Thompson River (Fa)	2001	100
195			Middle Shuswap River (Su)	1986, 1997	125
196			Birkenhead River (Sp)	1997, 1999, 2001, 2002, 2003	91
197			Harrison River	2002	96
198		Washington	Makah National Fish Hatchery (Fa)	2001, 2003	79
199			Forks Creek (Fa)	2005	149
200			Upper Skagit River (Su)	2006	89
201			Soos Creek Hatchery (Fa)	2004	117
202			Lyons Ferry Hatchery (Su/Fa)	2002, 2003	118
203			Hanford Reach	2000, 2004, 2006	107
204		Oregon	Lower Deschutes River (Fa)	2002	86
205			Carson Hatchery (Sp)	2001	95
206			McKenzie River (Sp)	2004	94
207			Alsea River (Fa)	2004	69
208			Siuslaw River (Fa)	2001	75
209		California	Klamath River	1990, 2006	52
210			Eel River (Fa)	2000, 2001	83
211			Sacramento River (Wi)	2005	95

[a] Sp=spring run; Su=summer run; Fa=fall run; Wi=winter run.

Table 2.–Samples collected and selected for mixed stock analysis from the Cook Inlet marine sport Chinook fishery 2014–2016.

Stratum			Collected			Selected for gcMSA		
				Heads				
Geographic	Temporal	Year	Genetic	Total collected	Known Origin	Genetic	Known Origin	Total
Central Cook Inlet	4/1–6/24 (Early)	2014	306	28	12	294	10	304
		2015	516	50	20	390	16	406
		2016	490	56	15	349	11	360
	6/25–9/30 (Late)	2014	30	5	2	N/A	N/A	N/A
		2015	27	3	2	N/A	N/A	N/A
		2016[a]	-	-	-	-	-	-
Lower Cook Inlet	4/1–9/30 (Summer)	2014	1,443	282	120	359	30	389
		2015	3,298	591	215	391	27	418
		2016[a]	-	-	-	-	-	-
	1/1–3/31 & 10/1–12/31 (Winter)	2014	326	42	18	309	18	327
		2015	868	190	66	391	23	414
		2016[a]	-	-	-	-	-	-

Note: Strata with inadequate sample sizes were not selected for gcMSA and are denoted as "N/A".

[a] Dashes indicate numbers that will be included in the final report.

Table 3.–Number by origin of Chinook salmon containing CWT by strata and year 2014–2016.

Year	Stratum	Alaska (outside Cook Inlet)	British Columbia	Washington	Oregon	Idaho
2014	CCI Early	1	8	1	2	0
	CCI Late	0	1	1	0	0
	LCI Summer	18	35	38	28	1
	LCI Winter	0	8	3	7	0
2015	CCI Early	0	10	7	3	0
	CCI Late	1	0	0	1	0
	LCI Summer	24	57	98	32	4
	LCI Winter	2	26	24	14	0
2016	CCI Early	1	10	3	1	0
	CCI Late[a]	-	-	-	-	-
	LCI Summer[a]	-	-	-	-	-
	LCI Winter[a]	-	-	-	-	-

[a] Dashes indicate numbers that will be included in the final report.

Table 4.–Source, observed heterozygosity (H_O), F_{IS}, and F_{ST} for the 42 single nucleotide polymorphisms used in baseline evaluation tests and mixed stock analysis.

Assay Name	Source [a]	H_o	F_{IS}	F_{ST}
Ots_arf-188	a	0.011	0.028	0.078
Ots_AsnRS-60	a	0.402	-0.004	0.064
Ots_C3N3[b]	b	-	0.000	0.568
Ots_E2-275	a	0.370	0.000	0.145
Ots_ETIF1A	c	0.416	0.018	0.122
Ots_FARSLA-220	d	0.263	0.002	0.302
Ots_FGF6A	e	0.384	0.004	0.217
Ots_GH2	b	0.271	-0.001	0.163
Ots_GPDH-338	a	0.152	-0.006	0.194
Ots_GPH-318	d	0.197	0.018	0.066
Ots_GST-207	d	0.158	-0.007	0.272
Ots_GST-375	d	0.028	0.019	0.143
Ots_GTH2B-550	e	0.412	-0.010	0.139
Ots_HGFA-446	a	0.008	0.028	0.137
Ots_hnRNPL-533	d	0.346	0.013	0.205
Ots_HSP90B-100	d	0.303	0.011	0.277
Ots_IGF-I.1-76	a	0.368	-0.004	0.187
Ots_Ikaros-250	a	0.098	0.002	0.072
Ots_il-1racp-166	a	0.435	-0.081	0.069
Ots_ins-115	a	0.037	-0.002	0.041
Ots_LEI-292	d	0.040	0.014	0.040
Ots_LWSop-638	a	0.079	0.013	0.073
Ots_MHC1	b	0.442	-0.005	0.090
Ots_MHC2	b	0.156	0.003	0.420
Ots_NOD1	e	0.390	0.003	0.196
Ots_P450	b	0.334	-0.002	0.238
Ots_Prl2	b	0.441	0.014	0.093
Ots_RAG3	e	0.244	0.005	0.328
Ots_RFC2-558	a	0.128	0.007	0.373
Ots_S7-1	e	0.324	0.010	0.224
Ots_SClkF2R2-135	a	0.427	0.002	0.119
Ots_SERPC1-209	d	0.114	0.065	0.072
Ots_SL	b	0.403	-0.008	0.144
Ots_SWS1op-182	a	0.433	-0.022	0.084
Ots_TAPBP	c	0.220	0.002	0.111
Ots_Tnsf	b	0.294	0.007	0.232

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Table 4.–Page 2 of 2.

Assay Name	Source [a]	H_o	F_{IS}	F_{ST}
Ots_u202-161	a	0.200	0.005	0.326
Ots_u211-85	a	0.191	0.010	0.351
Ots_U212-158	a	0.107	-0.018	0.060
Ots_u4-92	a	0.155	-0.002	0.104
Ots_u6-75	a	0.199	0.006	0.096
Ots_Zp3b-215	a	0.072	0.008	0.116
Average/Overall		0.245	0.000	0.179

Note: Summary statistics are based upon the 211 populations in the Cook Inlet coastwide baseline.

[a] Marker sources: (a) Smith et al. 2005a; (b) Smith et al. 2005b; (c) Washington State University Vancouver (Unpublished); (d) Smith et al. 2007; (e) Northwest Fisheries Science Center-NOAA (Unpublished).

[b] Mitochondrial SNP marker.

Table 5.–Average estimates of stock composition, bias, root mean square error (RMSE), and 90% credibility interval (CI) width for 10 replicates of 100% proof tests of the Cook Inlet coastwide Chinook salmon genetic baseline with 42 loci.

Reporting Group	Average	Bias	RMSE	CI Width	Average	Bias	RMSE	CI Width
	Outside CI				*West/Susitna*			
Outside CI	**98.7**	-1.3	1.4	3.0	0.1	0.1	0.1	0.6
West/Susitna	0.2	0.2	0.3	1.1	**92.9**	-7.1	8.7	21.4
CI Other	0.4	0.4	0.4	1.6	6.1	6.1	7.7	20.8
Kenai	0.7	0.7	0.9	2.2	0.8	0.8	1.0	2.9
	CI Other				*Kenai*			
Outside CI	0.3	0.3	0.4	1.4	0.3	0.3	0.4	1.1
West/Susitna	7.4	7.4	8.0	12.1	1.6	1.6	2.1	5.0
CI Other	**86.6**	-13.4	14.1	17.6	1.3	1.3	1.6	5.1
Kenai	5.7	5.7	7.2	12.7	**96.8**	-3.2	3.5	8.2

Note: Each replicate was a sample of 400 individuals removed from the genetic baseline. Bold indicates correct allocations. Stock composition estimates (percentage) may not sum to 100 due to rounding error. Stock composition estimates may not sum to 100% due to rounding error.

Table 6.–Estimates of stock composition (%) including mean, 90% credibility interval (CI), standard deviation (SD), and sample size (n) for mixtures of Chinook salmon harvested in the Central and Lower Cook Inlet marine sport fisheries in 2014.

	Central Cook Inlet				Lower Cook Inlet							
	Early (Dates: 4/1–6/24; n = 306)				Summer (Dates: 4/1–9/30; n = 387)				Winter (Dates: 1/1–3/31 & 10/1–12/31; n = 324)			
		90% CI				90% CI				90% CI		
Reporting Group	Mean	5%	95%	SD	Mean	5%	95%	SD	Mean	5%	95%	SD
Outside CI	75.3	71.1	79.4	2.5	97.9	96.6	99.0	0.7	99.8	99.2	100.0	0.3
West/Susitna	13.8	9.3	18.3	2.8	0.1	0.0	0.5	0.2	0.1	0.0	0.4	0.2
CI Other	10.4	6.7	14.9	2.5	1.5	0.4	2.9	0.8	0.1	0.0	0.4	0.2
Kenai	0.5	0.0	2.1	0.8	0.5	0.0	1.7	0.6	0.1	0.0	0.4	0.2

Note: Stock composition estimates may not sum to 100% due to rounding error.

Table 7.–Estimates of stock composition (%) including mean, 90% credibility interval (CI), standard deviation (SD), and sample size (n) for mixtures of Chinook salmon harvested in the Central and Lower Cook Inlet marine sport fisheries in 2015.

	Central Cook Inlet				Lower Cook Inlet							
	Early (Dates: 4/1–6/24; n = 404)				Summer (Dates: 4/1–9/30; n = 411)				Winter (Dates: 1/1–3/31 & 10/1–12/31; n = 414)			
		90% CI				90% CI				90% CI		
Reporting Group	Mean	5%	95%	SD	Mean	5%	95%	SD	Mean	5%	95%	SD
Outside CI	80.4	77.1	83.6	2.0	99.0	98.0	99.7	0.5	99.8	99.4	100.0	0.2
West/Susitna	6.4	3.7	9.7	1.8	0.7	0.0	1.6	0.5	0.1	0.0	0.3	0.1
CI Other	12.7	9.1	16.4	2.2	0.2	0.0	0.8	0.3	0.1	0.0	0.3	0.1
Kenai	0.4	0.0	2.0	0.7	0.1	0.0	0.6	0.2	0.1	0.0	0.3	0.1

Note: Stock composition estimates may not sum to 100% due to rounding error.

Table 8.–Estimates of stock composition (%) including mean, 90% credibility interval (CI), standard deviation (SD), and sample size (n) for mixtures of Chinook salmon harvested in the Central Cook Inlet marine sport fishery in 2016.

	Central Cook Inlet			
	Early (Dates: 4/1–6/24; n = 348)			
		90% CI		
Reporting Group	Mean	5%	95%	SD
Outside CI	89.9	87.0	92.6	1.7
West/Susitna	4.2	0.2	7.7	2.2
CI Other	4.2	1.1	9.1	2.5
Kenai	1.7	0.0	3.9	1.2

Note: Stock composition estimates may not sum to 100% due to rounding error.

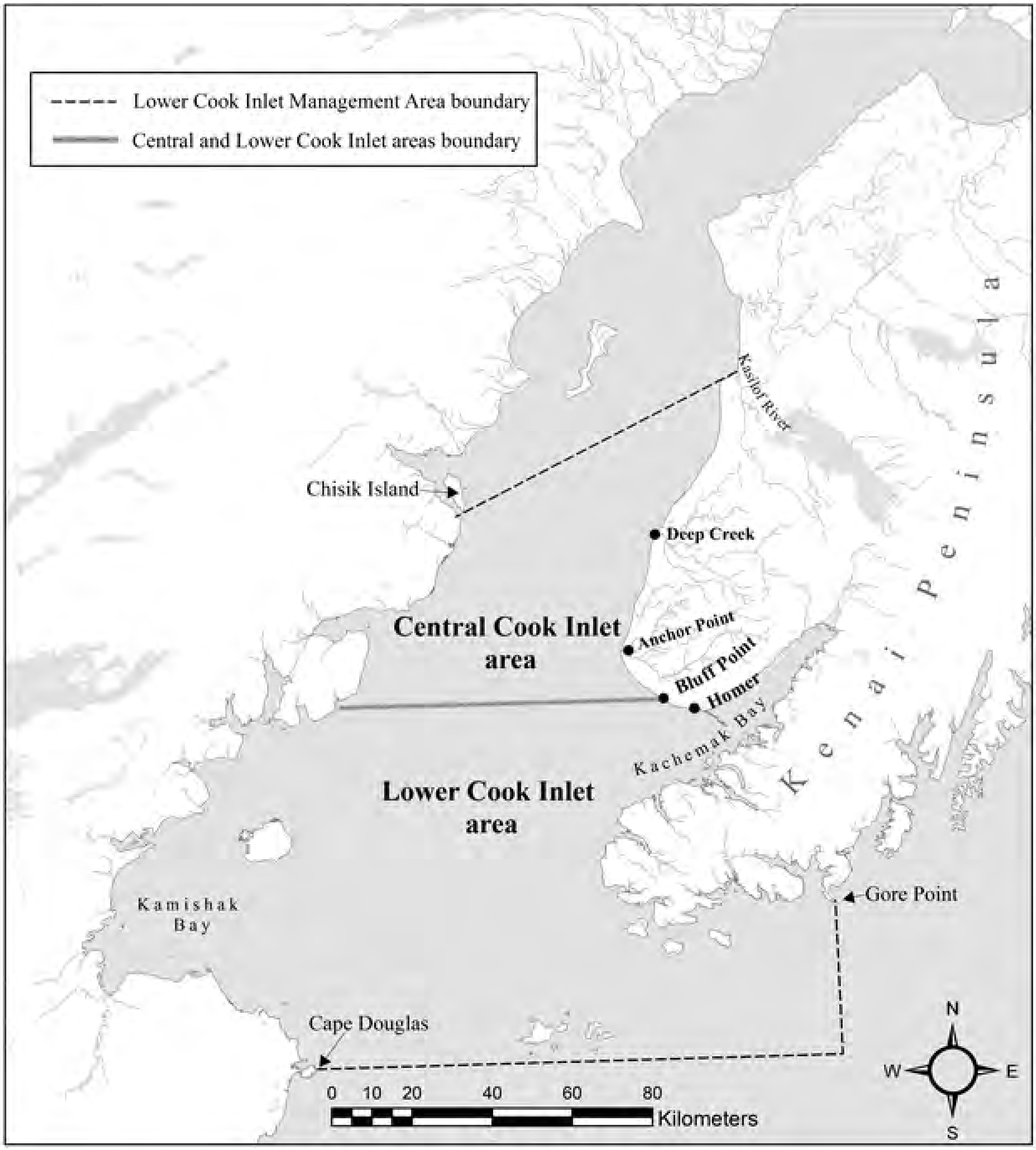

Figure 1.–Boundaries of the Lower Cook Inlet Management Area for Division of Sport Fish. This management area is further divided into Central Cook Inlet area (north of Bluff Point), and Lower Cook Inlet area (south of Bluff Point including Kachemak Bay).

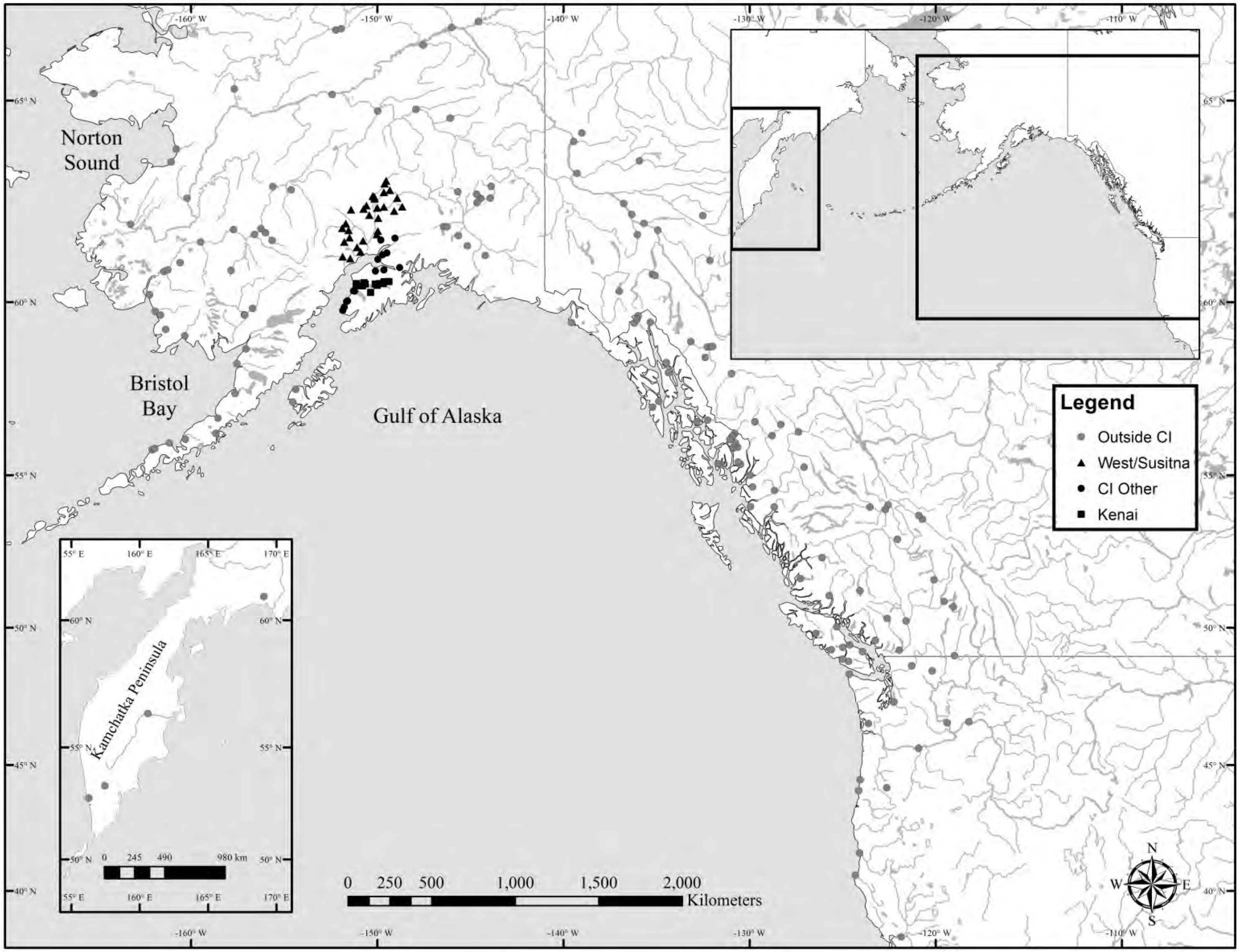

Figure 2.–Map of 211 sampling locations for Chinook salmon populations included in the Cook Inlet coastwide baseline. Location dot shape and color matches reporting group assignment.

Source: Adapted from Templin et al. 2011.

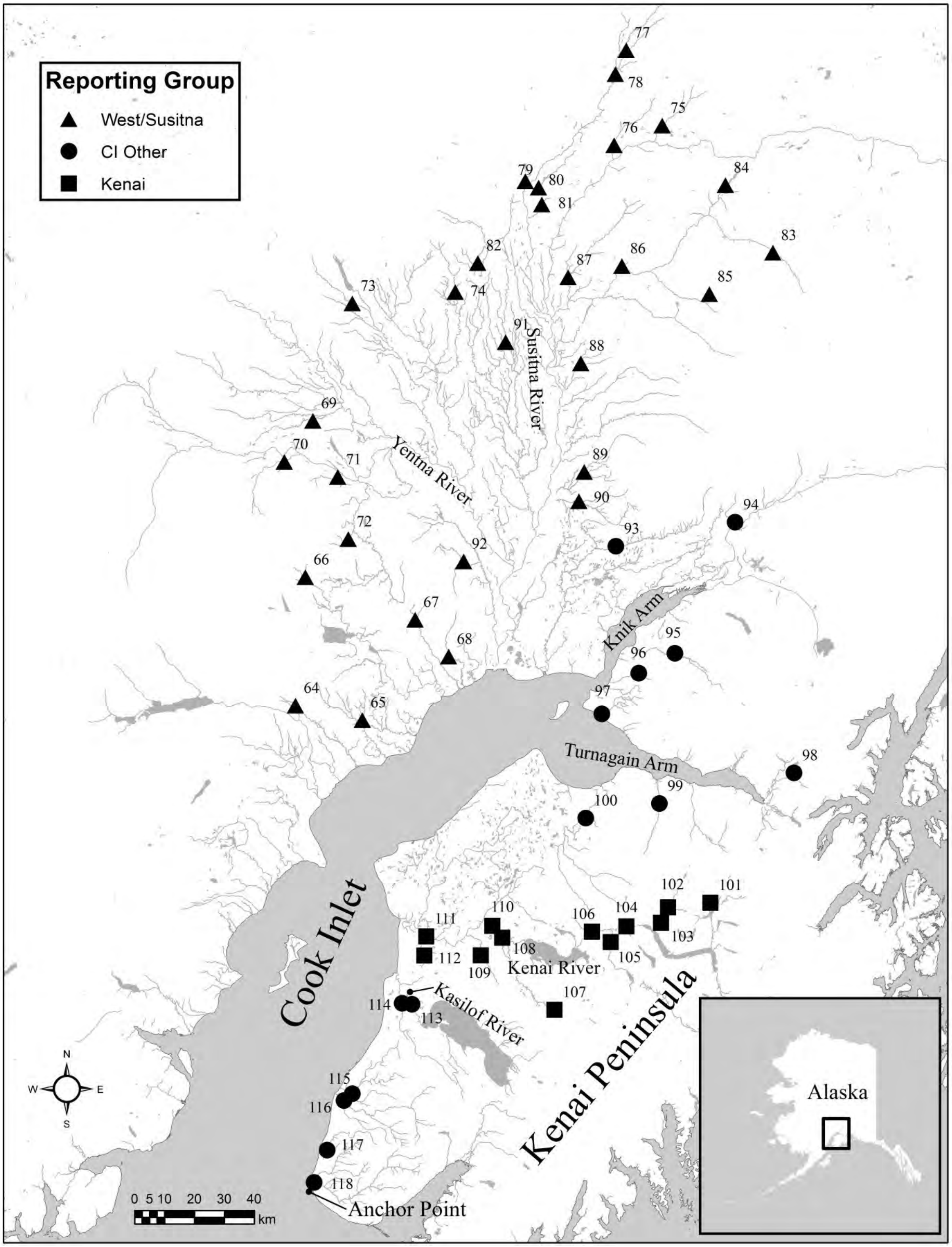

Figure 3.–Sampling locations for Chinook salmon populations from Cook Inlet included in the Cook Inlet coastwide genetic baseline. Numbers correspond to map numbers on Table 1. Location dot shape matches reporting group assignment.

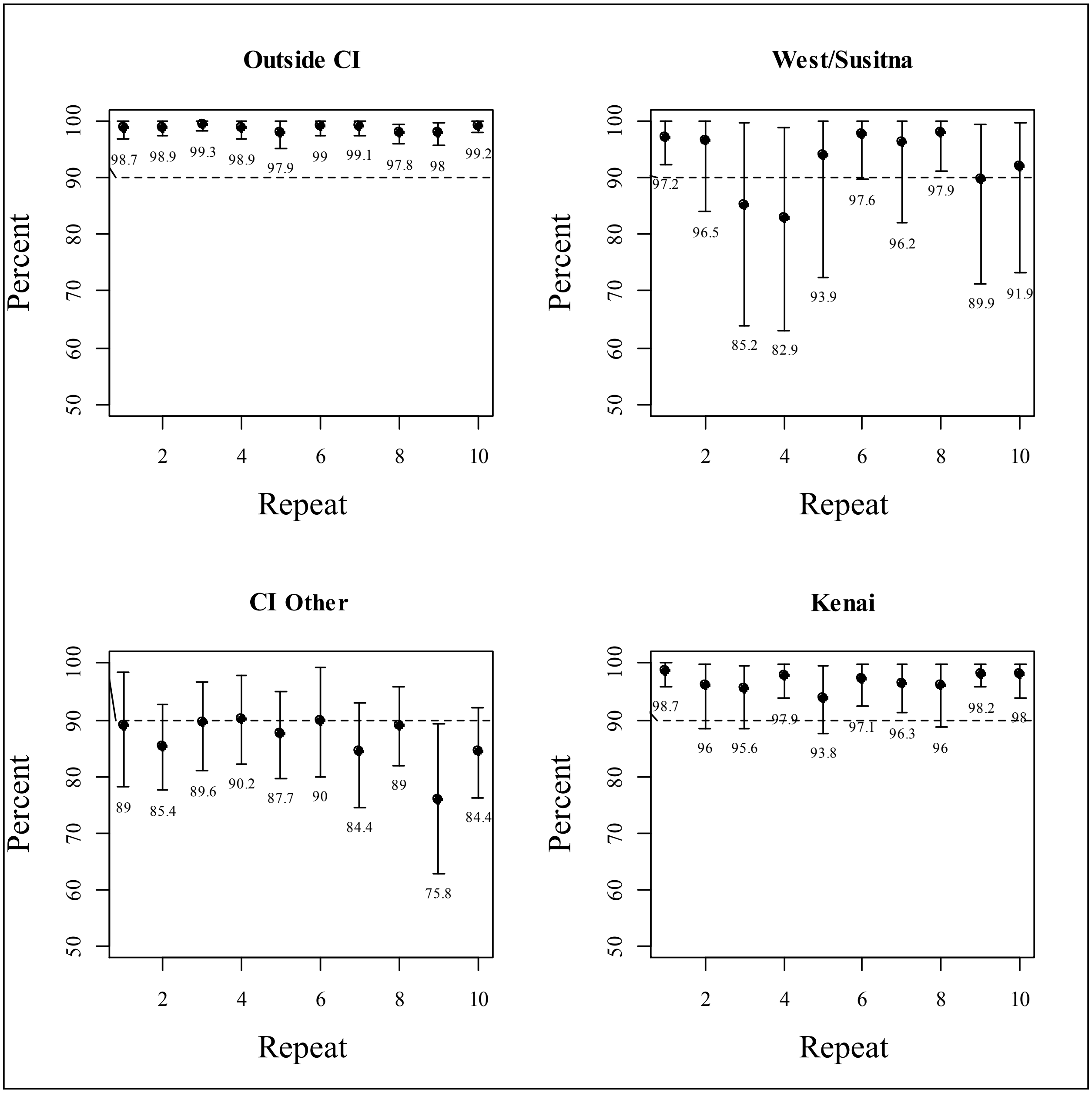

Figure 4.–Results of repeated proof tests for 4 reporting groups. The points represent the mean correct allocation from each repeat with 90% credibility intervals for each point. Point estimates for each repeat of the tests are included below the lower credibility interval.

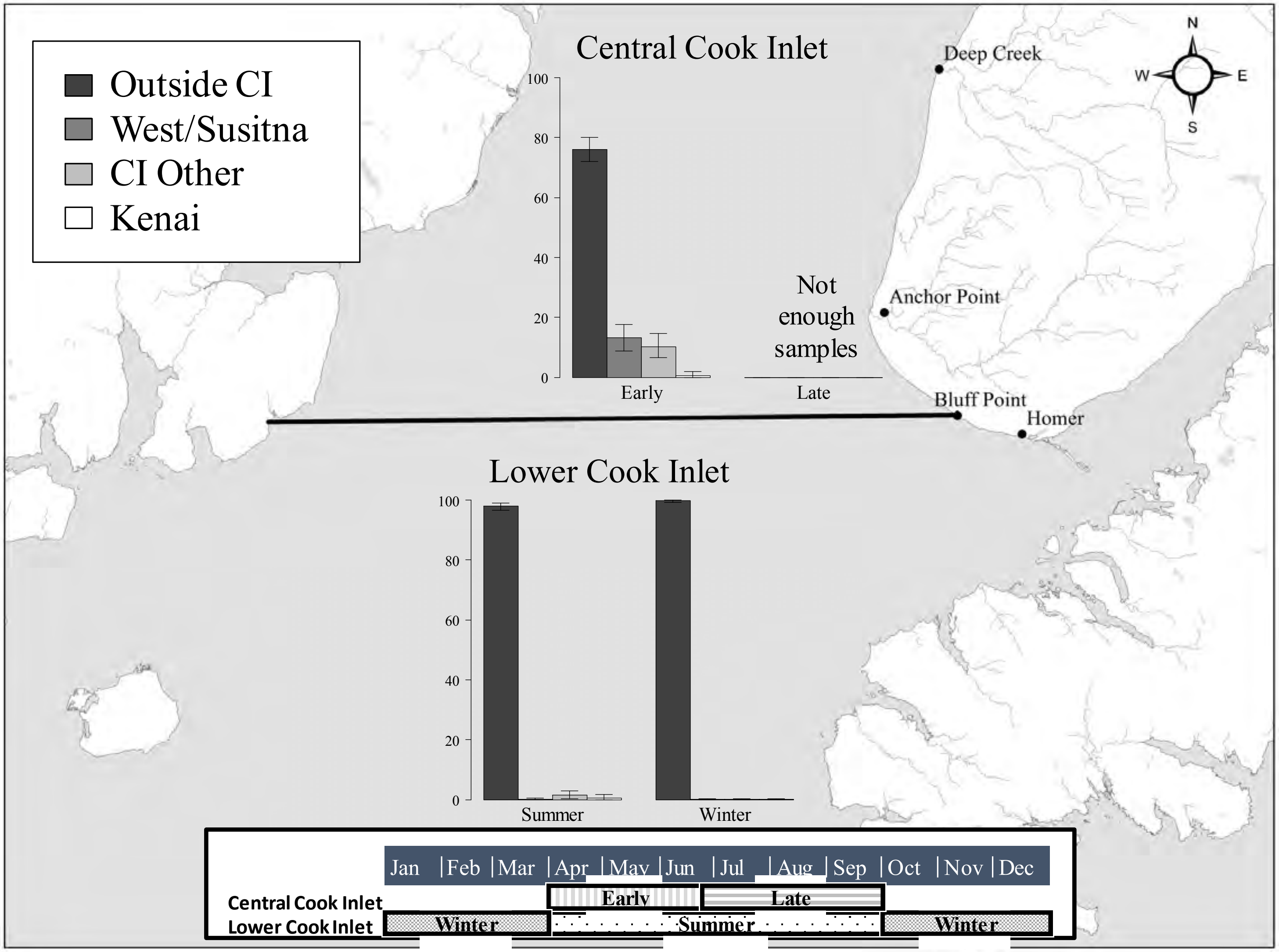

Figure 5.–Map of the Lower Cook Inlet Management Area with bar charts of stock composition estimates and 90% credibility intervals for the 2014 Cook Inlet marine sport harvest, including a timeline indicating the dates represented by each chart.

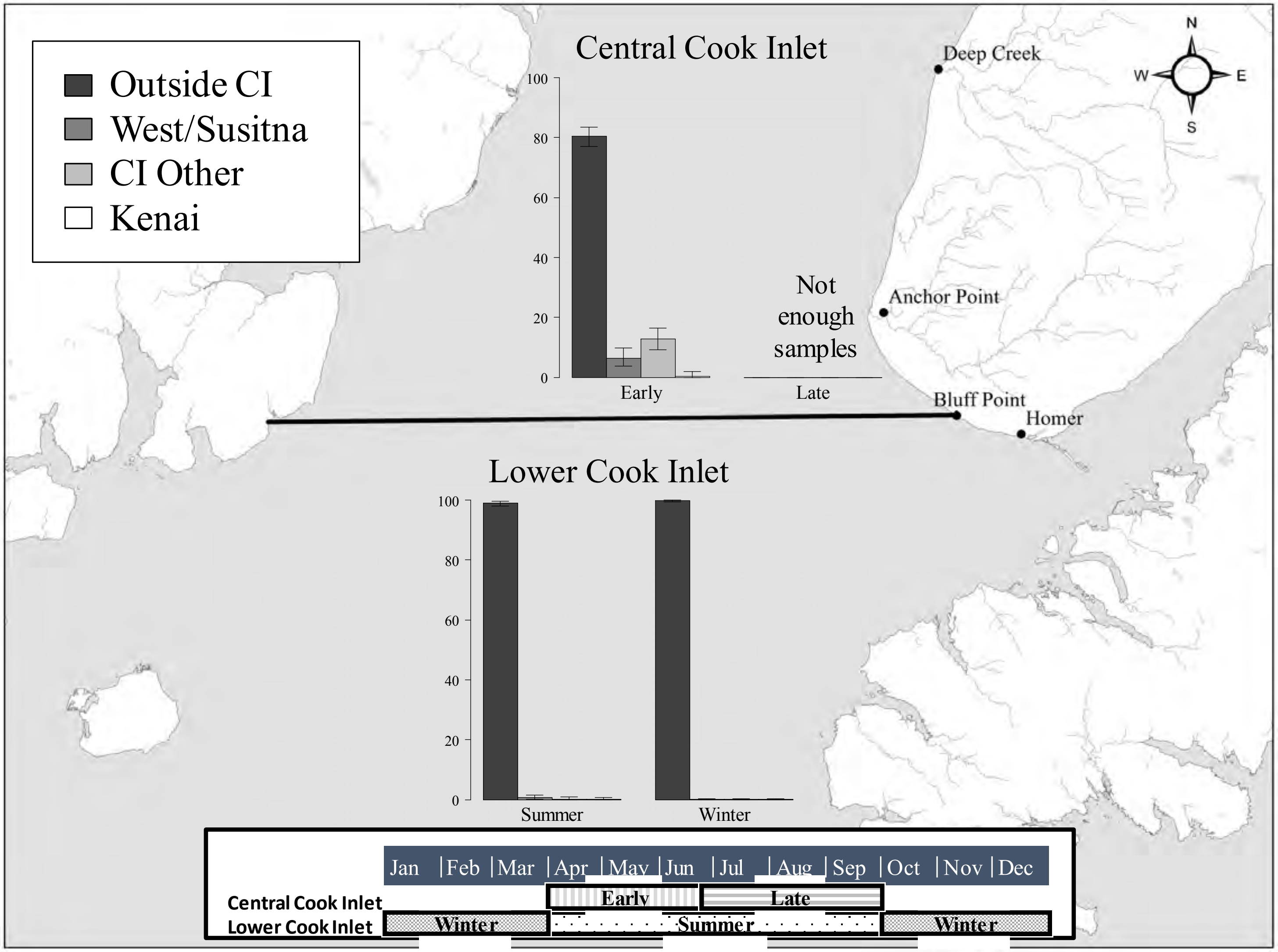

Figure 6.–Map of the Lower Cook Inlet Management Area with bar charts of stock composition estimates and 90% credibility intervals for the 2015 Cook Inlet marine sport harvest, including a timeline indicating the dates represented by each chart.

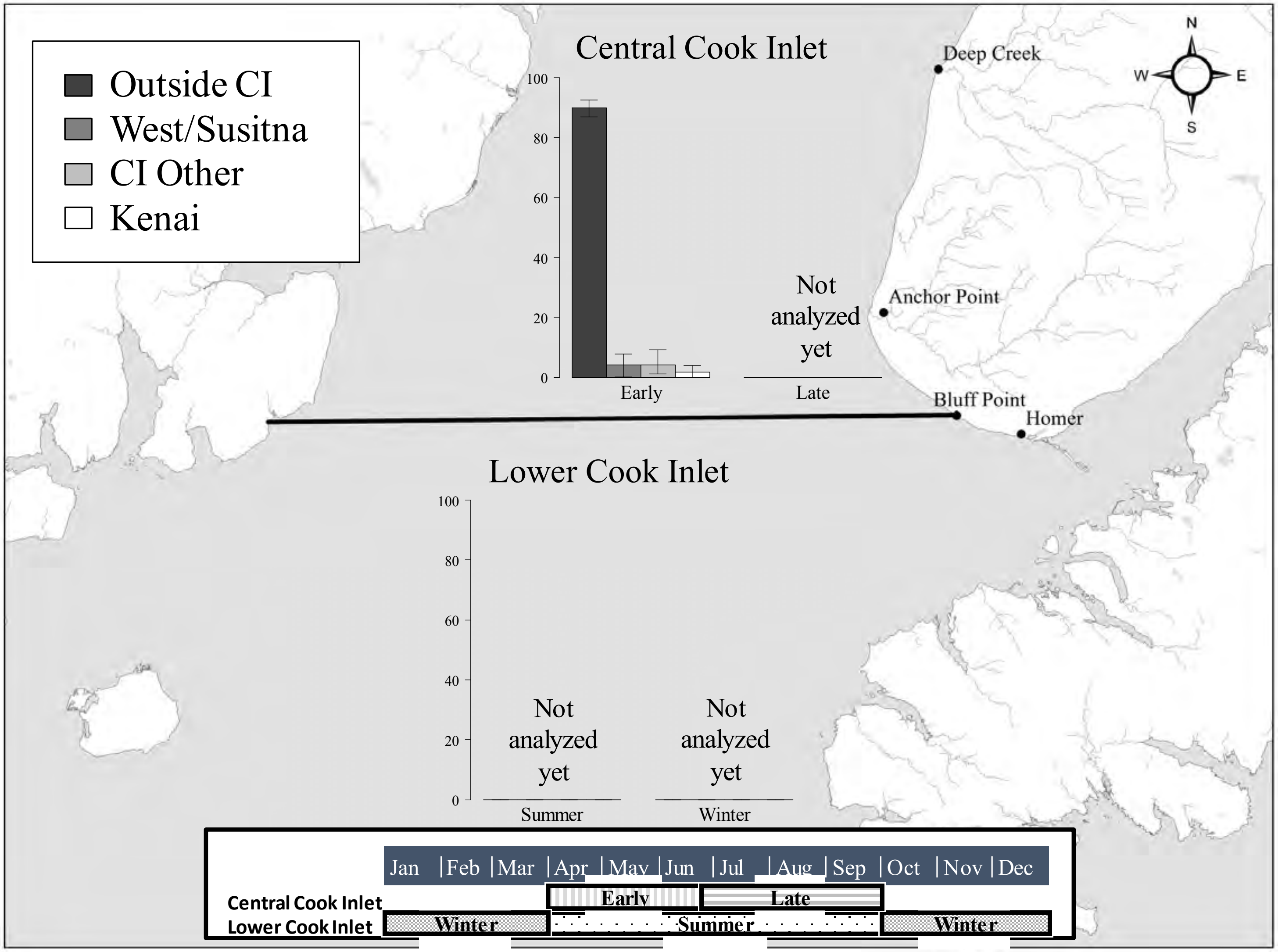

Figure 7.–Map of the Lower Cook Inlet Management Area with bar charts of stock composition estimates and 90% credibility intervals for the 2016 Cook Inlet marine sport harvest, including a timeline indicating the dates represented by each chart.

APPENDIX A. SUMMARY OF HARVEST SAMPLES COLLECTED BY PORT

Appendix A1.–Number of samples collected in the Lower Cook Inlet Management Area from the Cook Inlet marine sport harvest by port and year, 2014–2016.

Port	Collection Date	Samples Collected	Heads Collected
Anchor Point	2014	232	32
	2015	283	38
	2016[a]	97	7
Deep Creek	2014	125	9
	2015	163	14
	2016[a]	108	17
Homer	2014	2,059	327
	2015	4,406	794
	2016[a]	285	32
	Total	7,758	1,270

[a] CCI Early only; remaining 2016 strata collection numbers will be reported in the final report.

APPENDIX B. SUMMARY OF REPEATED PROOF TESTS

Appendix B1.–Estimates of stock composition (%) for 10 replicates of 100% proof tests for each of 4 reporting groups included as part of the Cook Inlet coastwide Chinook salmon genetic baseline with 42 loci. Each replicate was a sample of 400 individuals removed from the genetic baseline. Estimates for each replicate describe the posterior distributions by the median, 90% credibility interval (CI), and mean and standard deviation (SD).

	True		90% CI					90% CI			
Reporting Group	Percentage	Median	5%	95%	Mean	SD	Median	5%	95%	Mean	SD
		Outside CI Replicate 1					*Outside CI* Replicate 2				
Outside CI	100.0	98.9	96.7	99.9	98.7	1.0	99.0	97.3	99.9	98.9	0.8
West/Susitna	0.0	0.0	0.0	1.1	0.2	0.4	0.1	0.0	1.1	0.3	0.4
CI Other	0.0	0.2	0.0	2.4	0.6	0.8	0.2	0.0	1.5	0.4	0.5
Kenai	0.0	0.2	0.0	1.8	0.5	0.7	0.2	0.0	1.7	0.5	0.6
		Outside CI Replicate 3					*Outside CI* Replicate 4				
Outside CI	100.0	99.5	98.1	100.0	99.3	0.6	99.1	96.8	100.0	98.9	1.0
West/Susitna	0.0	0.1	0.0	1.0	0.2	0.4	0.0	0.0	0.7	0.1	0.3
CI Other	0.0	0.0	0.0	0.9	0.2	0.3	0.2	0.0	2.3	0.6	0.8
Kenai	0.0	0.1	0.0	1.2	0.3	0.4	0.1	0.0	1.9	0.4	0.7
		Outside CI Replicate 5					*Outside CI* Replicate 6				
Outside CI	100.0	98.1	95.2	99.8	97.9	1.5	99.2	97.4	100.0	99.0	0.8
West/Susitna	0.0	0.0	0.0	0.8	0.2	0.3	0.1	0.0	1.6	0.4	0.6
CI Other	0.0	0.1	0.0	1.4	0.3	0.5	0.1	0.0	1.3	0.3	0.5
Kenai	0.0	1.3	0.0	4.4	1.6	1.5	0.1	0.0	1.4	0.3	0.5
		Outside CI Replicate 7					*Outside CI* Replicate 8				
Outside CI	100.0	99.3	97.5	100.0	99.1	0.8	98.0	95.9	99.3	97.8	1.1
West/Susitna	0.0	0.0	0.0	0.6	0.1	0.3	0.1	0.0	1.3	0.3	0.5
CI Other	0.0	0.0	0.0	1.0	0.2	0.4	0.2	0.0	1.9	0.5	0.7
Kenai	0.0	0.3	0.0	2.0	0.6	0.7	1.3	0.1	3.1	1.4	0.9

Note: Stock composition estimates may not sum to 100% due to rounding error.

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	True		90% CI					90% CI			
Reporting Group	Percentage	Median	5%	95%	Mean	SD	Median	5%	95%	Mean	SD
		Outside CI Replicate 9					*Outside CI* Replicate 10				
Outside CI	100.0	98.2	95.7	99.8	98.0	1.3	99.3	97.8	99.9	99.2	0.7
West/Susitna	0.0	0.1	0.0	1.0	0.2	0.4	0.3	0.0	1.4	0.4	0.5
CI Other	0.0	0.1	0.0	1.9	0.5	0.7	0.0	0.0	0.9	0.2	0.4
Kenai	0.0	1.0	0.0	3.6	1.3	1.2	0.0	0.0	1.0	0.2	0.4
		West/Susitna Replicate 1					*West/Susitna* Replicate 2				
Outside CI	0.0	0.0	0.0	0.6	0.1	0.3	0.0	0.0	0.4	0.1	0.2
West/Susitna	100.0	97.8	92.4	99.9	97.2	2.6	98.9	84.0	100.0	96.5	5.6
CI Other	0.0	1.7	0.0	7.0	2.4	2.5	0.5	0.0	15.5	3.1	5.6
Kenai	0.0	0.1	0.0	1.6	0.3	0.7	0.1	0.0	1.6	0.3	0.6
		West/Susitna Replicate 3					*West/Susitna* Replicate 4				
Outside CI	0.0	0.0	0.0	0.4	0.1	0.2	0.0	0.0	0.5	0.1	0.2
West/Susitna	100.0	85.9	63.9	99.7	85.2	12.7	82.1	63.1	98.9	82.9	12.0
CI Other	0.0	12.7	0.0	34.6	13.3	12.7	16.0	0.0	35.2	15.1	12.2
Kenai	0.0	1.0	0.0	4.4	1.4	1.5	1.5	0.0	5.3	1.9	1.8
		West/Susitna Replicate 5					*West/Susitna* Replicate 6				
Outside CI	0.0	0.0	0.0	1.0	0.2	0.4	0.0	0.0	0.6	0.1	0.2
West/Susitna	100.0	98.7	72.4	100.0	93.9	9.5	99.0	89.7	100.0	97.6	3.6
CI Other	0.0	0.5	0.0	27.1	5.7	9.5	0.2	0.0	9.6	1.7	3.6
Kenai	0.0	0.1	0.0	1.3	0.3	0.5	0.1	0.0	2.6	0.5	0.9

Note: Stock composition estimates may not sum to 100% due to rounding error.

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Reporting Group	True Percentage	Median	90% CI 5%	90% CI 95%	Mean	SD	Median	90% CI 5%	90% CI 95%	Mean	SD
		West/Susitna Replicate 7					*West/Susitna* Replicate 8				
			90% CI					90% CI			
Outside CI	0.0	0.0	0.0	0.7	0.1	0.3	0.0	0.0	0.5	0.1	0.2
West/Susitna	100.0	98.4	82.0	99.9	96.2	6.2	99.1	91.3	100.0	97.9	3.3
CI Other	0.0	0.4	0.0	17.3	2.7	6.2	0.4	0.0	8.4	1.8	3.3
Kenai	0.0	0.3	0.0	3.6	0.9	1.3	0.0	0.0	1.3	0.3	0.5
		West/Susitna Replicate 9					*West/Susitna* Replicate 10				
Outside CI	0.0	0.0	0.0	1.2	0.2	0.5	0.0	0.0	0.4	0.1	0.2
West/Susitna	100.0	91.8	71.4	99.5	89.9	8.5	95.0	73.1	99.6	91.9	8.4
CI Other	0.0	7.3	0.0	27.8	9.3	8.5	3.0	0.0	25.7	6.5	8.5
Kenai	0.0	0.2	0.0	2.8	0.7	1.0	1.2	0.0	4.3	1.5	1.5
		CI Other Replicate 1					*CI Other* Replicate 2				
Outside CI	0.0	0.3	0.0	1.3	0.4	0.6	0.6	0.0	2.5	0.8	0.9
West/Susitna	0.0	5.0	0.0	11.8	5.2	3.8	11.5	5.0	18.4	11.6	4.0
CI Other	100.0	89.7	78.1	98.4	89.0	6.1	85.6	77.5	92.7	85.4	4.6
Kenai	0.0	3.1	0.0	16.2	5.4	5.8	1.2	0.0	8.2	2.2	2.8
		CI Other Replicate 3					*CI Other* Replicate 4				
Outside CI	0.0	0.0	0.0	2.1	0.4	0.8	0.0	0.0	0.7	0.1	0.3
West/Susitna	0.0	8.2	0.9	14.3	8.1	3.9	8.3	0.6	15.1	8.2	4.3
CI Other	100.0	89.9	81.0	96.8	89.6	4.7	90.3	82.3	97.8	90.2	4.6
Kenai	0.0	0.3	0.0	11.1	2.0	3.8	0.3	0.0	6.7	1.5	2.4

Note: Stock composition estimates may not sum to 100% due to rounding error.

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Reporting Group	True Percentage	Median	90% CI 5%	90% CI 95%	Mean	SD	Median	90% CI 5%	90% CI 95%	Mean	SD
		CI Other Replicate 5					*CI Other* Replicate 6				
Outside CI	0.0	0.4	0.0	1.7	0.6	0.5	0.0	0.0	0.8	0.2	0.4
West/Susitna	0.0	7.8	2.2	13.8	7.9	3.5	3.1	0.0	9.2	3.6	3.0
CI Other	100.0	87.9	79.7	95.1	87.7	4.6	90.2	79.9	99.1	90.0	5.9
Kenai	0.0	3.2	0.0	10.1	3.8	3.3	6.2	0.0	15.3	6.3	5.3
		CI Other Replicate 7					*CI Other* Replicate 8				
Outside CI	0.0	0.0	0.0	1.1	0.2	0.4	0.1	0.0	2.3	0.4	0.8
West/Susitna	0.0	11.4	4.8	19.2	11.6	4.4	6.5	0.3	12.8	6.6	3.7
CI Other	100.0	84.8	74.6	93.1	84.4	5.6	89.2	82.0	95.9	89.0	4.2
Kenai	0.0	2.9	0.0	11.4	3.8	3.8	3.4	1.0	8.3	3.9	2.3
		CI Other Replicate 9					*CI Other* Replicate 10				
Outside CI	0.0	0.0	0.0	0.5	0.1	0.2	0.0	0.0	0.6	0.1	0.3
West/Susitna	0.0	9.6	2.7	16.8	9.7	4.2	1.0	0.0	6.5	1.9	2.3
CI Other	100.0	75.6	62.9	89.4	75.8	8.1	84.5	76.3	92.1	84.4	4.8
Kenai	0.0	14.9	0.4	26.6	14.4	7.8	13.5	6.4	21.0	13.6	4.4
		Kenai Replicate 1					*Kenai* Replicate 2				
Outside CI	0.0	0.0	0.0	1.5	0.3	0.6	0.0	0.0	0.7	0.1	0.3
West/Susitna	0.0	0.1	0.0	2.3	0.5	0.9	0.9	0.0	6.2	1.8	2.2
CI Other	0.0	0.1	0.0	2.4	0.5	0.9	1.2	0.0	7.6	2.0	2.6
Kenai	100.0	99.1	95.9	100.0	98.7	1.4	96.9	88.5	99.8	96.0	3.6

Note: Stock composition estimates may not sum to 100% due to rounding error.

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	True		90% CI					90% CI			
Reporting Group	Percentage	Median	5%	95%	Mean	SD	Median	5%	95%	Mean	SD
		Kenai Replicate 3					*Kenai* Replicate 4				
Outside CI	0.0	0.4	0.0	1.4	0.5	0.5	0.0	0.0	1.4	0.3	0.5
West/Susitna	0.0	0.1	0.0	1.9	0.4	0.8	0.2	0.0	3.5	0.8	1.3
CI Other	0.0	2.4	0.0	10.4	3.5	3.5	0.3	0.0	4.2	1.0	1.6
Kenai	100.0	96.6	88.5	99.7	95.6	3.6	98.5	93.8	99.9	97.9	2.1
		Kenai Replicate 5					*Kenai* Replicate 6				
Outside CI	0.0	0.0	0.0	0.4	0.1	0.2	0.4	0.0	1.6	0.5	0.5
West/Susitna	0.0	5.0	0.0	10.4	5.0	3.2	0.8	0.0	6.0	1.7	2.1
CI Other	0.0	0.2	0.0	5.0	1.1	1.8	0.1	0.0	3.1	0.6	1.2
Kenai	100.0	94.0	87.6	99.6	93.8	3.6	97.8	92.3	99.7	97.1	2.4
		Kenai Replicate 7					*Kenai* Replicate 8				
Outside CI	0.0	0.0	0.0	0.5	0.1	0.2	0.0	0.0	0.8	0.2	0.4
West/Susitna	0.0	2.5	0.0	7.5	2.8	2.5	0.5	0.0	5.7	1.5	2.0
CI Other	0.0	0.2	0.0	3.6	0.8	1.3	1.2	0.0	8.8	2.4	3.0
Kenai	100.0	96.7	91.3	99.9	96.3	2.8	96.9	88.7	99.9	96.0	3.6
		Kenai Replicate 9					*Kenai* Replicate 10				
Outside CI	0.0	0.7	0.1	2.8	1.0	0.9	0.0	0.0	0.6	0.1	0.3
West/Susitna	0.0	0.1	0.0	2.1	0.4	0.8	0.2	0.0	4.0	0.9	1.4
CI Other	0.0	0.1	0.0	1.5	0.3	0.6	0.2	0.0	4.5	1.0	1.6
Kenai	100.0	98.5	95.7	99.8	98.2	1.3	98.6	94.0	100.0	98.0	2.0

Note: Stock composition estimates may not sum to 100% due to rounding error.

APPENDIX C. SUMMARY OF HATCHERY CHINOOK SALMON IN COOK INLET, 2009–2015

Appendix C1.–Cook Inlet hatchery Chinook salmon smolt release information including release year, potential marine sport fish harvest years through 2016, number of adipose fin clipped smolt released with coded wire tags and thermal marks (CWT & TM) and only thermally marked (TM), number of smolt released without adipose fins that were thermally marked only, and the total number of smolt released, 2009-2015.

		Adipose Finclipped		Not Adipose Finclipped	
Year Released	Potential Harvest Years[a]	CWT & TM	TM	TM	Total Released
2009	2011, 2012, 2013, **2014**, 2015, 2016, 2017	281,202	0	604,306	885,508
2010	2011, 2012, 2013, **2014**, **2015**, 2016, 2017	319,567	0	923,669	1,243,236
2011	2011, 2012, 2013, **2014**, **2015**, **2016**, **2017**	0	264,306	867,663	1,131,969
2012	2011, 2012, 2013, **2014**, **2015**, **2016**, 2017	0	258,759	917,029	1,175,788
2013	2011, 2012, 2013, **2014**, **2015**, **2016**, 2017	0	199,356	759,018	958,374
2014	2011, 2012, 2013, 2014, 2015, **2016**, 2017	0	405,723	1,120,618	1,526,341
2015	2011, 2012, 2013, 2014, 2015, 2016, 2017	511,505	0	1,175,865	1,687,370

[a] black years = available for harvest; bold years = available for harvest during this study; gray years = not available for harvest.