Coded Wire Tag Augmented Genetic Mixed Stock Analysis of Chinook Salmon Harvested in Cook Inlet Marine Sport Fishery, 2014–2017

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Divisions of Sport Fish and Commercial Fisheries



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.

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FISHERY MANUSCRIPT NO. 19-04

CODED WIRE TAG AUGMENTED GENETIC MIXED STOCK ANALYSIS OF CHINOOK SALMON HARVESTED IN COOK INLET MARINE SPORT FISHERY, 2014–2017

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 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 2017. Results of the baseline tests indicated adequate genetic variation to distinguish among 4 reporting groups of interest to management (*Outside CI, Northern CI, Kenai*, and *S. Kenai Pen*.). The gcMSA results were obtained from 4,780 Chinook salmon sampled from the Cook Inlet marine sport fishery. Stock composition and stock-specific harvests were estimated for the Upper Cook Inlet early fishery and Lower Cook Inlet summer and winter fisheries for all 4 years and Upper Cook Inlet late fishery for 2016 and 2017 only. The *Outside CI* reporting group dominated all fisheries. The contribution of Cook Inlet Chinook salmon stocks was greatest in Upper Cook Inlet and ranged from 10.1% to 24.7% in the early fishery and from 3.5% to 18.0% in the late fishery. In Lower Cook Inlet, Cook Inlet stocks contributed 1.0 to 3.9% in the summer fishery and less than 1.0% of the harvest in the winter fishery in all 4 years.

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 1,000 fish for personal use (1997–2015; Fall et al. 2018). Sport fishing for Chinook salmon occurs in both salt and fresh waters of Cook Inlet, where an estimated 46,388 fish are harvested annually.¹ Commercial harvests occur in the Northern District set gillnet Chinook salmon fishery, and as a nontargeted species in Northern, Central, and Lower districts set gillnet and drift gillnet fisheries, averaging 13,302 fish annually (1997–2016; Shields and Frothingham 2018; Hollowell et al. 2017).

The Cook Inlet marine sport fishery occurs in the Lower Cook Inlet Management Area (LCIMA; Kerkvliet et al. 2016). 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 vessels trolling in nearshore and offshore waters, and harvests average roughly 16,000 Chinook salmon annually (2013–2017; Kerkvliet et al. 2016). Immature Chinook salmon feeding in the Cook Inlet management area support the year-round harvest, and mature Chinook salmon migrating through the area provide additional harvest opportunity.

Cook Inlet marine waters are divided into 2 major geographic areas, Upper Cook Inlet (UCI) and Lower Cook Inlet (LCI), with the latitude of 59°40.0'N (commonly referred to as Bluff Point) being the boundary. At the 2016 October Board of Fisheries (BOF) meeting, the BOF modified regulations used to manage Cook Inlet Chinook salmon marine sport fisheries by aligning them to the months when mature Cook Inlet stocks are migrating through the LCIMA. As a result, beginning in 2017, Cook Inlet fisheries were divided into 2 summer fisheries (April 1–August 31) and a winter fishery (January 1–March 31 and September 1–December 31). The UCI and LCI summer fisheries were separated by the Bluff Point boundary and the winter fishery included all Cook Inlet marine waters. Before 2017, the summer fishery in UCI was divided into an early run

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

fishery (April 1–June 24) and a late run fishery (June 25–September 30). From 2002 to 2010, the winter fishery (October 1–March 31) encompassed only LCI waters south of Bluff Point, but from 2011–2016, the boundary was shifted north to the Anchor Point Light.

Harvest, catch, and effort for Cook Inlet marine Chinook salmon sport fisheries is estimated through the Statewide Harvest Survey (SWHS; e.g., Jennings et al. 2004, 2006a, 2006b, 2007, 2009a, 2009b, 2010a, 2010b, 2011a, 2011b, 2015). The SWHS is a mail survey that is used to estimate annual sport fishing harvest, catch, and effort (in angler days) by location. Although harvest and catch are estimated for individual species, the SWHS is not designed to estimate directed effort towards individual species. In Cook Inlet marine waters, Chinook salmon harvest was estimated annually for each Cook Inlet fishery. In 2017, the SWHS was modified to incorporate regulatory changes to these fisheries, resulting in estimates for each of the UCI summer, LCI summer and winter fisheries, but not for UCI early- and late-run fisheries.

The Cook Inlet marine sport fishery 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 Cook Inlet 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, most 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, 2017). With the development of comprehensive genetic baselines for UCI Chinook salmon (Barclay et al. 2012; Barclay and Habicht 2015), this method has 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, 2017, 2018). These analyses estimated stock-specific commercial fishery harvests in UCI 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 UCI 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, and 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 broadscale MSA of fishery harvests on the high seas and only contained 16 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, hereafter referred to as the Cook Inlet coastwide baseline.

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.

In 2013, the State of Alaska funded a 3-year MSA study of Chinook salmon harvested in the Cook Inlet marine sport fishery with the primary goal of estimating the stock-specific harvests of Kenai River and Susitna River Chinook salmon. The initial results of the study were reported to the BOF at the 2016 LCI finfish BOF meeting prior to project completion (Barclay et al. 2016). The report included results from genetic baseline evaluation tests for MSA and select MSA results using genetic and CWT data (gcMSA) from Chinook salmon harvested from January 2014 to June 2016 in the Cook Inlet marine sport fishery. Adequate samples were available to report stock composition estimates for the UCI (referred to as Central Cook Inlet [CCI] in Barclay et al. 2016) early fishery (2014–2016), the LCI summer fisheries (2014 and 2015) and the winter fishery (2014 and 2015) for 4 reporting groups: (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); and (4) Kenai (Kenai River populations). Results of the baseline tests indicated adequate genetic variation to distinguish among the 4 reporting groups. The Outside CI reporting group dominated all mixture samples and the proportion of Cook Inlet Chinook salmon stocks was highest in the UCI early fishery. Although the MSA results reported in Barclay et al. (2016) were an important first glimpse into the stock composition of fisheries in the LCIMA, the composition of the UCI late fishery was still unknown, and stock-specific harvest estimates were not included in the report. Also, the 2014-2016 analysis did not include stock composition estimates for southern Kenai Peninsula streams, which might have relatively high exploitation rates given their proximity to the fishery.

Here we report an update to MSA results reported in Barclay et al. (2016) and all new stock composition estimates for previously unreported 2016 and 2017 fishery strata. Updates in this report include genetic baseline evaluation tests of the Cook Inlet coastwide baseline for a new set of MSA reporting groups and stock composition estimates for UCI early (2014–2016), LCI summer (2014 and 2016), and Cook Inlet winter (2014 and 2015) fisheries for the new reporting groups. Previously unreported fishery estimates in this report include UCI early 2017, UCI late 2016 and 2017, LCI summer 2016 and 2017, and Cook Inlet winter 2016 and 2017. This report also adds stock-specific harvest estimates for all analyzed Cook Inlet marine sport fishery strata from 2014 to 2017.

OBJECTIVES

- 1. Evaluate the Cook Inlet Chinook salmon coastwide baseline for MSA.
- 2. Sample the Cook Inlet Chinook salmon marine sport fishery, 2014–2017.
- 3. Determine location of origin for fish containing CWTs.

- 4. Analyze a subset of Chinook salmon marine sport 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 the LCI summer and winter fisheries 2014–2017, UCI early fishery 2014–2017, and the UCI late fishery 2016–2017.
- 6. Using statewide harvest survey information, estimate the stock-specific harvest of Chinook salmon harvested in the Cook Inlet marine sport fishery for the LCI summer and winter fisheries 2014–2017, UCI early fishery 2014–2017, and the UCI late fishery 2016–2017.
- 7. Estimate the overall annual stock-specific harvest of Chinook salmon harvested in the Cook Inlet marine sport fishery for analyzed strata, 2014–2017.

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.
- Mixture sample. A sample of fish of unknown origin selected for MSA.
- *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 sample 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 (populations) 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; see 5 AAC 39.222(f).

METHODS

HARVEST SAMPLING

Field Sampling

Angler surveys and biological sampling occurred primarily at the Homer small boat harbor and Anchor Point or Deep Creek tractor launches from April to late August during the summer fisheries (Figure 1). Anglers were intercepted at the end of their fishing trip. Sampling schedules were designed to maximize the number of anglers surveyed and the number of Chinook salmon sampled. Four technicians were assigned to the project, working 7.5 hours each scheduled workday, 5 days per week. Technicians were generally stationed in each port from early May to late August, encompassing the majority of the marine sport fishing season. Sampling was scheduled during periods each day to maximize the number of anglers encountered, salmon were examined and sampled, and sampling effort was distributed throughout the area (e.g., inclusion of the Homer small boat harbor).

Additional angler surveys and biological data were collected by area staff and volunteers during fishing derbies held in March (Homer Chamber) and October (Elks Club)—by area staff at the Homer small boat harbor, and by volunteer anglers fishing in the derbies. Volunteer anglers were provided kits to collect genetic, biological, and effort information during the winter fishery.

Genetic Tissues

Genetic tissue samples were collected from harvests of Chinook salmon in the marine sport fishery in 2014, 2015, 2016, and 2017. 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 and 2017, 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 examined for the presence/absence of an adipose fin. Fish missing an adipose fin may have a CWT in their head. With permission from the angler, the head of all adipose finclipped fish were collected and frozen. Heads were then sent to the ADF&G Mark, Tag and Age Laboratory in Juneau for CWT extraction and decoding to determine release location. If collected heads could not be assigned to a fishery (i.e., missing date or location data), they were not used in the CWT analysis.

Subsampling for Genetic/Coded Wire Tag Mixed Stock Analysis

Samples were stratified geographically and temporally into 4 strata: (1) Upper Cook Inlet April 1 to June 24, 2014–2017 (UCI early); (2) Upper Cook Inlet June 25 to September 30, 2014–2016, and June 25 to August 31, 2017 (UCI late); (3) Lower Cook Inlet April 1 to September 30, 2014–2016, and April 1 to August 31, 2017 (LCI summer); and (4) Cook Inlet January 1 to March 31, 2014–2017, October 1 to December 31, 2014–2016, and September 1 to December 31, 2017 (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 random sample of the unknown samples (target 300 fish) was identified and stratified by user group (private or charter fishermen) using SAS software². 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 fishery, 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 fisheries from year to year depending on the samples available for analysis among strata. For example, if fewer tissue samples were collected for a fishery 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 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 fishery (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

Genomic DNA was extracted from tissue samples using a NucleoSpin 96 Tissue Kit by Macherey-Nagel (Düren, Germany). DNA was screened for 42 SNP markers for all 4 years; however, to ensure that DNA concentrations were high enough with the dry sampling method used to preserve samples in 2016 and 2017, 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 GTXpres Master Mix (Applied Biosystem), 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 polymerase chain reaction (PCR) protocol as follows: an initial "Hot-Start" denaturation of 95°C for 2 min followed by 40 cycles of denaturation at 95°C for 2 s and annealing at 60°C for 20 s, with a final "Cool-Down" at

² SAS Institute Inc., Cary, NC, USA. Available from: <u>https://www.sas.com/en_us/home.html</u> (Accessed October 2019).

25°C for 10 s. 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 and 2017 samples was increased using a multiplexed preamplification PCR of 42 screened SNP markers. Reactions were conducted in 10 μ L volumes consisting of 4 uL of genomic DNA, 5 μ L of 2X Multiplex PCR Master Mix (QIAGEN) and 1 μ L each (2 μ M 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.

A total of 158 of 1,199 preamplified DNA samples were screened from the 2016 samples using the same methods as described for the 2014 and 2015 samples. The remaining 1,041 preamplified DNA samples from 2016 and all 2017 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 μ L volume consisting of 6–40 ng/ μ l 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

Genotypes from LOKI were retrieved and imported into R^3 with the *RJDBC* package.⁴ 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 genotypes in 95% of their overlapping, nonmissing loci. The individual 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

We selected reporting groups for this study that would likely meet our 90% correct allocation criterion in baseline evaluation tests and allow for accurate MSA estimates for populations in close proximity to the marine sport fishery (Table 1; Figures 2 and 3). In our selection, we retained the well-performing reporting groups from the previous study (Outside CI and Kenai) and combined West/Susitna stocks and northern Cook Inlet stocks included in the CI Other group to form a single broadscale reporting group for northern and western Cook Inlet (Northern CI; Barclay et al. 2016). Baseline analyses in Barclay and Habicht (2015) suggested that the remaining baseline populations (Kasilof, Anchor, and Ninilchik rivers; and Deep and Stariski creeks) previously included in the CI Other reporting group might perform well as a separate MSA reporting group. Chinook salmon from these populations migrate through the LCIMA from April through mid-July (Kerkvliet et al. 2016). In the previous study, the contributions of the CI Other reporting group were highest in the early summer fishery (April 1-June 24) in all 3 years analyzed, with stock composition estimates ranging from 4.2% to 12.7% (Barclay et al. 2016). Given the proximity of these populations to the fishery and their early run timing, the estimates suggested that these populations may make up a large portion of Cook Inlet Chinook salmon in the early fishery harvest. To investigate the harvest of these populations, they were combined to form the S. Kenai Pen. reporting group for this study.

The 4 reporting groups chosen for this study are the following:

- (1) *Outside CI* (Populations outside of Cook Inlet)
- (2) Northern CI (Western Cook Inlet, Yentna River, Susitna River, Knik Arm, and Turnagain Arm populations)
- (3) Kenai (Kenai River populations)
- (4) S. Kenai Pen. (Kenai Peninsula populations south of the Kenai River)

³ The R project for statistical computing, Vienna, Austria. Available from <u>https://www.R-project.org/</u> (accessed June 20, 2019).

⁴ Simon Urbanek. April 16, 2018. RJDBC: Provides Access to Databases Through the JDBC Interface. R package version 0.2-7.1. Available from <u>https://cran.r-project.org/package=RJDBC</u> (accessed June 20, 2019).

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, mixture samples 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 mixture samples 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 and summing to 1 (i.e., a *flat* prior). Within each reporting group, the prior parameter was divided by its number of populations and spread evenly among them. Stock proportion estimates and the 90% credibility intervals for each proof test mixture were calculated by taking the median, 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 measures bias as well as variation of the posterior mean estimate among replicates (i.e., precision of the posterior among replicates), and mean 90% credibility interval 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 sample and reduced baseline each time. These tests provide an indication of the power of a baseline for MSA, assuming that all populations are represented in the baseline.

Mixed Stock Analysis

Two types of data were used to estimate the stock compositions of the harvest. The first type was genetic data from the fish of unknown origin encompassing (1 - r)% of the sample, and the second type was coded-wire-tagged data of known-origin fish encompassed the remaining r% of the sample. To incorporate the stock compositions of CWT samples of known origin with stock compositions of genetic samples of unknown origin into a combined gcMSA, mixture samples 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: The stock composition of the genetic samples selected for MSA was estimated using the same BAYES protocol 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 known-origin data: We partitioned the known component into 4 stocks, where k_i is the count of known fish from stock *i*. To account for sampling error in the known-origin

stock composition \mathbf{P}_{K} , we placed a unit Dirichlet distribution on them, resulting in the following conjugate Dirichlet posterior distribution:

$$\mathbf{P}_{K}|k\sim \text{Dirchlet}\left(k_{1}+\frac{1}{4},\ldots,k_{4}+\frac{1}{4}\right).$$
(1)

To allow for uncertainty in the known-origin proportion of the mixture r, we placed a uniform distribution on it resulting in the following conjugate beta posterior distribution:

$$r|n, k \sim \text{Beta}(k+1, n-k+1).$$
 (2)

The posterior outputs from both the known-origin CWT and unknown-origin genetic components were combined per iteration by the following equation to derive the full posterior distribution of the proportion of each stock (p_i) in the mixture:

$$p_i = r p_{K,i} + (1 - r) p_{U,i}, \tag{3}$$

where r is the known-origin proportion of the mixture, $p_{K,i}$ is stock *i*'s composition in the knownorigin portion of the mixture, and $p_{U,i}$ is stock *i*'s composition in the unknown-origin portion of the mixture. Stock proportion estimates and 90% CIs for each mixture analysis were calculated by taking the mean and 5th and 95th quantiles of the output from the full posterior distribution.

Stock-Specific Harvest

Estimates of stock-specific harvest were derived by applying the stock composition proportions p_i to the fishery harvest *H* following methods of Habicht et al. (2012):

$$H_i = H p_i. \tag{4}$$

The estimate and distribution of stock-specific harvest H_i for each reporting group (*i*) were obtained by Monte Carlo simulation. Independent realizations of the reporting group-specific harvest $H_i^{(k)}$ were drawn randomly from the joint distribution of the harvest $H^{(k)}$ and stock composition $p_i^{(k)}$ for each fishery (K observations):

$$H_i^{(k)} = H^{(k)} p_i^{(k)}.$$
 (5)

Descriptive statistics were estimated directly from the K realizations of $H_i^{(k)}$ with the mean used as the estimate of stock-specific harvest \hat{H}_i and the 5th and 95th quantiles determining the bounds of the 90% CI.

Generation of posterior stock-specific catch distributions required an estimate of the distribution of each component. The distributions of the stock compositions $p_i^{(k)}$ were the Bayesian posterior

distributions of stock proportions from output of the MSA described above. The harvest $H^{(k)}$ from each fishery were assumed to be approximated by a lognormal distribution with the mean and SD taken from the SWHS.

RESULTS

HARVEST SAMPLING

Angler Surveys

In 2014, angler interviews were collected from 1,240 vessels in LCIMA. A total of 1,884 angler days were recorded during the UCI early fishery with a reported harvest of 373 Chinook salmon. A total of 360 angler days were recorded during the UCI late fishery with a reported harvest of 26 Chinook salmon. A total of 2,355 angler days were recorded during the LCI summer fishery with a reported harvest of 1,936 Chinook salmon. A total of 644 angler days were recorded during the winter fishery with a reported harvest of 379 Chinook salmon.

In 2015, angler interviews were collected from 2,671 vessels in LCIMA. A total of 2,054 angler days were recorded during the UCI early fishery with a reported harvest of 956 Chinook salmon. A total of 56 angler days were recorded during the UCI late fishery with a reported harvest of 33 Chinook salmon. A total of 6,516 angler days were recorded during the LCI summer fishery with a reported harvest of 4,322 Chinook salmon. A total of 1,434 angler days were recorded during the winter fishery with a reported harvest of 1,266 Chinook salmon.

In 2016, angler interviews were collected from 2,045 vessels in LCIMA. A total of 1,967 angler days were recorded during the UCI early fishery with a reported harvest of 772 Chinook salmon. A total of 941 angler days were recorded during the UCI late fishery with a reported harvest of 424 Chinook salmon. A total of 3,728 angler days were recorded during the LCI summer fishery with a reported harvest of 2,543 Chinook salmon. A total of 1,751 angler days were recorded during the winter fishery with a reported harvest of 1,009 Chinook salmon.

In 2017, angler interviews were collected from vessels in LCIMA. A total of 2,225 angler days were recorded during the UCI early fishery with a reported harvest of 922 Chinook salmon. A total of 1,131 angler days were recorded during the UCI late fishery with a reported harvest of 423 Chinook salmon. A total of 3,650 angler days were recorded during the LCI summer fishery with a reported harvest of 1,707 Chinook salmon. A total of 858 angler days were recorded during the winter fishery with a reported harvest of 258 Chinook salmon.

Field Sampling

A total of 13,673 fish were examined by samplers (Table 2): 1,995 had genetic tissues, heads for CWTs, and ASL data collected from them; 11,154 had only genetic tissues and ASL data collected from them; 180 had only heads and ASL data collected from them; and 344 had only ASL data collected from them.

Genetic Tissues

From 2014 to 2017, a total of 13,149 genetic samples were collected at docks, during derbies, and through participation in voluntary catch sampling in the winter fishery (Table 2; Appendix A1).

Known-Origin Samples

Of the 13,673 fish examined by samplers, a total of 1,995 with a missing adipose fin had heads collected from them (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). All but 1 known-origin fish identified as originating from Alaska were from outside of Cook Inlet.

Subsampling for Genetic/Coded Wire Tag Mixed Stock Analysis

A total of 4,532 fish were selected for genetic analysis and 248 CWT fish of known origin were selected for gcMSA (Table 2). These samples include those from UCI early (2014–2017), UCI late (2016–2017), LCI summer (2014–2017), and LCI winter (2014–2017) fisheries. No samples were selected from the UCI late fishery in 2014 and 2015 due to insufficient sample sizes for gcMSA.

LABORATORY ANALYSIS

Assaying Genotypes

A total of 4,532 fish from the 2014–2017 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 12 collections ranged from 0.30% 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

Fifty-three of the assayed samples (1.17%) 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

As expected, all 4 reporting groups performed well in the baseline evaluation tests for MSA reporting groups (Table 5; Figures 2 and 3; Appendix B1). Each of the 40 proof tests (10 tests for each reporting group) exceeded our 90% correct allocation criterion for evaluating baseline reporting groups for MSA. The average correct allocation for all 10 proof tests for each of the 4 reporting groups ranged from 96.8% to 98.8% (Table 5; Appendix B1; Figure 4). The *Outside CI*, *Northern CI*, and *S. Kenai Pen.* reporting groups had the highest correct allocations across all repeated tests, averaging 98.8% (*Outside CI*; RMSE = 1.3%; 90% credibility interval width = 2.8%), 98.0% (*Northern CI*; RMSE = 2.3%; 90% credibility interval width = 4.8%), and 98.4% (*S. Kenai Pen.*; RMSE = 1.8%; 90% credibility interval width = 5.4%). The *Kenai* allocations had more variation, with correct allocations averaging 96.8% (RMSE = 3.7%; 90% credibility interval width = 8.5%). *Kenai* fish misallocated primarily and in similar proportions to Cook Inlet reporting groups Northern CI (1.6%) and *S. Kenai Pen.* (1.4%). *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 4,532 genetic samples and 248 known-origin CWT samples were subsampled from the 2014–2017 collections to create 14 mixture samples for which stock composition was estimated (Table 2). Mixture sample sizes ranged from 242 to 418 fish, with CWT samples comprising 3.1% to 7.7% of the mixture samples. All reporting groups had shrink factors of less than 1.2 for each mixture sample, 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).

Stock Composition and Stock-Specific Harvest of Analyzed Strata

Upper Cook Inlet Early

The *Outside CI* reporting group was the dominant reporting group in the UCI early harvest mixture samples in all 4 years, with harvest contributions ranging from 75.3% to 89.9% (2014–2017; Tables 6–9; Figures 5–8). The *Northern CI* (range: 5.5–14.8%) and *S. Kenai Pen.* (range: 2.17–9.4%) reporting groups were the second and third largest contributors to the harvest and the *Kenai* reporting group contributed less than 2.4% in all 4 years.

In 2014, the total UCI early Chinook salmon harvest was 1,554 fish (Table 6; Figure 5). Of this Chinook salmon harvest, 75.3% (1,171 fish; SD = 220) was attributed to the *Outside CI* reporting group, 14.8% (230 fish; SD = 57) to the *Northern CI* group, 9.4% (146 fish; SD = 42) to the *S. Kenai Pen.* group, and the remaining harvest (7 fish; SD = 13) to the *Kenai* group.

In 2015, the total UCI early Chinook salmon harvest was 2,658 fish (Table 7; Figure 6). Of this Chinook salmon harvest, 80.4% (2,137 fish; SD = 329) was attributed to the *Outside CI* reporting group, 11.5% (306 fish; SD = 66) to the *Northern CI* group, 7.7% (204 fish; SD = 52) to the *S. Kenai Pen.* group, and the remaining harvest (11 fish; SD = 20) to the *Kenai* group.

In 2016, the total UCI early Chinook salmon harvest was 2,430 fish (Table 8; Figure 7). Of this Chinook salmon harvest, 89.9% (2,185 fish; SD = 326) was attributed to the *Outside CI* group, 6.2% (152 fish; SD = 46) to the *Northern CI* group, and the remaining harvest (93 fish) to the *S. Kenai Pen.* (SD = 27) and *Kenai* (SD = 31) groups.

In 2017, the total UCI early Chinook salmon harvest was 1,999 fish (Table 9; Figure 8). Of this Chinook salmon harvest, 84.7% (1,693 fish; SD = 245) was attributed to the *Outside CI* reporting group, 7.5% (149 fish; SD = 46) to the *S. Kenai Pen.* group, 5.5% (109 fish; SD = 43) to the *Northern CI group*, and the remaining harvest (47 fish; SD = 40) to the *Kenai* group.

Upper Cook Inlet Late

The *Outside CI* reporting group was the dominant reporting group in the UCI late harvest mixture samples, contributing 96.5% to the harvest in 2016 and 82.0% to the harvest in 2017 (Tables 8 and 9; Figures 7 and 8). The *Northern CI, Kenai*, and *S. Kenai Pen.* reporting groups contributed less than 3.3% to the harvest in both years, except in 2017 when the *Kenai* group contributed 12.7%

In 2016, the total UCI late Chinook salmon harvest was 1,333 fish (Table 8; Figure 7). Of this Chinook salmon harvest, 96.5% (1,286 fish; SD = 239) was attributed to the *Outside CI* reporting group and the remaining harvest (47 fish) to the *Northern CI*, *S. Kenai Pen.*, and *Kenai* groups.

In 2017, the total UCI late Chinook salmon harvest was 1,157 fish (Table 9; Figure 8). Of this Chinook salmon harvest, 82.0% (948 fish; SD = 235) was attributed to the *Outside CI* reporting group and the remaining harvest (289 fish) to the *Northern CI*, *S. Kenai Pen.*, and *Kenai* groups.

Lower Cook Inlet Summer

The *Outside CI* reporting group was the dominant reporting group in the LCI summer harvest mixture samples in all 4 years, with harvest contributions ranging from 96.1% to 99.0% (2014–2017; Tables 6–9; Figures 5–8). The combined contribution of *Northern CI, Kenai*, and *S. Kenai Pen*. reporting groups was less than 4.0% in all 4 years.

In 2014, the total LCI summer Chinook salmon harvest was 5,059 fish (Table 6; Figure 5). Of this Chinook salmon harvest, 97.9% (4,955 fish; SD = 538) was attributed to the *Outside CI* reporting group and the remaining harvest (104 fish) to the *Northern CI*, *S. Kenai Pen.*, and *Kenai* groups.

In 2015, the total LCI summer Chinook salmon harvest was 8,066 fish (Table 7; Figure 6). Of this Chinook salmon harvest, 99.0% (7,988 fish; SD = 785) was attributed to the *Outside CI* reporting group and the remaining harvest (78 fish) to the *Northern CI*, *S. Kenai Pen.*, and *Kenai* groups.

In 2016, the total LCI summer Chinook salmon harvest was 9,868 fish (Table 8; Figure 7). Of this Chinook salmon harvest, 96.1% (9,487 fish; SD = 739) was attributed to the *Outside CI* reporting group and the remaining harvest (381 fish) to the *Northern CI*, *S. Kenai Pen.*, and *Kenai* groups.

In 2017, the total LCI summer Chinook salmon harvest was 8,687 fish (Table 9; Figure 8). Of this Chinook salmon harvest, 96.7% (8,398 fish; SD = 683) was attributed to the *Outside CI* reporting group and the remaining harvest (289 fish) to the *Northern CI*, *S. Kenai Pen.*, and *Kenai* groups.

Winter

The *Outside CI* reporting group was the dominant reporting group in the LCI winter harvest mixture samples and contributed 99.8% to the harvest in all 4 years (2014–2017; Tables 6–9; Figures 5–8). The combined contribution of *Northern CI, Kenai*, and *S. Kenai Pen.* reporting groups was 0.2% in all 4 years.

In 2014, the total LCI winter Chinook salmon harvest was 3,173 fish (Table 6; Figure 5). Of this Chinook salmon harvest, 99.8% (3,165 fish; SD = 648) was attributed to the *Outside CI* reporting group and the remaining harvest (8 fish) to the *Northern CI*, *S. Kenai Pen.*, and *Kenai* groups.

In 2015, the total LCI winter Chinook salmon harvest was 5,179 fish (Table 7; Figure 6). Of this Chinook salmon harvest, 99.8% (5,170 fish; SD = 865) was attributed to the *Outside CI* reporting group and the remaining harvest (9 fish) to the *Northern CI*, *S. Kenai Pen.*, and *Kenai* groups.

In 2016, the total LCI winter Chinook salmon harvest was 5,106 fish (Table 8; Figure 7). Of this Chinook salmon harvest, 99.8% (5,095 fish; SD = 857) was attributed to the *Outside CI* reporting groups and the remaining harvest (11 fish) to the *Northern CI*, *S. Kenai Pen.*, and *Kenai* groups.

In 2017, the total LCI winter Chinook salmon harvest was 4,518 fish (Table 9; Figure 8). Of this Chinook salmon harvest, 99.8% (4,507 fish; SD = 788) was attributed to the *Outside CI* reporting groups and the remaining harvest (11 fish) to the *Northern CI*, *S. Kenai Pen.*, and *Kenai* groups.

All strata combined

In 2014, the total Cook Inlet marine sport Chinook salmon harvest from fishing areas and periods analyzed was 9,786 fish (Table 10; Figure 9). Of this Chinook salmon harvest, 94.9% (9,292 fish;

SD = 866) was attributed to the *Outside CI* reporting group, and the remaining harvest (494 fish) was attributed to the *Northern CI*, *Kenai*, and *S. Kenai Pen.* groups.

In 2015, the total Cook Inlet marine sport Chinook salmon harvest from fishing areas and periods analyzed was 15,903 fish (Table 10; Figure 9). Of this Chinook salmon harvest, 96.2% (15,295 fish; SD = 1,214) was attributed to the *Outside CI* reporting group and the remaining harvest (608 fish) to the *Northern CI, Kenai*, and *S. Kenai Pen.* groups.

In 2016, the total Cook Inlet marine sport Chinook salmon harvest from fishing areas and periods analyzed was 18,737 fish (Table 10; Figure 9). Of this Chinook salmon harvest, 96.3% (18,052 fish; SD = 1,199) was attributed to the *Outside CI* reporting group, and the remaining harvest (685 fish) to the *Northern CI, Kenai*, and *S. Kenai Pen.* groups.

In 2017, the total Cook Inlet marine sport Chinook salmon harvest from fishing areas and periods analyzed was 16,361 fish (Table 10; Figure 9). Of this Chinook salmon harvest, 95.0% (15,547 fish; SD = 1,095) was attributed to the *Outside CI* reporting group, and the remaining harvest (814 fish) to the *Northern CI, Kenai*, and *S. Kenai Pen.* groups.

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 with 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 CWT data. Analyses were performed on harvest samples collected from the Cook Inlet marine sport harvest in the LCI summer and winter, the UCI early fisheries from 2014 to 2017, and the UCI late fishery in 2016 and 2017. These results represent the most comprehensive analysis to date using genetic information of Chinook salmon captured in the Cook Inlet marine sport fishery.

MANAGEMENT IMPLICATIONS

This project provides fisheries managers and the BOF with a snapshot of the Cook Inlet marine sport Chinook salmon harvest stock composition from 2014–2017. Determining which fisheries are most likely to harvest Cook Inlet stocks provides valuable information in assessing sport fishing regulations. These results suggest that the regulation structure for Cook Inlet fisheries has been adequate to restrict the harvest of Cook Inlet stocks and maintain harvest opportunity on nonlocal stocks. Understanding the local stock composition within each fishery independently could also help to better understand the effects of shifts in effort and harvest between fisheries.

Study results from 2014–2016 (Barclay et al. 2016) were used at the 2016 BOF meeting to help evaluate impacts of proposals seeking to liberalize sport fishing regulations. As a result, the BOF adopted proposals that better aligned regulations with the timing of when Cook Inlet stocks are present in Cook Inlet marine waters. Study results also highlight that the harvest of Cook Inlet stocks in the LCI summer fishery is low. In 2014 and 2015, preseason and inseason Emergency Order restrictions were used for the UCI fisheries but none were issued in the LCI summer fishery. Restricting the LCI summer fishery in these years would not have resulted in appreciable increases in any Cook Inlet stock escapements. However, this management approach may or may not be

appropriate in future years as different productivity regimes may affect the proportion of Cook Inlet stocks present in the LCI summer fishery.

REPRESENTATIVENESS OF HARVEST SAMPLES

Sampling the Chinook salmon harvest in the LCIMA marine sport fishery presented some unique challenges, including unsampled landing sites, the large size of the Homer harbor, and inseason restrictions.

Some landing sites on the south side of Kachemak Bay were not sampled as they are accessible only via boat. The Homer harbor (the largest of 3 ports sampled in the LCIMA) presented some difficulties due to the 3 public fish cleaning stations, dozens of vessels cleaning fish on the docks, and approximately 10 cleaning facilities used by charter operators. Ideally, due to the high volume of charter-caught fish, approximately 4 or 5 charter vessels 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. Due to varying levels of effort amongst the charter fleet and the size of the Homer harbor, some charters may have been sampled more often than others. On days of low harvest all Chinook salmon returned to the harbor were sampled, and on days of very high harvest the inevitable maximum sampling effort was reached—this could have resulted in the undersampling of peak harvest days and subsequent underrepresentation of these days in the gcMSA.

Additionally, in 2014 and 2015, the Chinook salmon marine sport fishery north of Bluff Point was restricted by emergency order in response to below-average outlooks of Chinook salmon escapement to the Anchor River, Deep Creek, and Ninilchik River (Kerkvliet et al. 2016). During these years, concerned anglers shifted their efforts south of Bluff Point where they could target apparently plentiful feeder (nonlocal) Chinook salmon. Restrictions and changes in angler behavior due to conservation concerns affected the ability of samplers to collect genetic data in the UCI late fishery during these years, preventing an adequate sample for gcMSA in both years.

The LCIMA winter Chinook salmon fishery was not sampled on a daily basis. However, interested anglers were provided either kits to sample their harvest or contact information so that project staff could sample Chinook salmon when they returned to port. Additionally, 2 winter Chinook salmon derbies presented concentrations of effort that were high enough to justify field sampling and were sampled during all 4 years of this study. A high rate of voluntary data reporting and lower fishing effort allowed project staff to sample the winter Chinook salmon fishery in a representative manner.

The aforementioned challenges, inherent in most sport fishery port sampling projects, required high levels of sampling effort and an in-depth understanding of angler behavior in LCIMA.

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 from 2011 to 2014, Cook Inlet hatchery fish were 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). Beginning in the 2015 UCI 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. Coded wire tagging for some of the Cook Inlet hatchery releases resumed in 2015, and 1 Cook Inlet hatchery fish was sampled in the 2017 harvest. Cook Inlet hatchery fish probably also make up some proportion of the heads without CWTs.

DIFFERENCES IN REPORTING GROUPS BETWEEN STUDIES

A key objective of the previous MSA study (Barclay et al. 2016) was to estimate harvest for indicator stocks identified by the Chinook Salmon Research Initiative (ADF&G 2013). Data available when the previous study was proposed (Barclay et al. 2012) indicated that 1 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 the northern Cook Inlet stocks contained in the CI Other reporting group. At the time, both reporting groups were missing baseline populations and we anticipated improved MSA performance once the baseline was augmented. During the period of the previous study, the baseline for these areas was augmented by a new study (Barclay and Habicht 2015). This augmented baseline was used for the baseline evaluation tests in the previous study and misallocations between West/Susitna and CI Other persisted, but both Kenai and Outside CI continued to perform well. Although our standard criteria for defining reporting groups is greater than 90% correct allocation in 100% proof tests, all 4 reporting groups were retained despite the subpar performance of CI Other (86.6%) because of the value of this reporting group to meeting key objectives of the Chinook Salmon Research Initiative.

The objectives of this study did not require estimates for the Chinook Research Initiative indicator stocks, and the *West/Susitna* and *CI Other* reporting groups from the previous study were not retained due to their subpar performance. For this study, *West/Susitna* populations and *CI Other* populations from Knik Arm and Turnagain Arm were combined to form the *Northern CI* reporting group, and the *CI Other* populations from the Kasilof, Ninilchik, and Anchor rivers and Deep and Stariski creeks were combined to form the *S. Kenai Pen.* reporting group. The increased performance of the Cook Inlet reporting groups (*Northern CI, Kenai*, and *S. Kenai Pen.*) in this study provide for more accurate stock composition and stock-specific harvest estimates of Cook Inlet marine sport fishery harvests.

BASELINE EVALUATION TESTS

The biases in misallocations observed in the baseline evaluation tests provide valuable information when interpreting results from this study (Table 5). Estimates for the *Outside CI* reporting group contain the lowest bias, whereas estimates for the 3 Cook Inlet reporting groups suggest they may be trading misallocations with each other; *Kenai* misallocates to *Northern CI* and *S. Kenai Pen.* reporting groups, and *Northern CI* and *S. Kenai Pen.* misallocate to the *Kenai* reporting group. These differences in MSA performance among these reporting groups is captured in the increased credibility intervals observed for the 3 Cook Inlet reporting groups' estimates compared to the *Outside CI* reporting group estimates.

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, although this 4-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.

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 4 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; CTC 2018). 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 annual harvests increased in the LCI summer and the Cook Inlet winter fisheries. The increase was primarily attributed to the following: (1) shifts in effort and harvest from the UCI early fishery to the LCI summer fishery resulting from emergency orders restricting UCI 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 and 2017, fishing success for feeder Chinook salmon 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 actual 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.

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TABLES AND FIGURES

| Pop. | Reporting | Geographic | | | |
|------|------------|------------|--------------------------|------------------------|-----|
| No. | Group | Region | Location ^a | Sample Year(s) | п |
| 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 | Pilgrim River | 2005, 2006 | 72 |
| 6 | | Alaska | 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 |

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. | Reporting | Geographic | | | |
|------|-------------|------------|---------------------------|------------------------|-----|
| No. | Group | Region | Location ^a | Sample Year(s) | n |
| 36 | Outside CI | Western | Eek River | 2002, 2005 | 171 |
| 37 | | Alaska | 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 | Northern CI | West Side | Straight Creek | 2010 | 95 |
| 65 | | Cook Inlet | 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 | Red Creek | 2012, 2013 | 111 |
| 70 | | River | 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 |

Table 1.–Page 3 of 6.

| Pop. No. | Reporting Group | Geographic Region | Location ^a | Sample Year(s) | 11 |
|-------------|--------------------|----------------------|----------------------------|--------------------------------------|-----------------|
| 75 | Northern CI | Susitna | Portage Creek | 2009, 2010, 2011, 2013 | $\frac{n}{162}$ |
| 76 | nonmern Ci | River | Indian River | 2009, 2010, 2011, 2013 2013 | 79 |
| 77 | | | Chulitna River middle fork | 2009, 2010 | 169 |
| 78 | | | Chulitna River east fork | 2009, 2010, 2011, 2013 | 77 |
| 79 | | | Byers Creek | 2003, 2010, 2011, 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 | | 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 | Campbell Creek | 2010, 2011, 2012 | 110 |
| 98 | | Arm | 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 |

Table 1.–Page 4 of 6.

| Pop. | Reporting | Geographic | | | |
|------|---------------|---------------|--------------------------------------|-------------------|-----|
| No. | Group | 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 | S. Kenai Pen. | Kasilof River | Kasilof River mainstem | 2005 | 316 |
| 114 | | | Crooked Creek | 2005, 2011 | 306 |
| 115 | | Coastal | Ninilchik River | 2006, 2010 | 209 |
| 116 | | Kenai | Deep Creek | 2009, 2010 | 196 |
| 117 | | Peninsula | 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 | Situk River | 1988, 1990, 1991, | 127 |
| | | Gulf of | | 1992 | |
| 131 | | Alaska | Big Boulder Creek | 1992, 1993, 1995, | 171 |
| | | | | 2004 | |
| 132 | | | Tahini River | 1992, 2004 | 168 |
| 133 | | | Tahini River - Pullen Creek | 2005 | 78 |
| 134 | | | Kelsall River | 2004 | 153 |
| 135 | | Southeast | King Salmon River | 1989, 1990, 1993 | 142 |
| 136 | | Alaska | King Creek | 2003 | 172 |
| 137 | | | Chickamin River | 1990, 2003 | 134 |
| 138 | | | Chickamin River - Little Port Walter | 1993, 2005 | 217 |
| | | | Chickamin River - Whitman Lake | 1992, 1998, 2005 | |
| 139 | | | Hatchery | | 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 |

| Pop. | Reporting | Geographic | т | | |
|------------|------------|---------------------|---|------------------|----------|
| <u>No.</u> | Group | Region Southeast | Location ^a | Sample Year(s) | <u>n</u> |
| 145 | Outside CI | Alaska | Kerr Creek Unuk River - Little Port Walter | 2003, 2004 | 151 |
| 146 | | | | 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 | |
| 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 | · · · · | 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 | Kateen River | 2005 | 94 |
| 163 | | Columbia | 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 |
| | | | continued | | |

Table 1.–Page 5 of 6.

Table 1.–Page 6 of 6.

| Pop. | Reporting | Geographic | | | |
|------|------------|------------|-----------------------------------|------------------------------|-----|
| No. | | Region | Location ^a | Sample Year(s) | n |
| 182 | Outside CI | Diffusii | Nanaimo River | 2002 | 78 |
| 183 | | Columbia | 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.

| Fishery | | | | Genetic tis | sue/Head | ∄/ASL | | Samp | les collected | l | Select | ted for gcN | /ISA |
|---------------------|---|-------|-------------------|-------------|----------|-------|--------|-------------------|---------------|--------|---------|-------------|-------|
| | | - | Genetic/ Head/ | Genetic/ | Head/ | | | Genetic tissue | He | Known | | Known | |
| Geographic | Temporal | Year | ASL | ASL | ASL | ASL | Total | Total | Total | origin | Genetic | origin | Total |
| Upper Cook Inlet | 4/1–6/24 (Early) | 2014 | 28 | 278 | 1 | 0 | 307 | 306 | 29 | 12 | 294 | 10 | 304 |
| | | 2015 | 50 | 466 | 1 | 11 | 528 | 516 | 51 | 20 | 390 | 16 | 406 |
| | | 2016 | 56 | 434 | 2 | 0 | 492 | 490 | 58 | 15 | 349 | 11 | 360 |
| | | 2017 | 55 | 486 | 3 | 0 | 544 | 541 | 58 | 20 | 300 | 11 | 311 |
| | 6/25-9/30 | 2014 | 5 | 25 | 0 | 34 | 64 | 30 | 5 | 2 | N/A | N/A | N/A |
| | (Late) | 2015 | 3 | 24 | 1 | 2 | 30 | 27 | 4 | 2 | N/A | N/A | N/A |
| | | 2016 | 33 | 209 | 2 | 0 | 244 | 242 | 35 | 14 | 228 | 14 | 242 |
| | 6/25–8/31 (Late) | 2017 | 38 | 289 | 2 | 0 | 329 | 327 | 40 | 11 | 299 | 10 | 309 |
| Lower | 4/1-9/30 | 2014 | 282 | 1161 | 25 | 76 | 1,544 | 1,443 | 307 | 120 | 359 | 30 | 389 |
| Cook Inlet | (Summer) | 2015 | 591 | 3022 | 15 | 33 | 3,661 | 3,613 | 606 | 215 | 391 | 27 | 418 |
| | | 2016 | 251 | 1654 | 23 | 0 | 1,928 | 1,905 | 274 | 90 | 311 | 16 | 327 |
| - | 4/1-8/31 (Summer) | 2017 | 171 | 981 | 24 | 0 | 1,176 | 1,152 | 195 | 66 | 300 | 18 | 318 |
| Cook Inlet | 1/1-3/31 & | 2014 | 42 | 284 | 5 | 151 | 482 | 326 | 47 | 18 | 309 | 18 | 327 |
| | 10/1-12/31 | 2015 | 190 | 681 | 56 | 12 | 939 | 871 | 246 | 66 | 391 | 23 | 414 |
| | (Winter) | 2016 | 121 | 595 | 14 | 25 | 755 | 716 | 135 | 53 | 311 | 25 | 336 |
| | 1/1-3/31 & 9/1-12/31 (Winter) | 2017 | 79 | 565 | 6 | 0 | 650 | 644 | 85 | 36 | 300 | 19 | 319 |
| | , | Total | 1,995 | 11,154 | 180 | 344 | 13,673 | 13,149 | 2,175 | 760 | 4,532 | 248 | 4,780 |

Table 2.-Number of fish sampled for genetic tissue, heads for CWT recovery and/or ASL data, and samples collected and selected for mixed stock analysis from the Cook Inlet marine sport Chinook salmon fishery 2014–2017.

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

| | | | | CWT Origi | n | | |
|-------|------------|--------------------------------|-----------------|---------------------|--------------|--------|-------|
| | | | Alaska | | | | |
| Year | Fishery | Alaska (outside Cook Inlet) | (Cook Inlet) | British Columbia | Washington | Oragon | Idaho |
| i eai | | | | | w asinington | Oregon | |
| | UCI early | 1 | 0 | 8 | 1 | 2 | 0 |
| 2014 | UCI late | 0 | 0 | 1 | 1 | 0 | 0 |
| 2011 | LCI Summer | 18 | 0 | 35 | 38 | 28 | 1 |
| | Winter | 0 | 0 | 8 | 3 | 7 | 0 |
| | UCI Early | 0 | 0 | 10 | 7 | 3 | 0 |
| 2015 | UCI Late | 1 | 0 | 0 | 0 | 1 | 0 |
| 2015 | LCI Summer | 24 | 0 | 57 | 98 | 32 | 4 |
| | Winter | 2 | 0 | 26 | 24 | 14 | 0 |
| | UCI Early | 1 | 0 | 10 | 3 | 1 | 0 |
| 2016 | UCI Late | 1 | 0 | 4 | 6 | 3 | 0 |
| 2010 | LCI Summer | 12 | 0 | 25 | 39 | 14 | 0 |
| | Winter | 6 | 0 | 29 | 11 | 7 | 0 |
| | UCI Early | 5 | 0 | 7 | 7 | 1 | 0 |
| 2017 | UCI Late | 2 | 0 | 3 | 3 | 3 | 0 |
| 2017 | LCI Summer | 10 | 1 | 16 | 25 | 14 | 0 |
| | Winter | 6 | 0 | 12 | 12 | 6 | 0 |
| | Total | 89 | 1 | 251 | 278 | 136 | 5 |

Table 3.-Number by origin of Chinook salmon containing CWT by fishery and year 2014–2017.

| Assay Name | Source ^a | Ho | F_{IS} | F_{ST} |
|------------------|---------------------|-------|----------|----------|
| Ots_arf-188 | а | 0.011 | 0.028 | 0.078 |
| Ots_AsnRS-60 | а | 0.402 | -0.004 | 0.064 |
| Ots_C3N3^b | b | - | 0.000 | 0.568 |
| Ots_E2-275 | а | 0.370 | 0.000 | 0.145 |
| Ots_ETIF1A | с | 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 | а | 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 | а | 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 | а | 0.368 | -0.004 | 0.187 |
| Ots_Ikaros-250 | a | 0.098 | 0.002 | 0.072 |
| Ots_il-1racp-166 | а | 0.435 | -0.081 | 0.069 |
| Ots_ins-115 | а | 0.037 | -0.002 | 0.041 |
| Ots_LEI-292 | d | 0.040 | 0.014 | 0.040 |
| Ots_LWSop-638 | а | 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 | а | 0.128 | 0.007 | 0.373 |
| Ots_S7-1 | e | 0.324 | 0.010 | 0.224 |
| Ots_SClkF2R2-135 | а | 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_SWS10p-182 | а | 0.433 | -0.022 | 0.084 |
| Ots_TAPBP | с | 0.220 | 0.002 | 0.111 |
| Ots Tnsf | b | 0.294 | 0.007 | 0.232 |

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 | Ho | F_{IS} | F_{ST} |
|------------------|---------------------|-------|----------|----------|
| Ots_u202-161 | а | 0.200 | 0.005 | 0.326 |
| Ots_u211-85 | а | 0.191 | 0.010 | 0.351 |
| Ots_U212-158 | а | 0.107 | -0.018 | 0.060 |
| Ots_u4-92 | а | 0.155 | -0.002 | 0.104 |
| <i>Ots_u6-75</i> | а | 0.199 | 0.006 | 0.096 |
| Ots_Zp3b-215 | а | 0.072 | 0.008 | 0.116 |
| Average/Overall | | 0.245 | 0.000 | 0.179 |

Table 4.–Page 2 of 2.

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.

| Reporting Group | Average | Bias | RMSE | CI Width | | Average | Bias | RMSE | CI Width | | |
|-----------------|---------|------------|------|----------|--|-------------|--------|----------|----------|--|--|
| | _ | Outside CI | | | | Northern CI | | | | | |
| Outside CI | 98.8 | -1.2 | 1.3 | 2.8 | | 0.4 | 0.4 | 0.7 | 1.5 | | |
| Northern CI | 0.3 | 0.3 | 0.3 | 1.1 | | 98.0 | -2.0 | 2.3 | 4.8 | | |
| Kenai | 0.4 | 0.4 | 0.5 | 1.6 | | 1.1 | 1.1 | 1.3 | 3.9 | | |
| S. Kenai Pen. | 0.6 | 0.6 | 0.7 | 1.8 | | 0.5 | 0.5 | 0.5 | 1.8 | | |
| | | Ke | enai | | | | S. Ker | nai Pen. | | | |
| Outside CI | 0.2 | 0.2 | 0.2 | 0.9 | | 0.1 | 0.1 | 0.1 | 0.5 | | |
| Northern CI | 1.6 | 1.6 | 2.0 | 5.3 | | 0.6 | 0.6 | 0.8 | 2.3 | | |
| Kenai | 96.8 | -3.2 | 3.7 | 8.5 | | 0.9 | 0.9 | 1.0 | 4.3 | | |
| S. Kenai Pen. | 1.4 | 1.4 | 1.7 | 5.2 | | 98.4 | -1.6 | 1.8 | 5.4 | | |

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.

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.

| | Upj | per Cook | Inlet Ear | ly | | | | |
|------------------------------|---------|-----------|---------------|-----|--------|-----------|-------|-----|
| Dates: 4/1-6/24 | Stock C | Compositi | ion $(n = 3)$ | 04) |] | Harvest = | 1,554 | |
| | | 90% | 6 CI | | _ | 90% | CI | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 75.3 | 71.1 | 79.4 | 2.5 | 1,171 | 847 | 1,564 | 220 |
| Northern CI | 14.8 | 10.9 | 18.9 | 2.4 | 230 | 147 | 333 | 57 |
| Kenai | 0.5 | 0.0 | 2.1 | 0.8 | 7 | 0 | 33 | 13 |
| S. Kenai Pen. | 9.4 | 6.2 | 12.9 | 2.1 | 146 | 86 | 222 | 42 |
| | Up | per Cook | Inlet Lat | e | | | | |
| Dates: 6/25–9/30 | Stock | Composi | ition ($n =$ | 0) | | Harvest = | = 985 | |
| | | 90% | 6 CI | | _ | 90% | CI | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | - | - | - | - | - | - | - | - |
| Northern CI | - | - | - | - | - | - | - | - |
| Kenai | - | - | - | - | - | - | - | |
| S. Kenai Pen. | - | - | - | - | - | - | - | - |
| | Lowe | er Cook I | nlet Sum | mer | | | | |
| Dates: 4/1–9/30 | Stock C | Compositi | ion $(n = 3)$ | 89) |] | Harvest = | 5,059 | |
| | | 90% | 6 CI | | _ | 90% | CI | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 97.9 | 96.6 | 99.0 | 0.7 | 4,955 | 4,121 | 5,882 | 538 |
| Northern CI | 0.2 | 0.0 | 0.7 | 0.3 | 8 | 0 | 35 | 13 |
| Kenai | 0.5 | 0.0 | 1.7 | 0.6 | 23 | 0 | 86 | 30 |
| S. Kenai Pen. | 1.4 | 0.3 | 2.8 | 0.8 | 72 | 16 | 144 | 40 |
| | | Win | ter | | | | | |
| Dates: 1/1-3/31 & 10/1-12/31 | Stock C | Compositi | ion $(n = 3)$ | 27) |] | Harvest = | 3,173 | |
| | | 90% | 6 CI | | 90% CI | | | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 99.8 | 99.2 | 100.0 | 0.3 | 3,165 | 2,225 | 4,330 | 648 |
| Northern CI | 0.1 | 0.0 | 0.5 | 0.2 | 4 | 0 | 16 | 6 |
| Kenai | 0.1 | 0.0 | 0.4 | 0.2 | 3 | 0 | 13 | 4 |
| S. Kenai Pen. | 0.0 | 0.0 | 0.2 | 0.1 | 1 | 0 | 6 | 3 |

Table 6.–Upper and Lower Cook Inlet marine sport fisheries, **2014**: Stock composition (%) and stock-specific harvest estimates, including mean, 90% credibility interval (CI), sample size (n), and standard deviation (SD).

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

Note: Estimates from strata with inadequate sample sizes for gcMSA are denoted with a dash.

| | Upp | per Cook | Inlet Ear | ly | | | | |
|------------------------------|---------|-----------|---------------|------|-------|-----------|-------|-----|
| Dates: 4/1-6/24 | Stock C | Composit | ion ($n = 4$ | 06) |] | Harvest = | 2,658 | |
| | | 90% | 6 CI | | | 90% | CI | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 80.4 | 77.1 | 83.6 | 2.0 | 2,137 | 1,645 | 2,719 | 329 |
| Northern CI | 11.5 | 8.8 | 14.5 | 1.8 | 306 | 209 | 425 | 66 |
| Kenai | 0.4 | 0.0 | 2.0 | 0.7 | 11 | 0 | 53 | 20 |
| S. Kenai Pen. | 7.7 | 5.2 | 10.3 | 1.5 | 204 | 128 | 296 | 52 |
| | Up | per Cook | x Inlet Lat | te | | | | |
| Dates: 6/25–9/30 | Stock C | Composit | ion $(n = N)$ | NA) |] | Harvest = | 1,528 | |
| | | 90% | 6 CI | | | 90% | CI | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | - | - | - | - | - | - | - | - |
| Northern CI | - | - | - | - | - | - | - | - |
| Kenai | - | - | - | - | - | - | - | - |
| S. Kenai Pen. | - | - | - | - | - | - | - | - |
| | Lowe | er Cook I | nlet Sum | mer | | | | |
| Dates: 4/1–9/30 | Stock C | Composit | ion $(n = 4)$ | -18) | | Harvest = | 8,066 | |
| | | 90% | 6 CI | | _ | 90% | CI | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 99.0 | 98.0 | 99.7 | 0.5 | 7,988 | 6,764 | 9,340 | 785 |
| Northern CI | 0.8 | 0.2 | 1.7 | 0.5 | 65 | 12 | 142 | 41 |
| Kenai | 0.1 | 0.0 | 0.6 | 0.2 | 10 | 0 | 51 | 20 |
| S. Kenai Pen. | 0.0 | 0.0 | 0.2 | 0.1 | 3 | 0 | 18 | 9 |
| | | Win | iter | | | | | |
| Dates: 1/1–3/31 & 10/1–12/31 | Stock C | Composit | ion $(n = 4$ | -14) | | Harvest = | 5,179 | |
| | | 90% | 90% CI | | | | | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 99.8 | 99.4 | 100.0 | 0.2 | 5,170 | 3,878 | 6,708 | 865 |
| Northern CI | 0.1 | 0.0 | 0.4 | 0.2 | 5 | 0 | 21 | 8 |
| Kenai | 0.1 | 0.0 | 0.3 | 0.1 | 3 | 0 | 15 | 6 |
| S. Kenai Pen. | 0.0 | 0.0 | 0.1 | 0.1 | 1 | 0 | 8 | 4 |

Table 7.–Upper and Lower Cook Inlet marine sport fisheries, **2015**: Stock composition (%) and stock-specific harvest estimates, including mean, 90% credibility interval (CI), sample size (n), and standard deviation (SD).

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

Note: Estimates from strata with inadequate sample sizes for gcMSA are denoted with a dash.

| | Up | per Coo | k Inlet Ea | rly | | | | |
|------------------------------|---------|----------|---------------|------|--------|-----------|--------|-----|
| Dates: 4/1-6/24 | Stock C | omposit | ion $(n = 3)$ | 60) | | Harvest = | 2,430 | |
| | | 90% | 6 CI | | | 90% | 6 CI | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 89.9 | 87.0 | 92.6 | 1.7 | 2,185 | 1,693 | 2,759 | 326 |
| Northern CI | 6.2 | 3.7 | 9.1 | 1.6 | 152 | 85 | 234 | 46 |
| Kenai | 1.7 | 0.0 | 4.0 | 1.2 | 40 | 0 | 98 | 31 |
| S. Kenai Pen. | 2.2 | 0.7 | 4.1 | 1.0 | 53 | 17 | 102 | 27 |
| | U | pper Coc | ok Inlet La | ate | | | | |
| Dates: 6/25–9/30 | Stock C | omposit | ion $(n = 2)$ | .42) | | Harvest = | 1,333 | |
| | | 90% | 6 CI | | | 90% | 6 CI | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 96.5 | 94.3 | 98.2 | 1.2 | 1,286 | 935 | 1,715 | 239 |
| Northern CI | 0.3 | 0.0 | 1.3 | 0.5 | 4 | 0 | 17 | 6 |
| Kenai | 1.6 | 0.0 | 4.5 | 1.6 | 21 | 0 | 62 | 21 |
| S. Kenai Pen. | 1.6 | 0.0 | 4.4 | 1.5 | 22 | 0 | 61 | 21 |
| | Low | er Cook | Inlet Sun | nmer | | | | |
| Dates: 4/1–9/30 | Stock C | omposit | ion $(n = 3)$ | 27) | | Harvest = | 9,868 | |
| | | 90% | 6 CI | | - | 90% | 6 CI | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 96.1 | 94.2 | 97.8 | 1.1 | 9,487 | 8,323 | 10,751 | 739 |
| Northern CI | 1.0 | 0.2 | 2.3 | 0.7 | 99 | 15 | 229 | 68 |
| Kenai | 0.2 | 0.0 | 0.9 | 0.4 | 20 | 0 | 91 | 35 |
| S. Kenai Pen. | 2.7 | 1.2 | 4.4 | 1.0 | 262 | 119 | 444 | 100 |
| | | Wi | nter | | | | | |
| Dates: 1/1-3/31 & 10/1-12/31 | Stock C | omposit | ion $(n = 3)$ | 36) | | Harvest = | 5,106 | |
| | | 90% | 6 CI | | 90% CI | | | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 99.8 | 99.3 | 100.0 | 0.3 | 5,095 | 3,823 | 6,604 | 857 |
| Northern CI | 0.1 | 0.0 | 0.5 | 0.2 | 6 | 0 | 25 | 10 |
| Kenai | 0.1 | 0.0 | 0.4 | 0.1 | 4 | 0 | 18 | 8 |
| S. Kenai Pen. | 0.0 | 0.0 | 0.2 | 0.1 | 2 | 0 | 10 | 5 |

Table 8.–Upper and Lower Cook Inlet marine sport fisheries, **2016**: Stock composition (%) and stock-specific harvest estimates, including mean, 90% credibility interval (CI), sample size (n), and standard deviation (SD).

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

| | Upj | per Cook | Inlet Ear | ly | | | | |
|-----------------------------|---------|-----------|---------------|-----|--------|-----------|-------|-----|
| Dates: 4/1-6/24 | Stock C | Composit | ion ($n = 3$ | 11) | | Harvest = | 1,999 | |
| | | 90% | 6 CI | | _ | 90% | CI | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 84.7 | 81.2 | 88.0 | 2.0 | 1,693 | 1,321 | 2,122 | 245 |
| Northern CI | 5.5 | 2.5 | 8.9 | 2.0 | 109 | 47 | 186 | 43 |
| Kenai | 2.3 | 0.0 | 6.2 | 2.0 | 47 | 0 | 126 | 40 |
| S. Kenai Pen. | 7.5 | 4.3 | 10.9 | 2.0 | 149 | 82 | 230 | 46 |
| | Up | per Cook | Inlet Lat | e | | | | |
| Dates: 6/25-8/31 | Stock C | Composit | ion $(n = 3)$ | 09) | | Harvest = | 1,157 | |
| | | 90% | 6 CI | | _ | 90% | CI | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 82.0 | 78.1 | 85.6 | 2.3 | 948 | 617 | 1,374 | 235 |
| Northern CI | 2.2 | 0.0 | 7.1 | 2.4 | 25 | 0 | 85 | 29 |
| Kenai | 12.7 | 6.8 | 17.9 | 3.4 | 147 | 69 | 243 | 54 |
| S. Kenai Pen. | 3.2 | 1.0 | 6.3 | 1.6 | 37 | 11 | 78 | 22 |
| | Lowe | er Cook I | nlet Sum | ner | | | | |
| Dates: 4/1-8/31 | Stock C | Composit | ion $(n = 3)$ | 18) | | Harvest = | 8,687 | |
| | | 90% | 6 CI | | _ | 90% | CI | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 96.7 | 94.8 | 98.2 | 1.0 | 8,398 | 7,321 | 9,566 | 683 |
| Northern CI | 1.6 | 0.4 | 3.1 | 0.8 | 137 | 37 | 272 | 73 |
| Kenai | 0.2 | 0.0 | 1.1 | 0.4 | 21 | 0 | 94 | 35 |
| S. Kenai Pen. | 1.5 | 0.5 | 3.0 | 0.8 | 131 | 39 | 260 | 69 |
| | | Win | ter | | | | | |
| Dates: 1/1-3/31 & 9/1-12/31 | Stock C | Composit | ion $(n = 3)$ | 19) |] | Harvest = | 4,518 | |
| | | 90% | 6 CI | | 90% CI | | | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 99.8 | 99.2 | 100.0 | 0.3 | 4,507 | 3,338 | 5,906 | 788 |
| Northern CI | 0.1 | 0.0 | 0.4 | 0.2 | 4 | 0 | 18 | 7 |
| Kenai | 0.1 | 0.0 | 0.4 | 0.2 | 4 | 0 | 18 | 7 |
| S. Kenai Pen. | 0.1 | 0.0 | 0.4 | 0.2 | 4 | 0 | 18 | 7 |

Table 9.–Upper and Lower Cook Inlet marine sport fisheries, **2017**: Stock composition (%) and stock-specific harvest estimates, including mean, 90% credibility interval (CI), sample size (n), and standard deviation (SD).

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

| Year: 2014 | Stock Composition ($n = 1,020$) | |) | | Harvest ^a | = 9,786 | | |
|-----------------|-----------------------------------|-----------|--------------|-----|----------------------|------------------------|--------|-------|
| | | 90% | CI | | | 90% | CI | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 94.9 | 94.0 | 95.8 | 0.6 | 9,292 | 7,954 | 10,802 | 866 |
| Northern CI | 2.5 | 1.8 | 3.2 | 0.4 | 242 | 156 | 349 | 59 |
| Kenai | 0.3 | 0.0 | 1.0 | 0.3 | 33 | 1 | 100 | 33 |
| S. Kenai Pen. | 2.2 | 1.4 | 3.1 | 0.5 | 219 | 132 | 323 | 58 |
| Year: 2015 | Stock Co | mposition | (n = 1,238) |) | | Harvest ^a = | 15,903 | |
| | | 90% | CI | | | 90% | CI | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 96.2 | 95.4 | 96.8 | 0.4 | 15,295 | 13,402 | 17,363 | 1,214 |
| Northern CI | 2.4 | 1.8 | 3.0 | 0.4 | 376 | 259 | 513 | 78 |
| Kenai | 0.2 | 0.0 | 0.5 | 0.2 | 25 | 0 | 85 | 29 |
| S. Kenai Pen. | 1.3 | 0.9 | 1.8 | 0.3 | 208 | 130 | 302 | 53 |
| Year: 2016 | Stock Co | mposition | (n = 1, 265) |) | | Harvest = 18,737 | | |
| | _ | 90% | CI | | _ | 90% | o CI | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 96.3 | 95.2 | 97.3 | 0.6 | 18,052 | 16,181 | 20,106 | 1,199 |
| Northern CI | 1.4 | 0.8 | 2.2 | 0.4 | 261 | 145 | 412 | 83 |
| Kenai | 0.5 | 0.1 | 0.9 | 0.3 | 85 | 17 | 180 | 52 |
| S. Kenai Pen. | 1.8 | 1.0 | 2.8 | 0.5 | 338 | 184 | 528 | 105 |
| Year: 2017 | Stock Co | mposition | (n = 1,257) |) | | Harvest = | 16,361 | |
| | _ | 90% | CI | | 90% CI | | | |
| Reporting Group | Mean | 5% | 95% | SD | Mean | 5% | 95% | SD |
| Outside CI | 95.0 | 93.9 | 96.0 | 0.6 | 15,547 | 13,834 | 17,420 | 1,095 |
| Northern CI | 1.7 | 0.9 | 2.6 | 0.5 | 275 | 143 | 437 | 90 |
| Kenai | 1.3 | 0.7 | 2.1 | 0.4 | 218 | 110 | 359 | 77 |
| S. Kenai Pen. | 2.0 | 1.2 | 2.9 | 0.5 | 321 | 196 | 475 | 86 |

Table 10.–Cook Inlet marine sport fishery, **2014–2017**: annual stock composition (%) and stock-specific harvest estimates, including mean, 90% credibility interval (CI), sample size (n), and standard deviation (SD).

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

^a Harvest estimates do not include harvest from UCI Late fishery in 2014 (985 fish) and 2015 (1,528 fish) because insufficient samples were collected for gcMSA.

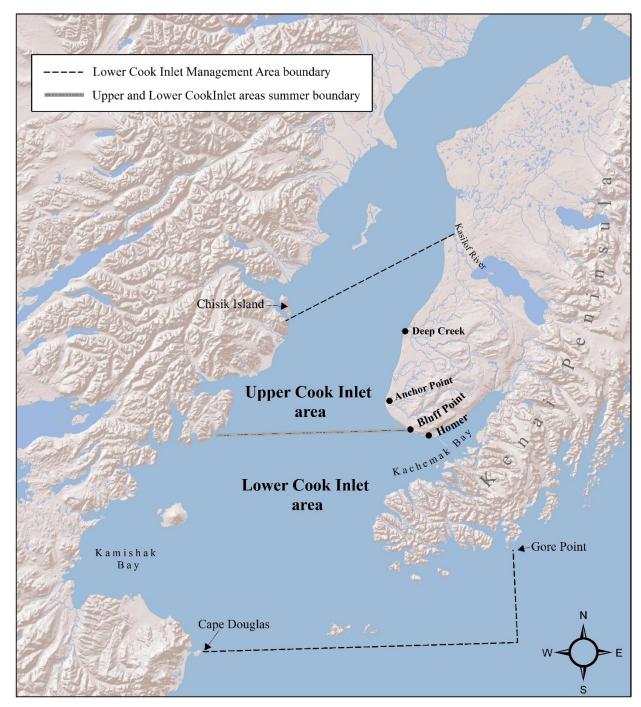


Figure 1.–Boundaries of the Lower Cook Inlet Management Area for the Division of Sport Fish. In the summer the management area is further divided into 2 fisheries, Upper Cook Inlet (north of Bluff Point) and Lower Cook Inlet (south of Bluff Point including Kachemak Bay). The winter fishery encompasses the entirety of the Lower Cook Inlet Management Area.

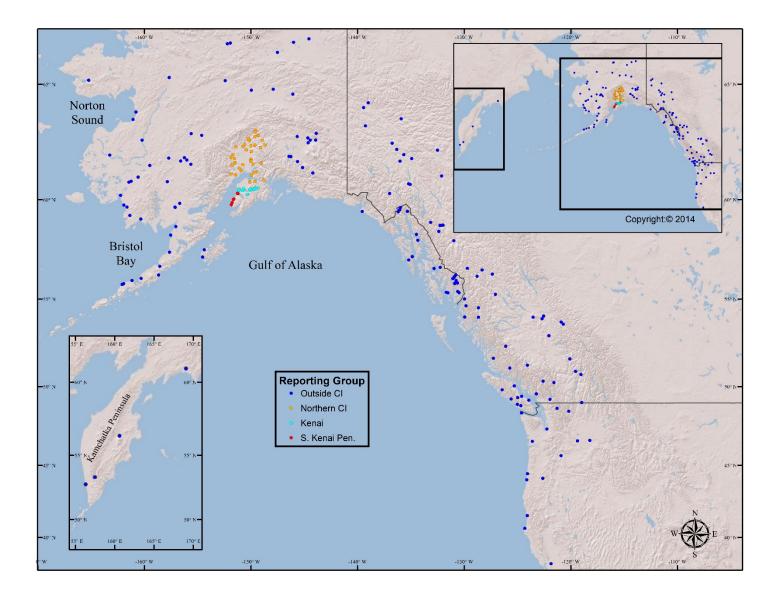


Figure 2.-Map of 211 sampling locations for Chinook salmon populations included in the Cook Inlet coastwide baseline. Location dot color matches reporting group assignment.

Source: Adapted from Templin et al. 2011.

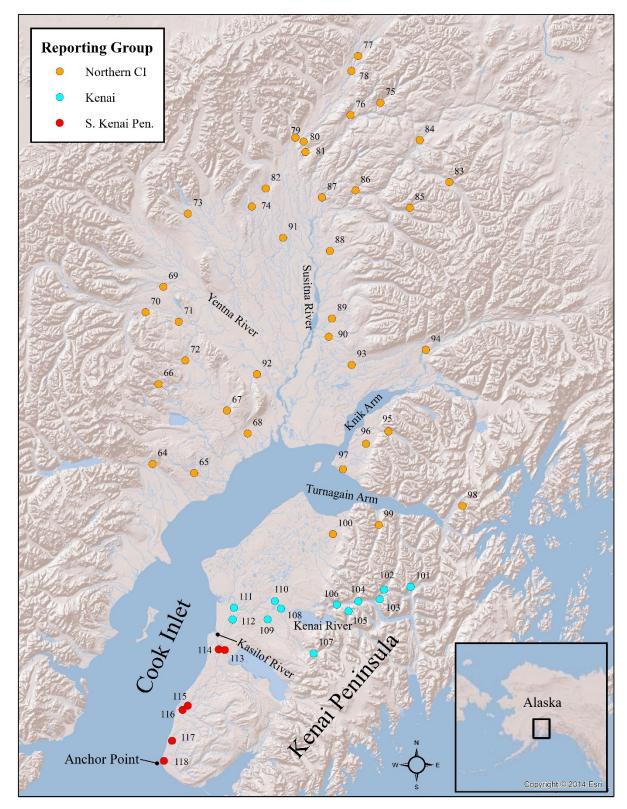


Figure 3.–Sampling locations for Chinook salmon populations from Cook Inlet included in the Cook Inlet coastwide genetic baseline.

Note: Numbers correspond to map numbers on Table 1. Location color matches reporting group assignment.

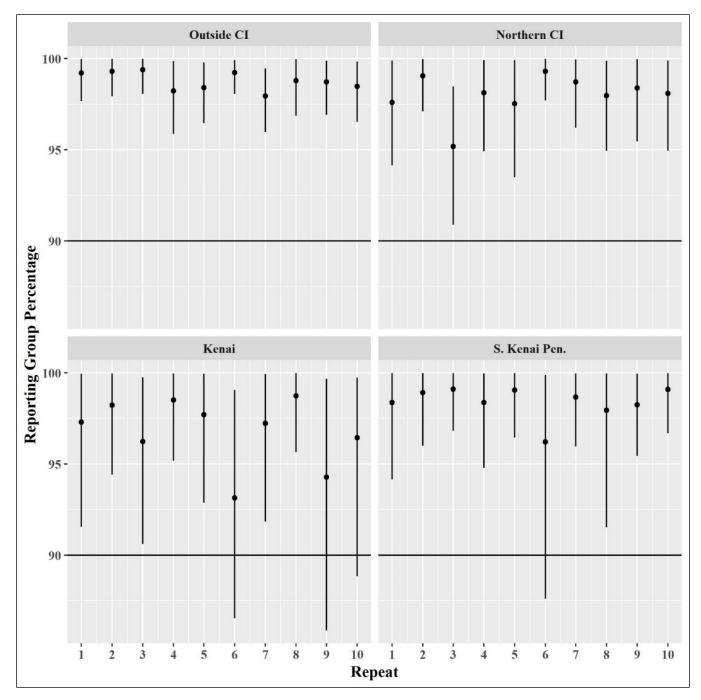


Figure 4.–Results of repeated proof tests for 4 reporting groups. The points represent the mean correct allocation from each repeat with 90% credibility intervals for each point.

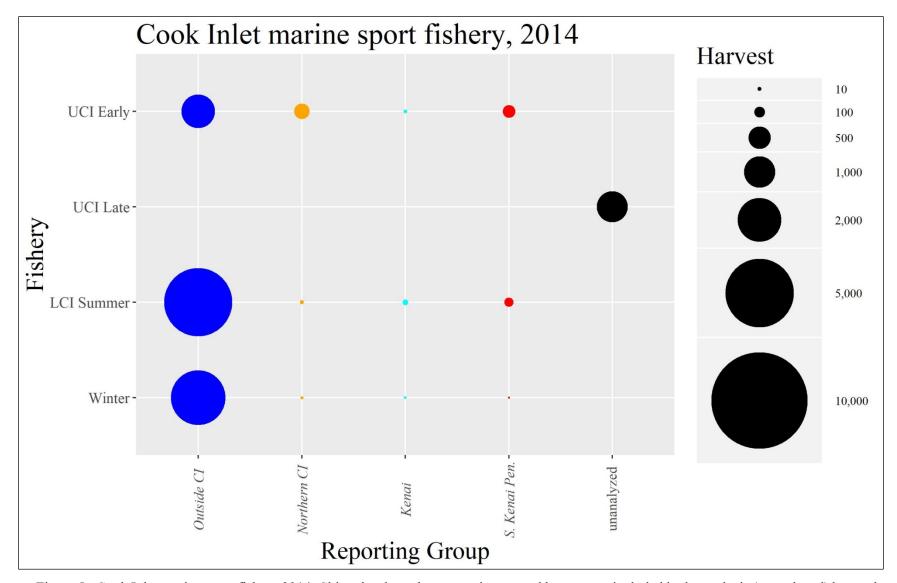


Figure 5.–Cook Inlet marine sport fishery **2014**: Chinook salmon harvest estimates and harvest not included in the analysis (unanalyzed) by stock (reporting group). Black circles indicate the portion of the total harvest from each fishery not included in the analysis (unanalyzed).

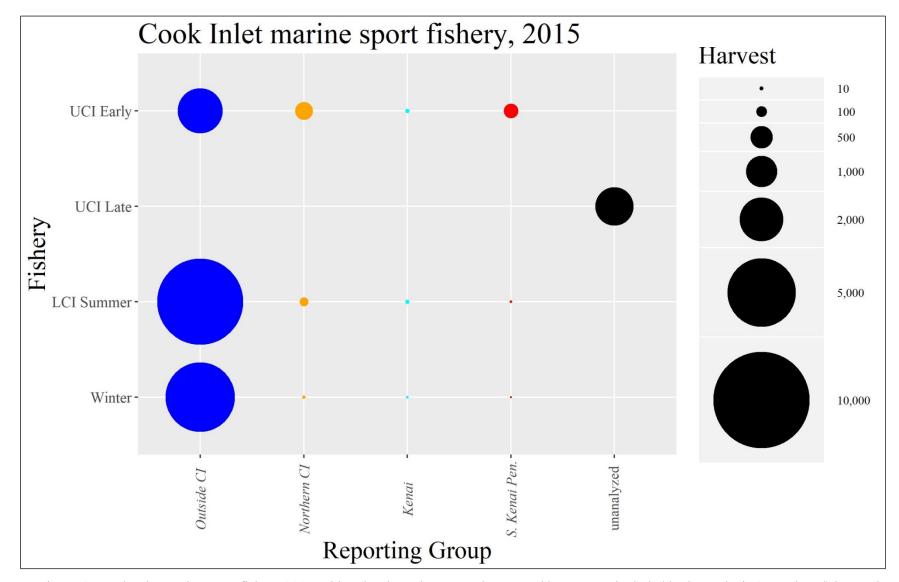


Figure 6.–Cook Inlet marine sport fishery **2015**: Chinook salmon harvest estimates and harvest not included in the analysis (unanalyzed) by stock (reporting group). Black circles indicate the portion of the total harvest from each fishery not included in the analysis (unanalyzed).

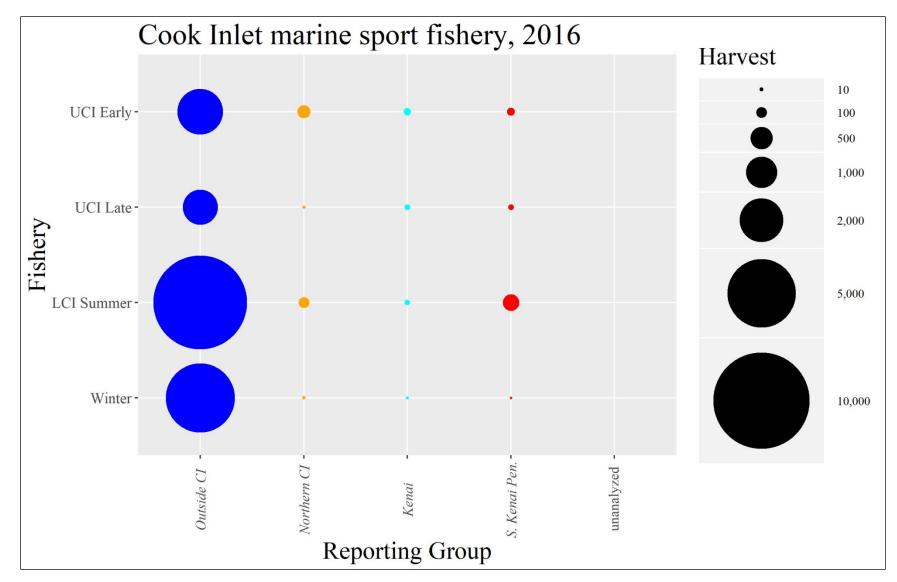


Figure 7.–Cook Inlet marine sport fishery **2016**: Chinook salmon harvest estimates and harvest not included in the analysis (unanalyzed) by stock (reporting group). Black circles indicate the portion of the total harvest from each fishery not included in the analysis (unanalyzed).

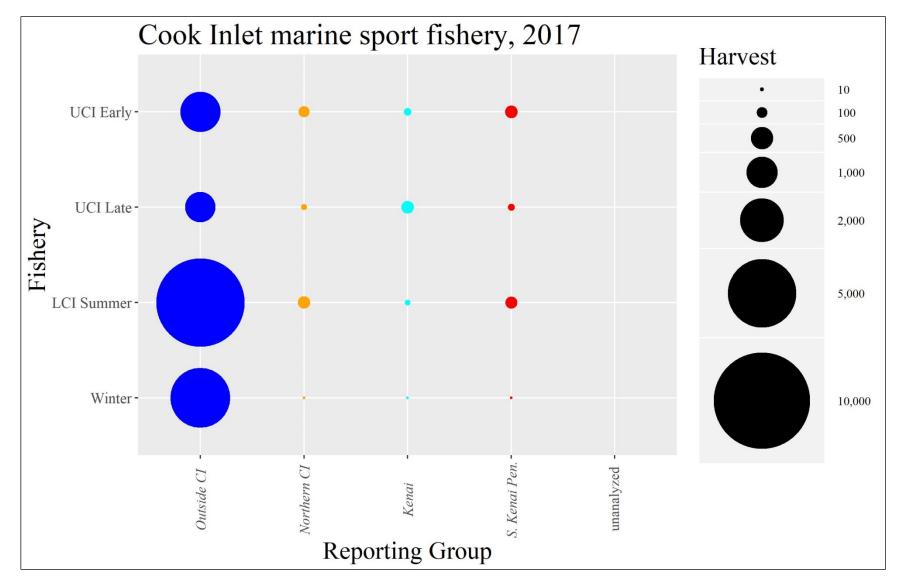


Figure 8.–Cook Inlet marine sport fishery **2017**: Chinook salmon harvest estimates and harvest not included in the analysis (unanalyzed) by stock (reporting group). Black circles indicate the portion of the total harvest from each fishery not included in the analysis (unanalyzed).

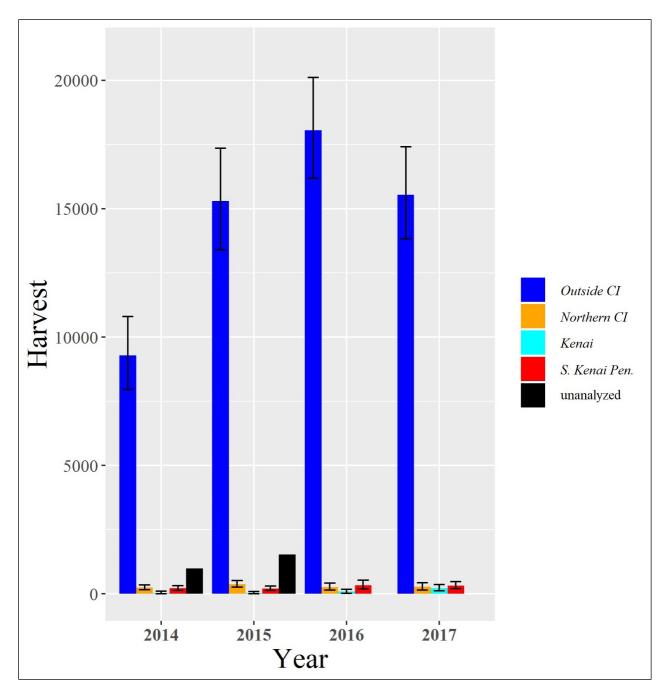


Figure 9.–Overall Cook Inlet marine sport fishery Chinook salmon harvest estimates and credibility intervals by reporting group for 2014, 2015, 2016, and 2017.

APPENDIX A. SUMMARY OF HARVEST SAMPLES COLLECTED BY PORT

| Port | Collection Date | Samples Collected | Heads Collected |
|--------------|-----------------|-------------------|-----------------|
| Anchor Point | 2014 | 231 | 32 |
| | 2015 | 272 | 38 |
| | 2016 | 156 | 10 |
| | 2017 | 251 | 18 |
| Deep Creek | 2014 | 123 | 9 |
| | 2015 | 163 | 14 |
| | 2016 | 148 | 16 |
| | 2017 | 143 | 19 |
| Homer | 2014 | 1,751 | 327 |
| | 2015 | 4,592 | 794 |
| | 2016 | 3,049 | 433 |
| | 2017 | 2,270 | 306 |
| | Total | 13,149 | 2,016 |

Appendix A1.–Number of samples collected in the Lower Cook Inlet Management Area from the Cook Inlet marine sport harvest by port and year, 2014–2017.

Note: If collected heads could not be assigned to a fishery (i.e. missing date or location data) they were not used in CWT analysis.

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% | 6 CI | | | | 90% | 6 CI | | | |
|-----------------|------------|---|---|------------|------|-----|--------|------------|------------|-------------|-----|--|
| Reporting Group | Percentage | Median | 5% | 95% | Mean | SD | Median | 5% | 95% | Mean | SD | |
| | | Outside CI Replicate 1 Outside CI Replica | | | | | | CI Replica | te 2 | | | |
| Outside CI | 100.0 | 99.4 | 97.7 | 100.0 | 99.2 | 0.8 | 99.5 | 97.9 | 100.0 | 99.3 | 0.7 | |
| Northern CI | 0.0 | 0.1 | 0.0 | 1.4 | 0.3 | 0.5 | 0.1 | 0.0 | 1.1 | 0.2 | 0.4 | |
| Kenai | 0.0 | 0.1 | 0.0 | 1.5 | 0.3 | 0.6 | 0.1 | 0.0 | 1.2 | 0.3 | 0.4 | |
| S. Kenai Pen. | 0.0 | 0.0 | 0.0 | 0.6 | 0.1 | 0.3 | 0.0 | 0.0 | 0.9 | 0.2 | 0.4 | |
| | | | Outside (| CI Replica | te 3 | | | Outside (| CI Replica | | | |
| Outside CI | 100.0 | 99.6 | 98.1 | 100.0 | 99.4 | 0.7 | 98.4 | 95.9 | 99.9 | 98.2 | 1.3 | |
| Northern CI | 0.0 | 0.0 | 0.0 | 1.0 | 0.2 | 0.4 | 0.1 | 0.0 | 1.2 | 0.3 | 0.4 | |
| Kenai | 0.0 | 0.0 | 0.0 | 0.9 | 0.2 | 0.4 | 0.6 | 0.0 | 3.4 | 1.0 | 1.2 | |
| S. Kenai Pen. | 0.0 | 0.0 | 0.0 | 1.1 | 0.2 | 0.4 | 0.1 | 0.0 | 2.1 | 0.5 | 0.7 | |
| | | | Outside (| CI Replica | te 5 | | | Outside (| CI Replica | Replicate 6 | | |
| Outside CI | 100.0 | 98.6 | 96.5 | 99.8 | 98.4 | 1.0 | 99.4 | 98.1 | 99.9 | 99.2 | 0.6 | |
| Northern CI | 0.0 | 0.3 | 0.0 | 1.9 | 0.5 | 0.7 | 0.3 | 0.0 | 1.4 | 0.5 | 0.5 | |
| Kenai | 0.0 | 0.2 | 0.0 | 2.1 | 0.5 | 0.8 | 0.0 | 0.0 | 0.7 | 0.1 | 0.3 | |
| S. Kenai Pen. | 0.0 | 0.3 | 0.0 | 1.7 | 0.5 | 0.6 | 0.0 | 0.0 | 0.8 | 0.2 | 0.3 | |
| | | | Outside CI Replicate 7 Outside CI Repli | | | | | CI Replica | te 8 | | | |
| Outside CI | 100.0 | 98.1 | 96.0 | 99.5 | 97.9 | 1.1 | 99.0 | 96.9 | 100.0 | 98.8 | 1.0 | |
| Northern CI | 0.0 | 0.1 | 0.0 | 1.3 | 0.3 | 0.5 | 0.0 | 0.0 | 0.5 | 0.1 | 0.2 | |
| Kenai | 0.0 | 0.1 | 0.0 | 1.5 | 0.3 | 0.6 | 0.1 | 0.0 | 1.3 | 0.3 | 0.5 | |
| S. Kenai Pen. | 0.0 | 1.3 | 0.1 | 3.1 | 1.4 | 0.9 | 0.6 | 0.0 | 2.6 | 0.8 | 0.9 | |

| | True | _ | 90% CI | | | | 90% CI | | | | | |
|-----------------|------------|-------------------------|-----------|-----------|-----------------------|-----|-------------------------|-------------------------|-------|-----------|-----|--|
| Reporting Group | Percentage | Median | 5% | 95% | Mean | SD | Median | 5% | 95% | Mean | SD | |
| | | (| Outside C | I Replica | ate 9 | | (| Outside C | e 10 | | | |
| Outside CI | 100.0 | 98.9 | 96.9 | 99.9 | 98.7 | 0.9 | 98.6 | 96.5 | 99.9 | 98.5 | 1.0 | |
| Northern CI | 0.0 | 0.0 | 0.0 | 0.8 | 0.2 | 0.3 | 0.0 | 0.0 | 0.6 | 0.1 | 0.2 | |
| Kenai | 0.0 | 0.0 | 0.0 | 1.2 | 0.2 | 0.5 | 0.2 | 0.0 | 1.9 | 0.5 | 0.7 | |
| S. Kenai Pen. | 0.0 | 0.7 | 0.0 | 2.3 | 0.9 | 0.7 | 0.8 | 0.0 | 2.5 | 0.9 | 0.8 | |
| | | N | orthern (| CI Replic | cate 1 Northern CI Re | | | | | olicate 2 | | |
| Outside CI | 0.0 | 0.0 | 0.0 | 0.6 | 0.1 | 0.3 | 0.0 | 0.0 | 0.7 | 0.1 | 0.3 | |
| Northern CI | 100.0 | 97.9 | 94.1 | 99.9 | 97.6 | 1.9 | 99.4 | 97.1 | 100.0 | 99.1 | 1.0 | |
| Kenai | 0.0 | 1.6 | 0.0 | 5.3 | 1.9 | 1.7 | 0.1 | 0.0 | 2.1 | 0.5 | 0.8 | |
| S. Kenai Pen. | 0.0 | 0.1 | 0.0 | 1.5 | 0.3 | 0.6 | 0.1 | 0.0 | 1.5 | 0.3 | 0.5 | |
| | | Northern CI Replicate 3 | | | | | Northern CI Replicate 4 | | | | | |
| Outside CI | 0.0 | 1.7 | 0.3 | 3.8 | 1.8 | 1.1 | 0.1 | 0.0 | 1.7 | 0.4 | 0.6 | |
| Northern CI | 100.0 | 95.5 | 90.9 | 98.5 | 95.2 | 2.4 | 98.5 | 94.9 | 99.9 | 98.1 | 1.6 | |
| Kenai | 0.0 | 1.2 | 0.0 | 6.4 | 1.9 | 2.2 | 0.2 | 0.0 | 3.8 | 0.9 | 1.4 | |
| S. Kenai Pen. | 0.0 | 0.7 | 0.0 | 3.6 | 1.1 | 1.2 | 0.3 | 0.0 | 2.5 | 0.6 | 0.9 | |
| | | | | | | | | Northern CI Replicate 6 | | | | |
| Outside CI | 0.0 | 0.0 | 0.0 | 1.0 | 0.2 | 0.4 | 0.0 | 0.0 | 0.4 | 0.1 | 0.2 | |
| Northern CI | 100.0 | 98.0 | 93.5 | 99.9 | 97.5 | 2.1 | 99.6 | 97.7 | 100.0 | 99.3 | 0.8 | |
| Kenai | 0.0 | 1.6 | 0.0 | 6.1 | 2.1 | 2.0 | 0.1 | 0.0 | 1.5 | 0.3 | 0.6 | |
| S. Kenai Pen. | 0.0 | 0.0 | 0.0 | 0.8 | 0.2 | 0.3 | 0.1 | 0.0 | 1.4 | 0.3 | 0.5 | |

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| | True | 90% CI | | | | | 90% CI | | | | | |
|-----------------|------------|--------|-------------------|------------|-------------------|-----|-------------------|-----------|------------|-------|-----|--|
| Reporting Group | Percentage | Median | 5% | 95% | Mean | SD | Median | 5% | 95% | Mean | SD | |
| | | 1 | Northern | CI Replica | ate 7 | | 1 | Northern | CI Replica | ate 8 | | |
| | | | 90% | 6 CI | | | | | | | | |
| Outside CI | 0.0 | 0.0 | 0.0 | 0.5 | 0.1 | 0.2 | 0.2 | 0.0 | 2.3 | 0.6 | 0.8 | |
| Northern CI | 100.0 | 99.1 | 96.2 | 100.0 | 98.7 | 1.2 | 98.3 | 95.0 | 99.9 | 98.0 | 1.6 | |
| Kenai | 0.0 | 0.2 | 0.0 | 3.2 | 0.8 | 1.1 | 0.6 | 0.0 | 3.9 | 1.1 | 1.4 | |
| S. Kenai Pen. | 0.0 | 0.2 | 0.0 | 1.7 | 0.4 | 0.6 | 0.1 | 0.0 | 1.8 | 0.4 | 0.7 | |
| | | 1 | Northern | CI Replica | nte 9 | | N | orthern (| CI Replica | te 10 | | |
| Outside CI | 0.0 | 0.2 | 0.0 | 3.2 | 0.8 | 1.1 | 0.0 | 0.0 | 1.0 | 0.2 | 0.4 | |
| Northern CI | 100.0 | 98.8 | 95.4 | 100.0 | 98.4 | 1.5 | 98.5 | 94.9 | 99.9 | 98.1 | 1.6 | |
| Kenai | 0.0 | 0.1 | 0.0 | 2.9 | 0.6 | 1.1 | 0.3 | 0.0 | 3.8 | 0.9 | 1.4 | |
| S. Kenai Pen. | 0.0 | 0.0 | 0.0 | 1.0 | 0.2 | 0.4 | 0.5 | 0.0 | 2.6 | 0.8 | 0.9 | |
| | | | Replicate | 1 | Kenai Replicate 2 | | | | | | | |
| Outside CI | 0.0 | 0.0 | 0.0 | 0.9 | 0.2 | 0.4 | 0.0 | 0.0 | 0.8 | 0.2 | 0.3 | |
| Northern CI | 0.0 | 0.5 | 0.0 | 6.6 | 1.6 | 2.3 | 0.1 | 0.0 | 1.9 | 0.4 | 0.8 | |
| Kenai | 100.0 | 98.3 | 91.6 | 99.9 | 97.3 | 3.2 | 98.8 | 94.4 | 100.0 | 98.2 | 1.9 | |
| S. Kenai Pen. | 0.0 | 0.2 | 0.0 | 3.9 | 0.9 | 1.8 | 0.5 | 0.0 | 4.8 | 1.2 | 1.7 | |
| | | | Kenai Replicate 3 | | | | Kenai Replicate 4 | | | | | |
| Outside CI | 0.0 | 0.0 | 0.0 | 1.1 | 0.2 | 0.4 | 0.0 | 0.0 | 0.5 | 0.1 | 0.2 | |
| Northern CI | 0.0 | 0.4 | 0.0 | 3.7 | 0.9 | 1.3 | 0.3 | 0.0 | 3.8 | 0.9 | 1.4 | |
| Kenai | 100.0 | 96.8 | 90.6 | 99.7 | 96.2 | 2.9 | 99.1 | 95.2 | 100.0 | 98.5 | 1.6 | |
| S. Kenai Pen. | 0.0 | 2.0 | 0.0 | 7.8 | 2.6 | 2.5 | 0.1 | 0.0 | 2.2 | 0.5 | 0.9 | |

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| | True | 90% CI | | | | | | 90% | 6 CI | | |
|-----------------|------------|---|-------|-----------|------|-----|-------------------|---------|-------------|------|-----|
| Reporting Group | Percentage | Median | 5% | 95% | Mean | SD | Median | 5% | 95% | Mean | SD |
| | ~~~~~ | | Kenai | Replicate | 5 | | | Kenai | 6 | | |
| Outside CI | 0.0 | 0.0 | 0.0 | 0.9 | 0.2 | 0.4 | 0.0 | 0.0 | 0.7 | 0.2 | 0.4 |
| Northern CI | 0.0 | 0.2 | 0.0 | 5.1 | 1.1 | 1.8 | 4.9 | 0.0 | 10.6 | 4.8 | 3.4 |
| Kenai | 100.0 | 98.5 | 92.9 | 99.9 | 97.7 | 2.4 | 93.3 | 86.5 | 99.0 | 93.1 | 3.8 |
| S. Kenai Pen. | 0.0 | 0.4 | 0.0 | 4.2 | 1.0 | 1.5 | 1.3 | 0.0 | 5.7 | 1.9 | 2.0 |
| | | | Kenai | Replicate | 7 | | Kenai Replicate 8 | | | | |
| Outside CI | 0.0 | 0.0 | 0.0 | 1.6 | 0.3 | 0.6 | 0.0 | 0.0 | 0.6 | 0.1 | 0.3 |
| Northern CI | 0.0 | 0.9 | 0.0 | 6.5 | 1.8 | 2.2 | 0.2 | 0.0 | 3.4 | 0.7 | 1.3 |
| Kenai | 100.0 | 98.0 | 91.8 | 99.9 | 97.2 | 2.7 | 99.3 | 95.6 | 100.0 | 98.7 | 1.5 |
| S. Kenai Pen. | 0.0 | 0.2 | 0.0 | 3.2 | 0.7 | 1.2 | 0.1 | 0.0 | 1.9 | 0.4 | 0.7 |
| | | | Kenai | Replicate | 9 | | | Kenai I | Replicate 1 | 0 | |
| Outside CI | 0.0 | 0.0 | 0.0 | 0.7 | 0.1 | 0.3 | 0.3 | 0.0 | 1.5 | 0.5 | 0.5 |
| Northern CI | 0.0 | 2.2 | 0.0 | 8.9 | 3.0 | 3.0 | 0.1 | 0.0 | 2.8 | 0.6 | 1.1 |
| Kenai | 100.0 | 95.2 | 85.9 | 99.7 | 94.3 | 4.4 | 97.6 | 88.8 | 99.7 | 96.4 | 3.5 |
| S. Kenai Pen. | 0.0 | 1.7 | 0.0 | 8.9 | 2.6 | 3.0 | 1.1 | 0.0 | 9.8 | 2.5 | 3.3 |
| | | S. Kenai Pen. Replicate 1 S. Kenai Pen. I | | | | | en. Replic | ate 2 | | | |
| Outside CI | 0.0 | 0.0 | 0.0 | 0.5 | 0.1 | 0.2 | 0.0 | 0.0 | 0.5 | 0.1 | 0.2 |
| Northern CI | 0.0 | 0.1 | 0.0 | 3.0 | 0.6 | 1.1 | 0.0 | 0.0 | 1.4 | 0.3 | 0.6 |
| Kenai | 0.0 | 0.1 | 0.0 | 5.0 | 0.9 | 1.9 | 0.1 | 0.0 | 3.3 | 0.7 | 1.3 |
| S. Kenai Pen. | 100.0 | 99.1 | 94.1 | 100.0 | 98.4 | 2.1 | 99.4 | 96.0 | 100.0 | 98.9 | 1.4 |

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| | True | | 90% | ó CI | | | | 90% | 6 CI | | | |
|-----------------|------------|--|-----------|------------|-------|-----|---------------------------|-------------|-------------|--------|-----|--|
| Reporting Group | Percentage | Median | 5% | 95% | Mean | SD | Median | 5% | 95% | Mean | SD | |
| | | S. Kenai Pen. Replicate 3 S. Kenai Pen | | | | | | Pen. Replic | ate 4 | | | |
| Outside CI | 0.0 | 0.0 | 0.0 | 0.4 | 0.1 | 0.2 | 0.0 | 0.0 | 0.8 | 0.2 | 0.4 | |
| Northern CI | 0.0 | 0.1 | 0.0 | 1.8 | 0.4 | 0.7 | 0.0 | 0.0 | 1.3 | 0.3 | 0.5 | |
| Kenai | 0.0 | 0.1 | 0.0 | 2.1 | 0.4 | 1.0 | 0.4 | 0.0 | 4.7 | 1.2 | 1.7 | |
| S. Kenai Pen. | 100.0 | 99.5 | 96.8 | 100.0 | 99.1 | 1.2 | 99.0 | 94.8 | 100.0 | 98.4 | 1.7 | |
| | | S | . Kenai P | en. Replic | ate 5 | | S | . Kenai F | Pen. Replic | ate 6 | | |
| Outside CI | 0.0 | 0.0 | 0.0 | 0.5 | 0.1 | 0.2 | 0.0 | 0.0 | 0.4 | 0.1 | 0.2 | |
| Northern CI | 0.0 | 0.0 | 0.0 | 1.3 | 0.3 | 0.5 | 1.8 | 0.0 | 4.8 | 2.0 | 1.6 | |
| Kenai | 0.0 | 0.1 | 0.0 | 3.0 | 0.6 | 1.2 | 0.2 | 0.0 | 9.6 | 1.7 | 3.3 | |
| S. Kenai Pen. | 100.0 | 99.5 | 96.5 | 100.0 | 99.1 | 1.4 | 97.3 | 87.6 | 99.9 | 96.2 | 3.8 | |
| | | S | . Kenai P | en. Replic | ate 7 | | S. Kenai Pen. Replicate 8 | | | | | |
| Outside CI | 0.0 | 0.0 | 0.0 | 0.7 | 0.1 | 0.3 | 0.0 | 0.0 | 0.4 | 0.1 | 0.2 | |
| Northern CI | 0.0 | 0.2 | 0.0 | 2.5 | 0.6 | 0.9 | 0.1 | 0.0 | 1.9 | 0.4 | 0.7 | |
| Kenai | 0.0 | 0.1 | 0.0 | 2.8 | 0.6 | 1.1 | 0.3 | 0.0 | 8.0 | 1.6 | 2.7 | |
| S. Kenai Pen. | 100.0 | 99.1 | 96.0 | 100.0 | 98.7 | 1.4 | 99.1 | 91.5 | 100.0 | 97.9 | 2.8 | |
| | | S | . Kenai P | en. Replic | ate 9 | | S. | Kenai P | en. Replica | ate 10 | | |
| Outside CI | 0.0 | 0.0 | 0.0 | 0.7 | 0.1 | 0.4 | 0.0 | 0.0 | 0.5 | 0.1 | 0.2 | |
| Northern CI | 0.0 | 1.0 | 0.0 | 3.7 | 1.3 | 1.3 | 0.0 | 0.0 | 1.2 | 0.3 | 0.5 | |
| Kenai | 0.0 | 0.1 | 0.0 | 1.7 | 0.4 | 0.8 | 0.1 | 0.0 | 2.7 | 0.6 | 1.1 | |
| S. Kenai Pen. | 100.0 | 98.5 | 95.4 | 99.9 | 98.2 | 1.5 | 99.5 | 96.7 | 100.0 | 99.1 | 1.2 | |

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

APPENDIX C. SUMMARY OF HATCHERY CHINOOK SALMON IN COOK INLET, 2009–2017

Appendix C1.–Cook Inlet hatchery Chinook salmon smolt release information including release year, potential marine sport fish harvest years through 2019, 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, 2009–2017.

| | | Adipose Fin Clipped | | Not Adipose Fin Clipped | <u>.</u> |
|------------------|--|---------------------|---------|-------------------------|----------------|
| Year Released | Potential Harvest Years ^a | CWT & TM | TM | TM | Total Released |
| 2009 | 2011, 2012, 2013, 2014 , 2015, 2016, 2017, 2018, 2019 | 281,202 | 0 | 604,306 | 885,508 |
| 2010 | 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019 | 319,567 | 0 | 923,669 | 1,243,236 |
| 2011 | 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019 | 0 | 264,306 | 867,663 | 1,131,969 |
| 2012 | 2011, 2012, 2013, 2014 , 2015 , 2016 , 2017 , 2018, 2019 | 0 | 258,759 | 917,029 | 1,175,788 |
| 2013 | 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019 | 0 | 199,356 | 759,018 | 958,374 |
| 2014 | 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019 | 0 | 405,723 | 1,120,618 | 1,526,341 |
| 2015 | 2011, 2012, 2013, 2014, 2015, 2016, 2017 , 2018, 2019 | 511,505 | 0 | 1,175,865 | 1,687,370 |
| 2016 | 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019 | 360,723 | 0 | 1,221,113 | 1,581,836 |
| 2017 | 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019 | 206,120 | 147,953 | 1,165,132 | 1,519,205 |

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