Fishery Manuscript Series No. 17-09

Genetic Stock Composition of the Commercial Harvest of Chinook Salmon in Copper River District, 2013–2017

by

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November 2017

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

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Weights and measures (metric)

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

Weights and measures (English)

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

Time and temperature

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

Physics and chemistry

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

General

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

Mathematics, statistics

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

FISHERY MANUSCRIPT SERIES NO. 17-09

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by

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November 2017

This investigation was funded by State of Alaska general funds through the Chinook Salmon Research Initiative.

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This document should be cited as follows:
Gilk-Baumer, S., K. Shedd, H. A. Hoyt, C. Habicht, W. D. Templin, S. Haught, and D. F. Evenson. 2017. Genetic stock composition of the commercial harvest of Chinook salmon in Copper River District, 2013–2017. Alaska Department of Fish and Game, Fishery Manuscript Series No. 17-09, Anchorage.

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ABSTRACT

Chinook salmon are harvested in subsistence, commercial, sport, and personal use fisheries throughout the Copper River drainage and in nearshore marine waters. This project was designed to estimate the stock-specific harvest of Chinook salmon in the Copper River District commercial drift gillnet fishery using genetics samples from 2013 through 2017. The Chinook Salmon Research Initiative identified the Copper River as 1 of 12 indicator stocks representing the diverse life history and migratory characteristics of Alaska Chinook salmon. Adult abundance information was identified as a fundamental knowledge gap, including the absence of programs to estimate stock-specific harvest in mixed stock commercial fisheries. This project applied the available baseline of genetic information representing Chinook salmon populations from within the Copper River drainage, around the Gulf of Alaska, and from southern populations to estimate the relative stock compositions of Chinook salmon harvests in the Copper River District commercial fishery. The results show that most of the fish in the Copper River commercial fishery originated from Copper River populations, which is consistent with findings from previous studies. A consistent temporal pattern in the composition of the commercial fishery harvests was observed across the 5-year study. As the season progressed, the proportion of *Upper Copper River* Chinook salmon decreased, and the proportion of *Lower Copper River* Chinook salmon increased. The unusually high proportions of *nonlocal* Chinook salmon in the commercial harvest occurring during 2 of the study years (2014 and 2015) align with other reports of large numbers of out-of-area Chinook salmon in commercial fisheries throughout the southern and southeastern seaboards of Alaska. The results support the historical commercial management approach of providing inriver passage for all temporal components of the run. Genetic data allow for estimating the stock-specific harvests of wild stocks or stocks (with and without coded wire tags) from other areas.

Key words: Copper River, Chinook salmon, *Oncorhynchus tshawytscha*, mixed stock analysis, MSA, commercial fishery, SNP, Chinook Salmon Research Initiative, CSRI

INTRODUCTION

Chinook salmon *Oncorhynchus tshawytscha* are harvested in subsistence, commercial, sport, and personal use fisheries throughout the Copper River drainage and nearshore marine waters. Decreased returns of Chinook salmon in the region and throughout Alaska have prompted statewide concern about the health of Chinook salmon stocks (ADF&G Chinook Salmon Research Team 2013). To address these concerns, the Chinook Salmon Research Initiative (CSRI) implemented stock assessment programs targeting 12 indicator stocks from around the state, including the Copper River. In addition to basic research estimating adult spawning abundances and juvenile abundance in these indicator streams, one of the major knowledge gaps identified by the CSRI was the stock of origin in fishery catches.

The Copper River District commercial drift gillnet fishery takes place in the marine waters of the Gulf of Alaska (GOA) off the mouth of the Copper River (Figure 1), and harvests include fish from non-Copper River stocks. Thus, scientific knowledge of the temporal and spatial presence of both *local* and *nonlocal* Chinook salmon in these catches is of regional, statewide, and international importance. Genetic mixed stock analysis (MSA) of the Chinook salmon catch in Copper River District commercial salmon fisheries had been conducted from 2005 to 2008 (Templin et al. 2011a); however, the genetic baseline used to estimate the composition of catches has been improved since that time.

The Alaska Department of Fish and Game (ADF&G) management strategy for the Copper River District sockeye and Chinook salmon commercial drift gillnet fishery is to provide inriver passage from all time segments (and presumably stocks) of the overall run, and thus has typically been managed with 2 evenly spaced fishery openers each week (Botz and Somerville 2011; Russell et al. 2017). From 2013 to 2017, the total annual commercial harvests of Chinook salmon ranged from 8,826 to over 22,506, and averaged 13,544 salmon (Figure 2; Vega et al. *In prep*). Commercial drift gillnet harvest in the Copper River District accounts for about 75% of the total

Copper River area Chinook salmon harvest (the remainder is harvested in subsistence, personal use, and sport fisheries) and has an estimated average annual harvest rate of 33% (Vega et al. *In prep*). Run timing of Copper River Chinook salmon through the commercial fishery is relatively compressed; from 2007 through 2017, an average of 90% of the commercial harvest of Chinook salmon occurred by June 15 (within 30 days, May 15 to June 15).

The commercial fishery in the Copper River District harvests fish from mixtures of population groups (stocks) returning to a variety of tributaries in the drainage and from other areas (Brase and Sarafin 2004). The Copper River currently has 49 documented spawning locations for Chinook salmon (Johnson and Blanche 2011). However, the organization of spawning locations into stocks and the existence of run-timing differences among stocks have only recently been demonstrated (Savereide 2005; Seeb et al. 2006; Templin et al. 2008). Understanding patterns of stock composition in the harvest is important information for the management of sustainable fisheries on Copper River Chinook salmon and is necessary to estimate the exploitation and productivity of the stock.

The first studies to examine run timing in Copper River Chinook salmon were radiotelemetry projects that provided information on inriver timing to many systems in the Upper Copper River (Wuttig and Evenson 2001; Savereide 2005). These studies provided information on spawning distribution, abundance, and run timing of Chinook salmon within the drainage and demonstrated that upriver populations were present in the river earlier than downriver populations. However, whereas radiotagging studies described run timing of populations within the Copper River, the run timing in commercial harvests were only partially understood from recoveries of coded wire tags in 2001 and 2002 (Brase and Sarafin 2004) from juveniles tagged in 1997–1999 (Sarafin 2000). A more comprehensive picture was not available until 2011 when the first genetic MSA study was published. This study provided highly precise stock-specific estimates of harvest compositions of Chinook salmon in the Copper River District commercial fishery on a weekly basis over multiple years (2005 to 2008; Templin et al. 2011a). Patterns of stock composition in the harvest confirmed the findings of the previous radiotagging work with respect to stock-specific run timing.

The central location of the Copper River in the GOA and long migrations undertaken by Chinook salmon throughout their range require a comprehensive baseline of populations across the North Pacific Ocean to provide accurate MSA estimates for the Copper River District commercial fishery. The original baseline completed in 2008 (Seeb et al. 2009) used the standardized set of 13 microsatellites surveyed across the range of the species so that the data from many baseline development projects could be combined—such as the comprehensive baseline already developed for the Pacific Salmon Commission (Seeb et al. 2007) and the Kenai River (Begich et al. 2010). This baseline was used from 2005 to 2008 for the first genetic MSA analyses of Chinook salmon harvests in the Copper River District (Templin et al. 2011a). The baseline included approximately 1,650 individuals from 16 locations across the Copper River drainage, and indicated that Chinook salmon populations could be separated into 3 broad geographical groups: 1) a heterogeneous group of populations in the *Upper Copper River*, 2) a relatively homogeneous group in the *Middle Copper River* (Gulkana River drainage and Mendeltna Creek), and 3) a diverse set of populations in the *Lower Copper River* glacial lakes. The utility of this baseline for MSA was demonstrated with samples from Baird Canyon and the 2005 Copper River District commercial fishery (Seeb et al. 2009). By 2010, a rangewide baseline using single nucleotide polymorphisms (SNPs) was developed (Templin et al. 2011b) and applied to marine samples (Larson et al. 2013; Figures 3–4). For many reasons, including efficiency and adaptability, SNPs have become the standard marker for analysis of fishery mixtures. The SNP baseline used for this study included an updated set of collections within the Copper River drainage reported from a study by Fox (2014) in which both Mendeltna Creek and Gulkana River populations were demonstrated to be highly identifiable in standard proof tests (96.7% Mendeltna Creek; 98.6% Gulkana River). To better understand productivity within the system, the Gulkana River collections were defined as a standalone reporting group (*Gulkana*) and the Mendeltna Creek population (a much smaller population) was merged with the *Lower Copper River* reporting group for this study.

The project reported herein applied the current baseline of genetic information representing Chinook salmon populations from within the Copper River drainage and from California to the Alaska Peninsula (Figures 3–4) to estimate the relative stock compositions of Chinook salmon harvests in the Copper River District commercial fishery during the years 2013 to 2017. This information will be useful for reconstructing runs, building accurate brood tables to define escapement goals, and refining management by identifying temporal harvest patterns of local and nonlocal stocks.

OBJECTIVES

As part of the CSRI, the goal of this project was to estimate the stock-specific contribution of Copper River Chinook salmon to the drift gillnet commercial fishery harvest in marine waters of the Copper River District. This was to be accomplished using genetic MSA to estimate the stock proportions and stock-specific harvests of Chinook salmon to 8 reporting groups (listed in analysis section) originating from within the Copper River drainage, around the GOA, and from the Pacific Northwest. Estimates would be provided by statistical week from 2013 to 2017 such that estimates are within 5% of the true value 90% of the time.

DEFINITIONS

To reduce confusion associated with the methods, results, and interpretation of this study, basic definitions of commonly used genetic and salmon management terms are offered here.

Allele. Alternative form(s) of a given gene or DNA sequence.

Brood (year). All salmon in a stock that were spawned in a specific year.

Credibility Interval. In Bayesian statistics, a credibility interval is a posterior probability interval. A credibility interval differs from a confidence interval in frequentist statistics in that it is a statement of probability: i.e., a 90% credibility interval has a 90% chance of containing the true answer.

District. A portion of a body of water, areas of which may be open to commercial salmon fishing. Districts are subdivided into statistical areas and used to document the spatial origin of fishery harvests. Commercial fishing districts, subdistricts, and sections in Copper River commercial fishing areas are defined in statutes listed below under *Salmon administrative area*.

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

Genetic Marker. A genetic variant showing Mendelian inheritance, such as a DNA sequence that can be identified by a simple assay.

Genotype. The set of alleles for 1 or more loci for an individual.

Harvest. The number of salmon or weight of salmon taken of a run from a specific stock.

Local. A salmon stock originating within the management area where it is caught.

Locus (Loci, plural). A fixed position or region on a chromosome that may contain more than 1 genetic marker.

Microsatellite. A locus with repetitive nucleotide elements that vary in number. The length of the repetitive section defines an allele.

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

Nonlocal. A salmon stock originating outside of the management area where it is caught.

Polymerase Chain Reaction (PCR). A method to amplify a single or few copies of a locus across several orders of magnitude, generating millions of copies of the DNA.

Reporting Group. A group of populations in a genetic baseline to which portions of a mixture are allocated with mixed stock analyses; constructed based on a combination of stakeholder needs and genetic distinction.

Run. The total number of salmon in a stock surviving to adulthood and returning to the vicinity of the natal stream in any calendar year, composed of both the harvest of adult salmon plus the escapement; the annual run in any calendar year. Except for pink salmon, a run is composed of several age classes of mature fish from the stock derived from the spawning of a number of previous brood years (from 5 AAC 39.222(f)).

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

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

METHODS

FISHERY SAMPLING

Fish captured in the commercial drift gillnet fishery in the Copper River District were sampled from landed catch at processors in Cordova, Alaska, as part of standard catch–sampling operations (Moffitt et al. 2015; Brenner and Moffitt 2014). While the original study design was to provide estimates by statistical week, sample sizes collected were sufficient to represent harvests within each fishing period (Table 1). Sampling was conducted over 5–6 weeks each year, beginning with statistical week 20 or 21. However, Chinook salmon continued to be harvested, but harvests were small or tapered off during this period.

The target sample size for each period was 200 fish, but strata represented by at least 100 fish were included in the analysis. Traditionally, sample sizes for estimating stock compositions have been set at 400 individuals per stratum for fishery samples from highly mixed locations where many stocks contribute to the harvest (e.g., Seeb et al. 2000). Under worst-case conditions, point estimates based on sample sizes of 400 will be within 5% of the true value 90% of the time (Thompson 1987) due to sampling error alone. However, for this study, this level of precision is not required for each stratum because 1) the fishery is not highly mixed (3 reporting groups dominate most mixtures); 2) the strata are designed to investigate patterns in stock composition within years (not stand-alone estimates); and 3) the annual estimates are based on the rollup of multiple strata (therefore based on much larger sample sizes). For strata with sample sizes above 100 fish, relative error for most estimates for the 3 primary reporting groups will be less than or equal to 20%, a criterion originally established for use in the Yukon River (JTC 1997). Given the number of strata per year, rollup annual estimates will be based on samples in excess of 400 fish.

Tissue samples for genetic analysis were collected from Chinook salmon caught in the commercial catch without regard to size, sex, or condition from the start of the fishery in mid-May (statistical week 20 or 21) through mid-June (statistical week 24 or 25). Age, sex, and length (ASL) sampling was conducted every other fishing period starting with period 4. ASL sampling was also conducted during the first 2 periods, when logistically feasible. During periods when fish were sampled for ASL, an axillary process (the modified and elongated structure found at the anterior base of the pelvic fin) was excised from each fish and placed in a 2 mL cryovial in at least 95% denatured ethanol or dried on Whatman paper (GE Healthcare Life Sciences, Buckinghamshire, United Kingdom). For data continuity, individual tissue samples were paired with ASL information collected from each fish. During periods when Chinook salmon were not sampled for ASL, 200 tissue samples were collected from mixed tender loads (Moffitt et al. 2015; Brenner and Moffitt 2014). These tissues were placed bulk in ethanol in a labeled 250 mL plastic bottle (with at least 1 bottle per fishery opening) or dried on Whatman paper. These data were collated and archived by Division of Commercial Fisheries staff at the ADF&G office in Cordova.

LABORATORY ANALYSIS

Assaying Genotypes

DNA extraction and genotyping was completed at the ADF&G Gene Conservation Laboratory and generally followed the methods in Seeb et al. (2009). Briefly, genomic DNA was extracted from individual tissue samples using either a DNAeasy 96 Tissue kit (QIAGEN, Valencia, CA) or a NucleoSpin 96 Tissue Kit by Macherey-Nagel (Düren, Germany). The set of 43 SNP markers used in Templin et al. (2011b) was screened using 2 Fluidigm 192.24 Dynamic Array Integrated Fluidic Circuits (IFCs), each of which systematically combined up to 24 assays and 192 samples into 4,608 parallel reactions. The components were pressurized into the IFC using the IFC Controller RX (Fluidigm). Each reaction was conducted in a 9 nL volume chamber consisting of a mixture of 20X Fast GT Sample Loading Reagent (Fluidigm), 2X TaqMan GTXpress Master Mix (Applied Biosystems), Custom TaqMan SNP Genotyping Assay (Applied Biosystems), 2X Assay Loading Reagent (Fluidigm), 50X ROX Reference Dye (Invitrogen), and 60–400 ng/µl DNA. Thermal cycling was performed on a Fluidigm FC1 Cycler using a Fast-PCR protocol as follows: an initial "Hot-Start" denaturation of 95ºC for 2 min, followed by 40 cycles of denaturation at 95ºC for 2 sec, and annealing at 60ºC for 20 sec, with a final "Cool-

Down" at 25ºC for 10 sec. The Dynamic Array IFCs were read on a Biomark or EP1 System (Fluidigm) after amplification and scored using Fluidigm SNP Genotyping Analysis software.

Assays that failed to amplify on the Fluidigm system were reanalyzed with the QuantStudio 12K Flex Real-Time PCR System (Life Technologies). Each reaction was performed in 384-well plates in a 5 µL volume consisting of 6–40 ng/µl of DNA, 2X TaqMan GTXpress Master Mix (Applied Biosystems), and Custom TaqMan SNP Genotyping Assay (Applied Biosystems). Thermal cycling was performed on a Dual 384-well GeneAmp PCR System 9700 (Applied Biosystems) as follows: an initial "Hot-Start" denaturation of 95°C for 10 min, followed by 40 cycles of denaturation at 92°C for 1 sec, and annealing at 60°C for 1 min, with a final "Cool-Down" hold at 10°C. The plates were scanned on the system after amplification and scored using the Life Technologies QuantStudio 12K Flex Software.

Genotypes produced on both platforms were imported and archived in the Gene Conservation Laboratory Oracle database, LOKI.

Laboratory Quality Control

We conducted quality control (QC) analyses to identify laboratory errors and to measure the background discrepancy rate of the genotyping process. The QC analyses were performed as a separate event from the original genotyping, with staff duties altered to reduce the likelihood of repeated human errors. All samples were subject to the following QC protocol: re-extraction of 8% of project fish and genotyping them for the same SNPs assayed in the original project. Discrepancy rates were calculated as the number of conflicting genotypes divided by the total number of genotypes compared. These rates describe the difference between original project data and QC data for all SNPs, and are capable of identifying extraction, assay plate, and genotyping errors. Error rates in the original project data are half the rate of discrepancies, assuming that errors are equally likely to occur in original and QC genotyping. This QC method is the best representation of the error rate of our current genotype production.

STATISTICAL ANALYSIS

Data Retrieval and Genotype Quality Control

We retrieved genotypes from LOKI and imported them into the statistical software *R* version 3.3.1.[1] All subsequent analyses were performed in *R* unless otherwise noted. Prior to MSA, we conducted 2 statistical QC analyses to ensure that only quality genotypic data was included in the estimation of stock compositions. First, we removed individuals that were missing substantial genotypic data from further analyses using what we refer to as the *80% rule*, which excludes individuals missing genotypes for 20% or more of loci, because these individuals likely have poor quality DNA. The inclusion of individuals with poor quality DNA might introduce genotyping errors into the catch samples and reduce the accuracy and precision of MSA (Dann et al. 2012).

Secondly, we 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 genotype in 95% of markers screened. The individual with the most missing data from each duplicate pair was removed from

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

further analyses. If both samples had the same amount of genotypic data, the first sample was removed from further analyses.

Each year, the following were tabulated: 1) the number of Chinook salmon initially selected for analysis; 2) the number of fish genetically screened, and excluded from statistical analysis because of missing loci, duplicate fish, or strata represented by an insufficient sample size (<100 fish); and 3) the final number of Chinook salmon statistically analyzed in MSA.

Estimating Stock Compositions and Stock-Specific Harvests

Reporting group designation

Populations were combined into the following reporting groups, following Templin et al. (2011b):

1. *Northwest Gulf of Alaska* (*NW Gulf of AK*) – populations in the western GOA (Chignik, Kodiak Island and Cook Inlet);
2. *Upper Copper River (Upper Copper)* – populations spawning within the Copper River upstream of the confluence with the Gulkana River;
3. *Gulkana* – populations spawning in the Gulkana River;
4. *Lower Copper River (Lower Copper)* – populations spawning in the Copper River drainage from Tazlina River (including Mendeltna Creek) downstream to the mouth;
5. *Northeast Gulf of Alaska (NE Gulf of AK)* – populations in the eastern GOA (Situk and Alsek rivers);
6. *Coastal Southeast Alaska (Coastal SEAK)* – populations spawning in Southeast Alaska and the Taku and Stikine rivers;
7. *British Columbia* – populations spawning in British Columbia south of the Alaska border; and
8. *West Coast U.S.* – populations spawning south of the Canada border.

These populations were grouped based on genetic similarity, geographic location, and proximity to the fishery at the mouth of the Copper River, and all perform well in genetic MSA (Templin et al. 2011b). The 3 reporting groups within the Copper River were originally identified using microsatellites by Seeb et al. (2009) and confirmed in SNP baseline (Figures 3–4; Templin et al. 2011a). Outside the Copper River, 5 large-scale groups were identified in the rest of the GOA and south (Figure 3). These groups are almost identical with the reporting groups test. These populations were grouped based on genetic similarity, geographic location, management needs, and proximity to the fishery at the mouth of the Copper River, and all perform well in genetic MSA (Templin et al. 2011b; Fox 2014).

Model

The stock compositions of Copper River fishery harvests were estimated using a Bayesian approach to genetic MSA, the Pella-Masuda Model, as implemented in the program *BAYES* (Pella and Masuda 2001). The Bayesian method of MSA estimates the proportion of stocks caught within each fishery using 4 pieces of information: 1) a baseline of allele frequencies for each population, 2) the grouping of populations into reporting groups desired for MSA, 3) prior information about the stock proportions of the fishery, and 4) the genotypes of fish sampled from the fishery. The baseline of allele frequencies for Chinook salmon populations and the reporting groups outside of the Copper River into which the populations were combined are described in Templin et al. (2011b).

Prior choice

The Bayesian model implemented by *BAYES* uses a Dirichlet distribution as the prior distribution for the stock proportions, and the parameters for this distribution must be specified. The choice of prior information about the stock proportions in a fishery, or the prior probability distribution (referred to hereafter as a *prior*) is important to the outcome of the MSA (Habicht et al. 2012). For the first period in the first year (2013), we defined prior parameters for each reporting group to be equal (a *regionally flat* prior) with the prior for each reporting group subsequently divided equally to populations within that reporting group. Following this initial set of stock composition estimates, subsequent periods in the same year were given a *sequential prior* (Jasper et al. 2012), such that the prior for each period was equal to the stock composition from the preceding period. For subsequent years, the prior for the first period was equal to the stock compositions from the first period of the previous year. We set the sum of all prior parameters to 1 (prior weight), which is equivalent to adding 1 fish to each mixture (Pella and Masuda 2001). We defined a minimum value of 0.01 for all priors for each reporting group. Reporting groups with estimates below this value were set to 0.01 by normalizing the sum of priors for all reporting groups to 1 after adjusting the values of the small proportion stocks.

BAYES protocol

For each period, we ran 5 independent Markov Chain Monte Carlo chains of 40,000 iterations with different starting values and discarded the first 20,000 iterations (burn-in) to remove the influences of the initial start values. We defined the starting values for the first chain such that the first 1/5 of the baseline populations summed to 0.9 and the remaining populations summed to 0.1. Each chain had a different combination of 1/5 of baseline populations summing to 0.9. We combined the second halves of these chains to form the posterior distribution and tabulated median and mean estimates, 90% credibility intervals, the probability of an estimate being equal to zero, and standard deviations from a total of 100,000 iterations. For each tabulated measure, summary statistics were based upon the raw posterior, which was calculated out to 6 significant digits.

We also assessed the within- and among-chain convergence of these estimates using the Raftery-Lewis (within-chain) and Gelman-Rubin (among-chain) diagnostics. These values measure the convergence of each chain to stable estimates (Raftery and Lewis 1996), as well as measure the variation of estimates within a chain to the total variation among chains (Gelman and Rubin 1992), respectively. If the Gelman-Rubin diagnostic for any stock group estimate was greater than 1.2 we reanalyzed the mixture with 80,000-iteration chains following the same protocol.

Applying stock compositions to harvests

Stock-specific estimated harvest was calculated in the manner described by Dann et al. (2009). Briefly, median and mean harvest estimates, credibility intervals, and standard deviations for each period were calculated by multiplying the harvest from that stratum by the unrounded estimates of reporting group stock proportions. Period estimates were combined (rolled up) into annual estimates by weighting them by their respective harvests. Credibility intervals for stock-specific harvests in a period were estimated by resampling 100,000 draws of the posterior output of stock proportions from each of the constituent periods and multiplying the harvest by the drawn proportions.

RESULTS

TISSUE SAMPLING

Tissues suitable for genetic analysis were collected from 8,113 fish in the Copper River District commercial harvest from 40 fishing periods between 2013 and 2017 (Table 1; Appendix B.). With the exceptions of period 3 in 2013, period 6 in 2015, and period 5 and 9 in 2016, sufficient sample sizes (>100 per period) were obtained to represent the harvest from all periods targeted for sampling. Details of the sampling (i.e., dates of fishing periods, tabulation of catch, samples successfully genotyped) for all years are provided in Table 1.

In 2013, samples were collected from May 16 to June 15 from Chinook salmon harvested in the Copper River District drift gillnet fishery and landed in Cordova. Tissues samples were successfully genotyped from 931 Chinook salmon during 5 of 6 fishing periods targeted for sampling (periods 1 to 5; Table 1). Too few fish were sampled (n=14) from fishing period 3 occurring on May 27 (harvest of 2,919). This resulted in a 21-day gap where fishery harvests were not sampled between period 2 (May 20) and period 4 (June 10–11). Additionally, the fishery was closed during statistical week 23 and there was only 1 fishing period per week in statistical weeks 21 to 23.

In 2014, samples were collected from May 15 to June 11 from Chinook salmon harvested in the Copper River District drift gillnet fishery and landed in Cordova. Tissues samples were successfully genotyped from 1,579 Chinook salmon during 8 of 8 fishing periods targeted for sampling. Sufficient sample sizes were collected to generate stock composition estimates for all 8 periods targeted for sampling (Table 1).

In 2015, samples were collected from May 14 to June 15 from Chinook salmon harvested in the Copper River District drift gillnet fishery and landed in Cordova. Tissues samples were successfully genotyped from 1,967 Chinook salmon during 10 of 11 fishing periods targeted for sampling. No samples were collected from fishing period 6 (May 30–31; harvest of 1,599). Sufficient sample sizes were collected for each period sampled to generate stock composition estimates (Table 1).

In 2016, samples were collected from May 16 to June 14 from Chinook salmon harvested in the Copper River District drift gillnet fishery and landed in Cordova. Tissues samples were successfully genotyped from 1,777 Chinook salmon during 8 of 10 fishing periods targeted for sampling. No samples were collected from fishing period 5 (May 28–29; harvest of 1,017), and too few fish were sampled (*n* = 69) from fishing period 9 (June 9–10; harvest of 346) which was insufficient to generate stock composition estimates for this stratum. Sufficient sample sizes were collected to generate stock composition estimates for 8 periods (Table 1).

In 2017, samples were collected from May 18 to June 13 from Chinook salmon harvested in the Copper River District drift gillnet fishery and landed in Cordova. Tissues samples were successfully genotyped from 1,503 Chinook salmon during 8 of 8 fishing periods targeted for sampling. Sufficient sample sizes were collected to generate stock composition estimates for all 8 periods (Table 1).

LABORATORY ANALYSIS

Assaying Genotypes

A total of 8,113 fish were selected for genotyping from 40 strata, 38 of which had enough samples to analyze, representing harvests across the 5 years of this project. (Table 1; Appendix B1)

Laboratory Quality Control

Laboratory QC identified errors in tissue and DNA handling. After these errors were corrected, we measured low levels of nonsystematic discrepancies between the original and QC analyses (Table 2). There were 31,734 genotypes compared between these analyses. The majority of discrepancies were between homozygote and heterozygote genotypes (0.35%), but some discrepancies between alternate homozygotes were observed (0.01%). Assuming all errors are equally likely to have occurred in the production and QC genotyping process, error rates for both error types was 0.18%. This level of error was well below the standard set by the laboratory as acceptable (1%).

STATISTICAL ANALYSIS

Data Retrieval and Genotype Quality Control

Of the 8,113 fish genotyped, 250 were excluded from analysis because they were missing genotypes for more than 20% of loci and 24 were excluded because they appeared to represent duplicate individuals (Appendix B1). In addition, the 82 fish that were successfully genotyped from the 2 strata with insufficient sample sizes (<100 fish) were excluded from analyses. In the end, a total of 7,757 fish were used to produce stock composition estimates for 38 strata (Table 1). Average sample size of strata was 204 fish with a minimum of 129 fish and a maximum of 370 fish.

Stock Composition and Stock-Specific Harvest Estimates

2013

In 2013, adequate genetic samples were collected in fishing periods where 49% of the commercial harvest of Chinook salmon in the Copper River District occurred (4,337 of 8,826 harvested fish; Table 1). During this period, 80% of the fish in these harvests came from the Copper River drainage and represented 3,482 fish (Tables 3–4;). Fish originating from the *Lower Copper River* reporting group contributed to more than 1/3 (35%) of the commercial harvest, followed by fish from the *Upper Copper River* (24%) and *Gulkana* (21%) reporting groups (Table 3). Of the 20% of harvests sampled attributable to *nonlocal* stocks, the majority originated from the *Northwest Gulf of Alaska* reporting group (11%; 473 fish).

Over the 4 fishing periods sampled, the proportions of *Upper Copper River* fish demonstrated a declining trend during each successive fishing period (range: 44–3%) that was mirrored by increasing proportions of *Lower Copper River* fish (range: 9–69%; Figure 5–6; Appendix A1). The proportion of *Gulkana* fish was relatively steady during the first 2 fishing periods sampled on May 16 (36%) and May 20 (38%), then dropped off (5%) during the next fishing period sampled 21 days later on June 11. The proportion of *Northwest Gulf Alaska* fish in fishing periods 4 (22%) and 5 (19%) was abnormally high relative to prior (2005–2008) and subsequent years (2014–2017) where it typically was less than 4% during each stratum sampled.

2014

In 2014, adequate genetic samples were collected in fishing periods where 92% of the commercial harvest of Chinook salmon in the Copper River District occurred (9,363 of 10,207 fish harvested; Table 1). During this period, 70% of the fish in these harvests came from the Copper River drainage and represented 6,569 fish (Tables 3–4). Fish originating from the *Gulkana* reporting group contributed the largest proportion of the commercial harvest (32%), followed by fish from the *Lower Copper River* (28%) and *Upper Copper River* (10%) reporting groups (Table 3). Of the 30% of harvests sampled attributable to nonlocal stocks, the majority originated from the *British Columbia* reporting group (12%), followed by the *West Coast U.S.* (10%) and all other reporting groups (≤5% each).

Over the 8 sequential fishing periods sampled, the proportions of *Upper Copper River* fish declined during each successive fishing period (range: 24 to <1%) that was mirrored by increasing proportions of *Lower Copper River* fish (range: 14–56%; Figure 7; Appendix A2). The proportion of *Gulkana* fish was large across the first 5 fishing periods (range: 38–46%), decreased beginning in period 6 (23%), and continued to decrease across the remainder of the season. The proportion of *British Columbia* and *West Coast U.S.* fish was unusually large with proportions reaching 27% each in fishing period 7.

2015

In 2015, adequate genetic samples were collected in fishing periods where 84% of the commercial harvest of Chinook salmon in the Copper River District occurred (19,346 of 22,506 fish harvested; Table 1). During this time period, only 64% of the fish in these harvests came from the Copper River drainage and represented 12,329 fish (Tables 3–4). Fish originating from the *Lower Copper River* reporting group contributed the largest proportion of the commercial harvest (35%), followed by fish from the *Gulkana* reporting group (21%). Fish from the *Upper Copper River* reporting group contributed a low proportion (8%; Table 3). Of the 36% of sampled harvests attributable to nonlocal stocks, the majority originated from the *British Columbia* reporting group (16%), followed by the *West Coast U.S.* (16%) and all other reporting groups (≤3% each).

Over the 10 fishing periods sampled, the proportions of *Upper Copper River* fish demonstrated a declining trend across the season (range: 17% to <1%) that was mirrored by increasing proportions of *Lower Copper River* fish (range: 7–67%; Figure 8; Appendix A3). The proportion of *Gulkana* fish was largest across the first 7 fishing periods (range: 13–39%) and decreased beginning in period 9 through the remainder of the season. The proportion of *British Columbia* and *West Coast U.S.* fish was unusually large in the early part of the fishing season with *British Columbia* fish reaching 32% during period 2, and *West Coast U.S.* fish reaching 30% during period 3.

2016

In 2016, adequate genetic samples were collected in fishing periods where 80% of the commercial harvest of Chinook salmon in the Copper River District occurred (10,182 of 12,348 fish harvested; Table 1). During this time period, 86% of the fish in these harvests came from the Copper River drainage and represented 8,782 fish (Tables 3–4). Fish originating from the *Gulkana* reporting group contributed the largest proportion of the commercial harvest (34%), followed by fish from the *Lower Copper River* (33%) and *Upper Copper River* (19%) reporting groups (Table 3). Of the 14% of harvests sampled attributable to nonlocal stocks, the majority originated from the *British Columbia* reporting group (7%), followed by all other reporting groups (≤4% each).

Over the 9 fishing periods sampled, the proportions of *Upper Copper River* fish demonstrated a declining trend across the season (range: 42–1%) that was mirrored by increasing proportions of *Lower Copper River* fish (range: 15–63%; Figure 9; Appendix A4). The proportion of *Gulkana* fish was largest across the first 5 fishing periods sampled (range: 33–46%) and decreased beginning in period 7 for the remainder of the season. The proportion of *British Columbia* fish was 9% in periods 2 and 3, and then decreased with the exception of period 10 (13%). No discernable harvest was attributable to the *Coastal Southeast Alaska* or *Northeast Gulf Alaska* reporting groups (Table 3).

2017

In 2017, adequate genetic samples were collected in fishing periods where 92% of the commercial harvest of Chinook salmon in the Copper River District occurred (12,780 of 13,834 fish harvested; Table 1). During this time period, 93% of the fish in these harvests came from the Copper River drainage and represented 11,824 fish (Tables 3–4). Fish originating from the *Lower Copper River* reporting group contributed the largest proportion of the commercial harvest (38%), followed by fish from the *Gulkana* (34%) and *Upper Copper River* (21%) reporting groups (Table 3). Of the 7% of harvests sampled attributable to nonlocal stocks, the majority originated from the *British Columbia* reporting group (4%), followed by all other reporting groups (≤2% each).

Over the 8 consecutive fishing periods sampled, the proportions of *Upper Copper River* fish demonstrated a declining trend across the season (range: 37% to <3%; Figure 10; Appendix A5); the proportions of *Gulkana* fish demonstrated a similar declining trend across the season (range: 43–12%). These trends were mirrored by increasing proportions of *Lower Copper River* fish (range: 15–72%). The proportion of all other reporting groups was low across the season with no discernable harvest attributable to the *Coastal Southeast Alaska* or *Northeast Gulf Alaska* reporting groups (Table 3).

DISCUSSION

Genetic MSA was successfully used to provide highly precise stock-specific estimates of the composition of the Chinook salmon commercial drift gillnet fishery harvests in the Copper River District across multiple years (2013–2017). These estimates demonstrate temporal variation in the composition of the harvest across fishing periods within each season and across years.

However, some aspects of these stock composition results should be interpreted with care, understanding that 1) relative errors of the estimates are inversely correlated with the proportional contribution to the harvest (i.e., small contributions have large relative errors), and 2) not all strata were sampled. Additionally, specific comparisons between analyses using the most recent baseline (this report) versus the previous study for years 2005 to 2008 (Templin et al. 2011a) can be made, but must be interpreted carefully as the number of populations and the definitions of reporting groups changed between the studies. Within the Copper River drainage, the Mendeltna Creek population was previously assigned to the *Middle Copper River* reporting group, but is in the *Lower Copper River* reporting group in this study. Furthermore, the *Gulkana* reporting group is more comprehensively represented by additional samples from within the

Gulkana River drainage (Fox 2014). Because of these changes in the genetic baselines, comparisons across years prior to 2013 are more reliable at the broad scale than at finer scale levels. Nonetheless, these caveats do not detract from the major trends observed in the MSA.

PATTERNS IN FISHERY STOCK COMPOSITIONS AND HARVESTS

Chinook salmon commercial harvests from the Copper River District were sampled on a per-period basis—generally from statistical week 20 to statistical week 25, 2013–2017, representing 49% (2013), 92% (2014), 84% (2015), 80% (2016), and 92% (2017) of the total commercial harvest in these years (Table 1). The results of this study show that most of the fish in the Copper River commercial fishery originated from populations spawning within the Copper River (Figures 11–12). These results are consistent with the 2005–2008 results (Templin et al. 2011a; Figure 11).

Stocks originating from the Copper River consistently dominated the harvest across all years and temporal strata with the exception of period 7 in 2014 and periods 2 and 3 in 2015 (Figures 6–10; Appendices A2 and A3). The highest annual non-Copper River contributions among the 9 years of available data occurred when 30% (2014) and 36% (2015) of the sampled harvests were attributable to *nonlocal* stocks (Figure 11). The *British Columbia* reporting group contributed 12% in 2014 and 16% in 2015, and the *West Coast U.S.* reporting group contributed 10% in 2014 and 16% in 2015. (Table 3). This anomalously large contribution of southern-origin stocks was also observed in Southeast Alaska troll and sport fisheries and in Chinook salmon bycatch in the GOA trawl fisheries during the same time frame (Gilk-Baumer et al. *In prep* [a], [b], [c]; Guthrie et al. 2016; 2017). These trends observed in 2014 and 2015 correspond with an increase in productivity of some British Columbia and Pacific Northwest stocks, in particular stocks originating from the Columbia River, North and Central British Columbia, and the west coast of Vancouver Island (Gilk-Baumer et al. *In prep* [a], [b], [c]; CTC 2017). In 2016 and 2017, the composition of the harvest reverted to lower proportions of *nonlocal* stocks (12% in 2016 and 7% in 2017), similar to proportions observed during 2005 to 2008 (range: 3–14%; Figure 11; Templin et al 2011a).

The *Lower Copper River* was the largest contributor to the fishery in periods sampled during all years except 2014 (range: 28–38%), followed by the *Gulkana* (range: 21–34%) and *Upper Copper River* (range: 8–24%) reporting groups (Table 3). The contribution from the *NW Gulf of Alaska* reporting group was largest in 2013 (11%), but only corresponded to an estimated harvest of 473 fish as overall harvest was low in 2013 (Tables 3–4). The proportions of *NE Gulf of Alaska* and *Coastal Southeast Alaska* reporting groups were low in 2013 to 2015 (<4%) with almost no discernable contributions in 2016 and 2017 (<1%; Table 3; Figure 12). For the *Coastal Southeast Alaska* reporting group, this low contribution is consistent with low productivities observed for these stocks across all years in this study (CTC 2017).

TRENDS IN RUN TIMING

A consistent temporal trend appeared in the composition of the commercial fishery harvests over the 5 years of this study. The proportion of *Upper Copper River* Chinook salmon was large in the beginning of each fishing season and tended to decline as the season progressed, but the proportion of *Lower Copper River* Chinook salmon increased (Figure 5). This trend was expected, given the early run timing of the *Upper Copper River* fish relative to the *Lower*

Copper River fish, as observed at the Baird Canyon fish wheel using radio tags (Savereide 2005; Wade et al. 2008) and as indicated by previous MSA (Templin et al. 2011a).

The results of this study provide information valuable for management of the commercial Chinook salmon fishery in the Copper River District. The results support the historical commercial management approach of providing inriver passage for all of the temporal components of the run by evenly spacing fishery openers each week throughout the Chinook salmon run.

PRESENCE OF *NONLOCAL* STOCKS

While annual Copper River District commercial Chinook salmon harvest is predominately of Copper River origin, outside stocks were present in all years sampled. The Copper River flows directly into the highly productive nearshore marine waters of the northeast Gulf of Alaska. Increased proportions of *nonlocal* Chinook salmon were observed in the commercial harvest during 2014 and 2015. Feeding Chinook salmon, originating from stocks across the Pacific Northwest and British Columbia, outnumbered Copper River stocks during 3 fishing periods across these 2 seasons (2014 and 2015). Large numbers of out-of-area Chinook salmon were also reported in commercial fisheries throughout the southern and southeastern seaboards of Alaska during 2014 and 2015 (Gilk-Baumer et al. *In prep* [a], [b], [c]; Guthrie et al. 2016, 2017). Harvest of *nonlocal* Chinook salmon may have also increased due to conservative management actions that closed the inside waters of the Copper River. This has served to increase effort in offshore areas where migratory fish are more likely to be present. It is assumed that most *nonlocal* Chinook salmon are foraging during migration. However, occasionally *nonlocal* coded-wire-tagged Chinook salmon are recovered well up into the Copper River drainage (Brase and Sarafin 2004). Furthermore, environmental factors likely play a significant role in the proportion of *nonlocal* Chinook salmon present in the Copper River District. Pacific Decadal Oscillation values were positive beginning in 2014, corresponding with above average sea surface temperatures throughout the GOA (http://research.jisao.washington.edu/pdo/PDO.latest).

APPLICATION TO CHINOOK SALMON RESEARCH INITIATIVE

Chinook salmon spawning within the Copper River drainage make up 1 of 12 stocks intensively studied under the CSRI to provide statewide indices of productivity and abundance trends across the many systems in Alaska. As part of the stock assessment for each of these indicator systems it was necessary to estimate total annual harvest of the stock. For the Copper River this meant using genetic MSA of harvests in the Copper River District commercial fishery to estimate harvest rates, production trends, and contributions of nonlocal harvest. These MSA results will provide much better estimates of Copper River fish harvested in the commercial fishery, especially in 2014 and 2015, when unusually high proportions of *nonlocal* fish were harvested. In combination with information from other CSRI studies, including coded wire tag recoveries, ASL measurements, escapement estimates, subsistence use patterns, and juvenile studies, these stock composition estimates will provide a more comprehensive understanding of the Chinook salmon spawning within the Copper River and potentially a broader understanding of the reasons for recent declines in the abundance of this species across Alaska.

CONCLUSIONS

1. This study provides highly precise stock-specific estimates of the composition of the Chinook salmon harvest in the Copper River District commercial fishery for each fishing period sampled over multiple years (2013–2017).
2. Stock composition estimates from MSA can serve to improve the understanding of stock productivity by providing information on the stock-specific harvests of Copper River Chinook salmon.
3. The run timing patterns demonstrated in these results support the historical commercial management approach of providing inriver passage for all of the temporal components of the run.
4. Even when local runs were uncharacteristically small and nonlocal runs were unusually large (2014 and 2015) most of the harvest in the Copper River commercial fishery originated from populations in the Copper River.

ACKNOWLEDGEMENTS

This study, from concept to completion, required the efforts of a large number of dedicated individuals. The authors acknowledge the work of the personnel in ADF&G's Gene Conservation Laboratory, including Paul Kuriscak, Erica Chenoweth, Zac Grauvogel, Chase Jalbert, and Zach Pechacek. We thank a large number of dedicated staff who collected tissue samples in addition to many other duties. Specifically, we thank ADF&G's Cordova sampling crew led by Jim O'Rourke (2013–2015), Angie Kelly (2016), and Scott Prevatte (2017) for their diligent work that enabled us to estimate stock proportions with a high degree of accuracy. Thanks to Jeremy Botz and Stacy Vega for input concerning Copper River District fisheries management and to Steve Moffitt for insight and guidance for study design. Jack Erickson, Mark Somerville, Jeremy Botz, and Bert Lewis provided thoughtful review and comment leading to a greatly improved report. This project benefited from the 2011–2013 baseline samples collected and analyzed under AKSSF project 44516.

All project costs were funded by the State of Alaska under the Chinook Salmon Research Initiative.

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TABLES AND FIGURES

Table 1.–Summary of commercial harvests of Chinook salmon in Copper River District by statistical week and period, and number of fish sampled and genotyped by period, 2013–2017.

Year	Stat. Week	Period[a]	Date(s)	Harvest	Sample Date(s)	Genotyped
2013	20	1[b]	5/16	801	5/16	200
	21	2[b]	5/20	1,530	5/20	193
	22	3[b]	5/27	2,919	5/27	14[c]
	24	4[b]	6/10–11	846	6/11	171
		5	6/13–14	1,160	6/14–15	367
	25–37	6–31	6/17–9/12	1,570	Not Sampled	0
			Total	8,826		931
2014	20	1[b]	5/15	1,264	5/15	165
	21	2[b]	5/19	851	5/19–20	197
		3[b]	5/22–23	1,470	5/23	178
	22	4[b]	5/26–27	1,210	5/27	195
		5[b]	5/29–30	1,182	5/31	233
	23	6[b]	6/2–3	1,283	6/3–4	199
		7[b]	6/5–7	1,281	6/7	219
	24	8[b]	6/9–11	822	6/11	193
	24–36	9–30	6/12–14	844	Not Sampled	0
			Total	10,207		1,579
2015	20	1[b]	5/14	1,517	5/14	194
	21	2[b]	5/18–19	2,959	5/19	199
		3[b]	5/21–22	2,460	5/22	194
	22	4[b]	5/25–26	3,002	5/26	197
		5[b]	5/28–29	1,932	5/29	198
		6[b]	5/30–31	1,599	Not sampled	0
	23	7[b]	6/1–2	1,882	6/3	199
		8[b]	6/4–6	1,523	6/6–7	195
	24	9[b]	6/8–9	872	6/10	198
		10[b]	6/11–13	2,219	6/12	198
	25	11	6/15–17	980	6/15	195
	25–37	12–33	6/18–9/7	1,561	Not Sampled	0
			Total	22,506		1,967
2016	21	1[b]	5/16	1,367	5/16	223
		2[b]	5/19–20	1,968	5/19–20	370
	22	3[b]	5/23–25	2,912	5/24–25	198
		4[b]	5/26–27	1,116	5/27	318
		5[b]	5/28–29	1,017	Not Sampled	0
	23	6[b]	5/30–31	988	5/31–6/1	198
		7[b]	6/2–3	904	6/3	143
	24	8[b]	6/6–7	624	6/7	198
		9[b]	6/9–10	346	6/10	68[c]
	25	10[b]	6/13–14	303	6/14	129
	25–35	11–30	6/16–8/25	803	Not sampled	0
			Total	12,348		1,777

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Table 1.–Page 2 of 2.

Year	Stat. Week	Period[a]	Date(s)	Harvest	Sample Date(s)	Genotyped
2017	20	1[b]	5/18	2,066	5/18	201
	21	2[b]	5/22	1,981	5/22–23	197
		3[b]	5/25	1,205	5/25	137
	22	4[b]	5/29	2,141	5/30	189
		5[b]	6/1	2,198	6/1–2	192
	23	6[b]	6/5	1,482	6/6	197
		7[b]	6/8	1,221	6/8	192
	24	8[b]	6/12	486	6/13	198
	24–36	11–30	6/22–9/4	1,054	Not Sampled	0
			Total	13,834		1,503

[a] The waters of the Copper River District were open for all periods. Unless otherwise noted, all waters available to commercial salmon fishing were open in the Copper River District.

[b] Waters of the inside closure area described in 5 AAC 24.350(1)(B) were closed for all or a portion of the fishing period.

[c] Collected, but not used for stock composition estimates; these are excluded from the totals.

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Table 2.–Quality control (QC) results including the number of genotypes compared, discrepancy rates, and estimated error rates of the collections genotyped for the Copper River District Chinook salmon commercial fishery samples.

	Discrepancy rate[a]			
Genotypes Compared	Homo-homo	Homo-het	Overall	Error Rate[b]
31,734	3 (0.01%)	111 (0.35%)	114 (0.36%)	0.18%

[a] Discrepancy rates include the rate due to differences of alternate homozygote genotypes (Homo-homo), of homozygote and heterozygote genotypes (Homo-het), and the total discrepancy rate.

[b] Error rate assumes that discrepancies are the result of errors that are equally likely to have occurred in the production and QC genotyping process.

Table 3.– Stock-specific contribution, standard deviation (SD), and 90% credibility intervals calculated using a stratified estimator (see text) for combined temporal strata and based on genetic analysis of mixtures of Chinook salmon harvested in the Copper River District, 2013–2017.

	Reporting Group							
	NW Gulf of AK	*Upper Copper*	*Gulkana*	*Lower Copper*	*NE Gulf of AK*	*Coastal SEAK*	*British Columbia*	*West Coast US*
2013								
Mean	11%	24%	21%	35%	1%	2%	4%	2%
SD	1%	2%	2%	2%	1%	1%	1%	0%
Lower 90% CI	9%	21%	18%	32%	0%	1%	3%	1%
Upper 90% CI	13%	27%	25%	39%	4%	3%	5%	2%
2014								
Mean	5%	10%	32%	28%	1%	2%	12%	10%
SD	1%	1%	2%	1%	1%	1%	1%	1%
Lower 90% CI	4%	8%	29%	26%	0%	1%	11%	9%
Upper 90% CI	6%	12%	34%	31%	3%	3%	14%	12%
2015								
Mean	3%	8%	21%	35%	0%	2%	16%	16%
SD	0%	1%	1%	1%	0%	1%	1%	1%
Lower 90% CI	2%	7%	19%	33%	0%	1%	14%	14%
Upper 90% CI	4%	9%	23%	37%	1%	3%	18%	17%
2016								
Mean	3%	19%	34%	33%	0%	0%	7%	4%
SD	0%	1%	2%	2%	0%	0%	1%	1%
Lower 90% CI	2%	17%	31%	30%	0%	0%	5%	3%
Upper 90% CI	3%	22%	37%	36%	1%	1%	8%	5%
2017								
Mean	2%	21%	34%	38%	0%	0%	4%	1%
SD	1%	1%	2%	2%	0%	0%	1%	0%
Lower 90% CI	2%	19%	31%	35%	0%	0%	3%	0%
Upper 90% CI	3%	23%	37%	40%	1%	1%	5%	1%

Table 4.– Stock-specific harvest, standard deviation (SD), and 90% credibility intervals calculated using a stratified estimator (see text) for combined temporal strata and based on genetic analysis of mixtures of Chinook salmon harvested in the Copper River District, 2013–2017.

	Reporting Group								
	NW Gulf of AK	*Upper Copper*	*Gulkana*	*Lower Copper*	*NE Gulf of AK*	*Coastal SEAK*	*British Columbia*	*West Coast US*	Not Sampled
2013									
Harvest	473	1,029	922	1,531	35	102	176	68	4,489
SD	47	82	91	85	52	29	33	18	
Lower 90% CI	400	895	774	1,395	0	55	125	41	
Upper 90% CI	552	1,165	1,075	1,676	155	150	235	101	
2014									
Harvest	435	925	2,993	2,651	102	150	1,138	970	844
SD	60	105	142	134	71	51	92	76	
Lower 90% CI	340	758	2,759	2,434	5	72	989	847	
Upper 90% CI	539	1,104	3,228	2,874	235	237	1,291	1,098	
2015									
Harvest	528	1,504	4,069	6,756	33	381	3,072	3,003	3,160
SD	97	154	250	241	60	101	195	183	
Lower 90% CI	380	1,258	3,660	6,363	0	225	2,757	2,707	
Upper 90% CI	697	1,764	4,482	7,157	165	556	3,398	3,308	
2016									
Harvest	268	1,976	3,461	3,345	12	26	667	426	2,166
SD	45	135	186	166	32	33	79	59	
Lower 90% CI	201	1,758	3,157	3,077	0	0	543	335	
Upper 90% CI	346	2,203	3,767	3,624	80	96	801	527	
2017									
Harvest	313	2,673	4,327	4,824	20	58	460	105	1,054
SD	64	169	215	195	36	26	67	34	
Lower 90% CI	215	2,398	3,976	4,505	0	22	356	55	
Upper 90% CI	425	2,953	4,684	5,147	82	107	575	167	

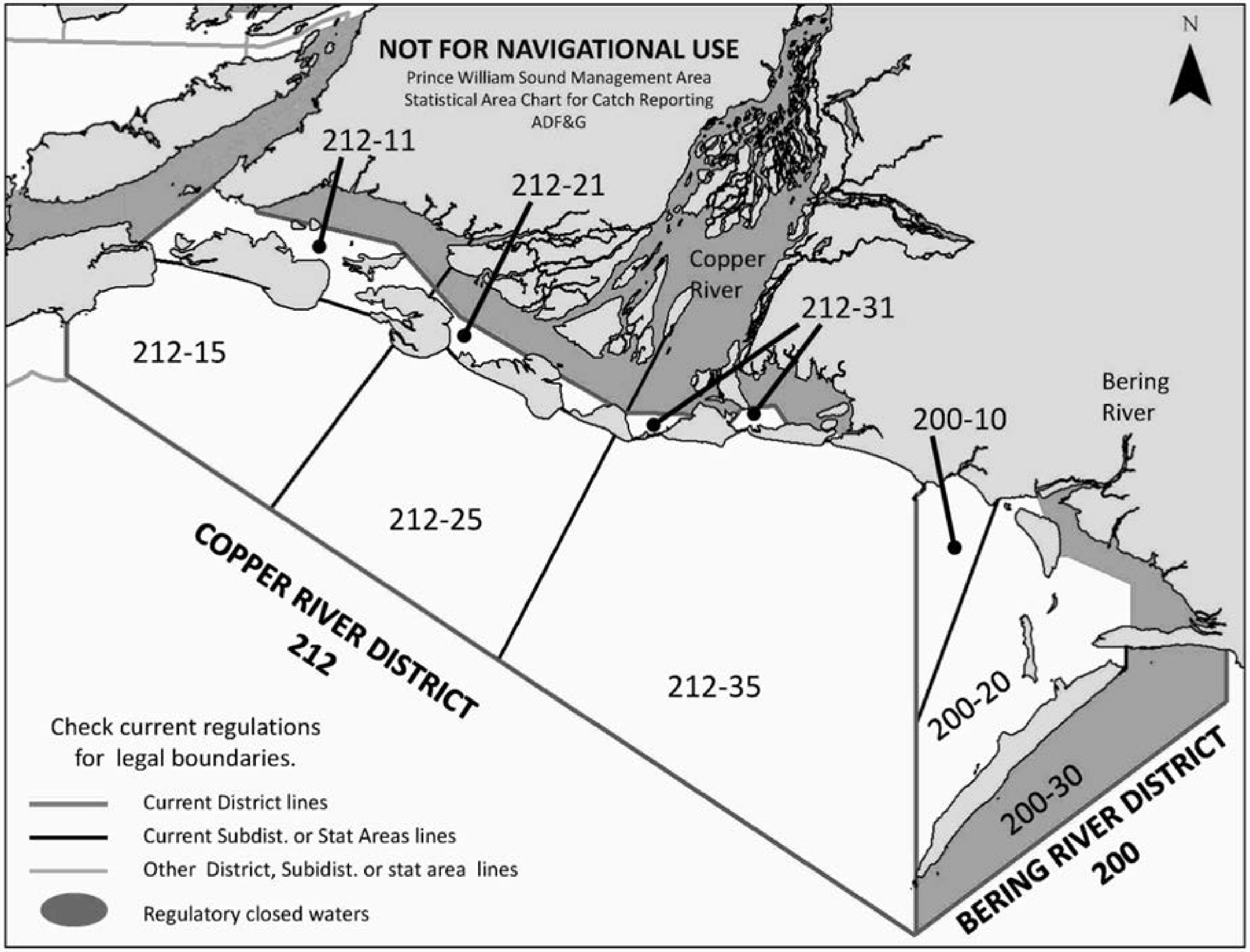

Figure 1.–Map depicting the commercial salmon fishery districts of the Copper River District management area.

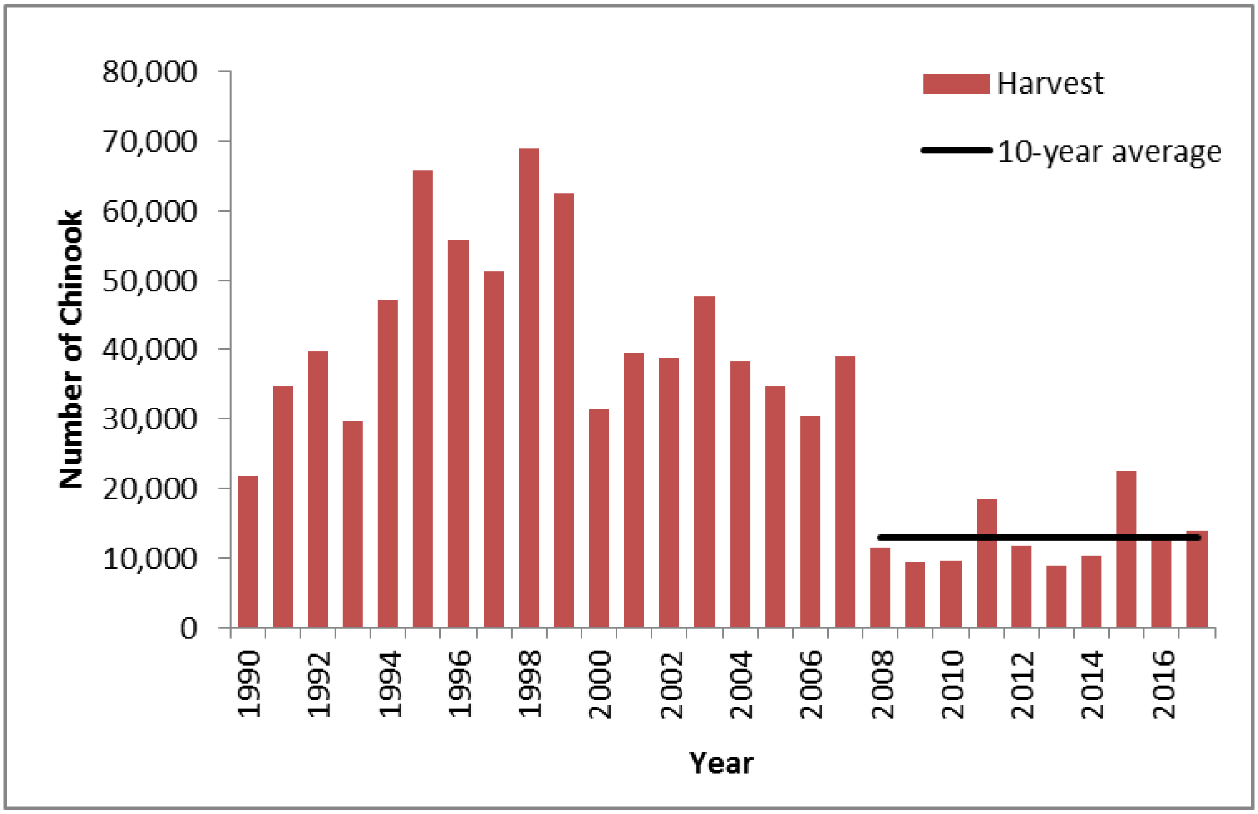

Figure 2.–Chinook salmon harvest in the Copper River District management area commercial fisheries by year and recent 10-year average, 1990–2017.

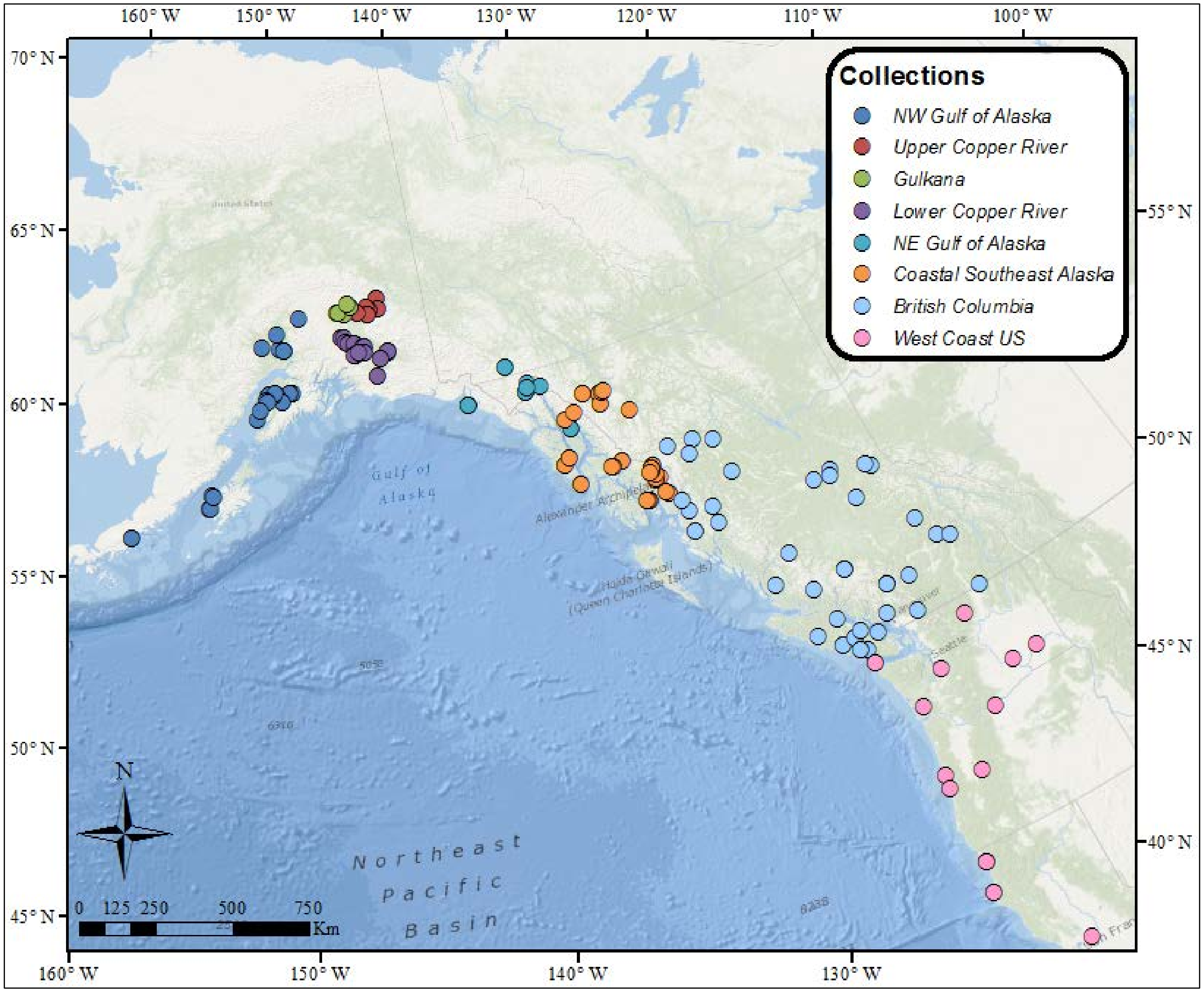

Figure 3.–The location and reporting group affiliation of 211 collections of Chinook salmon included in the coastwide genetic baseline grouped as 118 populations for genetic mixed stock analysis of commercial harvest of Chinook salmon in the Copper River District, 2013–2017.

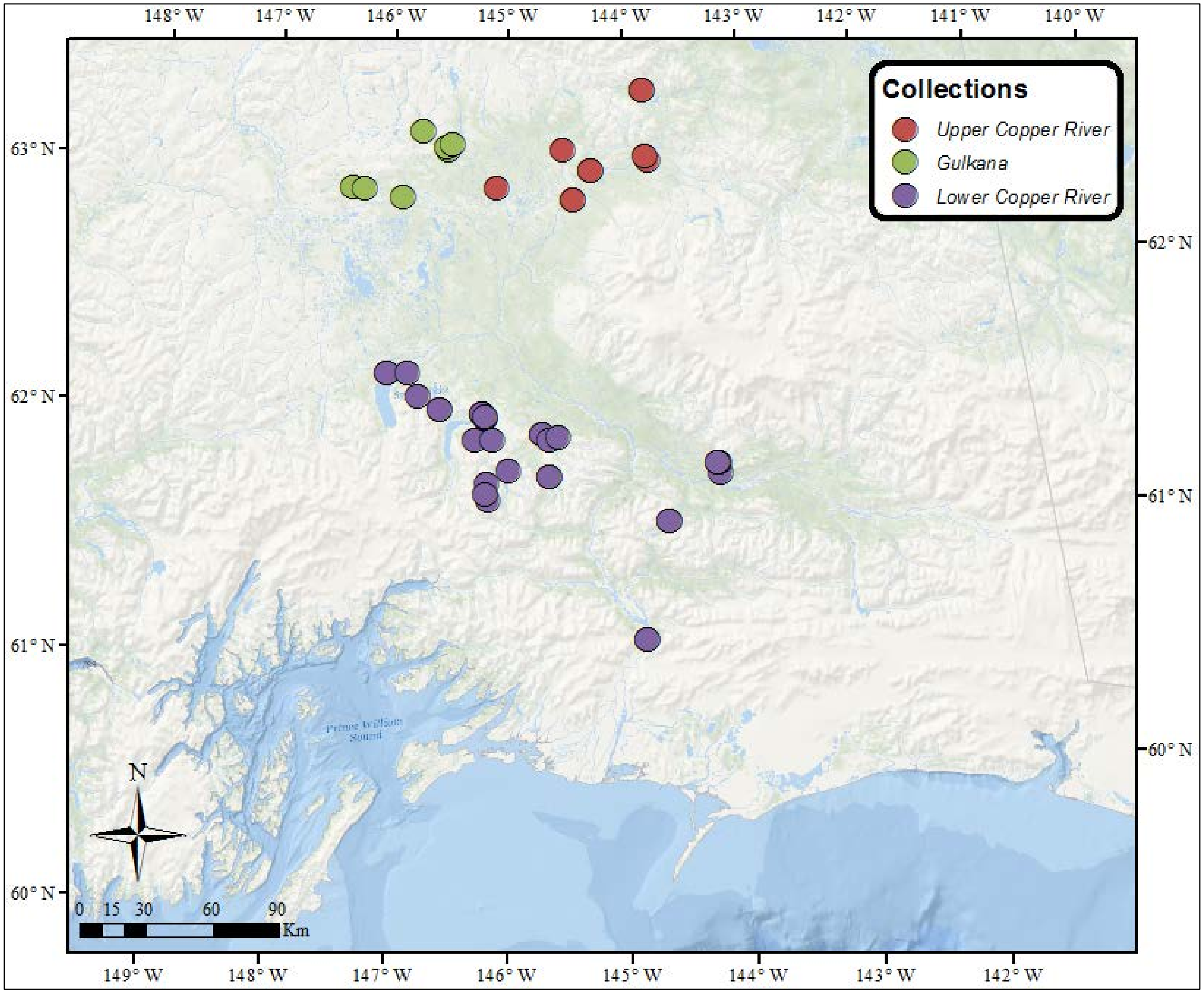

Figure 4.–The location and reporting group affiliation of 50 collections of Copper River Chinook salmon in the baseline grouped as 17 populations for genetic mixed stock analysis of commercial harvest of Chinook salmon in the Copper River District, 2013–2017 (Table 3).

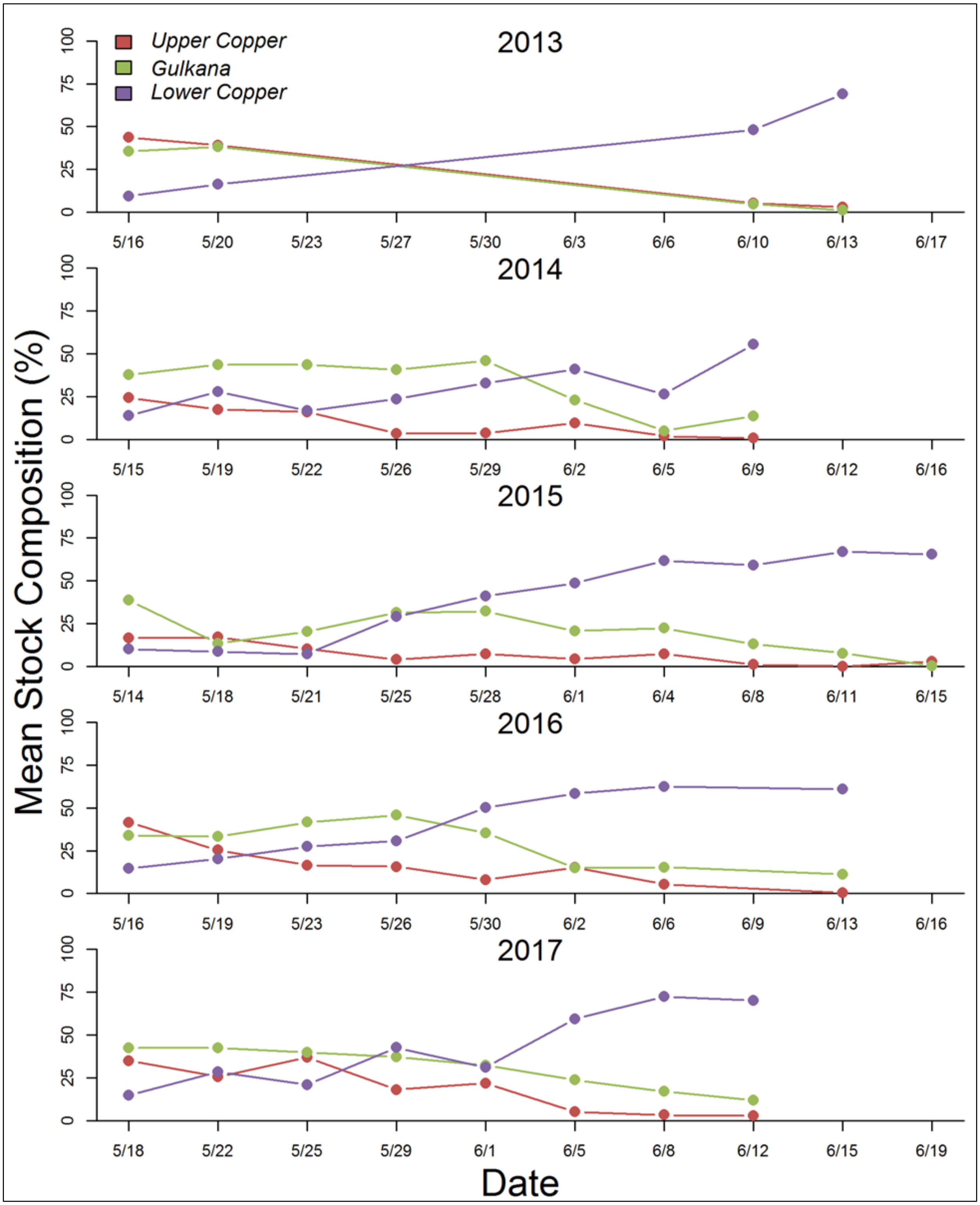

Figure 5.–Run-timing of Copper River origin Chinook salmon harvested in the Copper River District Chinook salmon fishery by date, 2013–2017.

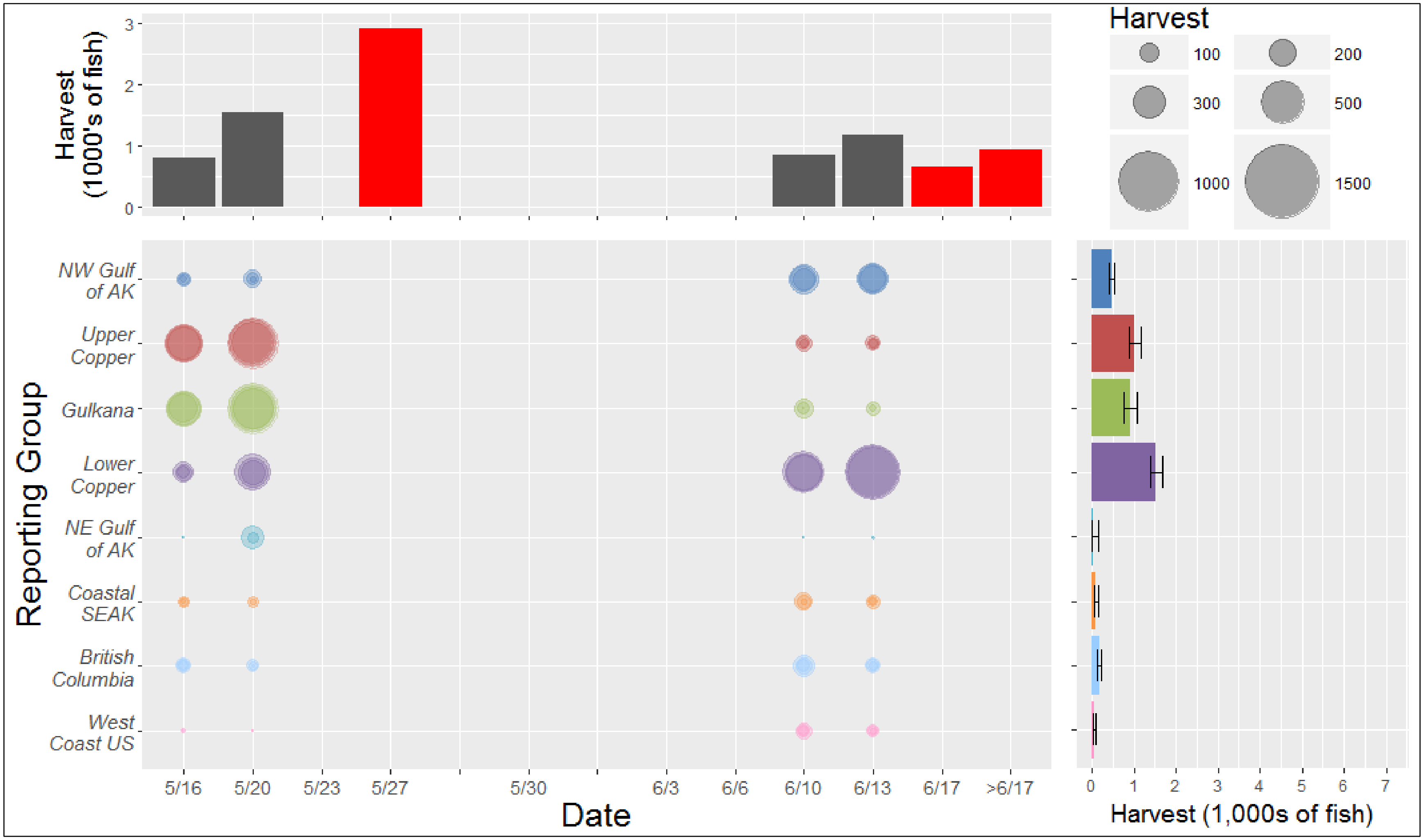

Figure 6.–Stock-specific harvest of Chinook salmon commercial harvest in the Copper River District by date, 2013.

Key: The bubble plot shows stock-specific harvest estimates (means) of Chinook salmon for all periods (*x*-axis) for all 8 reporting groups (*y*-axis). The size of the circle represents the stock-specific harvest for a sampling area (see legend, top right). Reporting groups are denoted by color. The top bar plot shows the total harvest during each period, with unsampled periods in red. The right bar plot shows the stock-specific harvest and 90% credibility intervals for the entire year across all sampled periods.

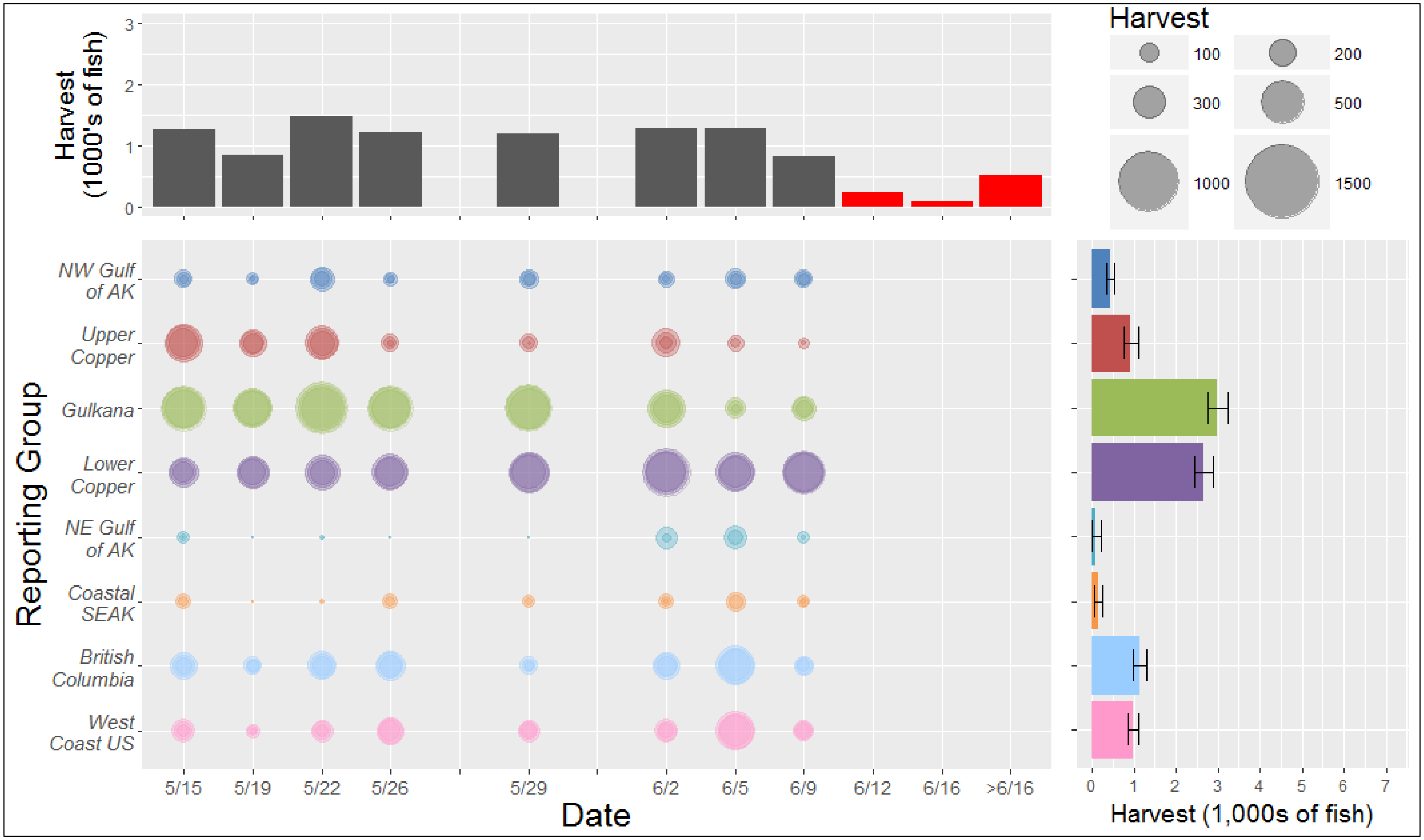

Figure 7.–Stock-specific harvest of Chinook salmon commercial harvest in the Copper River District by date, 2014.

Key: The bubble plot shows stock-specific harvest estimates (means) of Chinook salmon for all periods (*x*-axis) for all 8 reporting groups (*y*-axis). The size of the circle represents the stock-specific harvest for a sampling area (see legend, top right). Reporting groups are denoted by color. The top bar plot shows the total harvest during each period, with unsampled periods in red. The right bar plot shows the stock-specific harvest and 90% credibility intervals for the entire year across all sampled periods.

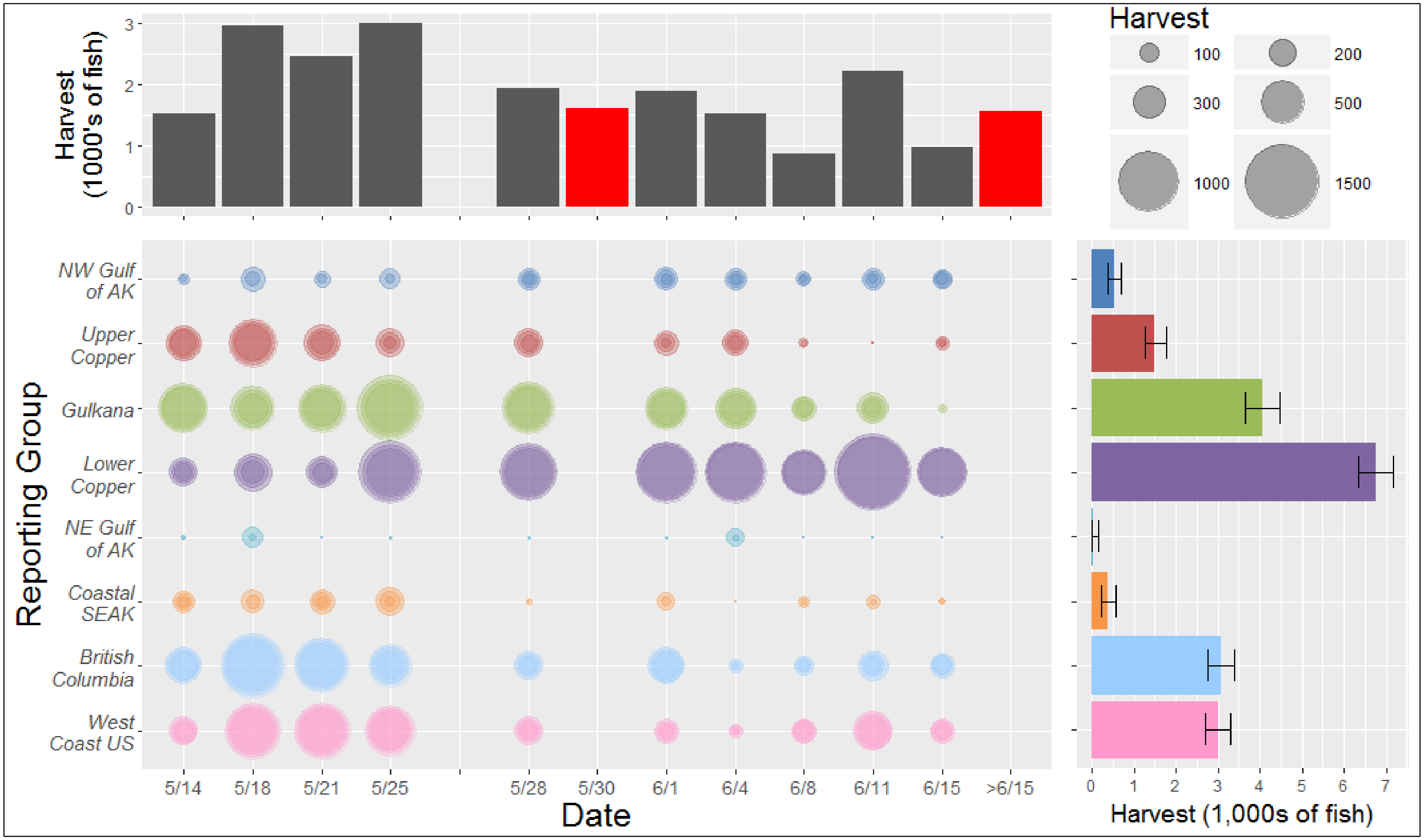

Figure 8.–Stock-specific harvest of Chinook salmon commercial harvest in the Copper River District by date, 2015.

Key: The bubble plot shows stock-specific harvest estimates (means) of Chinook salmon for all periods (*x*-axis) for all 8 reporting groups (*y*-axis). The size of the circle represents the stock-specific harvest for a sampling area (see legend, top right). Reporting groups are denoted by color. The top bar plot shows the total harvest during each period, with unsampled periods in red. The right bar plot shows the stock-specific harvest and 90% credibility intervals for the entire year across all sampled periods.

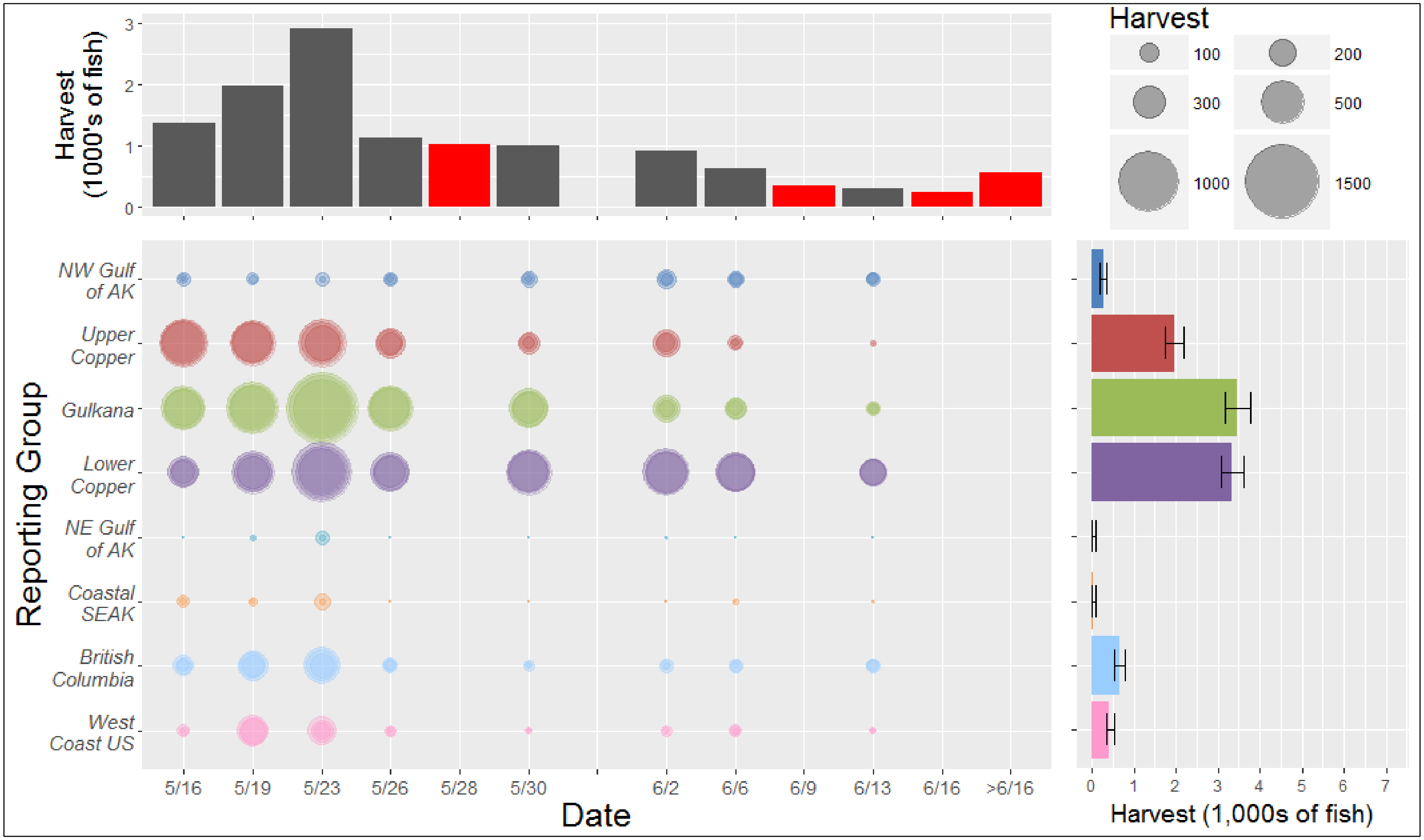

Figure 9.–Stock-specific harvest of Chinook salmon commercial harvest in the Copper River District by date, 2016.

Key: The bubble plot shows stock-specific harvest estimates (means) of Chinook salmon for all periods (*x*-axis) for all 8 reporting groups (*y*-axis). The size of the circle represents the stock-specific harvest for a sampling area (see legend, top right). Reporting groups are denoted by color. The top bar plot shows the total harvest during each period, with unsampled periods in red. The right bar plot shows the stock-specific harvest and 90% credibility intervals for the entire year across all sampled periods.

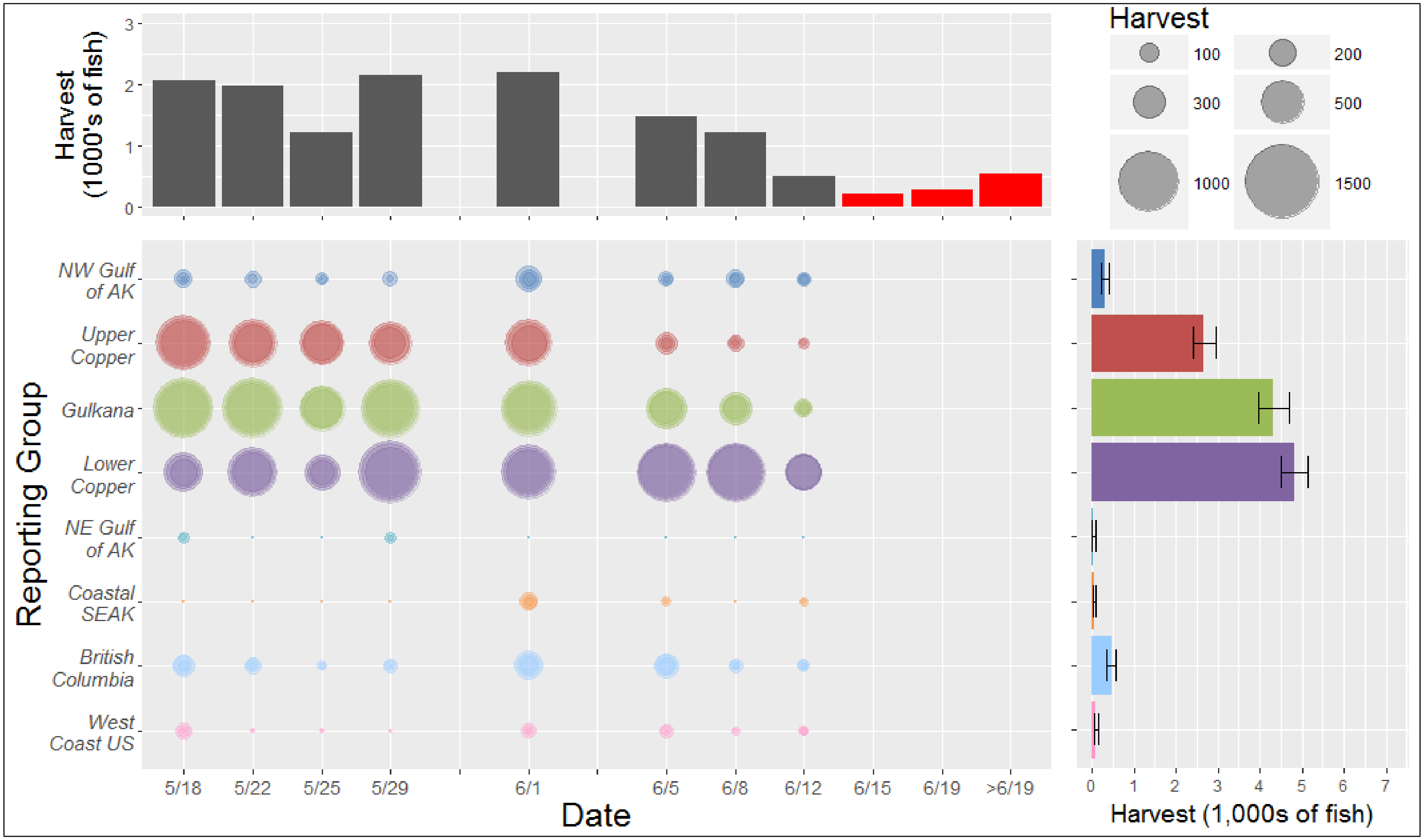

Figure 10.–Stock-specific harvest of Chinook salmon commercial harvest in the Copper River District by date, 2017.

Key: The bubble plot shows stock-specific harvest estimates (means) of Chinook salmon for all periods (*x*-axis) for all 8 reporting groups (*y*-axis). The size of the circle represents the stock-specific harvest for a sampling area (see legend, top right). Reporting groups are denoted by color. The top bar plot shows the total harvest during each period, with unsampled periods in red. The right bar plot shows the stock-specific harvest and 90% credibility intervals for the entire year across all sampled periods.

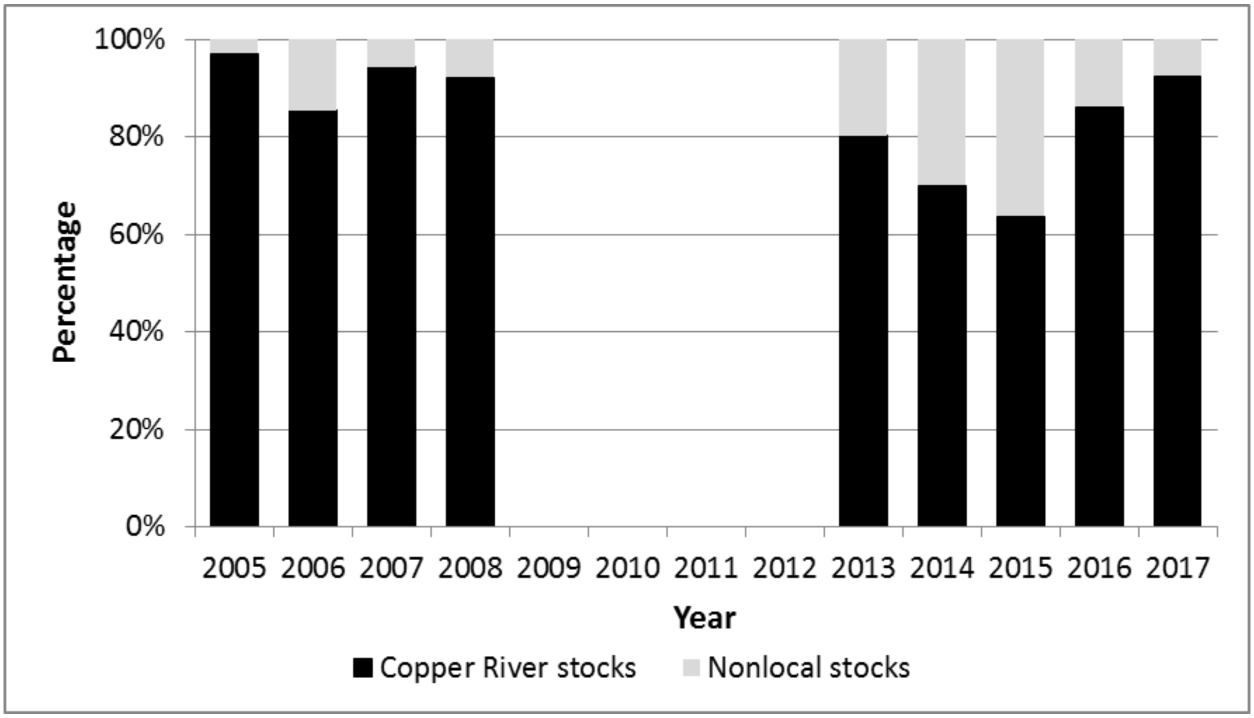

Figure 11.–Proportion of Copper River origin Chinook salmon sampled from the commercial harvest from the Copper River District, 2005–2017.

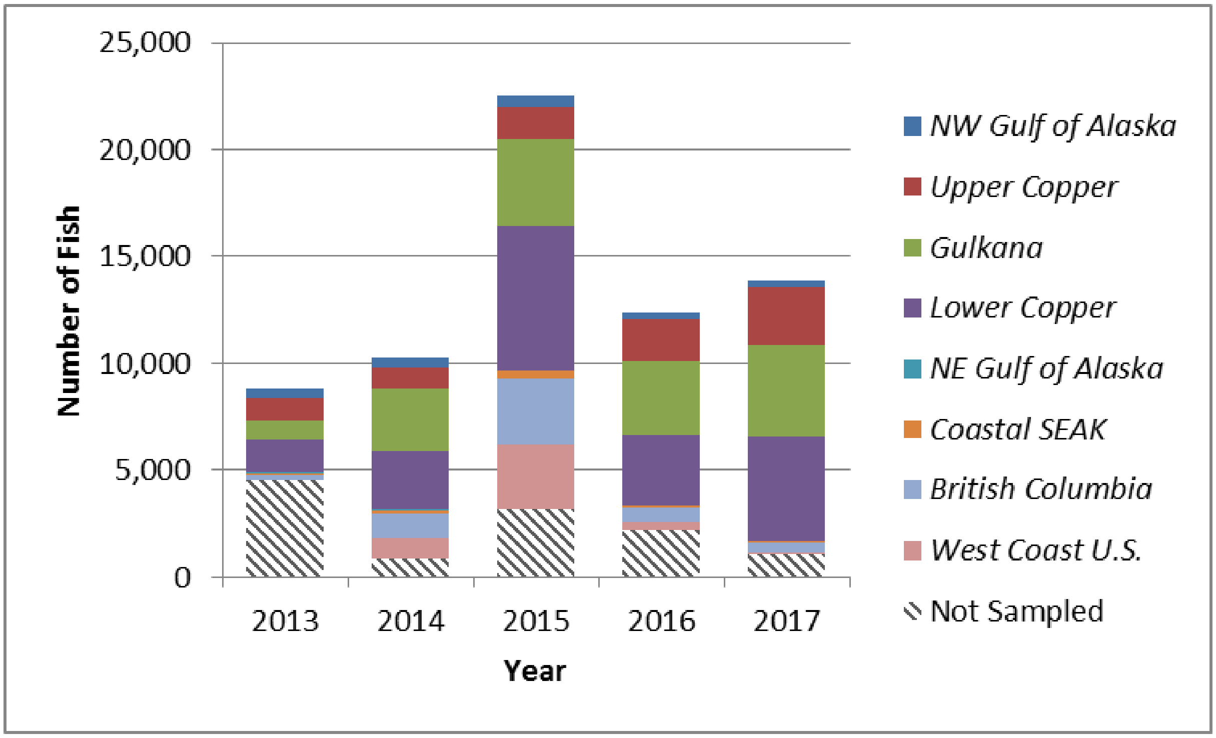

Figure 12.–Stock-specific harvest estimates in the Copper River District Chinook salmon fishery calculated using a stratified estimator for all weeks within years, 2013–2017.

APPENDIX A: DETAILED STOCK COMPOSITION AND STOCK-SPECIFIC HARVEST ESTIMATES

Appendix A1.–Estimates of stock composition (%) and stock-specific harvest for the Copper River District commercial fishery for each period, 2013.

Period 1 (5/16)	Stock Composition (n = 200)				Stock-specific Harvest (C = 801)			
			90% CI				90% CI	
Reporting Group	Mean	SD	5%	95%	Mean	SD	5%	95%
NW Gulf of Alaska	3.8%	1.6%	1.6%	6.8%	31	13	12	54
Upper Copper River	43.7%	4.1%	37.0%	50.5%	350	33	296	404
Gulkana	35.5%	4.4%	28.4%	42.8%	284	35	227	343
Lower Copper River	9.4%	2.9%	5.2%	14.5%	76	23	41	116
NE Gulf of Alaska	0.1%	0.5%	0.0%	0.0%	0	4	0	0
Southeast Alaska	2.2%	1.1%	0.7%	4.3%	18	9	6	35
British Columbia	5.1%	1.6%	2.8%	8.1%	41	13	22	65
West Coast U.S.	0.1%	0.3%	0.0%	0.6%	1	2	0	5

Period 2 (5/20)	Stock Composition (n = 193)				Stock-specific Harvest (C = 1,530)			
NW Gulf of Alaska	2.5%	1.4%	0.7%	5.2%	38	22	10	79
Upper Copper River	39.1%	4.7%	31.6%	46.9%	599	72	483	718
Gulkana	38.2%	5.0%	30.0%	46.4%	584	76	459	710
Lower Copper River	16.2%	4.0%	10.1%	23.4%	248	62	155	358
NE Gulf of Alaska	2.2%	3.3%	0.0%	10.0%	34	51	0	153
Southeast Alaska	0.6%	0.8%	0.0%	2.2%	9	12	0	34
British Columbia	1.2%	0.8%	0.2%	2.7%	18	12	3	42
West Coast U.S.	0.0%	0.1%	0.0%	0.0%	0	1	0	0

Period 3 (5/27)	Stock Composition (n = 14)	Unsampled Harvest (C = 2,919)

Period 4 (6/10-6/11)	Stock Composition (n = 171)				Stock-specific Harvest (C = 846)			
NW Gulf of Alaska	21.7%	3.5%	16.2%	27.7%	184	30	137	234
Upper Copper River	5.2%	2.2%	2.0%	9.3%	44	19	17	78
Gulkana	4.7%	3.6%	0.0%	11.4%	40	30	0	96
Lower Copper River	48.2%	5.0%	39.9%	56.2%	407	42	337	476
NE Gulf of Alaska	0.1%	0.4%	0.0%	0.1%	1	4	0	1
Southeast Alaska	5.6%	2.6%	0.9%	9.8%	47	22	8	83
British Columbia	9.2%	3.0%	5.0%	14.7%	78	25	42	124
West Coast U.S.	5.3%	1.9%	2.7%	8.7%	45	16	23	74

Period 5 (6/13-6/14)	Stock Composition (n = 367)				Stock-specific Harvest (C = 1,160)			
NW Gulf of Alaska	19.1%	2.2%	15.5%	22.8%	221	26	180	265
Upper Copper River	3.1%	1.1%	1.5%	5.1%	36	13	17	59
Gulkana	1.2%	1.6%	0.0%	4.5%	14	18	0	52
Lower Copper River	69.0%	2.9%	64.0%	73.6%	800	34	742	854
NE Gulf of Alaska	0.0%	0.2%	0.0%	0.1%	0	2	0	1
Southeast Alaska	2.3%	1.0%	0.9%	4.1%	27	11	11	48
British Columbia	3.4%	1.1%	1.7%	5.4%	39	13	20	62
West Coast U.S.	1.9%	0.8%	0.9%	3.3%	22	9	10	39

Period 6-31 (6/17-9/12)	Stock Composition (n = 0)	Unsampled Harvest (C = 1,570)

Note: Estimates include mean, standard deviation (SD), and 90% credibility interval (CI).
Note: n = successfully analyzed sample size and C = catch.

Appendix A2.–Estimates of stock composition (%) and stock-specific harvest for the Copper River District commercial fishery for each period, 2014.

Period 1 (5/14)	Stock Composition (*n* = 165)				Stock-specific Harvest (*C* = 1,264)			
			90% CI				90% CI	
Reporting Group	Mean	SD	5%	95%	Mean	SD	5%	95%
NW Gulf of Alaska	4.0%	1.8%	1.5%	7.2%	50	22	19	91
Upper Copper River	24.3%	3.9%	18.1%	31.0%	308	50	228	392
Gulkana	37.6%	4.6%	30.1%	45.3%	476	58	381	572
Lower Copper River	14.0%	3.1%	9.2%	19.4%	177	39	117	245
NE Gulf of Alaska	1.0%	1.3%	0.0%	3.0%	12	16	0	38
Southeast Alaska	1.9%	1.6%	0.0%	4.8%	24	20	0	60
British Columbia	10.5%	2.9%	5.9%	15.5%	133	37	74	196
West Coast U.S.	6.8%	2.3%	3.5%	11.1%	86	29	44	140

Period 2 (5/19)	Stock Composition (*n* = 197)				Stock-specific Harvest (*C* = 851)			
NW Gulf of Alaska	2.1%	1.3%	0.5%	4.5%	18	11	4	39
Upper Copper River	17.5%	3.6%	11.8%	23.8%	149	31	101	202
Gulkana	43.6%	4.5%	36.2%	51.1%	371	38	308	435
Lower Copper River	27.7%	3.9%	21.5%	34.2%	236	33	183	291
NE Gulf of Alaska	0.0%	0.1%	0.0%	0.0%	0	1	0	0
Southeast Alaska	0.0%	0.1%	0.0%	0.1%	0	1	0	0
British Columbia	6.2%	1.9%	3.4%	9.6%	53	16	29	82
West Coast U.S.	2.9%	1.4%	0.9%	5.5%	24	12	8	47

Period 3 (5/22-5/23)	Stock Composition (*n* = 178)				Stock-specific Harvest (*C* = 1,470)			
NW Gulf of Alaska	7.3%	2.3%	3.9%	11.5%	108	35	57	169
Upper Copper River	16.0%	3.4%	10.7%	21.9%	235	50	158	322
Gulkana	43.6%	4.7%	35.8%	51.3%	640	70	526	754
Lower Copper River	16.7%	3.8%	11.0%	23.3%	246	55	161	343
NE Gulf of Alaska	0.1%	0.6%	0.0%	0.2%	1	8	0	4
Southeast Alaska	0.1%	0.4%	0.0%	0.2%	1	6	0	3
British Columbia	10.7%	2.5%	6.9%	14.9%	157	36	101	220
West Coast U.S.	5.6%	1.8%	3.0%	8.7%	82	26	44	128

Period 4 (5/26-5/27)	Stock Composition (*n* = 195)				Stock-specific Harvest (*C* = 1,210)			
NW Gulf of Alaska	2.3%	1.2%	0.7%	4.6%	28	14	9	55
Upper Copper River	3.4%	1.8%	0.8%	6.6%	41	22	10	80
Gulkana	40.8%	4.3%	33.7%	47.8%	493	52	408	578
Lower Copper River	23.6%	3.8%	17.6%	30.0%	285	45	214	363
NE Gulf of Alaska	0.0%	0.2%	0.0%	0.0%	0	2	0	0
Southeast Alaska	1.8%	1.8%	0.0%	5.4%	22	22	0	66
British Columbia	15.2%	3.0%	10.4%	20.2%	184	36	126	245
West Coast U.S.	12.9%	2.5%	9.1%	17.2%	157	30	110	209

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Appendix A2.–Page 2 of 2.

Period 5 (5/29-5/30)	Stock Composition (*n* = 233)				Stock-specific Harvest (*C* = 1,182)			
			90% CI				90% CI	
Reporting Group	Mean	SD	5%	95%	Mean	SD	5%	95%
NW Gulf of Alaska	5.0%	1.7%	2.6%	8.0%	59	20	30	94
Upper Copper River	3.6%	2.1%	0.2%	7.5%	43	25	2	89
Gulkana	46.0%	4.3%	38.9%	53.2%	544	51	459	629
Lower Copper River	32.8%	3.8%	26.7%	39.2%	387	45	315	463
NE Gulf of Alaska	0.1%	0.6%	0.0%	0.1%	1	7	0	1
Southeast Alaska	1.0%	1.1%	0.0%	3.1%	12	13	0	37
British Columbia	3.8%	1.6%	1.4%	6.7%	45	19	17	80
West Coast U.S.	7.7%	1.8%	4.9%	10.9%	91	21	58	129

Period 6 (6/2-6/3)	Stock Composition (*n* = 199)				Stock-specific Harvest (*C* = 1,283)			
NW Gulf of Alaska	3.3%	1.6%	1.1%	6.1%	42	20	14	78
Upper Copper River	9.4%	4.5%	3.4%	17.9%	121	57	43	230
Gulkana	22.9%	4.7%	15.3%	30.9%	294	61	197	396
Lower Copper River	41.0%	5.4%	32.2%	50.0%	526	69	414	642
NE Gulf of Alaska	1.7%	3.5%	0.0%	10.2%	21	45	0	130
Southeast Alaska	1.9%	1.3%	0.4%	4.4%	25	16	5	56
British Columbia	11.9%	2.5%	8.0%	16.1%	152	32	103	207
West Coast U.S.	8.0%	2.0%	5.0%	11.5%	102	25	64	147

Period 7 (6/5-6/7)	Stock Composition (*n* = 219)				Stock-specific Harvest (*C* = 1,281)			
NW Gulf of Alaska	5.4%	1.9%	2.7%	8.7%	70	24	34	112
Upper Copper River	1.9%	1.9%	0.0%	5.6%	24	25	0	72
Gulkana	4.9%	2.3%	1.4%	8.9%	62	29	18	113
Lower Copper River	26.4%	3.5%	20.8%	32.4%	338	45	266	416
NE Gulf of Alaska	4.7%	3.8%	0.0%	10.8%	60	49	0	139
Southeast Alaska	3.6%	2.5%	0.0%	7.8%	46	32	0	100
British Columbia	26.6%	3.8%	20.5%	33.1%	341	49	262	424
West Coast U.S.	26.6%	3.3%	21.2%	32.2%	340	43	272	413

Period 8 (6/9-6/11)	Stock Composition (*n* = 193)				Stock-specific Harvest (*C* = 822)			
NW Gulf of Alaska	7.4%	2.1%	4.3%	11.0%	61	17	35	91
Upper Copper River	0.6%	1.4%	0.0%	3.8%	5	11	0	31
Gulkana	13.7%	3.3%	8.5%	19.5%	113	27	70	160
Lower Copper River	55.5%	4.2%	48.4%	62.4%	456	35	398	513
NE Gulf of Alaska	0.7%	1.7%	0.0%	4.7%	5	14	0	39
Southeast Alaska	2.6%	1.4%	0.6%	5.1%	21	11	5	42
British Columbia	8.9%	2.2%	5.6%	12.9%	73	18	46	106
West Coast U.S.	10.6%	2.3%	7.2%	14.6%	87	19	59	120

Period 9-30 (6/12-9/1)	Stock Composition (*n* = 0)	Unsampled Harvest (*C* = 844)

Note: Estimates include mean, standard deviation (SD), and 90% credibility interval (CI).
Note: *n* = successfully analyzed sample size and *C* = catch.

Appendix A3.–Estimates of stock composition (%) and stock-specific harvest for the Copper River District commercial fishery for each period, 2015.

Period 1 (5/14)	Stock Composition (*n* = 194)				Stock-specific Harvest (*C* = 1,517)			
			90% CI				90% CI	
Reporting Group	Mean	SD	5%	95%	Mean	SD	5%	95%
NW Gulf of Alaska	0.7%	0.7%	0.0%	2.1%	10	11	0	32
Upper Copper River	16.7%	3.3%	11.4%	22.4%	253	50	174	339
Gulkana	38.8%	4.3%	31.8%	45.8%	588	65	483	695
Lower Copper River	10.1%	2.8%	6.0%	15.2%	154	43	91	231
NE Gulf of Alaska	0.1%	0.5%	0.0%	0.4%	1	7	0	6
Southeast Alaska	5.2%	2.0%	2.3%	8.5%	78	30	35	129
British Columbia	18.2%	3.1%	13.5%	23.5%	277	46	205	356
West Coast U.S.	10.3%	2.3%	6.8%	14.2%	156	34	103	216

Period 2 (5/18-5/19)	Stock Composition (*n* = 199)				Stock-specific Harvest (*C* = 2,959)			
NW Gulf of Alaska	2.2%	1.7%	0.0%	5.4%	64	50	0	160
Upper Copper River	17.1%	3.1%	12.2%	22.3%	505	90	362	659
Gulkana	13.4%	3.2%	8.4%	19.0%	398	95	248	561
Lower Copper River	8.7%	2.7%	4.7%	13.4%	256	79	139	397
NE Gulf of Alaska	0.5%	1.4%	0.0%	3.9%	14	41	0	117
Southeast Alaska	1.7%	1.8%	0.0%	5.1%	49	52	0	150
British Columbia	32.2%	3.7%	26.1%	38.3%	951	109	773	1134
West Coast U.S.	24.4%	3.1%	19.4%	29.7%	721	92	574	877

Period 3 (5/21-5/22)	Stock Composition (*n* = 194)				Stock-specific Harvest (*C* = 2,460)			
NW Gulf of Alaska	1.0%	1.0%	0.0%	2.9%	23	24	0	71
Upper Copper River	10.2%	2.7%	6.1%	14.9%	251	66	150	367
Gulkana	20.3%	3.4%	15.0%	26.1%	500	83	369	642
Lower Copper River	7.2%	2.3%	3.9%	11.2%	178	56	96	277
NE Gulf of Alaska	0.0%	0.1%	0.0%	0.0%	0	3	0	0
Southeast Alaska	3.7%	1.6%	1.4%	6.6%	90	39	34	162
British Columbia	28.0%	3.6%	22.2%	34.1%	688	89	545	839
West Coast U.S.	29.6%	3.6%	23.8%	35.7%	728	89	586	878

Period 4 (5/25-5/26)	Stock Composition (*n* = 197)				Stock-specific Harvest (*C* = 3,002)			
NW Gulf of Alaska	0.8%	1.3%	0.0%	3.7%	25	40	0	111
Upper Copper River	4.0%	1.9%	1.4%	7.5%	121	57	42	225
Gulkana	31.4%	4.8%	23.5%	39.4%	943	145	705	1181
Lower Copper River	29.1%	4.6%	21.8%	37.1%	874	140	653	1112
NE Gulf of Alaska	0.1%	0.5%	0.0%	0.1%	2	16	0	2
Southeast Alaska	3.8%	2.0%	0.8%	7.4%	115	60	23	222
British Columbia	12.1%	3.0%	7.5%	17.4%	364	90	224	521
West Coast U.S.	18.6%	3.0%	13.8%	23.7%	557	90	415	711

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Period 5 (5/28-5/29)	Stock Composition (*n* = 198)				Stock-specific Harvest (*C* = 1,932)			
			90% CI				90% CI	
Reporting Group	Mean	SD	5%	95%	Mean	SD	5%	95%
NW Gulf of Alaska	4.0%	1.5%	1.9%	6.7%	77	29	36	129
Upper Copper River	7.3%	2.2%	4.0%	11.2%	141	43	76	217
Gulkana	32.2%	4.7%	24.7%	40.0%	622	90	476	773
Lower Copper River	41.1%	4.8%	33.3%	49.1%	794	92	644	948
NE Gulf of Alaska	0.2%	0.9%	0.0%	0.1%	3	18	0	2
Southeast Alaska	0.1%	0.3%	0.0%	0.4%	1	5	0	7
British Columbia	7.8%	2.1%	4.7%	11.4%	151	40	91	221
West Coast U.S.	7.4%	2.0%	4.4%	11.0%	143	39	84	212

Period 6 (5/30-5/31)	Stock Composition (*n* = 0)	Unsampled Harvest (*C* = 1,599)

Period 7 (6/1-6/2)	Stock Composition (*n* = 199)				Stock-specific Harvest (*C* = 1,882)			
NW Gulf of Alaska	4.2%	1.8%	1.6%	7.5%	80	34	30	141
Upper Copper River	4.3%	2.2%	1.1%	8.3%	82	41	22	155
Gulkana	20.7%	3.6%	15.1%	26.8%	390	67	283	505
Lower Copper River	48.6%	4.0%	42.0%	55.3%	915	76	790	1041
NE Gulf of Alaska	0.1%	0.8%	0.0%	0.1%	2	15	0	2
Southeast Alaska	1.4%	1.6%	0.0%	4.4%	25	30	0	83
British Columbia	15.2%	2.8%	10.8%	20.1%	287	53	203	378
West Coast U.S.	5.4%	1.7%	2.9%	8.5%	101	32	54	159

Period 8 (6/4-6/6)	Stock Composition (*n* = 195)				Stock-specific Harvest (*C* = 1,523)			
NW Gulf of Alaska	4.9%	2.0%	2.0%	8.4%	74	30	30	129
Upper Copper River	7.4%	2.5%	3.7%	11.9%	113	38	57	182
Gulkana	22.3%	4.3%	15.4%	29.5%	339	65	235	449
Lower Copper River	61.7%	4.3%	54.5%	68.7%	939	66	830	1047
NE Gulf of Alaska	0.6%	2.0%	0.0%	5.4%	9	31	0	82
Southeast Alaska	0.0%	0.1%	0.0%	0.0%	0	1	0	0
British Columbia	1.4%	0.9%	0.3%	3.1%	21	14	5	47
West Coast U.S.	1.8%	1.0%	0.5%	3.6%	27	15	7	55

Period 9 (6/8-6/9)	Stock Composition (*n* = 198)				Stock-specific Harvest (*C* = 872)			
			90% CI				90% CI	
Reporting Group	Mean	SD	5%	95%	Mean	SD	5%	95%
NW Gulf of Alaska	3.8%	1.6%	1.6%	6.7%	34	14	14	58
Upper Copper River	1.1%	1.1%	0.0%	3.2%	9	9	0	28
Gulkana	13.1%	3.0%	8.3%	18.4%	114	27	73	160
Lower Copper River	59.2%	3.9%	52.7%	65.5%	516	34	459	571
NE Gulf of Alaska	0.0%	0.4%	0.0%	0.0%	0	3	0	0
Southeast Alaska	1.1%	1.2%	0.0%	3.5%	10	11	0	31
British Columbia	7.5%	2.3%	4.0%	11.6%	65	20	35	101
West Coast U.S.	14.2%	3.0%	9.5%	19.4%	123	26	83	170

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Period 10 (6/11-6/13)	Stock Composition (*n* = 198)				Stock-specific Harvest (*C* = 2,219)			
NW Gulf of Alaska	3.1%	1.4%	1.1%	5.7%	68	32	24	128
Upper Copper River	0.0%	0.2%	0.0%	0.1%	1	5	0	1
Gulkana	7.7%	2.6%	3.8%	12.3%	171	58	84	272
Lower Copper River	67.1%	3.7%	60.8%	73.1%	1488	83	1349	1621
NE Gulf of Alaska	0.0%	0.2%	0.0%	0.0%	0	4	0	0
Southeast Alaska	0.4%	0.8%	0.0%	2.2%	8	18	0	49
British Columbia	6.8%	2.1%	3.6%	10.5%	150	47	79	234
West Coast U.S.	15.0%	2.7%	10.7%	19.7%	332	61	237	437

Period 11 (6/15-6/17)	Stock Composition (*n* = 195)				Stock-specific Harvest (*C* = 980)			
NW Gulf of Alaska	7.3%	1.9%	4.4%	10.7%	71	19	43	105
Upper Copper River	2.9%	1.4%	0.9%	5.4%	28	14	9	53
Gulkana	0.3%	0.8%	0.0%	2.0%	3	8	0	19
Lower Copper River	65.5%	3.5%	59.6%	71.2%	642	35	584	697
NE Gulf of Alaska	0.0%	0.1%	0.0%	0.0%	0	1	0	0
Southeast Alaska	0.4%	0.5%	0.0%	1.5%	4	5	0	14
British Columbia	12.0%	2.5%	8.2%	16.3%	118	24	80	160
West Coast U.S.	11.7%	2.4%	7.9%	15.9%	115	24	78	156

Period 12-33 (6/18-9/7)	Stock Composition (*n* = 0)	Unsampled Harvest (*C* = 1,561)

Note: Estimates include mean, standard deviation (SD), and 90% credibility interval (CI).
Note: *n* = successfully analyzed sample size and *C* = catch.

Appendix A4.–Estimates of stock composition (%) and stock-specific harvest for the Copper River District commercial fishery for each period, 2016.

Period 1 (5/16)	Stock Composition (*n* = 223)				Stock-specific Harvest (*C* = 1,367)			
			90% CI				90% CI	
Reporting Group	Mean	SD	5%	95%	Mean	SD	5%	95%
NW Gulf of Alaska	1.6%	0.9%	0.4%	3.4%	22	13	6	46
Upper Copper River	41.6%	4.1%	35.0%	48.4%	569	56	478	661
Gulkana	34.0%	4.3%	27.1%	41.1%	465	58	371	562
Lower Copper River	14.7%	2.9%	10.2%	19.8%	202	40	139	270
NE Gulf of Alaska	0.0%	0.2%	0.0%	0.0%	0	2	0	0
Southeast Alaska	0.8%	1.1%	0.0%	3.0%	11	15	0	41
British Columbia	5.7%	1.8%	3.1%	8.8%	78	24	42	121
West Coast U.S.	1.4%	0.9%	0.3%	3.1%	20	12	5	42

Period 2 (5/19-5/20)	Stock Composition (*n* = 370)				Stock-specific Harvest (*C* = 1,968)			
NW Gulf of Alaska	0.8%	0.7%	0.0%	2.1%	16	13	0	40
Upper Copper River	25.3%	2.7%	21.0%	29.9%	498	53	413	588
Gulkana	33.4%	3.5%	27.6%	39.3%	657	70	544	773
Lower Copper River	20.3%	3.1%	15.3%	25.4%	399	61	301	501
NE Gulf of Alaska	0.1%	0.6%	0.0%	0.4%	2	13	0	9
Southeast Alaska	0.2%	0.4%	0.0%	1.0%	4	7	0	20
British Columbia	9.3%	1.6%	6.7%	12.1%	182	32	132	238
West Coast U.S.	10.6%	1.7%	8.0%	13.6%	210	34	157	267

Period 3 (5/23-5/25)	Stock Composition (*n* = 198)				Stock-specific Harvest (*C* = 2,912)			
NW Gulf of Alaska	0.3%	0.7%	0.0%	1.8%	8	21	0	53
Upper Copper River	16.5%	3.3%	11.4%	22.2%	481	95	332	646
Gulkana	41.6%	4.8%	33.7%	49.6%	1212	140	982	1444
Lower Copper River	27.6%	4.3%	20.8%	34.9%	803	125	605	1016
NE Gulf of Alaska	0.2%	0.9%	0.0%	1.8%	7	27	0	52
Southeast Alaska	0.3%	1.0%	0.0%	2.6%	10	28	0	76
British Columbia	8.8%	2.2%	5.5%	12.6%	257	63	159	367
West Coast U.S.	4.6%	1.5%	2.4%	7.3%	134	44	71	213

Period 4 (5/26-5/27)	Stock Composition (*n* = 318)				Stock-specific Harvest (*C* = 1,116)			
NW Gulf of Alaska	2.7%	1.1%	1.1%	4.8%	31	12	13	53
Upper Copper River	15.7%	3.1%	10.9%	21.0%	175	35	122	235
Gulkana	45.8%	4.7%	38.1%	53.4%	511	52	425	596
Lower Copper River	30.7%	4.1%	24.2%	37.6%	343	46	271	420
NE Gulf of Alaska	0.0%	0.3%	0.0%	0.0%	0	4	0	0
Southeast Alaska	0.0%	0.1%	0.0%	0.0%	0	1	0	0
British Columbia	3.6%	1.1%	2.0%	5.5%	40	12	22	62
West Coast U.S.	1.5%	0.7%	0.5%	2.8%	16	8	5	31

Period 5 (5/28-5/29)	Stock Composition (*n* = 0)	Unsampled Harvest (*C* = 1,017)

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Period 6 (5/30-5/31)	Stock Composition (*n* = 198)				Stock-specific Harvest (*C* = 988)			
			90% CI				90% CI	
Reporting Group	Mean	SD	5%	95%	Mean	SD	5%	95%
NW Gulf of Alaska	4.1%	1.9%	1.5%	7.5%	41	18	14	74
Upper Copper River	8.1%	2.7%	4.1%	13.0%	80	27	40	128
Gulkana	35.4%	4.6%	27.9%	43.0%	350	45	276	424
Lower Copper River	50.2%	4.4%	43.0%	57.5%	496	44	425	568
NE Gulf of Alaska	0.1%	0.8%	0.0%	0.0%	1	8	0	0
Southeast Alaska	0.0%	0.1%	0.0%	0.0%	0	1	0	0
British Columbia	1.6%	0.9%	0.4%	3.2%	15	9	4	32
West Coast U.S.	0.5%	0.5%	0.0%	1.5%	5	5	0	15

Period 7 (6/2-6/3)	Stock Composition (*n* = 143)				Stock-specific Harvest (*C* = 904)			
NW Gulf of Alaska	6.9%	2.4%	3.5%	11.3%	63	22	32	102
Upper Copper River	15.2%	3.7%	9.6%	21.6%	137	33	87	195
Gulkana	15.0%	4.4%	8.2%	22.7%	136	40	74	205
Lower Copper River	58.5%	5.0%	50.3%	66.6%	529	45	454	602
NE Gulf of Alaska	0.1%	0.8%	0.0%	0.1%	1	7	0	1
Southeast Alaska	0.0%	0.1%	0.0%	0.0%	0	1	0	0
British Columbia	2.7%	1.4%	0.8%	5.3%	24	13	7	48
West Coast U.S.	1.5%	1.1%	0.2%	3.7%	14	10	2	33

Period 8 (6/6-6/7)	Stock Composition (*n* = 198)				Stock-specific Harvest (*C* = 624)			
NW Gulf of Alaska	8.1%	2.1%	4.9%	11.9%	51	13	30	74
Upper Copper River	5.3%	2.1%	2.3%	9.0%	33	13	14	56
Gulkana	15.4%	3.4%	10.0%	21.3%	96	22	62	133
Lower Copper River	62.6%	3.9%	56.0%	69.0%	390	25	349	430
NE Gulf of Alaska	0.0%	0.2%	0.0%	0.0%	0	1	0	0
Southeast Alaska	0.2%	0.5%	0.0%	1.2%	1	3	0	7
British Columbia	4.9%	1.7%	2.4%	7.9%	31	10	15	49
West Coast U.S.	3.5%	1.4%	1.5%	6.2%	22	9	10	39

Period 9 (6/9-6/10)	Stock Composition (*n* = 0)	Unsampled Harvest (*C* = 346)

Period 10 (6/13-6/14)	Stock Composition (*n* = 129)				Stock-specific Harvest (*C* = 303)			
NW Gulf of Alaska	12.6%	3.3%	7.6%	18.4%	38	10	23	56
Upper Copper River	0.6%	1.1%	0.0%	2.9%	2	3	0	9
Gulkana	11.2%	3.8%	5.3%	17.9%	34	12	16	54
Lower Copper River	60.9%	5.0%	52.6%	69.0%	184	15	159	209
NE Gulf of Alaska	0.1%	0.7%	0.0%	0.0%	0	2	0	0
Southeast Alaska	0.1%	0.3%	0.0%	0.4%	0	1	0	1
British Columbia	12.9%	2.9%	8.4%	18.1%	39	9	26	55
West Coast U.S.	1.7%	1.2%	0.3%	4.0%	5	4	1	12

Period 11-30 (6/16-8/25)	Stock Composition (*n* = 0)	Unsampled Harvest (*C* = 803)

Note: Estimates include mean, standard deviation (SD), and 90% credibility interval (CI).
Note: *n* = successfully analyzed sample size and *C* = catch.

Appendix A5.–Estimates of stock composition (%) and stock-specific harvest for the Copper River District commercial fishery for each period, 2017.

Period 1 (5/18)	Stock Composition (*n* = 201)				Stock-specific Harvest (*C* = 2,066)			
			90% CI				90% CI	
Reporting Group	Mean	SD	5%	95%	Mean	SD	5%	95%
NW Gulf of Alaska	1.9%	1.2%	0.4%	4.1%	39	24	8	85
Upper Copper River	34.9%	4.0%	28.5%	41.5%	721	82	589	858
Gulkana	42.4%	4.4%	35.3%	49.6%	876	90	728	1025
Lower Copper River	14.7%	3.0%	10.0%	20.0%	304	63	207	413
NE Gulf of Alaska	0.6%	0.7%	0.0%	1.7%	12	14	0	36
Southeast Alaska	0.0%	0.1%	0.0%	0.0%	0	2	0	0
British Columbia	3.9%	1.5%	1.7%	6.5%	80	30	36	135
West Coast U.S.	1.6%	1.1%	0.3%	3.6%	33	22	6	75

Period 2 (5/22)	Stock Composition (*n* = 197)				Stock-specific Harvest (*C* = 1,981)			
NW Gulf of Alaska	1.3%	1.1%	0.0%	3.4%	25	23	0	67
Upper Copper River	25.6%	3.7%	19.7%	32.0%	508	74	390	634
Gulkana	42.5%	4.7%	34.9%	50.3%	842	93	690	996
Lower Copper River	28.5%	4.1%	22.0%	35.4%	564	81	435	701
NE Gulf of Alaska	0.0%	0.4%	0.0%	0.0%	1	7	0	0
Southeast Alaska	0.0%	0.1%	0.0%	0.0%	0	2	0	0
British Columbia	2.0%	1.0%	0.7%	3.9%	40	20	13	77
West Coast U.S.	0.0%	0.2%	0.0%	0.2%	1	4	0	5

Period 3 (5/25)	Stock Composition (*n* = 137)				Stock-specific Harvest (*C* = 1,205)			
NW Gulf of Alaska	1.3%	1.1%	0.0%	3.5%	16	14	0	43
Upper Copper River	37.0%	4.6%	29.5%	44.7%	446	56	355	539
Gulkana	40.0%	5.2%	31.6%	48.6%	482	62	380	585
Lower Copper River	20.9%	4.3%	14.2%	28.4%	252	52	171	342
NE Gulf of Alaska	0.0%	0.2%	0.0%	0.0%	0	3	0	0
Southeast Alaska	0.0%	0.1%	0.0%	0.0%	0	1	0	0
British Columbia	0.7%	0.7%	0.0%	2.2%	8	9	0	26
West Coast U.S.	0.1%	0.3%	0.0%	0.4%	1	3	0	4

Period 4 (5/29)	Stock Composition (*n* = 189)				Stock-specific Harvest (*C* = 2,141)			
NW Gulf of Alaska	0.6%	1.1%	0.0%	2.9%	14	23	0	62
Upper Copper River	18.1%	3.4%	12.8%	23.8%	387	72	274	510
Gulkana	37.2%	4.9%	29.3%	45.4%	797	105	628	972
Lower Copper River	42.7%	5.0%	34.4%	50.9%	913	107	736	1089
NE Gulf of Alaska	0.3%	1.5%	0.0%	1.5%	7	32	0	32
Southeast Alaska	0.0%	0.1%	0.0%	0.0%	0	2	0	0
British Columbia	1.0%	0.8%	0.1%	2.5%	22	16	2	53
West Coast U.S.	0.0%	0.3%	0.0%	0.1%	1	5	0	2

Period 5 (6/1)	Stock Composition (*n* = 192)				Stock-specific Harvest (*C* = 2,198)			
NW Gulf of Alaska	4.8%	1.8%	2.2%	8.0%	105	39	49	176
Upper Copper River	21.8%	3.6%	16.0%	28.0%	479	80	353	615
Gulkana	32.3%	4.4%	25.2%	39.6%	711	96	554	871
Lower Copper River	31.2%	3.9%	24.9%	37.7%	685	86	547	829
NE Gulf of Alaska	0.0%	0.1%	0.0%	0.0%	0	3	0	0
Southeast Alaska	2.2%	1.1%	0.7%	4.2%	48	24	16	92
British Columbia	6.5%	1.8%	3.8%	9.8%	144	40	84	215
West Coast U.S.	1.2%	0.9%	0.2%	2.8%	26	19	4	62

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Period 6 (6/5)	Stock Composition (*n* = 197)				Stock-specific Harvest (*C* = 1,482)			
			90% CI				90% CI	
Reporting Group	Mean	SD	5%	95%	Mean	SD	5%	95%
NW Gulf of Alaska	2.0%	1.1%	0.6%	3.9%	29	16	8	58
Upper Copper River	5.2%	2.0%	2.2%	8.8%	76	30	33	131
Gulkana	23.7%	3.9%	17.6%	30.3%	352	57	261	449
Lower Copper River	59.5%	4.0%	52.7%	66.0%	881	60	781	978
NE Gulf of Alaska	0.0%	0.2%	0.0%	0.0%	0	3	0	0
Southeast Alaska	0.4%	0.6%	0.0%	1.7%	6	9	0	25
British Columbia	7.8%	2.0%	4.8%	11.4%	116	30	71	169
West Coast U.S.	1.5%	1.0%	0.1%	3.3%	22	15	2	49

Period 7 (6/8)	Stock Composition (*n* = 192)				Stock-specific Harvest (*C* = 1,221)			
NW Gulf of Alaska	4.5%	1.7%	2.1%	7.5%	55	20	26	92
Upper Copper River	3.4%	1.6%	1.1%	6.3%	41	20	14	77
Gulkana	17.1%	3.5%	11.7%	23.1%	209	42	142	282
Lower Copper River	72.4%	3.8%	66.0%	78.4%	884	46	806	957
NE Gulf of Alaska	0.0%	0.1%	0.0%	0.0%	0	1	0	0
Southeast Alaska	0.0%	0.1%	0.0%	0.0%	0	1	0	0
British Columbia	2.2%	1.1%	0.7%	4.2%	27	13	9	51
West Coast U.S.	0.5%	0.6%	0.0%	1.6%	6	7	0	19

Period 8 (6/12)	Stock Composition (*n* = 198)				Stock-specific Harvest (*C* = 486)			
NW Gulf of Alaska	6.1%	1.9%	3.3%	9.5%	30	9	16	46
Upper Copper River	2.8%	1.9%	0.0%	6.3%	14	9	0	31
Gulkana	11.9%	3.2%	6.8%	17.4%	58	16	33	85
Lower Copper River	70.1%	4.0%	63.4%	76.6%	341	19	308	372
NE Gulf of Alaska	0.0%	0.3%	0.0%	0.0%	0	1	0	0
Southeast Alaska	0.9%	1.2%	0.0%	3.4%	4	6	0	17
British Columbia	5.0%	2.1%	1.9%	8.7%	25	10	9	42
West Coast U.S.	3.3%	1.4%	1.3%	5.9%	16	7	6	28

Period 9-30 (6/15-9/4)	Stock Composition (*n* = 0)	Unsampled Harvest (*C* = 1,054)

Note: Estimates include mean, standard deviation (SD), and 90% credibility interval (CI).
Note: *n* = successfully analyzed sample size and *C* = catch.

APPENDIX B: QUALITY CONTROL RESULTS

Appendix B1.–Results of the statistical quality control by year for Chinook salmon catch samples analyzed to estimate the stock composition of Copper River District commercial harvests in 2013–2017.

	Number of Fish				
		Fish Removed			
Year	Genotyped	Missing Loci	Duplicate	Unanalyzed strata (insufficient samples)	Final
2013	1,097	151	1	14	931
2014	1,614	32	3		1,579
2015	1,989	16	6		1,967
2016	1,881	31	5	68	1,777
2017	1,532	20	9		1,503
Total	8,113	250	24	82	7,757

Note: The number of fish genetically screened, and excluded from statistical analysis because of 1) missing loci, 2) duplicate fish, and 3) strata represented by an insufficient sample sizes (< 100 fish), and the final number statistically analyzed are provided.