Fishery Data Series No. 22-35

Genetic Stock Composition of the Commercial Harvest of Chinook Salmon in Copper River District, 2018–2021

by

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

Symbols and Abbreviations

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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

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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 2018 through 2021. 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. The consistent temporal pattern in the composition of the commercial fishery harvests observed in previous studies was also observed across the 4 years of this 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 results support a 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.

Keywords: Copper River, Chinook salmon, *Oncorhynchus tshawytscha*, mixed stock analysis, MSA, commercial fishery, SNP

INTRODUCTION

Chinook salmon *Oncorhynchus tshawytscha* are harvested in subsistence, commercial, sport, and personal use fisheries throughout the Copper River drainage and nearshore marine waters. The Copper River District commercial drift gillnet fishery takes place in the marine waters of the Gulf of Alaska (GOA) surrounding the mouth of the Copper River (Figure 1). Harvests include fish representing an array of Copper River watershed stocks and 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. The first genetic mixed stock analysis (MSA) of the Chinook salmon catch in Copper River District commercial salmon fisheries analyzed harvest samples from 2005 to 2008 (Templin et al. 2011a); however, the genetic baseline used to estimate the composition of catches has been improved (updated markers and set of collections) since that time.

The most recent MSA of Cooper River District Chinook catches analyzed harvests from 2013 to 2017 and used the improved genetic baseline to estimate the composition of the catches (Gilk-Baumer et al. 2017a). The results from that study showed that most of the fish in the Copper River commercial fishery originated from Copper River populations (stocks), which was largely consistent with findings from previous studies (Templin et al 2011a). The study also observed a consistent temporal pattern in the Copper River stock composition of the commercial fishery harvests across the 5-year study. As the season progressed, the proportion of Chinook salmon from the *Upper Copper River* reporting group decreased, and the proportion of *Lower Copper River* Chinook salmon increased. The 2013–2017 study also observed unusually high proportions of nonlocal Chinook salmon in the commercial harvest in 2 of the study years (2014 and 2015), which aligned with other reports of large numbers of out-of-area Chinook salmon in commercial fisheries throughout the southern and southeastern seaboards of Alaska (Gilk-Baumer et al. 2017a, 2017b, 2017c). The results from that study supported the historical commercial management approach of providing inriver passage for all temporal components of the run.

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 2021; Botz et al.

2021). However, the number of fishing openers may be reduced to allow more fish to enter the river when salmon runs are weak. Waters near the mouth of the Copper River inside of the barrier islands, known as the "inside closure area", are closed by regulation for all but 1 fishing period during the first 2 weeks of the fishery. Beyond these first 2 weeks, the inside closure area may be closed to fishing, all or in part, to reduce the harvest of Chinook salmon (Figure 1). The extent to which these inside waters are closed is tied to the level of conservation concern, and, in recent years of small Chinook salmon runs, this has meant continued closure of these waters well into June. From 2012 to 2021, the total annual commercial harvests of Chinook salmon ranged from 6,105 to over 23,651 and averaged 12,577 salmon[1] (Figure 2). Commercial drift gillnet harvest in the Copper River District accounts for about 69.6% 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 42.8% (Botz et al. 2021). Run timing of Copper River Chinook salmon through the commercial fishery is relatively compressed; from 2012 through 2021, an average of 88.2% 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 amongst stocks was not demonstrated until the mid-2000s (Savereide 2005; Seeb et al. 2006; Templin et al. 2008). Understanding patterns of stock composition in the harvest is important for the management of sustainable fisheries on Copper River Chinook salmon and is necessary to estimate the exploitation and productivity of stocks.

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) because the project only tagged juveniles from 4 stocks and only 1 stock was tagged in all 3 years, resulting in very few recoveries in the fishery harvests. 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 a standardized set of 13 microsatellites surveyed across the range of the species so that the data from many baseline

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[1] Statewide electronic fish ticket database. Alaska Department of Fish and Game, Division of Commercial Fisheries. 1985 to present. (Accessed October 19, 2021). [URL not publicly available because some information is confidential.]

development projects could be combined—such as the comprehensive baseline already developed for stocks of interest under the Pacific Salmon Commission (Seeb et al. 2007) and for 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 range-wide 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 the previous MSA study (Gilk-Baumer et al. 2017a) 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 stand-alone reporting group (*Gulkana*) and the Mendeltna Creek population (a much smaller population) was merged with the *Lower Copper River* reporting group for the previous MSA study.

The project reported herein applied the current SNP genetic baseline representing Chinook salmon populations from within the Copper River drainage and from California to the Alaska Peninsula (Templin et al. 2011b; Figures 3 and 4) to estimate the relative stock compositions of Chinook salmon harvests in the Copper River District commercial fishery during the years 2018 to 2021. 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.

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.

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 or weight of salmon caught in a fishery.

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, 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 amongst 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. Although 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 2–4 weeks each year, beginning with statistical week 20 or 21. Sampling ended around mid-June each year; 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, with a minimum sample size goal of 100 fish per stratum. However, strata with sample sizes less than 100 fish were included in the analysis if they were temporally adjacent to other strata, providing some context to assume that estimates with low sample sizes were not outliers. 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). Point estimates based on sample sizes of 400, under worst-case conditions, 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 was not required for each stratum because (1) the fishery was not highly mixed (3 reporting groups dominate most mixtures); (2) the strata were designed to investigate patterns in stock composition within years (not stand-alone estimates); and (3) the annual estimates were 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 were expected to 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 for most years were based on samples close to, or in excess of, 400 fish.

Tissue samples for genetic analysis were collected concurrently with age, sex, and length (ASL) samples 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). There are typically 2 fishing periods per statistical week. ASL sample goals are set based on a weekly sampling window schedule for the first 3 statistical weeks of fishing (typically statistical weeks 20, 21, and 22). The ASL sample size goal for the first 3 statistical weeks of fishing was 200 individuals per week. For the 3 remaining statistical weeks (weeks 23–26), the sampling goal was to collect a total of 200 individuals. During sampling, an axillary process (the modified and elongated structure found at the anterior base of the pelvic fin; sampled in 2018) or piece of pelvic fin (sampled in 2019–2021) was excised from each fish and 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 some periods, tissues were collected from mixed tender loads and ASL data was not collected. In those cases, tissues were placed bulk in ethanol in a labeled 250 mL plastic bottle containing at least 95% denatured ethanol (with at least 1 bottle per fishery opening). 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 Gilk-Baumer et al. (2017a). Briefly, genomic DNA was extracted from individual tissue samples using 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 probable 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 4.1.0.[2] 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 most likely have poor quality DNA. The inclusion of individuals with poor quality DNA might introduce

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[2] R Core Team. 2021. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. Available from https://www.R-project.org/.

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 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
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; Fox 2014). The 3 reporting groups within the Copper River were originally identified using microsatellites by Seeb et al. (2009) and confirmed in the SNP baseline (Figures 3 and 4; Templin et al. 2011a). Outside the Copper River, 5 large-scale groups were identified for the remainder of the GOA and south (Figure 3).

Model

The stock compositions of Copper River fishery harvests were estimated using the *R* package *rubias* (Moran and Anderson 2019). The *rubias* package is a Bayesian approach to the conditional genetic stock identification model based upon computationally efficient C code implemented in *R*. 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).

rubias protocol

For each stratum, we ran a single Markov Chain Monte Carlo chain of 25,000 iterations and discarded the first 5,000 iterations (burn-in) to remove the influences of the initial start values. 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. 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. We used random starting values for each population in the chain, with starting values summing to 1 over all populations. The posterior distribution of 20,000 iterations was formed after removing the burn-in from the chain output. Stock proportion estimates and the 90% credibility intervals for each stratum were calculated by taking the mean and 5% and 95% quantiles of the posterior distribution from the posterior distribution.

Applying stock compositions to harvests

Stock-specific estimated harvest was calculated in the manner described by Dann et al. (2009). Briefly, mean harvest estimates, credibility intervals, and standard deviations for each stratum were calculated by multiplying the harvest from that stratum by the unrounded estimates of reporting group stock proportions. Stratum estimates were combined (rolled up) into annual estimates by weighting them by their respective harvests. Credibility intervals for annual stock-specific harvests were estimated by resampling 20,000 draws of the posterior output of stock proportions from each of the constituent stratum and multiplying the harvest by the drawn proportions.

RESULTS

TISSUE SAMPLING

Tissues suitable for genetic analysis were collected from 1,862 fish in the Copper River District commercial harvest from 14 fishing periods between 2018 and 2021 (Table 1, Appendix A1). With the exceptions of the test fish period in 2018, period 9 in 2019, period 1 in 2020, and period 2 in 2021, all periods targeted for sampling met the minimum sample size goal of 100 fish. However, period 9 from 2019 and period 1 from 2020 were considered to have sufficient sample size because they were temporally close to periods with sample sizes >100 fish (see *Fishery Sampling* methods). 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 2018, samples were collected from May 17 to June 25 from Chinook salmon harvested in the Copper River District drift gillnet fishery and landed in Cordova. Tissues samples were successfully genotyped from 178 Chinook salmon during 1 of 2 fishing periods targeted for sampling (Table 1). No fish were sampled from periods 2 and 3 (May 21–28), the fishery was closed during statistical weeks 23–27, and too few fish were sampled (*n* = 40) from the test fish period occurring on June 25 (harvest of 40). Because of this, only period 1 had sufficient sample size to generate stock-composition estimates.

In 2019, 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 (Table 1). Tissues samples were successfully genotyped from 743 Chinook salmon during 5 of 5 fishing periods targeted for sampling. Sufficient sample sizes were collected to generate stock-composition estimates for all 5 periods targeted for sampling.

In 2020, samples were collected from May 14 to May 26 from Chinook salmon harvested in the Copper River District drift gillnet fishery and landed in Cordova (Table 1). Tissues samples were successfully genotyped from 452 Chinook salmon during 3 of 3 fishing periods targeted for sampling. Sufficient sample sizes were collected to generate stock-composition estimates for all 3 periods targeted for sampling.

In 2021, samples were collected from May 17 to June 15 from Chinook salmon harvested in the Copper River District drift gillnet fishery and landed in Cordova (Table 1). Tissues samples were successfully genotyped from 424 Chinook salmon during 3 of 4 fishing periods targeted for sampling. Too few fish were sampled (*n* = 25) from fishing period 2 occurring on May 21 (harvest of 1,303). Sufficient sample sizes were collected to generate stock-composition estimates for 3 periods targeted for sampling.

LABORATORY ANALYSIS

Assaying Genotypes

A total of 1,862 fish were selected for genotyping from 14 strata, 12 of which had enough samples to analyze, representing harvests across the 4 years of this project (Table 1, Appendix A1).

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 7,632 genotypes compared between these analyses. Most discrepancies were between homozygote and heterozygote genotypes (0.3%), but some discrepancies between alternate homozygotes were observed (0.1%). Assuming all errors are equally likely to have occurred in the production and QC genotyping process, error rate for both error types was 0.2%. This level of error was well below the standard set by the laboratory as acceptable (1.0%).

STATISTICAL ANALYSIS

Data Retrieval and Genotype Quality Control

Of the 1,862 fish genotyped, 111 were excluded from analysis because they were missing genotypes for more than 20% of loci, and 9 were excluded because they appeared to represent duplicate individuals (Appendix A1). In addition, the 65 fish that were successfully genotyped from the 2 strata with insufficient sample sizes were excluded from analyses. In total, 1,677 fish were used to produce stock-composition estimates for 12 strata (Table 1). Average sample size of strata after excluding individuals was 140 fish with a minimum of 89 fish and a maximum of 200 fish.

Stock Composition and Stock-Specific Harvest Estimates

2018

In 2018, adequate genetic samples were collected from a single fishing period where 39% of the commercial harvest of Chinook salmon in the Copper River District occurred (2,989 of 7,703 harvested fish; Table 1). This fishing period was near the start of the Chinook salmon fishery and not necessarily representative of harvest through the historical peak and tail of the harvest timing curve. During this fishing period, 91.0% of the fish in this harvest came from the Copper River drainage and represented 2,720 fish (Table 3, Appendix B1). Fish originating from the *Upper Copper River* reporting group contributed to more than half (50.5%) of the commercial harvest, followed by fish from the *Gulkana* (27.4%) and *Lower Copper River* (13.1%) reporting groups (Table 3, Figures 5 and 6, Appendix B1). Of the 8.9% of harvests sampled attributable to nonlocal stocks, the majority originated from the *British Columbia* reporting group (4.8%; 145 fish).

There was no discernable harvest attributable to the *Northwest Gulf of Alaska*, *Northeast Gulf of Alaska*, *Coastal Southeast Alaska*, *British Columbia*, and *West Coast U.S.* reporting groups for the single fishing period analyzed (period 1; Table 3).

2019

In 2019, adequate genetic samples were collected from fishing periods where 46.4% of the commercial harvest of Chinook salmon in the Copper River District occurred (9,220 of 19,888 fish harvested; Table 1). Sampling did not occur during the first week of June when harvest historically remains high following the previous week's peak harvest timing (Figure 7). During the sampled periods, 80.3% of the fish in these harvests came from the Copper River drainage and represented 7,397 fish (Table 3). Fish originating from the *Upper Copper River* contributed the largest proportion of the commercial harvest (28.0%), followed by fish from the *Lower Copper River* (27.6%) and *Gulkana River* (24.7%) reporting groups (Table 3). Of the 19.7% of harvests sampled attributable to nonlocal stocks, the largest component originated from the *British Columbia* reporting group (8.1%), followed by all other reporting groups (≤5.0% each).

Over the 5 fishing periods analyzed (periods 1, 3, 5, 8, and 9), the proportions of *Upper Copper River* fish declined during each successive fishing period (range: 60.6% to <1.0%) that was mirrored by generally increasing proportions of *Lower Copper River* fish (range: 3.3–68.0%; Figures 5 and 7, Appendix B2). The proportion of *Gulkana* fish was low in period 1 (14.1%), increased and stayed relatively constant for fishing periods 3 (36.0%) and 5 (36.7%), then decreased in periods 8 (18.0%) and period 9 (9.2%). The proportion of *British Columbia* fluctuated and was highest in periods 1 (13.8%) and 5 (11.3%). The proportion of all other reporting groups was low across the season with no discernable harvest attributable to the *Coastal Southeast Alaska* reporting group (Table 3).

2020

In 2020, adequate genetic samples were collected from fishing periods where 81.9% of the commercial harvest of Chinook salmon in the Copper River District occurred (5,003 of 6,105 fish harvested; Table 1). Sampling occurred from the beginning of the Copper River Chinook salmon run through peak commercial harvest timing, but the latter half of the historical harvest timing curve was not sampled (Figure 8). During this time period, 74.5% of the fish in these harvests came from the Copper River drainage and represented 3,730 fish (Table 3). Fish originating from the *Gulkana River* reporting group contributed the largest proportion of the commercial harvest

(31.4%), followed by fish from the *Upper Copper River* (27.2%) and *Lower Copper River* (15.9%) reporting groups (Table 3). Of the 25.4% of sampled harvests attributable to nonlocal stocks, the largest contributor was the *British Columbia* reporting group (11.1%), followed by *West Coast U.S.* (6.9%), *Coastal Southeast Alaska* (6.2%), and all other reporting groups (≤1.0% each).

Over the 3 consecutive fishing periods analyzed (periods 1–3), the proportions of *Upper Copper River* fish demonstrated a declining trend across the season (range: 43.2–20.3%) that was mirrored by generally increasing proportions of *Lower Copper River* fish (range: 11.3–27.5%; Figures 5 and 8, Appendix B3). The proportion of *Gulkana* fish was largest in fishing period 1 (37.6%), decreased in period 2 (24.1%), then increased in period 3 (33.7%). The proportions of *British Columbia, Coastal Southeast Alaska,* and *West Coast U.S.* fish were low in period 1 (≤5.0% each), unusually large in period 2 (12.5%, 22.0%, and 10.5%), and then decreased in period 3 (4.8%, 7.6%, and 5.0%). There was no discernable harvest attributable to the *Northwest Gulf of Alaska* and *Northeast Gulf of Alaska* reporting groups (Table 3).

2021

In 2021, adequate genetic samples were collected from fishing periods where 61.7% of the commercial harvest of Chinook salmon in the Copper River District occurred (4,807 of 7,790 fish harvested; Table 1). Sampling occurred from the beginning of the Copper River Chinook salmon run into peak commercial harvest timing, but 3 consecutive weeks following peak harvest timing were not sampled (Figure 9). During this time period, only 57.0% of the fish in these harvests came from the Copper River drainage and represented 2,738 fish (Table 3). Fish originating from the *Gulkana* reporting group contributed the largest proportion of the commercial harvest (31.2%), followed by fish from the *Upper Copper River* (16.7%) and *Lower Copper River* (9.1%) reporting groups (Table 3). Of the 43.1% of harvests sampled attributable to nonlocal stocks, the majority originated from the *British Columbia* reporting group (20.7%), followed by *West Coast U.S.* (8.0%), *Coastal Southeast Alaska* (6.0%), and all other reporting groups (≤5.0% each).

Over the 3 fishing periods analyzed (periods 1, 3, and 5), the proportions of *Upper Copper River* fish demonstrated a declining trend across the season (range: 24.3% to <1.0%) that was mirrored by increasing proportions of *Lower Copper River* fish (range: 1.3–32.1%; Figures 5 and 9, Appendix B4). The proportion of *Gulkana* fish was largest in periods 1 (31.7%) and 3 (35.9%), then decreased in period 5 (6.0%). The proportion of *British Columbia* fish was unusually high in all 3 periods and increased over the season (range: 18.9–23.3%). The proportion of Coastal Southeast Alaska fish was highest in period 1, then declined over the periods analyzed (range: 7.9–3.1%). There was no discernable harvest attributable to the *Northwest Gulf of Alaska* and *Northeast Gulf of Alaska* reporting groups (Table 3).

DISCUSSION

Genetic MSA was successfully used to provide precise stock-specific estimates of the composition of the Chinook salmon commercial drift gillnet fishery harvests in the Copper River District across multiple years (2018–2021). 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), (2) not all fishing periods were sampled, and (3) prolonged fishery closures in 3 of 4 years resulted in extended time periods without samples. The unsampled fishing periods and fishery closures resulted in portions of the Copper River Chinook salmon run not being represented in the MSA. Additionally, specific comparisons between analyses using the most recent baseline (Gilk-Baumer et al. 2017a; this report) versus the original study for years 2005–2008 (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 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, 2018–2021, representing 38.8% (2018), 46.4% (2019), 81.9% (2020), and 61.7% (2021) 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 10 and 11). These results are generally consistent with the 2005–2008 (Templin et al. 2011a) and 2013–2017 (Gilk-Baumer et al. 2017a) results (Figure 10).

Stocks originating from the Copper River consistently dominated the sampled harvest across all years and temporal strata, except for period 5 in 2021 (Figures 6–9, Appendices B1–B4). The highest annual non-Copper River contributions from the 13 years of available data occurred in 2021, when 43.1% of the sampled harvests were attributable to nonlocal stocks (Figure 10). However, high non-Copper River contributions were also observed in 2014 and 2015, when 30.0% and 36.3% of the sampled harvests were attributable to nonlocal stocks (Gilk-Baumer et al. 2017a). The *British Columbia* reporting group contributed 12% in 2014, 16% in 2015, and 20.7% in 2021; and the *West Coast U.S.* reporting group contributed 10% in 2014, 16% in 2015, and 8% in 2021 (Table 3). These large contributions of southern-origin stocks were also observed in Southeast Alaska troll and sport fisheries during the same years (Gilk-Baumer et al. 2017b, 2017c, 2017d; Shedd et al. 2021a, 2021b, 2022) and in Chinook salmon bycatch in the GOA trawl fisheries in 2014 and 2015 (Guthrie et al. 2016, 2017). The stock composition of the GOA trawl fisheries Chinook salmon bycatch continued to be dominated by southern-origin stocks in 2016–2019 (Guthrie et al. 2018, 2019, 2020, 2021), and although estimates from 2020 and 2021 were unavailable to confirm, it's likely that this pattern continued into 2021. The 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. 2017b, 2017c, 2017d; CTC 2022). However, this was not the case for the trend observed in 2021 because most British Columbia and Pacific Northwest stocks had declined in productivity. The higher contributions of non-Copper River stocks in 2021 was most likely attributed to a combination of Lower Copper River Chinook salmon abundance in 2021 (Figure 2) and onshore distribution of nonlocal stocks feeding on abundant forage fish.

The composition of stocks in the periods sampled varied throughout the years of this study. *Upper Copper River* group made up the largest contribution in 2018 and 2019 and was the second largest contributor in 2020 and 2021 (range: 16.7–50.5%; Table 3). *Gulkana* was the second largest contributor in 2018, the third largest contributor in 2019, and the largest contributor in 2020 and 2021 (range: 24.7–31.4%). *Lower Copper River* was the second largest contributor in 2019, the third largest contributor in 2018 and 2020, and fourth largest contributor in 2021 (range: 9.1–27.6%). The contribution from the *NW Gulf of Alaska* reporting group was low in all 4 years (<4%) with almost no discernable contribution in 2020 (<1%; Table 3, Figure 11). The contribution from the *NE Gulf of Alaska* reporting group was low in 2018–2020 (<4%), with almost no discernable contribution in 2020 (<1%) and was 5.3% in 2021. The contribution from the *Coastal SEAK* reporting group was low in 2018 and 2019 (<2%) with almost no discernable contribution in 2019 (<1%), then increased in 2020 by 6.2%, and 6.0% in 2021. The low contributions from the *Coastal Southeast Alaska* reporting group are consistent with the decline in productively of these stocks over the last decade (CTC 2022).

TRENDS IN RUN TIMING

Due to the proximity of the Copper River District fishery to the mouth of the Copper River, fishery harvest patterns have historically been used to infer the run timing of Copper River Chinook salmon. In general, about 90% of the commercial harvest and inferred run through the district occurs between mid-May and mid-June (Botz and Somerville 2021). The fishery is typically prosecuted on a semi-weekly basis (2 regular fishing periods per week), and samples collected from these regular fishing periods are thought to be representative of stocks as they pass though the district. Sampling goals for this study were set at 200 samples per week for the first 3 weeks of the fishery and 200 samples total for the remaining 3 weeks of the fishery. These goals were thought to be sufficient to represent the majority of the Chinook salmon run because they give greater weight the early part of the run (generally statistical weeks 20–22), when most of the harvest occurs, and less weight to the later portion of the run (generally statistical weeks 23–25), when harvests are low.

However, during most years of this study, prolonged fishery closures, other sampling priorities, or low harvest reduced the number of samples that could be collected for each sample window. Consequently, sampling goals were not met in some statistical weeks and samples collected for this study may not be representative of the run. Peak periods of abundance for individual stock groups are probably underrepresented in some years due to unsampled statistical weeks, causing overall reporting group proportions reported here (Table 3) to be divergent from the overall run. For example, in 2018, a historically low sockeye salmon run prompted extensive fishery closures, and sufficient samples were only collected to represent the first statistical week (week 20; Table 1). Unsampled Chinook salmon harvest in the second and third statistical weeks of the fishery represented 61.2% of the total harvest and ended up being a significant sampling gap in a year with limited fishery openings. In 2019, a two-fishing-period-per-week commercial fishing schedule was implemented throughout the Chinook salmon run, yet 53.6% of the harvest was unsampled. One unsampled statistical week (week 23) near peak run timing in the commercial fishery represented 25.4% of the total harvest. In 2020, the Chinook salmon run was one of the weakest on record, and sufficient samples were collected to represent the first 3 statistical weeks (weeks 20–22); no samples were collected from the last 3 weeks of the fishery due to low fishery harvests. In 2021, sufficient samples were collected to represent statistical weeks 21, 22, and 25; however, no samples were collected to represent the third week of the fishery (week 24) due to low harvest. Due to the unsampled portions of the run each year, the overall stock-composition estimates from this study may not be good indicators of annual stock-specific run strength and should only be used to describe the commercial harvest in which sampling occurred.

Although information was not available throughout the season for some years of this study, a consistent temporal trend appeared in the composition of the commercial fishery harvests. The proportion of *Upper Copper River* Chinook salmon was largest in the beginning of each fishing season, except for 2021, 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; Gilk-Baumer et al. 2017a).

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

PRESENCE OF NONLOCAL STOCKS

Although annual Copper River District commercial Chinook salmon harvest is predominately of Copper River origin, outside stocks were present at variable contributions 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 2021, where 43% of the commercial harvest sampled originated from nonlocal stocks. However, the only fishing period from that year where Chinook salmon, originating from stocks across the Pacific Northwest and British Columbia, outnumbered Copper River stocks was in period 5 of 2021, where nonlocal stocks made up 61.6% of the 443 fish harvested. This fishing period was late in the Copper River run when local stock abundance was expected to be low, resulting in a relatively small harvest of nonlocal stocks making up a large proportion of the harvest. Harvest proportions 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 outside the barrier islands where migratory fish are more likely to be present. It is assumed that most nonlocal Chinook salmon are foraging during migration. Furthermore, the abundance of foraging fish nearshore in the Copper River District probably plays a significant role in the proportion of nonlocal Chinook salmon present in the harvest.

CONCLUSIONS

1. This study provides 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 (2018–2021).
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 a historical commercial management approach of providing inriver passage for all the temporal components of the run.
4. Over all years, most of the harvest in the Copper River commercial fishery originated from populations in the Copper River.

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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, 2018–2021.

Year	Stat. week	Period[a]	Date(s)	Harvest[f]	Sample date(s)	Genotyped	Used
2018	20	1[b]	5/17	2,989	5/17–18	178	176
	21–22	2–3[b]	5/21–28	4,598	Not sampled	–	–
	26	TF[c]	6/25	40	6/26	40[g]	–
	28–37	4–16	7/9–9/11	76	Not sampled	–	–
			Total	7,703		178	176
2019	20	1[b]	5/16	2,585	5/16	127	121
	21	2[b]	5/20	1,842	Not sampled	–	–
		3[b]	5/23–24	2,569	5/24	201	196
	22	4[b]	5/27–28	2,247	Not sampled	–	–
		5[b]	5/30–31	1,761	5/31	210	200
	23	6–7[d]	6/3–8	5,056	Not sampled	–	–
	24	8[d]	6/10–11	1,476	6/12	110	107
		9	6/13–14	829	6/14	95	89
	25–36	10–29	6/17–9/3	1,523	Not sampled	–	–
			Total	19,888		743	713
2020	20	1[b]	5/14	1,659	5/14–15	93	93
	21	2[b]	5/18	1,875	5/18–19	156	139
	22	3	5/25	1,469	5/25–26	203	191
	23–38	4–14[e]	6/1–9/15	1,102	Not sampled	–	–
			Total	6,105		452	423
2021	21	1[b]	5/17	2,232	5/17–18	167	138
		2[b]	5/20	1,303	5/21	25[g]	–
	22	3[b]	5/24	2,132	5/24–25	138	122
	24	4[b]	6/9	607	Not sampled	–	–
	25	5[b]	6/14	443	6/15	119	105
	26–37	6–26[e]	6/17–9/7	1,073	Not sampled	–	–
			Total	7,790		424	365

Note: En dash (–) = no data available.

[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 (Figure 1) described in 5 AAC 24.350(1)(B) were closed for all or a portion of the fishing period.

[c] This was not a normal fishing period; a single test fish boat was allowed to harvest on 6/25/2018.

[d] Waters of the inside closure area (Figure 1) described in 5 AAC 24.350(1)(B) was expanded and in effect for the fishing period.

[e] Waters of the inside closure area (Figure 1) described in 5 AAC 24.350(1)(B) was expanded and in effect for the 6/1/20, and 6/18/20 fishing periods and for fishing periods 6/17/21–7/2/21.

[f] Harvest numbers from: Statewide electronic fish ticket database. Alaska Department of Fish and Game, Division of Commercial Fisheries. 1985 to present. (Accessed October 19, 2021). [URL not publicly available because some information is confidential.]

[g] Genotyped, but not used for stock-composition estimates; these are excluded from the totals.

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]
7,632	4 (0.1%)	23 (0.3%)	27 (0.4%)	0.2%

[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.–Estimates of stock-specific harvest and stock compostion (%), including standard deviation (SD) and 90% credibility intervals (CRI) calculated using a stratified estimator (Gilk-Baumer et al. 2017a) for combined temporal strata and based on genetic analysis of mixtures of Chinook salmon harvested in the Copper River District, 2013–2021.

		Stock-specific harvest				Stock composition			
				90% CRI				90% CRI	
Year	Reporting group	Mean	SD	5%	95%	Mean	SD	5%	95%
2013	NW Gulf of AK	473	47	400	552	10.9%	1.1%	9.2%	12.7%
	Upper Copper	1,029	82	895	1,165	23.7%	1.9%	20.6%	26.9%
	Gulkana	922	91	774	1,075	21.3%	2.1%	17.8%	24.8%
	Lower Copper	1,531	85	1,395	1,676	35.3%	2.0%	32.2%	38.6%
	NE Gulf of AK	35	52	0	155	0.8%	1.2%	0.0%	3.6%
	Coastal SEAK	102	29	55	150	2.3%	0.7%	1.3%	3.5%
	British Columbia	176	33	125	235	4.1%	0.8%	2.9%	5.4%
	West Coast U.S.	68	18	41	101	1.6%	0.4%	1.0%	2.3%
	Sampled harvest	4,337							
	Unsampled harvest	4,489							
	Total harvest	8,826							
2014	NW Gulf of AK	435	60	340	539	4.7%	0.6%	3.6%	5.8%
	Upper Copper	925	105	758	1,104	9.9%	1.1%	8.1%	11.8%
	Gulkana	2,993	142	2,759	3,228	32.0%	1.5%	29.5%	34.5%
	Lower Copper	2,651	134	2,434	2,874	28.3%	1.4%	26.0%	30.7%
	NE Gulf of AK	102	71	5	235	1.1%	0.8%	0.1%	2.5%
	Coastal SEAK	150	51	72	237	1.6%	0.5%	0.8%	2.5%
	British Columbia	1,138	92	989	1,291	12.2%	1.0%	10.6%	13.8%
	West Coast U.S.	970	76	847	1,098	10.4%	0.8%	9.1%	11.7%
	Sampled harvest	9,363							
	Unsampled harvest	844							
	Total harvest	10,207							
2015	NW Gulf of AK	528	97	380	697	2.7%	0.5%	2.0%	3.6%
	Upper Copper	1,504	154	1,258	1,764	7.8%	0.8%	6.5%	9.1%
	Gulkana	4,069	250	3,660	4,482	21.0%	1.3%	18.9%	23.2%
	Lower Copper	6,756	241	6,363	7,157	34.9%	1.2%	32.9%	37.0%
	NE Gulf of AK	33	60	0	165	0.2%	0.3%	0.0%	0.9%
	Coastal SEAK	381	101	225	556	2.0%	0.5%	1.2%	2.9%
	British Columbia	3,072	195	2,757	3,398	15.9%	1.0%	14.2%	17.6%
	West Coast U.S.	3,003	183	2,707	3,308	15.5%	0.9%	14.0%	17.1%
	Sampled harvest	19,346							
	Unsampled harvest	3,160							
	Total harvest	22,506							

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		Stock-specific harvest				Stock composition			
				90% CRI				90% CRI	
Year	Reporting group	Mean	SD	5%	95%	Mean	SD	5%	95%
2016	NW Gulf of AK	268	45	201	346	2.6%	0.4%	2.0%	3.4%
	Upper Copper	1,976	135	1,758	2,203	19.4%	1.3%	17.3%	21.6%
	Gulkana	3,461	186	3,157	3,767	34.0%	1.8%	31.0%	37.0%
	Lower Copper	3,345	166	3,077	3,624	32.9%	1.6%	30.2%	35.6%
	NE Gulf of AK	12	32	0	80	0.1%	0.3%	0.0%	0.8%
	Coastal SEAK	26	33	0	96	0.3%	0.3%	0.0%	0.9%
	British Columbia	667	79	543	801	6.6%	0.8%	5.3%	7.9%
	West Coast U.S.	426	59	335	527	4.2%	0.6%	3.3%	5.2%
	Sampled harvest	10,182							
	Unsampled harvest	2,166							
	Total harvest	12,348							
2017	NW Gulf of AK	313	64	215	425	2.4%	0.5%	1.7%	3.3%
	Upper Copper	2,673	169	2,398	2,953	20.9%	1.3%	18.8%	23.1%
	Gulkana	4,327	215	3,976	4,684	33.9%	1.7%	31.1%	36.6%
	Lower Copper	4,824	195	4,505	5,147	37.7%	1.5%	35.3%	40.3%
	NE Gulf of AK	20	36	0	82	0.2%	0.3%	0.0%	0.6%
	Coastal SEAK	58	26	22	107	0.5%	0.2%	0.2%	0.8%
	British Columbia	460	67	356	575	3.6%	0.5%	2.8%	4.5%
	West Coast U.S.	105	34	55	167	0.8%	0.3%	0.4%	1.3%
	Sampled harvest	12,780							
	Unsampled harvest	1,054							
	Total harvest	13,834							
2018	NW Gulf of AK	41	30	3	99	1.4%	1.0%	0.1%	3.3%
	Upper Copper	1,508	128	1,308	1,720	50.5%	4.3%	43.8%	57.6%
	Gulkana	820	132	606	1,039	27.4%	4.4%	20.3%	34.8%
	Lower Copper	392	102	242	570	13.1%	3.4%	8.1%	19.1%
	NE Gulf of AK	19	43	0	111	0.6%	1.4%	0.0%	3.7%
	Coastal SEAK	43	41	0	117	1.4%	1.4%	0.0%	3.9%
	British Columbia	145	58	65	253	4.8%	2.0%	2.2%	8.5%
	West Coast U.S.	22	22	1	65	0.7%	0.7%	0.0%	2.2%
	Sampled harvest	2,989							
	Unsampled harvest	4,714							
	Total harvest	7,703							

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		Stock-specific harvest				Stock composition			
				90% CRI				90% CRI	
Year	Reporting group	Mean	SD	5%	95%	Mean	SD	5%	95%
2019	NW Gulf of AK	298	61	204	402	3.2%	0.7%	2.2%	4.4%
	Upper Copper	2,580	176	2,291	2,864	28.0%	1.9%	24.8%	31.1%
	Gulkana	2,276	192	1,970	2,603	24.7%	2.1%	21.4%	28.2%
	Lower Copper	2,542	152	2,298	2,793	27.6%	1.7%	24.9%	30.3%
	NE Gulf of AK	353	142	131	606	3.8%	1.5%	1.4%	6.6%
	Coastal SEAK	47	33	5	108	0.5%	0.4%	0.1%	1.2%
	British Columbia	748	110	573	940	8.1%	1.2%	6.2%	10.2%
	West Coast U.S.	377	83	253	522	4.1%	0.9%	2.7%	5.7%
	Sampled harvest	9,220							
	Unsampled harvest	10,668							
	Total harvest	19,888							
2020	NW Gulf of AK	16	22	0	59	0.3%	0.4%	0.0%	1.2%
	Upper Copper	1,362	132	1,145	1,579	27.2%	2.6%	22.9%	31.6%
	Gulkana	1,571	152	1,321	1,821	31.4%	3.0%	26.4%	36.4%
	Lower Copper	797	119	612	1,008	15.9%	2.4%	12.2%	20.1%
	NE Gulf of AK	46	49	0	139	0.9%	1.0%	0.0%	2.8%
	Coastal SEAK	312	73	195	433	6.2%	1.5%	3.9%	8.6%
	British Columbia	555	86	420	706	11.1%	1.7%	8.4%	14.1%
	West Coast U.S.	345	69	238	461	6.9%	1.4%	4.7%	9.2%
	Sampled harvest	5,003							
	Unsampled harvest	1,102							
	Total harvest	6,105							
2021	NW Gulf of AK	151	43	93	229	3.1%	0.9%	1.9%	4.8%
	Upper Copper	804	123	613	1,014	16.7%	2.5%	12.8%	21.1%
	Gulkana	1,499	166	1,231	1,773	31.2%	3.5%	25.6%	36.9%
	Lower Copper	436	111	281	641	9.1%	2.3%	5.8%	13.3%
	NE Gulf of AK	254	99	90	424	5.3%	2.1%	1.9%	8.8%
	Coastal SEAK	286	79	167	421	6.0%	1.7%	3.5%	8.8%
	British Columbia	994	121	802	1,196	20.7%	2.5%	16.7%	24.9%
	West Coast U.S.	384	72	270	509	8.0%	1.5%	5.6%	10.6%
	Sampled harvest	4,807							
	Unsampled harvest	2,983							
	Total harvest	7,790							

Note: unsampled harvest includes harvest from periods where samples were collected but were not used to produce stock-composition estimates.

Note: estimates for 2013–2017 were originally reported in (Gilk-Baumer et al. 2017a).

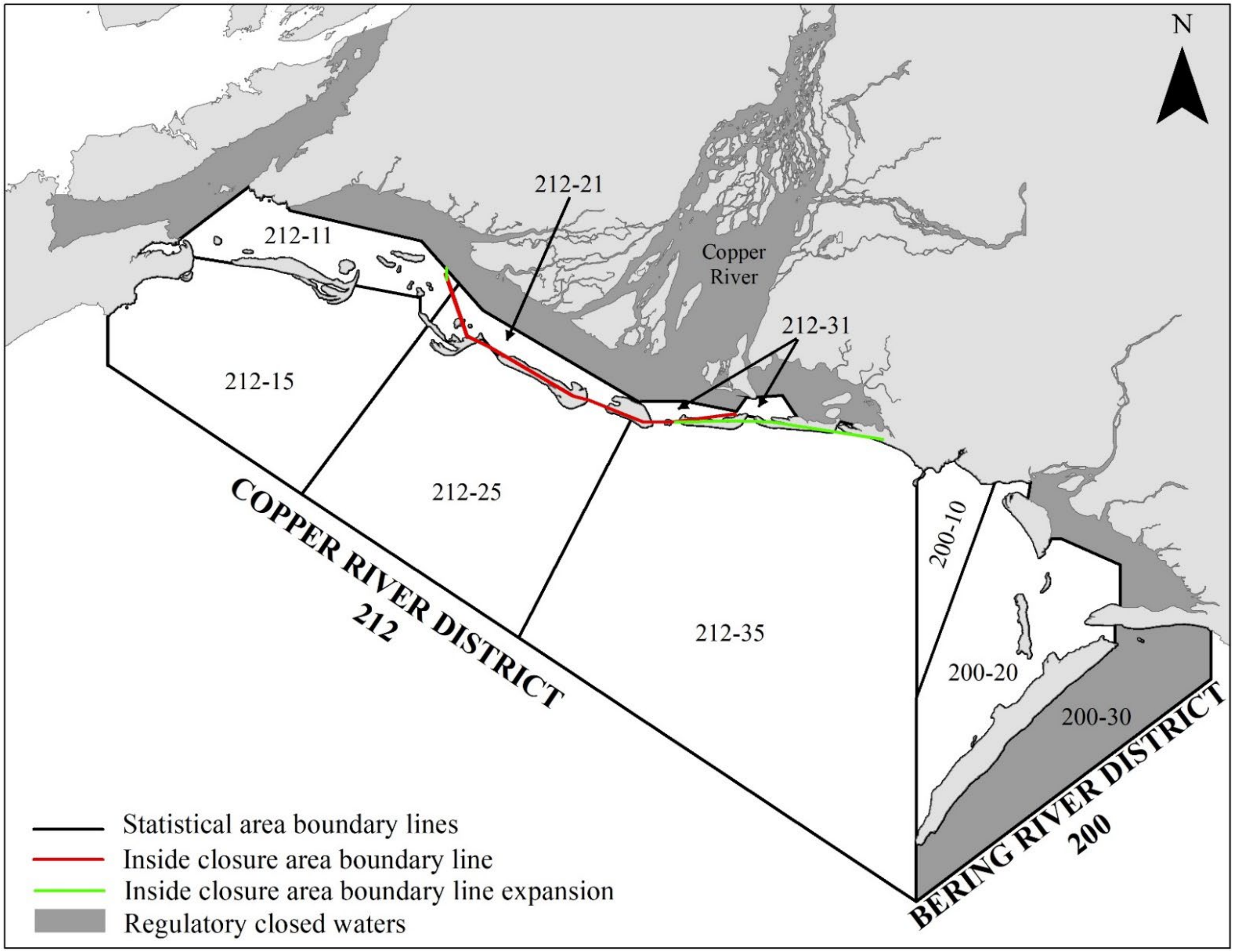

Figure 1.–Map depicting the commercial salmon fishery districts and statistical areas of the Copper River District management area.

Note: the inside closure area includes all waters north of the red boundary line and the inside closure area expansion includes all waters north of the red and green lines.

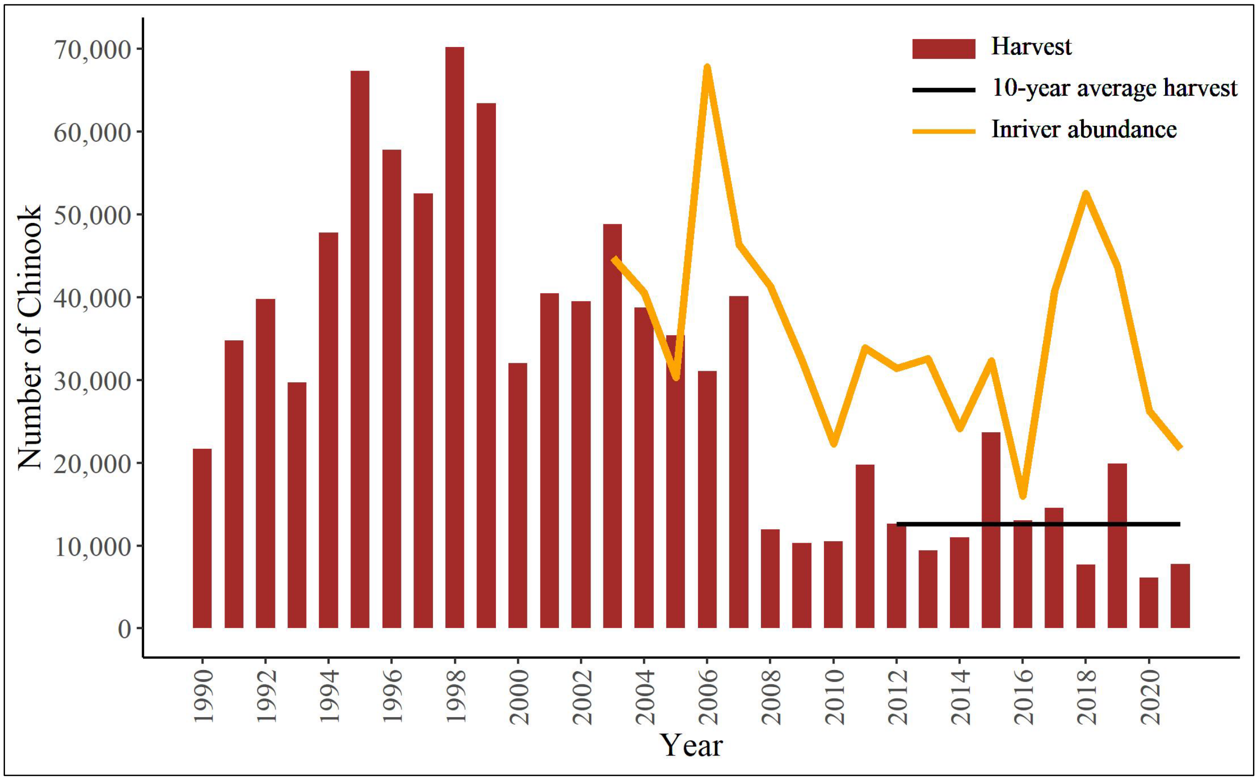

Figure 2.–Chinook salmon harvest in the Copper River District management area commercial fisheries by year, recent 10-year average harvest, and annual inriver abundance estimates, 1990–2021.

Note: Harvest numbers from: Statewide electronic fish ticket database. Alaska Department of Fish and Game, Division of Commercial Fisheries. 1985 to present. (Accessed October 19, 2021). [URL not publicly available as some information is confidential.]

Note: Annual abundance estimates are from Piche et al. (2022)

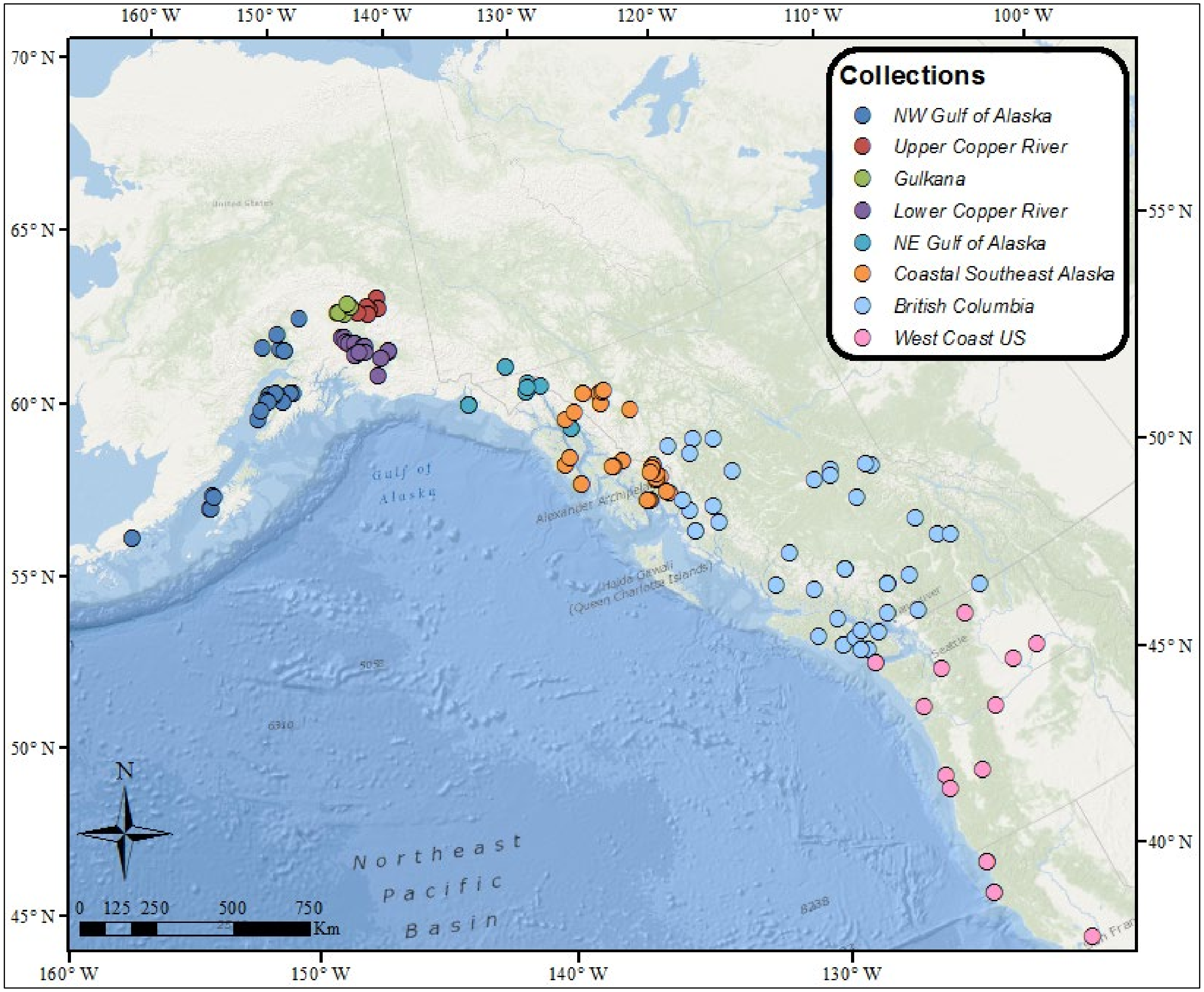

Figure 3.–The location and reporting group affiliation of 211 collections of Chinook salmon included in the coastwide genetic baseline grouped as 118 populations for genetic mixed stock analysis of commercial harvest of Chinook salmon in the Copper River District, 2018–2021.

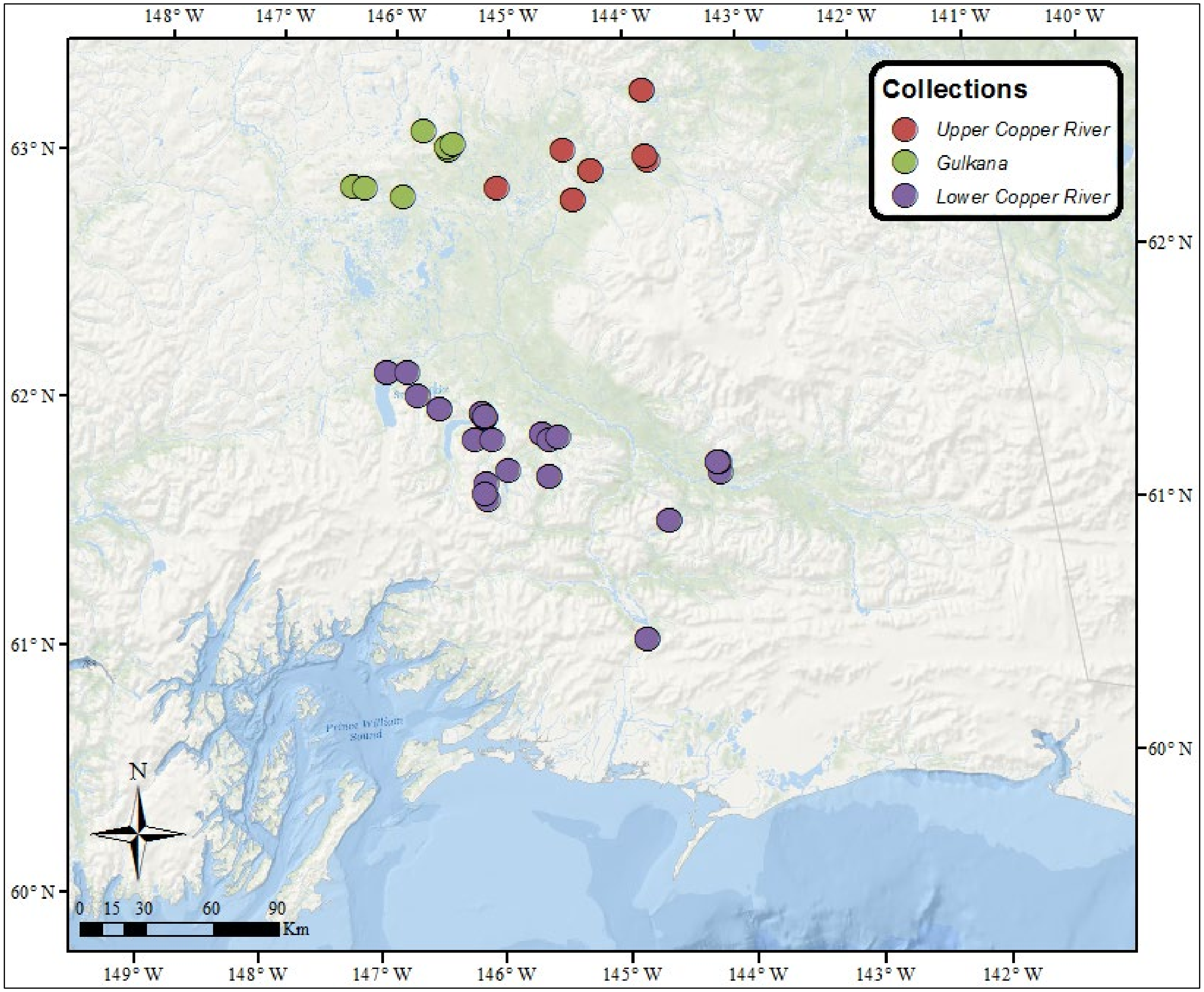

Figure 4.–The location and reporting group affiliation of 50 collections of Copper River Chinook salmon in the baseline grouped as 17 populations for genetic mixed stock analysis of commercial harvest of Chinook salmon in the Copper River District, 2018–2021 (Table 3).

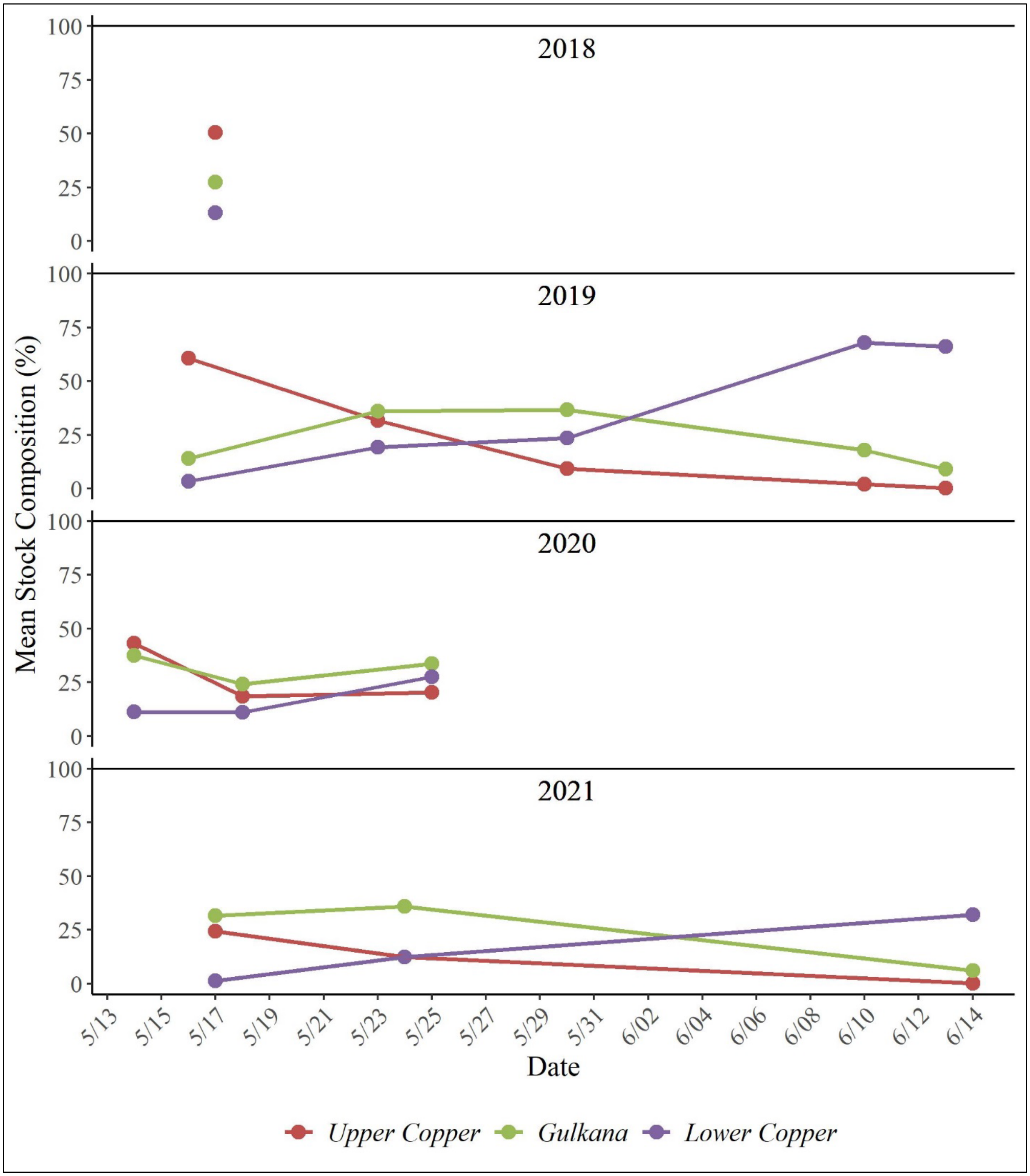

Figure 5.–Run timing of Copper River origin Chinook salmon harvested in the Copper River District Chinook salmon fishery by date, 2018–2021.

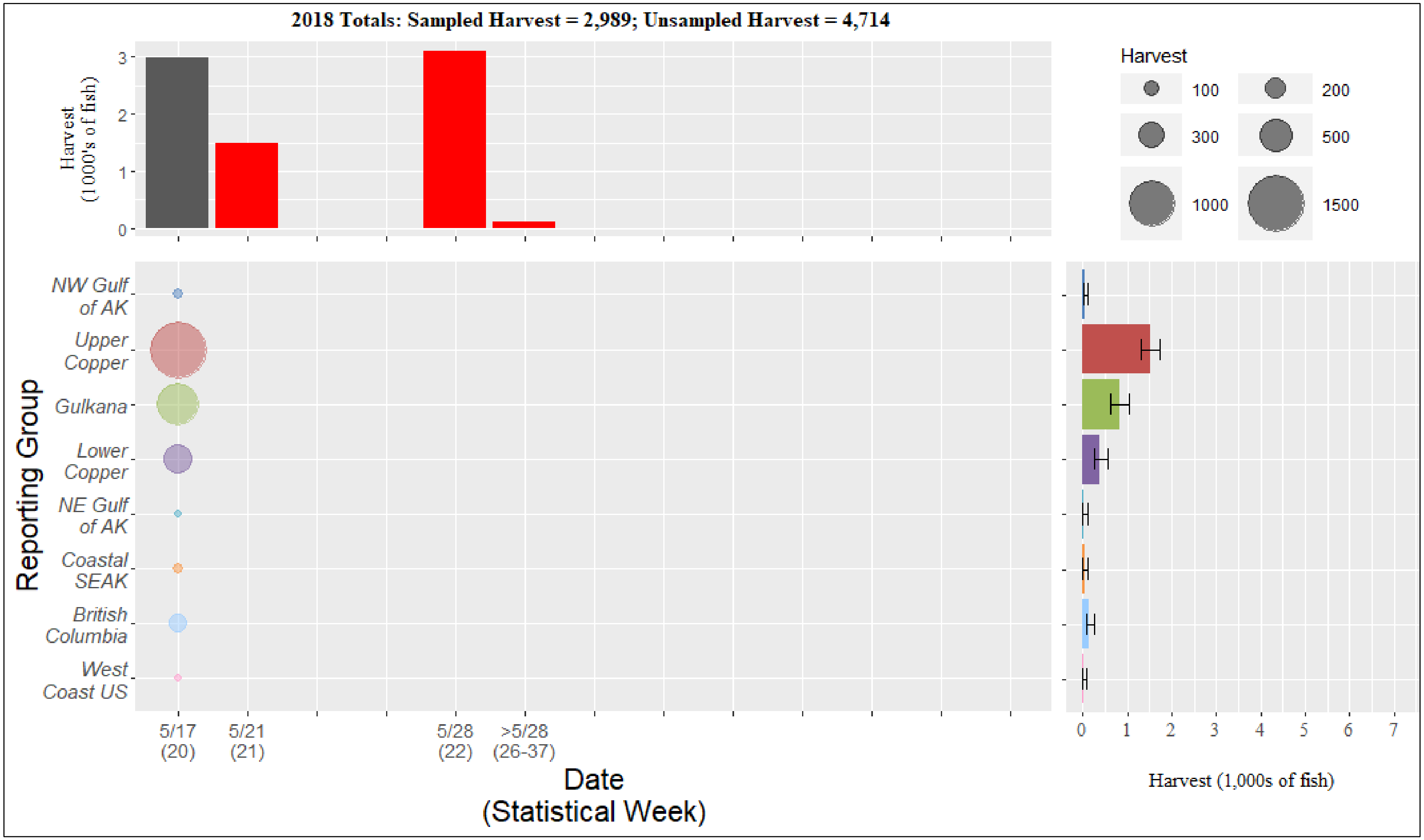

Figure 6.–Stock-specific harvest of Chinook salmon commercial harvest in the Copper River District by date, 2018.

Note: 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.

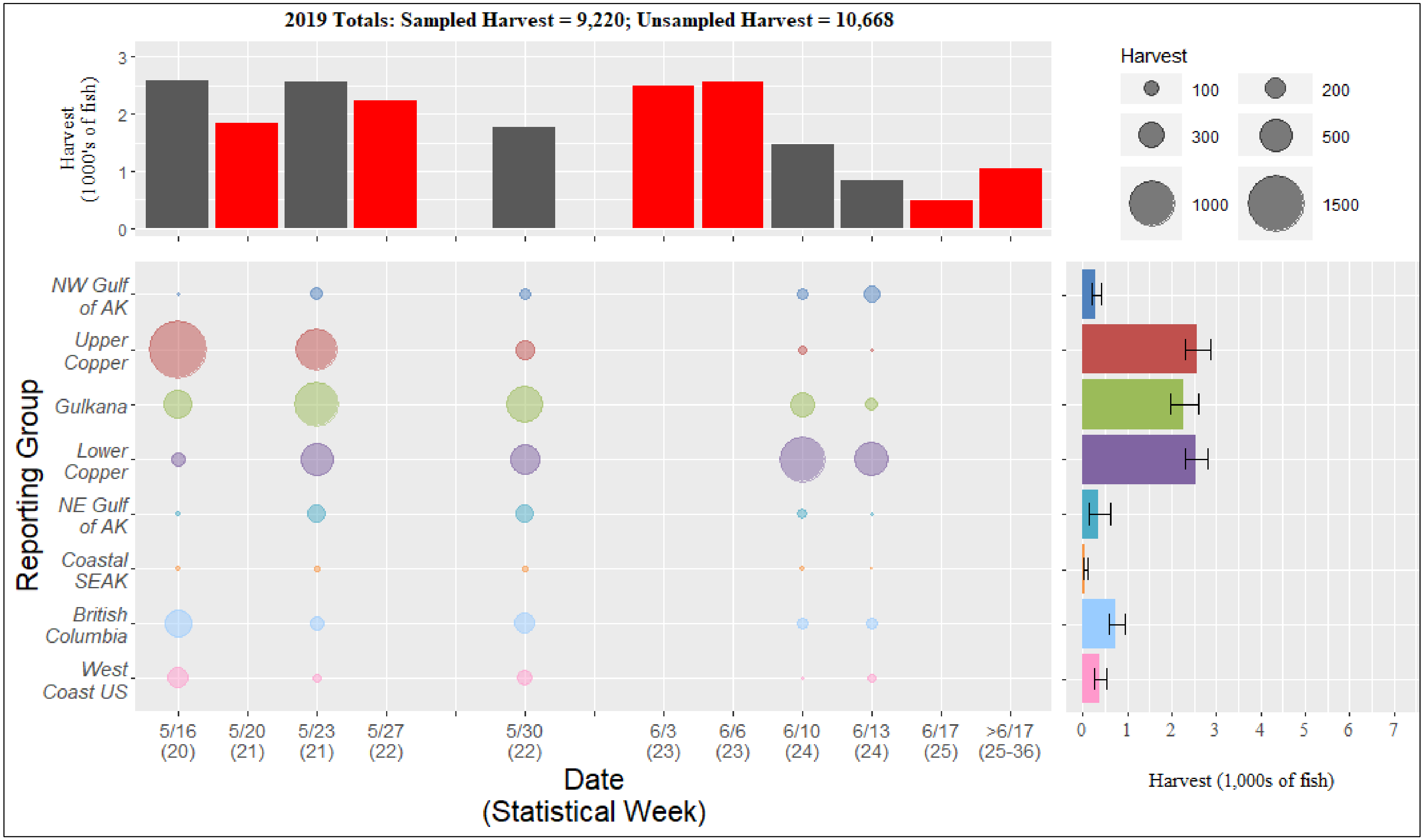

Figure 7.–Stock-specific harvest of Chinook salmon commercial harvest in the Copper River District by date, 2019.

Note: 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.

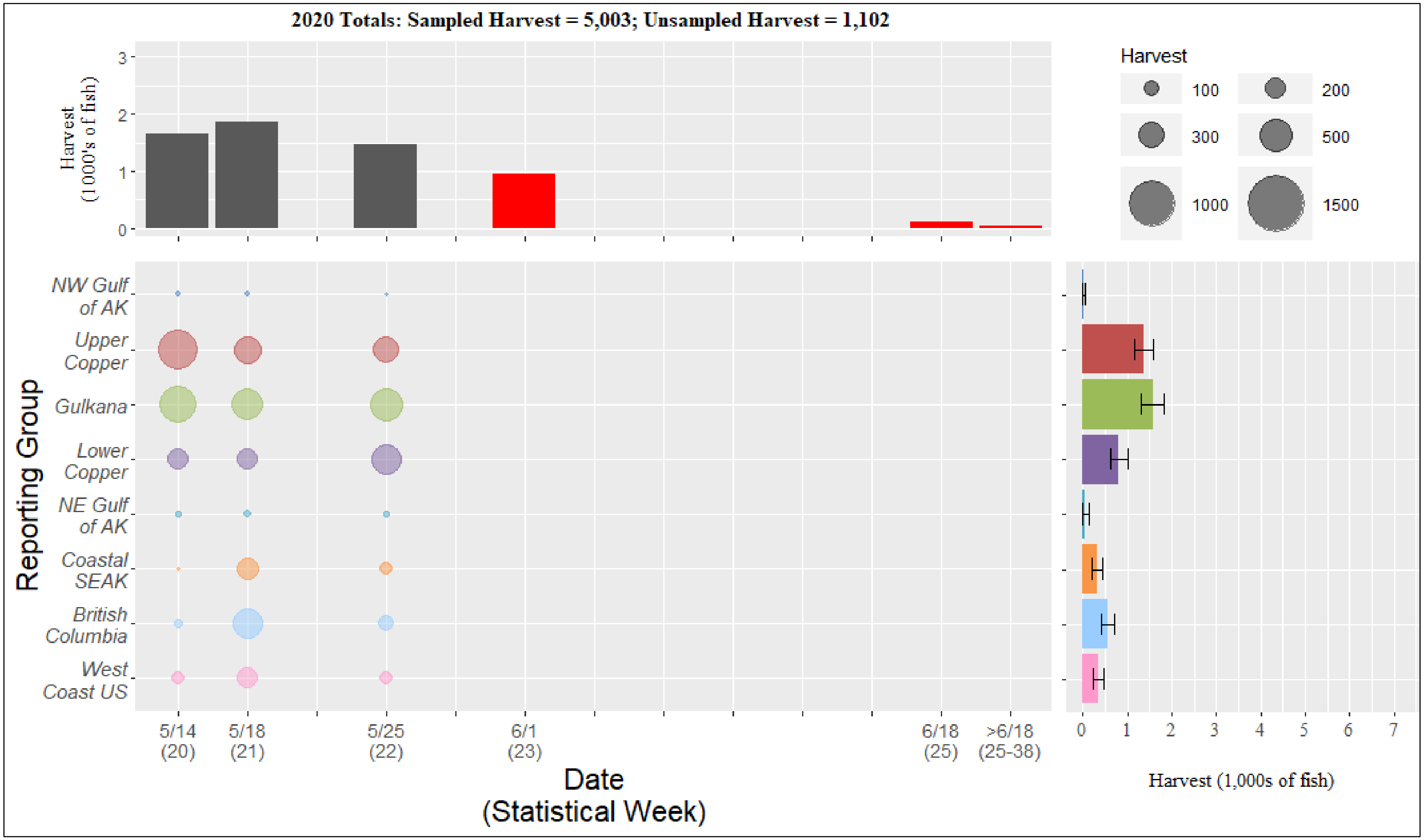

Figure 8.–Stock-specific harvest of Chinook salmon commercial harvest in the Copper River District by date, 2020.

Note: 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.

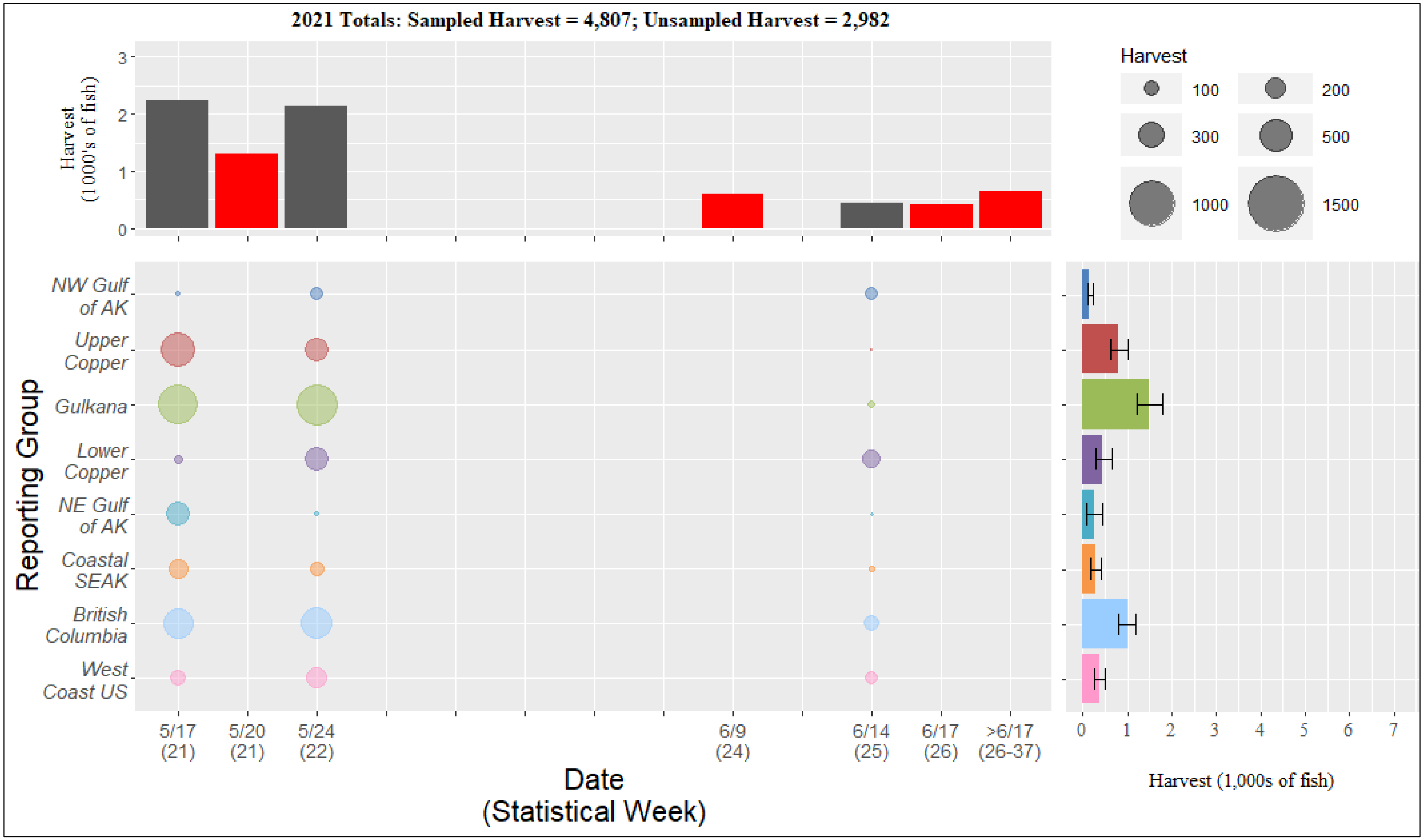

Figure 9.–Stock-specific harvest of Chinook salmon commercial harvest in the Copper River District by date, 2021.

Note: 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.

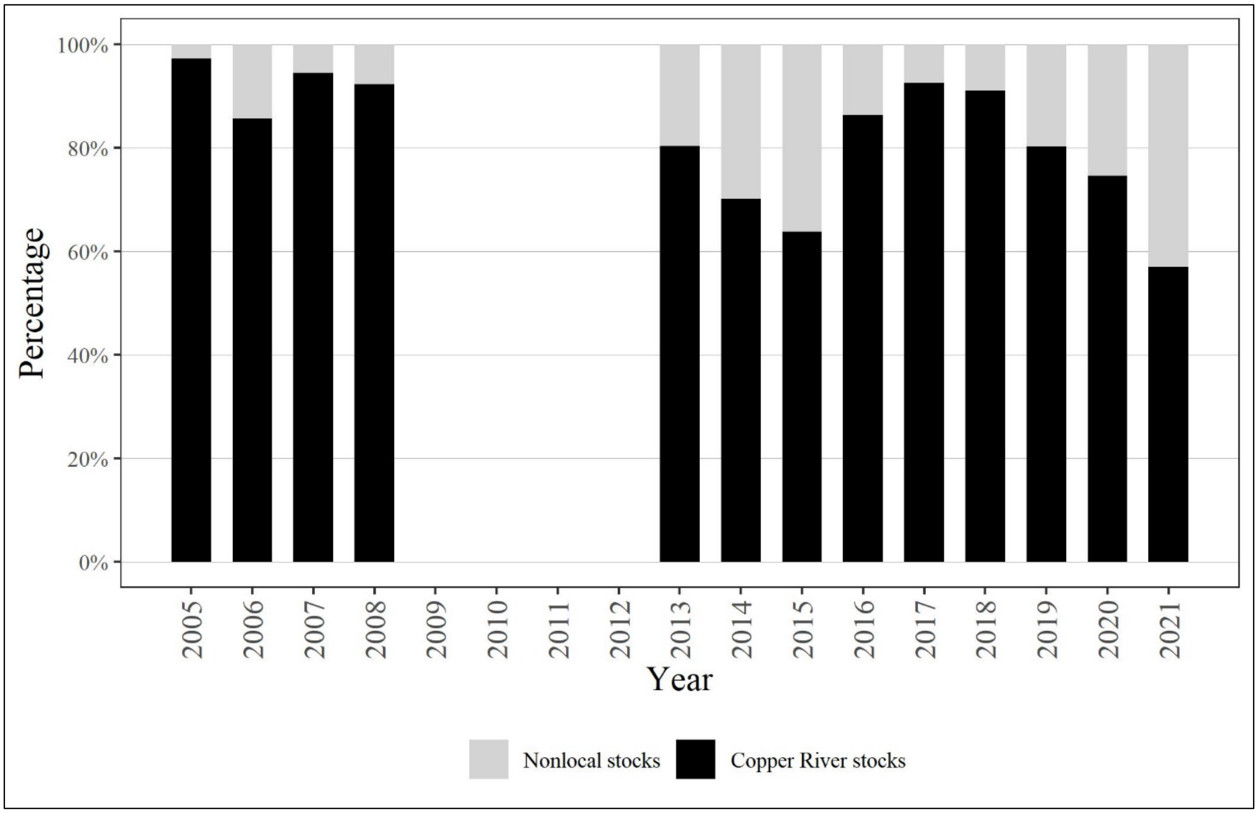

Figure 10.–Proportion of Copper River origin Chinook salmon sampled from the commercial harvest from the Copper River District, 2005–2021.

Notes: Genetic samples were not collected from the Copper River District Chinook salmon harvest in 2009–2012.

Note: 2005–2008 estimates from Templin et al. (2011a); 2013–2017 estimates from Gilk-Baumer et al. (2017a).

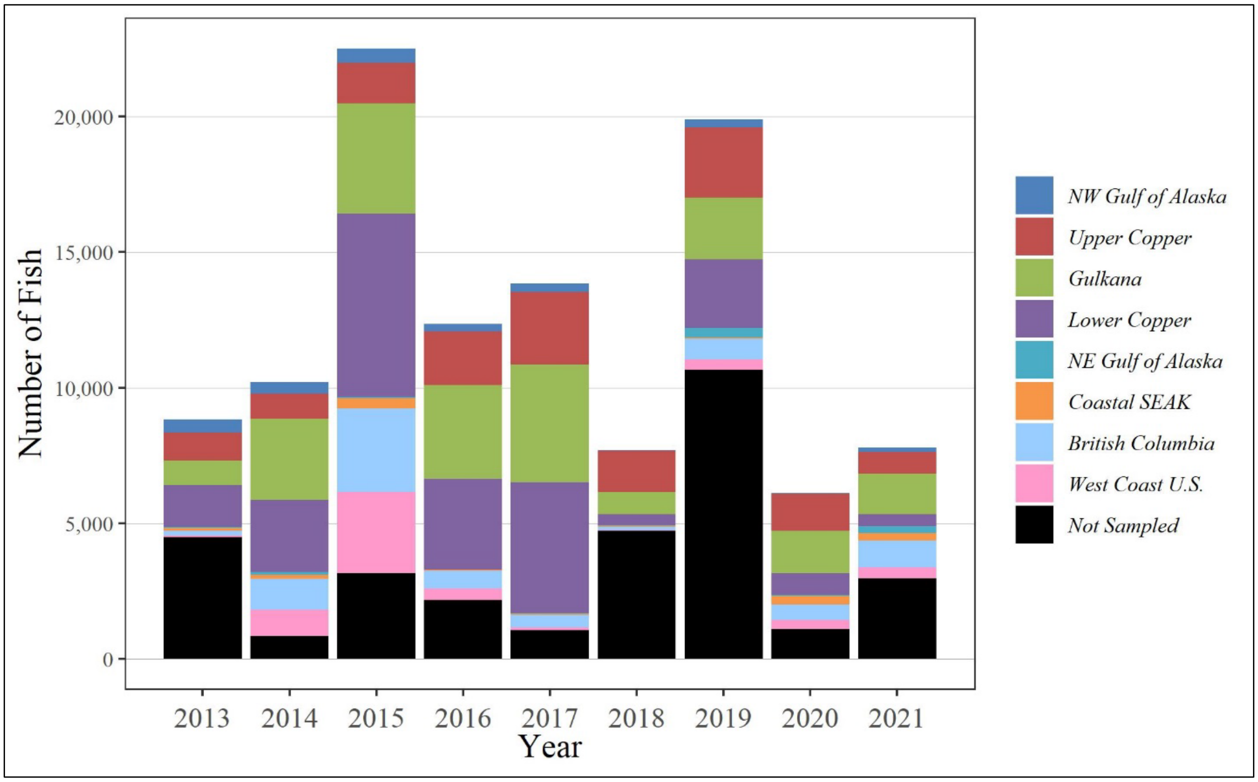

Figure 11.–Stock-specific harvest estimates in the Copper River District Chinook salmon fishery calculated using a stratified estimator for all weeks within years, 2013–2021.

Note: 2013–2017 estimates from Gilk-Baumer et al. (2017a)

APPENDIX A: QUALITY CONTROL RESULTS

Appendix A1.–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 2018–2021.

	Number of fish				
		Fish removed			
Year	Genotyped	Missing loci	Duplicate	Unanalyzed strata (insufficient samples)	Final
2018	218	1	1	40	176
2019	743	29	1		713
2020	452	28	1		423
2021	449	53	6	25	365
Total	1,862	111	9	65	1,677

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 size (< 89 fish), and the final number statistically analyzed are provided.

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

Appendix B1.–Estimates of stock-specific harvest and stock composition (%) for the Copper River District commercial fishery for each period, 2018.

Period 1 (5/17)	Stock-specific harvest (C = 2,989)				Stock composition (n = 176)			
			90% CRI				90% CRI	
Reporting group	Mean	SD	5%	95%	Mean	SD	5%	95%
NW Gulf of AK	41	30	3	99	1.4%	1.0%	0.1%	3.3%
Upper Copper	1,508	128	1,308	1,720	50.5%	4.3%	43.8%	57.6%
Gulkana	820	132	606	1,039	27.4%	4.4%	20.3%	34.8%
Lower Copper	392	102	242	570	13.1%	3.4%	8.1%	19.1%
NE Gulf of AK	19	43	0	111	0.6%	1.4%	0.0%	3.7%
Coastal SEAK	43	41	0	117	1.4%	1.4%	0.0%	3.9%
British Columbia	145	58	65	253	4.8%	2.0%	2.2%	8.5%
West Coast U.S.	22	22	1	65	0.7%	0.7%	0.0%	2.2%

Period 2–16 (5/21–9/11)	Unsampled harvest (C = 4,714)	Stock composition (n = 0)

Note: Estimates include mean, standard deviation (SD), and 90% credibility interval (CRI).

Note: n = successfully analyzed sample size and C = catch.

Appendix B2.–Estimates of stock composition (%) and stock-specific harvest for the Copper River District commercial fishery for each period, 2019.

Period 1 (5/16)	Stock-specific harvest (C = 2,585)				Stock composition (n = 121)			
			90% CI				90% CI	
Reporting group	Mean	SD	5%	95%	Mean	SD	5%	95%
NW Gulf of AK	4	11	0	24	0.2%	0.4%	0.0%	0.9%
Upper Copper	1,567	132	1,342	1,786	60.6%	5.1%	51.9%	69.1%
Gulkana	364	104	209	551	14.1%	4.0%	8.1%	21.3%
Lower Copper	85	49	23	178	3.3%	1.9%	0.9%	6.9%
NE Gulf of AK	7	21	0	34	0.3%	0.8%	0.0%	1.3%
Coastal SEAK	7	16	0	39	0.3%	0.6%	0.0%	1.5%
British Columbia	357	89	222	519	13.8%	3.4%	8.6%	20.1%
West Coast U.S.	194	70	90	319	7.5%	2.7%	3.5%	12.3%

Period 2 (5/20)	Unsampled harvest (C = 1,842)	Stock composition (n = 0)

Period 3 (5/23–5/24)	Stock-specific harvest (C = 2,569)				Stock composition (n = 196)			
NW Gulf of AK	65	33	22	128	2.5%	1.3%	0.9%	5.0%
Upper Copper	815	100	657	983	31.7%	3.9%	25.6%	38.3%
Gulkana	924	121	727	1,126	36.0%	4.7%	28.3%	43.8%
Lower Copper	492	85	358	645	19.2%	3.3%	13.9%	25.1%
NE Gulf of AK	151	111	0	339	5.9%	4.3%	0.0%	13.2%
Coastal SEAK	12	18	0	49	0.5%	0.7%	0.0%	1.9%
British Columbia	82	34	34	144	3.2%	1.3%	1.3%	5.6%
West Coast U.S.	29	20	5	70	1.1%	0.8%	0.2%	2.7%

Period 4 (5/27–28)	Unsampled harvest (C = 2,247)	Stock composition (n = 0)

Period 5 (5/30–5/31)	Stock-specific harvest (C = 1,761)				Stock composition (n = 200)			
NW Gulf of AK	60	27	23	108	3.4%	1.5%	1.3%	6.2%
Upper Copper	165	46	97	242	9.4%	2.6%	5.5%	13.8%
Gulkana	646	72	530	766	36.7%	4.1%	30.1%	43.5%
Lower Copper	414	63	310	518	23.5%	3.6%	17.6%	29.4%
NE Gulf of AK	144	59	54	249	8.2%	3.4%	3.1%	14.1%
Coastal SEAK	18	19	0	56	1.0%	1.1%	0.0%	3.2%
British Columbia	200	44	131	274	11.3%	2.5%	7.4%	15.5%
West Coast U.S.	114	33	64	174	6.5%	1.9%	3.6%	9.9%

Period 6–7 (6/3–6/8)	Unsampled harvest (C = 5,056)	Stock composition (n = 0)

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Period 8 (6/10–6/11)	Stock-specific harvest (C = 1,476)				Stock composition (n = 107)			
			90% CRI				90% CRI	
Reporting group	Mean	SD	5%	95%	Mean	SD	5%	95%
NW Gulf of AK	53	29	15	107	3.6%	2.0%	1.0%	7.3%
Upper Copper	31	33	0	97	2.1%	2.2%	0.0%	6.6%
Gulkana	265	71	154	386	18.0%	4.8%	10.4%	26.2%
Lower Copper	1,004	83	860	1,136	68.0%	5.6%	58.3%	77.0%
NE Gulf of AK	49	69	0	197	3.3%	4.7%	0.0%	13.3%
Coastal SEAK	9	13	0	36	0.6%	0.9%	0.0%	2.4%
British Columbia	59	30	17	113	4.0%	2.0%	1.1%	7.7%
West Coast U.S.	5	13	0	31	0.4%	0.9%	0.0%	2.1%

Period 9 (6/13–6/14)	Stock-specific harvest (C = 829)				Stock composition (n = 89)			
NW Gulf of AK	116	34	64	177	14.0%	4.2%	7.7%	21.4%
Upper Copper	2	6	0	14	0.3%	0.8%	0.0%	1.7%
Gulkana	76	35	23	139	9.2%	4.2%	2.8%	16.8%
Lower Copper	547	46	468	620	66.0%	5.5%	56.5%	74.8%
NE Gulf of AK	2	7	0	13	0.3%	0.8%	0.0%	1.5%
Coastal SEAK	1	3	0	6	0.1%	0.4%	0.0%	0.8%
British Columbia	50	21	20	88	6.0%	2.5%	2.4%	10.7%
West Coast U.S.	34	18	11	68	4.1%	2.2%	1.3%	8.2%

Period 10–29 (6/17–9/3)	Unsampled harvest (C = 1,523)	Stock composition (n = 0)

Note: Estimates include mean, standard deviation (SD), and 90% credibility interval (CRI).

Note: n = successfully analyzed sample size and C = catch.

Appendix B3.–Estimates of stock-specific harvest and stock composition (%) for the Copper River District commercial fishery for each period, 2020.

Period 1 (5/14)	Stock-specific harvest (C = 1,659)				Stock composition (n = 93)			
			90% CRI				90% CRI	
Reporting Group	Mean	SD	5%	95%	Mean	SD	5%	95%
NW Gulf of AK	7	16	0	40	0.4%	1.0%	0.0%	2.4%
Upper Copper	716	97	550	874	43.2%	5.9%	33.2%	52.7%
Gulkana	623	108	449	808	37.6%	6.5%	27.1%	48.7%
Lower Copper	187	85	65	343	11.3%	5.2%	3.9%	20.7%
NE Gulf of AK	13	32	0	70	0.8%	1.9%	0.0%	4.2%
Coastal SEAK	3	8	0	16	0.2%	0.5%	0.0%	1.0%
British Columbia	31	26	2	82	1.9%	1.5%	0.1%	5.0%
West Coast U.S.	78	37	27	145	4.7%	2.2%	1.6%	8.7%

Period 2 (5/18)	Stock-specific harvest (C = 1,875)				Stock composition (n = 139)			
NW Gulf of AK	6	13	0	35	0.3%	0.7%	0.0%	1.8%
Upper Copper	349	74	234	477	18.6%	3.9%	12.5%	25.4%
Gulkana	452	86	319	597	24.1%	4.6%	17.0%	31.8%
Lower Copper	206	61	118	314	11.0%	3.2%	6.3%	16.8%
NE Gulf of AK	18	28	0	79	1.0%	1.5%	0.0%	4.2%
Coastal SEAK	235	67	127	349	12.5%	3.6%	6.8%	18.6%
British Columbia	413	77	292	546	22.0%	4.1%	15.6%	29.1%
West Coast U.S.	196	52	117	287	10.5%	2.8%	6.2%	15.3%

Period 3 (5/25)	Stock-specific harvest (C = 1,469)				Stock composition (n = 191)			
NW Gulf of AK	2	6	0	14	0.2%	0.4%	0.0%	0.9%
Upper Copper	298	47	222	375	20.3%	3.2%	15.1%	25.5%
Gulkana	496	59	401	597	33.7%	4.0%	27.3%	40.6%
Lower Copper	404	57	311	497	27.5%	3.9%	21.2%	33.8%
NE Gulf of AK	14	21	0	59	1.0%	1.5%	0.0%	4.0%
Coastal SEAK	74	26	36	119	5.0%	1.8%	2.5%	8.1%
British Columbia	111	31	67	167	7.6%	2.1%	4.6%	11.4%
West Coast U.S.	70	25	35	116	4.8%	1.7%	2.4%	7.9%

Period 4–14 (6/1–9/15)	Unsampled harvest (C = 1,102)	Stock composition (n = 0)

Note: Estimates include mean, standard deviation (SD), and 90% credibility interval (CRI).

Note: n = successfully analyzed sample size and C = catch.

Appendix B4.–Estimates of stock-specific harvest and stock composition (%) for the Copper River District commercial fishery for each period, 2021.

Period 1 (5/17)	Stock-specific harvest (C = 2,232)				Stock composition (n = 138)			
			90% CRI				90% CRI	
Reporting group	Mean	SD	5%	95%	Mean	SD	5%	95%
NW Gulf of AK	7	14	0	38	0.3%	0.6%	0.0%	1.7%
Upper Copper	542	97	388	708	24.3%	4.4%	17.4%	31.7%
Gulkana	707	112	524	896	31.7%	5.0%	23.5%	40.1%
Lower Copper	29	56	0	153	1.3%	2.5%	0.0%	6.8%
NE Gulf of AK	241	97	82	397	10.8%	4.3%	3.7%	17.8%
Coastal SEAK	177	57	93	280	7.9%	2.6%	4.2%	12.6%
British Columbia	422	78	293	559	18.9%	3.5%	13.1%	25.1%
West Coast U.S.	107	41	48	180	4.8%	1.8%	2.2%	8.0%

Period 2 (5/20)	Unsampled harvest (C = 1,303)	Stock composition (n = 0)

Period 3 (5/24)	Stock-specific harvest (C = 2,132)				Stock composition (n = 122)			
NW Gulf of AK	69	36	21	134	3.2%	1.7%	1.0%	6.3%
Upper Copper	261	78	144	398	12.3%	3.7%	6.7%	18.7%
Gulkana	765	121	572	964	35.9%	5.7%	26.8%	45.2%
Lower Copper	264	96	131	440	12.4%	4.5%	6.2%	20.6%
NE Gulf of AK	8	19	0	44	0.4%	0.9%	0.0%	2.0%
Coastal SEAK	96	56	23	205	4.5%	2.6%	1.1%	9.6%
British Columbia	469	88	325	620	22.0%	4.1%	15.2%	29.1%
West Coast U.S.	200	57	113	302	9.4%	2.7%	5.3%	14.2%

Period 4 (6/9)	Unsampled harvest (C = 607)	Stock composition (n = 0)

Period 5 (6/14)	Stock-specific harvest (C = 443)				Stock composition (n = 105)			
NW Gulf of AK	76	17	49	105	17.0%	3.9%	11.0%	23.6%
Upper Copper	1	2	0	5	0.2%	0.5%	0.0%	1.2%
Gulkana	26	13	8	50	6.0%	2.9%	1.8%	11.3%
Lower Copper	142	21	110	179	32.1%	4.8%	24.8%	40.3%
NE Gulf of AK	4	7	0	20	0.9%	1.7%	0.0%	4.6%
Coastal SEAK	14	9	3	31	3.1%	2.0%	0.6%	7.1%
British Columbia	103	20	71	136	23.3%	4.5%	16.1%	30.8%
West Coast U.S.	77	18	49	106	17.3%	4.0%	11.0%	24.0%

Period 6–26 (6/17–9/7)	Unsampled harvest (C = 1,073)	Stock composition (n = 0)

Note: Estimates include mean, standard deviation (SD), and 90% credibility interval (CRI).

Note: n = successfully analyzed sample size and C = catch.