Fishery Data Series No. 13-64

Seasonal Stock Contributions of the Inriver Run and Sport Harvest for Tributary and Mainstem Spawning Chinook Salmon in the Kenai River, Alaska

by

Timothy R. McKinley

Andrew W. Barclay

and

Jim Jasper

December 2013

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

Symbols and Abbreviations

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

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 DATA SERIES NO. 13-64

SEASONAL STOCK CONTRIBUTIONS OF THE INRIVER RUN AND SPORT HARVEST FOR TRIBUTARY AND MAINSTEM SPAWNING CHINOOK SALMON IN THE KENAI RIVER, ALASKA

by

Timothy R. McKinley
Alaska Department of Fish and Game, Division of Sport Fish, Soldotna,

Andrew W. Barclay
Alaska Department of Fish and Game, Division of Commercial Fisheries, Anchorage

and

Jim Jasper
Alaska Department of Fish and Game, Division of Commercial Fisheries, Anchorage

Alaska Department of Fish and Game
Division of Sport Fish, Research and Technical Services
333 Raspberry Road, Anchorage, Alaska, 99518-1565

December 2013

This investigation was partially financed by the Federal Aid in Sport Fish Restoration Act (16 U.S.C. 777-777K) under Project F-10-19, Job No. S-2-5a, the Pacific Coastal Salmon Recovery Fund/Southeast Sustainable Salmon Fund (NOAA Grant # NA04NMF4380162), and the Alaska Sustainable Salmon Fund.

ADF&G Fishery Data Series was established in 1987 for the publication of Division of Sport Fish technically oriented results for a single project or group of closely related projects, and in 2004 became a joint divisional series with the Division of Commercial Fisheries. Fishery Data Series reports are intended for fishery and other technical professionals and are available through the Alaska State Library and on the Internet: http://www.adfg.alaska.gov/sf/publications/. This publication has undergone editorial and peer review.

Timothy R. McKinley,
Alaska Department of Fish and Game, Division of Sport Fish,
43961 Kalifornsky Beach Rd. Soldotna, AK, 99669-8276, USA

Andrew W. Barclay,
Alaska Department of Fish and Game, Division of Commercial Fisheries,
333 Raspberry Rd. Anchorage, AK 99518-1599, USA

and

Jim Jasper
Alaska Department of Fish and Game, Division of Commercial Fisheries,
333 Raspberry Rd. Anchorage, AK, 99518-1599, USA

This document should be cited as:
McKinley, T. R., A. W. Barclay, and J. Jasper. 2013. Seasonal stock contributions of the inriver run and sport harvest for tributary and mainstem spawning Chinook salmon in the Kenai River, Alaska. Alaska Department of Fish and Game, Fishery Data Series No. 13-64, Anchorage.

TABLE OF CONTENTS

Page

LIST OF TABLES

LIST OF FIGURES

LIST OF FIGURES (Continued)

Figure **Page**

LIST OF APPENDICES

ABSTRACT

The goal of this project was to describe the stock composition over the fishing season of the inriver run and sport harvest for Kenai River Chinook salmon by 3 different reporting groups (Lower Tributary, Upper Tributary, and Mainstem) using mixed stock analysis (MSA). Mixture samples from the inriver run were collected during 2003–2013 via an existing netting program as the salmon passed river mile 8.5 in the lower Kenai River; samples from the sport fishery were collected from creel (2006–2013) and roving (2007–2010) sample surveys. MSA results from the inriver run show that Upper Tributary fish were a small but protracted component of the run. Lower Tributary fish accounted for nearly all of the run prior to mid-June, but were near zero after the first week of July. Mainstem fish were not a significant component of the run until mid-June, and comprised nearly all of the run by the first week in July. MSA results from the sport harvest below the Soldotna Bridge demonstrate that prior to 1 July, the majority of the harvest in all stratified time periods in all years (2006–2013) was generally of Lower Tributary fish, but after 1 July, Lower Tributary fish were less than 20% of the harvest. Upper Tributary fish were under 20% of the harvest in all strata prior to 1 July and less than 15% in all strata after 1 July. The Mainstem component of the harvest became 50% or greater within the last June stratum prior to 1 July, and accounted for 75% or more of the harvest in all July strata for all years. MSA results from samples collected above the Soldotna Bridge show that prior to 1 July, the majority of the harvest in all strata in all years (2007–2010) was generally of Lower Tributary fish. In all years, the proportion of Lower Tributary fish peaked in the first stratum and declined in succeeding strata. Mainstem fish and Upper Tributary fish were 25% or less of the harvest in any of the strata prior to 1 July. From 1 July until the end of the season, Lower Tributary fish accounted for 25–50% of the harvest during 1–7 July and less than 25% in all strata after that in all years (2006–2013). Mainstem fish accounted for approximately 35–65% of the harvest during 1–7 July and 70% or greater during later strata. Fish sealed by the Alaska Department of Fish and Game as trophy fish (Chinook salmon 55 inches total length or greater) were primarily from the Mainstem reporting group. These results will be useful in generating estimates of escapement of tributary- and mainstem-bound Chinook salmon, escapement goal analyses for these stocks, as well as estimating harvest in mixed-stock fisheries outside of the Kenai River drainage.

Key words: Chinook salmon, *Oncorhynchus tshawytscha*, Kenai River, spawning abundance, age composition, escapement goal, run reconstruction, spawner–recruit analysis, maximum sustained yield, measurement error, serial correlation, missing data, Bayesian statistics, OpenBUGS, mixed stock analysis.

INTRODUCTION

The Kenai River (Figure 1) supports the largest freshwater sport fishery in Alaska. Radiotagging studies have shown that Chinook salmon (*Oncorhynchus tshawytscha*) bound for tributaries of the Kenai River (tributary spawners) enter the river from late April through early July, while Chinook salmon that spawn in the Kenai River itself (mainstem spawners) enter the river from mid-June through mid-August (Bendock and Alexandersdottir 1992; Burger et al. 1985; Reimer *In prep*). These populations of Kenai River Chinook salmon are highly prized by anglers for their size relative to other Chinook salmon stocks (Roni and Quinn 1995). A major inriver sport fishery occurs within the Kenai River and anglers expend in excess of 300,000 angler-days annually fishing for the prized salmon (Jennings et al. 2011: Table 2.69).

It has been useful to manage the inriver fisheries as 2 separate stocks: 1) the early run, which roughly corresponds to tributary-spawning fish, and 2) the late run, which roughly corresponds to mainstem-spawning fish. The fisheries are managed separately based on date; e.g., bait is allowed on 1 July, when most fish in the harvest are presumed to be late-run fish, and a slot limit, in place for the early run, is repealed on 1 July below the Soldotna Bridge and on 15 July above the Soldotna Bridge, when most fish in the harvest are presumed to be from the late run. In addition, to protect staging tributary-spawning Chinook salmon, there are also areas of the mainstem Kenai River adjacent to tributary mouths that are closed to Chinook salmon harvest, as well as the entire Upper Kenai River.

In 1988, the Alaska Board of Fisheries (BOF) first developed management plans for both the early and late runs of Kenai River Chinook salmon (McBride et al. 1989). These plans defined the early run as fish arriving at the river prior to 1 July and the late run as those arriving after 30 June.

In the original 1988 plan, the optimum spawning escapement for early-run Chinook salmon was set at 9,000 fish, with management directives centered around projected escapement levels of less than 5,300 fish; 5,300 to 9,000 fish; and greater than 9,000 fish (McBride et al. 1989). In 1999, the management plan was revised with a biological escapement goal (BEG; definition in Alaska Administrative Code 5 AAC 39.222 [f][3]) established as a range of 7,200–14,400 Chinook salmon. Prior to the 2005 season, a BEG of 4,000–9,000 early run Chinook salmon was recommended by the Alaska Department of Fish and Game (ADF&G), to which BOF set an optimal escapement goal (OEG; definition in 5 ACC 39.222 [f][25]) of 5,300–9,000 fish for this stock. The *Kenai River and Kasilof River Early-Run King Salmon Management Plan* (5 AAC 57.160) contains mandates that the inriver sport fishery be managed to achieve the OEG. In brief, bait, multiple hooks, and fishing from boats on Mondays was prohibited unless the projected spawning escapement exceeded 9,000 fish; if the projected spawning escapement was below 5,300 fish, ADF&G restricted the sport fishery in order to achieve a spawning escapement of at least 5,300 fish. In 2013, based on new sonar technologies and new run reconstructions for the years 1986–2012, ADF&G adopted a new sustainable escapement goal (SEG; definition in 5 ACC 39.222 [f] [36]) for early-run Kenai River Chinook salmon of 3,800–8,500 fish (McKinley and Fleischman 2013). This is the current SEG, although ADF&G still manages for the current OEG of 5,300–9,000 early-run Chinook salmon.

The Kenai River late-run Chinook salmon fishery is managed according to provisions of the *Kenai River Late-Run King Salmon Management Plan* (5 AAC 21.359). In the original plan developed in 1988, an optimum spawning escapement goal was set at 22,300 fish, with management directives centered around 3 projected escapement levels: less than 15,500 fish; 15,500 to 19,000 fish; and greater than 22,300 fish. In 1999, the management plan was revised with a BEG established as a range of 17,800–35,700 Chinook salmon. In 2011, the BEG was redefined as an SEG because of the uncertainty recognized in the escapement estimates due to the measurement error associated with split-beam target-strength-based (TS-based) sonar passage estimates of Chinook salmon entering the river. The current SEG of 15,000–30,000 Chinook salmon, adopted in 2013, is based on new run reconstructions, new sonar technologies, and new harvest apportionments in mixed stock fisheries in Cook Inlet for the years 1986–2012 (Fleischman and McKinley 2013). There is no OEG for the late run as there is for the early run.

In 2003, anticipating the future development of a genetic baseline for Chinook salmon in the Kenai River drainage, ADF&G began the collection and archiving of baseline and mixture tissue samples. Collection of mixture samples from the inriver netting project at river mile (RM) 8.5 began in 2003, by the inriver creel survey downstream of the Soldotna Bridge beginning in 2006, and from harvest sampling upstream of the Soldotna Bridge beginning in 2007. Using a complete genetic baseline and the mixture sample collections, run timing and composition of sport harvests across time for returning Kenai River Chinook salmon could then be estimated by stock (i.e. tributary- or mainstem-spawner) (Begich et al. 2010; Appendix C1).

The genetic baseline for Kenai River Chinook salmon has been developed and updated repeatedly over the past 20 years, beginning with mitochondrial DNA (mtDNA) and protein electrophoresis analyses (Adams et al. 1994), which identified genetic differences between

tributary- and mainstem-spawning Chinook salmon in the Kenai River drainage. Following this, microsatellite DNA was used to quantify genetic differences among populations within each spawning type as well as to provide better estimates of stock composition in samples taken at the sonar site (Begich et al. 2010). More recently, populations in the Kenai River were included in a larger-scale baseline describing genetic variation in Chinook salmon populations in all of Upper Cook Inlet (Barclay et al. 2012). This last version of the baseline used single nucleotide polymorphisms (SNPs) as genetic markers and was primarily concerned with describing broad-scale genetic variation and the potential for mixed stock analysis of samples taken from the marine waters of Cook Inlet. The application of the baseline for analysis of samples taken within the Kenai River was not fully developed, tested, or described.

In 2011, a preliminary Kenai River drainage Chinook salmon baseline was developed from a subset of populations and the same set of SNPs markers reported in Barclay et al. (2012) that were used for a Cook Inlet–wide baseline. The preliminary Kenai River Chinook salmon baseline included tissue samples from more than 2,000 Chinook salmon collected over 11 spawning locations between 2003 and 2009, representing 10 populations.

Rogers Olive et al. (2013) reported the most recent Kenai River baseline, which uses 42 SNP markers and samples of 2,205 Chinook salmon representing 11 populations. The baseline includes all Kenai River collections and a subset of the SNPs reported in Barclay et al. (2012); however, 3 additional collections were added, including Grant Creek, a new population. The baseline report includes an examination of population structure within the Kenai River and tests to determine how well the baseline performs for mixed stock analysis (MSA) using the same reporting groups used in this study.

MSA has the potential to inform important management decisions for Kenai River Chinook salmon, particularly regarding tributary- vs. mainstem-spawning stock questions. Kenai River stocks are harvested in sport and commercial fisheries in Cook Inlet (McKinley and Fleischman 2013; Fleischman and McKinley 2013) but the only fishery in Cook Inlet that has been sampled for MSA of Chinook salmon harvests is the commercial Eastside set net fishery (Eskelin et al. 2013). The goal of this study was to use the baseline reported in Rogers Olive et al. (2013) (Table 1) to conduct a MSA of samples collected by the Kenai River netting program and from the Kenai River sport harvests.

OBJECTIVES

The objectives of this study were as follows:

1) Estimate the stock composition of Kenai River Chinook salmon samples from fish captured in the lower river netting program between 16 May and 10 August.
2) Estimate the stock composition of the sport harvest of Kenai River Chinook salmon in the lower Kenai River downstream of the Soldotna Bridge between 16 May and 31 July.
3) Estimate the stock composition of the sport harvest of Kenai River Chinook salmon between Skilak Lake and the Soldotna Bridge between early June and 31 July.

METHODS

SAMPLE COLLECTION

Tissue collection from Chinook salmon for genetic analysis was nonlethal: a 1⅓-cm (half-inch) piece of tissue from the axillary process was removed from each sampled fish, placed in a 2-mL

cryovial, and completely covered with a Sigma Reagent Grade 95% Alcohol buffer solution (Sigma Cat. # R 8382)[1] such that the liquid to tissue ratio was approximately 3:1. Samples were transferred to the ADF&G Gene Conservation Laboratory in Anchorage and stored at room temperature until analyzed.

Mixture Samples

Mixture samples were taken from the Kenai River lower inriver netting project (inriver run), the lower river sport fishery, and the middle river sport fishery. Samples were also collected from Chinook salmon harvested by anglers and submitted to the ADF&G "Trophy Fish" program.

Inriver Run

Samples of fish captured in the lower river netting program, adjacent to the Kenai River Chinook salmon sonar site at RM 8.5 (Figure 2), were considered representative of the Kenai River Chinook salmon run. Little to no harvest occurs downstream of this site during the early run (Perschbacher 2012). In some years during the late run, up to 30% of the inriver harvest occurs downstream of this site. The primary objectives of the netting project were to collect representative age, sex, and length (ASL) data from adult Chinook salmon returning to the Kenai River, and to collect species composition data from fish that pass through the insonified area of the river channel. Tissue collection for genetic analysis was added in 2003 (Perschbacher 2012). Netting occurred daily from 16 May to mid-August. Gillnets of 2 mesh sizes (5.0 and 7.5 inches stretched mesh) were used. The nets were constructed of a multi-fiber mesh in colors that best matched Kenai River water. Two mesh sizes were fished with equal frequency:

1) 5.0 inch (stretched mesh) multi-fiber, 80 meshes deep, 10 fathoms long, Shade 1 (clear-steel blue), MS73 (14 strand) twine
2) 7.5 inch (stretched mesh) multi-fiber, 55 meshes deep, 10 fathoms long, Shade 1, MS93 (18 strand) twine

Since 2003, the netting schedule has changed twice to improve data collection relative to ASL and species composition. In 2003, netting was scheduled from 4 hours before low tide to 4 hours after low tide; from 2004 to 2006, netting was scheduled from 3 hours before low tide to 3 hours after low tide; and from 2007 to 2013, netting was scheduled from 5 hours before low tide to 1 hour after. The netting project area is approximately 0.3 mi in length and located just downstream of the Chinook salmon sonar site at RM 8.5. This location was chosen because it has relatively less impact by the sport fishery (Perschbacher 2012), and because it is not known as spawning habitat for Chinook salmon (Bendock and Alexandersdottir 1992; Reimer *In prep*). During the years 2002–2012, nets were drifted within the split-beam sonar insonified area that extended across the river from a point 15 m from the right-bank transducer to a point 10 m from the left-bank transducer. In 2013, the nets were drifted within the DIDSON insonified area that extended across the river from a point 3 m from the right-bank transducer to a point 3 m from the left-bank transducer. Nets were deployed at the upstream end of the study area (immediately downstream from the sonar transducers) and drifted downstream (Perschbacher 2012; Perschbacher *In prep*).

[1] Product names used in this publication are included for completeness but do not constitute product endorsement.

Lower River Sport Fishery

The lower river is defined as the section of the Kenai River downstream of the Soldotna Bridge (Figure 2). The lower river sport fishery was sampled during the existing Kenai River Chinook salmon creel survey beginning in 2006 (Perschbacher 2012). As part of this survey, tissue samples were collected from harvested fish with the angler's consent. Interviews were conducted at access locations during times that occurred between angler counts. Every attempt was made to interview all anglers exiting the fishery at the interview location.

Anglers were interviewed at the following 5 access locations:

1) Centennial Campground (RM 20.3)
2) Poacher's Cove (RM 17.4)
3) River Bend Campground (RM 14.0)
4) Stewart's Landing (RM 14.1)
5) Pillars Boat Launch (RM 12.3)
6) Eagle Rock Launch Area (RM 11.4)

Most anglers access the early-run fishery in May at Pillars Boat Launch and Stewart's Landing (Reimer 2003); more access locations are added to the schedule as boat traffic increases at each location (Perschbacher 2012).

Four angler counts were spaced equally throughout the sampling day, providing 3 periods between angler counts for conducting angler interviews, plus 1 additional period after the last count. Interviews were scheduled as follows with time and access location paired randomly: during May to early June (when fewer than 4 access locations were sampled) each location was sampled at least once before any were repeated; beginning in mid-June (when more access locations were available than sampling periods) 3–4 access locations were sampled without replacement from the five available (Perschbacher 2012).

In addition to the sampling that occurred as part of the creel survey, sampling was also scheduled for two 10-hour shifts per week from 15 May to 31 July in the years 2010–2013. The daily start and stop times varied during the season depending on previous sampling trends; varying the sample time is not likely to bias estimates of stock composition of the harvest. The sampling dates and locations were selected to ensure that the creel survey sampler and the supplementary harvest sampler were never assigned to the same place at the same time. All sampling days, times, and locations were chosen to maximize the number of fish sampled, except when they overlapped the creel survey or during special events that would otherwise go unsampled.

Middle River Sport Fishery

A roving sampling survey of harvest was conducted for the Kenai River Chinook salmon sport fishery in the middle Kenai River (between the Soldotna Bridge and the outlet of Skilak Lake) beginning in 2007. Historically, approximately 80% of the harvest above the Soldotna Bridge occurs between the Soldotna Bridge and the Moose River, and the remaining 20% occurs between the Moose River and Skilak Lake. However, in the first year of sampling (2007) it was found that the sport harvest in the Kenai River upstream of the Moose River confluence had become small enough in recent years (due to regulatory changes and social pressures) that sampling efforts produced very few samples, and sampling upstream of the confluence was discontinued. Additionally, because of low water and low fish abundance, very little harvest

occurs above the Soldotna Bridge in May; hence, our sampling there began as early as 12 June. Many anglers fishing this section of river access the fishery via numerous private docks, as well as several public access locations. Anglers were contacted while fishing or exiting the fishery by a crew of 2 technicians operating an outboard-powered skiff launched from Centennial Campground. Sampling was conducted daily on Tuesday through Saturday, from approximately 0900 to 1700 hours. The start and stop times varied somewhat during the season depending on previous days' sampling trends; varying the time of day for sampling was considered not likely to bias estimates of stock composition of the harvest.

Harvest in the middle river sport fishery is estimated via the ADF&G Statewide Harvest Survey (SWHS). Beginning in 1996, the SWHS began estimating and reporting harvests of Chinook salmon separately for the two time periods: "prior to 1 July" and "after 1 July." However, it has always been understood that after 1 July, some of the harvest, especially above the Soldotna Bridge, was of tributary fish. Sampling effort was distributed as equally as possible geographically within the reach. In order to distribute sampling effort more evenly within the Soldotna Bridge to Moose River section, the end of the section in which sampling began was alternated every other day within each week, and then alternated for the next week. With anglers' consent, a tissue sample was collected from sport harvested adult Chinook salmon for genetic analysis.

Trophy Fish

A special collection of fish was obtained voluntarily from a subset of Chinook salmon that were sport harvested from the Kenai River. Beginning in 2003, by regulation any Chinook salmon sport harvested in the Kenai River that was 55 inches total length or greater needed to be presented to ADF&G for sealing. "Sealing" is the attachment of a numbered cinch-type strap to the harvested fish as a way of logging and acknowledging the catch. As part of the sealing process, staff also collected ASL data and a tissue sample for MSA.

Sample Size Goals

Sample size goals were determined at the beginning of the project to meet specific precision and accuracy goals:

1) Lower river netting—to estimate stock composition of mainstem-origin and tributary-origin Chinook salmon in weekly or biweekly periods between 16 May and mid-August, sample size targets were set at 30–100 samples per stratum to achieve estimates that were within 0.15 of the true values 90% of the time.

2) Lower river sport fishery—to estimate the stock composition of mainstem-origin and tributary-origin Chinook salmon caught in the sport fishery downstream of the Soldotna Bridge between 16 May and 31 July, sample size targets were set at 26–50 samples per week to achieve estimates that were within 0.15 of the true values 90% of the time.

3) Middle river sport fishery—to estimate the stock composition of mainstem-origin and tributary-origin Chinook salmon caught in the sport fishery downstream of the Soldotna Bridge between 16 May and 31 July, sample size targets were set at 26–50 samples per week to achieve estimates that were within 0.15 of the true values 90% of the time.

LABORATORY ANALYSIS

Assaying Genotypes

Genomic DNA was extracted using a DNeasy 96 Tissue Kit by QIAGEN (Valencia, CA). Fluidigm 96.96 Dynamic Arrays (http://www.fluidigm.com) were used to screen 42 SNP markers (Rogers Olive et al. 2013). Genotypes for these SNPs were screened using 3 platforms.

For some collections, the Fluidigm 48.48 Dynamic Array platform was used. The Fluidigm 48.48 Dynamic Array contains a matrix of integrated channels and valves housed in an input frame. On one side of the frame are 48 inlets to accept the sample DNA from each individual fish, and on the other are 48 inlets to accept the assays for each of the SNP markers. Once in the wells, the components are pressurized into the array using the NanoFlex 4-IFC Controller. The 48 samples and 48 assays are then systematically combined into 2,304 parallel reactions. Each reaction was conducted in a 6.75 nL volume consisting of 1xTaqMan Universal Buffer (Applied Biosystems), 1.5 U AmpliTaq Gold DNA Polymerase (Applied Biosystems), 9 mM of each polymerase chain reaction (PCR) primer, 2 mM of each probe, 1xDA Assay Loading Buffer (Fluidigm), 12.5xROX (Invitrogen), and 0.01% Tween-20. Thermal cycling was performed on a BioMark IFC Cycler as follows: an initial denaturation of 10 min at 95°C followed by 50 cycles of 92°C for 15 seconds and 60°C for 1 minute. The Dynamic Arrays were read on a BioMark Real-Time PCR System after amplification and scored using Fluidigm SNP Genotyping Analysis software.

For other collections, the Fluidigm 96.96 Dynamic Array platform was used. The Fluidigm 96.96 Dynamic Array contains a matrix of integrated channels and valves housed in an input frame. On each side of the frame are 96 inlets, one side to accept sample DNA and the other to accept assays for a unique SNP marker. An IFC Controller HX (Fluidigm) was used to for mixing the sample DNA and assays under pressure to create 9,216 separate reactions. Each reaction consisted of a mixture of 4µl of assay mix (1× DA Assay Loading Buffer [Fluidigm], 10× TaqMan SNP Genotyping Assay [Applied Biosystems], and 2.5× ROX [Invitrogen]) and 5µl of sample mix (1× TaqMan Universal Buffer [Applied Biosystems], 0.05× AmpliTaq Gold DNA Polymerase [Applied Biosystems], 1× GT Sample Loading Reagent [Fluidigm], and 60–400 ng/µl DNA) combined in a 7.2 nL chamber. Thermal cycling was performed on an Eppendorf IFC Thermal Cycler as follows: 70°C for 30 minutes for "Hot-Mix" step, initial denaturation of 10 min at 96°C followed by 40 cycles of 96°C for 15 seconds and 60°C for 1 minute. The Dynamic Arrays were read on a Fluidigm EP1 System after amplification and scored using Fluidigm SNP Genotyping Analysis software.

Assays that failed to amplify on the Fluidigm system were reanalyzed on the Applied Biosystems platform. Each reaction on this platform was performed in 384-well reaction plates in a 5µL volume consisting of 5–40 ng/µl of template DNA, 1× TaqMan Universal PCR Master Mix (Applied Biosystems), and 1× 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 denaturation of 10 minutes at 95°C followed by 50 cycles of 92°C for 1 second and annealing-extension temperature for 1 minute. The plates were scanned on an Applied Biosystems Prism 7900HT Sequence Detection System after amplification and scored using Applied Biosystems Sequence Detection Software (SDS) version 2.2.

Laboratory Failure Rates and Quality Control

The overall failure rate was calculated by dividing the number of failed single-locus genotypes by the number of assayed single-locus genotypes. A single-locus genotype was considered a failure when it could not be satisfactorily scored for a fish.

Quality control (QC) measures were instituted to identify laboratory errors and to determine the reproducibility of genotypes. In this process, 8% of every extraction plate is re-extracted and reanalyzed for all markers by staff not involved in the original analysis.

Laboratory errors found during the QC process were corrected, and genotypes were corrected in the database. Inconsistencies not attributable to laboratory error were recorded, but original genotype scores were retained in the database.

Assuming that the inconsistencies among analyses (original vs. QC genotyping) were due equally to errors in original genotyping and errors during the QC genotyping and that these analyses are unbiased, error rates in the original genotyping were estimated as one-half the rate of inconsistencies.

STATISTICAL ANALYSIS

Data Retrieval and Quality Control

Genotypes were imported from LOKI into *R* (*R* Development Core Team 2011) using the *RODBC* package (Ripley 2010). All subsequent genetic analyses were performed in *R* unless otherwise noted.

Two statistical analyses were performed to confirm the quality of the data. First, individuals missing substantial genotypic data were removed following the 80% rule (Dann et al. 2009) which requires individuals included in the analysis to have complete genotypes for at least 80% of the loci surveyed. The inclusion of individuals with poor quality DNA might introduce genotyping errors and reduce the accuracy of MSA.

Second, individuals with duplicate genotypes were identified and removed from further analysis. Duplicate genotypes can occur as a result of sampling or extracting the same individual twice, and were defined as pairs of individuals sharing the same alleles in 95% of screened loci. The sample with the most missing genotypic data from each duplicate pair was removed from further analyses. If both samples had the same amount of genotypic data, the first sample was removed from further analyses.

Mixed Stock Analysis

Sampling goals were set to independently estimate stock proportions of temporal strata (roughly by week and year) within the inriver run, lower river sport fishery, and middle river sport fishery for 3 reporting groups (Mainstem, Lower Tributary, and Upper Tributary). If sample goals were met in all temporal strata, mixed stock analysis the of mixture samples was performed for each stratum independently using the program BAYES (Pella and Masuda 2001). However, it was anticipated that meeting the sample goals for all strata would be difficult to achieve, and that a modeling effort might have to be used to estimate stock proportions for each stratum.

Inriver Run and Sport Harvest

Mixed stock analysis of the inriver run and sport harvests was performed using a hierarchical Bayesian model. Because the model can estimate stock proportions for each temporal stratum with greater precision than independent estimates in BAYES, we estimated stock compositions for 3 reporting groups: Upper Tributary, Mainstem, and Lower Tributary. In baseline tests, Rogers Olive et al. (2013) found that the baseline has sufficient variation within these reporting groups for use in MSA.

The objective of the current model is to develop an informative prior distribution for stock proportions as an extension of the method developed by Pella and Masuda (2001) for conducting MSA, in which a noninformative prior for the stock proportions is used. The parameterization used here for the stock proportions was first described by Okuyama and Bolker (2005), in which group proportions $(\mathbf{R})$ are defined for groups of populations, and within-group subproportions $(\mathbf{S})$ are defined for the individual populations. However, unlike Okuyama and Bolker (2005), who used a noninformative prior for the group proportions and an informative prior for the subproportions, augmented by covariates, we took the opposite approach. The proposed model develops an informative prior for the group proportions, and a noninformative prior for the subproportions. The informative prior that we used provides context in which to link together an entire suite of stratified mixture samples, whose stock proportions can be viewed as related.

In the present setting, samples were stratified by fishery ($f \in \{1,2,...,F\}$), year ($t \in \{1,2,...,T\}$), and week ($w \in \{1,2,...,W\}$). The group proportions within fishery *f*, year *t*, and week *w* were defined as follows:

$$\mathbf{R}_{f,t,w} = \left\{R_{f,t,w,1}, R_{f,t,w,2}, ..., R_{f,t,w,G}\right\} \tag{1}$$

such that

$$\sum_{g=1}^{G} R_{f,t,w,g} = 1. \tag{2}$$

The subproportions for group *g* were defined as follows:

$$\mathbf{S}_{f,t,w,g} = \left\{S_{f,t,w,g,1}, S_{f,t,w,g,2}, ...S_{f,t,w,g,\mathbf{C}_g}\right\} \tag{3}$$

such that

$$\sum_{k=1}^{\mathbf{C}_g} S_{f,t,w,g,k} = 1 \tag{4}$$

where $\mathbf{C}_g$ equals the number of populations within this group. The full set of population proportions $\mathbf{P}_{f,t,w}$ is then

$$\mathbf{P}_{f,t,w} = \left\{R_{f,t,w,1}\mathbf{S}_{f,t,w,1}, R_{f,t,w,2}\mathbf{S}_{f,t,w,2}, ...R_{f,t,w,G}\mathbf{S}_{f,t,w,G}\right\}. \tag{5}$$

As a prior for the subproportions of group *g*, a flat Dirichlet distribution was used with equal parameters set to $\frac{1}{\mathbf{C}_g}$. The informative prior used for the group proportions was also Dirichlet, parameterized in terms of its expectation

$$E\left(\mathbf{R}_{f,t,w}\right)=\left\{E\left(R_{f,t,w,1}\right),E\left(R_{f,t,w,2}\right),...,E\left(R_{f,t,w,G}\right)\right\}, \tag{6}$$

as well as a dispersion parameter $\rho^2\left(0<\rho^2<1\right)$, as follows:

$$\mathbf{R}_{f,t,w}\sim Dirichlet\left(\frac{\rho^2}{1-\rho^2}E\left(\mathbf{R}_{f,t,w}\right)\right). \tag{7}$$

Here, the expectation of $\mathbf{R}_{f,t,w}$ was constructed as a function of week *w* via a multiple logistic structure model:

$$E\left(R_{f,t,w,g}\right)=\frac{e^{\alpha_{f,t,g}+\beta_{f,t,g}\left(w-\overline{w}\right)}}{\sum_{g'=1}^{G}e^{\alpha_{f,t,g'}+\beta_{f,t,g'}\left(w-\hat{w}\right)}} \tag{8}$$

where $\alpha_{f,t,g}$ and $\beta_{f,t,g}$ are regression parameters and $\overline{w}=\frac{W+1}{2}$ is the mean week number. We made group *G* the base category required by the multiple logistic structure and set $\alpha_{f,t,G}=\beta_{f,t,G}=0$. By giving the dispersion parameter ρ^2 a noninformative uniform prior, it can be regarded as an approximation to the amount of variation in **R** accounted for by the model (Guo et al. 2008), whereas the quantity $\frac{\rho^2}{1-\rho^2}$ can be regarded as the prior "sample size."

The fisheries occur sequentially along the river such that, in year *t* for group *g*, the regression parameters for fishery *f* are expected to be similar to those of adjacent fisheries. Therefore, these parameters evolve according to the following prior distributions:

$$\alpha_{f,t,g}\sim N\left(\alpha_{f-1,t,g},\varsigma_\alpha^2\right):\ f>1, \tag{9}$$

and

$$\beta_{f,t,g}\sim N\left(\beta_{f-1,t,g},\varsigma_\beta^2\right):\ f>1. \tag{10}$$

where ς_α^2 and ς_β^2 are parameters of dispersion to be estimated (Congdon 2003). The initial fisheries' parameters for each group in each year are drawn from the following prior distributions:

$$\alpha_{1,t,g}\sim N\left(\dot{\alpha}_g,\sigma_\alpha^2\right), \tag{11}$$

and

$$\beta_{1,t,g}\sim N\left(\dot{\beta}_g,\sigma_\beta^2\right), \tag{12}$$

where α_g and β_g are the global average parameters for group g across years, and σ_α^2 and σ_β^2 are dispersion parameters. We continued to keep group G the base category, such that $\dot{\alpha}_G = \dot{\beta}_G = 0$.

The global average parameters α_g and β_g were given noninformative normal priors with means of zero and variances of 10^3. The dispersion parameter ρ^2 was given a noninformative uniform prior, whereas σ_α^2, σ_β^2, ς_α^2, and ς_β^2 were given noninformative inverse-gamma prior distributions with all hyper-parameters equal to 10^{-3}.

To estimate the stock composition of the inriver run, lower Kenai River sport harvest, and middle Kenai River sport harvest, we implemented the model described above in the package *rjags* (Plummer 2013; Appendix A1). The package *rjags* is an interface for the program JAGS, which employs Markov Chain Monte Carlo (MCMC) simulation for the analysis of Bayesian hierarchical models. Because implementation of this analysis was more difficult than our standard BAYES MSA protocol, we ran fewer than our typical 5 chains and increased the number of iterations per chain by 10,000 (Barclay et al. 2010; Eskelin et al. 2013). Subsequently, we ran 3 independent MCMC chains of 50,000 iterations with different starting values and discarded the first 25,000 iterations to remove the influence of the initial start values. We assessed among-chain convergence using the Gelman-Rubin shrink factors computed for all stock groups using the package *coda*. This shrink factor compared the variation within a chain to the total variation among chains (Gelman and Rubin 1992). A Gelman-Rubin shrink factor greater than 1.2 for a single reporting group may indicate lack of convergence. Estimates and 90% credibility intervals were tabulated from the combined set of the second half of three 50,000-iteration chains. Credibility intervals differ from confidence intervals in that they are a direct statement of probability: i.e., a 90% credibility interval has a 90% chance of containing the true answer (Gelman et al. 2004). The credibility intervals reflect both sampling error and genetic assignment error.

Even though the data were not balanced with respect to all strata, the model provides an expectation of stock proportions for all strata, which allowed for stock compositions to be estimated for all temporal strata in the inriver run, lower river sport fishery, and middle river sport fishery, even when few or no samples were available for a given stratum. To visualize stock composition trends for all 3 reporting groups, we plotted trend lines on the same plot using stock composition estimates for all strata for years when samples were collected for a given fishery (inriver run, lower river sport fishery, and middle river sport fishery; Figures 3–26). To show the error around the point estimates, we plotted the point estimates and 90% credibility intervals for each reporting group on separate plots; however, we did not plot estimates where no samples were available to inform the estimate. These estimates were not reported because the model used the global mean as the estimate when no samples were available and it would be inappropriate to give estimates for the sport harvests when the fishery was not open.

Trophy Fish

The stock composition of trophy fish for 2 reporting groups—Tributary and Mainstem—was estimated using the program BAYES (Pella and Masuda 2001). The Bayesian model implemented by BAYES places a Dirichlet distribution as the prior distribution for the stock proportions, and the parameters for this distribution must be specified. Prior parameters for each reporting group were defined to be equal (i.e., a "flat" prior). Within each reporting group, the prior population parameters were divided equally among populations within that reporting group.

We set the sum of the prior parameters to be 1 (prior weight), which is equivalent to adding 1 fish to the mixture (Pella and Masuda 2001). We ran 5 independent MCMC chains of 40,000 iterations with different starting values and discarded the first 20,000 iterations to remove the influence of the initial start values. Estimates and 90% credibility intervals were tabulated from the combined set of the second half of the five iteration chains. We examined the adequacy of burn-in for each chain with the Raftery and Lewis (1996) diagnostic. We assessed among-chain convergence using the Gelman-Rubin shrink factors that are computed for all stock groups in the program BAYES. A Gelman-Rubin shrink factor greater than 1.2 for a single reporting group may indicate lack of convergence.

RESULTS

LABORATORY ANALYSIS

Laboratory Failure Rates and Quality Control

A total of 8,892 fish were genotyped from the inriver run, lower Kenai River sport harvest, and middle Kenai River sport harvest from 2003 to 2013. Failure rates among collections ranged from 0.04% to 3.37% and discrepancy rates were uniformly low and ranged from 0.00% to 1.16%. Assuming equal error rates in the original and the quality-control analyses, estimated error rates in the samples are half of the discrepancy rate (0.00% to 0.58%).

STATISTICAL ANALYSIS

Data Retrieval and Quality Control

Based upon the 80% scorable marker rule, 0.76%, 1.10%, and 0.03% of individuals were removed from the inriver run, sport harvest, and trophy fish collections, respectively, before stock composition estimates were calculated.

INRIVER RUN

A total of 5,198 samples were collected between 2003 and 2013 during the months of May, June, July, and August. Fish from all 3 reporting groups (Mainstem, Upper Tributary, and Lower Tributary) occurred in strata before and after 1 July in all years (Figures 4–14, Appendix B1). Upper Tributary fish were a very small but protracted component of the run that generally peaked near the regulatory cut-off of 1 July between the early run and the late run (Figure 3). Lower Tributary fish accounted for nearly all of the run until mid-June, and were near zero during the first week of July and following (Figure 3). Mainstem fish were generally not a significant component of the run until mid-June, and comprised nearly all of the run by the first week in July (Figure 3). In 8 years out of the 11 sampled, the Mainstem component of the run became 50% or greater beginning in the 17–23 June stratum.

HARVEST

Lower River Sport Fishery

A total of 2,633 samples were collected between 2006 and 2013. Low harvest due to periods of low abundance and inseason fishery restrictions negatively impacted the number of samples collected, resulting in no samples and estimates for some strata and longer temporal strata in others (Figures 15–22, Appendix B2).

Prior to 1 July, the majority of the harvest in all strata in all years (2006–2013) was generally of Lower Tributary fish. Of the 8 years sampled for the lower river sport fishery, 6 years had samples representing at least 5 of the 6 strata prior to 1 July. In 5 of these 6 years, the Mainstem component of the harvest became 50% or greater within the last June stratum (24–30 June). Upper Tributary fish were under 20% of the harvest in all strata prior to 1 July (Figures 15–22).

From 1 July until the end of the season, Lower Tributary fish were less than 20% of the harvest in all strata and all years (2006–2013). Mainstem fish accounted for 75% or greater of the harvest in all strata and all years. Upper Tributary fish were less than 15% of the harvest in all strata from 1 July until the end of the season (Figures 15–22).

Middle River Sport Fishery

A total of 1,061 samples were collected between 2007 and 2010. Low harvest due to low abundance periods and inseason fishery restrictions negatively impacted the number of samples collected, resulting in no samples and estimates for some strata and longer temporal strata in others (Figures 23–26, Appendix B3).

Prior to 1 July, the majority of the harvest in all strata in all years (2007–2010) was generally of Lower Tributary fish. Mainstem fish and Upper Tributary fish were never the majority of the harvest in any of the strata prior to 1 July, and were always 25% of the harvest or substantially less (Figures 23–26).

From 1 July until the end of the season, Lower Tributary fish were between about 25% and 50% of the harvest in the first stratum and less than 25% in all strata after that in all years (2006–2013). Mainstem fish accounted for approximately 35–65% of the harvest in the first stratum and approximately 70% of the harvest or greater in later strata. In all 4 years sampled, the Mainstem component of the harvest became 50% or greater within the first July stratum (1–7 July). In all years, the proportion of Upper Tributary fish peaked in the first stratum and declined in succeeding strata (Figures 23–26).

Trophy Fish

The type of analyses currently conducted for MSA with Pacific salmon does not produce exact genetic assignments for individual fish; results are more appropriately reported for groups or samples of fish. Accordingly, while tissue was collected between 2003 and 2013 from 32 fish that were presented to ADF&G as a legal requirement for sealing as trophy fish (fish that are 55 inches total length or greater), results are for the group and not each individual. For this sample of fish, the Mainstem reporting group accounted for 95% of the sample.

DISCUSSION

INRIVER RUN

Run timing differences determined from MSA for Lower Tributary Chinook salmon (which compose most of the run until mid-June, and almost none of it beginning in July) vs. Upper Tributary Chinook salmon (run peak near 1 July) are loosely corroborated by passage timing at the Funny River (a lower tributary) weir and Quartz Creek (an upper tributary) weir (K. Gates, Fishery Biologist, United States Fish and Wildlife Service, Soldotna, personal communication). The midpoint of fish passage at the Quartz Creek weir is approximately 2 weeks later than the midpoint of fish passage at the Funny River weir. However, this difference in midpoint passage

time may not be directly related to river entry time and could simply be an artifact explained by the greater distance to Quartz Creek. Radio tags were applied to fish near the Kenai River sonar site RM 8.5 via the same netting program used to collect tissue samples for the study herein (for 4 years with only 2 complete years of late-run tagging; Reimer *In prep*) but none of the fish radiotagged in July used an upper Kenai River tributary as their ultimate spawning destination. Upper Tributary fish in the July strata estimates herein could be the result of either 1) the detection of a true occurrence of small proportions measurable through the power of genetic analysis and many years of samples, or 2) a statistical artifact caused by a small amount of misclassification applied to a large number of fish.

There has long been a question of whether Chinook salmon that enter the Kenai River in June and yet spawn in the mainstem (*early-run mainstem spawners*; based on radiotelemetry; Bendock and Alexandersdottir 1992) are a distinct population or simply the beginning of the late run. The analyses in this report used the current genetic baseline to identify and quantify a significant mainstem component that enters prior to 1 July for each year estimated. In recent radiotelemetry work (Reimer *In prep*), these fish spawn in the same general locations as radiotagged fish that entered in July. Both of these results point to the same conclusion: so-called *early-run mainstem spawners* are simply the beginning of the late-run mainstem spawning stock. For the project reported herein, fish captured in the existing netting program at RM 8.5 were treated as representative of the run of immigrating Chinook salmon. Harvest downstream of the sampling area likely does not alter the reporting group components of the run at the netting site; little-to-no harvest occurs downstream of this site during the early run (Perschbacher 2012). In the late run, however, up to 30% of the inriver harvest in some years occurs downstream of this site, but since fish entering in July are nearly all from the same reporting group, the harvest downstream is not likely to affect estimates of reporting groups substantially.

A pilot study to investigate Chinook salmon passage nearshore of the existing insonified area and netting areas was conducted in 2013. In the early run, Chinook salmon caught nearshore were younger and smaller than fish in the regular netting area (Perschbacher *In prep*). This suggests that the inriver MSA sample may not be representative because there are across-year differences in size and age between stocks. In the future, nearshore netting will likely be a part of the regular stock assessment to ensure a representive sample is collected and to investigate any potential biases.

HARVEST

For practical reasons, the sampling protocols for the middle river sport fishery were not as rigorous as those for the lower river sport fishery. Time of day and sampling location were not thought to affect the estimates of harvest by reporting group. Hence, time of day and days of the week expected for peak and for guided activity (and hence harvest) were chosen. Also, it takes approximately 40 minutes to get from one end of the sampling area to the other with the outboard jet-powered boat used by the sampling crew, so the roving, hot-spot approach was taken to minimize time spent in obviously slow fishing areas that varied during the season.

Lower Tributary fish would likely be a larger component of the harvest in the middle river sport fishery if not for the areas closed to sport fishing adjacent to the mouths of key middle river tributaries (Funny River and Killey River). Through radiotelemetry, natal fish have been shown to hold in these areas, sometimes for weeks (Reimer *In prep*).

While the sealing requirement for harvested Chinook salmon that were 55 inches total length or greater was enacted at the behest of the public to address early-run Chinook salmon issues, virtually all of the fish sealed so far have been mainstem (i.e., late-run) Chinook salmon.

Stock Assessment and Management Implications

Based on this work, future and historical estimates of inriver run, inriver harvest, and escapement by run can be estimated and stock-recruit analyses updated. The impact on estimates of S_{msy} (number of spawners to produce maximum sustained yield) is expected to be very small and likely will not affect a change in the current sustainable escapement goals (SEGs) for the two runs. However, the assessment of whether each escapement goal was achieved or exceeded annually could possibly differ for years when escapement is close to either end of the goal range.

Future MSA sampling is being planned for Cook Inlet marine sport and commercial fisheries. Currently, the only Cook Inlet marine fishery sampled for MSA is the Eastside setnet (ESSN) fishery, beginning in 2010. Annual estimates have been similar for the Kenai Mainstem harvest component for years that were successfully sampled (2010, 2011, and 2013; Eskelin et al. 2013); however, samples from these years are not representative of run size and fisheries. Sampling of the ESSN fishery during years of high Kenai River Chinook salmon run size, when they occur, would be prudent.

These are the first published estimates of the stock contribution of the harvest in the Kenai River using the now complete genetic baseline. Based on this work, the key regulatory dates seem to work well in balancing harvests between the less abundant early run (tributary) and the more abundant late run (mainstem) as the early-run fish move upstream: 1) no bait by regulation until 1 July (when the more abundant mainstem fish predominate in the lower river and lower river harvest), 2) removal of the slot limit on 1 July for the fishery below the Soldotna Bridge (the slot limit is meant to conserve older, larger early-run fish); and 3) removal of the slot limit on 15 July for the fishery above the Soldotna Bridge (the slot limit is meant to conserve older, larger early-run fish). Based on the tributary component of the harvest above the Soldotna Bridge between 1 July and 15 July, ADF&G is currently proposing changing the date on which bait is allowed by regulation above the Soldotna Bridge from 1 July to a later date of 15 July.

As expected, the 1 July cut-off for differentiating the early and late runs is imperfect, but still practical for management of both runs. Run estimates, apportioned by stratum estimates from this report, will be produced for a better comparison of the optimal run separation date.

Given the (1) genetic resolution of reporting groups for run assessment and harvests to Upper Tributary, Lower Tributary, and Mainstem spawners and not to finer-scale reporting groups; (2) the discrete run and harvest timing of early (tributary) and late (mainstem) spawners; (3) the observed protracted nature of Upper Tributary spawner passage; and (4) the relatively small contribution of Upper Tributary spawners to the overall run, this study and the previous genetic baseline work support continued management of Kenai River Chinook salmon as 2 runs (early and late). Management of finer-scale reporting groups (i.e. spawning aggregates representing individual tributaries) would not be possible or practical at this time, and would likely lead to greater management uncertainty. Management of mixed stock fisheries using defining biological characteristics for stock group discrimination, such as run timing, is not uncommon. Russian River sockeye salmon are managed separately as early and late runs. Likewise, Yukon River chum salmon are also managed separately as early (summer) and late (fall) runs as the most viable management units for these mixed stock fisheries, even though each of the runs is

comprised of many discrete tributary spawning groups. In these mixed stock fisheries, managing for an individual tributary stock is often impractical, unless areas are closed where a higher preponderance of natal fish are known to hold, typically in spawning tributaries or near mouths of tributaries.

ACKNOWLEDGEMENTS

This study required the efforts of a large number of incredibly dedicated people. Netting samples were collected by Nate Lockwood, Oralee Nudsen, Matt King, Amy Breakfield, Jodi Knudsen, Jason Pawluk, Bob Zeyer, Jim Boersma, Sherra Pritchard, Phillip Ischi, Tim Lybrand, Mike Lunde, Art Barboza, Kassie Johnson, Stan Westerman, Jamie McKellar, Samantha Collum, and Averee Amend. Harvest samples in the lower Kenai River were collected by Alyssa Stevens, Ivan Karic, Stacie Mallette, and Amanda Alaniz. Harvest samples in the middle Kenai River were collected by Ramona Baker, Julianne Pettey, Will Newberry, and Bristol Whitmore. Barry Stratton was key in initiating this study. Adam Reimer and Robert Begich lead some of the initial planning and sampling efforts. Jeff Perschbacher and Tony Eskelin supervised sampling crews for collections in many years. Anton Antonovich provided biometric support in planning. Jim Hasbrouck provided insight and direction where appropriate. Many staff from the Gene Conservation Lab were involved with this project including: Tara Harrington and Christina Cupp, who oversaw sampling kit assembly and processed incoming samples; Heather Liller, Zac Grauvogel, Serena Rogers Olive, Paul Kuriscak, Charles Thompson, and Wei Cheng, who oversaw DNA extractions, screened SNPs, and ensured quality control of laboratory data; Judy Berger for archiving samples; and Eric Lardizabal for database support.

REFERENCES CITED

Adams, N. S., W. J. Spearman, C. V. Burger, K. P. Currens, C. B. Schreck, and H. W. Li. 1994. Variation in mitochondrial DNA and allozymes discriminates early and late forms of Chinook salmon (*Oncorhynchus tshawytscha*) in the Kenai and Kasilof Rivers, Alaska. Canadian Journal of Fisheries and Aquatic Sciences 51 (Supplement 1): 172-181.

Barclay, A. W., C. Habicht, R. A. Merizon, and R. J. Yanusz. 2012. Genetic baseline for Upper Cook Inlet Chinook salmon: 46 SNPs and 5,279 fish. Alaska Department of Fish and Game, Fishery Manuscript Series No. 12-02, Anchorage. http://www.adfg.alaska.gov/FedAidpdfs/FMS12-02

Barclay, A. W., C. Habicht, W. D. Templin, H. A. Hoyt, T. Tobias, and T. M. Willette. 2010. Genetic stock identification of Upper Cook Inlet sockeye salmon harvest, 2005–2008. Alaska Department of Fish and Game, Fishery Manuscript No. 10–01, Anchorage. http://www.adfg.alaska.gov/FedAidpdfs/FMS10-01.pdf

Begich, R. N., W. D. Templin, A. W. Barclay, and L. W. Seeb. 2010. Development of microsatellite genetic markers for Kenai River Chinook salmon. Alaska Department of Fish and Game, Fishery Data Series No. 10-38, Anchorage. http://www.adfg.alaska.gov/FedAidpdfs/FDS10-38.pdf

Bendock, T. N., and M. Alexandersdottir. 1992. Mortality and movement behavior of hooked-and-released Chinook salmon in the Kenai River recreational fishery, 1989-1991. Alaska Department of Fish and Game, Fishery Manuscript No. 92-02, Anchorage. http://www.adfg.alaska.gov/FedAidPDFs/fms92-02.pdf

Burger, C. V., R. L. Wilmot, and D. B. Wangaard. 1985. Comparison of spawning areas and times for two runs of Chinook salmon (*Oncorhynchus tshawytscha*) in the Kenai River, Alaska. Canadian Journal of Fisheries and Aquatic Sciences 42(4):693-700.

Congdon, P. 2003. Applied Bayesian modelling. Wiley and Sons.

Dann, T. H., C. Habicht, J. R. Jasper, H. A. Hoyt, A. W. Barclay, W. D. Templin, T. T. Baker, F. W. West, and L. F. Fair. 2009. Genetic stock composition of the commercial harvest of sockeye salmon in Bristol Bay, Alaska, 2006-2008. Alaska Department of Fish and Game, Fishery Manuscript Series No. 09-06, Anchorage. http://www.adfg.alaska.gov/FedAidPDFs/FMS09-06.pdf

Eskelin, T., A. W. Barclay, and A. Antonovich. 2013. Mixed stock analysis and age, sex, and length composition of Chinook salmon in Upper Cook Inlet, Alaska, 2010–2013. Alaska Department of Fish and Game, Fishery Data Series No. 13-63, Anchorage. http://www.adfg.alaska.gov/FedAidpdfs/FDS13-63

Fleischman, S. J., and T. R. McKinley. 2013. Run reconstruction, spawner–recruit analysis, and escapement goal recommendation for late-run Chinook salmon in the Kenai River. Alaska Department of Fish and Game, Fishery Manuscript Series No. 13-02, Anchorage. http://www/adfg/alaska.gov/FedAidpdfs/FMS13-02

Gelman, A., J. B. Carlin, H. S. Stern, and D. B. Rubin. 2004. Bayesian data analysis. 3rd edition. Chapman and Hall, Boca Raton, Florida.

Gelman, A., and D. B. Rubin. 1992. Inference from iterative simulation using multiple sequences. Statistical Science 7:457-511.

Guo, F., D. K. Dey, and K. E. Holsinger. 2008. A hierarchical Bayesian approach for estimating the origin of a mixed population. Institute of Mathematical Statistics Collections 3:237-250.

Jennings, G. B., K. Sundet, and A. E. Bingham. 2011. Estimates of participation, catch, and harvest in Alaska sport fisheries during 2010. Alaska Department of Fish and Game, Fishery Data Series No. 11-60, Anchorage. http://www.adfg.alaska.gov/FedAidpdfs/FDS11-60

McBride, D. N., M. Alexandersdottir, S. Hammarstrom, and D. Vincent-Lang. 1989. Development and implementation of an escapement goal policy for the return of Chinook salmon to the Kenai River. Alaska Department of Fish and Game, Fishery Manuscript No. 8, Juneau. http://www.adfg.alaska.gov/FedAidPDFs/fms-008.pdf

McKinley, T. R., and S. J. Fleischman. 2013. Run reconstruction, spawner–recruit analysis, and escapement goal recommendation for early-run Chinook salmon in the Kenai River. Alaska Department of Fish and Game, Fishery Manuscript Series No. 13-03, Anchorage. http://www.adfg.alaska.gov/FedAidPDFs/FMS13-03.pdf

REFERENCES CITED (Continued)

Okuyama, T., and B. M. Bolker. 2005. Combining genetic data and ecological data to estimate sea turtle origins. Ecological Applications 15(1):315-325.

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

Perschbacher, J. 2012. Chinook salmon creel survey and inriver gillnetting study, lower Kenai River, Alaska, 2011. Alaska Department of Fish and Game, Fishery Data Series No. 12-84, Anchorage. http://www.adfg.alaska.gov/FedAidPDFs/FDS12-84.pdf

Perschbacher, J. *In prep.* Chinook salmon creel survey and inriver gillnetting study, lower Kenai River, Alaska, 2012. Alaska Department of Fish and Game, Fishery Data Series, Anchorage.

Plummer, M. 2013. R package version 3-11. rjags: Bayesian graphical models using MCMC. http://CRAN.R-project.org/package=rjags

R Development Core Team. 2011. *R:* A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL http://www.R-project.org/ (Accessed October 6, 2011).

Raftery, A. E., and S. M. Lewis. 1996. Implementing MCMC. Pages 115–130 [*In*] W. R. Gilks, S. Richardson, and D.J. Spiegelhalter, editors. Markov chain Monte Carlo in practice. Chapman and Hall, Inc., London.

Reimer, A. 2003. Chinook salmon creel survey and inriver gillnetting study, lower Kenai River, Alaska, 2001. Alaska Department of Fish and Game, Fishery Data Series No. 03-01, Anchorage. http://www.adfg.alaska.gov/FedAidPDFs/fds03-01.pdf

Reimer, A.M. *In prep*. Migratory timing and distribution of Kenai River Chinook salmon, 2010–2013. Alaska Department of Fish and Game, Fishery Data Series, Anchorage

Ripley, B. 2010. RODBC: ODBC Database Access. R package version 1.3-2. http://CRAN.R-project.org/package=RODBC (Accessed December 15, 2011).

Rogers Olive, S. D., A. W. Barclay, T. R. McKinley, and W. D. Templin. 2013. Genetic baseline of Kenai River Chinook salmon for mixed stock analyses, 2013. Alaska Department of Fish and Game, Fishery Manuscript Series No. 13-12, Anchorage. http://www.adfg.alaska.gov/FedAidPDFs/FMS13-12.pdf

Roni, P., and T. P. Quinn. 1995. Geographic variation in size and age of North American Chinook salmon. North American Journal of Fisheries Management 15:325-345

TABLES

Table 1.–Tissue collections of Chinook salmon throughout the Kenai River drainage, including the year sampled, number of samples collected, the number of individuals analyzed from each collection included in the baseline, and the assigned reporting group for each collection.

Reporting group	Collection location	Map no.	Collection year(s)	Sample size	Samples analyzed
Mainstem					
	Upper Kenai Mainstem[a]	1	2009	200	191
	Juneau Creek	2	2005–2007	147	141
	Lower Kenai Mainstem[b]	3	2003, 2004, 2006, 2011	393	380
Upper Tributary					
	Quartz/Dave's Creek	4	2006–2011	139	131
	Crescent Creek	5	2006	165	164
	Grant Creek	6	2011–2012	55	55
	Russian River	7	2005–2008	214	214
Lower Tributary					
	Benjamin Creek	8	2005–2006	206	204
	Killey River	9	2005–2006	266	254
	Funny River	10	2005–2006	220	219
	Slikok Creek	11	2004, 2005, 2008	200	136
Total				2,205	2,089

Note: map numbers correspond to populations on Figure 1.

[a] Samples collected between the Kenai Lake outlet and Skilak Lake.

[b] Samples collected between Skilak Lake outlet and Eagle Rock.

FIGURES

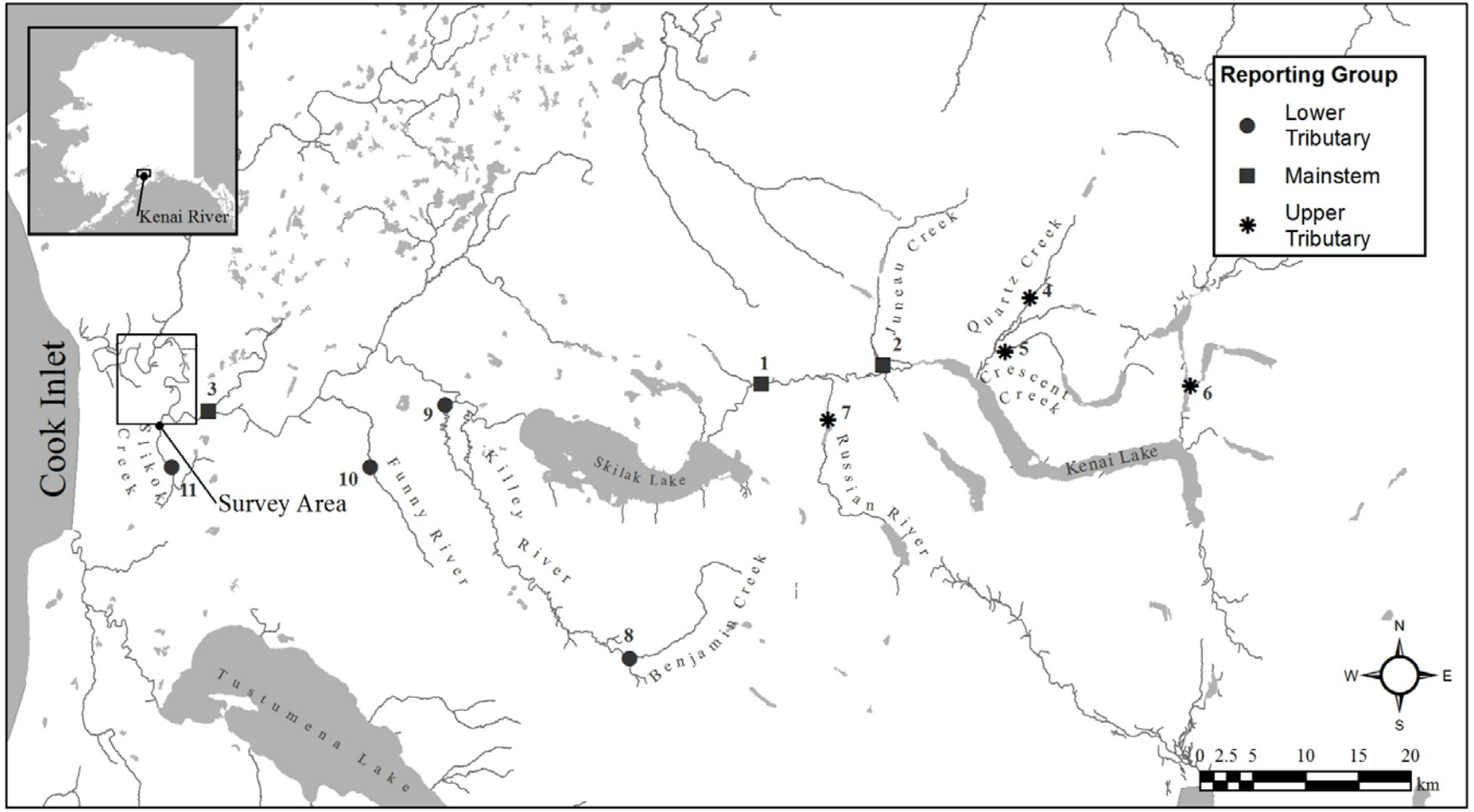

Figure 1.–Map of Kenai River drainage.

Note: "Survey Area" is depicted in Figure 2. Map numbers correspond to collection locations in Table1.

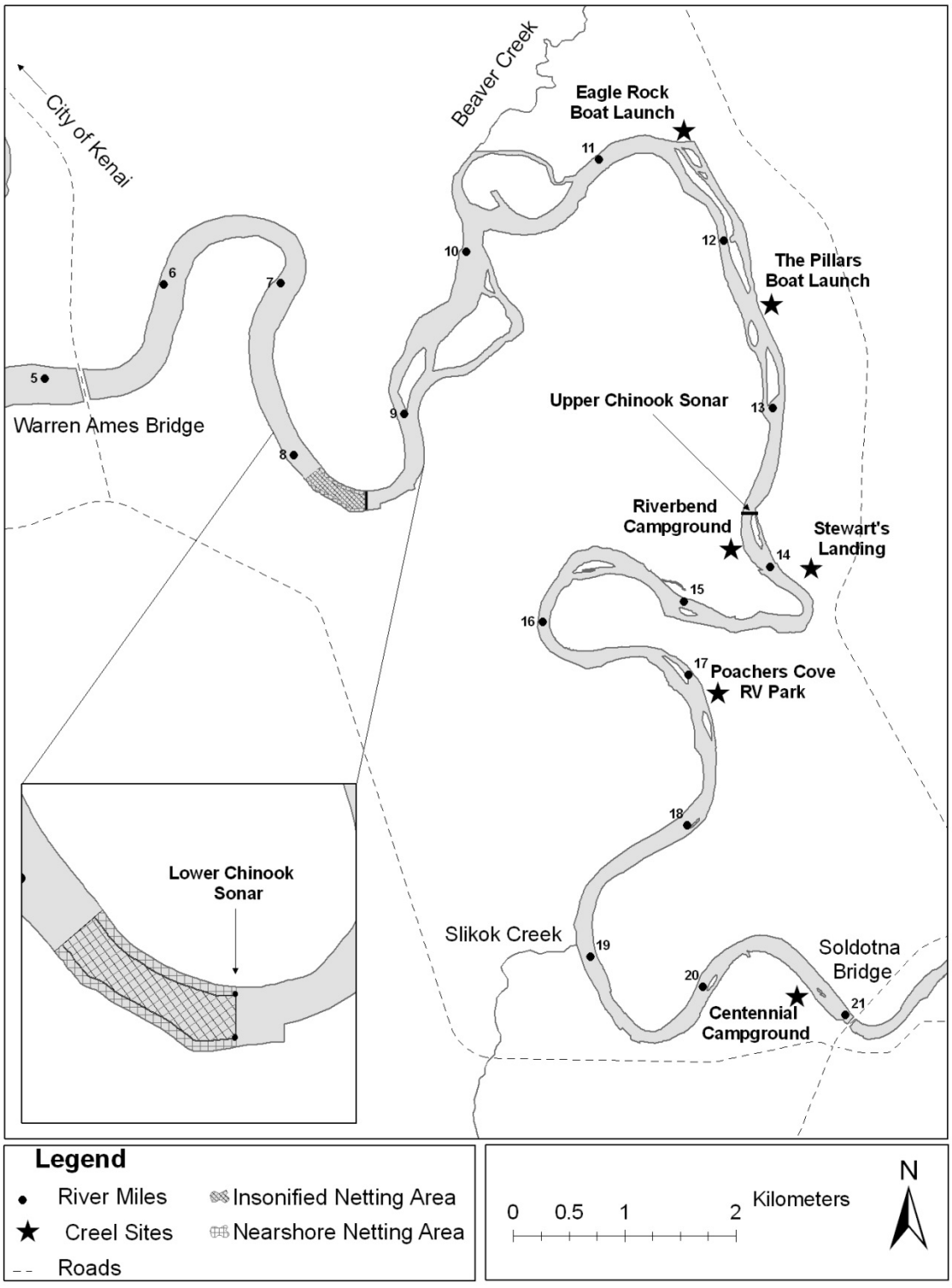

Figure 2.–Map of the Kenai River creel survey and inriver gillnetting study areas.

Note: see Figure 1 for location of survey area.

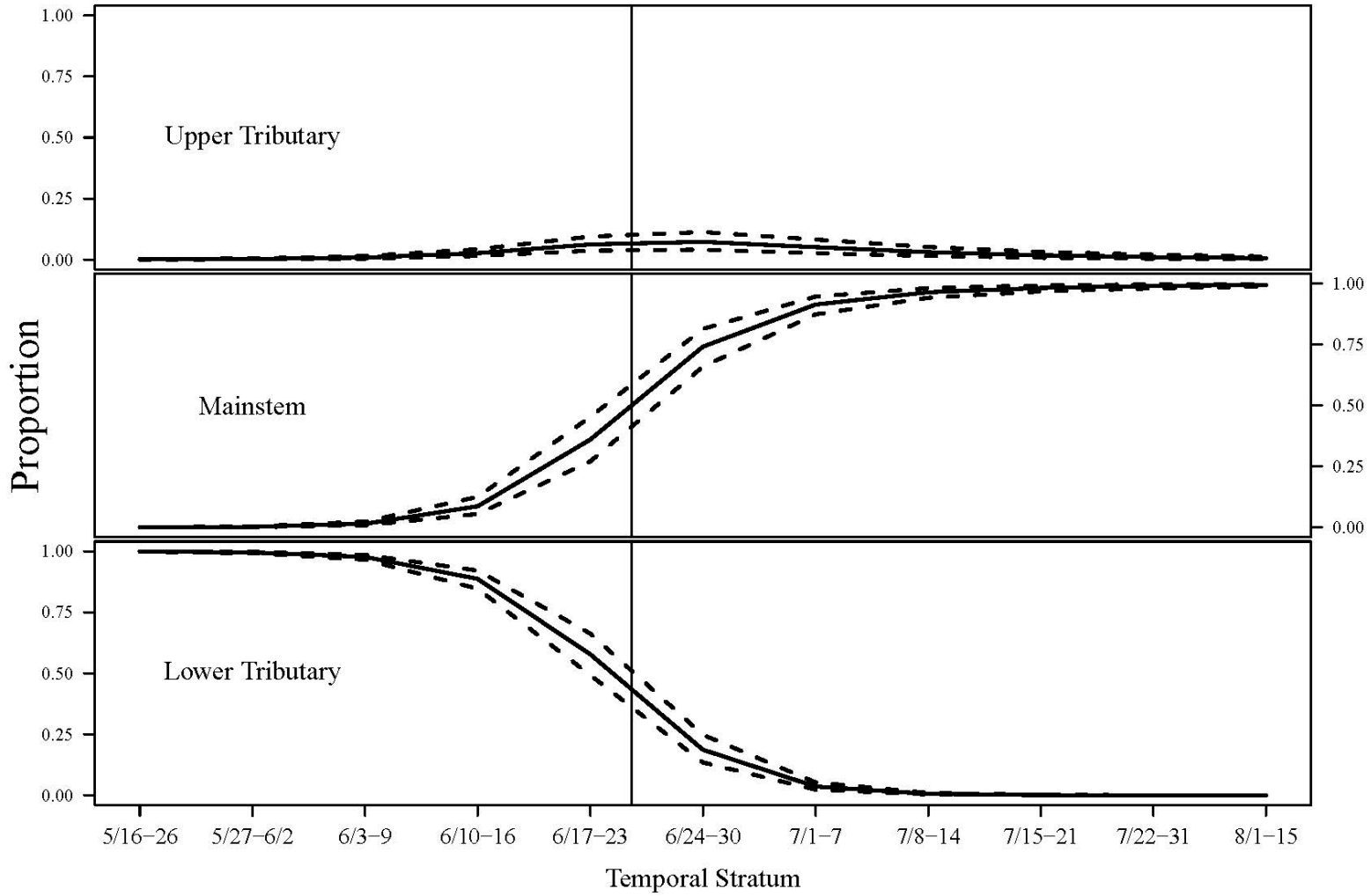

Figure 3.–Global mean proportions (solid lines) and 90% credibility intervals (dashed lines) for temporal strata from the inriver run from 2003–2013.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

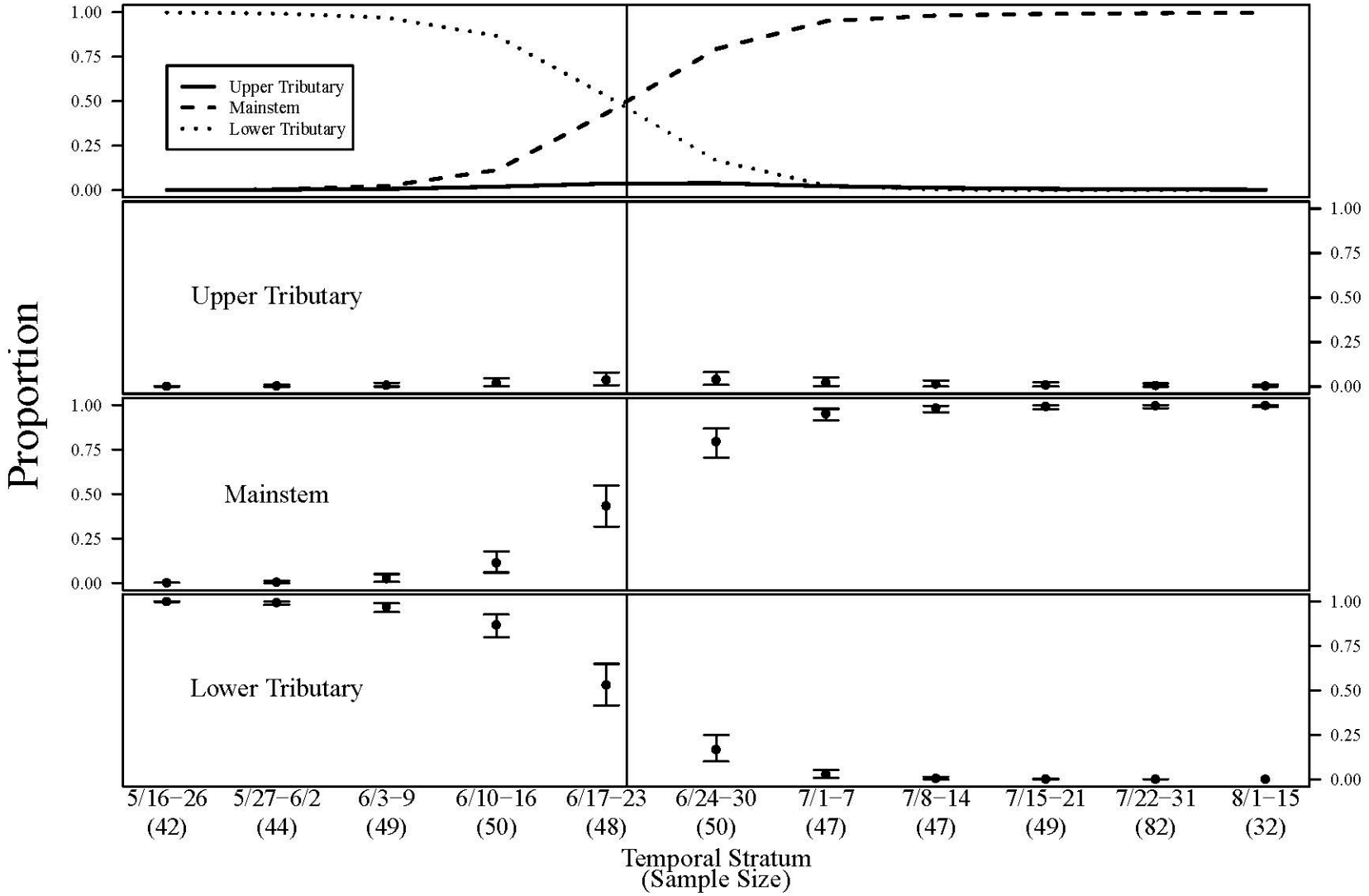

Figure 4.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish captured in the Kenai River netting program in 2003.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

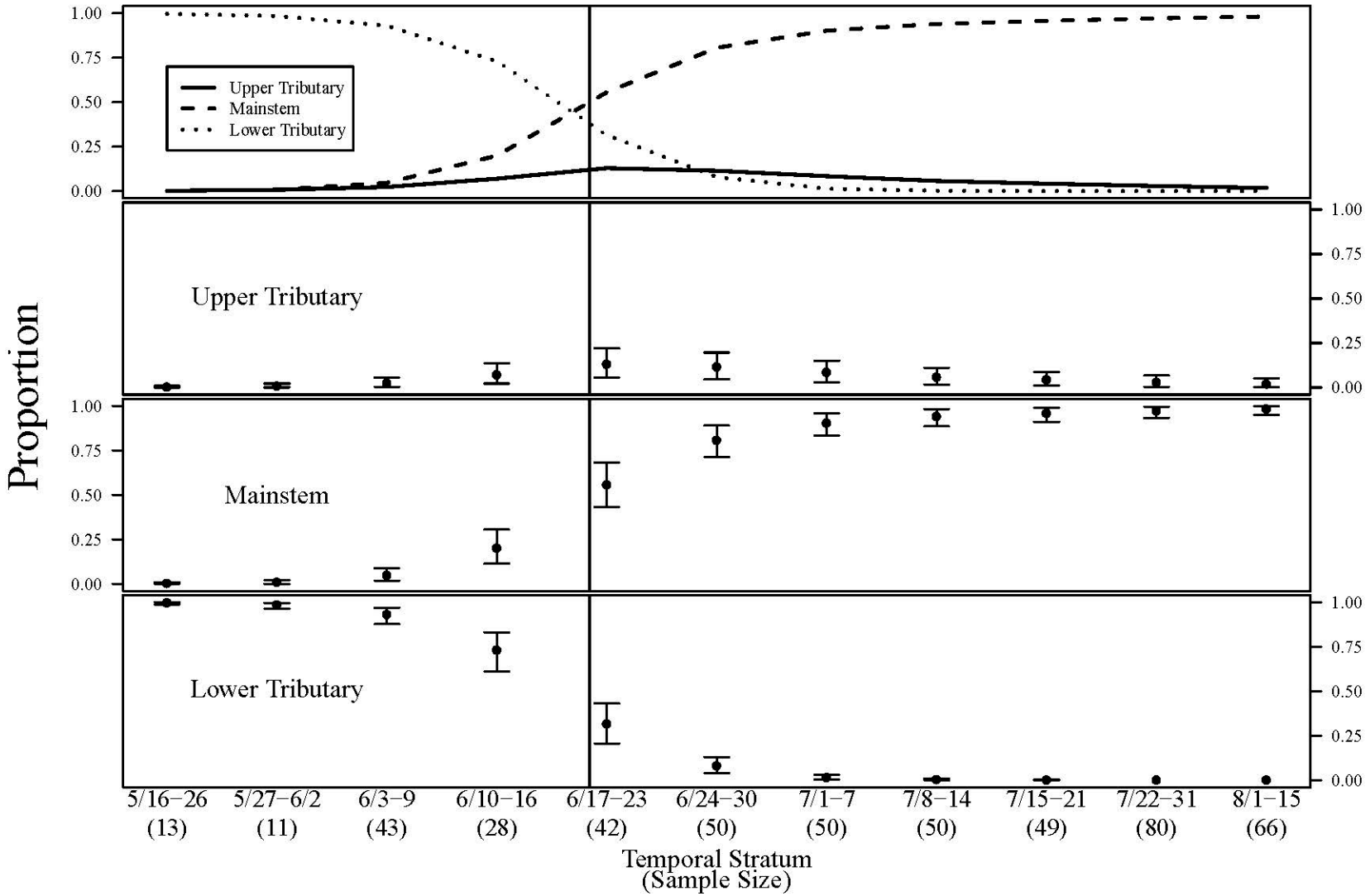

Figure 5.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish captured in the Kenai River netting program in 2004.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

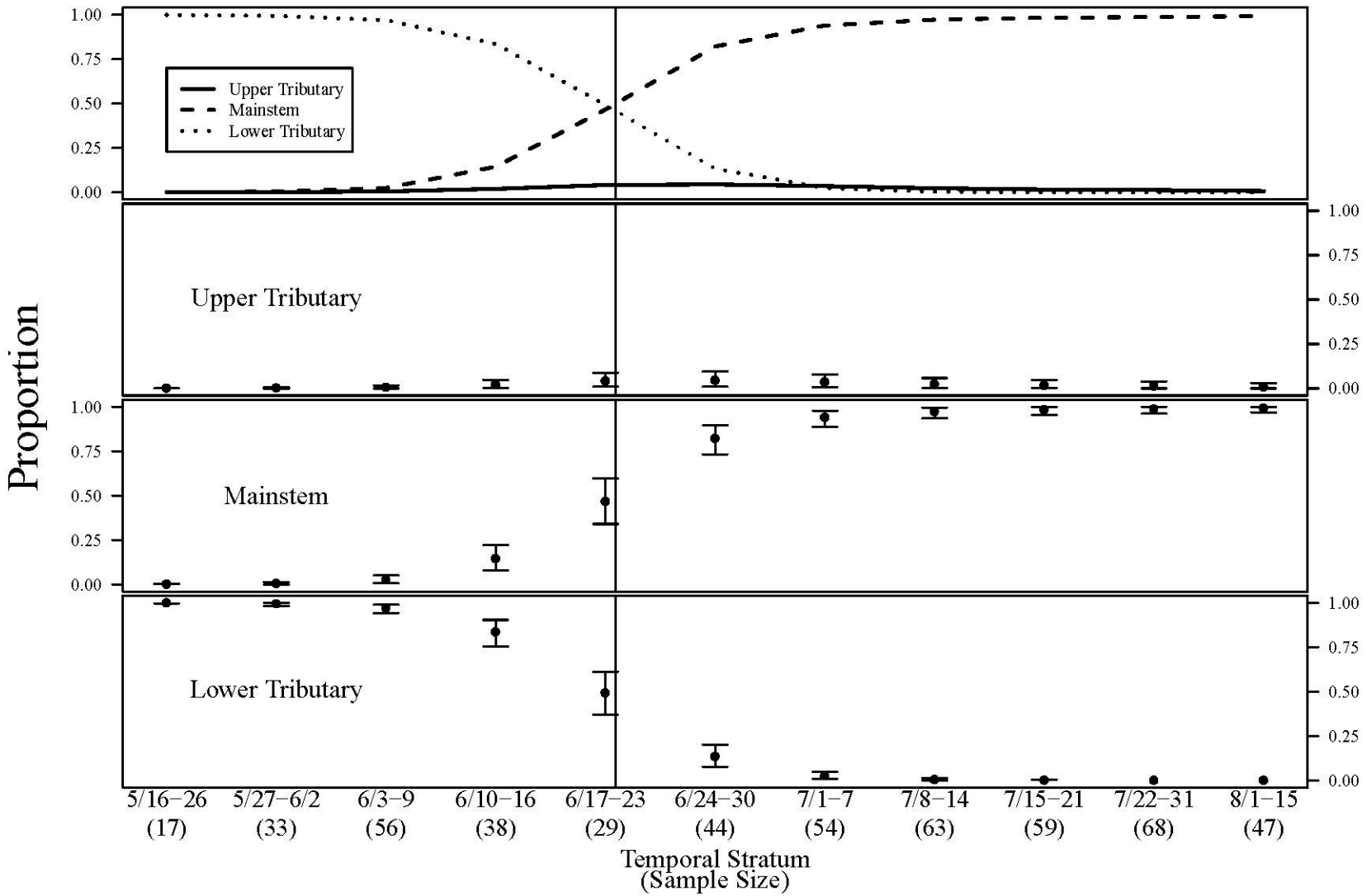

Figure 6.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish captured in the Kenai River netting program in 2005.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

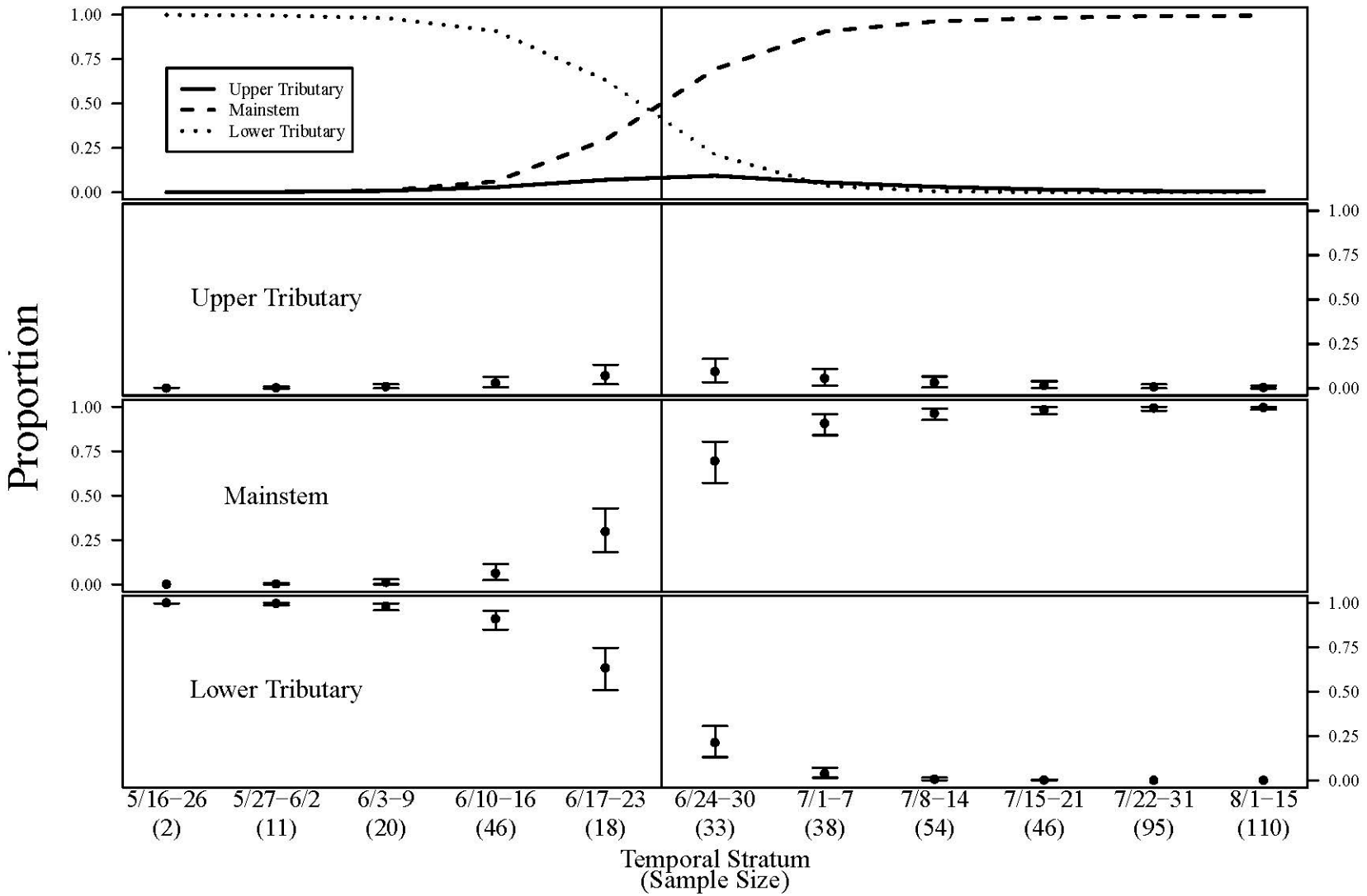

Figure 7.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish captured in the Kenai River netting program in 2006.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

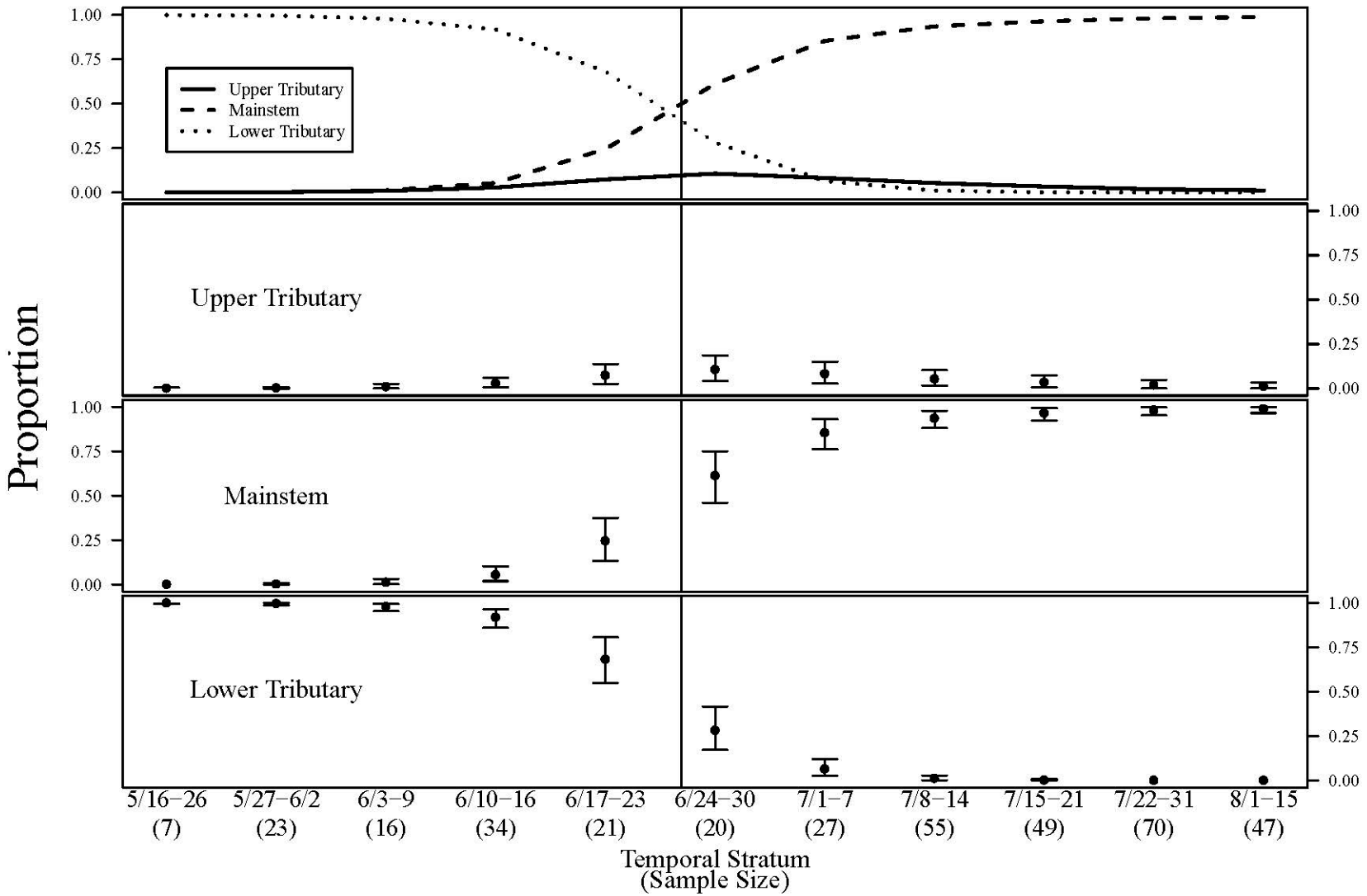

Figure 8.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish captured in the Kenai River netting program in 2007.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

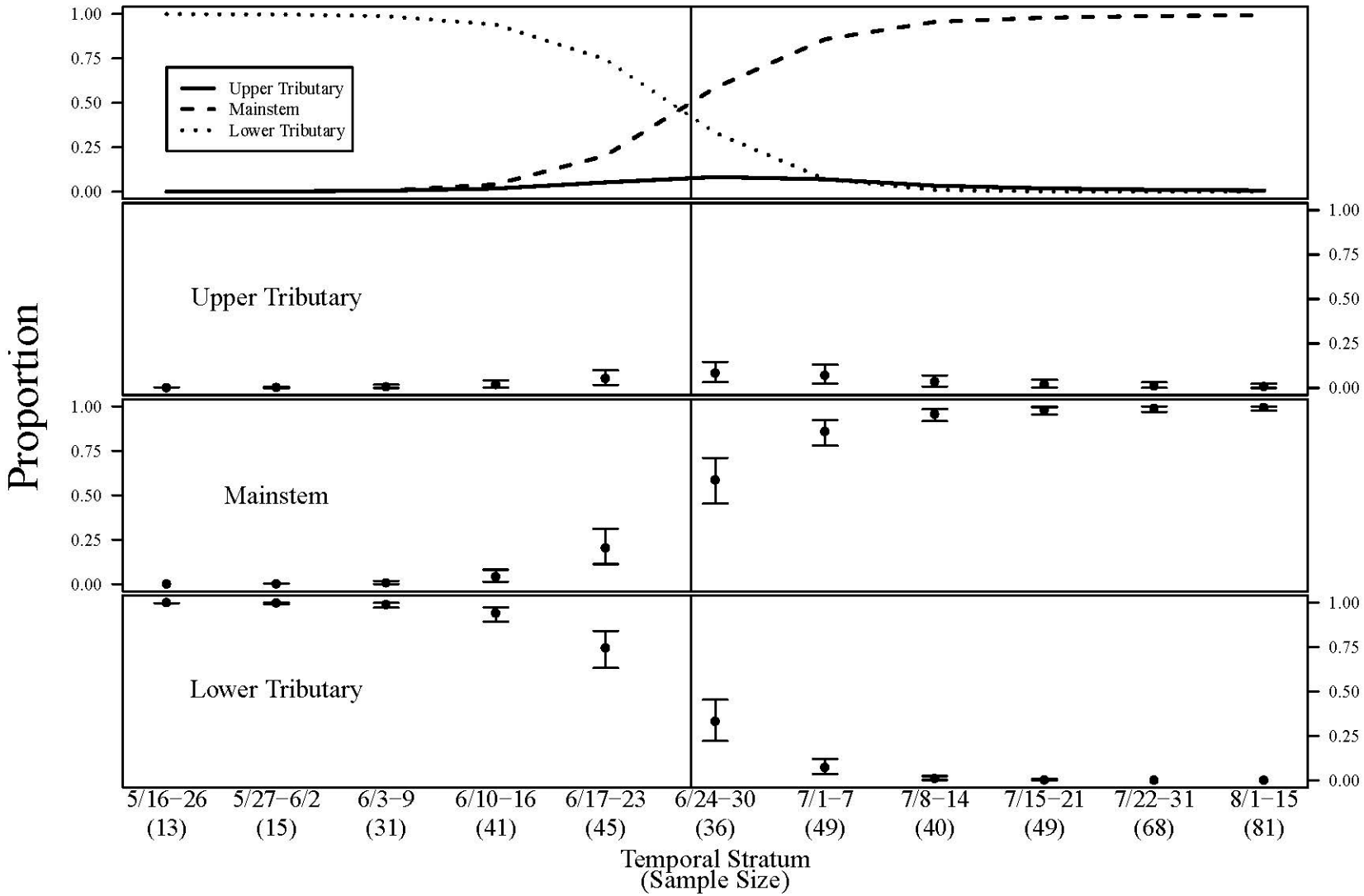

Figure 9.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish captured in the Kenai River netting program in 2008.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

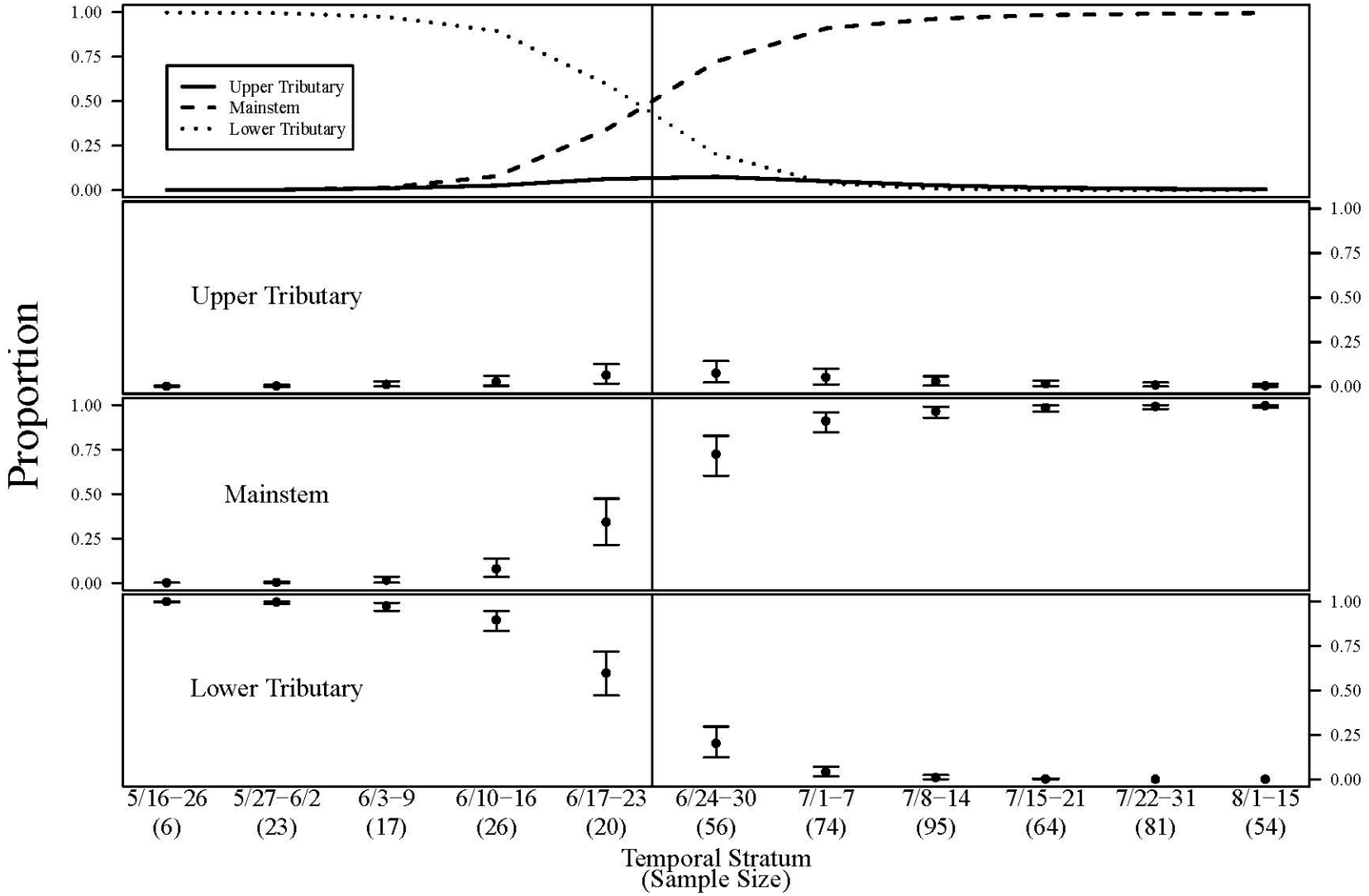

Figure 10.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish captured in the Kenai River netting program in 2009.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

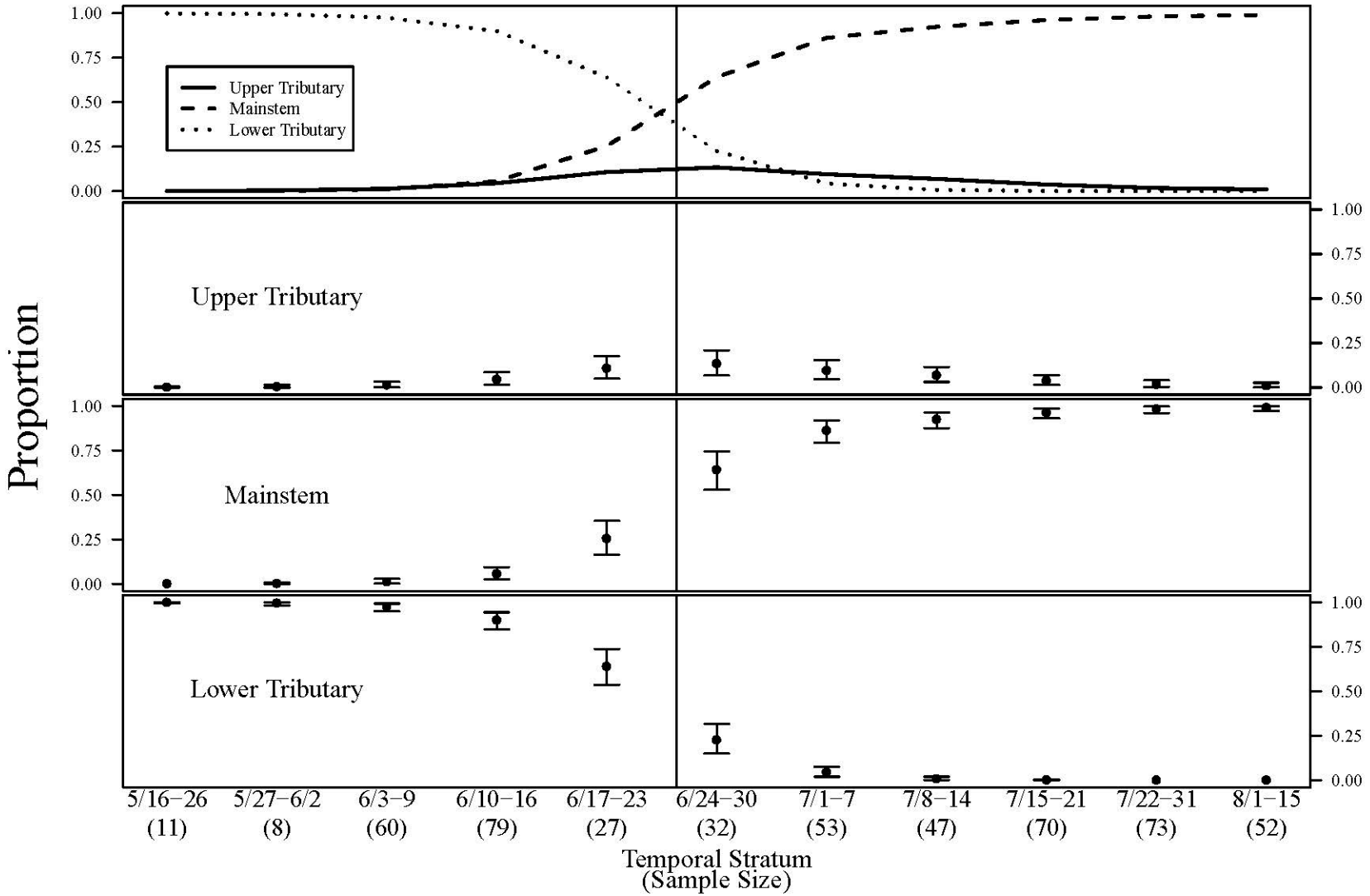

Figure 11.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish captured in the Kenai River netting program in 2010.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

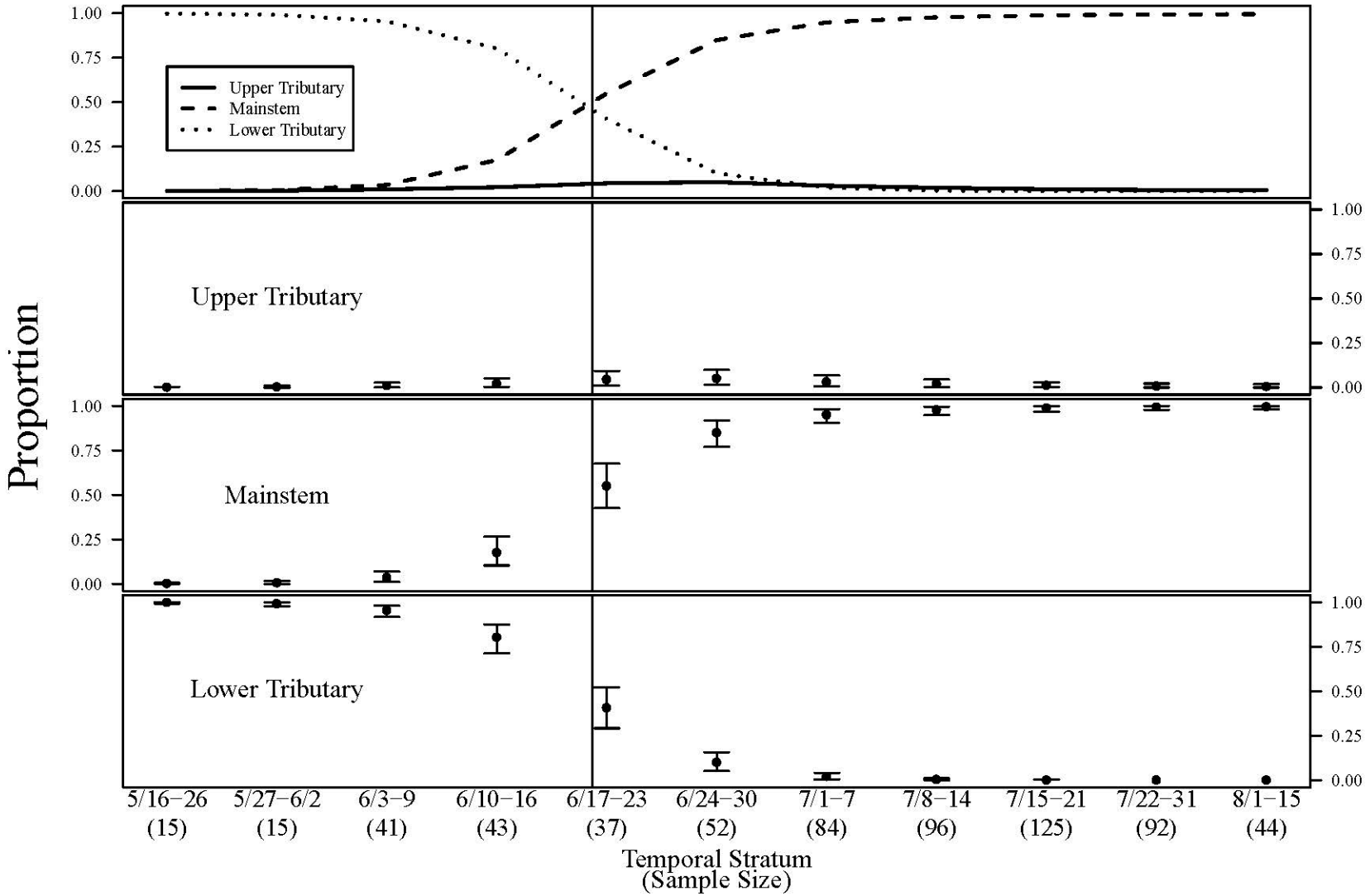

Figure 12.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish captured in the Kenai River netting program in 2011.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

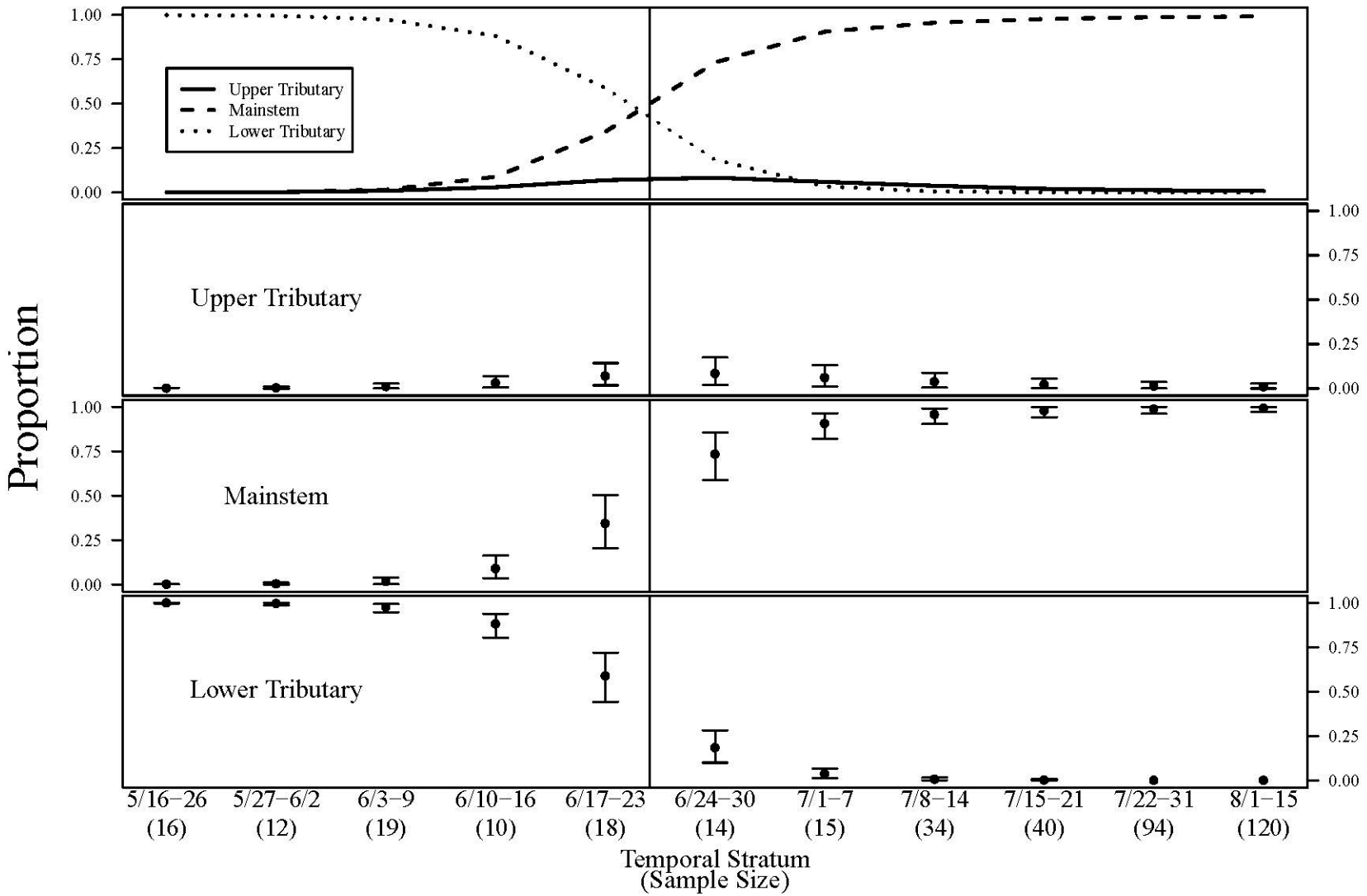

Figure 13.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish captured in the Kenai River netting program in 2012.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

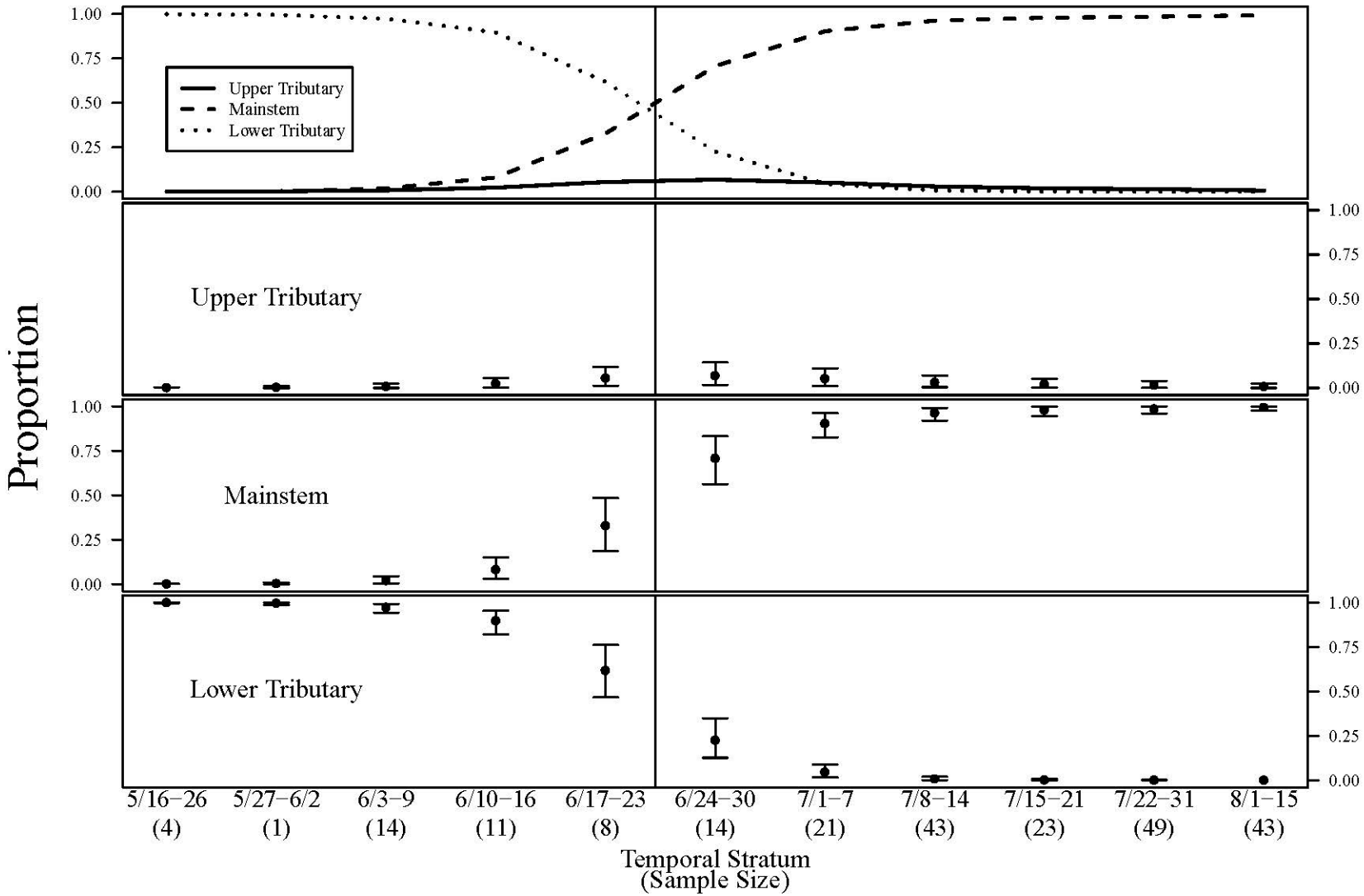

Figure 14.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish captured in the Kenai River netting program in 2013.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

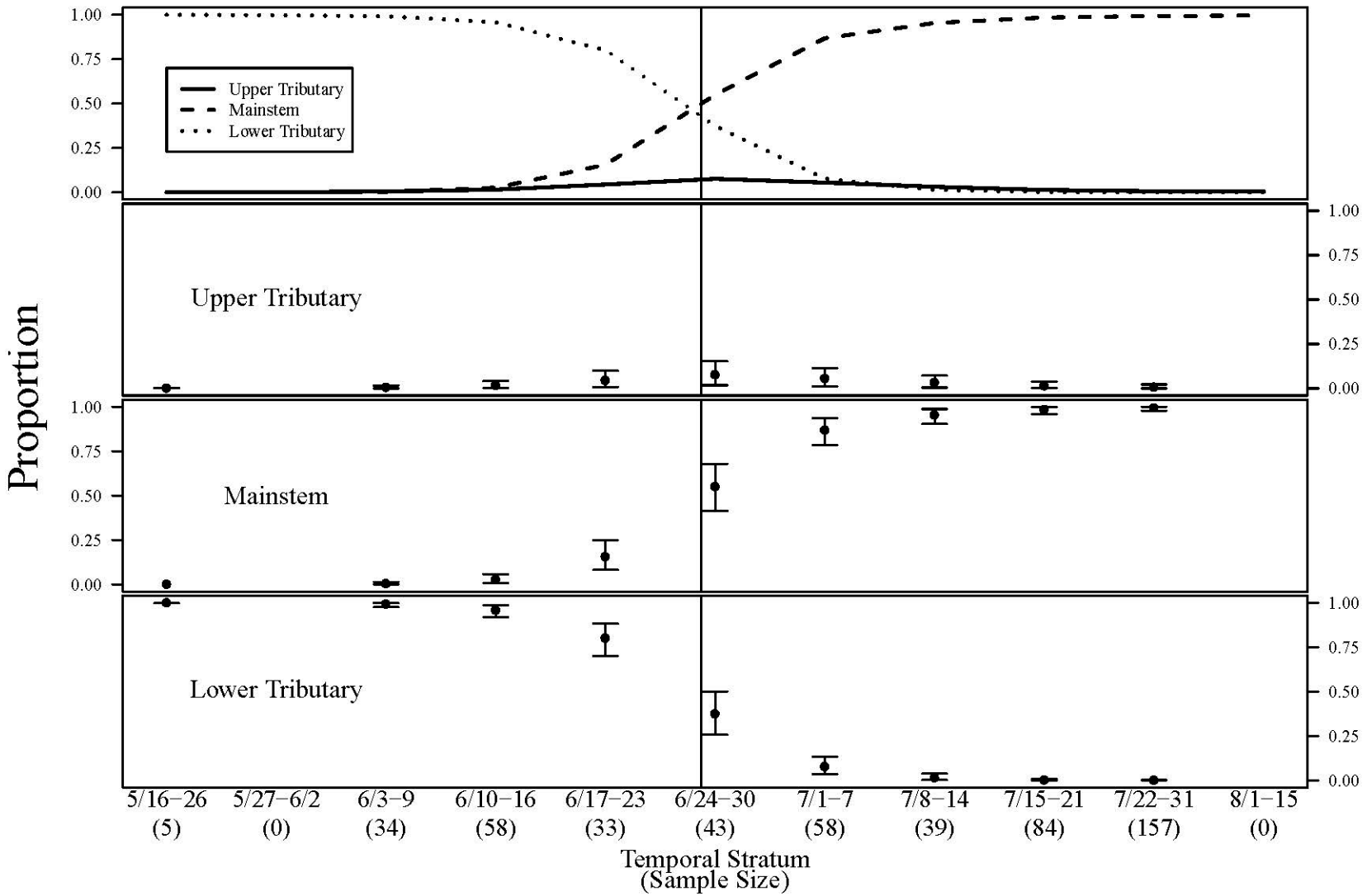

Figure 15.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish harvested in the lower Kenai River sport fishery in 2006.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

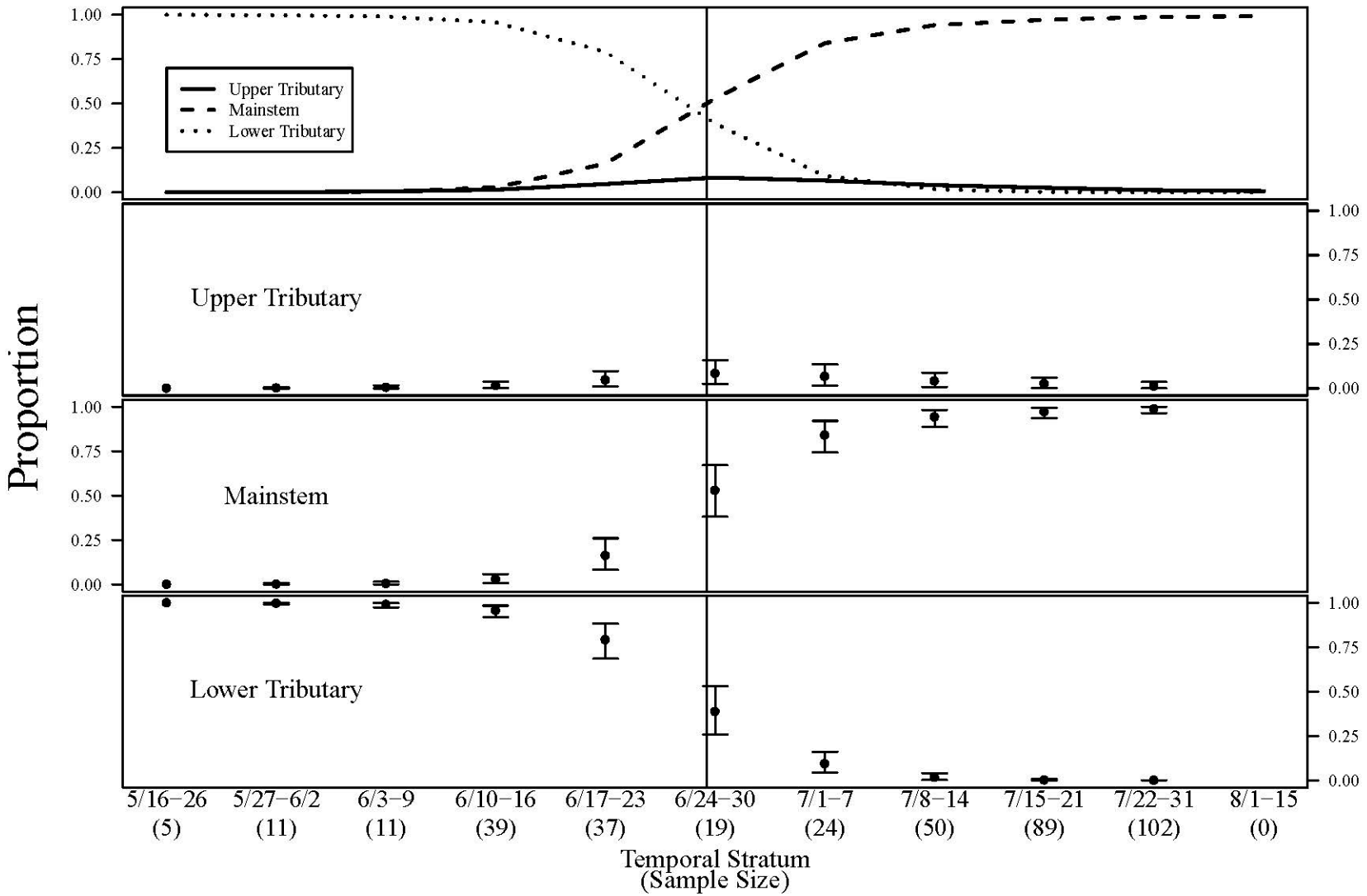

Figure 16.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish harvested in the lower Kenai River sport fishery in 2007.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

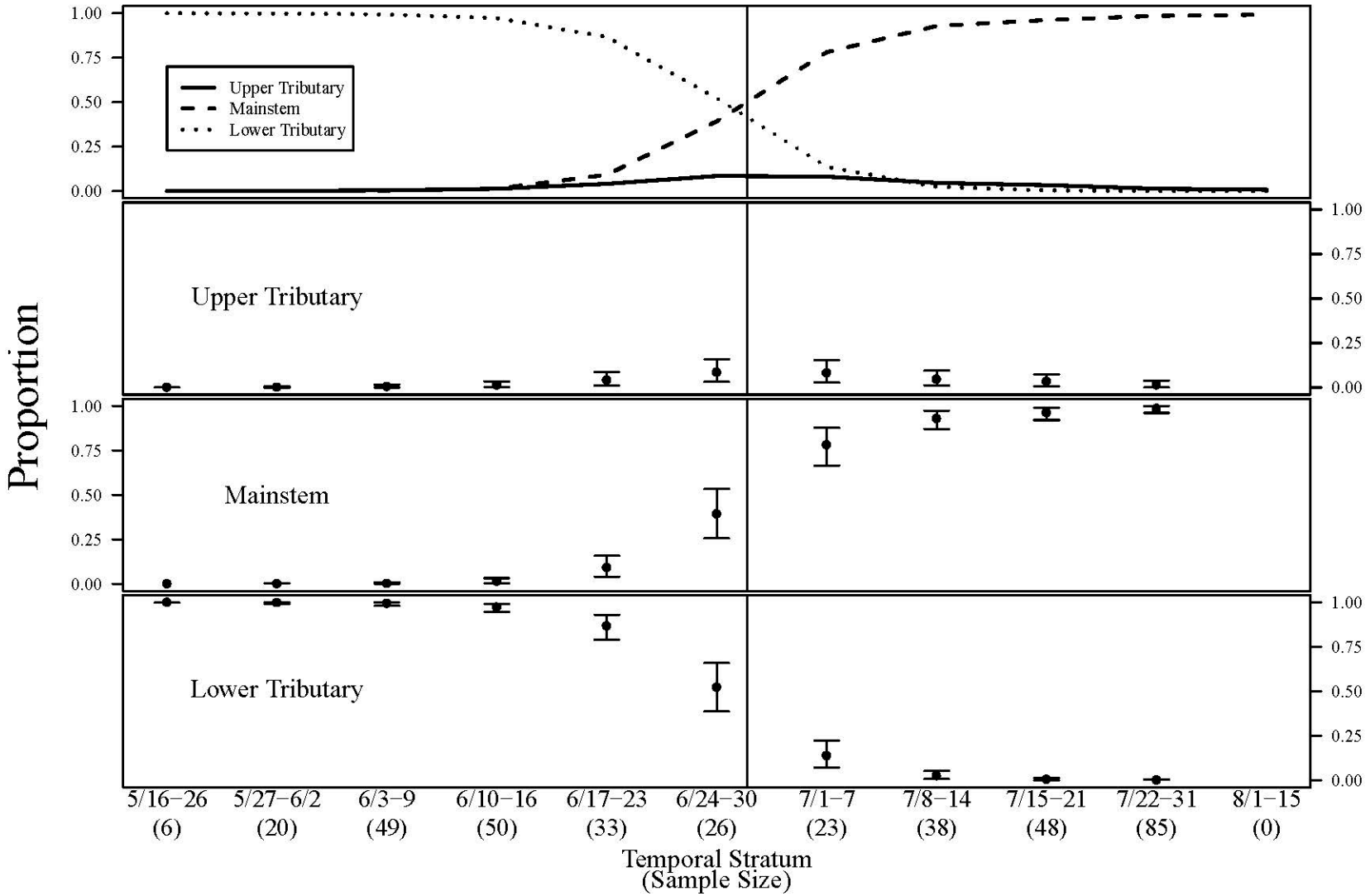

Figure 17.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish harvested in the lower Kenai River sport fishery in 2008.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

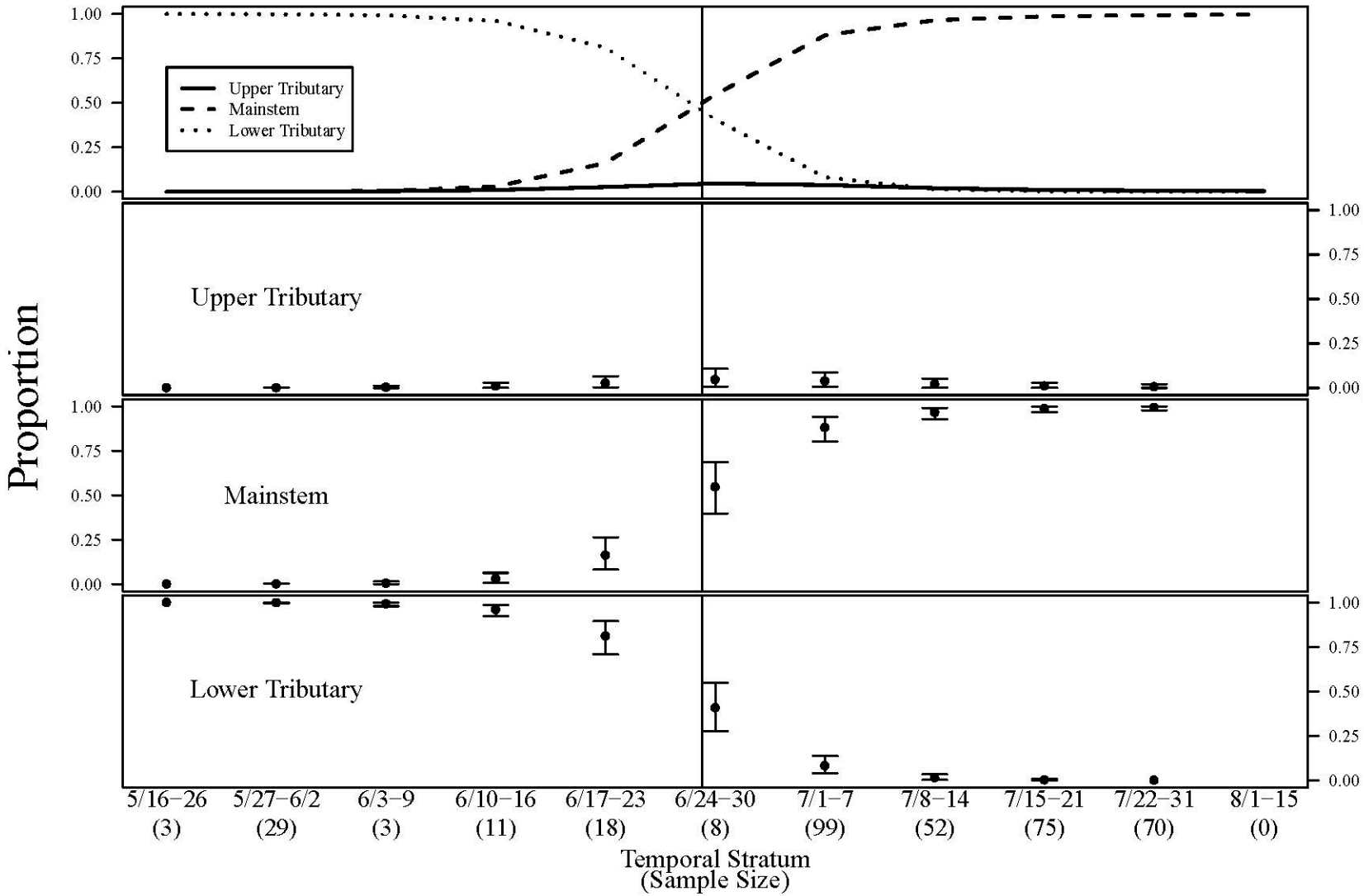

Figure 18.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish harvested in the lower Kenai River sport fishery in 2009.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

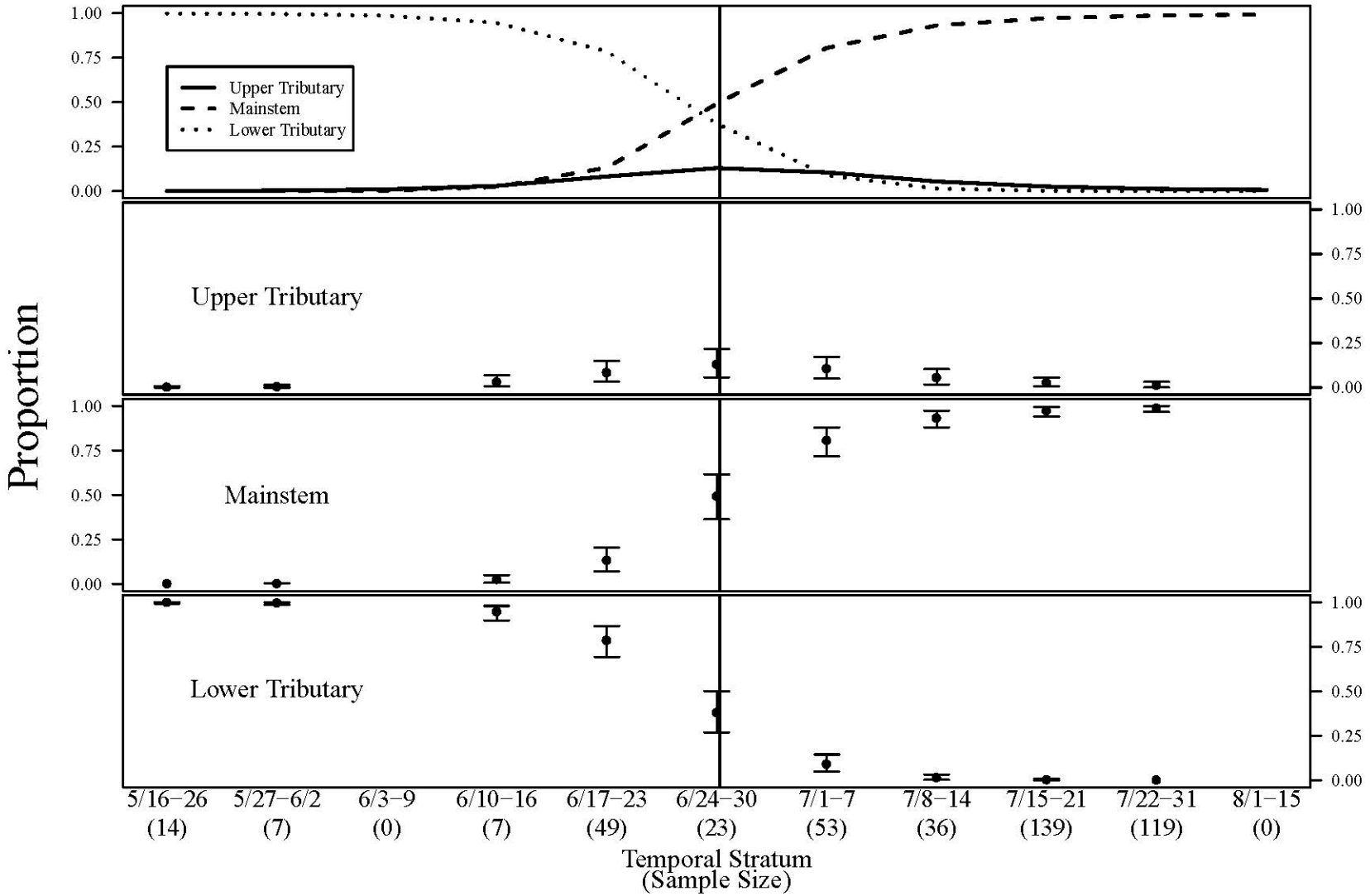

Figure 19.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish harvested in the lower Kenai River sport fishery in 2010.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

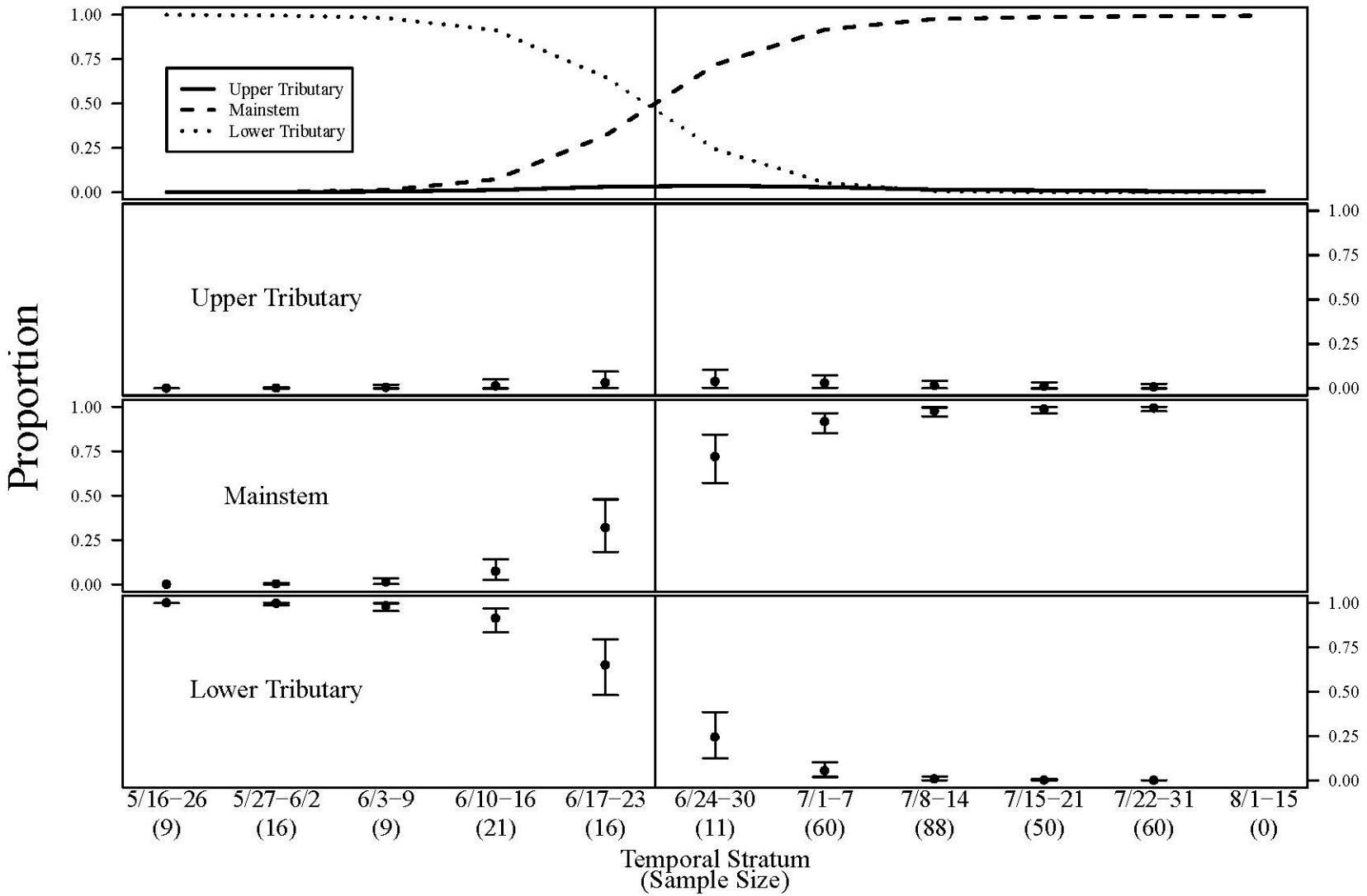

Figure 20.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish harvested in the lower Kenai River sport fishery in 2011.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

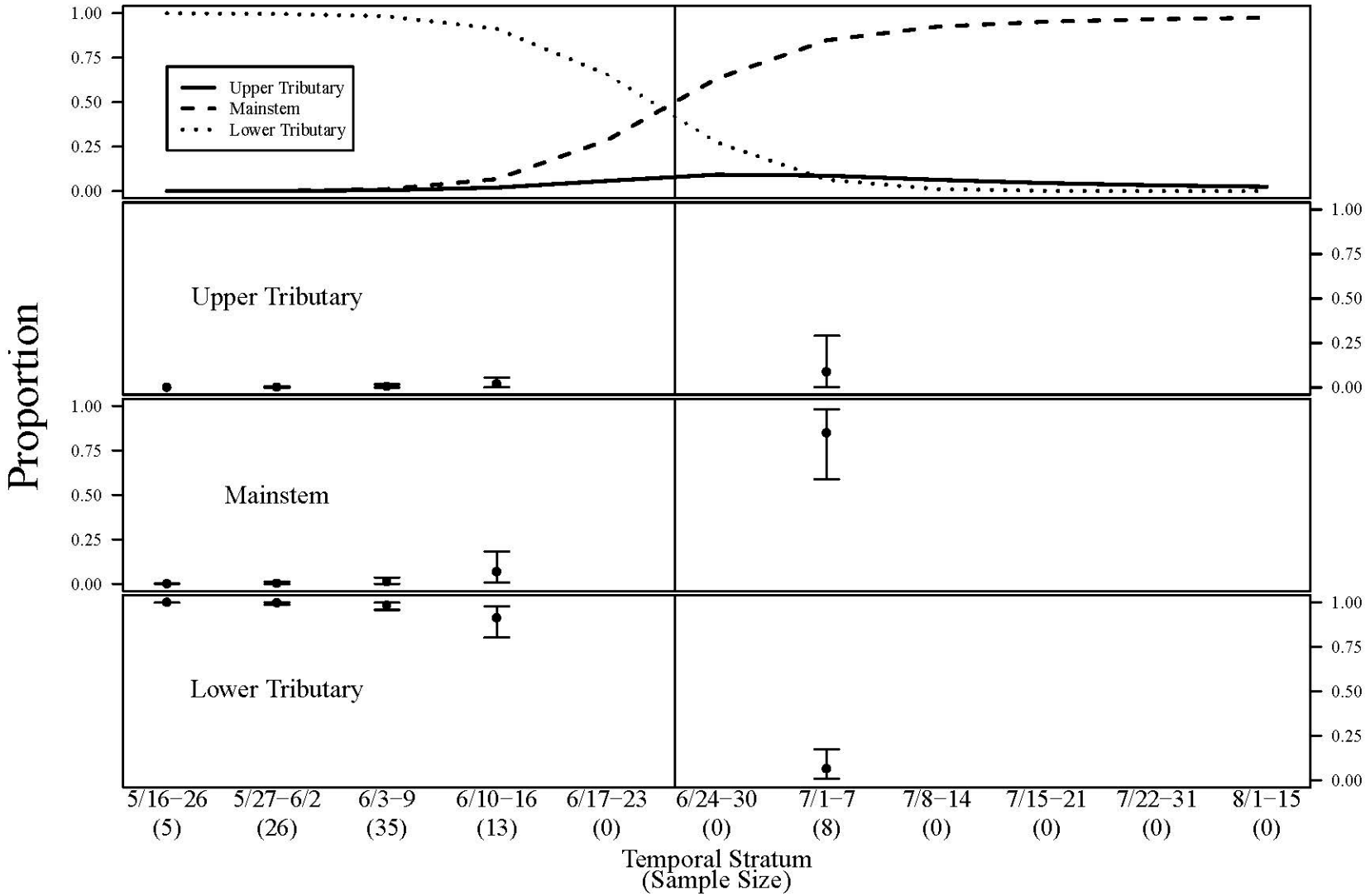

Figure 21.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish harvested in the lower Kenai River sport fishery in 2012.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

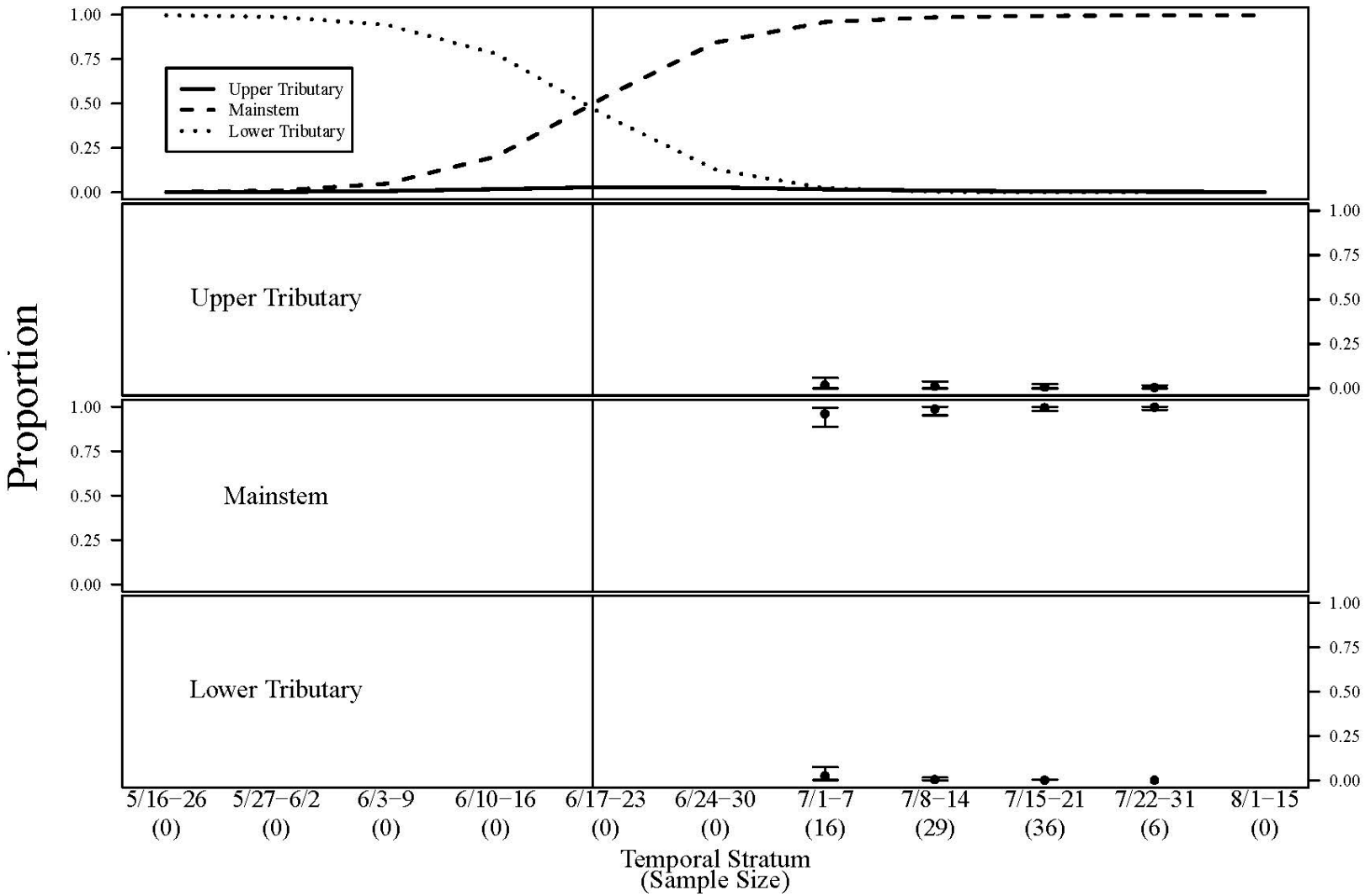

Figure 22.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish harvested in the lower Kenai River sport fishery in 2013.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

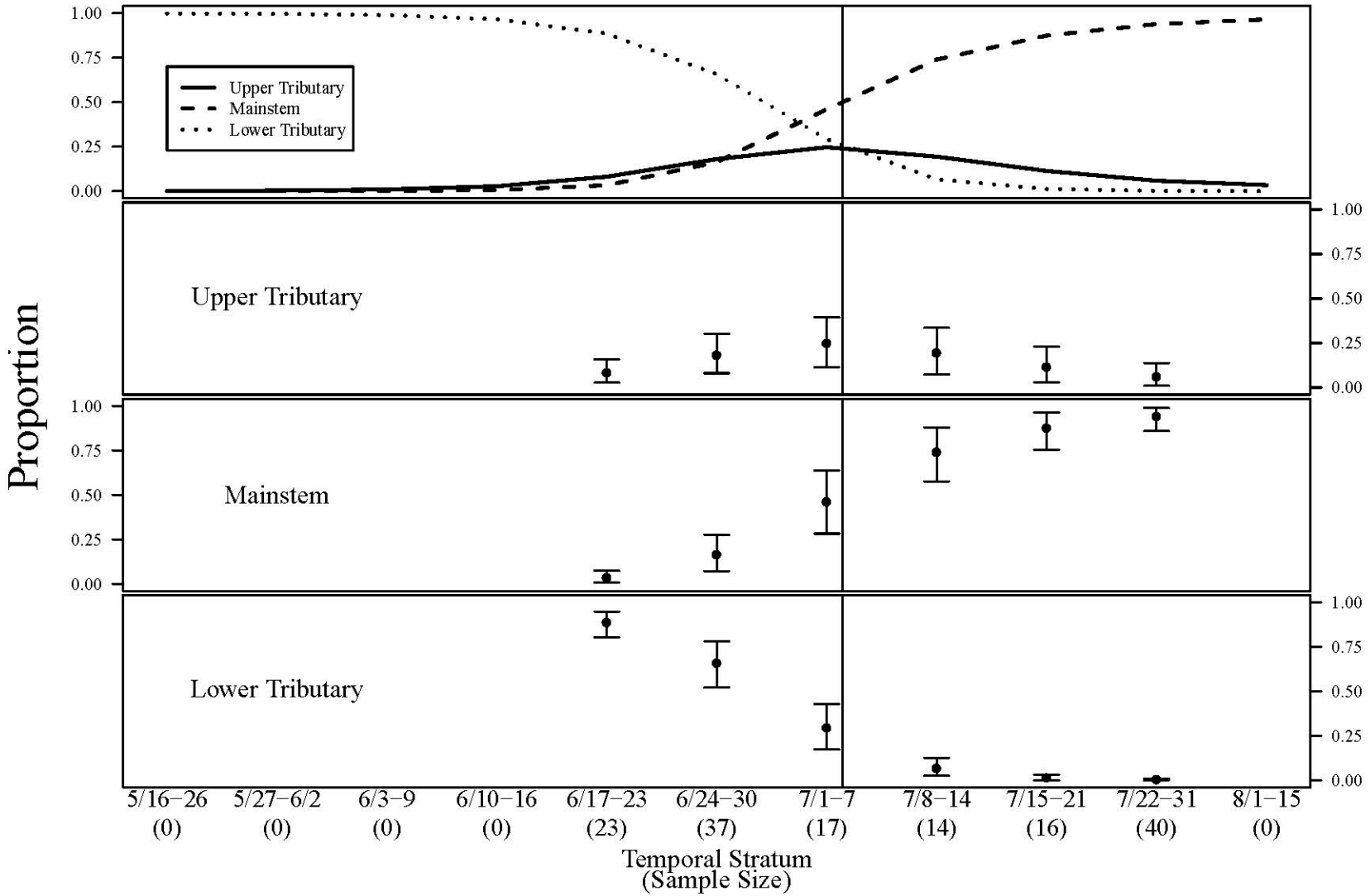

Figure 23.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish harvested in the middle Kenai River sport fishery in 2007.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

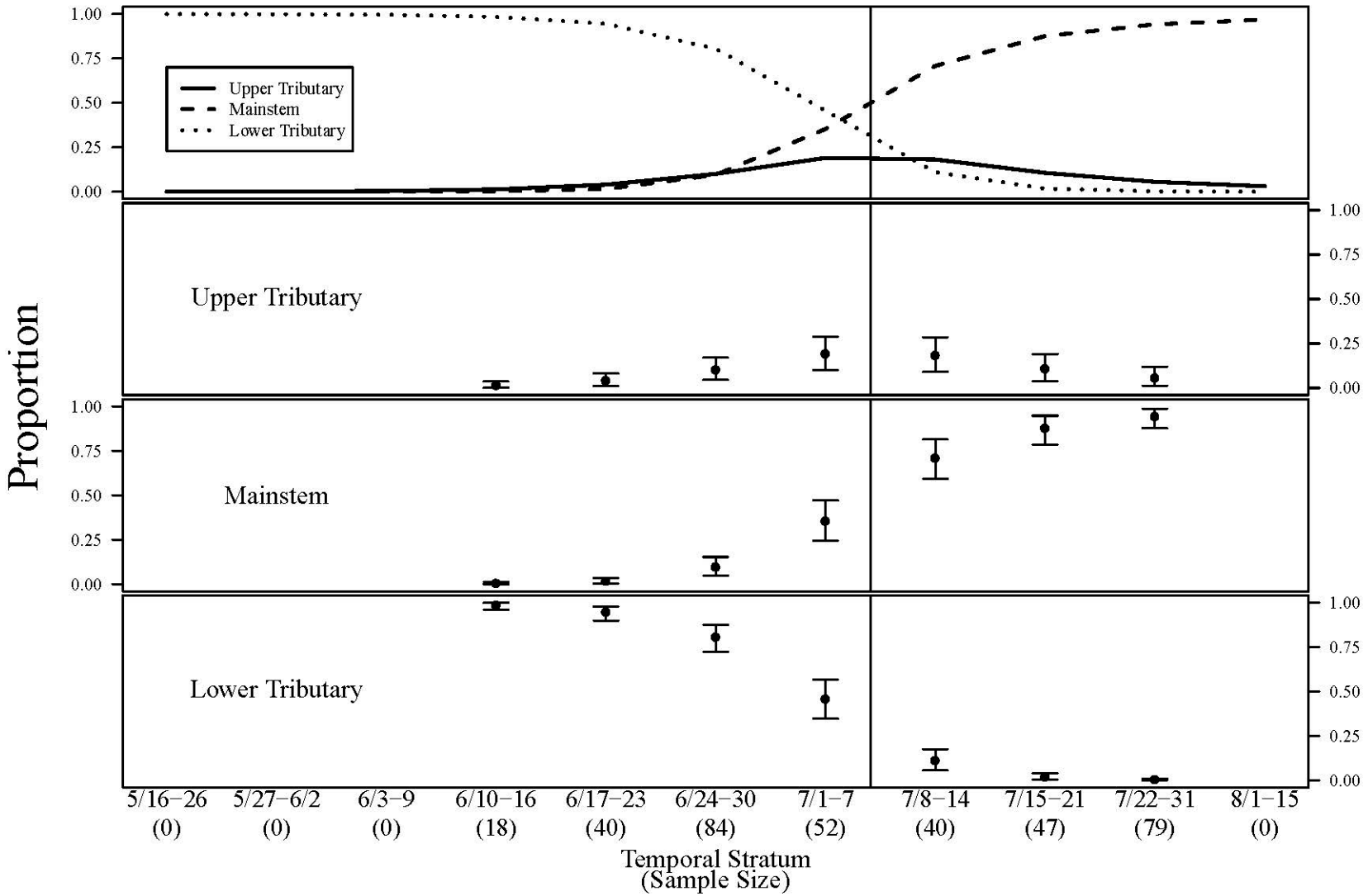

Figure 24.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish harvested in the middle Kenai River sport fishery in 2008.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

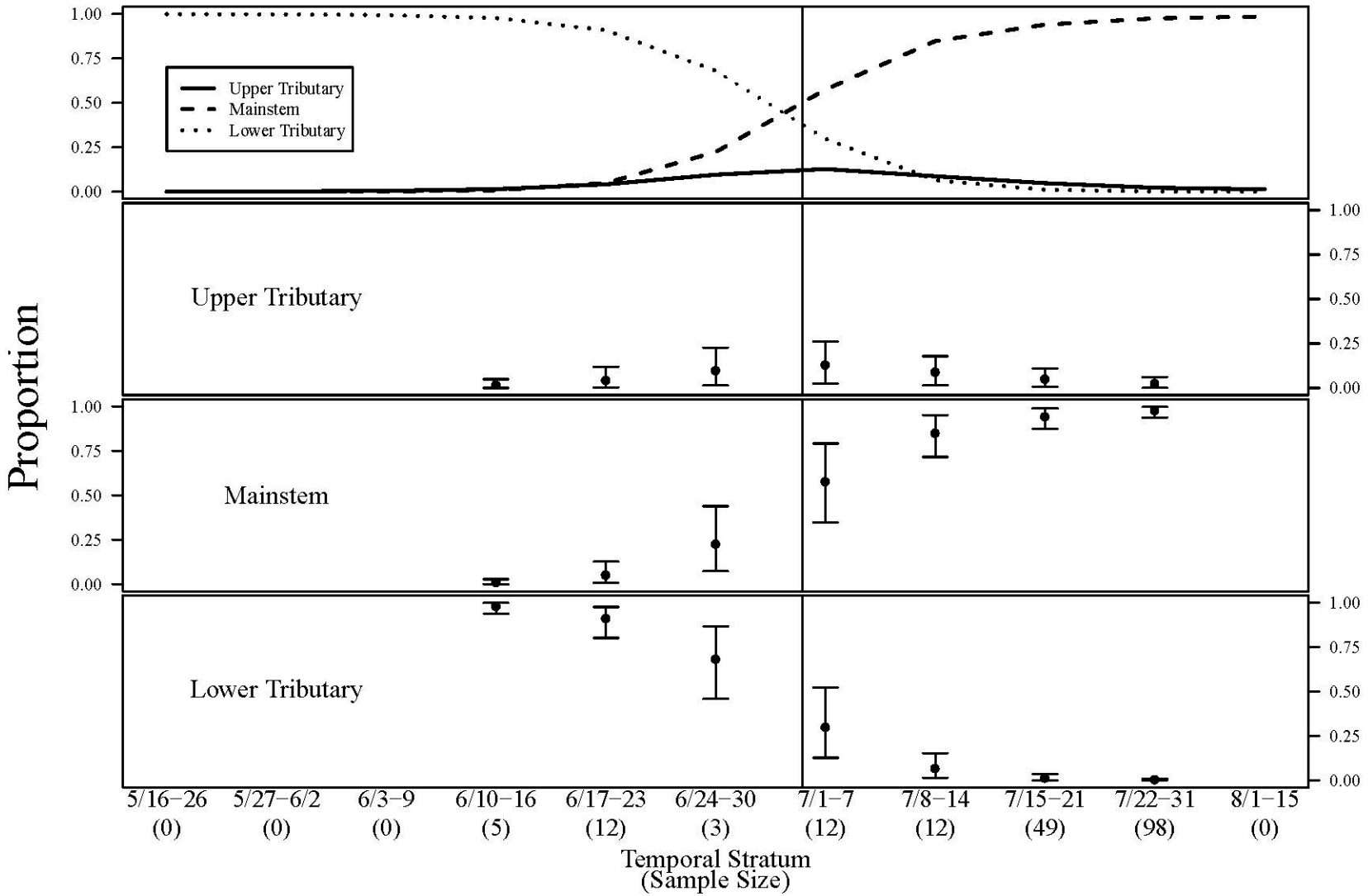

Figure 25.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish harvested in the middle Kenai River sport fishery in 2009.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

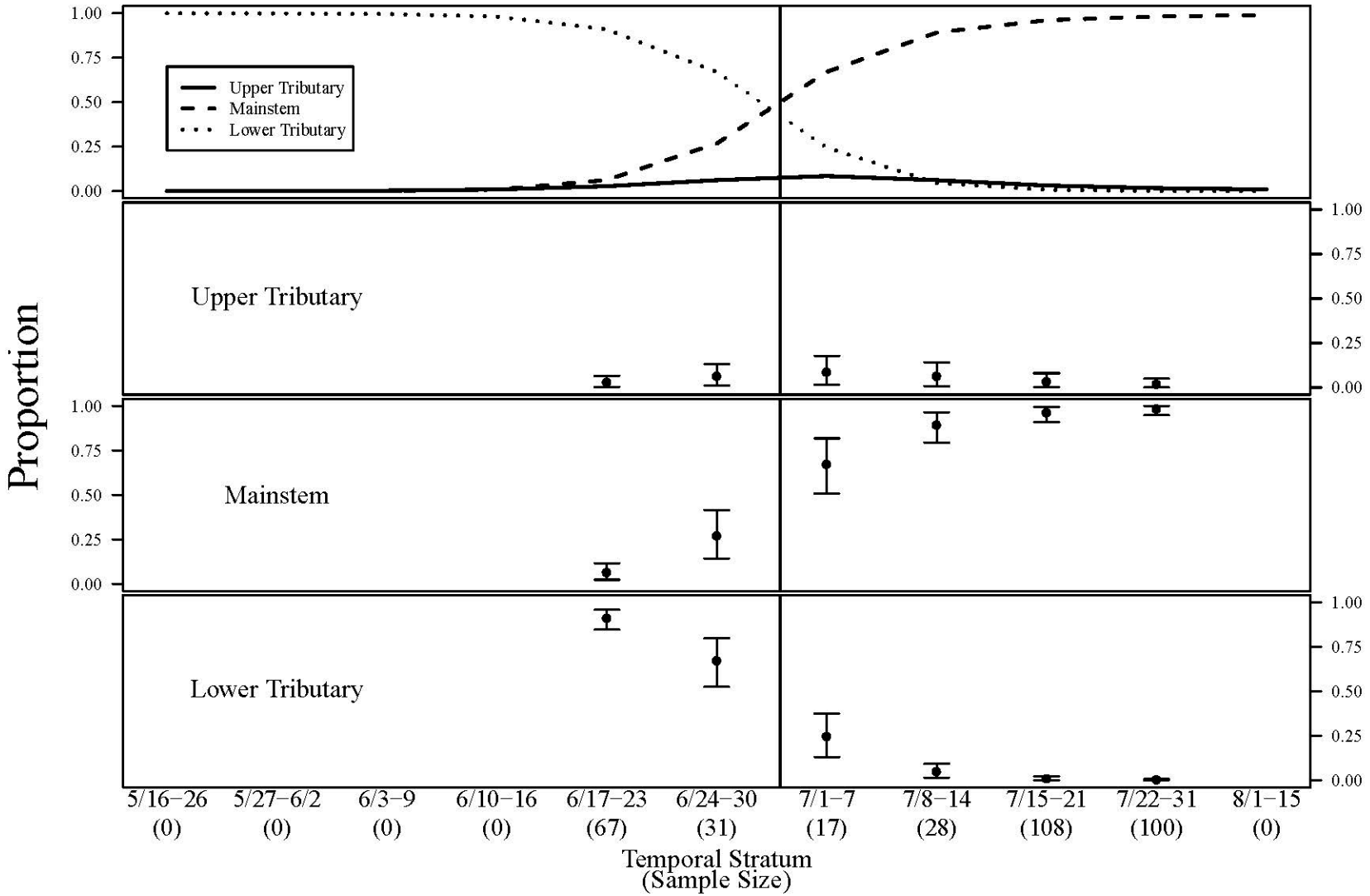

Figure 26.–Superimposed trend lines of stock composition estimates (top) and stock composition estimates (points) and 90% credibility intervals (bars) by reporting group (bottom 3) for fish harvested in the middle Kenai River sport fishery in 2010.

Note: vertical line indicates the approximate date when the stock composition of the inriver run is 50% Mainstem.

.

APPENDIX A: MODEL CODE FOR *RJAGS*

Appendix A1.–Model code for *rjags* used to estimate the stock composition of the inriver run, lower Kenai River sport harvest, and middle Kenai River sport harvest.

```
model{
 for(i in 1:C){
  for(l in 1:L){
   y[i,l]  ~ dbin(q[i,l],n[i,l])
   q[i,l] ~ dbeta(0.5,0.5)
  }#l
 }#i
 for(m in 1:M){
  z[m] ~ dcat(p[1:C,Fishery[m],Year[m],Week[m]])
  for(l in 1:L){
   x[m,l] ~ dbin(q[z[m],l],2)
  }#l
 }#m
 aveW <- (W+1)/2
 for(f in 1:F){
  for(t in 1:T){
   for(w in 1:W){
    for(g in 1:G){
     for(k in 1:Cg[g]){
      S0[g,k,f,t,w] ~ dgamma(SpriorPars[g,k],1)
      S[g,k,f,t,w] <- S0[g,k,f,t,w]/sum(S0[g,1:Cg[g],f,t,w])
      p[cmCg[g]+k,f,t,w] <- R[g,f,t,w]*S[g,k,f,t,w]
     }#k
    }#g
    for(g in 1:G){
     log(RpriorPars0[g,f,t,w]) <- alpha[g,f,t]+beta[g,f,t]*(w-aveW)
     RpriorPars[g,f,t,w] <- rho2/(1-rho2)*RpriorPars0[g,f,t,w]/sum(RpriorPars0[1:G,f,t,w])
     R0[g,f,t,w] ~ dgamma(RpriorPars[g,f,t,w],1)
     R[g,f,t,w] <- R0[g,f,t,w]/sum(R0[1:G,f,t,w])
    }#g
   }#w
  }#t
 }#f

 for(t in 1:T){
  for(g in 1:(G-1)){
   alpha[g,1,t] ~ dnorm(alphaDot[g],taualpha)
   beta[g,1,t] ~ dnorm(betaDot[g],taubeta)
  }#g
  alpha[G,1,t] <- 0
  beta[G,1,t] <- 0
 }#t
```

-continued-

Appendix A1.–Page 2 of 2.

```
for(f in 2:F){
   for(t in 1:T){
     for(g in 1:(G-1)){
       alpha[g,f,t] ~ dnorm(alpha[g,f-1,t],tauvaralpha)
       beta[g,f,t] ~ dnorm(beta[g,f-1,t],tauvarbeta)
     }#g
     alpha[G,f,t] <- 0
     beta[G,f,t] <- 0
   }#t
 }#f
 for(g in 1:(G-1)){
   alphaDot[g] ~ dnorm(0,0.001)
   betaDot[g] ~ dnorm(0,0.001)
 }#g
 alphaDot[G] <- 0
 betaDot[G] <- 0
 for(g in 1:G){
   for(k in 1:Cg[g]){
     SpriorPars[g,k] <- 1/Cg[g]
   }#k
 }#g
 rho2 ~ dbeta(1,1)
 taualpha ~ dgamma(0.001,0.001)
 taubeta ~ dgamma(0.001,0.001)
 tauvaralpha ~ dgamma(0.001,0.001)
 tauvarbeta ~ dgamma(0.001,0.001)
 sig2alpha <- 1/taualpha
 sig2beta <- 1/taubeta
 sigvar2alpha <- 1/tauvaralpha
 sigvar2beta <- 1/tauvarbeta
}#model
```

.

APPENDIX B: MEAN PROPORTIONAL RUN ESTIMATES FOR KENAI RIVER CHINOOK SALMON, 2003–2013

Appendix B1.–Mean proportional run estimates, standard deviations, and 95% confidence limits by year, stratum, and reporting group for Kenai River Chinook salmon, 2003–2013.

		Upper Tributary				Mainstem				Lower Tributary			
Year	Stratum	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%
2003													
	16–26 May	0.001	0.001	0	0.004	0	0.001	0	0.002	0.999	0.002	0.996	1
	27 May–2 Jun	0.003	0.004	0	0.012	0.004	0.005	0	0.014	0.993	0.007	0.980	1
	3–9 Jun	0.007	0.007	0	0.021	0.023	0.014	0.006	0.050	0.970	0.016	0.940	0.990
	10–16 Jun	0.020	0.014	0.002	0.047	0.113	0.036	0.059	0.177	0.868	0.039	0.799	0.926
	17–23 Jun	0.037	0.022	0.008	0.080	0.432	0.070	0.317	0.548	0.530	0.071	0.416	0.649
	24–30 Jun	0.040	0.022	0.009	0.081	0.793	0.050	0.704	0.868	0.167	0.046	0.101	0.250
	1–7 Jul	0.023	0.015	0.004	0.051	0.950	0.020	0.913	0.978	0.027	0.013	0.009	0.052
	8–14 Jul	0.014	0.011	0.001	0.034	0.982	0.012	0.959	0.996	0.005	0.005	0	0.014
	15–21 Jul	0.008	0.008	0	0.023	0.991	0.008	0.976	1	0.001	0.002	0	0.005
	22–31 Jul	0.005	0.006	0	0.018	0.995	0.006	0.982	1	0	0	0	0.001
	1–15 Aug	0.003	0.005	0	0.012	0.997	0.005	0.988	1	0	0	0	0
2004													
	16–26 May	0.002	0.004	0	0.009	0.002	0.003	0	0.007	0.996	0.005	0.987	1
	27 May–2 Jun	0.007	0.008	0	0.022	0.008	0.007	0.001	0.022	0.985	0.011	0.963	0.997
	3–9 Jun	0.023	0.017	0.004	0.056	0.047	0.022	0.017	0.088	0.930	0.028	0.877	0.969
	10–16 Jun	0.070	0.036	0.022	0.137	0.200	0.059	0.113	0.305	0.730	0.067	0.611	0.831
	17–23 Jun	0.129	0.051	0.055	0.220	0.556	0.077	0.432	0.682	0.315	0.068	0.207	0.431
	24–30 Jun	0.115	0.046	0.046	0.197	0.806	0.054	0.712	0.890	0.080	0.028	0.039	0.130
	1–7 Jul	0.084	0.037	0.030	0.151	0.902	0.039	0.833	0.960	0.014	0.008	0.003	0.030
	8–14 Jul	0.057	0.029	0.016	0.111	0.940	0.030	0.886	0.982	0.003	0.003	0	0.009
	15–21 Jul	0.042	0.025	0.009	0.088	0.957	0.025	0.911	0.990	0	0.001	0	0.002
	22–31 Jul	0.029	0.020	0.004	0.068	0.971	0.020	0.932	0.996	0	0	0	0
	1–15 Aug	0.018	0.016	0.001	0.052	0.982	0.016	0.948	0.999	0	0	0	0

-continued-

Appendix B1.–Page 2 of 6.

		Upper Tributary				Mainstem				Lower Tributary			
Year	Stratum	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%
2005													
	16–26 May	0	0.001	0	0.002	0.001	0.001	0	0.003	0.999	0.001	0.996	1
	27 May–2 Jun	0.002	0.003	0	0.008	0.004	0.005	0	0.014	0.994	0.006	0.982	1
	3–9 Jun	0.005	0.006	0	0.017	0.025	0.014	0.007	0.051	0.970	0.015	0.942	0.989
	10–16 Jun	0.020	0.015	0.003	0.048	0.145	0.044	0.080	0.222	0.835	0.045	0.755	0.904
	17–23 Jun	0.041	0.025	0.009	0.088	0.467	0.077	0.340	0.596	0.492	0.074	0.370	0.612
	24–30 Jun	0.045	0.027	0.010	0.095	0.822	0.050	0.732	0.896	0.133	0.038	0.077	0.202
	1–7 Jul	0.035	0.023	0.006	0.079	0.940	0.029	0.887	0.978	0.025	0.013	0.008	0.050
	8–14 Jul	0.023	0.018	0.002	0.058	0.972	0.019	0.936	0.995	0.004	0.005	0	0.013
	15–21 Jul	0.016	0.015	0.001	0.045	0.983	0.015	0.954	0.999	0.001	0.001	0	0.003
	22–31 Jul	0.013	0.013	0	0.038	0.987	0.013	0.962	1	0	0	0	0
	1–15 Aug	0.008	0.011	0	0.031	0.992	0.011	0.969	1	0	0	0	0
2006													
	16–26 May	0.001	0.002	0	0.004	0	0	0	0	0.999	0.002	0.996	1
	27 May–2 Jun	0.003	0.004	0	0.011	0.002	0.003	0	0.008	0.996	0.005	0.985	1
	3–9 Jun	0.009	0.008	0	0.024	0.010	0.009	0.001	0.028	0.981	0.012	0.958	0.995
	10–16 Jun	0.029	0.018	0.006	0.064	0.062	0.029	0.023	0.115	0.909	0.032	0.850	0.955
	17–23 Jun	0.071	0.034	0.023	0.134	0.297	0.076	0.181	0.428	0.633	0.072	0.508	0.747
	24–30 Jun	0.094	0.040	0.035	0.167	0.694	0.071	0.572	0.804	0.212	0.053	0.131	0.306
	1–7 Jul	0.056	0.029	0.016	0.110	0.906	0.036	0.840	0.958	0.038	0.017	0.015	0.070
	8–14 Jul	0.032	0.019	0.007	0.067	0.963	0.020	0.925	0.990	0.006	0.005	0	0.017
	15–21 Jul	0.016	0.012	0.002	0.040	0.982	0.013	0.958	0.998	0.001	0.003	0	0.006
	22–31 Jul	0.008	0.007	0	0.023	0.992	0.007	0.977	1	0	0	0	0
	1–15 Aug	0.005	0.006	0	0.016	0.995	0.006	0.984	1	0	0	0	0

-continued-

Appendix B1.–Page 3 of 6.

		Upper Tributary				Mainstem				Lower Tributary			
Year	Stratum	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%
2007													
	16–26 May	0.001	0.002	0	0.005	0	0	0	0	0.999	0.002	0.995	1
	27 May–2 Jun	0.002	0.003	0	0.009	0.002	0.004	0	0.008	0.996	0.005	0.986	1
	3–9 Jun	0.009	0.009	0.001	0.026	0.012	0.010	0.001	0.031	0.979	0.013	0.953	0.995
	10–16 Jun	0.028	0.017	0.006	0.061	0.054	0.026	0.019	0.103	0.918	0.032	0.859	0.964
	17–23 Jun	0.074	0.034	0.026	0.138	0.245	0.074	0.133	0.375	0.681	0.078	0.549	0.806
	24–30 Jun	0.106	0.044	0.043	0.186	0.612	0.088	0.460	0.750	0.282	0.076	0.172	0.417
	1–7 Jul	0.082	0.038	0.028	0.151	0.854	0.052	0.760	0.930	0.064	0.029	0.026	0.119
	8–14 Jul	0.053	0.027	0.016	0.104	0.936	0.030	0.881	0.977	0.011	0.009	0.001	0.028
	15–21 Jul	0.034	0.021	0.007	0.073	0.965	0.021	0.924	0.992	0.002	0.002	0	0.006
	22–31 Jul	0.019	0.015	0.002	0.047	0.981	0.015	0.953	0.998	0	0	0	0.001
	1–15 Aug	0.012	0.012	0	0.035	0.988	0.012	0.965	1	0	0	0	0
2008													
	16–26 May	0	0.001	0	0.003	0	0	0	0	0.999	0.001	0.997	1
	27 May–2 Jun	0.002	0.003	0	0.008	0.001	0.002	0	0.004	0.997	0.004	0.990	1
	3–9 Jun	0.006	0.006	0	0.018	0.006	0.006	0	0.018	0.988	0.009	0.971	0.998
	10–16 Jun	0.018	0.013	0.003	0.042	0.042	0.021	0.014	0.081	0.940	0.025	0.893	0.974
	17–23 Jun	0.053	0.026	0.017	0.100	0.203	0.061	0.112	0.311	0.744	0.064	0.632	0.840
	24–30 Jun	0.083	0.035	0.033	0.147	0.586	0.078	0.453	0.710	0.331	0.070	0.221	0.453
	1–7 Jul	0.070	0.033	0.025	0.130	0.858	0.045	0.778	0.922	0.072	0.026	0.035	0.120
	8–14 Jul	0.034	0.020	0.008	0.070	0.956	0.021	0.917	0.985	0.010	0.007	0.002	0.024
	15–21 Jul	0.019	0.013	0.003	0.045	0.979	0.014	0.952	0.997	0.002	0.003	0	0.007
	22–31 Jul	0.011	0.010	0.001	0.032	0.989	0.010	0.968	0.999	0	0	0	0
	1–15 Aug	0.007	0.008	0	0.023	0.993	0.008	0.977	1	0	0	0	0

-continued-

Appendix B1.–Page 4 of 6.

		Upper Tributary				Mainstem				Lower Tributary			
Year	Stratum	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%
2009													
	16–26 May	0.001	0.003	0	0.005	0	0.001	0	0.003	0.999	0.003	0.994	1
	27 May–2 Jun	0.003	0.004	0	0.010	0.002	0.004	0	0.009	0.995	0.005	0.985	1
	3–9 Jun	0.011	0.010	0.001	0.029	0.015	0.011	0.002	0.036	0.974	0.014	0.948	0.992
	10–16 Jun	0.026	0.018	0.005	0.060	0.078	0.032	0.033	0.137	0.895	0.035	0.834	0.946
	17–23 Jun	0.063	0.034	0.017	0.126	0.340	0.079	0.214	0.474	0.597	0.075	0.472	0.718
	24–30 Jun	0.075	0.037	0.024	0.143	0.723	0.068	0.603	0.827	0.202	0.053	0.123	0.297
	1–7 Jul	0.051	0.027	0.013	0.101	0.909	0.034	0.848	0.959	0.040	0.017	0.016	0.071
	8–14 Jul	0.027	0.017	0.005	0.058	0.964	0.019	0.929	0.990	0.009	0.008	0.001	0.025
	15–21 Jul	0.014	0.011	0.001	0.035	0.984	0.011	0.963	0.998	0.001	0.002	0	0.006
	22–31 Jul	0.008	0.008	0	0.023	0.992	0.008	0.977	1	0	0	0	0
	1–15 Aug	0.005	0.005	0	0.015	0.995	0.005	0.985	1	0	0	0	0
2010													
	16–26 May	0.001	0.002	0	0.006	0	0	0	0	0.999	0.002	0.994	1
	27 May–2 Jun	0.004	0.005	0	0.014	0.002	0.003	0	0.006	0.994	0.006	0.983	1
	3–9 Jun	0.013	0.010	0.002	0.033	0.011	0.009	0.001	0.028	0.976	0.014	0.950	0.993
	10–16 Jun	0.045	0.022	0.015	0.086	0.056	0.021	0.025	0.094	0.899	0.030	0.847	0.944
	17–23 Jun	0.107	0.038	0.050	0.176	0.254	0.058	0.163	0.354	0.639	0.061	0.537	0.738
	24–30 Jun	0.134	0.044	0.067	0.210	0.641	0.066	0.529	0.744	0.226	0.051	0.150	0.316
	1–7 Jul	0.095	0.032	0.047	0.153	0.861	0.039	0.793	0.919	0.043	0.017	0.020	0.076
	8–14 Jul	0.069	0.026	0.031	0.115	0.924	0.027	0.875	0.963	0.008	0.006	0.001	0.020
	15–21 Jul	0.037	0.017	0.014	0.069	0.962	0.017	0.930	0.986	0.001	0.002	0	0.005
	22–31 Jul	0.017	0.012	0.003	0.041	0.983	0.012	0.959	0.997	0	0	0	0
	1–15 Aug	0.010	0.009	0.001	0.027	0.990	0.009	0.973	0.999	0	0	0	0

-continued-

Appendix B1.–Page 5 of 6.

		Upper Tributary				Mainstem				Lower Tributary			
Year	Stratum	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%
2011													
	16–26 May	0.001	0.001	0	0.003	0.001	0.003	0	0.007	0.998	0.003	0.992	1
	27 May–2 Jun	0.003	0.004	0	0.010	0.006	0.006	0	0.018	0.992	0.007	0.977	0.999
	3–9 Jun	0.010	0.009	0.001	0.028	0.035	0.018	0.012	0.070	0.955	0.020	0.917	0.981
	10–16 Jun	0.022	0.015	0.004	0.051	0.175	0.049	0.104	0.265	0.802	0.050	0.712	0.876
	17–23 Jun	0.044	0.026	0.011	0.093	0.550	0.075	0.426	0.676	0.406	0.070	0.292	0.522
	24–30 Jun	0.051	0.026	0.015	0.099	0.849	0.045	0.770	0.918	0.100	0.032	0.052	0.158
	1–7 Jul	0.031	0.019	0.006	0.067	0.949	0.024	0.905	0.982	0.020	0.012	0.005	0.042
	8–14 Jul	0.019	0.014	0.002	0.046	0.977	0.015	0.949	0.996	0.004	0.004	0	0.012
	15–21 Jul	0.011	0.010	0.001	0.031	0.988	0.010	0.969	0.999	0	0.001	0	0.002
	22–31 Jul	0.007	0.008	0	0.022	0.993	0.008	0.977	1	0	0	0	0
	1–15 Aug	0.005	0.007	0	0.019	0.995	0.007	0.981	1	0	0	0	0
2012													
	16–26 May	0.001	0.001	0	0.004	0	0.001	0	0.002	0.999	0.002	0.996	1
	27 May–2 Jun	0.002	0.004	0	0.010	0.002	0.004	0	0.010	0.995	0.005	0.985	1
	3–9 Jun	0.010	0.009	0	0.027	0.016	0.012	0.002	0.039	0.975	0.015	0.947	0.993
	10–16 Jun	0.030	0.020	0.005	0.069	0.089	0.040	0.036	0.162	0.881	0.042	0.805	0.939
	17–23 Jun	0.069	0.039	0.018	0.143	0.343	0.091	0.203	0.503	0.588	0.085	0.442	0.72
	24–30 Jun	0.083	0.048	0.020	0.175	0.733	0.080	0.588	0.856	0.184	0.056	0.100	0.283
	1–7 Jul	0.060	0.038	0.012	0.132	0.905	0.044	0.821	0.965	0.035	0.017	0.012	0.068
	8–14 Jul	0.038	0.026	0.005	0.088	0.956	0.027	0.904	0.991	0.006	0.006	0	0.017
	15–21 Jul	0.021	0.017	0.001	0.055	0.977	0.018	0.942	0.998	0.001	0.003	0	0.006
	22–31 Jul	0.013	0.012	0	0.038	0.987	0.012	0.962	1	0	0	0	0
	1–15 Aug	0.008	0.009	0	0.027	0.992	0.009	0.973	1	0	0	0	0

-continued-

Appendix B1.–Page 6 of 6.

		Upper Tributary				Mainstem				Lower Tributary			
Year	Stratum	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%
2013													
	16–26 May	0.001	0.002	0	0.003	0	0.001	0	0.002	0.999	0.002	0.996	1
	27 May–2 Jun	0.002	0.004	0	0.009	0.002	0.004	0	0.010	0.995	0.006	0.985	1
	3–9 Jun	0.008	0.009	0	0.025	0.019	0.013	0.004	0.044	0.973	0.016	0.943	0.992
	10–16 Jun	0.023	0.017	0.003	0.057	0.080	0.037	0.030	0.150	0.896	0.041	0.821	0.954
	17–23 Jun	0.055	0.033	0.013	0.119	0.328	0.091	0.187	0.484	0.617	0.090	0.467	0.761
	24–30 Jun	0.068	0.040	0.017	0.143	0.707	0.083	0.563	0.832	0.225	0.068	0.127	0.349
	1–7 Jul	0.052	0.031	0.011	0.111	0.903	0.042	0.826	0.961	0.045	0.023	0.016	0.089
	8–14 Jul	0.030	0.021	0.004	0.069	0.963	0.023	0.919	0.991	0.008	0.007	0.001	0.021
	15–21 Jul	0.020	0.016	0.002	0.052	0.979	0.017	0.946	0.997	0.001	0.003	0	0.007
	22–31 Jul	0.015	0.013	0.001	0.039	0.985	0.013	0.960	0.999	0	0.001	0	0.002
	1–15 Aug	0.007	0.008	0	0.024	0.993	0.008	0.976	1	0	0	0	0

Appendix B2.–Mean proportional sport harvest estimates, standard deviations, and 95% confidence limits by year, stratum, and reporting group for Kenai River Chinook salmon downstream of the Soldotna Bridge, 2007–2010.

		Upper Tributary				Mainstem				Lower Tributary			
Year	Stratum	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%
2006													
	16–26 May	0	0.001	0	0.002	0	0	0	0	1	0.001	0.998	1
	27 May–2 Jun	–	–	–	–	–	–	–	–	–	–	–	–
	3–9 Jun	0.005	0.006	0	0.016	0.004	0.005	0	0.013	0.992	0.008	0.976	0.999
	10–16 Jun	0.016	0.013	0.001	0.041	0.027	0.016	0.007	0.058	0.958	0.021	0.919	0.985
	17–23 Jun	0.044	0.029	0.008	0.099	0.155	0.051	0.082	0.248	0.800	0.056	0.700	0.883
	24–30 Jun	0.076	0.042	0.018	0.153	0.550	0.081	0.415	0.679	0.374	0.074	0.257	0.501
	1–7 Jul	0.055	0.032	0.012	0.114	0.868	0.046	0.786	0.935	0.077	0.031	0.034	0.135
	8–14 Jul	0.032	0.021	0.005	0.072	0.954	0.026	0.904	0.987	0.015	0.012	0.002	0.038
	15–21 Jul	0.014	0.012	0.001	0.037	0.984	0.013	0.959	0.999	0.002	0.003	0	0.008
	22–31 Jul	0.007	0.008	0	0.022	0.993	0.009	0.977	1	0	0.001	0	0.002
2007													
	16–26 May	0	0	0	0.001	0	0	0	0	1	0	0.999	1
	27 May–2 Jun	0.002	0.003	0	0.007	0.001	0.002	0	0.008	0.997	0.004	0.989	1
	3–9 Jun	0.005	0.006	0	0.017	0.005	0.005	0	0.015	0.990	0.008	0.974	0.999
	10–16 Jun	0.015	0.011	0.002	0.037	0.028	0.016	0.008	0.059	0.957	0.020	0.919	0.984
	17–23 Jun	0.047	0.027	0.011	0.098	0.162	0.055	0.082	0.260	0.791	0.060	0.685	0.883
	24–30 Jun	0.084	0.041	0.025	0.158	0.529	0.089	0.381	0.671	0.387	0.083	0.259	0.531
	1–7 Jul	0.067	0.036	0.017	0.134	0.840	0.055	0.742	0.921	0.093	0.037	0.043	0.162
	8–14 Jul	0.041	0.025	0.008	0.088	0.942	0.029	0.887	0.982	0.017	0.012	0.003	0.040
	15–21 Jul	0.026	0.019	0.003	0.062	0.971	0.019	0.935	0.995	0.002	0.003	0	0.009
	22–31 Jul	0.012	0.012	0	0.036	0.987	0.012	0.964	1	0	0	0	0.001
2008													
	16–26 May	0	0.001	0	0.001	0	0	0	0	1	0.001	0.999	1
	27 May–2 Jun	0.001	0.003	0	0.007	0	0.001	0	0.002	0.998	0.003	0.992	1
	3–9 Jun	0.005	0.006	0	0.016	0.002	0.003	0	0.008	0.993	0.007	0.980	1
	10–16 Jun	0.014	0.011	0.002	0.035	0.014	0.009	0.002	0.032	0.973	0.014	0.946	0.991
	17–23 Jun	0.041	0.024	0.011	0.087	0.092	0.036	0.040	0.158	0.867	0.043	0.789	0.930
	24–30 Jun	0.085	0.039	0.031	0.158	0.393	0.084	0.256	0.533	0.522	0.083	0.386	0.659
	1–7 Jul	0.082	0.039	0.027	0.154	0.781	0.064	0.666	0.876	0.137	0.047	0.070	0.224
	8–14 Jul	0.047	0.026	0.012	0.096	0.928	0.032	0.869	0.973	0.025	0.015	0.007	0.053
	15–21 Jul	0.034	0.020	0.008	0.072	0.962	0.022	0.921	0.990	0.004	0.005	0	0.014
	22–31 Jul	0.014	0.012	0.001	0.038	0.985	0.012	0.961	0.999	0.001	0.002	0	0.004

-continued-

Appendix B2.–Page 2 of 3.

		Upper Tributary				Mainstem				Lower Tributary			
Year	Stratum	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%
2009													
	16–26 May	0	0	0	0	0	0	0	0	1	0	1	1
	27 May–2 Jun	0.001	0.001	0	0.003	0.001	0.002	0	0.004	0.999	0.002	0.994	1
	3–9 Jun	0.003	0.004	0	0.012	0.005	0.005	0	0.014	0.992	0.007	0.979	0.999
	10–16 Jun	0.010	0.010	0	0.029	0.030	0.018	0.008	0.063	0.960	0.020	0.923	0.987
	17–23 Jun	0.027	0.020	0.004	0.066	0.162	0.055	0.082	0.264	0.812	0.057	0.709	0.895
	24–30 Jun	0.046	0.031	0.009	0.108	0.546	0.088	0.397	0.686	0.407	0.082	0.276	0.548
	1–7 Jul	0.038	0.025	0.006	0.087	0.880	0.042	0.803	0.940	0.081	0.030	0.039	0.136
	8–14 Jul	0.021	0.016	0.002	0.052	0.965	0.020	0.927	0.991	0.015	0.010	0.003	0.033
	15–21 Jul	0.011	0.010	0	0.030	0.987	0.011	0.966	0.999	0.002	0.004	0	0.009
	22–31 Jul	0.007	0.008	0	0.022	0.993	0.008	0.978	1	0	0	0	0
2010													
	16–26 May	0.002	0.003	0	0.008	0	0	0	0	0.998	0.003	0.992	1
	27 May–2 Jun	0.003	0.005	0	0.014	0.001	0.001	0	0.004	0.996	0.005	0.985	1
	3–9 Jun	–	–	–	–	–	–	–	–	–	–	–	–
	10–16 Jun	0.030	0.020	0.006	0.069	0.024	0.014	0.006	0.050	0.946	0.025	0.899	0.979
	17–23 Jun	0.083	0.036	0.033	0.150	0.132	0.041	0.070	0.204	0.785	0.052	0.693	0.866
	24–30 Jun	0.129	0.049	0.057	0.216	0.491	0.077	0.363	0.615	0.379	0.071	0.269	0.501
	1–7 Jul	0.105	0.037	0.050	0.171	0.805	0.049	0.718	0.880	0.090	0.030	0.048	0.145
	8–14 Jul	0.054	0.027	0.017	0.103	0.931	0.029	0.879	0.973	0.014	0.009	0.003	0.031
	15–21 Jul	0.026	0.016	0.005	0.055	0.972	0.016	0.942	0.993	0.002	0.003	0	0.008
	22–31 Jul	0.013	0.010	0.001	0.033	0.987	0.010	0.967	0.999	0	0	0	0
2011													
	16–26 May	0	0.001	0	0.001	0	0	0	0	1	0.001	0.999	1
	27 May–2 Jun	0.001	0.003	0	0.008	0.002	0.004	0	0.009	0.996	0.005	0.986	1
	3–9 Jun	0.005	0.008	0	0.021	0.013	0.011	0.001	0.034	0.982	0.014	0.955	0.998
	10–16 Jun	0.014	0.017	0	0.050	0.073	0.036	0.026	0.141	0.913	0.042	0.834	0.968
	17–23 Jun	0.031	0.030	0.002	0.095	0.320	0.090	0.184	0.478	0.649	0.094	0.480	0.794
	24–30 Jun	0.038	0.033	0.003	0.105	0.718	0.084	0.571	0.844	0.244	0.079	0.125	0.385
	1–7 Jul	0.029	0.022	0.004	0.073	0.916	0.035	0.851	0.965	0.054	0.026	0.020	0.103
	8–14 Jul	0.016	0.014	0.001	0.042	0.976	0.016	0.945	0.996	0.008	0.007	0	0.022
	15–21 Jul	0.012	0.012	0	0.035	0.987	0.013	0.962	1	0.001	0.003	0	0.007
	22–31 Jul	0.007	0.009	0	0.025	0.992	0.009	0.975	1	0	0.001	0	0.001

-continued-

Appendix B2.–Page 3 of 3.

		Upper Tributary				Mainstem				Lower Tributary			
Year	Stratum	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%
2012													
	16–26 May	0	0	0	0	0	0	0	0.001	1	0	0.999	1
	27 May–2 Jun	0.001	0.003	0	0.007	0.002	0.005	0	0.011	0.996	0.006	0.986	1
	3–9 Jun	0.005	0.006	0	0.018	0.011	0.013	0	0.036	0.983	0.014	0.957	0.998
	10–16 Jun	0.020	0.018	0.001	0.056	0.068	0.057	0.009	0.181	0.912	0.057	0.802	0.978
	17–23 Jun	–	–	–	–	–	–	–	–	–	–	–	–
	24–30 Jun	–	–	–	–	–	–	–	–	–	–	–	–
	1–7 Jul	0.087	0.093	0.003	0.290	0.848	0.126	0.589	0.981	0.065	0.056	0.009	0.174
	8–14 Jul	–	–	–	–	–	–	–	–	–	–	–	–
	15–21 Jul	–	–	–	–	–	–	–	–	–	–	–	–
	22–31 Jul	–	–	–	–	–	–	–	–	–	–	–	–
2013													
	16–26 May	–	–	–	–	–	–	–	–	–	–	–	–
	27 May–2 Jun	–	–	–	–	–	–	–	–	–	–	–	–
	3–9 Jun	–	–	–	–	–	–	–	–	–	–	–	–
	10–16 Jun	–	–	–	–	–	–	–	–	–	–	–	–
	17–23 Jun	–	–	–	–	–	–	–	–	–	–	–	–
	24–30 Jun	–	–	–	–	–	–	–	–	–	–	–	–
	1–7 Jul	0.017	0.022	0	0.059	0.959	0.038	0.887	0.995	0.024	0.025	0.002	0.074
	8–14 Jul	0.010	0.014	0	0.038	0.986	0.017	0.952	1	0.004	0.006	0	0.016
	15–21 Jul	0.006	0.009	0	0.023	0.994	0.009	0.976	1	0	0.001	0	0.003
	22–31 Jul	0.004	0.007	0	0.017	0.996	0.007	0.983	1	0	0	0	0

Appendix B3.–Mean proportional sport harvest estimates, standard deviations, and 95% confidence limits by year, stratum, and reporting group for Kenai River Chinook salmon between the Moose River confluence and the Soldotna Bridge, 2007–2010.

		Upper Tributary				Mainstem				Lower Tributary			
Year	Stratum	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%	Mean	SD	CI 5%	CI 95%
2007													
	10–16 Jun	–	–	–	–	–	–	–	–	–	–	–	–
	17–23 Jun	0.081	0.041	0.027	0.158	0.034	0.021	0.007	0.074	0.885	0.045	0.803	0.948
	24–30 Jun	0.180	0.067	0.080	0.301	0.163	0.063	0.071	0.277	0.657	0.079	0.521	0.780
	1–7 Jul	0.247	0.085	0.114	0.394	0.460	0.107	0.282	0.636	0.293	0.078	0.172	0.428
	8–14 Jul	0.194	0.081	0.073	0.336	0.740	0.092	0.576	0.879	0.066	0.032	0.024	0.125
	15–21 Jul	0.114	0.061	0.030	0.228	0.874	0.064	0.754	0.962	0.012	0.010	0.001	0.032
	22–31 Jul	0.059	0.041	0.009	0.138	0.939	0.041	0.858	0.990	0.002	0.003	0	0.009
2008													
	10–16 Jun	0.013	0.012	0.001	0.036	0.003	0.005	0	0.011	0.984	0.013	0.959	0.998
	17–23 Jun	0.040	0.022	0.011	0.082	0.015	0.010	0.003	0.035	0.945	0.025	0.899	0.978
	24–30 Jun	0.101	0.038	0.045	0.170	0.095	0.032	0.048	0.153	0.804	0.046	0.723	0.875
	1–7 Jul	0.191	0.057	0.100	0.288	0.353	0.069	0.244	0.471	0.456	0.068	0.346	0.566
	8–14 Jul	0.182	0.059	0.091	0.284	0.708	0.067	0.592	0.815	0.110	0.036	0.057	0.175
	15–21 Jul	0.106	0.047	0.039	0.192	0.876	0.049	0.786	0.947	0.018	0.011	0.004	0.039
	22–31 Jul	0.056	0.034	0.012	0.118	0.941	0.034	0.878	0.986	0.003	0.004	0	0.010
2009													
	10–16 Jun	0.015	0.017	0	0.049	0.008	0.010	0	0.028	0.977	0.020	0.936	0.998
	17–23 Jun	0.042	0.037	0.003	0.119	0.049	0.039	0.008	0.126	0.909	0.055	0.801	0.975
	24–30 Jun	0.096	0.067	0.014	0.227	0.224	0.113	0.073	0.438	0.680	0.126	0.459	0.865
	1–7 Jul	0.128	0.072	0.026	0.260	0.575	0.136	0.346	0.791	0.297	0.122	0.127	0.522
	8–14 Jul	0.087	0.051	0.015	0.179	0.848	0.072	0.715	0.950	0.065	0.044	0.015	0.153
	15–21 Jul	0.048	0.032	0.006	0.108	0.940	0.036	0.874	0.988	0.012	0.011	0	0.034
	22–31 Jul	0.023	0.020	0.001	0.060	0.975	0.020	0.936	0.998	0.002	0.004	0	0.009
2010													
	10–16 Jun	–	–	–	–	–	–	–	–	–	–	–	–
	17–23 Jun	0.028	0.020	0.003	0.066	0.063	0.029	0.023	0.116	0.909	0.034	0.846	0.958
	24–30 Jun	0.062	0.038	0.011	0.131	0.268	0.084	0.143	0.415	0.670	0.083	0.524	0.798
	1–7 Jul	0.085	0.051	0.015	0.178	0.670	0.094	0.507	0.818	0.245	0.075	0.131	0.376
	8–14 Jul	0.062	0.042	0.007	0.141	0.892	0.053	0.794	0.964	0.047	0.025	0.015	0.093
	15–21 Jul	0.032	0.025	0.002	0.080	0.961	0.027	0.909	0.994	0.007	0.007	0	0.021
	22–31 Jul	0.017	0.016	0	0.050	0.982	0.017	0.948	0.999	0.001	0.002	0	0.007

.

APPENDIX C: ALASKA SUSTAINABLE SALMON FUND PROJECT COMPLETION REPORT

Appendix C1.–Alaska Sustainable Salmon Fund Project 45143–completion report.

Note: The following material is for reference only and has not been reviewed by an ADF&G regional editor or published elsewhere–Editor.

Alaska Sustainable Salmon Fund
Project Completion Report

NOAA Grant Number:	To be filled in by AKSSF Staff
AKSSF Project Number:	45143 (700)
Project Title:	KRSA:Kenai River Chinook GSI
Principal Investigator:	Timothy McKinley ADF&G, Division of Sport Fish 43961 Kalifornsky Beach Road, Suite B Soldotna, AK 99669 Phone: (907) 260-2913; Fax: (907) 262-4709 Email: timothy.mckinley@alaska.gov
ADF&G Contact:	above
Total Funding:	$163,534 (direct: $158,771; indirect or admin fee: $4,763)
NOAA Category:	RM&E
Congress Designated:	Yes
Award Period:	Start: 6/4/08 End: 3/31/11
Date Prepared:	3/21/11

Abstract:
The goal of this project was to continue to develop a genetic baseline for Kenai River Chinook salmon; and to examine the genetic structure among samples collected from spawning aggregates within the Kenai River drainage; and estimate and quantify overlap in the run timing of tributary and mainstem spawning Kenai River Chinook salmon prior to this project (2003 and 2004), during (2005-2007), and in subsequent years. The baseline genetics data will be added to the coast-wide genetic database maintained by the Pacific Salmon Commission Chinook Technical Committee. Chinook salmon in spawning condition were sampled in 10 different mainstem areas and tributaries of the Kenai River to develop a genetic baseline database. Additionally, mixture samples for tributary versus mainstem run timing estimates were collected via an existing netting program as they entered the lower Kenai River, during years prior to the project (2003 and 2004), during this project (2005-2007), and in subsequent years. The results from some of the lower river netting collections during years outside the scope of the project are included in this report. Based on the lower river mixture sampling, most of the Chinook salmon that enter the Kenai River prior to the middle of June are of tributary origin; depending on the year, after the second or third week in June mainstem fish become more predominant. Few tributary spawning Chinook salmon enter the Kenai in July. Results from the lower river sport fishery mixture sampling demonstrate that: (1) most of the harvest in May and June is of tributary-bound fish, and, (2) nearly all of the harvest in July is of mainstem-bound fish. The middle river sport fishery mixture sampling results indicate that: (1) most of the harvest in June is of tributary-bound fish; (2) the harvest in the first two weeks of July is nearly an equal mix of tributary- and mainstem-bound fish; and, (3) nearly all of the harvest in the last two weeks in July is of mainstem-bound fish. These results will be extremely useful in generating estimates of escapement of tributary and mainstem Chinook salmon, escapement goal analyses for these stocks, possibly changing regulatory dates relative to these stocks, as well as estimating harvest in mixed-stock fisheries outside of the Kenai River drainage.

-continued-

Methods

Sample collection

Baseline samples were collected from mainstem and tributary spawning locations within the Kenai River, Alaska (Table 1). Collecting tissue from Chinook salmon for genetic analysis was non-lethal; a ½ inch sized piece of tissue from the axillary process was removed from each fish sampled, placed in a 2mL cryovial and completely covered with a Sigma Reagent Grade 95% Alcohol (Sigma Cat. # R 8382) buffer solution such that the liquid/tissue ratio was approximately 3:1. Samples were transferred to the Alaska Department of Fish and Game Gene Conservation Laboratory in Anchorage and stored at room temperature until analyzed. All Chinook salmon sampled for tissue were also sampled for age, sex, and length. After sampling Chinook salmon were released alive back to the water.

Mixture samples were taken from the lower Kenai River (downstream of the Soldotna Bridge) sport fisher, and the netting project at rm 8.5, and from the middle Kenai River (between Moose River and the Soldotna Bridge) sport fishery (Table 2). For the netting samples, samples were collected daily during the duration of both runs from May 16 - August 10, using 5.0 and 7.5" stretched mesh gillnets. The tissue collected from adult Chinook salmon for genetic analysis followed the methods used for baseline collections. Each tissue was preserved following the methods used for baseline collections. All Chinook salmon sampled for tissue were also sampled for age, sex ,and length and the time and location of capture were recorded.

Initially sample size goals were determined at the beginning of the project to meet specific precision and accuracy goals. For baseline samples, the sample size goal for each spawning location was set to estimate allelic frequencies at each marker to within 5% of the true values 90% of the time under a worst-case scenario. This level of precision requires identification of 403 alleles (Thompson 1987). Given two alleles at each marker in each diploid individual, and assuming random mating, tissue samples from a total of approximately 200 fish (400 alleles) at each location were needed to meet the stated precision criteria. The same rationale was used to set the sample sizes for sampling the test and sport fisheries. The following sample size goals were set based on precision and accuracy goals stated in the project objectives:

i) Lower river netting – To estimate stock composition of mainstem- and tributary-origin Chinook salmon in weekly or biweekly periods downstream of the Soldotna Bridge between May 16 and August 10 sample size targets were set at 30-100 samples per stratum to achieve estimates that are within 10% of the true values 90% of the time.
ii) Lower river sport fishery – To estimate the stock composition of mainstem-origin and tributary-origin Chinook salmon caught in the sport fishery downstream of the Soldotna Bridge between May 16 and July 31 sample size targets were set at 26-50 samples per week to achieve estimates that are within 25% of the true values 90% of the time.
iii) Middle river sport fishery –To estimate stock composition of mainstem-origin and tributary-origin Chinook salmon harvested in the sport harvest between Moose River and the Soldotna Bridge in two-week intervals between approximately June 1 and July

-continued-

31 sample size targets were set at 45 samples per stratum to achieve estimates that are within 15 % of the true value 90% of the time.

Subsequently, minimum numbers of fish per strata required for analysis to meet the precision objectives were reduced by implementing hierarchical Bayesian methods (see Mixture Analyses under Data Analyses, below).

Laboratory Analysis

Genotyping

All Genomic DNA were extracted using a DNeasy® 96 Tissue Kit by QIAGEN® (Valencia, CA). Fifty-two SNP markers were assayed; 1 mitochondrial and 51 nuclear DNA. Genotypes for these SNPs were screened using 2 platforms.

For some of the samples, SNP genotyping was performed in 384-well reaction plates. Each reaction was conducted in a 5µL volume consisting of 5-40ng of template DNA, 1x TaqMan® Universal PCR Master Mix (Applied Biosystems) and 1x 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 denaturation of 10 min at 95°C followed by 50 cycles of 92°C for 1s and annealing/extension temperature for 1.0 or 1.5 min. The plates were scanned on an Applied Biosystems Prism 7900HT Sequence Detection System after amplification and scored using Applied Biosystems' Sequence Detection Software (SDS) version 2.2.

For the remaining samples,SNP genotyping was performed using a BioMark 48.48 Dynamic Array (Fluidigm http://www.fluidigm.com/biomark_ genotyping.htm). The BioMark 48.48 Dynamic Array contains a matrix of integrated channels and valves housed in an input frame. On one side of the frame are 48 inlets to accept the sample DNA from each individual fish, and on the other are 48 inlets to accept the assays for each of the SNP markers. Once in the wells, the components are pressurized into the chip using the NanoFlex 4-IFC Controller. The 48 samples and 48 assays are then systematically combined into 2,304 parallel reactions. Each reaction was conducted in a 6.75 nL volume consisting of 1xTaqMan Universal Buffer (Applied Biosystems), 1.5 U AmpliTaq Gold DNA Polymerase (Applied Biosystems), 9 mM of each polymerase chain reaction (PCR) primer, 2 mM of each probe, 1xDA Assay Loading Buffer (Fluidigm), 12.5xROX (Invitrogen), and 0.01% Tween-20. Thermal cycling were performed on a BioMark IFC Cycler as follows: an initial denaturation of 10 min at 95°C followed by 50 cycles of 92° for 15 s and 60° for 1 min. The Dynamic Arrays were read on a BioMark Real-Time PCR System after amplification and scored using BioMark Genotyping Analysis software (Fluidigm).

Data collection

Genetic data were collected as individual multi-marker genotypes for the 52 SNP markers. To reduce the number of makers analyzed, 2009 upper mainstem and Quartz Creek collections were not genotyped for markers *Ots_FGF6A* and *Ots_GNRH2-278*. In the previous baseline analysis, which did not included these collections, marker *Ots_FGF6A* showed significant linkage with marker *Ots_FGF6B* and was dropped from further analysis. Marker *Ots_GNRH2-278* was

-continued-

dropped from the previous analysis because it was invariant. Genotypes collected from both instruments were entered into the ADFG Oracle database, LOKI.

Laboratory failure rates and quality control

The overall failure rate was calculated by dividing the number of failed single-marker genotypes by the number of assayed single-marker genotypes.

Quality control measures were instituted to identify laboratory errors and to determine the reproducibility of genotypes. The process involved the reanalysis of 8 out of every 96 fish (one row per 96-well plate; 8%) for all markers by staff not involved with the original analysis. Assuming that the inconsistencies among analyses were due equally to errors in original genotyping and errors during the quality control, error rates in the original genotyping can be estimated as ½ the rate of inconsistencies. Because baseline and mixture collections were genotyped on many projects and have been subject to many quality control analyses, we report quality control results for representative baseline and mixture projects. These projects genotyped fish on the Fluidigm Dynamic Array platform, and were typical of our current genotyping process.

Data analysis

Data retrieval and quality control

Genotypic data were retrieved from LOKI and were imported into R (R Foundation for Statistical Computing, Vienna, Austria). Unless otherwise noted, all analyses were performed in R.

Two quality control measures were conducted once genotypes were retrieved from LOKI. The first one identified and excluded duplicate fish within collections. Duplicate fish can occur as a result of sampling or extracting the same fish twice. For each pair of duplicate fish, the fish with the most number of markers scored or, if both fish have equal number of scored markers, the first fish in the collection was retained for further analyses. The second quality control analysis excluded mixture and baseline individuals with an excessive rate of unscorable markers, or dropouts.

A threshold of 80% scorable markers per individual was established and all individuals that did not meet this threshold were excluded from MSA. This threshold was set to exclude individuals with poor quality DNA. Poor quality DNA leads to lower reproducibility and therefore adds error to the multi-marker genotype.

The value of 80% was chosen based upon the observation that many individuals with high quality DNA had some dropouts, but generally less than 20% of markers, while those with poor-quality DNA had higher dropout rates. As a result, there was little difference in which individuals were excluded from analysis when picking the threshold as long as it was within the 70% to 90% range. This rule (referred to as the "80% rule") was used for samples from mixtures to decrease errors and estimate variances caused by poor quality DNA and missing data. This approach was an attempt to balance the benefits from better data with the loss of power to accurately and precisely estimate stock proportions due to smaller sample sizes.

-continued-

Pooling collections

When multiple collections were available from the same population, these collections were combined to represent the population. A minimum sample size of 50 individuals was used for inclusion of a population in the population structure analysis. Because Chinook salmon are diploid organisms, this is a minimum of 100 samples from the gene pool for determining allele frequencies at each marker. Geographically proximate populations were tested for significant differences using a log likelihood ratio statistic (Weir 1990). If no significant differences were found, populations were pooled.

Linkage disequilibrium

Marker-specific allele frequencies were calculated for each collection. Some markers were found be invariant and were dropped from further analaysis. After pooling collections into populations, tests for gametic equilibrium (between all remaining pairs of markers) were performed using GENEPOP. All pairs of markers were tested for gametic disequiliburium within each population. We defined a pair of marker s to be significantly out of gametic equilibrium if tests for gametic disequilibrium were significant ($P<0.01$) for greater than half of all populations. When gametic linkage was significant, we produced composite gentoypes by ordering the alleles within each marker alphabetically and then stringing the alleles together by marker ordered alphanumerically. Markers that did not exhibit gametic disequilibrium with any other marker and markers that were combinded were defined as loci for the remaingin analyses. If the combined locus has a lower F_{ST} value than one of the uncombined loci, the single locus with the higher F_{ST} was kept and the other was dropped from the analysis.

Population structure

Locus-specific allele frequencies were calculated for each population. Observed and expected heterozygosity was calculated using *FSTAT* (Goudet 1995), and conformation of genotype frequencies to Hardy-Weinberg equilibrium (HWE) expected ratios was assessed using the exact test in *GENEPOP* (Raymond and Rousset 1995). The significance of departures from HWE for each locus in each population was determined using $\alpha=0.05$ adjusted for the number of loci ($n=40$) assayed in each population using the Bonferroni adjusted significance levels ($\acute{\alpha}= \alpha/n= 0.0013$).

Two measures of population subdivision were calculated from allele frequency differences: Cavalli-Sforza and Edwards' (CSE) chord distances (Cavalli-Sforza and Edwards 1967) and F_{ST} (Weir and Cockerham 1984). R was was used to calculate the CSE distances and *FSTAT* was used to calculate F_{ST} values. Population structure was visualized as a tree (Neighbor-Joining method, Saitou and Nei 1987) using the APE package (Paradis et al. 2004) in the program R to view genetic similarities between populations reflected in the interpopulation chord distances.

Mixture analysis testing

Proof tests were conducted to evaluate the accuracy and precision of the genetic baseline to provide compositional estimates of mixtures of Chinook salmon taken from within the Kenai River. These tests were used to help assess whether the baseline of allele frequencies at the 40 SNP loci would provide sufficient information to identify individual stocks or groups of stocks (reporting groups) in mixtures. Reporting groups for genetic stock identification of Chinook salmon in the Kenai River were defined by grouping the populations by whether they spawn in a

-continued-

tributary or the mainstem based on a previous report (Begich et al. 2010) and on management applications. Juneau Creek was included in the mainstem reporting group because it was genetically similar to both mainstem populations.

In these tests, we created test mixtures by sampling approximately 200 individuals from the baseline. For tributary and mainstem reporting groups, we created two 100% mixtures by sampling 200 fish from each group and a 50% mixture by sampling 100 fish from each reporting group. For all 3 tests we rebuilt the baseline excluding the sampled fish. These tests provided an indication of the power of the baseline for MSA assuming that all the populations were represented in the baseline.

The proof test mixtures were analyzed using the program BAYES (Pella and Masuda 2001). The Bayesian model implemented by BAYES places a Dirichlet distribution as the prior distribution for the stock proportions, and the parameters for this distribution must be specified. Prior parameters for each reporting group were defined to be equal (i.e., a "flat" prior) with the prior parameters for a reporting group divided equally among populations within that reporting group. We set the sum of all prior parameters to be 1 (prior weight), which is equivalent to adding 1 fish to each mixture (Pella and Masuda, 2001). We ran 5 independent Markov Chain Monte Carlo (MCMC) chains of 15,000 iterations with different starting values and discarded the first 7,500 iterations to remove the influence of the initial start values. Estimates and 90% credibility intervals from the second half of five 15,000 iteration chains were tabulated. Credibility intervals differ from confidence intervals in that they are a direct statement of probability: i.e. a 90% credibility interval has a 90% chance of containing the true answer (Gelman et al. 2000). We repeated this procedure for each of the three proof tests.

A critical level of 90% correct allocation was used to determine if the reporting group was acceptably identifiable (Seeb et al. 2000). We examined the adequacy of burn-in for each chain with the Rafferty and Lewis (1996) diagnostic. To ensure that the BAYES output was an acceptable approximation of the stationary posterior distribution and that the stock composition estimates were valid, we assessed the 5 independent (MCMC) chains for convergence among chains. We assessed among-chain convergence using the Gelman-Rubin shrink factors that are computed for all stock groups in the program BAYES. This shrink factor compared the variation within a chain to the total variation among chains (Gelman and Rubin, 1992).

Sport mixture analysis

We estimated the stock composition of the lower river (2006–2010) and middle river (2007–2010) sport fishery data for biweekly time strata. Since biweekly sample sizes were small, hierarchical Bayesian methods were used to model the prior structure. These methods provide the added benefit of making use of the intra- and inter-annual temporal relationship between stock proportions in adjacent weeks to add strength to the estimates in any one week. The prior for the group stock proportions were modeled with a logistic specification (Okuyama and Bolker 2005) using time as a covariate according to the following:

$$\varepsilon_{y,t,g} = \alpha_{y,g} + \beta_{y,g} t \,,$$

-continued-

$$e_{y,t,g} = \frac{e^{\varepsilon_{y,t,g}}}{1+\sum_{j=1}^{G-1} e^{\varepsilon_{y,t,j}}},$$

$$e_{y,t,G} = \frac{1}{1+\sum_{j=1}^{G-1} e^{\varepsilon_{y,t,j}}},$$

Where G is the number of stock groups. Hierarchical priors were specified for the parameters of the logistic curve according to:

$$\alpha_{y,g} \sim N(\mu_\alpha, \tau_\alpha),$$

$$\beta_{y,g} \sim N(\mu_\beta, \tau_\beta),$$

$$\mu_\alpha, \mu_\beta \sim N(0,1000),$$

$$\tau_\alpha, \tau_\beta \sim Exp(1000).$$

Regional stock proportions were given a Dirichlet prior distribution with parameters:

$$\eta_{y,t,g} = W e_{y,t,g},$$

Where W is the prior "weight" and is given a vague exponential prior dristribution with a mean of 1000. Within group sub-stock proportions were given a Dirichlet prior distribution with parameters equal to $1/C_g$, where C_g is the number of sub-stocks in group g.

Netting mixture analysis

We estimated the stock composition of the netting data for weekly time strata for 2003–2010. Since weekly sample sizes were small, we used hierarchical Bayesian methods augmented by weekly catch-per-unit-effort (CPUE) data to model the regional prior structure. These methods provide the added benefit of making use of the temporal relationship between stock proportions in adjacent weeks to add strength to the estimates in any one week. Weekly CPUE data show two distinct modes which we assume correspond to early and late run fish passage at the net. Fortunately, there is also a genetic distinction between early and late run fish, and we coupled weekly genetics samples with weekly CPUE data to improve estimation.

Weekly CPUE

-continued-

We model the observed weekly CPUE as the sum of two curves. We borrow the form of Student's t-distribution to capture the shape of each run, that is, the early run CPUE in year y at week t is modeled as:

$$E_{y,t} = \frac{a_{E,y}\Gamma\left(\frac{\upsilon_{E,y}+1}{2}\right)}{\Gamma\left(\frac{\upsilon_{E,y}}{2}\right)\sqrt{\pi\upsilon_{E,y}\sigma_{E,y}^2}}\left(1+\frac{(t-\mu_{E,y})}{\upsilon_{E,y}\sigma_{E,y}^2}\right)^{\frac{\upsilon_{E,y}+1}{2}}$$

Similarly, the late run CPUE in year y at week t is modeled as:

$$L_{y,t} = \frac{a_{L,y}\Gamma\left(\frac{\upsilon_{L,y}+1}{2}\right)}{\Gamma\left(\frac{\upsilon_{L,y}}{2}\right)\sqrt{\pi\upsilon_{L,y}\sigma_{L,y}^2}}\left(1+\frac{(t-\mu_{L,y})}{\upsilon_{L,y}\sigma_{L,y}^2}\right)^{\frac{\upsilon_{L,y}+1}{2}}$$

The observed CPUE in year y at week t ($O_{y,t}$) is given log-normal errors and is modeled as:

$$CPUE_{y,t} = (E_{y,t} + L_{y,t})e^{\varepsilon_{y,t}}$$

The errors, $\varepsilon_{y,t}$, come from a normal distribution with mean zero and variance σ_ε^2.
Prior distributions for each of the run's parameters are as follows:

$$a_{.,y} \sim logN(\theta_{a_.}, \tau_{a_.})$$
$$\upsilon_{.,y} \sim G(a_{\upsilon_.}, b_{\upsilon_.})$$
$$\sigma_{.,y} \sim G(a_{\sigma_.}, b_{\sigma_.})$$
$$\mu_{.,y} \sim N(\theta_{\mu_.}, \tau_{\mu_.})$$
$$\theta_{a_.}, \theta_{\mu_.} \sim N(0,1000)$$
$$a_{\upsilon_.}, b_{\upsilon_.}, a_{\sigma_.}, b_{\sigma_.}, \tau_{a_.}, \tau_{\mu_.}, \sigma_\varepsilon^2 \sim Exp(1000)$$

Here, the dot (.) is meant to represent either early (E) or late (L) run parameters.

Stock Proportions

The C stocks are broken-up into two groups: early run stocks and late run stocks. The early run is composed of C_E stocks and the late run is made up of C_L stocks, where C_E+C_L= C. Let $R_{E,y,t}$ and $R_{L,y,t}$ be the relative contributions in year y and week t for the early run and late run, respectively, where $R_{E,y,t}$+$R_{L,y,t}$=1. Since $\boldsymbol{R}_{y,t}$={$R_{E,y,t}$, $R_{L,y,t}$} is unknown, we place an informative Dirichlet prior on it of the form:

$$\boldsymbol{R}_{y,t} \sim Dirichlet\left(W\frac{E_{y,t}}{E_{y,t}+L_{y,t}}, W\frac{L_{y,t}}{E_{y,t}+L_{y,t}}\right)$$

This prior specification is motivated by the fact that, prior to observing the genotypic data in year y and week t, our best estimate of $R_{E,y,t}$ is the early component of the run ($E_{y,t}$) divided by the total run ($E_{y,t}$+$L_{y,t}$). Since the prior Dirichlet parameters sum to W, this term can be interpreted as the "prior count". It is given a vague prior distribution of:

$$W \sim Exp(1000)$$

We denote the within-group stock proportions for the C_E early stocks in year y and week t as the vector $\boldsymbol{S}_{E,y,t}$, such that:

-continued-

$$\sum_{i=1}^{C_E} S_{E,y,t,i} = 1$$

Likewise, denote the within-group stock proportions for the C_L late stocks in year y and week t as the vector $\boldsymbol{S}_{L,y,t}$, such that:

$$\sum_{i=1}^{C_L} S_{L,y,t,i} = 1$$

The priors for these within-group stock proportions are:

$$\boldsymbol{S}_{.,y,t} \sim Dirichlet(\boldsymbol{\alpha}_{.})$$

$$\alpha_{.,i} = \frac{1}{C_{.}}, \text{for } i = 1,2,\ldots,C_{.}$$

We specify the proportions for all C stock proportions in year y and week t as the vector $\boldsymbol{P}_{y,t}$, where:

$$\boldsymbol{P}_{y,t} = \{R_{E,y,t}S_{E,y,t,1}, R_{E,y,t}S_{E,y,t,2}, \ldots, R_{E,y,t}S_{E,y,t,C_E}, R_{L,y,t}S_{L,y,t,1}, R_{L,y,t}S_{L,y,t,2}, \ldots, R_{L,y,t}S_{L,y,t,C_L}\}$$

Notice that:

$$\sum_{i=1}^{C_E} R_{E,y,t}S_{E,y,t,i} + \sum_{i=1}^{C_L} R_{L,y,t}S_{L,y,t,i} = 1$$

Results

Sample collection

Samples were collected from a mix of projects specifically funded though this grant and the previous grant, and from existing projects such as the lower Kenai River netting, lower Kenai River sport creel survey, and the Funny River weir.

Baseline

Tissues samples from spawning populations of Chinook salmon were collected throughout the Kenai River drainage (Table 1). Over seven years (2003-2009), 24 individual collections were made with the majority of collections (13) made in 2005 and 2006. Collections were taken at 11 different locations; individuals from 8 of these locations were taken in multiple years. A total of 2,021 fish were analyzed for the baseline.

Mixture

i) Lower river netting - A total of 4,867 Chinook salmon were sampled for tissues suitable for genetic analysis from the lower Kenai River drift netting project from 2003to2010.

ii) Lower river sport- A total of 2,177 Chinook salmon were sampled for tissues suitable for genetic analysis from the lower Kenai River creel surveyfrom 2006 to2010.

-continued-

iii) Middle river sport- A total of 1,061 Chinook salmon were sampled for tissues suitable for genetic analysis from the middle Kenai River creel survey from 2007 to 2010.

Laboratory analysis

Genotyping and Data collection

Genotypes were assayed from a total of 2,021 individuals from 24 collections representing 10 putative populations (Table 1). A total of 8,105 individuals from 8 lower Kenai River netting collections, 5 lower Kenai River sport collections, and 4 middle Kenai River sport fishery collections were available for analysis (Table 2). From these, genotypes were assayed from 7,087 individuals.

Laboratory failure rates and quality control

For the baseline collections, the overall failure rate for successfully assaying genotypes was 3.87%. Most failures occurred in the samples from Slikok Creek (success rate approximately 80%) and were due to poor tissue quality. The representative baseline used to demonstrate baseline error rates consisted of 7 collections comprising 661 individuals (~ 37% of current baseline) that were genotyped as part of a recent baseline supplemental project. The quality control checks employed on this representative project demonstrated an error rate of 0.21%. The quality control checks also revealed pairs of individuals in some collections that had identical multi-marker genotypes. The following populations had individuals with duplicate genotypes: Benjamin Creek (1 pair), Funny River (1 pair), Crescent Creek (1 pair), Quartz Creek (2 pairs), and Juneau Creek (4 pairs). In most cases, duplicates appear to have been the result of sampling the same fish into neighboring vials.

For the mixture collections, the overall failure rate for successfully assaying genotypes was 1.18%. The representative mixture project used to demonstrate mixture error rates consisted of 6 collections comprising 2,291 individuals (~49% of the mixture samples genotyped). The quality control checks employed on this representative project demonstrated an error rate of 0.04%. Among all mixture samples, only one pair of individuals had duplicate genotypes.

Data analysis

Pooling collections

Multiple collections from the same population and geographically proximate populations that showed no significant differences in the log likelihood ratio tests were pooled to form 10 populations.

Linkage disequilibrium

Eleven markers were dropped from further analysis because they were invariant. These marker were: *Ots_E9BAC, Ots_META* (Northwest Fisheries Science Center-NOAA (Unpublished)), *Ots_ARF, Ots_HGFA, Ots_HGFA* (Smith et al. 2005a), *Ots_GST-375, Ots_PSMB1* (Smith et al. 2007), *Ots_C3N3, Ots_GNRH2-278, Ots_NRP, and Ots_RFC2* (Smith et al. 2005b). Marker *Ots_FGF6A* (Northwest Fisheries Science Center-NOAA (Unpublished)) was also dropped from further analysis because it showed significant linkage with *Ots_FGF6B* in 100% of populations in the previous baseline analysis. Linkage disequilibrium tests were performed on the remaining

-continued-

41 SNP markers. One set of markers was found to be significantly linked in greater than half of all popoulations. Markers *Ots_HSP90B-100* and *Ots_HSP90B-385* (Smith et al. 2007) showed significant linage in 60% of populations. After combining these two markers, the F_{ST} for *Ots_HSP90B-385* (F_{ST}=0.051) was greater than that of the combined locus (F_{ST}=0.040) and *Ots_HSP90B-100* (F_{ST}=0.022). After dropping *Ots_HSP90B-100*, a total of 40 snp loci were available for further analysis (Table 3).

Population structure

After correcting for multiple tests, no significant departures from HWE were found. Genetic differences between populations were measured using CSE distances calculated from allele frequencies at the 40 SNP loci. Visualizing these interpopulation distances with a Neighbor-Joining tree showed five major clusters of populations which appear to be structured largely by tributaries (Figure 2). Each of the major branches on the tree, with the exception of Juneau Creek and the 2 mainstem populations, corresponds to a subdrainage within the greater Kenai River drainage (considering the mainstem spawning locations to be a subset of the whole).

Mixture analysis testing

When prooftests were performed on mixtures of fish composed entirely from a single reporting group (tributary or mainstem) more than 97% were correctly identified to the group of origin (Table 4). When an additional proof test was performed with a mixture comprised of 50% mainstem and 50% tributary fish, the estimates for each reporting group were within 1% of their true value.

Mixture analyses

Results from lower river mixture sampling (Tables 5–12) show the majority of Chinook salmon that enter the Kenai River prior to the middle of June are of tributary origin; depending on the year, after the second or third week in June mainstem fish become more predominant. Very few tributary fish enter the Kenai in July. Results from the lower river sport fishery mixture sampling (Tables 13–17) demonstrate that most of the harvest in May and June is of tributary-bound fish, and that nearly all of the harvest in July is of mainstem-bound fish. Results from the middle river sport fishery mixture sampling (Tables 18–21) demonstrate that most of the harvest in June is of tributary-bound fish, the harvest in the first two weeks of July is approximately a 1:3 mix of tributary- and mainstem-bound fish, and that nearly all of the harvest in the last two weeks in July is of mainstem-bound fish.

Evaluation

Project objectives were addressed and exceeded. Strong genetic separation between tributary and mainstem spawning aggregates within the Kenai River drainage were found and will be useful in future examinations in mixed-stock fisheries within the Kenai River and outside. Lab results showed separation among spawning aggregates Kenai River drainage. The results from the mixture samples collected from the lower river netting and sport sampling will be very useful in future examinations of escapement goals, escapement estimates for the early (tributary) and late (mainstem) Kenai River stocks, and regulatory dates for these stocks.

Project Products

-continued-

Project results are ongoing as more baseline populations are sampled and analyzed as well as additional mixture samples collected. Results through 2010 will be reported in an FDS report with a draft by the Spring of 2012.

Key Words
Kenai River, Chinook salmon, GSI, baseline, mixture, SNP's.

-continued-

References

Begich, R. N., W. D. Templin, A. W. Barclay, and L. W. Seeb. 2010. Development of Microsatellite Genetic Markers for Kenai River Chinook Salmon. Alaska Department of Fish and Game, Fishery Data Series No. 10-38, Anchorage.

Cavalli-Sforza, L. L. and A. W. F. Edwards. 1967. Phylogenetic Analysis: Models and Estimation Procedures. Evolution. 19(3):233

Gelman, A. B., J. S. Carlin, H. S. Stern, and D. B. Rubin. 2000. Bayesian Data Analysis. Chapman and Hall, Boca Raton, Florida.

Gelman, A., and D. B. Rubin. 1992. Inference from iterative simulation using multiple sequences. Stat. Sci. 7:457–511.

Goudet J (1995) FSTAT (Version 1.2): A computer program to calculate F-statistics. Journal of Heredity. 86:485–486.

Okuyama, T. and B. M. Bolker. 2005. Combining Genetic and Ecological Data to Estimate Sea Turtle Origins. Ecological Applications. 15(1):315–325.

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

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

Rafferty. A.E., and S.M. Lewis. 1996. Implementing MCMC. Pages 115–130 [*In*] W.R. Gilks, S. Richardson, and D.J. Spiegelhalter, editors. Markov chain Monte Carlo in practice. Chapman and Hall, Inc., London.

Raymond, M. and F. Rousset. 1995. An exact test for population differentiation. Evolution 49:1280–1283.

Saitou, N. and M. Nei. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Molecular Biology and Evolution 4:406–425.

Seeb, L. W., C. Habicht, W. D. Templin, K. E. Tarbox, R Z. Davis, L. K. Brannian, and J. E. Seeb. 2000. Genetic diversity of sockeye salmon of Cook Inlet, Alaska, and its application to management of populations affected by the Exxon Valdez oil spill. Transactions of the American Fisheries Society 129: 1223–1249.

Smith C. T., J. E. Seeb, P. Schwenke, and L. W. Seeb. 2005a. Use of the 5 '-nuclease reaction for single nucleotide polymorphism genotyping in Chinook salmon. Transactions of the American Fisheries Society. 134:207–217.

Smith C. T., W. D. Templin, J. E. Seeb, and L. W. Seeb. 2005b. Single Nucleotide Polymorphisms (SNPs) provide rapid and accurate estimates of the proportions of U.S. and Canadian Chinook salmon caught in Yukon River fisheries. Nort American Journal of Fisheries Management. 25:944–953.

Smith C. T., A. Antonovich, W. D. Templin, and C. M. Elfstrom. 2007. Impacts of marker class bias relative to locus-specific variability on population inferences in Chinook salmon: a comparison of single-nucleotide polymorphisms with short tandem repeats and allozymes. Transactions of the American Fisheries Society. 136: 1674–1687.

Thompson, S. K. 1987. Sample size for estimating multinomial proportions. The American Statistician 41:42–46.

Weir, B. S. and C. C. Cockerham. 1984. Estimating F-statistics for the analysis of population structure. Evolution 38(6): 1358–1370.

-continued-

Table 1. Collection reporting group, locations, sampling years and sample sizes of Chinook salmon from the Kenai River used in the genetic baseline for mixed stock analysis. Each location represented a different population except for the two Lower Kenai mainstem locations which represented a single population.

Reporting Group	Location	Sample Year(s)	N
Tributary	Slikok Creek	2004, 2005, 2008	200
	Funny River	2005, 2006	220
	Killey River	2005, 2006	258
	Benjamin Creek	2005, 2006	206
	Russian River	2005, 2006, 2007, 2008	214
	Quartz Creek	2006, 2008, 2009	109
	Crescent Creek	2006	165
Mainstem	Lower Kenai River mainstem site1	2003, 2004	119
	Lower Kenai River mainstem site2	2006	183
	Juneau Creek	2005, 2006, 2007	147
	Upper Kenai River mainstem	2009	200
		Total	2021

-continued-

Table 2. Collection year, number of samples collected , and number of samples genotyped for Chinook salmon sampled for genetic studies taken from fish captured in the Kenai River lower river netting program and lower and middle sport fisheries.

		Samples	
Collection	Year	Collected	Genotyped
Lower river netting	2003	1,004	554
	2004	740	488
	2005	504	504
	2006	478	478
	2007	370	370
	2008	732	480
	2009	527	527
	2010	512	512
Lower river sport	2006	516	516
	2007	388	387
	2008	442	379
	2009	375	375
	2010	456	456
Middle river sport	2007	147	147
	2008	362	362
	2009	197	197
	2010	355	355

-continued-

Table 3. Assay name, source, range of common allele, observed and expected heterozygosity, and F_{ST} for each of the 40 SNP markers used in the analysis of Kenai River Chinook salmon.

Assay Name	Source[1]	Range of Common Allele	Heterozygosity		F_{ST}
			Observed	Expected	
Ots_GTH2B-550	a	(0.595 - 0.792)	0.451	0.436	0.016
Ots_NOD1	a	(0.274 - 0.770)	0.456	0.456	0.100
Ots_E2-275	b	(0.569 - 0.891)	0.325	0.324	0.039
Ots_AsnRS-60	b	(0.516 - 0.766)	0.419	0.436	0.037
Ots_ETIF1A	c	(0.363 - 0.678)	0.479	0.479	0.051
Ots_FARSLA-220	d	(0.602 - 0.891)	0.342	0.338	0.051
Ots_FGF6A	a	(0.371 - 0.804)	0.387	0.393	0.085
Ots_GH2	e	(0.755 - 0.888)	0.288	0.294	0.010
Ots_GPDH-338	b	(0.830 - 0.980)	0.105	0.104	0.033
Ots_GPH-318	d	(0.872 - 0.985)	0.122	0.128	0.026
Ots_GST-207	d	(0.878 - 1.000)	0.046	0.048	0.051
Ots_hnRNPL-533	d	(0.737 - 0.929)	0.284	0.288	0.021
Ots_HSP90B-385	d	(0.868 - 1.000)	0.054	0.053	0.048
Ots_IGF-I.1-76	b	(0.364 - 0.716)	0.501	0.472	0.043
Ots_Ikaros-250	b	(0.838 - 0.993)	0.143	0.142	0.052
Ots_il-1racp-166	b	(0.577 - 0.811)	0.456	0.419	0.031
Ots_LEI-292	d	(0.922 - 0.988)	0.080	0.083	0.010
Ots_MHC1	e	(0.511 - 0.766)	0.420	0.431	0.054
Ots_MHC2	e	(0.952 - 1.000)	0.031	0.032	0.010
Ots_LWSop-638	b	(0.901 - 1.000)	0.063	0.059	0.021
Ots_SWS1op-182	b	(0.557 - 0.748)	0.458	0.439	0.017
Ots_P450	e	(0.681 - 0.851)	0.349	0.353	0.020
Ots_P53	b	(0.559 - 0.778)	0.413	0.428	0.023
Ots_Prl2	e	(0.420 - 0.667)	0.488	0.490	0.020
Ots_ins-115	b	(0.950 - 1.000)	0.042	0.042	0.014
Ots_SClkF2R2-135	b	(0.448 - 0.835)	0.407	0.409	0.062
Ots_SERPC1-209	d	(0.797 - 0.998)	0.132	0.149	0.051
Ots_SL	e	(0.532 - 0.863)	0.412	0.386	0.037
Ots_TAPBP	c	(0.784 - 0.963)	0.231	0.229	0.024
Ots_Tnsf	e	(0.848 - 0.948)	0.186	0.183	0.008
Ots_u202-161	b	(0.926 - 1.000)	0.038	0.037	0.037
Ots_u211-85	b	(0.768 - 0.922)	0.201	0.193	0.020
Ots_U212-158	b	(0.857 - 1.000)	0.045	0.047	0.071
Ots_u4-92	b	(0.658 - 0.914)	0.277	0.284	0.041
Ots_u6-75	b	(0.875 - 0.965)	0.145	0.139	0.014
Ots_Zp3b-215	b	(0.914 - 0.995)	0.069	0.070	0.014
Ots_PGK-54	a	(0.975 - 1.000)	0.007	0.007	0.013
Ots_RAG3	a	(0.683 - 0.991)	0.230	0.245	0.068
Ots_S7-1	a	(0.807 - 0.915)	0.218	0.226	0.009
Ots_unkn-526	a	(0.797 - 0.995)	0.181	0.186	0.046

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

-continued-

Table 4. Proof test results for three known mixtures (see text for details). Sample sizes are provided for each mixture along with reporting group-specific allocation proportions (P), standard deviation (SD), and BAYES; 90% credibility interval (CI).

N	Reporing Group	P	SD	CI
		100% tributary mixture		
200	tributary	0.974	0.025	(0.924 - 1.000)
	mainstem	0.026	0.025	(0.000 - 0.076)
		100% mainstem mixture		
200	tributary	0.017	0.019	(0.000 - 0.055)
	mainstem	0.983	0.019	(0.945 - 1.000)
		50% tributary / 50% mainstem mixture		
200	tributary	0.509	0.063	(0.406 - 0.613)
	mainstem	0.491	0.063	(0.387 - 0.594)

-continued-

Table 5. Lower Kenai River netting program, 2003: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
5/16 - 5/26	42	T	0.980	0.026	(0.927 - 1.000)
		M	0.020	0.026	(0.000 - 0.073)
5/27 - 6/2	43	T	0.965	0.031	(0.905 - 1.000)
		M	0.035	0.031	(0.000 - 0.095)
6/3 - 6/9	48	T	0.913	0.046	(0.831 - 0.978)
		M	0.087	0.046	(0.022 - 0.170)
6/10 - 6/16	50	T	0.862	0.056	(0.765 - 0.949)
		M	0.138	0.056	(0.051 - 0.235)
6/17 - 6/23	48	T	0.508	0.081	(0.377 - 0.643)
		M	0.492	0.081	(0.358 - 0.623)
6/24 - 6/30	50	T	0.208	0.073	(0.101 - 0.338)
		M	0.792	0.073	(0.662 - 0.899)
7/1 - 7/7	46	T	0.026	0.023	(0.001 - 0.070)
		M	0.974	0.023	(0.930 - 0.999)
7/8 - 7/14	47	T	0.017	0.019	(0.000 - 0.055)
		M	0.983	0.019	(0.945 - 1.000)
7/15 - 7/21	49	T	0.013	0.020	(0.000 - 0.053)
		M	0.987	0.020	(0.947 - 1.000)
7/22 - 7/28	49	T	0.013	0.019	(0.000 - 0.054)
		M	0.987	0.019	(0.946 - 1.000)
7/29 - 8/4	47	T	0.009	0.013	(0.000 - 0.036)
		M	0.991	0.013	(0.964 - 1.000)
8/5 - 8/10	18	T	0.022	0.027	(0.000 - 0.073)
		M	0.978	0.027	(0.927 - 1.000)

[a]Reporting Groups: tributary (T) and mainstem (M).

-continued-

Table 6. Lower Kenai River netting program, 2004: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
5/16 - 5/26	13	T	0.980	0.028	(0.924 - 1.000)
		M	0.020	0.028	(0.000 - 0.076)
5/27 - 6/2	11	T	0.969	0.035	(0.902 - 1.000)
		M	0.031	0.035	(0.000 - 0.098)
6/3 - 6/9	43	T	0.937	0.044	(0.857 - 0.999)
		M	0.063	0.044	(0.002 - 0.143)
6/10 - 6/16	28	T	0.860	0.066	(0.744 - 0.962)
		M	0.140	0.066	(0.038 - 0.256)
6/17 - 6/23	42	T	0.420	0.088	(0.275 - 0.564)
		M	0.580	0.088	(0.436 - 0.725)
6/24 - 6/30	50	T	0.124	0.055	(0.044 - 0.223)
		M	0.876	0.055	(0.778 - 0.956)
7/1 - 7/7	50	T	0.044	0.032	(0.004 - 0.104)
		M	0.956	0.032	(0.896 - 0.996)
7/8 - 7/14	50	T	0.024	0.025	(0.000 - 0.072)
		M	0.976	0.025	(0.928 - 1.000)
7/15 - 7/21	48	T	0.027	0.028	(0.000 - 0.082)
		M	0.973	0.028	(0.918 - 1.000)
7/22 - 7/28	50	T	0.005	0.012	(0.000 - 0.028)
		M	0.995	0.012	(0.972 - 1.000)
7/29 - 8/4	49	T	0.007	0.016	(0.000 - 0.038)
		M	0.993	0.016	(0.962 - 1.000)
8/5 - 8/10	47	T	0.011	0.018	(0.000 - 0.049)
		M	0.989	0.018	(0.951 - 1.000)

[a]Reporting Groups: tributary (T) and mainstem (M).

-continued-

Table 7. Lower Kenai River netting program, 2005: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
5/16 - 5/26	17	T	0.989	0.018	(0.952 - 1.000)
		M	0.011	0.018	(0.000 - 0.048)
5/27 - 6/2	33	T	0.978	0.027	(0.923 - 1.000)
		M	0.022	0.027	(0.000 - 0.077)
6/3 - 6/9	56	T	0.977	0.023	(0.931 - 1.000)
		M	0.023	0.023	(0.000 - 0.069)
6/10 - 6/16	38	T	0.839	0.067	(0.718 - 0.935)
		M	0.161	0.067	(0.065 - 0.282)
6/17 - 6/23	29	T	0.594	0.091	(0.443 - 0.741)
		M	0.406	0.091	(0.259 - 0.557)
6/24 - 6/30	44	T	0.149	0.057	(0.062 - 0.249)
		M	0.852	0.057	(0.751 - 0.938)
7/1 - 7/7	54	T	0.052	0.037	(0.006 - 0.122)
		M	0.948	0.037	(0.878 - 0.994)
7/8 - 7/14	63	T	0.020	0.024	(0.000 - 0.067)
		M	0.980	0.024	(0.933 - 1.000)
7/15 - 7/21	61	T	0.010	0.018	(0.000 - 0.045)
		M	0.990	0.018	(0.955 - 1.000)
7/22 - 7/28	40	T	0.007	0.014	(0.000 - 0.032)
		M	0.993	0.014	(0.968 - 1.000)
7/29 - 8/4	51	T	0.009	0.016	(0.000 - 0.042)
		M	0.991	0.016	(0.958 - 1.000)
8/5 - 8/10	21	T	0.011	0.020	(0.000 - 0.049)
		M	0.989	0.020	(0.951 - 1.000)

[a]Reporting Groups: tributary (T) and mainstem (M).

-continued-

Table 8. Lower Kenai River netting program, 2006: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
5/16 - 5/26	2	T	0.989	0.021	(0.946 - 1.000)
		M	0.011	0.021	(0.000 - 0.054)
5/27 - 6/2	11	T	0.976	0.031	(0.914 - 1.000)
		M	0.024	0.031	(0.000 - 0.086)
6/3 - 6/9	20	T	0.971	0.033	(0.906 - 1.000)
		M	0.029	0.033	(0.000 - 0.094)
6/10 - 6/16	46	T	0.937	0.046	(0.853 - 0.998)
		M	0.063	0.046	(0.002 - 0.148)
6/17 - 6/23	18	T	0.674	0.099	(0.513 - 0.839)
		M	0.326	0.099	(0.161 - 0.487)
6/24 - 6/30	33	T	0.212	0.080	(0.095 - 0.355)
		M	0.788	0.080	(0.645 - 0.906)
7/1 - 7/7	38	T	0.033	0.028	(0.002 - 0.087)
		M	0.967	0.028	(0.913 - 0.998)
7/8 - 7/14	54	T	0.011	0.016	(0.000 - 0.044)
		M	0.989	0.016	(0.957 - 1.000)
7/15 - 7/21	46	T	0.006	0.013	(0.000 - 0.029)
		M	0.994	0.013	(0.971 - 1.000)
7/22 - 7/28	76	T	0.002	0.006	(0.000 - 0.009)
		M	0.998	0.006	(0.991 - 1.000)
7/29 - 8/4	55	T	0.002	0.006	(0.000 - 0.008)
		M	0.999	0.006	(0.992 - 1.000)
8/5 - 8/10	75	T	0.002	0.005	(0.000 - 0.009)
		M	0.999	0.005	(0.991 - 1.000)

[a]Reporting Groups: tributary (T) and mainstem (M).

-continued-

Table 9. Lower Kenai River netting program, 2007: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
5/16 - 5/26	7	T	0.993	0.017	(0.961 - 1.000)
		M	0.007	0.017	(0.000 - 0.039)
5/27 - 6/2	23	T	0.987	0.021	(0.943 - 1.000)
		M	0.013	0.021	(0.000 - 0.057)
6/3 - 6/9	16	T	0.973	0.035	(0.902 - 1.000)
		M	0.027	0.035	(0.000 - 0.098)
6/10 - 6/16	34	T	0.957	0.037	(0.886 - 1.000)
		M	0.043	0.037	(0.000 - 0.115)
6/17 - 6/23	21	T	0.761	0.093	(0.603 - 0.912)
		M	0.239	0.093	(0.088 - 0.397)
6/24 - 6/30	20	T	0.366	0.114	(0.198 - 0.575)
		M	0.634	0.114	(0.425 - 0.802)
7/1 - 7/7	27	T	0.097	0.065	(0.016 - 0.221)
		M	0.903	0.065	(0.779 - 0.984)
7/8 - 7/14	55	T	0.044	0.035	(0.004 - 0.111)
		M	0.956	0.035	(0.889 - 0.996)
7/15 - 7/21	49	T	0.011	0.018	(0.000 - 0.047)
		M	0.989	0.018	(0.953 - 1.000)
7/22 - 7/28	55	T	0.004	0.009	(0.000 - 0.020)
		M	0.996	0.009	(0.980 - 1.000)
7/29 - 8/4	35	T	0.005	0.010	(0.000 - 0.023)
		M	0.995	0.010	(0.977 - 1.000)
8/5 - 8/10	27	T	0.008	0.016	(0.000 - 0.037)
		M	0.992	0.016	(0.963 - 1.000)

[a]Reporting Groups: tributary (T) and mainstem (M).

-continued-

Table 10. Lower Kenai River netting program, 2008: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
5/16 - 5/26	13	T	0.996	0.012	(0.975 - 1.000)
		M	0.004	0.012	(0.000 - 0.025)
5/27 - 6/2	15	T	0.995	0.012	(0.972 - 1.000)
		M	0.005	0.012	(0.000 - 0.028)
6/3 - 6/9	31	T	0.989	0.018	(0.953 - 1.000)
		M	0.011	0.018	(0.000 - 0.047)
6/10 - 6/16	41	T	0.950	0.037	(0.879 - 0.996)
		M	0.050	0.037	(0.004 - 0.121)
6/17 - 6/23	45	T	0.843	0.070	(0.722 - 0.952)
		M	0.157	0.070	(0.048 - 0.278)
6/24 - 6/30	36	T	0.495	0.092	(0.351 - 0.653)
		M	0.505	0.092	(0.347 - 0.649)
7/1 - 7/7	49	T	0.156	0.067	(0.061 - 0.280)
		M	0.845	0.067	(0.720 - 0.939)
7/8 - 7/14	40	T	0.016	0.017	(0.000 - 0.050)
		M	0.984	0.017	(0.950 - 1.000)
7/15 - 7/21	49	T	0.006	0.011	(0.000 - 0.028)
		M	0.994	0.011	(0.972 - 1.000)
7/22 - 7/28	50	T	0.003	0.007	(0.000 - 0.016)
		M	0.997	0.007	(0.984 - 1.000)
7/29 - 8/4	49	T	0.004	0.011	(0.000 - 0.022)
		M	0.996	0.011	(0.978 - 1.000)
8/5 - 8/10	50	T	0.003	0.009	(0.000 - 0.017)
		M	0.997	0.009	(0.983 - 1.000)

[a]Reporting Groups: tributary (T) and mainstem (M).

-continued-

Table 11. Lower Kenai River netting program, 2009: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
5/16 - 5/26	6	T	0.982	0.027	(0.926 - 1.000)
		M	0.018	0.027	(0.000 - 0.074)
5/27 - 6/2	23	T	0.972	0.032	(0.908 - 1.000)
		M	0.028	0.032	(0.000 - 0.092)
6/3 - 6/9	17	T	0.928	0.057	(0.822 - 0.998)
		M	0.072	0.057	(0.002 - 0.178)
6/10 - 6/16	26	T	0.878	0.062	(0.768 - 0.972)
		M	0.122	0.062	(0.029 - 0.232)
6/17 - 6/23	20	T	0.533	0.098	(0.374 - 0.698)
		M	0.467	0.098	(0.303 - 0.626)
6/24 - 6/30	56	T	0.219	0.071	(0.116 - 0.347)
		M	0.781	0.071	(0.653 - 0.884)
7/1 - 7/7	74	T	0.049	0.036	(0.004 - 0.117)
		M	0.951	0.036	(0.883 - 0.996)
7/8 - 7/14	95	T	0.039	0.037	(0.000 - 0.113)
		M	0.961	0.037	(0.887 - 1.000)
7/15 - 7/21	64	T	0.024	0.030	(0.000 - 0.087)
		M	0.976	0.030	(0.913 - 1.000)
7/22 - 7/28	52	T	0.004	0.010	(0.000 - 0.022)
		M	0.996	0.010	(0.978 - 1.000)
7/29 - 8/4	54	T	0.004	0.008	(0.000 - 0.020)
		M	0.996	0.008	(0.980 - 1.000)
8/5 - 8/10	28	T	0.010	0.019	(0.000 - 0.046)
		M	0.990	0.019	(0.954 - 1.000)

[a]Reporting Groups: tributary (T) and mainstem (M).

-continued-

Table 12. Lower Kenai River netting program, 2010: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
5/16 - 5/26	11	T	0.992	0.016	(0.961 - 1.000)
		M	0.008	0.016	(0.000 - 0.039)
5/27 - 6/2	8	T	0.985	0.024	(0.934 - 1.000)
		M	0.015	0.024	(0.000 - 0.066)
6/3 - 6/9	60	T	0.967	0.035	(0.896 - 1.000)
		M	0.033	0.035	(0.000 - 0.104)
6/10 - 6/16	79	T	0.957	0.035	(0.890 - 0.999)
		M	0.043	0.035	(0.001 - 0.110)
6/17 - 6/23	27	T	0.783	0.089	(0.633 - 0.929)
		M	0.217	0.089	(0.071 - 0.367)
6/24 - 6/30	32	T	0.259	0.083	(0.131 - 0.404)
		M	0.741	0.083	(0.597 - 0.869)
7/1 - 7/7	53	T	0.089	0.040	(0.033 - 0.162)
		M	0.911	0.040	(0.838 - 0.967)
7/8 - 7/14	47	T	0.085	0.044	(0.026 - 0.169)
		M	0.915	0.044	(0.831 - 0.975)
7/15 - 7/21	70	T	0.035	0.023	(0.008 - 0.079)
		M	0.965	0.023	(0.921 - 0.992)
7/22 - 7/28	50	T	0.009	0.014	(0.000 - 0.037)
		M	0.991	0.014	(0.964 - 1.000)
7/29 - 8/4	52	T	0.009	0.015	(0.000 - 0.039)
		M	0.991	0.015	(0.961 - 1.000)
8/5 - 8/10	23	T	0.030	0.039	(0.000 - 0.109)
		M	0.970	0.039	(0.891 - 1.000)

[a]Reporting Groups: tributary (T) and mainstem (M).

-continued-

Table 13. Lower Kenai River sport fishery, 2006: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
5/16 - 5/29	5	T	1.000	0.001	(1.000 - 1.000)
		M	0.000	0.001	(0.000 - 0.000)
5/30 - 6/16	92	T	0.991	0.012	(0.966 - 1.000)
		M	0.009	0.012	(0.000 - 0.034)
6/17 - 6/30	76	T	0.683	0.064	(0.572 - 0.783)
		M	0.317	0.064	(0.217 - 0.428)
7/1 - 7/16	129	T	0.054	0.029	(0.014 - 0.107)
		M	0.946	0.029	(0.893 - 0.986)
7/17 - 7/31	209	T	0.002	0.005	(0.000 - 0.010)
		M	0.998	0.005	(0.990 - 1.000)

[a]Reporting Groups: tributary (T) and mainstem (M).

Table 14. Lower Kenai River sport fishery, 2007: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
5/16 - 5/29	4	T	1.000	0.001	(1.000 - 1.000)
		M	0.000	0.001	(0.000 - 0.000)
5/30 - 6/16	61	T	0.986	0.018	(0.948 - 1.000)
		M	0.014	0.018	(0.000 - 0.052)
6/17 - 6/30	56	T	0.704	0.070	(0.584 - 0.811)
		M	0.296	0.070	(0.189 - 0.416)
7/1 - 7/16	88	T	0.051	0.030	(0.011 - 0.108)
		M	0.949	0.030	(0.892 - 0.989)
7/17 - 7/31	173	T	0.003	0.010	(0.000 - 0.020)
		M	0.997	0.010	(0.980 - 1.000)

[a]Reporting Groups: tributary (T) and mainstem (M).

-continued-

Table 15. Lower Kenai River sport fishery, 2008: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
5/16 - 5/29	21	T	1.000	0.000	(1.000 - 1.000)
		M	0.000	0.000	(0.000 - 0.000)
5/30 - 6/16	104	T	0.996	0.007	(0.982 - 1.000)
		M	0.004	0.007	(0.000 - 0.018)
6/17 - 6/30	59	T	0.772	0.063	(0.665 - 0.873)
		M	0.228	0.063	(0.127 - 0.335)
7/1 - 7/16	81	T	0.057	0.032	(0.014 - 0.118)
		M	0.943	0.032	(0.883 - 0.986)
7/17 - 7/31	113	T	0.016	0.016	(0.001 - 0.050)
		M	0.984	0.016	(0.950 - 0.999)

[a]Reporting Groups: tributary (T) and mainstem (M).

Table 16. Lower Kenai River sport fishery, 2009: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
5/16 - 5/29	13	T	1.000	0.000	(1.000 - 1.000)
		M	0.000	0.000	(0.000 - 0.000)
5/30 - 6/16	33	T	0.991	0.015	(0.961 - 1.000)
		M	0.010	0.015	(0.000 - 0.039)
6/17 - 6/30	26	T	0.771	0.068	(0.655 - 0.881)
		M	0.229	0.068	(0.119 - 0.345)
7/1 - 7/16	178	T	0.049	0.024	(0.016 - 0.092)
		M	0.951	0.024	(0.908 - 0.985)
7/17 - 7/31	117	T	0.004	0.011	(0.000 - 0.021)
		M	0.996	0.011	(0.979 - 1.000)

[a]Reporting Groups: tributary (T) and mainstem (M).

-continued-

Table 17. Lower Kenai River sport fishery, 2010: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
5/16 - 5/29	18	T	1.000	0.000	(1.000 - 1.000)
		M	0.000	0.000	(0.000 - 0.000)
5/30 - 6/16	6	T	0.991	0.016	(0.962 - 1.000)
		M	0.009	0.016	(0.000 - 0.038)
6/17 - 6/30	45	T	0.701	0.067	(0.586 - 0.804)
		M	0.299	0.067	(0.196 - 0.415)
7/1 - 7/16	49	T	0.074	0.036	(0.027 - 0.142)
		M	0.926	0.036	(0.858 - 0.973)
7/17 - 7/31	168	T	0.005	0.011	(0.000 - 0.028)
		M	0.995	0.011	(0.972 - 1.000)

[a]Reporting Groups: tributary (T) and mainstem (M).

Table 18. Middle Kenai River sport fishery, 2007: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
6/17 - 6/30	60	T	0.878	0.051	(0.788 - 0.953)
		M	0.122	0.051	(0.047 - 0.212)
7/1 - 7/16	31	T	0.265	0.077	(0.147 - 0.397)
		M	0.735	0.077	(0.603 - 0.853)
7/17 - 7/31	56	T	0.010	0.014	(0.000 - 0.038)
		M	0.990	0.014	(0.962 - 1.000)

[a]Reporting Groups: tributary (T) and mainstem (M).

-continued-

Table 19. Middle Kenai River sport fishery, 2008: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
6/17 - 6/30	124	T	0.890	0.037	(0.825 - 0.946)
		M	0.111	0.037	(0.054 - 0.175)
7/1 - 7/16	114	T	0.355	0.061	(0.260 - 0.463)
		M	0.645	0.061	(0.537 - 0.740)
7/17 - 7/31	104	T	0.021	0.017	(0.002 - 0.053)
		M	0.980	0.017	(0.947 - 0.998)

[a]Reporting Groups: tributary (T) and mainstem (M).

Table 20. Middle Kenai River sport fishery, 2009: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
6/17 - 6/30	15	T	0.876	0.064	(0.759 - 0.966)
		M	0.124	0.064	(0.034 - 0.241)
7/1 - 7/16	44	T	0.223	0.066	(0.117 - 0.335)
		M	0.777	0.066	(0.665 - 0.883)
7/17 - 7/31	127	T	0.012	0.016	(0.000 - 0.044)
		M	0.988	0.016	(0.956 - 1.000)

[a]Reporting Groups: tributary (T) and mainstem (M).

Table 21. Middle Kenai River sport fishery, 2010: Sample size (N) and fitted stock composition estimates, standard deviations (SD), and 90% credibility intervals (CI) to reporting groups by date ranges.

Dates	N	RG[a]	Estimate	SD	CI
6/17 - 6/30	99	T	0.856	0.046	(0.774 - 0.925)
		M	0.144	0.046	(0.075 - 0.226)
7/1 - 7/16	88	T	0.191	0.055	(0.104 - 0.286)
		M	0.809	0.055	(0.714 - 0.896)
7/17 - 7/31	157	T	0.010	0.013	(0.000 - 0.037)
		M	0.990	0.013	(0.963 - 1.000)

[a]Reporting Groups: tributary (T) and mainstem (M).

-continued-

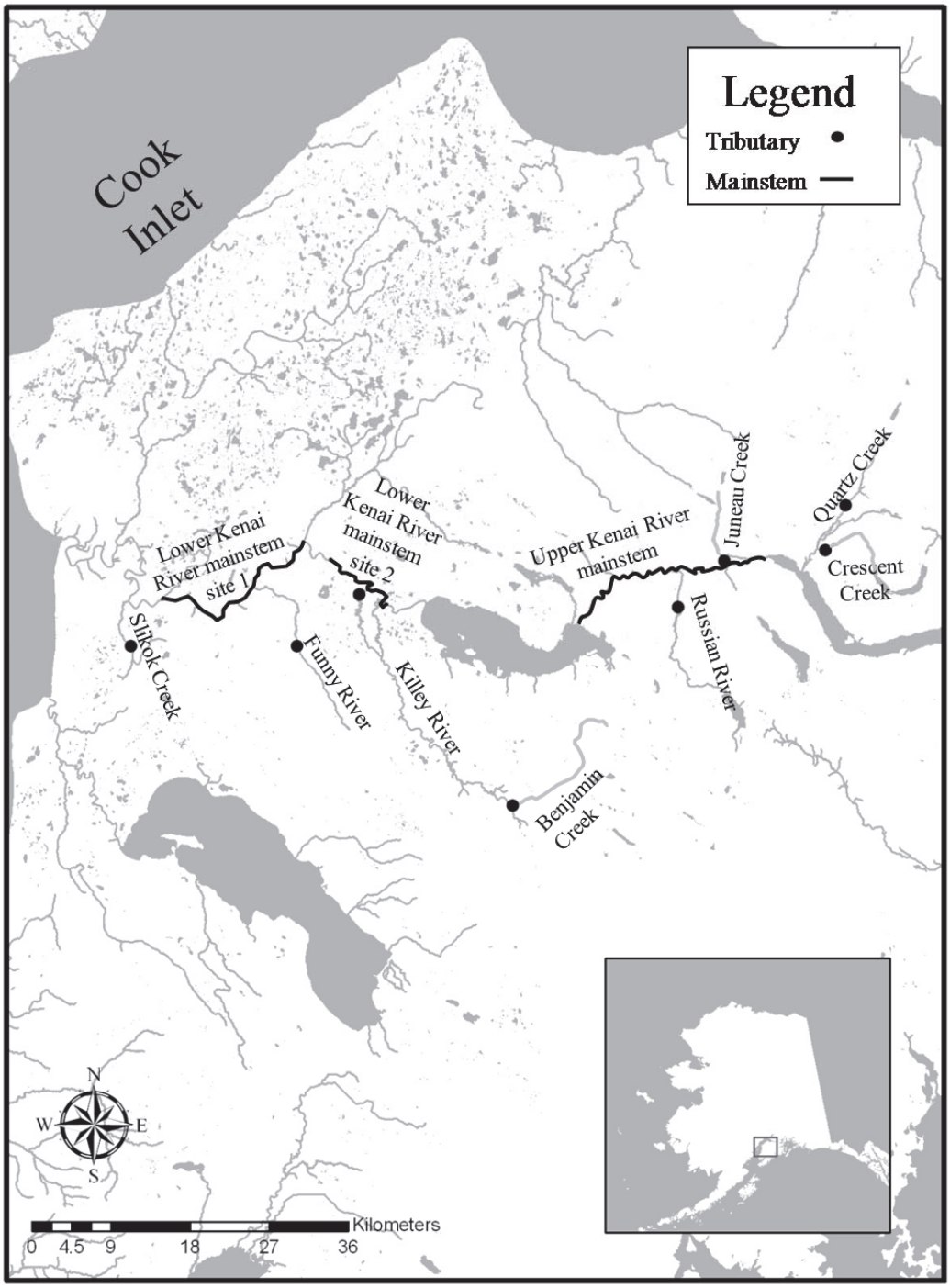

Figure 1.- Sampling locations for Chinook salmon in the Kenai River, Alaska, drainage used to compile a genetic baseline.

-continued-

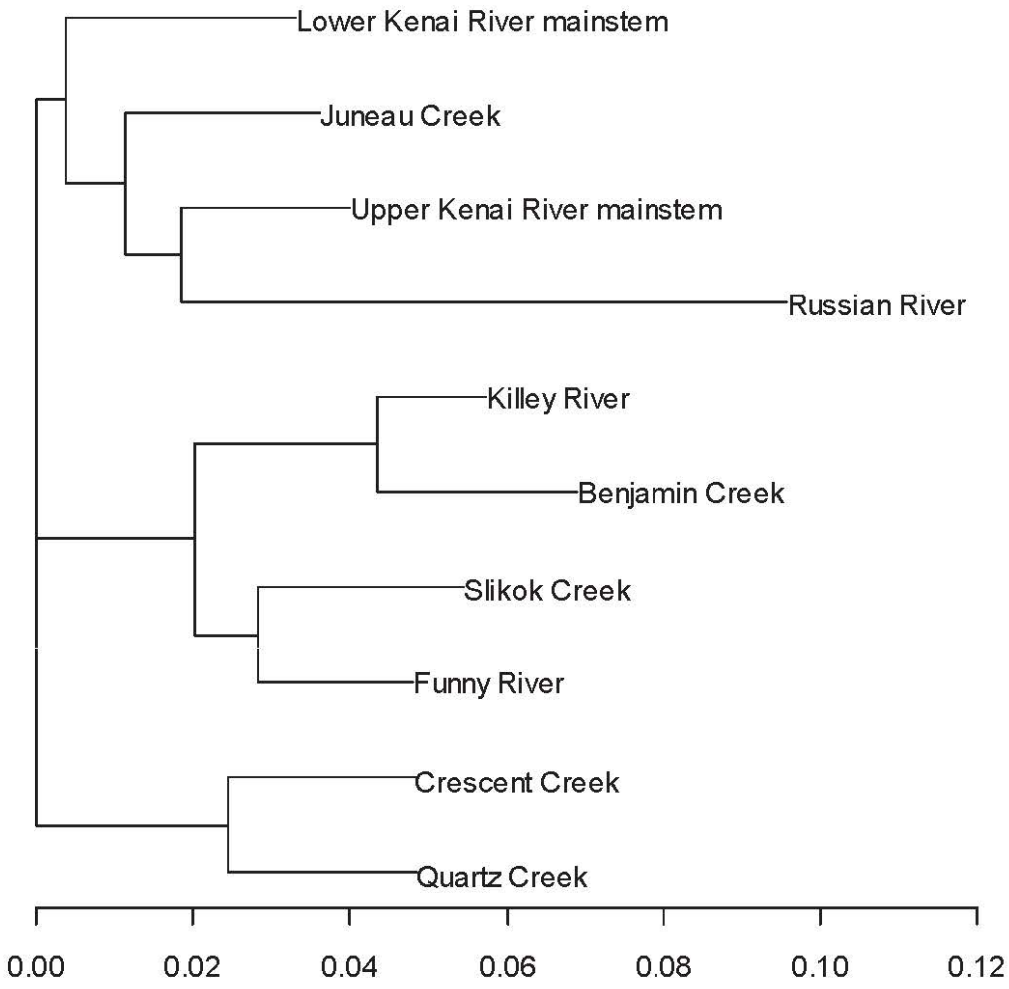

Figure 2.- Neighbor-Joining tree based on Cavalli-Sforza and Edwards (1967) chord distances among Chinook salmon populations sampled from spawning locations in the Kenai River, Alaska. drainage.