Regional Operational Plan SF.2A.2018.14

Operational Plan: Upper Cook Inlet Commercial Eastside Set Gillnet Chinook Salmon Harvest Composition Study

by

Tony Eskelin

and

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May 2018

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

Symbols and Abbreviations

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Weights and measures (metric)

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

Weights and measures (English)

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

Time and temperature

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

Physics and chemistry

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

General

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

Mathematics, statistics

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

REGIONAL OPERATIONAL PLAN SF.2A.2018.14

OPERATIONAL PLAN: UPPER COOK INLET COMMERCIAL EASTSIDE SET GILLNET CHINOOK SALMON HARVEST COMPOSITION STUDY

by
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May 2018

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ABSTRACT

Genetic tissue and age, sex, and length composition information will be collected from harvested Chinook salmon in the Upper Cook Inlet eastside set gillnet (ESSN) commercial fishery in 2018–2020. The primary goals of the study are to estimate the stock composition and stock-specific harvest of Chinook salmon in the ESSN commercial fishery by reporting group and size (2 categories: less than 75 cm METF [mid eye to tail fork] and 75 cm METF and longer) for each temporal and geographic stratum, and for each season (2018–2020). Harvest estimates will be apportioned into 4 reporting groups: Kenai River mainstem, Kasilof River mainstem, Kenai River tributaries, and Cook Inlet other. Age, sex, and length composition will also be estimated for each temporal and geographic stratum and for each season.

Key words: Chinook salmon, *Oncorhynchus tshawytscha*, Kenai River, eastside set gillnet, commercial fishery, ESSN, upper Cook Inlet, MSA, stock-specific harvest

INTRODUCTION

PURPOSE

Stock-specific harvest and age, sex, and length (ASL) composition of Chinook salmon harvest in the ESSN commercial fishery are needed for effective management of Chinook salmon stocks in Cook Inlet to improve understanding of stock productivity, for brood table development, and for setting and attaining escapement goals. Genetic samples are needed to estimate the stock-specific harvest of Chinook salmon in the ESSN commercial fishery temporally, geographically, and by size. ASL composition of the Chinook salmon harvest is needed to more accurately characterize the harvest and assess production and age at maturity trends. This project will collect and analyze ASL and genetic tissue samples of Chinook salmon harvested in the ESSN commercial fishery. The Alaska Department of Fish and Game (ADF&G) Division of Sport Fish (SF) will be responsible for the collection of genetic tissue samples and ASL data. Tissue samples will be sent to the Division of Commercial Fisheries (CF) Gene Conservation Lab (GCL), which will be responsible for mixed stock analysis (MSA).

BACKGROUND

All 5 species of Pacific salmon are harvested by the commercial fisheries in Upper Cook Inlet (UCI). Sockeye salmon (*Oncorhynchus nerka*) compose the majority of the harvest (Shields and Dupuis 2017) but Chinook salmon (*O. tshawytscha*) are also harvested. Harvest statistics are monitored by the Alaska Department of Fish and Game (ADF&G) from fish tickets (5 AAC 21.355). Harvest data are available and reported by 5-digit statistical areas (Shields and Dupuis 2017). Most of the UCI commercial Chinook salmon harvest occurs in the Upper Subdistrict of the Central District, commonly referred to as the Eastside set gillnet (ESSN) fishery, located along the eastern shore of Cook Inlet between Ninilchik and Boulder Point (Figures 1 and 2). On average since 1966, the ESSN fishery has accounted for 64.6% of all Chinook salmon harvested in UCI commercial fisheries (Table 1).

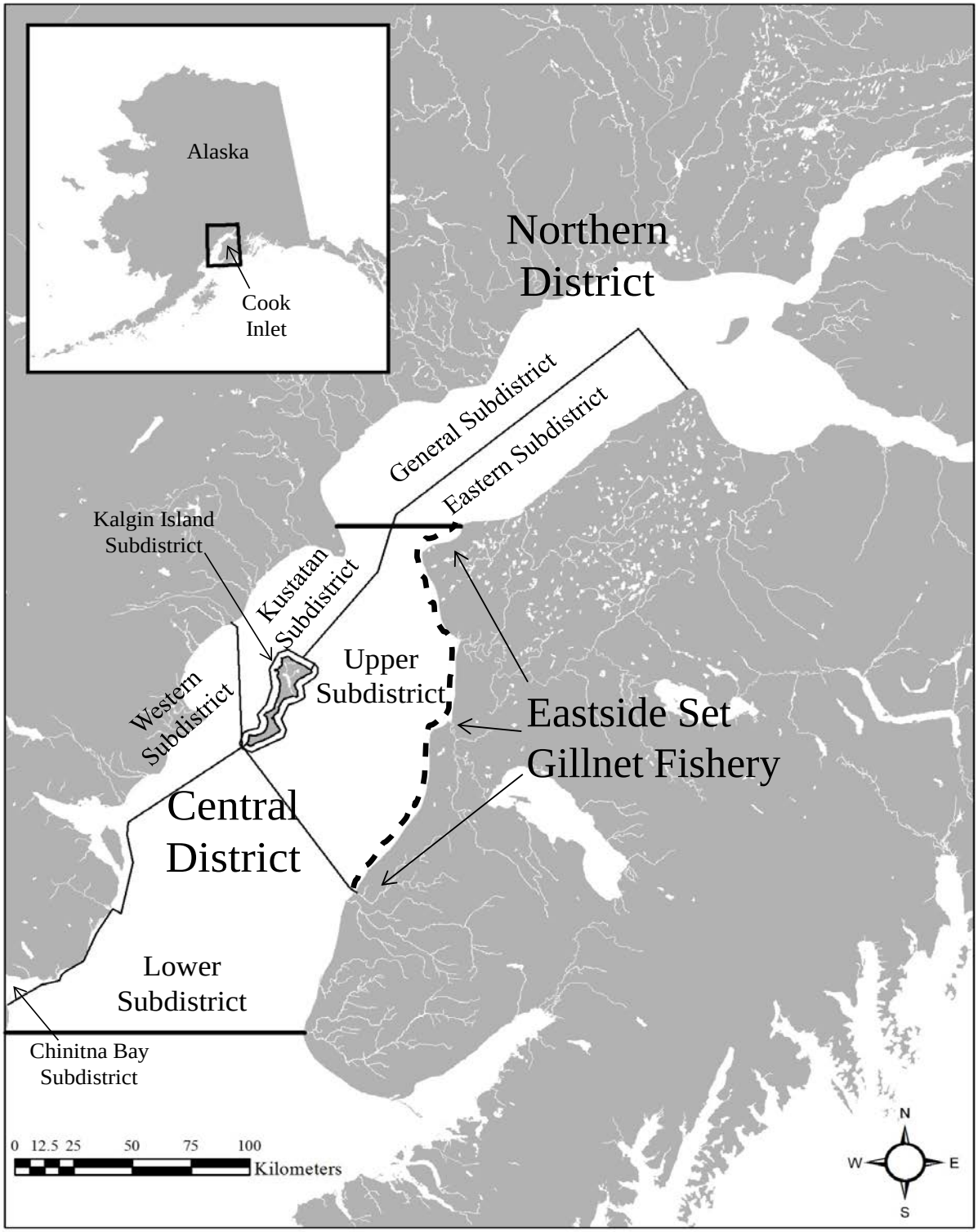

Figure 1.–Map of Upper Cook Inlet commercial fishing districts and subdistricts.

Note: Thick black lines indicate district borders and thin lines indicate subdistrict borders; the thick dashed line near the eastern shore of Cook Inlet denotes the Eastside set gillnet fishery.

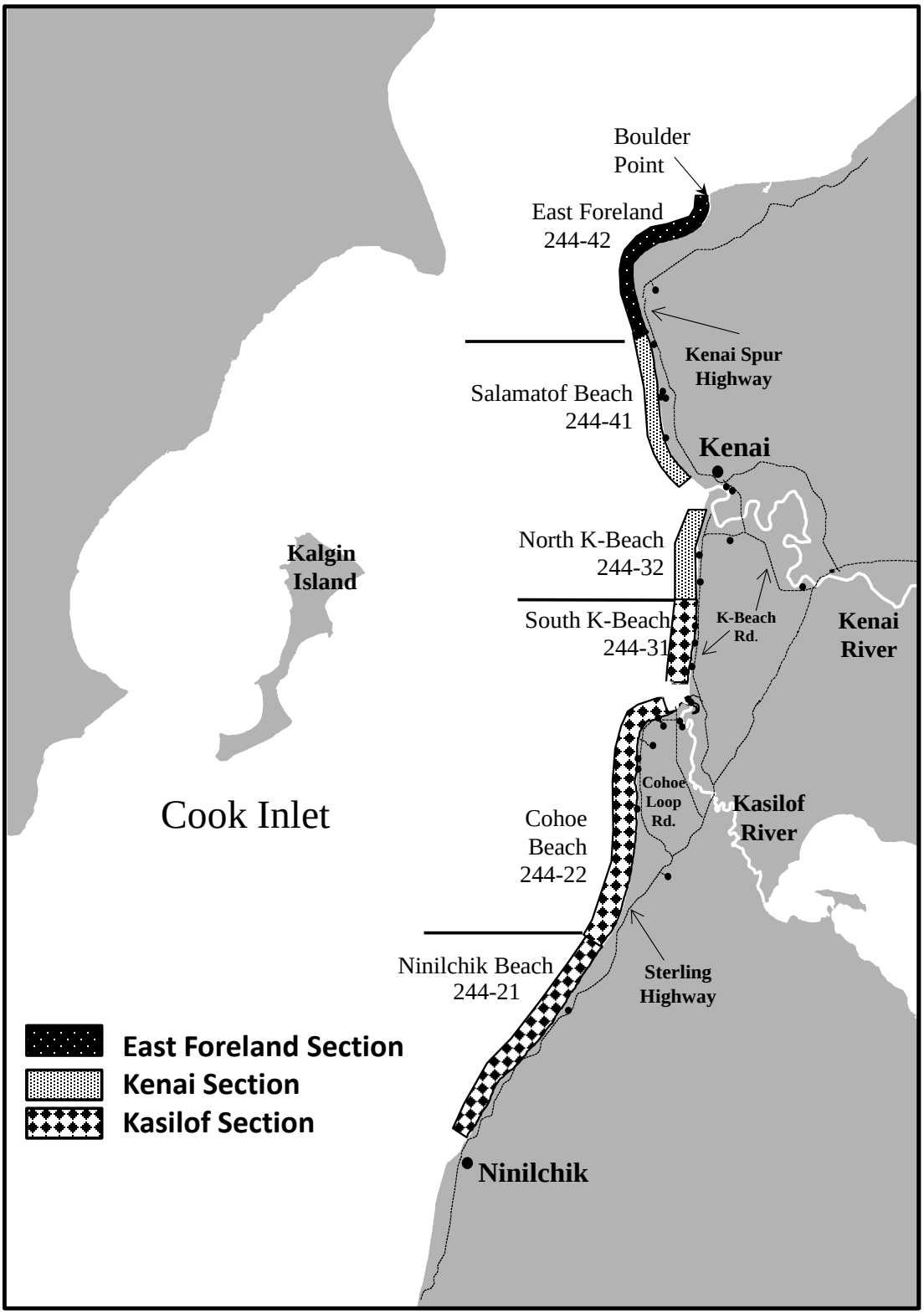

Figure 2.–Map of Upper Cook Inlet Eastside set gillnet commercial fishing statistical areas.

Note: Small circles represent approximate locations of processing plants or receiving sites.

Table 1.–Upper Cook Inlet commercial Chinook salmon gillnet harvest by gear type and area, 1966–2017.

	Central District								
	Eastside setnet		Drift		Kalgin–Westside setnet		Northern District setnet		
Year	Harvest	%	Harvest	%	Harvest	%	Harvest	%	Total
1966	7,329	85.8	392	4.6	401	4.7	422	4.9	8,544
1967	6,686	85.1	489	6.2	500	6.4	184	2.3	7,859
1968	3,304	72.8	182	4.0	579	12.8	471	10.4	4,536
1969	5,834	47.1	362	2.9	3,286	26.5	2,904	23.4	12,386
1970	5,368	64.4	356	4.3	1,152	13.8	1,460	17.5	8,336
1971	7,055	35.7	237	1.2	2,875	14.5	9,598	48.6	19,765
1972	8,599	53.5	375	2.3	2,199	13.7	4,913	30.5	16,086
1973	4,411	84.9	244	4.7	369	7.1	170	3.3	5,194
1974	5,571	84.5	422	6.4	434	6.6	169	2.6	6,596
1975	3,675	76.8	250	5.2	733	15.3	129	2.7	4,787
1976	8,249	75.9	690	6.4	1,469	13.5	457	4.2	10,865
1977	9,730	65.8	3,411	23.1	1,084	7.3	565	3.8	14,790
1978	12,468	72.1	2,072	12.0	2,093	12.1	666	3.8	17,299
1979	8,671	63.1	1,089	7.9	2,264	16.5	1,714	12.5	13,738
1980	9,643	69.9	889	6.4	2,273	16.5	993	7.2	13,798
1981	8,358	68.3	2,320	19.0	837	6.8	725	5.9	12,240
1982	13,658	65.4	1,293	6.2	3,203	15.3	2,716	13.0	20,870
1983	15,042	72.9	1,125	5.5	3,534	17.1	933	4.5	20,634
1984	6,165	61.3	1,377	13.7	1,516	15.1	1,004	10.0	10,062
1985	17,723	73.6	2,048	8.5	2,427	10.1	1,890	7.8	24,088
1986	19,826	50.5	1,834	4.7	2,108	5.4	15,488	39.5	39,256
1987	21,159	53.6	4,552	11.5	1,029	2.6	12,700	32.2	39,440
1988	12,859	44.2	2,237	7.7	1,148	3.9	12,836	44.1	29,080
1989	10,914	40.8	0	0.0	3,092	11.6	12,731	47.6	26,737
1990	4,139	25.7	621	3.9	1,763	10.9	9,582	59.5	16,105
1991	4,893	36.1	246	1.8	1,544	11.4	6,859	50.6	13,542
1992	10,718	62.4	615	3.6	1,284	7.5	4,554	26.5	17,171
1993	14,079	74.6	765	4.1	720	3.8	3,307	17.5	18,871
1994	15,575	78.0	464	2.3	730	3.7	3,193	16.0	19,962
1995	12,068	67.4	594	3.3	1,101	6.2	4,130	23.1	17,893
1996	11,564	80.8	389	2.7	395	2.8	1,958	13.7	14,306
1997	11,325	85.2	627	4.7	207	1.6	1,133	8.5	13,292
1998	5,087	62.6	335	4.1	155	1.9	2,547	31.4	8,124
1999	9,463	65.8	575	4.0	1,533	10.7	2,812	19.6	14,383
2000	3,684	50.1	270	3.7	1,089	14.8	2,307	31.4	7,350
2001	6,009	64.6	619	6.7	856	9.2	1,811	19.5	9,295
2002	9,478	74.5	415	3.3	926	7.3	1,895	14.9	12,714
2003	14,810	80.1	1,240	6.7	770	4.2	1,670	9.0	18,490

-continued-

Table 1.–Page 2 of 2.

	Central District								
	Eastside setnet		Drift		Kalgin–Westside setnet		Northern District setnet		
Year	Harvest	%	Harvest	%	Harvest	%	Harvest	%	Total
2004	21,684	80.5	1,104	4.1	2,208	8.2	1,926	7.2	26,922
2005	21,597	78.1	1,958	7.1	739	2.7	3,373	12.2	27,667
2006	9,956	55.2	2,782	15.4	1,030	5.7	4,261	23.6	18,029
2007	12,292	69.7	912	5.2	603	3.4	3,818	21.7	17,625
2008	7,573	56.8	653	4.9	1,124	8.4	3,983	29.9	13,333
2009	5,588	63.9	859	9.8	672	7.7	1,631	18.6	8,750
2010	7,059	71.3	538	5.4	553	5.6	1,750	17.7	9,900
2011	7,697	68.4	593	5.3	659	5.9	2,299	20.4	11,248
2012	704	27.9	218	8.6	555	22.0	1,049	41.5	2,526
2013	2,988	55.4	493	9.1	590	10.9	1,327	24.6	5,398
2014	2,301	49.4	382	8.2	507	10.9	1,470	31.5	4,660
2015	7,781	72.1	556	5.1	538	5.0	1,923	17.8	10,798
2016	6,759	67.4	606	6.0	460	4.6	2,202	22.0	10,027
2017	4,779	62.4	264	3.4	387	5.1	2,230	29.1	7,660
Average									
1966–2016[a]	9,395	64.6	935	6.3	1,253	9.3	3,228	19.9	14,811
2007–2016	6,074	60.2	581	6.8	626	8.4	2,145	24.6	9,427

[a] Data from 1989 were not used in averages because the drift fleet did not fish due to the Exxon Valdez oil spill, which affected all other fisheries.

Management of the Eastside Set Gillnet Fishery

The ESSN (commercial) fishery is divided into 3 sections (Kenai, Kasilof, and East Foreland) and 6 main statistical areas: Ninilchik Beach (244-22), Cohoe Beach (244-22), South K-Beach (244-31), North K-Beach (244-32), Salamatof Beach (244-41), and East Foreland Beach (244-42) (Figure 2). Management plans generally dictate the ESSN fishery be opened by sections, which are mostly groups of statistical areas. The Kasilof Section is composed of Ninilchik Beach, Cohoe Beach, and South K-Beach. The Kenai Section is composed of North K-Beach and Salamatof Beach. East Foreland Section is composed of East Foreland Beach and has always been opened concurrently with the Kenai Section.

The Kasilof Section opens on the first Monday or Thursday on or after 25 June, unless ADF&G estimates that 50,000 sockeye salmon are in the Kasilof River prior to that date, at which time the commissioner may open the Kasilof Section by emergency order (EO); however, the Kasilof Section may not open earlier than 20 June (Alaska Administrative Code 5 AAC 21.310 b. 2.C.[i]). The Kenai and East Foreland sections open by regulation on the first Monday or Thursday on or after 8 July (5 AAC 21.310). There is also a small area at the mouth of the Kasilof River designated the Kasilof River Special Harvest Area (KRSHA, 244-25). KRSHA has been opened separately from the Kasilof Section to concentrate harvest of Kasilof River sockeye salmon while minimizing harvest of other stocks. However, at the 2017 UCI Board of Fisheries (BOF) meeting, the management plan was changed to allow the possibility of much more (unlimited) fishing time in the Kasilof Section itself, with openings restricted to within 600 ft of

the mean high tide line. This change was intended to provide a management tool to maximize Kasilof River sockeye salmon harvest if necessary, but to limit the use of KRSHA. In addition, at the 2017 UCI BOF meeting, North K-Beach (Kenai Section) within 600 ft of the mean high tide line was also added as a management tool that can be fished concurrently with openings of the Kasilof Section restricted to within 600 ft of the mean high tide line if the ESSN fishery is closed to conserve Kenai River Chinook salmon or Kenai River sockeye salmon.

There are other restrictions to the ESSN fishery. After the Kenai and East Foreland sections open for the season, 2 mandatory no fishing windows per week are in place whereby the ESSN fishery will close for 36 continuous hours beginning sometime between 7:00 PM Thursday and 7:00 AM Friday and will also close for 24 continuous hours beginning sometime between 7:00 PM Monday and 7:00 AM Wednesday. Openings of the Kasilof Section and North K-Beach that are restricted to within 600 ft of the mean high tide line are not tied to the weekly no-fishing window restrictions. The ESSN fishery is also paired with the Kenai River sport fishery such that when the inriver sport fishery is restricted from the use of bait, the ESSN fishery may, by emergency order (EO), be allowed extra fishing periods up to 48 hours per week. Furthermore, when the Kenai River sport fishery is restricted to catch-and-release only fishing, the ESSN fishery may, by EO, be allowed extra fishing periods up to 24 hours per week.

The ESSN fishery closes on 15 August with only regular periods allowed after August 10. In addition, the ESSN fishery closes if less than 1% of the cumulative sockeye salmon harvest is harvested in consecutive fishery openings after 7 August. See Shields and Dupuis (2017) for more specific details regarding management of the ESSN fishery

Chinook Salmon Research

A recent downturn in Chinook salmon productivity and abundance statewide has created social and economic hardships for many communities in Alaska (ADF&G Chinook Salmon Research Team 2013). Fishery management has been responsive to lower run abundances to achieve escapement goals. This downturn has also heightened concerns about stock-specific harvest of Chinook salmon. In July 2012, ADF&G initiated a comprehensive Chinook Salmon Research Initiative (CSRI) to increase stock assessment capabilities, address knowledge gaps, and elucidate causal mechanisms behind the observed trend in Chinook salmon productivity and abundance. This research plan included Kenai River Chinook salmon as 1 of 12 statewide indicator stocks and represented an effort to address critical knowledge gaps that limit management capabilities, particularly during times of low abundance. The ESSN Chinook salmon sampling project was funded by CSRI during 2013–2016 to better assess Kenai River Chinook salmon adult abundance and gain a better understanding of stock-specific harvests of Chinook salmon in the ESSN fishery. This project continued in 2017 and was funded by the Pacific States Marine Fisheries Commission (PSMFC). The PSMFC issued grants to qualified research projects in Cook Inlet that addressed research themes to the “Alaska Chinook salmon Fishery Disaster” that was declared by the Secretary of Commerce on September 31, 2012 and the PSMFC awarded funding for this project in 2017. This project will be funded by ADF&G in 2018–2020.

Mixed Stock Analysis

Accurate estimation of adult abundance requires stock-specific information on the escapement and inriver run as well as marine and freshwater harvests. For mixed stock harvests from marine and freshwater fisheries, stock-specific harvest can be estimated by using genetic information in

a mixed stock analysis (MSA). This analysis requires a comprehensive genetic baseline that includes genetic data from fish representing all potential populations that may contribute to the harvest. In addition, for available genetic markers, there must be sufficient genetic variation among baseline populations to accurately estimate the contribution of population groups (stocks) in a MSA. These groups of populations are referred to as reporting groups. Stock compositions and stock-specific harvest estimates refer to compositions and harvest by reporting group.

Baseline and Reporting Groups

A Chinook salmon genetic baseline for UCI was first developed in 2012 that included 30 populations and 38 genetically variant single nucleotide polymorphism (SNP) loci (Barclay et al. 2012). Since then, the baseline has been augmented with additional collections and previously unrepresented populations, and it is now comprehensive, including 55 populations and 39 variant SNPs (Barclay and Habicht 2015). To minimize misallocation between MSA reporting groups, the Slikok Creek population from the Kenai River drainage was removed from the baseline because it represents a very small number of fish and is genetically similar to the Crooked Creek population from the Kasilof River drainage (Barclay et al. 2012). Therefore, the baseline only includes 54 of the 55 populations reported in Barclay and Habicht (2015). For more specific details regarding the UCI Chinook salmon baseline, see Barclay and Habicht (2015) or past reports detailing MSAs of the ESSN Chinook salmon harvest since 2010 (Eskelin et al. 2013; Eskelin and Barclay 2015-2017).

Genetic baselines are always evolving. This project has successfully used a baseline containing 54 populations genotyped for 39 SNP loci to estimate the composition of the ESSN Chinook salmon harvest since 2013 (Eskelin et al. 2013; Eskelin and Barclay 2015-2017). This vetted baseline will be the default for use in the 2018–2020 analyses. However, we will investigate ways to improve the accuracy and precision of estimates by incorporating novel, informative SNPs to the baseline prior to MSA each year. We will only use the improved baseline if its ability to discriminate among stocks is better than the default baseline.

Reporting groups chosen to apportion the harvest were selected based on 1 or more of the following criteria: 1) the genetic similarity among populations, 2) the expectation that proportional harvest would be greater than 5%, or 3) the applicability for answering fishery management questions. The 4 reporting groups chosen to apportion the ESSN Chinook salmon harvest were as follows: *Kenai River mainstem* (Kenai River mainstem populations and Juneau Creek), *Kenai River tributaries* (Kenai River tributary populations excluding Juneau Creek), *Kasilof River mainstem* (the Kasilof River mainstem population) and *Cook Inlet other* (all remaining UCI baseline populations).

Juneau Creek, a Kenai River tributary, was included in the *Kenai River mainstem* reporting group due to its genetic similarity with Kenai River mainstem populations (Barclay et al. 2012). The results of baseline evaluation tests (proof tests) for the 4 reporting groups are reported in Eskelin et al. (2013). Since that report, 12 additional northern Cook Inlet populations have been added to the baseline. Because northern Cook Inlet populations are included in the *Cook Inlet other* reporting group, which represents a very small component of the ESSN Chinook salmon harvest, the previous proof test results are still a good indicator of the performance of the updated baseline for ESSN Chinook salmon reporting groups.

Tissue and Age, Sex, and Length Sampling and Analyses

Age, sex, and length (ASL) samples have been collected from Chinook salmon harvested in the ESSN fishery since 1983 (Tobias and Willette 2002). Tissue samples for MSA were added to the collection effort beginning in 2010. Stock compositions and stock-specific harvest estimates were produced for 2010–2017 except for 2012 due to low sample size. During 2013–2017, increased funding provided annually by CSRI (2013–2016) and PSMFC (2017) amplified sampling effort which increased the sampling rate, provided for better coverage of the fishery and permitted stock compositions and stock-specific harvest estimates to be stratified by time and area.

In the meantime, management of Kenai River Chinook salmon has transitioned to assessment and management based on sonar estimates of Chinook salmon that are 75 cm from mid eye to tail fork (METF) and longer. This modification to the management plan was finalized at the 2017 UCI BOF meeting. To support the new management regime and to provide as much pertinent information as possible, we developed methods to estimate stock compositions and stock-specific harvest of ESSN Chinook salmon stratified by size (i.e., large and small fish as defined above), and provided size-stratified estimates for 2015–2017.

Results from MSA ESSN harvest studies have been published in Eskelin et al. (2013) for 2010, 2011, and 2013, and in Eskelin and Barclay (2015–2017) for 2014–2016, respectively. Results from the 2017 study will be published in 2018.

A new project set to begin in 2018 will assess inriver abundance of large late run *Kasilof River mainstem* Chinook salmon abundance using newest sonar technology. This ESSN Chinook salmon sampling project will have even more utility for the department in the future by continuing to provide ESSN harvest of large *Kasilof River mainstem* fish to better assess Kasilof River Chinook salmon.

OBJECTIVES

PRIMARY OBJECTIVES

1) Estimate the proportion of Chinook salmon harvested in the ESSN fishery by reporting group[1] and size[2] for each temporal and geographic stratum, and for the entire season, such that the estimated proportions are within 13 percentage points of the true values 90% of the time.
2) Estimate the harvest of *Kenai River mainstem* and *Kasilof River mainstem* Chinook salmon in the ESSN fishery by size for each temporal and geographic stratum, and for the entire season, such that the estimates are within 30% of the true value, 90% of the time[3].
3) Estimate the age composition of Chinook salmon harvested by the ESSN fishery such that the estimates are within 10 percentage points of the true values 95% of the time[4].

[1] Reporting groups to apportion the harvest will be *Kenai River mainstem, Kasilof River mainstem, Kenai River tributaries, and Cook Inlet other*.
[2] Size will be stratified by small fish (shorter than 75 cm METF) and large fish (75 cm METF and longer).
[3] This criterion is for harvest estimates of stocks that account for at least 20% of the total harvest within a stratum. It is not necessary nor realistic for harvest estimates that account for less than 20% to meet this criterion.
[4] The sample size goal for collection of age (scale) samples will be driven by Objectives 1 and 2.

SECONDARY OBJECTIVES

1) Estimate the harvest of Chinook salmon by size for the reporting groups *Kenai River tributaries* and *Cook Inlet Other* in the ESSN fishery for each temporal and geographic stratum, and for the entire season[5].
2) Sample 30% of the Chinook salmon harvested in the ESSN fishery for tissue, coded wire tags (CWTs), scales, sex, and METF length[6].
3) Estimate the age, sex, and length composition of the Chinook salmon harvest.
4) Determine the sex of sampled fish that are shorter than 75 cm METF length by internal examination[7].

METHODS

STUDY DESIGN

Reported Chinook Salmon Harvest

By regulation, all salmon harvested in the ESSN fishery must be recorded on fish tickets, including those not sold but kept for personal use (Alaska Administrative Code 5 AAC 21.355 *Reporting requirements*). Along with the number of fish harvested, the ticket includes information on the date and location of the harvest. Fish ticket information will be entered into the ADF&G fish ticket database by ADF&G commercial fisheries staff and reported to the project biologist the day after each fishery opening. Final harvest information from the ESSN fishery will be retrieved from this database and used for subsequent analyses postseason.

Sampling Fishery Openings

All regular (generally Monday and Thursday) fishing periods and most fishing periods opened by EO will be sampled. The particular openings by EO that are chosen for sampling will depend on recent harvests, collections to date for each proposed stratum, and insight from commercial fishery managers regarding upcoming fishery openings. All area-restricted openings in relation to the mean high tide line (i.e., within 600 ft, or one-half mile) will be sampled because there is limited stock composition information about that portion of the fishery. In addition, all openings in August will be sampled due to low harvest that generally occurs in August, subsequent low sample size, and that we have limited spatial information in MSAs of the August portion of the fishery. The fishery ends by regulation August 15, with only regular fishing periods allowed after August 10.

Sampling Strategy

During and after fishery openings, 3 ADF&G personnel will travel to the receiving sites for fish processing plants after each tide and sample harvested Chinook salmon for genetic tissue, scales, sex, length, and for CWT recovery. All Chinook salmon at each receiving site will be sampled if possible. If the technician is not able to sample all Chinook salmon at a receiving site due to time

[5] Based on previous MSA results, it is anticipated that Chinook salmon harvest of reporting groups *Kenai River tributaries* and *Cook Inlet Other* will be low (<150 fish) so no precision criteria are set for estimation of these reporting groups. Sample size is driven by Objectives 1 and 2.

[6] The goal to collect biological samples from 30% of the harvest is a rough guideline based on the sampling rate from previous years, whereas the actual goal is to collect as many representative samples distributed between statistical areas during each sampling day. Depending on harvest, it is very possible to meet precision criteria in Objectives 1 and 2, yet not sample 30% of the Chinook salmon harvest during this project.

[7] Sex of fish shorter than 75 cm METF will be determined by internal examination only if permission is granted by the processor.

constraints, Chinook salmon will be sampled for tissue and ASL composition with regard to size such that they sample approximately representative from the Chinook salmon that are available. Generally, as many Chinook salmon as possible will be sampled, but some areas will be sampled more vigorously than other areas. Based on past studies, it has been more difficult to collect sufficient tissue samples from the Ninilchik Beach and South K-Beach statistical areas to meet sample size requirements for MSA when stratified by time and beach, so more time may be spent sampling in those areas. North K-Beach may also be sampled more rigorously in order to collect enough samples to stratify the MSA by time period in July for that area. Salamatof Beach will be sampled less vigorously than other statistical areas due to MSA results consistently showing that nearly all (>95%) of the harvest has been composed of *Kenai River mainstem* fish and sample size goals for that area have been easily attained in previous years.

Each technician will be assigned a specific area to sample; however, there will be overlap in sampling areas among technicians and modifications to assigned areas may occur during the season. Inseason analyses of the number of samples collected and the sampling rate by statistical area will be conducted by the project biologist and modifications will be made to the sampling strategy as necessary to meet sample size requirements for each proposed stratum.

Technicians will begin sampling most often at the southern end of their sampling area after the first round of deliveries to each buying station. Sampling at the southern end first and moving northward usually follows the fish deliveries as they occur and will maximize the number of samples collected. This sampling strategy should not introduce bias. If technicians always started at the northern end and moved southerly, they would probably collect fewer samples due to the generally later timing of deliveries from the northern end of the fishery but it will be up to the technicians and project biologist to determine the best sampling strategy for each day. Technicians will sample during each opening at the receiving sites prior to harvested fish being transported to processing plants. The day following each fishing period, additional Chinook salmon samples may be collected at the fish processing plants, if deemed necessary by the project biologist.

There will probably be 20 or more receiving sites in total, spread throughout each statistical area, where Chinook salmon are delivered. The number and location of receiving sites can change from year to year so prior to each field season, the project biologist will develop a list with processor contact information and a map showing possible locations to sample, which will be distributed to each technician. There will be no set schedule for times to sample at each location. Sampling times will depend on tides and the times of fishing periods. Technicians will gauge when and where they need to be to maximize sample collections, yet still sample representatively.

Tissue Sampling for MSA

A 1⅓ cm (half-inch) piece of the axillary process will be removed from each fish and placed on a Whatman[8] paper card in its own grid space and then stapled in place. Whatman cards with tissue samples will be placed in an airtight case with desiccant beads to preserve the tissue for DNA extraction. Tissue sampling instructions are detailed in Appendix A1.

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

Scale, Sex, and Length Sampling

Three scales will be removed from the preferred area of each fish and placed on an adhesive-coated card (Clutter and Whitesel 1956; Welander 1940). Acetate impressions will be made of the scales on the card using a 25,000 PSI press, and the scale growth patterns will be viewed with a 40× microfiche reader to determine freshwater and marine residence times. Sex will generally be identified from external morphometric characteristics (i.e., protruding ovipositor on females or a developing kype on males). METF length will be measured to the nearest half-centimeter. Fish less than 75 cm METF will be examined internally to positively confirm sex by cutting a small slit in the anal opening using a plastic gut hook, if permission is granted by the personnel at the receiving site or processor.

Coded-Wire Tag Recovery

All sampled Chinook salmon will be examined for an adipose fin clip. Technicians will remove the head of all adipose finclipped Chinook salmon encountered. A cinch strap will be attached to the head, which will be returned to the office for storage in a freezer.

Sample Size of Selections for MSA

Subsampling of collections is required postseason to ensure analyses accurately represent the harvest by time, area, size, sex, and age. The goal will be to sample at least 30% of the reported harvest and to select between 800 and 900 samples for MSA, which has usually been about 10% of the total reported harvest each year. However, sampling goals will not drive the study design because the number of samples that are collected and the sampling rate is largely dependent on harvest. Strata to be used in the MSA will depend on the number of representative samples collected within each possible stratum.

Once the number of required samples for each day and statistical area is determined, samples will be selected randomly from all available tissues sampled on that date and statistical area. When insufficient samples are collected, to select samples in proportion to harvest by statistical area for a given day, excess samples from the same statistical area and from the next closest day will be used to represent the harvest, but only if samples were collected within 3 days of each other and are within the same stratum. Length will be incorporated into the sample selection such that the length distribution of fish selected for MSA will be approximately equivalent to the length distribution of all sampled fish within each stratum. Sampled fish within each stratum will be divided into length categories and the proportion required for each length category will be determined based on lengths of collected samples. Random MSA samples will then be proportionally selected from each length category.

The goal will be to use a total of 100 tissue samples for MSA for each stratum. Proof tests conducted by the GCL have demonstrated that with a ESSN Chinook salmon fishery mixture of 100 samples, we can estimate stock composition for the 4 reporting groups (*Kenai river tributaries, Kenai River mainstem, Kasilof River mainstem,* and *Cook Inlet other*) within 13 percentage points of the true values 90% of the time (Eskelin and Barclay. 2014). These tests followed the same protocol as reported in Eskelin et al. (2013) for baseline evaluation tests; however, instead of using test mixtures with 100% of 1 reporting group, test mixtures were created with proportions from each reporting group that represented a realistic scenario for what might be expected in these fisheries. Taking into account the reporting group proportions from the analyses of the 2010, 2011, and 2013 ESSN harvests (Eskelin et al. 2013), tests were

conducted under a realistic scenario for reporting group proportions in ESSN fishery mixtures: 0.02 for *Kenai tributary*, 0.58 for *Kenai Mainstem*, 0.38 for *Kasilof Mainstem*, and 0.02 for *Cook Inlet other*. With this precision for stock composition estimates and an anticipated sample size of 100 fish, we will be able to estimate the harvest of *Kenai River mainstem* and *Kasilof River mainstem* Chinook salmon in the UCI ESSN commercial fishery in each stratum within 30% of the true values 90% of the time if harvest estimates for the stock account for at least 20% of the total harvest within that stratum. If the harvest estimates account for less than 20% of the total harvest within the stratum, it is unnecessary and unrealistic to meet this criterion.

Stratification of Stock Compositions and Stock-Specific Harvest

Harvest samples will be stratified temporally, spatially (geographically), and by size into mixtures for MSA. The level of stratification will be dependent on several factors: how the ESSN fishery is prosecuted; the number of representative tissue samples of the harvest that are collected by date, area, time period, and size; the ability to provide new information; and the ability to provide comparative information from past studies. Judicious effort will be made to stratify the stock composition and stock-specific harvest estimates to maximize new information from this fishery, yet still provide comparative estimates for similar strata from previous years and remain within budgetary constraints. Since 2013, MSA estimates have been produced for 3 similar strata annually: 1) Kasilof Section "Early" prior to the Kenai and East Foreland sections open for the season, 2) Kasilof Section "Late" in July after the Kenai and East Foreland sections open for the season, and 3) Kenai and East Foreland sections "Late" in July. Since 2015, MSA estimates have also been produced from mixtures by beach (statistical area) for both the "Early" and "Late" time periods, although samples from East Foreland Beach have been combined with samples from Salamatof Beach due to low sample size from East Foreland Beach. An MSA from samples collected in August has been produced since 2014; however, stratification by area in August is dependent on sample size. In some years an "All areas, August" mixture was produced due to an insufficient number of samples collected by area, but in other years enough samples were collected for the MSA to be were separated into 2 mixtures (Kasilof Section and Kenai–East Foreland sections). Table 2 details all mixtures that were used for MSAs in 2015–2017.

Table 2.–Mixture number and stratum by time period, geographic area, and size for each mixture (nonshaded) and combined mixtures (grey shaded) in the Eastside set gillnet Chinook salmon fishery, Upper Cook Inlet, Alaska, 2015–2017.

Mixture no.(s)	Time period	Geographic area	Size
1	Early	Ninilchik Beach	Large/Small
2	Early	Cohoe Beach	Large/Small
3	Early	South K-Beach	Large/Small
1–3	Early	Kasilof Section	Large/Small
4	Late	Ninilchik Beach	Large/Small
5	Late	Cohoe Beach	Large/Small
6	Late	South K-Beach	Large/Small
4–6	Late	Kasilof Section	Large/Small
7	Late	North K-Beach	Large/Small
8	Late	Salamatof–East.Foreland beaches	Large/Small
7–8	Late	Kenai–East Foreland sections	Large/Small
9	August	Kasilof Section	Large/Small
10	August	Kenai–E.F. sections	Large/Small
1–10	Entire Season	All areas	Large/Small

If possible, the same mixtures will be used in the MSAs during 2018–2020, although mixture 8 (Salamatof and East Foreland beaches "Late") may not be included in future MSAs because past results show that essentially all the harvests in Salamatof and East Foreland beaches are *Kenai River mainstem* fish. Mixtures and MSA results will also be produced for KRSHA, Kasilof Section openings restricted to within one-half mile of the mean high tide line, Kasilof Section openings restricted to within 600 ft of the mean high tide line, and North K-Beach restricted to within 600 ft of the mean high tide line if those areas are fished and a sufficient number of samples are collected for each area. In addition, any other new genetic information will be provided from this fishery if possible.

Age, Sex, and Length Sample Size and Compositions

Only samples that are used in the MSA will be analyzed for ASL composition and reported by the same strata chosen for MSA and for the entire season. The objective criterion (± 0.10 with 95% confidence level) for estimating the overall age composition of Chinook salmon harvested in the ESSN fishery should be achieved with approximately 170 scale samples. To arrive at this sample size, we assumed a worst-case scenario of 25% scale regeneration rate with multinomial proportions of equality among ages (Thompson 1987). We plan to collect and analyze substantially more than 170 samples every year so we are likely to achieve much higher precision for the age composition estimates than the objective states.

Technicians will also verify sex of fish less than 75 cm METF by internal examination, if permission is given from the processor.

DATA COLLECTION

Tissue Collection

Each Whatman card will have a unique barcode and a numbered grid. Card barcodes (5-digit) and grid position numbers (1–10) will be recorded on data sheets for each sample (Appendix B1) and will also be entered into field computers. All Whatman cards will be stored at the Soldotna office until the end of the season then sent to the GCL for analysis and archiving.

Scale, Sex, and Length Collection

All scales, sex, and length information will be recorded on data sheets and handheld computers, including positive sex identification of small fish (Appendix B1). Data will be kept in the Soldotna ADF&G office.

Coded Wire Tag Collection

All heads collected from adipose finclipped Chinook salmon will be recorded on a tag recovery form (Appendix C1). The cinch strap number will also be recorded along with scale, sex, and length data (Appendix B1) to enable cross-referencing between datasets. Collected data will be returned to the Project Leader (Tony Eskelin). CWT forms and heads of all adipose finclipped fish will be shipped at the end of the season to the ADF&G Mark, Tag, and Age Laboratory for CWT recovery, determination of stock of origin, and for archiving data.

Laboratory Analysis

Assaying Genotypes

We will extract genomic DNA from tissue samples using a NucleoSpin 96 Tissue Kit by Macherey-Nagel (Düren, Germany). DNA will be screened for 39 SNP markers. To ensure that DNA concentrations are high enough with the dry sampling method used to preserve samples, preamplification will be conducted before screening the DNA.

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

We will screen the preamplified DNA for the 39 SNP markers using Fluidigm 192.24 Dynamic Array Integrated Fluidic Circuits (IFCs), which systematically combine up to 24 assays and 192 samples into 4,608 parallel reactions. The components are pressurized into the IFC using the IFC Controller RX (Fluidigm). Each reaction will be conducted in a 9 nL volume chamber consisting of a mixture of 20X Fast GT Sample Loading Reagent (Fluidigm), 2X TaqMan GTXpress Master Mix (Applied Biosystems), Custom TaqMan SNP Genotyping Assay (Applied Biosystems), 2X Assay Loading Reagent (Fluidigm), 50X ROX Reference Dye (Invitrogen), and 60–400 ng/μl DNA. Thermal cycling will be performed on a Fluidigm FC1 Cycler using a Fast PCR protocol as follows: an initial "Hot-Start" denaturation of 95°C for 2 min followed by 40 cycles of denaturation at 95°C for 2 s and annealing at 60°C for 20 s, with a final "Cool-Down"

at 25°C for 10 s. The Dynamic Array IFCs will be read on a Biomark or EP1 System (Fluidigm) after amplification and genotyped using Fluidigm SNP Genotyping Analysis software.

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

Laboratory Failure Rates and Quality Control

The overall failure rate will be calculated by dividing the number of failed single-locus genotypes by the number of assayed single-locus genotypes. An individual genotype will be considered a failure when a locus for a fish cannot be satisfactorily scored.

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

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

DATA REDUCTION

Technicians will return their genetic cards, scale cards, field data sheets, and field computers to the Soldotna office daily and will be responsible for ensuring the recorded data are legible and accurate. The project biologist will ensure all data are returned, legible, and entered correctly and will also download files from the field computer to the office computer. Age data will be entered upon scale reading analysis. CWT forms will be edited to ensure accuracy and mailed to the ADF&G Mark, Tag, and Age Laboratory in Juneau, Alaska for database entry. A final edited copy of all data files along with a data map will be sent to the Alaska Department of Fish and Game Research and Technical Services (RTS) for archiving.

DATA ANALYSIS

Mixed Stock Analysis and Stock Compositions

The stock compositions of the ESSN mixtures (Table 2) will be estimated in R using the Pella and Masuda (2001) model. The Pella–Masuda model employs a Gibbs sampling algorithm to estimate the most probable contribution of the baseline populations to explain the combination of genotypes in the mixture sample. Within each iterate of the algorithm, every individual is stochastically assigned a hypothetical stock-of-origin based on the statistical likelihood of its genotype in each population. After all assignments are made, they are summarized for deriving the stock composition for that iterate. The process of assigning individuals and deriving stock compositions is repeated many times. Output files will be written for composition estimates by reporting group for each iteration (RGN output) and reporting group assignments for each fish at each iteration (CLS output). We will run 8 Markov Chain Monte Carlo chains (MCMC) with 25,000 iterations for each mixture.

The prior distribution used for this analysis will be based upon the stock composition estimates of similar strata from the analyses of ESSN Chinook salmon samples from previous years. If no estimates are available from a similar stratum analyzed in a previous year, the prior parameters for each reporting group will be defined to be equal (i.e., a *flat* prior). Prior parameters will be set equal to 1, thus minimizing the overall influence of the prior distribution. Chains will be run until among-chain convergence is reached (shrink factor less than 1.2; Pella and Masuda 2001). The first 12,500 iterations from each MCMC chain will be discarded to reduce the influence of the starting values and the remaining iterations from each chain will be combined to form the posterior distribution (100,000 iterations). Stock composition estimates and 90% credibility intervals (CIs) for each stratum will be calculated by taking the mean and 5% and 95% quantiles of the posterior distribution from the RGN output (Gelman et al. 2004).

To estimate the stock composition by size and reporting group for each mixture, we will use the posterior distribution for the RGN output as well as the posterior distribution CLS output. Within each iterate, we will summarize the number of fish (n_i) that are assigned to reporting group i, along with how many of those are large (b_i). For that iterate, the proportion of this stock that is large fish (β_i), will be derived as a draw from a beta distribution with parameters $b_i + ½$ and $n_i - b_i + ½$, before it is multiplied by the reporting group's composition (p_i) in the same iterate. This produces the desired parameter $(s_i = p_i\beta_i)$. These proportions will be summarized across iterates to provide their estimates $(\hat{s}_i)$ for both large and small fish for each reporting group.

Stock-Specific Harvest Estimates

Stock-specific harvest estimates and 90% CIs will be calculated for each stratum (i.e., mixtures 1–10 as defined in Table 2). The stock-specific harvest estimate for each stratum will be calculated by multiplying the reported harvest from that stratum by its unrounded stock composition estimate (Equation 1):

$$\hat{H}_{g,i} = H_i \hat{p}_{g,i}, \tag{1}$$

where $\hat{H}_{g,i}$ is the stock-specific harvest estimate for reporting group *g* fish in stratum *i*, H_i is the reported harvest in stratum *i*, and $\hat{p}_{g,i}$ is the estimated proportion of reporting group *g* fish in stratum *i* (obtained from MSA). The 90% CI will be calculated by multiplying the reported harvest (H_i) by the upper and lower 90% bounds of the proportion estimate $\hat{p}_{g,i}$ from MSA. Results will be rounded to the nearest fish. The variance of $\hat{H}_{g,i}$ will be calculated using following equation:

$$\text{var}(\hat{H}_{g,i}) = H_i^2 \,\text{var}(\hat{p}_{g,i}), \tag{2}$$

where $\text{var}(\hat{p}_{g,i})$ is the variance estimate for $\hat{p}_{g,i}$ obtained from MSA.

The overall proportion of reporting group *g* fish for each of the combined mixture strata *c* (e.g., Kasilof Section "Early," Kasilof Section "Late," Kenai–East Foreland sections "Late," and the entire season) will be estimated as follows:

$$\hat{p}_g^c = \frac{\sum_{i=1}^{Sc} \hat{H}_{g,i}}{\sum_{i=1}^{Sc} H_i}, \quad (3)$$

where S_c equals the number of strata included in the combined mixture stratum *c*. The variance of $\hat{p}_g^c$ will be calculated as follows:

$$\text{var}(\hat{p}_g^c) = \frac{\sum_{i=1}^{Sc} \text{var}(\hat{H}_{g,i})}{(\sum_{i=1}^{Sc} H_i)^2}, \quad (4)$$

The overall number of Chinook salmon ($\hat{H}_g^c$) from reporting group *g* harvested in each combined mixture stratum *c* will be estimated by summing all the stock-specific harvest estimates from each of the constituent strata (Equation 5):

$$\hat{H}_g^c = \sum_{i=1}^{Sc} \hat{H}_{g,i} = \sum_{i=1}^{Sc} H_i \hat{p}_{g,i}, \quad (5)$$

To calculate the CI for $\hat{H}_g^c$, its distribution will be derived via MCMC by resampling 100,000 draws of the MSA posterior output from each of the constituent strata and applying the harvest to the draws according to Equation 5.

Age Composition

The age proportions of Chinook salmon harvested in the commercial ESSN fishery by stratum will be estimated as follows:

$$\hat{p}_i^{(z)} = \frac{n_i^{(z)}}{n_i}, \quad (6)$$

where $\hat{p}_i^{(z)}$ is the estimated proportion of salmon of age category *z* from sampling stratum *i*, $n_i^{(z)}$ is the number of fish sampled from sampling stratum *i* that were classified as age category *z*, and n_i is the number of Chinook salmon age determinations from stratum *i*.

The variance of $\hat{p}_i^{(z)}$ will be calculated as follows:

$$\text{var}\left[\hat{p}_i^{(z)}\right] = \left(1 - \frac{n_i}{H_i}\right) \frac{\hat{p}_i^{(z)}\left(1 - \hat{p}_i^{(z)}\right)}{n_i - 1}, \quad (7)$$

where H_i is the reported number of Chinook salmon harvested in stratum *i*.

The estimates of harvest by age category in each stratum will be calculated as follows:

$$\hat{H}_i^{(z)} = H_i \hat{p}_i^{(z)}, \tag{8}$$

with variance

$$\text{var}\left[\hat{H}_i^{(z)}\right] = H_i^2 \,\text{var}\left[\hat{p}_i^{(z)}\right]. \tag{9}$$

The total Chinook salmon harvest by age category and its variance will be estimated by the following summations:

$$\hat{H}^{(z)} = \sum_{i=1}^{S} \hat{H}_i^{(z)} \tag{10}$$

and

$$\text{var}\left[\hat{H}^{(z)}\right] = \sum_{i=1}^{S} \text{var}\left[\hat{H}_i^{(z)}\right], \tag{11}$$

where *S* equals the number of sampling strata.

Finally, the total proportion of the ESSN Chinook salmon harvest by age category and its variance will be estimated by the following:

$$\hat{p}^{(z)} = \frac{\hat{H}^{(z)}}{H} \tag{12}$$

and

$$\text{var}\left[\hat{p}^{(z)}\right] = \frac{\text{var}\left[\hat{H}^{(z)}\right]}{H^2}, \tag{13}$$

where *H* is the total reported Chinook salmon harvest for each year.

Sex Composition

Sex composition will be estimated using the same Equations 6–13 used to estimate age composition.

Length Composition

Mean length $\bar{l}_z$ of Chinook salmon in age class *z* will be estimated as follows:

$$\bar{l}_z = \frac{1}{n_z} \sum_{i=1}^{n_z} l_i \,, \tag{14}$$

where l_i is the length of fish *i* in sample n_z, and n_z is the number of Chinook salmon of age class *z*.

The variance $\text{var}(\bar{l}_z)$ of the mean length-at-age class *z* will be estimated as follows:

$$\text{var}(\bar{l}_z) = \frac{1}{n_z} \frac{\sum_{i=1}^{n_z} (l_i - \bar{l}_z)^2}{n_z - 1}. \quad (15)$$

Coded-Wire Tag Recovery

Low numbers of CWT recoveries are expected, so no direct estimates of CWT recoveries by stock will be made, but the data will be archived with Mark, Tag, and Age Laboratory in Juneau.

SCHEDULE AND DELIVERABLES

Dates [a]	Activity
Mid-late June	Hiring and preseason training (*Eskelin*)\
Late June–mid-August	ESSN Chinook salmon harvest sampling, collection of ASL data and genetic tissue (3 *FWT II*)
October	Data edited, tissue collection transferred to GCL (*Eskelin*)
November	Final harvest estimates by date and statistical area assembled (provided by *CF management staff*). Tissue, age, sex, and length subsamples selected for composition analysis (*Eskelin and Huang*).
December	Scales aged (*Eskelin*) Draft ASL composition estimates completed (*Eskelin and Huang*)
January–February following year of sample collection	Extract DNA and analyze tissues (*GCL and Barclay*)
February following year of sample collection	Draft MSA and harvest estimates complete by temporal and geographic stratum and overall by reporting group (*Barclay, Eskelin, and Huang*)
April following year of sample collection	FDS draft report summarizing draft results disseminated to regional editing staff (*Eskelin and Barclay*).
Based on need	Publication of final FDS report (*Eskelin and Barclay*)
October following year of sample collection	Archiving of data. All genetic tissue and associated data and analysis archived at the Anchorage ADF&G GCL lab (*Barclay)*. Tissue and ASL collection data (scales, acetates, data forms, electronic files, etc.) stored at the Soldotna ADF&G office (*Eskelin)*

[a] Timeline will be protracted after 2019 field season to produce 2019 MSA and ASL composition results prior to 2020 UCI BOF meeting.

RESPONSIBILITIES

Principal investigator: *Tony Eskelin, Project Leader, Fishery Biologist II*

Duties: As project leader, responsible for writing the operational plan. Serves as the project biologist, who is responsible hiring and training personnel, supervising data collection, collating data, and transferring tissue samples and associated data to Anchorage for MSA, and any CWT heads and data forms to the Mark, Tag and Age lab in Juneau. Responsible for all scale aging, ensuring all data is in proper format, and archiving data with RTS at the completion of the field season. Serves as the primary author on any reporting.

Coprinciple investigator: *Andy Barclay, Fishery Biologist III*

Duties: Represents the Gene Conservation Laboratory and is responsible for the analysis of tissue samples for MSA and providing estimates to the project biologist and biometrician. Serves as coauthor on FDS reports and memos.

Consulting Biometrician: *Jiaqi Huang, Biometrician III*

Duties: Provides guidance on sampling design and data analysis, selects samples for analysis, prepares estimates of harvest of Chinook salmon by reporting group and assisting with preparation and editing of the operational plan and any reports.

Sampling Crew:
Vacant, *Fish and Wildlife Technician II, 20 June–16 August*
Vacant, *Fish and Wildlife Technician II, 20 June–16 August*
Vacant, *Fish and Wildlife Technician II, 20 June–16 August*

Duties: Operates State of Alaska vehicles, adheres to sampling schedule, samples harvested Chinook salmon for ASL and tissue, records data accurately, enters data into a computerized database in a timely manner, and completes miscellaneous duties as assigned.

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APPENDIX A: INSTRUCTIONS FOR TISSUE SAMPLING

Adult Finfish Tissue Sampling for DNA Analysis

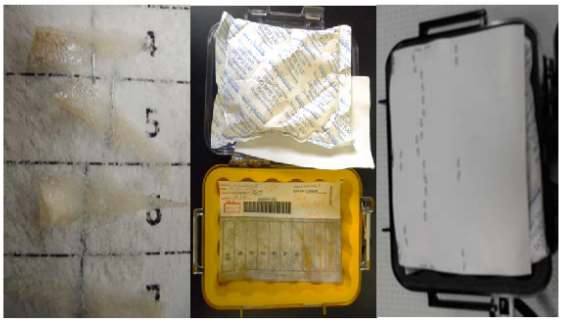
ADF&G Gene Conservation Lab, Anchorage

I. General Information

We use fin tissues as a source of DNA to genotype fish. Genotyped fish are used to determine the genetic characteristics of fish stocks or to determine stock compositions of fishery mixtures. The most important thing to remember in collecting samples is that **only quality tissue samples give quality results**. If sampling from carcasses: tissues need to be as "fresh" and as cold as possible.

Preservative used: Silica desiccant bead packet and salt dries and preserves tissues for later DNA extraction. Quality DNA preservation requires **Fast drying** (under 5 hours at 65°F); **Dry storage** (with 2 desiccant packs) in weathertight file box.

II. Sampling Method



III. Sampling Instructions

- **Every morning:** before sampling, rotate 3 desiccant packs (2-Pelican micro, 1-file box) into dehydrator @ **160^0 F** for 12 hrs. **(NOT SAMPLES)!**
- **Prior to sampling**: Set up work space, fill out required collection information (upper left hand corner only) and place Whatman genetics card (10WGC) flat for easy access; ready to sample.
- **Sampling:**
  - Wipe fin prior to sampling.
  - Briefly wipe or rinse clippers with water between samples to reduce cross contaminating.
  - Using clippers, cut one axillary fin per fish.
  - Place one clipped fin tissue onto appropriate grid space. Follow sampling order printed on card - do not deviate. If large tissue sample, center tissue diagonally on grid space.
  - **Only one fin clip per fish into each numbered grid space.**
  - Staple each sample to 10WGC (see photo).
  - Sampling complete, dust tissues with **1 tsp. non-iodized salt** to promote the preservation process.
  - Staple landscape cloth "rain fly" to paper edge (2 staples max).
- **Loading Pelican Case:**
  - 1st card: Remove blotter papers and desiccant packs from Pelican case. Place first card in Pelican case with tissues facing up. Next, place blotter paper directly over card and place one desiccant pack on top. Close and secure lid so drying begins.
  - Up to 4 cards can be added per case. Add them so **tissue samples always face the desiccant pack** through blotter paper: 2nd card facing down between desiccant packs; 3rd card facing up between desiccant packs; and 4th card facing down on top of second desiccant pack. Close and secure Pelican case after inserting each card.
  - All Whatman cards **remain in Pelican overnight** to dry flat.
- **Post-sampling storage:** Every morning, store dried tissue cards in weathertight file box at room temperature. Two desiccant packs are allocated for file box: every morning rotate 3 desiccant packs (2-Pelican, 1-file box) into dehydrator @ **160^0 F** for 12 hours. **(NOT SAMPLES)!**
- **Shipping at end of the season:** Pack 10 **dried cards** per plastic photo page, slide in manila envelope; pack inside priority mailing box. Tape box shut and tape return address on box.

IV. Supplies included in sampling kit:

1. Clippers - for cutting a portion of selected fin.
2. Whatman genetics card – holds 10 fish/card.
3. Pelican case - 1st stage of drying and holding card samples.
4. Non-iodized salt – distribute 1 tsp. non-iodized salt over each card.
5. Silica packs – desiccant removes moisture from samples.
6. Blotter paper – covers full sample card for drying; multiple use.
7. Watertight file box – dry storage prior to return shipment.
8. Plastic photo page – 10 cards per page for return shipment.
9. Manila envelope – pack dried cards in manila envelope.
10. Shipping box – put sealed manila envelope inside box.
11. Stapler – extra protection, secure sample to numbered grid.
12. Staples – only use staples provided, specific for stapler.
13. Dehydrator – oven-dry desiccant packs overnight (share w/CF).
14. Laminated "return address" labels.
15. Sampling instructions.
16. Pencil

V. Shipping: Address the sealed mailer box for return shipment to ADF&G Genetics lab.

Return to ADF&G Anchorage lab: ADF&G – Genetics
333 Raspberry Road
Anchorage, Alaska 99518

Lab staff: 907-267-2247
Judy Berger: 907-267-2175
Freight code: _____

APPENDIX B: SAMPLING FORMS

Appendix B1.–ESSN Chinook salmon harvest sampling form.

ESSN Chinook salmon sampling form

Date:__________ **Sampler(s):** ______________

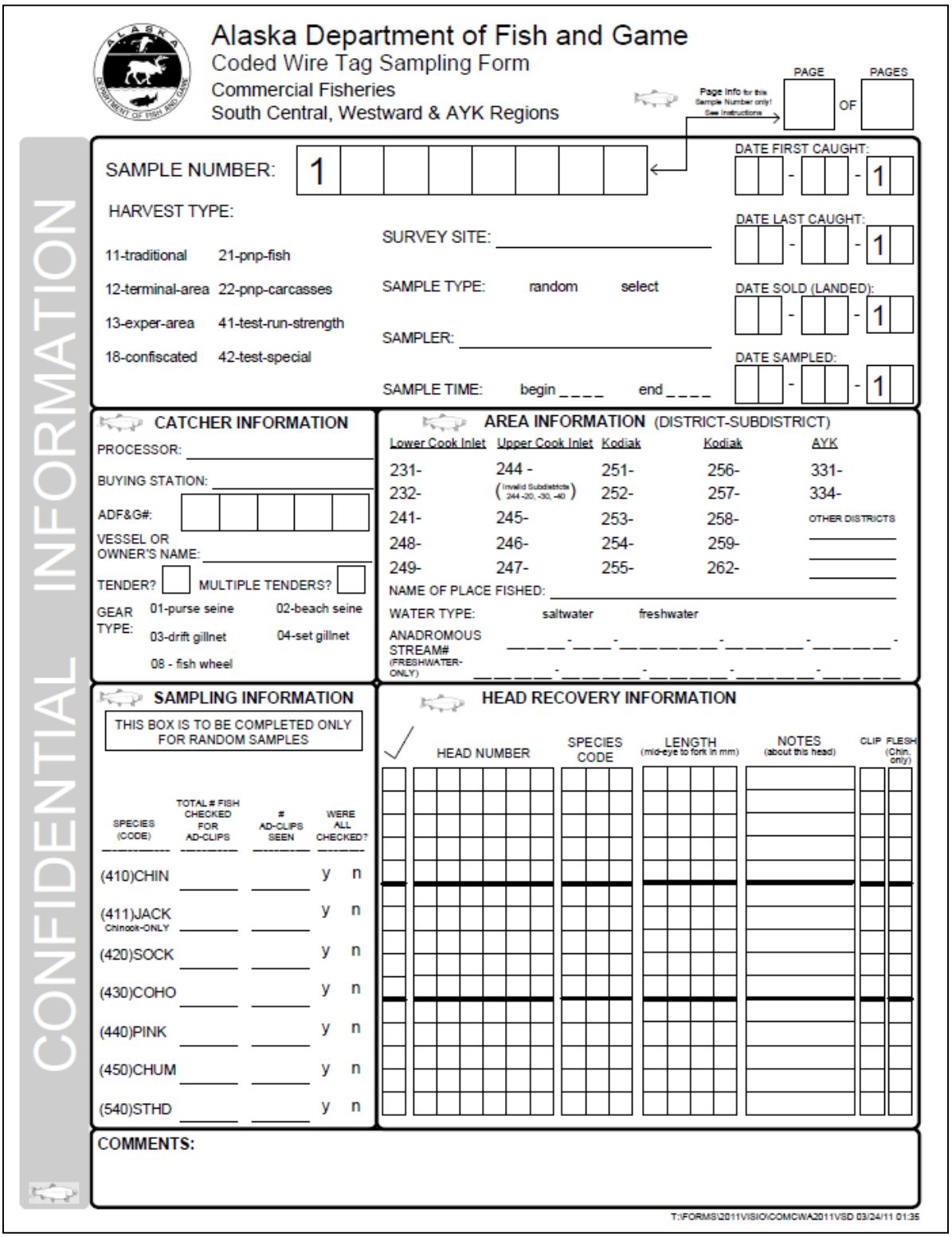
Start Time: ________ **End Time:**_______

Scale		METF		Sex	Genetics		Sample	Stat	
Card#	**Scale#**	**Length**	**Sex**	**Verify?**	**Card#**	**Box#**	**Location**	**Area**	**CWT #**
	1								
	2								
	3								
	4								
	5								
	6								
	7								
	8								
	9								
	10								
	1								
	2								
	3								
	4								
	5								
	6								
	7								
	8								
	9								
	10								
	1								
	2								
	3								
	4								
	5								
	6								
	7								
	8								
	9								
	10								

Sex: 1-male 2-female, verify sex for fish less than 750 cm METF (if granted permission).
Length: mid eye to fork-of-tail to nearest cm.

APPENDIX C: CODED-WIRE TAG SAMPLING FORM

Appendix C1.–Coded-wire tag sampling form.



Alaska Department of Fish and Game
Coded Wire Tag Sampling Form
Commercial Fisheries
South Central, Westward & AYK Regions

PAGE ____ OF PAGES ____

Page info for this Sample Number only! See Instructions

CONFIDENTIAL INFORMATION

SAMPLE NUMBER: 1 _____

DATE FIRST CAUGHT: __ - __ - 1

DATE LAST CAUGHT: __ - __ - 1

DATE SOLD (LANDED): __ - __ - 1

DATE SAMPLED: __ - __ - 1

HARVEST TYPE:

11-traditional 21-pnp-fish
12-terminal-area 22-pnp-carcasses
13-exper-area 41-test-run-strength
18-confiscated 42-test-special

SURVEY SITE: _____

SAMPLE TYPE: random select

SAMPLER: _____

SAMPLE TIME: begin ____ end ____

CATCHER INFORMATION

PROCESSOR: _____

BUYING STATION: _____

ADF&G#: _____

VESSEL OR OWNER'S NAME: _____

TENDER? ☐ MULTIPLE TENDERS? ☐

GEAR TYPE: 01-purse seine 02-beach seine 03-drift gillnet 04-set gillnet 08 - fish wheel

AREA INFORMATION (DISTRICT-SUBDISTRICT)

Lower Cook Inlet	Upper Cook Inlet	Kodiak	Kodiak	AYK
231-	244 - (Invalid Subdistricts 244-20, -30, -40)	251-	256-	331-
232-		252-	257-	334-
241-	245-	253-	258-	OTHER DISTRICTS
248-	246-	254-	259-	_____
249-	247-	255-	262-	_____
				_____

NAME OF PLACE FISHED: _____

WATER TYPE: saltwater freshwater

ANADROMOUS STREAM# (FRESHWATER-ONLY) ____-____-____-____-____-____-____

SAMPLING INFORMATION

THIS BOX IS TO BE COMPLETED ONLY FOR RANDOM SAMPLES

SPECIES (CODE)	TOTAL # FISH CHECKED FOR AD-CLIPS	# AD-CLIPS SEEN	WERE ALL CHECKED?
(410)CHIN			y n
(411)JACK Chinook-ONLY			y n
(420)SOCK			y n
(430)COHO			y n
(440)PINK			y n
(450)CHUM			y n
(540)STHD			y n

HEAD RECOVERY INFORMATION

✓	HEAD NUMBER	SPECIES CODE	LENGTH (mid-eye to fork in mm)	NOTES (about this head)	CLIP	FLESH (Chin. only)

COMMENTS:

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