Western Alaska Chum Salmon Bycatch Assessment in the Shoreside B-Season Bering Sea Aleutian Islands Walleye Pollock Trawl Fishery, 2024 Annual Report

Pilot Year to Develop Inseason Genetic Stock Composition Analysis

Bristol Bay Science and Research Institute
P.O. Box 1464, Dillingham, Alaska 99576
Contact: Jordan Head, Executive Director
jordan@bbsri.org

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Cover Photos:

F/V *Sovereignty* at the Trident Seafoods dock in Akutan (left); adult chum salmon being sampled at a processing plant (middle); and genetic sampling at BBSRI's laboratory in Dutch Harbor (right).

[1] Bristol Bay Science and Research Institute, Dillingham, Alaska, USA

[2] J. J. Smith and Associates Ltd., Nanaimo, British Columbia, Canada

[3] NOAA Alaska Fisheries Science Center, Auke Bay Laboratories, Juneau, Alaska, USA

EXECUTIVE SUMMARY

In 2024, the Bristol Bay Science and Research Institute (BBSRI) successfully implemented a pilot project to produce weekly inseason genetic stock composition estimates of the chum salmon (*Oncorhynchus keta*) bycatch in the shoreside B-season Bering Sea and Aleutian Islands (BSAI) walleye pollock (*Gadus chalcogrammus*) trawl fishery. The goal of the project was to provide more timely stock composition information than was currently available (i.e., post-season annual estimates) that could be used as a tool by the shoreside sector of the pollock trawl fleet to aid in the tracking and reduction of Western Alaska chum salmon bycatch.

Chum salmon bycatch caught in the shoreside sector during the 2024 B-season BSAI pollock trawl fishery totaled 21,710 fish. This was considerably lower than the most recent 5-year average (2019–2023: 189,820 fish). From June 13 to October 5, 2024, six BBSRI personnel tissue-sampled 7,034 chum salmon (32.4% of total bycatch) from 941 vessel offloads at five processors located in Dutch Harbor (Alyeska, Northern Victor, Unisea, and Westward) and Akutan (Trident). Of the samples collected, 3,531 (50.2%) were subsequently processed at a genetics laboratory established and operated by BBSRI in Dutch Harbor. Of the samples processed, 3,088 (87.5%) were successfully genotyped (i.e., ≥ 80% of loci scored). Weekly stock composition estimates were produced by the National Oceanographic and Atmospheric Administration's (NOAA's) Alaska Fisheries Science Center Auke Bay Laboratories (AFSC-ABL) Genetics Program in Juneau.

Based on all samples analyzed in 2024 (i.e., pooling all statistical weeks [StatWks]) and a total bycatch of 21,631 chum salmon through October 5, 2024 when sampling ended, the largest contributing genetic group to the chum salmon bycatch was Eastern Gulf of Alaska/Pacific Northwest (34.7%; point estimate of 7,516 fish), followed by Northeast Asia (29.7%; 6,430 fish), Southeast Asia (19.9%; 4,306 fish), Coastal Western Alaska (7.7%; 1,673 fish), Upper/Middle Yukon (5.1%; 1,109 fish), Southwest Alaska (1.8%; 397 fish), and Kotzebue Sound (0.9%; 200 fish). The Western Alaska (WAK) aggregate consisting of the Coastal Western Alaska, Kotzebue Sound, and Upper/Middle Yukon stock groups comprised 13.8% of the bycatch (2,982 fish). Weekly composition estimates for the WAK aggregate of stocks ranged from a low of 7.8% during StatWk 31 to a high of 19.2% during StatWk 34. The estimated contribution of the WAK aggregate of stocks was comparable to that produced independently by the AFSC-ABL Genetics Program using samples collected by the North Pacific Observer Program administered by the AFSC Fisheries Monitoring and Analysis Division (15.3%).

BBSRI worked closely with NOAA, Alaska Department of Fish and Game (ADF&G), industry, and regional stakeholders to implement this project. Funding was provided through a direct legislative grant from the State of Alaska and BBSRI, with additional in-kind support provided by NOAA and ADF&G.

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LIST OF ABBREVIATIONS

ADF&G	Alaska Department of Fish and Game
AKFIN	Alaska Fisheries Information Network
AFSC-ABL	Alaska Fisheries Science Center Auke Bay Laboratory
BBSRI	Bristol Bay Science and Research Institute
BSAI	Bering Sea/Aleutian Islands
DNA	Deoxyribonucleic acid
GCL	Gene Conservation Laboratory
GOA	Gulf of Alaska
IFC	Integrated Fluidic Circuit
MCMC	Markov Chain Monte Carlo
MTAL	Mark, Tag, and Age Laboratory (ADF&G)
NOAA	National Oceanographic and Atmospheric Administration
NPFMC	North Pacific Fishery Management Council
PCR	Polymerase Chain Reaction
QC	Quality Control
SNP	Single Nucleotide Polymorphism
StatWk	Statistical Week
WAK	Western Alaska

1 INTRODUCTION

The Bering Sea walleye pollock (*Gadus chalcogrammus*) fishery is the largest U.S. fishery by volume, with harvests by all sectors from 2011 to 2022 averaging 1.28 million metric tons (Happala and Shaftel 2024). The fishery is managed at the federal level by the North Pacific Fishery Management Council (NPFMC) with regulations that set seasonal catch limits for pollock. The fishery is separated into an A-season, which is open from January 1 to June 10, and a B-season, which is open from June 10 to November 1. The fishery is further separated into three fishing sectors: shoreside catcher vessel, catcher-processor, and mothership. The shoreside catcher vessel sector harvests fish at sea using pelagic trawl gear on smaller vessels and delivers to eligible processing plants in Alaska communities (i.e., Dutch Harbor, Akutan, King Cove, and Sand Point). Processors require catcher vessels to make deliveries within 48 hours of their first tow of fish to maintain high product quality, so the operational range of these vessels is limited. The catcher-processor sector includes vessels that catch and process fish at sea, while the mothership sector includes vessels that offload pollock for processing at sea.

Chum salmon (*Oncorhynchus keta*) are caught incidentally in the pollock fishery as bycatch, which is defined in the Magnuson-Stevens Fishery Conservation and Management Act as fish that are harvested in a fishery, but which are not sold or kept for personal use. Historically, approximately 99% of the chum salmon bycatch occurred during the B-season (Barry et al. 2024). Over the most recent 10-year period (2014–2023), chum salmon bycatch in the B-season Bering Sea and Aleutian Islands (BSAI) pollock fishery (all sectors combined) averaged 313,914 fish annually and ranged from 111,698 to 545,883 (Figure 1; Barry et al. 2024; NMFS 2024).

Since 2011, all chum salmon bycatch has been enumerated by the North Pacific Observer Program (Observer Program) and 1 in 30 fish are tissue-sampled for genetics analysis. Annual estimates of genetic stock composition for chum salmon bycatch in the pollock fishery are produced by the genetics program of the National Oceanographic and Atmospheric Administration's (NOAA's) Alaska Fishery Science Center Auke Bay Laboratories (AFSC-ABL) Genetics Program and presented to the North Pacific Fisheries Management Council (NPFMC) at their February or April meetings (~3–5 months after the official end of the B-season, but ~5–7 months after the majority of the fishery has been executed). Over the most recent 5-year period (2019–2023), the stock composition of chum salmon bycatch in the B-season BSAI pollock trawl fishery (all sectors combined) has averaged 42.4% Northeast Asia (NE Asia), 26.9% Eastern Gulf of Alaska/Pacific Northwest (E GOA/PNW), 13.9% Southeast Asia (SE Asia), 12.4% Coastal Western Alaska (W Alaska; including Kotzebue Sound stocks)[4], 3.1% Southwest Alaska (SW Alaska), and 1.2% Upper/Middle Yukon (Up/Mid Yukon; Kondzela 2021; Barry et al. 2022a, 2022b, 2023, 2024).

Most chum salmon bycatch in the B-season BSAI pollock fishery are from Asia (which includes Russia) and include a hatchery component, however, a portion are from Western Alaska river systems (Coastal Western Alaska, Kotzebue Sound, and the Up/Mid Yukon combined) which have seen declines in abundance in recent years (Happala and Shaftel 2024). As a result of these declines the NPFMC has proposed an action "*to minimize bycatch of Western Alaska origin chum salmon in the Eastern Bering Sea pollock fishery consistent with the Magnuson-Stevens Act, National Standards, and other applicable law*." (Happala and Shaftel 2024). Under this action, the NPFMC is currently analyzing the potential impacts of a proposed set of management alternatives that might "*have some positive benefit on the number of chum salmon that return to Western Alaska rivers.*" These additional chum salmon returns could improve "*the*

[4] NOAA typically pools Kotzebue Sound stocks with the Coastal Western Alaska stock group. For the 2024 BBSRI project, Coastal Western Alaska and Kotzebue Sound stock groups were reported separately.

ability to meet the State's spawning escapement goals which is necessary for the long-term sustainability of chum salmon fisheries."

During the B-season of 2024, the Bristol Bay Science and Research Institute (BBSRI) implemented the first year of a research project to quantify the stocks of origin of chum salmon bycatch in the shoreside sector of the Bering Sea pollock fishery. BBSRI targeted the shoreside sector for practical reasons (i.e., shore-based deliveries), but also because it typically catches a larger number of chum salmon bycatch, and a greater proportion of the Western Alaska stock groups than the catcher-processor or mothership sectors (Barry et al. 2024). Bycatch in the shoreside sector averaged 189,820 chum salmon annually from 2019 to 2023 (range: 66,776–341,433; Kondzela 2021; Barry et al. 2022a, 2022b, 2023, 2024). From 2019 to 2023, chum salmon bycatch in the shoreside B-season BSAI pollock fishery was comprised of 15.6% Western Alaska (range: 9.4–25.4% including Kotzebue Sound stocks)[4] and 1.6% Upper/Middle Yukon (range: 0.4–3.0%) stock groups (Kondzela 2021; Barry et al. 2022a, 2022b, 2023, 2024).

Genetic stock-composition estimates were to be generated inseason on a weekly basis and provide more timely information than was currently available (i.e., post-season annual estimates). It was hoped that more timely estimates could be used as a tool by the shoreside pollock fleet to aid in bycatch reduction of Western Alaska chum salmon. The specific nature of avoidance measures taken by the fleet might be informed by these near real-time results. At the most basic level, this project would provide inseason accounting of Western Alaska chum salmon catch, which may help guide decisions whether to move the fleet some distance away or reduce overall effort (e.g., when Western Alaska chum salmon catch is high). Conversely, if Western Alaska chum salmon catch was low, project information might reassure the fleet it would not need to move. There was no expectation that project information be used to guide hour-to-hour or even day-to-day fishing effort by the fleet.

1.1 Goals and Objectives

The primary objective of the 2024 pilot project was to produce weekly inseason genetic stock-composition estimates of the chum salmon bycatch in the shoreside B-season Bering Sea pollock fishery. The overall goal of producing these timely inseason estimates is to provide a tool to aid the fishing fleet in bycatch monitoring and reduction of Western Alaska chum salmon.

Three project components in 2024 were to:

1) Sample chum salmon landed as bycatch at shoreside processing plants in Dutch Harbor and Akutan for age (fish scales), length, and genetic composition (fin clip) in proportion to bycatch volume from June through October.
2) Use genetic methods to generate accurate, stock-specific estimates of chum salmon bycatch from the shoreside sector of the pollock fishery on a weekly basis; and
3) Estimate the age composition of chum salmon bycatch by analyzing scale samples collected at shoreside processing plants.

BBSRI's plan in this pilot year was to demonstrate the feasibility of providing weekly stock-composition estimates to industry, fisheries managers, and stakeholders. Project results were not made public inseason to provide time for BBSRI and its collaborators to overcome any challenges encountered in the first year of a project. BBSRI worked closely with the NOAA, Alaska Department of Fish and Game (ADF&G), industry, and regional stakeholders to implement this project. Funding in 2024 was provided through a direct legislative grant from the State of Alaska and BBSRI, with additional in-kind support provided by NOAA and ADF&G.

The following report summarizes the methods and results of the 2024 pilot year and provides recommendations for future efforts.

2 METHODS

2.1 Study Design

The 2024 project comprised three main components:

1) Port Sampling – Port samplers collected biological data (and associated metadata) from fishing vessel offloads at processors in Dutch Harbor (Unalaska) and Akutan from 13 June to 5 October.
2) Genetic Analysis – BBSRI personnel ("genotypers") stationed at a laboratory in Dutch Harbor genotyped fin-tissue samples on a weekly basis, and the NOAA's AFSC-ABL Genetics Program in Juneau produced weekly inseason stock-composition estimates.
3) Scale Analysis – BBSRI personnel pressed fish scale samples collected from genotyped chum salmon and ADF&G read the scales to determine fish ages.

Table 1 lists key project activities and their completion dates. The following sections describe the methods used to implement the three project components.

2.2 Port Sampling

In 2024, BBSRI port samplers sampled chum salmon bycatch offloaded by shoreside catcher vessels to processors in Dutch Harbor and Akutan during the B-season BSAI pollock trawl fishery. A map showing the National Marine Fisheries Service (NMFS) fishery management areas where chum salmon bycatch has historically occurred in the Bering Sea and Aleutian Islands is shown in Figure 2.

2.2.1 Port Samplers

BBSRI contracted six experienced fishery observers from Saltwater Inc. (Anchorage, AK) to work as BBSRI ports samplers to sample chum salmon at processing plants in Dutch Harbor and Akutan. Four of the port samplers were stationed in Dutch Harbor and sampled deliveries to three shore-based processors (Alyeska, Unisea, and Westward) and one floating processor (Northern Victor; Figure 3; Photo 1, Photo 2). The other two port samplers were stationed in Akutan and sampled deliveries to Trident Seafoods. In each port, crews were available to sample offloads 24 hours a day, 7 days a week. The Dutch Harbor crew stayed in a 3-bedroom house that BBSRI rented for the season, and they had access to two rental vehicles. BBSRI provided room and board for the Akutan crew at Trident's facility.

2.2.2 Vessel Offloads

Upon arrival in Dutch Harbor and Akutan in early June 2024, BBSRI's project team met with staff at each processor to discuss project logistics (e.g., conducting plant orientations, establishing protocols for communicating the timing of vessel offloads, designating sampling areas for BBSRI port samplers, fine-tuning sampling protocols, and reviewing safety procedures).

Processors communicated regularly with their associated fishing vessels while they were on the fishing grounds and staggered their offloads to keep the plants running as close to 24 hours a day as possible (Photo 3, Photo 4). Smaller vessels could take 4–6 hours to offload, whereas larger vessels could take 15 hours or more. North Pacific Observer Program Fishery Observers (Observers) were stationed at each processor, and they were present throughout the duration of each offload to collect data for scientific, management, and regulation-compliance purposes (AFSC 2024). As pollock were being offloaded, Observers separated all chum salmon bycatch and placed it in secured totes. Observers typically only sampled bycatch once all the pollock had been offloaded. Once they were done sampling, plant staff moved the totes to a separate, designated area for the BBSRI port samplers.

In contrast to Observers, BBSRI port samplers did not need to be on-site throughout the duration of each offload; they just had to be there when chum salmon were available to sample. Plant staff kept in regular communication with the port samplers to ensure sampling was conducted as soon as possible after an offload ended. If there were simultaneous deliveries at two or more processors in Dutch Harbor, the port samplers adjusted their site visits to minimize the length of time fish had to be held by the plants. After sampling, the bycatch was either processed for donation to a food-share program or discarded at sea on the next outgoing vessel depending on fish quality. Port samplers made every effort to avoid causing any unnecessary delays in plant operations. Early in the 2024 season, there were minor communication issues between BBSRI port samplers and Observers stationed at the processors (e.g., regarding equipment usage, sampling protocols, and the location of work areas); however, these issues were quickly resolved.

2.2.3 Selecting Fish to Sample

2.2.3.1 Target Sample Rate

To ensure sampled chum salmon were reflective of the stock composition of the bycatch encountered by the shoreside sector, all chum salmon were to be sampled in proportion to the number landed across each port, processor, and vessel offload for a given statistical week (StatWk; i.e., Sunday through Saturday). Sampling effort was based on an adaptive, weekly target sample rate (e.g., sampling every fish, every 5th fish, or every 10th fish), which was determined *a priori* (every Saturday afternoon) by the project management team and based on anticipated bycatch levels for the upcoming statistical week. If small numbers of chum salmon were expected, then the target sample rate would be set relatively high (e.g., every fish encountered was sampled) to ensure adequate sample sizes for genetic analysis. If large numbers of chum salmon were expected, then the target sample rate was reduced (e.g., every 10th fish encountered was sampled) to ensure port samplers were not overwhelmed with excessive sampling requirements.

2.2.3.2 Randomly Selecting Fish to Sample from an Offload

Chum salmon were randomly selected to ensure each fish had the same probability of being sampled. To achieve this, port samplers separated the chum salmon from each offload into two groups, those that had been previously sampled by Observers (all these fish had been cut open to determine sex from the gonads; Photo 5), if any, and those that had not yet been sampled (fish that were not cut open). As stated earlier, Observers sampled 1 in 30 chum salmon encountered for the entire season (AFSC 2024). Once separated, the port samplers proceeded to select fish for sampling at the target sample rate (1 in every *n* fish), working through each tote until empty; with the tote of already-sampled fish being treated in the same manner as the other totes.

2.2.4 Data Collection and Management

For each offload, various delivery-related data fields were recorded including the cruise number, processor permit number, vessel permit number, offload number, NMFS fishing area, offload start/end dates, and number of chum salmon landed. If any of these data were not available at the time of the offload (i.e., provided by plant staff or written on the fish ticket), then they were populated from data provided by AFSC Fisheries Monitoring and Analysis Division emailed to BBSRI every Monday morning. Other fields related to the specific sample session were also recorded, including session start/end times, target sample rate, and number of fish sampled.

Various biological data were recorded for each fish sampled, including the specimen number, fish length, scale book number, scale number, Whatman card number, and position on the Whatman card. The specimen number was also noted for all fish sampled by the port samplers that had previously been sampled by Observers. Fork lengths (distance from the tip of the snout to the end of the middle rays of the caudal fin) were measured to the nearest millimeter (mm) using digital calipers. One scale (for aging)

was collected from each fish from the preferred area (i.e., the left side of the fish approximately two rows above the lateral line in an area crossed by a diagonal from the posterior insertion of the dorsal fin to the anterior insertion of the anal fin). If no scales were available from the preferred area, a scale was taken from an alternative location, such as behind a pectoral fin where scales were less prone to have been lost during hauling and offloading. Scales were placed on pre-numbered, gummed cards for preservation (Photo 6).

For each fish sampled, a pectoral fin clip (for genetic analysis) was collected and stapled to the appropriate Whatman card for preservation (Photo 7, Photo 8; see Appendix Figure A-1 for tissue-sampling protocols for DNA analysis). New scale books and Whatman cards were used for each offload. To ensure quality DNA was available for genetic analysis, it was important that tissue samples be fully dried as soon as possible after collection and then stored in a warm and dry location. To achieve this, Whatman cards were placed in Pelican cases (Model 1150) and layered between desiccant packs and blotter paper for a minimum of 24 hours after being collected. BBSRI will archive the tissue samples for a minimum of three years.

Waterproof field datasheets were used to record all port-sampling data. Port samplers were equipped with laptop computers and entered field data daily into a cloud-based database. Daily inseason QA/QC measures were taken to check for potential errors in the database.

2.2.5 Transporting Tissue Samples from Akutan to Dutch Harbor

At the end of each week, port samplers in Akutan arranged for their tissue samples to be shipped to the BBSRI laboratory in Dutch Harbor. The M/V *Eastern Wind* was used most often for this purpose as it made regular supply runs for Trident between Akutan and Dutch Harbor. Various other vessels were also used to transport samples and supplies, including F/Vs *Arcturus*, *Dominator*, *Golden Dawn*, *Golden Pisces*, *Gladiator*, *Miss Leona*, and *Sovereignty, and T/B Gyrafalcon*.

2.3 Genetic Analysis

2.3.1 Genotyping

From late May to early June 2024, BBSRI personnel conducted pre-season genetics training in Anchorage in coordination with ADF&G's Gene Conservation Laboratory (GCL). Training involved reviewing genotyping procedures, establishing project-specific laboratory protocols, and testing laboratory equipment. In the first half of June, the genotypers setup BBSRI's remote genetics laboratory in Dutch Harbor. The laboratory space was rented from Makushin Bay Resources (Dutch Harbor, AK) and located near the airport. A technician from Standard Biotools (San Francisco, CA) visited Dutch Harbor in early June to install, calibrate, and test a BioMark X9 Real-Time PCR (polymerase chain reaction) System.

2.3.1.1 Selecting Tissue Samples to Genotype

If more than 380 tissue samples were collected by the port samplers in a week, a subsample was randomly selected for genotyping (up to a maximum of 380); otherwise, efforts were made to genotype all tissue samples collected in a week.

2.3.1.2 Sample Extraction and Analysis

All tissue samples collected for this project were genotyped at the BBSRI-staffed genetics laboratory in Dutch Harbor (Photo 9 to Photo 11). Genomic DNA was extracted from dried fin clips with Macherey-Nagel (Allentown, PA) NucleoSpin Tissue kits. Extracted DNA was amplified for 96 single nucleotide polymorphism (SNP) markers (Appendix Table B-1) with a BioMark X9 Real-Time PCR System using 96.96 Dynamic Array integrated fluidic circuits (IFCs). The BioMark X9 Real-Time PCR System is a microfluidics-based benchtop platform that integrates sample and reagent preparation, thermal cycling, and end point

amplification analysis IFCs. Each IFC plate (or "chip") contained a matrix of integrated channels and valves housed in an input frame. On one side of the frame, there were 96 inlets to accept DNA extracts from individual tissue samples and on the other were 96 inlets to accept the assay mixtures for each SNP marker. The well components are pressurized into an IFC, and the 96 samples (comprised of 95 DNA samples and 1 negative control) and 96 assays are systematically combined into 9,216 parallel reactions.

Each of 9,120 parallel reactions consisted of 50–500 ηg/μL DNA (96 of the 9,216 parallel reactions were negative controls with no DNA), 1X Fast GT Sample Loading Reagent (Standard Biotools), 1X TaqMan GTXpress Master Mix (Applied Biosystems), 10X Custom ABI TaqMan SNP Genotyping Assay (Applied Biosystems), 1X Assay Loading Reagent (Standard Biotools), and 2.5X ROX Reference Dye (Invitrogen). The temperature profile for amplification was thermal mixing at 60°C for 10 min and 70°C for 30 min followed by "Hot-Start" denaturation at 95°C for 2 min and 40 cycles of amplification (denaturation at 95°C for 2 s and annealing at 60°C for 20 s).

After amplification, Standard BioTools SNP Genotyping Analysis Software onboard the BioMark X9 Real-Time PCR System was used to score the IFCs. Individuals with low-quality multi-locus genotypes (<80% of the 96 loci scored) were noted. Data from all samples, regardless of genotype quality, were sent to AFSC-ABL for analysis. Analysis by AFBL-ABL used only 84 of the 96 SNPs amplified and scored by BBSRI. As such, samples that were low-quality according to BBSRI standards may not have been low quality for AFSC-ABL analysis (<80% of 84 loci). BBSRI chose to amplify 96 markers despite the lower SNP analysis needs of AFSC-ABL for two reasons: 1) ADF&G recommended using all 96 SNP markers in case the additional results would be of use in potential future analyses; and 2) IFCs suitable for use in the BioMark X9 Real-Time PCR System are designed to accept 96 assays.

2.3.1.3 Quality-control (QC) Measures

Quality-control (QC) measures were implemented to ensure genotypes were reproducible and to identify potential laboratory errors and rates of inconsistencies. Approximately 8% of the tissue samples genotyped inseason at the Dutch Harbor laboratory were re-run post-season for comparison. This level of duplication was like that typically used at ADF&G's GCL (8.3%; Jodi Estrada, ADF&G, personal communication) but less than that used by the AFSC-ABL Genetics Program to analyze the 2024 bycatch (11.3%; Barry et al. 2025).

Samples were selected for QC from each IFC run using a diagonal line from the A3 to the H10 wells on 96 well plates (sample plates) used to hold samples prior to loading IFCs. Selecting QC samples in this way allowed for identification of sample plate orientation errors, which would lead to downstream errors in assigning a genotype to an individual fish. This method also allowed for identification of possible systematic pipetting errors. All QC samples were run from the DNA extraction step through to the genotype assignment step using methods described in Section 2.3.1.2. Resulting QC genotypes were then compared to the original sample genotypes to assess reproducibility and to identify any potential systematic lab problems in generating genotypes.

In addition to BBSRI's in-house QC, samples were re-run for QC measures at both ADF&G GCL and AFSC-ABL using the genotyping methods of each respective lab.

2.3.1.4 Data Collection and Management

The genotyper was equipped with a laptop computer and entered IFC-tracking data daily into a cloud-based database, including the IFC plate ID, sample rate, number of samples, sampling start/end times, and output file name. Results for individual tissue samples were tracked using a unique identifier (WHAT_CARD-NO) which was formed by concatenating a sample's Whatman Card number and Whatman card position. All genotyping output referenced this identifier so that the results could be linked back to the delivery and biosampling data associated with that sample. Scored genotypes for each IFC run were

exported from the Standard Biotools SNP Genotyping Analysis Software and archived on a cloud-based server.

2.3.2 Stock Composition Estimates

Each week, BBSRI emailed the port sampling and genotyping data to the AFSC-ABL Genetics Program for mixed-stock analyses. The following paragraphs describe the methods used to produce the weekly stock-composition estimates.

Mixtures were created by grouping sampled fish into temporal groups (statistical week) from non-debriefed observer data provided by the Alaska Regional Office and linked to genetic samples by BBSRI. Individual samples with fewer than 80% of their multilocus genotype scored were dropped from analyses (based on 84 loci that the AFSC-ABL Genetics Program uses for their post-season analysis). Additionally, if individuals were identified to have matching multilocus genotypes (>95% similarity) the individuals with fewer scored loci were dropped. Genetic stock identification was performed with the conditional genetic stock identification model in the R package *rubias* (Moran and Anderson 2019) following the methods used in NOAA's annual reports (e.g., Barry et al. 2024). Briefly, baseline populations were grouped into seven regions (aka reporting groups): Southeast Asia (SE Asia), Northeast Asia (NE Asia), Kotzebue Sound, Western Alaska (W Alaska), Upper/Middle Yukon (Up/Mid Yukon), Southwest Alaska (SW Alaska), and the Eastern Gulf of Alaska/Pacific Northwest (E GOA/PNW; Appendix Table B-2 and Appendix Figure B-1). For all estimates, the Dirichlet prior parameters for the stock proportions were defined by region to be $1/(GC_g)$, where C_g is the number of baseline populations in region g, and G is the number of regions. To ensure convergence to the posterior distribution, seven separate MCMC chains of 100,000 iterations (burn-in of 50,000) of the non-bootstrapped model were run, which each chain starting at disparate values of stock proportions; configured such that for each chain 95% of the mixture came from a single designated reporting group (with probability distributed equally among the populations within that reporting group) and the remaining 5% equally distributed among remaining reporting groups. The convergence of chains for each reporting group estimate was assessed with the Gelman-Rubin statistic (Gelman and Rubin 1992) estimated with the gelman.diag function in the coda library (Plummer et al. 2006) within R. Once chain convergence was confirmed, inference was conducted with the conditional genetic stock identification model with bootstrapping over reporting groups (MCMC chains of 100,000 iterations, burn-in of 50,000, 100 bootstrap iterations).

The stock composition estimates were summarized by the mean, standard deviation, median, 95% credible interval (2.5^{th} and 97.5^{th} percentile of the MCMC iterates in the posterior distribution), and P = 0, which is the probability that a stock composition estimate is effectively zero (Munro et al. 2012). The P = 0 statistic is the frequency of the last half of the MCMC iterates of each chain for which the individual regional contribution to the mixture was less than a threshold of $0.5e^{-6}$. This statistic may be more useful than the credible interval for assessing the presence or absence of minor stocks. The estimated number of fish for each genetic group, and associated uncertainty, was estimated as the mean stock proportion and 95% credible intervals multiplied by the total bycatch in a given statistical week.

An automated weekly summary report was generated and distributed to the study team (this report was not released to the public in 2024).

2.4 Scale Analysis

Post-season, scales from a subsample of the genotyped chum salmon were pressed and imaged by BBSRI in Anchorage, and the individual images were then aged by ADF&G's Mark, Tag, and Age Laboratory (MTAL) in Juneau. To age individual chum salmon, a physical impression of the scales was made on a piece of acetate under heat and pressure. A customized, inverted microscope with a specialized camera (Nikon Eclipse Ti2 with a 2x objective lens) and software system (NIS Elements AR) was used to analyze the

impressions. Under magnification, patterns on the impression (i.e., circuli formed by ridges on the bony scale) revealed the number of winters a fish had lived (annuli). Growth slows in the winter and circuli are more tightly spaced. Fish ages are reported as total age, including the gravel year such that an age 0.2 (freshwater age.saltwater age) chum salmon is reported as an age 3 fish. Scale aging data were entered into a cloud-based database and included the sampling date, scale book number, scale number, age designation, and scale condition.

3 RESULTS

3.1 2024 Shoreside B-season BSAI Pollock Fishery (Dutch Harbor/Akutan offloads)

The 2024 shoreside B-season BSAI pollock trawl fishery opened on June 10. The first deliveries to processors in Akutan and Dutch Harbor were offloaded on June 11 and June 12, respectively. The final offloads for the season occurred on October 3 in Dutch Harbor and on October 29 in Akutan. From June 11 to October 29, 21,710 chum salmon were landed as bycatch in 1,032 offloads to the five processing plants in Dutch Harbor and Akutan (Table 2; Figure 4). Bycatch in the 2024 shoreside B-season BSAI pollock trawl fishery was considerably lower than the previous 5-year (2018–2023) average of 188,132 (range: 66,170–341,960). Weekly bycatch in 2024 averaged 1,034 fish and peaked at 4,168 in StatWk 27 (Table 2). In 2024, there were three periods of relatively high bycatch: July 2–4, August 15–16, and September 4–7 (Figure 5). Daily chum salmon bycatch peaked at 1,254 fish on July 2 (StatWk 27), and the midpoint (50%) of the season's chum salmon bycatch was reached on July 24 which fell within StatWk 30.

Nearly all chum salmon bycatch offloaded during the first week (StatWk 24) of the season was reported from NMFS fishing area 509 (Figure 6). Bycatch was more evenly distributed between NMFS fishing areas 509 and 517 during StatWks 25 and 26. For the remainder of the season (StatWks 27–44), most bycatch was reported from NMFS fishing area 517, with relatively minor landings from NMFS fishing areas 509, 513, 519, 521, and 523.

3.2 Port Sampling

Of the 1,032 vessel offloads at processors in Dutch Harbor and Akutan, 90 (8.7%; representing 1,518 chum salmon as bycatch) were not sampled by BBSRI port samplers (Figure 7), and included:

- Offloads from June 11–13 made prior to the onset of BBSRI's sampling program;
- Offloads made after BBSRI's sampling program had ended [Note: BBSRI stopped sampling in Akutan prior to the end of B-season because bycatch was extremely low and all processing plants in Dutch Harbor had ceased operations];
- Offloads from June 14 to July 18 at the Northern Victor were not sampled for administrative reasons (i.e., the project team was awaiting confirmation from NOAA that potential changes to fish-handling protocols due to BBSRI's activities were allowable); and
- An offload in September that was not sampled because of a miscommunication between BBSRI port samplers and personnel at one of the processing plants.

BBSRI's sampling program operated from June 13 to October 3 in Dutch Harbor and from June 14 to October 5 in Akutan. In total, 7,034 chum salmon were tissue-sampled from 942 vessel offloads (Table 2). The number of fish sampled represented 32.4% of the 21,710 chum salmon landed for the season, and 32.7% of the 21,520 chum salmon landed during BBSRI's operational period. During BBSRI's operational period, an average of 414 fish were tissue-sampled per week (range: 13–1,901 samples per week).

Three weekly target sample rates were used in 2024: sampling every fish landed, sampling every 5th fish, and sampling every 10th fish (Table 2; Figure 8). Despite efforts to keep target sample rates constant within

each statistical week, there were two occasions where this did not occur. Every chum salmon landed in the first 20 offloads available to BBSRI during StatWk 24 was sampled; however, the final offload was mistakenly sampled at a rate of 1 in 10 (June 15; 58 chum salmon landed, 6 sampled). Every chum salmon landed in the first portion of StatWk 33 was sampled (August 11–14 and 7 offloads on August 15); however, bycatch increased significantly over two consecutive offloads on August 15, so the project team reduced the target sample rate to 1 in 10 for the remaining 25 offloads during StatWk 33. Bycatch levels decreased following these two deliveries, and in hindsight, reducing the sample rate was unnecessary.

Sampled chum salmon measured 563 mm FL on average (range: 300–790 mm FL; n = 7,019; Figure 9).

3.3 Genetic Analysis

3.3.1 Genotyping

BBSRI's genetics laboratory in Dutch Harbor became operational on July 1 when the lead genotyper and ADF&G's genetics laboratory manager – who visited the Dutch Harbor lab for 3 days - began genotyping trials. Laboratory trials and fine-tuning of laboratory procedures continued through mid-July. The laboratory began sending genotyping data to NOAA on July 17. Staff subsequently began running the backlog of tissue samples that had accumulated by then. The laboratory was fully caught up on producing genotype data by the end of July; and from that point kept pace each week genotyping all designated tissue samples through to the end of the season (the last laboratory day was October 7). Once NOAA began analysis of the genotyping data it became evident that there were errors related to data scoring. These errors were determined to be due to inconsistencies in the X9 software. These issues were resolved quickly with no further problems related to genotyping results.

Of the 7,034 tissue samples collected in 2024, 3,531 (50.2%) were run on a total of 39 IFCs for the purpose of generating individual fish genotypes (Table 2). The weekly number of tissue samples run on IFCs ranged from 13 to 380 (avg = 208), which represented 20–100% of the tissue samples collected each week.

Of the 3,531 samples run on IFCs, 3,088 (87.5%) were successfully genotyped, while the remaining 443 (12.5%) were discarded because fewer than 80% of 95 loci scored (Table 2). The weekly proportion of samples run on IFCs that were successfully genotyped ranged from 0.45 (StatWk24) to 1.00 (StatWks 30 and 38–40).

The proportion of samples run on IFCs that were successfully genotyped was lower for tissue collected during StatWks 24–27 (848/1,210, or 70.1% success rate) than during StatWks 28–40 (2,240/2,321, or 96.5% success rate). This difference was attributed to changes in tissue preservation methods. Samples collected from StatWks 24–27 were not layered correctly with desiccant packs and blotter paper in Pelican cases immediately after being collection. During this early period, the same Pelican case was used for multiple offloads and often opened several times in a day. As a result, a portion of the tissue samples did not dry quickly enough to preserve the integrity of the DNA. In contrast, samples collected from StatWks 28–40 were layered correctly in the Pelican cases, one Pelican case was used for each offload, and the Pelican cases were kept closed for at least 24 hours after initially being sealed up following an offload. The revised protocols ensured the tissue samples dried quickly and high-quality DNA was available for genotyping.

3.3.2 Stock Composition Estimates

A total of 3,061 genotyped tissue samples were used to generate the weekly stock composition estimates (Table 2). A small number of individual samples were omitted from the mixed-stock analysis because they had high similarity (>98.5% matching loci) in genotypes to other samples indicating that they likely came from the same fish, or they had fewer than 80% of 84 loci scored (as per AFSC-ABL Genetics Program protocols).

A composite estimate based on the weighted average stock compositions across weeks showed that the largest contributing genetic group to the 2024 shoreside B-season BSAI pollock trawl fishery during BBSRI's sampling operations (June 11 to August 5) was the E GOA/PNW (34.7%), with a point estimate of 7,516 chum salmon (Figure 10; Appendix Table C-1). Contributions by other stock groups included NE Asia (29.7%; 6,430 fish), SE Asia (19.9%; 4,306 fish), W Alaska (7.7%; 1,673 fish), Up/Mid Yukon (5.1%; 1,109 fish), SW Alaska (1.8%; 397 fish), and Kotzebue Sound (0.01%; 200 fish).

The E GOA/PNW stocks showed the largest variation in weekly stock proportions, ranging from a high of 69.8% in StatWk 24 to a low of 17.0% in StatWk 30 (Figure 10; Figure 11; Appendix Table C-1). E GOA/PNW stocks were the largest contributor to the catch in StatWks 24, 25, 28, 29, 32, 34, and 35, and contributions remained relatively high throughout the season. NE Asia stocks steadily increased throughout the season, and they were the largest contributor in StatWks 30, 31, 33, and 36–40. SE Asia stocks increased from 9.2% in StatWk 24 to 33.1% in StatWk 27, remained high through StatWk 31, but then decreased and remained at moderate levels for StatWks 33–40 (10.0–15.6%). Contributions by the W Alaska, Kotzebue Sound, Up/Mid Yukon and SW Alaska stocks were relatively small throughout the season. SW Alaska and W Alaska stocks showed only minor increases from StatWk 33 onwards. Kotzebue Sound stocks were highest in StatWks 24 and 25 but decreased and remained low for the remainder of the season. Up/Mid Yukon stocks showed small increases in contributions early and late in the season but remained low from StatWks 27–33.

In aggregate, the three WAK stock groups (W Alaska, Up/Mid Yukon, and Kotzebue Sound) comprised 13.8% of the bycatch (2,982 fish). Weekly stock composition estimates for the WAK aggregate ranged from a low of 7.8% (StatWk 31) to a high of 19.2% (StatWk 34).

3.3.3 Quality-Control (QC) Measures

From September 17 to October 8, 2024, BBSRI re-ran 285 tissue samples (or 8.1% of all samples run on IFCs during the 2024 season) on 3 IFCs at the Dutch Harbor laboratory as part of their QC measures. Of the 285 samples run, 246 (86.3%) were successfully genotyped and the vast majority scored with the same genotype that they received during their initial inseason IFC run. These results indicate the genotyping process was accurate and reproducible, and that there were no significant or systematic inconsistencies in the laboratory.

In addition to BBSRI's in-house QC measures, a total of 495 samples (7.1% of samples run on IFCs during the 2024 season) in two different subsets were re-run at either the ADF&G GCL or AFSC-ABL for QC. In September, sample DNA extract used for 4 IFCs (380 samples) was sent to ADF&G GCL. These DNA samples were genotyped by ADF&G GCL staff using GCL genotyping methods. In July, tissue samples from StatWk 28 (115 samples) were sent to AFSC-ABL. In September, AFSC-ABL staff genotyped these tissue samples using AFSC-ABL genotyping methods. Staff from both external laboratories confirmed that the genotypes they produced were consistent with those produced by BBSRI which verified BBSRI's methods and results.

3.4 Scale Analysis

Scale images from a subsample of 307 genotyped chum salmon were sent to the MTAL for aging. Of these, 230 (74.9%) samples were successfully aged. Age classifications included Age 2 (0.4%), Age 3 (22.6%), Age 4 (61.3%), Age 5 (14.8%), and Age 6 (0.9%). The remaining samples could not be aged because they were not the "preferred" scale type (n = 43), scale impressions were inverted (n = 13), no scale was present on the impression (n = 10), the image was unreadable (n = 6), or the scale was not from a chum salmon (n = 5).

Port sampling crews found it time-consuming to sample chum salmon bycatch for scales. Very few scales could be found on fish upon delivery, and any scales that were present were typically not found in the

"preferred" area. Despite only collecting one scale per fish, a relatively high proportion of the samples were successfully aged (74.9%).

4 DISCUSSION

Despite numerous challenges, BBSRI successfully implemented the 2024 feasibility project and produced weekly inseason stock composition estimates for chum salmon bycatch in the shoreside B-season Bering Sea pollock fishery for StatWks 24–40. BBSRI's estimated contribution of the WAK aggregate stock groups was comparable to the post-season estimate produced independently by the AFSC-ABL Genetics Program which used samples collected by the Observer Program (15.3%; Barry et al. 2025). BBSRI and the AFSC-ABL Genetics Program sampled different fish (for the most part), sampled at different rates, sampled over slightly different time periods (BBSRI omitted the latest chum), and used different laboratory methods to analyze the tissue samples. Given these differences in methods, the fact that the WAK stock composition estimates generated by the two programs were comparable lends confidence to the results.

BBSRI's 2024 WAK aggregate stock composition estimate (13.8%) for the shoreside fleet was lower than both the 2023 post-season estimate produced by the AFSC-ABL Genetics Program (14.6%; Barry et al. 2024) and the recent 5-year average of post-season estimates (17.3% from 2019–2023; Barry et al. 2022a, 2022b, 2023, 2024; Kondzela et al. 2021). Total chum salmon bycatch in the shoreside B-season Bering Sea fishery has decreased annually since 2021 (341,433 in 2021, 131,849 in 2022, 66,776 in 2023 and 21,710 in 2024). Based on NOAA's post-season estimates, contributions of the WAK aggregate stock group to total bycatch have decreased annually since 2022 (28.0% in 2022, 14.6% in 2023, and 15.3% in 2024). These are certainly positive trends for a fishery in which reducing overall chum salmon bycatch, and WAK stocks in particular, is a high priority.

One of the main reasons BBSRI's 2024 feasibility project was a success was attributed to using an adaptive sampling rate when collecting tissue samples at the processing plants. Weekly sample rates varied from sampling every fish during weeks with low-volume bycatch to sampling 1 in 10 fish during weeks with high-volume bycatch. The sampling rate for a given statistical week was set by the project team on Saturday of the previous week and based on the anticipated bycatch volume. This adaptive approach ensured that BBSRI could meet weekly sample-size targets and produce accurate stock composition estimates during low-volume periods yet prevent their crews from being overwhelmed with sampling requirements during high-volume periods. If BBSRI had sampled at a rate of 1 in 30 (which is used by the Observer Program), then only about 720 chum salmon would have been sampled over then entire season. Despite chum salmon bycatch being extremely low in 2024 relative to previous years, BBSRI was still able to sample at a high enough rate to produce weekly stock composition estimates. If BBSRI did not use this adaptive approach, it would have failed to meet project objectives.

The goal of this project is to produce timely inseason stock composition estimates. In 2024, this occurred weekly and corresponded to statistical weeks of the fishery. Typically, chum salmon bycatch was sampled at processing plants from Sunday through Saturday, and then the tissue samples were shipped to BBSRI's Dutch Harbor laboratory on Sunday. Laboratory work started as soon as the samples were received and was completed by Wednesday or Thursday, depending on the number of samples being genotyped. Since 2024 was a feasibility year and no results were released to the public inseason, BBSRI was focused more on ensuring laboratory protocols were established and fine-tuned rather than expediting the results each week. Although BBSRI kept to a weekly schedule in 2024, there is nothing tying operations to this time frame in future years. The frequency that estimates will be generated in 2025 has yet to be determined, but at a minimum it will be done weekly. If it were deemed valuable to the fleet to increase the frequency of producing inseason stock composition estimates (e.g., twice a week), then BBSRI would certainly consider that option.

Given its success in 2024 producing timely stock-composition estimates, BBSRI is confident this project can be used as a tool by the shoreside fleet to aid in bycatch reduction of WAK chum salmon stocks. In its current structure, project results can be used to track the total number of WAK chum salmon being caught as the fishery is being executed, which in turn can inform the fleet on whether voluntary efforts should be made to reduce chum salmon bycatch. Looking ahead, BBSRI plans to build on the success of their 2024 efforts and explore ways to evolve the project to help drive meaningful, data-driven decision-making with respect to the avoidance of WAK chum salmon in the shoreside B-season pollock trawl fishery. This will only be achieved with continued involvement and collaboration with NOAA, ADF&G, industry, and numerous stakeholder groups who were all instrumental in the success of this project in 2024.

5 RECOMMENDATIONS

The following bullets summarize some of the challenges encountered in 2024 and the corrective measures that BBSRI will take to improve subsequent project years.

- As described in Section 2.2.2, BBSRI staff met with personnel from each processor in early June to discuss project logistics. These pre-season meetings were extremely helpful, but it still took several weeks to fine-tune communications between the processors and BBSRI port samplers. In 2025, BBSRI will confirm communication protocols with each processor prior to the onset of the fishing season.
- As described in Section 2.2.2, there were minor communication issues in early June between BBSRI port samplers and Observers. These issues largely stemmed from a lack of pre-season engagement between the two groups. BBSRI will coordinate with the NOAA Observer Program to ensure the project objectives and sampling protocols for both programs are communicated to everyone who is working at the ports.
- In 2024, BBSRI port samplers were not available for a handful of offloads at the start and end of the B-season fishery. In addition, due to an administrative issue (see Section 3.2), 58 offloads at the Northern Victor were not sampled by BBSRI port samplers. To ensure all chum salmon bycatch in a given statistical week has the same probability of being sampled, BBSRI will ensure their port samplers are available in both ports for the duration of the 2025 B-season fishery. Efforts will also be made to resolve any administrative issues between NOAA and the processors prior to the onset of the fishery.
- Some data that BBSRI required to produce weekly stock composition estimates was only recorded by Observers (e.g., offload number, NMFS fishing area, cruise number). Other data were recorded by both BBSRI port samplers and Observers (e.g., offload end date, chum salmon retention count). As stated earlier, NOAA provided all their delivery data to BBSRI once a week (every Monday morning). In 2024, there were occasional discrepancies in the data recorded by the two groups (e.g., due to differences in species identification or human error when counting large numbers of fish). These discrepancies were relatively minor and did not likely impact the stock composition estimates; however, in 2025, BBSRI will crossmatch the data sets prior sending any files to the AFSC-ABL Genetics Program for mixed-stock analysis.
- As described in Section 2.2.3.1, prior to the start of each statistical week, the BBSRI project team set a target sample rate (i.e., every fish, every 5th fish, every 10th fish) for the following week that it anticipated would provide enough samples for analysis, but not so many as to overwhelm the port samplers with sampling requirements. This proved to be a difficult task (see Section 3.2), even in a low bycatch year like 2024. In 2025, BBSRI will coordinate more closely with the processors and coop managers to better forecast short-term bycatch levels, as they are in contact with fishing vessels on the fishing grounds.

- Significant QC measures were taken by BBSRI throughout the 2024 season to validate laboratory methods and results. However, errors can occur in any given IFC run due to human error, equipment failure, DNA extraction failures, or chemistry failure. To ensure validation of genotyping results in real-time during the 2025 season, a single sample of known genotype from the 2024 season will be integrated into each IFC run to act as a positive control. As such, if errors occur due to human error or equipment malfunction, this will be evidenced prior to making data public. A positive control will also allow for the differentiation between DNA extraction failures and chemistry failures, aiding in troubleshooting and re-running samples such that the genotypes from such samples can still be used inseason.
- If scale sampling is done in subsequent years, it seems reasonable to continue collecting only one scale per fish. In 2024, collecting one scale per fish was time-consuming for the port samplers; however, as described in Section 3.4, a high proportion of the single-scale samples were successfully aged.
- In 2024, the composition of the chum salmon bycatch was reported using seven stock groups. Moving forward, BBSRI plans to remove Kotzebue Sound as one of these stock groups because its contributions to the overall bycatch were extremely small in 2024 (0.01%). This was consistent with the small proportion of Kotzebue Sound in the bycatch across all sectors (0.5%; Barry et al. 2024). Instead, Kotzebue Sound stocks will be pooled with the W Alaska stock group. All else being equal, reducing the number of stock groups may provide for more precise weekly stock composition estimates.
- In 2025, BBSRI will work NOAA and Sea State Inc. to conduct additional inseason stock-composition analyses that may assist with fishery management. These may include analyzing samples from lightning-strike events (i.e., when a large number of chum salmon bycatch is landed from on delivery), vessel aggregations, or hot-spot closure areas.

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Bristol Bay Science and Research Institute (BBSRI): Jordan Head, Executive Director, was principal investigator and provided technical oversight, administered contracts, managed project finances, and liaised with government agencies and industry representatives. Abby Duffy was the lead genotyper and field supervisor in Dutch Harbor; Natura Richardson assisted with genotyping; and Tami Matheny assisted with procurement, logistics, and administration. Sam Harris assisted with pre-season logistics, equipment calibration, and pressed/imaged all scale samples. Jason Smith was project manager; Jeff Regnart provided technical advice and inseason logistical support; Scott Rayborn assisted with the study design.

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8 TABLES

Table 1. List of key project activities and their completion dates in 2024.

Activity	Completion Date
Field crews and gear mobilized from Anchorage to Dutch Harbor	June 2–12
Remote genetics laboratory mobilized in Dutch Harbor	June 3 – July 17
Port sampler training and processing plant orientations	June 8–10
Port sampling chum salmon bycatch in Dutch Harbor and Akutan	June 13 – October 5
Genotyping chum tissue samples at the Dutch Harbor laboratory	July 2 – October 8
Prepared weekly internal progress reports for internal distribution	June – October
Last two port samplers done for the season and return to Anchorage	October 7
Demobilized laboratory equipment in Dutch Harbor; genotyper and select gear return to Anchorage to wrap-up project	October 8 – 14

Table 2. Number of offloads and chum salmon bycatch in the shoreside B-season BSAI pollock trawl fishery, as well as the number of chum salmon tissue samples collected, run on IFCs (integrated fluidic circuits), and successfully genotyped, by statistical week, 2024.

Stat. Week	Offload End Date From:	To:	Offloads in Dutch Harbor/ Akutan	Chum Bycatch	Chum Tissue Sampled	Tissue Samples Run on IFCs	Tissue Samples Successfully Genotyped	Samples Used to Estimate Stock Comp.	Proportion of Chum Landed Tissue Sampled	Proportion of Tissue Samples Run on IFCs	Proportion Run on IFCs Successfully Genotyped
24	Jun-11	Jun-15	32	879	578	366	165	154	0.658	0.633	0.451
25	Jun-16	Jun-22	81	1,538	144	144	115	113	0.094	1.000	0.799
26	Jun-23	Jun-29	76	2,209	408	380	320	320	0.185	0.931	0.842
27	Jun-30	Jul-6	66	4,168	764	320	248	247	0.183	0.419	0.775
28	Jul-7	Jul-13	72	865	115	115	114	113	0.133	1.000	0.991
29	Jul-14	Jul-20	79	1,103	176	176	173	171	0.160	1.000	0.983
30	Jul-21	Jul-27	76	223	220	220	220	219	0.987	1.000	1.000
31	Jul-28	Aug-3	73	216	214	214	206	206	0.991	1.000	0.963
32	Aug-4	Aug-10	64	1,349	1,343	380	341	334	0.996	0.283	0.897
33	Aug-11	Aug-17	79	3,229	1,901	380	375	375	0.589	0.200	0.987
34	Aug-18	Aug-24	56	761	155	155	152	151	0.204	1.000	0.981
35	Aug-25	Aug-31	60	475	93	93	92	92	0.196	1.000	0.989
36	Sep-1	Sep-7	59	3,569	715	380	360	360	0.200	0.531	0.947
37	Sep-8	Sep-14	48	539	107	107	106	106	0.199	1.000	0.991
38	Sep-15	Sep-21	34	345	65	65	65	100	0.188	1.000	1.000
39	Sep-22	Sep-28	31	63	13	13	13		0.206	1.000	1.000
40	Sep-29	Oct-5	23	115	23	23	23		0.200	1.000	1.000
41	Oct-6	Oct-12	9	44	-	-	-		-	-	-
42-44	Oct-13	Nov-2	14	20	-	-	-		-	-	-
Total			1,032	21,710	7,034	3,531	3,088	3,061	0.324	0.502	0.439

Notes:

B-season opened June 10; the first offload ended on June 11, and the last on October 29.

No. of offloads and chum bycatch reported here include those for all deliveries, even ones that BBSRI did not sample.

StatWk 24 - all bycatch during BBSRI operational period was sampled except for one offload (6/15, 58 fish; every 10th fish sampled).

StatWk 33 - every fish sampled Aug. 11-14, 7 offloads Aug. 15; every 10th fish sampled for 3 offloads Aug. 15 and all from Aug 16-17.

StatWks 38-40 - genotyped samples were pooled (n = 100) to estimate stock composition.

9 FIGURES

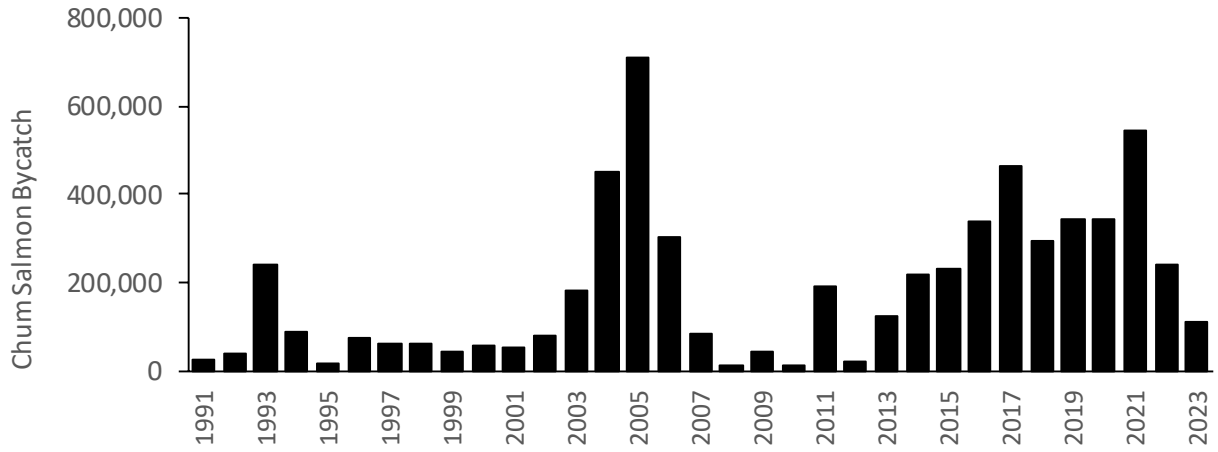


Figure 1. Chum salmon bycatch in the B-season BSAI pollock fishery, all sectors combined, 1991–2023 (NMFS 2024; Barry et al. 2024).

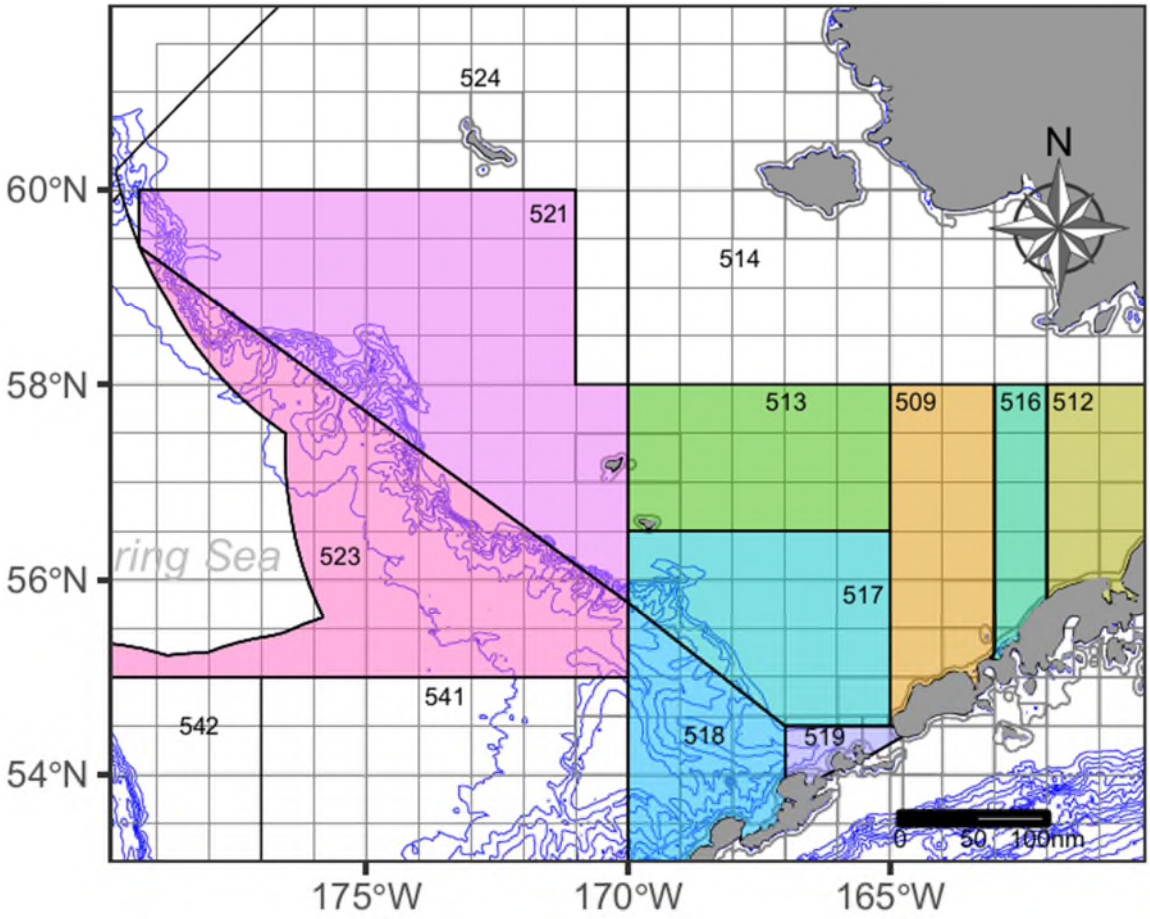


Figure 2. Map of National Marine Fisheries Service (NMFS) management areas within the Bering Sea and Aleutian Islands. Colored areas indicate those areas from which chum salmon bycatch has historically occurred.

Figure 3. Aerial imagery showing the location of four processors, BBSRI genetics laboratory, and crew bunkhouse in Dutch Harbor (top), and one processor in Akutan (bottom).

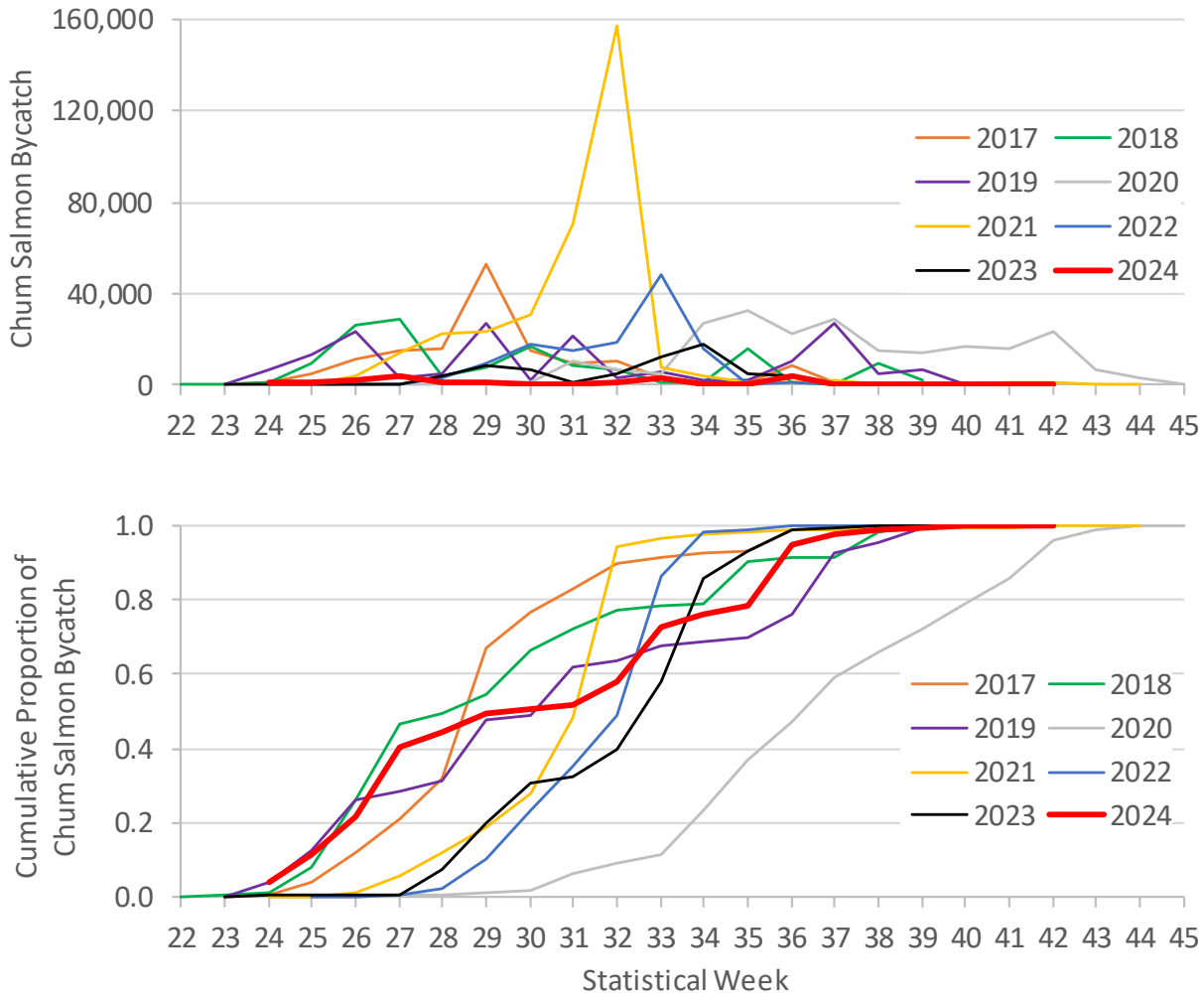


Figure 4. Weekly chum salmon bycatch at processors in Dutch Harbor and Akutan (top), and cumulative proportion of the bycatch (bottom), in the shoreside B-season BSAI pollock trawl fishery, 2017–2024 (2017–2023 data from S. Martell, Sea State Inc., pers. comm; 2024 data from G. Campbell, NOAA, pers. comm.). Data from StatWks 43–44 was excluded for confidentiality requirements.

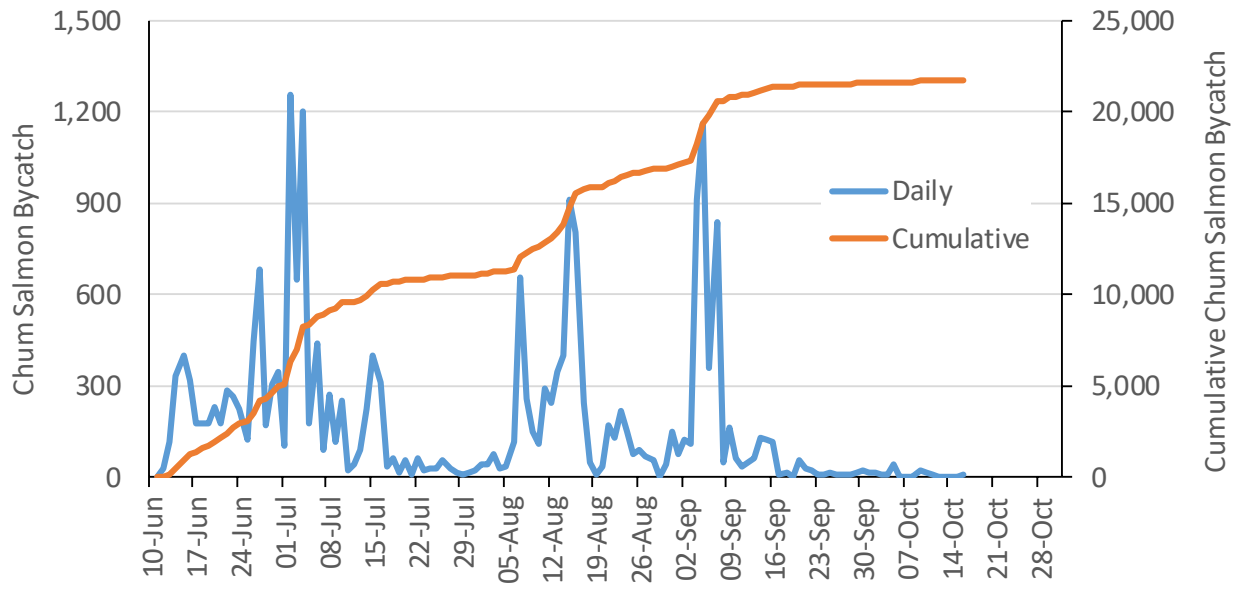


Figure 5. Daily and cumulative number of chum salmon landed as bycatch in Dutch Harbor and Akutan during the shoreside B-season BSAI pollock trawl fishery, 2024. Data from October 17–29 was excluded for confidentiality requirements.

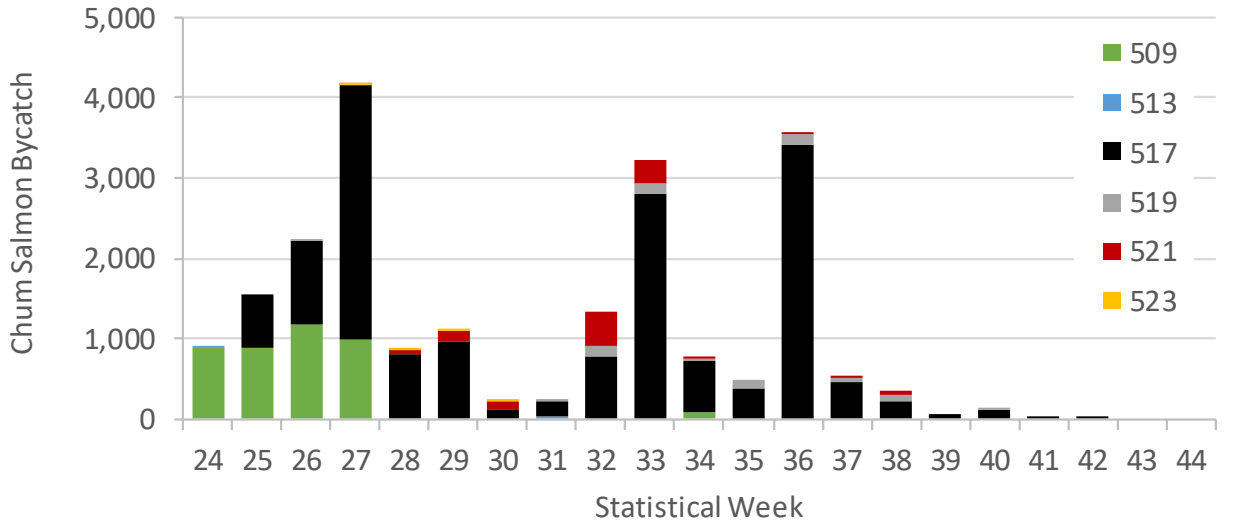


Figure 6. Weekly number of chum salmon landed as bycatch in Dutch Harbor and Akutan during the shoreside B-season BSAI pollock trawl fishery, by NMFS fishing area, 2024. Data from StatWks 43–44 was excluded for confidentiality requirements.

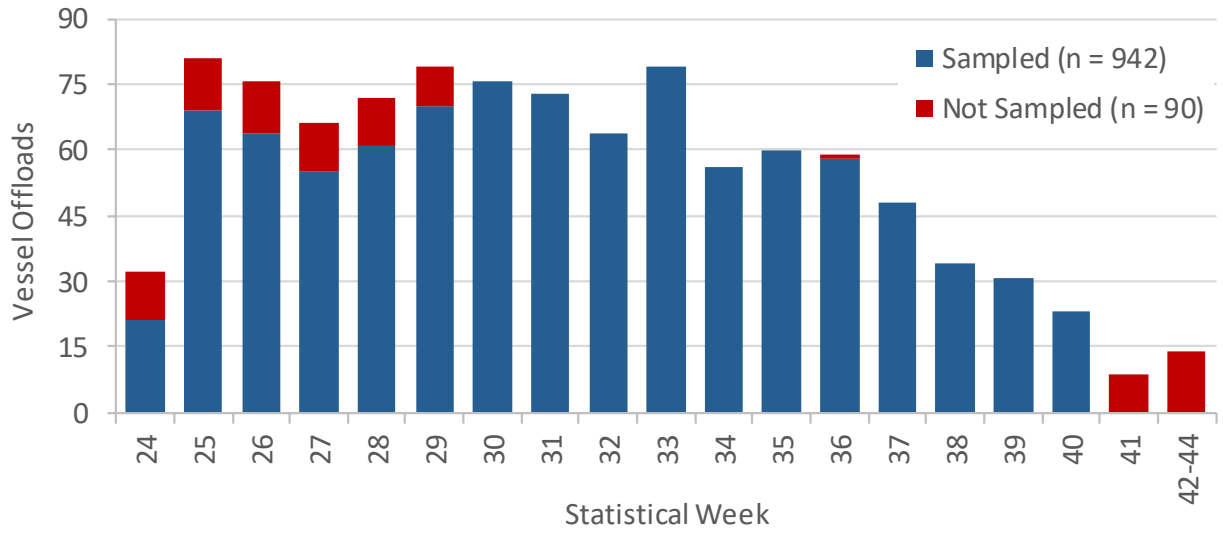


Figure 7. Number of vessel offloads from the shoreside B-season BSAI pollock trawl fishery (Dutch Harbor and Akutan only) sampled, and not sampled, by BBSRI port samplers, by statistical week, 2024. Data from StatWks 42–44 was pooled for privacy reasons.

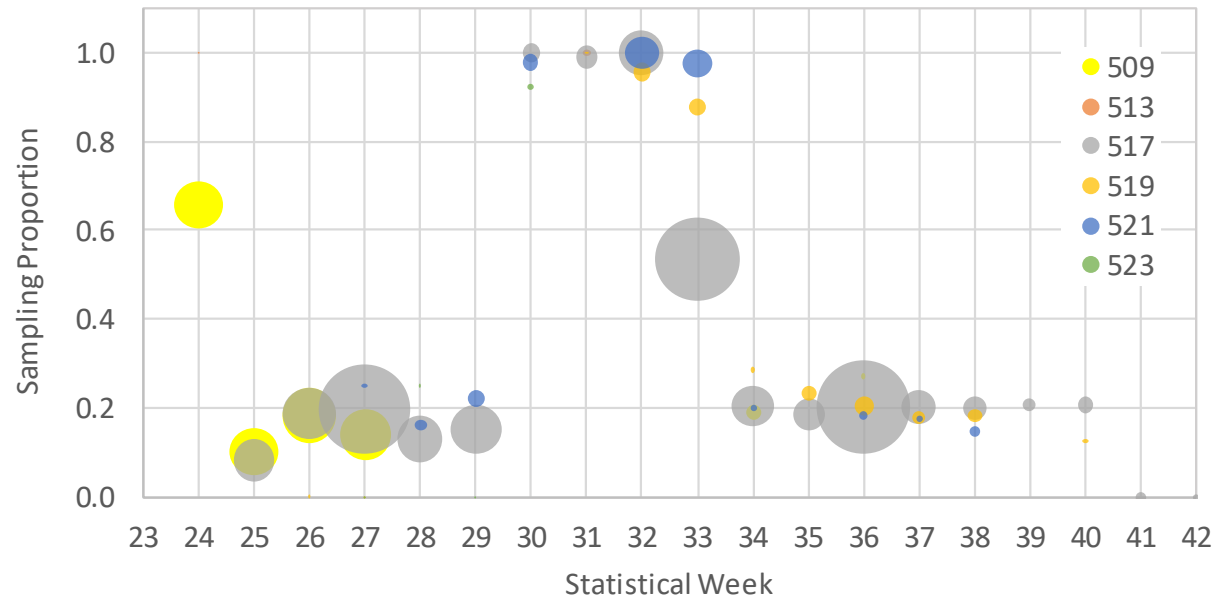


Figure 8. Proportion of chum salmon landed as bycatch in Dutch Harbor and Akutan during the shoreside B-season BSAI pollock trawl fishery that were sampled by BBSRI port samplers, by statistical week and NMFS fishing area. Circle size is proportional to the number of chum salmon landed as bycatch. Data from StatWks 43–44 was excluded for confidentiality requirements.

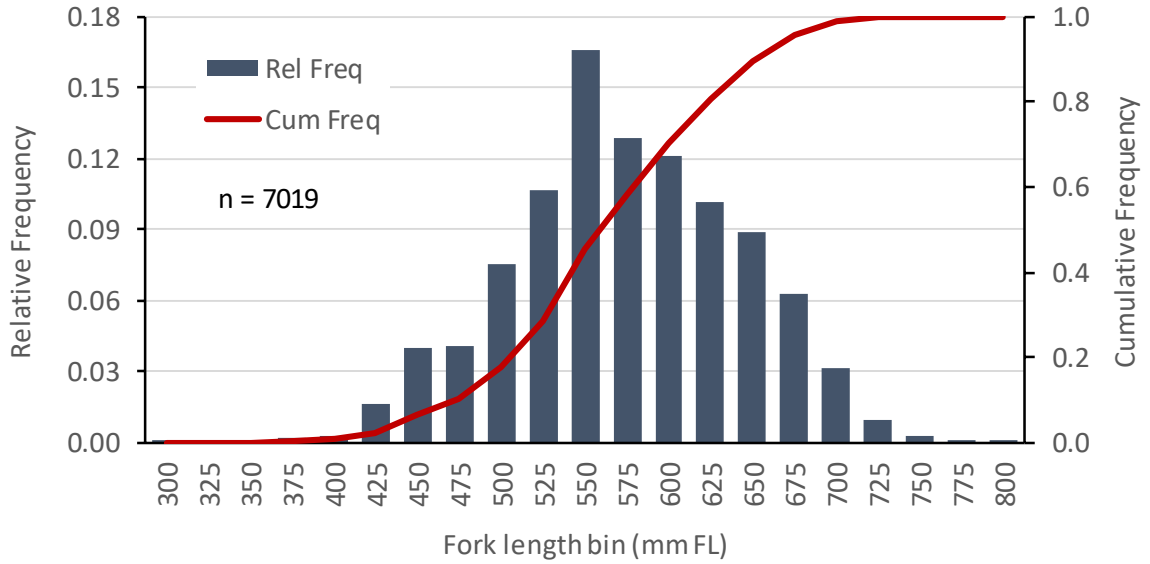


Figure 9. Length-frequency distribution for chum salmon landed as bycatch in Dutch Harbor and Akutan during the shoreside B-season BSAI pollock trawl fishery that were tissue-sampled by BBSRI port samplers, 2024.

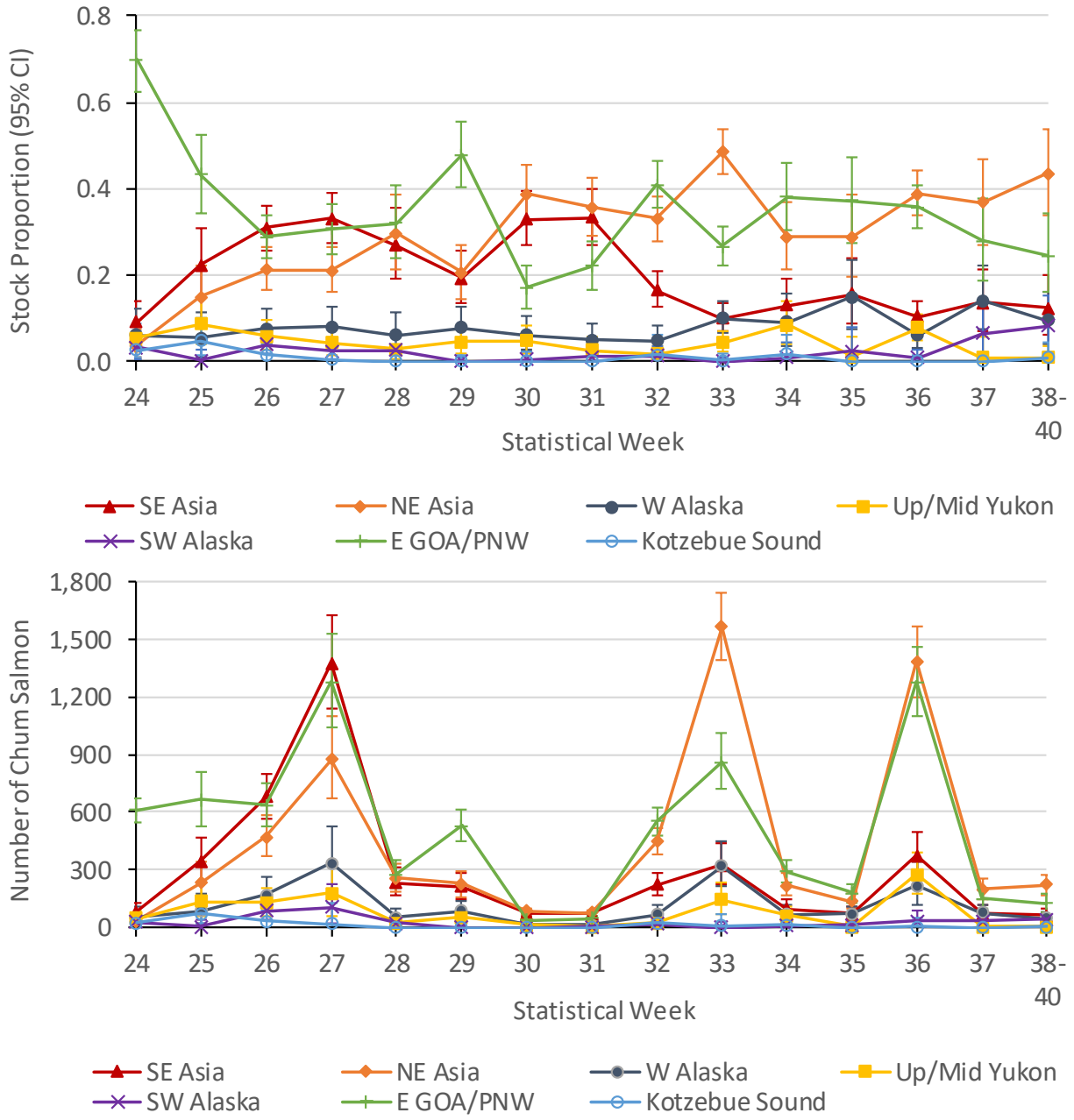


Figure 10. Stock proportions (top) and number of fish (bottom) as estimated using genetic analysis for chum salmon landed as bycatch in Dutch Harbor and Akutan during the shoreside B-season BSAI pollock trawl fishery, 2024.

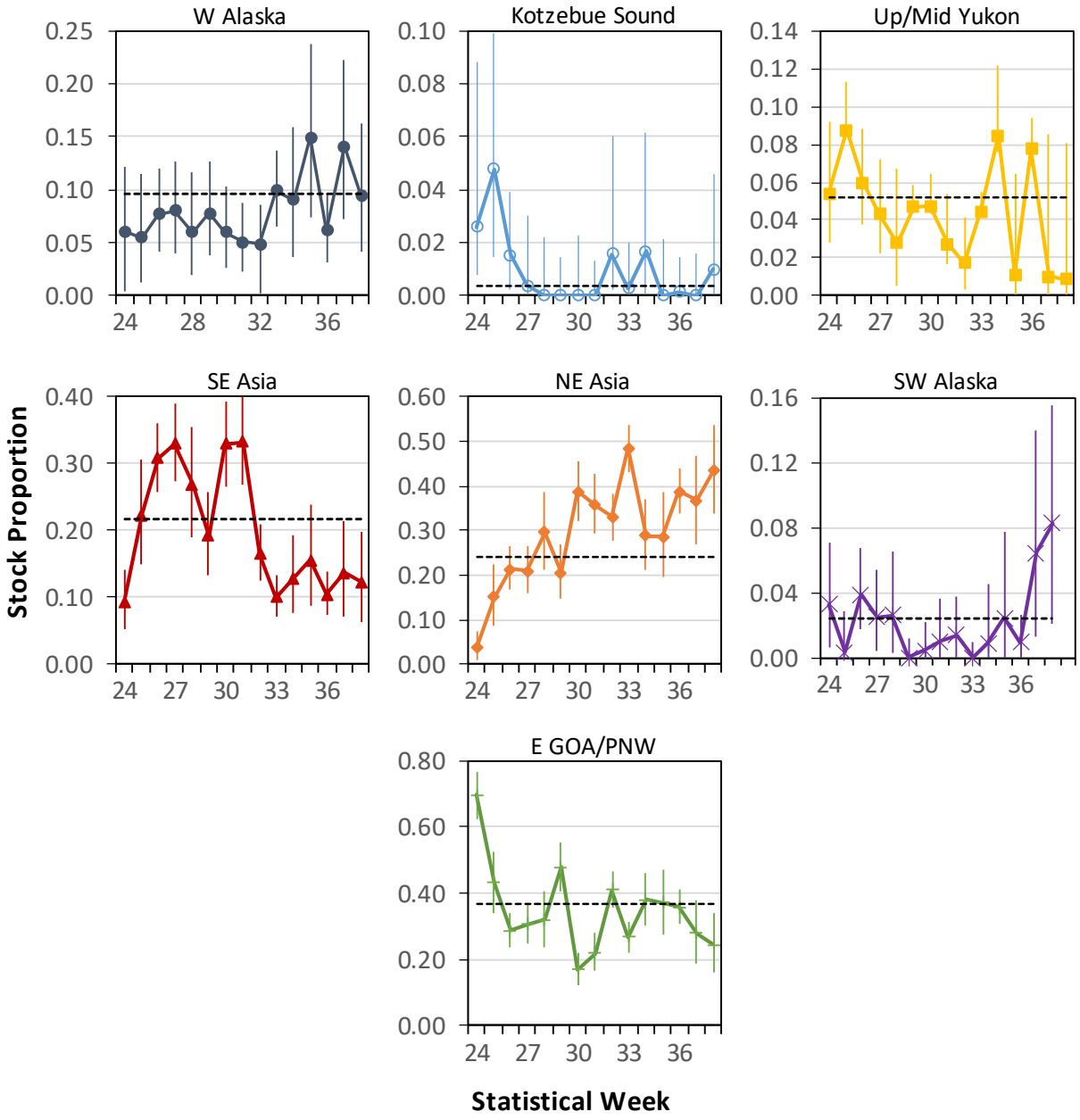


Figure 11. Stock proportions as estimated using genetic analysis for chum salmon landed as bycatch in Dutch Harbor and Akutan during the shoreside B-season BSAI pollock trawl fishery, 2024. Dotted lines show the 2024 post-season stock proportions estimated by the AFSC-ABL Genetics Program.

10 APPENDICES

APPENDIX A –TISSUE SAMPLING PROTOCOL

Appendix Figure A-1. Protocols used to tissue sample adult chum salmon for DNA analysis in 2024.

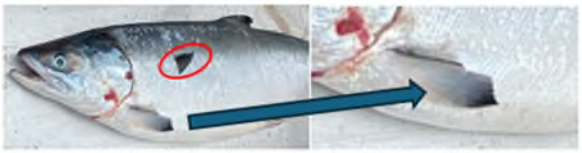
Adult Chum Salmon Tissue Sampling Protocol for DNA Analysis

1. General Information

Fin tissue is used as a source of DNA to genotype fish. For this project, genotyped fish tissue is used to determine the stock composition of chum salmon bycatch in the pollock fishery. The most important thing to remember in collecting and preserving samples is that **only quality tissue samples give quality results**.

Preservation used: Silica desiccant bead packets dry and preserve tissues for later DNA extraction. Quality DNA preservation requires dry storage in Pelican cases with desiccant packs.

2. Sampling Method



From tip of pectoral fin, cut a small clip of tissue ½-1" max and place on Whatman card, one fish per numbered cell. If fin is "feathery" at tip, clip off feathery portion before cutting the sample clip.

3. Sampling Instructions

- **Prior to sampling:** setup workplace, fill out required collection information on Whatman card and datasheet, fold landscape cloth so that cloth can be secured by clipboard – do not fold cloth behind Whatman card - and place Whatman card on clipboard, secure with clip; ready to sample.
- **Sampling:**
  - Wipe fin prior to sampling.
  - Briefly wipe or rinse scissors and forceps between samples to reduce cross-contamination.
  - Using scissors for cutting and forceps for handling, cut one fin clip per fish.
  - Place fin tissue onto #1 grid space. Follow numerical sampling order (# 1-48) printed on Whatman card.
  - **Only one fin clip per fish into each numbered grid space.**
  - Staple each sample to the Whatman card.
  - When sampling is complete, fold the landscape cloth "rain fly" over the samples to the papers edge protecting the tissue samples for storage/transport. DO NOT STAPLE LANDSCAPE CLOTH CLOSED.
- **Loading the Pelican case (Model 1150):**
  - First card: remove blotter papers and desiccant packs from Pelican case. Place first Whatman card in Pelican case with tissue samples facing up. Next, place blotter paper directly over the card and place one desiccant pack on top. Close and secure lid so drying begins (keep upright so weight of desiccant pack is on card, and it dries flat).
  - Up to 4 cards can be added per Pelican case. Add each card so the tissue samples always face a 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 cards.
  - Only use 1 Pelican case per offload.
  - DO NOT OPEN Pelican case for at least 24 hours after inserting cards to ensure tissue preserves properly.
- **Post-sampling Storage:**
  - All Whatman cards will remain in a Pelican case for a minimum of 24 hours after being sampled.
  - Once removed from a Pelican case, cards will be stored in a file box containing desiccant packs at room temperature.

4. Supplies required:

1) Scissors – for cutting fin clips
2) Forceps – for handling fin clips
3) Whatman genetics card – holds 48 fish/card
4) Bostitch Office B8 heavy duty stapler – secure tissue to card
5) Bostitch Office B8 PowerCrown staples
6) Pelican cases (Model 1150)
7) Desiccant packs – removes moisture from samples
8) Blotter paper (pre-cut) – covers full sample card in Pelican
9) Clipboard – holds Whatman card while sampling
10) Laminated sampling instruction sheet
11) Pencils
12) File box – long-term dry storage with desiccant packs
13) Paper towels – for wiping fin, scissors, and forceps.

APPENDIX B – GENETIC MARKERS AND BASELINE

Appendix Table B-1. List of SNPs in the 96-SNP panel used by BBSRI for chum salmon stock-composition analysis in 2024.

Locus Name	Ploidy	FAM	VIC	F Primer Sequence	Reporter 1 Sequence	Reporter 2 Sequence
Oke_ACOT-100	D	G	C	TCAGGGACGATAAAGGGATCATCTT	CTTCCGCTCTCTACTCC	TTCCGCTCTGTACTCC
Oke_AhR1-78	D	A	G	AGCAGAACCAGCACCTACAG	CAGCCTCGGTGCCAT	TCAGCCTCAGTGCCAT
Oke_arf-319	D	C	T	TGCAGAAACTGATCATTGGTAGTGG	CTGTGTGAATTGCCTC	CTGTGTGAACTGCCTC
Oke_ATP5L-105	D	G	C	GTGCACACCAATCCATTTCTGAAT	AGTATATTGAGATGAATCCCAC	ATATTGAGATGAATGCCAC
Oke_azin1-90	D	T	C	GGGAATAGTGTCATTTGGGATGCAT	CCTTTATCTGAGGAACTG	CCTTTATCTGAAGAACTG
Oke_brd2-118	D	T	C	CTCAAGCCCTCCACACTCA	ATGACGAAGCTCTCC	ATGACGAAACTCTCC
Oke_brp16-65	D	T	C	TCCACGTCACTCAGCATGATG	ACGTTGCCTGTCCAC	ACGTTGCCTATCCAC
Oke_CATB-60	D	T	C	GCTTCTATGGGTCCTACTACCGTAT	CAGGAACGGGTATGAG	CAGGAACGAGTATGAG
Oke_ccd16-77	D	C	A	TGTCTTCAGAATCCAATGCTTTCCT	CCAGCCCCCTCTGAAA	AGCCCCCGCTGAAA
Oke_CD81-108	D	T	G	CAGTATCATCATACAGCACAGATACAACA	TCCGGCATGTCCCAG	TCCGGCATTTCCCAG
Oke_CD81-173	D	C	A	GATGACTGGAGTCAGCTTGCA	CAGTCACAGAGAGTCAC	AGTCACAGCGAGTCAC
Oke_CKS1-94	D	T	G	TCTTCGACATGTTTAATCGAACAGAAGT	TCTGGATAAATTTGTGTATTC	TTCTGGATAAATTTTTGTATTC
Oke_CKS-389	D	A	G	GGGCCATTCTCTGAGTTCAGT	AAATGAATGATAATGTGTTCTG	AAATGAATGATAATATGTTCTG
Oke_Cr30	H	A	G	ACTACTCTCTGGCGGCTACA	CAAGTTATGGCATTTACA	TTACAAGTTATAGCATTTACA
Oke_Cr386	H	-	G	CTTAATGTAGTAAGAACCGACCAACGA	ATCGTATTAGGTCGCATCT	AAATCGTATTAGTCGCATCT
Oke_ctgf-105	D	A	G	TGAGTCCATGTACTACAAGAAGATGCT	TCATGGCGTAAACAA	ATCATGGCATAAACAA
Oke_DCXR-87	D	T	A	GTCACCCAGAACAATAGAATGAGTCT	CCTGTTTGTTGAAACCGTA	CCTGTTTGTTGTAACCGTA
Oke_e2ig5-50	D	T	C	GCACTGCTCATTCTGTCACATG	CATCTTTGTATCTGTGCCATT	TCATCTTTGTATCTATGCCATT
Oke_eif4g1-43	D	T	G	GCACCCAACAGTTCATCATGTAAGT	CTGAGATTCTTCATCTTTTAC	TGAGATTCTTCATATTTTAC
Oke_f5-71	D	T	C	CTCAAATTTCCCTTTGACATCAATTCATCA	CAGGTGCGTGCAGTAA	TCAGGTGCATGCAGTAA
Oke_FANK1-166	D	T	C	ACTCACGTGTGGTAGAGACAGA	CTACAGCCCGGCTGTG	CTACAGCCCAGCTGTG
Oke_FBXL5-61	D	A	G	TGGTGTGTAACGTCAGTGACTTAAG	TCTGAGGGAAACTGC	TCTGAGGAAAACTGC
Oke_gdh1-191	D	G	A	GTGGAGACCAAACCCAGTAGAAC	TGTGTTCCTCAGCACAAC	TGTTCCTCGGCACAAC
Oke_gdh1-62	D	T	C	CCACGTGATACAGGGAGATGTG	TTCTGTGTCCCGTGACCT	CTGTGTCCCATGACCT
Oke_GHII-3129	D	A	G	GTCAAGCTGATACCACTCAAATCTCA	CAGGGCGACTCTAT	ACAGGGCAACTCTAT
Oke_glrx1-78	D	T	C	CGCTCCGTCCAGTGATGTC	TGGGCATTTAGAGTTTATT	TGGGCATTTAGAATTTATT
Oke_GPDH-191	D	A	T	CCTGTACCTATAGGGCAACTTCAC	CGGAGCCACTTCCAGTA	CGGAGCCACTACCAGTA
Oke_GPH-105	D	G	T	CAGATCAACCCTGGAAAAATATCTGATGT	CCAGTAATTGGTATTTTGA	CCAGTAATTGGTCTTTTGA
Oke_HP-182	D	C	A	CCGATGACTCCAAAGAAGTTGCT	AGAAAAGGTGAGCTAGTATG	AAAAGGTGAGCTCGTATG
Oke_il-1racp-67	D	A	G	AATTGCTCCTCCTCGCTATTTCTC	CGTACGAGATGTAGATGT	CGTACGAGATATAGATGT
Oke_IL8r2-406	D	G	T	GGATGGACATTCACAGTCTGGTT	AAACACAAAACCCC	AAACACAAACCCCC
Oke_KPNA2-87	D	A	T	AGGCAGCCAGGTAAGTCAGTA	ACAGAACAGAAACAGTG	AACAGAACAGTAACAGTG

Appendix Table B-1 – Continued.

Locus Name	Ploidy	FAM	VIC	F Primer Sequence	Reporter 1 Sequence	Reporter 2 Sequence
Oke_LAMP2-186	D	G	A	TTCTAGCCATGACCCAATGAAAGG	CTAACTTTACAAAGACACTGC	AACTTTACAAAGGCACTGC
Oke_mgll-49	D	T	A	ACATTGTAATCTGTATTAGTCCAATGCAGAC	ATTTATGGGTGTTCCCC	TTATGGGAGTTCCCC
Oke_MLRN-63	D	A	G	CCATTTCAGCATTGCCAGATTTGAAA	CTGGTGATTGACGATCC	CTGGTGATTAACGATCC
Oke_Moesin-160	D	G	T	TTTCAGCAAATGAAGAGAACATCAAACTG	CATTTTGTAATTCTAATTTTAAGC	ATTTTGTAATTCTAATGTTAAGC
Oke_nc2b-148	D	C	A	CCAGCCTATTTCCTTTAGTGCATATGA	TTTAGTTCTAGTCAAAAGTAG	TAGTTCTAGTCCAAAGTAG
Oke_ND3-69	H	A	G	TGGTATTGAATTTGTCGTAGAAGGCAAA	CAGCCAGAAAGGTAGAG	CAGCCAGAAAAGTAGAG
Oke_NUPR1-70	D	T	G	AGACGGTGAACTCTGCTGTAGA	CTATGAGGACGGGTCACA	ACTATGAGGACTGGTCACA
Oke_pgap-111	D	T	C	TGCAGATCTCAATTTGAACGACCTAT	AGCTAGCAGGCTAAAG	AGCTAGCAAGCTAAAG
Oke_pgap-92	D	G	C	TGCAGATCTCAATTTGAACGACCTAT	CAAGAGGTAAGAAGCTAC	AAGAGGTAACAAGCTAC
Oke_PPA2-635	D	T	C	ACACAACTGACCATATTGACTTTCGA	TTGCCTCCCCCGCTC	TTATTGCCTCTCCCGCTC
Oke_psmd9-57	D	T	C	ACTGTAGTGACTGCATTTCATATTGCT	CATTGGCGGTGTAACG	TCATTGGCAGTGTAACG
Oke_rab5a-117	D	T	C	GGGAATAACAGTCATTGCAGCATTT	CAGCTGTTTTTCTTGTAGCCT	AGCTGTTTTTCTTATAGCCT
Oke_ras1-249	D	G	T	GGATGACTAAGAGCGACTGTATGTG	CACCAAGGTAAAAAT	CCAAGGGAAAAAT
Oke_RFC2-618	D	A	G	GACAATGTGTTAGTGTAGGCTTCACT	CAGCTCCTGGACTCA	CAGCTCCTAGACTCA
Oke_RH1op-245	D	T	C	TGGCCGATCTCTTCATGGTAATC	AGTGGTGAAGCCTC	TAGTGGTAAAGCCTC
Oke_RS27-81	D	A	G	GCAACAAAGTGGACTATCACATTGAA	TGTCCAGGCGTCATGA	TGTCCAGGCATCATGA
Oke_RSPRY1-106	D	T	A	GTCCTCCCTATTCTTCCACTTACCT	TAGTCTCTTTACATAATCTC	TAGTCTCTTTACTTAATCTC
Oke_serpin-140	D	T	A	TCCACAGTGAGTAATAAAGTTGCACAT	CAAGAACTGACCTTAGACAC	AAGAACTGACCTTTGACAC
Oke_slc1a3a-86	D	T	C	TGTCTTCATCTGTGGACTCCTACA	CCCAACGCGGTGATG	CCCAACGCAGTGATG
Oke_sylc-90	D	T	A	TTGAGGAAACCACTGGTCTTACAAG	ATATCTTTGAGACTAGATTAA	CTTTGAGACAAGATTAA
Oke_TCP1-78	D	G	A	CTCCAGGGCATCAGCAAATG	ATACTGCTCCAGAGACG	CTGCTCCAGGGACG
Oke_Tf-278	D	A	C	GCCACAATTGTAATTCTAGATCCAGAGT	ATTTTACAGTTGACATTCAA	TTTTACAGTTGAAATTCAA
Oke_thic-84	D	T	C	GCTGCTGTCTTAAACCACATTCTACA	ATGGAATGACAGCAATGT	ATGGAATGACAACAATGT
Oke_U1002-262	D	T	G	CCTAGACCACTCCAGACTGTTG	AAGCTTGATTTCTTTTCTT	AAGCTTGATTTATTTTCTT
Oke_U1008-83	D	G	A	GTCACCAAACATCCTGCGAATG	CCGTTCTCTTCTTGGACAC	CGTTCTCTTCCTGGACAC
Oke_U1010-251	D	G	A	CACCTCAATCAATCAAATGTATTTATAAAGCCA	ATAGAGGTGAGCATTGACAT	TAGAGGTGAGCACTGACAT
Oke_U1012-241	D	G	C	GCAGAGGTTATACCCATTTTAGATGCA	ATGGAAAAAGAACTGTTTACT	ATGGAAAAAGAACTCTTTACT
Oke_U1015-255	D	G	A	CAGAGTGCAGAGTAATACGCATACA	CAAACACACACAGAGCC	AACACACGCAGAGCC
Oke_U1016-154	D	T	C	GCAGGTTGCTAAGTCATGTTACACA	CCATGTTTGCGGTATGT	CCATGTTTGCAGTATGT
Oke_U1017-52	D	T	C	TGGCAATGGGATGTCAAGTTATGA	AGAGAGTTGTCGTTCATC	AGAGAGTTGTCATTCATC
Oke_U1018-50	D	T	C	TCCAGGTTGCTGACAATGTAAAAGT	CTGGGCACGTACAGCT	CTGGGCACATACAGCT
Oke_U1021-102	D	T	G	TCGAGGATTTGAGGATTAGGCTACT	TGTTTCCACAAGAACTGA	TGTTTCCACAATAACTGA
Oke_U1022-139	D	G	A	AACATTAAAACTGTGGTTTTGACCTCTTG	CTGGAACATGAAGCAAA	TGGAACATGGAGCAAA

Appendix Table B-1 – Continued.

Locus Name	Ploidy	FAM	VIC	F Primer Sequence	Reporter 1 Sequence	Reporter 2 Sequence
Oke_U1023-147	D	C	A	TCTTAAAATGGAGAGAGCGATTAATGAAGG	CATCAGGGAAAGCCTACAAA	AGGGAAAGCCGACAAA
Oke_U1024-113	D	G	A	CATGCTGGTGAATTATTGGACAATGT	CCAGAAACAACTTAATTAT	CAGAAACAACTCAATTAT
Oke_U1025-135	D	T	G	GGCTAGGGTTCTATTTGGACCAT	ACTTAGTCTATTTGTAACTTT	ACTTAGTCTATTTTTAACTTT
Oke_u200-385	D	T	G	CCCATAATTTTGCAACCCTAGTCACA	CATTATCTCCCTGAATGTA	CATTATCTCCATGAATGTA
Oke_U2006-109	D	T	G	CCAACACCACTTTCCATTAATAAGCA	AAACAAAGGCAAAGTC	AAAACAAAGGAAAAGTC
Oke_U2007-190	D	G	C	ACAGGCTGTGATGAGTTAACAATGTAAA	CTAAAAGCTGAGAATAAAT	AAAGCTGACAATAAAT
Oke_U2011-107	D	T	G	CCGTTTCTGTCAGACTCTGGTAAA	TTCTGTGAGAGATTTAG	TTTCTGTGAGATATTTAG
Oke_U2015-151	D	T	C	GCATTTTATCCTCAAACTTTTCAACTGACA	AATTGATCACGATCATTC	ATTGATCACAATCATTC
Oke_U2025-86	D	A	G	AAATCCCCATGGAGAAACACAATGA	ACTTTTTTGTCGTTTTTTT	ACTTTTTTGTCATTTTTTT
Oke_U2029-79	D	T	C	GGTTTGATTTCGTCGCGATTTGA	AGGTGTACTGAAGAGAC	AGGTGTACTAAAGAGAC
Oke_U2031-37	D	T	A	CACACTTTCAATCAAATGTTGTGCAG	CATTCACACTGATCTGC	TTCACACAGATCTGC
Oke_U2032-74	D	A	G	GCTATTCCAATGTAAATCCTGTACTGTGT	CAATAAAGTGCTAGGTGTCC	CAATAAAGTGCTAAGTGTCC
Oke_U2034-55	D	T	C	GGGAAGAAAAGCCTACCATAAACAG	ATGTCAAATCACGCTGATG	ATGTCAAATCACACTGATG
Oke_U2035-54	D	A	G	CGCCAATAACGCTCCAACAAC	CACCAATAACGTCCTAATC	CACCAATAACATCCTAATC
Oke_U2037-76	D	G	C	CATATCAGGTGTGTCTCAACAGTCT	TCGAGTCTGGAGTCTTGA	CGAGTCTGGACTCTTGA
Oke_U2041-84	D	T	G	CCAGACCATGTGCTTGTTTGTCATA	CAGATCCGGTGTATGC	ACAGATCCTGTGTATGC
Oke_U2043-51	D	A	G	CACAAACCTACTACAGACAGCAGTT	TCTGGAGGCGTATTGG	CTGGAGGCATATTGG
Oke_U2048-91	D	C	A	AGTTGGGTCTTAAAGATGATCATTTGCT	CAGCCTCATAAGATGTTTA	CAGCCTCATAAGCTGTTTA
Oke_U2050-101	D	T	C	CTCTGAGTGTCACAATCACATATCGT	AATTGATCTACAGCTGCACG	AATTGATCTACAACTGCACG
Oke_U2053-60	D	T	C	TCTGCTTTTGTCGTCTCACCAA	CACACATATGAGATGCC	CACACATATAAGATGCC
Oke_U2054-58	D	T	C	CGTCTCATTCAGCTCTTTGATGTC	ATGCCCAATTACGTCAGCA	TGCCCAATTACATCAGCA
Oke_U2056-90	D	T	G	CCATCACGTCACCATTACACTGT	CGAAGTGATGAAGGTGACAA	CGAAGTGATGAATGTGACAA
Oke_U2057-80	D	G	A	GCAGTTGTCATGGCAGTAAGG	CACGTTTTCTCTTTTCTC	ACGTTTTCTCCTTTCTC
Oke_U212-87	D	A	C	TTGATTCATACTCAAGGTGAGCAGATT	CTTGTGACATTCCTCTCT	CTTGTGACATTACTCTCT
Oke_u217-172	D	C	T	GGATGGAAGAAGTTAGTTGTGTCAGA	CACTCTTACAAAAACA	CACTCTTACGAAAACA
Oke_U302-195	D	A	C	GACCCTCAGCTATTTTAAGAACCTCAA	TTGTCAAAGGAATCATTT	TGTCAAAGGAATAATTT
Oke_U502-241	D	A	G	ATGATCATTACACAGATGCACCTTGT	CCACTCTCCGTTTTAT	CCACTCTCCATTTTAT
Oke_U504-228	D	G	A	CTTAACTCAGTCACACCAACTCACT	TGGCTCAAACTTG	TTGGCTCGAACTTG
Oke_U506-110	D	T	C	CGTGGTTGGTTTCATTGACTCTCA	TTGTAAGTTGTGGCTAAAA	TTGTAAGTTGTGACTAAAA
Oke_U507-286	D	G	T	TGGTCATAGCTTGCACTGTACAAA	CTGCTGTTCATAAAAGTA	CTGCTGTTCATACAAGTA
Oke_U509-219	D	T	C	GCACCCCACCTGGCTT	CCTCTCTGCAGGGCT	CCCTCTCTACAGGGCT

Appendix Table B-2. Chum salmon populations in the ADF&G single nucleotide polymorphism baseline grouped by six regional reporting groups (from Appendix B in Barry et al. 2022). Kotzebue Sound populations are pooled with the W Alaska reporting group in this table.

Population	Reporting Group	Samples	Population	Reporting Group	Samples
Abashiri River	SE Asia	80	Pymta	NE Asia	147
Chitose River - early	SE Asia	80	Tauy	NE Asia	41
Gakko River – early	SE Asia	78	Tym River	NE Asia	53
Kushiro River	SE Asia	79	Udarnitza River	NE Asia	44
Namdae River	SE Asia	90	Vorovskaya	NE Asia	101
Nishibetsu River	SE Asia	79	Agiapuk River	W Alaska	94
Sasanai River	SE Asia	77	Alagnak River	W Alaska	92
Shari River	SE Asia	75	American River	W Alaska	86
Shinzunai River	SE Asia	78	West Fork Andreafsky River	W Alaska	85
Teshio River	SE Asia	80	Andreafsky River - East Fork weir	W Alaska	94
Tokachi River	SE Asia	78	Aniak River	W Alaska	92
Tokoro River	SE Asia	69	Yellow River – Anvik	W Alaska	80
Tokushibetsu River	SE Asia	80	Otter Creek - Anvik	W Alaska	156
Yurappu River - early	SE Asia	80	Big River	W Alaska	94
Yurappu River - late	SE Asia	75	Black River	W Alaska	93
Amur River – summer run	NE Asia	60	Big Creek - Naknek River	W Alaska	69
Bistraya River	NE Asia	66	Chulinak	W Alaska	92
Bolshaya River	NE Asia	93	Clear Creek	W Alaska	94
Hairusova River	NE Asia	85	Eldorado River	W Alaska	89
Kamchatka River	NE Asia	49	Fish River	W Alaska	92
Kanchalan	NE Asia	77	George River	W Alaska	95
Kol River	NE Asia	123	Gisasa River	W Alaska	95
Magadan	NE Asia	77	Goodnews River	W Alaska	137
Naiba	NE Asia	98	Henshaw Creek - early	W Alaska	94
Oklan River	NE Asia	75	Holokuk River	W Alaska	103
Ola River - Hatchery	NE Asia	78	Huslia River, Koyukuk - Set B	W Alaska	95
Ossora	NE Asia	87	Inmachuk River	W Alaska	91
Ozerki Hatchery	NE Asia	93	Iowithla River	W Alaska	95
Palana River	NE Asia	90	Kaltag River	W Alaska	92
Paratunka River	NE Asia	94	Kanektok River weir	W Alaska	94
Penzhina	NE Asia	43	Kasigluk River	W Alaska	55

Appendix Table B-2 – Continued.

Population	Reporting Group	Samples	Population	Reporting Group	Samples
Kelly Lake - Noatak River	W Alaska	95	Stony River	W Alaska	150
Kobuk River - at Kiana	W Alaska	95	Stuyahok River	W Alaska	86
Kisaralik River - (Set F)	W Alaska	93	Sunshine Creek	W Alaska	47
Klutuspak Creek	W Alaska	70	Takotna River - 2 mile above Takotna Village	W Alaska	94
Kobuk - Salmon River (Mile 4)	W Alaska	99	Tatlawiksuk River weir	W Alaska	95
Kogrukluk River weir	W Alaska	95	Togiak River	W Alaska	175
Kokwok River	W Alaska	131	Tozitna River	W Alaska	92
Koyuk River	W Alaska	43	Tubutulik River	W Alaska	93
Kwethluk River	W Alaska	143	Tuluksak River Weir	W Alaska	92
Kwiniuk River	W Alaska	94	Unalakleet	W Alaska	188
Mekoryuk River	W Alaska	104	Ungalik River	W Alaska	144
Melozitna River	W Alaska	91	Wandering Creek - tributary of Dog Salmon River	W Alaska	50
Mulchatna River - Upper Nushagak River	W Alaska	91	Whale Mountain Creek, (King Salmon River, Egegik Bay)	W Alaska	189
Necons River	W Alaska	95	Windy Fork Kuskokwim	W Alaska	93
Niukluk River	W Alaska	93	Innoko River (Yukon A)	W Alaska	85
Noatak River - above hatchery	W Alaska	92	American River	SW Alaska	95
Nome River	W Alaska	94	Foster Creek - Balboa Bay	SW Alaska	182
Nulato River	W Alaska	189	Dog Bay	SW Alaska	95
Nunsatuk River - (Set A)	W Alaska	92	Kizhuyak River	SW Alaska	174
Upper Nushagak	W Alaska	97	Peterson Lagoon	SW Alaska	181
Osviak River	W Alaska	88	Uganik River	SW Alaska	175
Pikmiktalik River	W Alaska	95	Alligator Hole	SW Alaska	183
Pilgrim River	W Alaska	75	Main Creek - Amber Bay	SW Alaska	85
Pumice Creek	W Alaska	95	Barling Bay Creek	SW Alaska	92
Salmon River	W Alaska	95	Belkovski River	SW Alaska	87
Selby Slough	W Alaska	90	Big River (Hallo Bay)	SW Alaska	95
South Fork Koyukuk River - Early	W Alaska	90	Big Sukhoi	SW Alaska	189
South Fork Kuskokwim - fall	W Alaska	95	Canoe Bay	SW Alaska	186
Shaktoolik River	W Alaska	94	Chichagof Bay	SW Alaska	180
Snake River	W Alaska	90	Chiginagak Bay River	SW Alaska	159
Solomon River	W Alaska	62	Coal Valley	SW Alaska	94

Appendix Table B-2 – Continued.

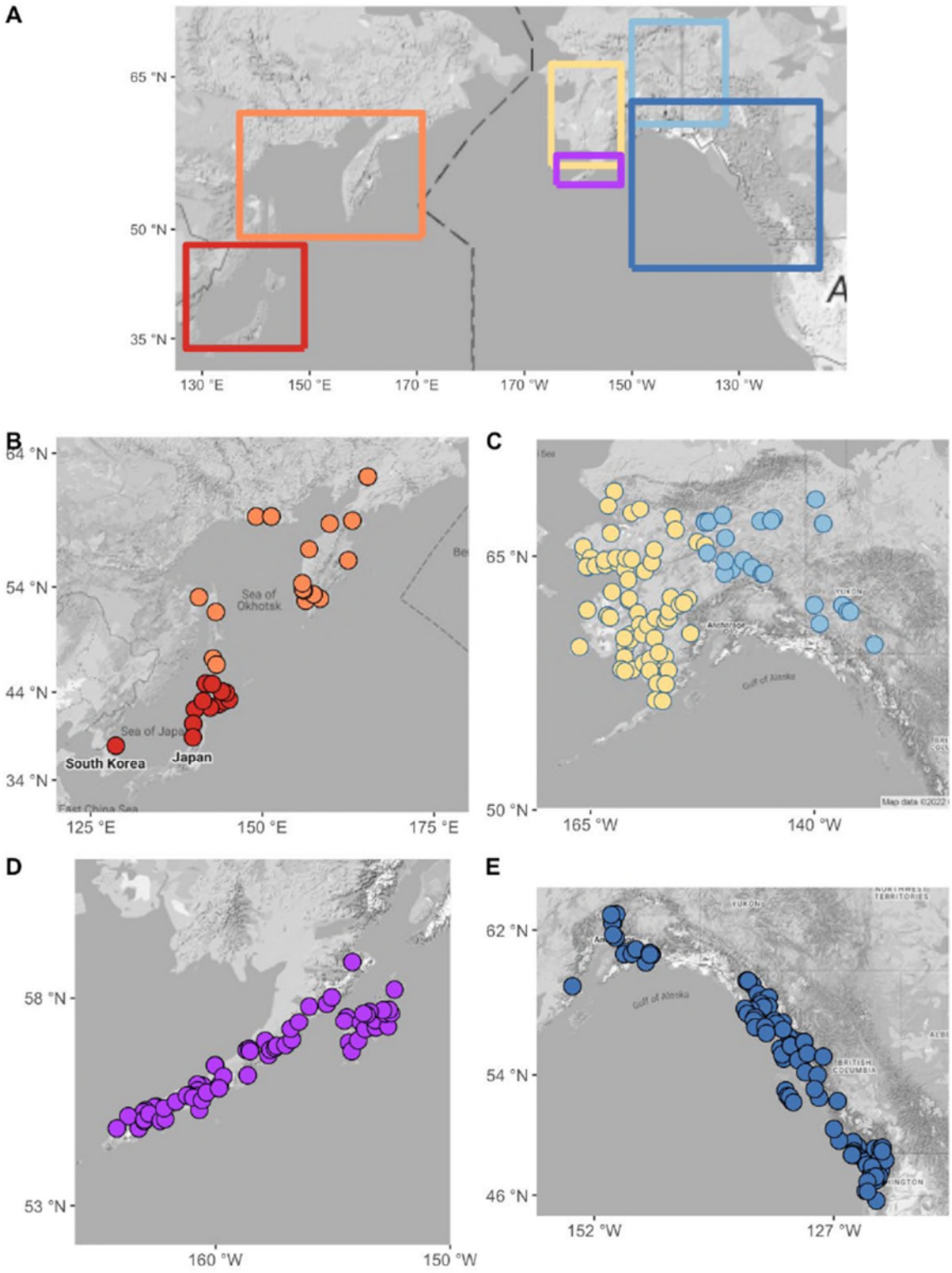
Population	Reporting Group	Samples	Population	Reporting Group	Samples
Coleman Creek	SW Alaska	95	Russell Creek	SW Alaska	185
Coxcomb Creek	SW Alaska	89	Russian River	SW Alaska	185
Deadman River	SW Alaska	95	Sandy Cove	SW Alaska	186
Deer Valley	SW Alaska	91	Sitkinak Island	SW Alaska	93
Delta Creek (Cold Bay)	SW Alaska	95	Spiridon River - Upper	SW Alaska	89
Dry Bay River	SW Alaska	71	St. Catherine Cove	SW Alaska	171
Eagle Harbor	SW Alaska	94	Big River - Stepovak Bay	SW Alaska	143
Frosty Creek	SW Alaska	190	Stepovak River	SW Alaska	94
Gull Cape Creek	SW Alaska	186	Sturgeon River	SW Alaska	109
Three Hills River	SW Alaska	49	Traders Cove	SW Alaska	76
Ivanof River	SW Alaska	181	Volcano Bay (Cold Bay)	SW Alaska	95
Joshua Green	SW Alaska	92	Bear Bay Creek	SW Alaska	187
Karluk Lagoon	SW Alaska	83	North Fork Creek, Aniakchak River	SW Alaska	94
Kialagvik Creek (Wide Bay)	SW Alaska	177	Alagogshak River	SW Alaska	94
Kitoi Hatchery	SW Alaska	194	Portage Creek	SW Alaska	190
Lawrence Valley Creek	SW Alaska	190	North Fork Creek, Kujulik Bay	SW Alaska	164
Little John Lagoon	SW Alaska	172	Wiggly Creek - Cinder	SW Alaska	177
Meshik River	SW Alaska	78	West Kiliuda Creek	SW Alaska	87
Braided Creek (Meshik River)	SW Alaska	94	Zachary Bay	SW Alaska	76
Moffet Creek	SW Alaska	95	Zachar River	SW Alaska	66
Nakililock River	SW Alaska	95	17 Mile Slough (Nenana) - fall run	Up/Mid Yukon	90
North of Cape Seniavin	SW Alaska	96	Big Creek - Canadian Mainstem (Yukon)	Up/Mid Yukon	100
Northeast Creek	SW Alaska	94	Black River	Up/Mid Yukon	95
Sapsuk River, Nelson Lagoon	SW Alaska	144	Bluff Cabin	Up/Mid Yukon	99
Ocean Bay	SW Alaska	78	Big Salt River	Up/Mid Yukon	69
Pass Creek - Wide Bay	SW Alaska	94	Chandalar River	Up/Mid Yukon	92
Plenty Bear Creek (Meshik River)	SW Alaska	138	Chena River	Up/Mid Yukon	77
NE Portage - Alitak	SW Alaska	94	Delta River - Fairbanks	Up/Mid Yukon	149
Right Hand Moller Bay	SW Alaska	94	Donjek River	Up/Mid Yukon	60
Rough Creek	SW Alaska	77	Fishing Branch	Up/Mid Yukon	90
Ruby's Lagoon (Cold Bay)	SW Alaska	92	Henshaw Creek - late	Up/Mid Yukon	60

Appendix Table B-2 – Continued.

Population	Reporting Group	Samples	Population	Reporting Group	Samples
Henshaw Creek - late	Up/Mid Yukon	60	Dosewallips River - summer run	EGOA/PNW	86
Jim River	Up/Mid Yukon	146	Dry Bay Creek	EGOA/PNW	94
Kantishna River	Up/Mid Yukon	94	Ecstall	EGOA/PNW	50
Kluane River	Up/Mid Yukon	114	Elwha River	EGOA/PNW	93
Minto Slough	Up/Mid Yukon	91	Fish Creek - early	EGOA/PNW	131
Old Crow - Porcupine River	Up/Mid Yukon	92	DIPAC Hatchery	EGOA/PNW	281
Pelly River	Up/Mid Yukon	84	Fish Creek - late	EGOA/PNW	49
Salcha River	Up/Mid Yukon	83	Ford Arm Lake - fall	EGOA/PNW	95
South Fork Koyukuk River - Late	Up/Mid Yukon	92	Goldstream River	EGOA/PNW	95
Sheenjek River	Up/Mid Yukon	93	Grays River - fall run	EGOA/PNW	93
Tanana River Mainstem	Up/Mid Yukon	95	Hamma Hamma River - summer	EGOA/PNW	108
Tatchun Creek	Up/Mid Yukon	92	Hamma Hamma River	EGOA/PNW	94
Teslin River	Up/Mid Yukon	92	Harding River	EGOA/PNW	45
Toklat River - Geiger Ck. (Set A) -Mainstream	Up/Mid Yukon	95	Herman Creek - Chilkat River	EGOA/PNW	94
Keta Creek	EGOA/PNW	95	Hidden Falls Hatchery	EGOA/PNW	95
Admiralty Creek	EGOA/PNW	64	Hidden Inlet	EGOA/PNW	82
Aloutte River	EGOA/PNW	95	I-205 Seeps - fall run	EGOA/PNW	72
Bag Harbor	EGOA/PNW	49	Inch Creek	EGOA/PNW	181
Beartrap Creek	EGOA/PNW	582	Jimmy Creek - summer run	EGOA/PNW	92
Big Qualicum River	EGOA/PNW	72	Johns Creek - summer run	EGOA/PNW	92
Big Mission Creek Fall Run	EGOA/PNW	55	Kalama Creek - winter run	EGOA/PNW	54
Carmen Lake	EGOA/PNW	67	Karta River	EGOA/PNW	56
Carroll River	EGOA/PNW	85	Kitasoo Creek	EGOA/PNW	169
Chilkat - mainstem	EGOA/PNW	76	Kitimat River	EGOA/PNW	104
Chunilna River	EGOA/PNW	83	Kitwanga River	EGOA/PNW	74
Constantine Creek	EGOA/PNW	594	Klahini River	EGOA/PNW	50
Conuma River	EGOA/PNW	96	Klehini River - Chilkat River	EGOA/PNW	92
Dewatto River - fall chum	EGOA/PNW	74	Lagoon Creek - fall run	EGOA/PNW	166
Diru Creek - Tribal Hatchery	EGOA/PNW	45	Little Creek - fall run	EGOA/PNW	92
Disappearance Creek - fall run	EGOA/PNW	162	Lilliwaup River - summer run	EGOA/PNW	45
Disappearance Creek	EGOA/PNW	143	Lilliwaup River - fall run	EGOA/PNW	92

Appendix Table B-2 – Continued.

Population	Reporting Group	Samples	Population	Reporting Group	Samples
Long Bay	EGOA/PNW	159	Sarita River	EGOA/PNW	63
Little Qualicum River	EGOA/PNW	98	Satsop River	EGOA/PNW	95
Lower Skagit River - fall run	EGOA/PNW	91	Sawmill Creek - Berners Bay	EGOA/PNW	95
Little Susitna River weir	EGOA/PNW	95	Sedgewick	EGOA/PNW	50
McNeil River Lagoon	EGOA/PNW	108	Sherwood Creek - fall run	EGOA/PNW	87
Medvejie Hatchery	EGOA/PNW	119	Sherwood Creek - summer run	EGOA/PNW	88
Mill Creek - fall run	EGOA/PNW	80	Sisters Lake	EGOA/PNW	86
Nahmint River	EGOA/PNW	95	Siwash Creek	EGOA/PNW	362
Nakat Inlet - summer	EGOA/PNW	95	Skamokawa Creek - fall run	EGOA/PNW	76
Nakwasina River	EGOA/PNW	93	Skykomish River - fall run	EGOA/PNW	87
North Arm Creek	EGOA/PNW	97	Snootli Creek	EGOA/PNW	190
North Creek - fall run	EGOA/PNW	93	Snoqualmie River	EGOA/PNW	84
Neets Bay - fall	EGOA/PNW	95	Sooke River	EGOA/PNW	50
Neets Bay - Summer	EGOA/PNW	145	Spink Creek	EGOA/PNW	44
Nimpkish River	EGOA/PNW	187	Stagoo	EGOA/PNW	49
Nisqually River Hatchery	EGOA/PNW	94	Sugsaw River	EGOA/PNW	60
Nitinat River	EGOA/PNW	113	Surprise	EGOA/PNW	50
Norrish Creek	EGOA/PNW	91	Susitna River (Slough 11)	EGOA/PNW	94
Pallant Creek	EGOA/PNW	209	Swan Cove Creek	EGOA/PNW	88
Prospect Creek	EGOA/PNW	89	Taku River - fall	EGOA/PNW	93
Puntledge River	EGOA/PNW	99	Talkeetna River	EGOA/PNW	50
Olsen Creek (PWS) - Set A	EGOA/PNW	94	Traitors Cove Creek	EGOA/PNW	91
Quilcene - summer run	EGOA/PNW	63	Union River - summer	EGOA/PNW	109
Ralph's Creek	EGOA/PNW	95	Upper Sauk River - fall run	EGOA/PNW	86
Saginaw Creek	EGOA/PNW	41	West Arm Creek	EGOA/PNW	186
Salmon Creek - summer run	EGOA/PNW	82	West Crawfish	EGOA/PNW	92
Salmon River	EGOA/PNW	47	Weaver Creek	EGOA/PNW	96
Saltery Bay	EGOA/PNW	48	Wells River	EGOA/PNW	597
Sample Creek	EGOA/PNW	74	Wells Bridge	EGOA/PNW	46
Sanborn Creek	EGOA/PNW	94	Wally Noerenberg Hatchery	EGOA/PNW	385
Saook Bay	EGOA/PNW	94	Willow Creek	EGOA/PNW	89



Appendix Figure B-1. Six regional groups of baseline chum salmon populations used in this report (circles represent individual populations in the baseline. Panels include: (A) range-wide distribution of the six regions; (B) SE Asia (red) and NE Asia (orange); (C) W Alaska (yellow) and Up/Mid Yukon (light blue); (D) SW Alaska (purple); and (E) EGOA/PNW (dark blue). Kotzebue Sound populations are pooled with the W Alaska reporting group. A complete list of the populations is provided in Appendix Table B-2.

APPENDIX C – STOCK COMPOSITION ESTIMATES

Appendix Table C-1. Stock composition estimates, by statistical week, for chum salmon bycatch sampled by BBSRI port samplers in Dutch Harbor and Akutan during the 2024 shoreside Bering Sea and Aleutian Island (BSAI) B-season pollock trawl fishery.

Stat. Wk.	Region	Est. Number	Lower 95% CL	Upper 95% CL	Mean Prop.	2.5% CL	97.5% CL	P = 0	SF
24	Kotzebue Sound	23	7	77	0.026	0.008	0.088	0.00	1.01
24	W Alaska	53	4	107	0.061	0.004	0.122	0.02	1.00
24	E GOA/PNW	614	550	674	0.698	0.625	0.767	0.00	1.00
24	NE Asia	32	9	64	0.036	0.010	0.073	0.00	1.00
24	SE Asia	81	46	124	0.092	0.053	0.141	0.00	1.00
24	SW Alaska	29	6	63	0.033	0.007	0.071	0.00	1.00
24	Up/Mid Yukon	47	19	86	0.054	0.022	0.098	0.00	1.00
25	Kotzebue Sound	74	23	153	0.048	0.015	0.099	0.00	1.00
25	W Alaska	84	18	175	0.055	0.012	0.114	0.00	1.00
25	E GOA/PNW	666	527	806	0.433	0.342	0.524	0.00	1.00
25	NE Asia	231	136	344	0.150	0.089	0.224	0.00	1.00
25	SE Asia	344	230	473	0.224	0.149	0.307	0.00	1.00
25	SW Alaska	5	0	43	0.003	0.000	0.028	0.57	1.00
25	Up/Mid Yukon	135	63	231	0.088	0.041	0.150	0.00	1.00
26	Kotzebue Sound	34	5	86	0.015	0.002	0.039	0.00	1.00
26	W Alaska	170	91	266	0.077	0.041	0.121	0.00	1.00
26	E GOA/PNW	634	524	749	0.287	0.237	0.339	0.00	1.00
26	NE Asia	471	370	582	0.213	0.168	0.264	0.00	1.00
26	SE Asia	682	570	800	0.309	0.258	0.362	0.00	1.00
26	SW Alaska	86	38	149	0.039	0.017	0.067	0.00	1.00
26	Up/Mid Yukon	132	64	209	0.060	0.029	0.095	0.00	1.00
27	Kotzebue Sound	16	0	125	0.004	0.000	0.030	0.55	1.00
27	W Alaska	335	164	527	0.080	0.039	0.126	0.00	1.00
27	E GOA/PNW	1,277	1,040	1,528	0.306	0.249	0.367	0.00	1.00
27	NE Asia	877	670	1,104	0.210	0.161	0.265	0.00	1.00
27	SE Asia	1,378	1,139	1,627	0.331	0.273	0.390	0.00	1.00
27	SW Alaska	105	18	226	0.025	0.004	0.054	0.01	1.00
27	Up/Mid Yukon	180	61	346	0.043	0.015	0.083	0.00	1.00
28	Kotzebue Sound	0	0	19	0.000	0.000	0.022	0.79	1.00
28	W Alaska	52	17	100	0.060	0.020	0.116	0.00	1.00
28	E GOA/PNW	277	205	353	0.320	0.237	0.408	0.00	1.00
28	NE Asia	256	185	334	0.296	0.213	0.386	0.00	1.00
28	SE Asia	233	166	308	0.269	0.192	0.356	0.00	1.00
28	SW Alaska	23	3	57	0.026	0.003	0.066	0.00	1.00
28	Up/Mid Yukon	24	4	58	0.028	0.005	0.068	0.00	1.00

Appendix Table C-1 – Continued.

Stat. Wk.	Region	Est. Number	Lower 95% CL	Upper 95% CL	Mean Prop.	2.5% CL	97.5% CL	P = 0	SF
29	Kotzebue Sound	0	0	16	0.000	0.000	0.015	0.77	1.00
29	W Alaska	86	43	140	0.078	0.039	0.127	0.00	1.00
29	E GOA/PNW	527	446	610	0.478	0.404	0.553	0.00	1.00
29	NE Asia	226	161	298	0.205	0.146	0.270	0.00	1.00
29	SE Asia	212	149	284	0.192	0.135	0.257	0.00	1.00
29	SW Alaska	0	0	13	0.000	0.000	0.012	0.77	1.00
29	Up/Mid Yukon	52	21	94	0.047	0.019	0.086	0.00	1.00
30	Kotzebue Sound	0	0	5	0.000	0.000	0.022	0.76	1.00
30	W Alaska	13	6	23	0.060	0.025	0.103	0.00	1.00
30	E GOA/PNW	38	28	50	0.170	0.124	0.223	0.00	1.00
30	NE Asia	87	72	102	0.388	0.323	0.456	0.00	1.00
30	SE Asia	74	60	88	0.330	0.267	0.394	0.00	1.00
30	SW Alaska	1	0	5	0.004	0.000	0.021	0.31	1.00
30	Up/Mid Yukon	11	5	18	0.047	0.021	0.082	0.00	1.00
31	Kotzebue Sound	0	0	3	0.000	0.000	0.013	0.78	1.00
31	W Alaska	11	5	19	0.051	0.022	0.088	0.00	1.00
31	E GOA/PNW	48	36	60	0.220	0.167	0.279	0.00	1.00
31	NE Asia	77	63	92	0.358	0.292	0.427	0.00	1.00
31	SE Asia	72	58	86	0.334	0.270	0.400	0.00	1.00
31	SW Alaska	2	0	8	0.010	0.000	0.037	0.17	1.00
31	Up/Mid Yukon	6	2	12	0.027	0.008	0.056	0.00	1.00
32	Kotzebue Sound	21	3	81	0.016	0.002	0.060	0.00	1.00
32	W Alaska	65	3	116	0.049	0.002	0.086	0.02	1.00
32	E GOA/PNW	553	479	627	0.410	0.355	0.465	0.00	1.00
32	NE Asia	446	376	518	0.330	0.279	0.384	0.00	1.00
32	SE Asia	223	170	281	0.165	0.126	0.208	0.00	1.00
32	SW Alaska	18	0	51	0.014	0.000	0.038	0.08	1.00
32	Up/Mid Yukon	23	7	48	0.017	0.006	0.035	0.00	1.00
33	Kotzebue Sound	9	0	65	0.003	0.000	0.020	0.43	1.00
33	W Alaska	321	212	445	0.100	0.066	0.138	0.00	1.00
33	E GOA/PNW	862	719	1,011	0.267	0.223	0.313	0.00	1.00
33	NE Asia	1,568	1,397	1,739	0.486	0.433	0.539	0.00	1.00
33	SE Asia	324	226	435	0.100	0.070	0.135	0.00	1.00
33	SW Alaska	0	0	33	0.000	0.000	0.010	0.75	1.00
33	Up/Mid Yukon	144	69	235	0.045	0.022	0.073	0.00	1.00

Appendix Table C-1 – Continued.

Stat. Wk.	Region	Est. Number	Lower 95% CL	Upper 95% CL	Mean Prop.	2.5% CL	97.5% CL	P = 0	SF
34	Kotzebue Sound	13	0	47	0.017	0.000	0.061	0.27	1.00
34	W Alaska	69	27	121	0.091	0.036	0.159	0.00	1.00
34	E GOA/PNW	290	232	351	0.381	0.304	0.462	0.00	1.00
34	NE Asia	220	163	281	0.289	0.214	0.369	0.00	1.00
34	SE Asia	98	58	146	0.129	0.076	0.192	0.00	1.00
34	SW Alaska	7	0	35	0.009	0.000	0.046	0.34	1.00
34	Up/Mid Yukon	64	31	106	0.085	0.041	0.139	0.00	1.00
35	Kotzebue Sound	0	0	10	0.000	0.000	0.022	0.80	1.00
35	W Alaska	71	35	113	0.150	0.074	0.237	0.00	1.00
35	E GOA/PNW	177	131	225	0.372	0.275	0.474	0.00	1.00
35	NE Asia	136	94	183	0.287	0.197	0.385	0.00	1.00
35	SE Asia	74	42	113	0.156	0.088	0.239	0.00	1.00
35	SW Alaska	11	0	37	0.024	0.000	0.077	0.07	1.00
35	Up/Mid Yukon	5	0	28	0.011	0.000	0.059	0.34	1.00
36	Kotzebue Sound	5	0	52	0.001	0.000	0.015	0.65	1.00
36	W Alaska	219	114	342	0.061	0.032	0.096	0.00	1.00
36	E GOA/PNW	1,278	1,101	1,459	0.358	0.308	0.409	0.00	1.00
36	NE Asia	1,384	1,201	1,572	0.388	0.337	0.441	0.00	1.00
36	SE Asia	374	265	500	0.105	0.074	0.140	0.00	1.00
36	SW Alaska	33	0	93	0.009	0.000	0.026	0.05	1.00
36	Up/Mid Yukon	276	179	391	0.077	0.050	0.110	0.00	1.00
37	Kotzebue Sound	0	0	9	0.000	0.000	0.016	0.80	1.00
37	W Alaska	76	39	120	0.141	0.073	0.222	0.00	1.00
37	E GOA/PNW	151	102	204	0.280	0.190	0.379	0.00	1.00
37	NE Asia	198	146	253	0.368	0.271	0.470	0.00	1.00
37	SE Asia	74	39	116	0.137	0.073	0.215	0.00	1.00
37	SW Alaska	35	7	75	0.064	0.014	0.140	0.00	1.00
37	Up/Mid Yukon	5	0	31	0.010	0.000	0.058	0.40	1.00
38-40	Kotzebue Sound	5	0	23	0.010	0.000	0.046	0.27	1.00
38-40	W Alaska	48	21	83	0.095	0.041	0.163	0.00	1.00
38-40	E GOA/PNW	124	82	173	0.245	0.162	0.341	0.00	1.00
38-40	NE Asia	221	171	272	0.435	0.337	0.537	0.00	1.00
38-40	SE Asia	63	32	101	0.123	0.062	0.199	0.00	1.00
38-40	SW Alaska	42	11	78	0.083	0.021	0.155	0.00	1.00
38-40	Up/Mid Yukon	5	0	19	0.009	0.000	0.037	0.18	1.00
All*	Kotzebue Sound	200	38	771	0.009				
All	W Alaska	1,673	799	2,697	0.077				
All	E GOA/PNW	7,516	6,202	8,880	0.347				
All	NE Asia	6,430	5,214	7,738	0.297				
All	SE Asia	4,306	3,250	5,482	0.199				
All	SW Alaska	397	83	966	0.018				
All	Up/Mid Yukon	1,109	525	1,912	0.051				

* Composites estimate based on the weighted average stock compositions across statistical weeks.

11 PHOTOS

Photo 1. Alyeska Seafoods Inc. processing plant in Dutch Harbor.

Photo 2. Aerial view of the Northern Victor, a floating processing plant in Dutch Harbor.

Photo 3. F/V *Westward 1* at Westward Seafoods in Dutch Harbor.

Photo 4. F/V *Northern Patriot* at Trident Seafoods in Akutan.

Photo 5. Sampling a chum salmon previously cut open and sampled by NOAA Fishery Observers.

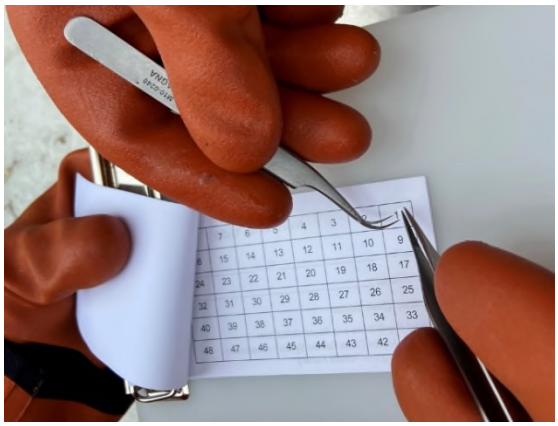


Photo 6. Chum salmon scale sample being placed on a gummed scale card for preservation.

Photo 7. Chum salmon with pectoral fin tissue removed to be used for genetic analysis.

Photo 8. Chum salmon fin tissue samples stapled to a Whatman card for preservation.

Photo 9. Incubation phase during DNA extraction, BBSRI genetics laboratory in Dutch Harbor.

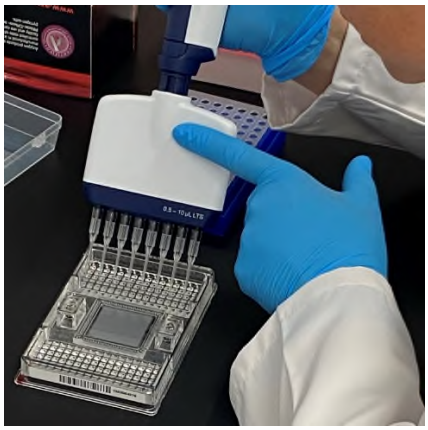


Photo 10. Sample mix being loaded into an IFC (integrated fluidic circuit) using an 8-channel pipette.

Photo 11. Loading an IFC (integrated fluidic circuit) into the BioMark X9 PCR System for genotyping.