Klukshu Sockeye 2016 Field Studies

Summary Report

5 September 2017

Submitted to: **Champagne & Aishihik First Nations**

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ACKNOWLEDGEMENTS

Dedicated to the memory of Kimberly Chambers, who was a crucial force in making these projects happen.

Many individuals and organizations contributed to the successful implementation of the two projects documented in this report. We are very grateful for their contributions. The projects could not have achieved this much without their help.

Champagne and Aishihik First Nations

Linaya Workman coordinated and guided these projects from early scoping discussions to final reporting. Kimberly Chambers, Dixie Smeeton, Michael Jim, and Lawrence Joe took care of project administration, assisted with field work, and organized support for the field crew.

Fisheries and Oceans Canada

Bill Waugh, Ian Boyce, and Sean Stark of DFO Whitehorse contributed to project planning, loaned equipment to our projects (nets and traps for juvenile sampling, radio telemetry equipment), provided accommodation at the weir site, and helped coordinate sampling at the weir (tags, DNA) with regular weir operation (scales, measurements). DFO also shared data including temperatures and water levels at Klukshu weir and scale reading results from the DFO Sclerochronology Lab in Nanaimo.

John Candy and Janine Supernault of the DFO Molecular Genetics Lab in Nanaimo provided practical and analytical support from project inception to final analysis, covering topics as diverse as sample sizes, sample packaging and shipping, software for genotype aanalyses, and interpretation of results. The Genetics Lab also shared baseline data for Alsek Sockeye, and Janine Supernault contributed an analysis of family structure.

Alaska Department of Fish and Game

Steve Heinl of ADFG Ketchikan contributed to project planning and coordinated feedback from ADFG experts on different project components. Sara Gilk-Baumer of ADFG Anchorage provided extensive advice on tissue sampling and packaging for the DNA analyses.

SOLV Consulting

Tatiana Tunon assisted with project design and logistics, and contributed extensively to the final report to improve communication of the work, with a focus on report structure, readability, and plot layouts.

Executive Summary

Two linked projects were implemented in 2016 to investigate the population structure of Klukshu Sockeye. Adult Sockeye were sampled on the spawning grounds and at Klukshu weir, where radio tags were applied and tissue samples for DNA analysis were collected. Sockeye fry and smolts were sampled for DNA at various sites throughout the watershed using different gears. Adult and juvenile Sockeye were successfully sampled at sites identified based on traditional and local knowledge, earlier studies, and observations during the 2016 project.

The total run size of Sockeye past Klukshu weir in 2016 was 7,584. 820 adults (11%) were sampled at the weir for sex, length, and scales as part of DFO's regular weir operation. For most of these we obtained DNA samples and valid genotype readings. We tagged a subset of the weir sample (165 tags), and a final destination could be determined for most of the tags. Weekly DNA samples and tags were spread to cover the full migration period, but with a proportionally larger sampling effort during the early migration before August 15th.

Our results clearly point to two distinct populations of Sockeye in the Klukshu, because phylogenetic tree fits are very robust across sensitivity analyses and assignment probabilities in genetic stock ID are generally high. When we split our tag movement data based on stock ID or tag fate, clear differences emerge in preferred spawning areas and migration behaviour. Early migrating adults were genetically matched to the river spawners and tag movements predominantly were classified as river fate, while late migrating adults were matched to lake spawners and assigned lake tag fates. Lake spawners moved up the Klukshu mainstem much faster than river spawners.

Sockeye fry were genetically matched to the site where they were caught. Fry from the Klukshu mainstem were matched to the river spawners, while juveniles caught in Klukshu Lake and at the lake outlet were matched to lake spawners. Interestingly, all of the smolts caught at the lake outlet were also matched to lake spawners, indicating that juvenile Klukshu River Sockeye either don't migrate upstream into the lake for rearing, or leave the lake at a different time and weren't caught in any of our smolt sampling.

Based on genetic stock matches, River Sockeye accounted for about 33% of a total run of 7,584, giving approximate abundances of 2,500 River Sockeye and 5,081 Lake Sockeye in 2016. Both populations returned over the full 3 months of weir operation, but the River population had a long, protracted migration pattern while the Lake population had a very pronounced peak migration period of 3 weeks from late August to early September. Overall, roughly half of the River population returned before August 15th, but for the Lake population roughly 90% returned after August 15th.

Weir records and scale readings offered some potential evidence for differences between the two populations in terms of age composition, size distribution, and sex ratio, but the majority of DNA results were for weekly pooled tissue samples, and couldn't be conclusively matched to individual weir records. In addition, observed size differences could simply reflect different stages of maturation.

Based on our results, we recommend that:

(1) the Early/Late terminology used for Klukshu Sockeye since the 1990s be discontinued, and the more accurate labels of *Klukshu River* population and *Klukshu Lake* population should be adopted.

(2) the Transboundary Technical Committee consider the implications of these project results for bilateral management of Alsek Sockeye (e.g. use as indicator stock), and

(3) DFO Science incorporate our results into the next review of conservation units for transboundary Sockeye salmon.

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1. Introduction

1.1. Purpose

Alsek River Sockeye Salmon (*Oncorhynchus nerka*) are a high priority for local, domestic, and international management.In 2015 a Working Group (WG) with representation from the Champagne & Aishihik First Nation (CAFN), Fisheries and Oceans Canada (DFO), and Alaska Department of Fish & Game (ADFG) was formed to review available information, identify crucial information gaps, and develop a shortlist of high-priority research topics.

The WG reviewed the current state of knowledge for Sockeye Salmon in the Alsek-Tatshenshini drainage, identified unresolved questions, established specific research priorities for 2015 to 2020, and compiled an inventory of project ideas.

The WG identified 3 overarching long-term priorities:

(1) better understand population structure of Alsek Sockeye,

(2) better understand differences between Alsek sockeye populations, and

(3) better understand differential harvest effects on Alsek Sockeye populations.

The work presented in this report falls under Priority 1 and is intended to build the foundation for subsequent work under Priorities 2 and 3.

Specific research priorities related to the population structure of Alsek sockeye are to (1) complete the genetic baseline and (2) improve adult and juvenile migration data. The information collected can then be used to finalize the definition of Conservation Units (CUs) under Canada's Wild Salmon Policy (WSP). This is consistent with the objectives developed by the Transboundary Panel (TRP) for their Strategic Salmon Plan (2009), which includes the following high-priority action item: "Continue collaborative TTC effort to identify and fill priority genetic baseline data gaps". Work on genetic baselines for Alsek sockeye has continued since then, and the current baseline inventory covers 26 population groups (labelled stocks in the GSI database).

Among the potential projects related to the population structure of sockeye salmon in the Alsek- Tatshenshini drainage, the WG considered improved information about population structure and status of early and late run populations of Klukshu River Sockeye Salmon (Figure 1) the highest priority. Klukshu River sockeye are an important component of the Alsek Sockeye stock complex:

- CAFN harvest Klukshu Sockeye for Food, Social, and Ceremonial 9FSC) purposes). The early run is most valued for food fisheries, but CAFN have raisedconcerns regarding recent declines in abundance and potential changes in spawning distribution of the early run. CAFN has not been able to harvest the early run in any significant numbers for many years because of conservation concerns, and in several years CAFN even had to altogether close the food fishery, which traditionally targets primarily the early run on the upper Klukshu River close to the lake outlet.
- CAFN, DFO, and ADFG rely on Klukshu as the main indicator of run size for the whole drainage via the GSI-based run estimates (Gazey 2010), and use Klukshu run sizes as the main input for historical run reconstructions (Eggers and Bernard 2011). Klukshu sockeye weir estimates are also used for post-season verification of the CPUE-based in-season harvest management of Alaska's Dry Bay commercial fishery.

Objective 1.3 of the TRP Strategic Plan (2009) is to "continue to fully develop and implement abundance-based management" for 3 stock groups, including Alsek River sockeye. The strategic plan also lists specific actions/projects including:

- *Develop Klukshu-specific Biological Escapement Goals (BEG), with early and late run targets*. Eggers and Bernard (2011) estimated a BEG for total Klukshu sockeye, but did not include separate targets for early and late components in their analysis. Rather, they recommended to continue managing fisheries "so that exploitation occurs as evenly as possible over the entire Alsek sockeye salmon run."
- *Monitor Canadian Wild Salmon Policy conservation units' abundance*. For DFO, finalizing CU delineations is also Action Step 1.1 of WSP implementation.

The population structure of Klukshu sockeye needs to be resolved before these steps can be completed. If distinct populations are confirmed, this will need to be reflected in status assessments and management targets. If, however, the genetic and tagging results indicate a single population, then the current total BEG estimate and CU delineation are adequate.

Differences in timing, spawning locations, and life history between the two runs are not well understood, and previous work is inconclusive. Fillatre (2002) and Petkovich (2000) document differences between early and late components, but Eggers and Bernard (2011) developed biological escapement goals for total Klukshu sockeye, because (a) they considered the evidence for biologically distinct sub-populations insufficient, and (b) catch could not be separated into early and late components. DFO has been using a cut-off date of August 15th to track weir counts for early and late components, but Fillatre (2002) showed that the timing of migration pulses varies substantially between years. Some years show two clear peaks with variable timing and different degrees of overlap (1977, 1991, 1992, 2002, 2006), but years with 3 peaks or 1 peak have also occurred (Figure 6, Appendix L).

If migration timing is closely correlated with spawning location (e.g. early migrating river spawners, later migrating lake spawners), this may be sufficient reason for separate CUs under the WSP. If the river spawners turn out to be river-type sockeye (i.e. age 0.X, do not rear in a lake) then they would automatically fall into a distinct CU based on the definitions used by Holtby and Ciruna (2007).

The WG identified the following shortlist of questions for urgent investigation:

(1) Are there genetic and physiological differences between early and late Klukshu sockeye?

(2) Are there differences in spawning and rearing habitats used by early-migrating vs. late-migrating Klukshu sockeye?

(3) Are early and late Klukshu different enough to warrant 2 separate CUs?

During the planning stage of this project, our working hypothesis by the WG is that there are two distinct populations: (1) Early migrating river-spawners with unknown juvenile rearing behaviour, and (2) Late migrating lake spawners, which are true lake-type sockeye. However, the annual migration timing is strongly influenced by hydrology making it difficult to accurately assign samples collected at the weir (genetic baseline, scales) purely based on the timing curve.

Earlier work on differences was confounded by having to classify the samples into early and late populations first. For example, Fillatre (2002) applied cluster analysis to weir-count patterns and estimated year-specific break-points using a 2-stock mixing model, then compared genetic and physiological differences. Until annual weir counts can be meaningfully separated into population components, status and differences (e.g. age composition) cannot be properly assessed.

1.2. Project Overview

Funding

The WG sketched out a series of potential projects related to the population structure of Sockeye Salmon in the Klukshu watershed, then selected 3 linked projects for submission to the Northern Endowment Fund (NEF) of the Pacific Salmon Commission (PSC) in September 2015. Two of the project proposals received NEF funding in the spring of 2016, and the field work was conducted from May to October 2016. Appendix A summarizes project costs and in-kind contributions by the participating organizations and individuals.

Objectives – Adult Project

The purpose of the adult project was to improve information regarding the population structure, migration behaviour, and status of early and late run Klukshu River sockeye salmon.

The adult project had 3 components: (1) collect systematic tissue and scale samples at Klukshu weir capturing all observed migration pulses; (2) apply radio tags to a systematic subsample to identify spawning locations of early and late-migrating Klukshu sockeye; (3) collect tissue and scale samples at spawning locations in Klukshu River and Klukshu Lake to establish an unambiguous baseline and cross-check the telemetry observations.

The adult project combined the approaches from several earlier studies to link run timing to spawning location, and allow reclassification of data (genetic, scale, size) based on both criteria simultaneously, then comparing the characteristics of the more homogenous samples (e.g. compare age composition estimates for weir samples matched to different spawning ground samples). Previous studies on the differences between early and late runs

focused on either genetic sampling at Klukshu weir (Fillatre 2002) or radio tagging to track fish from the weir to their spawning locations (Petkovich 2000). Both studies found clear differences between the earlier migrants and later migrants.

Our project built on this earlier work by combining both sampling methods so that each sampled fish can be classified as an early or late migrant as well as river spawner or lake spawner, which in turn can: (1) improve run-timing estimates for the two populations; (2) establish an improved genetic baseline for future identification of early run and late run fish (e.g. in Dry Bay harvest, and in juvenile samples); (3) improve age class estimates for the early and late populations (e.g. to check for differences); (4) document differences in life history and physiology between early run and late run Klukshu sockeye (spawning areas, sex ratio, size).

The main brood year for the 2016 returns (2011) had good abundance of both early and late run (based on visual interpretation of pattern in sockeye weir counts; Appendix L). Note, however, that 2011 likely had a high degree of timing overlap between the early and late populations.

Objectives – Juvenile Project

The purpose of the juvenile project was to improve information regarding the distribution of juveniles from lake spawning and river spawning juvenile sockeye in the Klukshu watershed.

The juvenile project had 3 components: (1) scale and tissue sampling of 1+ smolts at the outlet of Klukshu Lake in May/June; and (2) scale and tissue sampling of fry in May below Klukshu weir at the Klukshu/Tatshenshini confluence; and (3) attempt scale and tissue sampling of recently-emerged fry near confirmed sockeye spawning locations in May.

Our project expanded upon the juvenile sampling described in Fillatre (2002) by covering different locations and a longer time window (i.e. starting in early May).

Field Work

Sampling for sockeye salmon juveniles (fry and smolts) was initiated in early May, 2016. Sampling was conducted, generally, on a weekly basis through early June with an additional sampling event conducted at the end of June/early July. Juvenile Sockeye were sampledat 4 locations, using 1 or 2 gear types selected based on local conditions from 4 alternative gears (beach seine, Wolf-type incline plane trap, Fyke net, Gee-type minnow trap).

Adult sampling at Klukshu weir was coordinated with DFO's regular weir operations running from early July to early October (statistical weeks 28 to 41). The DFO weir crew took morphometric measurements and scales from a sample of passing Sockeye. Our project team collected tissue samples from all the handled Sockeye, and applied radio tags to a subsample of the DFO sample.

Radio tags were tracked with 4 stationary receivers (Figure 1) along the Klukshu River mainstem and 1 helicopter survey.

Spawning sockeye were sampled along the Klukshu River mainstem and in Klukshu Lake between early August and early October, for a total of 11 sampling events covering 5 locations.

Analysis

Our work-up of the data collected in 2016 went through 3 phases:

- Exploratory Data Analysis (EDA) of the biological information (i.e. age composition and sex ratio of adults at weir, size distributions of adult and juvenile sample groups, juvenile length-weight relationships) to establish the context for interpreting the tagging and DNA results.
- Preliminary analysis of tag detections and genotypes results to identify promising lines of inquiry (e.g. checking the properties of DFO's genetic baseline samples for Alsek sockeye, checking sensitivity of tree fits to alternative combinations of our 2016 DNA sample groups).
- Final analysis of radio tag detections and genotype results. Analyses of radio tag data looked at movement patterns, migration speeds, and tag fates. Analyses of DNA samples looked at phylogenetic trees, genetic stock ID, and family structure. Results from the radio tag and genotype analyses were then combined to cross-check the accuracy of tag fates vs. genetic stock ID, and to develop two alternative estimates of weekly run composition. Figure 2 maps out the radio tag and genotype analyses and how they are connected. Figure 3 shows the components of the genetic analyses in more detail.

1.3. Report Overview

This report describes two closely related projects with many inter-connected components, and seeks a balance between clearly documenting the various pieces and assisting the reader with linking the information.

We decided to break the material into fairly self-contained sections with extensive cross-referencing. For example, we have 4 separate methods chapters to document the adult sampling, juvenile sampling, sample processing, and quantitative analyses. Similarly, we have 2 separate results chapters, one for field work and sample processing, and the other for quantitative analyses.

A lot of details that are supplementary to the main objectives of this work are covered in the figure and table captions of the Appendices (e.g. brief commentaries on length-weight relationships for various sample groups of juvenile sockeye, suitability of different gears for sampling juvenile Sockeye at different sites on the Klukshu).

This produces some overlap between sections and replicates some content, but we consider it necessary to make the detailed information easily accessible to different target audiences while keeping the main narrative tractable, and allowing a general reader to browse through various parts without having to read the whole report in sequence.

Our description of methods focuses on the operational side of the field work and quantitative analyses. For example, for the work-up of genetic data we describe the software and settings used, so that readers can replicate the calculations, rather than delving into the theoretical background for alternative approaches.

2. Methods - Sampling Adults

2.1. Sampling at Klukshu Weir

Klukshu Weir

A temporary rigid fish weir has been operated on the lower Klukshu each year since the 1976 (Photo 1), first by the Fisheries and Marine Service of Environment Canada, then by DFO.

The original objective of the weir project was to assess the run size of Chinook, Sockeye, and Coho Salmon entering the Klukshu River, as well as recording age, size, and sex ratio for a subsample of passing fish. The weir also served as a centralized monitoring site to assess fish harvest by CAFN and the growing sport fishery (Elson and Steigenberger 1977).

As the annual weir counts and associated age, sex and size data accumulated, biologically-based spawning escapement goals were generated for Chinook and Sockeye (Clarke and Etherton 2000, McPherson et al. 1998, Eggers and Benard 2009, Eggers and Jones 2013, McBride and Bernard 1983).

In addition, building on the long-term series of run size and run timing, the weir has served as an indicator of salmon abundance since the early 1980s, used by Canadian and Alaskan fishery managers to support their in-season salmon management decisions (e.g. fishery openings). The weir also serves as the key data source in assessing total Alsek River Chinook and Sockeye run size using expansion factors based on radio and spaghetti tagging projects and genetic stock identication. On average, the Klukshu River Sockeye return accounts for about 20% of the total Alsek River Sockeye population (TTC 2017).

The basic weir design has been consistent since 1976, but some aspects of the weir configuration have been adapted over time, and the weir site has moved twice.

The current weir is approximately 18.3 m (60ft) long. It consists of two “picket style” wings set at an approximate 30^{o} angle leading to a counting chamber, trap, and eventually a video camera counting apparatus. The pickets consist of 2.54 cm (1”) diameter by 2.4m (8’) electrical conduit pipe spaced at 5 cm (2”) centres. The conduit is supported by 3 m (10’) aluminum stringers drilled to accommodate the pipe. The fence is supported by 7 tripods spaced at 3m (10’) intervals. The tripods are constructed of two 1.7m (5.5’) rear legs, one 1.8m (6’) front leg consisting of a 7.6cm (3’) pipe. The tripod is supported latterly by 3 lengths of 7.6cm (3’”) channel iron. The rectangular counting chamber and trap configuration consists 1.2 m (4’) vertically mounted picket fences. The counting chamber measure 1.2m (4‘) by 2.4m (8’); the trap which also houses the video counting chamber measures 2.4m (8’) by 3m (10’). The counting chamber is covered by a heated plywood shack for the comfort and safety of the field crew.

The current weir site is about 680 metres upstream from the Klukshu-Tatshenshini confluence (Figure 1). The initial site was located approximately 100 metres upstream from the mouth of the Klukshu, but due to a change in the flow regime of the Tatshenshini River the weir was moved upstream approximately 270 metres in 1991, immediately above the Klukshu River bridge. In order to faciiliate the placement of the weir at this new site, heavy equipment was used to widen the stream by approximate 6m (30’). In 2001 the weir was once again moved. The new location and current site of operations was chosen by CAFN and DFO to minimise the possibility of the salmon moving out of the system due to the presence of the weir. The underlying assumption was that if the weir is further up the Klukshu River, then salmon are more committed to the Klukshu system and more likely to pass the weir rather than leaving the Klukshu and moving into another system. Note that there was no quantitative data showing that the earlier weir location had causef fish to move to other non-natal streams in this particular watershed, but observations show that there isa potential weir effect (e.g. see overview of Chinook weirs in Appendix A of Pestal et al. 2016). It is also important to note that some fish appear to stage at locations below the weir before passing the structure, but it is unknown whether this staging behaviour is inherent or caused by the presense of the weir.

2016 Sampling Approach at Klukshu Weir

Klukshu weir was continuously in operation (counting and trapping mode) from 06 June to 04 October. Adult sampling for this project was coordinated with DFO's routine weir operation:

- Fish were extracted from the trap using a dipnet measuring approximately 40 cm (16in) by 60 cm (24in) opening with a shaft measuring approximately 1.5 m (4.5ft). The dipnet mesh measurement was approximately 5 cm (2in) stretched between knots. Samples were removed from the dipnet and placed on a sampling table located within the trap.
- From there fish were measured to the nearest 0.5 cm (¼") for fork length (from the snout to the fork of tail), identified as to sex, date recorded, and five scales were taken from the preferred area (Koo 1995) and mounted on standard DFO scale cards (numbered gum cards). MacLellan (2004) describes DFO's scale sampling approach. Sex was assessed primarily based on the size of the snout in contrast to body length; presence of an ovipositor was also used to determine sex.
- In addition to this routine sampling, our project added two additional steps:
    1) *All Sampled Fish (820)*: To collect tissue for DNA analysis, the left axillary process was excised from all sampled fish and fixed in 95% ethanol. Tissue samples were collected over the course of a statistical week (Sunday-Saturday) and fixed in a single sample bottle per week (i.e. weekly composite samples).
    2) *Tag Subsample (165):* Radio tags were applied to a subsample (see below) of fish handled at the weir. Subsampling of adults handled at the weir was based on a goal to tag about 50 female sockeye salmon per month from July to September. Tagging focused on female Sockeye, due to their typically higher fidelity to the spawning sites than males. However, some male Sockeye were tagged when no females were available during the early component of the run. Up to four radio tags were applied roughly every other day. Radio tags recovered in the FSC fishery or on the spawning grounds were re-deployed. The right axillary appendage was taken as an additional tissue sample, and fixed in 95% ethanol in individual vials to allow matching the DNA results to tag detections. This work sequence resulted in tagged fish being sampled twice for DNA (i.e. 1 in individual vial and 1 in pooled jar), but duplicate genotypes were later identified, and excluded from the analyses.

Table 1 summarizes the sample groups and outlines the information collected for each group. Table 2 shows the sample sizes by statistical week for the different study components (scales, radio tags, DNA samples). Table 3 summarizes the radio tag application by timing group and categories of tag patterns (e.g. clear pattern vs. interpretation of mixed signals required).

Appendix B summarizes the weir operation and water conditions (temperature, level). Appendix C documents the tag tracking, and Appendix H summarizes tag fates by time of application. Appendix J documents each tag, including a brief description of movements throughout the Klukshu watershed, resulting tag fates assigned to each fish, and results from genetic stock ID (Section 5.8). Appendix K summarizes the match between tag fates and genetic stock ID for different subsets of the 165 tagged fish (e.g. early migrating females) and various movement patterns (e.g. straight to lake vs. moved to lake then dropped back to Vand).

Tag Applications at Klukshu Weir

The radio-tags were manufactured by Sigma Eight Inc., Newmarket, Ontario. 150 Pisces model TX-PSC1-160© tags, measuring 40 mm by 10 mm were programmed to make them compatible with LOTEK SRX-400© receivers. A Pisces Programmer from Sigma Eight Inc was used for the conversion. The radio tags were programmed to emit a signal every 2.0 seconds (burst rate) continuously for a period of approximately 200 days from the time of activation. A total of seven frequencies (149.360, 149.380, 149.400, 149.420, 149.440, 149.460, and 149.500 MHz) and about 22 codes per frequency were used.

Each tagged fish was also marked with a 6.3 mm (¼") inch hole punched into the upper portion of the left operculum. This was done to readily identify it as a tagged fish when observed on the spawning grounds, and also to assess tag loss. Radio tags were generally applied as follows: the radio tag was made "ready" by threading the antenna of the radio tag through a PVC tube measuring 30.5 cm (12") x 5 mm (¼"); tag frequency and code and date was recorded ensuring the information matched with other fish sampling metrics (length, sex, DNA, scales); the fish was then secured on the sampling board by staff member "A" while staff member "B" slowly inserted the wetted radio-tag into the gut of specimen (insertion distance was approximately 10 cm (4 in). Approximately 30 cm (12") of the antenna protruded outside of the specimen after the insertion was concluded.

2.2. Radio-Tag Tracking

Stream-side towers and a single aerial survey were used to track the movement of radio tagged fish. A few foot surveys were also conducted, but they yielded little information and are not documented in this report.

Stationary Receivers (towers)

Four tower-mounted stationary receivers were set up along the Klukhsu River to monitor the movement of radio-tagged fish (Photo 3). Table C 1 describes the 4 sites and identifies challenges encountered in the field. Figure 1 shows tower locations. In summary:

- *Tower 1:* located immediately above the weir (Good Site)
- *Tower 2:* near the mouth of Motheral Creek (Ideal Site)
- *Tower 3:* near the mouth of Vand Creek (Good Site)
- *Tower 4:* at the outlet of Klukshu Lake (Fair Site).

All towers were equipped with a LOTEK SRX-400 receiver powered by a 12 volt battery under continual charge generated by an 80 watt solar panel. The receivers were programmed to monitor, in 5 second intervals, for the presence of each of the seven frequencies. Data transmitted to the receiver included frequency, tag code, antenna power, time, and date. Except for tower one which only housed one antenna, the fish signals were transmitted to the towers via two Yagi antennas with four elements each, mounted on the towers with one antenna pointing upstream and the second pointing downstream to provide information about the direction of tag movement.

Towers were checked weekly or occasionally on a fortnight basis. Data was transferred to a laptop computer and converted into an MS Excel spreadsheet for manipulation.

Section 5.4 describes how the raw signal detections were converted into tag movement patterns. Section 6.3 summarizes the observed tag movements. Table C 2 and Table C 3 document the details. Appendix J describes the observed movement pattern for each tagged fish.

Aerial Tracking Survey

A single aerial tracking survey was conducted on 28 Oct 2016. The survey was conducted using a Bell 206B Jet Ranger helicopter flown at 20-80 m altitude and 10-20 km/h. Occasionally the helicopter hovered to provide adequate time to receive signals from large groups of radio-tagged sockeye salmon. Two researchers, each equipped with a LOTEK SRX-400, participated with one researcher scanning four frequencies, while the second researcher scanned the balance of the frequencies. A single, two element Yagi antenna mounted on the fore of helicopter provided directional information, i.e. strongest signal arrived from ahead of the helicopter (Photo 4).

2.3. Spawning Ground Sampling

A total of 110 adult sockeye was sampled at spawning sites along the Klukshu mainstem, and 136 adult sockeye were sampled at spawning sites on Klukshu Lake. Appendix D documents the sampling events by date and location, and classifies samples by spawning condition.

Fishing poles, gillnets, and spears were made ready for the project (spears of course were limited to collecting post-spawning fish only). The gillnets were specially ordered with specification to hang the 13cm (5’”) mesh at a 3:1 ratio, i.e loosely hung thus serve as a tangle net more so than a gillnet; gillnet length ranged from 4.6m (15’) to 9m (30’). The spears were 15cm (6”) and 13cm (5”) with four sharp, barbed prongs. Fishing poles available for the study had heavy duty spin cast Diawa ©reels and rigid, heavy, two-piece Ugly Sticks© rod. Fish were captured primarily with a heavy fishing line (ca. 18kg /40lb) affixed to a weighted 50mm (2in) treble hook, which facilitated the snagging of target specimens. Only fishing poles were actually used, but field crew consider the gillnet likely more appropriate for years with larger abundances.

All live fish were released after sampling, which took approximately 30-60 seconds to complete. In some instances, carcasses were sampled. DNA samples were collected even if length measurements were not available (predation or too decomposed).

Fish were sampled from select spawning sites identified by a combination of:

- traditional and local knowledge
- presence of redds
- capture of ripe and post-spawning fish
- radio tag distribution records from the towers
- observed spawning distribution in previous studies (Petkovich 1997; Smith et. al 2005)

Access to spawning fish on Klukshu Lake required boating to potential sites with a 4m (12') Zodiac rubber raft powered by a 15 hp Honda outboard motor.

Fork length (tip of nose to fork in tail, measured to the nearest 0.5 cm), date, sex, and DNA samples were collected from spawning or post-spawning sockeye salmon.

DNA samples were stored in individually labelled vials, fixed in 95% ethanol, and cross-referenced with each specimen's fork-length, and sex. Scale samples were not collected due to the prospect of unreliable ages driven by scale resorption. Ages derived from radio-tagged fish spawning at select spawning sites were used as a proxy.

Radio tags were extracted from post spawning fish and were redeployed. Radio-tag channel number, code, fork length, sex, and date were recorded.

3. Methods - Sampling Juveniles

3.1. Overview

Sampling for Sockeye Salmon juveniles (fry and smolts) started in early May, 2016. Samples were taken, generally, on a weekly basis through early June with an additional sampling event conducted at the end of June/early July. Four locations were sampled:

A. Klukshu Lake at its outlet (including current boat launch area at Klukshu Village)
B. Klukshu River (at Klukshu Village ca. 300m downstream of the lake outlet on the Klukshu River)
C. Klukshu River mainstem approximately 500m downstream of Vand Creek confluence.
D. Lower Klukshu River approximately 500m upstream of its confluence with the Tatshenshini River.

The following sampling devices were deployed to capture representative samples at each location:

- Beach Seine – sites A, C, D
- Wolf-type Incline Plane Trap (IPT) – site B
- Fyke Net – site D
- Gee-type Minnow Traps – sites A, C and D

3.2. Beach Seine

Beach seining was conducted primarily at sites A and C. Some additional seining was conducted at site D, on the lower Klukshu River at the Tatshenshini River confluence and just upstream of the lower Klukshu River Bridge. Seining at site A was done primarily at the boat launch located near the outlet of Klukshu Lake in Klukshu Village. Seining at site C was done primarily in a back-eddy on the Klukshu River situated immediately to the north where the access road from Haines Highway intersects the river.

The beach seine consisted of a 3.0 m x 2.0 m deep, 3.2 mm (1/8 “) mesh panel fitted with weighted (lead) line along the bottom edge and floating line on upper edge (Photo 7, p.120). Short sweeps (lasting 30 s or less) were used to capture fish. Seining was conducted in relatively shallow water (< 0.5 m) at site C and D and in water approximately 1.0 m deep or less at site A. Live captured fish were transferred to a 20 l plastic bucket filled to approximately 50% with river or lake water for holding and processing. Small groups of fish (20-30) were processed at a time and were first anaesthetized using MS222. Whole sockeye fry retained for genetic analysis were placed in small glass or plastic vials and preserved in 95% ethanol alcohol. Processed fish that were not being retained were transferred to a 20 l bucket containing fresh river water for recovery. After fish were observed to fully recover from the anaesthetic they were released back to the river or lake.

3.3. Wolf-type Incline Plane Trap (IPT)

The Wolf-type incline plane trap (IPT) was deployed on the Klukshu River at Klukshu Village approximately 300m downstream of the lake outlet. The trap consisted of a rectangular metal mesh (6.4mm, 1/4“) box and plywood capture chamber attached to the downstream end. The metal mesh box (2.4 m length) was secured to the river bottom using rebar. The rectangular trap opening (30 cm wide x 40 cm deep) was oriented in the creek such that there was swift flow through the upper end (metal mesh portion) of the device. Flow was directed into a wooden floating box (2.5 m length) trapping fish. The box was secured in a pool close to the stream bank thus reducing flow and turbulence in the holding chamber and stress on fish being held. A baffle was situated between the metal mesh and wooden box to increase flow at this point and prevent fish from escaping upstream from the capture box.

Vexar mesh screen (6.4mm, 1/4 “) and sandbags slightly angled upstream were used to deflect a portion of the flow and out-migrating fish towards the trap. This resulted in approximately 40 % cross-sectional coverage of the river (Photo 8, p.120) by the vexar mesh while the sand bags used to create a back-flood extended across approximately 75% of the river. Actual coverage varied from week to week depending on river discharge and water level. This variability, however, was not substantial as river discharge was relatively stable throughout the sampling period. Sampling typically occurred over a nominal 24 hour period once/week from early May to late June. The main trapping structure (i.e. steel mesh and collection box) was removed after each weekly sampling event and re-deployed the following week.

Five sampling events occurred between 05 May and 02 June 2017. Two additional sampling events were conducted on 23 June and 30 June – 02 July 2017 to observe fish movement in the system but not to take samples for genetic profiling.

Live captured fish to be processed were transferred to a 20 l bucket (half-filled with river water). Fish were anaesthesized using MS222. Fish to be retained for genetic sampling were given a lethal dose of MS222. Fish to be processed and released were given a less concentrated dose and immediately after processing these fish were transferred to a 20 l recovery bucket filled to half with river water. Once fish had fully recovered they were released back into the Klukshu River.

3.4. Fyke Trap

The Fyke trap was deployed under the bridge, situated on the lower Klukshu River approximately 500m upstream of the Tatshenshini River confluence. The Fyke trap is composed of 3.2 mm (1/8“) mesh with a square opening (1.2 m x 1.2 m) tapering to a 7.6 cm (3”) PVC pipe connected to a floating collection box constructed of plywood and vexar screen. The net was secured near the river margin where flow rates were tempered in order to reduce stress on captured fish (Photo 9, p.121). The net was secured using rebar pounded into the stream bottom and tied off at points upstream along the shore and on the bridge structure. The floating collection box was secured to the bank such that it was out of the main flow of the river.

3.5. Gee-type Minnow traps

Gee-type minnow traps (Photo 10) with 6.5 mm (1/4 “) mesh were deployed at three locations (sites A, C and D) throughout the sampling period (early May to early June). Sampling at site A occurred between the boat launch at Klukshu Village and the foot bridge immediately at the lake outlet. Traps were set for a nominal 24 hours and were baited initially (until 18th May) with cat food, after which sockeye smolt carcasses were used. Traps were set along stream bank or in eddy pools in slack flow and secured to the bank with cord. Traps were fully submerged.

3.6. Sample Collection and Morphometric Measurements

All juvenile salmon captured using trapping methods described above were identified and enumerated. Most fish captured were released alive except for sockeye salmon fry and smolts. A portion of these fish were retained for genetic analysis. If the number of sockeye captured exceeded the number targeted for genetic sampling during a particular sampling event, those fish were released alive.

Most of the salmon captured (including Coho and Chinook) during sampling were weighed in milligrams (+/- .01 g) using a Smart Weigh GEM20 High Precision Digital jewellery scale and measured for fork-length (mm) prior to release or prior to being preserved in absolute alcohol for genetic sampling.

Scale samples (smears) were taken from most of the Sockeye smolts that were sacrificed and from a sample of the Chinook smolts captured. Collected scales were mounted on coded gum cards.

4. Methods - Sample Processing

4.1. Scale Samples

Adult Scale Samples Collected at Klukshu Weir

As part of DFO's regular weir operation (Section 2.1), scales were collected from all adults sampled at the weir. Scales were sent to DFO's Sclerochronology Lab in Nanaimo, for processing and reading according to current departmental standard procedure.

Hudson and Crosby (2010) describe the steps and equipment. Briefly, impressions were made on cellulose acetate under a specific heat and pressure regimes. Ages were assessed visually under approximately 20-50 power magnification. Ages are presented in the Gilbert-Rich format showing overall age in standard text, and freshwater age in subscript. For example an age 5_2 fish indicates a five year old specimen that spent two years in freshwater, including its incubation time.

Note that scales were not collected from adults sampled on the spawning grounds, due to their condition (i.e. scale resorption).

Juvenile Scale Samples

Scales were also collected from sockeye smolts at the outlet of Klukshu Lake. Scales were processed and read by Peter Etherton using available equipment using the following approach:

- Scale samples were collected from the preferred area as described by MacLellan (2004). Due to the small size of the individual scales, a "smear" was scraped off the specimen using a scalpel blade and placed on a coded scale gum card provided by DFO. Date and location were recorded on the back of individual gum cards for cross referencing the scale sample with the specimen's weight and length.
- The scale card was taped to an identically-sized cellulose acetate card. The card and acetate were placed between two rectangular heated (200^0 C) steel plates measuring 14cm (5.5") by 12cm (4.7") by 4cm (1.6"). A conventional gas barbecue was used to heat the steel; a standard kitchen thermometer was used to measure the heat. A stainless steel plate and a piece of baker's sheet covered the acetate, a second plate of stainless steel covered the back of the scale card. The scale card/acetate and steel plates were pressed for approximately 3 minutes using a 10cm (4") bench vise with an estimated force of 105 kg/sqcm (1,500 psi). Photo 13 shows the vise set-up.
- Ages were assessed by viewing the acetate scale impression under a magnification of 30 power. Ages are presented in the Gilbert-Rich format. An age-0 reading indicates the specimen did not yet spend a winter in freshwater, whereas an age of 1 and 2 indicates that the specimen spent 1 and 2 years in a freshwater environment including its incubation period.

Note that this was done as additional work outside the original scope of the project, and readings were not verified by the DFO scale lab. The intent was to check whether some clues about differences in juvenile life histories of lake spawners and river spawners could be extracted from the available samples.

4.2. DNA Samples

Tissue samples were fixed in 95% ethanol and shipped to DFO's Molecular Genetics Lab in Nanaimo for processing. DNA extraction and genotype reading followed the current standard DFO protocol for genotyping Pacific salmon (Beacham et al. 2001, Withler et al. 2000, Beacham, McIntosh and Wallace 2010). Briefly, DNA was extracted from the samples, the products of Polymerase Chain Reaction (PCR) at 14 microsatellite loci (Table I 1) were size-fractionated on denaturing polyacrylamide gels, and allele sizes were determined with the ABI 377 automated DNA sequencer.

Ruzzante (1998) describes the rationale for using microsatellite loci: They are widespread in the genome and are believed to be selectively neutral (i.e. have no effect on survival and reproduction). They can be isolated relatively easily from small amounts of fresh ore preserved tissue. Ruzzante (1998) concludes that "*these qualities of microsatellites make them very useful as genetic markers for studies of population differentiation and stock identification*".

Note that the DFO lab provided readings for 14 loci identified by Beacham, McIntosh and Wallace (2010), but more recent work indicates that 6 loci may be sufficient for stock ID of some Salmon stocks (Beacham and Wood 2011). In general, more markers (e.g. loci) provide more resolution, and the requirements for stock ID depend on the characteristics of the species and stock being studied as well as the assessment objectives. For example, in the 1990s the Chum Salmon stock ID program implemented by Washington State agencies used a 30 locus baseline to monitor timing and abundance, while DFO was using a 7 locus baseline to monitor catch composition in Southern BC fisheries (Winans et al. 1998).

Godbout et al. (2011) and Withler et al. (2014) describe recent genetics work on BC Sockeye salmon and document the sample processing methods.

5. Methods - Quantitative Analyses

5.1. Software

Most of the data summaries, exploratory analyses, statistical tests, and figures in this report were implemented with the R language for statistical computing (R Core Team 2015), using a suite of custom-developed functions and available code packages for specialized tasks. Notable R packages we used for genotype analyses are {ape}, {adegenet}, and {phangorn}. The R program and extension packages are free open source software, and can be downloaded at https://www.r-project.org/. Custom R functions for this project are available on the GitHub repository at https://github.com/SOLV-Code/Klukshu-Sockeye-2016.

Four additional programs were used for analyzing genotype data:

- *TreeFit* to estimate genetic distances between samples, fit alternative phylogenetic trees, and run bootstrap tests of tree fits (Kalinowski 2009). Treefit is a free program available at http://www.montana.edu/kalinowski/software/treefit.html.
- *FigTree* to view and polish trees created by TreeFit. FigTree is a free program available at http://tree.bio.ed.ac.uk/software/figtree/.
- *ONCOR* to estimate probabilities of genetic stock matches against a baseline sample (Kalinowksi et al. 2007). ONCOR is a free program available at http://www.montana.edu/kalinowski/software/oncor.html.
- *COLONY* to estimate sibling relationships (Jones and Wang 2010). COLONY is a free program available at https://www.zsl.org/science/software/colony.

5.2. Timing Groups and Sample Weights (Run, Tags, DNA)

Samples collected at Klukshu weir can be subdivided by date to explore patterns over time (i.e. treat as a stratified sample). We used two alternative aggregations:

- *Statistical Week*: Combine samples into calendar weeks (e.g. Week 28 started on 03 July in 2016).
- *Timing Group:* Combine samples into 3 groups based on the 15 August cut-off between early run and late run used by DFO since the 1990s. The Early group includes samples collected in statistical weeks 28 to 33 (03 July to 13 August). The Mix group includes samples collected in week 34 (14 August to 20 August). The Late group includes samples collected in weeks 35 to 41 (21 August to 08 October).

Weights or expansion factors are required for some analyses of these stratified data. For example, to estimate the overall proportion of river-spawning fish, the weekly proportion of tags that were assigned a river fate needs to be weighted by the abundance that the tags represent (i.e. how many fish passed the weir that week?)

One common approach is to expand the tag counts based on run size, and work with the expanded counts in subsequent analyses. For each weak, calculate the number of fish represented by a tag as weekly run / number of tags, then expand the weekly tag count by that number. For example, 30 fish were successfully tagged (i.e. tag fate could be determined) out of 154 adults that passed the weir in Week 31. Each of the tags represents 154/30=5.13 fish. Of these tags, 14/30=47% were assigned to a river spawning destination. When calculating the overall proportion of river spawners, these counts would then be expanded to 14*5.13= 71.82 river-fate tags and 16*5.13=82.08 lake-fate tags. These expanded tag count incorporate both the relative weekly run size and the proportion of the weekly run that was sampled.

We chose a slightly different approach, working with the weekly proportions (i.e. 47%), and calculating a weighted average across weeks using run size (i.e. weight 47% by 154/7584=2% of the total run). Technically, this weighted average includes only one of the two components in the above tag expansion, but in our data set the weekly sample sizes are quite similar, and the calculations produce essentially the same results. However, this second approach using weekly run proportions as weights has two practical advantages: (1) Run proportions are always the same, but expansion factors would have to be adjusted for each sensitivity test (e.g. all tags vs. females only), and for different analyses (e.g. tags vs. DNA samples); (2) Actual sample sizes are retained throughout the analysis, avoiding potential confusion about which number to use for which test (e.g. use expanded numbers for overall proportions, but need to use raw numbers for Chi-Squared test comparing the proportion of river-tag fates in the early run vs. the late run, because the sample sizes affects the statistical test).

Table 4 summarizes weekly run proportion, sample ratios, and expansion factors.

5.3. Statistical Tests Used in Exploratory Data Analyses (EDA)

Outline

The first step in the analysis was to explore the biological information and establish the context for interpreting the tagging and DNA results.

EDA of the juvenile data covered the following (Appendix F):

- distribution of fork lengths by sample group and by sample date
- distribution of weights by sample group and by sample date
- log-linear regression fits for length-weight relationships by sample group
- pairwise test of differences in fork length between lake and river sockeye fry
- size distribution of smolts by age class

EDA of the adult data covered the following (Appendix G):

- distribution of fork lengths by sample group and sex
- 4-way pairwise bootstrap comparisons of fork length (Early Weir, Late Weir, River Spn, Lake Spn)
- weekly pattern in sex ratio and test of difference between early weir and late weir sex ratio
- weekly pattern in age composition and test of difference between early weir and late weir age composition

The rest of this section describes the statistical methods used in these analyses. Custom R functions for this project are available on the GitHub repository at https://github.com/SOLV-Code/Klukshu-Sockeye-2016.

Test to Compare 2 Sample Means

We used Welch's modification of Student's t-test (Welch 1947, Devore 1991) to check whether two samples have the same average or are significantly different from each other.

We implemented the test with the custom R function *TwoSample.comp.test()*, which calculates summary statistics for both samples (e.g. kurtosis), applies R's built-in *t.test()* function for a two-sided comparison (i.e. is the mean of sample 1 either larger or smaller than the mean of sample 2?), and replicates the *t.test()* call for bootstrapped subsamples. Our bootstrap test used 1,000 replicates, each dropping 10% of the sample.

Table F 5 shows an example, comparing fork length for river fry and lake fry.

Test to Compare 4 Sample Means

We applied the 2-sample comparison test (above) to sets of 4 samples. The custom R function *FourSample.comp.test()* loops through all possible pairwise comparisons of the 4 input samples, applies the *TwoSample.comp.test()* as above, and tracks the bootstrapped proportion of p-values <0.05.

Table G 2 shows an example, comparing fork length for early weir females, late weir females, female river spawners, and female lake spawners.

Test to Compare 2 Sample Proportions

We used Pearson's Chi-squared test (Chernoff and Lehmann 1954, Devore 1991) to check whether two samples have the same proportional composition or are significantly different from each other.

We implemented the test with the custom R function *chi.boot()*, which creates bootstrap subsamples and then applies R's built-in *prop.test()* function for a two-sided comparison (i.e. is the ratio in sample 1 either larger or smaller than the ratio in sample 2?), and tracks the bootstrapped proportion of p-values<0.05. Our bootstrap test used 1,000 replicates, each dropping 10% of the sample.

Table G 8 shows an example, comparing age composition of early and late sockeye passing Klukshu weir.

Linear Regression

We used linear regressions to capture the relationship between 2 variables, and implemented the regression fits with R's built-in *lm()* function.

Figure 17 shows an example of a simple linear regression fitted to the changing weekly proportion of weir adults genetically matched to river spawners. The function call is *lm(prop.river ~ stat.week)*, where *prop.river* is a vector of weekly proportions and *stat.week* is a vector of week numbers.

Figure F 2 shows an example of a log-linear regression fitted to the length and weight data for river and lake Sockeye fry. The function call is *lm(ln.river.fry.wt ~ river.fry.len)*, where *ln.river.fry.wt* is a vector of natural logs of fry weights and *river.fry.len* is a vector of with the corresponding fry weights.

Partitioning Around Medoids (PAM)

We used PAM (Kaufman and Rousseeuw 1990) to identify data clusters in one of the sockeye fry samples. PAM identifies center points for a user-specified number of clusters in the data, and assigns the remaining observations to the nearest center point.

We implemented PAM using the *pam()* function from the {cluster} package in R.

Figure F 3 shows clear length-weight clusters for Sockeye fry sampled on July 8 at Klukshu Lake outlet, but note that only 19 of the 64 fry sampled that day have both measurements, so the clustering may be an artefact of a small sample with incomplete records.

5.4. Radio Tag Destinations

The four towers and one overflight produced about 400,000 raw signal detections, which were synthesized into useable data in 5 steps:

- Translate each tower's signal detections into dates of entry and exit from the tower range. This yields distinct time windows where each tag was in different parts of the Klukshu watershed. For example, tag 804 was applied on 13 July and then detected by the weir tower many times until 15 July. All these detections were summarized as "exit weir tower: 15 July"
- Patterns of tower range entry and exit were further summarized into dates of first entry, to track progress up the river and establish migration times and speed. For example, tag 602 entered and exited the range of each tower along the river in quick sequence, then was detected by the lake tower many times between 03 August and 06 October, which translates into a very fast up-river migration rate. In contrast, tag 817 moved between weir tower range and Motheral tower range several times, before last detections in Vand tower range, which gives a very slow net migration rate from weir to Vand Creek confluence.
- Final tower detections were then cross-checked against the overflight detections, where available, given that only 92/150=56% of the tags were detected during the overflight. The aerial survey was done at the end of October, so detections had to be interpreted carefully. For example, tag 514 passed all the river towers in a few days and then was detected in the lake many times between 02 August and 06 October. However, during the overflight the tag was located in the Klukshu mainstem, and interpreted as a likely carcass drift of a lake spawner.
- These descriptions of individual movement patterns were the categorized into 1 of 15 pattern types (e.g. "straight to lake", "moved about mainstem and ended up in river") and classified based on pattern clarity (i.e. "clear", "interpretation").
- Based on the overall movement pattern, each tag was then assigned to a final fate: 56 river spawners, 97 lake spawners, and 12 undetermined.

Table 3 shows a general summary of the tag movement patterns by run timing group (Early, Mix, Late) Section 6.3 summarizes the observed tag movements. Table C 2 and Table C 3 document the details. Appendix J describes the observed movement pattern for each tagged fish.

5.5. Cleaning and Reorganizing Genotype Data

The starting points for our genetic analyses were two raw data files with genotype readings provided by DFO's Molecular Genetics Lab in Nanaimo, which contained allele readings for 14 microsatellite loci (Table I 1). The data files are:

- *2016 Klukshu samples*: 1,690 raw records in 11 sample groups, with 1,536 usable records left after dropping 14 incomplete genotype records and 140 duplicate genotypes (Section 6.4).
- *DFO's Alsek Sockeye Baseline*: 4,075 raw records in 26 sample groups, with sample sizes ranging from 1 record for Takhanne_RT to 832 for Neskataheen. After dropping 144 incomplete genotype records and 8 sample groups with less than 50 records that are complete or mostly complete, the original baseline reference file contains 3,759 samples in 18 sample groups (Section 6.4). Note that 1,027 of these samples (27%) are Klukshu weir samples grouped by timing into Early, Mix, and Late. 832 (22%) of the samples are from the Neskataheen, which was found to be closely related to the Klukshu River spawners in our analysis (Section 7.5), so that 1,859 (49%) of all useable records in DFO's Alsek baseline are from the Klukshu/Neskatheen complex.

Section 6.4 describes the genotype records clean-up and Appendix I documents the details.

We used 2 custom-built R functions to manipulate the genotype data:

- *genepop.read()*: reads in a tab-delimited version of the genepop file, which we created by importing into MS Excel and exporting as a *.txt file from there. The function produces an output object with a matrix of individual allele readings (2 columns/locus), a list of column labels (e.g. loc_3dre_1, loc_3dre_2), and a list of loci labels (e.g. loc_3dre). In this matrix format, the data can be easily manipulated within R.
- *genepop.write()*: takes an object created by *genepop.read()* and modified in R, and writes the records back into the original genepop format as a *.gen file for use with programs like TreeFit (Section 5.7), ONCOR (Section 5.8), or COLONY (Section 5.9).

Using these functions, we organized the available genotypes records into 12 alternative sets for sensitivity analyses, as listed in Table 8. In addition, we used these functions to create 100 bootstrapped versions of sets G11 and G12, which were the focus for the final set of analyses. Each bootstrapped version dropped 10% of the records from each sample group.

The functions are available on the GitHub repository at https://github.com/SOLV-Code/Klukshu-Sockeye-2016.

5.6. Allele Frequencies

Some researchers explore allele frequencies for the different loci to establish a context for more formal analyses like fitting phylogenetic trees (next section). We used the custom R function *allele.diagnostics()* to produce 3 summaries of allele frequencies in the 2016 Klukshu sockeye samples and the revised baseline for Alskek Sockeye:

- Calculate total number of alleles observed at each locus, as in Table 1 of Beacham *et al.* (2008)
- Calculate mean number of alleles in 1000 bootstrapped samples of size = 100, similar to the multi-sample summary in Table 2 of Beacham *et al.* (2008).
- Calculate the allele frequencies in each sample group for each locus, as in Table 3 of Scribner *et al.* (1996), Figure 4 of Withler *et al.* (2000), Figure 2 of Beacham and Wood (1999), and Figure 3 of Pavey *et al.* (2007).
- Compare allele frequencies for 2 sample groups in a profile plot as follows: Select most prevalent allele for each sample group, plus alleles with the biggest differences in frequency between the sample groups, for up to 10 alleles. Rescale allele frequencies so that the highest observed frequency =100%, and plot the index profiles.

The functions are available on the GitHub repository at https://github.com/SOLV-Code/Klukshu-Sockeye-2016.

5.7. Phylogenetic Trees

Phylogenetic trees show how different sample groups are related to each other through a series of binary splits (i.e each node of the tree has 2 branches). Tree fitting has 2 basic steps:

- *Step 1: Calculate genetic distances*. For each pair of sample groups in the data set, calculate how different the genotypes for all records are. This is conceptually analogous to calculating sample means and standard deviations for size data, and then calculating a measure of difference between the size distributions. Genetic distances are calculated between each pair of sample groups, and therefore are not affected by what is included on the full set of sample groups being analyzed. For example, the genetic distance between the Klukshu River fry sample and the Klukshu Lake spawner sample is the same whether we are only working with the samples collected in 2016 or whether we include the Alsek baselines in the analysis.
- *Step 2: Fit a Tree*. Given a set of pairwise genetic distances between all sample groups in a data file, this step searches for a tree that best divides the sample groups into a series of binary branches. The tree fitting algorithms use some combination of maximizing the amount of variability explained by the tree and minimizing the complexity of the tree (i.e. conceptually similar to testing alternative multi-variate regressions).The final tree depends on how the program searches for potential tree fits and which criteria are used to compare alternative fits. Also, this step is influenced by the full set of sample groups being analyzed. For example, the linkage between early weir samples and river spawner samples collected in 2016 can be influenced by whether the mixed-timing weir samples (week 34) are included in the data set.

Many alternative approaches have been developed for both steps, and we implemented extensive sensitivity testing of the options available within the programs we used (Section 5.1). We checked the sensitivity of tree fits to 4 alternative measures of genetic distance and 2 alternative tree fitting algorithms, implemented across 2 different software applications. Table 9 summarizes the 11 alternative tree fitting approaches we tested.

Measures of Genetic Distance

There is an extensive and long-running debate among genetics researchers regarding the strengths and limitations of alternative distance measures and their underlying assumptions. For example, Ruzzante (1998) tested 7 alternative distance measures on samples of cod (*Gadus morhua*) scored on 6 microsatellite loci.

Sorting through all of these theoretical arguments to choose a single most appropriate measure for the Klukshu Sockeye data is beyond the scope of this project, so we opted instead to do a sensitivity test using all the available options in the TreeFit program (Kalinowksi 2009), which is commonly used for genetic studies of Pacific salmon.

The TreeFit program includes 4 alternative measures of genetic distance:

- *Fst* (Weir and Cockerham 1984), which is labelled *Theta* in TreeFit
- *Ds* (Nei 1978)
- *Dc* (Cavalli-Sforza and Ewdards 1967)
- *Da* (Nei 1987).

As an additional test, we also cross-checked the first 3 distance measures using the R package {adegenet}.

Most recent CJFAS papers with phylogenetic trees for Pacific Salmon genetics seem to use the *Dc* metric (Table 25). Section 8.5 compares our methods and results to these other studies.

Tree Fitting Algorithms

As for measures of genetic distance, there is a lot of active research and debate regarding the strengths and limitations of alternative tree fitting algorithms and their underlying assumptions. Felsenstein (2004) provides an extensive review.

The TreeFit program includes 2 alternative tree fitting measures: *Neighbour-Joining* (Saitou and Nei 1987, Gascuel and Steel 2006) and *UPGMA* (Sokal and Michener 1958).

As above, we opted to do a sensitivity test using both of them, and cross-checked the neighbour-joining tree fits using the R package {phangorn}. Most recent CJFAS papers with phylogenetic trees for Pacific Salmon genetics seem to use the *Neighbour-Joining* method (Table 25). Section 8.5 compares our methods and results to these other studies.

Summarizing Tree Shapes and Testing Goodness-Of-Fit

Our final set of tree fits covers 19 variations: The 8 method variations listed in Table 9 were applied to two alternative genotype sets (G11 and G12; Table 8), and 3 variations were then replicated for 1 genotype set (G12) in R.

We used two approaches to compare these alternative trees:

- *R^2 measure*: Analogous to the coefficient of determination in regression analysis, this measure describes how much of the sample variation is explained by the fitted tree. The better the tree branches match the structure of genetic distances between samples, the closer R^2 is to 1.
- *Bootstrap support for key nodes*: For this test, drop parts of the data set, fit a tree, and compare the resulting tree to the tree with all the data. By replicating this many times, we can get a proportion of trees that have a node of interest (if 850 of 1000 replication put 2 groups onto the same branch, then there is 85% bootstrap support for these samples being more closely related to each other than to the rest of the sample groups. We implemented 2 alternative bootstrap approaches to test the sensitivity of tree fits to our data:
    - *Test 1*: In R, fit trees to 100 random subsamples of records (e.g. drop 10% of samples in each group).
    - *Test 2*: In TreeFit, fit trees to 1000 random subsamples of alleles (e.g. remove a portion of the data at the locus level).

Kalinowski (2009) explains how the two approaches fit together: *"Bootstrapping is frequently used to measure statistical confidence in the topology of evolutionary trees (for example, Felsenstein (2004), chapter 20, and references therein). High bootstrap support and high R^2 values are desirable if a tree is to be used to describe population structure, but they measure different quantities and the distinction is important. The goal of bootstrapping is to assess the statistical support for each interior branch in the tree. The concern is that the topology of the tree has been influenced by sampling error caused by sampling a limited number of loci. If the number of loci genotyped is increased, trees should approach the correct topology and the level of support is expected to increase. The goal of calculating R^2 is to determine whether a tree's topology and branch lengths accurately reflect the genetic distances in the genetic distance matrix. The concern is that imposing a bifurcating topology onto the populations distorts the actual relationships among populations. This value is not expected to increase if more loci are genotyped. A tree could have high bootstrap values, but a low R^2."*

5.8. Genetic Stock Identification (GSI)

We used the ONCOR program (Kalinowski et al. 2007) to match the 2016 samples to reference populations. The program takes 2 inputs: (1) a sample file with genotypes to be matched, and (2) a baseline file with reference samples from different populations. For each individual genotype record in the sample file, it calculates the probabilities of matching to the different baseline groups (e.g. fish 1 has probabilities of 85% Pop 1, 7% Pop 2, 3% Pop 3, etc).

The ONCOR program was specifically developed for Pacific Salmon GSI, and we used it with all the built-in settings described by Kalinowski et al. (2007) to implement 4 analyses:

- Match each of the 2016 sample groups to DFO's baseline (Set G5; Table 8) for Alsek Sockeye (after data clean-up, Section 5.5)
- Match 2016 samples from weir adults and juveniles to a revised baseline for Alsek Sockeye (Set G10; Table 8), which uses the 2016 river spawners and lake spawners instead of the early/mix/late weir samples in DFO's original baseline)
- Leave-one-out test of DFO's original baseline (i.e. remove 1 record, run a stock ID, and check if it gets assigned back to the sample it was taken from).
- Leave-one-out test of the revised baseline.

5.9. Genetic Family Structure

In samples from small populations or in confined conditions, the sampled individuals could be closely related, which affects estimates of genetic diversity in the larger population (e.g. if a sample happens to contain a lot of siblings).

In our project this is a potential concern with the juvenile samples, especially the newly emerged fry. The COLONY program by Jones and Wang (2010) estimates sibling relationships by linking samples with similar genotypes to a set of constructed source genotypes (i.e. virtual parents). Janine Supernault of DFO's Molecular Genetics Lab ran the ONCOR analysis with settings and assumptions as described in Withler et al. (2014), and provided summary results.

Note that our samples cover 3 brood years (2016 returns, fry from 2015 spawners, smolts from 2014 spawners), and this analysis does not establish actual brood lineages across samples. However, the interpretation of common parentage is valid within each sample group.

6. Results – Sampling and Sample Processing

6.1. Sample Overview

This report covers two field projects completed in 2016 (Section 1.2). One project sampled adult Sockeye at Klukshu weir throughout the full migration, and at spawning sites in Klukshu River and in Klukshu Lake. The other project sampled juvenile Sockeye throughout the Klukshu watershed.

Budget Summary

The total budget for both projects was Can$200,000, with roughly 2/3 for the adult project and 1/3 for the juvenile project. In addition, there were substantial in-kind contributions by participating organizations and individuals. Appendix A has a budget overview.

Adult Project

Adult Sockeye were successfully sampled at Klukshu weir and at spawning sites identified based on traditional and local knowledge, earlier studies (Petkovich 2000, Fillatre 2002), and radio tag tracking during the 2016 project.

Table 2 summarizes the adult samples by location (weir, river, lake), and further splits the weir samples by statistical week.

The total run size of Sockeye past Klukshu weir in 2016 was 7,584. 820 adults (11%) were sampled at the weir for sex, length, and scales as part of DFO's regular weir operation. For most of these we obtained DNA samples and valid genotype readings (809, 99% of sampled adults, 10% of run). We tagged a subset of the weir sample (165 tags, 20% of sampled adults, 2% of run), and a final destination could be determined for most of the tags (153, 93% of tags, 2% of run). Weekly samples were spread to cover the full migration period, but with a focus on early migrants (Figure 7).

Appendix B documents sampling at the weir. Table B 1 lists weekly notes on weir operation and sockeye observations. Figure B 1 shows daily water temperatures near the weir relative to observed temperatures since 1986 and water levels for 2016. Temperatures in 2016 were consistently above average, and frequently exceeded the previously recorded maximum. Historical information on water levels is not currently available in electronic format, but weir crew consider 2016 water levels below average (Sean Stark, pers. comm.). Field crew speculated that migration through the weir in 2016 may have been delayed because of the observed water conditions.

Section 6.3 summarizes radio tag application, detection, and signal interpretation.

Adult sampling at spawning grounds was designed to collect roughly equal samples sizes for river spawners and lake spawners, so that samples do not reflect relative abundance observed at these sites. Overall, 246 adults were sampled. For most of these we obtained DNA samples and valid genotype readings (235, 96% of sampled adults).

Appendix D documents sampling events on the spawning grounds. Potential sampling sites were identified using information compiled from traditional and local knowledge, DFO records, and past spawning distribution studies (Petkovich et al. 1997, Pacific Salmon Commission 1997, Etherton 1997). A total of 110 river spawners was sampled at two locations throughout Klukshu River on five different dates. Samples included 57 males and 53 females. A total of 136 lake spawners was sampled at three locations throughout Klukshu Lake on four different dates. Samples included 61 males, 51 females, and 24 unidentified (23 skeletal samples, 1 undetermined carcass).

Juvenile Project

Five species of fish were captured during sampling for juvenile salmon in the Klukshu River system from early May to early July 2017. This included three species of Pacific salmon; Sockeye (*Onchorhynchus nerka*), Chinook (*Onchoryhnchus tshawyscha*), Coho (*Onchorhynchus kitsutch),* one additional salmonid, Dolly Varden charr (*Salvelinus malma*), and slimy sculpin (*Cottus cognatus*). Fry were caught for all three salmon species, smolts for Sockeye and Chinook.

Table 5 summarizes the juvenile sample sizes by species and life stage. 535 juvenile Sockeye samples were collected, 167 smolts and 368 fry, with a roughly even split across locations and life stages (214 river fry, 154

lake and lake outlet fry, 167 lake outlet smolts). For most of these we obtained DNA samples and valid genotype readings (492, 92%)

A comparable number of Coho fry were also caught (602) and a few Chinook juveniles (24 fry, 18 smolts). Length and weight were measured for juvenile Chinook and Coho, but no DNA samples were collected.

Juvenile sampling was identified as a potential challenge during the planning stage for this project, with high uncertainty about the best locations and timing for catching fry, and alternative gear types under consideration:

- *Gear:* The field crew prepared 5 alternative sampling gears, and deployed 4 of them depending on local conditions at each of the 4 sampling sites. 3 types of traps and beach seines were tested, and achieved sample sizes that exceeded our original budget for DNA processing. Therefore it was not necessary to deploy electrofishing gear, which had also been prepared as a backup option.
- *Location:* Potential sampling sites were identified using information compiled from traditional and local knowledge, DFO records, and past spawning distribution studies (Petkovich et al. 1997, Pacific Salmon Commission 1997, Etherton 1997).
- *Timing:* Emergence of Sockeye fry has been linked to temperature, specifically accumulated thermal units (ATU) since spawning (DFO 2011). Based on measured temperatures at the weir (Figure B 1) during the summer, and some assumptions about daily temperatures for the rest of the year, a plausible time window for Klukshu sockeye emergence in 2016 was 28 May to 18 June (Figure E 1). Given the large number of successfully sampled fry and their observed size distributions (Figure F 6), this rough approximation seems to have been accurate for 2016.

Appendix E documents the individual sampling events, sampling effort, and fish captures by each of the four sampling methods at the four sites sampled. In summary:

- *Wolf-type Incline Plane Trap (IPT):* Near the lake outlet (Site B), the IPT caught highly variable numbers of juvenile salmon. Overall, most of them were Sockeye smolts (472/633, 75%). However, the sample composition varied greatly with date, time of day, and soak time. In May, sampling events during the day captured few or no Sockeye juveniles (<2 smolts and 0 fry for daytime samples on May 5, May 12, and May 18), while overnight sampling caught large numbers (138 smolts on May 12/13 and 236 smolts on May 18/19). In early June, daytime and overnight sampling caught roughly the same number of sockeye smolts (21 on June 1, 27 on June 1/2). A multi-day set in late June was the only IPT sampling event that caught any sockeye fry, and in this case they were more abundant than sockeye smolts (64 fry, 26 smolts).
- *Beach Seine:* Short sweeps in shallow water with a 1/8“ mesh net reliably captured Sockeye fry at the lake outlet (Site A) and on the Klukshu mainstem near Vand Creek (Site C), but seining on the lower Klukshu near the Tatshenshini confluence (site C, near weir) only caught salmon fry in one of the 2 sets. Fry caught at the lake outlet were almost entirely Sockeye (125 Sockeye, 1 Coho), while all 3 species were caught on the Klukshu mainstem near Vand Creek (214 Sockeye, 342 Coho, and 24 Chinook). Seining in the lower Klukshu caught mostly Coho fry (12 Sockeye, 47 Coho, no Chinook).
- *Fyke Trap:* On the Lower Klukshu River, near the Tatshenshini confluence, the Fyke trap caught a lot of Coho fry in overnight sets in early May to mid-May (313 on May 5/6 and 488 on May 12/13), as well as a few Chinook and Sockeye (<4). On the same dates, evening sets from mid-afternoon to about 11pm did not catch any juvenile salmon. In late May, short sets on the evening or morning caught a few Coho fry and no other juvenile salmon. Additional sampling in early June caught no juvenile salmon.
- *Gee-Type Minnow Trap:* Minnow traps caught no juvenile Sockeye over 13 sampling events spread over 3 locations. Coho fry were reliably caught on the Klukshu mainstem near Vand Creek, but only a few were caught on the lower Klukshu River (13 fry over 5 overnight sets with 1-6 traps each) , and almost none at the lake outlet (4 fry over 5 overnight sets, with 2-3 traps each).

6.2. Scale Sampling and Processing

Scales from 817 adult Sockeye were collected as part of DFO’s routine weir operation (Section 2.1) and processed at the DFO Sclerochronology Lab in Nanaimo (Section 4.1). Full age readings were possible for 748 of the 817 samples (92%; Table 2). Marine age could be determined for another 26 (3%) samples, and freshwater age for another 28 (3%). 15 samples (2%) could not be aged at all. This is a typical outcome for scale readings.

Scales from Sockeye smolts sampled at Klukshu Lake outlet were processed and read by Peter Etherton using available equipment (Section 4.1). Note that this was done as additional work outside the original scope of the project, and readings were not verified by the DFO scale lab. Of 167 smolt scale samples, 133 (83%) could be read clearly and yielded a freshwater age determination (Table 5). An additional 9 samples could be read, but age determinations were classified as highly uncertain due to poor sample quality or unclear annuli. These were excluded from subsequent analyses. 25 samples (15%) could not be read.

Note that 7 of the 133 smolt samples with an age reading of good quality were classified as age 0 smolts. This presents an interpretation challenge, and will be discussed in Section 8.3.

6.3. Radio Tagging and Determining Tag Destinations

A total of 165 radio tags was applied to adult sockeye at Klukshu weir (20% of adults sampled at the weir, 2% of run), and a final destination could be determined for most of the tags (153, 93% of tags, 2% of run) using 4 stationary receivers and 1 helicopter overflight. 150 tags were applied to females, and 15 tags to males. 12 tags recovered by harvesters or on the spawning grounds were re-deployed, but they had very short tracking histories, and were excluded from our final analysis of run composition.

Tag application worked well, and there was no evidence of tag regurgitation. However, there were some minor inconveniences with record keeping due to the very small print on individual tags and the amount of other data being collected during tagging (i.e. scales, lengths, sex, tissue samples).

The stationary towers worked reasonably well over the season, but we did encounter some equipment challenges:

- Some minor malfunctions occurred at Vand, where the upstream antenna failed to report for short time periods.
- As the season progressed and daylight hours shortened, there was an issue with power supply at the lake tower. The tower was moved to a site with more sun exposure on 12 Sept; one day of monitoring was lost.
- The tower located at the weir malfunctioned from 18-30 September due to low power which was due to a loose connection.
- The relatively small percentage of the tags located during the aerial survey (92/150=61% of active tags;Table C 3) was most probably due to a measure of the post-spawning tagged fish sinking to undetectable depths at Klukshu Lake (i.e. signal strength weakens in proportion to water depth). The detection of mainstem fish was more efficient. Additional aerial surveys would have been useful to better refine spawning areas, but given the cost of air charters, this was not considered cost-efficient, given the large amount of data already provided by the four stationary towers.

The Sigma-8 tags worked well and were the least expensive on the market, but programming the tags and constantly cross-referencing the tags with Lotek SRX-400 receiver's output was both frustrating and time consuming. In hindshight, this extra work on processing the results was not worth the cost savings in the tag purchase.

Another challenge we encountered was the handling of tag recoveries in fisheries.There was no reward offered for recovered tags, to avoid creating an incentive for harvesters to specifically target tagged fish. However, the interpretation of tag detections would have been easier if recovered tags, complete with recovery details, had been quickly delivered to CAFN fisheries staff. For example, given how shallow the sockeye spawning grounds are at the lake outlet coupled with the fact that many CAFN harvesters camp there and process fish there, it was a challenge to determine whether a tag signal from the lake outlet spawning site was an acutal spawning fish or a harvested fish at the CAFN camp.

Finally, it would have assisted signal interpretation to create set of reference signals for each tower by placing active tags at various points upstream and downstream and at different water depths. This should be planned into the effort allocation in future telemetry studies.

Appendix C documents the tag tracking results:

- Table C 2 shows the number of tags detected entering each tower's range, and splits the total records based on time of application (early/late, by statistical week), tag fate, and genetic stock ID. 62% of all tags were detected within range of the lake tower at least once. Tag fates, which are derived from the movement pattern in combination with an aerial survey late in the season, line up closely with the tower detections. Almost all of the fish assigned a lake fate were recorded entering the lake, and only a few of

the fish assigned a river fate were ever recorded by the lake tower. However, only about 3/4 of the fish genetically matched to Klukshu lake spawners in the revised Alsek baseline were detected by the lake tower and almost half of the fish matched to the Klukshu River / Neskataheen genetic group were detected at least once by the lake. Of these 27 River/Neskataheen fish, only about half went straight to the lake, while the others either moved about the mainstem for a long time or had various types of mixed signals.

- Table C 3 summarizes the distribution of tags during the aerial survey. Roughly half of the tags (92/165, 56%) were detected during the overflight, which took place about 3 months after the first tag application and 1 month after the latest tag application. Of these, most tags applied early (before August 14) were detected somewhere along the Klukshu mainstem (67%), and most of the tags applied late (after Aug 20) were detected in the lake (70%).

Observed tag movement patterns were grouped into 15 categories and classified based on clarity (i.e. clear pattern vs. interpretation of mixed signals required). Table 3 list the number of tags for these various classifications. Appendix J describes the observed movement of each tagged fish and identifies the corresponding genetic stock ID.

6.4. DNA Sampling and Processing

Tissue samples from most of the adult and juvenile Sockeye sampled for these 2 projects were successfully collected, prepared, shipped to the DNA Lab in Nanaimo, processed, and genotyped. Table 2 lists the number of tissue samples, valid genotype readings, and unique genotypes for adult samples, and Table 5 lists the juvenile samples. Valid genotype readings were obtained for 809 adults at the weir (99% of adults sampled at weir, 10% of run), 238 adults on the spawning grounds (97% of sampled spawners), and 492 juveniles (92% of sampled juveniles).

Tissue samples from adults at Klukshu weir were collected with combination of strategies (Section 2.1):

- *Tagged*: individually packed in labelled vials
- *Untagged*: pooled in jars by statistical week

This was necessary to increase the sample size. It would not have been feasible to individually track the tissue samples from untagged fish without disrupting the standard weir operating procedure. Note that the axillary processes from all fish sampled at the weir were collected in the weekly pooled sample. Tag application and individual tissue sampling happened after, resulting in duplicate tissue samples from the tagged fish. Duplicate genotypes were later identified, and excluded from the analyses.

Genotype data for Sockeye salmon in the Alsek watershed was used as a baseline reference (Section 5.7) for the 2016 Klukshu samples.

Genotype data was cleaned in 3 steps, which are documented in Appendix I:

- *Filter out incomplete records*: DNA sample processing (Section 4.2) produced genotype sequences for 14 loci (i.e. allele pairs), but not all alleles could be fully read (i.e. one or both records in a pair may be missing). The first step in the data clean-up was to remove records with too many missing pieces. The cut-off was to allow no more than 8 incomplete alleles (out of 28). The proportion of records that had to be dropped from the 2016 sample groups was small, with the largest filtering on the lake spawner sample (5/123,4%). However, for several of the Alsek baselines the proportion of records that were filtered out was quite high, especially for baselines with small sample sizes (e.g. for Kane filtered out 9/59 records, 15%).
- *Filter out small baselines*: After filtering incomplete records, the Alsek baselines were checked for sample size. The cut-off was to retain only baseline groups with 50 samples or more. As a result, 8 of 26 baseline samples were dropped from subsequent analyses.
- *Remove duplicate genotypes:* The final step in the DNA data clean-up was to check for duplicate genotypes and remove those records. Duplicate genotypes can arise at different steps during sampling, packing, or processing. The main source of duplicates in the 2016 sampling arose due to the sampling set-up at the weir, with weekly pooled DNA samples being collected from all sampled fish, and additional samples being taken and individually stored when some of those fish were subsequently subsampled for radio tagging. In addition, duplicate genotypes arose from fish that were sampled at the weir and then encountered again on the spawning grounds. Duplicates were removed using 3 rules: (1) if duplicates are 1 tagged and 1 non-tagged from weir, remove non-tagged; (2) if duplicates are 1 from spawning grounds and 1 from weir,

remove weir sample; (3) if duplicates are from same sample group, remove later one. Overall, 140 duplicate samples were excluded, all from the weekly pooled weir samples (70 Early, 13 Mix, 56 Late).

There were no practical challenges collecting tissue samples, other than allocating effort between all the different components of the field work (i.e. number of trips, dates, locations for spawning ground samples from lake vs. river sites, while keeping the radio towers maintained). The timing for collecting tissue samples from Klukshu Lake spawners located upstream of the lake outlet turned out to be too late in the season, after peak spawning had passed. Only a few active spawners were encountered at the selected lake shoal areas, but samples from carcasses and skeletal remains were taken to increase sample size. Table D 2 lists spawner conditions at each sample site.

The storage and shipping of tissues samples did not pose any serious challenges. Note that our prepared supply of vials and fixative at the weir site fell short, because sample size was larger than anticipated. However, the DFO crew operating the weir provided supplies to make up the shortfall.

7. Results – Quantitative Analyses

7.1. Exploratory Data Analysis - Juveniles

We collected size, weight, and age data for juvenile Klukshu Salmon in 2016. Table 5 lists sample sizes. Appendix F documents the observations.

Sockeye Fry

The size of Sockeye fry varied by sample location (Table F 1, Table F 2, Figure F 1). 340 fork length records ranged from 24mm to 57mm. 311 weight records ranged from 0.1g to 1.7g. Ranges and medians by sample group were:

- *River Fry*: 202 length obs = 30mm (27-42mm) ; 202 weight obs = 0.21g (0.1-0.7g)
- *Lake Fry*: 90 obs = 28mm (24-35mm); 90 obs = 0.17g (0.1-0.4g)
- *Lake Outlet Fry*: 48 obs = 46mm (34-57mm); 19 obs = 1.01g (0.6-1.7g)

Log-linear regressions describe the observed length-weight relationship for the fry samples well, with an adjusted R^2 for the "All Fry" fit =0.919 and R^2 for individual sample group fits ranging from 0.719 to 0.879 (Table F 3, Figure F 2).

Clear differences between River fry and Lake fry were observed:

- River Fry had a much narrower length distribution than Lake Fry (K = 3.09 >1.96; Table F 4)
- River Fry were significantly longer than Lake fry (95% confidence interval for difference in means = 1.4 to 2.6mm, 100% of bootstrap tests had p-value << 0.05; Table F 5)
- River fry were similar size in over time, but Lake fry caught later were smaller (Figure F 6).

Lake Outlet fry were much larger than both River fry and Lake fry, and the distribution of length and weight data was much wider (Figure F 1). Scatter plots of weight vs. length show two potential clusters within the Lake Outlet fry sample (Figure F 2, Figure F 3). If these are true clusters, then they could represent a mix of populations or spawning areas with different emergence times, but the observed pattern may be due to a small sample with incomplete records (64 samples, 48 length measures, and 19 weight measures).

Sockeye Smolts

The size of 167 Sockeye smolts sampled at the outlet of Klukshu Lake varied widely (Table F 1, Table F 2). 167 fork length records ranged from 56mm to 119mm with a median of 98mm. 160 weight measurements ranged from 1.1g to 15.8g with a median of 8.92mm. Both distributions were roughly normal (S,K << 1.96; Table F 4). A log-linear regression describes the observed length-weight relationship for the smolt samples fairly well (R^2 = 0.719; Table F 3), but there is 1 outlier from an otherwise narrow scatter around the regression line (Figure F 4).

Age classes could be determined for most of the sampled smolts (167 smolts, 161 scale samples, 133 valid age readings). Figure F 5 shows the length and weight distributions for all samples and by age class. Most smolts were age 1 (121/133, 91%), but there were a few age 0 smolts (7/133, 5%) and age 2 smolts (5/133, 4%). The length and weight distributions for the 3 age classes do overlap, but medians are significantly different between Age 0 and Age 1 smolts, supporting the age classifications despite the small sampl size of Age 0 smolts (Table F 6).

The size of age 1 smolts increased from mid-May to early June, but smolts caught in early July were much smaller (Figure F 7).

Other Juvenile Salmon

Sampling with beach seine, Fyke trap, and minnow trap captured a large number of juvenile Coho (Appendix E). Of 1,361 captured Coho fry, fork length was measured for 602 fry (44%) and ranged from 31mm to 75mm with a median of 39mm (Table F 1. Weight was measured for 548 Fry (40%) and ranged from 0.2g to 4.2g with a median of 0.52g (Table F 2).

A few Chinook juveniles were also captured. Size ranges for fry and smolts overlapped a lot. Fork length for 24 Chinook Fry ranged from 32mm to 43mm with a median of 36mm, and for 18 Chinook smolts range from 33mm

to 142mm with a median of 118mm, indicating that the small Chinook smolts may have actually been misclassified fry.

7.2. Exploratory Data Analysis - Adults

DFO collected size, sex, and age data for adult Sockeye passing Klukshu weir in 2016. In addition, we collected size, sex and condition data from live spawners and carcasses at various spawnig sites. Table 2 lists sample sizes by sample group and type of observation. Table D 1 and Table D 2 list the spawner conditions by sampling site and date.

Fork Length

The size of adult sockeye varied across sample groups, and showed some potentially interesting patterns (Table G 1 , Figure G 1):

- Fork length (mm) for all sample groups had a roughly normal distribution (S,K << 1.96; Table G 1).
- Males were substantially larger than females in each sample group.
- Median fork length for river spawners was slightly larger than for lake spawners in both females and males, but distributions mostly overlapped.
- Mean fork length of males increased slightly over time (Early = 594, Mix = 600, Late=609), but the change is less pronounced in median length (600,600,610).
- Male size became more variable later in the migration (i.e. standard deviation increased: Early=30, mix= 32, Late=42; Table G 1).

Some of these patters are confirmed in the bootstrap test for significant differences (Table G 2) between early migrants, late migrants, river spawners, and lake spawners:

- For females, the only consistently significant size difference was between early migrants (median = 559mm) and River spawners (median = 571mm).
- For males, there are 3 consistently significant size differences. Early migrants (median=600mm) were smaller than late migrants (610mm) and smaller than River spawners. Note that early migrants were also smaller than Lake spawners (620mm), but lake spawners had a much wider distribution (i.e. much higher SD), so that the statistical test did not detect a significant difference. Late migrants (610mm) were significantly smaller than River spawners, and smaller than Lake spawners (but again the comparison test with Lake spawners was not significant due to the large SD)

Sex Ratio

The sex ratio of adult Sockeye migrating past Klukshu weir in 2016 varied substantially over time (Table G 3), ranging from 27% females in mid-July (week 29) up to 76% females in late September (week 40), excluding the first and last week of sampling with only 1 and 2 fish sampled. The overall average, weighted by weekly run size, is 58% females.

Sex ratio increased steadily from week 29 to week 37 (early Sep), then became more variable (i.e. dropped for two weeks and spiked again in the final week). Figure G 2 shows the pattern. A simple linear regression fit to the pattern estimates a weekly increase of roughly 3.5% females (p-value <<0.05, R^2=0.6)

The sex ratio of early migrants was significantly different from later migrants (Table G 4), with 100% of the bootstrap tests having p-value << 0.05. Note that this test showed essentially the same result for raw sex ratios and ratios weighted by weekly run size within a timing group, but the estimated confidence intervals are different. The weighted sex ratios are 45% female in the early migrants and 63% females in the late migrants, with a 95% confidence interval for the difference in sex ratio ranging from 11% to 25%.

Observed sex ratio in the spawning ground samples is purely a result of the survey objective to collect roughly equal number of DNA samples from males and females (Table G 5).

Age Composition

The age composition of varied substantially between males and females, and over time (Table G 6, Table G 7). Almost all females and most males were 5 years old who spent 1 year rearing in freshwater (Gilbert-Rich age class = 5.2). Age 4.2 were also present, but much more among males than females. For males, the weekly % age 4.2 ranged from 5% to 27% for weeks with more than 10 full age readings. For females it ranged from 0% to 7.5%.

Table G 8 summarizes statistical tests of differences in age composition. Early migrating males had significantly fewer age 4.2 (8% avg weighted by run size) than late migrating males (18% wt avg), with 94% of the bootstrap tests having p-value <0.05). However, the age composition of early and late migrating females was very similar, and none of the bootstrap tests had p-value<0.05.

Linear regression fits to the weekly % age 4.2 produce the same result. For females, the regression line (Figure G 3) is a very poor fit ($p >> 0.05$) and explains none of the the observed pattern (adjusted R^2 essentially 0). For males, the linear regression fit (Figure G 4) is better ($p < 0.05$), but doesn't explain much of the observed variation (adjusted $R^2 = 0.33$). The fit could probably be improved by dropping weeks with small sample sizes (first and last week) and fitting non-linear models, but wasn't considered necessary for our analyses.

7.3. Radio Tag Analysis

Tags Applied

We radio tagged 165 adult sockeye at Klukshu weir in 2016. Table 3 summarizes the sample sizes and observed patterns. Appendix J describes the observed movement of each tagged fish.

70 tags were applied to the early part of the run (before 14 August, weeks 28 to 33), 19 tags during the mixed period (14 -20 August), and 76 tags during the late run (after 20 August, weeks 35-41). 150 fish were tagged with new tags, and 15 with redeployed tags. Note that redeployed tags all had very short tracking histories and a very poor match between tag fates and genetic stock ID, and were excluded from some analyses (Section 7.8).

Table 4 shows weekly run sizes, tag fates, and tag expansion factors if all tags are used in the analyses. Note that our analyses don't use the tag expansion factors, but use the weekly run proportion to weight estimates instead, which basically amounts to the same thing (Section 5.2).

Movement Patterns

Table 3 shows that 83 tags had a clear pattern, 70 required interpretation, and 12 were either harvested, lost, or not recorded.Overall, the most common pattern was tags rapidly passing all towers and entering the lake (56/165,34%), but the frequency of patterns differed by timing group:

- *Early:* 14 different movement patterns were observed for the early migrants. The two most common are fish that moved about the mainstem then ended up at a river spawning site (18/70, 26% of Early) and fish that migrated straight to the lake and stayed there (16/70,22% of Early). Note that a substantial number of early tags were detected by the lake tower. Some moved back down the mainstem after, but others didn't.
- *Late:* Most of the late migrants either moved straight to the lake or were only detected in the lake (i.e. no detections at the river towers). Only 6 of the 76 late tags moved about the mainstem (i.e. detected at different river towers at different times) and half of those still ended up in the lake as a final destination. 12 of the late tags had a short tracking history that ended in the river, but half of those were redeployed tags, which we excluded from the final analyses.

Run Composition based on Tag Fates

Table 6 shows the weekly estimated proportion of River sockeye based on tag fate, using either all tags (females and males, new and redeployed tags), or new tags only. The proportion of tags assigned to a river fate varied substantially over time, ranging from high of 73% in mid-July (week 29) to a low of 7% at the end of August (week 36) among those weeks with more than 10 tags. If redeployed tags are excluded, the proportion assigned to a river fate is much lower in week 39, and no estimate is available for week 40. This affects statistical tests and regression fits.

The run composition of early migrants was significantly different from later migrants (Table 7), with 100% of the bootstrap tests having p-value << 0.05. Note that this test showed essentially the same result for raw ratios and ratios weighted by weekly run size within a timing group, but the estimated confidence intervals are different. The weighted run compositions 52% river fate in the early migrants and 18% river fate in the late migrants, with a

95% confidence interval for the difference in run composition ranging from 19% to 50%. Repeating the test without the redeployed tags gives almost the same results.

Figure 8 shows the weekly pattern in tag fate composition, and the corresponding tag counts and tag ratios. The % river fates decreased steadily over the course of the run until early September (week 37), then became highly variable as number of tags decreased and redeployed tags were used. Tag counts and tag ratios were fairly stable over most of the run, except for 2 early weeks when extra tags were applied to increase the chances of detecting two run components, if they are present.

The early/late comparison and weekly pattern described above might be sensitive to a few inconsistent or misinterpreted tags, given the relatively small weekly sample sizes. To ensure that results are robust, we also check the proportion test and regression fit for several variations. Table H 1 lists weekly proportions of tag fates for tagged females only, and Table H 2 further excludes redeployed tags. Table H 3 replicates the Chi-Squared test from Table 7 for these alternative data sets. Table H 4 lists tag fates for males only.

Figure 9 shows a simple linear regression fit to the weekly stock composition (i.e. % tags assigned to the river spawners), using only results for new tags applied to females, and excluding statistical weeks with less than five valid tag fates. The regression fit is highly significant (p-value << 0.05) and has strong predictive power (adj. R^2 =0.76, the regression line explains about ¾ of the observed variability in stock composition). The regression fit shows that in 2016, the run consisted of about 60-70% River spawners early on, and the % River spawners dropped roughly 6% per week.

Figure H 4 shows regression fits to four alternative subsets of the data (e.g. including results for redeployed tags). The general pattern is always the same, but cleaning up the data by excluding redeployed tags and dropping weeks with few tag results does improve the regression fits (i.e. Figure 9 vs. Figure H 4).

Migration Times and Speeds

Table H 5 summarizes migration times from the weir tagging event to the 3 towers along Klukshu River, and breaks the observations out into different subsamples (by timing group, by statistical week, by tag fate, and by genetic match). Overall, the median time was 2 days to reach Motheral, 4 days to reach Vand, and 6 days to reach the lake tower. However, migration times differed substantially by subgroup:

- Early migrants took almost 3 times as long as late migrants to reach Vand Tower (8d vs. 3d).
- Fish with a tag fate assigned to the river took more than twice as long to reach Vand (10.5 vs. 4 days) compared to fish with a lake fate.

Table H 6 shows the same information, but converted to migration speed in km/day. Overall, the median speed was about 5 km/day to Motheral, 3 km/day to Vand, and 4 km/day to the lake tower.

Figure H 1, Figure H 2, and Figure H 3 show distribution in migration times to each radio tower along the Klukshu, broken out into different sample groups .

Section 7.8 describes the match between tagging results and genetic stock ID, and Section 7.9 discusses differences in migration for 3 subsamples of the tagged fish: grouped by weir timing, grouped by tag fate, and grouped by GSI match.

7.4. Genotype Analysis - Allele Frequencies

Note that sample groups used for the summaries in this section are based on later analyses, which fitted phylogenetic trees (Section 7.5) and assigned probabilities of genetic stock matches (Section 7.6). These later analyses linked the following samples together:

- *Lake Group*: 2016 samples of lake spawners, late weir migrants, and juveniles sampled at the lake outlet.
- *River Group:* 2016 samples of river spawners, early weir migrants, and juveniles sampled on the Klukshu mainstem.

Table 10 summarizes allele distributions using two different metrics for 4 alternative sample groups (Lake Group, River Group, Neskataheen baseline, and all 2016 samples combined with the revised baseline samples for the Alsek (Set G11; Table 8). Allele variability, expressed as the average number of unique alleles in 1000 bootstrapped samples of 100 alleles (similar to Table 2 in Beacham et al. 2008), differs substantially across loci and between sample groups, from 3-4 alleles/100 samples for *oki1a* to 19-29 alleles/100 samples for *oki10*.

More detailed summaries for each group of samples are included as Table I 5 to Table I 8. These show the number of samples and number of unique alleles for each locus. Note that the avg. alleles / 100 samples can be much lower than the total number of unique alleles in the sample.

We summarized allele frequencies in a diagnostic plot showing rescaled allele frequencies for the most prevalent allele in each sample group, plus other alleles with the largest differences in frequency between the two sample groups, up to 10 alleles (Section 5.6). Figure 10 compares the allele frequency profiles for the 2016 Lake Group and 2016 River Group at 14 loci, and Table 11 summarizes the observed patterns:

- 10 of the 14 loci show little obvious difference between allele frequencies for the River Group and and the Lake Group of samples collected in 2016. For these 10 loci, both sample groups have the same predominant allele, and the remaining alleles have similar frequencies of occurrence (i.e. pattern types 1, 2, and 3 in Table 11). Note that the average numbers of unique alleles in the bootstrapped samples for these loci are also similar for the two groups of 2016 samples (first 2 columns of Table 10).
- 4 of the loci have substantially different patterns of allele frequencies for the River Group and and the Lake Group. One locus, *oki10*, has the same predominant allele for both groups, but very different pattern for the remaining alleles. Note that *oki10* also has the largest variety of alleles among the 14 loci used in this analysis (Table 10). The other 3 loci (*i1*, *oki6*, and *3dre*) have different predominant alleles, but the avg. number of unique alleles / 100 samples is very similar in the two sample groups.

7.5. Genotype Analysis - Trees

We explored the genetic relationships between the 2016 samples and the DFO baseline samples for Alsek Sockeye populations by fitting phylogenetic trees to different groups of genotype sets. Table 8 lists the alternative genotype sets we worked with, and Table 9 lists the alternative tree fitting approaches we tried. Section 5.7 describes the methods in detail.

Figure 11 shows a stylized phylogenetic tree summarizing the key results from all these alternative tree fits. The diagram shows genotype samples that were consistently grouped together:

- *Klukshu River*: Adults sampled at the weir early in the run (before Aug 14) and fry sampled on the Klukshu mainstem were consistenly grouped with the Klukshu River spawner sample.
- *Klukshu River / Neskataheen Complex:* Klukshu River spawners, early migrating adults, and river fry were consistently grouped with the Neskataheen baseline sample.
- *Klukshu Lake*: Adults sampled at the weir late in the run (after Aug 20) and juveniles sampled at Klukshu Lake outlet were consistenly grouped with the Klukshu Lake spawner sample.
- The group of adults sampled around mid-August, the cut-off point between early run and late run used since the late 1990s, was assigned to different sample groups depending on the genotype set and fitting method used. Note that these samples were split into roughly two halves in the genetic stock ID (Section 7.6), one half assigned to the Klukshu River / Neskataheen Complex, the other to Klukshu Lake.

Figure 12 shows the actual tree fit and bootstrap probabilities for the base case (T4 in Table 9). The bootstrap probabilities show how consistently each binary split shows up across 1000 resampled tests (i.e. drop some allele readings and refit the tree). 100% of the bootstraps grouped the early weir samples, river spawners, river fry, and Neskataheen together. 100% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. 89% of the tests put all the Klukshu samples and Neskataheen on a separate branch from all the other Alsek samples (some of these tests had Kwatine or some other population grouped with the Klukshu samples). Note that this is one of 16 alternative trees produced with Treefit. Appendix M and Appendix N show the alternative tree fits explored in the sensitivity analyses and list the estimates of genetic distance used to fit the trees. Note that for a specific set of genetic distance measure and tree fitting algorithm, the fitted trees are similar between TreeFit and R, but estimated values of genetic distances differ (e.g. Table M 4 vs. Table N 3). One recommendation for future work is to further explore methodological differences between the available software tools (Section 9.4).

Table 12 categorizes the 16 alternative fits generated with the TreeFit program into five types, and lists a measure of how well they fit the sample. The tree shown in Figure 12, using the *Dc* measure of genetic distance (Cavalli-Sforza and Edwards 1967) and the *Neighbour Joining* algorithm for tree fitting, has the best overall fit (i.e. highest R^2). All 16 variations combine all the Lake group samples. 14 of the 16 variations combine all the River group samples, but 2 cases move the river spawners to a separate branch within the Klukshu /

Neskataheen aggregate. Trees based on the neighbour-joining algorithm have better fits (i.e. higher R^2) than trees based on the UPGMA algorithm.

Table 13 compares bootstrap results for the 11 different fitting methods and two alternative genotype sets. The alternative fotting approaches include four alternative measures of genetic distance and two alternative tree fitting algorithms, implemented across two different software applications (TreeFit, and the R packages {ape} , {adegenet} , and {phangorn}). Table 9 lists the alternative approaches.

Note that bootstrap tests differ between the two software applicationsL

- *TreeFit:* 1000 resamples of individual loci (reshuffling parts of a genotype), with automated summary of bootstrap probabilities for key nodes.
- *R:* 100 resamples each dropping 10% of the records in each sample group (i.e. excluding whole fish), and visually checked for key nodes.

Bootstrap support for the River Group and Lake Group is very high across all 11 alternative approaches (Median values are 98% for the River group of samples and 100% for the Lake Group of samples. Most alternative tree fits separate the Klukshu samples and Neskataheen baseline from all the other Alsek baselines (G12; T1-T8 and T11). In two cases, the baseline for Kwatine Creek moves between different nodes, resulting in low bootstrap probablities for any particular arrangement of branches (Table 13).

7.6. Genotype Analysis – Genetic Stock ID

We used the ONCOR program (Kalinowski et al. 2007), which was specifically developed for Salmon stock ID, two implement two types of analysis:

- Calculate probabilities of assignment to different baselines for each sample (i.e. each genotype record)
- Calculate the probability of assigning baseline samples back to the group they are in (“leave-one-out” test)

Section 5.8 outlines the methods.

Assignment Probabilities

Table 14 summarizes genetic matches of the 2016 samples to Alsek sockeye baselines, using the revised baseline set, which substitutes the 2016 spawning ground samples as baselines for Klukshu (Klukshu_River, Klukshu_Lake). Table 15 replicates the analysis with the original baselines for Klukshu (weir samples split into Early, Mix, Late; mostly from early 2000s; Table I 3). Table 16 replicates the analysis with a trimmed baseline, which includes only 3 samples: 2016 Klukshu River spawners, 2016 Klukshu Lake spawners, and DFO’s Neskataheen baseline. Each table shows the number of samples which have each baseline group as the best match (i.e. highest probability; Section 5.8). Klukshu samples matched to the Neskataheen baseline were interpreted as part of a Klukshu River / Neskataheen genetic group (Section 7.5). Appendix J lists the best and 2nd best match for all the tagged samples. Section 8.5 discusses alternative interpretations of Klukshu samples matched to non-Klukshu baselines.

Using the revised baseline (Table 14), most of the early Sockeye (i.e. passed Klukshu weir before August 14th) were matched to the Klukshu River / Neskataheen group. Conversely, most of the late sockeye (i.e. passed Klukshu weir after August 20th) were matched to the Lake spawners. Roughly half of the sockeye during the mixed period (i.e. passing Klukshu weir Aug 14-20) were matched with the Klukshu River / Neskataheen group. Juvenile samples collected in 2016 matched up very closely with the spawning ground samples Only 1 of 278 juveniles sampled at Klukshu Lake outlet and in the lake was matched to the Klukshu River / Neskataheen group (less than 1%). Conversely, only 1 of 214 fry sampled at on the Klukshu mainstem at Vand Creek was genetically matched to the Lake spawners. Both of these numbers are much smaller than the number of samples matched to other baselines (e.g. 14 of the lake outlet fry, 22 of the mainstem fry). Note that almost 10% of the 2016 Klukshu samples were matched to other baselines, such as U_Tatshensh_RT, Alsek_T_down, or Tweedsmuir_RT.

Using the original baseline (Table 15), the matches for adult samples are less clear than with the revised baseline (Table 14). Most sample groups had more assignments to “other” baselines, and only about 50% of samples from river spawners were matched to the Early Klukshu/Neskataheen group. However, the results are still broadly similar to the matches for the revised baseline in Table 14. Most of the early-returning adults and most of the mainstem fry were matched to the Early Klukshu/Neskataheen group. Very few of the late-returning adults and almost none of the lake juveniles were matched to the Early Klukshu/Neskataheen group.

Using the trimmed baseline (Table 16), the matches for adult samples are similar to the results for the revised baseline (Table 14). Most of the early-returning adults and most of the mainstem fry were matched to the Klukshu River / Neskataheen group. Few of the late-returning adults and almost none of the lake juveniles were matched to the Klukshu River / Neskataheen. Note that for comparisons like this, which match individual samples to only 3 baselines, even a random assignment would be correct 33% of the time.

Table 14 to Table 16 summarize the genetic stock ID results in terms of the number of samples assigned to each baseline group (i.e. the highest probability), using three alternative baseline sets.

Figure 16 plots the resulting stock composition for the revised and trimmed baselines. Observed compositions are consistent with the tree fitting results (e.g. Figure 12). Adults sampled at the weir early (before Aug 14) and fry sampled on the Klukshu mainstem near Vand Creek were mostly assigned to the Klukshu River spawning ground sample. Adults sampled at the weir late (after Aug 20) and juveniles sampled at the lake outlet were mostly assigned to the Klukshu Lake spawning ground sample. Adults sampled during the mixed period (Aug 14 to 20) had a substantial proportion of fish matched to both of the spawning ground samples, but a bit higher proportion assigned to the Klukshu River / Neskataheen group. This caused the tree fits for the Mix samples to be unstable (i.e. grouped with different baselines depending on fitting method) and caused some of the other branches to shift around as well (e.g. river spawners split from river fry in 2 of 16 test cases; Table 12). Estimated genetic composition for each sample group is similar for the two alternative baselines, but proportions are not identical.

Figure 13 to Figure 15 look at a different aspect of the stock ID results by plotting the distribution of assignment probabilities. For example, two samples might be assigned to one of the Klukshu baselines, but one with probability 95% (high confidence), and the other with probability 65% (moderate confidence).

Figure 13 summarizes the assignment probabilities for genetic stock ID against the revised baseline. All of the sample groups have some samples with very low assignment probabilities (i.e. matched the sample to a baseline outside the Klukshu with a very high probability), but most samples in each group were clearly assigned to one of the baselines in the All Klukshu / Neskataheen group. Lake outlet smolts had the highest proportion of samples with low assignment probability to Klukshu or Neskataheen.Table 17 lists the number of samples in the different probability ranges.

Figure 14 shows assignment probabilities against the original Alsek baseline, which uses Early/Mix/Late weir samples for the Klukshu. Assignments to the All Klukshu / Neskataheen group are less clear (i.e. lower probabilities) for several of the sample groups. This is particularly pronounced for the early weir sample, the untagged late weir samples, and Vand Creek Fry. Conversely, lake outlet smolt matches are improved using this baseline. The 2016 river spawner sample turned out to be hard to match up against any of the populations in the original baseline, with about half the samples having a less than 50% probability match to the All Klukshu / Neskataheen group. Basically, the stock ID calculation concludes it's a coin toss whether the sample is from the Klukshu or elsewhere). Note, however, that the 2016 river spawner sample serves as an informative sample in the revised baseline (i.e. can assign many weir adults and juveniles quite clearly to either the river or lake spawners; see Table 14).

Figure 15 shows assignment probabilities against a trimmed baseline, which includes only the 2016 spawning ground samples from the river and lake, plus Neskataheen baseline samples. Assignments to the Klukshu River / Neskataheen group or the Lake baseline are very clear for most of the sample groups. Early migrating fish in the untagged sample and the Vand Creek fry sample are mostly matched to the River spawners or the Neskataheen baseline with a high probability. Late migrating fish with tags and Lake juveniles are mostly matched to Lake spawners with a high probability (i.e. low probability match to Klukshu River / Neskataheen). The remaining sample groups have a wider distribution of assignment probabilities.

Table 18 summarizes stock ID assignments to baselines outside of the All Klukshu / Neskataheen complex, using the revised baseline. About 10% of the valid genotype readings from adults sampled at the weir and juveniles sampled throughout the Klukshu were genetically matched one of the non-Klukshu baselines. Note that these are the best matches (i.e. highest probability), but they are not necessarily good matches (i.e. assignment probability could be 40% for the best match, and 25% for the second best match, and a few percent for many other matches). Appendix J lists the best and 2nd best match for all the tagged samples, as well as the assignment probabilities. Upper Tatshenshini River Type, Alsek / Tatshenshini Downstream, and O'Connor River Type Sockeye are the most frequent non-Klukshu matches, accounting for about 60% of all the non-Klukshu assignments. Section 8.5 discusses alternative interpretations of Klukshu samples matched to non-Klukshu baselines.

Leave-one-out Test of Baselines

The ONCOR program (Kalinowski et al. 2007) includes a sensitivity test for assessing the properties of a genetic baseline set by taking individual records out of each baseline and estimating the probability with which the sample would be assigned back to its baseline.

Table 19 shows the results for this leave-one-out test applied to the revised baseline set, which substitutes the 2016 spawning ground samples as baselines for Klukshu (Klukshu_River, Klukshu_Lake). Table 20 replicates the analysis with the original baselines for Klukshu (weir samples split into Early, Mix, Late; mostly from early 2000s; Table I 3), as well as with a trimmed baseline (only 2016 Spawner samples and Neskataheen baseline), and a test using only the 2016 spawing ground samples.

The probability of correct assignments is similar or identical in the revised and original baselines for all the sample groups that are in both baselines, and most of the baselines have low to very low % correct assignments (e.g. Alsek_T_down with 5.9%). Note that the probability of correct assignment can be low for different reasons, such as sample baseline sample size (e.g. Kane) or similar other baseline populations (Klukshu River vs. Neskataheen).

Correct assignments are moderate for the Klukshu Lake spawners and low for Klukshu River spawners if they are combined with the other Alsek baseline set. Only about 1/3 of the Klukshu River spawners spawning ground samples are reassigned to their source sample, and about a quarter are misclassified as Neskataheen fish. Re-assignments perform even poorer with the original baseline, where only 15% of Early Klukshu weir samples are reassigned correctly. However, when focusing the test only on Klukshu and Neskataheen, re-assignment probabilities are much better at about 80% for Klukshu Lake spawners and Neskataheen baseline, and about 60% for Klukshu River. Also note that Klukshu River samples have a combine probability of assignment to either Klukshu River or Neskataheen of almost 90%, indicating that 9 of every 10 samples are clearly distinguished from the Klukshu Lake spawner sample.

Using only the 2016 spawning ground samples, the reassignment probabilities in the leave-one-out test are also around 80%.

Note that the reassignment probabilities in the leave-one-out test tend to be much lower than the stock match probabilities in the earlier analysis (Figure 13 to Figure 15), even though both analyses were implemented with the ONCOR software package (Section 5.8), but that assignment probabilities here are much lower than the stock ID results in Table 14 and Table 17 . An investigation into the cause for this difference between analyses falls outside the scope of the current project, but is listed as priority item for future work (Section 9.4).

Run Composition based on Genetic Stock ID

Table 21 shows the weekly estimated proportion of River sockeye based on genetic stock ID, using all valid samples and a revised baseline for Alsek Sockeye. DNA samples were collected from most of the adults sampled at the weir (Table 2). Samples with valid genotype include only those where a tissue sample could be matched to a statistical week and the genotype reading was both mostly complete and not a duplicate (Appendix I). Genetic stock ID matches (Section 5.8) were classified into 3 categories, base on the fitted phylogenetic trees (Section 7.5): Klukshu River / Neskataheen, Klukshu Lake, and Other. Note that these observations can't be separated into males and females, because only weekly sex ratio is available for the pooled DNA samples. Individuals can only be matched up within the much smaller sample of tagged fish. The proportion of adults matched to the River spawners varied substantially over time, ranging from high of 93% in mid-July (week 29) to a low of 4% at the end of September (week 40) among those weeks with more than 10 valid genotype samples.

The run composition of early migrants was significantly different from later migrants (Table 22), with 100% of the bootstrap tests having p-value << 0.05. Note that this test showed essentially the same result for raw ratios and ratios weighted by weekly run size within a timing group, but the estimated confidence intervals are slightly different. The weighted run composition was 87% matched to River spawners in the early migrants and 18% River matches in the late migrants, with a 95% confidence interval for the difference in run composition ranging from 63% to 74%.

Figure 17 shows the weekly pattern in genetic stock composition, and the corresponding number of weekly DNA samples and sampling ratios. The number of weekly DNA samples was were fairly stable over most of the run, except for one week in mid-July (week 30) with few samples (see weir operation notes in Table B 1) and another week in early August (week 32) with a larger sample near the assumed peak of the early run. The corresponding sampling ratio decreased over time, as abundance increased. The % river matches decreased

over the course of the run until late September (week 40), but two alternative relationships fit the observed pattern:

- *Two distinct time periods*: treat early samples as one group and late samples as another group, then fit a moving average or estimate a weighted average for the time period. The weighted averages are 87% river match for the early run, and 18% river match for the late run (see Table 22).
- *Linear regression*: The regression fit is highly significant (p-value <<0.05) and predictive (adj. R^2=86%). and estimates a roughly 10% decrease in % river matches by week. The regression fit shows that in 2016, the run consisted of about 80-90% River spawners early on, and the % River spawners dropped roughly 10% per week.

7.7. Genotype Analysis – Family Structure

Table 23 summarizes sibling relationships in the 2016 Klukshu samples, reconstructed using the COLONY program (Section 5.9). This analysis links samples with similar genotypes to a set of constructed source genotypes (i.e. virtual parents). Note that our samples cover 3 brood years, and this analysis does not establish actual brood lineages across samples. However, the interpretation of common parentage is valid within each sample group. The table focuses on full siblings (e.g.likely share both parents).

Overall, most of the samples are not full siblings (1293 virtual parent pairs for 1536 samples; 84%). Also most of the sample groups have very few or no full siblings in the sample (99% or more unique parent pairs). Notable exceptions are adults migrating past the weir early (87% unique parents) and fry sampled on the Klukshu mainstem near Vand Creek (63% unique parents). The fry sample had a total of 135 unique parent pairs for 214 fry, but 35 of those parent pairs account for 114 of the samples, and 1 pair of virtual parents accounts for 15 full siblings in the Vand Creek fry sample.

Figure 18 shows a heatmap of the reconstructed sibling relationships within and across sample groups. The heatmap shows the same thing as the summary in Table 23: Most of the full siblings were identified within the newly emerged fry on the Klukshu mainstem, but there were some among the early weir returns as well.

Additional analyses could include looking at half-sibling relationships (i.e. 1 parent in common) and developing a more formal family reconstruction. This exceeds the scope of the current project, but has been noted as a suggested priority for future work (Section 9.4).

7.8. Cross-Check: Tag destination vs. Genetic Stock ID

Adult Sockeye passing the weir were radio tagged and sampled for DNA. The total sample sizes were 820 tissue samples and 165 tag applications. After sample processing and data clean-up (Sections 5.4 and 5.5), there were 124 samples which had both a valid genotype reading and an assigned tag fate. For those 124 samples, we can cross-check the two methods to assess their performance. Appendix J describes movement patterns and genetic stock ID results for each tagged fish.

Table 24 summarizes the observed matches, broken out based on the observed pattern of movement. The proportion of matching assignments varied for different tag movement patterns and by timing group. For example, the 16 fish that moved about the mainstem and then spent an extended period in the river were classified as river spawner based on tag fate, and 15 of them were genetically matched to either the Klukshu River spawner sample from 2016 or the the Neskatheen baseline (i.e. Klukshu River / Neskataheen Complex). In contrast, 52 fish rapidly migrated to the lake tower range and then were detected there for an extended period. These were classified as lake spawners based on tag fate, but the genetic stock match changed over time: Of the 12 fish tagged early, only 4 are genetically matched to the lake spawners (25% agreement between tags and DNA). Of the 32 late migrating fish with the same observed tag pattern, 25 are genetically matched to the lake spawners (78% agreement between tags and DNA).

Note that short radio tracking records that ended in the river were genetically matched to river spawners among the early and mixed sample groups, but genetically matched to lake spawners among the late group (i.e. radio tag pattern looks like a river spawner, but genetically it is a lake spawner). Note that these results are for new tags only. Redeployed tags had very low proportion of tag vs. GSI match and were excluded from most analyses.

Appendix K compares the tag fates and genetic stock ID (GSI) for different subsets of the 2016 weir samples. GSI matches used the the revised Alsek baseline (see Sec. 7.5). All the tables are organized the same way, with columns showing the count of samples with a particular combination of results using the following notation (T =

Tag, G = GSI, R = River, L = Lake, O = Other, NA = tag fate and/or stock ID not available. For example, “T:R /G:L” denotes a river tag fate that was genetically matched to the lake spawners.

Table K 1 shows the tag vs. GSI match for all adults tagged at Klukshu weir.The proportion of samples where radio tagging and GSI produced consistent classifications (termed “% correct” below), varied by timing group. Early migrants accounted for 42% of the tags and were 57% correct (i.e. 33 of 58 tags in this timing group were either T:R/G:R or T:L/G:L). Late migrants accounted for 46% of the tags and were 64% correct. Female samples were correctly interpreted more frequently than male samples (F: 86/135=64% / M: 6/13=46%). Tag movement patterns classified as “Clear” (68% correct) were correct more often than those classified as “Interpretation” (55% correct).

Table K 2 to Table K 4 show the same summary, just for females separated by timing group (56 Early, 17 Mix, 62 Late). Table K 5 shows results for the 13 tagged males, and Table K 6 splits out the redeployed tags. Overall, the 12 redeployed tags for which tag fates were assigned were only 36% correct, but a closer look shows that performance was even worse than that: 1 tag was assumed lost, 5 were assigned a lake tag fate and 6 were assigned a river tag fate. Genetically they were mostly matched to the lake spawners, which is consistent with other analyses, because the redeployed tags were applied very late in the run. In summary, the redeployed tags all had short tracking histories, and tage fates were assigned roughly half to river spawners and half to lake spawners which makes it basically a coin toss.

Note that these matches could possibly be improved by using the trimmed baseline consisting only of Klukshu and Neskataheen samples and thereby eliminating the “other” category for genetic matches. However, the current comparison is probably more broadly relevant in terms of understanding the performance of these two methods, because most tagging studies would be done in a setting with more than two populations.

7.9. Differences in Migration Up the Klukshu River

Results presented so far allow us to split the tagging data three different ways to explore differences in migration behaviour: grouped by weir timing, grouped by tag fate, and grouped by GSI match.

Figure 19 shows differences in migration time to the 3 stationary towers, from last detection at the weir tower to first detection at the upstream towers. All three alternative groupings show a clear difference in migration timing:

- Early migrants took about twice as long as the late migrants to reach Vand and Lake towers, and migration times of early migrants were much more variable (long whiskers).
- Tags assigned a River fate took about twice as long as the fish assigned Lake fate to reach Vand, and 4 times as long to reach the lake tower (i.e. among those river fate fish that were detected at the lake tower).
- Fish that were genetically matched to river spawners took about twice as long as those matched to lake spawners to reach Vand and Lake towers, and migration times of the river-matched fish were much more variable (long whiskers).

Figure 20 shows the distribution of migration speeds until first detection at Vand tower split into males and females, and further split based on tag fate and GSI match. Females migrated much faster than males, and lake fish migrated faster than river fish. Note, however, that these are net migration speeds, from the weir to the Vand tower, and do not reflect actual swimming speed. For example, many river fish seem to spend a lot of their time moving up and down stretches of the mainstem, while the lake fish tend to move straight upstream.

Appendix H tabulates migration times (Table H 5) and migration speeds (Table H 6), and plots distribution of migration times to each radio tower along the Klukshu, broken out into different sample groups (Figure H 1 to Figure H 3).

7.10. Composition of 2016 Run at Klukshu Weir

The sampling program in 2016 produced two alternative estimates of stock composition for the Sockeye run at Klukshu Weir, one using radio tags and the other using genetic stock ID (GSI). Results for both went through substantial data clean-up (Sections 5.4 and 5.5) and sensitivity analyses (Sections 7.3 and 7.6), but the final results in terms of stock composition are mostly consistent between the two assessment methods.

Both radio tags (Table 7) and the GSI matches (Table 22) showed a significant difference in composition between early and late migrants, but DNA results estimate a much higher proportion assigned to the Klukshu River / Neskataheen group (87% weighted average for the early run) than the radio tag fates (52% weighted average for the early run). Note that the genetic stock ID had a much larger sample size than the tagging

program (656 vs. 136), and different tag movement patterns had different levels of consistency with the GSI matches (Section 7.8).

Weekly run composition estimated from tags (Figure 9; details in Section 7.3) followed the same pattern as the genetics-based estimates of run composition (Figure 17; details in Section 7.6). However, the genetics-based estimates are higher than the tag-based estimates for the early run and lower for the late run.

Figure 21 compares the two alternative estimates of run composition, excluding tags with unknown fate and genetic matches to "other" populations. The estimates are roughly similar for 8 of the 11 statistical weeks with both estimates, but there is large difference for the early part of the run: For weeks 31 to 33 (late July/early August), the estimated proportion of river spawners is almost 90% based on the genetic stock ID, but only about 45% based on the radio tags. However, when converting these composition estimates into actual abundances (i.e. multiply by weekly weir count total), both methods produce a similar pattern: River spawners returned earlier, but were still present in similar abundances later on when the bulk of the lake spawners passed the weir.

Figure 22 shows the corresponding run timing curves. The Klukshu River population, identified either by tag fate or by genetic match (i.e. matched to 2016 river spawner sample or to closely related Neskataheen baseline), started to migrate in larger numbers past Klukshu weir in late July (week 31), with the bulk of the run arriving between end of July and end of August (weeks 32-35), and the tail-end of the run extending until the end of September. The run of the Klukshu Lake population, identified either by tag fate or by genetic match to the 2016 lake spawner sample, started to build up to similar abundances as the River run towards the end of the early time window (i.e. in early August, week 33), but the bulk of the run came through in a 3-week window in late August to early September, and substantial numbers continued to pass the weir until early October.

Both populations returned over the full 3 months of weir operation, but the River population had a long, protracted migration pattern while the Lake population had a very pronounced peak migration period of 3 weeks.

Figure 23 compares three alternative estimates of total run composition. Based on genetic stock matches, River Sockeye accounted for about 33% (Table 21) of a total run of 7,584 Sockeye (Table 2), giving approximate abundances of 2,503 River Sockeye and 5,081 Lake Sockeye in 2016. Based on tag fates, River spawners accounted for about 23% of the run (Table H 2; females with new tags only), giving approximate abundances of 1,744 River Sockeye and 5,840 Lake Sockeye in 2016. Finally, using the August 15th cut-off date used by DFO since the 1990s, the early run was 1,381 (18%) and the late run was 6,203.

8. Discussion

8.1. Field Observations – Sampling Methods

Project Design

During the planning stages for this work, the Working Group (Section 1.1) extensively debated alternative fish capture methods for the the different project components. Sampling adult sockeye at Klukshu weir was considered straight forward and only required coordination of the subsampling approach with the DFO weir crew. However, the capture of the juveniles and of adult spawners at different locations in the watershed was expected to be more challenging. To increase the odds of achieving adequate sample sizes, we prepared gear for multiple capture methods, and planned for multiple sampling events at several different locations. Candidate sampling locations for adults and juveniles were pre-identified by combining traditional and local knowledge with observed spawning distribution in previous studies (Petkovich 1997; Smith et. al 2005). Site selections and sampling effort at different sites were then adjusted based on in-season field observations such as presence of redds, capture of ripe and post-spawning fish, and radio tag distribution records from the stationary towers.

Sampling Juveniles

The field crew prepared 5 alternative sampling gears for juveniles, and deployed 4 of them depending on local conditions at each of the 4 sampling sites. 3 types of traps and beach seines were tested, and achieved sample sizes that exceeded our original budget for DNA processing (Appendix E). Therefore it was not necessary to deploy electrofishing gear, which had also been prepared as a backup option.

The Wolf-type Incline Plane Trap (IPT) caught a large number of sockeye smolts and quite a few fry (Sockeye, Coho) at the outlet of Klukshu Lake, but most of these were caught in two of the 14 sampling events (374/472 smolts = 80% of samples; Table E 1). The IPT was most effective at capturing fish during evening or early morning hours.

Beach seining netted consistent numbers of sockeye fry on multiple dates in 2 of 3 locations, and a large number of coho fry at 1 of 3 locations. The small mesh worked very well in the capture of recently ermerged sockeye fry, especially in back-eddies located within or near spawning sites. Beach seining was facilitated by the high water clarity, with fry clearly visible at all sampling sites. In addition, recently emerged fry are not strong swimmers and thus are easily captured with a beach seine.

The Fyke trap and Gee-type minnow trap both caught large numbers of Coho fry, but catches were highly variable over time with the Fyke trap and between sites for the minnow trap. Fyke trap and IPT required field staff to be vigilant in clearing any debris buildup, especially in periods of high flow. It was expected that they would not be effective for capturing sockeye fry or smolts but instead were used to monitor other species of fish in the system, some which may be considered predatory to sockeye and other salmon. The traps were effective in capturing coho fry at site C but very few were captured at the other sites sampled. The only potential predatory fish captured in the traps were Dolly Varden which were captured in low numbers throughout the sampling period.

Overall, the variability of juvenile sample sizes confirms that projects need to budget for multiple gears, multiple sites, and multiple sampling events.

We calculated an approximate time window for fry emergence using accumulated thermal units (based on river temperature data; Figure E 1), and given the large sample of recently emerged fry, the calculation seems to have been sufficiently accurate.

Sampling Adults at the Weir

Handling of adult Sockeye at Klukshu weir in 2016 worked very well. Our project crew implemented extensive sampling steps in addition to regular weir operation, working in close coordination with the DFO weir crew. The DFO crew sampled 820 adults (11% of the run) for sex, condition, fork length, and scales. Our crew obtained valid DNA samples for almost all the handled fish (809 valid genotype readings, 99%) and applied 165 radio tags (20% of handled fish). Table 4 lists the weekly sampling ratios, which are also plotted in Figure 8 for radio tags and Figure 17 for DNA samples.

There was one operational challenge which we addressed with a two step sample handling approach, but which created extra costs and analytical challenges later on. The pace of fish handling at the weir exceeded our crew's

ability to individually label and pack the tissue samples for all the handled fish, so we took weekly pooled samples from all fish, and an additional individually-labelled tissue sample from the tagged fish (Section 2.1). This approach allowed our weir sampling to integrate smoothly with DFO's weir operation, but resulted in 145 duplicate tissue samples (out of 1,196 total tissue samples) that had to be packed, shipped to Nanaimo, and processed, for a total extra cost of about $4,000. Once samples were processed, duplicate genotypes could be easily identified and removed before using the data (Table I 4).

Sampling Adult Spawners

Gillnets, fishing poles, and spears were prepared for the project, with spears of course limited to collecting post-spawning fish only. During field operations, only fishing poles were actually used for spawning and post-spawning capture of sockeye. Gillnets or spears were not required at the river sites or lake sites. Lake spawning fish, primarily at the outlet, were easily accessible for snagging; there were very few live fish observed on spawning grounds along shorelines in the main body of the lake. Only carcasses were recovered from these sites (sampling effort at the lake was probably late). It should be noted that in years of larger run sizes or sampling at an earlier date, these tangle gillnets would have most probably been effective in capturing shore spawning sockeye.

Radio Telemetry

Tag application worked well, and there was no evidence of tag regurgitation. However, there were some minor inconveniences with record keeping due to the very small print on individual tags and the amount of other data being collected during tagging (i.e. scales, lengths, sex, tissue samples).

Two aspects of the tagging study design created challenges, and could be improved in future projects:

- *Tag recoveries*: There was no reward offered for recovered tags, to avoid creating an incentive for harvesters to specifically target tagged fish, but in some cases the tag movement pattern was difficult to interpret, given possible transport and storage of tagged fish within tower range, especially at the lake outlet where CAFN harvesters set up camp.
- *Reference Signals*: It would have helped signal interpretation to create set of reference signals for each tower by placing active tags at various points upstream and downstream and at different water depths. This should be planned into the effort allocation in future telemetry studies.

Section 6.3 describes the details.

8.2. Sample Processing

DFO Labs – Weir Scales and all DNA

The collection, storage and shipping of tissue samples did not pose any serious practical challenges. Storing and shipping of scale samples was handled by DFO as part of their weir operation.

Scales and tissue samples and scales were successfully processed at the DFO labs in Nanaimo. Sections 6.2 and 6.4 have the details. Full age readings were possible for 748 of the 817 scale samples collected at the weir (92%). Genotype readings were possible for 1184 of the 1196 tissue samples (99%), which included adults at the weir, plus adults and juveniles from different sites throughout the Klukshu River and Klukshu Lake. For both types of samples, these are typical success rates at these labs. Table 2 lists the different sample sizes.

Etherton Barn – Smolt Scales

We collected scale samples from Sockeye smolts caught at the outlet of Klukshu Lake. Processing these scales at the DFO lab was not part of the project budget, so one of us (Peter Etherton) used a homestyle set-up with a barbecue, steel bricks, and bench vise (Photo 13; Section 4.1). This produced 133 valid age readings from 161 scale samples (83%), which is almost as high as the success rate in the DFO lab.

8.3. Exploratory Data Analysis

Juvenile Size and Age Composition

Section 7.1 describes the observed distributions for length, weight, and age of juvenile salmon sampled in the Klukshu system in 2016.

We observed clear size differences between Sockeye fry sampled at different locations. Fry sampled on the Klukshu River mainstem near Vand Creek were significantly larger than fry sampled in Klukshu Lake (Table F 5), and fry sampled at the lake outlet were much larger than both of the other samples (Figure F 1). Some of these size differences are likely a result of rapid growth and different times between emergence and capture. This could explain difference between lake outlet fry and lake fry. Given the sample timing (Figure F 6), and the genetic matches (almost all matched to lake spawners; Figure 16), it is plausible that the lake sample contained recently emerged fry, and the lake outlet sample contained older fry that have already spread out further away from the spawning site. However, the size difference between river fry and lake fry could point to real population differences, because the samples were matched to different genetic baselines (almost all river fry to river spawners, and almost all lake fry to lake spawners; Figure 16) and the size distribution of river fry was fairly consistent over four different sampling events (Figure F 6), which indicates that these were all fry of similar age. In contrast, the size of lake fry decreased over time, indicating that the early samples were a bit older than the later samples. The largest lake fry were only about the size of average river fry, and later lake fry samples were even smaller.

Adaption to different spawning ground characteristics could be a biological explanation for the size difference between river fry and lake fry. The river spawning sites have faster water flow, so salmon eggs can be larger (less surface area per volume) and still receive sufficient oxygen. Also, in faster flowing water the emerging fry need to be stronger swimmers. Anecdotally, this is the case for Tahltan Lake Sockeye (Peter Etherton observations), and a survey of egg sizes throughout the Klukshu could provide some additional clues. However, rapid early growth could also account for the observed size difference. Our sampling location for river fry was about 300m downstream from the main spawning site. Conversely, we sampled lake fry at the exact location of spawning, which the newly emerged fry probably left quickly to head for the additional cover and food supply in the lakeshore habitat. Also note that spring was early in 2016, and the water was hitting 18°C at the lake outlet in May, which may have accelerated early growth and magnified observed differences.

The size of Sockeye smolts sampled at the outlet of Klukshu Lake varied widely, with smolt size increasing over time from mid-May to early June, but another sample from early July has smaller sizes (Figure F 7). Age classes could be determined for most of the sampled smolts (80%). Most smolts were age 1 (91%), but there were a few age 0 smolts (5%) and age 2 smolts (4%). The length and weight distributions for the 3 age classes overlapped, but medians are significantly different between Age 0 and Age 1 smolts (Table F 6), supporting the age classifications despite the small sample size of Age 0.

The 7 observed Age 0 smolts present an interesting interpretation challenge. Conceptually, these would be consistent with a river-type life history (i.e. no lake rearing), but we cannot conclusively link these samples to the river spawning population, because smolt tissue samples were not individually labelled. The number of age 0 smolts is similar to the number of smolt samples genetically matched to the river spawners (Table 16), but the genetic stock ID has an inevitable error rate (e.g. rare genotypes), and the lake fry sample has the same low number matched to the river spawners. Setting aside a few juvenile samples which are difficult to interpret (10 genetic matches to River spawners, 7 age 0 scale readings, 5 age 2), almost all of the roughly 500 juvenile samples support the following hypothesis about juvenile life history of Klukshu Sockeye:

- *Lake*: Offspring from the Lake spawning population rears in Klukshu lake, and mostly migrates out after 1 year (i.e. smolts sampled in 2016 are the offspring of the 2015 brood).
- *River*: Offspring from the River spawning population moves out of the spawning area quickly after emergence. The unresolved question is whether they move upstream to the lake for rearing, or leave the Klukshu soon after emergence. If they move into the lake, they would have to migrate out at a different time from the lake spawner offspring, because almost none of those lake juvenile samples were genetically matched to the River population. The alternative hypothesis is that they are adapted to a river rearing habitat, and move out of the Klukshu system soon after emergence.

Other Juvenile Salmon

Sampling with beach seine, Fyke trap, and minnow trap captured a large number of juvenile Coho (Appendix E). Of 1,361 captured Coho fry, fork length was measured for 602 fry (44%) and ranged from 31mm to 75mm with a median of 39mm (Table F 1. Weight was measured for 548 Fry (40%) and ranged from 0.2g to 4.2g with a median of 0.52g (Table F 2).

A few Chinook juveniles were also captured. Size ranges for fry and smolts overlapped a lot, indicating that the small Chinook smolts may have actually been misclassified fry.

In general Sockeye fry captured were smaller than Coho fry. This was consistent throughout the sampling period and might reflect an earlier emergence of coho fry compared to Sockeye fry. However, as discussed above the majority of Sockeye fry captured seem to be recently emerged fry and few older (in terms of days after emergence) fry were captured. Sockeye fry seem to have moved from sites A and C shortly after emergence and were not using those areas for rearing.

In addition to Sockeye smolts the Incline Plane Trap (IPT) captured Coho fry and Chinook smolts. Chinook smolts were captured during two sampling events with the highest capture occurring in early June (Table E 1). It is interesting to note that the IPT trap location was just downstream of the outlet of Klukshu Lake. Therefore the Chinook smolts were likely migrating out of the lake when captured, possibly after they reared in the lake. Adult Chinook salmon in the Klukshu system have not been observed migrating into Klukshu Lake or spawning in streams that flow into the lake. Thus it appears that Chinook juveniles spawned in the Klukshu River and at some stage migrated upstream to rear in the lake prior to smolting. This is not typical behavior for Chinook salmon and has only been noted on one other Chinook Salmon spawning system.

Adult Sizes

The size of adult Sockeye varied across sample groups, and showed some potentially interesting patterns (Figure G 1, Section 7.2):

- Males were substantially larger than females in each sample group.
- River spawners were slightly larger than lake spawners, but distributions mostly overlapped.
- Size of males at the weir increased slightly as the run progressed, but also became more variable later in the migration.
- Sizes at the weir were smaller than on the spawning grounds (some with statistical significance; Section 7.2)

Most of these size differences can probably explained by increasing maturity as fish come in later and then reach fully developed dimorphism on the spawning grounds, rather than identify a real size differences between the populations. Note, however, that all adults passing the weir were categorized as condition 2.

Given observed size difference between river fry and lake fry, and the difference in adult migration behaviour (River population migrates into Klukshu earlier), it is conceivable that there are adult size differences. It's just not possible to tell from the 2016 samples collected so close to the spawning grounds when Sockeye are changing rapidly. A larger sample of size measurements linked to individual genetic stock ID at the weir could potentially reveal some size differences (i.e. try to separate out the confounding effect of timing), but given the large observed variability this is probably not worth the cost of DNA sample processing unless it is done as part of larger study. Another approach would be to collect individually-tracked tissue samples in the marine area, use genetic stock ID to identify Klukshu River and Klukshu Lake fish, and compare their sizes. Again, however, this would only be cost-effective as part of a larger project.

Sex Ratio

The sex ratio of adult Sockeye migrating past Klukshu weir in 2016 varied substantially over time (Table G 3, Figure G 2), increasing steadily from about 30% in mid-July to about 70% in early September, then fluctuating for the last part of the run. The sex ratio of early migrants was significantly different from later migrants (Table G 4).

Given that both radio tags and genetic stock ID matched the early run mostly to river spawners and the late run mostly to lake spawners (Figure 21), it is tempting to interpret this as a difference in sex ratios between the 2 populations. However, the available data are not conclusive, and there are other plausible explanations. The radio tags were applied mostly to females (150/165 total tags applied, 91%), so the tag fates have no information about sex ratio. Most of the genetic stock ID results are from the weekly pooled samples (650/809 valid genotypes, 80%; Table 14), which can't be matched to the individual records of size, age, and sex. Spawning ground samples were collected with a survey objective of roughly equal numbers of DNA samples from males and females (Table G 5), so those samples provide no information about sex ratio either. If females truly tend to migrate later in both populations, then the observed run timing curves (Figure 22) could produce the observed overall pattern: First the river males pass the weir, then as the river females start to come in after that, they are mixed with the lake males, and then the end of the run is mostly a combination of river females and lake females.

Note that these observations are for the specific returns and conditions in 2016 (see water temperature and level in Figure B 1). Run timing curves of Sockeye past Klukshu weir vary a lot from year to year (Figure 6), and are likely the result of a complex interaction between Sockeye behaviour and river conditions.

A plausible hypothesis is that:

- The two populations have different preferences in terms of return timing, with river spawners tending to come in earlier.
- In both populations, males and females behave differently during the final stretch of the migration and on the spawning grounds, with females tending to pass the weir later, and moving about the Klukshu system differently (some clues in the tagging results, see Section 8.4)

A future project could take weekly pooled tissue samples at the weir, just separating males and females (i.e. two jars instead of one). The populations could then be separated out in each of the pooled samples to calculate sex ratios for each population.

Adult Age Composition

The age composition of adult Sockeye at Klukshu weir varied substantially between males and females, and over time (Table G 6, Table G 7). Almost all females and most males were 5 year olds who spent 1 year rearing in freshwater (Gilbert-Rich age class = 5.2). Age 4.2 were also present, but much more among males (ca. 16%) than females (ca. 4%). Early migrating males had significantly fewer age 4.2 (8%) than late migrating males (18%), but the age composition of early and late migrating females was very similar (Table G 8).

As with size and sex ratio in the previous section, this observation has alternative plausible explanations:

- if the younger males tend to come in earlier for both early migrating river spawners and late migrating lake spawners, then the % 4.2 is higher for the lake spawners, and this observation is a clue for biological differences between the two populations.
- An alternative explanation would be that younger males come in later for both populations, and that the two populations have similar proportion of Age 4.2 males. such that the early run has a few Age 4.2 from river spawners, then the bulk of the river 4.2 males returns together with the lake 4.2, then at the end of the run get the most of the lake 4.2 with some straggling river 4.2.

The 2016 data does not allow us to rule out one or the other of these explanations, because most of the tagged fish, where we can match destination to age reading, are females, and the larger sample of genetic stock IDs is from the weekly pooled samples, where we can't match up individual results.

A comparison to age composition data from other Sockeye runs may offer some insight (i.e. do younger males typically return earlier or later in transboundary Sockeye stocks?), as would a look at the age composition of Neskataheen Sockeye (i.e. even if age readings can't be separated out by timing, it would be interesting to check whether the age composition is similar to the early Klukshu migrants, which are mostly matched to the Klukshu River / Neskataheen complex based on genetics).

However, to really resolve the question a future project could take a larger number of individually-tracked tissue and scale samples at the weir, to get an estimate of population-specific age composition.

8.4. Radio Tag Analysis

We radio tagged 165 adult sockeye at Klukshu weir in 2016, with most tags applied to females (Table 3), which are assumed to show more affinity to their spawning area of origin. Tags were spread roughly evenly throughout the entire run, such that a similar number of early migrants and late migrants was tagged, but weekly tagging ratio varied with run size (Table 4). Four stationary towers were used to track tag movement along the Klukshu River to Klukshu Lake, and a helicopter survey at the end of October was used to gain a final snapshot of tag distribution.

Tag movement patterns varied a lot, and we categorized them into 15 distinct types (Table 3). Overall, the most common pattern was tags rapidly passing all towers and entering the lake, but the frequency of patterns differed by timing group. For early migrants, the two most common patterns were (1) fish that moved about the mainstem and then ended up at a river spawning site, and (2) fish that migrated straight to the lake and stayed there. A substantial number of early tags were detected by the lake tower. Some moved back down the mainstem after, but others didn't. Most of the late migrants either moved straight to the lake or were only detected in the lake (i.e. no detections at the river towers).

These observed movement patterns offer a glimpse into the complex spawning behaviour of Klukshu Sockeye, despite the challenges of interpreting the journey of any one particular tag. We discuss these observations and interpretation challenges in Section 8.6 below, where they are linked to genetic stock ID results (e.g. tags that moved rapidly up the Klukshu River and then stayed in the lake, but were genetically matched up with River spawners).

Based on the observed movement patterns, most tags could be assigned to a likely spawning area either on Klukshu River or in Klukshu Lake (Table 6, Table H 2). Only 12 of the 165 applied tags were lost or assumed lost, or didn't have a record. The proportion of tags assigned to a river fate started high and then dropped as the run progressed, ranging from about 3/4 in mid-July to about 1/14 at the end of August, with variations in the estimates depending on the data treatment (e.g. including/excluding redeployed tags). The general pattern is always the same, but cleaning up the data does improve the regression fits (e.g. using only females, excluding redeployed tags, and dropping weeks with few tag results; Figure 9 vs. Figure H 4). Results of statistical tests for the difference in tag fate proportions between early migrants and late migrants are highly robust (i.e. six alternative data treatments all show a significant difference, confirmed in 100% of bootstrap tests; Table 7 and Table H 3). Tagged fish assigned a lake fate also moved up the Klukshu River about twice as fast as those spawning in the river.

In summary, these radio telemetry results very strongly support the working hypothesis that the early run predominantly consists of fish staying in Klukshu River to spawn, while those fish returning later mostly head to Klukshu Lake for spawning.

A fundamental concern that arises with any tagging study is whether the final location for a fish is where it was actually trying to get to. In our case, fish heading to Klukshu Lake for spawning may have died along the way, or they may have run out of energy and decided to spawn further downstream. The additional stress of tag application could have actually decreased a fish's chances of making it further up the river. All of these are potential mechanisms for inflating the proportion of river spawners in a tag-based estimate, but they are probably not a concern with our project, because:

- The distance from weir to lake is only 23km.
- Many of the fish assigned a river fate moved about the mainstem quite a bit before settling into a spawning area (e.g. detected at lake outlet, then later downstream at Vand Creek). Some even moved into the lake for a while (Table K 1).
- Tags with very short tracking histories that ended in the river were mostly assigned a river fate, but a closer look reveals that most of these were redeployed tags applied late in the run (Table K 6). Given this observation, redeployed tags were excluded from most of our analyses, as described in the plots and tables
- The DNA-based estimate of the proportion of river spawners is actually quite a bit higher than the tag-based estimate during the early run, and similar during the late run (Section 8.6, Figure 21)

8.5. Genotype Analysis

Overview of Genetic Data and Analyses

Tissue samples collected during the 2016 field projects yielded 1,536 unique genotype readings from adults at the weir, adults on the spawning grounds, and juveniles throughout the Klukshu watershed (Table I 4). Adult DNA results were split into eight sample groups based on location, timing, and whether they were tagged. For example, *AdWeir_EarlyNoTag2016* includes 274 genotype records collected at Klukshu weir in 2016 before August 14th and stored in a weekly pooled sample. Juvenile samples were split into 3 groups based on location and life history stage.

We implemented three types of genetic analysis, and completed extensive sensitivity tests for two of them (Figure 3):

- *Phylogenetic Trees*: This analysis maps out how the different sample groups are related to each other, and to reference samples from other Alsek populations (called the "baseline"). Tree fits first compare each possible pair of sample groups to check how different they are (i.e. the genetic distance) and then build a tree by linking those groups with smaller genetic differences closer together. Many alternative calculation approaches are available for fitting phylogenetic trees, and we applied 11 variations (Table 9) to several alternative subsets of the available data (Table 8). The resulting trees show the populations structure of a

set of populations. For example, most of the tree fits showed that Klukshu River spawners sampled in 2016 are closely related to the available samples from the Neskataheen River collected in previous years, in what we call the Klukshu River / Neskataheen complex.

- *Genetic Stock ID*: This analysis takes individual samples (i.e. 1 fish) and estimates which sample group it most likely comes from. Stock assignments are expressed as a set of probabilities. For example, a female tagged on 11 July 2016 at Klukshu weir with tag 314 had a 54.5% probability match to the river spawner sample (*AdSpn_KlukshuRiver2016*) and a 45.2% match to the Neskataheen baseline sample, for an overall 99.7% probability match to the Klukshu River / Neskataheen complex (see 3rd record in Table J 1). Note that the tag movement pattern for this fish was very clear and was assigned a river fate (Section 8.6 compares tag fates and genetic stock IDs).
- *Family Structure*: This analysis looks for closely related individuals (i.e. siblings and half-siblings) in a sample, and estimates the number of unique parents. In our 2016 samples, most of the siblings were found among the newly-emerged fry on the Klukshu mainstem at Vand Creek.

Population Structure

Key results for phylogenetic tree fits and genetic stock ID were consistent across analyses, and sensitivity tests (Figure 12, Figure 15):

- *Klukshu River / Neskataheen Complex:* The Neskataheen baseline sample was consistently linked with Klukshu River spawners in the tree fits, and stock ID assigned many samples to either the Klukshu River spawners or the Neskataheen baseline. Basicallly, the tree fits put these two sample groups close together, and the stock ID had trouble telling the difference between the two.
- *Klukshu River Population:* Adults sampled at the weir early in the run (before Aug 14) and fry sampled on the Klukshu mainstem were consistenly grouped with the Klukshu River spawner sample or the Neskataheen baseline in the tree fits, and most of the individual fish in those samples were assigned to the Klukshu River / Neskataheen complex with high probability.
- *Klukshu Lake Population:* Adults sampled at the weir late in the run (after Aug 20) and juveniles sampled at Klukshu Lake outlet were consistenly grouped with the Klukshu Lake spawner sample, and most of the individual fish in those samples were assigned to the Klukshu Lake spawners with high probability.

Early weir samples had a much higher proportion of individuals assigned to the Klukshu River / Neskataheen complex (87% vs. 18%) in the genetic stock ID, and the tree links up samples based on the predominant component (i.e. River matches among the early migrants, lake matches among the late migrants).

Figure 13 summarizes these results in a stylized diagram of Klukshu Sockeye population structure. The bootstraps tests are an especially strong confirmation, with 100% of the alternative fits showing these sample groupings (Table 13). Individual assignment probabilities to either river spawners or lake spawners are also very high for most of the 1,536 samples (Figure 13). Such a consistent result across methods and sensitivity tests means that genetic differences between river spawners and lake spawners are very pronounced. This does not necessarily mean that they are reproductively isolated from each other, but genetic exchange between the populations is small enough for them to retain distinct genetic “fingerprints” (i.e. allele frequencies on 14 loci used in this analysis, Table 11). In contrast, genetic stock ID can’t really tell the difference between the Klukshu River population and the Neskataheen, indicating that there may be substantial gene flow between the two populations. Section 9.3 summarizes the observed population structure and outlines a plausible gene flow hypothesis.

The group of adults sampled around mid-August, the cut-off point between early run and late run used since the late 1990s, was assigned to different sample groups during the sensitivity tests, and individual samples were split into roughly two halves in the genetic stock ID, one half assigned to the Klukshu River / Neskataheen Complex, the other to Klukshu Lake. This shows that the traditional cut-off date actually fits the observed run timing well in 2016, but note that this only captures the relative contribution to the total run. The run consisted mostly of river spawners before mid-August, mostly of lake spawners after that, and both populations were about equally abundant around mid-August. However, this does not mean that the return migration of the river spawners was over by the end of August. In fact, only about half of the river spawners passed Klukshu weir before August 15th in 2016 (see run timing curves discussed in Section 8.7 below).

Samples Matched to Other Baselines

A portion of the individuals in each sample group were genetically matched to some baseline population outside of the Klukshu or Neskataheen (Table 14, Table 18). Overall, about 10 out of every 100 samples (129/1301) were matched to other systems when using the revised baseline with 2016 spawning ground samples. With the original baseline using weir samples from earlier years, the number of "other" matches was a bit higher (14/100; Table 15). Percentages differed by sample group (Figure 16).

There are three possible explanations for these genetic matches:

- The genetic stock ID estimates may have an element of random error. Out of a thousand probability calculations, some portion will inevitably be wrong. This would mean that even a pure population sample would have some assignment errors, given the inherent properties of the estimation method.
- Each sample group may have some unusual individuals, which belong to that population but are different from the the typical genetic fingerprint. This would mean that there is just some natural variation in the alleles, and the analysis has trouble assigning non-typical genetic fingerprints.
- Some of the sampled individuals may have actually been from a different population and strayed into the Klukshu. This would indicate some potential gene flow between populations that are further apart.

All three of these mechanisms may be contributing to the observed results, and further analysis to resolve the questions will have to tackle two parallel lines of inquiry:

- Work with experts in genetic analysis to compare these results to other case studies and identify a base rate of misclassifications inherent in the calculations of individual assignment probabilities as implemented in the ONCOR program (Kalinowski et al. 2007).
- Work with experts on Alsek Sockeye to review the non-Klukshu matches in Table 18, and discuss which of them might be plausible sources for straying into the Klukshu. Note that Kwatine Creek and Goat Creek River-Type are the only two non-Klukshu stock ID matches that also are linked to the Klukshu populations in some of the alternative tree fits (Table 13), indicating some potential common ancestry or current genetic exchange.

Leave-One-Out Test

A leave-one-out sensitivity test assesses the properties of a genetic baseline set by taking individual records out of each baseline and estimating the probability with which the sample would be assigned back to its baseline. Reassignment probabilities were low to very low for most of the samples when the full Alsek baseline is used (Table 19). There are different potential explanations, such as a small sample size (e.g. Kane) or similar other baseline populations (Klukshu River vs. Neskataheen), but nevertheless this is an unexpected observation given the highly robust tree fits and the high probabilities of stock match in the genetic stock ID, expecially because the leave-one-out test was implemented with the same software as the genetic stock ID (Kalinowski et al. 2007). An investigation into the cause for this difference between analyses falls outside the scope of the current project, but is listed as priority item for future work (Section 9.4). Reassignment probabilities improve a lot when looking only at the Klukshu populations (i.e. the trimmed baseline results in Table 20).

Calculation Methods

Many alternative methods are available for calculating genetic distances and fitting phylogenetic trees. We tested 4 genetic distances and 2 tree fitting methods, covering most of the variations used in a selection of recent papers (Table 25). Most papers published in the Canadian Journal of Fisheries and Aquatic Sciences since January 2000 use the *Dc* metric and the *Neighbour-Joining* algorithm. In our sensitivity tests, that is the combination with the highest R^2 (Table 12,Table 13) for the final set of genotype data (G12;Table 8).

Despite differences in statistical performance, like the R^2 measure listed in Table 12, the results most relevant to our analysis are highly consistent across these alternative methods, grouping early Klukshu migrants and juveniles sampled on the Klukshu mainstem with the Klukshu River / Neskataheen complex, and grouping late Klukshu migrants and juveniles samples in the lake with the Klukshu Lake spawners.

Given this robustness of results, it is not necessary for our project to weigh the relative strengths and limitations of the alternative methods, but formal guidance on best practices or current standards for genetic analysis of transboundary systems would be helpful for future work (e.g. a workshop hosted by the TTC bringing together experts from DFO and ADFG).

Allele Frequencies

All of the genetic analyses discussed so far in this section build on a common set of information, which is how often different genetic variations show up in different samples. In technical terms, the sample groups are described based on the frequency of different alleles at 14 different locations. One way to visualize this is to think of a page with 14 labelled boxes, where each box can take different colours. Each box corresponds to a *locus*, and the colour of the box corresponds to an *allele* (i.e. a unique snip of DNA). Some of the boxes can have many different colours, while other boxes have only a few possible variations. Table 10 lists the average number of alleles observed in 100 samples from different genotype sets. The tree fitting analysis is equivalent to taking a stack of pages, and sorting them into binders based on similar colour patterns. Those with more matches on the coloured boxes are more closely related to each other. The genetic stock ID analysis is then equivalent to taking 1 page with 14 coloured boxes, and checking which binder (i.e. group of baseline samples) to file it under. For example, if the page you are trying to match up has Blue-Red-Green in the first three boxes, and in your selection of binders there is only one that has a lot of pages with Blue-Red-Green, then you would add it to that binder with a high confidence.

When trying to understand why some populations are grouped together or split apart in the genetic analysis, it is helpful to explore the underlying allele frequencies. We used a diagnostic plot showing the relative frequency of up to 10 most common alleles to compare the 2016 Lake Group (lake spawners, late migrants, and lake juveniles) and the 2016 River Group (river spawners, early migrants, and river juveniles). Figure 10 shows the resulting profiles of allele frequency, and Table 11 summarizes the observed patterns. 10 of the 14 loci show little obvious difference between allele frequencies for the River Group and and the Lake Group of samples collected in 2016. Only four of the loci have substantially different patterns of allele frequencies.

At first glance, this could be interpreted as an opportunity for cost savings by focusing future sample processing and analyses only on those 4 loci. While this could somewhat reduce processing costs and the size of resulting data sets, the actual savings would likely be marginal in projects like ours. Also, when looking at a new set of samples or a different population, researchers wouldn't know ahead of time which of the 14 loci will eventually turn out to be the most informative *in that particular study*. One possible setting where it could be worthwhile to focus on a smaller number of loci identified through earlier work would be a large-scale annual stock ID program. For example, if thousands of sockeye tissue samples were being collected on the lower Alsek year after year, then it might make sense to streamline the genotyping to only those loci required to separate out stock groups relevant to management and stock assessment. However, even then the cost savings would have to be balanced against the potential information (e.g. ability to spot unusual individuals which might be strays from another system).

Genotype Analysis – Family Structure

An analysis of family structure in a genotype sample can provide clues about mating behaviour and reproductive success (e.g. number of parents contributing to the next generation), but also may flag potential sources of bias in other analyses like tree fitting and genetic stock ID (e.g. if a sample has a lot of siblings, it may not represent the full range and relative frequency of alleles in the source population). This potential source of bias is a particular concern with samples of newly-emerged fry, because they have not had much time to disperse throughout their habitat and mix with fry from other spawning sites in the same population.

Our 2016 juvenile DNA samples include 366 fry (Table 5), which were collected near spawning sites and are assumed to be recently emerged (based on size, Section 8.3). As a quick check for potential concerns, Janine Supernault (DFO Molecular Genetics Lab, Nanaimo) reconstructed sibling relationships in all of out 2016 Klukshu Sockeye samples using the COLONY program (Section 5.9). Table 23 summarizes the results. Most of the sample groups had sufficient genetic variability to have more than 90% unique parent pairs (i.e. more than 9 out of every 10 fish in the sample had a pair of reconstructed parents that was different from all the other parent pairs in the sample). Notable exceptions are adults migrating past the weir early (87% unique parents) and fry sampled on the Klukshu mainstem near Vand Creek (63% unique parents). The heatmap in Figure 18 shows the same thing as the summary in Table 23: Most of the full siblings were identified within the newly emerged fry on the Klukshu mainstem, but there were some among the early weir returns as well.

These results confirm that family structure is not a concern for most most of our 2016 sample groups, and should not affect the conclusions based on phylogenetic tree fits and genetic stock ID. Specifically, the two most influential samples are the Klukshu River spawners and Klukshu Lake spawners, which are used as reference samples in the revised baseline set, and both of these have very few identified siblings.

In addition, these results are a starting point for some interesting speculations that could form the basis of future work on spawning behaviour of Klukshu Sockeye. For example, the unexpectedly high number of full siblings among the early migrants (non-tagged sample) could indicate a highly competitive spawning event for the River population, with a comparatively few prime redds having much better survival rates and producing a larger proportional contribution to the returning run than many other redds in more marginal sites. The large amount of tag movement up and down the mainstem (e.g. Table 3) could be another clue, potentially indicating females that were searching and competing for sites. Finally, quite a few tagged fish that were genetically matched to Klukshu River spawners seemed to move into the lake and stay there (Section 8.6), potentially indicating females that were displaced from their their preferred spawning area altogether.

Additional analyses could include looking at half-sibling relationships (i.e. 1 parent in common) and developing a more formal family reconstruction. This exceeds the scope of the current project, but has been noted as a suggested priority for future work (Section 9.4).

8.6. Cross-Check: Tag Destinations vs. Genetic Stock ID

During the planning phase for this project, we expected the tagging study to face a potential bias towards river sites as final destination due to natural mortality during upstream migration. Observed movement patterns turned out to be complex, and the match between tag fate and genetic stock ID varied by movement pattern and statistical week.

About 11% of the 7,584 adult Sockeye passing Klukshu weir were measured and sampled for scales as part of DFO's routine weir operation. Most of the fish handled by the DFO weir crew were also sampled for DNA, and 1/5 of those were radio tagged as well. The total sample sizes were 820 tissue samples and 165 tag applications. After sample processing and data clean-up (Sections 5.4 and 5.5), there were 124 samples which had both a valid genotype reading and an assigned tag fate. For those 124 samples, we can cross-check the two methods to assess their performance. Appendix J describes movement patterns and genetic stock ID results for each tagged fish. Appendix K compares the tag fates and genetic stock ID (GSI) for different subsets of the 2016 weir samples.

The proportion of matching assignments varied for different tag movement patterns and by timing group (Table 24). For example, 52 fish rapidly migrated to the lake tower range and then were detected there for an extended period. These were classified as lake spawners based on tag fate, but the genetic stock match changed over time, with early migrants mostly matched to river spawners and late migrants mostly matched to lake spawners.

Roughly 2/3 of the samples had matching results for tag fate and genetic stock ID (Table K 1). Early migrants (57% matches) matched less often than late migrants (64%) , female samples (64%) matched more often than male samples (46%), and tag movement patterns classified as "Clear" (68%) matched more often than those classified as "Interpretation" (55%).

In cases where tag fate and genetic stock ID differ, which is correct? Several points need to be considered when trying to answer that question:

- Both methods are subject to technical errors (e.g. record keeping, telemetry signal readings, genotype readings), but possibly at different rates.
- Genetic stock ID only provides information about the likely origin of a fish, but has no information about where it was trying to go or where it actually went.
- Tag movement only provides information about the likely destination of a fish, but has little information about where it was trying to get to or where it came from.
- Neither genetic stock ID nor tag movement have any information about spawning success and actual contribution to the next generation.
- Genetic stock ID has less subjective interpretation than the tag movement patterns.
- Sockeye Salmon exhibit complex spawning behaviour with strongly territorial females, and larger fish displacing smaller fish (Burgner 1991).

Assuming that the number of actual errors is small, this leaves two alternative interpretations:

- Given that the classification of tag movements is more subjective, assume that the genetic stock ID is more often correct.

- Given the complex spawning behaviour, both methods could be correct. Any mismatches simply identify fish that did not spawn in the same place as their parents, and reflect either gene flow between the populations or unsuccessful spawners. For example, a fish from the lake population returning very late in the run may not have the energy reserves to migrate all the way to Klukshu Lake, and try to spawn in Klukshu River instead. Similarly, a smaller-than-average female from the river population may not be able to hold territory in the preferred spawning habitat, and move into the lake instead and try to set up a redd there.

Both of these mechanisms likely contribute to the observed results, but further work would be required to figure out which one has the larger effect. A starting point would be to use our project results and look at size distributions for the mismatched vs. matched weir samples (e.g. if those fish where genetic stock ID and tag fate disagree tend to be smaller, then density-dependent competition on the spawning grounds is a plausible mechanism). A review of other studies that applied both radio telemetry and genetic stock ID might establish typical base rate of errors and plausible mechanisms identified in other systems. For example, two studies from the 1990s checked genetic stock ID against stock composition estimates based on mark-recovery sampling with coded-wire tags. A Nass River Sockeye study by Beacham and Wood (1999) estimated the proportion of Medziadin fish in a marine test fishery using genetic stock ID, scales and coded-wire tags (GSI = 73% Meziadin, tags = 73%, scales=61%). Brodziak et al. (1991) estimated an error rate of less than 3% for genetic stock ID of Chinook salmon sampled from fisheries in California and Oregon, based on a check against coded-wire tags.

Two specific examples illustrate the interpretation challenges:

- *Lake outlet spawners*: Ten fish with tagging histories ended up at the lake outlet (Appendix J). Seven of 8 females were classified as river spawners, because the signal was stronger on the downstream side of the radio tower at the lake outlet. Six of them were genetically matched to the Klukshu River / Neskataheen complex, one to the lake spawners, and two to non-Klukshu baselines. The two males with this tag movement pattern were both assigned to a river fate based on signal strength, but both were genetically matched to lake spawners. This could be interpreted as an indication of population mixing at edge of the two spawning areas, but we don't know whether these are successful spawners or marginal sites contributing little to the next generation. If they do contribute, the next question is which population they tend to contribute to (i.e. do offspring of lake outlet spawners prefer river sites or lake sites when they return?). Also, we don't know if this is a regular occurrence, or driven by density (i.e. more fish pushed into marginal habitat when run is large or water levels reduce spawning area.
- *Redeployed tags*: Some recovered tags were re-deployed near the end of the run, and there are tracking histories for 11 of those redeployed tags. All of the tracking histories are very short, and half of them ended in the river (Table J 5). Genetically, most of these were matched to the Klukshu Lake spawners. Given this discrepancy, we excluded the redeployed tags from the final analyses. However, there are actually two alternative interpretations: (1) the redeployed tags failed soon after application (e.g. battery life), (2) the fish were trying to get to the lake, but as very late migrants didn't make it (e.g. possible sign of higher en-route mortality among late-migrating fish).
- *Interactions with other species*: Other species introduce additional complexities. For example, some of the sockeye spawning sites were later inundated by spawning Coho Salmon. Our study did not collect any quantitative information on this, and potential effects on reproductive success of Klukshu Sockeye are unknown.

In summary, there are substantial interpretation challenges and unresolved questions regarding the individual cases where genetic stock ID and radio tagging give different results. However, the resulting estimates of total run composition and weekly run composition are mostly similar (except for late July to mid-August; see Section 8.7 and Figure 21).

Despite the complexity of individual tag movement patterns, there were also clear differences in the speed of net migration from Klukshu weir upstream, which were consistent when splitting the data based on tag fate or based on genetic stock ID matches (Figure 19). Fish linked to the river spawners either based on tags or genetics took much longer to reach the upstream towers than fish linked to lake spawners, and their migration times were much more variable. A plausible mechanism for this observation is that river spawners move about on the mainstem, with females choosing sites and trying to defend them, and males moving around looking for mates. Over time, these river spawners will disperse throughout the system, leading to detections further upstream. Lake spawners, on the other hand, probably don't linger in the mainstem, but rather try to reach their preferred spawning habitat in the lake, and do move up the mainstem quickly. Note that our tagging study focused mainly on females, because the primary objective was to determine population structure, and females are assumed to stray less. A study looking more closely at the spawning behaviour of Klukshu sockeye would need to also tag

more males throughout the whole run (compared to the 12 early migrating males and 1 late migrating male tagged with new tags in our study; Table J 4). This observation also has implications for harvest impacts in the Kukshu River, because river spawners are exposed longer to fisheries along the mainstem, but harvests in the lake or at the lake outlet are more selective towards the larger population of lake spawners.

The usefulness radio tags vs. genetic stock ID depends on the specific situation:

- Radio tags will be more informative if there is more spatial separation between the target populations. For example, if radio tags are applied on the lower Alsek or in the marine area, and then are detected at various milestones along the upstream migration, and then finally enter the Klukshu, then interpretation is very clear. However, larger distances also increase interpretation challenges due to en-route mortality events, and exhausted fish taking an “off-ramp” into another system along the way. Within a single system we expect mortality to be less of an issue, but movement becomes more complex as the fish compete for spawning sites.
- Genetic stock ID is much cheaper per sample than the radio tagging, but relies on having a solid set of population baselines for comparison. However, once the overhead cost of creating the baselines has been incurred, genetic stock ID will get clearer stock composition results (but keep in mind the earlier point regarding origin vs. destination).

8.7. Stock Composition at Weir

Radio tags and genetic stock ID have both been used to estimate stock composition of Pacific Salmon stocks, and both approaches have strengths and limitations (previous section). Both were applied in our project, and can be used to determine stock composition of Sockeye returning to the Klukshu. Results for both went through substantial data clean-up (Sections 5.4 and 5.5) and sensitivity analyses (Sections 7.3 and 7.6), but the final results in terms of stock composition are mostly consistent between the two assessment methods (Section 7.10). In summary:

- Both radio tags and genetic stock ID showed that in 2016 early migrants had a higher proportion of river spawners and late migrants had a higher proportion of lake spawners, with genetics-based estimates estimating more river spawners (Table 7, Table 22).
- Weekly run composition estimated from tags followed the same pattern as the genetics-based estimates of run composition, and estimates are roughly similar for 8 of the 11 statistical weeks with both estimates, but in late July and early August the genetics-based estimate is twice as high (90% river spawners vs. 45% river spawners; Figure 21).
- However, when converting these composition estimates into actual abundances (i.e. multiply by weekly weir count total), both methods produce similar run timing curves: River spawners returned earlier, but were still present in similar abundances later on when the bulk of the lake spawners passed the weir (Figure 22). Both populations returned over the full 3 months of weir operation, but the River population had a long, protracted migration pattern while the Lake population had a very pronounced peak migration period of 3 weeks. The migration peak of of the lake population may be linked to water levels, because in 2016 water level spiked in early September (Figure B 1) during the same week as the run size of the Lake population dropped drastically (Figure 22. Overall, roughly half of the River population returned before August 15th, but for the Lake population roughly 90% returned after August 15th.
- Estimates of overall stock proportion and total abundance differ substantially between survey methods. Genetic stock ID estimated 2,503 (33%) River population and 5,081 (67%) Lake population, while radio tags produced estimates of 1,744 (23%) River population and 5,840 (77%) Lake population (Figure 23). Both of these estimates for the River population are higher than the portion of the run that passed the weir before August 15th (i.e. the cut-off date in use since the 1990s) which was 1,381 (18%) early Sockeye and 6,203 (82%) late Sockeye.

Together, all these observations are strong evidence of behavioural differences in adult migration between the 2 populations which were identified based on phylogenetic trees and tag fates. These individual migration patterns, interacting with environmental factors like water level, could account for the many observed patterns in run timing curves (Figure 6). Two approaches could be used to further investigate difference in migration behaviour. One option would be to implement future studies similar to this one, and check whether the observed differences are persistent, or were specific to 2016. Another option might be to attempt extracting DNA from archived scale samples for some past years with interesting overall run timing curves (e.g. 2005; Figure 6) and then reconstruct separate timing curves for the two populations based on genetic stock ID (as in Figure 22).

9. Conclusions

9.1. Achievement of Project Objectives

Clearly defined measures of success were defined in the proposals for the two projects documented in this report, with project implementation evaluated against the sampling plan, and the analytical component requiring a final project report.

The sampling plan for the adult project was to collect representative samples from each timing group (early, mixed, late) and location (river, lake), for a total of 450 to 1200 scale samples, 200 to 600 tissue samples, and 60 to 150 radio tags. Actual sample sizes were 817 scale samples, 1196 tissue samples collected at the weir and on the spawning grounds, and 165 radio tags applied (Table 2). Sampling and tagging at the weir covered most of the 2016 Klukshu Sockeye run timing, and spawning ground samples covered key sites identified based on traditional and local knowledge, previous studies, and field observations. Scale samples were collected by DFO as part of routine weir operations and met the target range. The planned 150 radio tags were successfully deployed, and later in the run 15 recovered tags were redeployed, so that implementation of the tagging study exceeded the original objective. Note, however, that the redeployed tags had only short tracking histories and were excluded from most analyses.

The sampling plan for the juvenile project was to collect at least 100 scale samples and 50 tissue samples from each of the 3 planned locations. Actual sample size was 494 tissue samples of Sockeye fry and smolts covering multiple sites and different times (Table 5). Scale samples could only be collected from smolts (161).

Overall the radio tagging component met the project objectives and the DNA sampling component far exceeded the planned number for both adult and juvenile tissue samples. Funds were re-allocated within the projects to cover the additional DNA processing (e.g. fewer helicopter overflights used for the telemetry component).

The analytical component of both projects is documented in this report, which describes the field work for the juvenile and adult studies, documents our analyses of tag movements and genotype readings, and links the results of both into an overall picture of population structure for Klukshu Sockeye, and observed differences between the two populations (e.g. run timing, spawning behaviour)

9.2. Sampling Methods

Juvenile Sampling

The field crew prepared 5 alternative sampling gears for juveniles, and deployed 4 of them depending on local conditions at 4 sampling sites. 3 types of traps and beach seines were tested, and achieved sample sizes that exceeded our original budget for DNA processing (Appendix E). Therefore it was not necessary to deploy electrofishing gear, which had also been prepared as a backup option.

Beach seining netted consistent numbers of sockeye fry on multiple dates in 2 of 3 locations, and a large number of coho fry at 1 of 3 locations. The Wolf-type Incline Plane Trap (IPT) caught a large number of sockeye smolts and quite a few fry (Sockeye, Coho) at the outlet of Klukshu Lake, but most of these were caught in two of the 14 sampling events. The Fyke trap and Gee-type minnow trap both caught large numbers of Coho fry, but catches were highly variable over time with the Fyke trap and between sites for the minnow trap.

Overall, the variability of juvenile sample sizes confirms that projects need to budget for multiple gears, multiple sites, and multiple sampling events.

After scales and tissues from smolts at the lake outlet were processed and analyzed, it turned out that the sample did not include any smolts matched to the River population. This could be because river juveniles don't spend a year rearing in Klukshu Lake, or because they migrate out of the lake at a different time and were missed by our 2016 sampling events. Future projects sampling smolts on the Klukshu should consider a longer time window and more frequent sampling events, in order to either find river-origin smolts or rule out that they rear in Klukshu Lake.

Sampling Adults at the Weir

Handling of adult Sockeye at Klukshu weir in 2016 worked very well. Our project crew implemented extensive sampling steps (i.e. tag application, tissue sampling) in addition to regular weir operation, working in close coordination with the DFO weir crew. Due to the pace of fish handling at the weir, most of the tissue samples had to be pooled weekly, rather than packed individually. This created some extra costs for DNA processing, but

once samples were processed, duplicate genotypes could be easily identified and removed before using the data (Table I 4).

To be successful, any future radio tagging or DNA study on Klukshu Sockeye will require similar levels of coordination and contribution by DFO, particularly in terms of access to sampled fish and all the biological data (e.g. size, sex).

Sampling Adult Spawners

Gillnets, fishing poles, and spears were prepared for the project, with spears of course limited to collecting post-spawning fish only. During field operations, only fishing poles were actually used. There were very few live fish observed on spawning grounds along shorelines in the main body of the lake, so carcasses and skeletons were sampled for DNA instead.

Future studies looking at Klukshu Lake spawners (e.g. to expand the baseline for stock ID), should consider starting the lakeshore sampling earlier, and conducting boat surveys to identify other potential sites.

DNA processing and genotype reading worked well, even for the carcass and skeleton samples (Table 2), so the late timing of the 2016 spawning ground survey did not affect the subsequent analyses.

Radio Telemetry

Tag application worked well, and there was no evidence of tag regurgitation. However, there were some minor inconveniences with record keeping due to the very small print on individual tags and the amount of other data being collected during tagging (i.e. scales, lengths, sex, tissue samples).

All the components of the telemetry equipment worked well with each other (Section 6.3), and the only major challenges were with practical implementation (e.g. finding tower sites with sufficient sun exposure to power the receiver unit). Most of the tower units were operational most of the time (Table C 1).

Based on our experience, the study design for future projects should include a clearer plan for handling tag recoveries (e.g. to mimimize misleading signal detection as a tagged fish is caught, packed, driven to camp, and stored near the lake outlet).

Future projects should also create set of reference signals for each tower by placing active tags at various points upstream and downstream and at different water depths. This information would greatly help with signal interpretation.

9.3. Population Structure

Our results clearly point to two distinct populations of Sockeye in the Klukshu, because phylogenetic tree fits are very robust across sensitivity analyses and assignment probabilities in genetic stock ID were generally high. When we split our data based on stock ID or tag fate, clear differences emerged in spawning areas, migration behaviour, and juvenile behaviour.

Table 26 summarizes relevant clues from the results and discussion sections:

- Strong evidence of genetic differences between the Klukshu River population and the Klukshu Lake population (i.e. phylogenetic trees, genetic stock ID, tag fates).
- Strong evidence of difference in run timing, based on weekly stock composition estimates at the weir (both radio tags and genetic stock ID).
- Strong evidence of difference in spawning behaviour (i.e. movement along the Klukshu mainstem).
- Moderate evidence for differences in spawning location, but implied in the genetic results (i.e. wouldn't see this level genetic distinction if there were regular mixing).
- Some potential differences in male age composition, adult sizes, and sex ratio, but our data are inconclusive given other factors (e.g. size distributions affected by maturity level.)
- In addition there was strong evidence that Klukshu River Sockeye are closely related to Neskataheen Sockeye, more closely even than to Klukshu Lake Sockeye (Figure 11).

Based on these results, we conclude that there is strong support for the working hypothesis that Klukshu Sockeye consist of two distinct populations, river spawners that tend to migrate early and lake spawners that tend to migrate later.

Given the genetic similarities between Klukshu River Sockeye and Neskataheen, and the observed tag movement patterns, a plausible model of directional gene flow between these populations is:

- Klukshu River and Neskataheen are either two closely related populations, or a single population with a variable portion entering the Kukshu (e.g. depending on river conditions). Either way, some portion of the Neskataheen fish regularly "tops up" the Klukshu River Sockeye population.
- Some of the river spawners push upstream close to or into the lake (e.g. getting chased off the good in-river spawning sites). Note, however, that we don't know how many of these spawn successfully in the lake.

Based on these conclusions, we recommend the following next steps:

- Discontinue the Early/Late terminology used for Klukshu Sockeye since the 1990s, and adopt the more accurate labels of *Klukshu River* population and *Klukshu Lake* population.
- Work with TTC to consider implications of these project results for bilateral management of Alsek Sockey
- Work with DFO Science to consider our project results in the next review of conservation units (CU) for Transboundary Sockeye Salmon. Given that migration timing is closely correlated with spawning location (e.g. early migrating river spawners, later migrating lake spawners), this may be sufficient reason for separate CUs under Canada's *Wild Salmon Policy*. In addition, juveniles from the Klukshu River population probably don't migrate upstream to rear in Klukshu Lake, but they may also not be true river type Sockeye (i.e. age 0.X, do not rear in a lake). If they do turn out to be river-type Sockeye in future studies, then they would automatically fall into a distinct CU based on the definitions used by Holtby and Ciruna (2007).

9.4. Ideas for Future Work

<u>Projects Involving Field Work or Sample Processing</u>

The following potential projects could be used to investigate questions about Klukshu Sockeye that arose during our field work and analyses:

1. *Expand Klukshu baselines:* Collect tissue samples from river spawners and lake spawners, and add the genotype readings to the revised baseline for Alsek Sockeye. This would strengthen future genetic stock ID analyses.
2. *Cross-check Klukshu baselines, tree fits, and genetic stock ID:* Send the archived tissue samples from the 2016 projects to the ADFG scale lab, and replicate the analyses in this paper with their genotype readings (i.e. use different loci and baseline samples). This would ensure consistency between future work by the two agencies.
3. *Run composition at Klukshu Weir - Future years:* Collect tissue samples from adults at Klukshu weir, estimate weekly run composition, and calculate run timing curves for each population. This would provide information about whether the 2016 observations are generally applicable. For example, in 2016 the river population had a protracted return migration, and the lake population had a fairly narrow peak. If similar patterns are observed in a few other years, then these patterns are a strong indicator for persistent biological differences between the two populations.
4. *Run composition at Klukshu Weir – Past years:* Try to extract DNA from scale samples collected in previous years, compare to the revised baselines developed in this project, and estimate the weekly run composition. Once the proportion of river spawners in the early and late run for each return year are categorized properly, this information can be used to estimate abundance trends and status for the two populations.
5. *Catch composition*: Management of fisheries intercepting Klukshu Sockeye in the marine area or on the lower Klukshu can not be directly linked to the observed run timing patterns at Klukshu weir. A larger-scale program would be required to collect Sockeye tissue samples in key fisheries, and use genetic stock ID to calculate stock composition by time and area. This would allow for a review of fishing plans, given objectives of targeting some populations and avoiding others.
6. *Spawning Behaviour:* Our study focused on population structure, and we tagged mostly females, because they are assumed to stick more closely to their spawning area of origin. However, to get a better picture of spawning behaviour, a more even mix of males and females would need to be radio tagged. This would help with investigating differences in spawning behaviour between males and females, and between the two populations.

7. *Sex ratio differences:* A future project could take weekly pooled tissue samples at the weir, just separating males and females (i.e. two jars instead of one). The populations could then be separated out in each of the pooled samples to calculate sex ratios for each population.

Note that some of these project ideas could be easily combined into a larger study (e.g. 1,2, and 3)

Projects Involving Data Compilation, Literature Review, and Analysis

The following potential projects could be used to investigate methodological questions that arose during our analyses of the genotype data:

- *Fitting phylogenetic trees – Methods review*: We tested the 4 alternative genetic distances and 2 alternative tree fitting algorithms included in the *TreeFit* program, and replicated 3 of the estimation approaches using R (Section 5.7). We also reviewed recent papers to check current practices (Table 25). However, we did not comprehensively review the theoretical foundations, strengths, and limitations of the approaches. For example, based on the software documentation and papers we reviewed, it seems that terminology and implementation of genetic distance calculations can be inconsistent. For example, Fst and Theta are either the same, or closely linked versions of genetic distance, can be applied within and across samples, and go by different names (e.g. co-ancestry coefficient, fixation index, genetic differentiation index). Progress toward resolving these method issues would require working with experts in salmon genetics to scope out large-scale comparisons. A literature review of methods could be coordinated with the TTC to develop guidelines for future analyses.
- *Fitting phylogenetic trees – Code tools*: Current R tools developed for this project were useful to check, clean, and rearrange genotypes samples, and quickly explore a large number of alternative tree fits. This helped focus the analyses that were then done using TreeFit, ONCOR and COLONY (Section 5.7). However, a more fully developed suite of R-based tools could greatly speed up and diversify the analyses presented in this report. This would build on the existing packages, but adapt the components to match the TreeFit analyses which are commonly used for Pacific Salmon. Custom R functions for this project are available on the GitHub repository at https://github.com/SOLV-Code/Klukshu-Sockeye-2016.
- *Genetic Stock ID:* We used two of the standard analysis functions in the ONCOR program. The main analysis estimates probability assignments for each individual sample. In addition, the program includes a sensitivity test of the baseline. Both of these analyses essentially take an individual sample and try to match it up against a set of reference samples in the baseline. However, the probability estimates from the two analyses are quite different, and this discrepancy should be resolved, or at least explained. One possible approach would be set up a working group with experts in genetic analysis to compare these results to other case studies and identify a base rate of misclassifications inherent in the calculations of individual assignment probabilities as implemented in the ONCOR program (Kalinowski et al. 2007). Another angle would be to work with experts on Alsek Sockeye to review the non-Klukshu matches in Table 18, and discuss which of them might be plausible sources for straying into the Klukshu.
- *Radio Tagging vs. Genetic Stock ID*: Cases where tag fate and genetic stock ID differ could either indicate that one of the methods gave a wrong result, or that both are correct and the individual fish exhibited a more complex behaviour. Both of these mechanisms likely contribute to the observed results, but further work would be required to figure out which one has the larger effect. A starting point would be to use our project results and look at size distributions for the mismatched vs. matched weir samples (e.g. if those fish where genetic stock ID and tag fate disagree tend to be smaller, then density-dependent competition on the spawning grounds is a plausible mechanism). A review of other studies that applied both radio telemetry and genetic stock ID might establish typical base rate of errors and plausible mechanisms identified in other systems.
- *Family structure:* Janine Supernault (DFO-Nanaimo) used the COLONY program to implement a virtual family analysis of our 2016 samples (i.e. reconstruct common parents). Further work on this aspect of the data could involve splitting our sample groups different ways (e.g split smolts by age class), and looking for persistent lineages. Another angle would be to identify and exclude siblings, then re-run the genetic stock ID and phylogenetic trees. Additional analyses could also include looking at half-sibling relationships (i.e. 1 parent in common) and developing a more formal family reconstruction.

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Tables

Table 1: Overview of 2016 Klukshu Sockeye Sample Groups.
The seven sample groups used in this report combine data from 2 CAFN projects (see Sec. 1.2) and DFO's annual Klukshu weir program. Valid genotype samples include only those where samples could be processed, at least 10 of 14 loci could be read, and that were not duplicates (See Section 5.7). Note that the valid genotype samples do not correct for family structure (i.e. siblings, Section 5.9). Radio tags were applied to a subset of fish sampled at the weir, with proportional focus on early migrating fish and a preference for tagging females. Samples with successful fate include only those where a final spawning destination could be identified based on stationary radio towers and a helicopter overflight. Note that sex, fork length, and scale samples were collected by DFO staff as part of routine weir operation, while DNA sampling and radio tagging was funded through the CAFN projects.

Sample Group	Field records	Unique Genotype
Adults/ Weir/ Tagged	**165** samples. daily date, fork length, gender, condition, tag freq, tag code, DNA vial ID, scale book #, in-river movement, final location (70 Early, 19 Mix, 76 Late)	**159** samples. Genotype for 14 loci, sample ID linked to individual record (65 Early, 19 Mix, 75 Late)
Adults/ Weir/ Weekly Samples	**655** samples. Daily date, fork length, gender, condition, scale book #, DNA samples packed as a weekly composite.	**650** samples. Genotype for 14 loci, batch processed by stat week.
Adults/ River Spawners	**110** samples. Location (102 Vand, 8 Motheral), daily date, fork length, condition, gender, recaptured	**117** samples. Genotype for 14 loci, merged into a single "River Spawner" group.
Adults/ Lake Spawners	**136** samples. Location(52 shoreline, 84 outlet), daily date, fork length, condition, gender, recaptured tag	**118** samples. Genotype for 14 loci, merged into a single "Lake Spawner" group.
Juveniles/ Lake / Fry	**154** samples. Location (90 Lake, 64 Outlet), Fork length, weight, capture method	**152** samples. Genotype for 14 loci, merged into a single "Lake Fry" group
Juveniles/ Lake Outlet / Smolt	**167** samples. Fork length, weight, capture method	**126** samples. Genotype for 14 loci.
Juvenile/ River/ Fry	**214** samples. Fork length, weight, capture method	**214** samples. Genotype for 14 loci.
Total Adults	1066	1044
Total Juveniles	535	492
Grand Total	1601	1536

Table 2: Overview of Adult Sample Sizes for 2016 Klukshu Sockeye Sampling.
First row shows total sample sizes. Rows 2-4 summarize samples collected by location (weir, river spawning sites, lake spawning sites), and the rest shows samples by statistical week. Run size is a count of all sockeye passing Klukshu weir. "All samples" includes those with records of biological measurements taken in the field. Scales were sent to the DFO Scale Lab in Nanaimo for aging. Fully aged scale samples include only those for which both a freshwater and marine age could be determined. DNA samples were sent to the DFO Genetics Lab in Nanaimo. Unique genotype (GT) samples include only those where samples could be processed, at least 10 of 14 loci could be read, and that were not duplicates. The number of processed DNA samples exceeds the number of field observations in several cases where tissue samples were pooled, rather than tracked individually (e.g. 117 unique genotypes from river spawners vs. 110 biological measurements), or where multiple samples were taken from the same fish (e.g. in tagged sample, pooled weekly sample, and spawning ground sample). Duplicate genotypes were removed and only unique genotypes retained (Section 5.7), while "GT Read" includes valid genotyping results that turned out to be duplicates. Appendix I summarizes the DNA data clean-up. Note that even after vlean-up, the DNA data set includes more unique genotype readings than sample records in some statistical weeks, but not in terms of total sample size at the weir. Radio tags were applied to a subset of fish sampled at the weir, with proportional focus on early migrating fish and a preference for tagging females. Samples with successfully determined fate include only those where a final spawning destination could be identified based on stationary radio towers and a helicopter overflight. Note that sex, fork length, and scale samples were collected by DFO staff as part of routine weir operation, while DNA sampling and radio tagging was funded through this project. Note that the valid genotype samples do not correct for family structure (i.e. siblings, Section 5.9).

									DNA Samples						Success Rate		
	Run Size	All Samples	% Run	Sex	Fork Len	% FL	Scales	Full Age	Proc-essed	GT Read	Uniq. GT	%GT	Radio Tags	Fate	Age	GT	Tag
Total	-	1066	-	1042	1023	96	817	748	1196	1184	1044	98	165	153	92	99	93
All Weir	7584	820	11	820	816	100	817	748	954	949	809	99	165	153	92	99	93
River	-	110	-	110	104	95	0	0	119	117	117	106	0	0	-	98	-
Lake	-	136	-	112	103	76	0	0	123	118	118	87	0	0	-	96	-
W28	1	1	100	1	1	100	1	1			-	0	0	0	92		-
W29	82	79	96	79	79	100	79	73			74	94	14	11	78		79
W30	108	9	8	9	9	100	9	7	425	423	6	67	3	3	96	100	100
W31	154	73	47	73	70	96	71	68			75	103	32	30	95		94
W32	429	130	30	130	130	100	130	123			127	98	9	8	93		89
W33	573	43	8	43	43	100	43	40			57	133	12	11	89		92
W34	492	98	20	98	98	100	98	87	100	100	87	89	19	17	89	100	89
W35	1776	111	6	111	110	99	110	101			94	85	18	17	93		94
W36	1292	70	5	70	70	100	70	65			73	104	14	14	88		100
W37	1414	59	4	59	59	100	59	52			70	119	11	11	89		100
W38	411	70	17	70	70	100	70	62	429	426	68	97	12	12	83	99	100
W39	563	41	7	41	41	100	41	34			43	105	11	10	97		91
W40	234	34	15	34	34	100	34	33			34	100	9	8	100		89
W41	55	2	4	2	2	100	2	2			1	50	1	1	92		100

Table 3: General Summary of Radio Tags Applied to Adult Sockeye at Klukshu Weir, July-Oct 2016. 165 tags were applied throughout the migration period (70 "Early" tags up to Aug 13, 19 "Mix" tags from Aug 14 to Aug 20, and 76 "Late" tags after Aug 20. Tags were applied mostly to females (150F, 15M). 153 of the 165 tagged fish could be assigned to a spawning destination, with 83 tag histories classified as "clear pattern" (e.g. fish rapidly passed all the river towers, then detected in lake many times), while the signal detections for 70 fish required more interpretation (e.g. moved about the mainstem, but were also detected by lake tower several times). 9 tagged fish were harvested or otherwise lost from the sample. 3 fish in the tagged sample (i.e. have fish ID and DNA sample) did not have an associated tag record. Appendix J describes the observed pattern for each tagged fish, and Appendix K summarizes the match between the assigned tag fate and the genetic stock identification (Section 7.5). Note that there were 12 late tags with a short tracking history that ended in in river, and 6 of these were from redeployed tags, which were excluded fromn some analyses.

Variable	Value	Early	Mix	Late	Total	%
	All tags	70	19	76	165	100
Sex	F	56	19	75	150	91
Sex	M	14	0	1	15	9
Tag_Use	New	70	17	63	150	91
Tag_Use	No Record	0	2	1	3	2
Tag_Use	Redeployed	0	0	12	12	7
TagHist_Class	Clear	36	10	37	83	50
TagHist_Class	Harvested or Lost	7	0	2	9	5
TagHist_Class	Interpretation	27	7	36	70	42
TagHist_Class	No Record	0	2	1	3	2
TagHist_Pattern	Lake and drop	5	1	0	6	4
TagHist_Pattern	Lake only	1	1	3	5	3
TagHist_Pattern	Lake outlet	4	1	3	8	5
TagHist_Pattern	Loss - Assumed	3	0	2	5	3
TagHist_Pattern	Loss - Harvested	4	0	0	4	2
TagHist_Pattern	Moved about mainstem and ended up at lake outlet	1	0	0	1	1
TagHist_Pattern	Moved about mainstem and ended up in lake	4	1	3	8	5
TagHist_Pattern	Moved about mainstem and ended up in river	18	2	2	22	13
TagHist_Pattern	Moved about mainstem, but stayed in lower river	1	0	1	2	1
TagHist_Pattern	Moved about mainstem, but with mixed signals	4	0	0	4	2
TagHist_Pattern	No Record	0	2	1	3	2
TagHist_Pattern	Short track ends in lake	1	2	9	12	7
TagHist_Pattern	Short track ends in river	3	1	12	16	10
TagHist_Pattern	Straight to lake	16	8	32	56	34
TagHist_Pattern	Straight to lake, but with mixed signals	5	0	8	13	8

Table 4: Sample Weights (Run,Tag, DNA) by Timing Group and Statistical Week.
Weights and expansion factors are required for some analyses (e.g. to calculate overall proportion of river-spawning fish based on proportion of weekly tags that were assigned a river fate). Section 5.2 summarizes the rationale for different weights and how they are used. Run is the total sockeye count at Klukshu weir. Tag Fates is the number of tags for which a fate could be assigned (see Appendix J for details). Unique genotype (GT) samples include only those where samples could be processed, at least 10 of 14 loci could be read, and that were not duplicates (Section 5.5). Prop Run is the proportion of the total run observed in a week. TF/Run is the proportion of the weekly run that was successfully tagged (i.e. tag fate assigned). GT/Run is the proportion of the weekly run that was successfully genotyped (i.e. baseline match assigned). 4 alternative weights were derived from these proportions: Run (overall) is Prop Run rescaled to a sum of 1. Run (within group) is the weekly contribution to each timing group. Tag = 1 / (TF/Run), which expands each tag based on weekly tag ratio (e.g. 1 tag in W29 represents about 7.5 fish, but 1 tag in W37 represents about 128 fish. Genotype is the same as Tag, just using the DNA sample ratio (GT/Run). Tag application was by design spread roughly evenly across all weeks to cover the full run, but as a result the tag ratios vary a lot (5 to 128).

							Weights			
	Run	Tag Fates	Unique GT	Prop Run	TF / Run	GT / Run	Run (over-all)	Run (within Group)	Tag	Geno-type
Early	1347	63	339	17.76	4.68	25.17	0.18	-	21.37	3.97
Mix	492	17	87	6.49	3.46	17.68	0.06	-	28.90	5.66
Late	5745	73	383	75.75	1.27	6.67	0.76	-	78.74	15.00
W28	1	0	-	0.01	0	0.00	0.00	0.00	0.00	0.00
W29	82	11	74	1.08	13.41	90.24	0.01	0.04	7.46	7.45
W30	108	3	6	1.42	2.78	5.56	0.01	0.06	35.97	36.00
W31	154	30	75	2.03	19.48	48.70	0.02	0.08	5.13	5.13
W32	429	8	127	5.66	1.86	29.60	0.06	0.23	53.76	53.63
W33	573	11	57	7.56	1.92	9.95	0.08	0.31	52.08	52.09
W34	492	17	87	6.49	3.46	17.68	0.06	1.00	28.90	28.94
W35	1776	17	94	23.42	0.96	5.29	0.23	0.31	104.17	104.47
W36	1292	14	73	17.04	1.08	5.65	0.17	0.22	92.59	92.29
W37	1414	11	70	18.64	0.78	4.95	0.19	0.25	128.21	128.55
W38	411	12	68	5.42	2.92	16.55	0.05	0.07	34.25	34.25
W39	563	10	43	7.42	1.78	7.64	0.07	0.10	56.18	56.30
W40	234	8	34	3.09	3.42	14.53	0.03	0.04	29.24	29.25
W41	55	1	1	0.73	1.82	1.82	0.01	0.01	54.95	55.00
	7584	*153*	*809*							

Table 5: Overview of Juvenile Sample Sizes for 2016 Klukshu Sockeye Sampling.
First row shows total sockeye sample sizes. Rows 2-4 summarize sockeye samples collected by location and life stage, and the rest shows samples from other species caught incidentally. Scales were processed and aged by Peter Etherton using available equipment. Aged scale samples include only those where annuli could be clearly identified. DNA samples were sent to the DFO Genetics Lab in Nanaimo. Unique genotype (GT) samples include only those where samples could be processed, at least 10 of 14 loci could be read, and were not duplicates (See Section 5.7), while "GT Read" includes valid genotyping results that turned out to be duplicates. Appendix I summarizes the DNA data clean-up. Note that the valid genotype samples do not correct for family structure (i.e. siblings, Section 5.9). Genetic sample processing pooled the Sockeye fry collected in Klukshu Lake and at Klukshu Lake outlet.

		Fork Length		Weight				DNA Samples				Success Rate	
	All	Num	%	Num	%	Scales	Aged	Proc-essed	GT Read	Uniq. GT	%GT	Age	GT
Sockeye - Total	535	507	95	471	88	161	133	494	492	492	92	83	100
Sockeye - River Fry	214	202	94	202	94	0	0	214	214	214	100	-	100
Sockeye - Lake Fry	90	90	100	90	100	0	0	154	152	152	99	-	99
Sockeye - Lake Outlet Fry	64	48	75	19	30	0	0						
Sockeye - Lake Outlet Smolt	167	167	100	160	96	161	133	126	126	126	75	83	100
Chinook - Fry	24	24	100	24	100	0	0	-	-	-	-	-	-
Chinook - Smolt	18	18	100	7	39	10	0	-	-	-	-	0	-
Coho - Fry	602	602	100	548	91	5	0	-	-	-	-	0	-

Table 6: Overview of Final Destination for <u>All</u> Adult Sockeye Tagged at Klukshu Weir in 2016.
Radio tags were applied to a subset of fish sampled at the weir, with proportional focus on early migrating fish and a preference for tagging females. Samples with successful fate include only those where a final spawning destination could be identified based on stationary radio towers and a helicopter overflight. 3 overall averages are listed (Section 5.2). Note that the bottom table uses raw totals for the timing groups. Table 7 shows ratios based on alternative weightings. Table H 1 and Table H 4 show the same data split into female and male tagged fish. Appendix C summarizes the radio tag detections and Appendix J has the details for each tag. Two versions of the tag summary are shown, with columns on the left including all tag records and columns on the right excluding 15 tags that were redeployed after recovery in a fishery or on the spawning grounds. This affects estimated proportion of river spawners in 3 statistical weeks, highlighted in green. The estimates using only new tags are used in subsequent analyses (e.g. the regression fits in Figure 9 and the timing curves in Figure 22), because redeployed tags had short tracking histories and movement patterns were difficult to interpret (Table J 5).

	All Tags					New Tags Only				
Stat Week	Tags	River	Lake	Un-known	Perc River*	Tags	River	Lake	Un-known	Perc River*
28	-	-	-	-	-	-	-	-	-	-
29	14	8	3	3	73	14	8	3	3	73
30	3	3	0	0	100	3	3	0	0	100
31	32	14	16	2	47	32	14	16	2	47
32	9	4	4	1	50	9	4	4	1	50
33	12	5	6	1	45	12	5	6	1	45
34	19	5	12	2	29	17	5	12	0	29
35	18	4	13	1	24	18	4	13	1	24
36	14	1	13	0	7	14	1	13	0	7
37	11	1	10	0	9	11	1	10	0	9
38	12	3	9	0	25	11	3	8	0	27
39	11	2	8	1	20	8	1	7	0	13
40	9	5	3	1	63	-	-	-	-	-
41	1	1	0	0	100	1	1	0	0	100
Total	***165***	***56***	***97***	***12***		***150***	***50***	***92***	***8***	
			Wt Avg (run)	**25**						**24**
			Wt Avg (#tags)	37						35
			Raw Avg	46						44

	All Tags					New Tags Only				
Timing Group	Tags	River	Lake	Un-known	Perc River*	Tags	River	Lake	Un-known	Perc River*
Early	70	34	29	7	54	70	34	29	7	54
Mixed	19	5	12	2	29	17	5	12	0	29
Late	76	17	56	3	23	63	11	51	1	18
Total	***165***	***56***	***97***	***12***		***150***	***50***	***92***	***8***	

* Percent River includes only tags with tag fate (i.e. excludes tags with unknown destination)

Table 7: Chi-Squared Test for Final Destination of <u>All</u> Adult Sockeye Tagged at Klukshu Weir in 2016. Tagging data from Table 6 were subset to focus only on the tags for which a final destination could be determined, which were then grouped as early migrants (W28-W33) or late migrants (W35-W41). This leaves out 29 samples, because they passed the weir during the "mixed" week 34, or tag destination couldn't be determined. Pearson's chi-squared test without continuity correction was applied to all 136 remaining observations using the R function prop.test(), and replicated 1,000 times on random subsamples of 90% of the data. Tests were replicated using proportions adjusted based on weighted average of weekly proportion using run size (see Section 5.2), and excluding redeployed tags. All three versions of the test show essentially the same result: the sample proportions are very different, with a p value smaller than 0.05 in all of the bootstrap tests (100%).

<u>All Tags – Raw Ratios</u>

Timing Group	Tag Destination Lake	River	% River	p.value	percent p.values ≤0.05	95% Conf Int. (Diff in Prop)
Early	29	34	54%	2.3e-4	100	Early tagged adults have between 15% and 46% <u>lower</u> proportion of lake spawners
Late	56	17	23%			

<u>All Tags– Weighted within a timing group by run size</u>

Timing Group	Tag Destination Lake	River	% River	p.value	percent p.values ≤0.05	95% Conf Int. (Diff in Prop)
Early	30	33	52%	2.1e-5	100	Early tagged adults have between 19% and 50% <u>lower</u> proportion of lake spawners
Late	60	13	18%			

<u>New Tags Only – Weighted within a timing group by run size</u>

Timing Group	Tag Destination Lake	River	% River	p.value	percent p.values ≤0.05	95% Conf Int. (Diff in Prop)
Early	30	33	52%	8.9e-6	100	Early tagged adults have between 21% and 51% <u>lower</u> proportion of lake spawners
Late	61	12	16%			

Table 8: Alternative Genotype Sets.
The genotype readings for the DNA samples collected for this project in 2016 (1,044 adults and 492 juveniles with unique genotypes; Table 2 and Table 5) were organized into alternative sets. This table outlines the different sets. Section 7.5 describes the details. Appendix I documents the data clean-up. These different combinations of genotype samples were used for different analyses. For example, sets G1 to G5 were used in sensitivity analyses for fitting phylogenetic trees (e.g. Figure 11), while sets G5 and G10 were used as baselines for genetic stock identification (e.g. Table 14).

Set ID	Description
G1	2016 Klukshu samples, cleaned
G2	2016 Klukshu samples (cleaned) and all large Alsek baseline samples (50+ samples)
G3	2016 Klukshu samples, all
G4	Alsek baselines, all
G5	Alsek baselines, large samples only (50+ samples)
G6	Klukshu baselines only
G7	2016 Klukshu samples (cleaned) and Klukshu baseline
G8	2016 Klukshu weir samples only (cleaned)
G9	2016 Klukshu weir samples (cleaned) and all large Alsek baseline samples (50+ samples)
G10	Revised Alsek Baseline (2016 Klukshu spawning gr. samples, large baselines for other systems)
G11	2016 Samples and Revised Alsek Baseline
G12	2016 Samples (excl. from Mixed Period, Aug 14-20) and Revised Alsek Baseline
G13	Trimmed Klukshu baseline (2016 river spawners and lake spawners, Neskataheen baseline)
G14	2016 spawners only (2016 river spawners and lake spawners)

Table 9: Alternative Methods for Fitting Phylogenetic Trees.
The process of fitting phylogenetic trees has 2 steps: first, calculate a measure of genetic distance between all possible pairs of individuals in your sample. Then apply a fitting algorithm that uses some combination of maximizing the amount of variability explained by the tree and minimizing the complexity of the tree (i.e. conceptually similar to testing alternative multi-variate regressions). Many alternative methods are available for both of these steps. We checked the sensitivity of tree fits to 4 alternative measures of genetic distance and 2 alternative tree fitting algorithms, implemented across different software applications (TreeFit, and the R packages {ape} , {adegenet} , and {phangorn}. Section 5.7 describes the methods.

Tree ID	Genetic Distance	Tree Fitting	Software
T1	Theta	Neighbour Joining	TreeFit
T2	Ds	Neighbour Joining	TreeFit
T3	Da	Neighbour Joining	TreeFit
T4	Dc	Neighbour Joining	TreeFit
T5	Theta	UPGMA	TreeFit
T6	Ds	UPGMA	TreeFit
T7	Da	UPGMA	TreeFit
T8	Dc	UPGMA	TreeFit
T9	Theta	UPGMA	R
T10	Ds	UPGMA	R
T11	Dc	UPGMA	R

Table 10: Allele Distributions for 2016 Klukshu Sockeye Samples And Alsek Baseline.
This table summarizes allele distributions using two different metrics for 4 alternative sample groups. Loci with the lowest value in a column are highlighted in green. Loci with the highest avg. alleles in a column are highlighted in yellow. Sample groups used in this table are based on later analyses, which fitted phylogenetic trees (Section 7.5) and assigned probabilities of genetic stock matches (Section 7.6). The Lake Group includes lake spawners, late weir migrants, and juveniles sampled at the lake outlet. The River Group includes river spawners, early weir migrants, and juveniles sampled on the Klukshu mainstem. The baselines (BL) include those samples left after filtering out incomplete genotypes and exclusing baselines with fewer than 50 samples (Set G11; Table 8). The average number of unique alleles is calculated based on 1000 bootstrapped samples of 100 alleles from the sample group (similar to Table 2 in Beacham et al. 2008). Allele variability differs substantially across loci, from 3-4 alleles /100 samples for *oki1a* to 19-29 alleles/100 samples for *oki10*. The proportion of allele samples captured by the 5 most frequent alleles summarizes the shape of the frequency distribution (i.e. higher proportion = more concentrated on a few alleles). In these samples, the locus with the highest avg number of alleles, *oki10*, also has the lowest proportion of samples in the top 5, indicating that these additional alleles are not just a few extremely rare cases (e.g. potential outliers or errors), but are rarer alleles in the population. Table I 1 lists the source references for each locus. More detailed summaries for each group of samples are included as Table I 5 to Table I 8. These show the number of samples and number of unique alleles for each locus. Note that the avg. alleles / 100 samples can be much lower than the total number of unique alleles in the sample. For example, Table I 8 shows that in the complete set of samples and baselines (Set G11), *oki10* has 77 unique alleles, but in the bootstrap samples of size 100 the number of unique alleles ranged from 20 to 37, with an average of 29, as listed below. Figure 10 compares the allele frequency profiles for the 2016 Lake Group and 2016 River Group at 14 loci, and Table 11 summarizes the observed patterns. 4 loci for which the profile patterns in Figure 10 are very different are highlighted in **bold font**.

	Avg. Alleles / 100				Prop in Top 5 Alleles			
Locus	2016 Lake	2016 River	Neskata-heen BL	All 2016 & Rev BL	2016 Lake	2016 River	Neskata-heen BL	All 2016 & Rev BL
loc_1b	5.1	4.6	4.3	5.4	0.997	0.999	1	0.995
loc_3dre	12.3	13.1	11.8	14.3	0.65	0.671	0.751	0.598
loc_i1	11.8	11.8	10.4	13.5	0.805	0.763	0.792	0.741
loc_oki10	27.9	23.5	18.7	29.0	0.381	0.572	0.645	0.417
loc_oki16	8.6	8.1	13.3	13.6	0.92	0.945	0.815	0.841
loc_oki1a	3.8	3.6	2.9	3.8	1	1	1	1
loc_oki1b	3.8	3.8	3.5	3.8	1	1	1	1
loc_oki29	12.5	13.6	11.8	16.0	0.775	0.745	0.782	0.68
loc_oki6	7.6	7.9	7.2	8.8	0.942	0.916	0.936	0.932
loc_omy77	8.0	9.6	7.9	9.6	0.921	0.919	0.953	0.9
loc_one8	8.0	8.0	8.5	10.0	0.955	0.915	0.928	0.909
loc_ots103	13.7	14.2	12.4	16.4	0.724	0.762	0.794	0.642
loc_ots2	6.9	7.0	6.1	7.6	0.892	0.956	0.982	0.925
loc_ots3	4.9	5.5	5.7	6.2	0.998	0.993	0.983	0.986
Min	*3.8*	*3.6*	*2.9*	*3.8*	*0.381*	*0.572*	*0.645*	*0.417*
Max	*27.9*	*23.5*	*18.7*	*29.0*	*1*	*1*	*1*	*1*

Table 11: Comparison of Allele Frequency Patterns – Klukshu River vs. Klukshu Lake.
Figure 10 shows profiles of allele frequencies for 2 sets of samples, grouped based on later analyses which fitted phylogenetic trees (Section 7.5) and assigned probabilities of genetic stock matches (Section 7.6). The Lake Group includes lake spawners, late weir migrants, and juveniles sampled at the lake outlet. The River Group includes river spawners, early weir migrants, and juveniles sampled on the Klukshu mainstem. This table summarizes the observed patterns. Allele frequency patterns fall into 5 types, with 10 of the 14 loci showing little difference between the two sample groups.

Type	Comparison	Description	Loci
1	River and Lake similar	Few alleles, 1 allele clearly predominant, little difference between sample groups	**3 loci:** *1b*, *oki1a*, *ots3*
2	River and Lake similar	Few alleles, 1 allele predominant, another allele also common, little difference between sample groups	**1 locus:** *oki1b*
3	River and Lake similar	10 or more alleles, both groups have same allele predominant, remaining alleles have similar frequencies	**6 loci:** *oki16, oki29, omy77, one8, ots103, ots2*
4	River and Lake different	10 or more alleles, both groups have same allele predominant, remaining allele frequencies very different	**1 locus:** *oki10*
5	River and Lake different	More than 10 alleles, most frequent allele differs between sample groups	**3 loci:** *i1, oki6, 3dre*

Table 12: Overview of Fitted Phylogenetic Trees - TreeFit.
The structure of phylogenetic trees estimated with Treefit varies depending on fitting method and the suite of samples included. This table summarizes the tree fits for all 2016 Klukshu samples and the revised Alsek baselines (G11), or excluding samples from the mixed weir timing (G12).
Table 8 lists the alternative genotype sets, and Section 5.7 describes the alternative tree fitting methods (NJ= Neighbour Joining, UP= UPGMA = Unweighted Pair Group Method with Arithmetic Mean). The 16 fitted trees (2 genotype sets * 4 genetic distance measures * 2 tree fitting methods) can be categorized into 5 types. Cells with numbers show which tree types were produced by which fitting method, and the cell values show the R^2 for the fitted tree (0-1, Higher $R^2 \approx$ better fit). The highest R^2 for each genotype set and tree fitting method is highlighted. All 16 variations combine all the Lake group samples. 14 of the 16 variations combine all the River group samples, but 2 cases move the river spawners to a separate branch within the Klukshu/Neskataheen aggregate (Type C: G11 with T3 and T4). Figure 12 and Appendix M show the fitted trees and bootstrap values for key branches.

			Method Genetic Distance/ Tree Fitting							
			T1 Theta	**T2** Ds	**T3** Da	**T4** Dc	**T5** Theta	**T6** Ds	**T7** Da	**T8** Dc
Gtype Set	**Tree Type**	**Description**	NJ	NJ	NJ	NJ	UP	UP	UP	UP
G11	**Type A**	**Lake Group:** Lake / Late Weir / LakeOutlet Fry & Smolt **River Group:** River / Early Weir / Vand Cr. Fry / Neskatah. Mix Weir with River Group	**0.914**	**0.918**	-	-	**0.648**	**0.643**	-	-
G11	**Type B**	**Lake Group:** Lake / Late Weir / LakeOutlet Fry & Smolt **River Group:** River / Early Weir / Vand Cr. Fry / Neskatah. Mix Weir: NoTag with River Group, Tagged on sep branch	-	-	-	-	-	-	**0.680**	**0.727**
G11	**Type C**	**Lake Group:** Lake / Late Weir / LakeOutlet Fry & Smolt **Neskatheen Group**: Early Weir / Vand Cr. Fry / Neskatah. River Spn on separate branch within Klukshu/Neskataheen Mix Weir with Neskataheen Group	-	-	**0.924**	**0.910**	-	-	-	-
G12	**Type D**	**Lake Group:** Lake / Late Weir / LakeOutlet Fry & Smolt **River Group:** River / Early Weir / Vand Cr. Fry / Neskatah. Mix Weir not included in sample	**0.933**	**0.932**	**0.932**	**0.946**	-	-	**0.692**	**0.739**
G12	**Type E**	**Lake Group:** Lake / Late Weir / LakeOutlet Fry & Smolt **River Group:** River / Early Weir / Vand Cr. Fry / Neskatah. Mix Weir not included in sample Kwatine Cr. with Lake Group	-	-	-	-	**0.656**	**0.642**	-	-

Table 13: Bootstrap sensitivity test of genetic trees.
This table summarizes key observations from a sensitivity analysis of alternative tree fitting approaches, using 3 alternative measures of genetic distance and 2 alternative tree fitting algorithms, implemented across different software applications (TreeFit, and the R packages {ape} , {adegenet} , and {phangorn}. Section 5.7 describes the methods. Table 9 lists the alternative approaches (e.g. T2 = Theta distance and neighbour-joining tree). Genepop sets are summarized in Table 8 (e.g. G12 = 2016 samples and revised Alsek Baselines with 50+ samples). Treefit bootstraps are 1000 resamples of individual loci (reshuffling parts of a genotype), with automated summary of bootstrap probabilities for key nodes. R bootstraps are based on 100 resamples each dropping 10% of the records in each sample group (i.e. excluding whole fish), and visually checked for key nodes. The Treefit trees with the highest R^2 for each genotype set are highlighted. Bootstrap support for the River Group and Lake Group is very high across all 11 alternative approaches (Median values are 98% for the River group of samples and 100% for the Lake Group of samples). For Set G12, 9 of the 11 alternative fits have a high bootstrap probability (72% to 96%) separating all the Klukshu samples from all the other Alsek baselines (except Neskataheen, which is part of the River Group). However, bootstrap values for T9 and T10 are low, because in these two ftree fitting approaches, Kwatine_Cr moves about between the river group, lake group, overall Klukshu, or a separate branch.

		TREEFIT Trees								R Trees		
Set	Tree Node	T1	T2	T3	T4	T5	T6	T7	T8	T9	T10	T11
	Set G12 R-Sq	0.93	0.93	0.93	**0.95**	0.67	0.64	0.69	0.74			
G12	**Full River Group***	99	98	98	**100**	83	82	83	96	100	100	100
G12	**Full Lake Group****	100	100	100	**100**	100	100	100	100	100	100	100
G12	All Klukshu samples separate from other Alsek	72	72	96	**89**	-	-	77	96	1	4	96
G12	Full River Group with Kwatine	-	-	-	**-**	-	-	-	-	55	40	-
G12	Full Lake Group with Kwatine	-	-	-	**-**	41	43	-	-	40	57	-
G12	All Klukshu samples with Goat and Kwatine	34	36	61	**81**	-	-	-	-	-	-	-
G12	All Klukshu samples with Kwatine	-	-	-	**-**	-	-	37	33	3	-	4
	Set G11 R-Sq	0.91	0.92	**0.92**	0.91	0.65	0.64	0.68	0.73			
G11	**Full River Group***	59	55	**-**	-	-	-	-	53			
G11	**Full Lake Group****	98	94	**98**	100	87	87	100	98			
G11	All Klukshu samples separate from other Alsek	98	98	**99**	99	-	-	76	94			
G11	All Klukshu samples with Kwatine	-	-	**-**	-	43	47	-	-			
G11	Full River Group with both Mix Weir samples	62	65	**-**	-	53	56	-	-			
G11	Partial River Group (without River Spn)	-	-	**56**	-	-	-	-	-			
G11	Full River Group and MixNoTag	-	-	**-**				67	71			
G11	Partial River Group and both Mix samples	-	-	**73**	-	-	-	-	-			

* **Full River Group:** River Spawners (AdSpn_KlukRiver), River Fry (Juv_KlukVandCrFry), Early Weir (AdWeir_EarlyTag, AdWeir_EarlyNoTag), Neskataheen baseline.

** **Full Lake Group:** Lake Spawners (AdSpn_KlukLake), Lake Fry and Smolt (Juv_KlukOutFry, Juv_KlukOutSm), Late Weir (AdWeir_LateTag, AdWeir_LateNoTag).

Table 14: DNA sample assignment to Klukshu / Neskataheen baselines – Revised Baselines

Genetic matches of 2016 samples to Alsek sockeye baselines. Tables show the number of samples which have each baseline group as the best match (i.e. highest probability; Section 5.8). In this case the 2016 samples are matched up against the revised baselines for Alsek Sockeye, which uses the 2016 spawning ground samples as baselines for Klukshu: Klukshu_River, Klukshu_Lake. Table 15 shows the corresponding results for the original baselines. Based on the phylogenetic tree fits (Figure 11), Klukshu samples matched to the Neskataheen baseline were interpreted as part of a Klukshu River / Neskataheen genetic group. Most of the early sockeye (i.e. passed Klukshu weir before August 14th) were matched to the River / Neskataheen group (85% of weekly pooled samples, 75% of tagged samples, 83% of all early samples). Conversely, most of the late sockeye (i.e. passed Klukshu weir after August 20th) were matched to the Lake spawners (227/308 =74% of weekly pooled samples, 57/75=76% of tagged samples, 74% of all late samples). Roughly half of the sockeye during the mixed period (i.e. passing Klukshu weir Aug 14-20) were matched with the River / Neskataheen group. Juvenile samples collected in 2016 matched up very closely with the spawning ground samples Only 1 of 278 juveniles (152 fry, 126 smolt) sampled at Klukshu Lake outlet and in the lake was matched to the River / Neskataheen group (less than 1%). Conversely, only 1 of 214 fry sampled at on the Klukshu mainstem at Vand Creek was genetically matched to the Lake spawners. Both of these numbers are much smaller than the number of samples matched to other baselines (e.g. 14 of the lake outlet fry, 22 of the mainstem fry). Note that almost 10% of the 2016 Klukshu samples were matched to other baselines, such as U_Tatshensh_RT, Alsek_T_down, or Tweedsmuir_RT. Appendix J lists the best and 2nd best match for all the tagged samples. Table 19 shows a leave-one-out sensitivity test for the original and revised Alsek baselines. Table 18 shows a breakdown of the 129 “other” baseline matches. Section 8.5 discusses alternative interpretations of Klukshu samples matched to non-Klukshu baselines.

	Baseline Groups						
Sample Group	Klukshu Lake Spawners	Klukshu River Spawners	Neska-taheen	Other	n	Percent River/Nesk Group	Percent Neska-taheen
AdWeir_EarlyNoTag2016	25	91	142	16	274	85.0%	51.8%
AdWeir_EarlyTagged2016	12	19	30	4	65	75.4%	46.2%
AdWeir_LateNoTag2016	227	32	14	35	308	14.9%	4.5%
AdWeir_LateTagged2016	57	3	4	11	75	9.3%	5.3%
AdWeir_MixNoTag2016	30	11	23	4	68	50.0%	33.8%
AdWeir_MixTagged2016	7	3	6	3	19	47.4%	31.6%
Juv_KlukLkOutFry2016	138	0	0	14	152	0.0%	0.0%
Juv_KlukLkOutSmolt2016	105	0	1	20	126	0.8%	0.8%
Juv_KlukVandCrFry2016	1	74	117	22	214	89.3%	54.7%
Adult Total	*358*	*159*	*219*	*73*	*809*	*46.7%*	*27.1%*
Juvenile Total	*244*	*74*	*118*	*56*	*492*	*39.0%*	*24.0%*
Grand Total	***602***	***233***	***337***	***129***	***1301***	***43.8%***	***25.9%***

Table 15: DNA sample assignment to Klukshu / Neskataheen baselines – Original Baselines

Table structure and context description are the same as for Table 14, but in this case the 2016 samples are matched up against the original baselines for Alsek Sockeye. The original baseline uses weir samples (mostly from early 2000s, Table I 3) grouped by timing to establish 3 baselines for Klukshu: Early, Mix, and Late. Based on the phylogenetic tree fits (Figure 11), Klukshu samples matched to the Neskataheen baseline were interpreted as part of an Early / Neskataheen genetic group. The matches for adult samples are less clear against the original baseline. Most sample groups had more assignments to "other" baselines, and only about 50% of samples from river spawners were matched to the Early/Neskataheen group. However, the results are still broadly similar to the matches for the revised baseline in Table 14. Most of the early-returning adults and most of the mainstem fry were matched to the Early/Neskataheen group (79% of weekly pooled adult samples, 63% of tagged adult samples, 80% of fry at Vand Creek confluence). Very few of the late-returning adults and almost none of the lake juveniles were matched to the Early/Neskataheen group (10% of weekly pooled adult samples, 7% of tagged adult samples, 1% of lake outlet juveniles). Section 8.5 discusses alternative interpretations of Klukshu samples matched to non-Klukshu baselines.

	Baseline Groups						Percent	Percent
Sample Group	Klukshu Late	Klukshu Early	Klukshu Mix	Neska-taheen	Other	n	Early Group	Neska-taheen
AdSpn_KlukshuLake2016	38	0	66	10	4	118	8.5%	8.5%
AdSpn_KlukshuRiver2016	3	0	0	59	55	117	50.4%	50.4%
AdWeir_EarlyNoTag2016	0	4	24	212	34	274	78.8%	77.4%
AdWeir_EarlyTagged2016	2	0	13	41	9	65	63.1%	63.1%
AdWeir_LateNoTag2016	140	0	93	31	44	308	10.1%	10.1%
AdWeir_LateTagged2016	36	1	31	4	3	75	6.7%	5.3%
AdWeir_MixNoTag2016	16	0	12	33	7	68	48.5%	48.5%
AdWeir_MixTagged2016	6	5	1	6	1	19	57.9%	31.6%
Juv_KlukLkOutFry2016	89	0	59	0	4	152	0.0%	0.0%
Juv_KlukLkOutSmolt2016	90	0	24	3	9	126	2.4%	2.4%
Juv_KlukVandCrFry2016	0	11	0	160	43	214	79.9%	74.8%
Adult Total	*241*	*10*	*240*	*396*	*157*	*1044*	*38.9%*	*37.9%*
Juvenile Total	*179*	*11*	*83*	*163*	*56*	*492*	*35.4%*	*33.1%*
Grand Total	***420***	***21***	***323***	***559***	***213***	***1536***	***37.8%***	***36.4%***

Table 16: DNA sample assignment to Klukshu / Neskataheen baselines – Trimmed Baselines
Table structure and context description are the same as for Table 14, but in this case the 2016 samples are matched up against a trimmed baseline using only the 2016 spawning ground samples for Klukshu River and Klukshu Lake, plus the Neskataheen baseline samples. Based on the phylogenetic tree fits (Figure 11), Klukshu samples matched to the Neskataheen baseline were interpreted as part of a Klukshu River / Neskataheen genetic group. The matches for adult samples are similar to the results for the revised baseline (Table 14). Most of the early-returning adults and most of the mainstem fry were matched to the Klukshu River/Neskataheen group (88% of weekly pooled adult samples, 67% of tagged adult samples, 100% of fry at Vand Creek confluence). Few of the late-returning adults and almost none of the lake juveniles were matched to the Klukshu River/Neskataheen group (19% of weekly pooled adult samples, 8% of tagged adult samples, 3-4% of lake outlet juveniles). Note that for comparisons like this, which match individual samples to only 3 baselines, even a random assignment would be correct 33% of the time.

Sample Group	Klukshu Lake	Klukshu River	Neska-taheen	n	Percent River/Nesk Group	Percent Neska-taheen
AdWeir_EarlyNoTag2016	34	107	133	274	88	49
AdWeir_EarlyTagged2016	26	23	29	78	67	37
AdWeir_LateNoTag2016	249	49	10	308	19	3
AdWeir_LateTagged2016	57	2	3	62	8	5
AdWeir_MixNoTag2016	31	13	24	68	54	35
AdWeir_MixTagged2016	9	6	4	19	53	21
Juv_KlukLkOutFry2016	147	5	0	152	3	0
Juv_KlukLkOutSmolt2016	121	5	0	126	4	0
Juv_KlukVandCrFry2016	1	109	104	214	100	49
Adult Total	*406*	*200*	*203*	*809*	*50*	*25*
Juvenile Total	*269*	*119*	*104*	*492*	*45*	*21*
Grand Total	***675***	***319***	***307***	***1301***	***48***	***24***

Table 17: Probability of assigning samples to Klukshu River / Neskataheen Complex.
Table shows the total number of samples in each group after data clean-up (Appendix I), and then categorizes them by assignment probability. For example, the 2nd row of the top table shows that 6 of 65 samples from early tagged adults had less than 80% probability of being matched to one of the Klukshu baselines or the Neskataheen baseline (i.e. for each of these 6 samples, the genetic stock ID estimated a chance of 1 in 5 or higher that it was from a population outside the Klukshu River /Neskataheen Complex (KR/N). For 3 of these 6 samples, the probabilities were less than 1/4 of a match to KR/N and more than 3/4 of a match to other populations. Using 80% probability as the cut-off for a high-confidence GSI match to KR/N, most of the sample groups have a substantial proportion of samples with a low to moderate-confidence GSI match (10% and higher are highlighted in yellow). Note that the proportions of low to moderate-confidence GSI matches are much higher for several of the sample groups when using the original baseline (e.g. early adults, mainstem fry), but lower for other sample groups (e.g. lake outlet fry and smolts). Figure 13 and Figure 14 show the distributions of assignment probability. Note that there are 2 different types of cases lumped together in the category of low to moderate-confidence assignment to KR/N: Some samples have very diffuse GSI match (i.e. some probability assigned to many different baselines), while others simply have a high-probability assignment to some other baseline (i.e. estimate a high probability that this sample is from one specific non-Klukshu population). Section 8.5 discusses alternative interpretations of Klukshu samples matched to non-Klukshu baselines.

A) Revised Baseline (2016 spawning ground samples for Klukshu)

		Number of Samples			Proportion of Samples		
Sample Group	n	<80%	<50%	<25%	<80%	<50%	<25%
AdWeir_EarlyNoTag2016	274	25	16	13	9	6	5
AdWeir_EarlyTagged2016	65	6	4	3	9	6	5
AdWeir_LateNoTag2016	308	57	36	26	19	12	8
AdWeir_LateTagged2016	75	16	11	8	21	15	11
AdWeir_MixNoTag2016	68	5	4	3	7	6	4
AdWeir_MixTagged2016	19	3	3	2	16	16	11
Juv_KlukLkOutFry2016	152	21	14	9	14	9	6
Juv_KlukLkOutSmolt2016	126	28	20	14	22	16	11
Juv_KlukVandCrFry2016	214	31	23	20	14	11	9
Adult Total	*809*	*112*	*74*	*55*			
Juvenile Total	*492*	*80*	*57*	*43*			
Grand Total	***1301***	***192***	***131***	***98***			

B) Original Baseline (Using weir samples for Klukshu, mostly from early 2000s)

		Number of Samples			Proportion of Samples		
Sample Group	n	<80%	<50%	<25%	<80%	<50%	<25%
AdSpn_KlukshuLake2016	118	9	4	3	8	3	3
AdSpn_KlukshuRiver2016	117	64	61	52	55	52	44
AdWeir_EarlyNoTag2016	274	56	33	26	20	12	9
AdWeir_EarlyTagged2016	65	14	10	8	22	15	12
AdWeir_LateNoTag2016	308	67	42	28	22	14	9
AdWeir_LateTagged2016	75	3	3	3	4	4	4
AdWeir_MixNoTag2016	68	8	6	3	12	9	4
AdWeir_MixTagged2016	19	3	1	0	16	5	0
Juv_KlukLkOutFry2016	152	7	4	3	5	3	2
Juv_KlukLkOutSmolt2016	126	10	8	4	8	6	3
Juv_KlukVandCrFry2016	214	54	43	33	25	20	15
Adult Total	*1044*	*224*	*160*	*123*			
Juvenile Total	*492*	*71*	*55*	*40*			
Grand Total	***1536***	***295***	***215***	***163***			

Table 18: Frequency of Non-Klukshu Baseline Matches Using Revised Baseline.
This table is based on the same set of results as Table 14, for details refer to the caption there. About 10% of the valid genotype readings from adults sampled at the weir and juveniles sampled throughout the Klukshu were genetically matched one of the non-Klukshu baselines. Note that these are the best matches (i.e. highest probability), but they are not necessarily good matches (i.e. assignment probability could be 40% for the best match, and 25% for the second best match, and a few percent for many other matches). Appendix J lists the best and 2nd best match for all the tagged samples, as well as the assignment probabilities. Upper Tatshenshini River Type, Alsek / Tatshenshini Downstream, and O'Connor River Type Sockeye are the most frequent non-Klukshu matches. Section 8.5 discusses alternative interpretations of Klukshu samples matched to non-Klukshu baselines.

BASELINE	MATCHES	
AdSpn_KlukshuLake2016	**602**	
Neskataheen	**337**	
AdSpn_KlukshuRiver2016	**233**	
U_Tatshensh_RT	33	
Alsek_T_down	22	
OConnor_RT	21	
Tweedsmuir_RT	14	
Kwatine_Cr	13	
Kudwat_Cr_RT	7	
Stinky_Cr_RT	5	
Goat_Cr_RT	4	
Bridge_Silver	3	
BorderSlough_RT	2	
Kane	2	
L_Tatshenshi_RT	2	
VernRichie_RT	1	
Klukshu / Neskataheen	1172	90.08%
Other	129	9.92%
Total	***1301***	

Table 19: Leave-one-out test of Alsek Sockeye genotype baselines – Revised Baseline.
This table shows a sensitivity analysis of the revised Alsek sockeye baseline data set, which uses 2016 spawning ground samples for the Klukshu. The information in this table differs from the results in Table 14 and Table 17, which match samples from 2016 to the Alsek baseline. In contrast, this analysis takes individual records out of each baseline and estimates the probability with which the sample would be assigned back to its baseline. The proportion of correct assignments is colour-coded, with 80% and better shaded green and worse than 50% shaded deep orange. Most of the baselines have low to very low % correct assignments. The probability of correct assignment can be low for different reasons, such as sample baseline sample size (e.g. Kane) or similar other baseline populations (Klukshu River vs. Neskataheen). Note that the sample size here is smaller, because only complete genotype records are used, as opposed to the criterion of "no more than 8 incomplete alleles" we used to filter the records (Table I 2). Also note that both types of analyses were implemented with the ONCOR software package (Section 5.8), but that assignment probabilities here are much lower than for the stock ID results in Table 14 and Table 17 . An investigation into the cause for this difference between analyses falls outside the scope of the current project, but is listed as priority item for future work (Section 9.4).

			Largest Misidentification	
Group	**n**	**% Correct**	**Group**	**%**
AdSpn_KlukshuLake2016	74	68.9%	AdSpn_KlukshuRiver2016	6.8%
AdSpn_KlukshuRiver2016	94	36.2%	Neskataheen	26.6%
Alsek_T_down	51	5.9%	Blanchard	33.3%
Blanchard	204	81.9%	Alsek_T_down	4.4%
BorderSlough_RT	162	67.3%	VernRichie_RT	15.4%
Bridge_Silver	96	33.3%	U_Tatshensh_RT	17.7%
Goat_Cr_RT	44	81.8%	AdSpn_KlukshuLake2016	2.3%
Kane	32	3.1%	U_Tatshensh_RT	15.6%
Kudwat_Cr_RT	230	20.9%	Stinky_Cr_RT	15.2%
Kwatine_Cr	55	54.5%	U_Tatshensh_RT	10.9%
L_Tatshenshi_RT	92	39.1%	U_Tatshensh_RT	12.0%
Neskataheen	714	81.1%	AdSpn_KlukshuRiver2016	9.9%
OConnor_RT	45	6.7%	Blanchard	20.0%
Stinky_Cr_RT	80	31.3%	Bridge_Silver	17.5%
Tweedsmuir_RT	130	47.7%	L_Tatshenshi_RT	6.9%
U_Tatshensh_RT	281	15.7%	Bridge_Silver	13.2%
VernRichie_RT	146	39.0%	BorderSlough_RT	17.1%

Table 20: Leave-one-out test of Alsek Sockeye genotype baselines – Original & Trimmed Baselines. Table structure and context description are the same as for Table 19, but with the original baselines for Alsek Sockeye. The original baseline uses weir samples (mostly from early 2000s; Table I 3) grouped by timing to establish 3 baselines for Klukshu: Early, Mix, and Late. Most of the baselines have low to very low % correct assignments

Original Baseline

			Largest Misidentification	
Group	**n**	**% Correct**	**Group**	**%**
Alsek_T_down	51	5.9%	Blanchard	33.3%
Blanchard	204	81.4%	Alsek_T_down	4.4%
BorderSlough_RT	162	67.3%	VernRichie_RT	16.0%
Bridge_Silver	96	34.4%	U_Tatshensh_RT	18.8%
Goat_Cr_RT	44	81.8%	Tweedsmuir_RT	4.5%
Kane	32	3.1%	U_Tatshensh_RT	18.8%
Klukshu_Early	192	15.1%	**Neskataheen**	**21.4%**
Klukshu_Late	231	55.4%	**Klukshu_mix**	**15.6%**
Klukshu_mix	425	25.4%	**Klukshu_Late**	**30.4%**
Kudwat_Cr_RT	230	20.9%	U_Tatshensh_RT	13.9%
Kwatine_Cr	55	56.4%	U_Tatshensh_RT	9.1%
L_Tatshenshi_RT	92	35.9%	U_Tatshensh_RT	12.0%
Neskataheen	714	85.6%	**Klukshu_Early**	**4.5%**
OConnor_RT	45	6.7%	Blanchard	20.0%
Stinky_Cr_RT	80	31.3%	Bridge_Silver	17.5%
Tweedsmuir_RT	130	47.7%	L_Tatshenshi_RT	6.9%
U_Tatshensh_RT	281	16.7%	Bridge_Silver	13.5%
VernRichie_RT	146	39.7%	BorderSlough_RT	17.8%

Trimmed Baseline

			Largest Misidentification	
Group	**n**	**% Correct**	**Group**	**%**
AdSpn_KlukshuLake2016	74	81.1%	AdSpn_KlukshuRiver2016	10.8%
AdSpn_KlukshuRiver2016	94	58.5%	Neskataheen	28.7%
Neskataheen	714	83.1%	AdSpn_KlukshuRiver2016	13.0%

2016 Spawners Only

			Largest Misidentification	
Group	**N**	**% Correct**	**Group**	**%**
AdSpn_KlukshuLake2016	74	82.4%	AdSpn_KlukshuRiver2016	17.6%
AdSpn_KlukshuRiver2016	94	83.0%	AdSpn_KlukshuLake2016	17.0%

Table 21: Overview of GSI Match for <u>All</u> Adult Sockeye Sampled at Klukshu Weir in 2016.
DNA samples were collected from most of the adults sampled at the weir (Table 2). Samples with valid genotype include only those where a tissue sample could be matched to a statistical week and the genotype reading was both mostly complete and not a duplicate (Appendix I). Genetic stock ID matches (Section 5.8) were classified into 3 categories, base on the fitted phylogenetic trees (Section 7.5): River/Neskataheen, Lake, and Other. 2 overall averages are listed (Section 5.2). The proportion of samples assigned to the River/Neskataheen group was high during the early run (80-93% up to week 33), and much lower during the late migration period (0-30% for week 34 and later). Note that the bottom table uses raw totals for the timing groups. Table 22 shows ratios based on alternative weightings and a formal test of differences between early and late migrants. Figure 17 plots the weekly proportions and fits a regression line. Note that these observations can't be separated into males and females, because only weekly sex ratio is available for the pooled DNA samples. Individuals can only be matched up within the much smaller sample of tagged fish.

Stat Week	Valid Genotypes	Klukshu River / Neskataheen	Klukshu Lake	Other	Perc River*
28	-	-	-	-	-
29	74	63	5	6	93
30	6	4	1	1	80
31	75	59	9	7	87
32	127	109	14	4	89
33	57	47	8	2	85
34	87	43	37	7	54
35	94	26	60	8	30
36	73	7	58	8	11
37	70	12	49	9	20
38	68	3	56	9	5
39	43	4	35	4	10
40	34	1	25	8	4
41	1	0	1	0	0
Total	*809*	*378*	*358*	*73*	
			Wt Avg (run)		**33**
			Raw Avg		44

Timing Group	Valid Genotypes	Klukshu River / Neskataheen	Klukshu Lake	Other	Perc River*
Early	339	282	37	20	83
Mixed	87	43	37	7	49
Late	383	53	284	46	14
Total	*809*	*378*	*358*	*73*	*47*

* Perc River includes only those samples genetically matched to one of the Klukshu baselines (i.e exclude "other" records)

Table 22: Chi-Squared Test for GSI Match of All Adult Sockeye Sampled at Klukshu Weir in 2016. Genetic matches from Table 21 were subset to focus only on the samples assigned to either the River/Neskataheen group or the lake spawner baseline, which were then grouped as early migrants (W28-W33) or late migrants (W35-W41). This leaves out 153 samples, because they passed the weir during the "mixed" week 34, or for which the best match was some non-Klukshu baseline. Pearson's chi-squared test without continuity correction was applied to all 656 remaining observations using the R function prop.test(), and replicated 1,000 times on random subsamples of 90% of the data. Tests were replicated using proportions adjusted based on weighted average of weekly proportion using run size (see Section 5.2). Both versions of the test show essentially the same result: the sample proportions are very different, with a p value smaller than 0.05 in all of the bootstrap tests (100%). Both the GSI matches (this table) and radio tags (Table 7) showed a significant difference in composition between early and late migrants, but DNA results estimate a much higher proportion assigned to the River/Neskataheen group (87% weighted average for the early run) than the radio tag fates (52% weighted average). Note that the genetic stock ID had a much larger sample size than the tagging program (656 vs. 136).

All – Raw Ratios

	GSI Match				percent	
Timing Group	Lake	River	% River	p.value	p.values ≤0.05	95% Conf Int. (Diff in Prop)
Early	37	282	89%	2.6e-77	100	Early migrants at the weir have between 67% and 78% lower proportion of lake spawners
Late	284	53	16%			

All – Weighted within a timing group by run size

	GSI Match				percent	
Timing Group	Lake	River	% River	p.value	p.values ≤0.05	95% Conf Int. (Diff in Prop)
Early	43	276	87%	9.4e-69	100	Early migrants at the weir have between 63% and 74% lower proportion of lake spawners
Late	276	61	18%			

Table 23: Summary of Sibship Reconstruction of 2016 Klukshu DNA Samples – Full Siblings. Sibling relationships were reconstructed using the COLONY program (Section 5.9), which links samples with similar genotypes to a set of constructed source genotypes (i.e. virtual parents). Note that our samples cover 3 brood years, and this analysis does not establish actual brood lineages across samples. However, the interpretation of common parentage is valid within each sample group. *Samples* is the total number of valid genotypes (Table I 4). *Unique Parent Pairs* is the number of different pairs of virtual parents in each sample group. *All* is the number of samples matched to at least one other sample as a full sibling (i.e. share both parents). *Max* is the largest number of full siblings for a parent pair in that sample group. *Parent Pairs* is the number of parent pairs that have at least 1 pair of full siblings in that sample group. *Single Match* is the number of parent pairs which have only 1 full sibling represented in this sample group (i.e. the other sibling is in a different sample group). An example helps to illustrate the interpretation of this summary: Of the 118 lake spawner samples with valid genotype readings (AdSpn_KlukLake), 17 (14%) have a full sibling among the grand total of 1536 samples, from 14 distinct pairs of virtual parents. 11 of the 14 parent pairs have only a single offspring represented in the AdSpn_KlukLake sample group, which means that the virtual siblings are in a different sample group. In some cases, these could be actual siblings (e.g. if both are from the weir samples, but one was tagged and the other wasn't) or close relatives (e.g. if one is from the 2016 adult returns and the other is from the fry sample which are the offspring of the 2015 spawners). Most samples have a high proportion of unique parent pairs, with the notable exception of newly emerged fry sampled on the Klukshu mainstem near the Vand Creek confluence, which have only 135 unique parent pairs for 214 samples. Within that group, 35 parent pairs account for 114 samples, with up to 15 fry from a single pair of parents. Figure 18 shows a heatmap of the reconstructed sibling relationships within and across sample groups. Additional analyses could include looking at half-sibling relationships (i.e. 1 parent in common) and developing a more formal family reconstruction. This exceeds the scope of the current project, but has been noted as a suggested priority for future work (Section 9.4).

				Full Sibling Matches			
Sample Group	Samples	All Parent Pairs	% Unique Parents	All	Max	Parent Pairs	Single Match
AdSpn_KlukLake	118	115	97%	17	2	14	11
AdSpn_KlukRiv	117	109	93%	33	3	25	18
AdWeir_EarlyNoTag	274	238	87%	97	5	61	35
AdWeir_EarlyTag	78	78	100%	33	1	33	33
AdWeir_LateNoTag	308	304	99%	46	2	42	38
AdWeir_LateTag	62	62	100%	18	1	18	18
AdWeir_MixNoTag	68	64	94%	21	2	17	13
AdWeir_MixTag	19	19	100%	5	1	5	5
Juv_KlukLkOutFry	152	150	99%	6	2	4	2
Juv_KlukLkOutSm	126	125	99%	6	2	5	4
Juv_KlukVandCrFry	214	135	63%	114	15	35	5
Adult Total	1044	-	-	270	17	215	171
Juvenile Total	492	-	-	126	19	44	11
Grand Total	**1536**	**1293***	**84%**	**396**	**36**	**259**	**182**

***** Note that parent pairs show up in multiple sample groups, so this column can't just be added up.

Table 24: Comparison of Tag Fate and Genetic Stock ID for New Tags Applied to Females.
Tag fates and genetic stock ID were successfully determined for 124 females migrating past Klukshu weir in 2016. This table shows the number of tags by timing group that showed various migration patterns, and also shows the proportion where the tag fate matched the genetic stock ID (i.e. "tag = river and GSI = river" or "tag = lake and GSI = lake". Note that these results are for new tags only. Redeployed tags had very low proportion of tag vs. GSI match and were excluded. Full comparisons are summarized in Appendix K. Detailed tag histories are listed in Appendix J. Two patterns were common among females tagged up to Aug 13 (Early Group): (a) moving about mainstem and settling in the river, with most of these fish (11/12, 92%) genetically matched to the river spawners; (b) moving past all the river towers straight to the lake, with only a few of these fish genetically matched to the lake spawners (3/12, 25%). The most common pattern of movement among the fish tagged from Aug 14 to Aug 20 (Mixed Group) was moving straight to the lake, but only half of these fish were genetically matched to lake spawners (4/8, 50%). Among the late group, tagged after Aug 20, the most common pattern of movement was to head straight to the lake, with 25 of these 32 genetically matched to lake spawners (78%). Another common pattern among late migrants was fish heading straight to the lake, but with some mixed signals (8 fish, all matched to lake spawners). Short tracking records that ended in the river were matched to river spawners among the early and mixed sample groups, but matched to lake spawners among the late group (i.e. radio tag pattern looks like a river spawner, but genetically it is a lake spawner) .

Tag History Pattern	Early Count	Early % Match	Mix Count	Mix % Match	Late Count	Late % Match
Lake and drop	3	33	1	100	0	-
Lake only	1	100	1	0	3	100
Lake outlet	3	0	1	100	3	33
Moved about m-stem, ended up at lake outlet	1	100	0	-	0	-
Moved about mainstem and ended up in lake	1	0	1	100	3	67
Moved about mainstem and ended up in river	12	92	2	100	2	100
Moved about m-stem, but stayed in lower river	1	100	0	-	1	0
Moved about mainstem, but with mixed signals	4	100	0	-	0	-
Short track ends in lake	1	0	2	100	3	67
Short track ends in river	3	100	1	100	6	0
Straight to lake	12	25	8	50	32	78
Straight to lake, but with mixed signals	4	50	0	-	8	100
Total	46		17		61	

Table 25: Methods used in some recent papers with phylogenetic trees for Pacific Salmon.
The examples summarized here are based on a keyword search through the *Canadian Journal of Fisheries and Aquatic Sciences* for papers since January 2000 that contain "Pacific Salmon" and either "Neighbour Joining" or "UPGMA". Search results were then reviewed for relevance, and included in addition to references already used elsewhere in this report. This is not intended as a comprehensive literature review, but still gives a good sense of common practices. We tested four alternative measures of genetic distance: *Fst* (Weir and Cockerham 1984), *Ds* (Nei 1978), *Dc* (Cavalli-Sforza and Ewdards 1967), and *Da* (Nei 1987). We also tested teo alternative tree fitting algorithms: *Neighbour-Joining* (Saitou and Nei 1987, Gascuel and Steel 2006) and *UPGMA* (Sokal and Michener 1958). Most papers use the *Dc* metric and the *Neighbour-Joining* algorithm. In our sensitivity tests, that is the combination with the highest R^2 (Table 12,Table 13) for the final set of genotype data (G12;Table 8). One paper used the *Das* metric (Bowcock et al. 1994) in a sensitivity test. Note that *Fst* is labelled *Theta* in the TreeFit program, and in our results produced from TreeFit output.

Paper	*Ds*	*Dc*	*Da*	*Fst (Theta)*	*Das*	*NJ*	*UPGMA*
Scribner *et al.* 1996	**X**		**X**		**X**		**X**
Beacham & Wood 1999		**X**				**X**	
Withler *et al*. 2000		**X**		**O**		**X**	
Banks *et al.* 2000		**X**		**O**		**X**	**X**
Irvine *et al.* 2000		**O**		**X**		**X**	
Heath *et al.* 2006		**X**		**O**		**X**	
Bucklin *et al.* 2007		**X**		**O**		**X**	
Olsen *et al.* 2008		**X**		**O**		**X**	
Pavey *et al.* 2007		**X**		**O**		**X**	
Beacham *et al.* 2008		**X**		**O**		**X**	
Dann *et al.* 2013				**X**		**X**	
Withler *et al*. 2014				**X**		**X**	
This report	**X**	**X**	**X**	**X**		**X**	**X**

X = used to fit a phylogenetic tree
O = calculated for a different purpose

Table 26: Inventory of Results Relevant to Population Structure of Klukshu Sockeye.
This table pulls together key results from the different analyses, roughly sorted by weight of evidence.

Observation	Weighth of Evidence	Key Results
Genetic differences between River spawners and Lake spawners are large enough for a clear distinction.	**Strong.** Phylogenetic trees consistently linked these sample groups (e.g. river fry and river spawners), and genetic stock ID had high average probabilities of assignment.	Figure 12, Figure 16
Spawners from the two populations have different run timing curves.	**Strong.** Adults migrating into the Klukshu early were predominantly matched to River spawners based on genetics and radio tagging. Late migrants predominantly matched up to the Lake spawners.	Figure 22
Spawners from the two populations behave differently once they enter the Klukshu.	**Strong.** Tag detections show that river females tend to move about the mainstem before choosing a spawning site, while lake females tend to migrate upstream rapidly to get to the lake.	Figure 19
Spawners from the two populations have different spawning site preferences.	**Moderate.** Adults matched to the River population predominantly had river tag fates as well, and similarly for the Lake population. However, the proportion of samples where tags and DNA agree is only a moderate 60-70%, or about 2/3. Indirectly, the strong genetic differences indicate that the two populations mostly stick to separate spawning areas.	Table K 1
Juvenile life history may differ between the two populations	**Moderate.** None of the 278 juveniles sampled at Klukshu Lake outlet were genetically matched to the River spawners, so river juveniles either don't rear in the lake, or they migrate out of the lake at different time from the lake juveniles, and were missed altogether by our sampling program.	Table 14
Male age composition at the weir may differ between the two populations	**Weak.** Males migrating later in the season had more age 4.2 fish, but the weekly pooled DNA samples can't be matched to the individual scale readings and there are other plausible explanations.	Figure G 4, Section 8.3
Adult size composition at the weir may differ between the two populations for both females and males	**Weak.** River spawners were slightly larger than lake spawners, and early migrants were slightly smaller than later migrants (looking at males and females separately). These two results are contradictory as first, but can be explained by changing maturity level.	Figure G 1, Table G 2
Sex ratio may differ between the two populations	**Weak.** Adults migrating later in the season had more females, but the weekly pooled DNA samples can't be matched to the individual records and there are other plausible explanations.	Table G 4, Figure G 2

Figures

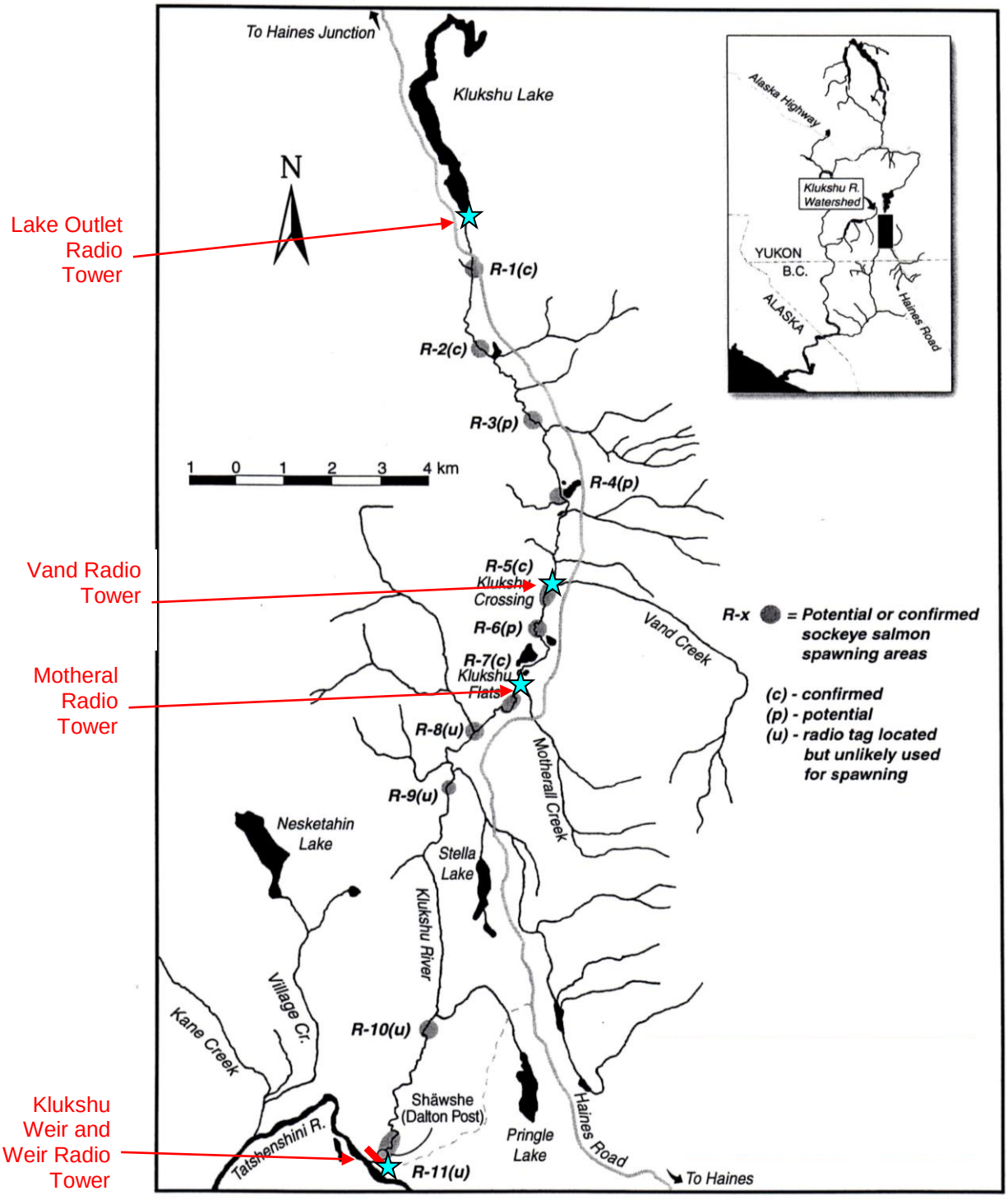


Figure 1: Overview Map of Klukshu Watershed and 2016 Stationary Radio Receivers.
Map adapted from Petkovich (2000).

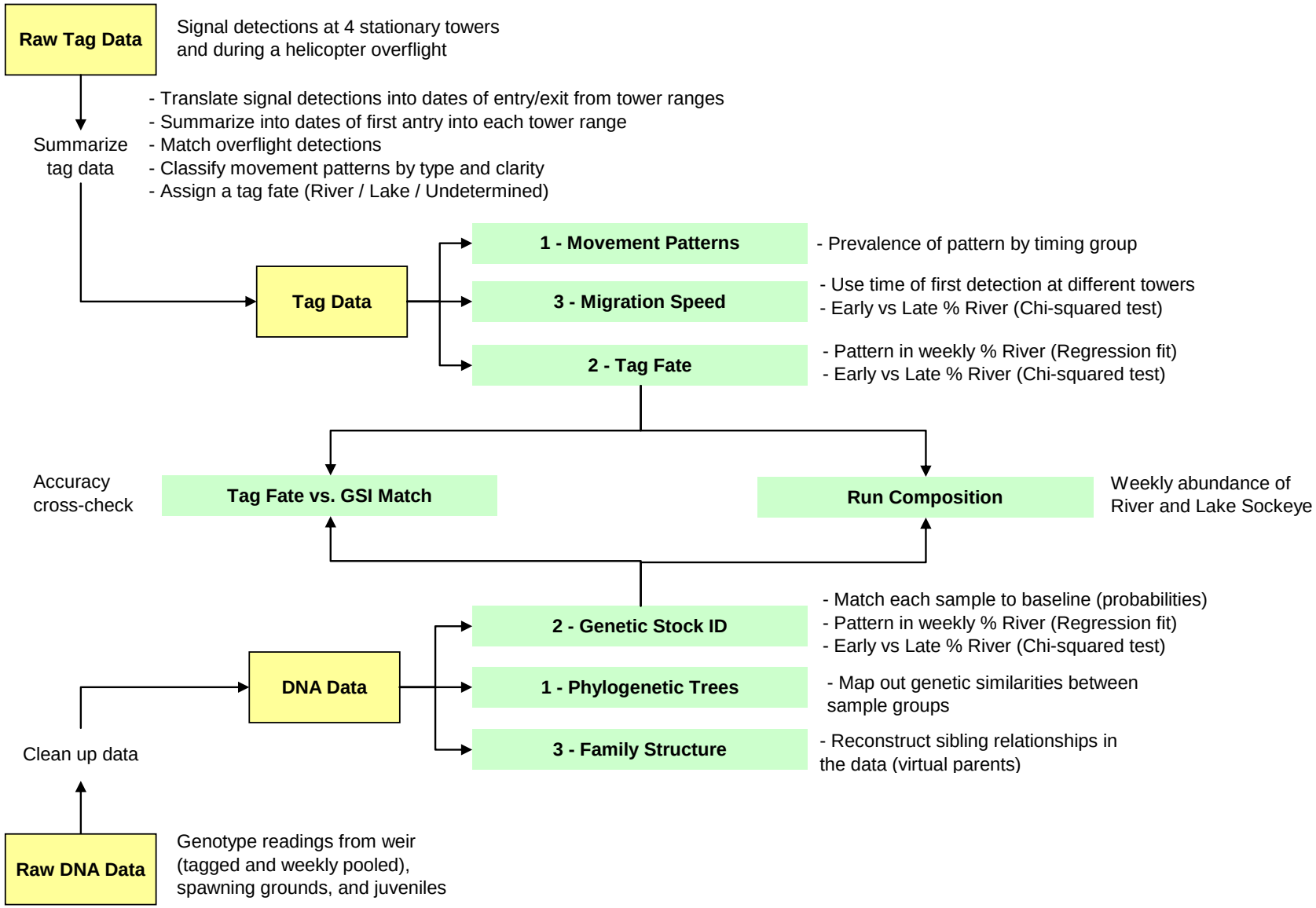


Figure 2: Overview of Radio Tag and Genotype Analyses.
This figure maps out the main steps in the analysis. Figure 3 describes the analyses of genotype data in more detail.

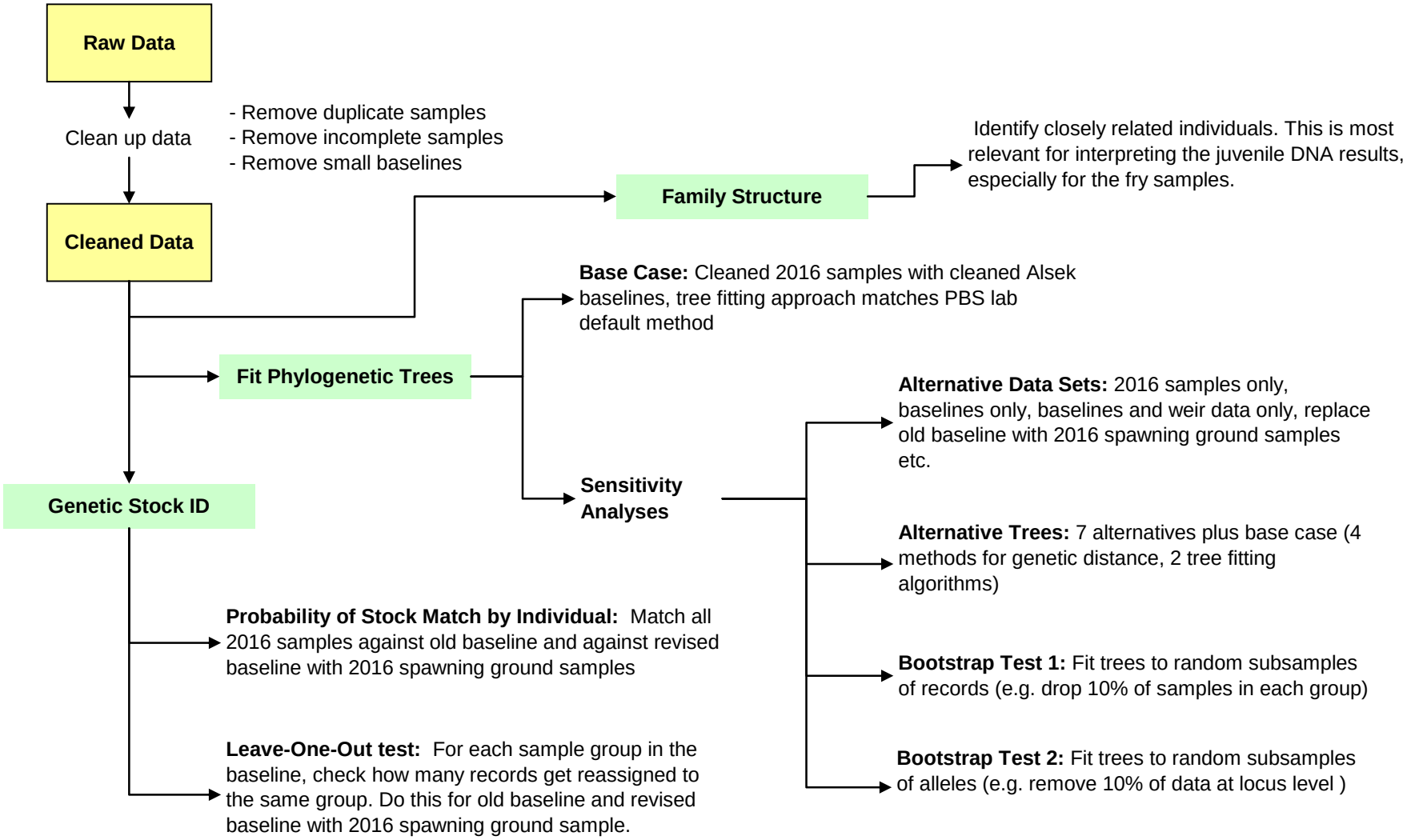


Figure 3: Components of the Genotype Analyses.
This flowchart summarizes the methods described in Sections 5.7, 5.8, and 5.9.

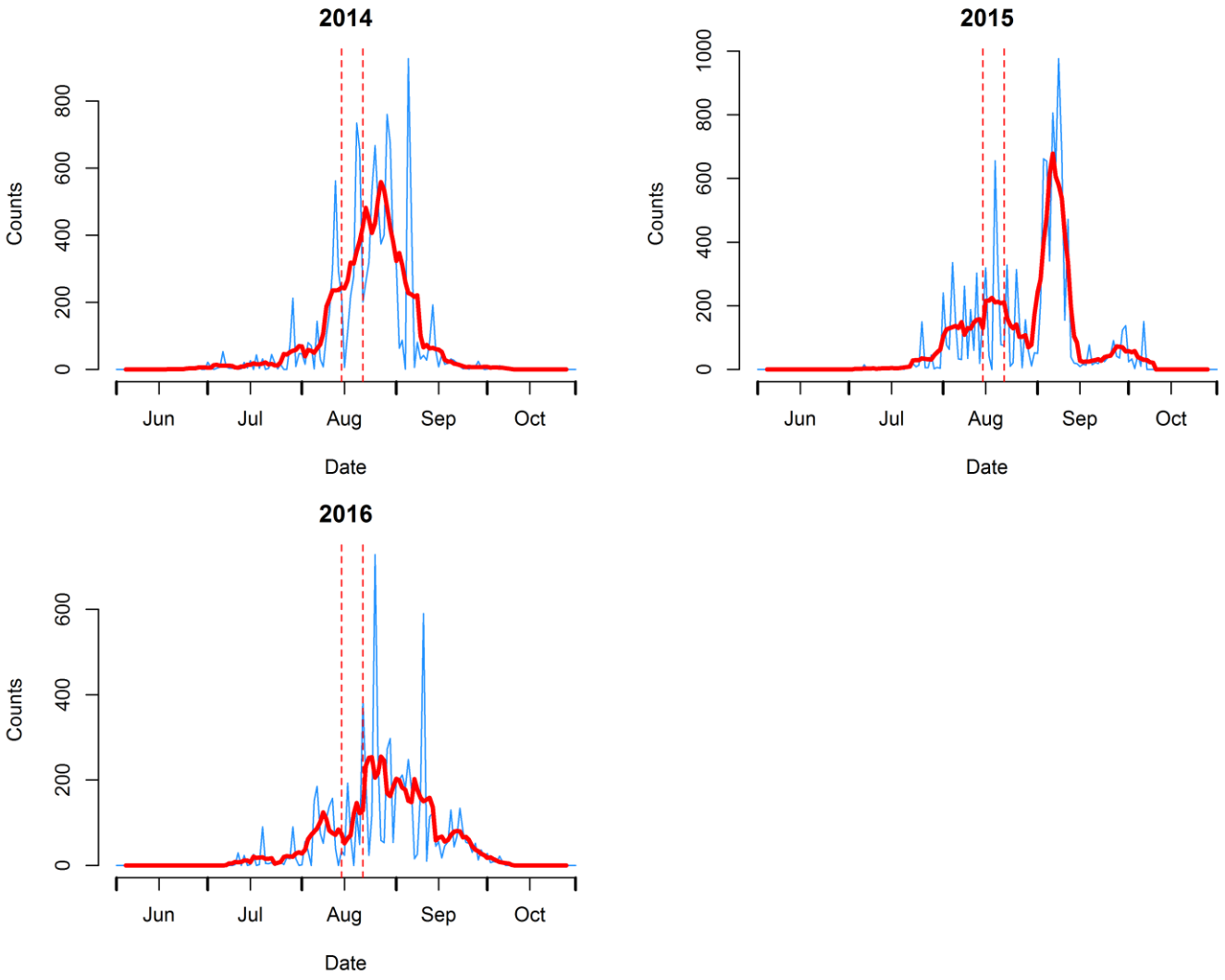


Figure 4: Timing Curves of Sockeye Migration at Klukshu Weir 2014-2016.
Blue lines show daily counts of sockeye at Klukshu weir. Solid red lines are the smoothed 7-day average centered on the day. Vertical dashed red lines mark statistical week 34 in 2016 (Aug 14 to Aug 20), which has been used to delineate the Early and Late timing groups. The three panels show the return years most relevant to this project. Adult samples at the weir were collected in 2016, which had clear early and late migration peaks. Fry samples collected in 2016 are the offspring of 2015 spawners, which also migrated past the weir in 2 clear peaks, but had a more distinct first peak that occurred later than in 2016. Smolt samples collected in 2016 are the offspring of 2014 spawners, which returned in a single peak, indicating that the early group either had very low abundance or returned together with the early part of the late run. Appendix L shows all the annual smoothed timing curves for 1976 to 2016.

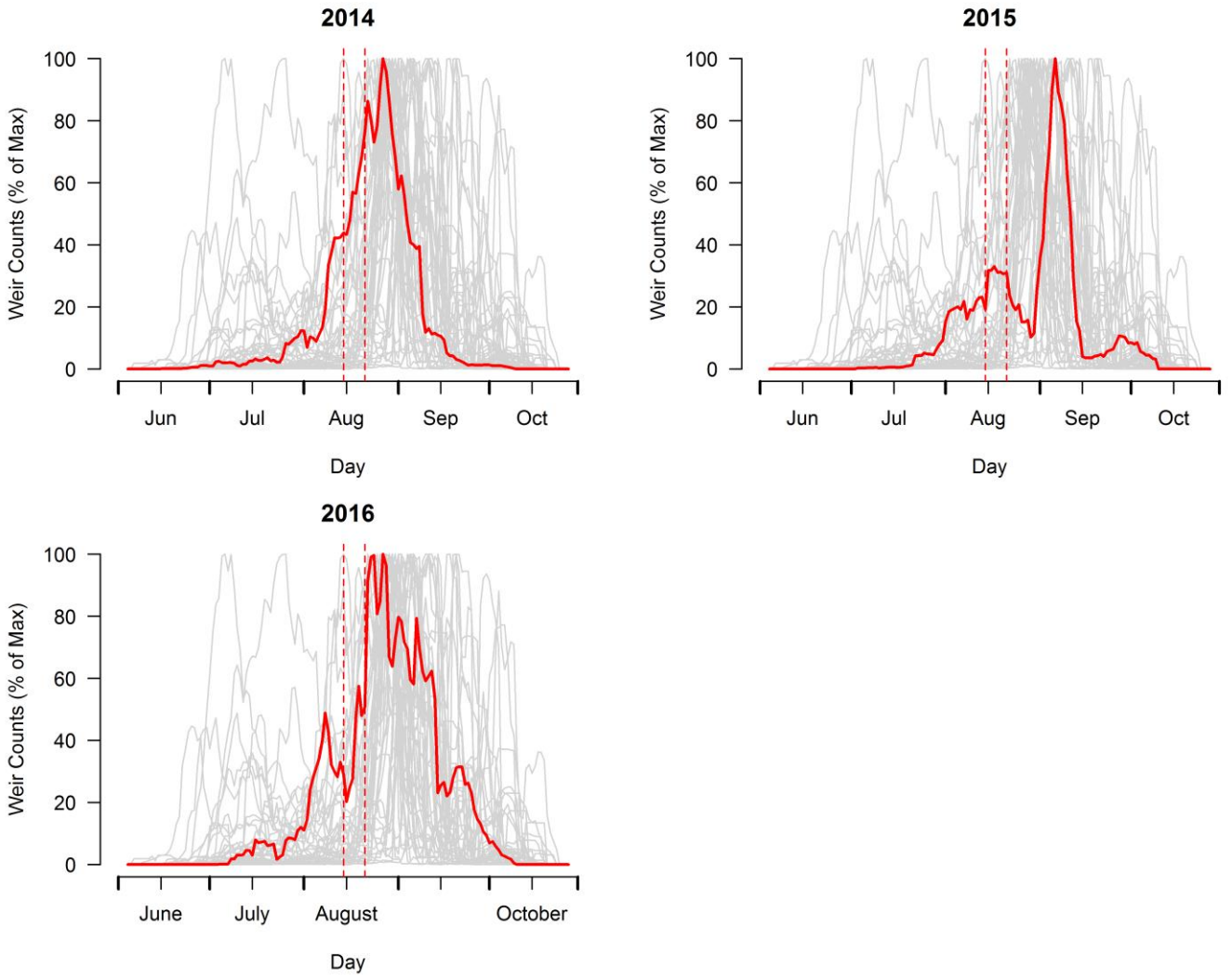


Figure 5: Recent Timing Curves of Sockeye Migration at Klukshu Weir 2014-2016 Compared to All Years . Panels correspond to Figure 4, but in this figure the smoothed timing curves are standardized relative to the largest observed value, so that patterns across years can be more easily compared. Migration past Klukshu weir in the 3 most recent years peaked around the same time as most of the earlier years (i.e. many overlapping grey lines). Note hover, that there are 2 years which had the largest peak much earlier in the season, and several years with more distinct peaks early on, reaching 40-60% of the largest value for that year (i.e. peaks on left half of each panel). Figure 6 summarizes the different timing patterns observed between 1976 and 2016. Appendix L shows all the annual smoothed timing curves for 1976 to 2016.

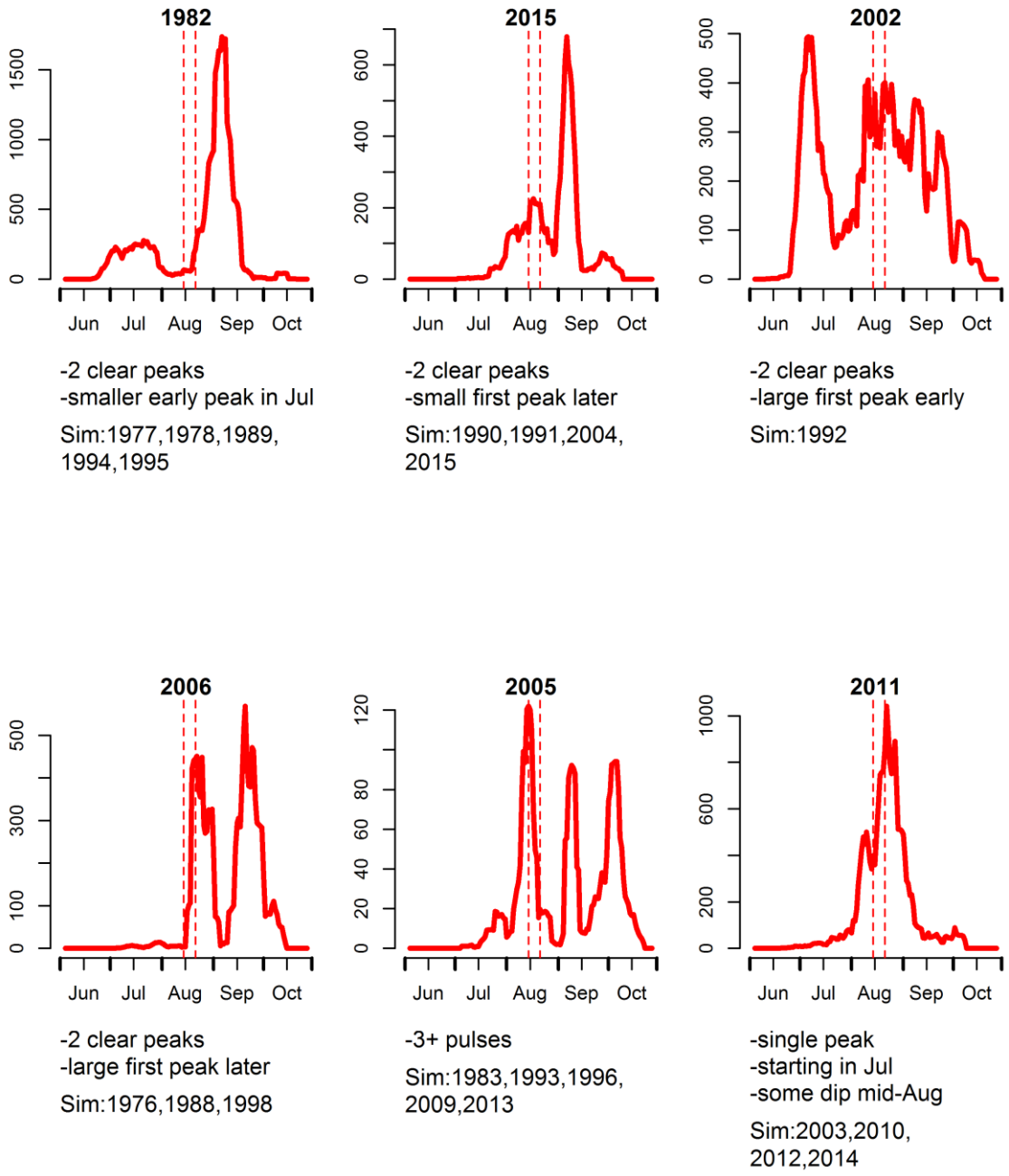


Figure 6: Observed Types of Timing Curves for Sockeye Migration at Klukshu Weir 1976-2016. Solid red lines are the smoothed 7-day average centered on the day. Vertical dashed red lines mark statistical week 34 in 2016 (Aug 14 to Aug 20), which has been used to delineate the Early and Late timing groups. Each panel shows one illustrative year for each type of pattern. Appendix L shows all the annual smoothed timing curves for 1976 to 2016.The key observation is that neither the timing pattern nor the mid-August cut-off point allow for a clear identification of the run composition. For example, in 2006 was there no early run, or a delayed return for both components? Radio tags and DNA samples collected in 2016 were used to estimate the weekly composition of the run for that year (Sec. 7.10).

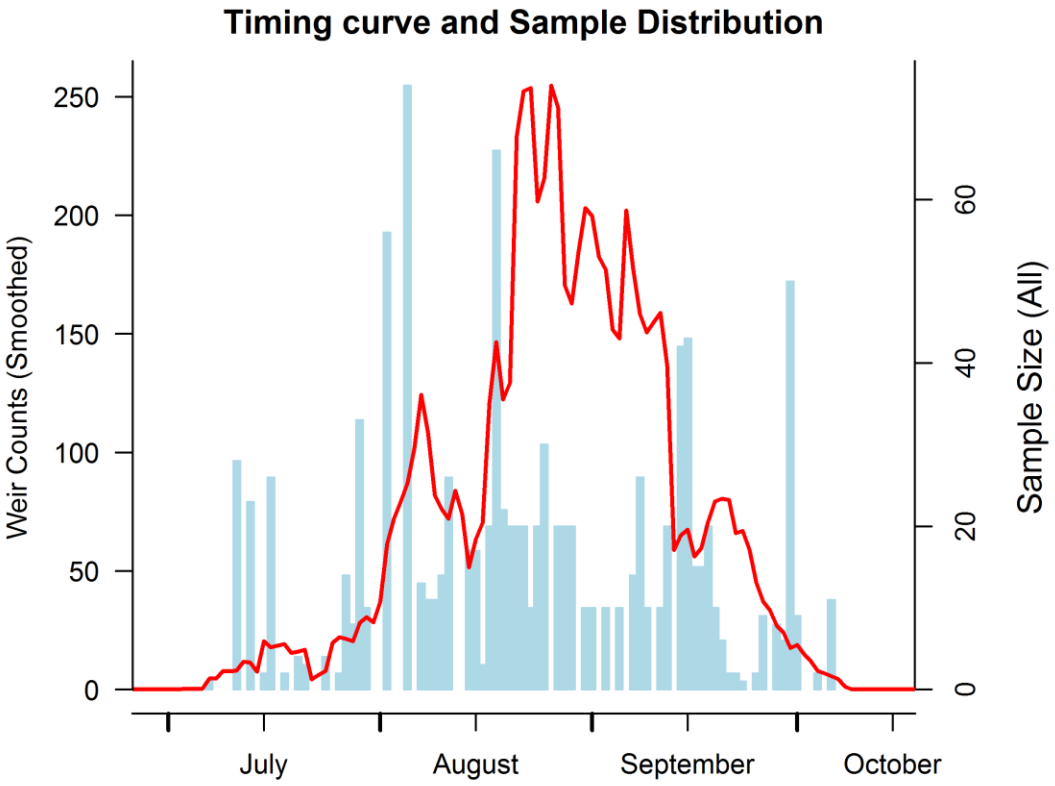


Figure 7: Timing of Adult Sockeye Samples Collected at Klukshu Weir in 2016.
The blue bars show the total number of adults sample on a date (i.e. "All Samples" category in Table 2) matched up against the smoothed run timing curve (i.e. 7d average of daily sockeye counts at Klukshu weir). On sample objective was to ensure a good representation of the early run component, which accounts for the proportionally larger sampling effort in July and early August.

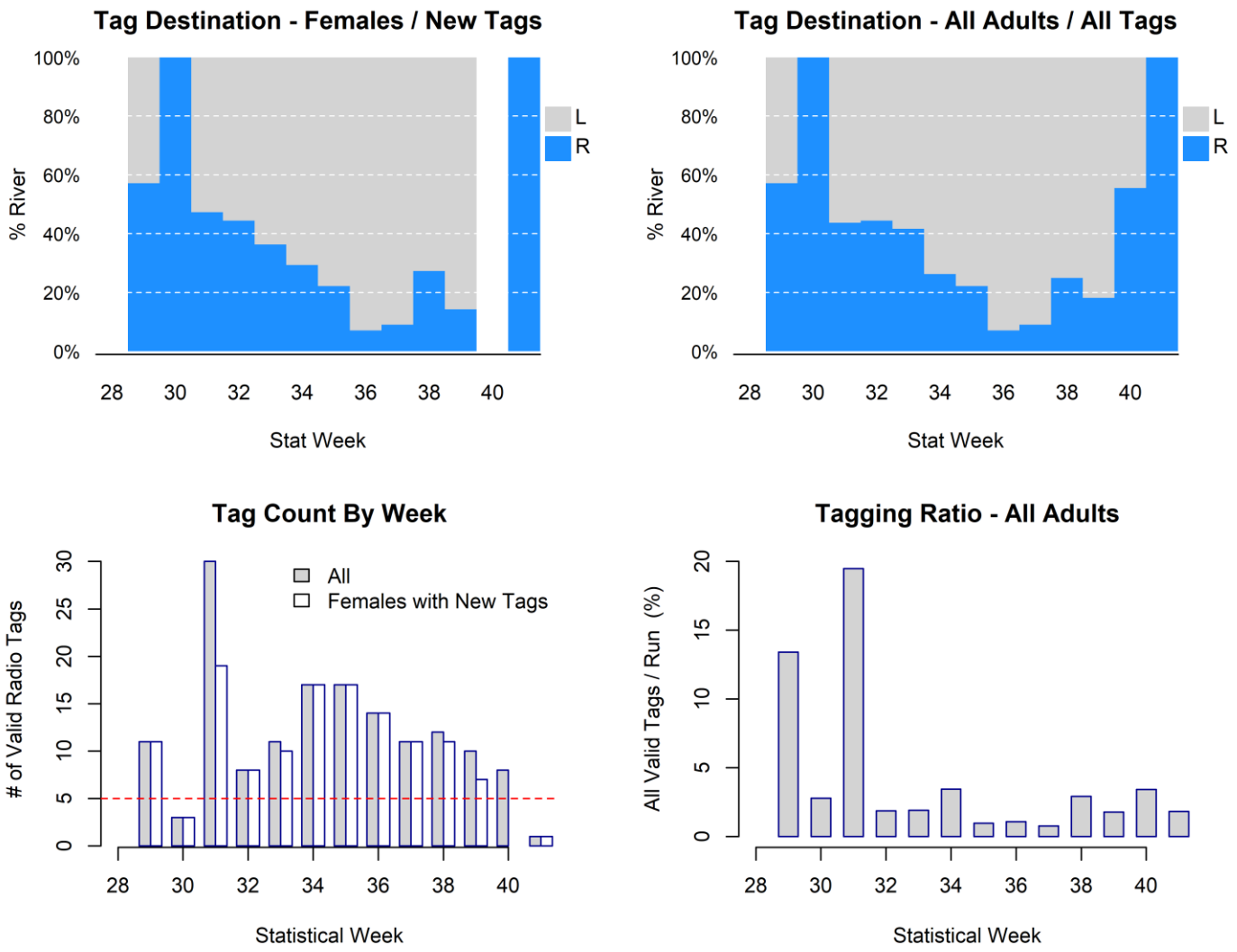


Figure 8: Weekly Tagging Ratio and Tag Destination for Adult Sockeye at Klukshu Weir in 2016.
Top panels both show the weekly proportion of tags that were assigned the river spawners. The top left panel shows results for 135 females with new tags (weekly counts listed in Table H 2), while the top right panel shows results for all 165 tagged fish (Table 6). Table H 3 and Table 7 summarize the corresponding chi-squared tests for difference between early and late migrants. Bottom panels show the number of samples and the tagging ratio by week, using only valid tags (i.e. tags where a final destination could be assigned). Weekly tag application focused on females, and prioritized early migrants (i.e. higher tag ratios in weeks 29 and 31). In most weeks, most of the tags were new tags applied to females, with two notable exceptions: (1) 13 males were tagged in week 13, with 11 valid tag destinations assigned. (2) No new tags were applied in week 40. Both top panels show the same pattern, with the proportion of tags assigned to river spawners higher early in the season, and decreasing steadily when the bulk of the run returned (weeks 35-39, mid-August to mid-September).

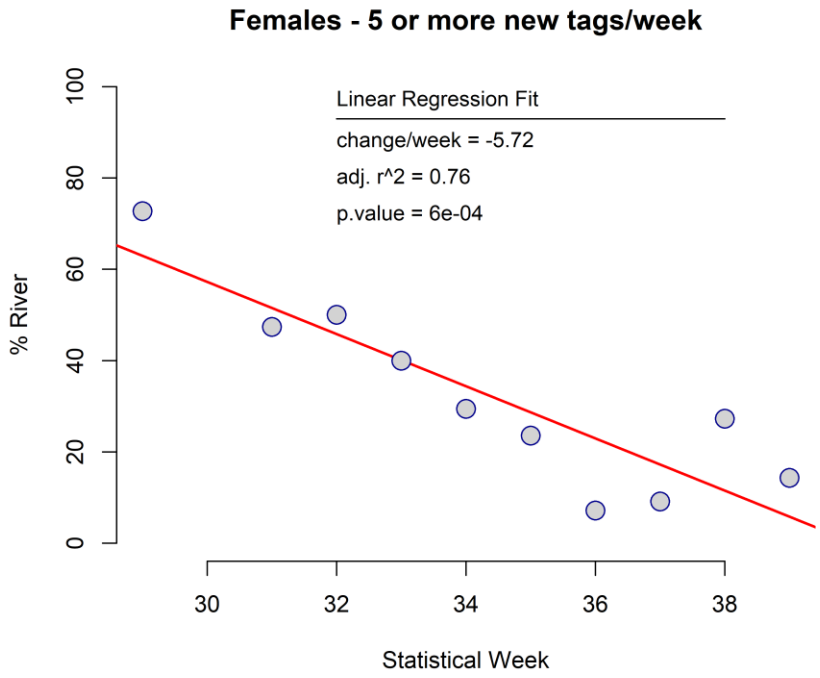


Figure 9: Regression Fits to Weekly Tag Fate (% River) for Female Sockeye at Klukshu Weir in 2016. This figure shows a simple linear regression fit to the weekly stock composition (i.e. % tags assigned to the river spawners), using only results for new tags applied to females, and excluding statistical weeks with less than five valid tag fates. Figure H 4 shows regression fits to alternative subsets of the data (e.g. including results for redeployed tags). Table 6, Table H 1, and Table H 2 list weekly tag counts. Table H 3 and Table 7 summarize the corresponding chi-squared tests for difference between early and late migrants. The regression fit is highly significant (p-value << 0.05) and has strong predictive power (adj. r^2 =0.76, the regression line explains about ¾ of the observed variability in stock composition). The regression fit shows that in 2016, the run consisted of about 60-70% River spawners early on, and the % River spawners dropped roughly 6% per week.

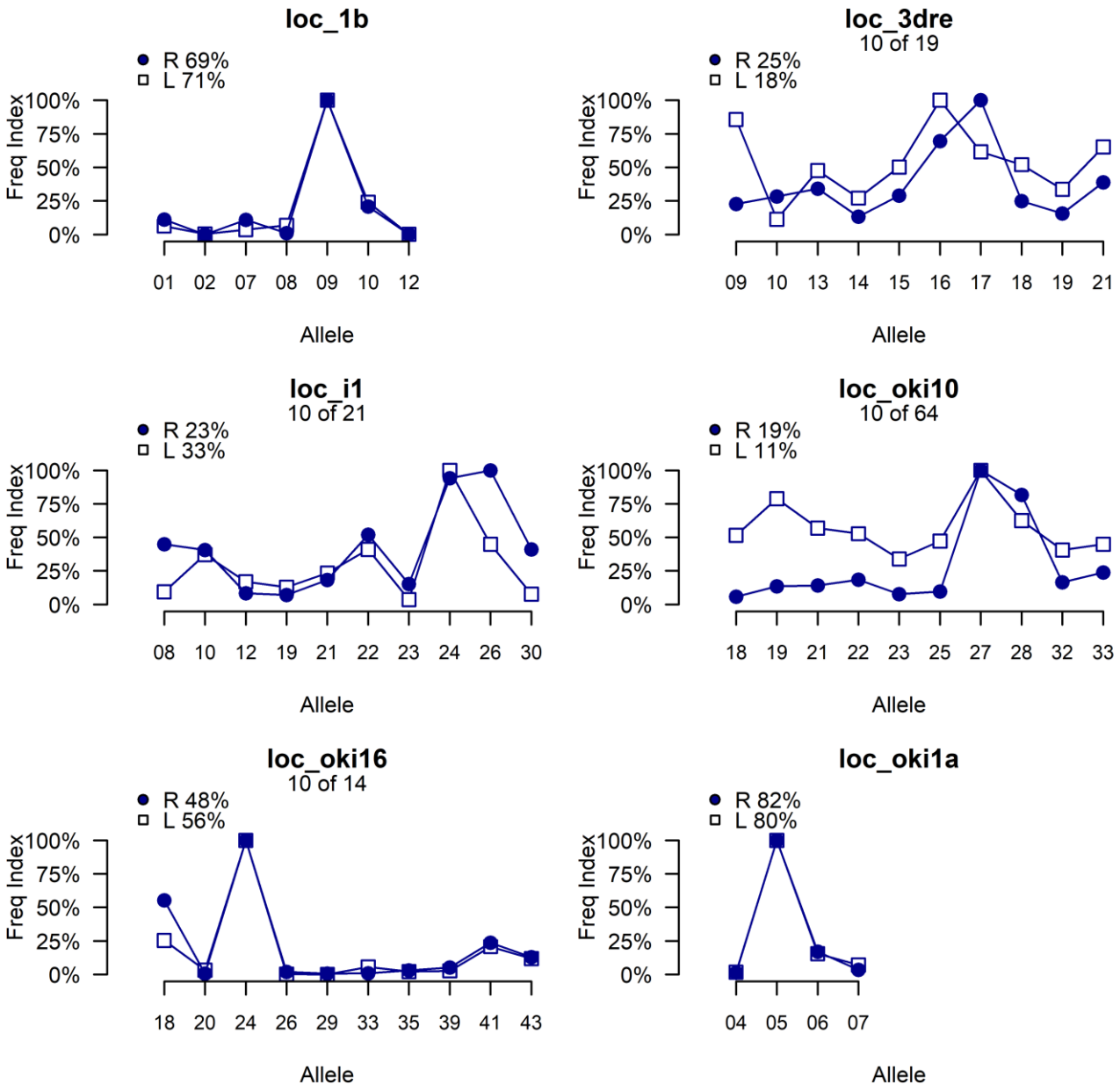
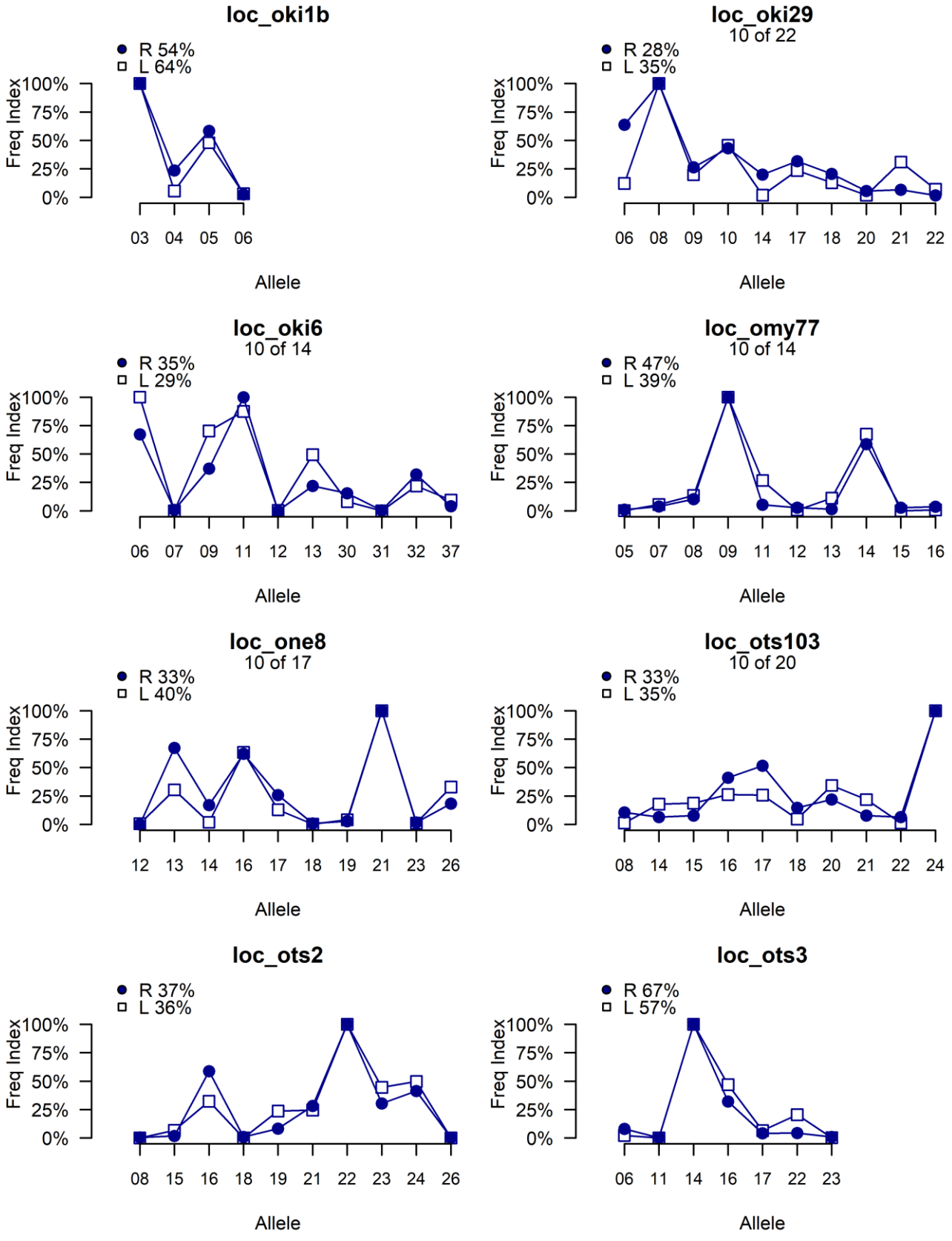


Figure 10: Allele Frequency Profile for 14 Loci – River Group vs. Lake Group
Each panel shows profiles of allele frequencies for two sample groups, which are grouped based on later analyses which fitted phylogenetic trees (Section 7.5) and assigned probabilities of genetic stock matches (Section 7.6). The Lake Group (L) includes lake spawners, late weir migrants, and juveniles sampled at the lake outlet. The River Group (R) includes river spawners, early weir migrants, and juveniles sampled on the Klukshu mainstem. The profiles show rescaled allele frequencies for the most prevalent allele in each sample group, plus other alleles with the largest differences in frequency between the two sample groups, up to 10 alleles (Section 5.6). Subtitles for panels list the total number of unique alleles between the two sample groups, where the number exceeds the plot limit of 10. Legends in each panel list the un-scaled allele frequencies for the most prevalent allele in each sample group. For example, the most common allele in the Lake Group for locus *3dre* is allele 16 (18% of samples, 100% in the rescaled index plot). Allele 09 is the second most common allele, with an index value of about 80% (i.e. 18% * 80% = 14.5% of samples). Table 11 summarizes the observed patterns and differences between sample groups.

Figure 10 continued…



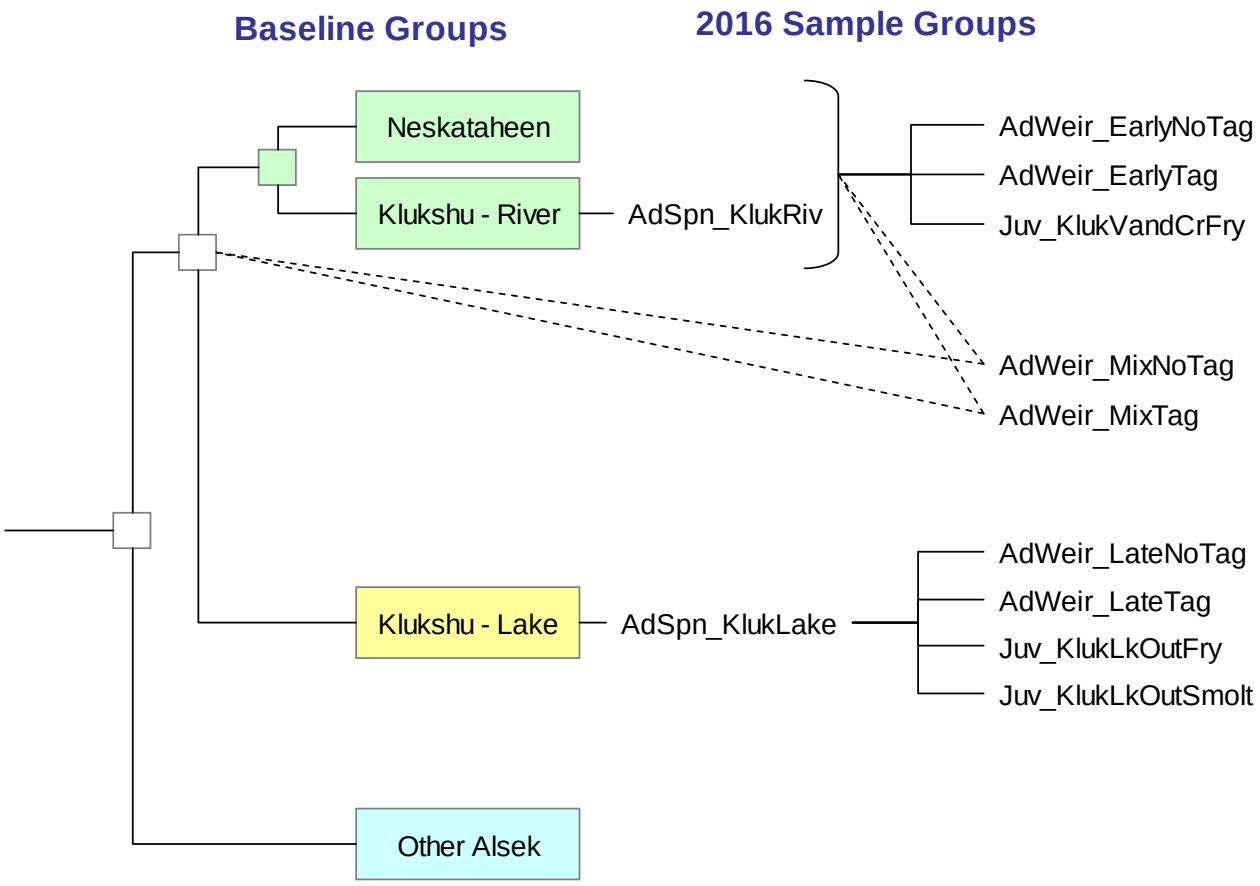


Figure 11: Stylized Phylogenetic Tree for Klukshu Sockeye
This diagram summarizes genotype samples that were consistently grouped together across alternative tree fitting methods (Table 9) and bootstrap tests (Table 13), using the revised baseline set (i.e. use 2016 spawning ground samples for Klukshu baseline rather than the Early/Mix/Late weir samples). Figure 12 shows the actual tree fit and bootstrap probabilities for the base case (T4 in Table 9). Appendix M illustrates the alternative tree fits explored in the sensitivity analyses. Figure 16 shows composition of each sample group based on genetic stock ID using the revised baseline. Samples of Klukshu River spawners were closely grouped with Neskataheen, a neighbouring watershed where sockeye also tend to return early. Adults sampled at the weir early in the season (before Aug 14) and fry sampled on the Klukshu mainstem near Vand Creek were grouped with the River / Neskataheen samples. Figure 17 shows the weekly run composition based on genetic stock ID (GSI) for the individual samples, which is consistent with the observed tree fits shown here: Early weir samples had a much higher proportion of individuals assigned to the River/Neskataheen group (87% vs. 18%), and the tree links up samples based on the predominant component (i.e. River matches among the early migrants, lake matches among the late migrants. Weir samples from the mix period were grouped with either the river or as a separate branch within the Klukshu/Neskataheen complex, depending on the specific tree fitting approach (Table 9), which is consistent with the GSI results showing large proportion of fish assigned to both the Klukshu River and Klukshu Lake spawner samples (Figure 16).

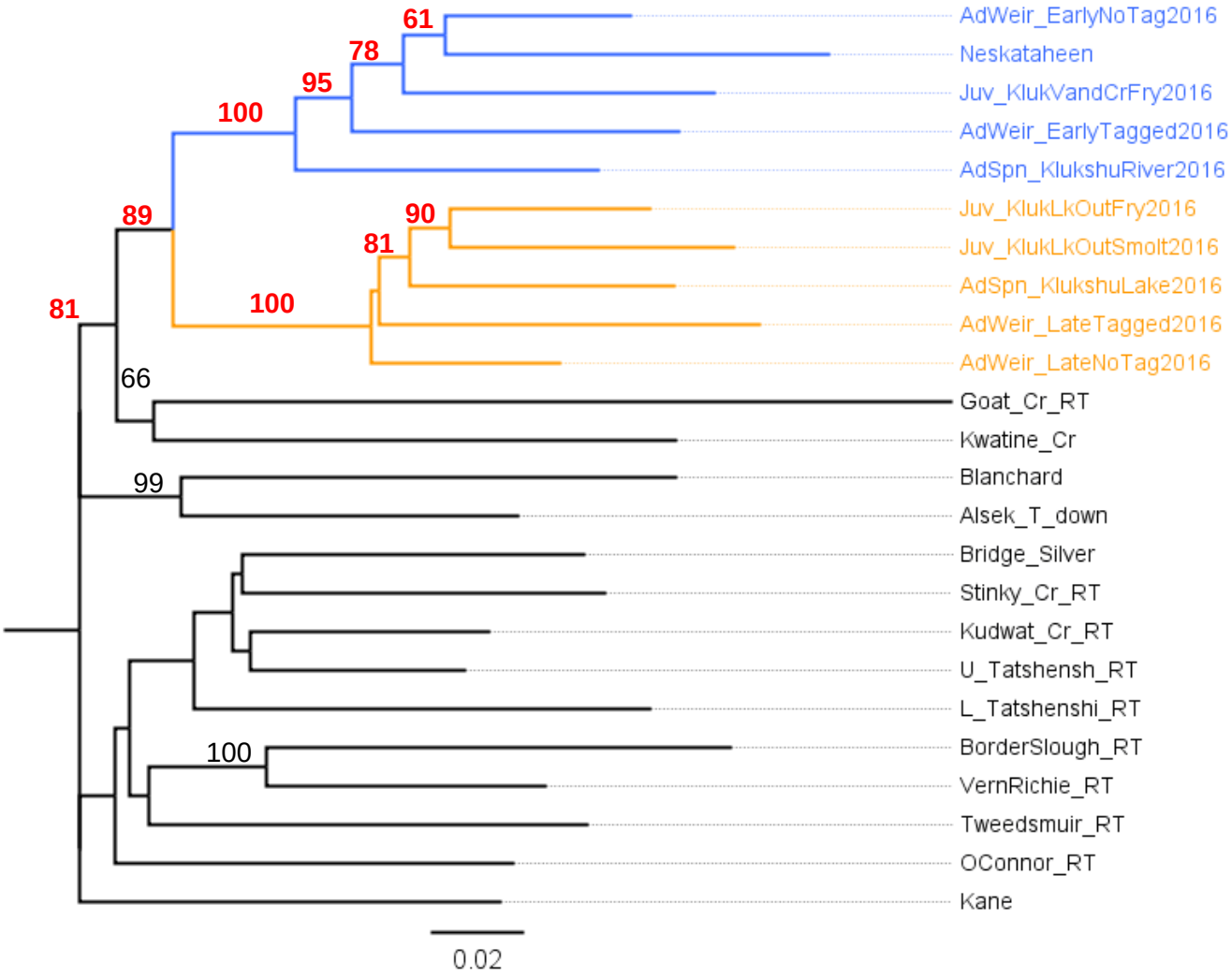


Figure 12: Fitted Phylogenetic Tree and Bootstrap Probabilities for 2016 Klukshu Sockeye Samples. This tree was constructed with the TREEFIT program (Section 5.7) using the *Dc* measure of genetic distance (Cavalli-Sforza and Edwards 1967) and the *Neighbour Joining* algorithm for tree fitting. The genotype set included all samples collected in 2016, except adults sampled at the weir during the Mix timing group (Aug 14-20, stat week 34), and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years). Numbers on the tree branches show the proportion of fits among 1000 bootstrap tests which grouped that particular set of samples together. 100% of the bootstraps grouped the early weir samples, river spawners, river fry, and Neskataheen together. 100% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. 89% of the tests put all the Klukshu samples and Neskataheen on a separate branch from all the other Alsek samples (some of these tests had Kwatine or some other population grouped with the Klukshu samples). Note that this is one of 16 alternative trees produced with TREEFIT (Set G12, Method T4). Table 8 and Table 9 list the components of the sensitivity analyses. Table 12 categorizes the resulting types of tree, and lists a measure of how well they fit the sample. This version of the tree has the best overall fit (i.e. highest R2). Table 13 compares bootstrap results for the different fitting methods. Appendix M shows the other 15 tree fits. Bootstrap values varied a little when the 1000 tests were replicated (± a few percent).

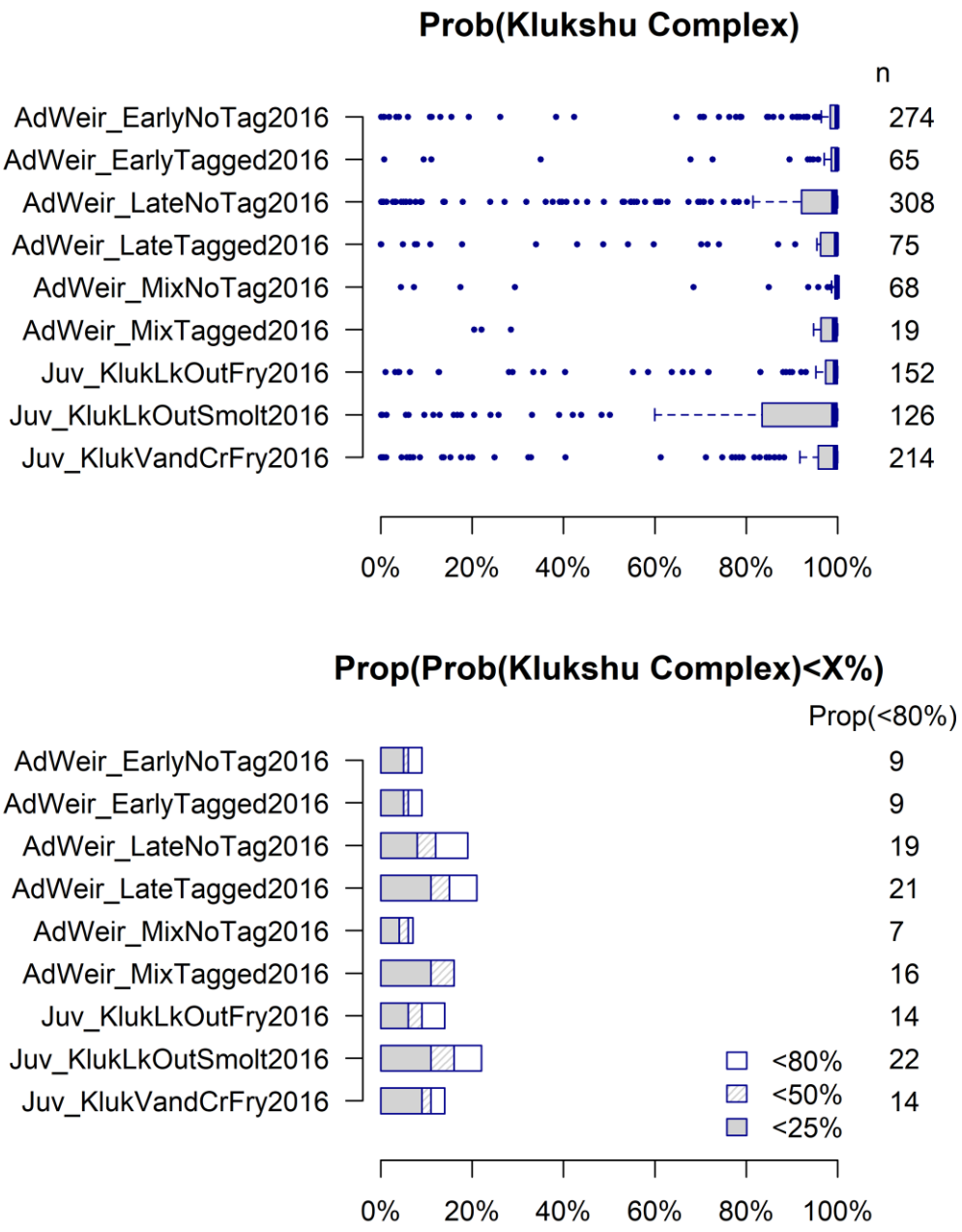


Figure 13: Probability of Assigning Samples to Klukshu / Neskataheen Group Using <u>Revised</u> Baseline. This figure summarizes the assignment probabilities for genetic stock ID against the revised baseline, which uses the river and lake spawning ground samples from 2016 as the reference populations for the Klukshu, instead of the Early/Mix/Late weir samples used in the original baseline (Figure 14). The top panel shows a boxplot and extreme values. Each point represents 1 DNA sample with an assignment probability outside of the range covering most of the sample (i.e. whiskers of the boxplot). All of the sample groups have some samples with very low assignment probabilities (i.e. matched the sample to a baseline outside the Klukshu with a very high probability), but most samples in each group were clearly assigned to one of the baselines in the Klukshu / Neskataheen group (i.e. boxes on the right of the plot). Lake outlet smolts had the highest proportion of samples with low assignment probability to Klukshu / Neskataheen (i.e. the boxplot stretches further to the left). The bottom panel shows the same information, just converted to the proportion of the sample falling in different probability ranges. Table 17 lists the number of samples in the different categories.

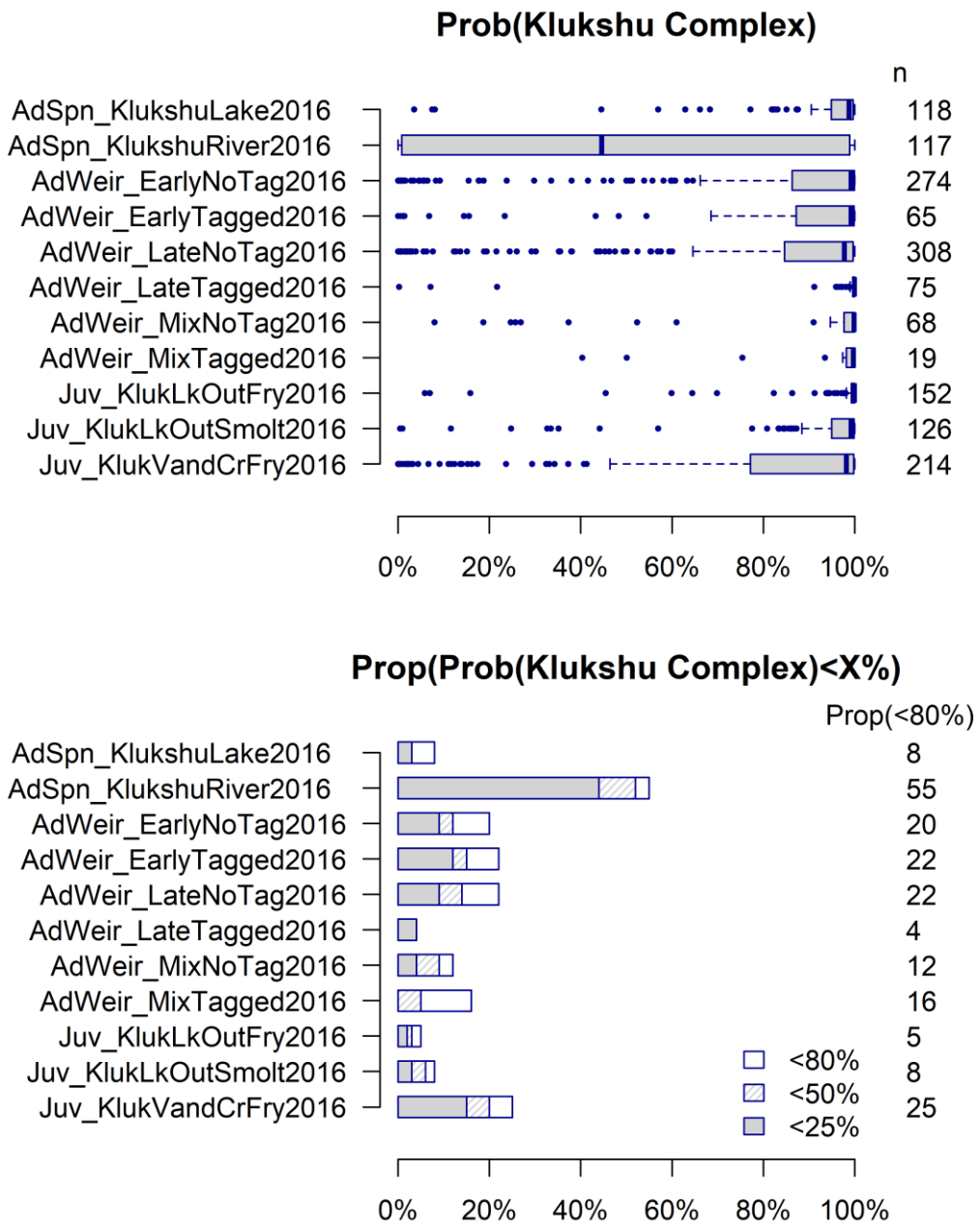


Figure 14: Probability of Assigning Samples to Klukshu / Neskataheen Group Using <u>Original</u> Baseline. Layout and definitions of this figure are the same as in Figure 13, but this plot shows assignment probabilities against the original Alsek baseline, which uses Early/Mix/Late weir samples for the Klukshu. Assignments to the Klukshu / Neskataheen group are less clear (i.e. lower probabilities, boxes stretching further left than in Figure 13) for several of the sample groups. This is particularly pronounced for the early weir sample, the untagged late weir samples, and Vand Creek Fry. Conversely, lake outlet smolt matches are improved using this baseline. The 2016 river spawner sample turned out to be hard to match up against any of the populations in the original baseline, with about half the samples having a less than 50% probability match to the Klukshu / Neskataheen group (GSI result basically concludes it's a coin toss whether the sample is from the Klukshu or elsewhere). Note, however, that the 2016 river spawner sample serves as an informative sample in the revised baseline (i.e. can assign many weir adults and juveniles quite clearly to either the river or lake spawners; see Table 14). Table 17 lists the number of samples in the different categories.

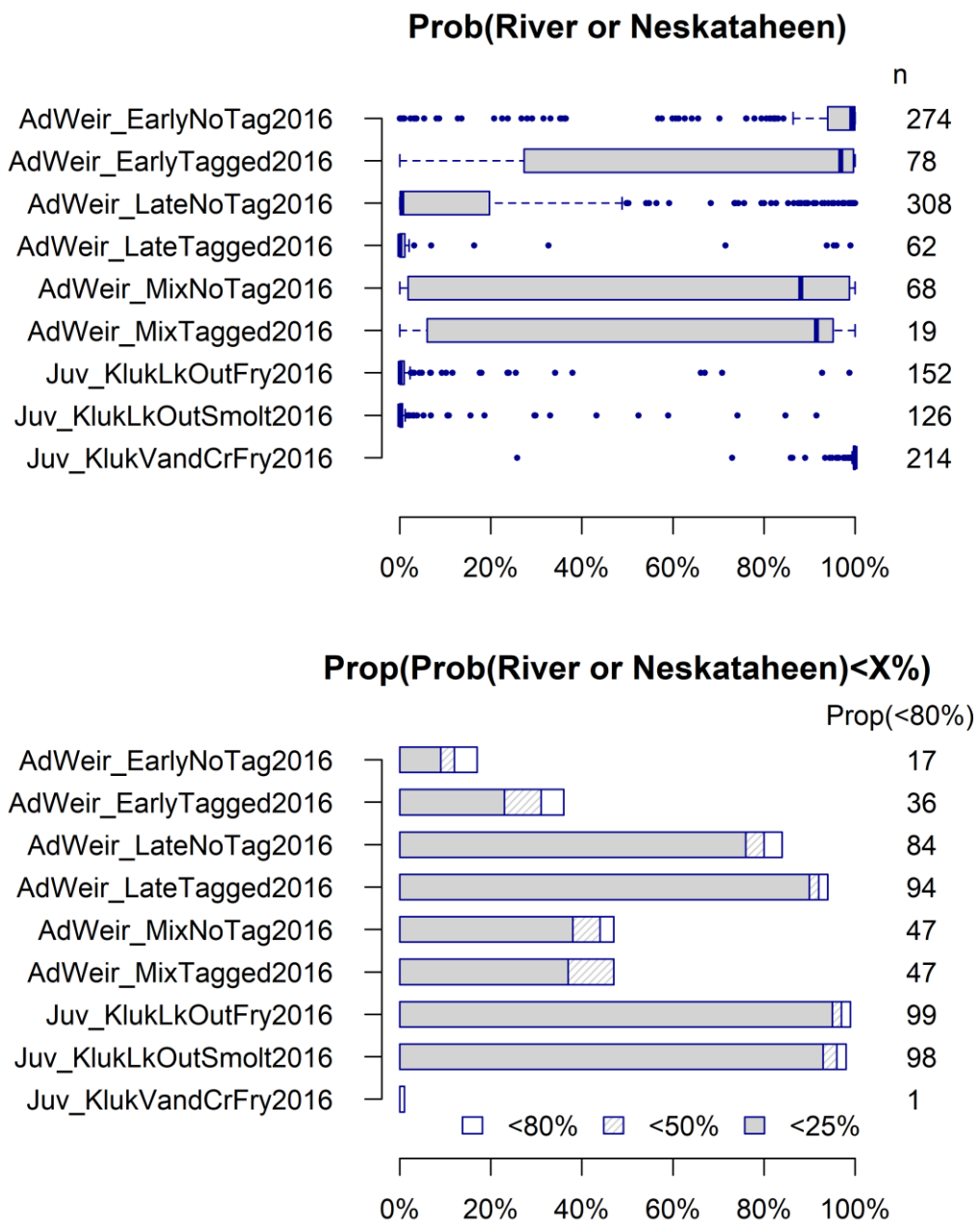


Figure 15: Probability of Assigning Samples to Klukshu / Neskataheen Group Using <u>Trimmed</u> Baseline. Layout and definitions of this figure are the same as in Figure 13, but this plot shows assignment probabilities against a trimmed baseline, which includes only the 2016 spawning ground samples from the river and lake, plus Neskataheen baseline samples. Assignments to the River / Neskataheen group or the Lake baseline are very clear for most of the sample groups. Early migrating fish in the untagged sample and the Vand Creek fry sample are mostly matched to the River spawners or the Neskataheen baseline with a high probability (i.e. narrow box on the right side of the boxplot). Late migrating fish with tags and Lake juveniles are mostly matched to Lake spawners with a high probability (i.e. low probability match to River/ Neskataheen; box pushed to the left). The remaining sample groups have a wider distribution of assignment probabilities (wide boxplots).

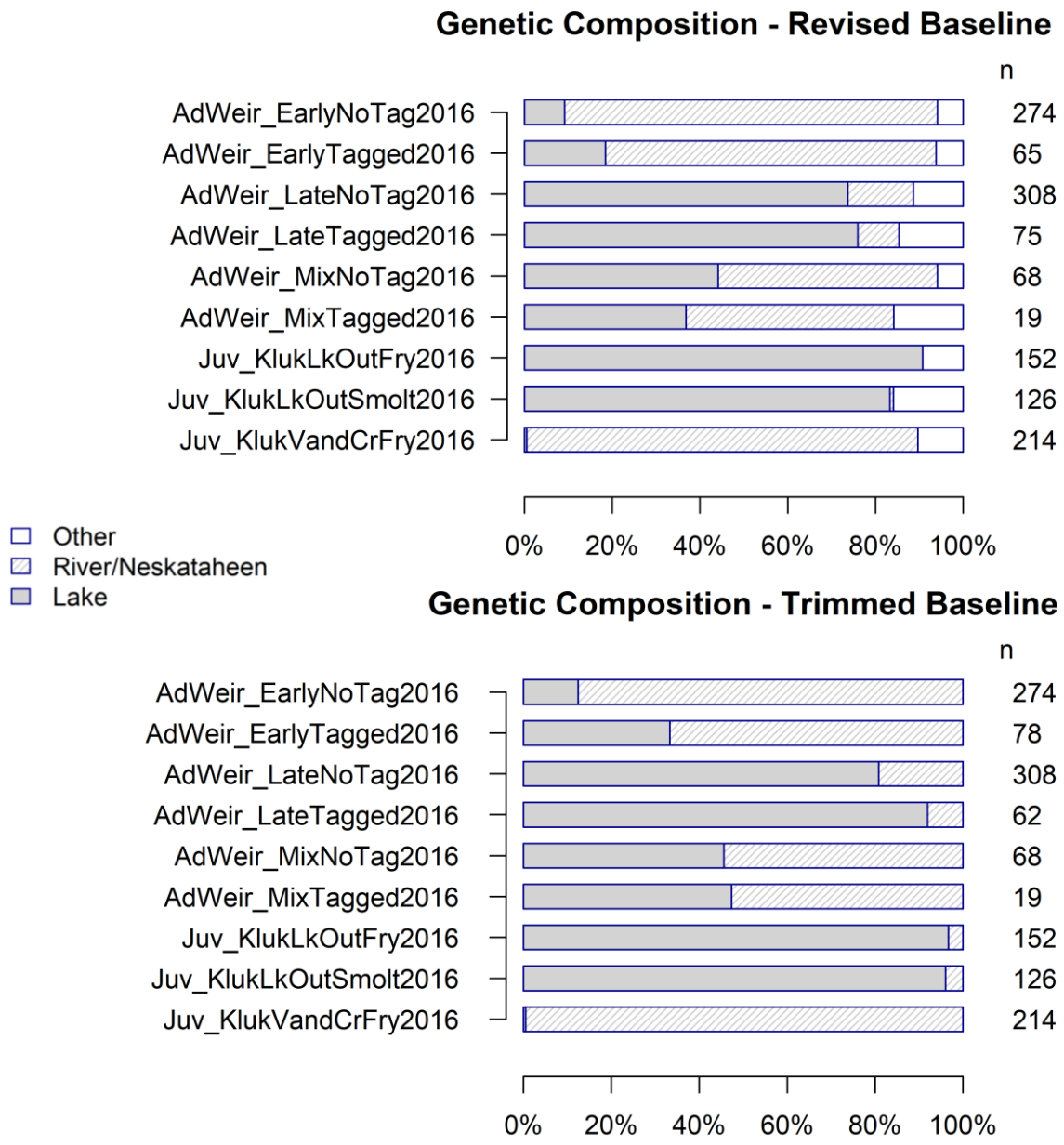


Figure 16: Genetic Composition of 2016 Klukshu Sample Groups Using Revised or Trimmed Baseline. This top panel of this figure shows the proportion of samples in each group matched to different populations in the revised Alsek baseline (large samples only, 2016 spawner samples instead of weir sampled from previous years). Samples were assigned to a baseline based on “best match” (i.e. highest probability across baselines), without a specific lower benchmark (i.e. assignment probability could be low). Figure 13 shows the distribution of assignment probabilities. Observed compositions shown in this figure are consistent with the tree fitting results (e.g. Figure 12). Adults sampled at the weir early (before Aug 14) and fry sampled on the Klukshu mainstem near Vand Creek were mostly assigned to the Klukshu River spawning ground sample. Adults sampled at the weir late (after Aug 20) and juveniles sampled at the lake outlet were mostly assigned to the Klukshu Lake spawning ground sample. Adults sampled during the mixed period (Aug 14 to 20) had a substantial proportion of fish matched to both of the spawning ground samples, but a bit higher proportion assigned to the Klukshu River / Neskataheen group. This caused the tree fits for the Mix samples to be unstable (i.e. grouped with different baselines depending on fitting method) and caused some of the other branches to shift around as well (e.g. river spawners split from river fry in 2 of 16 test cases; Table 12). The bottom panel is the same, except that samples are matched to a trimmed baseline including only 3 samples: 2016 Klukshu River Spawners, 2016 Klukshu Lake Spawners, and existing DFO baseline for Neskataheen. Estimated genetic composition for each sample group is similar for the two alternative baselines, but proportions are not identical.

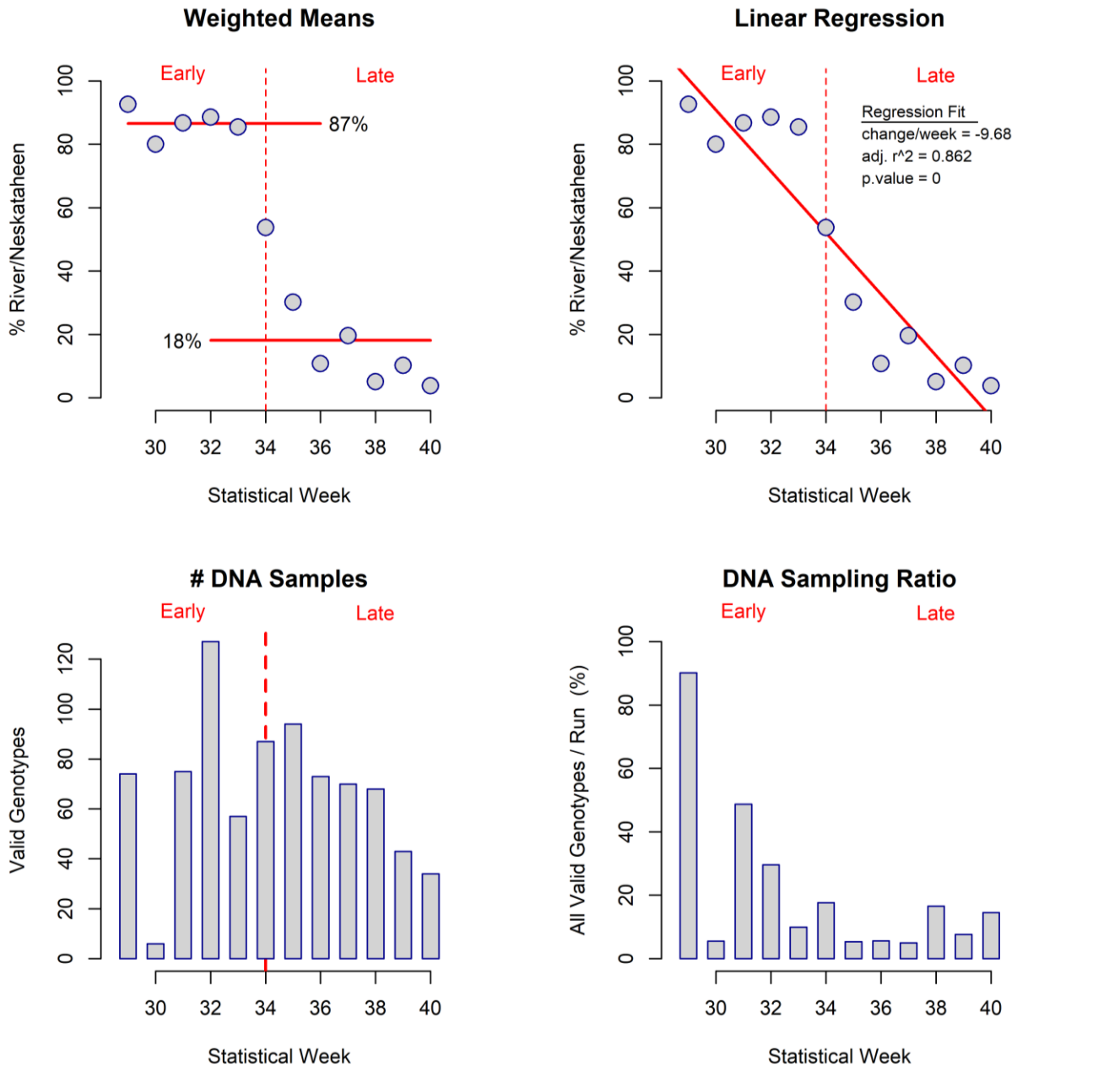


Figure 17: Weekly DNA Sampling Ratio and Run Composition for Sockeye at Klukshu Weir in 2016. Top panels both show the weekly proportion of samples assigned to the River / Neskataheen group in the genetic stock ID (Table 21). The top left panel overlays the weighted average proportion for each timing group, and the top right panel shows a regression fit for the change in composition over time. The regression fit is highly significant (p-value <<0.05) and predictive (adj. R^2=86%), and estimates a roughly 10% decrease in % river matches by week. Bottom panels show the number of samples and the DNA sampling ratio by week. Table 22 summarizes chi-squared tests for difference between early and late migrants. Note that these proportions use only the samples assigned to either “River/Neskataheen” or “Lake” (i.e. samples matched to non-Klukshu baselines were excluded). The number of DNA samples per week is fairly stable throughout the season, except for week 30 (July 17-23), which had very few samples (see weir operation notes in Table B 1). The corresponding sampling ratio decreased over time, as abundance increased.

Figure 18: Heatmap of Sibship Reconstruction – Full Siblings.
This plot shows reconstructed sibling relationships within and across sample groups. Table 23 summarizes the reconstruction and explains the definitions. In this plot, each column corresponds to a sample group, and each row corresponds to a unique pair of virtual parents. Each cell is colour-coded based on the number of full siblings in that sample from that pair of parents. Example A highlights 1 pair of virtual parents which accounts for 5+ samples among the Klukshu mainstem fry sampled near Vand Creek, but no full siblings in any other sample group (i.e. no other shaded cells). Example B illustrates the more typical case where 1-2 full siblings were identified in two different sample groups, in this case the lake spawners and the weir sample from the mixed time period (Aug 14-20). Overall, most of the full siblings were identified within the newly emerged fry on the Klukshu mainstem, but there were some among the early weir returns as well.

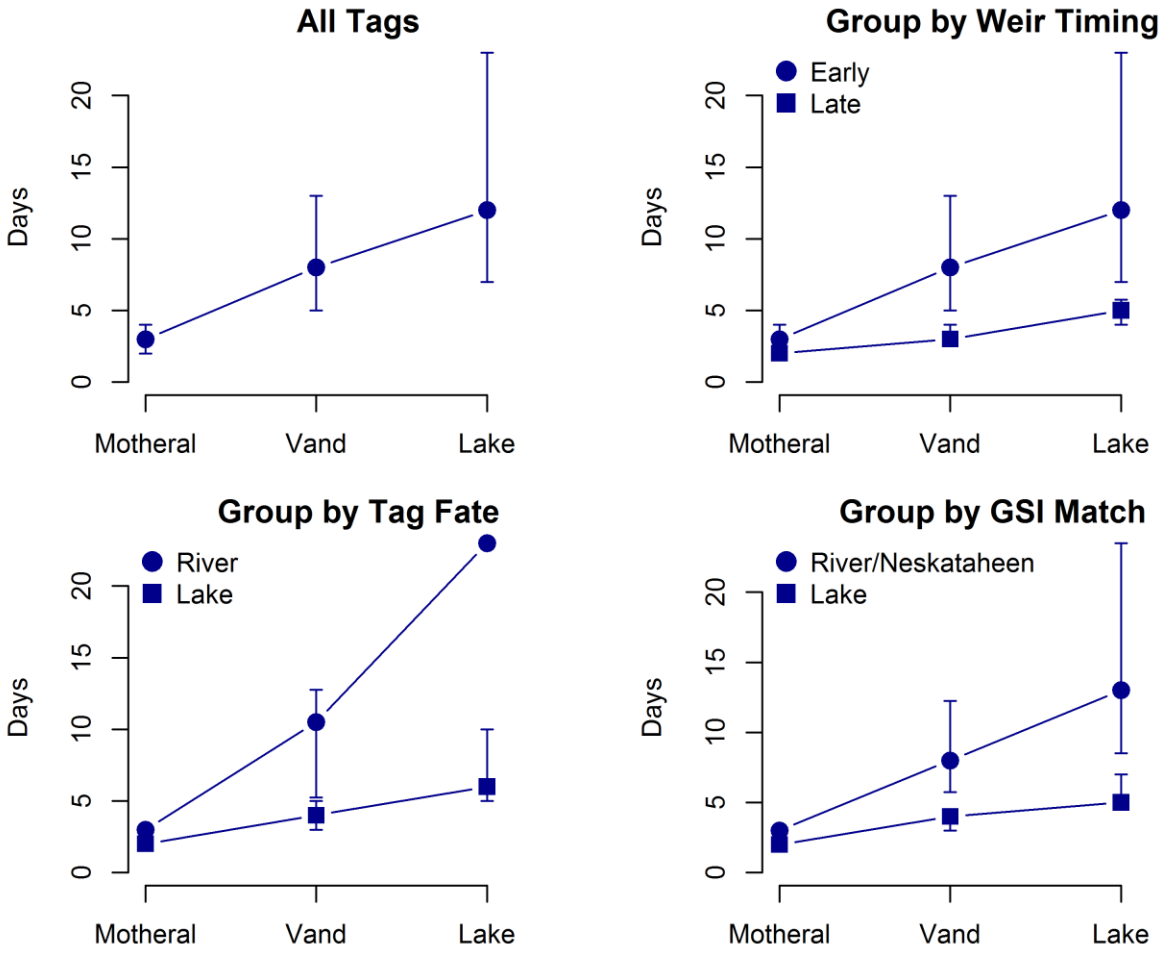


Figure 19: Differences in Migration Time Along Klukshu River Based on Stationary Receivers. Plots show days elapsed between last detection at the weir tower to first detection at the upstream towers (median and 25th to 75th percentile). The top left panel plots all tags detected at the weir tower and at least 1 upstream tower. The remaining panels show the total sample split into groupings based on weir timing, tag fate (Sec. 6.3), and genetic stock identification (Section 6.4). All three alternative groupings show the same result: Fish associated with the lake population migrate up Klukshu River much faster than those associated with the river population. The three alternative groupings are ordered by increasing accuracy (Section 7.8). Sample sizes, medians and ranges are listed in Table H 5.

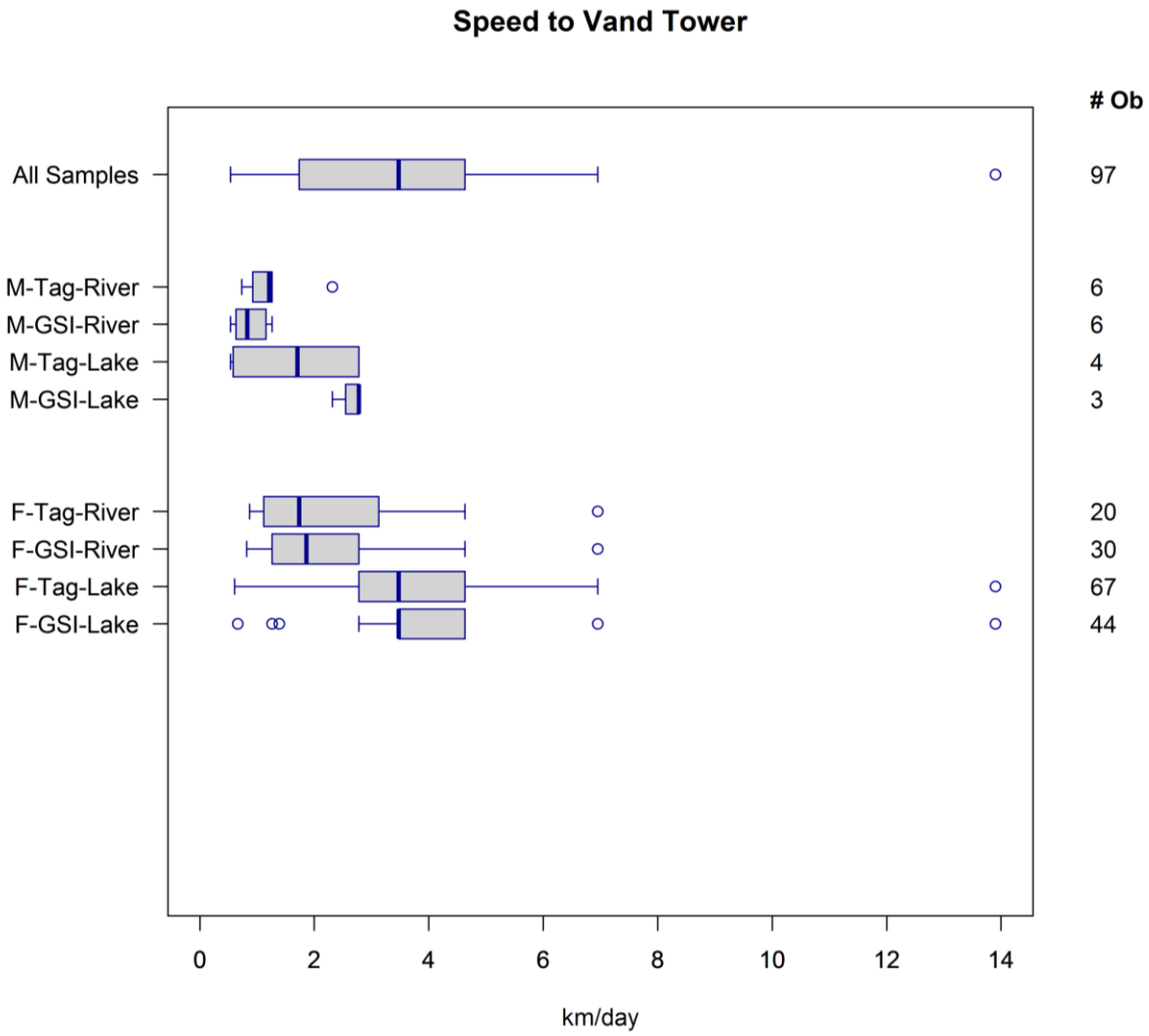


Figure 20: Differences in Migration Speed from Klukshu Weir to Vand Tower Based on Stationary Receivers.
Plots show km/day from last detection at the weir tower to first detection at Vand Tower 13.9km upstream. Refer to Table H 5 for further notes regarding the data (e.g. observed movement patterns) and to Table C 1 for a description of the tracking towers. Figure H 1 to Figure H 3 show the same data expressed as migration time in days, and with some alternative groupings (e.g. by timing of migration past the weir). The extreme value at 14 km/day was from a female tagged on Sep 7, detected by Motheral and Vand towers on Sep 8, and entered lake tower range on Sep 9, covering the full 22.6 km upstream migration in 2 days. The second fastest value, at about 7km/day, was observed for 8 females tagged between Aug 2 and Sep 12, which all took 2 days to reach Vand tower. 7 of these 8 were assigned a lake fate based on the tag movement pattern, but only half were genetically matched to the lake spawners, while 2 were matched to River / Neskataheen group and 2 matched to baseline samples elsewhere in the Alsek system. Overall, females migrated much faster than males, and lake fish migrated faster than river fish.

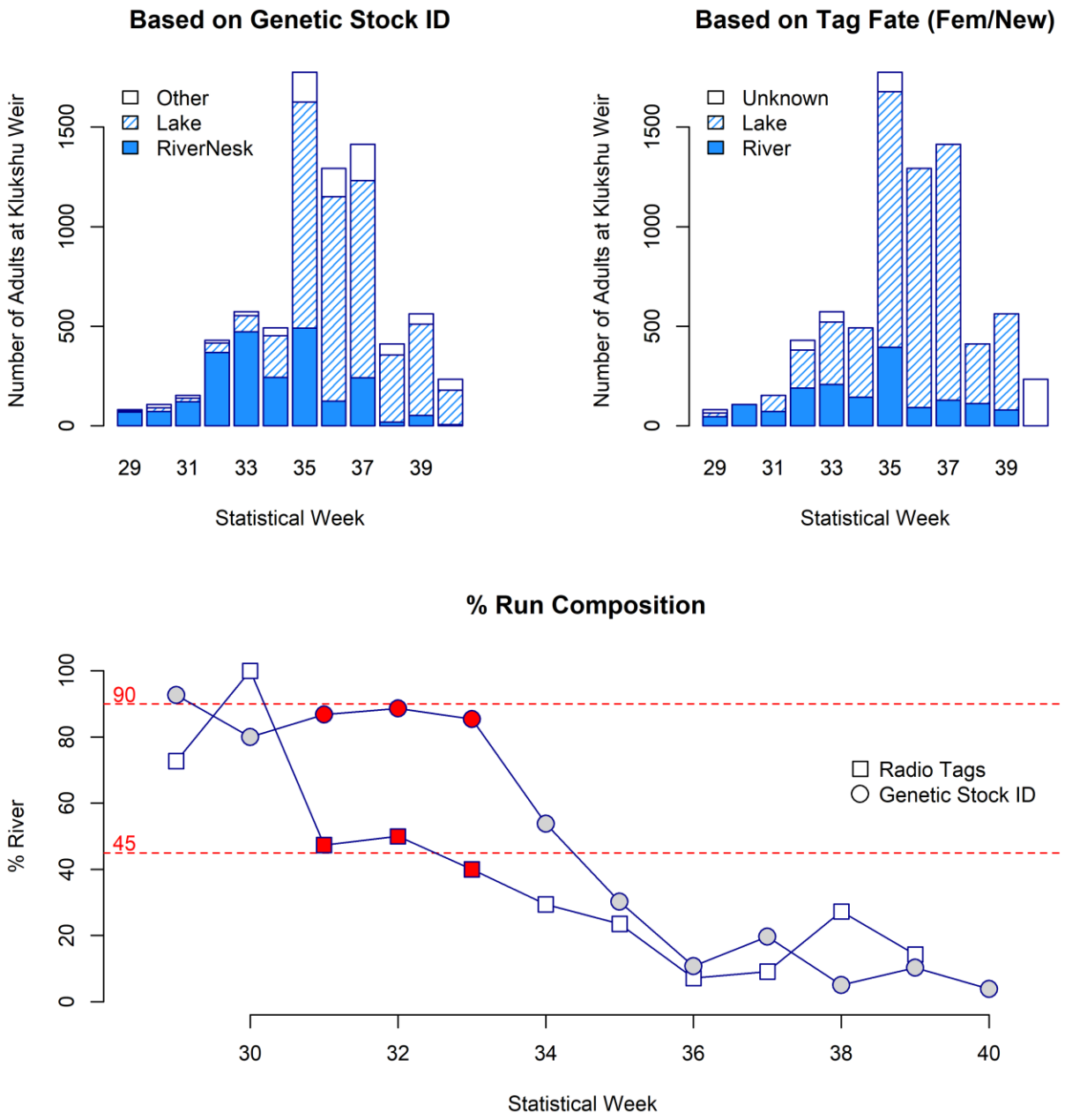


Figure 21: Weekly Run Composition based on Radio Tags and DNA.
Top two panels show the run composition based on sample proportions. The top left panel uses sample proportions for 3 categories based on genetic stock ID (Table 21): River/Neskataheen, Lake, or some other Alsek baseline. The right panel uses sample proportions for 3 categories based on radio tag fates for females with new tags (Table H 2): River, Lake, Unknown. The bottom panel shows estimated run composition, excluding tags with unknown fate and genetic matches to "other" populations. Both top panels show that the river spawners returned earlier, but were still present in similar abundances later on when the bulk of the lake spawners passed the weir. The estimated abundance of river spawners in the weekly run differs between the two sampling methods, with the DNA samples showing higher abundance of river spawners in the earlier part of the run, and the radio tags showing higher abundance of river spawners in the later part of the run. Figure 22 shows the corresponding run timing curves. The bottom panel emphasizes the large difference between the two methods in estimated stock composition for the early part of the run: For weeks 31 to 33 (late July/early August), the estimated proportion of river spawners is almost 90% based on the genetic stock ID, but only about 45% based on the radio tags.

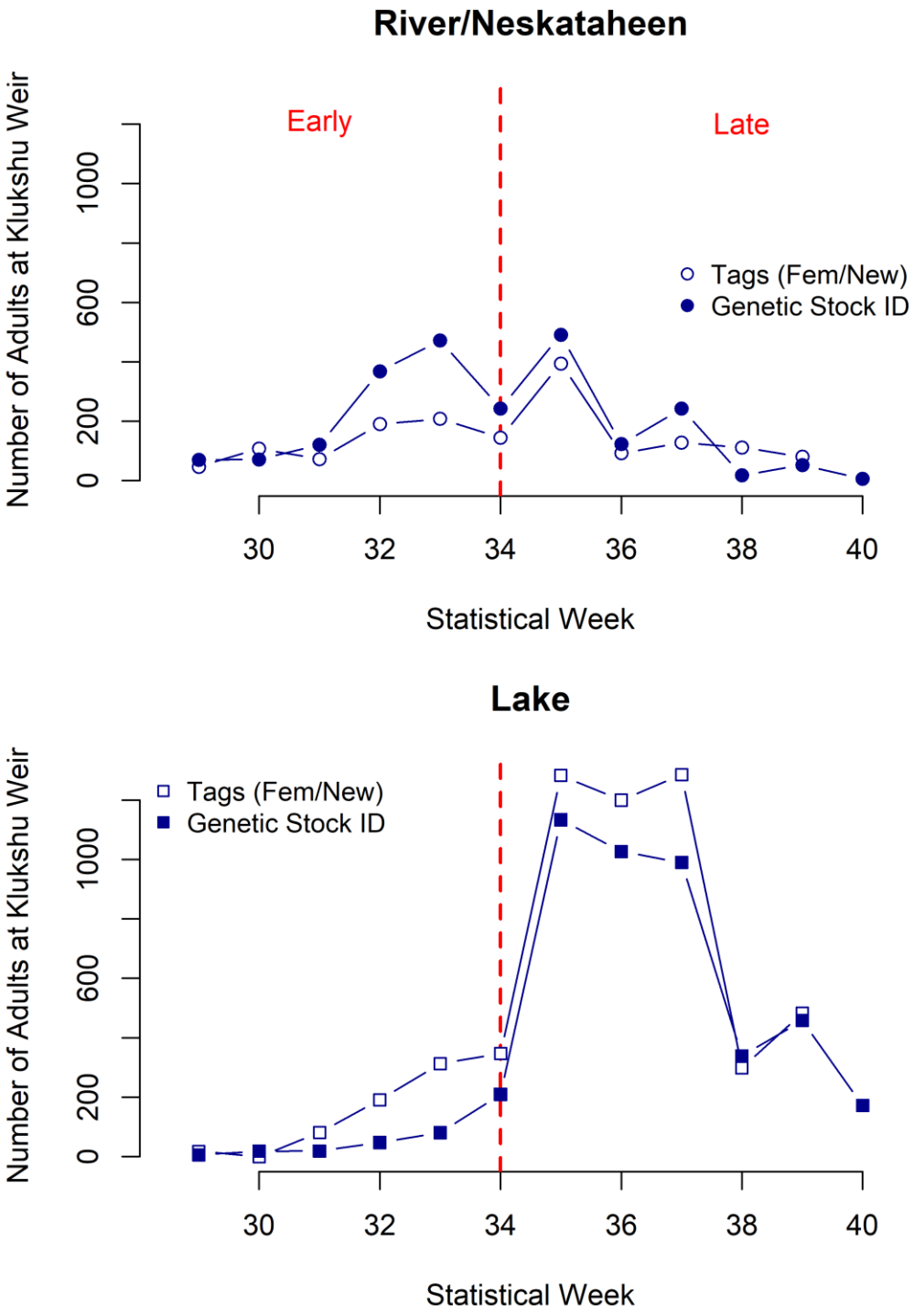


Figure 22: Run Timing Curves for River and Lake Sockeye at Klukshu Weir in 2016 – Weekly Estimates. This plot shows the same data as Figure 21, just presented as run timing curves for the two groups of spawners.

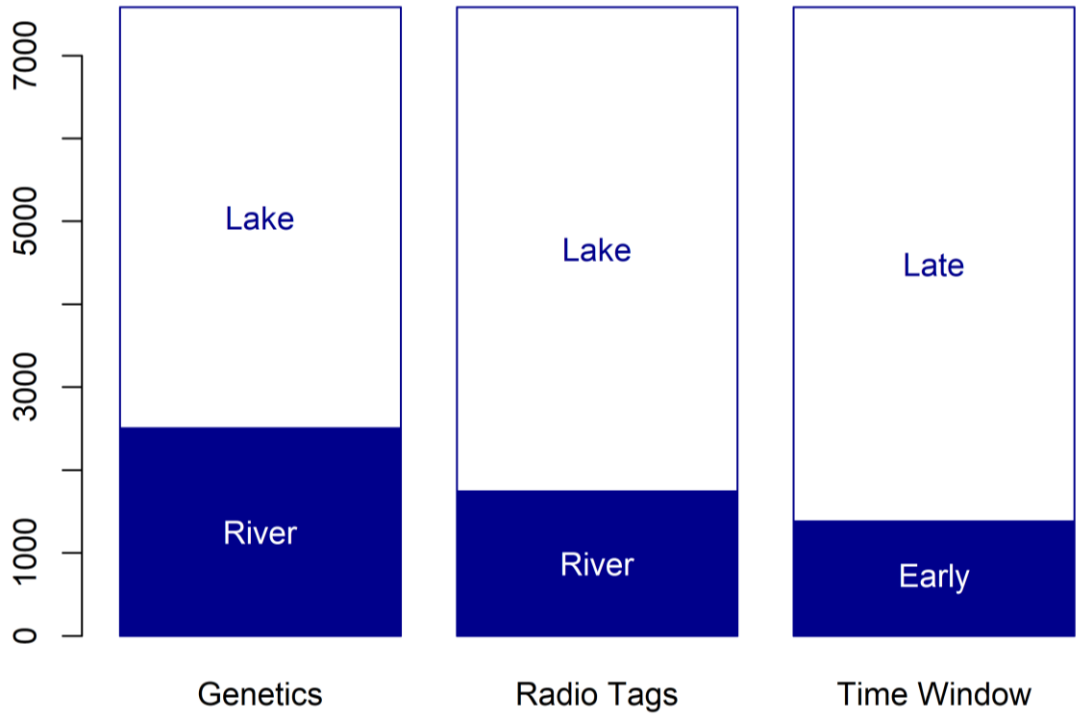


Figure 23: 3 Alternative Estimates of Total Run Composition of Klukshu Sockeye in 2016. compares three alternative estimates of total run composition.Based on genetic stock matches, River Sockeye accounted for about 33% (Table 21) of a total run of 7,584 Sockeye (Table 2), giving approximate abundances of 2,503 River Sockeye and 5,081 Lake Sockeye in 2016. Based on tag fates, River spawners accounted for about 23% of the run (Table H 2; females with new tags only), giving approximate abundances of 1,744 River Sockeye and 5,840 Lake Sockeye in 2016. Finally, using the August 15th cut-off date used by DFO since the 1990s, the early run was 1,381 (18%) and the late run was 6,203.

Photos

Photo 1: Klukshu Weir in August, 2011.
Picture faces upstream, showing the two “picket style” wings set at an approximate 30^{o} angle leading to a counting chamber, trap, and eventually a video counter, located underneath the plywood shack.

Photo 2: Tag Application.
Photo shows insertion of a Sigma-8 radio tag into a female Sockeye Salmon in August 2016. The inset shows the radio tag and antenna.

Photo 3: Stationary Radio Telemetry Receiving Tower Tower.
This photo shows the tower mounted on a bluff above the Klukshu River near Motheral Creek. Photo shows tripod support structure, receiver housing (containing receiver, 12V battery power supply and voltage regulator components) and solar panel for battery charging. Two directional antennas, one directed upstream and one downstream, were secured near the top of the tripod structure (not in photo). Photo taken on June 15th, 2016.

Photo 4: Helicoper Setup for Aerial Tag Detection.
The aerial survey on Oct 28, 2016,survey was conducted using a Bell 206B Jet Ranger helicopter flown at 20-80 m altitude and 10-20 km/h. Occasionally the helicopter hovered to provide adequate time to receive signals from large groups of radio-tagged sockeye salmon. Two researchers, each equipped with a LOTEK SRX-400, participated with one researcher scanning four frequencies, while the second researcher scanned the balance of the frequencies. A single, two element Yagi antenna mounted on the fore of helicopter provided directional information, i.e. strongest signal arrived from ahead of the helicopter. Note the Lotek SRX-400 recevier in the upper right inset used for aerial tracking radio tagged Klukshu River sockeye.

Photo 5: Collecting tissue sample from an adult Sockeye radio-tagged at Klukshu weir in August 2016. Picture shows excision of right axillary.

Female

Male

Photo 6: Female and Male Sockeye Salmon Spawning Adults.
Fish captured (snagged via hook and line) during adult sampling on Klukshu River spawning site just upstream of Vand Creek. Photos taken August 25th, 2016.

Photo 7: Beach seine used to capture juvenile salmon on Klukshu River and on Klukshu Lake.
Picture taken May 18, 2016, at site C (Section 3.1), on the Klukshu River mainstem downstream of Vand Creek.

Photo 8: Wolf-type Incline Plane Trap (IPT) deployed on the upper Klukshu River.
Picture taken on May 5, 2016, at site B (Section 3.1) on the Klukshu River mainstem downstream of Klukshu Lake outlet.

Photo 9: Retrieving captured fish from the Fyke trap deployed in the lower Klukshu River.
Picture taken May 4th, 2016, at site D (Section 3.1) on the Klukshu River mainstem 500m upstream of its confluence with the Tatshenshini River.

Photo 10: Gee-type minnow traps used at Sockeye rearing sites from May to July 2016.

Photo 11: Fry sampled at Vand Creek.
Coho salmon fry (top) and sockeye fry (bottom) captured with Beach Seine at Vand Creek during sampling on 02 May, 2017.

Photo 12: Sockeye Smolt sampled at Klukshu Lake Outlet.
Sockeye salmon smolt captured in the Wolf-type Incline Plane Trap on the upper Klukshu River near the outlet of Klukshu Lake, 18 May, 2017.

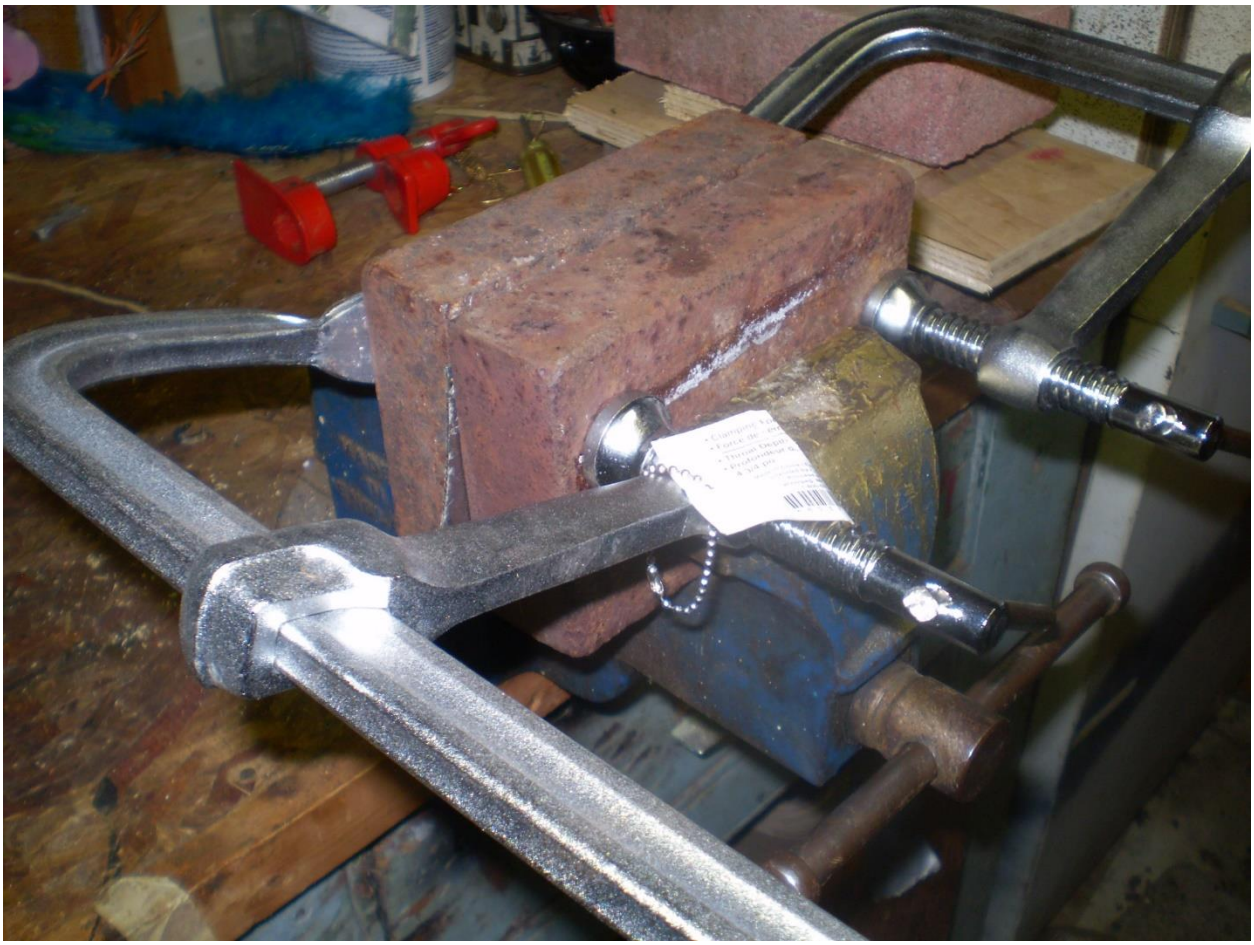


Photo 13: Pressing smolt scales using a bench vise.
Note the rectangular steel bricks and the stainless steel plate where the scale card and acetate is enclosed, Steel bricks were heated to 200° C with a conventional gas barbecue. Picture taken in January 2017.

Appendix A: Budget Overview

Table A 1: Budget Summary - Adult Project
Sampling of adult sockeye at Klukshu weir and throughout Klukshu watershed from July to August 2016 was administered through CAFN Project 247, using funds allocated by the Northern Endowment Fund of the Pacific Salmon Commission.

	Adult Project	%
Contract biologists	$41,033.76	31%
Statistical Consultant	$13,345.50	10%
Helicopter Charter	$5,089.56	4%
DNA samples (Materials, Shipping, Processing)	$28,550.00	21%
Radio Tags	$27,639.50	21%
Crew supplies (food, safety gear)	$2,410.03	2%
Fuel, Travel, Boat Rental	$2,709.20	2%
Administrative	$12,078.00	9%
Total	$132,855.55	

Table A 2: Budget Summary – Juvenile Project
Sampling of juvenile sockeye throughout Klukshu watershed from July to August 2016 was administered through CAFN Project 247, using funds allocated by the Northern Endowment Fund of the Pacific Salmon Commission.

	Juvenile Project	%
Contract biologists	$29,501.80	44%
Statistical Consultant	$13,166.80	20%
DNA samples (Materials, Shipping, Processing)	$12,450.00	18%
Crew supplies (food, safety gear)	$2,619.79	4%
Fuel, Travel, Boat Rental	$3,469.00	5%
Administrative	$6,121.00	9%
	$67,328.39	

Table A 3: Overview of In-Kind Contributions
These projects could not have been successfully implemented and documented to this level without substantial in-kind contributions by participating organizations and individuals.

Contributor	Contribution
CAFN	Staff time, accommodation for field crew, field crew support
DFO	Juvenile sampling gear loan (nets, traps), radio telemetry equipment loan (towers, receivers), accommodation at weir site, coordination of weir sampling (tags, DNA) with regular weir operation (scales, measurements), scale age readings, telemetry software, Genetics Lab technical advice and family structure analysis
ADFG	Staff time for feedback during planning, implementation, and analysis
SOLV Consulting Ltd.	Analytical and writing services
Peter Etherton	Juvenile scale aging, radio telemetry signal interpretation, writing services
David Petkovich	Juvenile sample analysis, writing services

Appendix B: Weir Samples – Sampling Effort and Field Notes

Table B 1: Summary of Weir Operations and Observations
This table summarizes the weekly sampling for this project at Klukshu Weir in 2016. Table 2 lists the weekly run sizes, number of samples collected, and number of samples that were successfully processed (i.e. full age reading, tag fate, valid genotype). Figure 7 shows total sample size matched up with the run timing curve. Figure 8 and Figure 17 plot weekly sampling ratios for radio tagging and DNA sampling. It was initially very difficult to find female sockeye, but the sex ratio approached roughly 50:50 later in the run (Figure G 2). Field crew speculated that migration through the weir in 2016 may have been delayed because the Klukshu was warmer and had lower water levels than average (Figure B 1). Some of the tagged fish were trapped during the early morning hours and held till 0800 hrs when tagging occurred.

Timing Group	Stat Week	Weir Operation Notes	Sockeye Observations
EARLY	W28	Below avg flow; water temp 2.2° C above 1986-15 avg	Slow; no evidence of sockeye numbers building below weir
	W29	Below avg flow; water temp 3.6° C above 1986-15 avg	Sockeye run starting to build, evidence of fish holding at eddy sites below weir
	W30	Below avg flow; water temp 2.4° C above 1986-15 avg	Bears showed up at weir; sow, two cubs; large boar; actively fishing at weir site; sockeye numbers building in back eddies below weir
	W31	Below avg flow; water temp 1.5° C above 1986-15 avg	Bear activity waning; sockeye numbers continue to build in downstream eddies; number through weir building
	W32	Below avg flow; water temp 3.0° C above 1986-15 avg	No bear activity; sockeye migration proceeding as normal
	W33	Below avg flow; water temp 2.7° C above 1986-15 avg	Sockeye migration proceeding as normal
MIX	W34	Below avg flow; water temp 1.7° C above 1986-15 avg	Sockeye migration proceeding as normal
LATE	W35	Below avg flow; water temp 2.0° C above 1986-15 avg	Sockeye migration proceeding as normal
	W36	Below avg flow; water temp 2.0° C above 1986-15 avg	Sockeye migration proceeding as normal
	W37	Below avg flow; water temp 2.1° C above 1986-15 avg	Tagged sockeye washed against the weir; recovered tag; located sockeye spawning site 300 m upstream from weir
	W38	Below avg flow, but rising due to rains; water temp 1.8° C above 1986-15 avg; first frost	Strong pulse of sockeye during increase in flow; observed sockeye spawning activity (one female two males immediately (1m) above weir
	W39	Below avg flow; water temp 1.7° C above 1986-15 avg	Sockeye migration proceeding as normal
	W40	Below avg flow; water temp 0.5° C above 1986-15 avg	Sockeye migration proceeding as normal
	W41	Below avg flow; water temp 0.2° C above 1986-15 avg	Very few sockeye present; termination of run

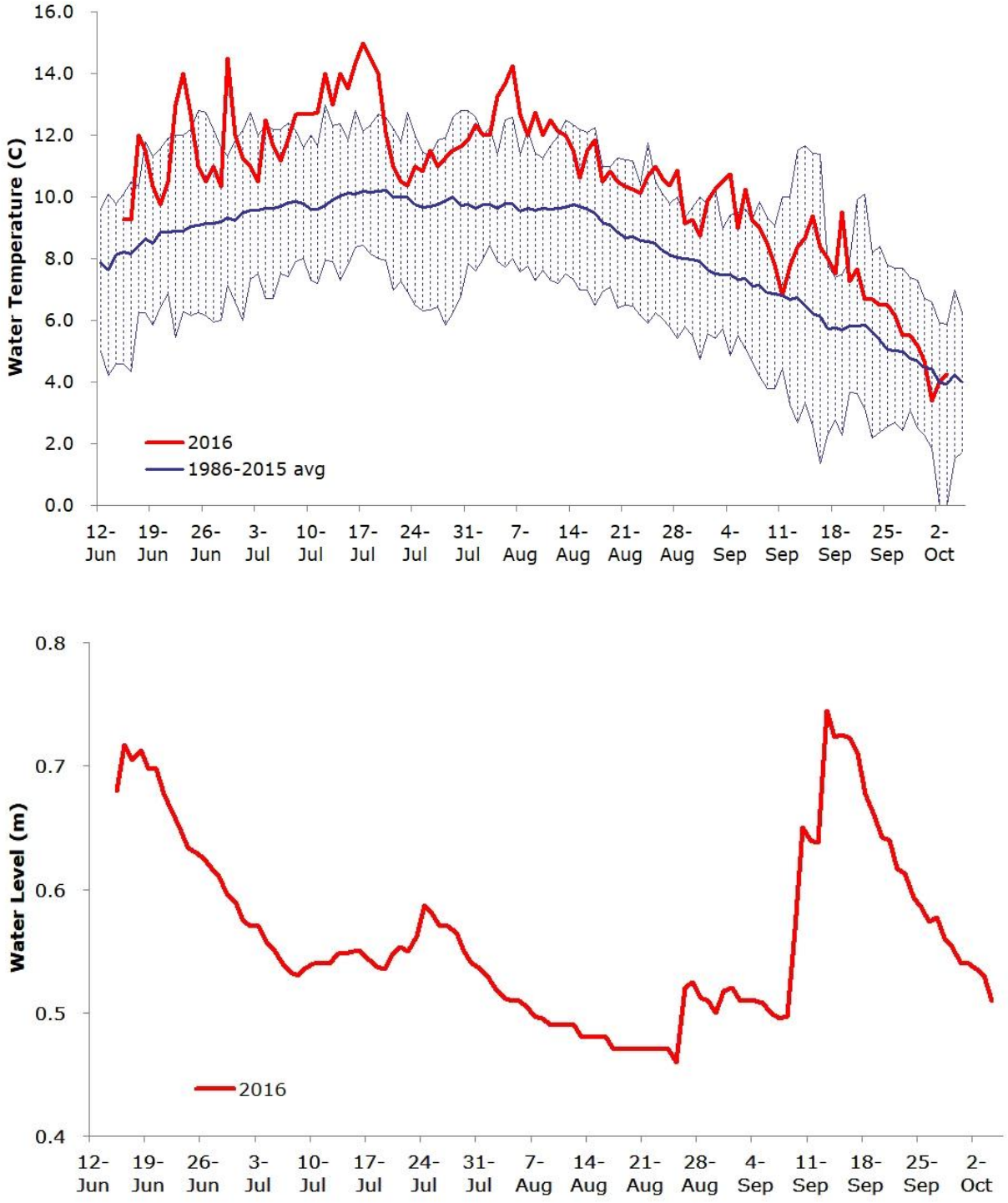


Figure B 1: 2016 Water Temperature and Water Level at Klukshu Weir.
Temperatures are measured in stream flow approximately 500 metres from the mouth of the Klukshu River during weir operations. Daily average temperatures are available since 1986. Water levels are measured at the weir gauge. Data provided by Sean Stark (DFO). Temperatures in 2016 were consistently above average, and frequently exceeded the previously recorded maximum. Historical information on water levels is not currently available in electronic format, but weir crew consider 2016 water levels below average (Sean Stark, pers. comm.)

Appendix C: Radio Telemetry – Sampling Effort and Field Notes

Table C 1: Field Notes on Stationary Receivers
Four stationary receivers (i.e. towers) were mounted along the Klukshu River to detect tagged fish as they moved about the Klukshu mainstem and into the lake. Section 2.2 describes the equipment. This table summarizes field observations on suitability of sites and equipment, as well as practical challenges encountered during the project. The 3 tower sites along the Klukshu mainstem were selected based on vehicle access and known spawning sites in the Klukshu River drainage, using information compiled from traditional and local knowledge, DFO records, and past spawning distribution studies (Petkovich et al. 1997, Pacific Salmon Commission 1997, Etherton 1997). The 4th tower was at the weir with the sole function of detecting passage upstream after tag application. The 4 tower locations worked well for the study design, but the tower sites at Motheral and Vand Creek posed two challenges: risk of dangerous bear encounters and physical demands of packing the tower pieces to the site from the nearest vehicle access point. Some fish moved up and down the Klukshu mainstem, and some entered the lake beyond the detection of the lake tower, but returned to the detection zone which included a major spawning ground located at the lake outlet. (see summary in Table 3, details in Appendix K).

Site	Description	Suitability	Field Challenges
Weir	Immediately above Klukshu weir (60.11983N -137.0306W)	**Good site**; sufficient sun exposure to activate solar panel; utilized only one antenna as this tower's function was to monitor upstream movement only.	Technical issues with downloading at the trial period, before the bulk of the tags were at large; lost power and therefore tag detection function, due to loose battery clamp from 18-30 September. A local spawning group c/w some radio tags near the weir resulted in large weekly data files
Motheral	Near mouth of Motheral Creek, 9.6km upstream of weir tower. (60.19605N -136.9996W)	**Ideal site**: located on a high bank with good downstream and upstream vantage; good sun exposure to activate solar panel through the field season	Required backpacking the tower to the site from the Motheral Creek Road, approximately 500 metres.
Vand	Near mouth of Vand Creek, 13.9 km upstream of weir tower. (60.22632N -136.9679W)	**Good site**; sufficient sun to activate the solar panel throughout the season; only fair vantage upstream and downstream due to river bends and thick foliage.	Required backpacking the tower to the site from the Vand Creek Road (Klukshu Crossing), approximately 600 metres; thick foliage and fair measure of bear activity walking to the site. There were miscellaneous technical issues with the receiver, but were rectified w/o major consequences.
Lake	At the outlet of Klukshu Lake, 22.6km upstream of weir tower. (60.29427N -137.0023W)* *tower moved on 12 Sept	**Fair site**; insufficient sunlight to activated solar panel post 11 Sept (due to thick foliage and solar panel angle); moved tower upstream approximately 200 metres to a treeless knoll overlooking the lake outlet on 12 Sept	The tower collected very large weekly data files due to the abundance of sockeye spawning at the outlet of the lake; tags recovered by CFN fishers were detected at this tower when harvesters returned to Klukshu Village located at the lake outlet. Very "busy" and sometimes confounding weekly data files

Table C 2: Radio Tag Tracking Overview – Stationary Receivers

Of 820 adult sockeye sampled at Klukshu weir in 2016, 165 were subsampled for radio tagging. Tag application was spread over the entire migration period, with a plan to tag roughly equal numbers during the early period (before Aug 14) and the late period (After Aug 20), and to tag mostly females. Note that no tags were applied 15-20 Sept. The table shows the number of tags recorded in each tower's range, split into different groupings (e.g. based on time of tag application). "Tags with Records" shows the number of tags with at least 1 record at one of the towers. Note that a tag recorded to enter the range of the lake tower does not automatically mean that the tagged fish spawned in the lake: Some moved back downstream later, others were only detected by downstream-facing antenna of the lake tower. Refer to Table 3 for a summary of the observed movement patterns, and to Appendix J for a description of the details for each tag. Tag fates, which are derived from the movement pattern in combination with an aerial survey late in the season, line up closely with the tower detections. Almost all of the fish assigned a lake fate were recorded entering the lake (96/97,99%). Conversely, only a few of the fish assigned a river fate were ever recorded by the lake tower (5/56,9%). However, the patterns are much less distinct if tagged fish are grouped based on genetic stock matches (Sec. 5.8). Only about 3/4 of the fish matched to Klukshu lake spawners in the revised Alsek baseline were detected by the lake tower (60/77,78%), and almost half of the fish matched to the Klukshu River / Neskataheen genetic group were detected at least once by the lake tower (River: 11/23,48%; Neskataheen: 16/40,40%). Of these 27 River/Neskataheen fish, only about half went straight to the lake (15/27), while the others either moved about the mainstem for a long time or had various types of mixed signals.

	All	Tags with Records	Exit Weir Tower	Enter Motheral	Enter Vand	Enter Lake	Perc Entered Lake
All	165	162	113	138	132	101	62
Early	70	70	51	58	52	32	46
Mixed	19	17	14	15	14	12	71
Late	76	75	48	65	66	57	76
Stat Week 29	14	14	2	10	10	3	21
Stat Week 30	3	3	3	3	1	0	0
Stat Week 31	32	32	28	27	26	18	56
Stat Week 32	9	9	8	8	6	5	56
Stat Week 33	12	12	10	10	9	6	50
Stat Week 34	19	17	14	15	14	12	71
Stat Week 35	18	18	16	15	16	14	78
Stat Week 36	14	14	12	12	12	13	93
Stat Week 37	11	11	8	10	10	10	91
Stat Week 38	12	12	9	10	11	9	75
Stat Week 39	11	10	0	9	9	8	80
Stat Week 40	9	9	2	8	8	3	33
Stat Week 41	1	1	1	1	0	0	0
Tag_Fate – Undet.	12	9	0	0	0	0	0
Tag_Fate - River	56	56	40	50	42	5	9
Tag_Fate - Lake	97	97	73	88	90	96	99
GSI Klukshu Lake	79	77	52	65	67	60	78
GSI Klukshu River	24	23	15	19	18	11	48
GSI Alsek_T_down	3	3	3	3	3	2	67
GSI - Kane	1	1	0	1	1	0	0
GSI Kudwat_Cr_RT	1	1	0	1	1	0	0
GSI - Neskataheen	40	40	32	36	28	16	40
GSI - OConnor_RT	3	3	3	3	3	3	100
GSI - Stinky_Cr_RT	3	3	2	1	2	2	67
GSI - Tweedsmu_RT	3	3	2	3	3	3	100
GSI - U_Tatshen_RT	2	2	1	1	1	2	100
GSI - Undetermined	6	6	3	5	5	2	33

Table C 3: Distribution of Radio-Tagged Klukshu River Sockeye based on Aerial Survey, Oct 28 2016. Of 820 adult sockeye sampled at Klukshu weir in 2016, 165 were subsampled for radio tagging. Tag application was spread over the entire migration period, with a plan to tag roughly equal numbers during the early period (before Aug 14) and the late period (After Aug 20), and to tag mostly females. Note that no tags were applied 15-20 Sept. The table shows the number of tags recorded in different locations during a helicopter overflight, split time of tag application. Note that a tag recorded in the river in late October does not automatically mean that the tagged fish was a river spawner: Some tags stayed in the lake for a long period, then were detected downstream later, and were classified as carcass drifts. Refer to Table 3 for a summary of the observed movement patterns, and to Appendix J for a description of the details for each tag. Tag fates were derived from the full movement pattern combining information from the stationary receivers with the aerial survey results. Roughly half of the tags (92/165, 56%) were detected during the overflight, which took place about 3 months after the first tag application and 1 month after the latest tag application.

	Timing of Tag Application			
Detected at	Early	Mix	Late	Total
River - Weir	7	0	7	14
River Motheral Confluence	8	2	0	10
River – Vand Confluence	5	1	5	11
River - Highway Crossing	6	2	0	8
Lake	13	8	28	49
Total	39	13	40	**92**
% Lake	33%	62%	70%	**53%**
% River	*77%*	*38%*	*30%*	***47%***

* Note that these are raw tag counts by time period, not weighted by run size.

Appendix D: Spawning Ground Samples – Sampling Effort and Field Notes

Table D 1: Spawning Ground Sampling Events – Klukshu River
110 adult spawning sockeye were sampled at 2 locations throughout Klukshu River on 5 different dates. Samples included 57 males and 53 females. Table values show the number of samples cross-tabulated by sampling event and spawner condition. Most of the samples were collected mid-August at Vand Creek confluence on the Klukshu mainstem (92/110, 84%), and most of those were fish that were either actively spawning or fully spawned out (77/92, 84%). Only a few spawners were sampled at Motheral confluence in mid-August and at Vand in late August. Section 2.3 summarizes the sampling methods. Fish were selected for these samples if they were clearly in spawning mode (i.e. over a redd or in spawning colours and shape). Fresh looking fish were ignored. Selected fish were snagged. This did not pose too much of challenge as sexual dimorphism was often pronounced and gametes were visible on most fish snagged at the river sites. Potential sampling sites were identified using information compiled from traditional and local knowledge, DFO records, and past spawning distribution studies (Petkovich et al. 1997, Pacific Salmon Commission 1997, Etherton 1997). Sampling sites were then prioritized based on a survey of likely spawning habitat. The major river spawning sites are located approximately 200 metres upstream from the Vand/Klukshu confluence, and consisted of deep pools with requisite spawning gravels at the head and foot, and in some instances latter areas of the pools (classic spawning sites which afford protection predators in close proximity to the actual spawning substrate). The spawning sites of the few fish sampled near Motheral Creek were of similar characteristics. Most of the river section between Motheral and Vand was surveyed on foot, and classified as poor spawning habitat based on lack of suitable gravel. Two foot surveys were covered about 2km downstream from the Motherall tower, and found only a few spawners. Given that access to these sites was onerous, and spawner numbers would likely have been small, sampling effort was instead focused on the Vand Creek site. Additional spawning sites might have been detected with a boat survey, which should be considered for future projects. Note that in October spawning Coho were observed digging in the spawning gravels near Vand Creek.

Date	**Aug 10**	**Aug 11**	**Aug 18**	**Aug 19**	**Aug 25**	
Location	**Motheral**	**Vand**	**Vand**	**Motheral**	**Vand**	***Total***
Spawner Condition						
Green, But Preparing	6	0	0	0	0	**6**
Milting	0	0	0	0	5	**5**
Other	0	1	3	1	0	**5**
Ripe	0	0	2	1	0	**3**
Ripe - Eggs Released	0	0	0	0	1	**1**
Spawned - Almost Complete	0	1	0	0	0	**1**
Spawned - Fully	0	2	31	0	4	**37**
Spawned - Partially	0	1	5	0	0	**6**
Spawning - Active	0	21	25	0	0	**46**
Total	**6**	**26**	**66**	**2**	**10**	**110**

Table D 2: Spawning Ground Sampling Events – Klukshu Lake

136 adult spawning sockeye were sampled at 3 locations throughout Klukshu Lake on 4 different dates. Potential sampling sites were identified using information compiled from traditionaland local knowledge, DFO records, and past spawning distribution studies (Petkovich et al. 1997, Pacific Salmon Commission 1997, Etherton 1997). Samples included 61 males, 51 females, and 24 unidentified (23 skeletal samples, 1 undetermined carcass). Table values show the number of samples cross-tabulated by sampling event and spawner condition. Most of the samples were collected mid- to late September (125/136, 92%). Samples in mid-September were mostly ripe or fully spawned, but at the end of September all samples were taken from dead animals at different stages of decay. Additional fully spawned fish were sampled in early October at the lake outlet. Section 2.3 summarizes the sampling methods. Any sockeye observed at the lake outlet or interior of the lake was subject to potential sampling. Spawner sampling in the interior of the lake (i.e. Gribbles Gultch and select shoreline areas) was probably too late in the year, given the number of skeletal remains present, and failure of sampling even a single live fish at these sites. Only a few live fish were observed near Gribbles and no spawning activity was observed along select sites on the west shore of the lake where spawning was documented by past researchers (Petkovich 1997; Etherton 1997). Note that in some instances that wind action was corralling sockeye carcasses to certain parts of the lake; hence, the location of spawner samples did not necessarily match the spawning site.

Date / *Location*	**Sep 14 Klukshu Lake Outlet**	**Sep 15 Klukshu Lake Outlet**	**Sep 30 East Shore Lake**	**Sep 30 Gribbles Gultch**	**Oct 6 Gribbles Gultch**	**Oct 6 Klukshu Lake Outlet**	***Total***
Spawner Condition							
Full Eggs	0	1	0	0	0	0	**1**
Ripe	18	20	0	0	0	0	**38**
Ripe & Full Eggs	2	0	0	0	0	0	**2**
Spawned - Fully	18	8	0	0	0	9	**35**
Spawned - Partially	1	5	0	0	0	0	**6**
Spent	0	2	0	0	0	0	**2**
UNK - Carcass	0	0	14	13	2	0	**29**
UNK - Skeletal	0	0	0	23	0	0	**23**
Total	**39**	**36**	**14**	**36**	**2**	**9**	**136**

Appendix E: Juvenile Samples – Sampling Effort and Field Notes

Table E 1: Juvenile Sampling Events with Wolf-type Incline Plane Trap (IPT).
IPT sampling from 05 May, 2016, to 02 July, 2016, on the upper Klukshu River 300 m downstream of the outlet of Klukshu Lake (site B) resulted in the capture of 472 Sockeye smolts, 59 Chinook salmon smolts and 38 Coho fry. A number of slimy sculpins were captured during most sampling events but were not enumerated. No practical challenges were encountered during implementation of the IPT sampling. The IPT have a large holding area within the trap, so few mortalities occurred. Note that initially the IPT was not fished too long due to concerns regarding potential mortality of sockeye smolts due to over crowding, but as project proceed and a better understanding of outmigration timing was gained the IPT trap was fished unattended for extended periods.

			Type / Number of Fish captured			
Deployment date/time	Recovery date/time	Soak Time (h)	Sockeye Fry	Sockeye Smolt	Coho Fry	Chinook Smolt
May 5, 13:30	May 5, 19:50	6.33 h	0	1	1	0
May 5, 19:50	May 6, 13:50	17.5 h	0	2	15	0
May 12, 11:30	May 12, 18:00	6.5 h	0	0	0	0
May 12, 18:00	May 12, 22:30	4.5 h	0	0	0	0
May 12, 22:30	May 13, 11:00	12.5 h	0	138	10	0
May 18, 12:25	May 18, 17:30	5.0 h	0	0	0	0
May 18, 17:30	May 19, 13:00	19.5 h	0	236	9	9
May 25, 12:20	May 26, 11:00	22.6 h	0	17	0	0
June 1, 12:00	June 1, 19:45	9.75 h	0	21	1	47
June 1, 19:45	June 2, 12:00	16.75 h	0	27	0	2
June 22, 21:35	June 23, 08:00	10.25 h	0	0	4	0
June 29, 12:00	June 30, 13:00	23.00 h	29	6	2	1
July 7, 14:00	July 8, 10:00	20.00 hr	19	20	0	0
		Other	16	0	0	0
		Total Caught	64	472	38	59
		Field Measurements	64	167	-	-
		Valid Genotype	64	126	-	-

Table E 2: Juvenile Sampling Events with Beach Seine.
Beach seine sampling from 06 May, 2016, to 02 June, 2016, captured Sockeye, Coho, and Chinook fry. Species composition differed by site. Beach seines on the Klukshu mainstem at Vand Creek (site C) captured numerous Sockeye and Coho fry as well as some Chinook fry. Except for 1 Coho fry, only Sockeye salmon fry were captured at site A (boat launch at Klukshu Lake outlet). Sockeye Fry were captured during all sampling events at sites A and C with higher catches per effort occurring after mid-May. Sockeye and Coho Fry were captured on the lower Klukshu River near the Tatshenshini confluence (Site D) during 1 of 2 sampling events. The beach seine worked well for sampling juveniles, and no practical challenges were encountered.

			Type / Number of Fish Captured		
Date / Time	Site	Sweeps	Sockeye Fry	Coho Fry	Chinook Fry
06 May, 14:30	A	2	35	0	0
13 May, 13:50	A	2	33	0	0
19 May, 15:00	A	2	24	0	0
26 May, 12:45	A	1	21	0	0
02 June, 13:30	A	1	12	1	0
Total Caught		8	125	1	0
Field Measurements			90	-	-
Valid Genotypes			88	-	-
06 May, 13:30	C	4	12	7	0
12 May, 15:30	C	4	22	89	12
18 May, 13:30	C	3	119	193	1
25 May, 13:15	C	1	25	29	6
*01 June, 13:50	C	1	36	24	5
Total Caught		13	214	342	24
Field Measurements			214	-	-
Valid Genotypes			214	-	-
12 May, 14:45	D	3	0	0	0
26 May, 13:00	D	1	12	47	0
Total Caught		4	12	47	0
Field Measurements			-	-	-
Valid Genotypes			-	-	-
Grand Total		25	351	390	24
Field Measurements			304	-	-
Valid Genotypes			302	-	-

* Note that on June 1, 2016, an additional 213 fry (mixed species) were captured and released at Site C (Vand Creek).

Table E 3: Juvenile Sampling Events with Fyke Trap.
Fyke trap sampling from 05 May, 2016, to 02 June, 2016, on the Lower Klukshu River approximately 500 m upstream of its confluence with the Tatshenshini River(site D) captured high numbers of coho fry and only low numbers of other salmon species. Like the IPT, a number of slimy sculpin were captured during each sampling event but these fish were not counted and were released without taking morphometric measurements. Only 1 sockeye smolt and no sockeye fry were captured using the Fyke trap. During the overnight set on 12-13 May a number of coho fry perished as flow velocities in the trap increased throughout the night resulting in conditions that many of the small fry could not sustain themselves in. Following the fish loss during the 12-13 May sampling event the Fyke trap was only deployed for shorter sets which likely impacted its sampling effectiveness.

			Type / Number of Fish Captured *					
Deployment date/time	Recovery date/time	Soak Time	Coho Fry	Coho Fry 1+	Chinook Fry	Chinook Smolt	Sockeye Smolt	Sockeye Fry
May 5, 15:10	May 5, 22:30	7.33 h	0	0	0	0	0	0
May 5, 22:30	May 6, 08:30	10.0 h	313	0	3	2	0	0
May 12, 14:20	May 12, 23:00	8.67 h	0	0	0	0	0	0
May 12, 23:00	May 13, 08:00	9.0 h	488	5	0	4	1	0
May 25, 20:15	May 25, 22:00	1.45 h	7	0	0	0	0	0
May 26, 07:20	May 26, 09:50	2.5 h	5	0	0	0	0	0
June 1, 21:40	June 1, 22:30	0.5 h	0	0	0	0	0	0
June 2, 07:20	June 2, 9:20	2.0 h	0	0	0	0	0	0
		Total	813	5	3	6	1	0

Table E 4: Juvenile Sampling Events with Gee-type Minnow Traps.
Gee Trap sampling from 05 May, 2016, to 01 June, 2016, at 3 of the 4 sample sites captured mostly Coho Fry and a few Chinook Smolts, but no juvenile Sockeye. As with Wolf-type incline plane trap and Fyke Trap, some slimy sculpin were captured, but at a much lower number than with the other trap. In addition, the Gee Trap also caught a few Dolly Varden Charr. Sculpins and Dolly Varden were enumerated and released without taking morphometric measurements. Gee Traps were deployed at Klukshu Lake Outlet (Site A), Klukshu River mainstem near Vand Creek (Site C), and Lower Klukshu near its confluence with the Tatshenshini River (Site D). Gee traps worked as expected, i.e. succeeded in catching non target species such as coho and chinook, but failed to yield sockeye. Sockeye appear to have an aversion to gee traps; a passive trap (i.e. non-baited) could be tested in future projects.

					Type / Number of Fish Captured				
Site	Deployment date/time	Recovery date/time	# traps set	Nominal Soak Time (h)	Coho Fry	Coho Fry 1+	Chinook Smolt	Slimy Sculpin	Dolly Varden
A	5 May, 12:45	6 May, 14:00	2	22.75	0	1	0	1	0
A	12 May, 12:15	13 May, 13:00	3	24.75	1	0	0	2	0
A	18 May, 12:45	19 May, 09:00	3	20.25	0	0	1	0	2
A	25 May, 12:30	26 May, 12:30	3	24.00	0	0	0	1	1
A	1 June, 12:45	2 June, 13:00	3	24.25	2	0	0	0	0
C	18 May, 18:15	19 May, 11:15	2	17.00	26	0	0	0	0
C	25 May, 15:00	26 May, 10:30	2	19.30	18	0	0	0	3
C	1 June, 13:45	2 June, 11:00	3	21.25	56	0	0	0	0
D	5 May, 14:45	6 May, 10:30	4	19.75	2	0	0	0	1
D	12 May, 14:00	13 May, 09:00	6	19.00	1	0	0	1	0
D	18 May, 21:00	19 May, 15:00	3	18.00	1	0	0	0	0
D	25 May, 19:30	26 May, 09:45	1	21.50	1	1	0	0	2
D	1 June, 16:45	2 June, 09:00	1	14.25	7	0	0	0	0
		Total Site A	14		3	1	1	4	3
		Total Site C	18		100	0	0	0	3
		Total Site D	2		12	1	0	1	3
		Grand Total	34		115	2	1	5	9

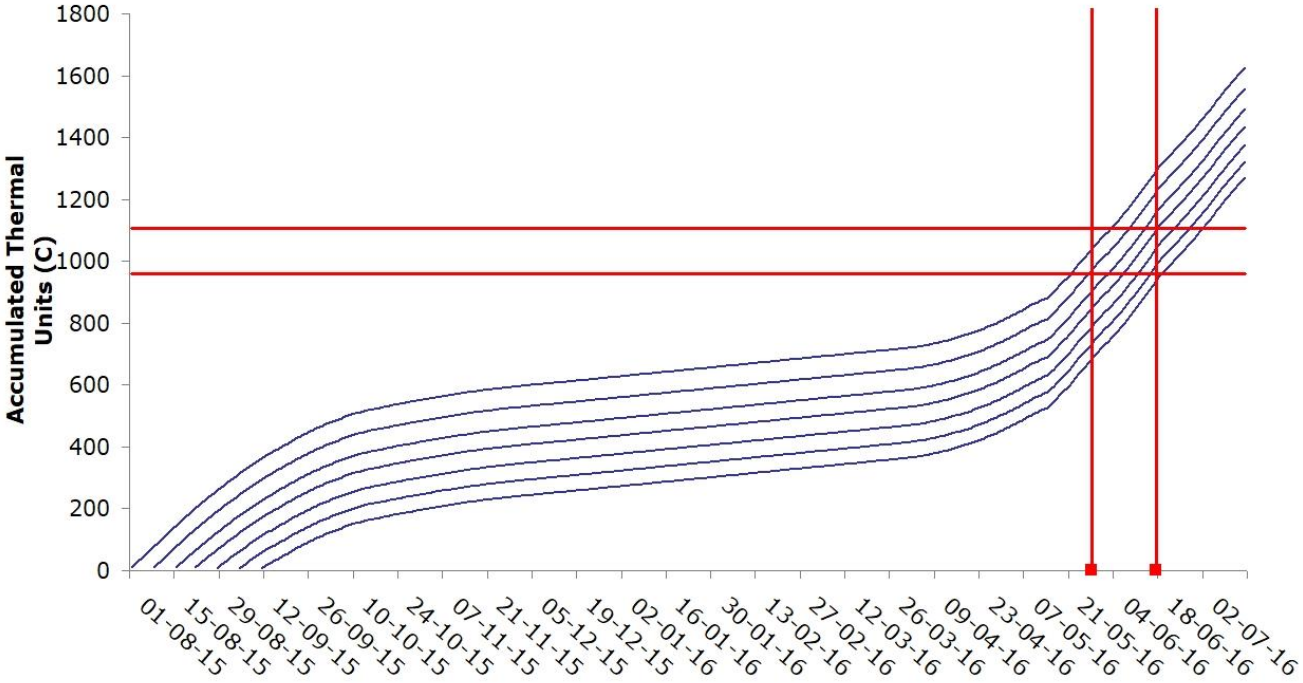


Figure E 1: Approximating Sockeye Emergence Based on Accumulated Thermal Units (ATU). Daily temperatures measured during weir operation (Figure B 1), assumed to be 1C in the winter, and interpolated for April, Oct, and Nov. Curves show accumulated thermal units for spawning events at weekly intervals from 1 Aug 2015 to 11 Sep 2015. Horizontal lines mark a plausible ATU range for sockeye emergence (960-1015 ATU, from DFO 2011), and vertical line show the corresponding time window for plausible fry emergence (28 May to 18 June).

Appendix F: Exploratory Data Analysis - Juveniles

Table F 1: Distribution of Fork Lengths for Juvenile Salmon Sampled in 2016.
Juvenile salmon were sampled in the Klukshu watershed from May to July, 2016. Sampling methods are summarized in Section 3. Sample sizes, dates, and field observations for the different gears are summarized in Appendix E. This table shows the medians, ranges, and percentiles of fork lengths (mm)by species, life stage, and location. Sockeye fry caught in the river and in the lake were substantially smaller on average than fry sampled at the lake outlet (30 and 28mm vs. 46mm). Sockeye smolts at the lake outlet were about 10cm on average (98mm). Coho fry were the most-encountered non-sockeye juveniles. Individual sampling events are detailed in Appendix E. Table F 4 summarizes sample statistics for the Sockeye samples (e.g. skewness).

Sample Group	**n**	Min	p10	p20	p30	p40	**Med**	p60	p70	p80	p90	Max
Sk - Total	**507**	24	28	29	30	30	**32**	42	75	95	103	119
Sk - River Fry	**202**	27	29	29	30	30	**30**	30	31	32	33	42
Sk - Lake Fry	**90**	24	26	27	27	28	**28**	29	29	30	32	35
Sk- Lake Outlet Fry	**48**	34	39	42	43	45	**46**	47	50	51	53	57
Sk - Lake Outlet Smolt	**167**	56	76	87	94	95	**98**	101	103	105	108	119
Chinook - Fry	**24**	32	33	34	34	35	**36**	37	38	38	40	43
Chinook - Smolt	**18**	33	34	58	70	74	**118**	121	132	135	137	142
Coho - Fry	**602**	31	36	37	38	39	**39**	40	40	41	41	75

Table F 2: Distribution of Weights for Juvenile Salmon Sampled in 2016.
Juvenile salmon were sampled in the Klukshu watershed from May to July, 2016. Sampling methods are summarized in Section 3. Sample sizes, dates, and field observations for the different gears are summarized in Appendix E. This table shows the medians, ranges, and percentiles of weight (g) by species, life stage, and location. Sockeye fry caught in the river and in the lake were substantially smaller on average than fry sampled at the lake outlet (0.21 and 0.17g vs. 1g). Sockeye smolts at the lake outlet were about 9g on average (8.92g). Coho fry were the most-encountered non-sockeye juveniles. Note that this table shows weights in g, but subsequent figures and regression fits retain the original mlg units for precision (1000 mlg = 1 g). Individual sampling events are detailed in Appendix E. Table F 4 summarizes sample statistics for the Sockeye samples (e.g. skewness).

Sample Group	**n**	Min	p10	p20	p30	p40	Med	p60	p70	p80	p90	Max
Sk - Total	**471**	0.1	0.2	0.2	0.2	0.2	**0.26**	0.4	5.2	8.4	10.0	15.8
Sk - River Fry	**202**	0.1	0.2	0.2	0.2	0.2	**0.21**	0.2	0.2	0.3	0.3	0.7
Sk - Lake Fry	**90**	0.1	0.1	0.1	0.2	0.2	**0.17**	0.2	0.2	0.2	0.3	0.4
Sk- Lake Outlet Fry	**19**	0.6	0.7	0.8	0.9	0.9	**1.01**	1.2	1.3	1.3	1.4	1.7
Sk - Lake Outlet Smolt	**160**	1.1	4.7	7.0	7.7	8.2	**8.92**	9.3	10.0	10.6	11.5	15.8
Chinook - Fry	**24**	0.3	0.3	0.3	0.3	0.3	**0.34**	0.4	0.4	0.4	0.4	0.5
Chinook - Smolt	**7**	0.3	0.3	0.3	0.3	6.3	**15.39**	16.1	16.8	17.4	17.7	17.8
Coho - Fry	**548**	0.2	0.4	0.5	0.5	0.5	**0.52**	0.5	0.6	0.6	0.6	4.2

Table F 3: Parameters for Length-Weight Relationships for Juvenile Sockeye Sampled in 2016.
Length-weight relationships for juvenile sockeye were fitted using a log-linear regression, where Wt_mlg = exp(Intercept + Slope * Length_mm). Section 5.3 describes the methods. 1000 mlg =1 g. Figure F 1 shows the distribution of lengths and weights. Percentile values are listed in Table F 1 and Table F 2. Regression fits are plotted in Figure F 2. The adjusted R^2 describes how much of the differences between observations in the sample are explained by the regression line (i.e. the proportion of observed variance). This measure or predictive value is high for all the alternative fits, but highest when combining all fry samples (larger sample size!).

Sample Group	Intercept	Slope	Adj. R^2
All Fry	2.675	0.089	0.919
River Fry	2.421	0.098	0.805
Lake Fry	1.958	0.113	0.746
Lake Outlet Fry	4.252	0.056	0.879
Lake Outlet Smolt	6.095	0.030	0.719

Table F 4: Sample Statistics for Fork Length and Weight of Juvenile Sockeye Sampled in 2016.
SD is the standard deviation. S and K are skewness and kurtosis, divided by SD. Values of S,K > 1.96 indicate a large difference from a normal distribution). The only sample group flagged by these diagnostics is fork length of River Fry.

	n	Mean	Median	SD	Skewness	S	Kurtosis	K
Fork Length (mm)								
River Fry	202	30.65	30	2.45	1.82	0.74	7.56	**3.09**
Lake Fry	90	28.63	28	2.21	0.62	0.28	3.34	1.52
Lake Outlet Fry	48	46.25	45.5	5.44	0.00	0.00	2.32	0.43
Lake Outlet Smolts	167	95.63	98	12.18	-0.91	-0.07	3.50	0.29
Total	***507***							
Smolts – Age 0	7	70.14	74	8.61	-0.83	-0.10	2.02	0.23
Smolts – Age 1	121	97.56	98	8.90	-0.83	-0.09	3.78	0.42
Smolts – Age 2	5	109.60	112	7.73	-0.24	-0.03	1.84	0.24
Weight (mlg)								
River Fry	202	234.45	212.5	77.75	2.57	0.03	11.62	0.15
Lake Fry	90	190.66	172.5	60.32	1.27	0.02	4.39	0.07
Lake Outlet Fry	19	1069.47	1010	302.83	0.24	0.00	2.03	0.01
Lake Outlet Smolts	160	8620.03	8915	2685.45	-0.32	0.00	3.52	0.00
Total	***471***							
Smolts – Age 0	7	3516.57	3730	1271.40	-0.10	0.00	2.01	0.00
Smolts – Age 1	121	8727.84	8810	2223.41	-0.40	0.00	3.89	0.00
Smolts – Age 2	5	12228.00	11480	2562.64	0.37	0.00	1.82	0.00

Table F 5: Pairwise Test of Differences in Fork Length (mm) between Lake and River Sockeye Fry.
To test the difference in average fork length, we calculated the p-value for Welch's t-test, then replicated the test for 1000s subsamples of 90% of the observations. Values in the table show the proportion of subsample tests with a p-value ≤ 0.05, so that a value of 99 means that 990 of 1000 subsample pairings had a significant difference. All the bootstrap test showed a significant difference. On average, River Fry were about 2mm larger, with a 95% confidence interval of +/- 0.5mm.

Statistic	Value
Mean Difference	2mm
p-value	5.4e-11
Confidence interval for difference between samples	1.4-2.6mm
% significant p-values in bootstrap	100

Table F 6: Pairwise Tests of Size Differences between Age Classes of Lake Outlet Sockeye Smolts.
To test the difference in average fork length (mm) and average weight (g), we calculated the p-value for Welch's t-test, then replicated the test for 1000s subsamples of 90% of the observations. Values in the table show the proportion of subsample tests with a p-value ≤ 0.05, so that a value of 99 means that 990 of 1000 subsample pairings had a significant difference. Smolts classified as Age 0 were significantly smaller than smolts classified as Age 2 (19 to 35mm shorter fork length; 4.0 to 6.4g lighter), with 100% of the bootstrap tests producing a p-value <0.05, despite the small sample size of 7 fish for Age 0 smolts (Table F 4). Using all 5 smolts classified as Age 2, the t-test also indicates as significant size difference between smolts classified as Age1 and those classified as Age 2 (3 to 22mm longer, 0.3 to 6.7g heavier), but this is not confirmed by the majority of bootstrap tests. Given the small sample size, each bootstrap test drops one of the observations from the Age 2 sample, and the difference between Age 1 and Age 2 smolts disappears. Figure F 5 shows that the value ranges mostly overlap. In summary, the observed size differences between smolts classified as Age 0 and those classified as Age 1 supports the results of the scale readings. However, the number of Age 2 smolts encountered was too low to draw the same conclusion Age 1 and Age 2 smolts, given the range of observed sizes and small sample size for Age 2s.

	Fork Length (mm)		Weight (g)	
Statistic	Age 0 vs Age1	Age 1 vs Age 2	Age 0 vs Age1	Age 1 vs Age 2
Mean Difference	27mm	12mm	5.2g	3.5g
p-value	9.6e-5	0.0233	6.5e-6	0.0367
Confidence interval for difference between samples	19-35mm	3-22mm	4.0-6.4g	0.3-6.7g
% significant p-values in bootstrap	100	40	100	19

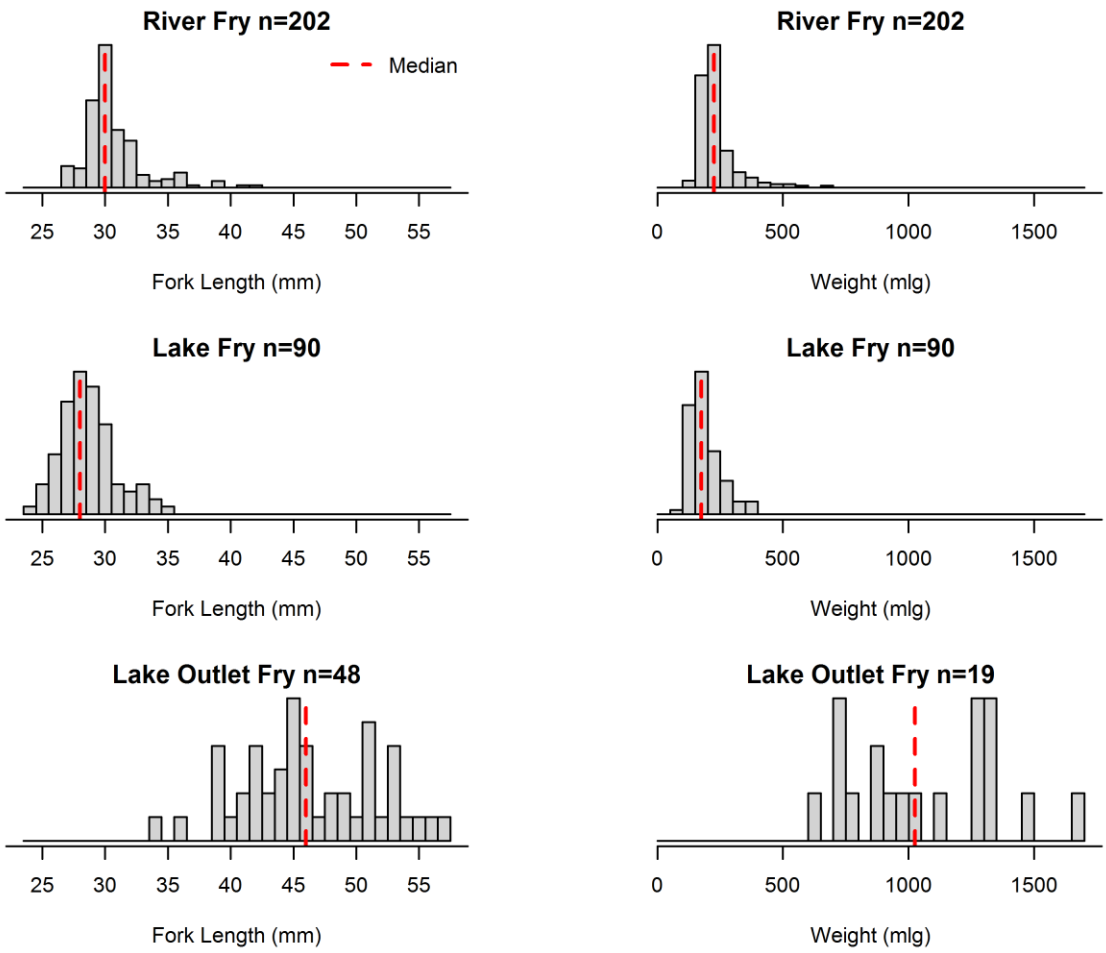


Figure F 1: Distribution of Fork Length and Weight for Klukshu Sockeye Fry Sampled in 2016.
Distributions of fork length (left panels) and weight (right panels) for 3 sample groups of Sockeye Fry. Each panel shows the median for that sample group and a density histogram, such that the area corresponds to number of observations in a bin. Individual sampling events are detailed in Appendix E. River fry were larger than lake fry (also see Table F 1 and Table F 2). Table F 5 shows a formal test of size difference between lake and river fry. Note that lake outlet fry were much larger than either river or lake fry, but were sampled much later in the season (30 June and 8 July) than the lake fry (13 May to 2 June) and river fry (12 May to 1 June). Figure F 6 shows the range of observations by date. Individual sampling events are detailed in Appendix E.

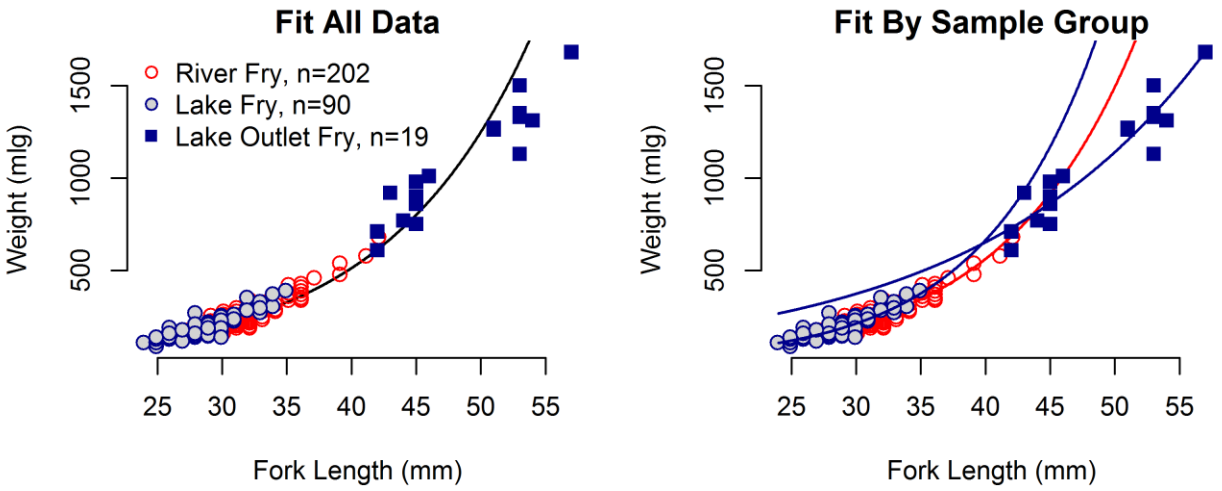


Figure F 2: Length-Weight Relationships for Klukshu Sockeye Fry Sampled in 2016.
Points show all records for which both length and weight measurements are available. Points are slightly offset on the horizontal axis, because sample values are integers and points would be masked otherwise. Lines show log-linear regression fits as described in Table F 3, which lists parameter estimates. Note that lake outlet fry were much larger than either river or lake fry, but were sampled much later in the season (30 June and 8 July) than the lake fry (13 May to 2 June) and river fry (12 May to 1 June). Figure F 6 shows the range of observations by date. Individual sampling events are detailed in Appendix E.

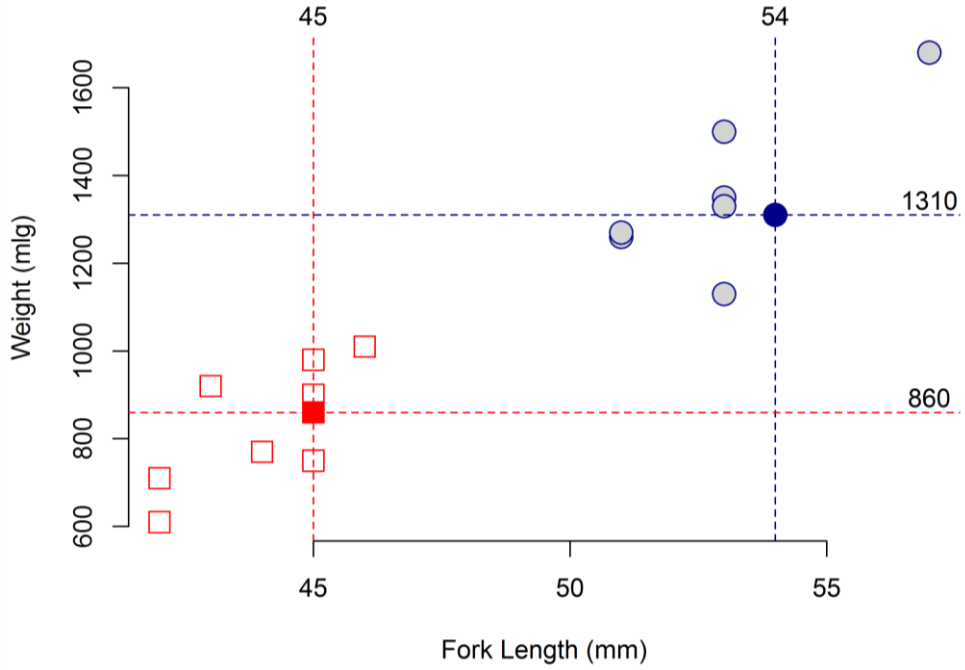


Figure F 3: Length-Weight Clusters of Sockeye Fry Sample on 8 July 2016 at Klukshu Lake outlet.
The Lake outlet fry sample shows two clusters, which were confirmed with a statistical partitioning test (PAM, Section 5.3). Note that only a few samples in this subset have both length and weight observations. Of the 64 fry sampled, 48 have fork-length measurements, and 19 have both fork length and weight measures. More specifically, there are 8 records with length measurements falling between the 2 clusters identified in this plot (see Figure F 1), but corresponding weight measurements are not available. Therefore the observed clustering, while quite distinct, may be simply an artefact of a small sample with incomplete records. Individual sampling events are detailed in Appendix E.

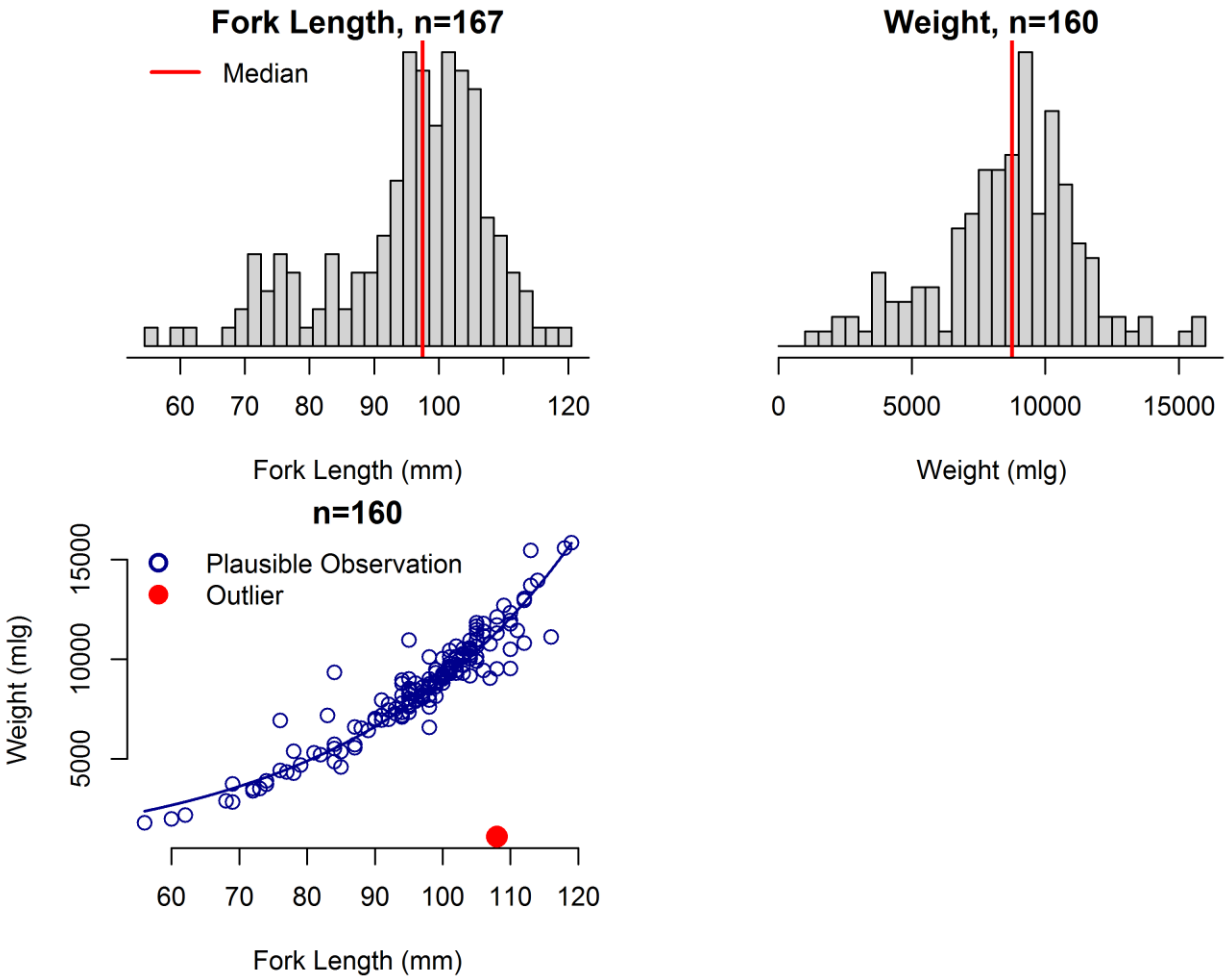


Figure F 4: Fork Length, Weight, and Length-Weight Relationship for Sockeye Smolts Sampled in 2016. Top row shows distributions of fork length (mm) and weight (mlg) for Sockeye Smolts. Each panel shows the median for that sample group and a density histogram, such that the area corresponds to number of observations in a bin. Bottom panel shows the length-weight scatterplot. Points are all records for which both length and weight measurements are available. Points are slightly offset on the horizontal axis, because sample values are integers and points would be masked otherwise. The line shows a log-linear regression fits as described in Table F 3, which lists parameter estimates. Individual sampling events are detailed in Appendix E. The scatterplot highlights 1 unusual record, which is within plausible range on weight and length separately, but in the scatterplot falls far from all the other observations. Given the large overall sample size, the effect of this outlier on sample summaries and regression fit were considered negligible.

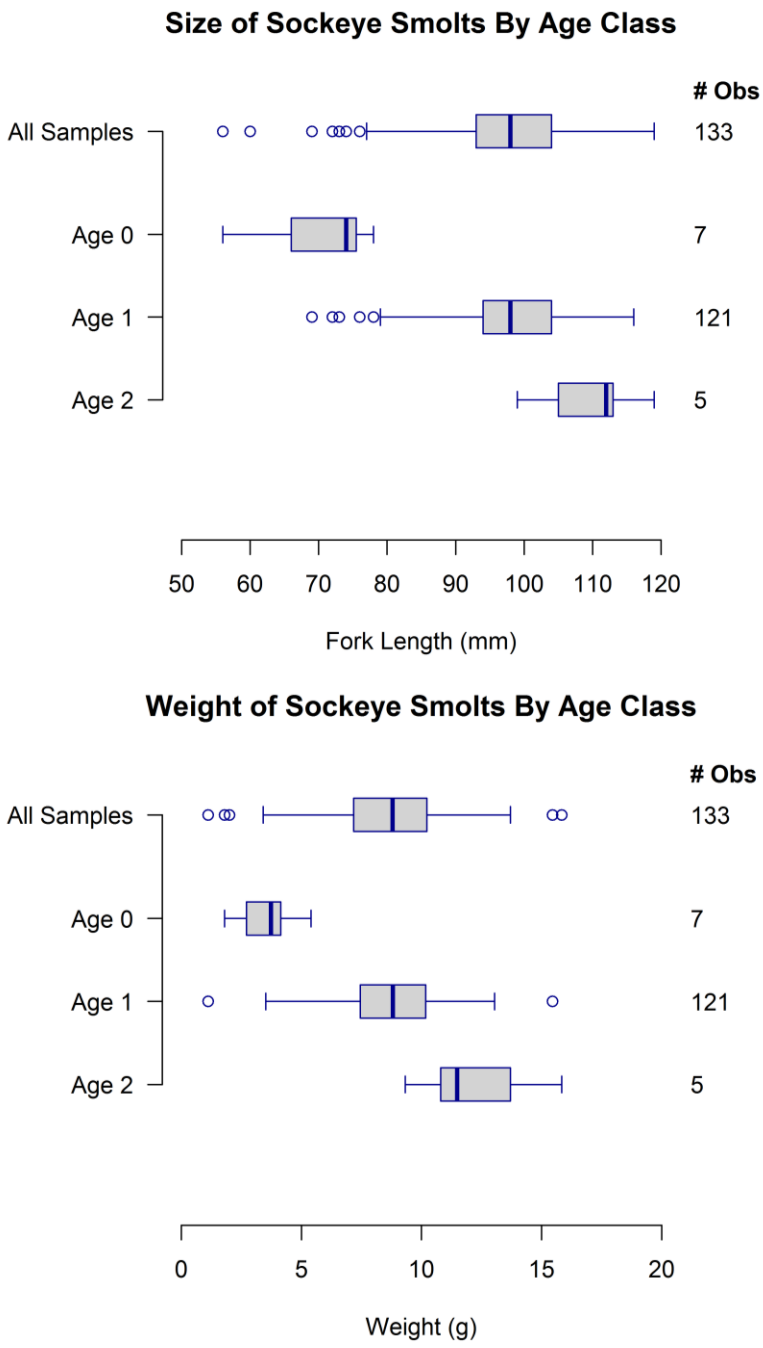


Figure F 5: Fork Length and Weight by Age Class for Klukshu Sockeye Smolts Sampled in 2016. Good-quality scale reading were possible for most of the Sockeye Smolts sampled the outlet of Klukshu Lake (133/167, 80%). Overall, length and weight measures were consistent with the age readings, and median size increased with age. However, the ranges overlap, indicating either large variability in early sockeye growth, observation error (either in size measure or age class assignment), or a combination of both.

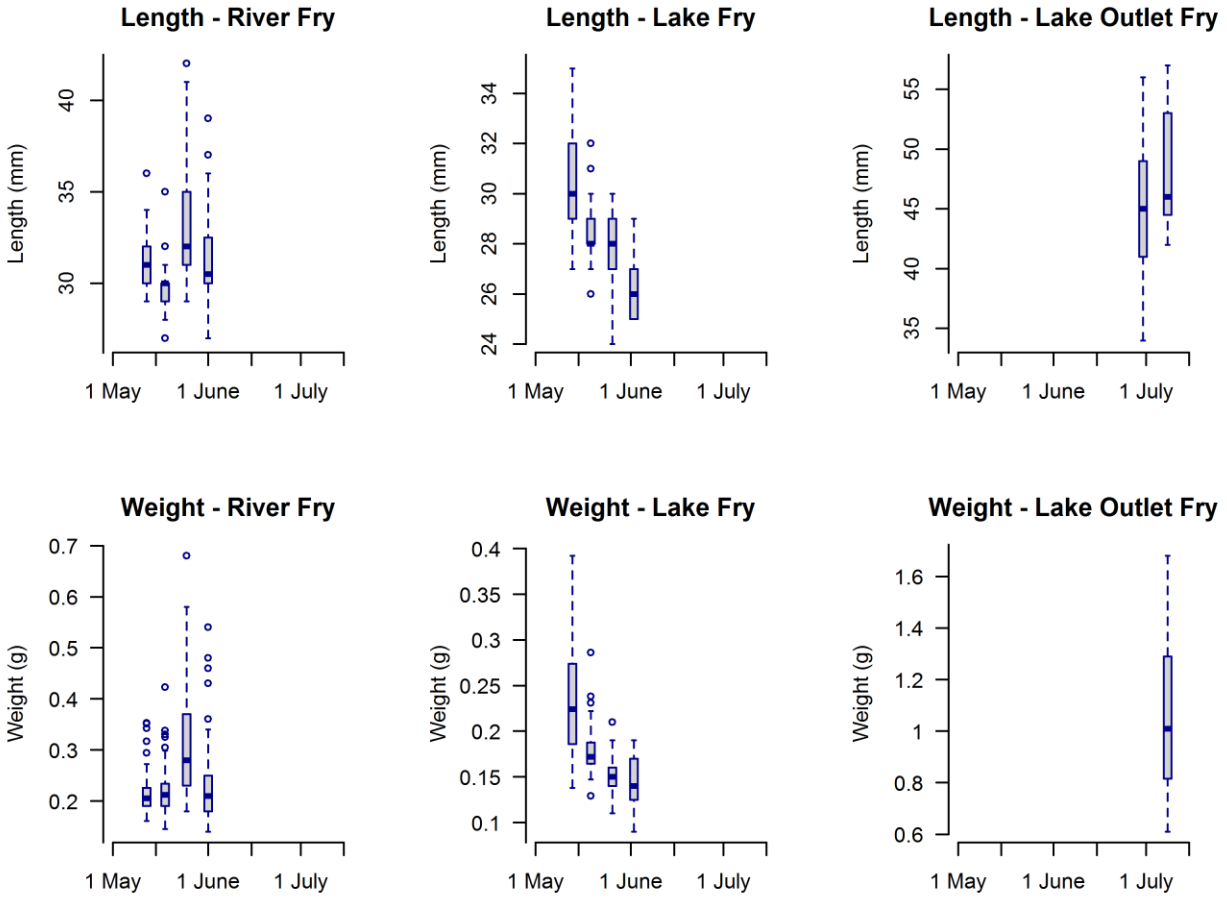


Figure F 6: Size and Weight Distribution of Sockeye Fry by Sample Date.
This figure shows the same samples as Figure F 1, but separated by date. Sample sizes by date are listed in Appendix E. River fry were similar size in over time, but lake fry caught later were smaller. Note that plot axes vary across sample groups, because each plot is scaled to emphasize the within-sample variation over time.

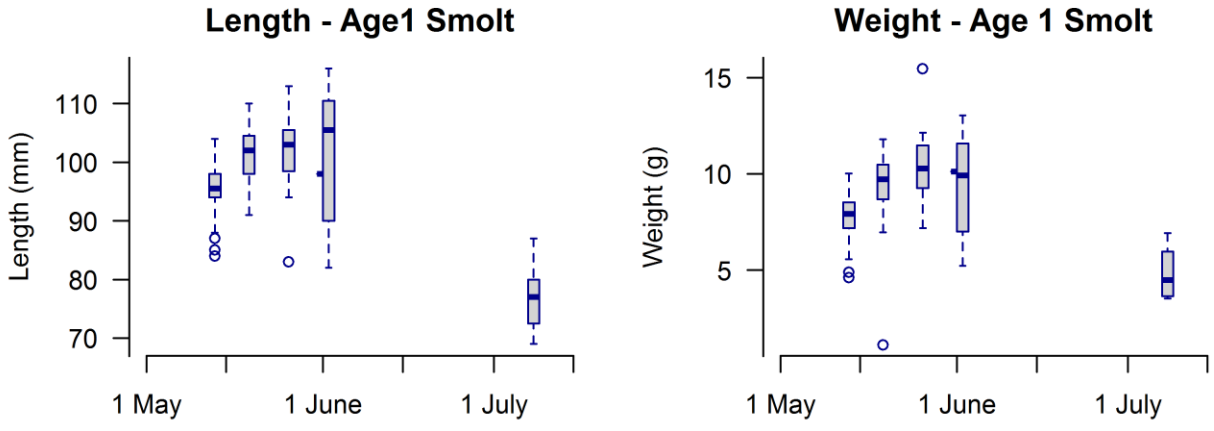


Figure F 7: Size and Weight Distribution of Age-1 Sockeye Smolts by Sample Date.
This figure shows the same samples as the age-1 bars in Figure F 5, but separated by date. Sample sizes by date are listed in Appendix E. Size of age-1 smolts increased from mid-May to early June, but smolts caught in early July were much smaller.

Appendix G: Exploratory Data Analysis - Adults

Table G 1: Summary of Fork Length (mm) For Adult Sockeye Sampled in 2016.
Adult samples at the weir were split into early (W28-W33), mix (W34), and late (W35-W41) migrants. SD is the standard deviation. S and K are skewness and kurtosis, divided by SD. Values of S,K > 1.96 show indicate a large difference from a normal distribution. Fork lengths not available for 39 of 1,063 adults sampled (3.7%). Note the large standard deviation in the sample of male lake spawner fork lengths.

	n(FL)	Mean	Median	SD	Skewness	S	Kurtosis	K
Females								
Weir - Early	127	559	560	22.08	-0.30	-0.01	4.28	0.19
Weir - Mix	45	567	570	21.65	-0.46	-0.02	4.21	0.19
Weir - Late	237	563	565	25.66	-0.49	-0.02	3.09	0.12
River	47	571	575	23.39	-0.12	-0.01	2.60	0.11
Lake	48	566	569	32.44	0.17	0.01	3.58	0.11
	504							
Males								
Weir - Early	205	594	600	30.02	-0.65	-0.02	4.96	0.17
Weir - Mix	53	600	600	31.58	-0.47	-0.015	4.44	0.14
Weir - Late	149	609	610	41.96	1.53	0.04	15.63	0.37
River	57	625	626	30.27	-0.79	-0.03	5.45	0.18
Lake	55	608	620	**64.27**	-2.21	-0.03	8.04	0.13
	519							
Females –Tagged Only								
Weir Early Tag	54	559	560	22.31	0.196	0.01	2.91	0.13
Weir Mix Tag	19	569	570	15.32	-0.455	-0.03	2.44	0.16
Weir Late Tag	74	567	568	25.11	-0.652	-0.03	2.85	0.11
	147							
Males – Tagged Only								
Weir Early Tag	13	588	600	28.76	-1.53	-0.05	4.19	0.15
Weir Mix Tag	0	-	-	-	-	-	-	-
Weir Late Tag	1	600	600	-	-	-	-	-
	14							

Table G 2: Pairwise Test of Differences in Fork Length (mm) for Adult Sockeye Samples.
Adult samples at the weir were split into early (W28-W33), mix (W34), and late (W35-W41) migrants. For each pair of samples, we calculated the p-value for Welch's t-test for 1000s subsamples of 90% of the observations (Section . Values in the table show the proportion of subsample tests with a p-value ≤ 0.05, so that a value of 99 means that 990 of 1000 subsample pairings had a significant difference. Among the female samples, the only persistently significant difference was between the early weir samples (mean=559mm) and the river spawners (571mm). Among the male samples, early weir samples, late weir samples, and river spawners were all clearly different from each other (100% of the bootstrapped sample comparisons were significantly different), but the fork length of the lake samples was much more variable (larger standard deviation in Table G 1), so that most of the pairwise test showed no significant differences.

Females

	Weir Late	River	Lake
Weir Early	8	99	2
Weir Late		36	0
River			0

Males

	Weir Late	River	Lake
Weir Early	100	100	12
Weir Late		100	0
River			9

Table G 3: Overview of % Females in Samples of Adult Sockeye at Klukshu Weir in 2016.
Sex was recorded for all 820 fish tags sampled at the weir. 2 overall averages are listed (Section 5.2). Note that the bottom table uses raw totals for the timing groups. Sex ratio varied substantially over time from a minimum of 27% females in week 29 to maximum of 76% females in week 40, and a general increase as the season progressed. Table G 4 shows ratios based on alternative weightings and statistical test of difference in sex ratio between early and late migrants. Figure G 2 shows the weekly pattern and regression fit.

Stat Week	n	Female	Male	Unk	%Fem
28	1	0	1	0	0%
29	79	21	58	0	27%
30	9	3	6	0	33%
31	73	27	46	0	37%
32	130	55	75	0	42%
33	43	23	20	0	53%
34	98	45	53	0	46%
35	111	67	44	0	60%
36	70	43	27	0	61%
37	59	42	17	0	71%
38	70	40	30	0	57%
39	41	18	23	0	44%
40	34	26	8	0	76%
41	2	2	0	0	100%
Total	820	412	408	0	

Wt Avg (run)	**58%**
Raw Avg	51%

Timing Group	n	Female	Male	Unk	%Fem
Early	335	129	206	0	39%
Mixed	98	45	53	0	46%
Late	387	238	149	0	61%
Total	820	412	408	0	

Table G 4: Chi-Squared Test for Sex Ratio of Adult Sockeye at Klukshu Weir in 2016.
Sex ratio data from Table G 3 were grouped as early migrants (W28-W33) or late migrants (W35-W41). This leaves out 98 samples, because they passed the weir during the "mixed" week 34. Pearson's chi-squared test without continuity correction was applied to all 722 remaining observations using the R function prop.test(), and replicated 1,000 times on random subsamples of 90% of the data. Tests were replicated using proportions adjusted based on weighted average of weekly proportion using run size (see Section 5.2). Both versions of the test show essentially the same result: the sample proportions are very different, with a p value smaller than 0.05 in all of the bootstrap tests (100%).

Raw Ratios

Timing Group	F	M	% F	p.value	percent p.values ≤0.05	95% Conf Int. (Diff in Prop)
Early	129	206	39%	7.2e-10	100	Early run has between 16% and
Late	238	149	61%			30% less Females)

Weighted within Timing Group By Run Size

Timing Group	F	M	% F	p.value	percent p.values ≤0.05	95% Conf Int. (Diff in Prop)
Early	150	185	45%	1.8e-06	100	Early run has between 11% and
Late	242	145	63%			25% less Females)

Table G 5: Overview of % Females in Spawning Site Samples of Adult Sockeye.
Note that the sampling objective for spawning grounds was to collect roughly equal numbers of DNA samples from males and females, so the observed % females does not reflect actual sex ratio of the spawning population.

Sample Group	n	n M/F	Female	Male	Unk	%Fem
River	110	110	53	57	0	48%
Lake	136	112	51	61	24	46%
Total	246	246	104	118	0	

Table G 6: Overview of Age Composition of Adult <u>Female</u> Sockeye at Klukshu Weir in 2016.
Scales were sampled and read for most of the 412 females sampled at the weir. 2 overall averages are listed (Section 5.2). Note that the bottom table uses raw totals for the timing groups. Age composition of females varied very little, with most females returning at age 5.2. Table G 8 shows ratios based on alternative weightings and statistical test of difference in age composition between early and late migrating females. Figure G 3 shows the weekly pattern and regression fit. Note that of the 31 females assigned to "Other" age class, 18 were partial scale readings (e.g. 3M)

Stat Week	n	4.2	5.2	Other	NA	Perc 4.2
28	0	0	0	0	0	-
29	21	0	21	0	0	0.0%
30	3	0	2	0	1	0.0%
31	27	0	24	1	2	0.0%
32	55	2	51	2	0	3.6%
33	23	1	21	1	0	4.3%
34	45	1	37	6	1	2.3%
35	67	1	61	3	2	1.5%
36	43	3	34	6	0	7.0%
37	42	3	31	6	2	7.5%
38	40	1	36	3	0	2.5%
39	18	0	15	1	2	0.0%
40	26	0	25	1	0	0.0%
41	2	0	1	1	0	0.0%
Total	412	12	359	31	10	
				Wt Avg (run)		**3.8%**
				Raw Avg		2.2%

Timing Group	n	4.2	5.2	Other	NA	Perc 4.2
Early	129	3	119	4	3	2.4%
Mixed	45	1	37	6	1	2.3%
Late	238	8	203	21	6	3.5%
Total	412	12	359	31	10	

Table G 7: Overview of Age Composition in Samples of Adult Male Sockeye at Klukshu Weir in 2016. Scales were sampled and read for most of the 408 males sampled at the weir. 2 overall averages are listed (Section 5.2). Note that the bottom table uses raw totals for the timing groups. Age composition of males varied throughout the season, with some increase in later weeks, but overall most males returned at age 5.2. Table G 8 shows ratios based on alternative weightings and statistical test of difference in age composition between early and late migrating females. Figure G 3 shows the weekly pattern and regression fit. Note that of the 40 males assigned to "Other" age class, 36 were partial scale readings (e.g. 3M)

Stat Week	n	4.2	5.2	Other	NA	Perc 4.2
28	1	0	1	0	0	0.0%
29	58	9	43	3	3	16.4%
30	6	0	5	1	0	0.0%
31	46	3	40	2	1	6.7%
32	75	4	65	6	0	5.3%
33	20	2	15	2	1	10.5%
34	53	6	40	7	0	11.3%
35	44	5	32	7	0	11.4%
36	27	7	19	0	1	26.9%
37	17	2	12	3	0	11.8%
38	30	4	21	3	2	14.3%
39	23	4	13	6	0	17.4%
40	8	5	3	0	0	62.5%
41	0	0	0	0	0	-
Total	408	51	309	40	8	
				Wt Avg (run)		**15.7%**
				Raw Avg		15.0%

Timing Group	n	4.2	5.2	Other	NA	Perc 4.2
Early	206	18	169	14	5	9.0%
Mixed	53	6	40	7	0	11.3%
Late	149	27	100	19	3	18.5%
Total	408	51	309	40	8	

Table G 8: Chi-Squared Test for Age Composition of Adult Sockeye at Klukshu Weir in 2016.
Age data from Table G 6 and Table G 7 were subset to focus only on the two main age classes (Gilbert-Rich 4.2 and 5.2), which were split into male and female samples, and further grouped as early migrants (W28-W33) or late migrants (W35-W41). This leaves out 94 of the 408 male samples and 79 of the 412 female samples from the weir, because they passed the weir during the "mixed" week 34, or scales couldn't be fully read, or individuals fell into one of the rarer age class. Pearson's chi-squared test without continuity correction was applied to the remaining observations using the R function *prop.test()*, and replicated 1,000 times on random subsamples of 90% the data. Tests were replicated using proportions adjusted based on weighted average of weekly proportion using run size (see Section 5.2). Both versions of the test show essentially the same result: age composition does not differ between early and late migrating females, but is significantly different for males, with a p value smaller than 0.05 in most of the bootstrap tests (94.3%-99.7%).

Females - Raw Ratios

Timing	Gilbert-Rich Age Class				percent p.values	
Group	4.2	5.2	% 4.2	p.value	≤0.05	95% Conf Int. (Diff in Prop)
Early	3	119	2.5%	0.51	0	No difference in % 4.2 between
Late	8	203	3.8%			early and late migrating females

Females – Weighted within a timing group by run size

Timing	Gilbert-Rich Age Class				percent p.values	
Group	4.2	5.2	% 4.2	p.value	≤0.05	95% Conf Int. (Diff in Prop)
Early	4	118	3.3%	0.65	0	No difference in % 4.2 between
Late	9	202	4.3%			early and late migrating females

Males - Raw Ratios

Timing	Gilbert-Rich Age Class				percent p.values	
Group	4.2	5.2	% 4.2	p.value	≤0.05	95% Conf Int. (Diff in Prop)
Early	18	169	9.6%	0.004	99.7	Early run has between 3% and
Late	27	100	21.3%			20% fewer age 4.2.

Males – Weighted within a timing group by run size

Timing	Gilbert-Rich Age Class				percent p.values	
Group	4.2	5.2	% 4.2	p.value	≤0.05	95% Conf Int. (Diff in Prop)
Early	15	172	8%	0.007	94.3	Early run has between 2% and
Late	23	104	18%			18% fewer age 4.2.

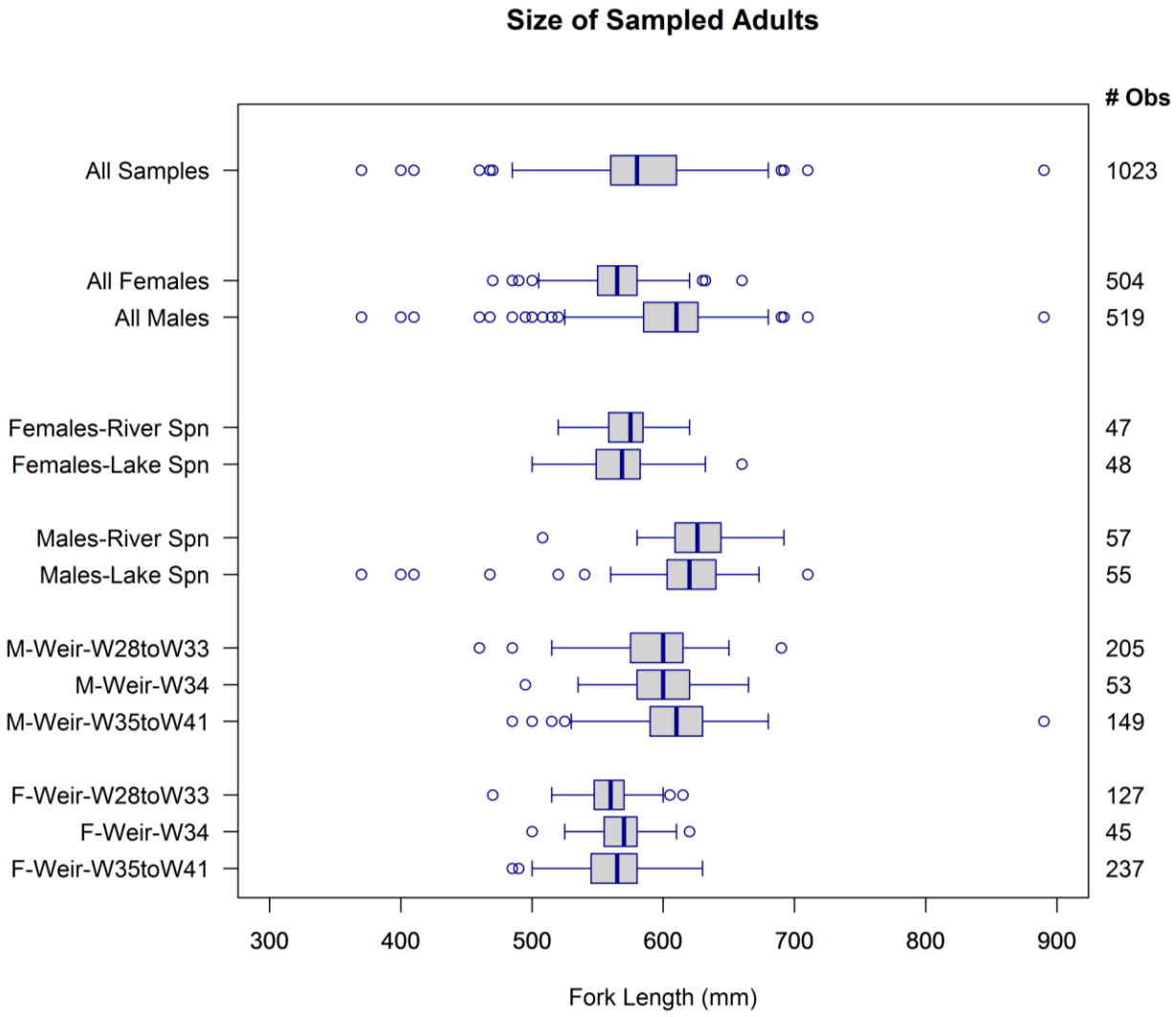


Figure G 1: Distribution of Fork Lengths for Adult Sockeye Samples.
The plot shows fork lengths (mm) for various subsets of the adult samples. Sampling locations are described in Section 2. In each boxplot, the thick vertical line marks the sample median, the grey box spans the interval from lower to the upper quarter if observations (25th and 75th percentiles). The circles show extreme values. Males were consistently larger than females. River spawners were larger than lake spawners, for both males and females. Males sampled at the weir were larger later in the season.

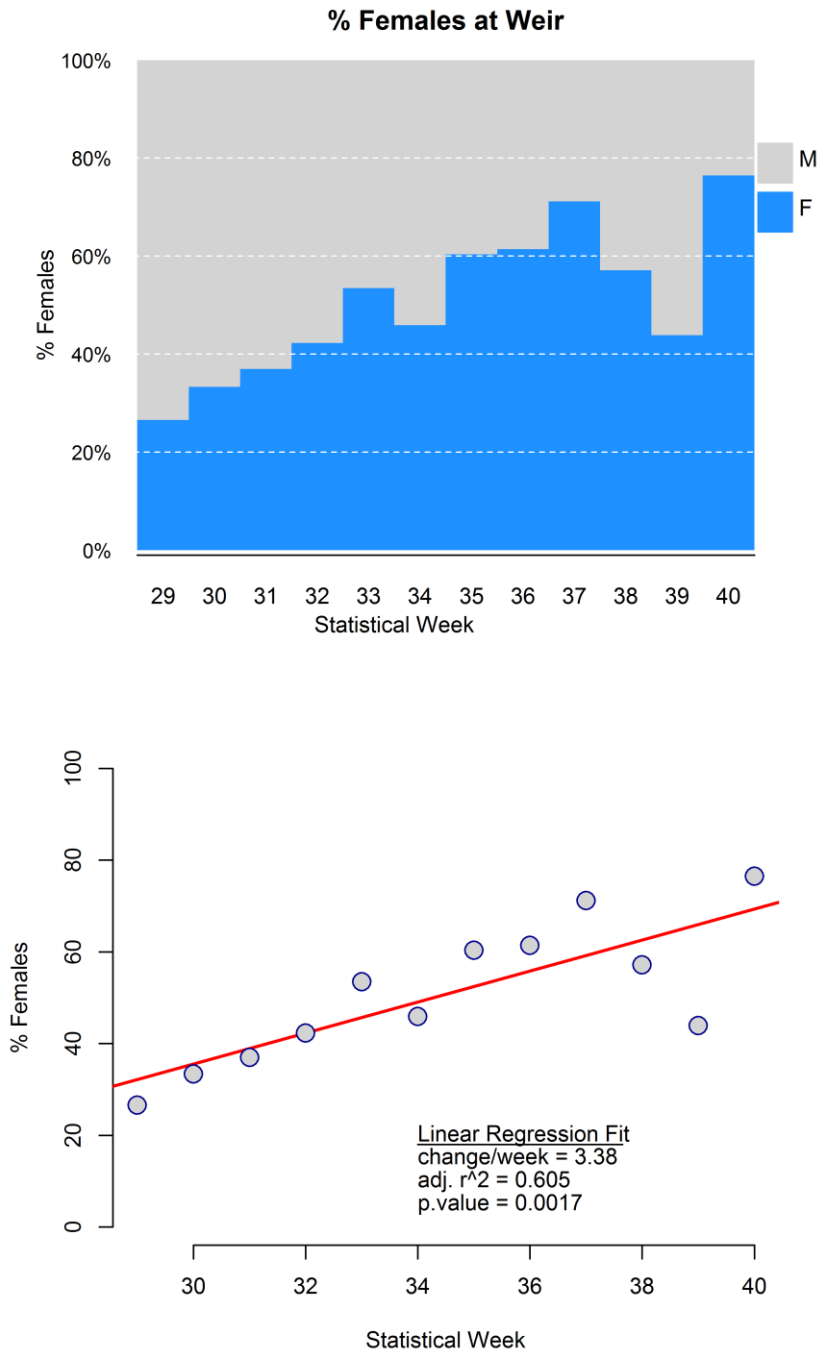


Figure G 2: Pattern in Weekly % Females in Samples of Adult Sockeye at Klukshu Weir in 2016.
Table G 3 describes the sample and lists the weekly observations, and Table G 4 summarizes a chi-squared test for difference in sex ratio between early and late migrants. The % females in the weir sample increased steadily throughout the season from about 30% in early July to about 70% in early September. It drops after that, and picks up again in week 40 (26/ females out of 40 sampled fish, 76%).

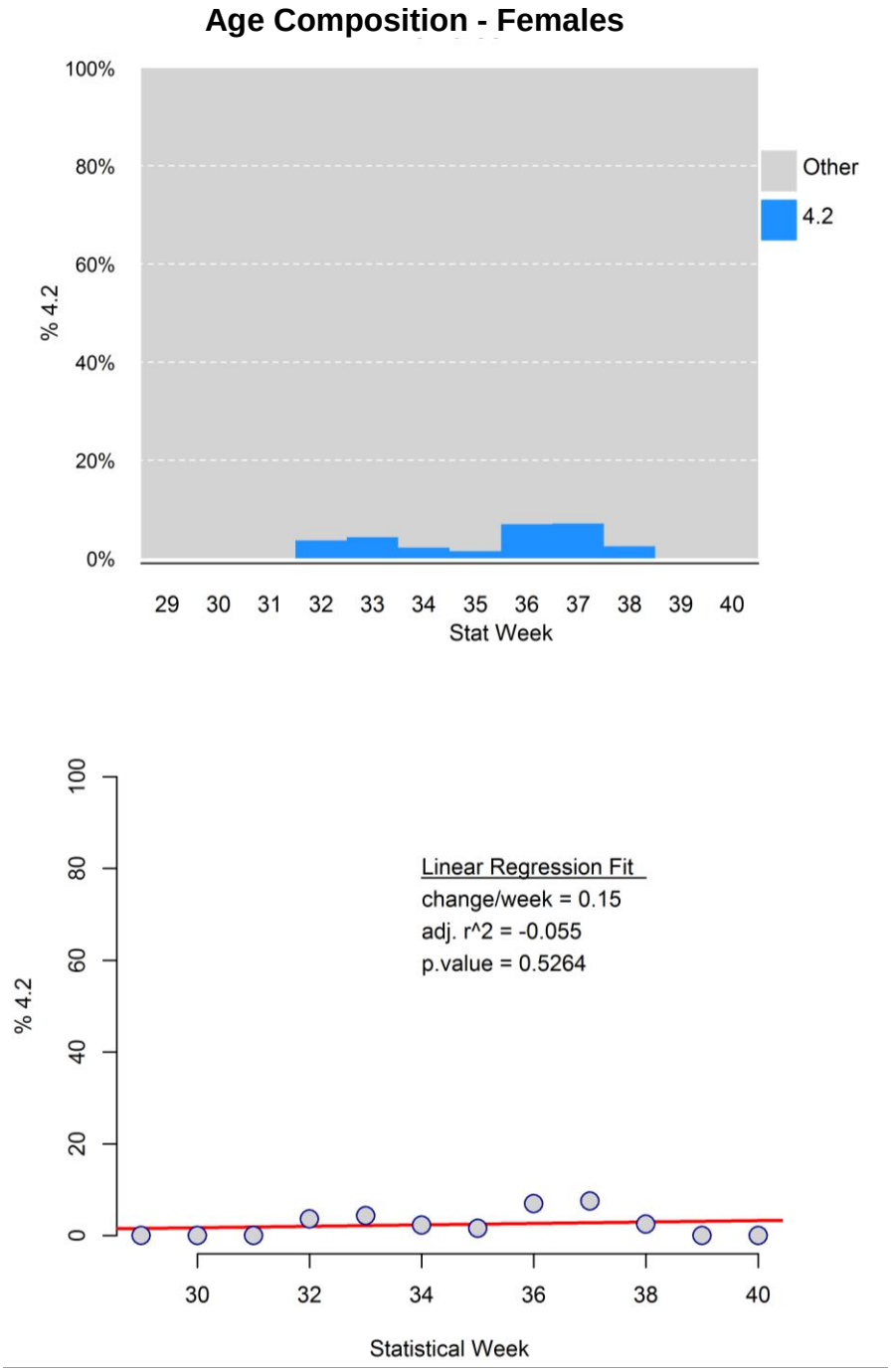


Figure G 3: Pattern in Weekly Age Composition in Samples of Female Sockeye at Klukshu Weir in 2016. Table G 6 describes the sample and lists the weekly observations. Table G 8 summarizes chi-squared tests for difference between early and late migrants. The proportion of age 4.2 females is very small and doesn't change throughout the season (i.e. regression line is flat, with very large p-value, both consistent with the results in Table G 8).

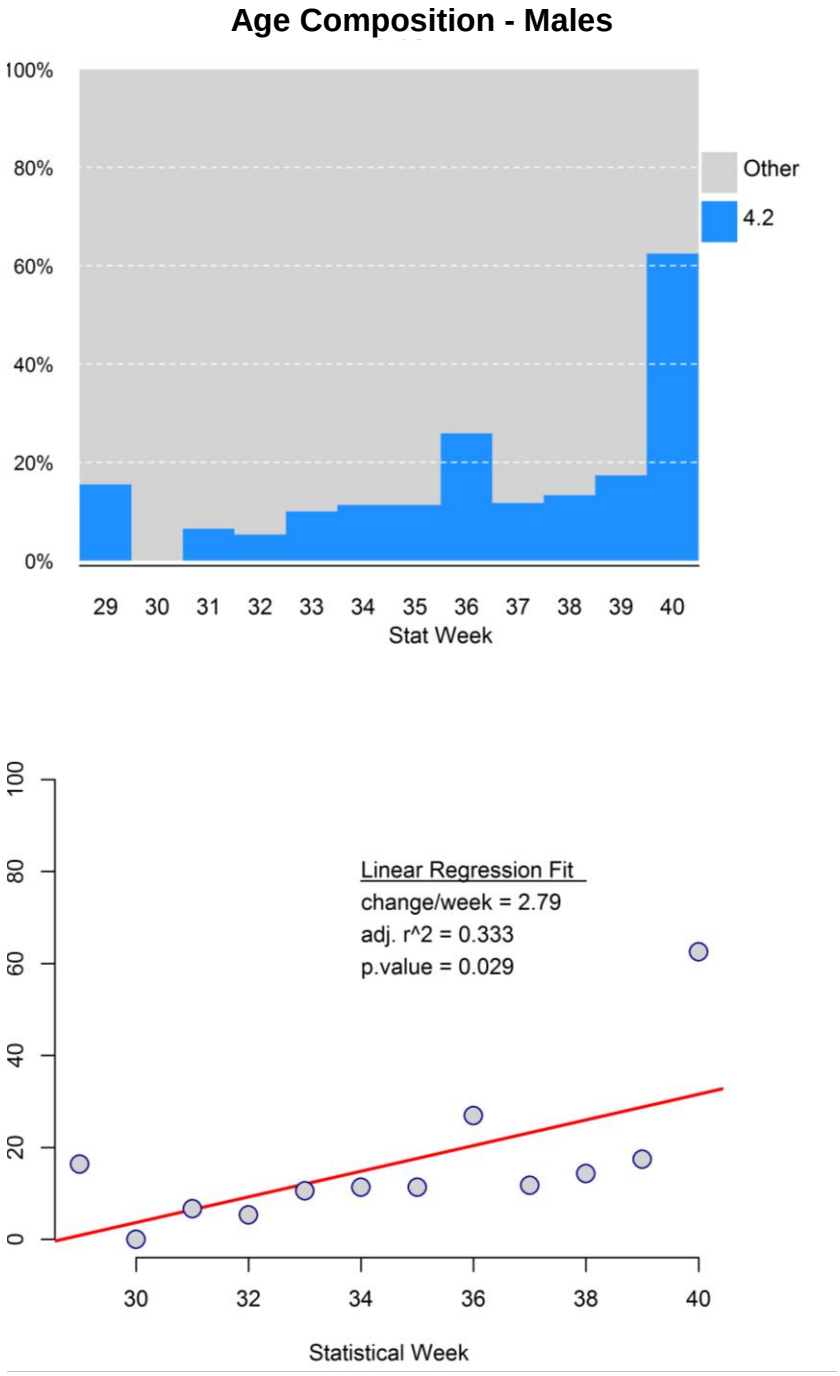


Figure G 4: Pattern in Weekly Age Composition in Samples of Male Sockeye at Klukshu Weir in 2016. Table G 7describes the sample and lists the weekly observations. Table G 8 summarizes chi-squared tests for difference between early and late migrants. The proportion of age 4.2 fish is larger for males than for females, and male 4.2s become more prevalent later in the season. The simple regression line shows an increase, but with a very low R^2 value, which indicates that the regression fit only explains about 30% of the observed variation in age composition. Part of the issue is the very large % 4.2 in week 40, which pulls the regression line up, and increases the variance estimate, but is based on a very small sample size of 8 fish (Table G 7).
The difference is more pronounced when observations are grouped by timing group, as shown in Table G 8.

Appendix H: Radio Telemetry – Additional Summaries

Table H 1: Overview of Final Destination for Adult Female Sockeye Tagged at Klukshu Weir in 2016. Radio tags were applied to a subset of fish sampled at the weir, with proportional focus on early migrating fish and a preference for tagging females. This table summarizes female samples only. Samples with successful fate include only those where a final spawning destination could be identified based on stationary radio towers and a helicopter overflight. 3 overall averages are listed (Section 5.2). Refer to Table 3 for a summary of the observed movement patterns, and to Appendix J for a description of the details for each tag. The proportion of tagged fish that were assigned a river fate varied substantially between statistical weeks. Table H 3 summarizes formal tests of differences in proportion of tags with river fate.

Stat Week	Tags	River	Lake	Unknown	Perc River
28	-	-	-	-	-
29	14	8	3	3	73
30	3	3	0	0	100
31	19	9	10	0	47
32	9	4	4	1	50
33	11	4	6	1	40
34	19	5	12	2	29
35	18	4	13	1	24
36	14	1	13	0	7
37	11	1	10	0	9
38	12	3	9	0	25
39	10	2	7	1	22
40	9	5	3	1	63
41	1	1	0	0	100
Total	***150***	***50***	***90***	***10***	

Wt Avg (run)	**25**
Wt Avg (#tags)	36
Raw Avg	45

Timing Group	Tags	River	Lake	Unknown	Perc River
Early	56	28	23	5	55
Mixed	19	5	12	2	29
Late	75	17	55	3	24
Total	***150***	***50***	***90***	***10***	

Table H 2: Overview of Final Destination for Adult Female Sockeye Tagged with New Tags.
Same as Table H 1, except excluding redeployed tags, wich had short tracking histories and a poor match with the genetic stock ID.

Stat Week	Tags	River	Lake	Unknown	Perc River
28	-	-	-	-	-
29	14	8	3	3	73
30	3	3	0	0	100
31	19	9	10	0	47
32	9	4	4	1	50
33	11	4	6	1	40
34	17	5	12	0	29
35	18	4	13	1	24
36	14	1	13	0	7
37	11	1	10	0	9
38	11	3	8	0	27
39	7	1	6	0	14
40	-	-	-	-	-
41	1	1	0	0	100
Total	***135***	***44***	***85***	***6***	

Wt Avg (run)	**23**
Wt Avg (n)	35
Raw Avg	43

Timing Group	Tags	River	Lake	Unknown	Perc River
Early	56	28	23	5	55
Mixed	17	5	12	0	29
Late	62	11	50	1	18
Total	***135***	***44***	***85***	***6***	

Table H 3: Chi-Squared Test for Final Destination of Female Sockeye Tagged at Klukshu Weir in 2016. Tagging data from Table H 1 were subset to focus only on the tags for which a final destination could be determined, which were then grouped as early migrants (W28-W33) or late migrants (W35-W41). This leaves out 27 samples, because they passed the weir during the "mixed" week 34, or tag destination couldn't be determined. Pearson's chi-squared test without continuity correction was applied to all 123 remaining observations using the R function prop.test(), and replicated 1,000 times on random subsamples of 90% of the data. Tests were replicated using proportions adjusted based on weighted average of weekly proportion using run size (see Section 5.2), and excluding redeployed tags. All three versions of the test show essentially the same result: the sample proportions are very different, with a p value smaller than 0.05 in all of the bootstrap tests (100%).

Females – All Tags – Raw Ratios

Timing Group	Tag Destination Lake	River	% River	p.value	percent p.values ≤0.05	95% Conf Int. (Diff in Prop)
Early	23	28	55%	3.9e-5	100	Early tagged females have between 14% and 48% lower proportion of lake spawners
Late	55	17	24%			

Females – All Tags – Weighted by run size

Timing Group	Tag Destination Lake	River	% River	p.value	percent p.values ≤0.05	95% Conf Int. (Diff in Prop)
Early	25	26	51%	1.1e-5	100	Early tagged females have between 17% and 50% lower proportion of lake spawners
Late	59	13	18%			

Females – New Tags Only – Weighted by run size

Timing Group	Tag Destination Lake	River	% River	p.value	percent p.values ≤0.05	95% Conf Int. (Diff in Prop)
Early	25	26	51%	9.5e-5	100	Early tagged females have between 17% and 50% lower proportion of lake spawners
Late	51	10	16%			

Table H 4: Overview of Final Destination for Adult Male Sockeye Tagged at Klukshu Weir in 2016.
Radio tags were applied to a subset of fish sampled at the weir, with proportional focus on early migrating fish and a preference for tagging females. Samples with successful fate include only those where a final spawning destination could be identified based on stationary radio towers and a helicopter overflight. Refer to Table 3 for a summary of the observed movement patterns, and to Appendix J for a description of the details for each tag. The proportion of tagged fish that were assigned a river fate varied substantially between statistical weeks. Table 7 summarizes formal tests of differences in proportion of tags with river fate, using all tags (male and female). Summaries by timing group and a formal test comparing tag destination ratios between the early and late runs (like Table H 3) for male fish only are not included, because the sample size is too small.

Stat Week	Tags	River	Lake	Unknown	Perc River
28	-	-	-	-	-
29	-	-	-	-	-
30	-	-	-	-	-
31	13	5	6	2	45
32	-	-	-	-	-
33	1	1	0	0	100
34	-	-	-	-	-
35	-	-	-	-	-
36	-	-	-	-	-
37	-	-	-	-	-
38	-	-	-	-	-
39	1	0	1	0	0
40	-	-	-	-	-
41	-	-	-	-	-
Total	15	7	8	0	

Table H 5: Migration Times based on Stationary Receivers

The table shows the number of days between last tag detection at the weir tower and first entry into the range of each upstream towers. Not all tags were detected at all en-route towers (e.g. some tags detected at Vand but not Motheral). Rows show the total sample split into different groupings (e.g. based on time of tag application). Note that a tag recorded to enter the range of the lake tower does not automatically mean that the tagged fish spawned in the lake: Some moved back downstream later, others were only detected by downstream-facing antenna of the lake tower. Refer to Table 3 for a summary of the observed movement patterns, and to Appendix J for a description of the details for each tag. Of 162 tags with at least 1 detection (Table C 2), 105 were detected at Motheral, 97 at Vand, and 73 at the lake tower. Overall, the median time was 2 days to reach Motheral, 4 days to reach Vand, and 6 days to reach the lake tower. However, migration times differ substantially by subgroup: Fish with a tag fate assigned to the river took more than twice as long to reach Vand (10.5 vs. 4 days) and almost 4 times as long to reach the lake tower (single obs of 23 vs. median of 6 days) compared to fish with a lake fate. The same observation holds when tags are split based on genetic stock ID (Sec. 5.8): Fish matched to the River / Neskataheen group took about twice as long to reach Vand (7 and 8.5 vs. 4 days) and more than twice as long to reach the lake (11.5 and 13 vs. 5 days) compared to fish genetically matched to the lake spawners.

	Days To Motheral				Days To Vand				Days To Lake			
	n	Min	Med	Max	n	Min	Med	Max	n	Min	Med	Max
All	105	1	2	20	97	1	4	26	73	2	6	44
Early	49	1	3	15	41	2	8	26	25	3	12	44
Mixed	13	1	2	20	12	2	4.5	21	10	4	6	24
Late	43	1	2	4	44	1	3	10	38	2	5	13
Stat Week 29	2	4	4	4	2	6	9	12	1	8	8	8
Stat Week 30	3	2	7	15	1	16	16	16	0	NA	NA	NA
Stat Week 31	26	2	3	4	23	4	9	26	15	7	13	33
Stat Week 32	8	2	3	4	6	2	5	6	4	7	7	19
Stat Week 33	10	1	2	3	9	2	13	17	5	3	21	44
Stat Week 34	13	1	2	20	12	2	4.5	21	10	4	6	24
Stat Week 35	14	2	2	3	15	3	4	10	12	4	5	13
Stat Week 36	11	2	2	4	11	3	3	5	11	4	5	11
Stat Week 37	7	1	2	3	8	1	3	4	8	2	6.5	7
Stat Week 38	8	1	2	3	8	2	3	5	6	2	4.5	10
Stat Week 39	0	NA	NA	NA	0	NA	NA	NA	0	NA	NA	NA
Stat Week 40	2	2	2.5	3	2	3	3.5	4	1	4	4	4
Stat Week 41	1	1	1	1	0	NA	NA	NA	0	NA	NA	NA
Tag_Fate - Undet.	0	NA	NA	NA	0	NA	NA	NA	0	NA	NA	NA
Tag_Fate - River	35	1	3	15	26	2	10.5	19	1	23	23	23
Tag_Fate - Lake	70	1	2	20	71	1	4	26	72	2	6	44
GSI - Klukshu Lake	46	1	2	20	47	1	4	21	40	2	5	24
GSI - Klukshu River	15	1	2	7	14	2	7	22	10	3	11.5	44
GSI - Alsek_T_down	3	1	2	4	3	2	3	11	1	4	4	4
GSI - Neskataheen	31	1	3	15	22	3	8.5	26	13	6	13	27
GSI - OConnor_RT	3	2	2	3	3	2	3	5	3	4	6	10
GSI - Stinky_Cr_RT	1	2	2	2	2	3	3	3	2	5	5	5
GSI - Tweedsmu_RT	2	2	2	2	2	3	3	3	2	4	4.5	5
GSI - U_Tatshen_RT	1	4	4	4	1	7	7	7	1	8	8	8
GSI - Undetermined	3	1	2	3	3	13	16	23	1	20	20	20
		Min	1				3				4	
		Med	2				4.25				6	
		Max	7				16				23	

Table H 6: Migration Speeds based on Stationary Receivers

The table shows the migration speed (km/day) between last tag detection at the weir tower and first entry into the range of each upstream towers. Not all tags were detected at all en-route towers (e.g. some tags detected at Vand but not Motheral). Rows show the total sample split into different groupings (e.g. based on time of tag application). Note that a tag recorded to enter the range of the lake tower does not automatically mean that the tagged fish spawned in the lake: Some moved back downstream later, others were only detected by downstream-facing antenna of the lake tower. Refer to Table 3 for a summary of the observed movement patterns, and to Appendix J for a description of the details for each tag. Of 162 tags with at least 1 detection (Table C 2), 105 were detected at Motheral, 97 at Vand, and 73 at the lake tower. Overall, the median speed was about 5 km/day to Motheral, 3 km/day to Vand, and 4 km/day to the lake tower. However, migration speeds differ substantially by subgroup: Fish with a tag fate assigned to the lake were more than twice as fast than those assigned to River fate. The same observation holds when tags are split based on genetic stock ID (Sec. 5.8): Fish matched to the Lake spawners were about twice as fast to Vand (3.5 vs 2 and 1.6 km/day) and more than twice as fast reach the lake (4.5 vs. 2 and 1.7 km/day) compared to fish genetically matched to the River / Neskataheen group.

	Speed To Motheral				Speed To Vand				Speed To Lake			
	n	Min	Med	Max	n	Min	Med	Max	n	Min	Med	Max
All	105	0.5	4.8	9.6	97	0.5	3.5	13.9	73	0.5	3.8	11.3
Early	49	0.6	3.2	9.6	41	0.5	1.7	7	25	0.5	1.9	7.5
Mixed	13	0.5	4.8	9.6	12	0.7	3.1	7	10	0.9	3.8	5.7
Late	43	2.4	4.8	9.6	44	1.4	4.6	13.9	38	1.7	4.5	11.3
Stat Week 29	2	2.4	2.4	2.4	2	1.2	1.7	2.3	1	2.8	2.8	2.8
Stat Week 30	3	0.6	1.4	4.8	1	0.9	0.9	0.9	0	NA	NA	NA
Stat Week 31	26	2.4	3.2	4.8	23	0.5	1.5	3.5	15	0.7	1.7	3.2
Stat Week 32	8	2.4	3.2	4.8	6	2.3	2.8	7	4	1.2	3.2	3.2
Stat Week 33	10	3.2	4.8	9.6	9	0.8	1.1	7	5	0.5	1.1	7.5
Stat Week 34	13	0.5	4.8	9.6	12	0.7	3.1	7	10	0.9	3.8	5.7
Stat Week 35	14	3.2	4.8	4.8	15	1.4	3.5	4.6	12	1.7	4.5	5.7
Stat Week 36	11	2.4	4.8	4.8	11	2.8	4.6	4.6	11	2.1	4.5	5.7
Stat Week 37	7	3.2	4.8	9.6	8	3.5	4.6	13.9	8	3.2	3.5	11.3
Stat Week 38	8	3.2	4.8	9.6	8	2.8	4.6	7	6	2.3	5.1	11.3
Stat Week 39	0	NA	NA	NA	0	NA	NA	NA	0	NA	NA	NA
Stat Week 40	2	3.2	4	4.8	2	3.5	4.1	4.6	1	5.7	5.7	5.7
Stat Week 41	1	9.6	9.6	9.6	0	NA	NA	NA	0	NA	NA	NA
Tag_Fate – Undet.	0	NA	NA	NA	0	NA	NA	NA	0	NA	NA	NA
Tag_Fate - River	35	0.6	3.2	9.6	26	0.7	1.3	7	1	1	1	1
Tag_Fate - Lake	70	0.5	4.8	9.6	71	0.5	3.5	13.9	72	0.5	3.8	11.3
GSI Klukshu Lake	46	0.5	4.8	9.6	47	0.7	3.5	13.9	40	0.9	4.5	11.3
GSI Klukshu River	15	1.4	4.8	9.6	14	0.6	2	7	10	0.5	2	7.5
GSI Alsek_T_down	3	2.4	4.8	9.6	3	1.3	4.6	7	1	5.7	5.7	5.7
GSI - Kane	0	NA	NA	NA	0	NA	NA	NA	0	NA	NA	NA
GSI Kudwat_Cr_RT	0	NA	NA	NA	0	NA	NA	NA	0	NA	NA	NA
GSI - Neskataheen	31	0.6	3.2	9.6	22	0.5	1.6	4.6	13	0.8	1.7	3.8
GSI - OConnor_RT	3	3.2	4.8	4.8	3	2.8	4.6	7	3	2.3	3.8	5.7
GSI - Stinky_Cr_RT	1	4.8	4.8	4.8	2	4.6	4.6	4.6	2	4.5	4.5	4.5
GSI - Tweedsmu_RT	2	4.8	4.8	4.8	2	4.6	4.6	4.6	2	4.5	5.1	5.7
GSI - U_Tatshen_RT	1	2.4	2.4	2.4	1	2	2	2	1	2.8	2.8	2.8
GSI - Undetermined	3	3.2	4.8	9.6	3	0.6	0.9	1.1	1	1.1	1.1	1.1
		Min	1.4				0.9				1	
		Med	4.8				3.3				3.8	
		Max	9.6				4.6				5.7	

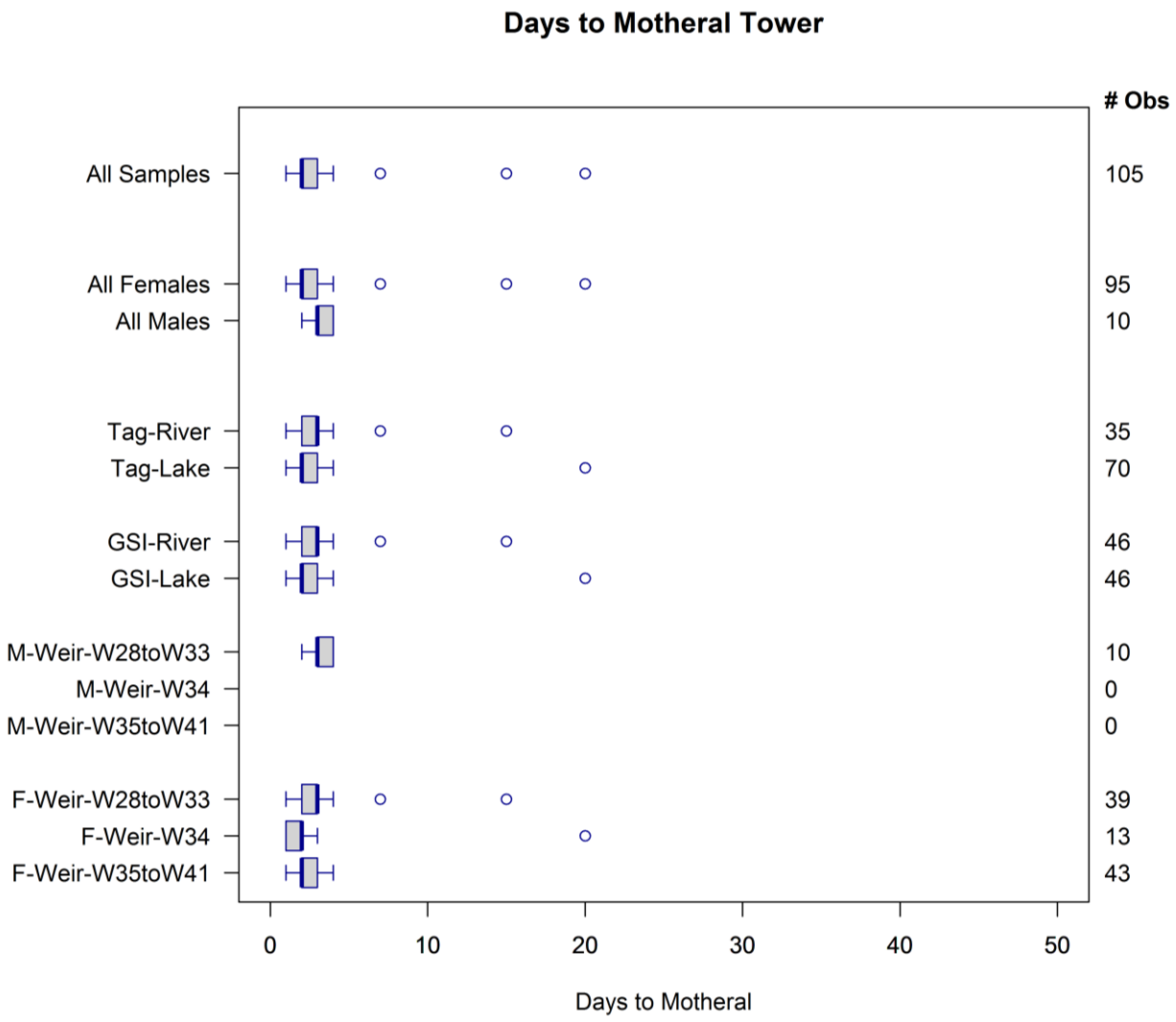


Figure H 1: Distribution of migration times – To Motheral
The figure shows the number of days between last tag detection at the weir tower and first entry into the range of Motheral Tower. Each boxplot shows the median (vertical line), interquartile range (box), distribution range (whiskers), and extreme values (open circles). Different boxplots show the total sample split into different groupings (e.g. based on sex and time of migration past the weir). Note that the GSI-River group includes fish matched to either River spawners or Neskataheen in the revised baseline (Section 5.8). Refer to Table H 5 for further notes regarding the data (e.g. observed movement patterns) and to Table C 1 for a description of the tracking towers. Motheral tower was a bit less than halfway between the weir tower and the lake tower (9.6/22.6km,42%). Over this first part of the upstream migration, there was little difference in migration time between the various subsets, with medians either 2 or 3 days. However, fish matched to lake spawners either through tag fate or genetic stock identification tended to reach Motheral a bit faster (median = 2 days) than fish matched to river spawners (median =3 days). Table H 5 lists the values.

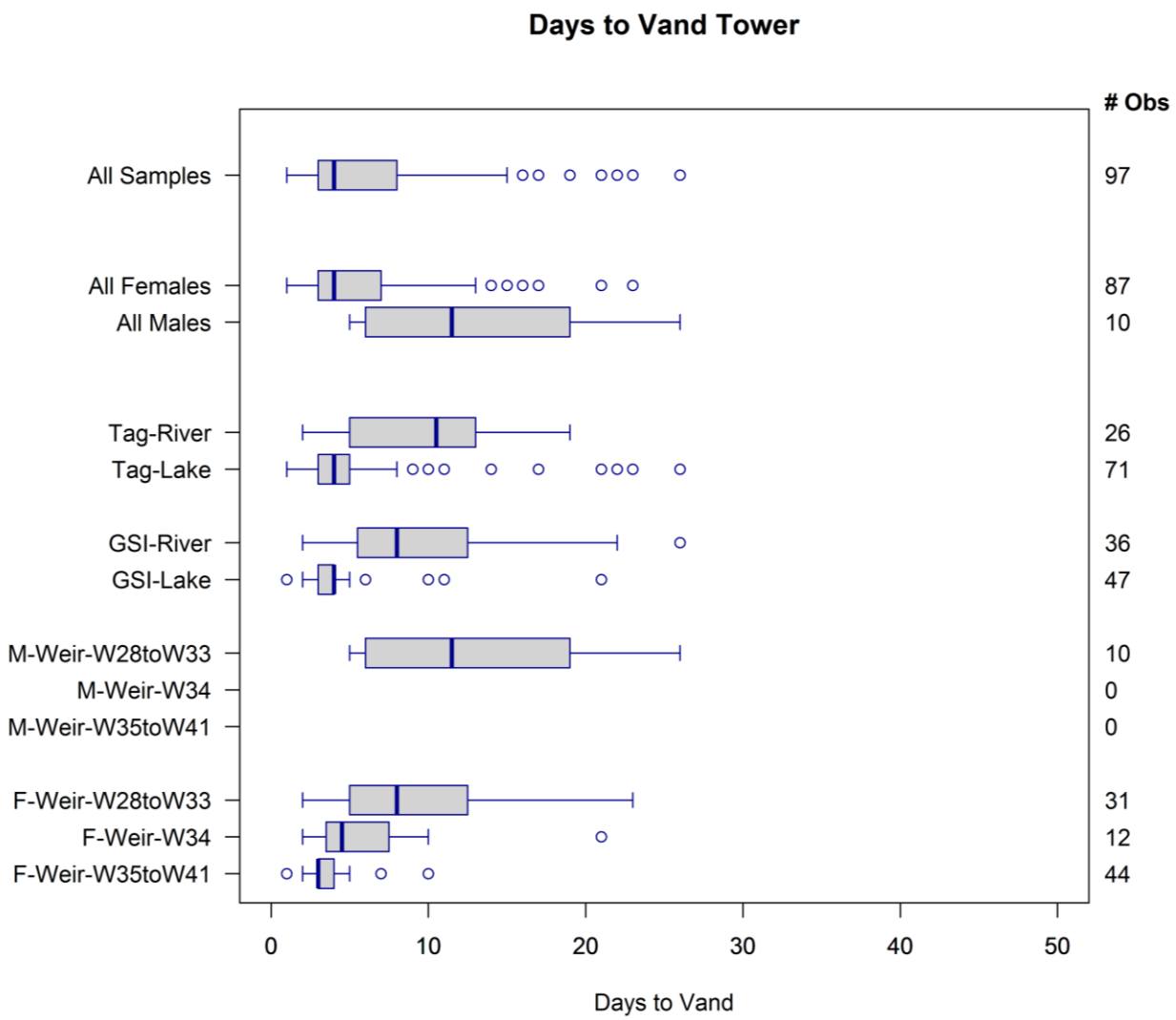


Figure H 2: Distribution of migration times – To Vand
The figure shows the number of days between last tag detection at the weir tower and first entry into the range of Vand Tower. Each boxplot shows the median (vertical line), interquartile range (box), distribution range (whiskers), and extreme values (open circles). Different boxplots show the total sample split into different groupings (e.g. based on sex and time of migration past the weir). Note that the GSI-River group includes fish matched to either River spawners or Neskataheen in the revised baseline (Section 5.8). Refer to Table H 5 for further notes regarding the data (e.g. observed movement patterns) and to Table C 1 for a description of the tracking towers. Vand tower was a bit more than halfway between the weir tower and the lake tower (13.9/22.6km, 61%). Over this second stretch of the upstream migration, marked differences in migration time between the various subsets emerged. Fish matched to lake spawners either through tag fate or genetic stock identification tended to reach Vand much faster than fish matched to river spawners. Table H 5 lists the values. Given that river spawners tend to migrate past Klukshu weir earlier (Table 7), this pattern of migration times also shows up when the sample is split into 3 timing groups based on statistical week (Early = W28-W33, Mix = W34, Late = W35-W41). Also note that splitting samples based on GSI produces fewer outliers in migration time than the grouping based on tag fate. The Tag-Lake group has 9 outlier values (some fish have identical values due to daily time step in records), but 6 of the extreme values (i.e. very slow migrants) were genetically matched to river spawners, which have a much wider observed distribution.

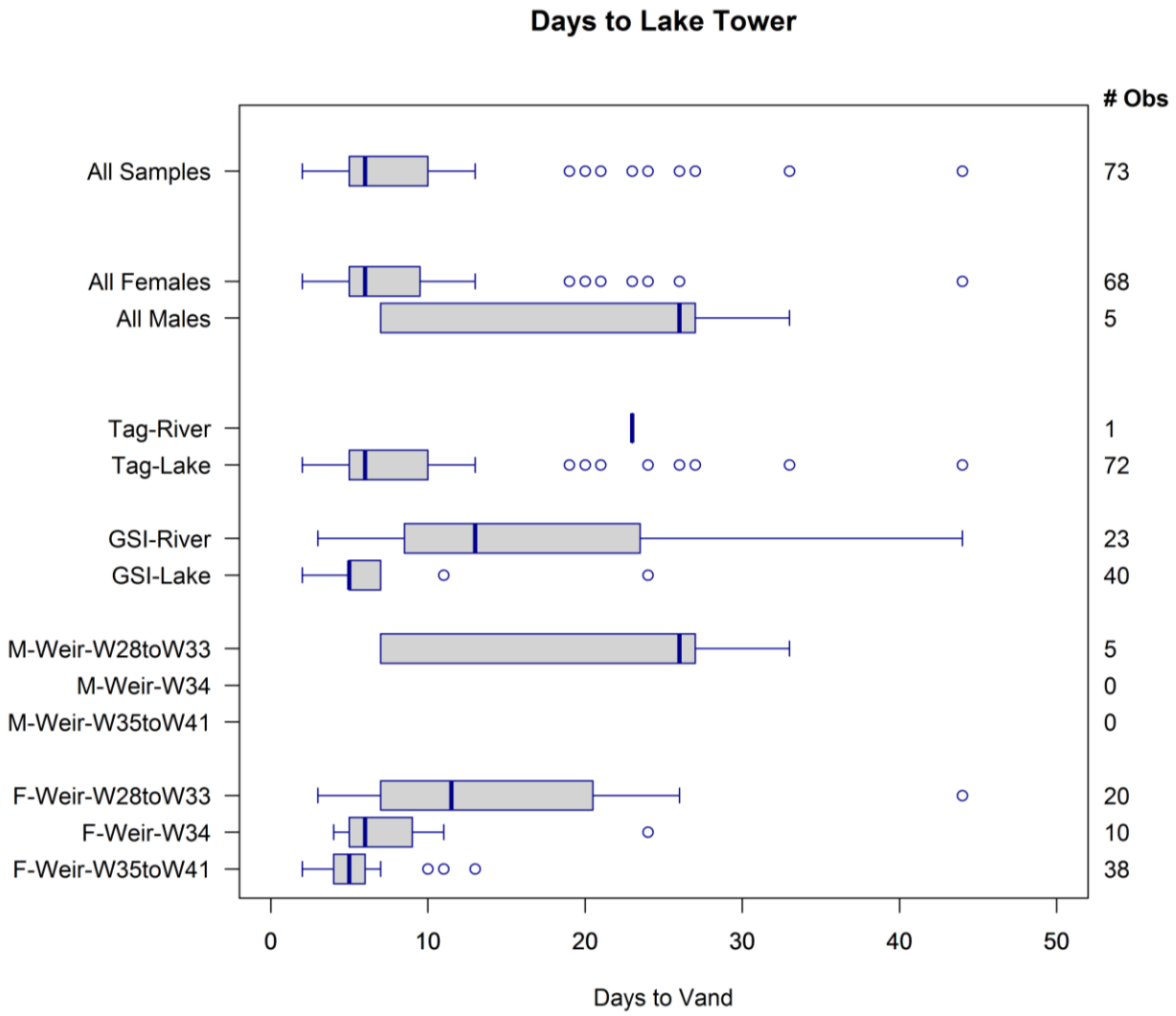


Figure H 3: Distribution of migration times – To Lake
The figure shows the number of days between last tag detection at the weir tower and first entry into the range of the Lake Tower. Each boxplot shows the median (vertical line), interquartile range (box), distribution range (whiskers), and extreme values (open circles). Different boxplots show the total sample split into different groupings (e.g. based on sex and time of migration past the weir). Note that the GSI-River group includes fish matched to either River spawners or Neskataheen in the revised baseline (Section 5.8). Refer to Table H 5 for further notes regarding the data (e.g. observed movement patterns) and to Table C 1 for a description of the tracking towers. The Lake tower was 22.6km upstream from the weir tower. Over this full upstream migration, marked differences in migration time between the various subsets emerged among those fish that were detected at least once at the Lake Tower. Fish matched to lake spawners either through tag fate or genetic stock identification tended to reach the lake much faster than fish matched to river spawners. Table H 5 lists the values. Given that river spawners tend to migrate past Klukshu weir earlier (Table 7), this pattern of migration times also shows up when the sample is split into 3 timing groups based on statistical week (Early = W28-W33, Mix = W34, Late = W35-W41). Also note that splitting samples based on GSI produces fewer outliers in migration time than the grouping based on tag fate. The Tag-Lake group has 8 high outlier values (some fish have identical values due to daily time step in records), and the Tag-River group only had a single fish that was detected at the Lake Tower. However, most of the extreme values (i.e. very slow migrants) were genetically matched to river spawners, resulting in a much narrower distribution of migration times for the GSI-Lake subset than the Tag-Lake subset.

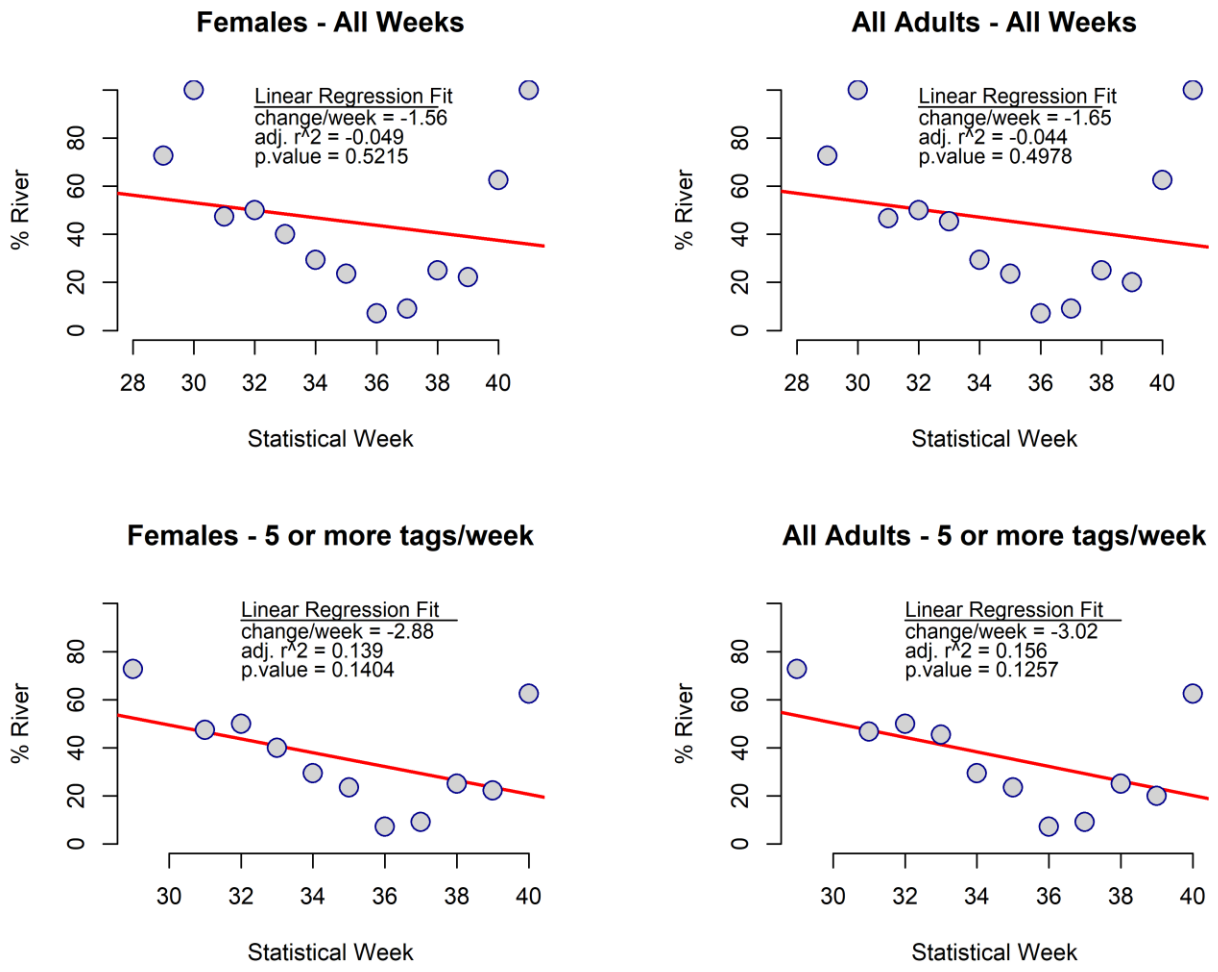


Figure H 4: Regression Fits to Weekly Tag Destination (% River) for Adult Sockeye at Klukshu Weir in 2016.

This figure shows 4 alternative regression fits to the weekly stock composition (i.e. % tags assigned to the river spawners). These represent intermediate steps in the exploratory analysis. The final regression fit is based on a cleaned data set using only females with new tags, shown in Figure 9. Table 6 and Table H 1 list weekly tag counts. Table H 3 and Table 7 summarize the corresponding chi-squared tests for difference between early and late migrants. All 4 of these alternative fits result in a similar trendlines, and regression fits are improved by using only weeks with 5 or more tags (i.e. drop week 30 which had 3 tags and week 41 which had only a single tag). Neither one of these linear fits was statically significant (i.e. p-value > 0.05) and all had poor predictive power (i.e. adjusted r2 very low). Rather than fitting some non-linear models, we instead excluded the observations in week 40, which relied on tags that were recovered in the fishery or on the spawning grounds, and then redeployed. These redeployed tags had short tracking histories and poor match with the genetic stock ID (Table J 5). Focusing the regression fit only on females with new tags produces a highly siginificant and predicitive linear relationship (Figure 9).

Appendix I: Genotype Analyses – Additional Summaries

Table I 1: Microsatellite Loci Used for Sockeye Salmon by DFO's Molecular Genetics Lab.
This table list the 14 polymorphic unlinked microsatellite loci currently used by DFO's Sclerochronology Lab in Nanaimo for Sockeye Salmon and source references for each locus given in Withler et al. 2014 and Withler et al. 2000.

Locus	Source
loc_1b	
loc_3dre	
loc_i1	
loc_oki10	Smith et al. 1998
loc_oki16	Smith et al. 1998
loc_oki1a	Smith et al. 1998
loc_oki1b	Smith et al. 1998
loc_oki29	Smith et al. 1998
loc_oki6	Smith et al. 1998
loc_omy77	Morris et al. 1996
loc_one8	Scribner et al. 1996
loc_ots103	Beacham et al. 1998; Nelson and Beacham 1999
loc_ots2	Banks et al. 1999
loc_ots3	Banks et al. 1999

Table I 2: DNA data cleaning – Filter out incomplete records.
DNA sample processing (Section 4.2) produced genotype sequences for 14 loci (i.e. allele pairs), but not all alleles could be fully read (i.e. one or both records in a pair may be missing). The first step in the data clean-up was to remove records with too many missing pieces. The cut-off was to allow no more than 8 incomplete alleles (out of 28). The proportion of records that had to be dropped from the 2016 sample groups was small, with the largest filtering on the lake spawner sample (5/123,4%). However, for several of the Alsek baselines the proportion of records that were filtered out was quite high, especially for baselines with small sample sizes (e.g. for Kane filtered out 9/59 records, 15%).

	Before	After	N Drop	% Drop
2016 Samples				
AdSpn_KlukshuLake2016	123	118	5	4
AdSpn_KlukshuRiver2016	119	117	2	2
AdWeir_EarlyNoTag2016	346	344	2	1
AdWeir_EarlyTagged2016	79	79	0	0
AdWeir_LateNoTag2016	367	364	3	1
AdWeir_LateTagged2016	62	62	0	0
AdWeir_MixNoTag2016	81	81	0	0
AdWeir_MixTagged2016	19	19	0	0
Juv_KlukLkOutFry2016	154	152	2	1
Juv_KlukLkOutSmolt2016	126	126	0	0
Juv_KlukVandCrFry2016	214	214	0	0
11 Groups, Total	1690	1676	14	
Original Baselines				
Alsek_T_down	73	65	8	11
Alsek_T_up	46	43	3	7
Basin_Cr_RT	39	36	3	8
Blanchard	249	238	11	4
BorderSlough_RT	182	181	1	1
Bridge_Silver	105	104	1	1
Detour_Cr_RT	26	26	0	0
Goat_Cr_RT	59	59	0	0
Kane	59	50	9	15
Klukshu_Early	**226**	**222**	**4**	**2**
Klukshu_Late	**306**	**289**	**17**	**6**
Klukshu_mix	**524**	**516**	**8**	**2**
Kudwat_Cr_RT	249	246	3	1
Kwatine_Cr	65	64	1	2
L_Tatshenshi_RT	112	109	3	3
LowFog_RT	3	2	1	33
Neskataheen	**832**	**819**	**13**	**2**
OConnor_RT	74	65	9	12
Sediment_Cr_RT	11	11	0	0
Stanley_Cr_RT	24	20	4	17
Stinky_Cr_RT	103	101	2	2
Takhanne_RT	1	1	0	0
Tweedsmuir_RT	151	150	1	1
U_Tatshensh_RT	318	316	2	1
Uknown_Alsek	35	33	2	6
VernRichie_RT	203	165	38	19
26 Groups, Total	4075	3931	144	

Table I 3: DNA data cleaning – Filter out small baselines.
After filtering incomplete records (Table I 2), the Alsek baselines were checked for sample size. The cut-off was to retain only baseline groups with 50 samples or more. Groups highlighted in orange were dropped from subsequent analyses. The 3rd column lists the years in which the baseline samples were collected.

Group	Samples	Sample Years
Alsek_T_down	65	2001/2002/2003
Alsek_T_up	43	2001/2002/2003
Basin_Cr_RT	36	2002/2003
Blanchard	238	2001/2002/2003/2007/2008/2009
BorderSlough_RT	181	2007/2008/2009/2011/2012
Bridge_Silver	104	2011/2012
Detour_Cr_RT	26	2001/2011
Goat_Cr_RT	59	2007/2012
Kane	50	2001/2002/2003
Klukshu_Early	**222**	**2000/2001/2002**
Klukshu_Late	**289**	**2000/2001/2002**
Klukshu_mix	**516**	**1992/2000/2007/2008**
Kudwat_Cr_RT	246	2001/2007/2009/2010/2011/2012
Kwatine_Cr	64	2011
L_Tatshenshi_RT	109	2000/2001/2002/2003/2010
LowFog_RT	2	2002/2003
Neskataheen	**819**	**2000/2001/2002/2003/2007**
OConnor_RT	65	2001/2002/2003
Sediment_Cr_RT	11	2010
Stanley_Cr_RT	20	2001/2002/2003
Stinky_Cr_RT	101	2001/2011
Takhanne_RT	1	2002
Tweedsmuir_RT	150	2003/2007/2009/2010/2011/2012
U_Tatshensh_RT	316	2001/2002/2003
Uknown_Alsek	33	2001
VernRichie_RT	165	2007/2008/2009/2010
18 Groups, Total	***3759***	

Table I 4: DNA data cleaning – Remove duplicate genotypes.
The final step in the DNA data clean-up was to check for duplicate genotypes and remove those records. Duplicate genotypes can arise at different steps during sampling, packing, or processing. The main source of duplicates in the 2016 sampling arose due to the sampling set-up at the weir, with weekly pooled DNA samples being collected from all sampled fish, and additional samples being taken and individually stored when some of those fish were subsequently subsampled for radio tagging. In addition, duplicate genotypes arose from fish that were sampled at the weir and then encountered again on the spawning grounds.

Duplicate Removal Rules
1) if duplicates are 1 tagged and 1 non-tagged from weir, remove non-tagged
2) if duplicates are 1 from spawning grounds and 1 from weir, remove weir sample
3) if duplicates are from same sample group, remove later one

2016 Samples	Records left after removing Incompletes	Duplicate Genotypes	Final Sample
AdSpn_KlukshuLake2016	118	0	118
AdSpn_KlukshuRiver2016	117	0	117
AdWeir_EarlyNoTag2016	344	70	274
AdWeir_EarlyTagged2016	79	1	78
AdWeir_LateNoTag2016	364	56	308
AdWeir_LateTagged2016	62	0	62
AdWeir_MixNoTag2016	81	13	68
AdWeir_MixTagged2016	19	0	19
Weir Total	949	140	809
Spawning Ground Total	235	0	235
Adult Total	1,184	140	1,044
Juv_KlukLkOutFry2016	152	0	152
Juv_KlukLkOutSmolt2016	126	0	126
Juv_KlukVandCrFry2016	214	0	214
Juvenile Total	492	0	492
Grand Total	1,676	140	1,536

Table I 5: Overview of Allele Distributions for 2016 River Group Samples.
The River Group includes river spawners, early weir migrants, and juveniles sampled on the Klukshu mainstem. This table summarizes allele distributions using various metrics. The total number of genotype readings is the sample size used for subsequent analyses (tree fitting, stock ID). For each genotype, there are two allele readings for each locus. The average number and range of unique alleles is calculated based on 1000 bootstrapped samples of 100 alleles from the sample group (similar to Table 2 in Beacham et al. 2008). The proportion of allele samples captured by the 5 most frequent alleles summarizes the shape of the frequency distribution (i.e. higher proportion = more concentrated on a few alleles). Allele variability differs substantially across loci, from 3.6 alleles /100 samples for *oki1a* to 23.5 alleles/100 samples for *oki10*. The total number of unique alleles is much larger than the bootstrap average for some loci (e.g. 46 vs. 23.5 for *oki10*).

Number of Genotypes = 683

Locus	n Valid Alleles	n Invalid Alleles	Lowest Allele	Highest Allele	Unique alleles	**Alleles / 100** (Bootstrap) Avg	Min	Max	Prop in Top 5 Alleles
loc_1b	1344	22	1	12	6	4.59	4	6	0.999
loc_3dre	1354	12	5	27	18	13.056	10	17	0.671
loc_i1	1340	26	5	32	15	11.846	9	15	0.763
loc_oki10	1356	10	15	93	46	23.51	16	32	0.572
loc_oki16	1352	14	10	45	12	8.082	4	11	0.945
loc_oki1a	1358	8	4	7	4	3.609	2	4	1
loc_oki1b	1358	8	3	6	4	3.757	3	4	1
loc_oki29	1354	12	6	27	21	13.647	9	18	0.745
loc_oki6	1358	8	6	37	12	7.924	6	11	0.916
loc_omy77	1352	14	3	17	14	9.634	6	13	0.919
loc_one8	1356	10	13	28	11	7.993	6	11	0.915
loc_ots103	1360	6	8	26	19	14.195	10	18	0.762
loc_ots2	1348	18	8	26	10	6.988	5	10	0.956
loc_ots3	1342	24	6	23	7	5.505	4	7	0.993
				Min	*4*	*3.609*			
				Max	*46*	*23.51*			

Table I 6: Overview of Allele Distributions for 2016 Lake Group Samples.
The Lake Group includes lake spawners, late weir migrants, and juveniles sampled at the lake outlet. Column descriptions and notable loci are the same as for Table I 5.

Number of Genotypes = 766

Locus	n Valid Alleles	n Invalid Alleles	Lowest Allele	Highest Allele	Unique alleles	**Alleles / 100** (Bootstrap) Avg	Min	Max	Prop in Top 5 Alleles
loc_1b	1518	14	1	12	7	5.139	3	7	0.997
loc_3dre	1530	2	5	25	15	12.308	10	15	0.65
loc_i1	1460	72	6	32	20	11.827	8	17	0.805
loc_oki10	1518	14	13	93	58	27.919	21	36	0.381
loc_oki16	1518	14	15	47	12	8.585	5	11	0.92
loc_oki1a	1524	8	4	7	4	3.773	2	4	1
loc_oki1b	1524	8	3	6	4	3.836	2	4	1
loc_oki29	1522	10	6	27	18	12.496	9	17	0.775
loc_oki6	1522	10	6	37	11	7.58	5	11	0.942
loc_omy77	1464	68	5	17	12	8.026	6	11	0.921
loc_one8	1518	14	12	30	17	7.987	5	12	0.955
loc_ots103	1526	6	8	27	18	13.692	9	17	0.724
loc_ots2	1520	12	15	24	7	6.901	6	7	0.892
loc_ots3	1526	6	6	23	7	4.866	3	7	0.998
				Min	*4*	*3.773*			
				Max	*58*	*27.919*			

Table I 7: Overview of Allele Distributions for Neskataheen Baseline Samples.
The baselines include those samples left after filtering out incomplete genotypes and exclusing baselines with fewer than 50 samples (Set G11; Table 8). This table shows only the Neskataheen baseline, because it is the largest basline on the Alsek (Table I 3), and was found to be closely related to the Klukshu River Group in fitted phylogenetic trees (Section 7.5) and genetic stock matches (Section 7.6). Column descriptions and notable loci are the same as for Table I 5.

Number of Genotypes = 819

Locus	n Valid Alleles	n Invalid Alleles	Lowest Allele	Highest Allele	Unique alleles	Alleles / 100 (Bootstrap) Avg	Min	Max	Prop in Top 5 Alleles
loc_1b	1632	6	1	10	5	4.303	3	5	1
loc_3dre	1620	18	5	27	15	11.802	8	14	0.751
loc_i1	1590	48	6	32	13	10.35	8	13	0.792
loc_oki10	1604	34	17	93	34	18.724	13	24	0.645
loc_oki16	1614	24	14	46	25	13.263	8	19	0.815
loc_oki1a	1634	4	4	7	4	2.938	2	4	1
loc_oki1b	1624	14	3	6	4	3.536	3	4	1
loc_oki29	1598	40	6	27	16	11.794	9	16	0.782
loc_oki6	1616	22	6	37	10	7.207	5	10	0.936
loc_omy77	1604	34	5	17	13	7.855	4	12	0.953
loc_one8	1614	24	13	28	13	8.536	5	12	0.928
loc_ots103	1618	20	8	26	17	12.436	9	16	0.794
loc_ots2	1634	4	15	24	8	6.099	5	8	0.982
loc_ots3	1628	10	6	23	8	5.727	3	8	0.983
				Min	*4*	*2.938*			
				Max	*34*	*18.724*			

Table I 8: Overview of Allele Distributions for All 2016 Samples and Revised Alsek Baseline.
The baselines include those samples left after filtering out incomplete genotypes and exclusing baselines with fewer than 50 samples (Set G11; Table 8). Column descriptions and notable loci are the same as for Table I 5.

Number of Genotypes = 4268

Locus	n Valid Alleles	n Invalid Alleles	Lowest Allele	Highest Allele	Unique alleles	Alleles / 100 (Bootstrap) Avg	Min	Max	Prop in Top 5 Alleles
loc_1b	8456	80	1	14	10	5.358	4	7	0.995
loc_3dre	8420	116	5	27	21	14.272	10	19	0.598
loc_i1	8274	262	1	32	25	13.485	10	19	0.741
loc_oki10	8414	122	13	93	77	28.969	20	37	0.417
loc_oki16	8374	162	1	49	39	13.625	8	19	0.841
loc_oki1a	8498	38	2	7	5	3.828	2	5	1
loc_oki1b	8480	56	3	7	5	3.833	3	5	1
loc_oki29	8374	162	4	38	28	15.961	12	21	0.68
loc_oki6	8466	70	1	37	20	8.827	6	13	0.932
loc_omy77	8368	168	3	17	14	9.634	6	13	0.9
loc_one8	8438	98	8	30	20	9.968	6	16	0.909
loc_ots103	8468	68	7	27	21	16.416	12	20	0.642
loc_ots2	8486	50	8	27	14	7.569	5	12	0.925
loc_ots3	8456	80	5	23	15	6.216	4	9	0.986
				Min	*5*	*3.828*			
				Max	*77*	*28.969*			

Appendix J: Tag History Details and GSI Matches

Table J 1: Tagged Females – New Tags / Tag Fate / Early Weir Timing.
51 females were successfully tagged (i.e. have a tag fate) during the Early Timing group (Stat Weeks 28-33, Jul 11 to Aug 10). Tag fates could be clearly assigned for a bit more than half of these (29/51), while the rest required some interpretation of mixed signals. A tag fate could not be determined for 7 additional females tagged during this time window (Table J 6). Tag histories are summarized briefly, then grouped into patterns (e.g. "Loss – Harvested" or "Straight to Lake") and assigned a quality classification (e.g. "Clear", "Interpretation", "Harvested or Lost"). Genetic Stock ID lists the two best matches in the revised Alsek baseline (see Sec. 7.5) and associated probabilities. Agreement between tag fate and genetic stock ID is summarized in Appendix K. Table K 2 shows that the most common patterns were (1) 12 fish moved about the mainstem and ended up in the river, and (2) another 12 migrated straight to the lake. The genetic match for the first groups was very high (11/12 river tag fates were genetically matched to the river spawner baseline, 92% match). However, the genetic match for the second group was very low (3/12 lake tag fate were genetically matched to the lake spawner baseline, 25% match). 10 other tag patterns were observed for 1-4 fish each, with variable matches rates to the GSI results ranging from 0% to 100% with small sample sizes. Table 24 compares match rates by timing group for different tag movement patterns.

TAG HISTORY					GENETIC STOCK IDENTIFICATION				
Date/Code	**Fate**	**Class**	**Pattern**	**Description**	**ID**	**Best Match**	**Prob**	**2nd Best match**	**Prob**
11/07/2016 - - 214	River	Interpretation	Moved about mainstem and ended up in river	Passed Vand Creek tower July 21, but did not enter lake. Was in and out of weir tower range, and also heard on aerial surveys near the weir. Possibly spawning at a spawning site located ~ 300 metres upstream from weir	2	AdSpn_KlukshuRiver2016	59.5%	Stinky_Cr_RT	14.7%
11/07/2016 - - 720	River	Clear	Moved about mainstem and ended up in river	In and out of Vand tower range until Sept. 14.	3	Undetermined	NA	NA	NA
11/07/2016 - - 314	River	Clear	Moved about mainstem and ended up in river	In Vand tower range July 21, but then dropped below Motheral tower July 24, and in weir tower range until Oct 17.	4	AdSpn_KlukshuRiver2016	54.5%	Neskataheen	45.2%
13/07/2016 - - 804	Lake	Interpretation	Lake and drop	Left weir tower range Jul 15, in Motheral tower range Jul 19, then in Vand range Jul 21 and heard at lake tower July 23, but then dropped back to Vand tower range Sep 7. Also heard a single weak signal at Vand on Sep 19. Signal at Vand was weak and late, therefore classified as lake fate.	5	Neskataheen	86.2%	AdSpn_KlukshuRiver2016	8.2%
13/07/2016 - - 101	Lake	Clear	Straight to lake	Detected in lake several times between July 23 and Oct 4.	7	Neskataheen	78.9%	AdSpn_KlukshuRiver2016	21.0%
13/07/2016 - - 610	River	Interpretation	Short track ends in river	Passed Vand Creek tower July 29, but did not enter lake.	8	AdSpn_KlukshuRiver2016	99.9%	Stinky_Cr_RT	0.1%
13/07/2016 - - 208	River	Interpretation	Moved about mainstem, but with mixed signals	Passed Vand Creek tower July 27, and detected in Lake Oct 4/6 (but signal was weak and only from 1 antenna, considered too weak to assign to lake). Located this tag at Vand during aerial surveys on 28 October.	9	Neskataheen	56.8%	AdSpn_KlukshuRiver2016	42.5%
13/07/2016 - - 721	River	Clear	Moved about mainstem and ended up in river	Detected in Vand tower range Aug 8/12/18. Recovered Vand spn Aug 18.	10	Neskataheen	91.6%	AdSpn_KlukshuRiver2016	6.9%

Table J 1 continued.

TAG HISTORY					GENETIC STOCK IDENTIFICATION				
Date/Code	**Fate**	**Class**	**Pattern**	**Description**	**ID**	**Best Match**	**Prob**	**2nd Best match**	**Prob**
16/07/2016 - - 308	River	Interpretation	Moved about mainstem and ended up in river	Passed all river towers, and several detections at Motheral. Furthest upstream signal at Vand Creek tower Aug 9, but did not enter lake.	11	AdSpn_KlukshuRiver2016	61.0%	Neskataheen	24.6%
16/07/2016 - - 816	Lake	Clear	Straight to lake, but with mixed signals	Detected in lake many times between July 25 and Oct 11. Heard at lake during 28 Oct aerial surveys, weak signals heard at Vand in twice mid Oct, but these were probably skip or atmosphere.	12	AdSpn_KlukshuLake2016	75.6%	AdSpn_KlukshuRiver2016	14.2%
21/07/2016 - - 703	River	Clear	Moved about mainstem and ended up in river	Detected in Vand tower range Aug 15/21/28. Strongest signals were from the motheral tower but several signals picked up at Vand. Aerial survyes indicated this fish entered the lake, lake tower did not pick up this tag. Mistaken locaction suspected during the aerial surveys.	16	AdSpn_KlukshuRiver2016	37.3%	Neskataheen	35.1%
16/07/2016 - - 407	River	Clear	Moved about mainstem and ended up in river	Detected in Vand tower range Aug 3/4/7/8/18. Recovered Vand spn Aug 18.	14	AdSpn_KlukshuRiver2016	98.3%	Alsek_T_down	1.3%
20/07/2016 - - 212	River	Clear	Moved about mainstem and ended up in river	Detected in Vand tower range Aug 6/17/18. Recovered Vand spawner Aug 18.	NA	Undetermined	NA	NA	NA
21/07/2016 - - 620	River	Interpretation	Moved about mainstem and ended up in river	Detected in Motheral tower range Aug 5, then dropped to weir tower range and detected there several times Aug 6 - Oct17. Could be a mortality.	15	Neskataheen	95.5%	AdSpn_KlukshuRiver2016	4.5%
24/07/2016 - - 514	Lake	Interpretation	Lake and drop	Passed all the river towers in few days, then detected in lake many times between Aug 2 and Oct 6 by towers. Detected in mainstem during Oct 28 aerial survey (likely carcass drift)	20	U_Tatshensh_RT	76.4%	AdSpn_KlukshuLake2016	8.8%
26/07/2016 - - 602	Lake	Clear	Straight to lake	Passed all river towers, then detected in lake many times between Aug 3 and Oct 6.	22	AdSpn_KlukshuLake2016	99.9%	U_Tatshensh_RT	0.1%
27/07/2016 - - 218	Lake	Clear	Straight to lake	Passed all river towers, then detected in lake several times between Aug 8 and Oct 6.	23	Neskataheen	83.4%	AdSpn_KlukshuRiver2016	16.4%
27/07/2016 - - 318	River	Interpretation	Lake outlet	Passed all the river towers quickly, then detected in lake tower range many times between Aug 5 and Oct 16 (but note: downstream antenna strength from the lake tower indicates lake outlet). Located downstream during aerial survey on Oct 28.	27	AdSpn_KlukshuLake2016	89.0%	Neskataheen	4.7%
27/07/2016 - - 814	River	Interpretation	Lake and drop	Heard at Motheral tower several times from Jul 30 to Sep 22 , then at lake tower Oct 3 (downstrean antenna only), but then dropped back to Motheral tower range Oct 15/16. Fish spent most of its time at Motheral. Signal heard above weir during the 28 Oct aerial survey, suspect this was a drifted carcass at that point.	28	Neskataheen	96.6%	AdSpn_KlukshuLake2016	2.2%
27/07/2016 - - 317	Lake	Clear	Straight to lake	Passed Motheral and Vand towers, then heard several times in lake Aug 7 to Sep 15.Very strong signal from 12-15 Sept as if fish dropped down to the shallows where spawning occurred. Recovered spawned out on Sep 15 at lake outlet.	NA	Undetermined	NA	NA	NA

Table J 1 continued.

TAG HISTORY					GENETIC STOCK IDENTIFICATION				
Date/Code	**Fate**	**Class**	**Pattern**	**Description**	**ID**	**Best Match**	**Prob**	**2nd Best match**	**Prob**
28/07/2016 - - 715	River	Interpretation	Moved about mainstem, but with mixed signals	In Vand tower range from Aug 5 to Sep 13, then in lake tower range Sep 22 and Oct 1, then dropped to Vand tower range Oct 19. Signal out of water at that point, probably picked up by harvester. Classified as river fate based on 5 weeks in Vand range.	29	Neskataheen	40.6%	AdSpn_Klukshu Lake2016	37.9%
28/07/2016 - - 711	River	Clear	Moved about mainstem, but stayed in lower river	Exited weir tower range July 28. Not detected by any other towers, but heard above weir during Oct 28 aerial survey.	36	Neskataheen	79.4%	AdSpn_Klukshu River2016	15.4%
28/07/2016 - - 811	River	Interpretation	Lake outlet	Passed all the river towers, then detected in lake tower range many times between Aug 12 and Oct 6 (but note that signal strength on downstream antenna indicates below lake). Detected in river during Oct 28 aerial survey. Assumed to be carcass drift.	35	AdSpn_Klukshu Lake2016	92.1%	AdSpn_Klukshu River2016	4.2%
29/07/2016 - - 617	Lake	Interpretation	Short track ends in lake	Passed all the river towers, then detected in lake once on Aug 9. No subsequent detections.	37	AdSpn_Klukshu River2016	71.5%	Neskataheen	27.2%
29/07/2016 - - 408	Lake	Interpretation	Straight to lake	Passed all the river towers, then detected in lake once on Aug 11. No subsequent detections.	39	Neskataheen	89.1%	AdSpn_Klukshu River2016	9.5%
29/07/2016 - - 513	River	Clear	Moved about mainstem and ended up in river	Detected several times at Motheral and Vand towers in Aug, then in weir tower range several times from Sep 4 to Oct 1. Heard above weir during Oct 28 aerial survey.	40	Neskataheen	42.2%	AdSpn_Klukshu River2016	32.0%
29/07/2016 - - 817	River	Clear	Moved about mainstem and ended up in river	In weir and Motheral tower range several times, then last detection in Vand tower range Aug 23.	42	AdSpn_Klukshu Lake2016	70.3%	Neskataheen	25.2%
29/07/2016 - - 704	Lake	Clear	Straight to lake	Passed all river towers, then detected in lake many times between Aug 11 and Sep 6, and during Oct 28 aerial survey.	43	Neskataheen	61.8%	AdSpn_Klukshu River2016	36.9%
29/07/2016 - - 607	Lake	Clear	Straight to lake	Passed all the river towers, then detected in lake several times from Aug 23 to Oct 9.	44	Neskataheen	92.7%	AdSpn_Klukshu River2016	7.1%
29/07/2016 - - 219	Lake	Interpretation	Moved about mainstem and ended up in lake	Passed all river towers, but moved between Vand tower and lake tower for several hits between Aug 19 to Sep 5, then in lake tower range until Oct 6	NA	Undetermined	NA	NA	NA
30/07/2016 - - 220	River	Interpretation	Moved about mainstem, but with mixed signals	Signal detected several times at different river towers, last detection at lake tower Aug 23/24 and on same day at Motheral tower. Originally classified as a lake fate, but revised based on multiple river detections, and conflicting signals on Aug 24	45	Neskataheen	78.3%	AdSpn_Klukshu River2016	21.7%
30/07/2016 - - 415	Lake	Clear	Straight to lake	Passed all the river towers, then detected in lake several times between Aug 13 to Sep 28.	46	Neskataheen	90.8%	AdSpn_Klukshu River2016	6.8%
30/07/2016 - - 502	River	Clear	Moved about mainstem and ended up in river	Heard at weir and Motheral towers, then detected at Vand tower Aug 15/18. Recovered Vand creek spawner Aug 18.	47	Neskataheen	62.5%	AdSpn_Klukshu River2016	35.5%

Table J 1 continued.

TAG HISTORY					GENETIC STOCK IDENTIFICATION				
Date/Code	**Fate**	**Class**	**Pattern**	**Description**	**ID**	**Best Match**	**Prob**	**2nd Best match**	**Prob**
02/08/2016 - - 806	Lake	Clear	Straight to lake, but with mixed signals	Detected in lake many times between Aug 11 and Oct 6. Weak signal heard at Vand tower in mid Oct., but tag heard at lake during the 28 Oct aerial surveys.	49	AdSpn_Klukshu Lake2016	99.7%	AdSpn_Klukshu River2016	0.2%
02/08/2016 - - 614	Lake	Clear	Straight to lake	Passed all the river towers and then detected in lake many times between Aug 9 and Oct 6.	51	Neskataheen	96.8%	AdSpn_Klukshu River2016	2.9%
02/08/2016 - - 205	River	Interpretation	Lake outlet	Passed all river towers, the detected by lake tower Aug 8/10, downstream antenna stronger signal, located downstream during Oct 28 aerial survey.	52	Alsek_T_down	90.8%	AdSpn_Klukshu Lake2016	4.6%
02/08/2016 - - 410	River	Interpretation	Moved about mainstem and ended up at lake outlet	Detected by lake tower Aug 26 to Oct 1, but, but no upstream signal some dates. Probably left lake and spawned in mainstem below lake within tower range.	53	Neskataheen	86.6%	AdSpn_Klukshu River2016	13.1%
02/08/2016 - - 710	Lake	Clear	Straight to lake	Passed all the river towers, then detected by lake tower Aug 9/16. Heard at lake during 28 Oct aerial surveys.	50	AdSpn_Klukshu Lake2016	95.0%	AdSpn_Klukshu River2016	5.0%
05/08/2016 - - 312	Lake	Interpretation	Straight to lake, but with mixed signals	Passed all river towers (slowly), then detected in lake from Aug 25 to Oct 5. Also detected at weir tower Sep 16. Possibly in harvesters vehicle?	55	AdSpn_Klukshu River2016	73.6%	Neskataheen	26.3%
05/08/2016 - - 801	River	Clear	Short track ends in river	Detected at weir tower Aug 5-8 and at Motheral tower Aug 10. No subsequent detections.	56	Neskataheen	70.9%	AdSpn_Klukshu River2016	28.7%
05/08/2016 - - 722	River	Clear	Moved about mainstem and ended up in river	In range of Motheral tower from Aug 9 to Sep 4. Signal heard at Motheral during the 28 Oct aerial survey.	57	Neskataheen	86.4%	AdSpn_Klukshu Lake2016	12.3%
07/08/2016 - - 612	Lake	Interpretation	Moved about mainstem and ended up in lake	Slow fish, hung out near Vand for 15 days in Aug and Sep, finally arrived at the lake on 21 sep. Located in lake via aerial surveys conducted on 28 Oct.	58	AdSpn_Klukshu River2016	59.7%	Neskataheen	39.1%
07/08/2016 - - 201	River	Interpretation	Short track ends in river	Heard at weir and Motheral towers, then in Vand tower range Aug 14/16. No subsequent detections.	59	AdSpn_Klukshu River2016	84.9%	Neskataheen	14.9%
08/08/2016 - - 512	Lake	Interpretation	Lake only	Detected by lake tower Aug 18 to Oct 6, but several signals out-of-water. Suspect fish was predated upon near lake outlet..very strong signals at lake, but no signal at any other towers?.	61	AdSpn_Klukshu Lake2016	95.5%	Neskataheen	3.5%
08/08/2016 - - 305	Lake	Clear	Straight to lake, but with mixed signals	Detected by lake tower Sep 4 to Sep 25. Phantom signal at weir on 19 Aug, no signals at Vand.	63	Neskataheen	89.5%	AdSpn_Klukshu Lake2016	9.7%
08/08/2016 - - 808	Lake	Clear	Straight to lake	Passed all river towers, then detected by lake tower many times between Aug 14 and Oct 6. Heard at lake during the 28 Oct aerial surveys	62	AdSpn_Klukshu Lake2016	34.8%	AdSpn_Klukshu River2016	32.8%
09/08/2016 - - 717	River	Clear	Moved about mainstem and ended up in river	Heard at all river towers. Slow migration from Motheral tower to Vand tower. In Vand range Aug 23/25.	64	Undetermined	NA	NA	NA

Table J 1 continued.

TAG HISTORY					GENETIC STOCK IDENTIFICATION				
Date/Code	**Fate**	**Class**	**Pattern**	**Description**	**ID**	**Best Match**	**Prob**	**2nd Best match**	**Prob**
09/08/2016 - - 608	Lake	Clear	Straight to lake	Passed all the river towers, then detected by lake tower several times between Aug 30 and Sep 29. Heard in lake during Oct 28 aerial survey.	65	AdSpn_Klukshu River2016	83.1%	Neskataheen	14.3%
10/08/2016 - - 508	River	Clear	Moved about mainstem and ended up in river	Detected at Vand tower Aug 24/26. Heard closer to Motheral during 28 Oct aerial survey. Probably drifting carcass by then.	67	Neskataheen	53.1%	AdSpn_Klukshu River2016	45.7%
10/08/2016 - - 812	River	Interpretation	Moved about mainstem, but with mixed signals	In Vand tower range several times between Aug 23 to Sep 15. Weak signal at the lake on 26 Sept. Skip from the Vand zone?	69	AdSpn_Klukshu River2016	79.6%	Neskataheen	18.1%
10/08/2016 - - 303	Lake	Clear	Straight to lake	Passed all the river towers, then detected in lake several times between Aug 14 and Sep 13.	68	AdSpn_Klukshu River2016	95.6%	U_Tatshensh_RT	2.7%

Table J 2: Tagged Females – New Tags / Tag Fate / Mix Weir Timing.

17 females were successfully tagged (i.e. have a tag fate) during the Mixed Timing group (Stat Week 34, Aug 14 to Aug 20). Tag fates could be clearly assigned for a bit more than half of these (10/17), while the rest required some interpretation of mixed signals. A tag fate could not be determined for 1 additional female tagged during this time window (Table J 6). Tag histories are summarized briefly, then grouped into patterns (e.g. "Loss – Harvested" or "Straight to Lake") and assigned a quality classification (e.g. "Clear", "Interpretation", "Harvested or Lost"). Genetic Stock ID lists the two best matches in the revised Alsek baseline (see Sec. 7.5) and associated probabilities. Agreement between tag fate and genetic stock ID is summarized in Appendix K. Table K 3 shows that the most common pattern was a migration straight to the lake, but only half (4/8) of these fish were genetically matched to the lake spawner baseline. 7 other tag patterns were observed for 1-2 fish each, and all except 1 fish had tag fates that match the genetic stock ID. Table 24 compares match rates by timing group for different tag movement patterns.

TAG HISTORY					GENETIC STOCK IDENTIFICATION				
Date/Code	Fate	Class	Pattern	Description	ID	Best Match	Prob	2nd Best match	Prob
14/08/2016 -- 621	River	Interpretation	Lake outlet	Passed Motheral tower, then in Vand tower range Aug 21/23/27, and in lake tower range from Sep 2 to Oct 6, with downstream signal stronger. Identified as a river spawner below lake during the aerial survey.	71	Neskataheen	93.7%	AdSpn_KlukshuLake2016	3.9%
14/08/2016 -- 216	River	Interpretation	Lake and drop	Sig at lake from Sep 23 to Oct 1, but strongest tower sigmal at Vand tower Aug 27 to Sep 1. Located tag at Vand via aerial surveys on 28 Oct.	72	Neskataheen	91.7%	AdSpn_KlukshuRiver2016	5.1%
14/08/2016 -- 403	Lake	Clear	Lake only	No signals picked up at weir, Motheral tor Vand towers, only strong signals at lake tower from Sep 2 to Oct 6.	73	U_Tatshensh_RT	41.6%	AdSpn_KlukshuLake2016	21.2%
15/08/2016 -- 515	Lake	Clear	Straight to lake	Passed all the river towers, then detected in lake many times between Aug 25 and Oct 6.	74	AdSpn_KlukshuRiver2016	96.2%	Stinky_Cr_RT	1.8%
15/08/2016 -- 319	Lake	Clear	Straight to lake	Passed all the river towers, then detected in lake many times between Aug 20 and Oct 19.	75	Alsek_T_down	51.1%	AdSpn_KlukshuRiver2016	34.0%
15/08/2016 -- 810	River	Interpretation	Moved about mainstem and ended up in river	In Motheral tower range Aug 17/18. Single hit at weir tower Sep 27 (ignore). Heard at Motheral during the 28 Oct aerial surveys.	76	Neskataheen	52.2%	AdSpn_KlukshuRiver2016	44.0%
16/08/2016 -- 706	Lake	Clear	Straight to lake	Passsed all river towers, then detected in lake tower range from Aug 28 to Sep 3. Signal heard at lake during aerial surv on 28 Oct.	77	AdSpn_KlukshuLake2016	98.1%	Neskataheen	1.1%
16/08/2016 -- 619	Lake	Interpretation	Short track ends in lake	Passed all the river towers, then detected in lake Aug 23/25.	78	AdSpn_KlukshuLake2016	51.2%	Alsek_T_down	20.4%
17/08/2016 -- 217	Lake	Clear	Straight to lake	Passed all the river towers, then detected in lake many times between Aug 24 and Oct 6.	79	AdSpn_KlukshuLake2016	61.4%	AdSpn_KlukshuRiver2016	34.6%
17/08/2016 -- 411	Lake	Clear	Straight to lake	Passed all the river towers, then detected in lake many times between Aug 25 and Oct 6. Signal strength suggests fish in the lake upstream of tower.	80	AdSpn_KlukshuLake2016	82.3%	AdSpn_KlukshuRiver2016	16.9%
17/08/2016 -- 419	River	Interpretation	Short track ends in river	Heard at weir and Motheral towers, then in Vand tower range Aug 25/26. No subsequent detections.	81	Neskataheen	99.4%	AdSpn_KlukshuRiver2016	0.6%
19/08/2016 -- 302	Lake	Clear	Straight to lake	Passed all the river towers, then detected in lake many times between Aug 25 and Oct 6.	82	Neskataheen	49.8%	AdSpn_KlukshuRiver2016	48.6%
19/08/2016 -- 521	Lake	Interpretation	Short track ends in lake	Heard at Motheral and Vand towers, then detected in lake Aug 25/28.	83	AdSpn_KlukshuLake2016	100.0%	U_Tatshensh_RT	0.0%

Table J 2 continued.

TAG HISTORY					GENETIC STOCK IDENTIFICATION				
Date/Code	Fate	Class	Pattern	Description	ID	Best Match	Prob	2nd Best match	Prob
19/08/2016 – 805	River	Interpretation	Moved about mainstem and ended up in river	Strong signal at Motheral Aug 20/21. Not heard at Vand or lake towers. Signal picked up at lake during the 28 Oct aerial surveys, but considered error.	84	Neskataheen	99.9%	AdSpn_KlukshuRiver2016	0.1%
20/08/2016 -- 712	Lake	Clear	Straight to lake	Passed the river towers, then detected in lake several times between Aug 25 and Oct 6.	86	AdSpn_KlukshuLake2016	98.6%	Neskataheen	1.3%
20/08/2016 -- 210	Lake	Clear	Straight to lake	Passed the river towers, then detected in lake several times between Aug 25 and Oct 6.	87	AdSpn_KlukshuRiver2016	88.2%	Neskataheen	5.9%
20/08/2016 -- 413	Lake	Clear	Moved about mainstem and ended up in lake	Slow fish, dropped back to weir 17 days after tagging and then moved past the river towers into lake (tag stress?). Detected in lake Sep 13 to Oct 5.	123	AdSpn_KlukshuLake2016	100.0%	Tweedsmuir_RT	0.0%

Table J 3: Tagged Females – New Tags / Tag Fate / Late Weir Timing.

61 females were successfully tagged (i.e. have a tag fate) during the Late Timing group (Stat Weeks 35-41, Aug 21 to Oct 4). Tag fates could be clearly assigned for a bit more than half of these (37/61), while the rest required some interpretation of mixed signals. A tag fate could not be determined for 2 additional female tagged during this time window (Table J 6). Tag histories are summarized briefly, then grouped into patterns (e.g. "Loss – Harvested" or "Straight to Lake") and assigned a quality classification (e.g. "Clear", "Interpretation", "Harvested or Lost"). Genetic Stock ID lists the two best matches in the revised Alsek baseline (see Sec. 7.5) and associated probabilities. Agreement between tag fate and genetic stock ID is summarized in Appendix K. Table K 4 shows that the most common pattern was a migration straight to the lake, and a clear majority (25/32, 78%) of these fish were genetically matched to the lake spawner baseline. The second most common pattern was migration straight to the lake, but with mixed signals, which had an even higher match rate to the genetic stock ID (8/8, 100%). 6 fish with short radio tracking that ended in the river were assigned a river tag fate, but all were genetically matched to the lake spawner baseline (0/6, 0% match). 7 other tag patterns were observed for 1-3 fish each, with variable matches rates to the GSI results ranging from 0% to 100% with small sample sizes. Table 24 compares match rates by timing group for different tag movement patterns.

TAG HISTORY					GENETIC STOCK IDENTIFICATION				
Date/Code	**Fate**	**Class**	**Pattern**	**Description**	**ID**	**Best Match**	**Prob**	**2nd Best match**	**Prob**
21/08/2016 -- 507	Lake	Interpretation	Straight to lake	Heard at river towers, then detected in lake between Sep 3 and Sep 9.	89	AdSpn_Klukshu River2016	76.5%	Neskataheen	22.4%
21/08/2016 -- 311	River	Interpretation	Lake outlet	Passed river towers, then in lake tower range between Sep 26 and Oct 1. Suspect below lake based on the two days (26 Sep and 01 Oct) of weak signals detected by the downstream antenna only. Also heard at weir tower on Oct 1, but assume to be phantom signal.	90	AdSpn_Klukshu River2016	57.7%	Alsek_T_down	33.6%
21/08/2016 -- 815	Lake	Clear	Straight to lake	Passed the river towers, then detected in lake tower range Aug 27 to Oct 1. Heard at lake during the 28 Oct aerial surveys.	91	AdSpn_Klukshu Lake2016	97.9%	Neskataheen	1.8%
21/08/2016 -- 418	River	Interpretation	Short track ends in river	Picked up at weir and Motheral towers, then detected at Vand tower Aug 25. No subsequent detections.	88	AdSpn_Klukshu Lake2016	99.9%	AdSpn_Klukshu River2016	0.0%
22/08/2016 -- 719	Lake	Interpretation	Short track ends in lake	Possibly tag record error based on timing to Motheral tower (4 weeks to Motheral, vs. typical few days). Standard pattern after first detection.	92	AdSpn_Klukshu Lake2016	96.0%	AdSpn_Klukshu River2016	3.0%
22/08/2016 -- 611	Lake	Clear	Straight to lake	Passed all the river towers, then detected in lake between Aug 27 and Sep 7.	93	AdSpn_Klukshu River2016	82.2%	U_Tatshensh_RT	14.6%
22/08/2016 -- 221	Lake	Clear	Straight to lake	Passed all the river towers, then detected in lake several times between Aug 26 and Sep 17.	94	AdSpn_Klukshu Lake2016	98.9%	AdSpn_Klukshu River2016	0.9%
23/08/2016 -- 310	Lake	Interpretation	Straight to lake, but with mixed signals	Confusing signal record. In lake tower range from Aug 28 to Oct 5, and heard at lake during aerial survey on Oct 28. However, also heard weak signal at Vand on 12 Oct (phantom?). Concluded a lake spawner	97	AdSpn_Klukshu Lake2016	95.2%	Neskataheen	3.5%
23/08/2016 -- 404	Lake	Clear	Straight to lake	Passed all the river towers, then detected in lake several times between Aug 28 and Sep 18.	95	AdSpn_Klukshu Lake2016	96.9%	AdSpn_Klukshu River2016	1.9%
23/08/2016 -- 509	River	Clear	Moved about mainstem and ended up in river	Heard at weir and Motheral towers, then in Vand tower range Sep 2 to Oct 14.	96	Neskataheen	75.5%	AdSpn_Klukshu River2016	22.9%
24/08/2016 -- 821	Lake	Interpretation	Short track ends in lake	Passed river towers, then detected in lake Aug 28. No subsequent detections. Significantly faster migration than other tagged fish.	98	AdSpn_Klukshu Lake2016	98.5%	AdSpn_Klukshu River2016	1.0%
24/08/2016 -- 714	Lake	Interpretation	Short track ends in lake	Heard at weir and Vand towers, then detected in lake tower range Aug 29. No subsequent detections.	99	Stinky_Cr_RT	73.6%	U_Tatshensh_RT	13.9%

Table J 3 continued.

TAG HISTORY					GENETIC STOCK IDENTIFICATION				
Date/Code	**Fate**	**Class**	**Pattern**	**Description**	**ID**	**Best Match**	**Prob**	**2nd Best match**	**Prob**
24/08/2016 - - 618	River	Interpretation	Short track ends in river	Never heard on any other towers besides the weir tower and left this site the same day. Heard during aerial survey on 28 Oct above weir.	100	AdSpn_KlukshuLake2016	46.4%	Neskataheen	41.7%
27/08/2016 - - 207	Lake	Clear	Straight to lake	Passed the river towers, then detected by lake tower many times from Sep 2 to Oct 1.	101	AdSpn_KlukshuLake2016	100.0%	Kudwat_Cr_RT	0.0%
27/08/2016 - - 406	Lake	Interpretation	Moved about mainstem and ended up in lake	Passed weir and Motheral towers, then detected by each of Vand tower and lake tower several times from Sep 2 to Oct 5. . Seems as if this tag may have been captured and redeployed or carried by a harvester after the original migration to spawning ground.	102	AdSpn_KlukshuLake2016	99.0%	Kudwat_Cr_RT	0.4%
27/08/2016 - - 517	Lake	Interpretation	Straight to lake	Heard at river towers, then detected by lake tower several times from Sep 3 to Sep 19. Signals mostly weak.	103	AdSpn_KlukshuLake2016	48.5%	Kudwat_Cr_RT	46.6%
27/08/2016 - - 306	Lake	Interpretation	Moved about mainstem and ended up in lake	In lake tower range from Sep 2 to Oct 1. Strong signal at Vand tower on Sep 12, and strong signal back at lake tower on Sep 15. Assume fish dropped down to Vand and returned to lake.	104	AdSpn_KlukshuLake2016	97.5%	OConnor_RT	0.8%
28/08/2016 - - 405	Lake	Interpretation	Straight to lake, but with mixed signals	Passed river towers, then in lake tower range from Sep 3 to Oct 18. Oddly, also picked up signal at weir on Sept 12, but consider it false hit given the strong sig at the lake in Sep and no record of it at Vand or Motheral on the way downstream.	105	AdSpn_KlukshuLake2016	99.7%	Tweedsmuir_RT	0.3%
28/08/2016 - - 501	Lake	Clear	Straight to lake	Passed the river towers, then detected by lake tower several times from Sep 2 to Oct 6.	106	Tweedsmuir_RT	67.0%	Kudwat_Cr_RT	15.0%
28/08/2016 - - 316	Lake	Clear	Straight to lake	Passed the river towers, then detected by lake tower several times from Sep 3 to Oct 19.	107	AdSpn_KlukshuLake2016	97.1%	Kane	2.5%
28/08/2016 - - 813	Lake	Clear	Straight to lake	Passed the river towers, then detected by lake tower many times from Sep 3 to Oct 6. Heard at lake during 28 Oct aerial surveys.	108	AdSpn_KlukshuLake2016	99.9%	Kudwat_Cr_RT	0.1%
29/08/2016 - - 709	Lake	Clear	Lake only	No signal from river towers (weir, Motheral, Vand), but detected several times in lake between Sep 3 and Sep 25. Tag malfunction or magnet left on but during the course of migration dislodged itself from tag?	109	AdSpn_KlukshuLake2016	100.0%	Stinky_Cr_RT	0.0%
29/08/2016 - - 606	River	Interpretation	Short track ends in river	located via aerial surveys on 28 Oct above weir, left the weir the day after tagging never heard again on any of the towers.	110	AdSpn_KlukshuLake2016	98.0%	Neskataheen	1.9%
29/08/2016 - - 204	Lake	Clear	Straight to lake	Heard at Motheral and Vand towers, then detected by lake tower many times from Sep 4 to Oct 2.	111	AdSpn_KlukshuLake2016	100.0%	Kudwat_Cr_RT	0.0%
29/08/2016 - - 414	Lake	Clear	Moved about mainstem and ended up in lake	Moved between Motheral and Vand towers, then detected in lake on Sep 9 and then again on Oct 6. Also located in lake via aerial surveys 28 Oct.	112	Neskataheen	58.2%	Tweedsmuir_RT	25.8%
31/08/2016 - - 323	Lake	Clear	Straight to lake	Moved between Motheral and Vand towers, then detected in lake on Sep 9 and then again on Oct 6. Also located in lake via aerial surveys 28 Oct.	113	AdSpn_KlukshuLake2016	97.3%	Neskataheen	1.1%
31/08/2016 - - 809	Lake	Clear	Straight to lake	Passed river towers, then detected in lake on Sep 6 and then again on Sep 14. Also located in lake via aerial surveys 28 Oct.	114	AdSpn_KlukshuLake2016	100.0%	Stinky_Cr_RT	0.0%
01/09/2016 - - 718	Lake	Clear	Straight to lake	Passed river towers, then detected by lake tower several times from Sep 6 to Oct 6.	115	Stinky_Cr_RT	93.7%	Kane	4.6%

Table J 3 continued.

TAG HISTORY					GENETIC STOCK IDENTIFICATION				
Date/Code	**Fate**	**Class**	**Pattern**	**Description**	**ID**	**Best Match**	**Prob**	**2nd Best match**	**Prob**
01/09/2016 - - 605	Lake	Interpretation	Straight to lake	Passed all river towers in quick succession, then in lake tower range from Sep 5 to Sept 18. Signal at Vand tower on 19 Sept (signal skip?), but fish located in lake during aerial surveys Oct 28.	116	AdSpn_KlukshuLake2016	100.0%	Kane	0.0%
03/09/2016 - - 203	Lake	Clear	Straight to lake	Passed all river towers in quick succession, then in lake tower range from Sep 9 to Sept 23.	118	AdSpn_KlukshuLake2016	99.7%	Tweedsmuir_RT	0.3%
03/09/2016 - - 209	Lake	Clear	Straight to lake	Passed all river towers in quick succession, then in lake tower range from Sep 9 to Sept 18.	117	Tweedsmuir_RT	80.6%	AdSpn_KlukshuLake2016	18.2%
05/09/2016 - - 807	Lake	Clear	Straight to lake	Passed all river towers in quick succession, then in lake tower range from Sep 9 to Sep 28.	120	OConnor_RT	52.6%	AdSpn_KlukshuLake2016	43.6%
05/09/2016 - - 708	Lake	Interpretation	Straight to lake, but with mixed signals	In Vand tower range Sep 9 and lake tower range Sep12/15. Then detected at Motheral tower Sept 22, and no subsequent detections.Assumed to be carcass drift.	119	AdSpn_KlukshuLake2016	99.7%	Stinky_Cr_RT	0.2%
07/09/2016 - - 613	Lake	Clear	Straight to lake	Detected at Motheral and Vand towers Sep 9/10, then in lake tower range from Sep 12 to Oct 6.	121	AdSpn_KlukshuLake2016	100.0%	OConnor_RT	0.0%
07/09/2016 - - 803	Lake	Clear	Straight to lake	Passed all river towers in quick succession, then in lake tower range from Sep 14 to Oct 6. Heard at lake during the 28 Oct aerial surveys.	122	AdSpn_KlukshuLake2016	98.5%	Tweedsmuir_RT	0.9%
07/09/2016 - - 417	Lake	Clear	Straight to lake	Passed all river towers in quick succession, then in lake tower range from Sep 9 to Sep 24.	124	AdSpn_KlukshuLake2016	99.9%	OConnor_RT	0.1%
07/09/2016 - - 506	Lake	Interpretation	Straight to lake, but with mixed signals	Odd tag history. Passed all river towers in quick succession, then detected by lake tower only once (weak signal), on same day as caught at lake outlet during spawning ground DNA sampling. Fish was spawned out, so looks like it spawned within a fortnight of tagging. Perhaps a tag malfunction?	125	AdSpn_KlukshuLake2016	98.3%	Kane	0.8%
08/09/2016 - - 320	Lake	Clear	Straight to lake, but with mixed signals	Passed all river towers in quick succession, then in lake tower range from Sep 15 to Sep 27.	126	AdSpn_KlukshuLake2016	99.9%	OConnor_RT	0.1%
08/09/2016 - - 802	Lake	Interpretation	Lake outlet	Passed all river towers, then in lake tower range from Sep 15 to Oct 3. Heard a weak signal at Vand tower on 12 Oct. Assumed to be spawning at lake outlet and then a carcass drift down to Vand.	127	OConnor_RT	67.0%	Tweedsmuir_RT	22.6%
08/09/2016 - - 705	Lake	Clear	Straight to lake, but with mixed signals	Passed all river towers, then in lake tower range from Sep 14 to Sep 22.	128	AdSpn_KlukshuLake2016	99.8%	Stinky_Cr_RT	0.1%
09/09/2016 - - 211	Lake	Clear	Lake only	No signal picked up from weir, Motheral or Vand towers. In lake tower range from Sep 14 to Oct 6. Suspect magnet left on and only dislodged after a while during migrations?	129	AdSpn_KlukshuLake2016	99.4%	Kane	0.2%
09/09/2016 - - 609	River	Clear	Moved about mainstem and ended up in river	Detected at Vand Sep 14, downstream at Motheral Oct 11, and then last detection at Vand tower Oct 13.	130	Neskataheen	96.6%	AdSpn_KlukshuLake2016	3.1%
11/09/2016 - - 412	River	Clear	Moved about mainstem, but stayed in lower river	In and out of weir tower range from Sep 11 to Oct 15, indicating it was not a mortality. Heard above weir during aerial surveys 28 Oct	131	AdSpn_KlukshuLake2016	99.9%	Kane	0.1%

Table J 3 continued.

TAG HISTORY					GENETIC STOCK IDENTIFICATION				
Date/Code	**Fate**	**Class**	**Pattern**	**Description**	**ID**	**Best Match**	**Prob**	**2nd Best match**	**Prob**
11/09/2016 - - 518	Lake	Clear	Straight to lake	Passed all river towers in quick succession, then in lake tower range from Sep 14 to Oct 4.	132	AdSpn_KlukshuLake2016	98.9%	Kane	1.0%
11/09/2016 - - 307	Lake	Clear	Straight to lake	Passed all river towers, then in lake tower range from Sep 23 to Sep 30.	133	AdSpn_KlukshuLake2016	99.5%	Stinky_Cr_RT	0.2%
11/09/2016 - - 819	Lake	Clear	Straight to lake	Passed all river towers in quick succession, then in lake tower range from Sep 16 to Oct 4.	134	AdSpn_KlukshuLake2016	99.2%	OConnor_RT	0.3%
12/09/2016 - - 707	Lake	Interpretation	Straight to lake, but with mixed signals	Passed all river towers in quick succession, then in lake tower range from Sep 19 to Oct 12. Signal also heard at Vand on Oct 13, but assumed to be a skip / .atmosphere). Tag heard during aerial surveys on 28 Oct at lake.	135	AdSpn_KlukshuLake2016	99.3%	OConnor_RT	0.3%
15/09/2016 - - 206	Lake	Clear	Straight to lake	Passed all river towers in quick succession, then in lake tower range from Sep 19 to Sep 28.	137	AdSpn_KlukshuLake2016	99.5%	Kane	0.4%
15/09/2016 - - 416	Lake	Clear	Straight to lake	Passed all river towers, then in lake tower range from Sep 26 to Oct 12.	138	OConnor_RT	99.8%	Kane	0.0%
16/09/2016 - - 504	Lake	Clear	Straight to lake	Passed all river towers, then in lake tower range from Sep 23 to Oct 3.	139	AdSpn_KlukshuLake2016	91.0%	Stinky_Cr_RT	4.2%
16/09/2016 - - 315	River	Interpretation	Lake outlet	Quickly passed all the river towers and in lake tower range from Sep 21 to Oct 5, but mostly weak signal at lake and only on the downstream antenna (<70). Concluded that it did not enter lake and prob spawned below lake	140	AdSpn_KlukshuLake2016	100.0%	Kane	0.0%
17/09/2016 - - 820	River	Interpretation	Short track ends in river	Heard at Motheral Sep 22/23 and Vand Sep 25/26. No subsequet detections.	141	AdSpn_KlukshuLake2016	97.2%	Tweedsmuir_RT	1.6%
17/09/2016 - - 716	Lake	Clear	Straight to lake	Passed all river towers, then in lake tower range from Sep 23 to Oct 6.	142	AdSpn_KlukshuLake2016	100.0%	Kane	0.0%
18/09/2016 - - 616	Lake	Clear	Straight to lake	Passed all river towers, then in lake tower range from Sep 23 to Oct 4.	143	AdSpn_KlukshuLake2016	99.5%	Kudwat_Cr_RT	0.5%
18/09/2016 - - 202	River	Interpretation	Short track ends in river	Heard at Motheral Sep 21 and Vand Sep 22. No subsequet detections.	144	AdSpn_KlukshuLake2016	99.8%	Kudwat_Cr_RT	0.1%
19/09/2016 - - 420	Lake	Clear	Straight to lake	Passed all river towers, then in lake tower range several times from Sep 25 to Oct 6 (last signal out of water).	145	AdSpn_KlukshuLake2016	100.0%	Kudwat_Cr_RT	0.0%
19/09/2016 - - 511	Lake	Clear	Straight to lake	Passed all river towers, then in lake tower range several times from Sep 25 to Oct 6.	146	AdSpn_KlukshuLake2016	95.6%	OConnor_RT	3.4%

Table J 3 continued.

TAG HISTORY					GENETIC STOCK IDENTIFICATION				
Date/Code	**Fate**	**Class**	**Pattern**	**Description**	**ID**	**Best Match**	**Prob**	**2nd Best match**	**Prob**
20/09/2016 - - 321	Lake	Clear	Straight to lake	Passed all river towers, then in lake tower range several times from Sep 23 to Oct 1. Heard during aerial survey on 28 Oct in lake	147	AdSpn_KlukshuLake2016	55.1%	Kudwat_Cr_RT	37.7%
20/09/2016 - - 822	Lake	Interpretation	Straight to lake, but with mixed signals	Passed all river towers, then in lake tower range several times from Sep 27 to Oct 3. Last lake tower detection probably downstream between lake and Vand. Heard at lake during the 28 Oct aerial surveys.	148	AdSpn_KlukshuLake2016	99.9%	Kudwat_Cr_RT	0.1%
22/09/2016 - - 213	Lake	Interpretation	Lake only	Signal not picked up at any river towers, but in lake tower range from Sep 26 to Oct 4. Suspect the magnet was left on the fish and it dislodged from the tag over time.	151	AdSpn_KlukshuLake2016	99.9%	OConnor_RT	0.1%
04/10/2016 - - 601	River	Interpretation	Short track ends in river	In Motheral tower range Oct 6 and Oct 19 Also picked signal up at lake on the date of application, but ignored.	163	AdSpn_KlukshuLake2016	99.9%	Neskataheen	0.1%

Table J 4: Tagged Males – New Tags / Tag Fate / All Timing.

13 males were successfully tagged (i.e. have a tag fate), mostly throughout the early part of the adult migration past Klukshu weir (13 from Jul 24 to Aug 9, 1 on Sep 21). Note that a tag history could not be associated with 1 additional tag (Table J 6), and that 1 male was also tagged with a redeployed tag late in the season (Table J 5). Tag fates could be clearly assigned for half of these (7/14), while the other half required some interpretation of mixed signals. Tag histories are summarized briefly, then grouped into patterns (e.g. "Loss – Harvested" or "Straight to Lake") and assigned a quality classification (e.g. "Clear", "Interpretation", "Harvested or Lost"). Genetic Stock ID lists the two best matches in the revised Alsek baseline (see Sec. 7.5) and associated probabilities. Agreement between tag fate and genetic stock ID is summarized in Appendix K. Table K 5 shows that less than half of the tagged males had tag fates that matched the genetic stock identification (7/15, 47%), but accuracy differed between tag history patterns. All 3 males that moved about the mainstem and ended up in the river were genetically matched to the river spawner baseline, but other tag patterns matched less (67%,50%,50%). Sample sizes are very small, so observations should not be generalized, but can help with shaping future research into spawning behaviour of male Sockeye in the Klukshu system.

TAG HISTORY						GENETIC STOCK IDENTIFICATION				
Sample Group	**Date/Code**	**Fate**	**Class**	**Pattern**	**Description**	**ID**	**Best Match**	**Prob**	**2nd Best match**	**Prob**
EarlyTag	24/07/2016 -- 301	Lake	Interpretation	Straight to lake, but with mixed signals	Detected at Vand Tower Aug 23/25 and in lake tower range Aug 24 and Sep 6. Assume moved about upper river then entered lake.	18	Neskataheen	60.4%	AdSpn_KlukshuRiver2016	38.9%
EarlyTag	24/07/2016 -- 818	River	Interpretation	Lake outlet	Passed Vand Jul31, then detected in lake tower range many times between Aug 1 and Oct 6 (but note: downstream antenna strength from the lake tower indicates lake outlet), then dropped to Vand tower range Oct 11/12. Likely carcass drift at that point.	19	AdSpn_KlukshuLake2016	99.4%	U_Tatshensh_RT	0.5%
EarlyTag	26/07/2016 -- 409	River	Clear	Moved about mainstem and ended up in river	Detected in Vand tower range many times between Aug 14 and Oct 14.	21	Neskataheen	82.0%	AdSpn_KlukshuRiver2016	17.8%
EarlyTag	27/07/2016 -- 519	Lake	Clear	Straight to lake	Detected in Lake Aug 3/4. Male fish did not roam, went directly into lake.	26	AdSpn_KlukshuLake2016	62.5%	AdSpn_KlukshuRiver2016	20.7%
EarlyTag	27/07/2016 -- 510	Lake	Clear	Moved about mainstem and ended up in lake	Detected in Lake Aug 30 and Sep 25. Male fish, seemed to roam in the mainstem Klukshu for all of August before entering the lake.	25	AdSpn_KlukshuRiver2016	99.0%	Neskataheen	0.7%
EarlyTag	28/07/2016 -- 503	Lake	Clear	Straight to lake	Passed weir and Motheral towers shortly after tag application, then detected in lake several times between Aug 23 and Oct 18	34	Neskataheen	99.7%	AdSpn_KlukshuRiver2016	0.3%
EarlyTag	28/07/2016 -- 604	River	Interpretation	Lake and drop	Spent most of August in Motheral tower range, then detected in lake Sep 17, and dropped back to Motheral Oct 19. Heard at Motheral during Oct 28 aerial survey.	30	Neskataheen	76.9%	AdSpn_KlukshuRiver2016	22.4%
EarlyTag	28/07/2016 -- 1	Lake	Clear	Straight to lake	Passed all the river towers then detected in lake many times between Aug 4 and Sep 19.	31	AdSpn_KlukshuLake2016	64.2%	AdSpn_KlukshuRiver2016	28.9%
EarlyTag	28/07/2016 -- 402	River	Interpretation	Lake and drop	In lake several times from Sep 28 and Oct 1, then dropped to Vand tower range Oct 1/6/19. even went back to weir on 18 August. Heard at Motheral area during aerial surveys on 28 Oct, assume drifted down from Vand as a carcass	32	Alsek_T_down	32.6%	AdSpn_KlukshuLake2016	25.4%

Table J 4 continued.

TAG HISTORY						GENETIC STOCK IDENTIFICATION				
Sample Group	**Date/Code**	**Fate**	**Class**	**Pattern**	**Description**	**ID**	**Best Match**	**Prob**	**2nd Best match**	**Prob**
EarlyTag	28/07/2016 -- 402	River	Interpretation	Lake and drop	In lake several times from Sep 28 and Oct 1, then dropped to Vand tower range Oct 1/6/19. even went back to weir on 18 August. Heard at Motheral area during aerial surveys on 28 Oct, assume drifted down from Vand as a carcass	32	Alsek_T_down	32.6%	AdSpn_KlukshuLake2016	25.4%
EarlyTag	28/07/2016 -- 318	River	Interpretation	Lake outlet	Passed river towers quickly, then detected in lake tower range many times between Aug 5 and Oct 16, but note that sometimes only weak signal on downstream antennna of lake tower, final detection downstream of lake outlet during aerial survey. Spawning near lake outlet tower.	33	AdSpn_KlukshuLake2016	95.7%	AdSpn_KlukshuRiver2016	2.6%
EarlyTag	29/07/2016 -- 304	River	Clear	Moved about mainstem and ended up in river	Detected many times at Vand tower from Aug 10 to Oct 19.Originally recorded as lake fate.	41	AdSpn_KlukshuRiver2016	99.9%	U_Tatshensh_RT	0.0%
EarlyTag	30/07/2016 -- 309	Lake	Interpretation	Moved about mainstem and ended up in lake	Passed all the river towers, then last detections in lake Aug 26, Sep 9, and Sep 16. However, long delay between Motheral and Vand (23 days). Wandering male?	48	Neskataheen	79.9%	AdSpn_KlukshuRiver2016	19.8%
EarlyTag	09/08/2016 -- 215	River	Clear	Moved about mainstem and ended up in river	Moving up and down on mainstem. Detected several times at each of the river towers. Last detection at Vand tower Sep 2.	66	Neskataheen	79.9%	AdSpn_KlukshuRiver2016	16.9%
LateTag	21/09/2016 -- 603	Lake	Interpretation	Short track ends in lake	Passed all river towers, then in lake tower range once on Sep 26.	150	Neskataheen	95.2%	AdSpn_KlukshuLake2016	4.5%

Table J 5: All Redeployed Tags – Female and Male.

Redeployed tags were applied to 11 females and 1 male late in the migration past Kluksu weir (Sep 12 to Oct 1). All 12 of these had short tracking record, but only 1 was not assigned a tage fate. Tag histories are summarized briefly, then grouped into patterns (e.g. "Loss – Harvested" or "Straight to Lake") and assigned a quality classification (e.g. "Clear", "Interpretation", "Harvested or Lost"). Genetic Stock ID lists the two best matches in the revised Alsek baseline (see Sec. 7.5) and associated probabilities. Agreement between tag fate and genetic stock ID is summarized in Appendix K. Table K 6 shows that 4 of 5 (80%) tags assigned to lake spawners based on the short tag history were genetically matched to the lake spawner baseline as well. However, none of the 6 (0%) tags classified as river destination were genetically matched to river spawner baseline, with 4 of them genetically identified as lake spawners. Overall, only 4 of the 11 (36%) redeployed tags had destinations that matched the genetic stock ID.

TAG HISTORY					GENETIC STOCK IDENTIFICATION				
Date/Code	**Fate**	**Class**	**Pattern**	**Description**	**ID**	**Best Match**	**Prob**	**2nd Best match**	**Prob**
12/09/2016 -- 201	Lake	Interpretation	Short track ends in lake	Passed all river towers in quick succession, then in lake tower range from Sep 17 to Sep 26.	136	AdSpn_KlukshuLake2016	99.7%	Kudwat_Cr_RT	0.1%
22/09/2016 -- 622	River	Interpretation	Short track ends in river	Heard at Motheral Sep 28/29 and Vand Sep 30. No subsequet detections.	152	AdSpn_KlukshuLake2016	100.0%	Neskataheen	0.0%
23/09/2016 -- 615	Lake	Interpretation	Short track ends in lake	Passed all river towers, then in lake tower range on Oct4/5.	153	AdSpn_KlukshuLake2016	100.0%	OConnor_RT	0.0%
25/09/2016 -- 407	River	Interpretation	Short track ends in river	Heard at Motheral Oct 3/4 and Vand Oct 6/7. No subsequet detections.	154	Kudwat_Cr_RT	64.5%	AdSpn_KlukshuLake2016	34.9%
25/09/2016 – 401 **MALE**	Lake	Interpretation	Short track ends in lake	Passed all river towers, then in lake tower range a few times from Sep 30 to Oct 2.	155	AdSpn_KlukshuLake2016	99.9%	Kudwat_Cr_RT	0.0%
26/09/2016 -- 212	Lake	Interpretation	Short track ends in lake	Passed all river towers, then in lake tower range a few times from Oct 1-5.	156	Tweedsmuir_RT	84.6%	Kudwat_Cr_RT	8.3%
26/09/2016 -- 502	Lake	Interpretation	Short track ends in lake	Passed all river towers, then in lake tower range a few times from Sep 30 to Oct 8.	157	AdSpn_KlukshuLake2016	74.5%	OConnor_RT	21.6%
26/09/2016 -- 505	River	Interpretation	Short track ends in river	Heard at Motheral Oct 2 and Vand Oct 4. No subsequet detections.	158	AdSpn_KlukshuLake2016	100.0%	Neskataheen	0.0%
28/09/2016 -- 721	River	Interpretation	Short track ends in river	Heard at Motheral (strong) and Vand (weak) on Oct 1. Signal heard in the lake during aerial surveys Oct 28, but assumed to be error, because signal not heard at lake tower.	159	Kane	99.6%	Tweedsmuir_RT	0.2%
29/09/2016 -- 520	River	Interpretation	Short track ends in river	Heard at Motheral Oct 4 and Vand Oct 5. No subsequet detections.	160	AdSpn_KlukshuLake2016	99.8%	OConnor_RT	0.1%
01/10/2016 -- 702	River	Interpretation	Short track ends in river	Heard at Motheral Oct 4 and Vand Oct 5. No subsequet detections.	162	AdSpn_KlukshuLake2016	47.5%	Kudwat_Cr_RT	37.0%
01/10/2016 -- 317	Undetermined	Harvested or Lost	Loss - Assumed	Strong signal at Motheral on Oct 7, no signal at Vand, and weak signal at lake tower on Oct 6 (assumed phantom signal) Motheral signal could be close to weir. Aerial survey picked it up above weir Oct 28. Assumed mortality or tag loss.	161	AdSpn_KlukshuLake2016	100.0%	OConnor_RT	0.0%

Table J 6: Tags with Undetermined Fate or Missing Record.

150 new tags were applied to adult salmon passing Klukshu weir in 2016. A clear spawning destination could not be determined for 8 of these tags. 3 of them were returned by harvesters, and 1 appears to have been caught and brought to Klukshu Village. 3 were lost to predation or migration mortality. An additional 3 fish in the tagged sample (i.e. have fish ID and DNA sample) did not have an associated tag record. Note that 1 of the redeployed tags also had an undetermined spawning destination (Table J 5). Tag histories are summarized briefly, then grouped into patterns (e.g. "Loss – Harvested" or "Straight to Lake") and assigned a quality classification (e.g. "Clear", "Interpretation", "Harvested or Lost"). Genetic Stock ID lists the two best matches in the revised Alsek baseline (see Sec. 7.5) and associated probabilities. Agreement between tag fate and genetic stock ID is summarized in Appendix K.

TAG HISTORY					GENETIC STOCK IDENTIFICATION				
Date/Code	**Fate**	**Class**	**Pattern**	**Description**	**ID**	**Best Match**	**Prob**	**2nd Best match**	**Prob**
11/07/2016 -- 615	Undetermined	Harvested or Lost	Loss - Harvested	Tag recovered before 5 Aug in fishery.	1	AdSpn_Klukshu River2016	94.0%	Alsek_T_down	3.6%
13/07/2016 -- 520	Undetermined	Harvested or Lost	Loss - Assumed	Found at culvert. No evidence of spawning. Might have been a mortality. Note: this tag was redeployed on 29 Sept and tracked to Vand	6	AdSpn_Klukshu River2016	74.0%	AdSpn_Klukshu Lake2016	17.9%
16/07/2016 -- 505	Undetermined	Harvested or Lost	Loss - Harvested	Caught in fishery Aug 5 at unknown site.	13	AdSpn_Klukshu River2016	98.8%	Neskataheen	0.9%
27/07/2016 -- 401	Undetermined	Harvested or Lost	Loss - Harvested	Harvested at or near Vand Creek.	24	Stinky_Cr_RT	98.3%	Alsek_T_down	0.9%
28/07/2016 -- NA	Undetermined	Harvested or Lost	Loss - Assumed	Undetermined	33	AdSpn_Klukshu Lake2016	95.7%	AdSpn_Klukshu River2016	2.6%
05/08/2016 -- 516	Undetermined	Harvested or Lost	Loss - Harvested	Signal out of water several times around lake tower. Probably harvested and brought to village.	54	Neskataheen	92.3%	AdSpn_Klukshu Lake2016	7.2%
07/08/2016 – 421	Undetermined	Harvested or Lost	Loss - Assumed	Too much confusion around this tag. Heard at lake with signal strength indicating it was out of the water from early to mid Oct; heard via aerial surveys above weir on Oct 28.	60	Neskataheen	75.6%	AdSpn_Klukshu River2016	21.1%
14/08/2016 -- 701	Undetermined	No Record	No Record	No tag details or detection records	70	AdSpn_Klukshu River2016	60.9%	Neskataheen	36.2%
20/08/2016 -- 622	Undetermined	No Record	No Record	Magnet left on tag therefore did not transmit. We recovered the tag from a prespawn carcass from the weir on 04 Sep. Originally classified as river fate.	85	AdSpn_Klukshu Lake2016	69.3%	AdSpn_Klukshu River2016	19.8%
22/08/2016 -- 713	Undetermined	Harvested or Lost	Loss - Assumed	Likely mortality, Sig indicates the tag was probably out of the water (Detections in weir tower range several times from Aug 22 to Oct 14, weak signal at lake tower Oct 8). Tag found near weir in area with heavy bear activity, so assume predation.	NA	Undetermined	NA	NA	NA
21/09/2016 -- NA	Undetermined	No Record	No Record	No tag details or detection records	149	AdSpn_Klukshu Lake2016	100.0%	Neskataheen	0.0%

Appendix K: Summaries of Tag Fate vs. GSI Match

Table K 1: Tag vs. GSI Match for All Adults Tagged at Klukshu Weir in 2016.
Cells in columns 3 to 9 show the count of tagged fish with a particular value for a grouping variable (rows) and the match between the fate assigned based on radio tags and genetic stock identification (GSI) using the revised Alsek baseline (see Sec. 7.5). T = Tag, G = GSI, R = River, L = Lake, O = Other, NA = tag fate and/or stock ID not available. For example, "T:R /G:L" denotes a river tag fate that was genetically matched to the lake spawners. Columns 3 and 7 show the cases where the two methods give matching results. Note that 3 fish in the tagged sample (i.e. have fish ID and DNA sample) did not have an associated tag record.

1	2	3	4	5	6	7	8	9	10	11	12	13
Variable	Value	T: R / G: R	T: R / G: L	T: R / G: O	T: L / G: R	T: L / G: L	T: L / G: O	NA	Total	Tag & GSI	% Tags	% Corr
Sample_Group	AdWeir_EarlyTagged2016	25	4	2	18	8	1	12	70	58	42	57
Sample_Group	AdWeir_MixTagged2016	5	0	0	3	7	2	2	19	17	12	71
Sample_Group	AdWeir_LateTagged2016	3	12	2	4	44	8	3	76	73	46	64
Sex	F	29	15	3	20	57	11	15	150	135	91	64
Sex	M	4	1	1	5	2	0	2	15	13	9	46
Tag_Use	New	33	12	2	25	55	10	13	150	137	91	64
Tag_Use	No Record	0	0	0	0	0	0	3	3	0	2	-
Tag_Use	Redeployed	0	4	2	0	4	1	1	12	11	7	36
TagHist_Class	Clear	15	2	0	16	39	7	4	83	79	50	68
TagHist_Class	Harvested or Lost	0	0	0	0	0	0	9	9	0	5	-
TagHist_Class	Interpretation	18	14	4	9	20	4	1	70	69	42	55
TagHist_Class	No Record	0	0	0	0	0	0	3	3	0	2	-

Table continued on next page.

Table K 1 continued.

1	2	3	4	5	6	7	8	9	10	11	12	13
Variable	Value	T: R / G: R	T: R / G: L	T: R / G: O	T: L / G: R	T: L / G: L	T: L / G: O	NA	Total	Tag & GSI	% Tags	% Corr
TagHist_Pattern	Lake and drop	3	0	1	1	0	1	0	6	6	4	50
TagHist_Pattern	Lake only	0	0	0	0	4	1	0	5	5	3	80
TagHist_Pattern	Lake outlet	2	4	1	0	0	1	0	8	8	5	25
TagHist_Pattern	Loss - Assumed	0	0	0	0	0	0	5	5	0	3	-
TagHist_Pattern	Loss - Harvested	0	0	0	0	0	0	4	4	0	2	-
TagHist_Pattern	Moved about mainstem and ended up at lake outlet	1	0	0	0	0	0	0	1	1	1	100
TagHist_Pattern	Moved about mainstem and ended up in lake	0	0	0	4	3	0	1	8	7	5	43
TagHist_Pattern	Moved about mainstem and ended up in river	18	1	0	0	0	0	3	22	19	13	95
TagHist_Pattern	Moved about mainstem, but stayed in lower river	1	1	0	0	0	0	0	2	2	1	50
TagHist_Pattern	Moved about mainstem, but with mixed signals	4	0	0	0	0	0	0	4	4	2	100
TagHist_Pattern	No record	0	0	0	0	0	0	3	3	0	2	-
TagHist_Pattern	Short track ends in lake	0	0	0	2	8	2	0	12	12	7	67
TagHist_Pattern	Short track ends in river	4	10	2	0	0	0	0	16	16	10	25
TagHist_Pattern	Straight to lake	0	0	0	15	34	6	1	56	55	34	62
TagHist_Pattern	Straight to lake, but with mixed signals	0	0	0	3	10	0	0	13	13	8	77

Table K 2: Tag vs. GSI Match for Females Tagged during the Early Timing Period

Cells in columns 3 to 9 show the count of tagged fish with a particular value for a grouping variable (rows) and the match between the fate assigned based on radio tags and genetic stock identification (GSI) using the revised Alsek baseline (see Sec. 7.5). T = Tag, G = GSI, R = River, L = Lake, O = Other, NA = tag fate and/or stock ID not available. For example, "T:R /G:L" denotes a river tag fate that was genetically matched to the lake spawners. Columns 3 and 7 show the cases where the two methods give matching results. Note that counts do not include the 3 fish without tag records (Table K 1).

1	2	3	4	5	6	7	8	9	10	11	12	13
Variable	Value	T: R / G: R	T: R / G: L	T: R / G: O	T: L / G: R	T: L / G: L	T: L / G: O	NA	Total	Tag & GSI	% Tags	% Corr
Sex	F	21	3	1	14	6	1	10	56	46	34	59
Tag_Use	New	21	3	1	14	6	1	10	56	46	34	59
Tag_Use	Redeployed	0	0	0	0	0	0	0	0	0	0	-
TagHist_Class	Clear	10	1	0	9	5	0	4	29	25	18	60
TagHist_Class	Harvested or Lost	0	0	0	0	0	0	5	5	0	3	-
TagHist_Class	Interpretation	11	2	1	5	1	1	1	22	21	13	57
TagHist_Class	No record	0	0	0	0	0	0	0	0	0	0	-
TagHist_Pattern	Lake and drop	1	0	0	1	0	1	0	3	3	2	33
TagHist_Pattern	Lake only	0	0	0	0	1	0	0	1	1	1	100
TagHist_Pattern	Lake outlet	0	2	1	0	0	0	0	3	3	2	0
TagHist_Pattern	Loss - Assumed	0	0	0	0	0	0	2	2	0	1	NA
TagHist_Pattern	Loss - Harvested	0	0	0	0	0	0	3	3	0	2	NA
TagHist_Pattern	Moved about mainstem and ended up at lake outlet	1	0	0	0	0	0	0	1	1	1	100
TagHist_Pattern	Moved about mainstem and ended up in lake	0	0	0	1	0	0	1	2	1	1	0
TagHist_Pattern	Moved about mainstem and ended up in river	11	1	0	0	0	0	3	15	12	9	92
TagHist_Pattern	Moved about mainstem, but stayed in lower river	1	0	0	0	0	0	0	1	1	1	100
TagHist_Pattern	Moved about mainstem, but with mixed signals	4	0	0	0	0	0	0	4	4	2	100
TagHist_Pattern	Short track ends in lake	0	0	0	1	0	0	0	1	1	1	0
TagHist_Pattern	Short track ends in river	3	0	0	0	0	0	0	3	3	2	100
TagHist_Pattern	Straight to lake	0	0	0	9	3	0	1	13	12	8	25
TagHist_Pattern	Straight to lake, but with mixed signals	0	0	0	2	2	0	0	4	4	2	50

Table K 3: Tag vs. GSI Match for Females Tagged during the Mixed Timing Period

Cells in columns 3 to 9 show the count of tagged fish with a particular value for a grouping variable (rows) and the match between the fate assigned based on radio tags and genetic stock identification (GSI) using the revised Alsek baseline (see Sec. 7.5). T = Tag, G = GSI, R = River, L = Lake, O = Other, NA = tag fate and/or stock ID not available. For example, "T:R /G:L" denotes a river tag fate that was genetically matched to the lake spawners. Columns 3 and 7 show the cases where the two methods give matching results. Note that counts do not include the 3 fish without tag records (Table K 1).

1	2	3	4	5	6	7	8	9	10	11	12	13
Variable	Value	T: R G: R	T: R G: L	T: R G: O	T: L G: R	T: L G: L	T: L G: O	NA	Total	Tag & GSI	% Tags	% Corr
Sex	F	5	0	0	3	7	2	0	17	17	10	71
Tag_Use	New	5	0	0	3	7	2	0	17	17	10	71
Tag_Use	Redeployed	0	0	0	0	0	0	0	0	0	0	-
TagHist_Class	Clear	0	0	0	3	5	2	0	10	10	6	50
TagHist_Class	Interpretation	5	0	0	0	2	0	0	7	7	4	100
TagHist_Pattern	Lake and drop	1	0	0	0	0	0	0	1	1	1	100
TagHist_Pattern	Lake only	0	0	0	0	0	1	0	1	1	1	0
TagHist_Pattern	Lake outlet	1	0	0	0	0	0	0	1	1	1	100
TagHist_Pattern	Moved about mainstem and ended up in lake	0	0	0	0	1	0	0	1	1	1	100
TagHist_Pattern	Moved about mainstem and ended up in river	2	0	0	0	0	0	0	2	2	1	100
TagHist_Pattern	Short track ends in lake	0	0	0	0	2	0	0	2	2	1	100
TagHist_Pattern	Short track ends in river	1	0	0	0	0	0	0	1	1	1	100
TagHist_Pattern	Straight to lake	0	0	0	3	4	1	0	8	8	5	50

Table K 4: Tag vs. GSI Match for Females Tagged during the Late Timing Period

Cells in columns 3 to 9 show the count of tagged fish with a particular value for a grouping variable (rows) and the match between the fate assigned based on radio tags and genetic stock identification (GSI) using the revised Alsek baseline (see Sec. 7.5). T = Tag, G = GSI, R = River, L = Lake, O = Other, NA = tag fate and/or stock ID not available. For example, "T:R /G:L" denotes a river tag fate that was genetically matched to the lake spawners. Columns 3 and 7 show the cases where the two methods give matching results. Note that counts do not include the 3 fish without tag records (Table K 1).

1	2	3	4	5	6	7	8	9	10	11	12	13
Variable	Value	T: R G: R	T: R G: L	T: R G: O	T: L G: R	T: L G: L	T: L G: O	NA	Total	Tag & GSI	% Tags	% Corr
Sex	F	3	8	0	3	40	7	1	62	61	38	70
Tag_Use	New	3	8	0	3	40	7	1	62	61	38	70
Tag_Use	Redeployed	0	0	0	0	0	0	0	0	0	0	-
TagHist_Class	Clear	2	1	0	2	27	5	0	37	37	22	78
TagHist_Class	Harvested or Lost	0	0	0	0	0	0	1	1	0	1	-
TagHist_Class	Interpretation	1	7	0	1	13	2	0	24	24	15	58
TagHist_Class	No record	0	0	0	0	0	0	0	0	0	0	-
TagHist_Pattern	Lake only	0	0	0	0	3	0	0	3	3	2	100
TagHist_Pattern	Lake outlet	1	1	0	0	0	1	0	3	3	2	33
TagHist_Pattern	Moved about mainstem and ended up in lake	0	0	0	1	2	0	0	3	3	2	67
TagHist_Pattern	Moved about mainstem and ended up in river	2	0	0	0	0	0	0	2	2	1	100
TagHist_Pattern	Moved about mainstem, but stayed in lower river	0	1	0	0	0	0	0	1	1	1	0
TagHist_Pattern	Short track ends in lake	0	0	0	0	2	1	0	3	3	2	67
TagHist_Pattern	Short track ends in river	0	6	0	0	0	0	0	6	6	4	0
TagHist_Pattern	Straight to lake	0	0	0	2	25	5	0	32	32	19	78
TagHist_Pattern	Straight to lake, but with mixed signals	0	0	0	0	8	0	0	8	8	5	100

Table K 5: Tag vs. GSI Match for Tagged Males with Tag Records

Cells in columns 3 to 9 show the count of tagged fish with a particular value for a grouping variable (rows) and the match between the fate assigned based on radio tags and genetic stock identification (GSI) using the revised Alsek baseline (see Sec. 7.5). T = Tag, G = GSI, R = River, L = Lake, O = Other, NA = tag fate and/or stock ID not available. For example, "T:R /G:L" denotes a river tag fate that was genetically matched to the lake spawners. Columns 3 and 7 show the cases where the two methods give matching results. Note that counts do not include the 3 fish without tag records (Table K 1).

1	2	3	4	5	6	7	8	9	10	11	12	13
Variable	Value	T: R G: R	T: R G: L	T: R G: O	T: L G: R	T: L G: L	T: L G: O	NA	Total	Tag & GSI	% Tags	% Corr
Sample_Group	AdWeir_EarlyTagged2016	4	1	1	4	2	0	2	14	12	8	50
Sample_Group	AdWeir_MixTagged2016	0	0	0	0	0	0	0	0	0	0	-
Sample_Group	AdWeir_LateTagged2016	0	0	0	1	0	0	0	1	1	1	0
Sex	M	4	1	1	5	2	0	2	15	13	9	46
Tag_Use	New	4	1	1	5	2	0	2	15	13	9	46
Tag_Use	Redeployed	0	0	0	0	1	0	0	1	1	1	100
TagHist_Class	Clear	3	0	0	2	2	0	0	7	7	4	71
TagHist_Class	Harvested or Lost	0	0	0	0	0	0	2	2	0	1	-
TagHist_Class	Interpretation	1	1	1	3	0	0	0	6	6	4	17
TagHist_Pattern	Lake and drop	1	0	1	0	0	0	0	2	2	1	50
TagHist_Pattern	Lake outlet	0	1	0	0	0	0	0	1	1	1	0
TagHist_Pattern	Moved about mainstem and ended up in lake	0	0	0	2	0	0	0	2	2	1	0
TagHist_Pattern	Moved about mainstem and ended up in river	3	0	0	0	0	0	0	3	3	2	100
TagHist_Pattern	Short track ends in lake	0	0	0	1	0	0	0	1	1	1	0
TagHist_Pattern	Straight to lake	0	0	0	1	2	0	0	3	3	2	67
TagHist_Pattern	Straight to lake, but with mixed signals	0	0	0	1	0	0	0	1	1	1	0

Table K 6: Tag vs. GSI Match for Redeployed Tags

Cells in columns 3 to 9 show the count of tagged fish with a particular value for a grouping variable (rows) and the match between the fate assigned based on radio tags and genetic stock identification (GSI) using the revised Alsek baseline (see Sec. 7.5). T = Tag, G = GSI, R = River, L = Lake, O = Other, NA = tag fate and/or stock ID not available. For example, "T:R /G:L" denotes a river tag fate that was genetically matched to the lake spawners. Columns 3 and 7 show the cases where the two methods give matching results. Note that counts do not include the 3 fish without tag records (Table K 1).

1	2	3	4	5	6	7	8	9	10	11	12	13
Variable	Value	T: R G: R	T: R G: L	T: R G: O	T: L G: R	T: L G: L	T: L G: O	NA	Total	Tag & GSI	% Tags	% Corr
Sample_Group	AdWeir_EarlyTagged2016	0	0	0	0	0	0	0	0	0	0	-
Sample_Group	AdWeir_MixTagged2016	0	0	0	0	0	0	0	0	0	0	-
Sample_Group	AdWeir_LateTagged2016	0	4	2	0	4	1	1	12	11	7	36
Sex	F	0	4	2	0	4	1	1	12	11	7	36
Sex	M	0	0	0	0	0	0	0	0	0	0	-
TagHist_Class	Clear	0	0	0	0	0	0	0	0	0	0	-
TagHist_Class	Harvested or Lost	0	0	0	0	0	0	1	1	0	1	-
TagHist_Class	Interpretation	0	4	2	0	4	1	0	11	11	7	36
TagHist_Class	No record	0	0	0	0	0	0	0	0	0	0	-
TagHist_Pattern	Loss - Assumed	0	0	0	0	0	0	1	1	0	1	-
TagHist_Pattern	Short track ends in lake	0	0	0	0	4	1	0	5	5	3	80
TagHist_Pattern	Short track ends in river	0	4	2	0	0	0	0	6	6	4	0

Appendix L: Annual Pattern of Sockeye Counts at Klukshu Weir 1976-2016

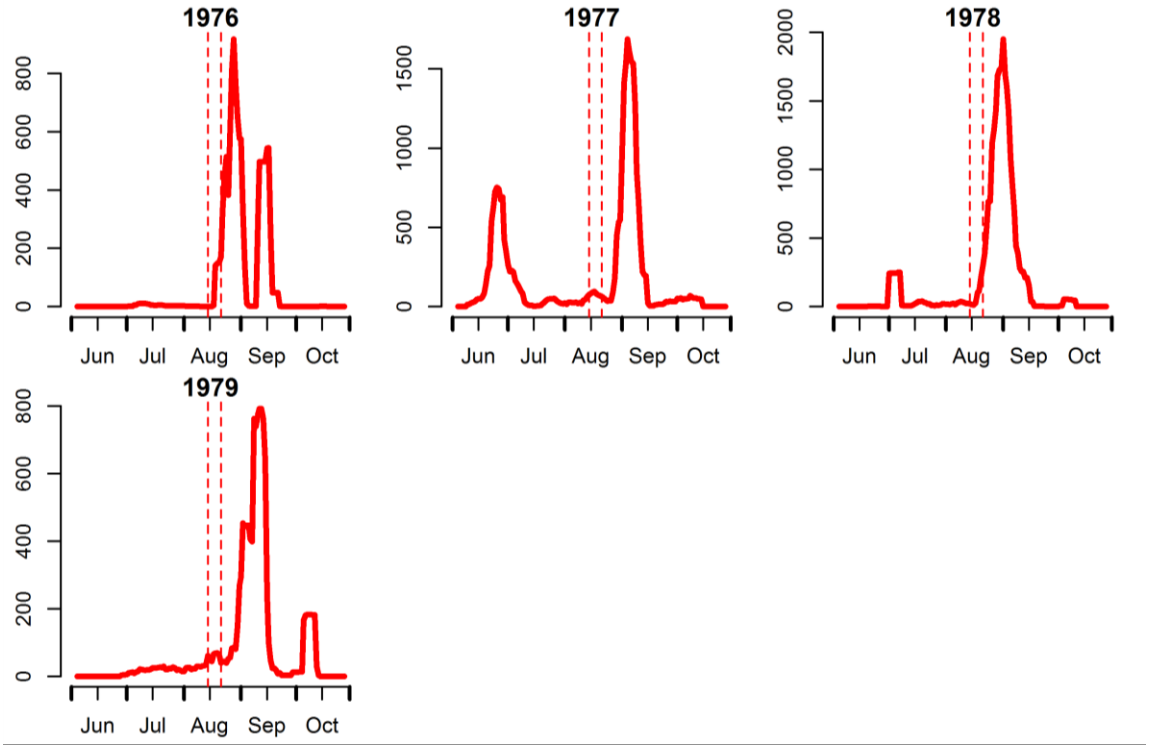


Figure L 1: Pattern of Sockeye Counts at Klukshu Weir – 1970s.
Each panel shows daily sockeye counts as smoothed 7-day average centered on the day. Vertical dashed red lines mark statistical week 34 in 2016 (Aug 14 to Aug 20), which has been used to delineate the Early and Late timing groups.

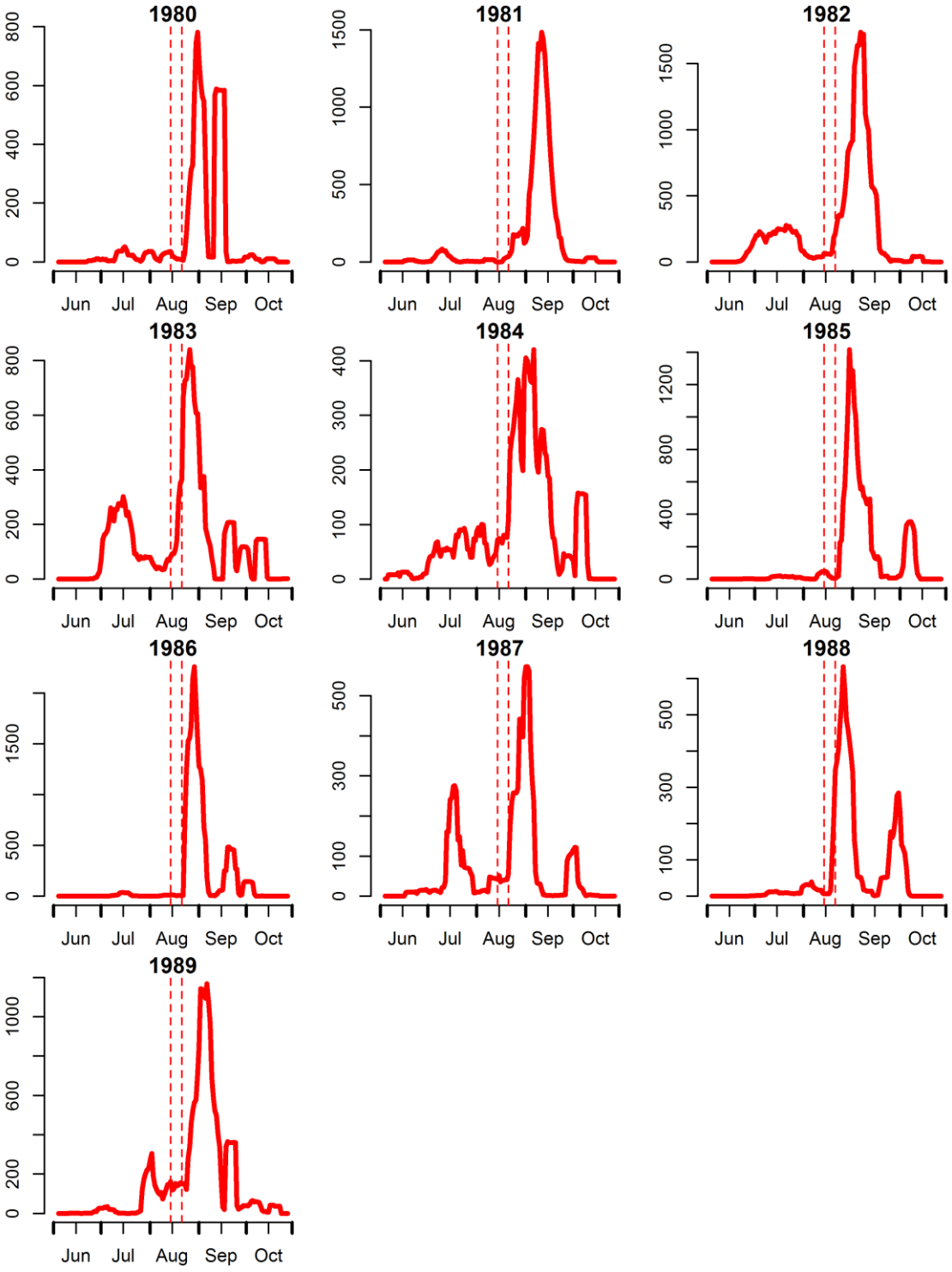


Figure L 2: Pattern of Sockeye Counts at Klukshu Weir – 1980s.
Each panel shows daily sockeye counts as smoothed 7-day average centered on the day. Vertical dashed red lines mark statistical week 34 in 2016 (Aug 14 to Aug 20), which has been used to delineate the Early and Late timing groups.

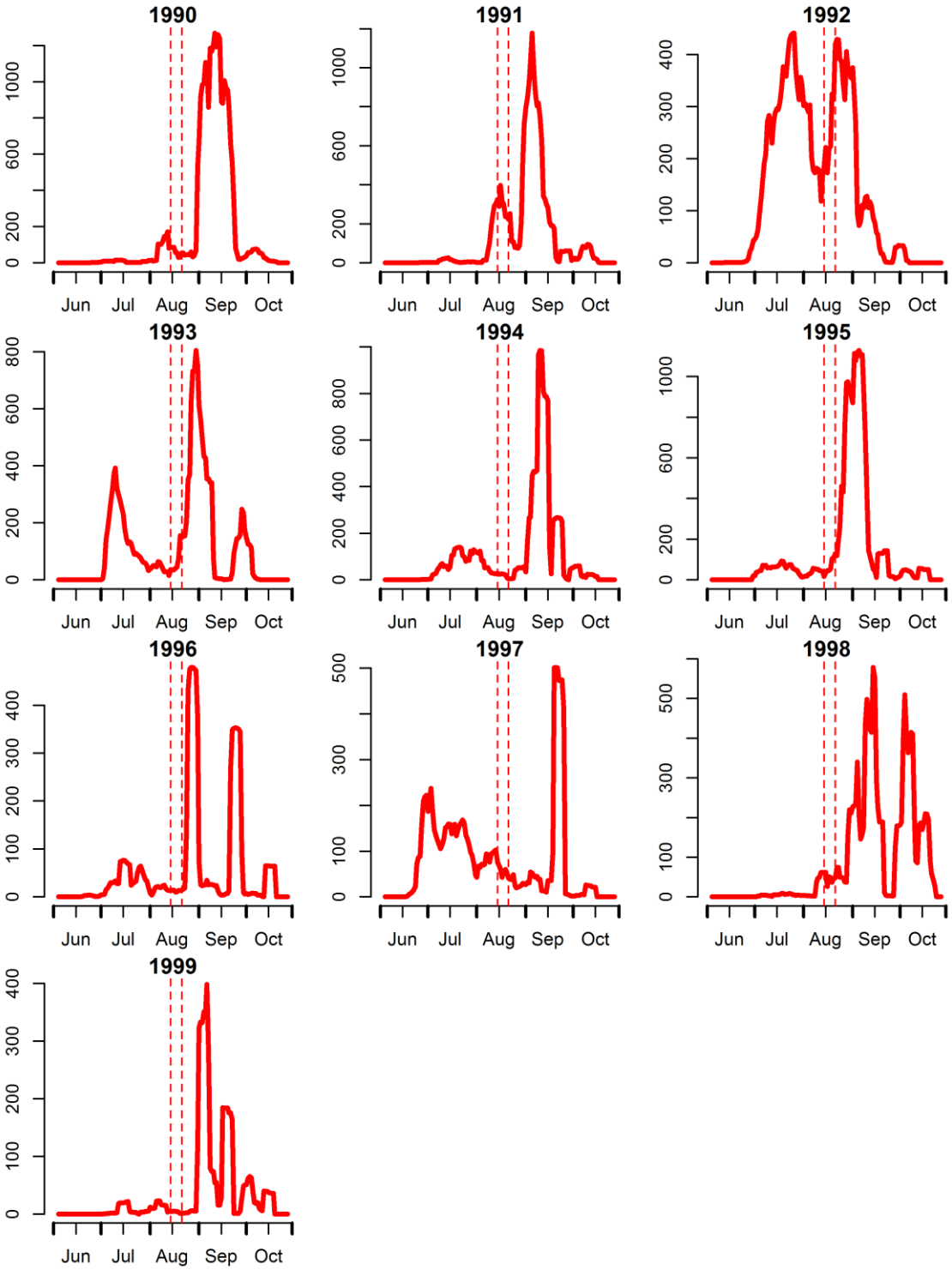


Figure L 3: Pattern of Sockeye Counts at Klukshu Weir – 1990s.
Each panel shows daily sockeye counts as smoothed 7-day average centered on the day. Vertical dashed red lines mark statistical week 34 in 2016 (Aug 14 to Aug 20), which has been used to delineate the Early and Late timing groups.

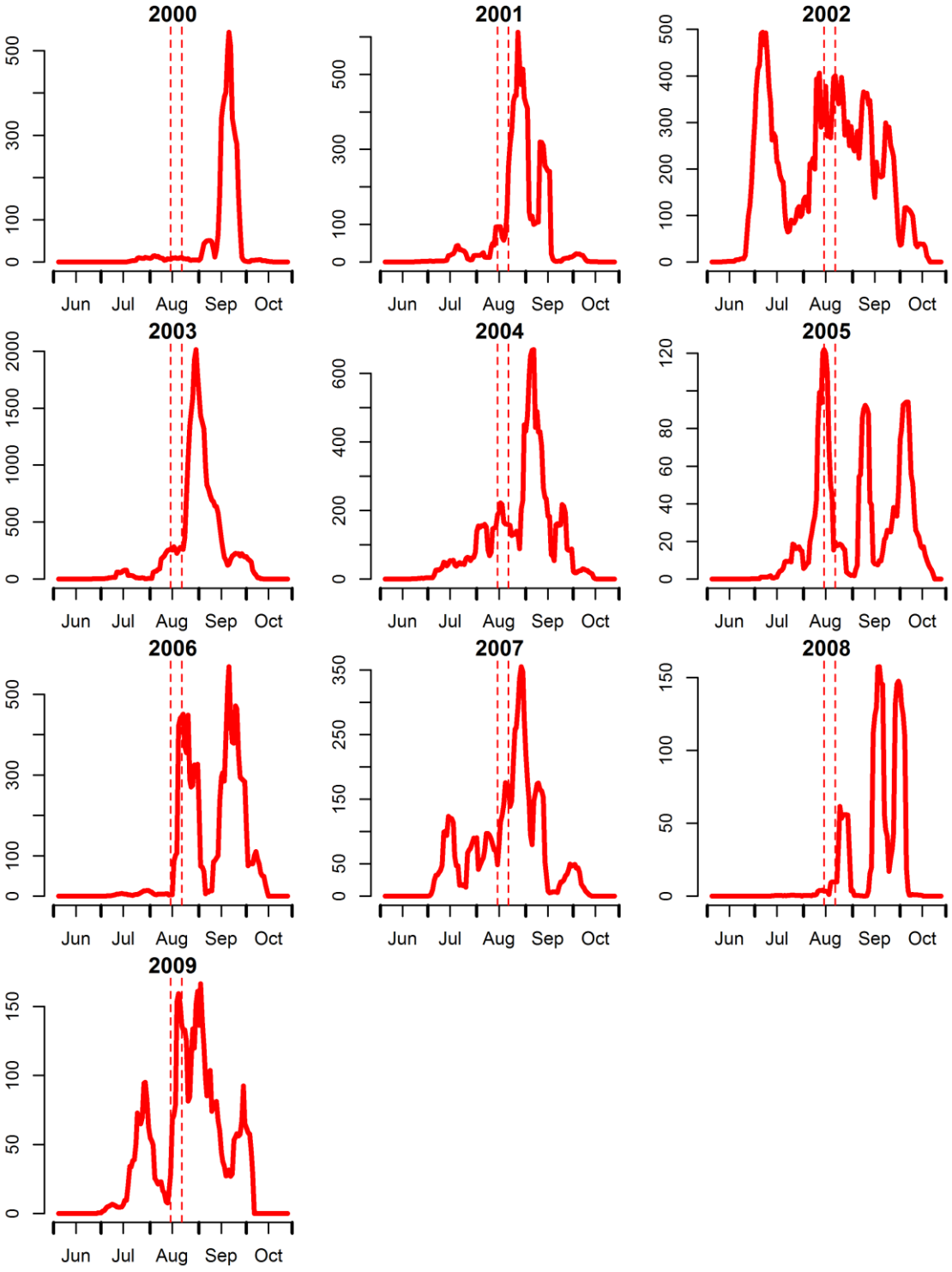


Figure L 4: Pattern of Sockeye Counts at Klukshu Weir – 2000s.
Each panel shows daily sockeye counts as smoothed 7-day average centered on the day. Vertical dashed red lines mark statistical week 34 in 2016 (Aug 14 to Aug 20), which has been used to delineate the Early and Late timing groups.

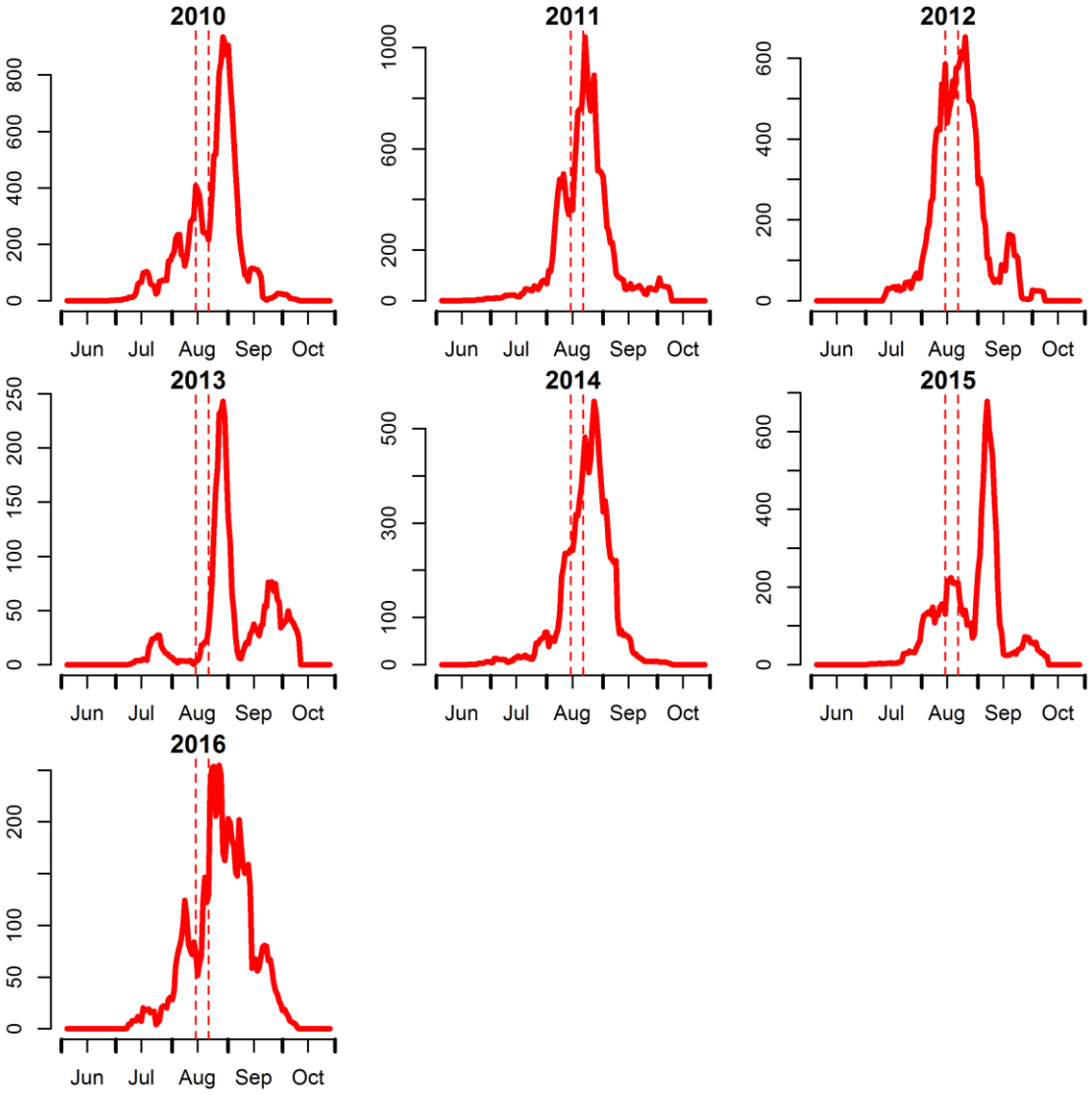


Figure L 5: Pattern of Sockeye Counts at Klukshu Weir – 2010s.
Each panel shows daily sockeye counts as smoothed 7-day average centered on the day. Vertical dashed red lines mark statistical week 34 in 2016 (Aug 14 to Aug 20), which has been used to delineate the Early and Late timing groups.

Appendix M: Additional Tree Fitting Outputs – TreeFit

Table M 1: Genetic Distances for 2016 Klukshu Samples and Revised Alsek Baselines - Dc

This table shows the *Dc* measure of genetic distance (Cavalli-Sforza 1967) for the 2016 Klukshu samples and the revised Alsek baseline (50+ samples only, 2016 Klukshu river and lake spawning ground samples instead of Early/Mix/Late weir samples from previous years). Genetic distances are based on pairwise sample comparisons, and are not affected by having other sample groups in the analysis. Therefore, the distances shown in this table apply to all the alternative genotype sets that were tested (Table 8). Tree fitting, however, is influenced by the full suite of sample groups, and alternative versions were tested (e.g. Figure 12 vs. figures in this appendix). Sample groups that are genetically close (i.e. smaller distance) are highlighted, with breakpoints set at 10% (Red), 20% (Orange), and 30% (Yellow) of the overall range of values across all pairwise comparisons for this distance measure. For example, the genetic distance between lake spawners and late untagged weir samples is 0.1107, which is very small relative to other pairwise comparisons.

	AdWeir_EarlyNoTag2016	AdWeir_EarlyTagged2016	AdWeir_LateNoTag2016	AdWeir_LateTagged2016	AdWeir_MixNoTag2016	AdWeir_MixTagged2016	Juv_KlukLkOutFry2016	Juv_KlukLkOutSmolt2016	Juv_KlukVandCrFry2016	AdSpn_KlukshuLake2016	AdSpn_KlukshuRiver2016
AdWeir_EarlyNoTag2016											
AdWeir_EarlyTagged2016	0.1131										
AdWeir_LateNoTag2016	0.1654	0.1682									
AdWeir_LateTagged2016	0.2123	0.2099	0.1238								
AdWeir_MixNoTag2016	0.1326	0.1493	0.1455	0.1832							
AdWeir_MixTagged2016	0.1843	0.1977	0.1882	0.2219	0.1950						
Juv_KlukLkOutFry2016	0.1902	0.1849	0.0918	0.1397	0.1598	0.1910					
Juv_KlukLkOutSmolt2016	0.2162	0.2101	0.1123	0.1469	0.1832	0.2199	0.1029				
Juv_KlukVandCrFry2016	0.1277	0.1608	0.1916	0.2304	0.1696	0.2112	0.2064	0.2326			
AdSpn_KlukshuLake2016	0.1797	0.1743	0.1107	0.1487	0.1536	0.1995	0.1082	0.1250	0.2068		
AdSpn_KlukshuRiver2016	0.1245	0.1510	0.1854	0.2377	0.1773	0.2148	0.2063	0.2357	0.1546	0.2116	
Alsek_T_down	0.2034	0.2195	0.2035	0.2555	0.2344	0.2507	0.2229	0.2414	0.2152	0.2355	0.2024
Blanchard	0.2297	0.2541	0.2388	0.2782	0.2561	0.2839	0.2595	0.2773	0.2412	0.2663	0.2257
BorderSlough_RT	0.2801	0.2796	0.2423	0.2824	0.2908	0.2927	0.2571	0.2689	0.2949	0.2658	0.2630
Bridge_Silver	0.2354	0.2304	0.2015	0.2451	0.2486	0.2652	0.2216	0.2343	0.2502	0.2238	0.2182
Goat_Cr_RT	0.2917	0.3107	0.2871	0.3086	0.3079	0.3385	0.3093	0.3178	0.3083	0.3104	0.2770
Kane	0.2088	0.2227	0.1900	0.2348	0.2296	0.2627	0.2117	0.2299	0.2146	0.2155	0.1981
Kudwat_Cr_RT	0.2106	0.2144	0.1853	0.2323	0.2262	0.2514	0.2028	0.2205	0.2266	0.2092	0.2003
Kwatine_Cr	0.2130	0.2257	0.2146	0.2526	0.2346	0.2724	0.2393	0.2530	0.2230	0.2444	0.2066
L_Tatshenshi_RT	0.2467	0.2488	0.2199	0.2638	0.2586	0.2780	0.2389	0.2489	0.2619	0.2378	0.2386
Neskataheen	0.1215	0.1604	0.2147	0.2561	0.1765	0.2242	0.2355	0.2581	0.1434	0.2260	0.1688
OConnor_RT	0.2002	0.2150	0.1907	0.2335	0.2256	0.2533	0.2091	0.2343	0.2178	0.2120	0.1944
Stinky_Cr_RT	0.2227	0.2272	0.2036	0.2344	0.2375	0.2529	0.2207	0.2364	0.2452	0.2288	0.2168
Tweedsmuir_RT	0.2271	0.2372	0.2131	0.2583	0.2493	0.2681	0.2368	0.2579	0.2422	0.2486	0.2115
U_Tatshensh_RT	0.2030	0.2083	0.1687	0.2179	0.2153	0.2386	0.1899	0.2012	0.2182	0.1930	0.1897
VernRichie_RT	0.2323	0.2365	0.2063	0.2536	0.2524	0.2697	0.2258	0.2493	0.2484	0.2337	0.2154

Breaks

Red	Orang	Yellow	White
0.11647	0.14114	0.16581	

Table M 2: Genetic Distances for 2016 Klukshu Samples and Revised Alsek Baselines - Da

This table shows the *Da* measure of genetic distance (Nei 1987) for the 2016 Klukshu samples and the revised Alsek baseline (50+ samples only, 2016 Klukshu river and lake spawning ground samples instead of Early/Mix/Late weir samples from previous years). Genetic distances are based on pairwise sample comparisons, and are not affected by having other sample groups in the analysis. Therefore, the distances shown in this table apply to all the alternative genotype sets that were tested (Table 8). Tree fitting, however, is influenced by the full suite of sample groups, and alternative versions were tested (e.g. Figure 12 vs. figures in this appendix). Sample groups that are genetically close (i.e. smaller distance) are highlighted, with breakpoints set at 10% (Red), 20% (Orange), and 30% (Yellow) of the overall range of values across all pairwise comparisons for this distance measure. For example, the genetic distance between lake spawners and late untagged weir samples is 0.0179, which is very small relative to other pairwise comparisons.

	AdWeir_EarlyNoTag2016	AdWeir_EarlyTagged2016	AdWeir_LateNoTag2016	AdWeir_LateTagged2016	AdWeir_MixNoTag2016	AdWeir_MixTagged2016	Juv_KlukLkOutFry2016	Juv_KlukLkOutSmolt2016	Juv_KlukVandCrFry2016	AdSpn_KlukshuLake2016	AdSpn_KlukshuRiver2016
AdWeir_EarlyNoTag2016											
AdWeir_EarlyTagged2016	0.0178										
AdWeir_LateNoTag2016	0.0381	0.0400									
AdWeir_LateTagged2016	0.0669	0.0631	0.0225								
AdWeir_MixNoTag2016	0.0258	0.0309	0.0311	0.0503							
AdWeir_MixTagged2016	0.0501	0.0562	0.0545	0.0745	0.0557						
Juv_KlukLkOutFry2016	0.0509	0.0478	0.0132	0.0293	0.0374	0.0563					
Juv_KlukLkOutSmolt2016	0.0638	0.0621	0.0179	0.0315	0.0470	0.0699	0.0164				
Juv_KlukVandCrFry2016	**0.0236**	0.0362	0.0495	0.0778	0.0404	0.0654	0.0584	0.0730			
AdSpn_KlukshuLake2016	0.0441	0.0421	0.0179	0.0326	0.0358	0.0588	0.0178	0.0239	0.0578		
AdSpn_KlukshuRiver2016	**0.0222**	**0.0302**	0.0472	0.0798	0.0436	0.0666	0.0596	0.0748	**0.0329**	0.0592	
Alsek_T_down	0.0566	0.0667	0.0593	0.0902	0.0756	0.0928	0.0729	0.0848	0.0638	0.0761	0.0556
Blanchard	0.0732	0.0902	0.0824	0.1150	0.0916	0.1157	0.0986	0.1122	0.0818	0.1006	0.0721
BorderSlough_RT	0.1112	0.1097	0.0853	0.1124	0.1196	0.1305	0.0979	0.1060	0.1221	0.1008	0.0983
Bridge_Silver	0.0783	0.0747	0.0572	0.0808	0.0865	0.1068	0.0702	0.0771	0.0868	0.0705	0.0666
Goat_Cr_RT	0.1315	0.1405	0.1189	0.1336	0.1397	0.1684	0.1345	0.1443	0.1401	0.1378	0.1185
Kane	0.0617	0.0699	0.0523	0.0780	0.0753	0.1042	0.0664	0.0772	0.0652	0.0664	0.0581
Kudwat_Cr_RT	0.0626	0.0644	0.0495	0.0756	0.0736	0.0968	0.0616	0.0707	0.0714	0.0621	0.0552
Kwatine_Cr	0.0631	0.0691	0.0635	0.0881	0.0751	0.1066	0.0791	0.0869	0.0714	0.0813	0.0622
L_Tatshenshi_RT	0.0881	0.0893	0.0708	0.0965	0.0952	0.1127	0.0823	0.0895	0.0981	0.0816	0.0812
Neskataheen	**0.0299**	0.0416	0.0671	0.0985	0.0492	0.0749	0.0794	0.0929	0.0386	0.0723	0.0469
OConnor_RT	0.0590	0.0655	0.0533	0.0788	0.0747	0.0971	0.0652	0.0795	0.0668	0.0635	0.0546
Stinky_Cr_RT	0.0703	0.0720	0.0575	0.0774	0.0790	0.0933	0.0680	0.0774	0.0828	0.0723	0.0646
Tweedsmuir_RT	0.0739	0.0792	0.0668	0.0949	0.0886	0.1093	0.0832	0.0960	0.0835	0.0882	0.0654
U_Tatshensh_RT	0.0561	0.0594	0.0414	0.0673	0.0643	0.0856	0.0532	0.0595	0.0658	0.0532	0.0498
VernRichie_RT	0.0759	0.0772	0.0615	0.0891	0.0891	0.1082	0.0732	0.0882	0.0855	0.0773	0.0654

Breaks				
Red	Orang	Yellow	White	
0.02895	0.0447	0.06045		

Table M 3: Genetic Distances for 2016 Klukshu Samples and Revised Alsek Baselines - Ds

This table shows the *Ds* measure of genetic distance (Nei 1978) for the 2016 Klukshu samples and the revised Alsek baseline (50+ samples only, 2016 Klukshu river and lake spawning ground samples instead of Early/Mix/Late weir samples from previous years). Genetic distances are based on pairwise sample comparisons, and are not affected by having other sample groups in the analysis. Therefore, the distances shown in this table apply to all the alternative genotype sets that were tested (Table 8). Tree fitting, however, is influenced by the full suite of sample groups, and alternative versions were tested (e.g. Figure 12 vs. figures in this appendix). Sample groups that are genetically close (i.e. smaller distance) are highlighted, with breakpoints set at 10% (Red), 20% (Orange), and 30% (Yellow) of the overall range of values across all pairwise comparisons for this distance measure. For example, the genetic distance between lake spawners and late untagged weir samples is 0.0014, which is very small relative to other pairwise comparisons.

	AdWeir_EarlyNoTag2016	AdWeir_EarlyTagged2016	AdWeir_LateNoTag2016	AdWeir_LateTagged2016	AdWeir_MixNoTag2016	AdWeir_MixTagged2016	Juv_KlukLkOutFry2016	Juv_KlukLkOutSmolt2016	Juv_KlukVandCrFry2016	AdSpn_KlukshuLake2016	AdSpn_KlukshuRiver2016
Breaks											
Red		0.01215									
Orang		0.0296									
Yellow		0.04705									
White											
AdWeir_EarlyNoTag2016											
AdWeir_EarlyTagged2016	0.0007										
AdWeir_LateNoTag2016	0.0345	0.0295									
AdWeir_LateTagged2016	0.0487	0.0380	0.0004								
AdWeir_MixNoTag2016	0.0078	0.0045	0.0079	0.0139							
AdWeir_MixTagged2016	0.0005	0.0035	0.0100	0.0210	-0.0053						
Juv_KlukLkOutFry2016	0.0439	0.0358	-0.0003	0.0022	0.0108	0.0107					
Juv_KlukLkOutSmolt2016	0.0564	0.0488	0.0031	0.0019	0.0226	0.0234	0.0018				
Juv_KlukVandCrFry2016	**0.0173**	**0.0201**	0.0418	0.0581	**0.0176**	**0.0136**	0.0450	0.0568			
AdSpn_KlukshuLake2016	**0.0322**	**0.0249**	**0.0014**	**0.0019**	**0.0050**	**0.0057**	**0.0018**	**0.0089**	0.0409		
AdSpn_KlukshuRiver2016	0.0062	0.0064	0.0354	0.0484	0.0138	0.0096	0.0408	0.0522	**0.0198**	0.0379	
Alsek_T_down	0.0383	0.0435	0.0370	0.0487	0.0357	0.0344	0.0417	0.0447	0.0506	0.0489	**0.0314**
Blanchard	0.0914	0.1047	0.0969	0.1098	0.0862	0.0988	0.1025	0.1032	0.1061	0.1093	0.0887
BorderSlough_RT	0.0971	0.0872	0.0768	0.0823	0.0918	0.0699	0.0810	0.0747	0.1175	0.0855	0.0787
Bridge_Silver	0.0708	0.0611	0.0557	0.0559	0.0597	0.0545	0.0627	0.0644	0.0947	0.0610	0.0564
Goat_Cr_RT	0.1218	0.1305	0.1025	0.1053	0.1144	0.1258	0.1158	0.1088	0.1446	0.1168	0.1000
Kane	0.0314	0.0296	0.0240	0.0285	0.0232	0.0325	0.0276	0.0305	0.0437	**0.0282**	**0.0230**
Kudwat_Cr_RT	0.0591	0.0517	0.0435	0.0453	0.0461	0.0456	0.0463	0.0482	0.0737	0.0517	0.0440
Kwatine_Cr	0.0346	0.0336	0.0327	0.0387	0.0286	0.0437	0.0445	0.0451	0.0494	0.0382	**0.0258**
L_Tatshenshi_RT	0.0841	0.0804	0.0622	0.0647	0.0683	0.0548	0.0639	0.0623	0.0965	0.0668	0.0698
Neskataheen	0.0220	0.0229	0.0668	0.0834	0.0317	0.0309	0.0755	0.0890	**0.0246**	0.0643	**0.0283**
OConnor_RT	0.0371	0.0393	0.0283	0.0340	0.0287	0.0217	0.0332	0.0386	0.0503	**0.0327**	**0.0302**
Stinky_Cr_RT	0.0702	0.0656	0.0536	0.0516	0.0581	0.0474	0.0534	0.0559	0.0839	0.0603	0.0544
Tweedsmuir_RT	0.0600	0.0567	0.0564	0.0586	0.0532	0.0502	0.0616	0.0666	0.0739	0.0633	0.0488
U_Tatshensh_RT	0.0535	0.0490	0.0380	0.0393	0.0407	0.0354	0.0403	0.0412	0.0687	0.0418	0.0409
VernRichie_RT	0.0614	0.0537	0.0480	0.0523	0.0560	0.0484	0.0531	0.0556	0.0824	0.0580	0.0528

Table M 4: Genetic Distances for 2016 Klukshu Samples and Revised Alsek Baselines - Theta

This table shows the *Theta* measure of genetic distance (Weir and Cockerham 1984) for the 2016 Klukshu samples and the revised Alsek baseline (50+ samples only, 2016 Klukshu river and lake spawning ground samples instead of Early/Mix/Late weir samples from previous years). Genetic distances are based on pairwise sample comparisons, and are not affected by having other sample groups in the analysis. Therefore, the distances shown in this table apply to all the alternative genotype sets that were tested (Table 8). Tree fitting, however, is influenced by the full suite of sample groups, and alternative versions were tested (e.g. Figure 12 vs. figures in this appendix). Sample groups that are genetically close (i.e. smaller distance) are highlighted, with breakpoints set at 10% (Red), 20% (Orange), and 30% (Yellow) of the overall range of values across all pairwise comparisons for this distance measure. For example, the genetic distance between lake spawners and late untagged weir samples is 0.0006, which is very small relative to other pairwise comparisons.

	AdWeir_EarlyNoTag2016	AdWeir_EarlyTagged2016	AdWeir_LateNoTag2016	AdWeir_LateTagged2016	AdWeir_MixNoTag2016	AdWeir_MixTagged2016	Juv_KlukLkOutFry2016	Juv_KlukLkOutSmolt2016	Juv_KlukVandCrFry2016	AdSpn_KlukshuLake2016	AdSpn_KlukshuRiver2016
Breaks											
Red		0.00618									
Orang		0.01236									
Yellow		0.01854									
White											
AdWeir_EarlyNoTag2016		0.0003	0.0141	0.0203	0.0036	0.0007	0.0177	0.0228	**0.0072**	0.0134	**0.0028**
AdWeir_EarlyTagged2016	0.0003		0.0120	0.0162	0.0022	0.0018	0.0144	0.0198	**0.0082**	0.0104	**0.0027**
AdWeir_LateNoTag2016	0.0141	0.0120		0.0003	0.0032	0.0040	0.0000	0.0013	0.0164	0.0006	0.0138
AdWeir_LateTagged2016	0.0203	0.0162	0.0003		0.0063	0.0098	0.0012	0.0009	0.0234	0.0008	0.0196
AdWeir_MixNoTag2016	0.0036	0.0022	0.0032	0.0063		0.0000	0.0042	0.0091	**0.0070**	0.0023	**0.0053**
AdWeir_MixTagged2016	0.0007	0.0018	0.0040	0.0098	0.0000		0.0041	0.0094	**0.0053**	0.0026	**0.0036**
Juv_KlukLkOutFry2016	0.0177	0.0144	0.0000	0.0012	0.0042	0.0041		0.0008	0.0174	0.0008	0.0156
Juv_KlukLkOutSmolt2016	0.0228	0.0198	0.0013	0.0009	0.0091	0.0094	0.0008		0.0222	0.0037	0.0202
Juv_KlukVandCrFry2016	**0.0072**	**0.0082**	0.0164	0.0234	**0.0070**	**0.0053**	0.0174	0.0222		0.0164	**0.0078**
AdSpn_KlukshuLake2016	0.0134	0.0104	0.0006	0.0008	0.0023	0.0026	0.0008	0.0037	0.0164		0.0152
AdSpn_KlukshuRiver2016	**0.0028**	**0.0027**	0.0138	0.0196	**0.0053**	**0.0036**	0.0156	0.0202	**0.0078**	0.0152	
Alsek_T_down	0.0159	0.0173	0.0143	0.0198	0.0129	0.0117	0.0155	0.0172	0.0191	0.0192	**0.0118**
Blanchard	0.0355	0.0399	0.0363	0.0421	0.0319	0.0360	0.0377	0.0388	0.0395	0.0414	0.0330
BorderSlough_RT	0.0365	0.0326	0.0282	0.0314	0.0321	0.0247	0.0290	0.0277	0.0417	0.0319	0.0283
Bridge_Silver	0.0283	0.0245	0.0218	0.0230	0.0230	0.0213	0.0241	0.0253	0.0359	0.0244	0.0219
Goat_Cr_RT	0.0471	0.0501	0.0389	0.0421	0.0425	0.0470	0.0430	0.0417	0.0531	0.0450	0.0377
Kane	0.0130	0.0120	0.0094	0.0120	0.0085	0.0109	0.0104	0.0120	0.0167	0.0114	**0.0087**
Kudwat_Cr_RT	0.0231	0.0200	0.0165	0.0180	0.0167	0.0163	0.0171	0.0183	0.0271	0.0200	0.0163
Kwatine_Cr	0.0143	0.0138	0.0130	0.0163	0.0113	0.0169	0.0172	0.0179	0.0194	0.0155	**0.0102**
L_Tatshenshi_RT	0.0322	0.0304	0.0233	0.0253	0.0244	0.0192	0.0234	0.0235	0.0351	0.0256	0.0253
Neskataheen	0.0092	0.0095	0.0261	0.0331	0.0127	0.0125	0.0291	0.0344	**0.0100**	0.0256	**0.0114**
OConnor_RT	0.0156	0.0158	0.0112	0.0144	0.0103	0.0067	0.0124	0.0151	0.0190	0.0134	**0.0113**
Stinky_Cr_RT	0.0283	0.0265	0.0212	0.0214	0.0227	0.0189	0.0209	0.0223	0.0324	0.0243	0.0214
Tweedsmuir_RT	0.0235	0.0219	0.0212	0.0230	0.0192	0.0176	0.0226	0.0250	0.0274	0.0242	0.0180
U_Tatshensh_RT	0.0212	0.0193	0.0147	0.0159	0.0153	0.0132	0.0153	0.0160	0.0259	0.0165	0.0155
VernRichie_RT	0.0240	0.0208	0.0182	0.0207	0.0202	0.0174	0.0195	0.0210	0.0301	0.0223	0.0194

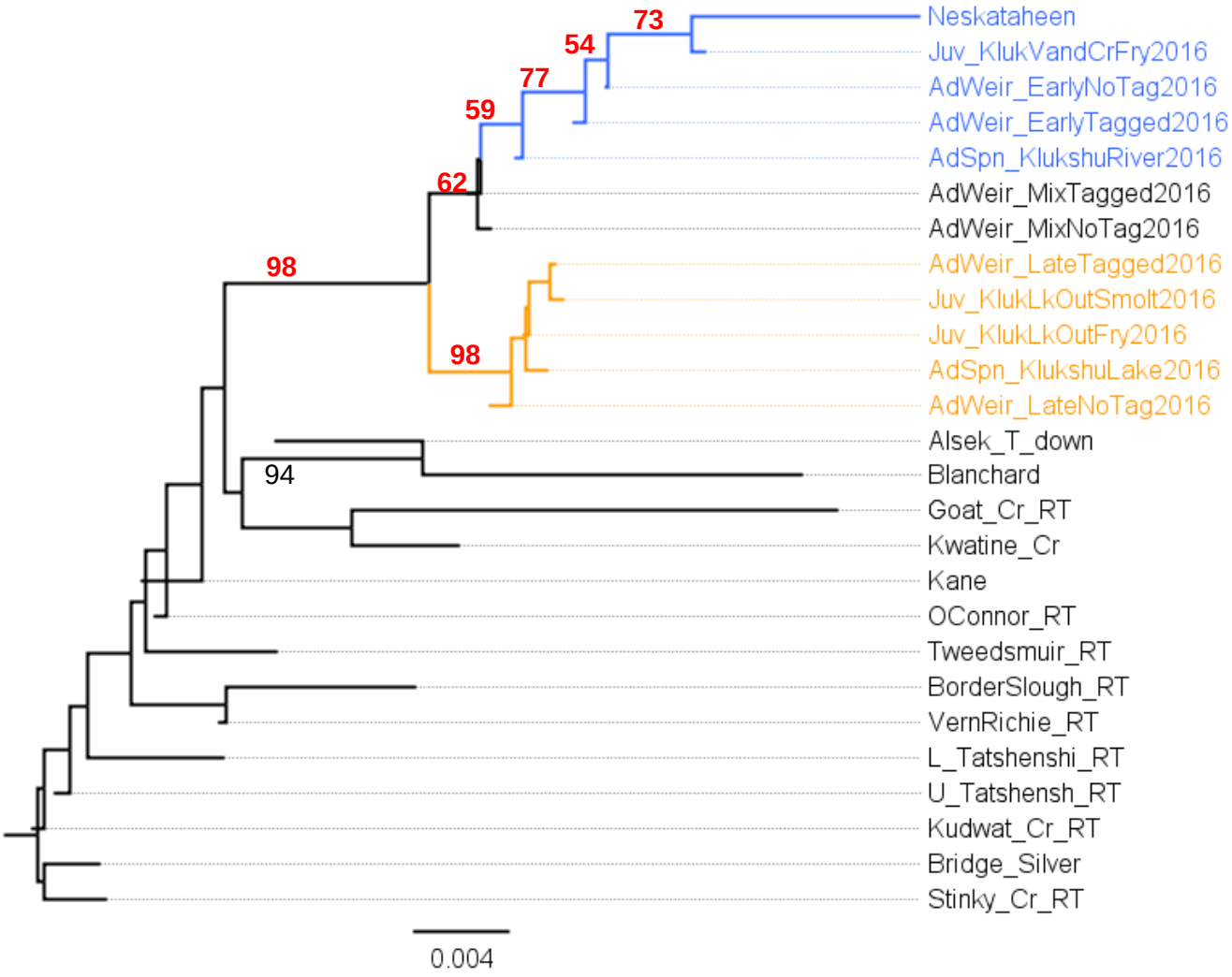


Figure M 1: Fitted Tree for 2016 Klukshu Samples and Revised Alsek Baselines – G11/T1
This tree was constructed with the TREEFIT program (Section 5.7) using the *Theta* measure of genetic distance (Weir and Cockerham 1984) and the *Neighbour Joining* algorithm for tree fitting. The genotype set included all samples collected in 2016 and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years). Numbers on the tree branches show the proportion of fits among 1000 bootstrap tests which grouped that particular set of samples together. 59% of the bootstrap tests grouped the early weir samples, river spawners, river fry, and Neskataheen together. 62% of the tests grouped both of the weir samples from the Mixed period (Aug 14-20) with the Early/River/Neskataheen samples. 98% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. 98% of the tests put all the Klukshu samples and Neskataheen on a separate branch from all the other Alsek samples. Note that this is one of 16 alternative trees produced with TREEFIT (Set G11, Method T1). Table 8 and Table 9 list the components of the sensitivity analyses. Table 12 categorizes the resulting types of tree, and lists a measure of how well they fit the sample. Table 13 compares bootstrap results for the different fitting methods. Bootstrap values varied a little when the 1000 tests were replicated (± a few percent).

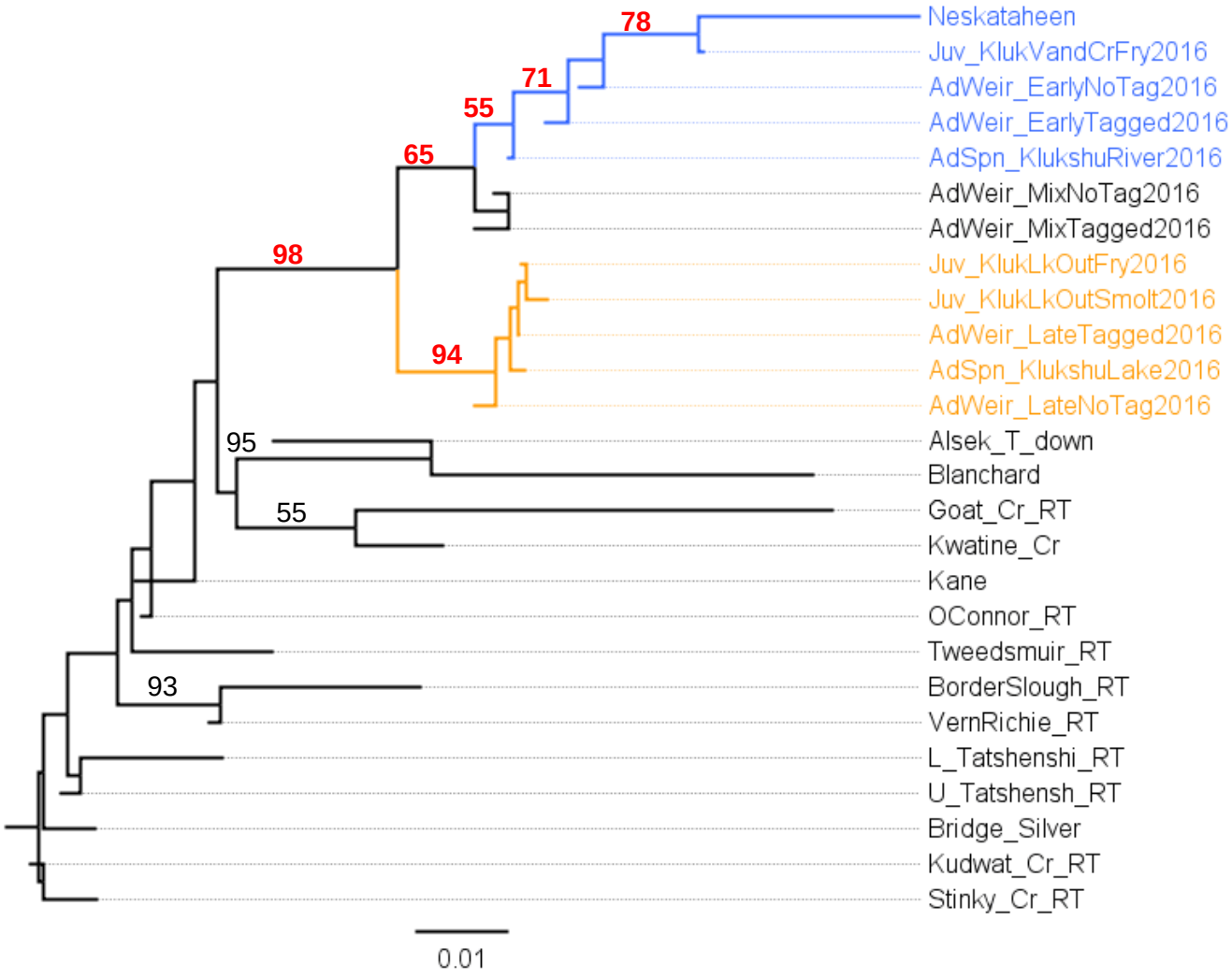


Figure M 2: Fitted Tree for 2016 Klukshu Samples and Revised Alsek Baselines – G11/T2
This tree was constructed with the TREEFIT program (Section 5.7) using the *Ds* measure of genetic distance (Nei 1978) and the *Neighbour Joining* algorithm for tree fitting. The genotype set included all samples collected in 2016 and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years). Numbers on the tree branches show the proportion of fits among 1000 bootstrap tests which grouped that particular set of samples together. 55% of the bootstrap tests grouped the early weir samples, river spawners, river fry, and Neskataheen together. 65% of the tests grouped both of the weir samples from the Mixed period (Aug 14-20) with the Early/River/Neskataheen samples. 94% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. 98% of the tests put all the Klukshu samples and Neskataheen on a separate branch from all the other Alsek samples. Note that this is one of 16 alternative trees produced with TREEFIT (Set G11, Method T2). Table 8 and Table 9 list the components of the sensitivity analyses. Table 12 categorizes the resulting types of tree, and lists a measure of how well they fit the sample. Table 13 compares bootstrap results for the different fitting methods. Bootstrap values varied a little when the 1000 tests were replicated (± a few percent).

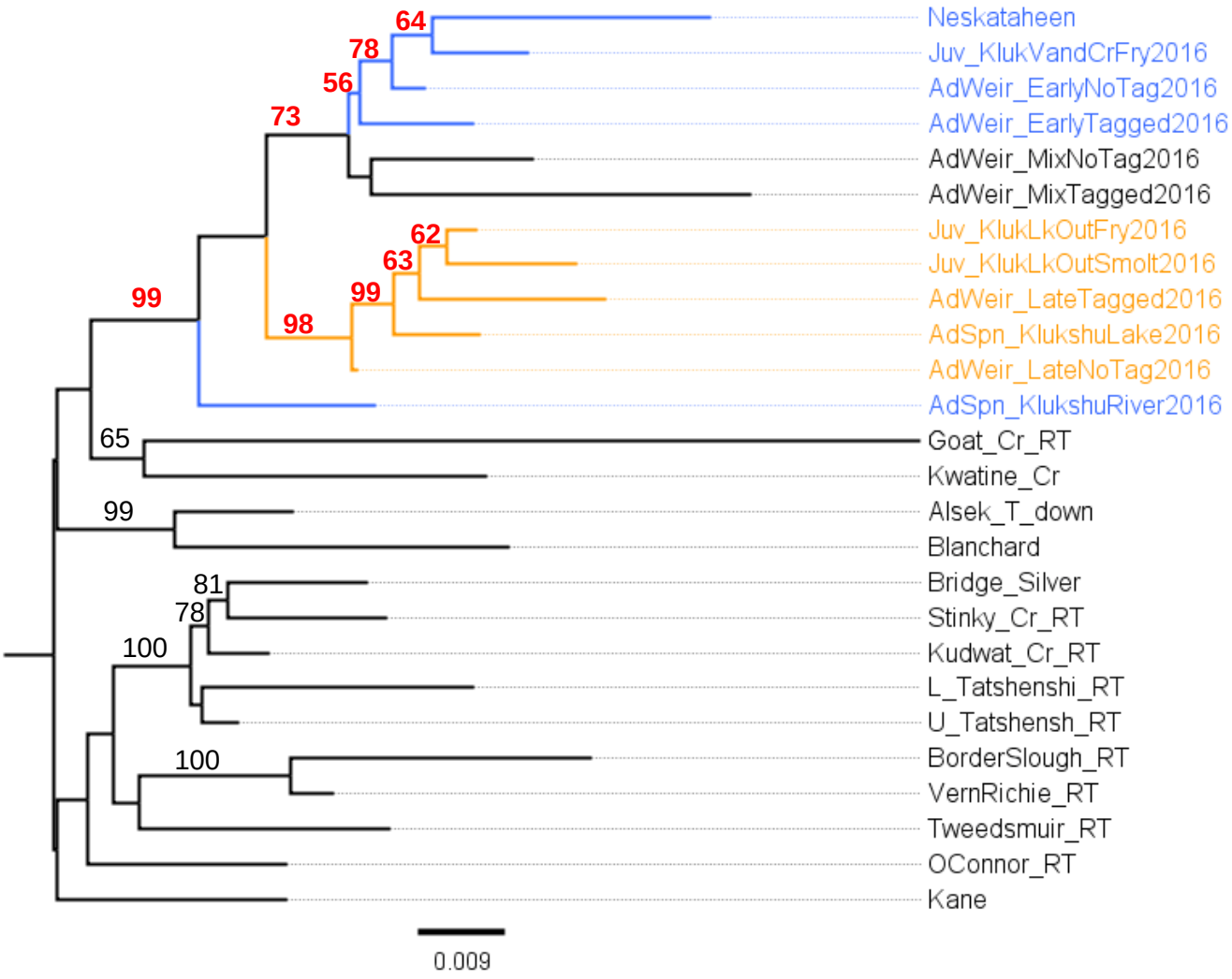


Figure M 3: Fitted Tree for 2016 Klukshu Samples and Revised Alsek Baselines – G11/T3
This tree was constructed with the TREEFIT program (Section 5.7) using the *Da* measure of genetic distance (Nei 1987) and the *Neighbour Joining* algorithm for tree fitting. The genotype set included all samples collected in 2016 and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years). Numbers on the tree branches show the proportion of fits among 1000 bootstrap tests which grouped that particular set of samples together. 56% of the bootstrap tests grouped the early weir samples, river fry, and Neskataheen together. 73% of the tests grouped both of the weir samples from the Mixed period (Aug 14-20) with the Early/River Juv/Neskataheen samples. 98% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. 99% of the tests put all the Klukshu samples and Neskataheen on a separate branch from all the other Alsek samples. However, the Klukshu River spawner sample ended up on a separate branch within the Klukshu/Neskataheen complex. Note that this is one of 16 alternative trees produced with TREEFIT (Set G11, Method T3). Table 8 and Table 9 list the components of the sensitivity analyses. Table 12 categorizes the resulting types of tree, and lists a measure of how well they fit the sample. Table 13 compares bootstrap results for the different fitting methods. Bootstrap values varied a little when the 1000 tests were replicated (± a few percent).

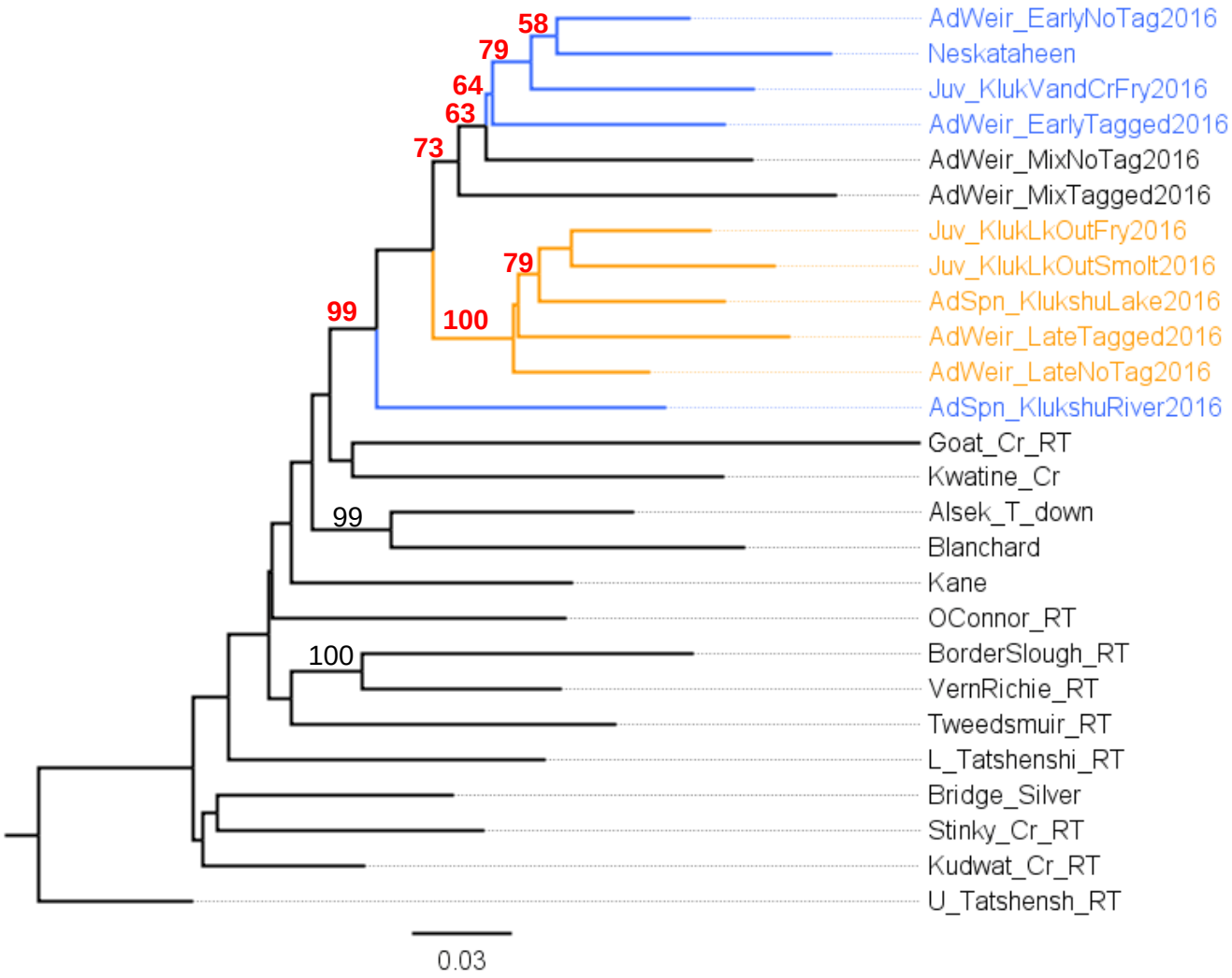


Figure M 4: Fitted Tree for 2016 Klukshu Samples and Revised Alsek Baselines – G11/T4
This tree was constructed with the TREEFIT program (Section 5.7) using the *Dc* measure of genetic distance (Cavalli-Sforza 1967) and the *Neighbour Joining* algorithm for tree fitting. The genotype set included all samples collected in 2016 and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years). Numbers on the tree branches show the proportion of fits among 1000 bootstrap tests which grouped that particular set of samples together. 64% of the bootstrap tests grouped the early weir samples, river fry, and Neskataheen together. 73% of the tests grouped both of the weir samples from the Mixed period (Aug 14-20) with the Early/River Juv/Neskataheen samples. 100% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. 99% of the tests put all the Klukshu samples and Neskataheen on a separate branch from all the other Alsek samples. However, the Klukshu River spawner sample ended up on a separate branch within the Klukshu/Neskataheen complex. Note that this is one of 16 alternative trees produced with TREEFIT (Set G11, Method T4). Table 8 and Table 9 list the components of the sensitivity analyses. Table 12 categorizes the resulting types of tree, and lists a measure of how well they fit the sample. Table 13 compares bootstrap results for the different fitting methods. Bootstrap values varied a little when the 1000 tests were replicated (± a few percent).

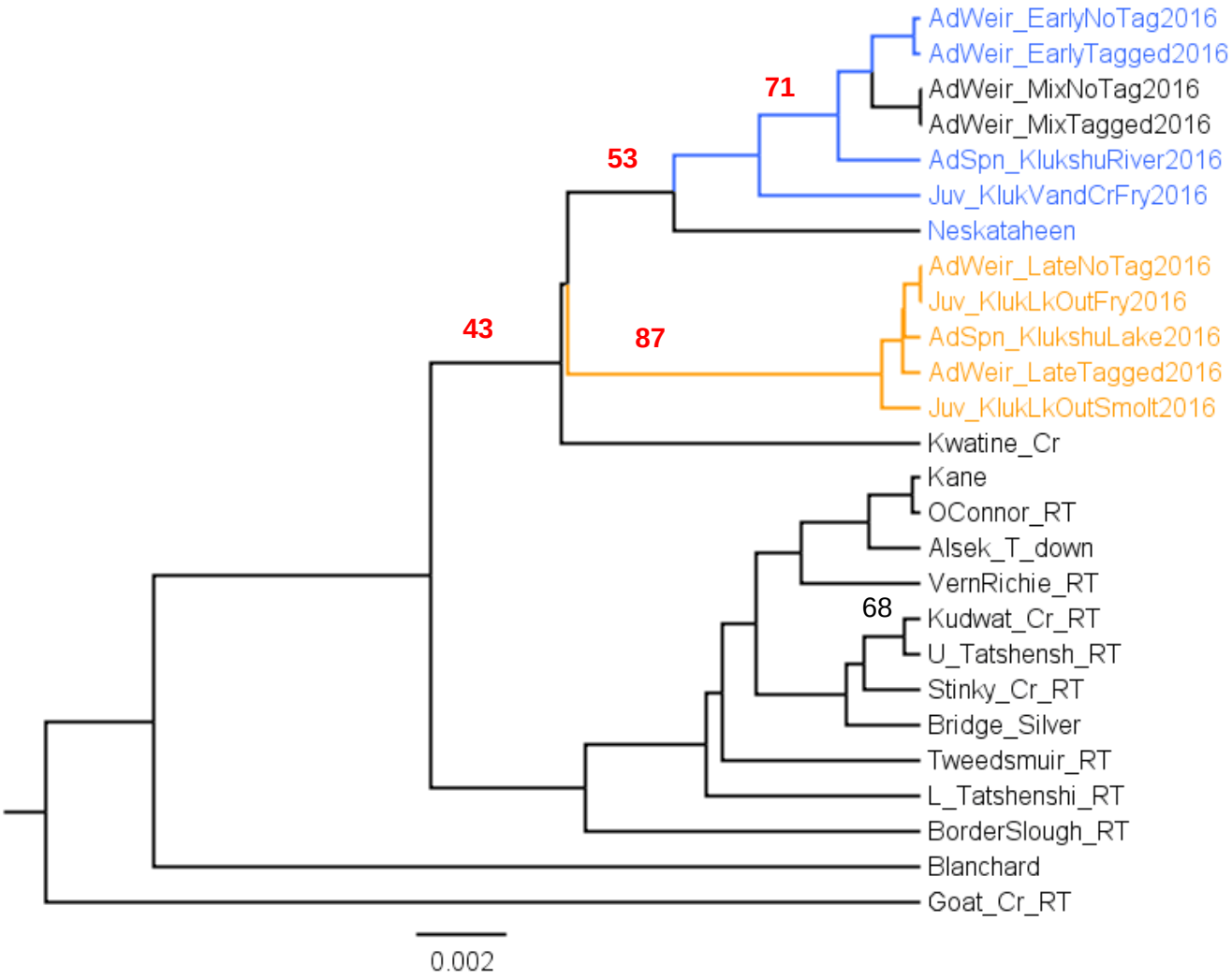


Figure M 5: Fitted Tree for 2016 Klukshu Samples and Revised Alsek Baselines – G11/T5
This tree was constructed with the TREEFIT program (Section 5.7) using the *Theta* measure of genetic distance (Weir and Cockerham 1984) and the *UPGMA* algorithm for tree fitting. The genotype set included all samples collected in 2016 and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years). Numbers on the tree branches show the proportion of fits among 1000 bootstrap tests which grouped that particular set of samples together. The UPGMA fits had overall lower bootstrap values (and lower R^2; Table 13), so only a few are highlighted. 53% of the bootstrap tests grouped the early weir samples, river spawners, river fry, mix-time weir samples, and Neskataheen together. 87% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. Only 43% of the tests put all the Klukshu samples with Neskataheen and Kwatine_Cr on a separate branch from all the other Alsek samples. Note that this is one of 16 alternative trees produced with TREEFIT (Set G11, Method T5). Table 8 and Table 9 list the components of the sensitivity analyses. Table 12 categorizes the resulting types of tree, and lists a measure of how well they fit the sample. Table 13 compares bootstrap results for the different fitting methods. Bootstrap values varied a little when the 1000 tests were replicated (± a few percent).

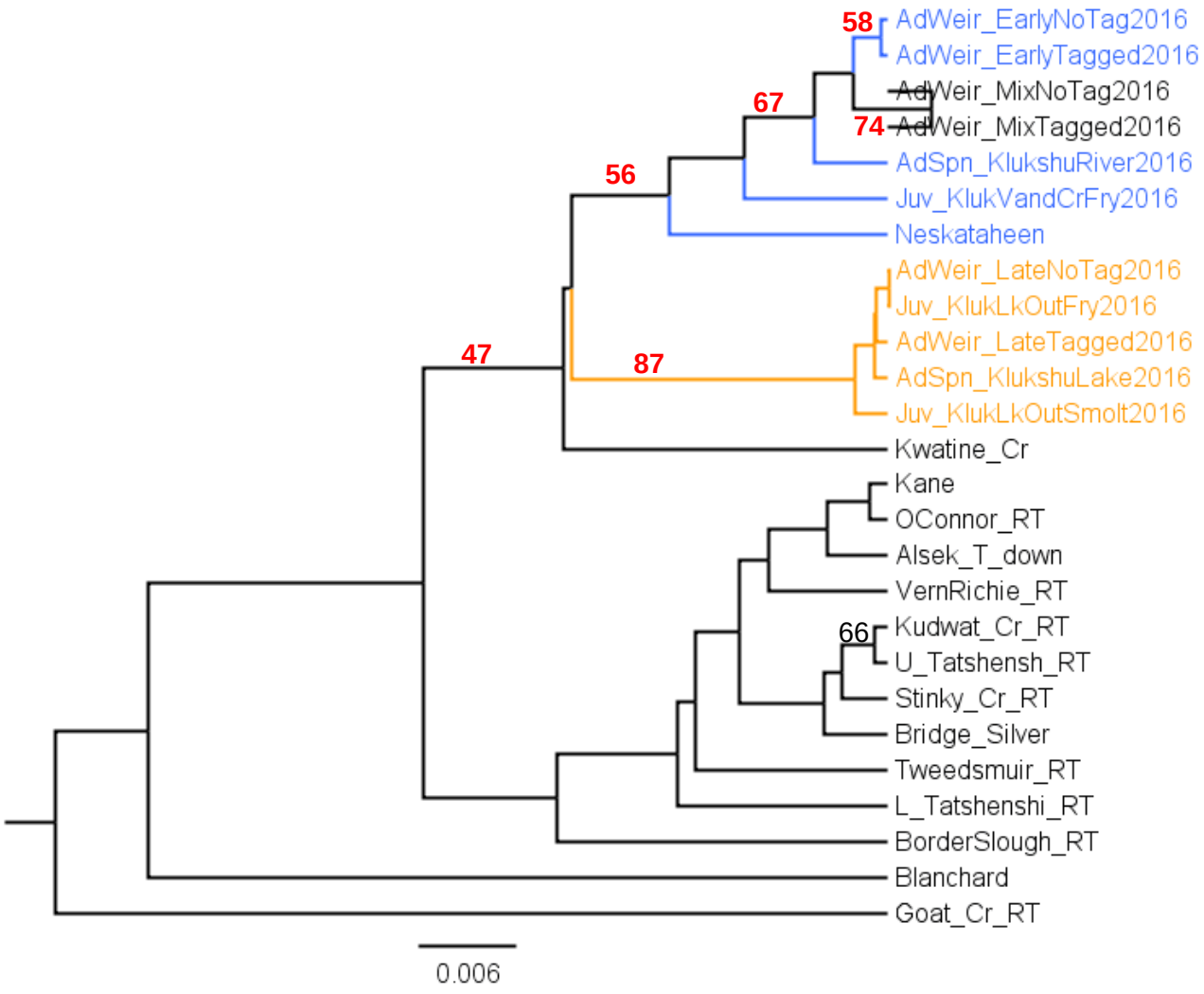


Figure M 6: Fitted Tree for 2016 Klukshu Samples and Revised Alsek Baselines – G11/T6
This tree was constructed with the TREEFIT program (Section 5.7) using the *Ds* measure of genetic distance (Nei 1978) and the *UPGMA* algorithm for tree fitting. The genotype set included all samples collected in 2016 and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years). Numbers on the tree branches show the proportion of fits among 1000 bootstrap tests which grouped that particular set of samples together. The UPGMA fits had overall lower bootstrap values (and lower R^2; Table 13), so only a few are highlighted. 56% of the bootstrap tests grouped the early weir samples, river spawners, river fry, mix-time weir samples, and Neskataheen together. 87% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. Only 47% of the tests put all the Klukshu samples with Neskataheen and Kwatine_Cr on a separate branch from all the other Alsek samples. Note that this is one of 16 alternative trees produced with TREEFIT (Set G11, Method T6). Table 8 and Table 9 list the components of the sensitivity analyses. Table 12 categorizes the resulting types of tree, and lists a measure of how well they fit the sample. Table 13 compares bootstrap results for the different fitting methods. Bootstrap values varied a little when the 1000 tests were replicated (± a few percent).

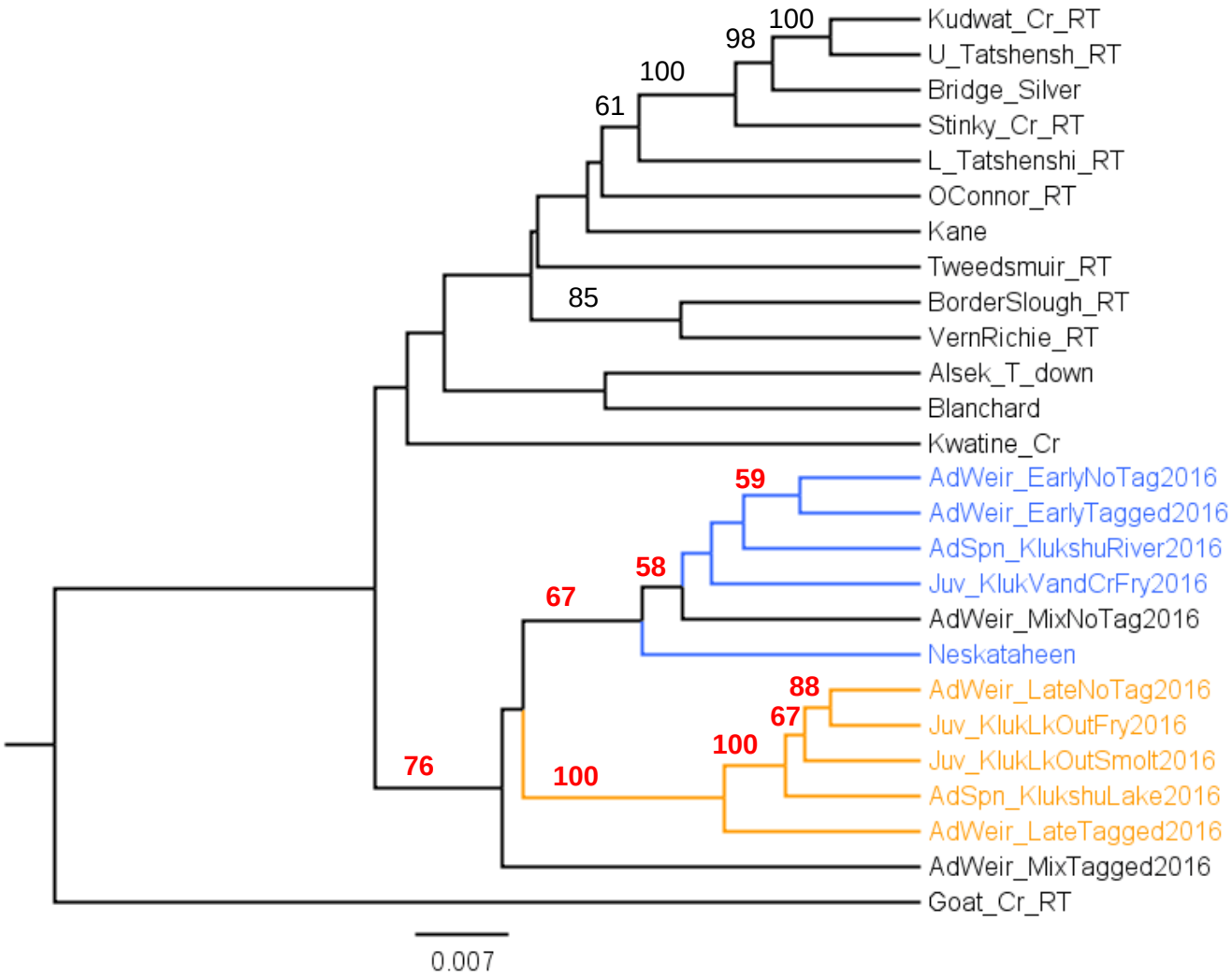


Figure M 7: Fitted Tree for 2016 Klukshu Samples and Revised Alsek Baselines – G11/T7
This tree was constructed with the TREEFIT program (Section 5.7) using the *Da* measure of genetic distance (Nei 1987) and the *UPGMA* algorithm for tree fitting. The genotype set included all samples collected in 2016 and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years). Numbers on the tree branches show the proportion of fits among 1000 bootstrap tests which grouped that particular set of samples together. The UPGMA fits had overall lower bootstrap values (and lower R^2; Table 13), so only a few are highlighted. 67% of the bootstrap tests grouped the early weir samples, river spawners, river fry, mix-time weir samples without tags, and Neskataheen together. 100% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. Only 76% of the tests put all the Klukshu samples with Neskataheen on a separate branch from all the other Alsek samples. The tagged sample from the Mixed period (Aug 14-20) ended up on a separate branch within the Klukshu/Neskataheen complex. Note that this is one of 16 alternative trees produced with TREEFIT (Set G11, Method T7). Table 8 and Table 9 list the components of the sensitivity analyses. Table 12 categorizes the resulting types of tree, and lists a measure of how well they fit the sample. Table 13 compares bootstrap results for the different fitting methods. Bootstrap values varied a little when the 1000 tests were replicated (± a few percent).

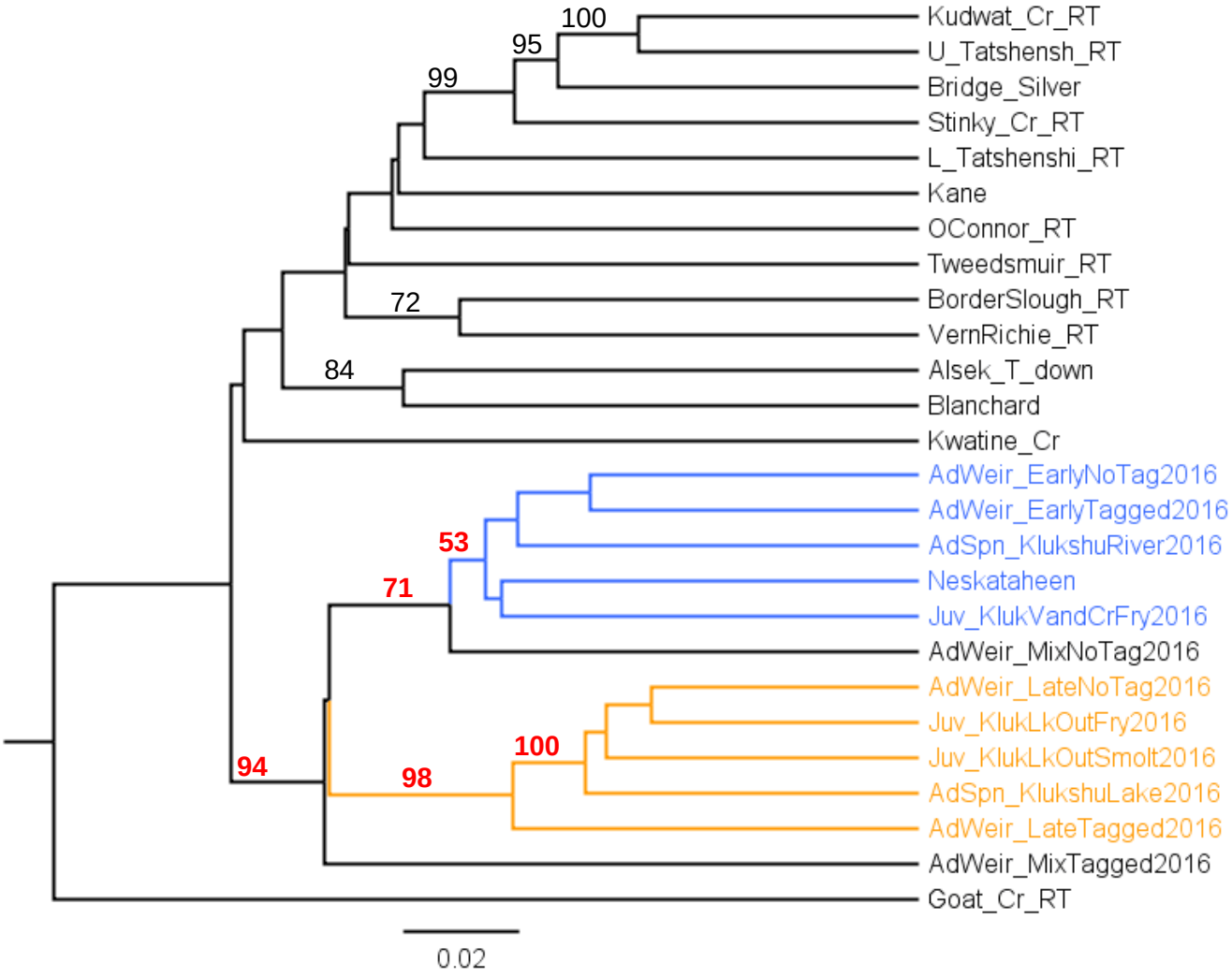


Figure M 8: Fitted Tree for 2016 Klukshu Samples and Revised Alsek Baselines – G11/T8
This tree was constructed with the TREEFIT program (Section 5.7) using the *Ds* measure of genetic distance (Cavalli-Sforza 1967) and the *UPGMA* algorithm for tree fitting. The genotype set included all samples collected in 2016 and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years). Numbers on the tree branches show the proportion of fits among 1000 bootstrap tests which grouped that particular set of samples together. The UPGMA fits had overall lower bootstrap values (and lower R^2; Table 13), so only a few are highlighted. 71% of the bootstrap tests grouped the early weir samples, river spawners, river fry, mix-time weir samples without tags, and Neskataheen together. 98% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. 94% of the tests put all the Klukshu samples with Neskataheen on a separate branch from all the other Alsek samples. The tagged sample from the Mixed period (Aug 14-20) ended up on a separate branch within the Klukshu/Neskataheen complex. Note that this is one of 16 alternative trees produced with TREEFIT (Set G11, Method T8). Table 8 and Table 9 list the components of the sensitivity analyses. Table 12 categorizes the resulting types of tree, and lists a measure of how well they fit the sample. Table 13 compares bootstrap results for the different fitting methods. Bootstrap values varied a little when the 1000 tests were replicated (± a few percent).

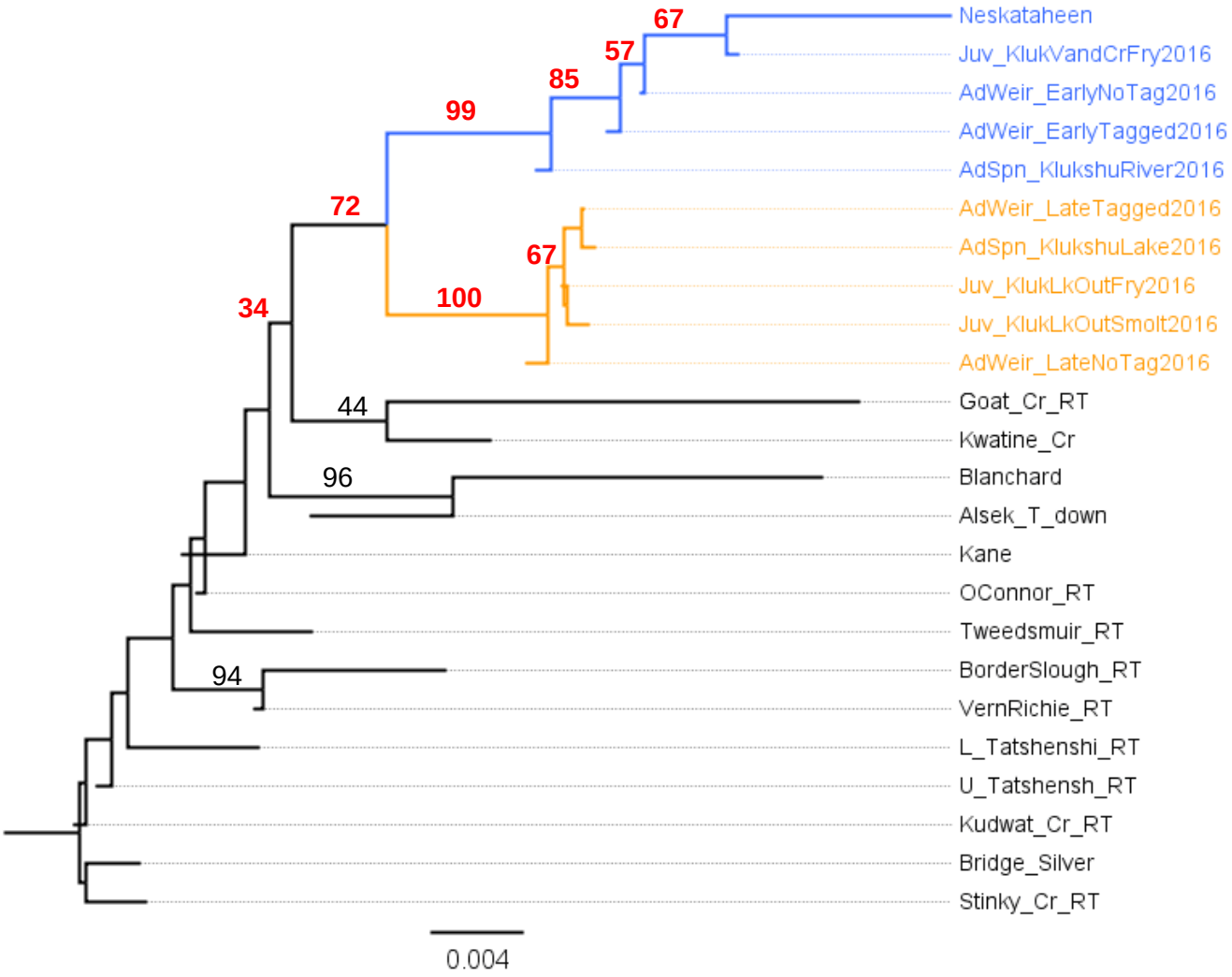


Figure M 9: Fitted Tree for 2016 Klukshu Samples (Excl. Mix) and Revised Alsek Baselines – G12/T1
This tree was constructed with the TREEFIT program (Section 5.7) using the *Theta* measure of genetic distance (Weir and Cockerham 1984) and the *Neighbour Joining* algorithm for tree fitting. The genotype set included all samples collected in 2016, except adults sampled at the weir during the Mix timing group (Aug 14-20, stat week 34), and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years). Numbers on the tree branches show the proportion of fits among 1000 bootstrap tests which grouped that particular set of samples together. 99% of the bootstrap tests grouped the early weir samples, river spawners, river fry, and Neskataheen together. 100% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. 72% of the tests put all the Klukshu samples and Neskataheen on a separate branch from all the other Alsek samples. Note that this is one of 16 alternative trees produced with TREEFIT (Set G12, Method T1). Table 8 and Table 9 list the components of the sensitivity analyses. Table 12 categorizes the resulting types of tree, and lists a measure of how well they fit the sample. Table 13 compares bootstrap results for the different fitting methods. Bootstrap values varied a little when the 1000 tests were replicated (± a few percent).

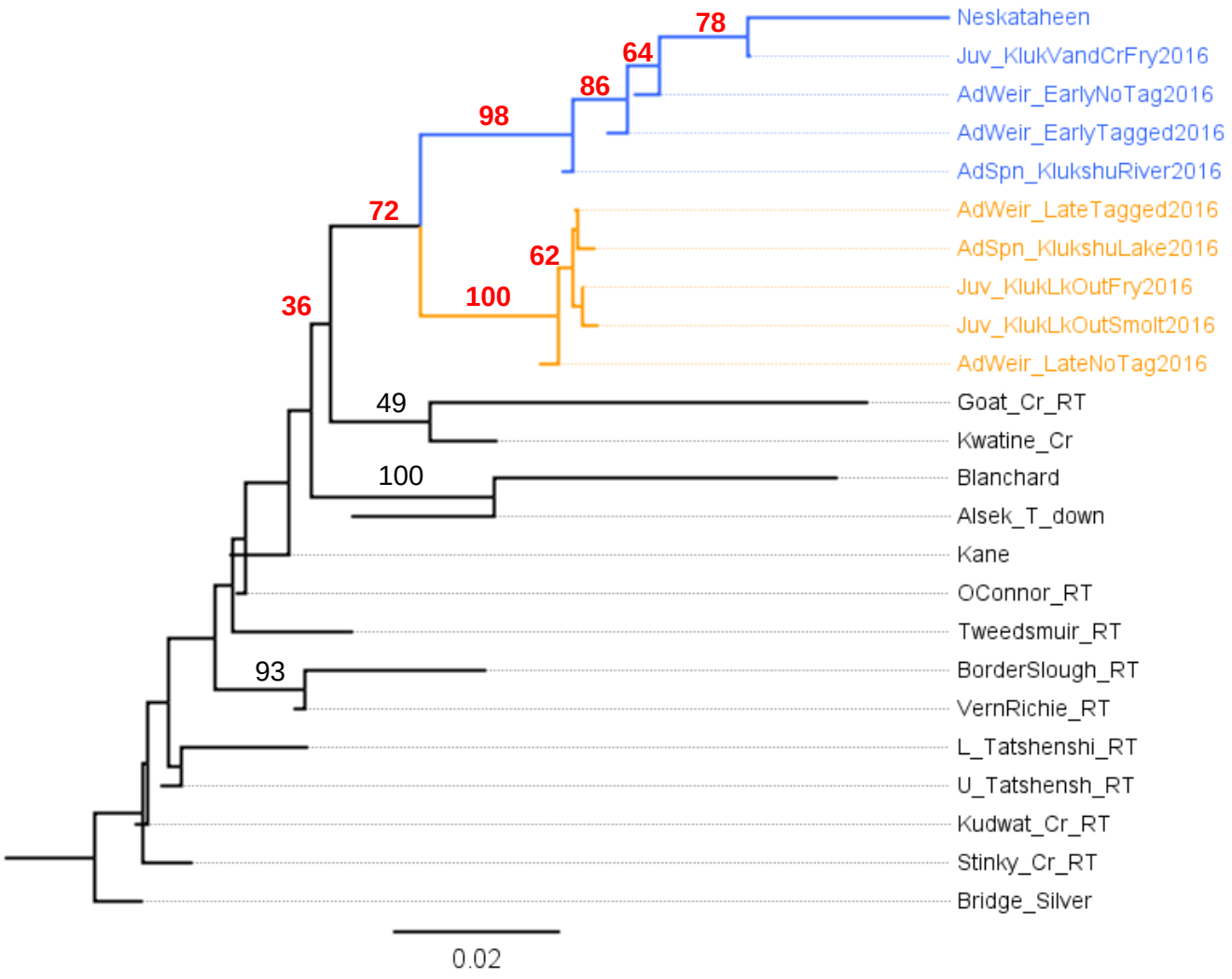


Figure M 10: Fitted Tree for 2016 Klukshu Samples (Excl. Mix) and Revised Alsek Baselines – G12/T2
This tree was constructed with the TREEFIT program (Section 5.7) using the *Ds* measure of genetic distance (Nei 1978) and the *Neighbour Joining* algorithm for tree fitting. The genotype set included all samples collected in 2016, except adults sampled at the weir during the Mix timing group (Aug 14-20, stat week 34), and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years). Numbers on the tree branches show the proportion of fits among 1000 bootstrap tests which grouped that particular set of samples together. 98% of the bootstrap tests grouped the early weir samples, river spawners, river fry, and Neskataheen together. 100% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. 72% of the tests put all the Klukshu samples and Neskataheen on a separate branch from all the other Alsek samples. Note that this is one of 16 alternative trees produced with TREEFIT (Set G12, Method T2). Table 8 and Table 9 list the components of the sensitivity analyses. Table 12 categorizes the resulting types of tree, and lists a measure of how well they fit the sample. Table 13 compares bootstrap results for the different fitting methods. Bootstrap values varied a little when the 1000 tests were replicated (± a few percent).

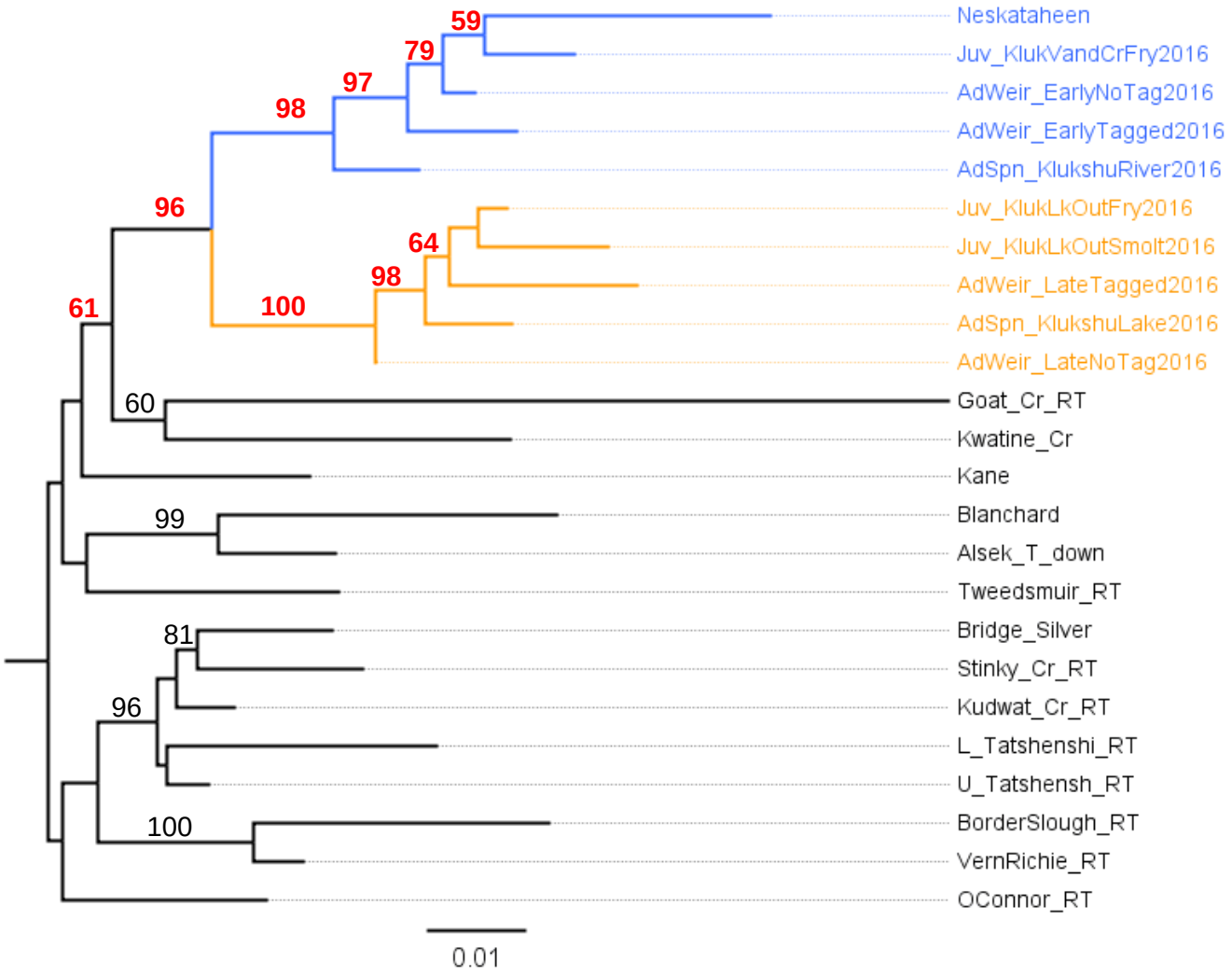


Figure M 11: Fitted Tree for 2016 Klukshu Samples (Excl. Mix) and Revised Alsek Baselines – G12/T3
This tree was constructed with the TREEFIT program (Section 5.7) using the *Da* measure of genetic distance (Nei 1987) and the *Neighbour Joining* algorithm for tree fitting. The genotype set included all samples collected in 2016, except adults sampled at the weir during the Mix timing group (Aug 14-20, stat week 34), and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years). Numbers on the tree branches show the proportion of fits among 1000 bootstrap tests which grouped that particular set of samples together. 98% of the bootstrap tests grouped the early weir samples, river spawners, river fry, and Neskataheen together. 100% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. 96% of the tests put all the Klukshu samples and Neskataheen on a separate branch from all the other Alsek samples.. Note that this is one of 16 alternative trees produced with TREEFIT (Set G12, Method T3). Table 8 and Table 9 list the components of the sensitivity analyses. Table 12 categorizes the resulting types of tree, and lists a measure of how well they fit the sample. Table 13 compares bootstrap results for the different fitting methods. Bootstrap values varied a little when the 1000 tests were replicated (± a few percent).

Included as Figure 12 in main report.

Figure M 12: Fitted Tree for 2016 Klukshu Samples (Excl. Mix) and Revised Alsek Baselines – G12/T4

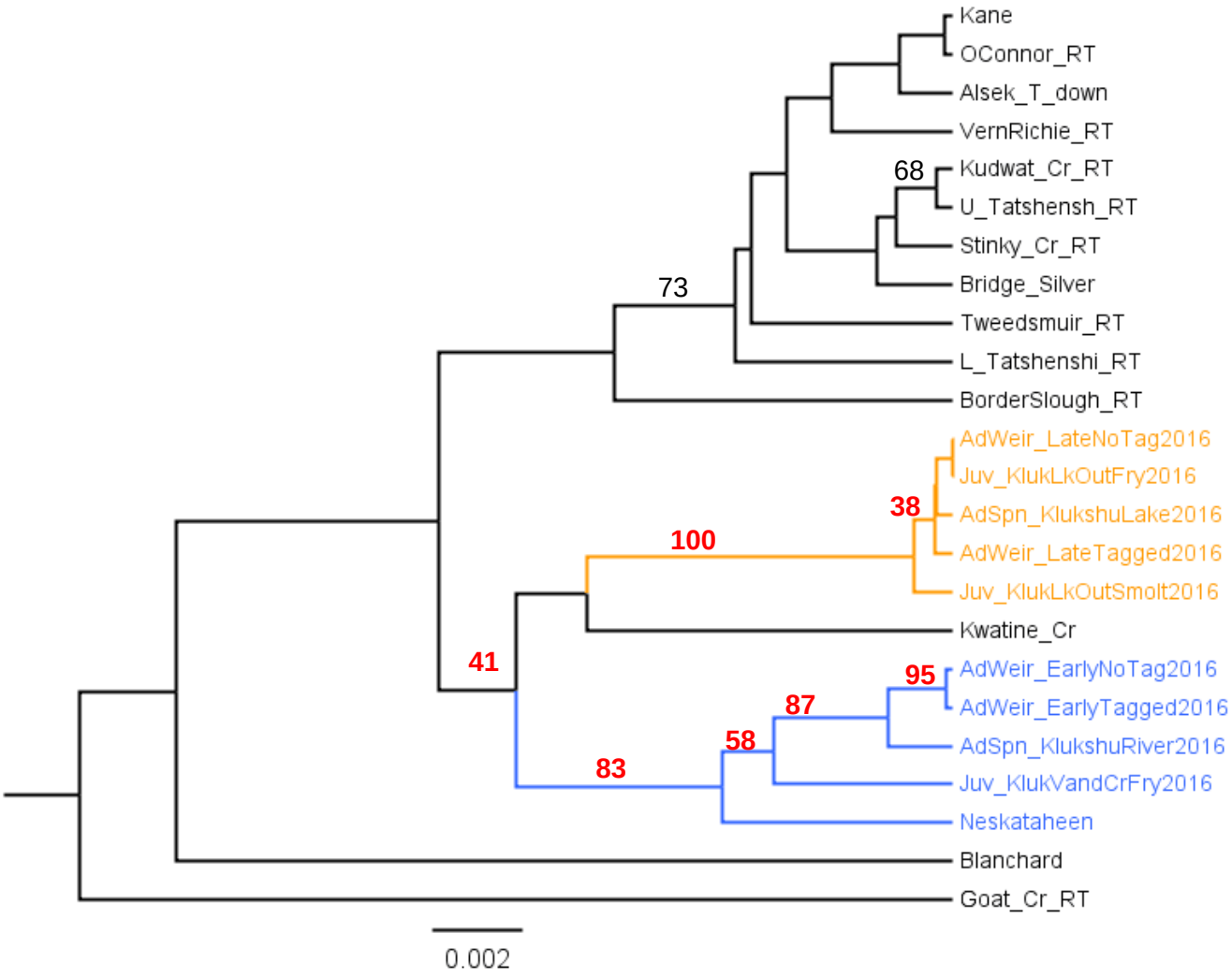


Figure M 13: Fitted Tree for 2016 Klukshu Samples (Excl. Mix) and Revised Alsek Baselines – G12/T5
This tree was constructed with the TREEFIT program (Section 5.7) using the *Theta* measure of genetic distance (Weir and Cockerham 1984) and the *UPGMA* algorithm for tree fitting. The genotype set included all samples collected in 2016, except adults sampled at the weir during the Mix timing group (Aug 14-20, stat week 34), and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years). Numbers on the tree branches show the proportion of fits among 1000 bootstrap tests which grouped that particular set of samples together. The UPGMA fits had overall lower bootstrap values (and lower R^2; Table 13). 83% of the bootstrap tests grouped the early weir samples, river spawners, river fry, and Neskataheen together. 100% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. Only 41% of the tests put all the Klukshu samples with Neskataheen and Kwatine_Cr on a separate branch from all the other Alsek samples. Note that this is one of 16 alternative trees produced with TREEFIT (Set G12, Method T5). Table 8 and Table 9 list the components of the sensitivity analyses. Table 12 categorizes the resulting types of tree, and lists a measure of how well they fit the sample. Table 13 compares bootstrap results for the different fitting methods. Bootstrap values varied a little when the 1000 tests were replicated (± a few percent).

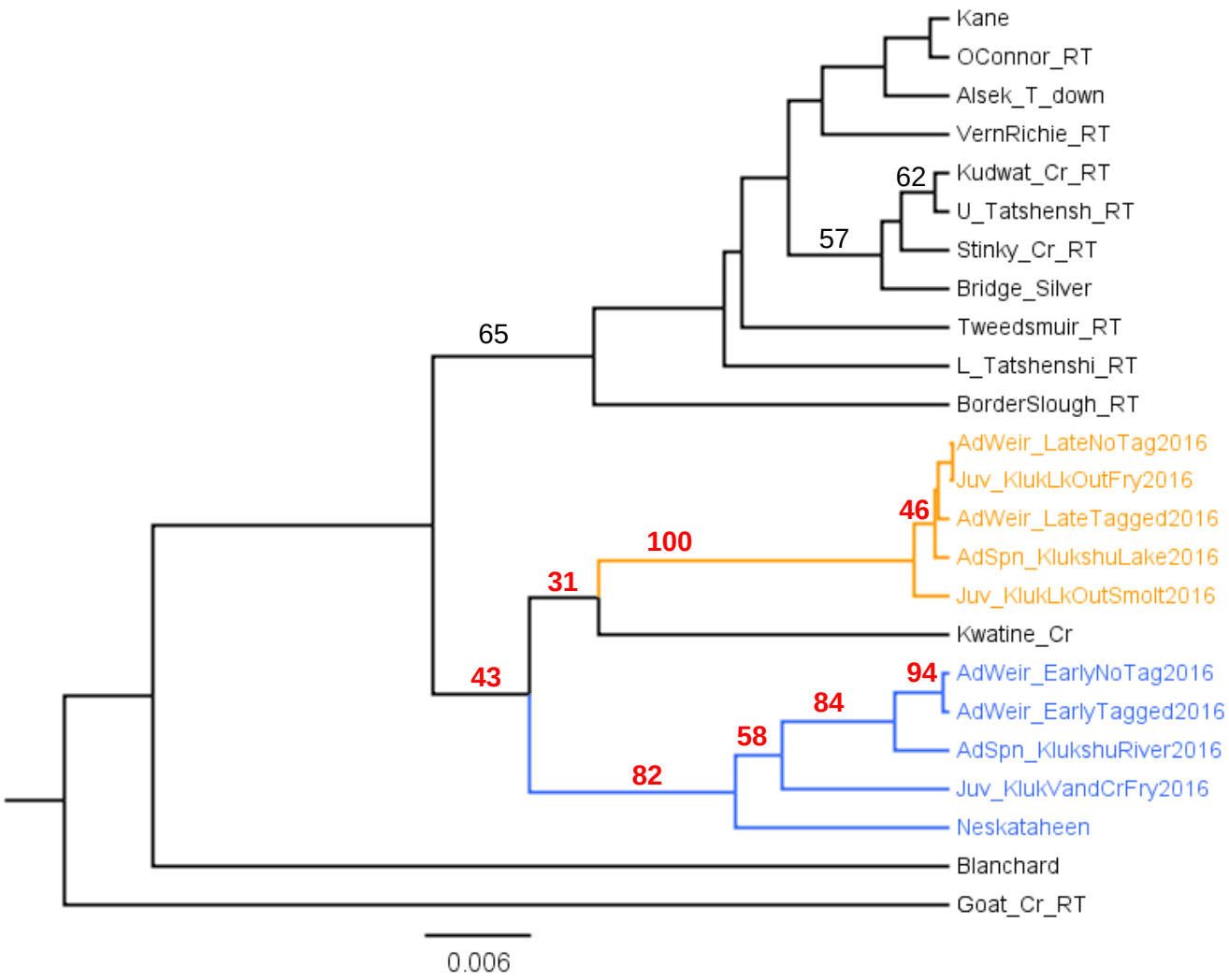


Figure M 14: Fitted Tree for 2016 Klukshu Samples (Excl. Mix) and Revised Alsek Baselines – G12/T6
This tree was constructed with the TREEFIT program (Section 5.7) using the *Ds* measure of genetic distance (Nei 1978) and the *UPGMA* algorithm for tree fitting. The genotype set included all samples collected in 2016, except adults sampled at the weir during the Mix timing group (Aug 14-20, stat week 34), and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years). Numbers on the tree branches show the proportion of fits among 1000 bootstrap tests which grouped that particular set of samples together. The UPGMA fits had overall lower bootstrap values (and lower R^2; Table 13). 82% of the bootstrap tests grouped the early weir samples, river spawners, river fry, and Neskataheen together.100% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. 31% of the tests grouped Kwatine_Cr with the Lake/Late group, and 43% of the tests put all the Klukshu samples with Neskataheen and Kwatine_Cr on a separate branch from all the other Alsek samples. Note that this is one of 16 alternative trees produced with TREEFIT (Set G12, Method T6). Table 8 and Table 9 list the components of the sensitivity analyses. Table 12 categorizes the resulting types of tree, and lists a measure of how well they fit the sample. Table 13 compares bootstrap results for the different fitting methods. Bootstrap values varied a little when the 1000 tests were replicated (± a few percent).

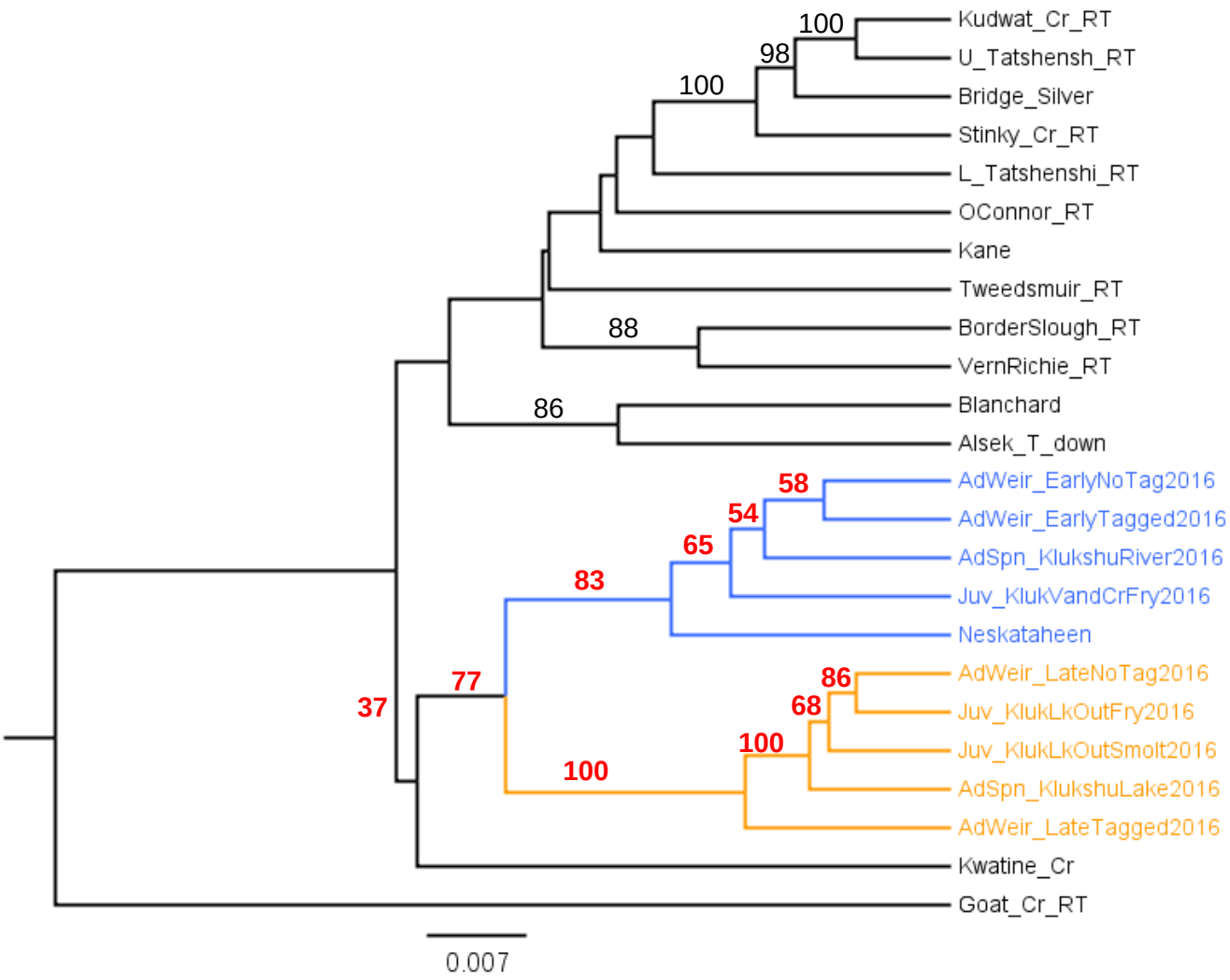


Figure M 15: Fitted Tree for 2016 Klukshu Samples (Excl. Mix) and Revised Alsek Baselines – G12/T7
This tree was constructed with the TREEFIT program (Section 5.7) using the *Da* measure of genetic distance (Nei 1987) and the *UPGMA* algorithm for tree fitting. The genotype set included all samples collected in 2016, except adults sampled at the weir during the Mix timing group (Aug 14-20, stat week 34), and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years). Numbers on the tree branches show the proportion of fits among 1000 bootstrap tests which grouped that particular set of samples together. The UPGMA fits had overall lower bootstrap values (and lower R^2; Table 13). 83% of the bootstrap tests grouped the early weir samples, river spawners, river fry, and Neskataheen together. 100% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. Only 77% of the tests put all the Klukshu samples with Neskataheen on a separate branch from all the other Alsek samples. Note that this is one of 16 alternative trees produced with TREEFIT (Set G12, Method T7). Table 8 and Table 9 list the components of the sensitivity analyses. Table 12 categorizes the resulting types of tree, and lists a measure of how well they fit the sample. Table 13 compares bootstrap results for the different fitting methods. Bootstrap values varied a little when the 1000 tests were replicated (± a few percent).

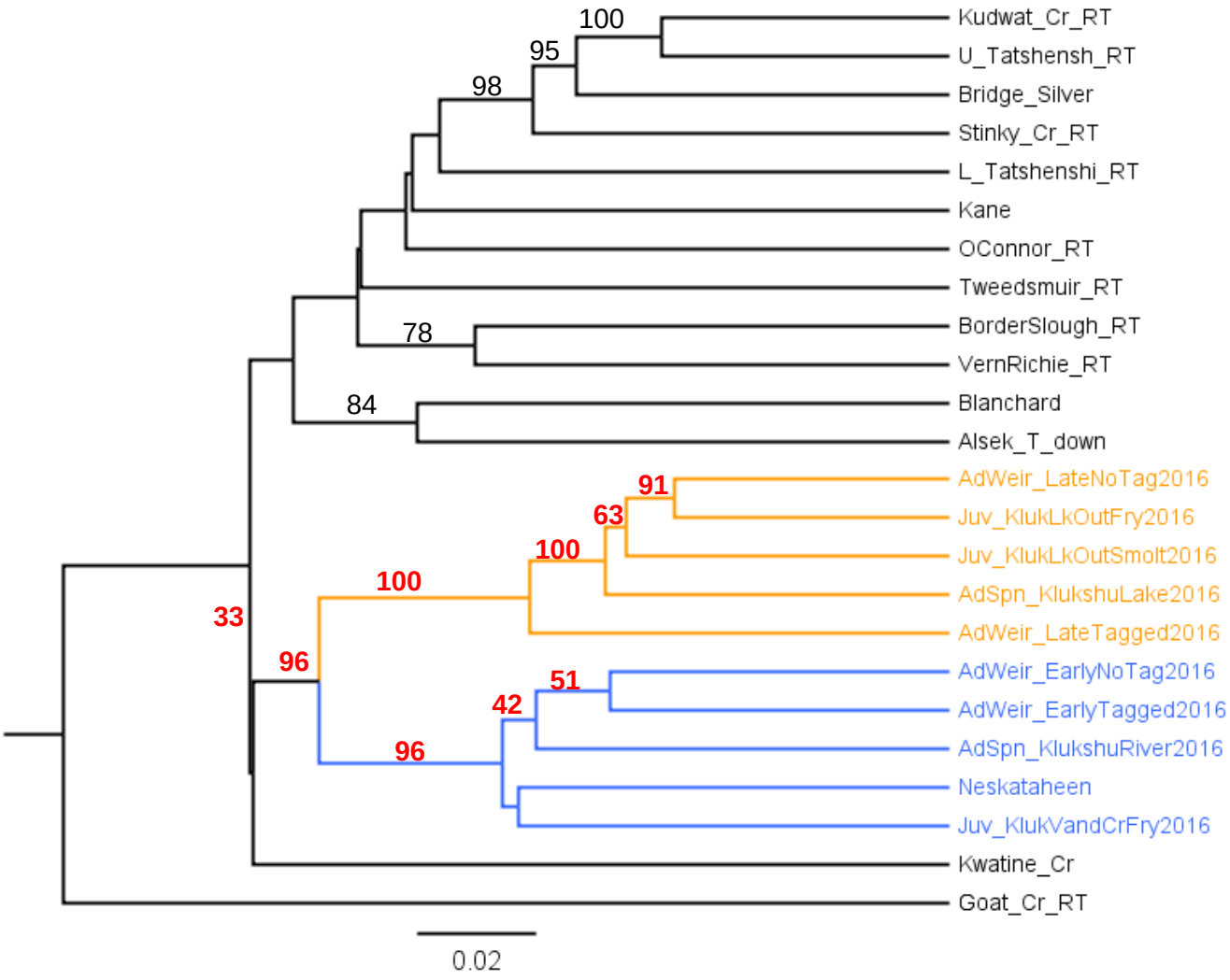


Figure M 16: Fitted Tree for 2016 Klukshu Samples (Excl. Mix) and Revised Alsek Baselines – G12/T8
This tree was constructed with the TREEFIT program (Section 5.7) using the *Dc* measure of genetic distance (Cavalli-Sforza 1967) and the *UPGMA* algorithm for tree fitting. The genotype set included all samples collected in 2016, except adults sampled at the weir during the Mix timing group (Aug 14-20, stat week 34), and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years). Numbers on the tree branches show the proportion of fits among 1000 bootstrap tests which grouped that particular set of samples together. The UPGMA fits had overall lower bootstrap values (and lower R^2; Table 13). 96% of the bootstrap tests grouped the early weir samples, river spawners, river fry, and Neskataheen together. 100% of the tests also grouped the late weir samples, lake spawners, lake outlet fry, and lake outlet smolts together. 96% of the tests put all the Klukshu samples with Neskataheen on a separate branch from all the other Alsek samples. Note that this is one of 16 alternative trees produced with TREEFIT (Set G12, Method T8). Table 8 and Table 9 list the components of the sensitivity analyses. Table 12 categorizes the resulting types of tree, and lists a measure of how well they fit the sample. Table 13 compares bootstrap results for the different fitting methods. Bootstrap values varied a little when the 1000 tests were replicated (± a few percent).

Appendix N: Additional Tree Fitting Outputs – R

Table N 1: Genetic Distances for 2016 Klukshu Samples and Revised Alsek Baselines – Dc (R)
This table shows the *Dc* measure of genetic distance (Cavalli-Sforza 1967) for the 2016 Klukshu samples and the revised Alsek baseline (50+ samples only, 2016 Klukshu river and lake spawning ground samples instead of Early/Mix/Late weir samples from previous years). *Dc* measures were calculated using the R package {adegenet}. Genetic distances are based on pairwise sample comparisons, and are not affected by having other sample groups in the analysis. Therefore, the distances shown in this table apply to all the alternative genotype sets that were tested (Table 8). Sample groups that are genetically close (i.e. smaller distance) are highlighted, with breakpoints set at 10% (Red), 20% (Orange), and 30% (Yellow) of the overall range of values across all pairwise comparisons for this distance measure.

	AdWeir_EarlyNoTag2016	AdWeir_EarlyTagged2016	AdWeir_LateNoTag2016	AdWeir_LateTagged2016	Juv_KlukLkOutFry2016	Juv_KlukLkOutSmolt2016	Juv_KlukVandCrFry2016	AdSpn_KlukshuLake2016	AdSpn_KlukshuRiver2016
AdWeir_EarlyNoTag2016		0.1336	0.1951	0.2587	0.2257	0.2525	0.1538	0.2099	0.1489
AdWeir_EarlyTagged2016	0.1336		0.1999	0.2513	0.2187	0.2492	0.1903	0.2052	0.1737
AdWeir_LateNoTag2016	0.1951	0.1999		0.1499	0.1149	0.1337	0.2225	0.1338	0.2172
AdWeir_LateTagged2016	0.2587	0.2513	0.1499		0.1712	0.1775	0.2789	0.1807	0.2824
Juv_KlukLkOutFry2016	0.2257	0.2187	0.1149	0.1712		0.1280	0.2416	0.1333	0.2441
Juv_KlukLkOutSmolt2016	0.2525	0.2492	0.1337	0.1775	0.1280		0.2701	0.1545	0.2734
Juv_KlukVandCrFry2016	0.1538	0.1903	0.2225	0.2789	0.2416	0.2701		0.2403	0.1813
AdSpn_KlukshuLake2016	0.2099	0.2052	0.1338	0.1807	0.1333	0.1545	0.2403		0.2432
AdSpn_KlukshuRiver2016	0.1489	0.1737	0.2172	0.2824	0.2441	0.2734	0.1813	0.2432	
Alsek_T_down	0.2379	0.2582	0.2435	0.3004	0.2700	0.2912	0.2527	0.2758	0.2358
Blanchard	0.2706	0.3003	0.2871	0.3391	0.3140	0.3350	0.2860	0.3172	0.2685
BorderSlough_RT	0.3334	0.3312	0.2921	0.3353	0.3129	0.3256	0.3495	0.3175	0.3136
Bridge_Silver	0.2798	0.2732	0.2392	0.2842	0.2649	0.2776	0.2946	0.2655	0.2581
Goat_Cr_RT	0.3626	0.3749	0.3448	0.3655	0.3667	0.3798	0.3743	0.3712	0.3442
Kane	0.2484	0.2643	0.2287	0.2793	0.2577	0.2779	0.2554	0.2577	0.2410
Kudwat_Cr_RT	0.2503	0.2538	0.2226	0.2749	0.2482	0.2660	0.2673	0.2491	0.2350
Kwatine_Cr	0.2512	0.2629	0.2520	0.2968	0.2813	0.2948	0.2671	0.2851	0.2495
L_Tatshenshi_RT	0.2968	0.2988	0.2661	0.3106	0.2869	0.2992	0.3132	0.2857	0.2849
Neskataheen	0.1728	0.2039	0.2590	0.3139	0.2817	0.3048	0.1964	0.2689	0.2165
OConnor_RT	0.2429	0.2559	0.2309	0.2806	0.2554	0.2819	0.2584	0.2521	0.2336
Stinky_Cr_RT	0.2650	0.2684	0.2398	0.2783	0.2607	0.2783	0.2878	0.2688	0.2542
Tweedsmuir_RT	0.2719	0.2814	0.2585	0.3080	0.2884	0.3098	0.2889	0.2970	0.2557
U_Tatshensh_RT	0.2368	0.2437	0.2035	0.2593	0.2306	0.2440	0.2566	0.2306	0.2231
VernRichie_RT	0.2755	0.2779	0.2480	0.2986	0.2706	0.2969	0.2924	0.2781	0.2557

Breaks				
Red	Orange	Yellow	White	
0.1216	0.1514	0.1813		

Table N 2: Genetic Distances for 2016 Klukshu Samples and Revised Alsek Baselines – Ds (R)

This table shows the *Ds* measure of genetic distance (Nei 1978) for the 2016 Klukshu samples and the revised Alsek baseline (50+ samples only, 2016 Klukshu river and lake spawning ground samples instead of Early/Mix/Late weir samples from previous years). *Ds* measures were calculated using the R package {adegenet}. Genetic distances are based on pairwise sample comparisons, and are not affected by having other sample groups in the analysis. Therefore, the distances shown in this table apply to all the alternative genotype sets that were tested (Table 8). Sample groups that are genetically close (i.e. smaller distance) are highlighted, with breakpoints set at 2% (Red), 7% (Orange), and 15% (Yellow) of the overall range of values across all pairwise comparisons for this distance measure.

	AdWeir_EarlyNoTag2016	AdWeir_EarlyTagged2016	AdWeir_LateNoTag2016	AdWeir_LateTagged2016	Juv_KlukLkOutFry2016	Juv_KlukLkOutSmolt2016	Juv_KlukVandCrFry2016	AdSpn_KlukshuLake2016	AdSpn_KlukshuRiver2016
AdWeir_EarlyNoTag2016									
AdWeir_EarlyTagged2016	0.0102								
AdWeir_LateNoTag2016	0.0387	0.0389							
AdWeir_LateTagged2016	0.0599	0.0545	0.0115						
Juv_KlukLkOutFry2016	0.0502	0.0473	0.0059	0.0154					
Juv_KlukLkOutSmolt2016	0.0633	0.0610	0.0099	0.0157	0.0107				
Juv_KlukVandCrFry2016	0.0223	0.0303	0.0467	0.0701	0.0520	0.0645			
AdSpn_KlukshuLake2016	0.0395	0.0376	0.0086	0.0161	0.0111	0.0189	0.0490		
AdSpn_KlukshuRiver2016	0.0138	0.0192	0.0429	0.0629	0.0505	0.0624	0.0282	0.0486	
Alsek_T_down	0.0515	0.0620	0.0501	0.0688	0.0570	0.0605	0.0646	0.0652	0.0480
Blanchard	0.0961	0.1146	0.1015	0.1215	0.1092	0.1106	0.1116	0.1171	0.0968
BorderSlough_RT	0.1030	0.0984	0.0825	0.0952	0.0889	0.0832	0.1241	0.0944	0.0880
Bridge_Silver	0.0787	0.0743	0.0635	0.0708	0.0726	0.0749	0.1034	0.0719	0.0677
Goat_Cr_RT	0.1340	0.1480	0.1146	0.1244	0.1300	0.1236	0.1575	0.1321	0.1156
Kane	0.0473	0.0508	0.0398	0.0513	0.0456	0.0491	0.0604	0.0473	0.0423
Kudwat_Cr_RT	0.0640	0.0618	0.0483	0.0571	0.0532	0.0558	0.0793	0.0597	0.0523
Kwatine_Cr	0.0462	0.0505	0.0442	0.0573	0.0580	0.0594	0.0618	0.0529	0.0408
L_Tatshenshi_RT	0.0924	0.0940	0.0704	0.0799	0.0743	0.0732	0.1055	0.0782	0.0815
Neskataheen	0.0248	0.0310	0.0696	0.0932	0.0804	0.0945	0.0282	0.0702	0.0345
OConnor_RT	0.0508	0.0583	0.0419	0.0546	0.0489	0.0549	0.0647	0.0495	0.0473
Stinky_Cr_RT	0.0783	0.0789	0.0615	0.0666	0.0635	0.0666	0.0927	0.0714	0.0659
Tweedsmuir_RT	0.0666	0.0685	0.0628	0.0721	0.0702	0.0758	0.0813	0.0729	0.0588
U_Tatshensh_RT	0.0577	0.0584	0.0420	0.0504	0.0465	0.0480	0.0736	0.0490	0.0484
VernRichie_RT	0.0676	0.0652	0.0542	0.0654	0.0614	0.0645	0.0894	0.0673	0.0624

Breaks

Red	Orange	Yellow	White
0.0218	0.0422	0.0576	

Table N 3: Genetic Distances for 2016 Klukshu Samples and Revised Alsek Baselines – Theta / Fst (R)

This table shows the *Fst* measure of genetic distance (Weir and Cockerham 1987), labelled *Theta* in the Treefit program, for the 2016 Klukshu samples and the revised Alsek baseline (50+ samples only, 2016 Klukshu river and lake spawning ground samples instead of Early/Mix/Late weir samples from previous years). *Ds* measures were calculated using the R package {adegenet}. Genetic distances are based on pairwise sample comparisons, and are not affected by having other sample groups in the analysis. Therefore, the distances shown in this table apply to all the alternative genotype sets that were tested (Table 8). Sample groups that are genetically close (i.e. smaller distance) are highlighted, with breakpoints set at 10% (Red), 20% (Orange), and 30% (Yellow) of the overall range of values across all pairwise comparisons for this distance measure.

	AdWeir_EarlyNoTag2016	AdWeir_EarlyTagged2016	AdWeir_LateNoTag2016	AdWeir_LateTagged2016	Juv_KlukLkOutFry2016	Juv_KlukLkOutSmolt2016	Juv_KlukVandCrFry2016	AdSpn_KlukshuLake2016	AdSpn_KlukshuRiver2016
AdWeir_EarlyNoTag2016									
AdWeir_EarlyTagged2016	0.0667								
AdWeir_LateNoTag2016	0.1259	0.1269							
AdWeir_LateTagged2016	0.1590	0.1525	0.0722						
Juv_KlukLkOutFry2016	0.1421	0.1389	0.0487	0.0832					
Juv_KlukLkOutSmolt2016	0.1601	0.1579	0.0640	0.0833	0.0665				
Juv_KlukVandCrFry2016	0.0965	0.1127	0.1356	0.1695	0.1421	0.1593			
AdSpn_KlukshuLake2016	0.1286	0.1260	0.0607	0.0845	0.0690	0.0891	0.1409		
AdSpn_KlukshuRiver2016	0.0766	0.0905	0.1295	0.1607	0.1392	0.1561	0.1059	0.1400	
Alsek_T_down	0.1427	0.1562	0.1372	0.1661	0.1446	0.1516	0.1550	0.1587	0.1336
Blanchard	0.1936	0.2105	0.1954	0.2180	0.2010	0.2046	0.2043	0.2116	0.1905
BorderSlough_RT	0.1964	0.1933	0.1740	0.1925	0.1790	0.1764	0.2101	0.1886	0.1784
Bridge_Silver	0.1775	0.1734	0.1581	0.1711	0.1676	0.1720	0.1986	0.1700	0.1625
Goat_Cr_RT	0.2283	0.2393	0.2100	0.2233	0.2213	0.2187	0.2422	0.2266	0.2102
Kane	0.1379	0.1434	0.1243	0.1459	0.1318	0.1388	0.1520	0.1376	0.1275
Kudwat_Cr_RT	0.1580	0.1564	0.1353	0.1528	0.1406	0.1464	0.1712	0.1528	0.1397
Kwatine_Cr	0.1382	0.1447	0.1333	0.1551	0.1512	0.1544	0.1566	0.1472	0.1279
L_Tatshenshi_RT	0.1875	0.1899	0.1622	0.1783	0.1652	0.1667	0.1959	0.1735	0.1728
Neskataheen	0.1021	0.1143	0.1648	0.1941	0.1755	0.1913	0.1070	0.1679	0.1177
OConnor_RT	0.1418	0.1519	0.1260	0.1498	0.1341	0.1447	0.1547	0.1398	0.1324
Stinky_Cr_RT	0.1779	0.1792	0.1567	0.1670	0.1585	0.1637	0.1900	0.1703	0.1614
Tweedsmuir_RT	0.1613	0.1643	0.1537	0.1702	0.1610	0.1695	0.1738	0.1680	0.1483
U_Tatshensh_RT	0.1515	0.1531	0.1276	0.1447	0.1332	0.1373	0.1669	0.1401	0.1361
VernRichie_RT	0.1621	0.1603	0.1429	0.1626	0.1505	0.1567	0.1810	0.1615	0.1520

Breaks				
Red	Orange	Yellow	White	
0.1127	0.1336	0.1545		

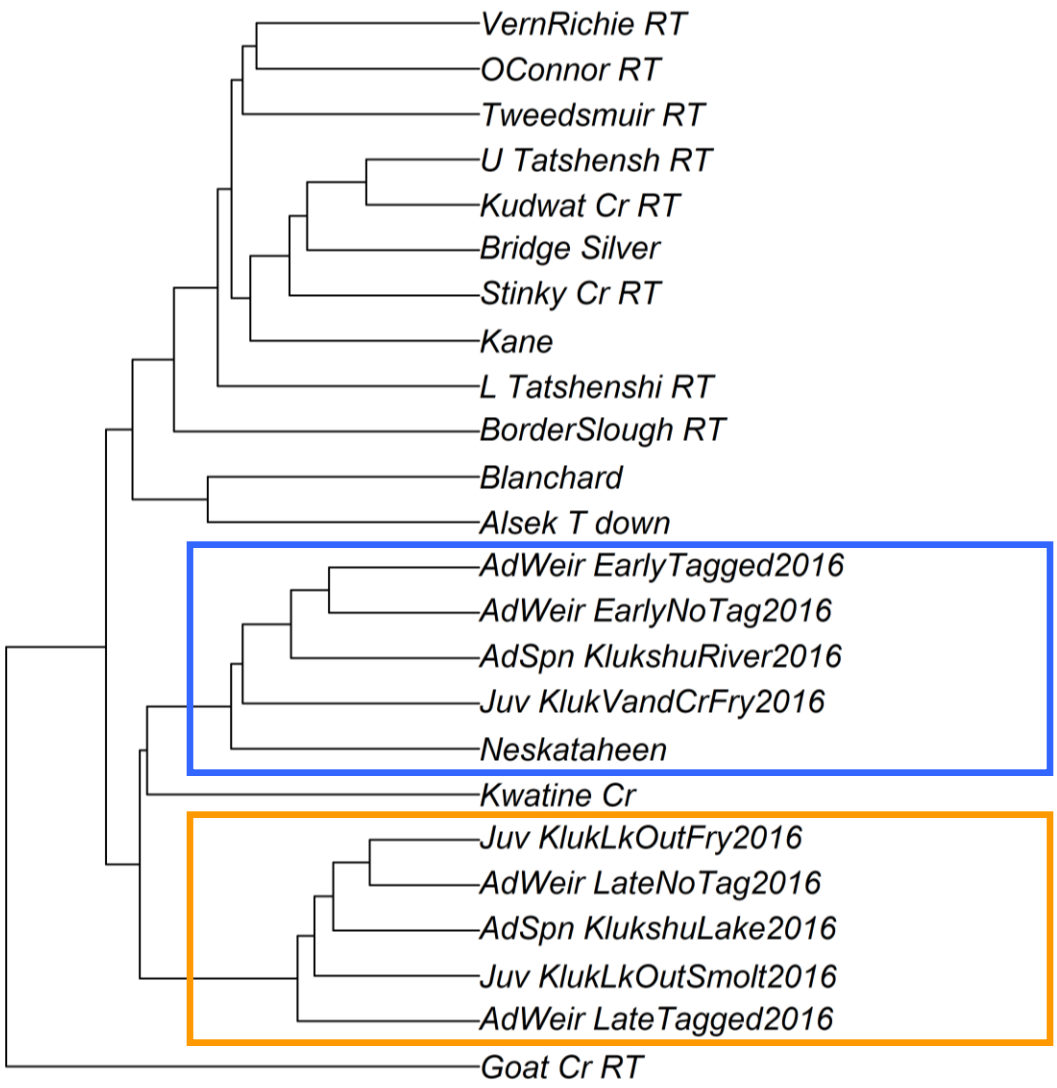


Figure N 1: Fitted Tree for 2016 Klukshu Samples (Excl. Mix) and Revised Alsek Baselines – G12/T9 (R) This tree was constructed with the R packages {adegenet}, {ape}, and {phangorn} (Section 5.7) using the *Theta* measure of genetic distance (Weir and Cockerham 1984) and the *UPGMA* algorithm for tree fitting. The genotype set included all samples collected in 2016, except adults sampled at the weir during the Mix timing group (Aug 14-20, stat week 34), and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years. Note that this is one of 3 alternative trees produced with R (Set G12, Method T9). Table 8 and Table 9 list the components of the sensitivity analyses. Table 13 compares bootstrap results for the different fitting methods. The structure of this tree is similar, but not identical, to the corresponding tree created with TREEFIT (Figure M 13). Early weir samples, river fry, river spawners, and Neskataheen are on one branch. Late weir samples, lake outlet juveniles, and lake spawners are on another branch. Kwatine_Cr is linked to the River/Neskataheen branch.

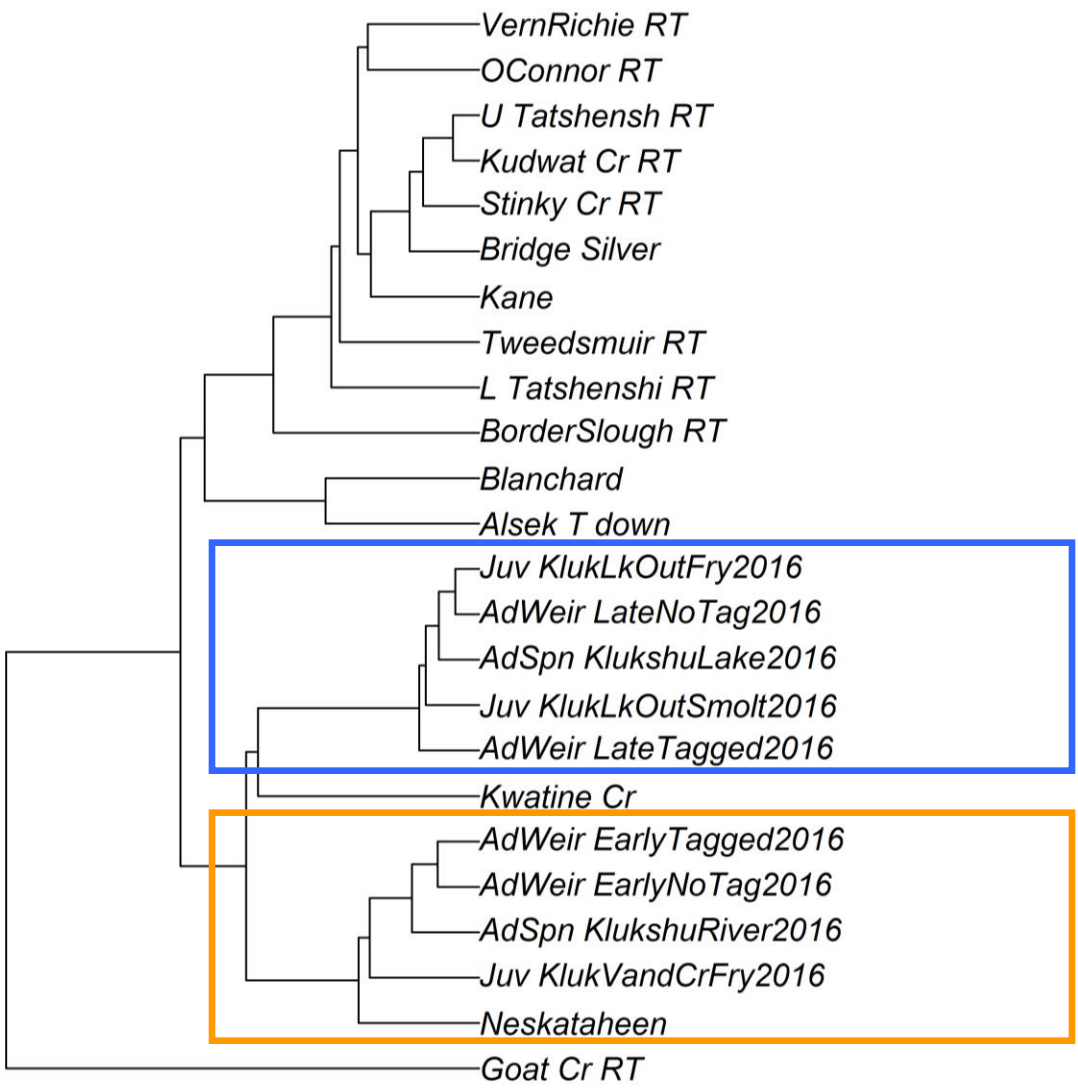


Figure N 2: Fitted Tree for 2016 Klukshu Samples (Excl. Mix) and Revised Alsek Baselines – G12/T10 (R) This tree was constructed with the R packages {adegenet}, {ape}, and {phangorn} (Section 5.7) using the *Ds* measure of genetic distance (Nei 1978) and the *UPGMA* algorithm for tree fitting. The genotype set included all samples collected in 2016, except adults sampled at the weir during the Mix timing group (Aug 14-20, stat week 34), and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years. Note that this is one of 3 alternative trees produced with R (Set G12, Method T10). Table 8 and Table 9 list the components of the sensitivity analyses. Table 13 compares bootstrap results for the different fitting methods. The structure of this tree is similar, but not identical, to the corresponding tree created with TREEFIT (Figure M 14). Early weir samples, river fry, river spawners, and Neskataheen are on one branch. Late weir samples, lake outlet juveniles, and lake spawners are on another branch. Kwatine_Cr is linked to the River/Neskataheen branch.

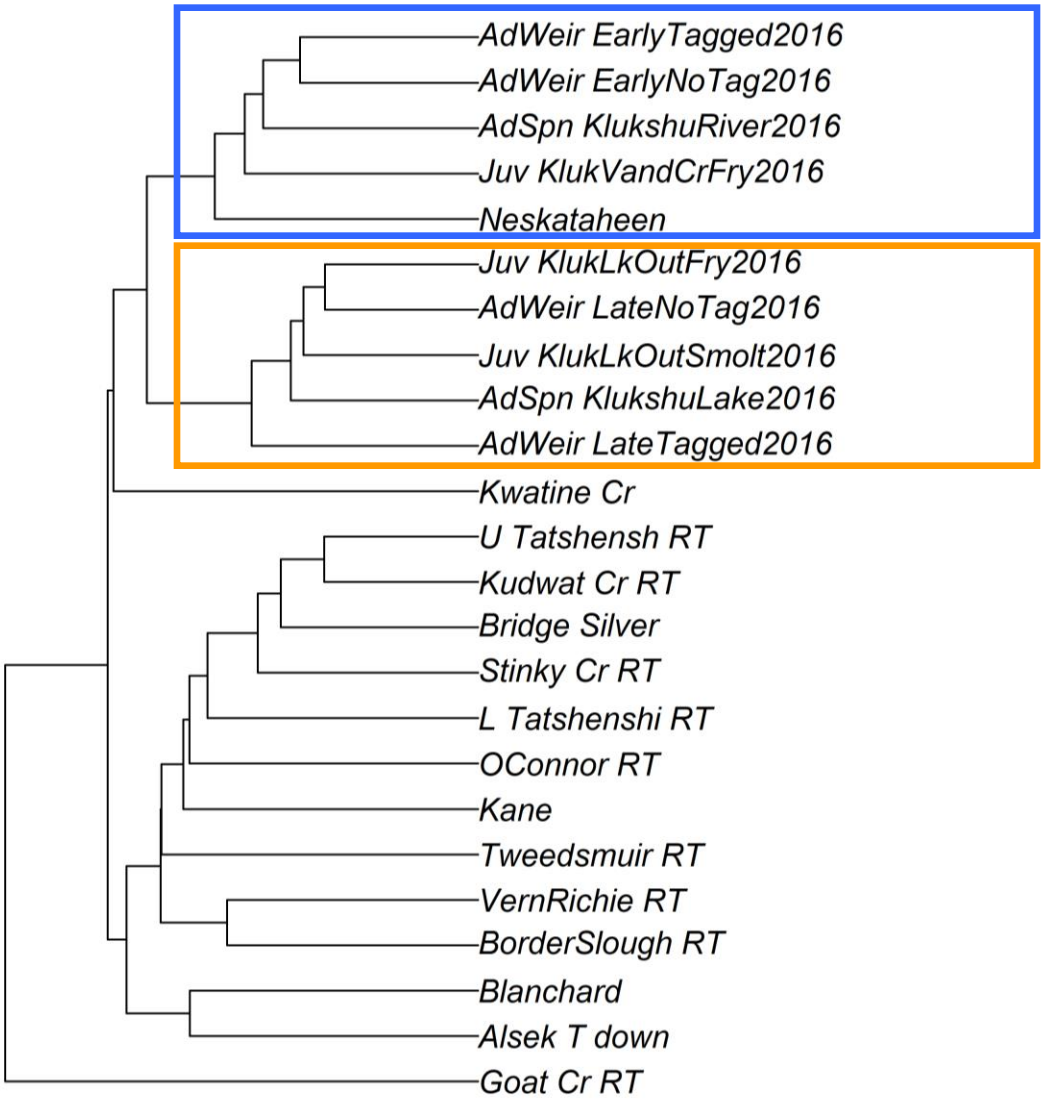


Figure N 3: Fitted Tree for 2016 Klukshu Samples (Excl. Mix) and Revised Alsek Baselines – G12/T11 (R) This tree was constructed with the R packages {adegenet}, {ape}, and {phangorn} (Section 5.7) using the *Dc* measure of genetic distance (Cavalli-Sforza 1967) and the *UPGMA* algorithm for tree fitting. The genotype set included all samples collected in 2016, except adults sampled at the weir during the Mix timing group (Aug 14-20, stat week 34), and the revised baseline for Alsek sockeye (sample groups with 50+ samples only, using 2016 river spawners and lake spawners instead of weir sampled from previous years. Note that this is one of 3 alternative trees produced with R (Set G12, Method 11). Table 8 and Table 9 list the components of the sensitivity analyses. Table 13 compares bootstrap results for the different fitting methods. The structure of this tree is similar, but not identical, to the corresponding tree created with TREEFIT (Figure M 16). Early weir samples, river fry, river spawners, and Neskataheen are on one branch. Late weir samples, lake outlet juveniles, and lake spawners are on another branch.