FISHERY RESEARCH

NATURAL-ORIGIN STEELHEAD AND CHINOOK SALMON LIFE HISTORY AND GENETIC DIVERSITY AT PIT TAG DETECTION LOCATIONS THROUGHOUT THE SNAKE RIVER BASIN

ANNUAL PROGRESS REPORT

January 1, 2022 — December 31, 2022

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IDFG Report Number 23-09
June 2023

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Project Progress Report

2022 Annual Report

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Project Number 2010-031-00
Contract Number 88216

IDFG Report Number 23-09
June 2023

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ABSTRACT

This report summarizes life history and genetic diversity information for wild adult steelhead (*Oncorhynchus mykiss*) and spring/summer Chinook Salmon (*O. tshawytscha*) sampled at Lower Granite Dam and later detected in a Distinct Population Segment (DPS) or Evolutionarily Significant Unit (ESU) in the Snake River basin for the 01/01/2022 to 12/31/2022 reporting period. This reporting period covers analysis of individuals crossing Lower Granite Dam in spawn year (SY) 2022. A total of 1,917 steelhead and 2,791 Chinook Salmon were sampled at Lower Granite Dam. Of the fish tagged at Lower Granite Dam, 930 steelhead and 1,732 Chinook Salmon were subsequently identified at a PIT tag array within the boundary of a population in the Snake River basin. Panels of up to 368 SNPs were genotyped at both Idaho Department of Fish and Game's Eagle Fish Genetics Lab and the Columbia River Inter-Tribal Fish Commission's Hagerman Genetics Lab, to assign these fish to hatchery parents or wild genetic stocks. We describe the life history variation and genetic diversity of steelhead and Chinook Salmon detected in Snake River populations for SY2022. The information presented in this report provides critical data for viable Salmonid population monitoring of the Snake River steelhead DPS and the Snake River spring/summer Chinook Salmon ESU.

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Suggested citation:

Hargrove, J. S., M. Davison, and M. R. Campbell. 2023. Natural-origin steelhead and Chinook Salmon life history and genetic diversity at PIT tag detection locations throughout the Snake River basin. Idaho Department of Fish and Game Report 23-09. Annual Report, BPA Project 2010-031-00.

INTRODUCTION

In this report we summarize life history and genetic diversity for 21 of the 24 extant steelhead (*Oncorhynchus mykiss*) populations in the Snake River Distinct Population Segment (DPS) (9/12 populations in Salmon River Major Population Group [MPG], 5/5 in Clearwater River MPG, 1/1 in Imnaha River MPG, 4/4 in Grande Ronde River MPG, 2/2 in Lower Snake River MPG). We provide similar information for 21 of the 30 extant populations of spring/summer Chinook Salmon (*O. tshawytscha*) within the Snake River Evolutionarily Significant Unit (ESU) (6/8 in Upper Salmon River, 3/9 in Middle Fork Salmon River, 3/4 in South Fork Salmon River, 7/7 in Grande Ronde/Imnaha Rivers, 2/2 in Lower Snake River). For spring/summer Chinook Salmon, we also report on five populations that were extirpated and subsequently re-founded with fish from either neighboring or out-of-basin populations. Extirpated populations of Chinook Salmon reported on here include Lookingglass Creek (Grande Ronde/Imnaha Rivers), two populations from the Clearwater River (Lolo Creek and the Lochsa River), one population from the Upper Salmon (Panther Creek), and one population from the Dry Clearwater (upper South Fork Clearwater River).

The data produced in this report are the product of multiple projects and agencies and are generated from the PIT tagging and biological sampling of adult steelhead and Chinook Salmon as they migrate through the Lower Granite Dam (LGR) fish ladder. Trapping at LGR is coordinated by National Marine Fisheries Service (NMFS; BPA Project 2005-002-00; Harmon 2003; Ogden 2016). The Idaho Salmon and Steelhead Monitoring and Evaluation Studies (ISSMES; BPA Project 1990-055-00) coordinated the biological sampling of adults at LGR and provided length, age, and passage timing data. The IDFG Genetic Monitoring of Snake River Salmon and Steelhead Stocks (BPA Project 2010-031-00) provided PBT baselines within the Snake River basin and SNP genotype data for population-level genetic diversity and structure analyses. The Integrated In-Stream PIT Tag Detection System Operations and Monitoring Project (ISEMP; BPA Project 2018-002-00) has historically developed and maintained much of the detection infrastructure throughout the Snake River basin.

METHODS

Adult Trap Operations and Sample Processing

Detailed methods describing sampling of adult steelhead and Chinook Salmon at the LGR adult trap are described in Lawry et al. (2020). Briefly, adult steelhead and spring/summer Chinook Salmon migrating upstream past LGR may be intercepted at a trapping facility, located on the adult fish ladder above the counting window, according to a predetermined trapping rate. A committee of collaborating management agencies determines the trapping rates that achieve sample requirements for multiple projects and balance fish handling concerns. Trapping rates are typically 10–20%. The trapping rate determines how long a trap gate remains open four times per hour; the trap is operational 24 hours per day.

Scale samples were taken from adults sampled in the LGR adult trap to assign freshwater and saltwater ages. Scales were processed in the IDFG Nampa Research Anadromous Ageing Laboratory according to protocols detailed in Wright et al. (2015). Ages are formatted using the European system where freshwater (FW) age is separated from saltwater (SW) age by a decimal. For steelhead repeat spawners, an ‘R’ is added to the saltwater age to designate the winter spent in freshwater while on the first spawning run. Age classes are defined as the unique combinations of SW, FW, and repeat spawning ages. Brood year (BY) is the migration year minus the total age

at spawning (sum of freshwater and saltwater ages, plus 1). Fish lacking either a freshwater or saltwater age were not used for analysis.

A fin clip was collected from each adult sampled in the LGR adult trap for genetic analysis. DNA was extracted using the nexttec™ Genomic DNA Isolation Kit from XpressBio (Thurmont, Maryland) or QIAGEN DNeasy Tissue Kits (Valencia, California). Once extracted, DNA was processed using "Genotyping-in-Thousands by sequencing" (GT-seq) technique at either the IDFG genetics laboratory in Eagle, Idaho (EFGL), or the Columbia River Inter-Tribal Fish Commission's genetics laboratory in Hagerman, Idaho. Protocols for library preparation associated with GT-seq can be found in Campbell et al. (2015). Library preparation begins with an initial multiplex PCR reaction that is used to ligate a pair of sequencing primers to the target sequences which contain a known single-nucleotide polymorphism (SNP). In a subsequent PCR reaction, the sample is "barcoded" by ligating an additional sequence to the target that identifies the sample's tray of origin (i7 barcode) and its position on the tray (i5 barcode). After barcoding, the quantity of DNA must be normalized for each sample. A SequalPrep™ Normalization Plate Kit (Applied Biosystems) is used to bind a standard amount of amplicon product and normalize concentrations. All 96 samples are then pooled into a single 'plate library'. All plate libraries are quantified by a Qubit fluorometer (Invitrogen), and concentrations are normalized again before being pooled. Loci are genotyped by sequencing the target location on the Illumina NextSeq. A bioinformatics pipeline is used to assign resulting sequences and the genotypes back to individual samples using the unique combination of i5 and i7 barcodes.

Data for the SNP marker panels can be accessed via the FishGen webpage (https://www.fishgen.net/Home.aspx). Once a user account has been set up with FishGen, the details of these panels can be accessed under the 'Marker Sets' > 'Export' tab once a user has logged in. Metadata for each marker include synonym of species, Vic probe, Vic allele, Fam probe, Fam allele, forward primer, and reverse primer. The current Chinook Salmon panel is 'CRITFC IDFG Chinook GTseq v4.0 343' and consists of 95 loci for parentage-based tagging (PBT) loci, 96 loci for genetic stock identification (GSI), 1 sex marker, and 151 additional SNP markers. The steelhead panel is 'CRITFC/IDFG Steelhead GTseq v5.0 368' consists of 95 PBT loci, 96 GSI loci, 1 sex marker, and 176 additional SNP markers.

In-Stream Pit Tag Detection Systems Spawning Site Estimation

Individual spawn sites associated with the in-stream pit tag detection systems (IPTDS) were determined with the R package PITcleanr (available at: https://github.com/KevinSee/PITcleanr) as described in Orme and Kinzer (2018).

Records of "valid" PIT tags implanted into, or detected in, putative natural-origin steelhead and Chinook Salmon at the LGR adult trap were downloaded from the Lower Granite adult trap database. In total, records of valid tags were downloaded for 1,917 for steelhead and 2,791 Chinook Salmon (Table 1).

Genetic and phenotypic data (fork length, scale age, and sample date at Lower Granite Dam) for each individual were downloaded from the Eagle Fish Genetic Lab Progeny database along with an individual's PIT tag number. The PIT tag detection data and life history and genetic datasets were joined using PIT tag numbers. When multiple records existed for an individual fish, all but the first record in each dataset were removed.

Pooling Arrays into Reporting Locations

We pooled PIT tag detection locations based on population delineations specified by the Snake River basin steelhead and Chinook Salmon recovery plans (NMFS 2017, steelhead: Table 2, Chinook Salmon: Table 3). Hereafter, reference to populations will refer to those described by the NMFS recovery plan as outlined in Table 2 and 3.

In past years, fish were classified as 'detected' if their final observed location occurred within the boundary of NMFS-defined populations or at locations that occur on the boundary of multiple populations. Most interrogation sites occur within a population boundary; however, there are multiple sites which occur at the boundary of more than one population and fish detected at these sites could have ultimately ended up in one of multiple upstream populations. In previous reports, fish that were detected at these sites were counted in reporting group summaries but were not attributed to any one population. In this report, fish that were detected at these arrays were treated as 'undetected'. For steelhead, we omitted observations at sites USE and USI which are on the main stem of the upper Salmon River (one station at river km 437 and another at river km 460) and fish last recorded at either of these locations could end up in one of multiple upstream populations (upper Salmon River, SRUMA; East Fork Salmon River, SREFS). For Chinook Salmon, we omitted observations at sites SC1 and SC2, which occur just above the confluence of the Middle and South Fork Clearwater rivers and fish could have ultimately contributed to either Lawyer Creek (SCLAW) or upper South Fork Clearwater River (SCUMA) populations. Sites SW1 and SW2 detected fish that could have contributed to either Meadow Creek (SEMEA), Moose Creek (SEMOO), or the upper Selway (SEUMA) populations. Site SFG is located within the boundary of the South Fork Salmon River (SFMAI), but fish could have also spawned in the Secesh River (SFSEC) or the East Fork South Fork Salmon River (SFEFS). Lastly, Chinook Salmon last detected at interrogation sites USE and USI could have traveled upstream and spawned in the Yankee Fork (SRYFS), Valley Creek (SRVAL), upper Salmon River mainstem (SRUMA), or East Fork Salmon River (SREFS) populations.

Life History (Sex, Length, Age, Run Timing)

Sex was determined using a sex-specific allelic discrimination assay (Campbell et al. 2012). Genomic DNA extraction and SNP genotyping (which includes sex-specific assays for *O. mykiss* and *O. tshawytscha*) are above. The steelhead and Chinook Salmon sex markers show high concordance (~99%) with phenotypic sex recorded at the hatchery in both species (Delomas et al. 2021).

We summarized fork length (cm), freshwater age, ocean (saltwater) age, and total age by DPS/ESU population. Population-specific descriptions were only presented for populations with a minimum of 20 samples detected at a PIT tag array within the respective population boundary. For a detailed description of aging methods and age descriptions see Wright et al. (2015). For steelhead, we also summarized the frequency and percentage of fish that meet A-run (<78 cm FL) and B-run (≥78 cm FL) length criteria. These size criteria are used to inform management processes and were adopted in the US vs. Oregon Management Agreement (NMFS 2018). Length at ocean age was also summarized by population.

Each returning adult steelhead and Chinook Salmon was assigned to a genetic stock of origin via genetic stock identification. Individuals were assigned to genetic stocks in which the probability of its genotype occurring was the greatest using the algorithms implemented in rubias (Moran and Anderson 2019) implemented in R (R Core Team 2020). Individual assignments (IA) were made using species-specific (steelhead or Chinook Salmon) Snake River SNP baselines

v3.1 which were developed by Powell et al. (2018a; section 2), and formally described in Appendix A of Hargrove et al. (2021).

Ten genetic stocks were used for natural-origin steelhead IA analyses. Genetic stocks include: 1) UPSALM: upper Salmon River; 2) MFSALM: Middle Fork Salmon River (including Chamberlain and Bargamin creeks); 3) SFSALM: South Fork Salmon River; 4) LOSALM: lower Salmon River; 5) UPCLWR: upper Clearwater River (Lochsa and Selway rivers); 6) SFCLWR: South Fork Clearwater River (including Clear Creek); 7) LOCLWR: lower Clearwater River; 8) IMNAHA: Imnaha River; 9) GRROND: Grande Ronde River; and 10) LSNAKE: Asotin Creek and tributaries to the Snake River downstream of the Clearwater River confluence.

Seven natural-origin Chinook Salmon genetic stocks were used during IA analyses. Genetic stocks include: 1) UPSALM: upper Salmon River; 2) MFSALM: Middle Fork Salmon River; 3) CHMBLN: Chamberlain Creek; 4) SFSALM: South Fork Salmon River; 5) HELLSC: an aggregate reporting group that includes the Little Salmon, Clearwater, Grande Ronde, and Imnaha rivers; 6) TUCANO: Tucannon River, and 7) FALL: Snake River fall Chinook Salmon.

We summarized passage timing at LGR for fish detected within the range of populations by calculating the 5th, 25th, 50th (median), 75th, and 95th quantile dates of passage for each group.

We calculated the proportion of fish crossing LGR each week of the spawn year that originated in each of the 10 steelhead or 7 Chinook Salmon GSI reporting units. We also estimated the proportion of the fish from each GSI reporting unit within a return week that were later detected within the range of a population in the Snake River basin.

Genetic Diversity and Structure

Genetic diversity and population structure were summarized for locations with a minimum sample size of 20 individuals. The observed and expected heterozygosity and the percent of SNPs that were polymorphic were calculated for each population as a proxy measure of genetic diversity. Observed heterozygosity directly measures the percentage of detected fish in a population that were heterozygotes (carry both alleles). The overall observed heterozygosity was calculated as the average across all SNPs. Expected heterozygosity is an estimate of the percentage of individuals in the population that are heterozygotes (average across SNPs) based on the allele frequency estimates from the population.

Tests for deviation from Hardy-Weinberg equilibrium (HWE) were performed across all SNPs for each population with at least 20 samples. Exact tests were performed for all nuclear SNPs in the R package pegas version 1.1 (Paradis 2010). Critical values were adjusted using the false discovery rate correction using the p.adjust function implemented in the R package stats (version 3.6.2).

Pairwise F_{ST} was estimated for each location with greater than 20 PIT tag detections using the R package genepop version 4.7.5 (https://cran.r-project.org/web/packages/genepop/index.html). Critical values were adjusted using the false discovery rate correction.

Genetic clustering of individuals detected within the ranges of DPS/ESU populations was examined using discriminant analysis of principal components (DAPC; Jombart 2008) using the R package adegenet version 1.3-1 (Jombart 2008, Jombart and Ahmed 2011). This method provides a multivariate based analysis of genetic clustering that is free of underlying genetic

models such as Hardy-Weinberg equilibrium or the absence of linkage disequilibrium (Jombart et al. 2009). Discriminant analysis of principal components is commonly used to discover the number of genetic clusters present in a collection of samples (i.e., estimation of genetic clusters is performed without prior knowledge), and we identified the optimal number of genetic clusters (K) based on Bayesian Information Criterion (BIC). Specifically, we generated 10 estimates of BIC for each K value across a range of values (K = 1-10) while retaining 160 and 150 principal components for steelhead and Chinook Salmon, respectively. The K which corresponded to the lowest BIC value was retained. The optimal number of discriminant analysis and principal components to retain was determined using the cross-validation function (*xvalDapc*) in adegenet.

Effective Number of Breeders (N_b)

We used two programs to estimate the effective number of breeders (N_b) by parental brood year (BY) for each population. The program COLONY 2 (Jones and Wang 2010) implements the sibship assignment (SA) method for calculating effective population size (N_e) and N_b proposed by Wang (2009). The SA method is a single-sample approach that uses sibship assignments to determine full-sibling and half-sibling relationships within the sample; estimates of N_e are then acquired from frequencies of full- and half-sibling dyads. The SA method has been shown to perform well both with simulated and empirical data (Wang 2005, Beebee 2009, Barker 2011, Phillipsen et al. 2011, Skrbinsek et al. 2012, Ackerman et al. 2016). When offspring from the same cohort (brood year) are analyzed as a single sample, estimates of N_e from the SA method are equivalent to N_b. We also used the program NeEstimator version 2.1 (Do et al. 2014) to estimate N_b using the bias corrected linkage disequilibrium (LD) method of Waples (2006) excluding all alleles with frequencies less than 0.03. The LD method is the most widely used method for estimating N_e from a single collection (Waples and England 2011) and provides estimates of N_b in a population when used on a single BY (Waples 2005).

We used scale age data to assign each fish back to a brood year. Offspring from the same population and BY were then analyzed as a single sample to estimate N_b. Because steelhead and Chinook Salmon reproductive strategies fall on a spectrum between monogamy and random mating, we calculated N_b assuming random mating. To generate a single N_b estimate per population, we used the harmonic mean of the SA and LD estimates of N_b. Waples and Do (2010) note that all N_e estimation techniques respond to a signal that is inversely related to N_e, and as a result an appropriate way to combine estimates across methods would be to take a weighted harmonic mean. Because the unweighted harmonic mean is the sample size divided by the sum of the reciprocal values, infinite estimates of N_b were replaced with the limit of the reciprocal of N_b, as N_b approaches infinity in the calculation of the harmonic mean N_b within a BY. The SA and LD methods were combined to increase precision of the estimated N_b (Waples and Do 2010). Finally, the unweighted harmonic mean was calculated across BY for each population. Future estimates of N_b will include individuals sampled from previous spawn years at Lower Granite Dam that originate from the same populations and BYs as those observed in the current spawn year. Estimates of N_b have been shown to be more accurate when sample sizes are near or greater than N_b (Ackerman et al. 2016).

Concordance and Genetic Origin of Detected and Non-Detected Fish

Individuals were assigned to genetic stocks using the methods described above. Individual assignments were used to examine concordance between genetic stock and PIT tag detections at arrays within different populations. The proportions of fish from a genetic reporting unit within a return year that were not detected within the range of a population were also calculated. Because the distribution of PIT tag arrays across the Snake River basin is not uniform it is possible

PIT tag detection probabilities vary across the landscape. For example, the number of arrays distributed across river systems is not standardized and some rivers are intrinsically difficult to monitor based on geography. As a result, calculating whether the proportion of that are detected in each reporting unit is higher or lower than proportions observed at Lower Granite Dam identifies areas where data derived from PIT tags may be more or less robust than others. We tested for differences between the observed frequencies of different genetic stocks at PIT tag arrays relative to expected frequencies based on the stock composition of fish passing LGR using a Pearson's Chi-squared test. To determine if fewer or greater numbers of fish were observed at PIT tag arrays relative to LGR, we performed a post hoc analysis, which used the standardized residuals to calculate p-values using the chisq.posthoc.test package in R. We performed the Chi-squared test to investigate whether non-detection rates varied among populations and reporting units or was a random process across the landscape.

Unless otherwise stated all analyses were performed in R version 3.6.3 (R Core Team 2020).

RESULTS

Steelhead

We present life history and genetic diversity information for 21 of the 24 extant Snake River steelhead DPS populations. A total of 14 steelhead populations had more than 20 observations which were used for summaries below. Details for the remaining populations can be found in Appendix A.

IPTDS Detection Query in PTAGIS

Records were downloaded for 1,917 valid PIT tags implanted into SY2022 adult steelhead at LGR (Table 1), 930 of which were subsequently detected within the range of a DPS population and 987 were never detected within the range of a DPS population. A total of 1,911 tagged fish were genotyped, including 927 that were later detected at an array.

Life History (Sex, Length, Age, Run Timing)

Life history diversity information including sex ratios, mean length (including large vs. small proportions), ocean (saltwater) age, total age, and LGR passage timing information for steelhead populations are summarized in Appendix A.

The upper Salmon River (SRUMA-s) population had the lowest percent females (36%), and the lower Middle Fork Salmon River (MFBIG-s) had the highest percent females (84%). Appendix A and Figure 1 summarize sex ratios for steelhead by population.

The South Fork Clearwater River population had the largest average adult steelhead (mean FL = 75.4 cm) while Asotin Creek had the smallest (59.8 cm). The highest percentage of large length (≥78 cm) detections occurred in the South Fork Salmon River (50% of fish). Six different populations had no detected fish ≥78 cm. Mean length (cm FL) and percentage of small versus large fish by location is summarized in Appendix A. Appendix B summarizes length frequencies (by ocean age) of populations.

We observed freshwater ages ranging from age-1 to age-4, and ocean ages ranging from age-1 to age-3 (Figure 2). Repeat spawners were observed in five of the 21 populations (23.8%; Appendix A). The South Fork Clearwater River populations had the oldest average ocean (saltwater) ages (1.8 years) and the lower Middle Fork Salmon River and Tucannon River populations were the youngest (1.3 years). Appendix A and Figure 2 summarize population specific freshwater, ocean-, and total-ages.

The date of median passage at LGR was September 29 across all populations (Figure 3). Panther Creek had the earliest median passage date at LGR (26 August), which was 34 days before the median passage date for the entire run. In contrast, the Tucannon River population had the latest median passage at LGR (13 October) which was 14 days after the median passage date for the entire run. Appendix A summarizes the distribution of LGR passage date by location, and Figure 3 summarizes the distribution of LGR passage date by GSI reporting unit.

We observed variation in the weekly genetic stock composition crossing Lower Granite Dam as well as the proportion of each stock that was detected within the range of a population in the Snake River basin (fall portion: Figure 4; spring portion: Figure 5).

Genetic Diversity and Structure

Expected heterozygosity ranged from a high of 0.313 in the Tucannon River population to a low of 0.283 in Lochsa River populations. The average percent polymorphic SNPs across all locations was high (96.7%), with a maximum of 100% in the Asotin Creek and Wallowa River populations. In contrast, the lowest percent of markers that were polymorphic was observed in the upper mainstem Salmon River (92.0%). Appendix A summarizes observed and expected heterozygosity and percentage of polymorphic SNPs by location.

Deviations from HWE at the population-level were observed in 9 of the 14 populations (Appendix A). The number of markers that deviated from HWE ranged from 1 to 4, which represented between 0.5 and 2.3% of the total number of markers (176) surveyed.

The level of mean pairwise genetic divergence (F_{ST}) among 14 populations of SY2022 steelhead (Figure 6) was 0.022. The highest pairwise values of genetic differentiation were observed in the Selway River (0.040), followed closely by the Lochsa River (0.038) and South Fork Clearwater River (0.035). In contrast, Asotin Creek had the lowest mean level of pairwise genetic differentiation (0.007). Other populations that displayed low levels of genetic differentiation included the Joseph Creek (0.012), upper Grande Ronde River (0.012) and lower Grande Ronde River (0.013) (Figure 6). In general, populations at terminal (upper) portions of drainages were more strongly differentiated, whereas populations in lower sections of drainages were weakly differentiated.

Returning adult steelhead were assigned to four potential genetic clusters via discriminant analysis of principal components (DAPC) based on the lowest Bayesian Information Criterion (BIC) value. Our final DAPC was performed using three discriminant functions and 160 principal components based on outputs from cross validation procedures (Figure 7). Steelhead from populations in the South Fork Clearwater, South Fork Salmon River, Middle Fork Salmon River, and the Upper Clearwater River were almost wholly assigned to a single genetic cluster (i.e., not partially assigned to multiple different clusters). In contrast, steelhead from the Grande Ronde, Imnaha, lower Snake, and upper Salmon rivers reporting units were assigned to multiple genetic clusters.

Effective Number of Breeders

There were sufficient samples to estimate N_b for 14 combinations of brood year and population (Table 4). The greatest number of estimates were made for brood year 2017 (8) and equal numbers of estimates were generated for 2016 and 2018 (3 each). The greatest number of estimates were available for populations in the Grande Ronde River system (5) followed by the Clearwater River (4) and Imnaha River (3). We observed infinite estimates of N_b for 7 brood year-population combinations via the linkage disequilibrium method implemented in NeEstimator and all 95% confidence interval estimates included infinity for this approach. In contrast, one N_b estimate approached infinity using the sibship estimation and five confidence intervals included infinity. Harmonic means ranged from a low of 70 (CRSFC-s 2017) to a high of 840 (SNASO-s 2017; Table 4). We removed one estimate of N_b for the upper Grande Ronde River as it was biologically infeasible (N_b = 4,294,967,294).

Concordance and Genetic Origin of Detected and Non-Detected Fish

Concordance between fish assigned to different genetic reporting groups via PIT tag detections relative to genetic stock identification varied by population (Table 5). Concordance was highest (100%) in the upper Middle Fork Salmon River. The next two highest assignment rates were for the Selway River (96%) and upper Mainstem Salmon River population (91%). The lowest concordance levels were observed in the Little Salmon River, Pahsimeroi River, and Hells Canyon populations (all 0%).

The difference in observed detections at PIT tag arrays was significantly different than expected based on observed counts at LGR overall (χ^2= 91.6, df = 9, p-value <0.001; Figures 4, 5). Post hoc tests identified the Imnaha River (p-value <0.001), Middle Fork Salmon River (p-value <0.001), and Upper Salmon River (p-value = 0.03) reporting units were detected at lower frequencies than expected based on observations at Lower Granite Dam. In contrast, more fish were detected at Upper Clearwater River arrays than observations at Lower Granite Dam (p <0.001). Detections at PIT arrays for fish belonging to the Grande Ronde River, lower Clearwater River, lower Salmon River, lower Snake River, South Fork Clearwater River, and South Fork Salmon River reporting groups occurred at numbers that were not significantly different from what was observed at LGR (all p-values >0.05)

Chinook Salmon

We present life history and genetic diversity information for 21 of the 30 extant Snake River spring/summer Chinook Salmon ESU populations. In addition, we provide information for five populations that were extirpated and subsequently re-founded. A total of 17 Chinook Salmon populations had more than 20 observations and summaries presented below focus on these populations. Details for the remaining populations can be found in Appendix C.

IPTDS Detection Query in PTAGIS

Records were downloaded for 2,791 valid PIT tags implanted into SY2022 adult Chinook Salmon at LGR (Table 1), 1,732 of which were subsequently detected within the range of an ESU population and 1,059 were never detected within the range of an ESU population. A total of 2,783 tagged fish were genotyped (8 fish failed to genotype), including 1,729 of the Chinook Salmon detected at an array.

Life History (Sex, Length, Age, Run Timing)

Life history diversity information including sex ratios, mean length (both including and excluding minijacks/jacks), ocean (saltwater) age, total age, and LGR passage timing information for Chinook Salmon populations are summarized in Appendix C.

Valley Creek (SRVAL) had the lowest percent females (28%), and Catherine Creek (GRCAT) had the highest percent females (66%). Appendix C and Figure 8 summarize sex ratios for Chinook Salmon by population.

The Secesh River (SFSEC) population had the largest average adult Chinook Salmon (jacks excluded; mean FL = 74.2 cm) and the Wenaha River had the smallest (68.5 cm). Appendix C summarizes mean lengths by location and Appendix D summarizes length frequencies (by ocean age) of populations.

We observed freshwater ages ranging from age-1 to age-2, and ocean ages ranging from age-1 to age-4 (Figure 8). Bear Valley Creek (MFBEA) had the oldest average ocean (saltwater) ages (2.1 years), and the Panther Creek population was the youngest (1.9 years). Appendix C and Figure 9 summarize population specific freshwater, ocean-, and total-ages.

The date of median passage at LGR was June 11 across all populations (Figure 10). Catherine Creek had the earliest median passage date at LGR (16 May), which was 26 days before the median passage date for the entire run. In contrast, the South Fork Salmon River main stem population had the latest median passage at LGR (28 June) which was 17 days after the median passage date for the entire run. Appendix C summarizes the distribution of LGR passage date by location, and Figure 10 summarizes the distribution of LGR passage date by GSI reporting unit.

We observed variation in the weekly genetic stock composition crossing Lower Granite Dam as well as the proportion of each stock that was detected within the range of a population in the Snake River basin (Figure 11).

Genetic Diversity and Structure

Expected heterozygosity ranged from a high of 0.249 in the Catherine Creek population to a low of 0.206 in Bear Valley Creek. The average percent polymorphic SNPs across all locations was 88.4% with a maximum of 95.9% in the South Fork Salmon River. In contrast, the lowest percent of markers that were polymorphic was observed in the Valley Creek population (80.0%). Appendix C summarizes observed and expected heterozygosity and percentage of polymorphic SNPs by location.

Deviations from Hardy-Weinberg Equilibrium (HWE) at the population-level were observed in 13 of the 17 populations with sufficient numbers of samples for analysis (Appendix C). The number of markers that deviated from HWE ranged from one to fifteen, which represented between 0.6 and 8.8% of the total number of markers (170) surveyed.

The mean level of pairwise genetic divergence (F_{ST}) among all 17 populations for SY2022 Chinook Salmon was 0.024 (Figure 12). As a function of reporting unit, the Middle Fork Salmon River was the most differentiated (mean F_{ST} across populations = 0.0262) followed by the Upper Salmon River (0.0257), the South Fork Salmon River (0.0254) and Hells Canyon River (0.0203). Among populations within reporting units there was notable variation in mean pairwise

differentiation. Specifically, many reporting units contained populations that displayed both high and low levels of pairwise genetic differentiation (Figure 12).

The optimal number of genetic clusters to describe returning adult Chinook Salmon via discriminant analysis of principal components (DAPC) was seven based on the lowest Bayesian Information Criterion (BIC) value. Membership probability varied as a function of population and reporting unit (Figure 13). The majority of individuals from the Middle Fork Salmon River were assigned to a single genetic cluster. In contrast, ~60% of Chinook Salmon from populations in the South Fork Salmon River were split between two genetic clusters, with the remaining individuals being assigned to various other genetic clusters. Similarly, individual Chinook Salmon from populations in the Hells Canyon reporting units were largely assigned to two genetic clusters.

Effective Number of Breeders

We estimated N_b for 16 Chinook Salmon populations, all of which were attributed to BY 2018 (Table 6). All estimates of N_b were all greater than 50 and ranged from 54 for Catherine Creek to 274 for the South Fork Salmon River main stem population.

Concordance and Genetic Origin of Detected and Non-Detected Fish

Concordance between fish assigned to different genetic reporting groups via PIT tag detections relative to genetic stock identification varied by population (Table 7). Concordance was highest in Lolo, Catherine, Lookingglass, and Big Sheep creeks. All fish detected in these populations were assigned to the Hells Canyon reporting unit. The next two highest assignment rates were for Lostine Creek (90%) and the Minam River population (89%). We observed the lowest concordance for Asotin Creek (0%) and the Tucannon River population (0%).

The difference in observed detections at PIT tag arrays was significantly different than expected based on observed counts at LGR overall (χ^2= 148.0, df = 5, p-value <0.001; Figure 11). Post hoc tests identified the Chamberlin Creek and Fall Chinook reporting unit were detected at significantly lower frequencies at PIT tag arrays (p-value <0.01) than expected based on expectations at LGR. In contrast, we observed far more fish from the South Fork Salmon River (p-value <0.01) than expected. Detections at PIT arrays for fish belonging to the Hells Canyon, Upper Salmon River, and Middle Fork Salmon River reporting groups occurred at numbers that were not significantly different from what was observed at LGR (all p-values >0.05).

DISCUSSION

Monitoring the life history variation and genetic diversity of populations of Snake River steelhead and spring/summer Chinook Salmon is important for determining their viability. McElhany et al. (2000) defined a viable salmonid population (VSP) as:

> An independent population of any Pacific salmonid (genus *Oncorhynchus*) that has a negligible risk of extinction due to threats from demographic variation (random or directional), local environmental variation, and genetic diversity changes (random or directional) over a 100-year time frame.

Four parameters were identified for determining whether a population is viable: population size, growth rate and related parameters, spatial structure, and diversity (McElhany et al. 2000). To assess the risk to population viability caused by the spatial structure and diversity of

populations the ICTRT developed 12 metrics, seven of which relate to maintaining natural patterns of phenotypic and genetic variation and gene flow (ICTRT 2007). Therefore, understanding the current and past patterns of life history diversity and genetic variation within a population is essential to assessing whether the population meets these metrics.

Life History (Sex, Length, Age, Run Timing)

We continued to observe a range of variation in life histories across the genetic stocks in the Snake River basin for both steelhead and Chinook Salmon. Examples include variation in sex ratios both among populations of the same species, but also among species (Figures 1, 8). The average percentage of fish that were female at the population level was lower for SY2022 adult steelhead (68% female) relative to SY2021 (79%; Hargrove et al. 2022). This value is in line with long-term averages; for SY2010-2019, the annual average percentage of female adults ranged from a low of 53% (SY2014) to a high of 73% (SY2017; IPTDSW 2020). In contrast, the percent of returning Chinook that were female at the population level increased from SY2021 (41%; Hargrove et al. 2022) to SY2022 (50%). In terms of size, we observed variation in the percentage of steelhead that returned as A-run vs. B-run across spawn years. In SY2022, on average 91% of individuals from each population were A-run, whereas this average was 78% for SY2021. The mean fork length of returning Chinook Salmon was also smaller for SY2022 (population average = 71.4 cm) than SY2021 (73.3 cm). Lastly, we note that SY2022 steelhead consisted of a more even split among 1- and 2-ocean fish, whereas SY2021 was dominated by the 2-ocean class. These data indicate that steelhead returning as adults in SY2022 were smaller and younger relative to SY2021. This pattern tracks with abundance estimates of 1- and 2-ocean steelhead of hatchery-origin returning to the Clearwater basin which have displayed a biennial trend since ~SY2013 (IDFG unpublished data). Work in other systems has identified a negative relationship between pink salmon abundance (*O. gorbuscha*) and the strength of sockeye salmon returns (*O. nerka*) with trophic competition in the ocean as a potential factor explaining variation in sockeye salmon productivity (Bugaev et al. 2001). At the population level, Chinook Salmon from SY2022 had a higher average percent of total age-4 fish (72%) when compared to SY2021 (63%). The life history data presented in this report and tracking associated changes through time represent critical information on populations of steelhead and Chinook Salmon of conservation concern in the Snake River basin.

Genetic Diversity and Structure

Overall, patterns of genetic diversity and differentiation in returning adult steelhead and Chinook Salmon mirrored those observed in previous years. Genetic diversity in steelhead populations varied as a function of drainage basin, management objectives, and the presence of steelhead hatchery programs. For example, steelhead populations in the Lochsa and Selway rivers showed below average levels of genetic diversity and higher degrees of genetic divergence relative to other populations (Figure 6). This pattern may in part be explained by a combination of greater distances between neighboring populations leading to genetic isolation and the absence of hatchery supplementation efforts (Powell and Campbell 2020; Hargrove et al. 2021). In contrast, populations located lower in the Snake River basin (e.g., lower Snake and Grande Ronde rivers) which are geographically close to neighboring populations and proximate to hatchery supplementation programs displayed higher levels of genetic diversity and lower levels of genetic divergence. Point estimates of genetic diversity and differentiation observed in SY2022 were generally consistent with historical estimates (e.g., SY2010–2019; IPTDSW 2020 Table 5). For SY2022 Chinook Salmon, genetic diversity among populations remained consistent with patterns observed for SY2010-2019 (IPTDSW 2020; Table 10). Most, but not all values of heterozygosity from SY2022 were lower relative to their long-term averages (SY2010-2019);

however, changes in heterozygosity were quite small (average change in H_e = 0.007; range = -0.055 to +0.003). Patterns of genetic divergence among Chinook Salmon populations were generally varied, and populations in the Hells Canyon reporting unit were below the basin wide average. In contrast, the most strongly differentiated populations were those associated with the Middle Fork Salmon River and Upper Salmon River reporting units.

For SY2022, we performed DAPC analysis *de novo* to discover the number of genetic clusters present in the data. As in previous years, steelhead from well-differentiated populations assigned well to individual genetic clusters. In other words, most individuals were assigned completely to one genetic cluster and not partially to multiple clusters or to a wide number of different clusters. This included populations from the South Fork Clearwater River, South Fork Salmon River, Middle Fork Salmon River, and upper Clearwater River. In contrast, populations from lower portions of major river drainages (Salmon, Clearwater, and Snake rivers) were assigned to multiple different clusters which likely reflects historical or ongoing gene flow occurring between neighboring populations. For SY2022 Chinook Salmon, individual assignments varied across populations, and in general, multiple different genetic clusters were present within each reporting unit. This pattern could be reflective of gene flow among neighboring populations, limited resolution with the current marker panel, limited sample sizes, the identification of genetic structure below the population level, or some combination thereof. Efforts to characterize a new GSI baseline for Snake River basin Chinook Salmon are currently underway. In the future, SY2022 samples could be compared to this new baseline to tease apart factors (gene flow vs. marker resolution) that might explain observed patterns.

Effective Number of Breeders

Effective population size is an important parameter to estimate because it is a measure of the relative contribution of individuals in a population to the next generation. Effective population size is usually smaller than census size (which biologists have traditionally attempted to measure) and determines the rate genetic drift and increase of inbreeding in a population (Wright 1931). Genetic drift refers to changes in allele frequencies in subsequent generations due to random sampling effects. Inbreeding refers to the mating of relatives. Theoretically, as a population decreases in size, the likelihood of inbreeding and genetic drift also increases, resulting in the loss of genetic variation. Franklin (1980) proposed minimum effective population sizes of 50 and 500 to prevent short-term inbreeding and to maintain sufficient long-term genetic diversity, respectively. An effective population size of 50 corresponds to an inbreeding rate of 1% per generation. An effective population size of 500 is aimed at maintaining genetic variation within a population by balancing the rate of loss of variation from genetic drift with the increase in variation from genetic mutations.

For SY2022, we generated estimates of N_b for 14 populations of steelhead (five with multiple brood years) and 16 populations of Chinook Salmon (all the same brood year). These estimates were all above the minimum effective size of 50. All estimates for Chinook Salmon were below 500, whereas four estimates for steelhead were above 500. Estimates of N_b for SY2022 steelhead were on average higher relative to those generated for SYs 2010–2019 (Table 4), but the extent of change varied by population (range of difference in N_b: -167 to +490). All estimates of Nb for Chinook Salmon were derived from a single brood year (2018), and nine of fifteen estimates of N_b for Chinook Salmon populations from SY2022 were lower relative to long-term averages (Table 6). Five populations experienced increases in N_b in SY2022. The average difference between SY2022 and SY2010-2019 was -45 (range of difference: -122 to +43). Variation in estimates of N_b across spawn years has been previously observed in the Snake River

basin and is likely influenced by multiple factors including run strength and the extent of contributions from resident or precocial males.

It is known that estimates of effective population size and effective number of breeders are biased downwards when effective population size is large, sample size is much smaller than effective population size, and when the number of genotyped loci is low (Wang 2009). We expect estimates of effective number of breeders reported in this paper, if biased, are likely biased low, especially in cases where sample size is low relative to true effective population size.

We are now generating estimates of N_b in brood years where abundance has also been estimated. These estimates could be directly compared to provide insight into a population's productivity. For example, a high N_b/N would suggest that most fish present for spawning are successful at producing returning adults. This may be suggestive of low density-dependent effects. A low N_b/N would suggest that few fish present on the spawning grounds are successful at producing returning adults. Currently, estimates of N are generated in a separate report authored by the Nez-Perce Tribe (in prep) and estimates of both N and N_b were presented for SYs 2010-2019 (IPTDSW 2020). In a future 5-year synopsis we will compare estimates of N_b directly with N.

Genetic Origin of Detected and Non-Detected Fish

Concordance between PIT tag detections occurring within the boundaries of steelhead and Chinook Salmon populations and GSI assignments varied by GSI reporting unit and may be explained by several potential mechanisms. First, the distribution of PIT tag arrays is nonuniform and varies as a function of both time and location. Within a given year, arrays are both added and decommissioned (see Table 1, IPTDSW 2020), and while most populations are represented by multiple arrays which operate consistently across years, in specific instances a population can be monitored by a single array. For example, the installation of an in-stream PIT tag detection array in the North Fork Salmon River in 2017 and Panther Creek in 2018 facilitated the description of life history characteristics for the associated populations. Thus, variation in detections on the landscape may be driven by array operation. Additionally, some genetic stocks have inherently lower self-assignment rates which may be driven by elevated rates of gene flow. Higher gene flow reduces genetic differentiation between populations and can be driven by natural (i.e., many populations in close proximity to one another) or anthropogenic processes (e.g., translocations and hatchery stockings, Powell and Campbell 2020). As mentioned above, reporting units encompassing lower sections of major river systems have consistently lower rates of self-assignment relative to other reporting units (Vu et al. 2015). Lastly, low concordance between GSI and PIT tag assignments may be an artifact of aligning genetic reporting units with Major Population Groups (MPG) to allow for evaluation of GSI at the MPG scale for VSP monitoring. For example, the Lower Snake reporting unit represents populations above (Alpowa and Asotin creeks) and below (Tucannon R) Lower Granite Dam, and fish originating from below Lower Granite Dam may never reach the dam or may ascend and subsequently fall back downstream (Ackerman et al. 2012). Thus, some combination of how management units were defined initially (i.e., with limited genetic data) and biological characteristics of specific steelhead populations (e.g., elevated rates of gene flow) may interact to explain why concordance is lower in specific regions in the Snake River basin. Moving forward, as GSI marker panels expand (e.g., Hargrove et al. 2021) and additional PIT tag arrays are placed on the landscape, there is potential for concordance to increase through time. Notably, Hargrove et al. 2021 described a new baseline for steelhead which utilized an increased number of molecular markers that resulted in substantially higher rates of concordance. For the current report, we performed GSI using baselines v3.1 for both steelhead and Chinook Salmon. In last year's report, Hargrove et al. (2021)

noted improved concordance for GSI results generated using steelhead baseline v4. A new Chinook Salmon baseline is currently in development, and we expect increased concordance associated with its future use. We maintained use of baselines v3.1 for SY2022 to maintain consistency with previous reports. In future reports, including 5-year summaries, we will perform GSI using the latest baseline versions.

For SY2022, 52% and 38% of PIT-tagged steelhead and Chinook Salmon were undetected in a population within the Snake River basin, respectively. To note, is that in past years we classified fish as being detected if their final observed location occurred within the boundary of NMFS-defined populations or at locations that occur on the boundary of multiple populations (see Methods section for a detailed description of arrays that were not included for SY2022). We excluded records for fish not detected within a population boundary in this report because the primary focus of this document is to generate population-level descriptions of life history characteristics and not a summary at the genetic stock level. While this decision increased the number of fish that were not detected at a PIT tag array, this represented only a small percentage of fish that were detected (e.g., ~2% of tagged steelhead). Regardless of how the percentage of fish detected on the landscape is calculated, a significant portion (generally 40-50%) of fish sampled at LGR are never detected again in the Snake River basin. Variable detection rates may be explained by some combination of the non-uniform distribution and density of PIT arrays in the Snake River basin (resulting in variable detection probabilities), variable straying rates from natal populations, and variation in pre-spawn mortality.

One benefit of approaches such as GSI is that it is capable of estimating abundance and diversity for all genetic stocks that return to the Snake River basin above LGR regardless of array coverage. However, there are specific management and conservation monitoring needs (fish-in/fish-out) that require collection of data at the scale of individual populations within genetic stocks. The results presented in this report demonstrate the strength of combining both technologies for providing VSP information at the multiple spatial scales needed for ESA status assessments.

ACKNOWLEDGEMENTS

The authors would like to thank the many individuals who contributed time and expertise towards implementing the life history and genetic diversity estimates (alphabetical):

Bonneville Power Administration
- Brady Allen

Columbia River Inter-Tribal Fish Commission:
- Shawn Narum
- Jon Hess
- Erin Collins
- Rebekah Horn
- Ilana Koch
- Stuart Willis
- Jeff Stephenson

Idaho Department of Fish and Game:
- Tim Copeland
- Lance Hebdon
- Luciano Chiaramonte
- John Powell

IDFG Eagle Fish Genetics Lab:
- Angie Chia (PSMFC)
- Kelly Heindel (PSMFC)
- Elizabeth Parkinson (PSMFC)
- Erika Alvarado (PSMFC)
- Natalie Beeken (PSMFC)

NOAA Northwest Fisheries Science Center:
- Darren Ogden

Nez Perce Tribe
- Ryan Kinzer

Primary funding for this project comes from the Bonneville Power Administration (Project #2010-031-00).

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TABLES

Table 1. Summary of total valid PIT tags implanted into adult steelhead at the Lower Granite Dam trapping facility and subsequent detection of these tags in the Snake River basin for SY2022. Genotyped tags represent the number of total tags that were successfully genotyped. Genotyped, detected tags represent the number of genotyped tags (and associated proportions) that were detected in the Snake River basin. Genotyped, undetected tags correspond to the number (and proportion) of genotyped tags that were never detected in the range of a Snake River basin population.

Species	Total tags	Detected tags	Undetected tags	Genotyped tags	Genotyped, detected tags	Genotyped, undetected tags
Steelhead	1,917	930 (48.5%)	987 (51.5%)	1,911 (99.7%)	927 (48.5%)	984 (51.5%)
Chinook Salmon	2,791	1,732 (62.1)	1,059 (37.9%)	2,783 (99.7%)	1,729 (62.1%)	1,054 (37.9%)

Table 2. Steelhead populations and PIT tag detection locations in the Snake River basin with observed steelhead in SY2022. The alphanumeric site code, site description, and location are shown. Fish detected at PIT array locations which were not associated with a population were considered undetected.

Population	Site code	Site description	Latitude	Longitude
SRUMA-s		*Upper Mainstem Salmon River*		
	SAWT	Sawtooth Hatchery	44.15068	-114.88366
	VC2	Valley Creek, upper site	44.21860	-114.94216
	YFK	Yankee Fork Salmon River	44.28761	-114.72075
SRPAH-s		*Pahsimeroi River*		
	PAHH	Pahsimeroi Hatchery	44.68414	-114.03947
SRPAN-s		*Panther Creek*		
	PCA	Panther Creek	45.29525	-114.3581
SRLEM-s		*Lemhi River*		
	HYC	Hayden Creek	44.86159	-113.63215
	EVU	Eagle Valley Ranch - Upper	45.10009	-113.72604
	KEN	Kenney Creek	45.02679	-113.65485
	LLR	Lower Lemhi River	45.17647	-113.88527
SRLSR-s		*Little Salmon and Rapid River*		
	WB1	White Bird Creek	45.75818	-116.30660
	RAPH	Rapid River Hatchery	45.35368	-116.39458
SRNFS-s		*North Fork Salmon River*		
	NFS	North Fork Salmon River	45.41756	-113.99409
MFUMA-s		*Upper Middle Fork Salmon River*		
	MAR	Marsh Cr at Lola Creek campground	44.40869	-115.17984
MFBIG-s		*Lower Middle Fork Salmon River*		
	TAY	Big Creek	45.10387	-114.84970
SFMAI-s		*South Fork Salmon River*		
	KRS	South Fork Salmon River, Krassel	44.97840	-115.72700
	ESS	East Fork South Fork Salmon River	44.95621	-115.53315
SFSEC-s		*Secesh River*		
	ZEN	Secesh River near Zena Creek Ranch	45.03330	-115.73302
CRLOC-s		*Lochsa River*		
	FISTRP	Fish Creek Weir	46.34011	-115.35513
	LRL	Lower Lochsa River	46.14573	-115.59650
	LRU	Upper Lochsa River	46.16382	-115.59000
CRSEL-s		*Selway River*		
	SW1	Lower Selway River	46.11032	-115.56589
	SW2	Upper Selway River	46.08593	-115.51553
CRLMA-s		*Lower Clearwater River*		
	EPR	East Fork Potlatch	46.79509	-116.41088
	SWT	Sweetwater Creek	46.36979	-116.79508
	WEB	Webb Creek	46.32599	-116.83197
	JA1	Jacks Creek	46.50386	-116.55000
	EFPW	East Fork Potlatch Weir	46.79848	-116.41933
CRLOL-s		*Lolo Creek*		
	LC1	Lolo Creek, river kilometer (rkm) 21	46.29443	-115.97612
	LC2	Lolo Creek, rkm 25	46.29056	-115.93415
CRSFC-s		*South Fork Clearwater River*		
	CRA	Crooked River	45.82149	-115.52766
	SC1	South Fork Clearwater, rkm 1	46.13685	-115.98091
	SC2	South Fork Clearwater, rkm 2	46.12749	-115.97730
	SC3	South Fork Clearwater, site 3	45.81415	-115.81597
	SC4	South Fork Clearwater, site 4	45.82350	-115.63410
GRJOS-s		*Joseph Creek*		
	JOC	Joseph Creek	46.03002	-117.01604
GRLMT-s		*Lower Grande Ronde*		
	WEN	Wenaha River Mouth	45.94615	-117.45412
GRUMA-s		*Upper Grande Ronde*		
	CCU	Catherine Creek at Union	45.21525	-117.90069

Table 2. Continued

Population	Site code	Site description	Latitude	Longitude
GRUMA-s		*Upper Grande Ronde (continued)*		
	CCW, CATHEW	Catherine Creek Ladder/Weir	45.19096	-117.82862
	LOOH	Lookingglass Hatchery	45.73154	-117.86441
	UGR	Upper Grande Ronde River	45.59334	-117.90312
	UGS	Upper Grande Ronde River, Starkey	45.24896	-118.38896
GRWAL-s		*Wallowa River*		
	WR1	Wallowa River, rkm 14	45.63368	-117.73376
	WR2	Wallowa River, rkm 32	45.59447	-117.57922
	WALH	Wallowa Hatchery	45.41757	-117.30157
	BCANF	Big Canyon Facility	45.61904	-117.69863
	MR1	Minam River, rkm 0.5	45.61962	-117.72657
IRMAI-s		*Imnaha River*		
	BSC	Big Sheep Creek	45.50649	-116.85067
	CMP	Camp Creek, rkm 2	45.55182	-116.86694
	COC	Cow Creek	45.76774	-116.74404
	CZY	Crazyman Creek	45.22930	-116.84478
	GCM	Grouse Creek Mouth	45.32802	-116.80664
	IR1	Imnaha R, rkm 7	45.76112	-116.75066
	IR2	Imnaha R, rkm 10	45.74284	-116.76456
	IR3	Imnaha R, rkm 41	45.49004	-116.80393
	IR4	Imnaha Weir downstream	45.19446	-116.86877
	IR5	Imnaha Weir upstream	45.19319	-116.86859
	LSHEEF	Little Sheep Facility	45.47782	-116.93025
SNASO-s		*Asotin Creek*		
	ACB	Asotin Creek, Cloverland	46.32545	-117.10852
	ACM	Asotin Creek, Mouth	46.34137	-117.05571
	AFC	Asotin Creek, NF/SF Junction	46.27230	-117.29243
	ALPOWC	Alpowa Creek, lower Snake River	46.40235	-117.39827
	GEORGC	George Creek, Asotin Creek watershed	46.19230	-117.19884
	TENMC2	Tenmile Creek, tributary to Snake River	46.19525	-117.04185
SNHCT-s		*Hells Canyon*		
	OXBO	Oxbow Hatchery	44.97254	-116.85466
SNTUC-s		*Tucannon River*		
	LTR	Lower Tucannon River	46.54419	-118.16290
	MTR	Middle Tucannon River	46.50526	-118.01628
	TFH	Tucannon Hatchery	46.30965	-117.65715
	TPJ	Panjab Creek	46.20459	-117.70617
	UTR	Upper Tucannon River	46.41592	-117.73834

Table 3. Chinook Salmon populations and PIT tag detection locations in the Snake River basin with observed Chinook Salmon in SY2022. The alphanumeric site code, site description, and location are shown. Fish detected at PIT array locations which were not associated with a population were considered undetected.

Population	Site code	Site description	Latitude	Longitude
SRUMA		*Upper Salmon River main stem*		
	SAWT	Sawtooth Hatchery	44.15068	-114.88366
SRVAL		*Valley Creek*		
	VC2	Valley Creek, upper site	44.21860	-114.94216
SRYFK		*Yankee Fork*		
	YFK	Yankee Fork Salmon River	44.28761	-114.72075
SRPAN		*Panther Creek*		
	PCA	Panther Creek	45.29525	-114.35810
SRNFS		*North Fork Salmon River*		
	NFS	North Fork Salmon River	45.41756	-113.99409
SRPAH		*Pahsimeroi River*		
	PAHH	Pahsimeroi Hatchery	44.68414	-114.03947
SRLEM		*Lemhi River*		
	EVU	Eagle Valley Ranch – upper	45.10008	-113.72604
	LRW	Lemhi River Weir	44.86612	-113.62475
	HYC	Hayden Creek	44.86159	-113.63215
	LBS	Big Eightmile Creek	44.73822	-113.46246
MFBEA		*Bear Valley Creek*		
	BRC	Bear Valley adult video weir	44.42793	-115.28417
MFMAR		*Marsh Creek*		
	MAR	Marsh Creek at Lola Creek campground	44.40868	-115.17984
MFBIG		*Big Creek*		
	TAY	Big Creek	45.10387	-114.84970
SFMAI		*South Fork Salmon River main stem*		
	KRS	South Fork Salmon River, Krassel	44.97840	-115.72700
	SALSFW	South Fork Salmon River weir	44.66687	-115.70295
SFSEC		*Secesh River*		
	ZEN	Secesh River near Zena Creek Ranch	45.03330	-115.73302
SFEFS		*East Fork South Fork Salmon River*		
	ESS	East Fork South Fork Salmon River	44.95621	-115.53315
	JOHNSC	Johnson Creek	44.73393	-115.54860
	YPP	Yellow Pine Pit Lake	44.92899	-115.33388
CRLOC		*Lochsa River*		
	LRL	Lower Lochsa River	46.14573	-115.59650
	LRU	Lochsa River upper site	46.16382	-115.58966
CRLOL		*Lolo Creek*		
	LC1	Lolo Creek, rkm 21	46.29436	-115.97616
	LC2	Lolo Creek, rkm 25	46.29056	-115.93415
SCUMA		*Upper South Fork Clearwater River*		
	CRA	Crooked River	45.82149	-115.52766
	SC3	South Fork Clearwater site 3	45.81414	-115.81597
	SC4	South Fork Clearwater site 4	45.82350	-115.63410
IRMAI		*Imnaha River*		
	IR2	Imnaha R, rkm 10	45.74270	-116.76430
	IR3	Imnaha R, rkm 41	45.49004	-116.80393
	IR4	Imnaha Weir downstream	45.19446	-116.86877
	IR5	Imnaha Weir upstream	45.19319	-116.86859
	IML	Imnaha River Weir	45.19428	-116.86866
	IMNAHW	Imnaha River Weir Adult Ladder	45.19428	-116.86866
IRBSH		*Big Sheep Creek*		
	BSC	Big Sheep Creek	45.50649	-116.85067
GRLOS		*Lostine River*		
	LOSTIW	Lostine River Weir	45.54327	-117.48450
	WR1	Wallowa River, rkm 14		
	WR2	Wallowa River, rkm 32		

Table 3. Continued

Population	Site code	Site description	Latitude	Longitude
GRLOO		*Lookingglass Creek*		
	LOOH	Lookingglass Hatchery	45.73154	-117.86441
GRCAT		*Catherine Creek*		
	CATHEW	Catherine Creek Weir	45.19096	-117.82862
	CCW	Catherine Creek Ladder/Weir*	45.19096	-117.82862
	CCU	Catherine Creek at Union	45.21525	-117.90069
GRUMA		*Upper Grande Ronde River*		
	GRANDW	Grande Ronde River Weir	45.24896	-118.38898
	UGS	Upper Grande Ronde - Starkey	45.24895	-118.38895
GRMIN		*Minam River*		
	MR1	Minam River, km 0.5	45.61962	-117.72657
GRWEN		*Wenaha River*		
	WEN	Wenaha River mouth	45.94615	-117.45412
SNTUC		*Tucannon River*		
	TFH	Tucannon Hatchery	46.30965	-117.65715
SNASO		*Asotin River*		
	AFC	North/South Fork Asotin Creek Junction	46.27249	-117.29215

Table 4. Effective number of breeders (N_b) for steelhead populations (see Table 2 for population description) assuming random mating. Harmonic means were estimated for brood year (BY) collections with more than 20 individuals. n = number of samples. Estimates of N_b for spawn years (SYs) 2010-2019 were taken from IPTDSW (2020).

Location	BY	n	Harmonic mean	SY2010-2019 harmonic mean
CRLOC-s	2016	27	312	276
CRLOC-s	2017	26	520	276
CRSEL-s	2017	46	278	325
CRSFC-s	2017	20	70	195
GRJOS-s	2017	21	420	373
GRJOS-s	2018	22	462	373
GRWAL-s	2017	26	804	314
GRWAL-s	2018	24	220	314
IRMAI-s	2016	20	506	459
IRMAI-s	2017	51	362	459
IRMAI-s	2018	72	292	459
SFMAI-s	2016	24	239	281
SNASO-s	2017	21	840	354

Table 5. Assignment concordance between populations and GSI reporting units for PIT-tagged steelhead from SY2022 using steelhead baseline v3.1. The GSI reporting unit of each population is highlighted in gray.

Population	n	LSNAKE	GRROND	IMNAHA	LOSALM	SFSALM	MFSALM	UPSALM	LOCLWR	UPCLWR	SFCLWR
SNASO-s	59	0.441	0.356	0.051	0	0	0	0.068	0.051	0.034	0
SNTUC-s	52	0.538	0.308	0.019	0	0	0	0.135	0	0	0
GRJOS-s	56	0.304	0.482	0.107	0	0	0	0.089	0.018	0	0
GRLMT-s	38	0.158	0.737	0.053	0	0	0	0	0.026	0.026	0
GRUMA-s	46	0.283	0.543	0.087	0.022	0	0	0.065	0	0	0
GRWAL-s	71	0.183	0.718	0.042	0	0	0.014	0.028	0.014	0	0
IRMAI-s	171	0.123	0.158	0.614	0	0	0	0.082	0.023	0	0
SNHCT-s	7	0	0	0.143	0	0	0	0.714	0.143	0	0
SRLSR-s	17	0.176	0.353	0.059	0	0	0	0.412	0	0	0
SFMAI-s	52	0.077	0	0	0.038	0.827	0.038	0	0	0.019	0
SFSEC-s	6	0	0	0.333	0.167	0.5	0	0	0	0	0
MFBIG-s	32	0.031	0.031	0.031	0	0.031	0.844	0.031	0	0	0
MFUMA-s	5	0	0	0	0	0	1	0	0	0	0
SRPAN-s	32	0.156	0.125	0.156	0	0	0.219	0.344	0	0	0
SRNFS-s	6	0.167	0	0	0	0	0	0.833	0	0	0
SRLEM-s	8	0.125	0.125	0	0	0	0	0.75	0	0	0
SRPAH-s	1	0	1	0	0	0	0	0	0	0	0
SRUMA-s	22	0	0.091	0	0	0	0	0.909	0	0	0
CRLMA-s	9	0.556	0.333	0	0	0	0	0	0.111	0	0
CRLOC-s	86	0.023	0	0	0	0	0	0.012	0.012	0.895	0.058
CRSEL-s	89	0	0	0	0	0	0	0.011	0.011	0.955	0.022
CRLOL-s	18	0.056	0	0	0	0	0	0.056	0.056	0.111	0.722
CRSFC-s	44	0.023	0	0	0	0	0	0.045	0.159	0.159	0.614

Table 6. Effective number of breeders (N_b) for Chinook Salmon populations (see Table 3 for population descriptions) assuming random mating. Harmonic means between multiple estimation algorithms were estimated for brood year (BY) collections with more than 20 individuals. n = number of samples. Estimates of N_b for spawn years (SYs) 2010-2019 were taken from IPTDSW (2020).

Location	BY	n	Harmonic mean	SY2010-2019
CRLOC	2018	40	150	228
GRCAT	2018	24	54	167
GRLOS	2018	112	215	199
GRMIN	2018	53	176	-
IRMAI	2018	72	107	209
MFBEA	2018	28	91	174
MFBIG	2018	85	106	228
MFMAR	2018	79	132	-
SCUMA	2018	54	190	177
SFEFS	2018	138	183	196
SFMAI	2018	237	274	255
SFSEC	2018	131	217	196
SRLEM	2018	93	171	128
SRPAH	2018	29	116	182
SRPAN	2018	45	129	250
SRVAL	2018	30	104	153

Table 7. Assignment concordance between populations and GSI reporting units for PIT-tagged Chinook Salmon from SY2022 using Chinook Salmon baseline v3.1. The GSI reporting unit of each population is highlighted in gray.

Population	n	HELLSC	MFSALM	SFSALM	TUCANO	UPSALM	CHMBLN	FALL
CRLOC	49	0.633	0.082	0.265	0	0.020	0	0
CRLOL	16	1.000	0	0	0	0	0	0
GRCAT	29	1.000	0	0	0	0	0	0
GRLOO	14	1.000	0	0	0	0	0	0
GRLOS	152	0.901	0.007	0.039	0	0.053	0	0
GRMIN	66	0.894	0.030	0.061	0	0.015	0	0
GRUMA	13	0.769	0	0.154	0	0.077	0	0
GRWEN	20	0.850	0	0.050	0	0.100	0	0
IRBSH	4	1.000	0	0	0	0	0	0
IRMAI	84	0.833	0.012	0.071	0	0.060	0.012	0.012
SCUMA	69	0.870	0.014	0.072	0	0.043	0	0
MFBEA	71	0.028	0.859	0.056	0	0.056	0	0
MFBIG	116	0.259	0.397	0.198	0	0.112	0.034	0
MFMAR	102	0.078	0.608	0.196	0	0.118	0	0
SFEFS	173	0.092	0.023	0.838	0	0.040	0.006	0
SFMAI	294	0.173	0.078	0.680	0	0.061	0.007	0
SFSEC	163	0.067	0.055	0.859	0	0.018	0	0
SNASO	1	0	0	0	0	0	0	1.000
SNTUC	1	1.000	0	0	0	0	0	0
SRLEM	110	0.255	0.055	0.100	0	0.582	0.009	0
SRNFS	19	0.211	0	0.053	0	0.737	0	0
SRPAH	42	0.071	0.024	0.024	0	0.881	0	0
SRPAN	59	0.475	0.034	0.373	0	0.085	0.034	0
SRUMA	17	0	0	0.118	0	0.882	0	0
SRVAL	40	0.075	0.050	0.075	0	0.800	0	0
SRYFS	5	0	0	0.400	0	0.600	0	0

FIGURES

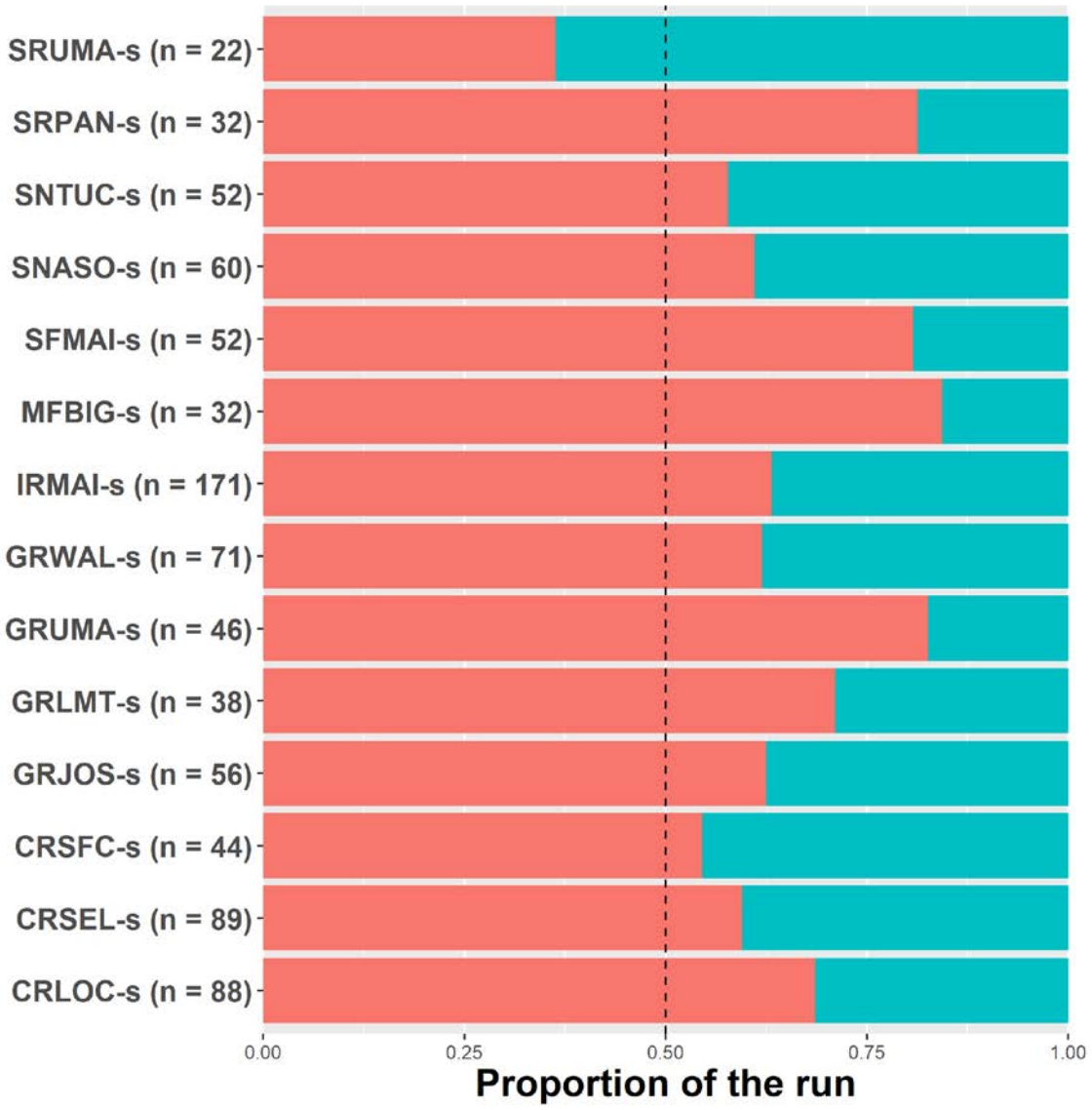


Figure 1. Sex ratios for Snake River steelhead populations (see Table 2 for a list of population names, codes, and composite Instream PIT Tag Detection Systems sites). Sample sizes are shown in the y-axis labels. The dotted vertical line indicates a 50:50 sex ratio and the proportion of females and males is given in red and blue, respectively.

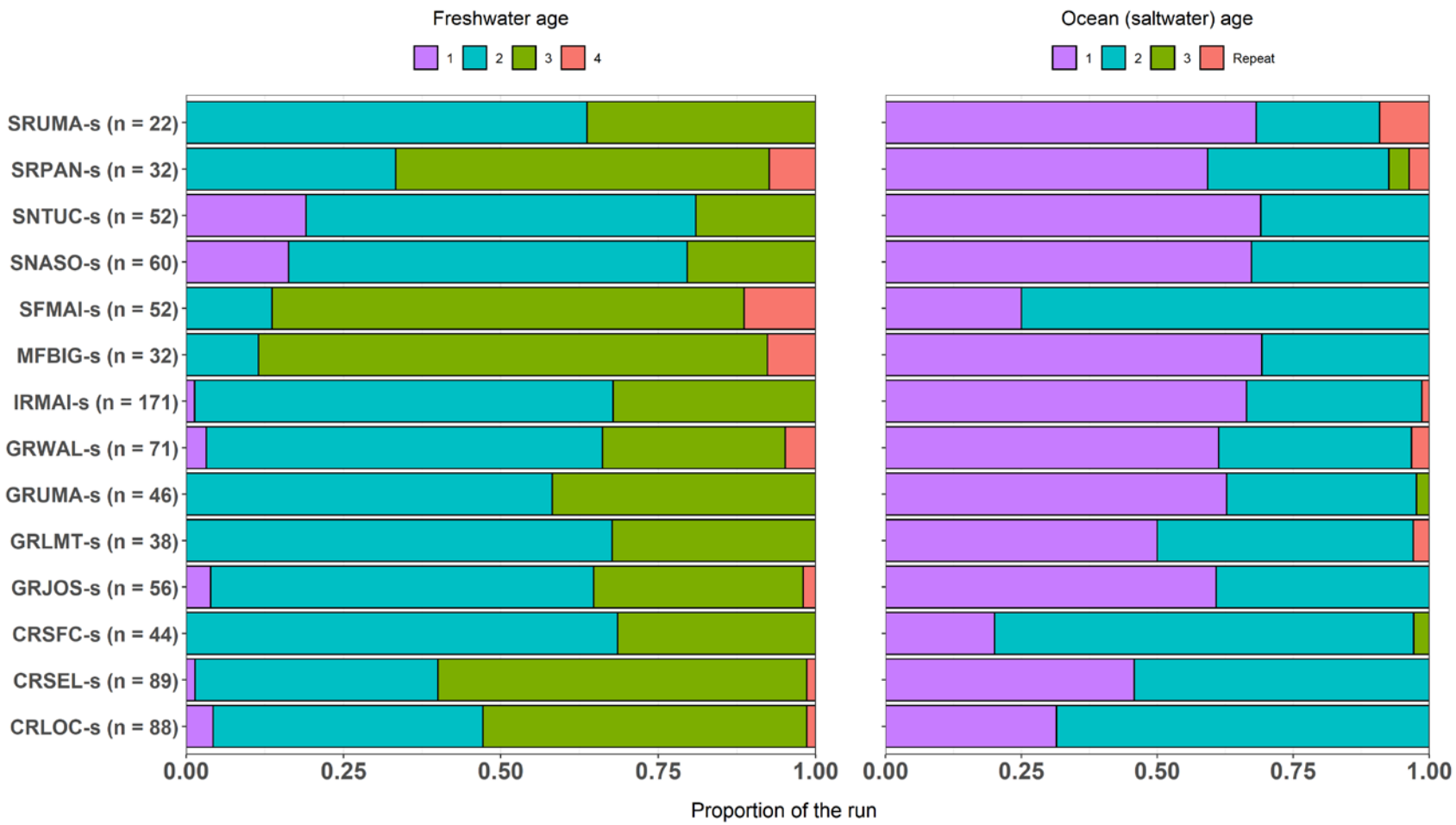


Figure 2. Distribution of freshwater and ocean (saltwater) ages for Snake River steelhead populations (see Table 2 for a list of population names, codes, and composite Instream PIT Tag Detection Systems sites). Sample sizes are shown in y-axis labels.

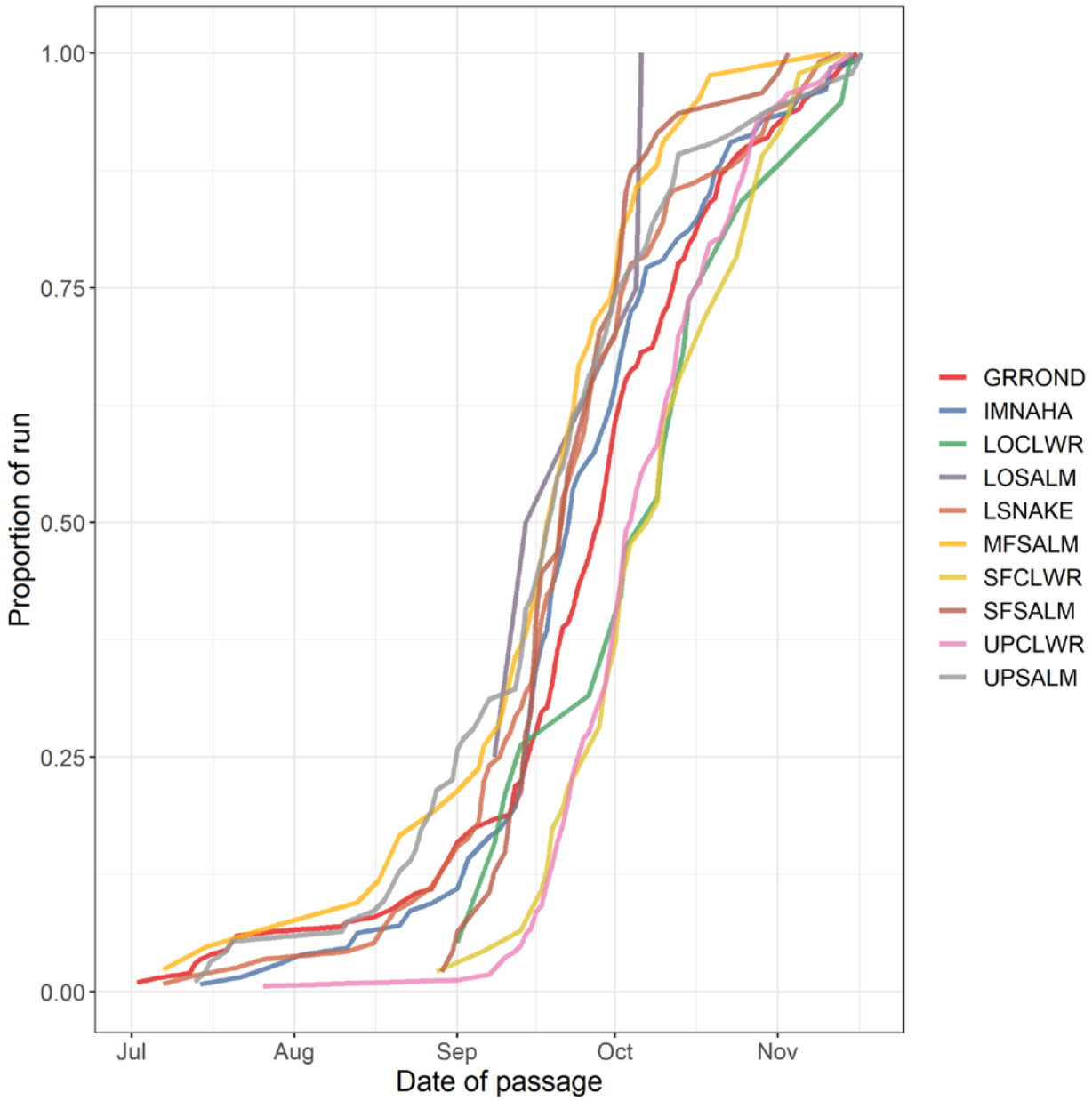


Figure 3. Date of passage for adult steelhead PIT tagged at Lower Granite Dam (LGR), Washington and later detected at Snake River Instream PIT Tag Detection Systems by GSI reporting unit. Steelhead migrating past LGR during the spring portion of the migration were removed from the analysis.

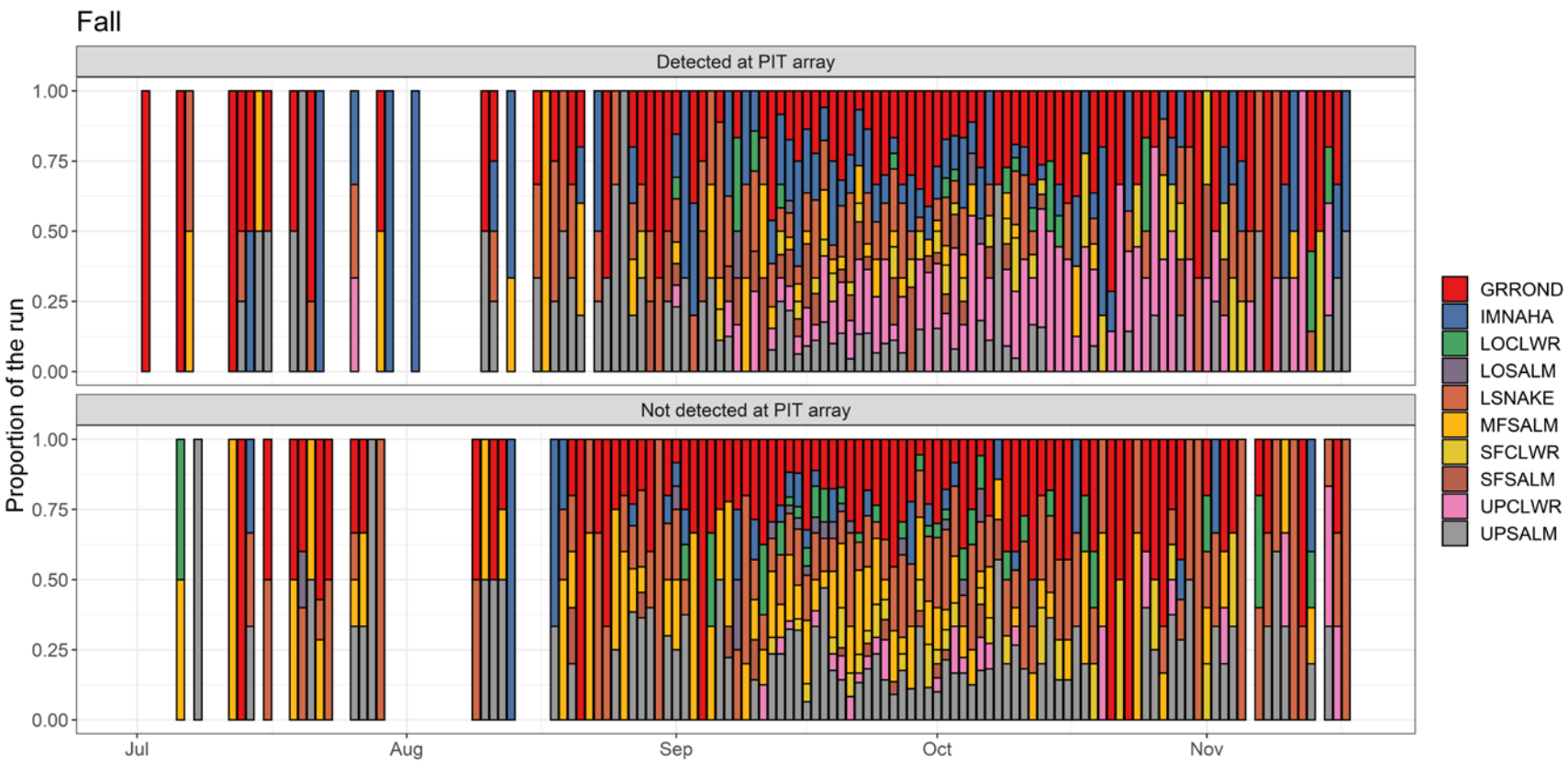


Figure 4. Relative contribution of genetic stocks to the weekly SY2022 steelhead run at Lower Granite Dam that were or were not detected at a PIT tag array in the Snake River basin for the fall portion of the run (prior to trap closure in November).

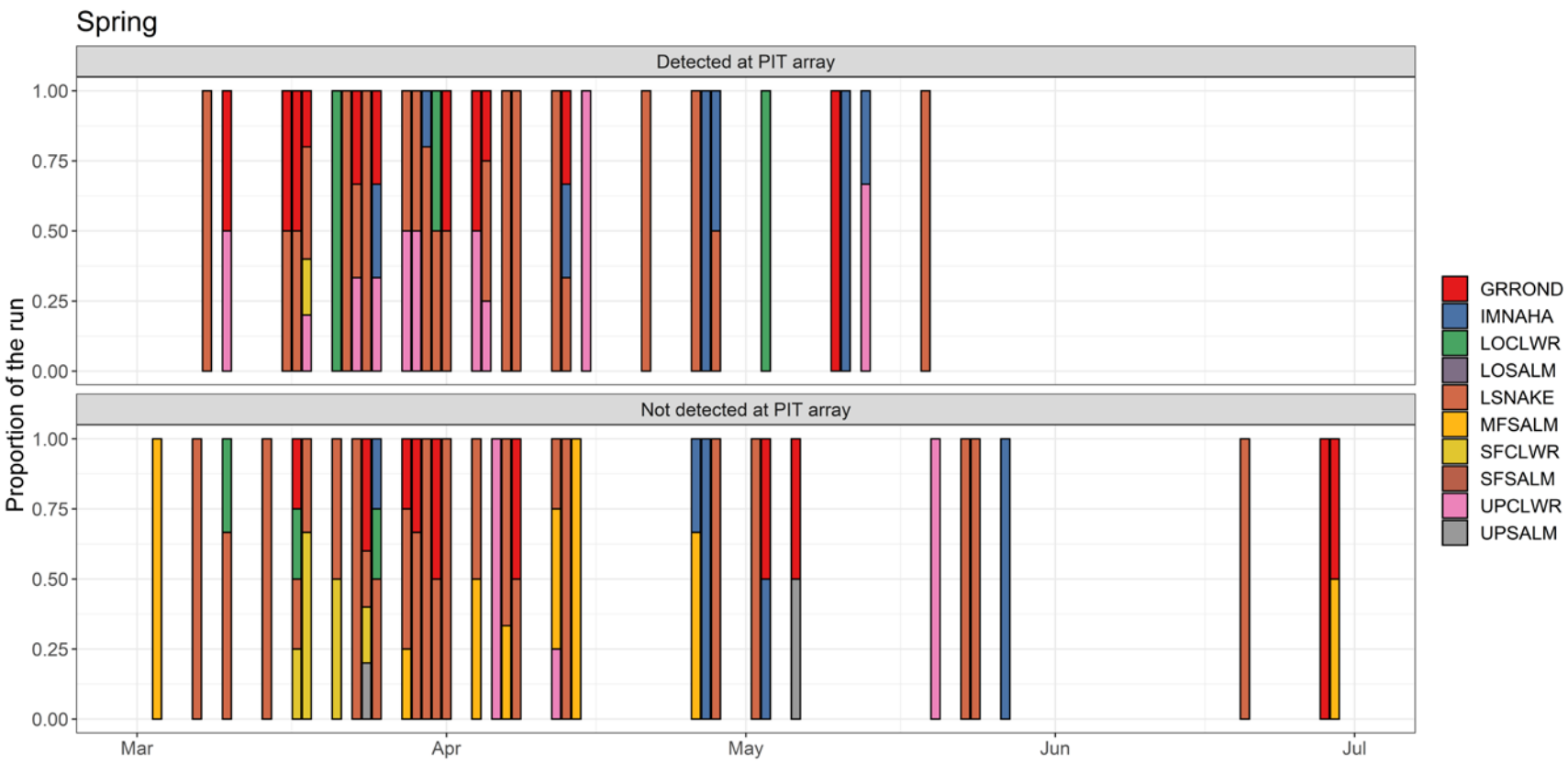


Figure 5. Relative contribution of genetic stocks to the weekly SY2022 steelhead run at Lower Granite Dam that were or were not detected at a PIT tag array in the Snake River basin during the spring portion of the run.

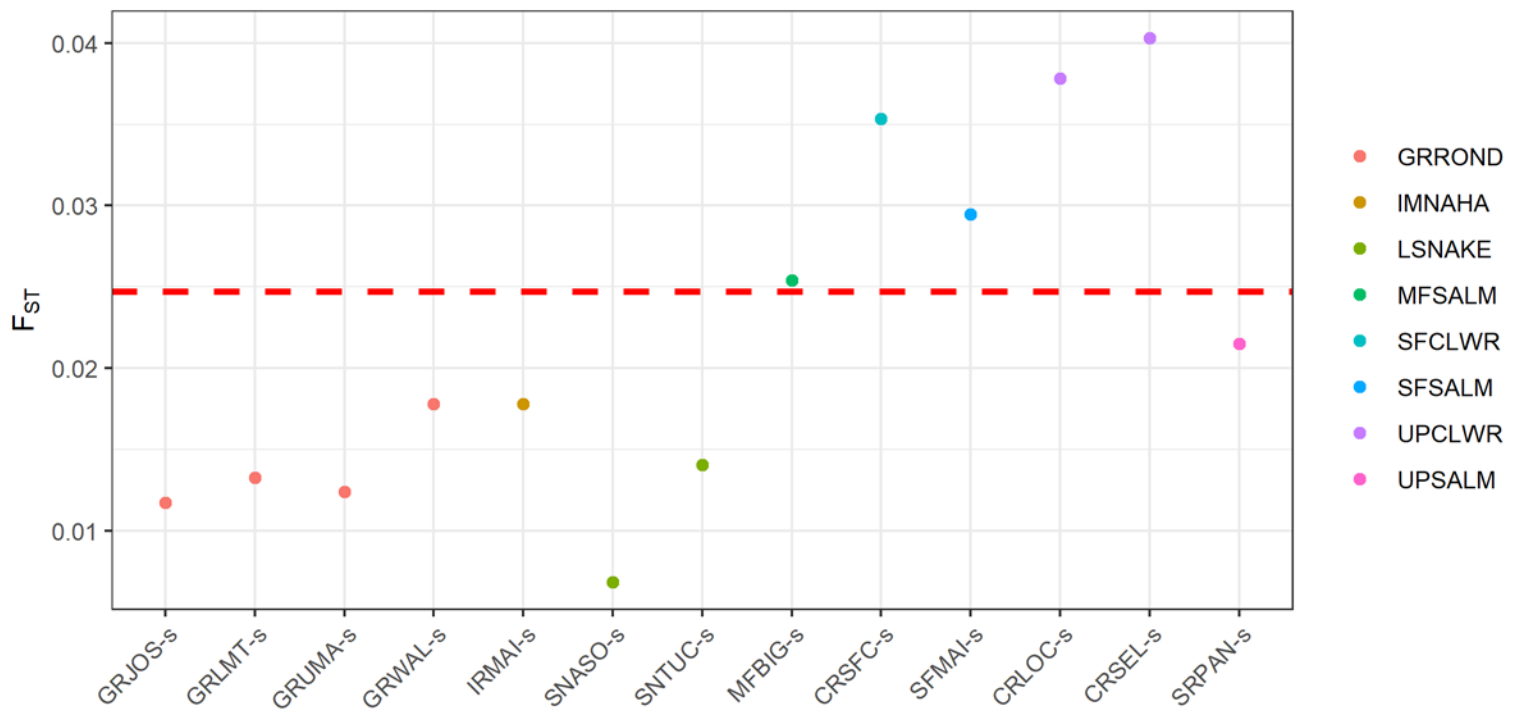


Figure 6. Estimates of mean pairwise F_{ST} for Snake River steelhead populations with ≥20 samples detected at In-Stream PIT Detection Systems sites for SY2022. The dashed line is the average pairwise F_{ST} estimate across all populations. Genetic stocks are coded by color and population descriptions can be found in Table 2.

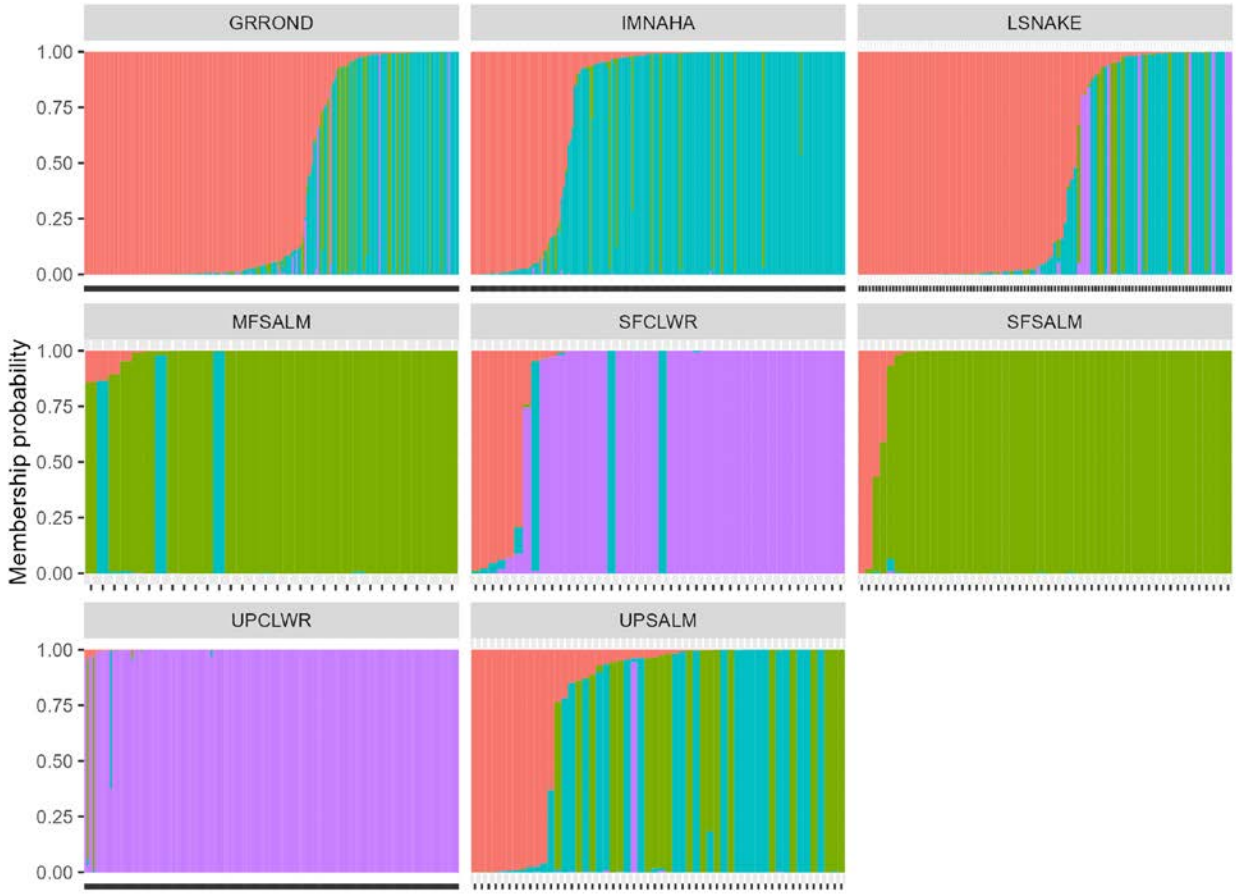


Figure 7. Bar charts of individual membership probability to four genetic clusters for SY2022 Snake River steelhead populations with ≥20 samples detected at In-Stream PIT Detection Systems sites organized by genetic reporting unit. Memberships of individuals to genetic clusters were identified by discriminant analysis of principal components. Each vertical line represents an individual fish and colors correspond to different genetic clusters. Individuals are grouped GSI reporting units for Snake River basin steelhead. No PIT tag detections occurred in the Lower Clearwater River or Lower Salmon River reporting units.

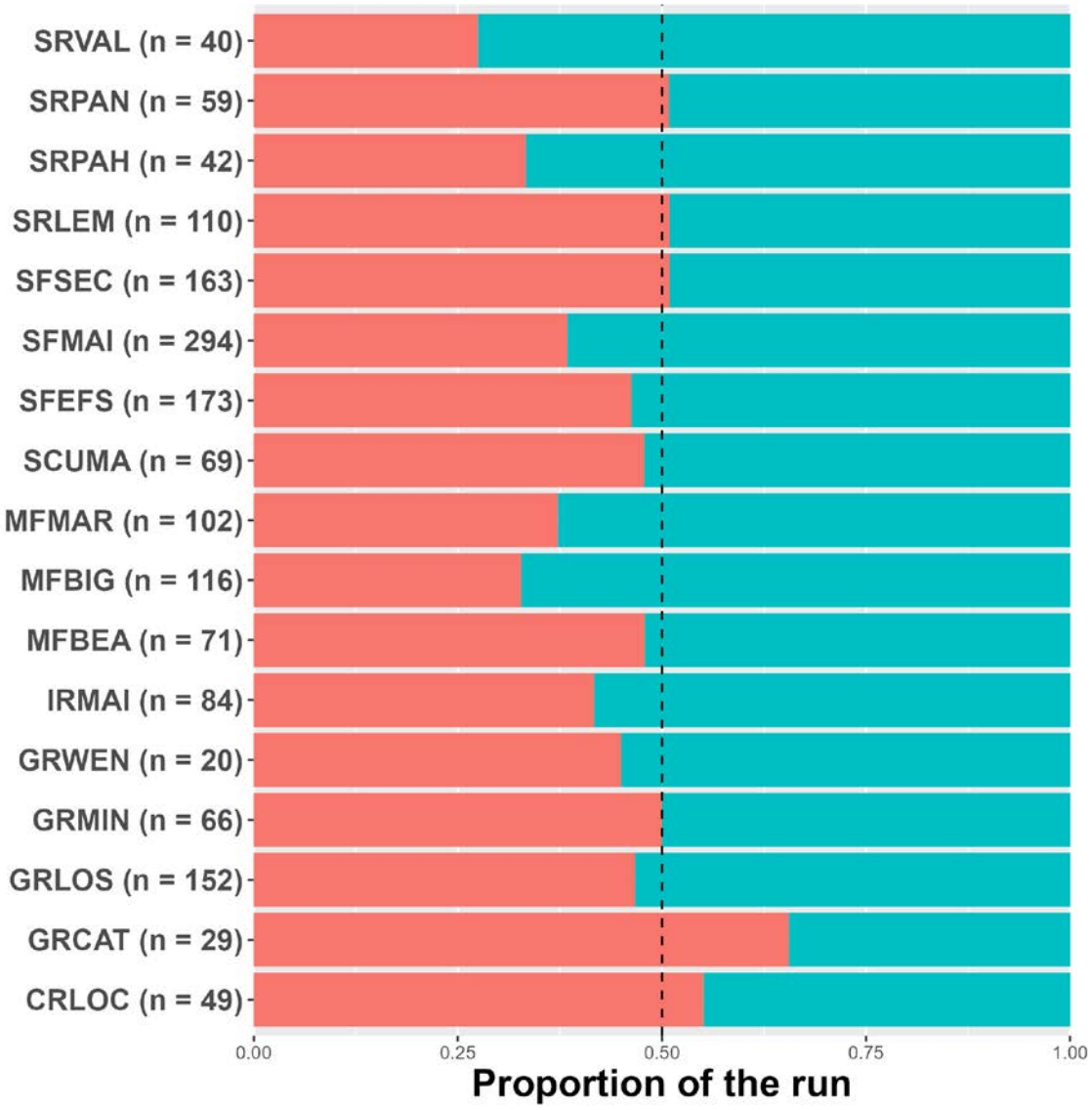


Figure 8. Sex ratios for Snake River Chinook Salmon populations (see Table 3 for a list of population names, codes, and composite IPTDS sites). Sample sizes are shown in the y-axis labels. The dotted vertical line indicates a 50:50 sex ratio and the proportion of females and males is given in red and blue, respectively.

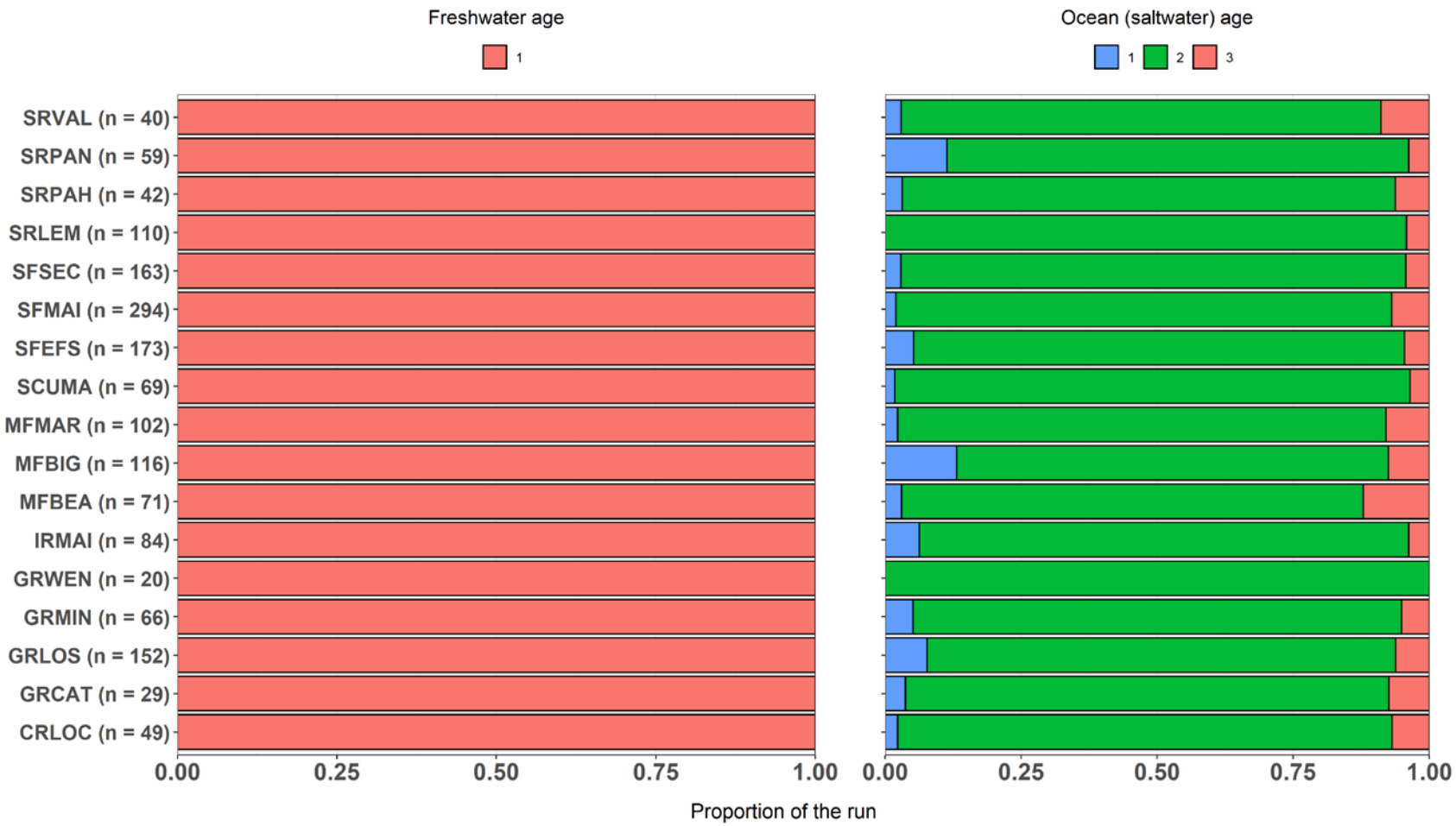


Figure 9. Distribution of freshwater and ocean (saltwater) ages for Snake River Chinook Salmon populations (see Table 3 for a list of population names, codes, and composite IPTDS sites). Sample sizes are shown in y-axis labels.

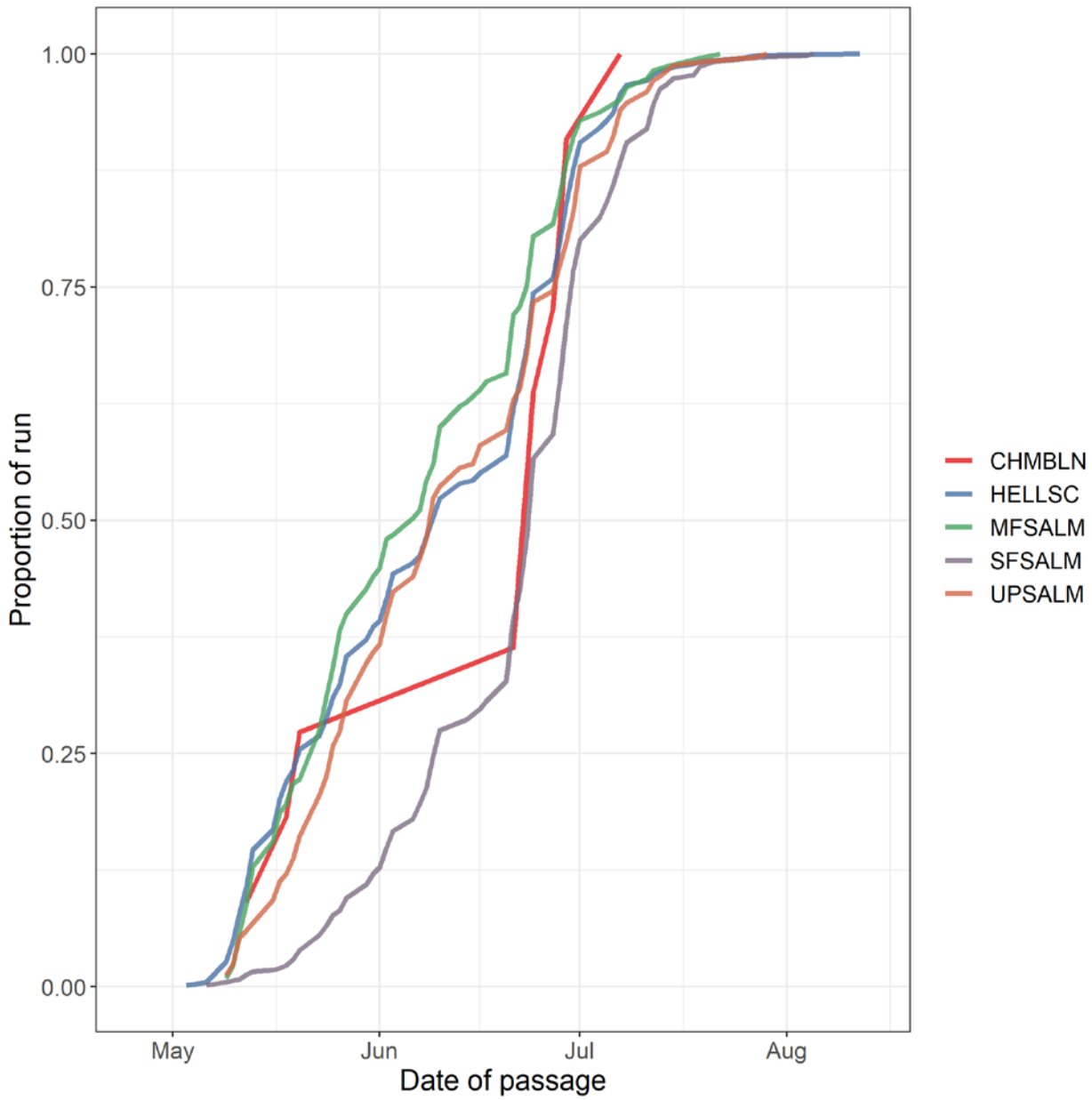


Figure 10. Date of passage for adult Chinook Salmon PIT-tagged at Lower Granite Dam , Washington and later detected at Snake River Instream PIT Tag Detection Systems site by GSI reporting unit.

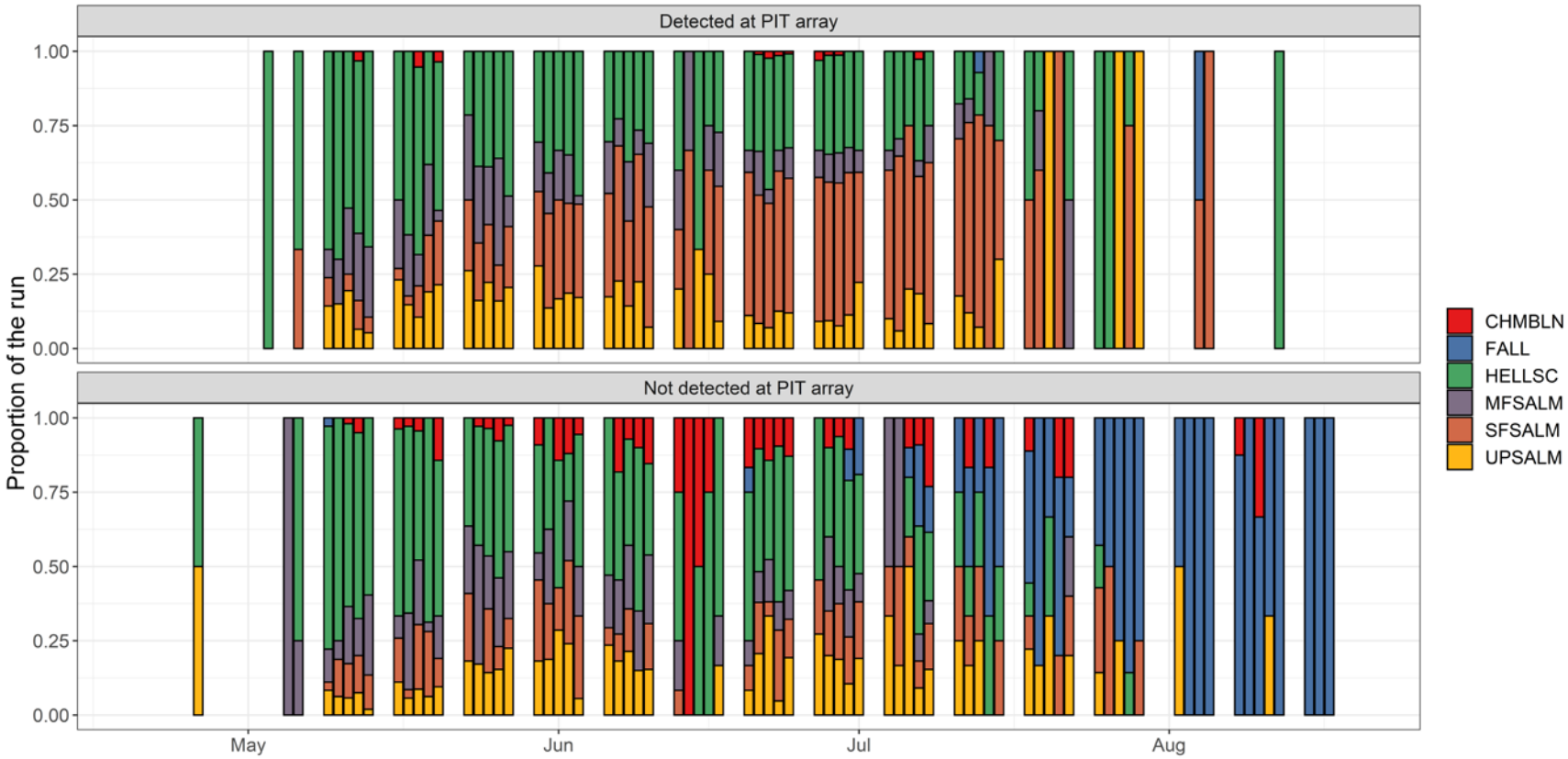


Figure 11. Relative contribution of genetic stocks to the weekly SY2022 Chinook Salmon run at Lower Granite Dam that were or were not detected at a PIT tag array in the Snake River basin.

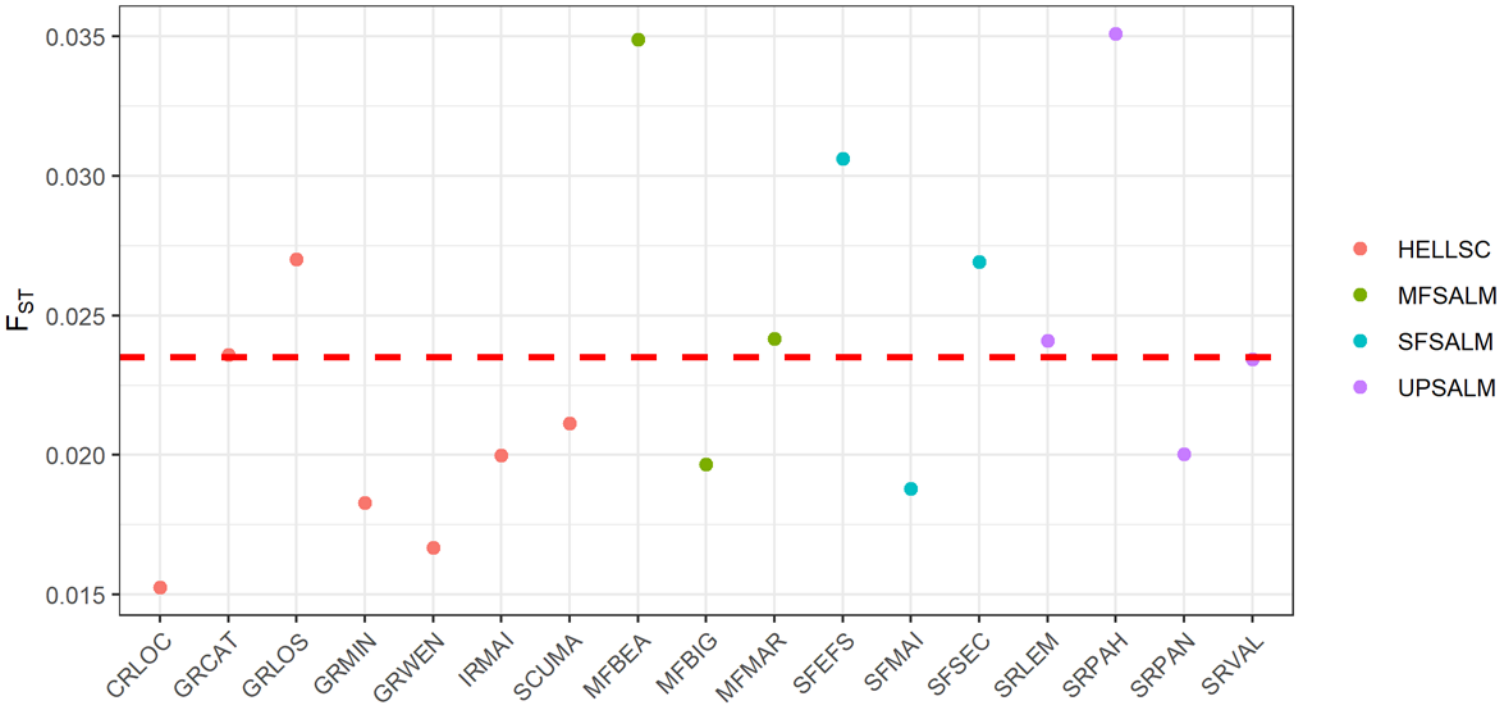


Figure 12. Estimates of mean pairwise F_{ST} for Snake River Chinook Salmon populations with ≥20 samples detected at In-Stream PIT Detection Systems sites for SY2022. The dashed line is the average pairwise F_{ST} estimate across all populations. Genetic stocks are coded by color and population names can be found in Table 3.

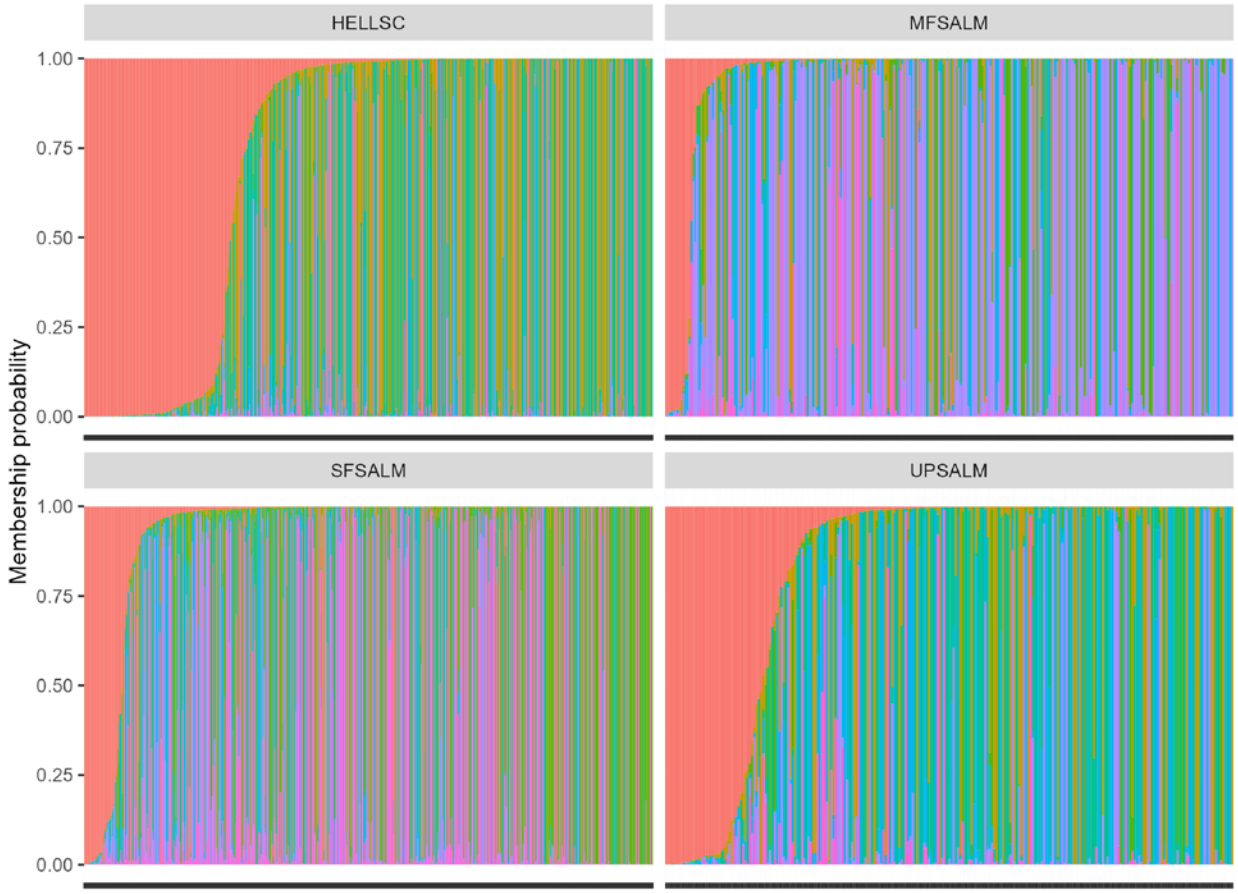


Figure 13. Bar charts of individual membership probability to seven genetic clusters for SY2022 Snake River Chinook Salmon populations with ≥20 samples detected at In-Stream PIT Detection Systems sites organized genetic reporting unit. Memberships of individuals to genetic clusters were identified by discriminant analysis of principal components. Each vertical line represents an individual fish and colors correspond to different genetic clusters. Individuals are grouped GSI reporting unit for Snake River Chinook Salmon. No PIT tag detections occurred in the Tucannon, Chamberlain Creek, or Fall Chinook reporting units.

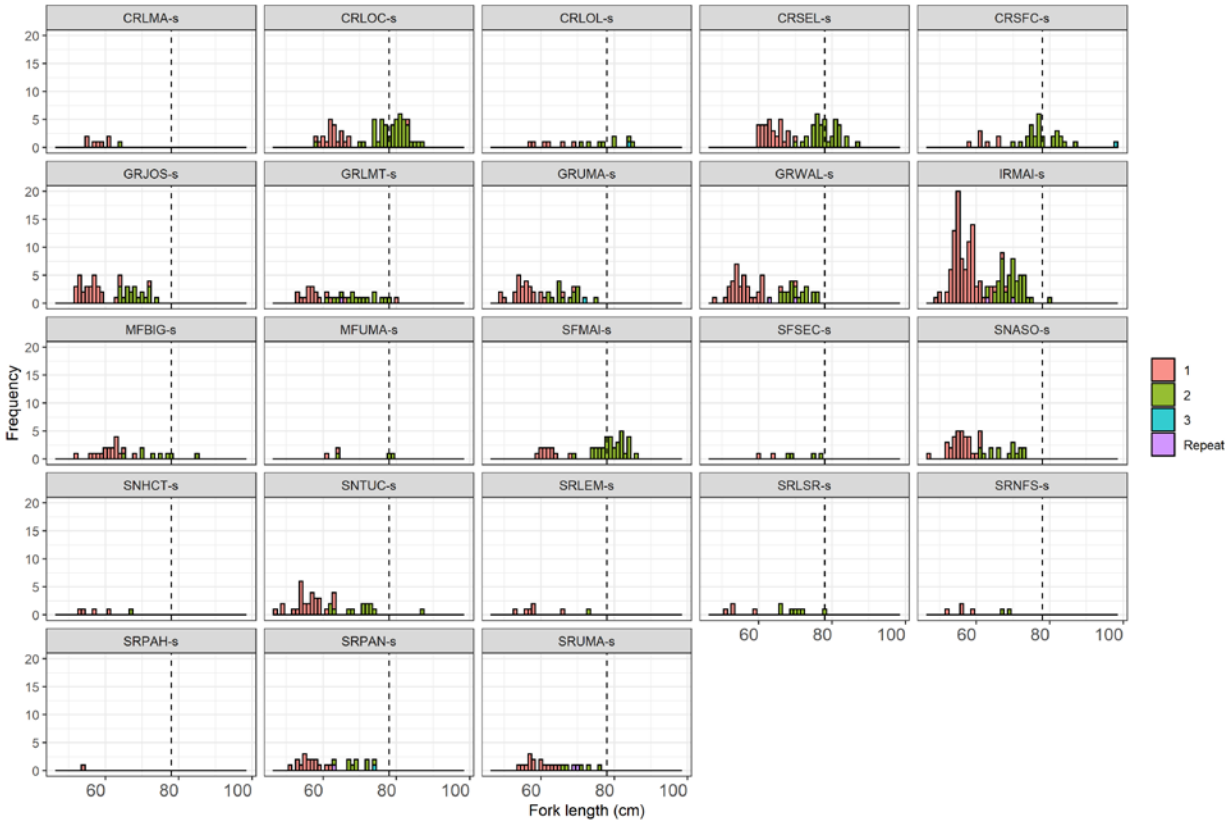
APPENDICES

Appendix A. Summary of life history diversity and genetic information for steelhead adults PIT tagged at Lower Granite Dam and later detected at Snake River instream PIT Tag Detection Systems (IPTDS; Table 2) by population for SY2022.

STEELHEAD			LIFE-HISTORY																																	GENETICS[b]			
			Genetic sex					Length[a]				Ocean (saltwater) age								Total age																HWE	Genetic diversity		
			Frequency			Percentage		Frequency			Percentage	Frequency				Percentage				Frequency						Percentage					Run timing								
Location	Arrays	Total detections	F	M	U	%F	%M	Mean fork length	A-Run	B-Run	%A-Run	%B-Run	1	2	3	Kelt	1	2	3	Kelt	3	4	5	6	7	U	3	4	5	6	7	5th % Run	25th % Run	50th % Run	75th % Run	95th % Run	Dev	Ho	He	%Poly SNPs
CRLMA-s	EPR, JA1, SWT, EFPW, WEB	9	7	2	-	78	22	58.8	8	0	100	0	7	1	-	-	88	12	-	-	-	6	2	-	-	1	-	67	22	-	-	9/18/2021	9/26/2021	10/3/2021	10/21/2021	3/24/2022	-	-	-	-
CRLOC-s	LRU, LRL, FISTRP	86	59	27	-	69	31	74	38	29	57	43	21	48	-	-	30	70	-	-	1	14	26	27	1	17	1	16	30	31	1	9/16/2021	9/29/2021	10/9/2021	10/24/2021	3/29/2022	1	0.279	0.283	94.9
CRLOL-s	LC2, LC1	18	11	7	-	61	39	72.2	10	5	67	33	6	8	1	-	40	53	7	-	-	4	8	3	-	3	-	22	44	17	-	9/6/2021	10/2/2021	10/10/2021	11/1/2021	5/13/2022	-	-	-	-
CRSEL-s	SW1, SW2	89	53	36	-	60	40	71.6	50	15	77	23	32	38	-	-	46	54	-	-	-	7	46	17	-	19	-	8	52	19	-	9/10/2021	9/24/2021	10/3/2021	10/19/2021	11/15/2021	-	0.282	0.288	92.6
CRSFC-s	SC3, SC1, SC2, SC4, CRA	44	24	20	-	55	45	75.4	23	10	70	30	7	27	1	-	20	77	3	-	-	5	20	10	-	9	-	11	45	23	-	9/8/2021	9/18/2021	10/7/2021	10/25/2021	3/18/2022	-	0.296	0.288	95.5
GRJOS-s	JOC	56	35	21	-	62	38	61.3	50	0	100	0	31	20	-	-	61	39	-	-	-	22	21	8	-	5	-	39	38	14	-	7/26/2021	9/12/2021	10/2/2021	10/19/2021	4/1/2022	-	0.303	0.304	99.4
GRLMT-s	WEN	38	27	11	-	71	29	64.1	32	1	97	3	17	16	-	1	50	47	-	3	-	13	14	6	1	4	-	34	37	16	3	7/21/2021	9/16/2021	9/27/2021	10/15/2021	4/4/2022	-	0.291	0.297	97.2
GRUMA-s	LOOH, UGR, CATHEW, UGS,	46	38	8	-	83	17	60.3	43	0	100	0	27	15	1	-	63	35	2	-	-	14	23	6	-	3	-	30	50	13	-	7/14/2021	9/1/2021	9/20/2021	10/7/2021	11/13/2021	1	0.301	0.306	97.7
GRWAL-s	MR1, WR2, WALH, BCANF,	71	44	27	-	62	38	61.7	62	0	100	0	38	22	-	2	61	35	-	3	2	24	26	6	4	9	3	34	37	8	6	7/16/2021	9/13/2021	9/25/2021	10/17/2021	11/14/2021	3	0.293	0.300	100
IRMAI-s	IR2, BSC, IR3, GCM, LSHEEF, COC, IR1, CZY, IR5, CMP,	171	108	63	-	63	37	61	145	1	99	1	97	47	-	2	66	32	-	1	1	72	51	20	2	25	1	42	30	12	1	8/27/2021	9/15/2021	9/24/2021	10/12/2021	11/16/2021	2	0.296	0.301	99.4
MFBIG-s	TAY	32	27	5	-	84	16	65	24	1	96	4	18	8	-	-	69	31	-	-	-	2	16	7	1	6	-	6	50	22	3	8/20/2021	9/12/2021	9/20/2021	10/2/2021	10/19/2021	-	0.285	0.292	93.8
MFUMA-s	MAR	5	3	2	-	60	40	69.2	3	1	75	25	2	3	-	-	40	60	-	-	-	1	-	3	1	-	-	20	-	60	20	9/1/2021	9/9/2021	9/22/2021	9/23/2021	10/17/2021	-	-	-	-
SFMAI-s	KRS, ESS	52	42	10	-	81	19	75	20	20	50	50	11	33	-	-	25	75	-	-	-	-	16	24	4	8	-	-	31	46	8	9/1/2021	9/13/2021	9/20/2021	10/2/2021	11/3/2021	4	0.301	0.301	95.5
SFSEC-s	ZEN	6	3	3	-	50	50	68.8	6	0	100	0	2	4	-	-	33	67	-	-	-	-	2	2	2	-	-	-	33	33	33	9/14/2021	9/23/2021	9/23/2021	10/7/2021	10/29/2021	-	-	-	-
SNASO-s	ACM, ACB, TENMC2, ALPOWC, GEORGC, AFC	59	36	23	-	61	39	59.8	48	0	100	0	32	16	-	-	67	33	-	-	7	18	21	2	-	11	12	31	36	3	-	8/11/2021	9/16/2021	10/2/2021	10/21/2021	4/12/2022	1	0.309	0.311	100
SNHCT-s	OXBO	7	3	4	-	43	57	58.4	5	0	100	0	4	1	-	-	80	20	-	-	-	4	1	-	-	2	-	57	14	-	-	9/13/2021	9/13/2021	9/23/2021	10/1/2021	10/12/2021	-	-	-	-
SNTUC-s	MTR, UTR, TFH, LTR, TPJ	52	30	22	-	58	42	60.5	41	1	98	2	29	13	-	-	69	31	-	-	8	15	17	2	-	10	15	29	33	4	-	9/1/2021	9/29/2021	10/13/2021	11/17/2021	4/5/2022	1	0.314	0.313	99.4
SRLEM-s	LLR, EVU, KEN, HYC	8	8	NA	-	100	-	60.1	7	0	100	0	6	1	-	-	86	14	-	-	-	3	3	1	-	1	-	38	38	12	-	7/13/2021	8/18/2021	9/6/2021	9/18/2021	11/13/2021	-	-	-	-
SRLSR-s	WB1, RAPH	17	9	8	-	53	47	64.4	10	0	100	0	4	7	-	-	36	64	-	-	-	4	5	2	-	6	-	24	29	12	-	7/15/2021	9/1/2021	9/26/2021	10/24/2021	4/12/2022	-	-	-	-
SRNFS-s	NFS	6	5	1	-	83	17	59.8	6	0	100	0	4	2	-	-	67	33	-	-	-	1	3	2	-	-	-	17	50	33	-	8/10/2021	8/16/2021	8/28/2021	9/22/2021	10/6/2021	-	-	-	-
SRPAH-s	PAHH	1	1	NA	-	100	-	54	1	0	100	0	1	-	-	-	100	-	-	-	-	1	-	-	-	-	-	100	-	-	-	8/24/2021	8/24/2021	8/24/2021	8/24/2021	8/24/2021	-	-	-	-
SRPAN-s	PCA	32	26	6	-	81	19	61.4	27	0	100	0	16	9	1	1	59	33	4	4	-	3	16	7	1	5	-	9	50	22	3	7/13/2021	8/16/2021	8/25/2021	9/17/2021	10/19/2021	1	0.302	0.306	97.7
SRUMA-s	YFK, VC2, SAWT	22	8	14	-	36	64	62.7	22	0	100	0	15	5	-	2	68	23	-	9	-	10	8	3	1	-	-	45	36	14	5	44427	44451	44458	44470	44477	1	0.29313	0.2945	92

a) A-run (<78 cm FL); B-run (≥78 cm FL).
b) Groups with <20 individuals were excluded from genetic analysis.

Appendix B. Length frequency histograms by ocean age of natural origin steelhead by population. All SY2022 individuals with ocean age and length data are shown. The vertical line denotes the traditional small versus large cutoff (78 cm).

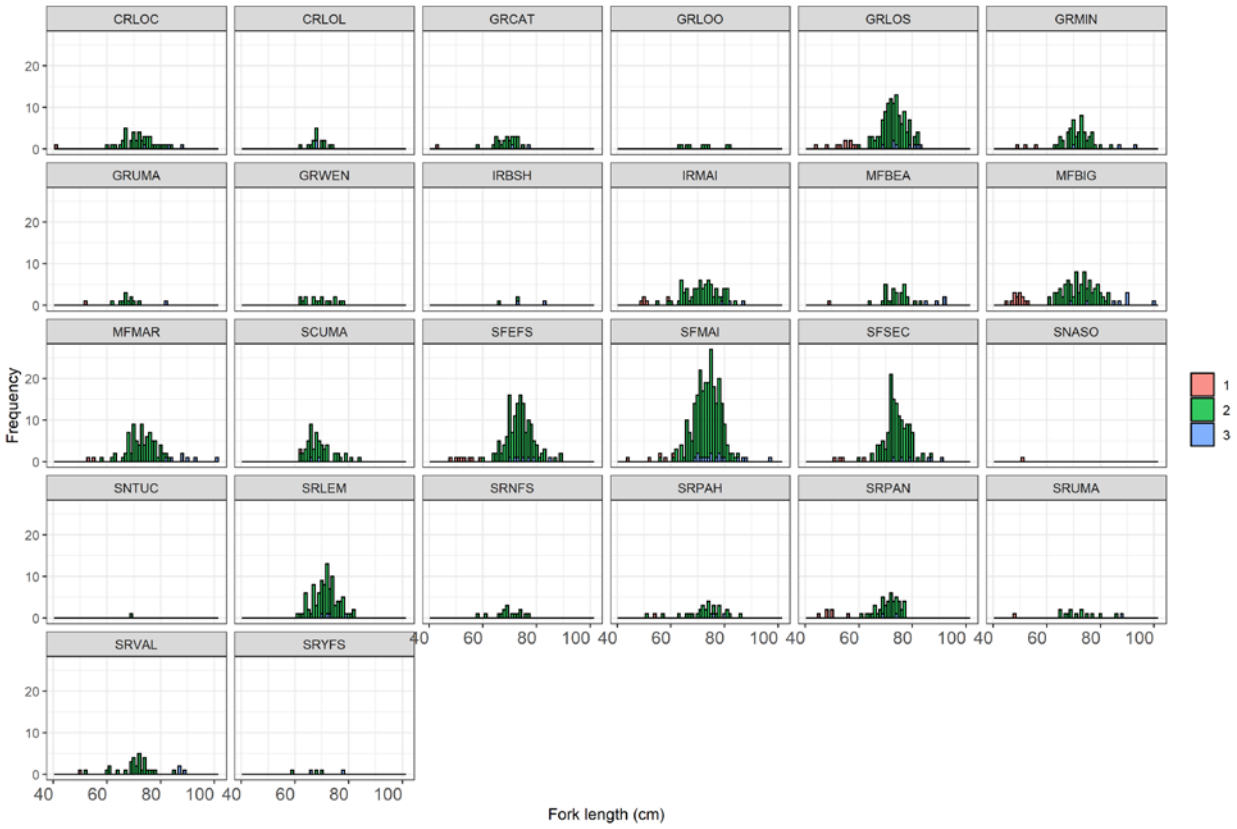


Appendix C Summary of life history diversity and genetic information for Chinook Salmon adults PIT tagged at Lower Granite Dam and later detected at Snake River instream PIT Tag Detection Systems (IPTDS; Table 3) by population for SY2022.

CHINOOK			LIFE-HISTORY																													GENETICS[b]			
			Genetic sex					Length		Ocean (saltwater) age								Total age								Run timing					HWE	Genetic diversity		
			Frequency			Percentage				Frequency				Percentage				Frequency				Percentage												
Location	Arrays	Total detections	F	M	U	%F	%M	Mean fork length	Mean fork length excl. jacks[a]	Minijack	1	2	3	U	% Age 1	% Age 2	% Age 3	% U	3	4	5	U	% Age 3	% Age 4	% Age 5	% Age U	5th % Run	25th % Run	50th % Run	75th % Run	95th % Run	Dev	Ho	He	%Poly SNPs
CRLOC	LRU, LRL	49	27	22	-	55	45	71.7	72.3	-	1	40	3	5	2	82	6	10	1	40	3	5	2	82	6	10	5/10/2022	5/20/2022	6/2/2022	6/22/2022	7/28/2022	-	0.23237	0.234	90.6
CRLOL	LC2, LC1	16	9	7	-	56	44	68.5	68.5	-	-	14	2	-	-	88	12	-	-	14	2	-	-	88	12	-	5/11/2022	5/12/2022	5/13/2022	5/17/2022	6/2/2022	-	-	-	-
GRCAT	CATHEW, CCU, CCW	29	19	10	-	66	34	68.1	69	-	1	24	2	2	3	83	7	7	1	24	2	2	3	83	7	7	5/9/2022	5/12/2022	5/16/2022	5/25/2022	6/3/2022	-	0.26166	0.249	84.7
GRLOO	LOOH	14	6	8	-	43	57	70.1	70.1	-	-	9	-	5	-	64	-	36	-	9	-	5	-	64	-	36	5/3/2022	5/10/2022	5/13/2022	5/24/2022	6/16/2022	-	-	-	-
GRLOS	WR2, LOSTIW, WR1	152	71	81	-	47	53	71.9	73.2	-	10	##	8	22	7	74	5	14	10	112	8	22	7	74	5	14	5/18/2022	6/8/2022	6/24/2022	6/30/2022	7/12/2022	2	0.23368	0.234	92.9
GRMIN	MR1	66	33	33	-	50	50	71.2	72.1	-	3	53	3	7	5	80	5	11	3	53	3	7	5	80	5	11	5/10/2022	5/18/2022	6/9/2022	6/24/2022	7/4/2022	-	0.23912	0.242	92.4
GRUMA	GRANDW, UGS	13	9	4	-	69	31	67.4	68.7	-	1	11	1	-	8	85	8	-	1	11	1	-	8	85	8	-	5/9/2022	5/17/2022	5/17/2022	5/30/2022	6/10/2022	-	-	-	-
GRWEN	WEN	20	9	11	-	45	55	68.5	68.5	-	-	17	-	3	-	85	-	15	-	17	-	3	-	85	-	15	5/10/2022	5/12/2022	5/16/2022	5/19/2022	6/6/2022	1	0.24236	0.246	89.4
IRBSH	BSC	4	3	1	-	75	25	73.8	73.8	-	-	2	2	-	-	50	50	-	-	2	2	-	-	50	50	-	5/27/2022	5/27/2022	6/6/2022	6/21/2022	7/1/2022	-	-	-	-
IRMAI	IMNAHW, IR5, IR4, IR3, IML, IR2	84	35	49	-	42	58	70.5	71.7	-	5	72	3	4	6	86	4	5	5	72	3	4	6	86	4	5	5/18/2022	6/10/2022	6/28/2022	7/1/2022	7/15/2022	15	0.23981	0.24	95.3
MFBEA	BRC	71	34	37	-	48	52	73.1	73.4	-	1	28	4	38	1	39	6	54	1	28	4	38	1	39	6	54	5/11/2022	5/17/2022	5/26/2022	6/13/2022	6/24/2022	1	0.20111	0.206	81.2
MFBIG	TAY	116	38	78	-	33	67	70.7	73.6	-	14	85	8	9	12	73	7	8	14	85	8	9	12	73	7	8	5/13/2022	5/30/2022	6/16/2022	6/27/2022	7/8/2022	4	0.21098	0.218	88.2
MFMAR	MAR	102	38	64	-	37	63	73.2	73.6	-	2	79	7	14	2	77	7	14	2	79	7	14	2	77	7	14	5/11/2022	5/19/2022	5/27/2022	6/10/2022	6/27/2022	2	0.21059	0.215	87.6
SCUMA	SC4, SC3, CRA	69	33	36	-	48	52	68.7	68.8	-	1	54	2	12	1	78	3	17	1	54	2	12	1	78	3	17	5/10/2022	5/13/2022	5/20/2022	6/3/2022	6/23/2022	-	0.23636	0.239	90.6
SFEFS	JOHNSC, ESS, YPP	173	80	93	-	46	54	72.5	73.4	-	8	##	7	20	5	80	4	12	8	138	7	20	5	80	4	12	6/1/2022	6/17/2022	6/27/2022	7/1/2022	7/12/2022	5	0.22122	0.222	91.8
SFMAI	KRS, SALSFW	294	113	181	-	38	62	73.4	73.7	-	5	##	18	34	2	81	6	12	5	237	18	34	2	81	6	12	5/27/2022	6/21/2022	6/28/2022	7/4/2022	7/15/2022	1	0.2256	0.225	95.9
SFSEC	ZEN	163	83	80	-	51	49	73.8	74.2	-	4	##	6	22	2	80	4	13	4	131	6	22	2	80	4	13	5/30/2022	6/10/2022	6/23/2022	6/29/2022	7/11/2022	1	0.21749	0.22	87.6
SNASO	AFC	1	-	1	-	-	100	51	-	-	1	-	-	-	100	-	-	-	1	-	-	-	100	-	-	-	8/4/2022	8/4/2022	8/4/2022	8/4/2022	8/4/2022	-	-	-	-
SNTUC	TFH	1	1	-	-	100	-	69	69	-	-	1	-	-	-	100	-	-	-	1	-	-	-	100	-	-	5/13/2022	5/13/2022	5/13/2022	5/13/2022	5/13/2022	-	-	-	-
SRLEM	LRW, HYC, EVU, LBS	110	56	54	-	51	49	71.5	71.5	-	-	93	4	13	-	85	4	12	-	93	4	13	-	85	4	12	5/11/2022	5/20/2022	5/30/2022	6/13/2022	6/29/2022	1	0.22475	0.227	87.1
SRNFS	NFS	19	9	10	-	47	53	69.7	69.7	-	-	16	-	3	-	84	-	16	-	15	1	3	-	79	5	16	5/9/2022	5/12/2022	5/20/2022	6/2/2022	7/11/2022	-	-	-	-
SRPAH	PAHH	42	14	28	-	33	67	73	73.5	-	1	29	2	10	2	69	5	24	1	29	2	10	2	69	5	24	5/27/2022	6/10/2022	6/24/2022	7/1/2022	7/15/2022	1	0.22094	0.223	81.8
SRPAN	PCA	59	30	29	-	51	49	68.6	70.8	-	6	45	2	6	10	76	3	10	6	45	2	6	10	76	3	10	5/12/2022	5/25/2022	6/8/2022	6/23/2022	7/1/2022	1	0.22735	0.228	85.3
SRUMA	SAWT	17	4	13	-	24	76	71.1	72.6	-	1	13	1	2	6	76	6	12	1	13	1	2	6	76	6	12	5/16/2022	5/30/2022	6/8/2022	6/24/2022	7/11/2022	-	-	-	-
SRVAL	VC2	40	11	29	-	28	72	71.7	72.2	-	1	30	3	6	2	75	8	15	1	30	3	6	2	75	8	15	5/10/2022	5/30/2022	6/20/2022	6/28/2022	7/12/2022	2	0.22318	0.23	80
SRYFS	YFK	5	3	2	-	60	40	68.2	68.2	-	-	3	2	-	-	60	40	-	-	3	2	-	-	60	40	-	5/16/2022	6/9/2022	6/24/2022	6/30/2022	7/1/2022	-	-	-	-

a) Excluded all individuals with an ocean age of one or an unknown ocean age
b) Groups with <20 individuals were excluded from genetic analysis.

Appendix D. Length frequency histograms by ocean age of natural origin Chinook Salmon by population. All SY2022 individuals with ocean age and length data are shown.



Appendix E. Details on where data on single nucleotide polymorphic (SNP) markers used to generate genetic summaries for steelhead (*Oncorhynchus mykiss*) and Chinook Salmon (*O. tshawytscha*) can be found.

Data for the SNP marker panels can be accessed via the FishGen webpage (https://www.fishgen.net/Home.aspx). Once a user account has been set up with FishGen, the details of these panels can be accessed under the 'Marker Sets' > 'Export' tab once a user has logged in. Metadata for each marker include synonym of species, Vic probe, Vic allele, Fam probe, Fam allele, forward primer, and reverse primer. The current Chinook Salmon panel is 'CRITFC IDFG Chinook GTseq v4.0 343' and consists of 95 loci for parentage-based tagging (PBT) loci, 96 loci for genetic stock identification (GSI), 1 sex marker, and 151 additional SNP markers. The steelhead panel is 'CRITFC/IDFG Steelhead GTseq v5.0 368' consists of 95 PBT loci, 96 GSI loci, 1 sex marker, and 176 additional SNP markers.

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