FISHERY RESEARCH

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

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Project Progress Report

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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) population in the Snake River basin for the 01/01/2021 to 12/31/2021 reporting period. This reporting period covers analysis of individuals crossing Lower Granite Dam in spawn year (SY) 2021. A total of 3,126 steelhead and 1,974 Chinook Salmon were sampled at Lower Granite Dam. Of the fish tagged at Lower Granite Dam, 1,659 steelhead and 1,034 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 379 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 SY2021. 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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INTRODUCTION

In this report we summarize life history and genetic diversity for 22 of the 24 extant Snake River steelhead (*Oncorhynchus mykiss*) Distinct Population Segment (DPS) populations (10/12 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 19 of the 30 extant Snake River spring/summer Chinook Salmon (*O. tshawytscha*) Evolutionarily Significant Unit (ESU) populations (5/8 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, 1/2 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 sampling rate. A committee of collaborating management agencies determines the trap sampling rates that achieve sample requirements for multiple projects and balance fish handling concerns. Sample rates are typically 10–20%. The sample 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 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 new larger Chinook Salmon panel known as 'CRITFC IDFG Chinook GTseq v4.0 343' consists of 95 PBT loci, 96 GSI loci, 1 sex marker, and 151 additional SNP markers. The new larger steelhead panel known as '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 at the LGR adult trap were downloaded from the Lower Granite adult trap database. In total, records of valid tags were downloaded for 3,126 for steelhead and 1,974 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, we have 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. For example, interrogation sites in the upper Salmon River (one station at river km 437 and another at river km 460) are located on the main stem of the river but do not correspond to an individual population. Fish detected at these locations may be subsequently detected at upstream arrays, but this is not always the case. With the exception of run timing and population clustering analysis, summaries in this document are produced at the population-level; as a result, we elected to exclude records for fish not detected within a population boundary.

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 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). By performing DAPC on an annual basis we may be able to detect temporal changes in genetic representation among sample collections from the comprehensive collection of individuals (i.e., a genetic baseline) that has historically been used to identify genetic structure across the landscape.

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).

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. We used a Pearson's Chi-squared test 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. 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 22 of the 24 extant Snake River steelhead DPS populations. A total of 16 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 3,126 valid PIT tags implanted into SY2021 adult steelhead at LGR (Table 1), 1,659 of which were subsequently detected within the range of a DPS population and 1,467 were never detected within the range of a DPS population. A total of 3,083 tagged fish were genotyped, including 1,644 of the steelhead 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 South Fork Clearwater (CRSFC-s) and Tucannon River (SNTUC-s) populations had the lowest percent females (69%) and the South Fork Salmon River (SFMAI-s), and Panther Creek (SRPAN-s) had the highest percent females (84%). Appendix A and Figure 1 summarize sex ratios for steelhead by population.

The Lochsa River population had the largest average adult steelhead (mean FL = 80.7 cm) while the Imnaha River had the smallest (67.1 cm). The highest percentage of large length (≥78 cm) detections occurred in the Lochsa River (80% of fish). The Asotin River and Upper Mainstem Salmon River all had 0% of 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-4 (Figure 2). Repeat spawners were observed in two of the 22 populations (9.1%; Appendix A). Lolo Creek and the South Fork Salmon River populations had the oldest average ocean (saltwater) ages (2 years) and the Tucannon River, lower Clearwater River, and Imnaha River populations were the youngest (1.8 years). Appendix A and Figure 2 summarize population specific freshwater, ocean-, and total-ages.

The date of median passage at LGR was September 28 across all populations (Figure 3). Panther Creek had the earliest median passage date at LGR (28 August), which was 31 days before the median passage date for the entire run. In contrast, the Lochsa River population had the latest median passage at LGR (13 October) which was 15 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 0.312 in the Tucannon River population to a low of 0.281 in Lolo Creek and the South Fork Clearwater River populations. The average percent polymorphic SNPs across all locations was high (97.5%), with a maximum of 100% in the Upper Grande Ronde River and Wallowa River populations. In contrast, the lowest percent of markers that were polymorphic was observed in the Lower Middle Fork Salmon River (89.2%). Appendix A summarizes observed and expected heterozygosity and percentage of polymorphic SNPs by location.

Deviations from HWE at the population-level were observed in 15 of the 16 populations with sufficient numbers of samples for analysis (Appendix A). The number of markers that deviated from HWE ranged from one to six, which represented between 0.5 and 3.4% of the total number of markers (176) surveyed.

Patterns of genetic divergence, estimated by mean pairwise F_{ST} for SY2021 steelhead (Figure 6) mirrored patterns observed across baseline samples (Vu et al. 2015). The highest pairwise values of genetic differentiation were observed in the upper Clearwater River, South Fork Clearwater River, and South Fork Salmon River reporting units. The Lower Clearwater River, Grande Ronde River, Imnaha River, upper Salmon River, and lower Snake River reporting units all exhibited levels of genetic differentiation that were lower than the basin wide average (Figure 6).

Discriminant analysis of principal components (DAPC) indicated the presence of six genetic clusters in returning adult steelhead. Retaining the first 29 principal components we assigned individuals detected at IPTDS to these six clusters. In general, we saw replication of the patterns of genetic divergence observed with F_{ST} across populations. Populations with greater mean levels of genetic differentiation (e.g., those in the upper Clearwater River, South Fork Salmon River, and South Fork Clearwater River) largely consisted of a single genetic cluster (Figure 7). In contrast, reporting units in the lower sections of major rivers (Lower Clearwater and Lower Salmon rivers) consisted of individuals assigned to multiple different genetic clusters. That we observed only six genetic clusters could be explained by incomplete or inadequate sampling of representative populations based on PIT tag detections or that the number of management units is not equal to the number of genetic clusters.

Effective Number of Breeders

We were able to estimate N_b for 14 populations, five of which included multiple parental BYs (Table 4). Harmonic means of N_b were presented for populations with multiple parental BYs. Estimates of N_b were all greater than 50 and ranged from a low of 173 for BY 2016 in Lolo Creek to a high of 504 for the lower Grande Ronde River BY 2016.

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 in the Pahsimeroi River, with 100% of the fish detected in the Pahsimeroi

population assigned to the upper Salmon River reporting unit. The next two highest assignment rates were for the Selway River (93%) and South Fork Salmon River population (90%). We observed the lowest concordance for the Little Salmon River (6%) and the mainstem lower Clearwater River population (6%).

The difference in observed detections at PIT tag arrays was significantly different than expected based on observed counts at LGR overall (χ^2= 143.85, df = 9, p-value <0.001). Post hoc tests identified that the Imnaha River (p-value = 0.002) and upper Clearwater River (p-value <0.001) reporting units were detected at greater frequencies than expected whereas the lower Clearwater River (p-value = 0.005), Middle Fork Salmon River (p-value <0.001), and upper Salmon River (p-value = 0.006) were detected at lower frequencies than expected. Detections at PIT arrays for fish belonging to the Grande Ronde 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 19 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 15 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 1,974 valid PIT tags implanted into SY2021 adult Chinook Salmon at LGR (Table 1), 1,034 of which were subsequently detected within the range of an ESU population and 940 were never detected within the range of an ESU population. A total of 1,970 tagged fish were genotyped, including 1,033 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.

The Bear Valley Creek (MFBEA-s) population had the lowest percent females (23%), and the Catherine Creek (GRCAT) population had the highest percent females (58%). Appendix C and Figure 7 summarize sex ratios for Chinook Salmon by population.

The Bear Valley Creek (MFBEA-s) population had the largest average adult Chinook Salmon (jacks excluded; mean FL = 77.1 cm) and the Wenaha River had the smallest (67.1 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-s) had the oldest average ocean (saltwater) ages (2.2 years), and the Big Creek population was the youngest (1.6 years). Appendix C and Figure 8 summarize population specific freshwater, ocean-, and total-ages.

The date of median passage at LGR was June 14 across all populations (Figure 10). Catherine Creek had the earliest median passage date at LGR (17 May), which was 28 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 (24 June) which was 10 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 0.271 in the Wenaha River population to a low of 0.210 in Bear Valley Creek. The average percent polymorphic SNPs across all locations was 87.6% with a maximum of 94.7% in the Minam River. In contrast, the lowest percent of markers that were polymorphic was observed in the Pahsimeroi River population (75.9%). 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 10 of the 15 populations with sufficient numbers of samples for analysis (Appendix C). The number of markers that deviated from HWE ranged from one to five, which represented between 0.6 and 2.9% of the total number of markers (170) surveyed.

Patterns of genetic divergence, estimated by mean pairwise F_{ST} for SY2021 Chinook Salmon (Figure 12) mirrored patterns observed across baseline samples (Vu et al. 2015). The highest pairwise values of genetic differentiation were observed in the Middle Fork Salmon River, but there was notable variation across all reporting units. Specifically, many reporting units contained populations that displayed both high and low levels of pairwise genetic differentiation (Figure 12).

Discriminant analysis of principal components (DAPC) indicated the presence of four genetic clusters in returning adult Chinook salmon. Retaining the first 27 principal components we assigned individuals detected at IPTDS to these four clusters. In general, populations of steelhead with above average levels of pairwise genetic differentiation (those in South Fork Clearwater, South Fork Salmon, and Upper Clearwater Rivers; Figure 6) were assigned to a single genetic cluster (Figure 7). The same pattern did not hold true for Chinook Salmon, however.

Effective Number of Breeders

We were able to estimate N_b for 12 populations, four of which included multiple parental BYs (Table 6). Harmonic means of N_b were presented for populations with multiple parental BYs. Estimates of N_b were all greater than 50 and ranged from a low of 59 for SY 2017 in the Lemhi River to a high of 177 for BY 2017 in South Fork Salmon River main stem population.

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 Creek, with 100% of the fish detected in the Lolo Creek population assigned to the Hells Canyon reporting unit. The next two highest assignment rates were for Catherine Creek (96%) and the Wenaha River population (92%). We observed the lowest concordance for Panther Creek (0%) and the Lemhi River population (2.5%).

The difference in observed detections at PIT tag arrays was significantly different than expected based on observed counts at LGR overall (χ^2= 87.3, df = 5, p-value <0.001). Post hoc tests identified the Fall Chinook (p-value <0.001) reporting unit was detected at lower frequencies than expected whereas the upper Salmon River (p-value = 0.01) and South Fork Salmon River (p-value <0.001) were detected at higher frequencies than expected. Detections at PIT arrays for fish belonging to the Chamberlain Creek, Hells Canyon, 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). Relative to SY2020, steelhead that returned during SY2021 had a larger percentage of returning fish that were female (Hargrove et al. 2021). Because of modifications to the trap during 2020, similar comparisons could not be made for Chinook Salmon. In addition to variation in sex ratios as a function of spawn year, we also note significant variation in age structure. Specifically, steelhead returning during SY2021 had a much higher proportion of individuals return as 2-ocean fish relative to SY2020. The life history data presented in this report represent critical information on populations of steelhead and Chinook Salmon of conservation concern in the Snake River basin.

Genetic Diversity and Structure

As was the case in previous years, we observed an inverse relationship between genetic diversity and differentiation among steelhead populations. Specifically, populations that had the highest levels of genetic diversity also tended to display the lowest levels of pairwise differentiation. For example, steelhead populations in the Lochsa and Selway rivers showed elevated genetic divergence relative to other populations (Figure 6), likely stemming from a combination of genetic isolation and an absence of hatchery stocking. Populations with hatchery releases involving broodstock from distant drainages (e.g., Upper Salmon River) displayed higher relative levels of genetic diversity (Appendix A) and lower levels of genetic differentiation (Figure 6). This trend is supported by previous work that evaluated levels of genetic differentiation between supplemented and non-supplemented steelhead populations (Powell and Campbell 2020; Hargrove et al. 2021). Estimates of genetic diversity observed in SY2021 were generally consistent with historical estimates (e.g., SY2010–2019; IPTDSW 2020 Table 5). For SY2021, DAPC analysis supported the presence of six genetic clusters, which was greater than the number supported for SY2020 (four clusters). Proposed mechanisms that might explain this trend include differences in sampling between years, which occurred at different rates throughout the season due to restrictions associated with the COVID-19 pandemic during SY2020. For example, there may have been systematic variation in samples sources due to altered sample rates and number of samples collected.

Patterns of genetic diversity among populations of Chinook Salmon remained largely consistent with patterns observed for SY2010-2019 (IPTDSW 2020; Table 10). Interestingly, all but one value of heterozygosity from SY2021 was lower relative to their long-term averages; however, changes in heterozygosity were quite small (average change in H_e = 0.006; range = -0.03 to +0.002). Chinook Salmon were not sampled because of the COVID-19 pandemic during SY2020, rendering a comparison of genetic structure (e.g., DAPC analyses) with the previous spawn year not possible. Results from DAPC for SY2018 Chinook Salmon identified two genetic clusters, whereas the best fit model for SY2016-2017 was three genetic clusters, both of which differ from this year's estimate of six genetic clusters. For SY2010-2019, genetic structure was evaluated via phylogenetic methods and not genetic clustering methods. Future work should consider analyzing long-term data sets via DAPC to determine if patterns in genetic clustering have changed through time.

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 that contribute offspring to the next generation. Effective population size is usually smaller than census size (which biologists have traditionally attempted to measure) and serves as an indicator of genetic drift and potential inbreeding in a population (Wright 1931). Genetic drift refers to changes 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 SY2021, we generated estimates of N_b for 14 populations of steelhead (five with multiple brood years) and 12 populations of Chinook Salmon (4 with multiple brood years). In general, these estimates were well above the minimum effective size of 50, but below 500. Estimates of N_b for SY2021 steelhead were on average lower (average decrease across populations: 18) relative to those generated for SYs 2010–2019 (Table 4), but the extent of change varied by population (range of difference in N_b: -152 to +157). In contrast, all estimates of N_b for Chinook Salmon populations from SY2021 were lower (average decrease across populations: 87; range: 1-157) relative to long-term averages (Table 6). Variation in estimates of N_b across spawn years has been previously observed in the Snake River basin and is likely influenced by a number of different 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 number of 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. Mechanisms to explain these discrepancies include the distribution and placement of PIT tag arrays on the landscape and GSI assignment accuracy. First, the number of PIT tag arrays varied as a function of population and their placement on the landscape and associated use varies temporally. Within a given year, arrays are both added and decommissioned. Thus, variation in detections on the landscape may be driven by the number and placement of arrays within a given population. Additionally, some genetic stocks have inherently lower self-assignment rates because of stocking and/or elevated rates of gene flow which reduces genetic differentiation between populations (e.g., 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). 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 SY2021 to maintain consistency with previous reports. In future reports, including 5-year summaries, we will perform GSI using the latest baseline versions.

For SY2021, 53% and 52% of PIT-tagged steelhead and Chinook Salmon were not detected in a population within the Snake River basin. 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 (e.g., arrays USE, USI, and SFG which occurred along the mainstem of the upper Salmon and South Fork Salmon Rivers). In this document, we elected to exclude records for fish not detected within a population boundary which likely increased the number of fish that were not detected at a PIT tag array. 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. Some of this can be explained by the non-uniform distribution and density of PIT arrays in the Snake River basin.

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.

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TABLES

Table 1. Summary of total valid PIT tags implanted into adult steelhead at the Lower Granite Dam (LGR) trapping facility and subsequent detection of these tags in the Snake River basin for SY2021. Genotyped tags represent the number of total tags that were successfully genotyped. Genotyped, detected tags represent the number of total tags (and associated proportions) that were genotyped and detected in the Snake River basin. Genotyped, undetected tags correspond to the number (and proportion) of total tags that were genotyped but 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	3,126	1,659 (53.1%)	1,467 (46.9%)	3,083 (98.6%)	1,644 (53.3%)	1,439 (46.7%)
Chinook Salmon	1,974	1,034 (52.4)	940 (47.6%)	1970 (99.8%)	1,033 (52.4%)	937 (47.6%)

Table 2. Steelhead populations and PIT tag detection locations in the Snake River basin with observed steelhead in SY2021. 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.

	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 F Salmon R	44.28761	-114.72075
SRPAH-s		*Pahsimeroi River*		
	PAHH	Pahsimeroi Hatchery	44.68414	-114.03947
SRPAN-s		*Panther Creek*		
	PCA	Panther Creek	45.29525	-114.35810
SRLEM-s		*Lemhi River*		
	LRW	Lemhi River Weir	44.86612	-113.62475
	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 R	45.17647	-113.88527
SRLSR-s		*Little Salmon and Rapid River*		
	WB1	White Bird Creek	45.75818	-116.30660
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	SF Salmon R, Krassel	44.97840	-115.72700
	ESS	EFSF Salmon R	44.95621	-115.53315
	YPP	Yellow Pine Pit Lake	44.92899	-115.33388
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	-115.58966
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 Array	46.79509	-116.41088
	LAP	Lapwai Creek	46.44327	-116.81254
	SWT	Sweetwater Creek	46.36979	-116.79508
	WEB	Webb Creek	46.32599	-116.83197
	JA1	Jacks Cr	46.50386	-116.54976
CRLOL-s		*Lolo Creek*		
	LC1	Lolo Creek, rkm 21	46.29443	-115.97612
	LC2	Lolo Creek, rkm 25	46.29056	-115.93415
CRSFC-s		*South Fork Clearwater River*		
	SC1	SF Clearwater, rkm 1	46.13685	-115.98091
	SC2	SF Clearwater, rkm 2	46.12749	-115.97730
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
	CCW, CATHEW	Catherine Creek Ladder/Weir	45.19096	-117.82862
	LOOH	Lookingglass Hatchery	45.73154	-117.86441

Table 2. Continued

	Site code	Site description	Latitude	Longitude
GRUMA-s		*Upper Grande Ronde (continued)*		
	LOOH	Lookingglass Hatchery	45.73154	-117.86441
	UGR	Upper Grande Ronde R	45.59334	-117.90312
	UGS	Upper Grande Ronde R, Starkey	45.24896	-118.38896
GRWAL-s		*Wallowa River*		
	WR1	Wallowa River at river km 14	45.63368	-117.73376
	WR2	Wallowa River at river km 32	45.59447	-117.57922
	WALH	Wallowa Hatchery	45.41757	-117.30157
	LOSTIW	Lostine River Weir	45.54327	-117.48450
	BCANF	Big Canyon Facility	45.61904	-117.69863
	MR1	Minam River at river km 0.5	45.61962	-117.72657
IRMAI-s		*Imnaha River*		
	COC	Cow Creek	45.76774	-116.74404
	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
	IR5	Imnaha Weir upstream array	45.19319	-116.86859
	LSHEEF	Little Sheep Facility	45.47782	-116.93025
	BSC	Big Sheep Creek	45.50649	-116.85067
	CMP, CAMP4C	Camp Creek at rkm 2 - Imnaha	45.55182	-116.86694
	GCM	Grouse Creek Mouth	45.32802	-116.80664
	CZY	Crazyman Creek	45.22930	-116.84478
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 R	46.54419	-118.16290
	MTR	Middle Tucannon R	46.50526	-118.01628
	TFH	Tucannon Hatchery	46.30965	-117.65715
	TPJ	Panjab Creek	46.20459	-117.70617
	UTR	Upper Tucannon R	46.41592	-117.73834

Table 3. Chinook Salmon populations and PIT tag detection locations in the Snake River basin with observed Chinook Salmon in SY2021. 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.

	Site code	Site description	Latitude	Longitude
SRUMA		*Upper Salmon River main stem*		
	RFL	Redfish Lake Creek	44.15472	-114.90504
	SAWT	Sawtooth Hatchery	44.15068	-114.88366
SRVAL		*Valley Creek*		
	VC2	Valley Creek, upper site	44.21860	-114.94216
SRYFK		*Yankee Fork*		
	YFK	Yankee F Salmon R	44.28761	-114.72075
SRPAN		*Panther Creek*		
	PCA	Panther Creek array	45.29525	-114.35810
SRPAH		*Pahsimeroi River*		
	PAHH	Pahsimeroi Hatchery	44.68414	-114.03947
SRLEM		*Lemhi River*		
	EVU	Eagle Valley Ranch – upper	45.10008	-113.72604
	EVL	Eagle Valley Ranch – lower	45.11507	-113.77402
	LLR	Lower Lemhi R	45.17635	-113.88512
	LRW	Lemhi River Weir	44.86612	-113.62475
	HYC	Hayden Creek	44.86159	-113.63215
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	SF Salmon R, Krassel	44.97840	-115.72700
	SALSFW	SF Salmon R 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	EFSF Salmon R	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*		
	LC2	Lolo Creek, rkm 25	46.29056	-115.93415
SCUMA		*Upper South Fork Clearwater River*		
	SC3	South Fork Clearwater site 3	45.81414	-115.81597
	SC4	South Fork Clearwater site 4	45.82350	-115.63410
IRMAI		*Imnaha River*		
	IR3	Imnaha R, rkm 41	45.49004	-116.80393
	IR4	Imnaha Weir downstream array	45.19446	-116.86877
	IR5	Imnaha Weir upstream array	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
GRLOO		*Lookingglass Creek*		
	LOOH	Lookingglass Hatchery	45.73154	-117.86441

Table 3. Continued

	Site code	Site description	Latitude	Longitude
GRCAT		*Catherine Creek*		
	CATHEW	Catherine Creek Weir	45.19096	-117.82862
	CCW	Catherine Creek Ladder/Weir*	45.19096	-117.82862
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 at river km 0.5	45.61962	-117.72657
GRWEN		*Wenaha River*		
	WEN	Wenaha River mouth	45.94615	-117.45412
SNTUC		*Tucannon River*		
	LTR	Lower Tucannon R	46.54419	-118.16290
	UTR	Upper Tucannon R	46.41584	-117.73832
	TFH	Tucannon Hatchery	46.30965	-117.65715

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
CRLMA-s	2016	27	184	276
CRLOC-s	2015	38	385	266
CRLOC-s	2016	44	300	266
CRLOL-s	2016	25	173	180
CRSEL-s	2015	49	267	325
CRSEL-s	2016	48	242	325
CRSFC-s	2016	21	239	195
GRJOS-s	2016	78	360	373
GRLMT-s	2016	36	504	353
GRUMA-s	2015	36	190	338
GRUMA-s	2016	80	275	338
GRWAL-s	2015	51	307	314
GRWAL-s	2016	89	353	314
IRMAI-s	2015	26	364	459
IRMAI-s	2016	83	302	459
SFMAI-s	2015	27	189	281
SNASO-s	2016	38	343	354
SNTUC-s	2016	30	368	346
SRUMA-s	2016	26	353	272

Table 5. Assignment concordance between populations and GSI reporting units for PIT-tagged steelhead from SY2021 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	SFCLWR	UPCLWR
SNASO-s	80	0.375	0.438	0.025	0.025	0	0	0.088	0.038	0.012	0
SNTUC-s	59	0.339	0.441	0.017	0.034	0	0.017	0.136	0.017	0	0
GRJOS-s	148	0.176	0.527	0.068	0.007	0.007	0.007	0.095	0.108	0	0.007
GRLMT-s	91	0.121	0.714	0.077	0.011	0	0.011	0.022	0.033	0.011	0
GRUMA-s	175	0.149	0.691	0.029	0.006	0.006	0.011	0.074	0.029	0	0.006
GRWAL-s	199	0.116	0.779	0.025	0.005	0	0.005	0.055	0.010	0	0.005
IRMAI-s	177	0.068	0.249	0.548	0.017	0	0.028	0.090	0	0	0
SRLSR-s	17	0.059	0.353	0.059	0.059	0	0.059	0.353	0.059	0	0
SFMAI-s	68	0.015	0.044	0	0.029	0.897	0.015	0	0	0	0
SFSEC-s	6	0	0	0.167	0	0.833	0	0	0	0	0
MFBIG-s	20	0	0.150	0	0	0	0.800	0	0	0	0.050
MFUMA-s	13	0	0.154	0	0.077	0	0.538	0.231	0	0	0
SRPAN-s	50	0.180	0.240	0.080	0.060	0	0.160	0.22	0.040	0.020	0
SRLEM-s	19	0.211	0.158	0.053	0.053	0	0	0.526	0	0	0
SRPAH-s	4	0	0	0	0	0	0	1.000	0	0	0
SRUMA-s	48	0.083	0.208	0.021	0.042	0	0	0.625	0.021	0	0
CRLMA-s	47	0.234	0.468	0.106	0.021	0.021	0	0.064	0.064	0.021	0
CRSFC-s	58	0	0.017	0	0	0	0	0	0.121	0.776	0.086
CRLOL-s	59	0.034	0.017	0	0	0	0	0	0.136	0.763	0.051
CRSEL-s	165	0.006	0.006	0	0	0	0	0.006	0	0.048	0.933
CRLOC-s	132	0.008	0.008	0	0	0	0	0	0.023	0.091	0.871

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 Harmonic mean
CRLOC	2017	33	71	228
GRLOS	2017	23	93	199
GRMIN	2017	56	112	-
IRMAI	2017	43	161	209
IRMAI	2018	26	104	209
MFBEA	2017	28	70	174
MFBIG	2017	39	157	228
MFBIG	2018	46	123	228
MFMAR	2017	30	96	-
SFEFS	2017	49	118	196
SFEFS	2018	29	124	196
SFMAI	2017	60	177	273
SFMAI	2018	51	117	273
SFSEC	2017	74	148	196
SRLEM	2017	24	59	128
SRUMA	2017	34	174	175

Table 7. Assignment concordance between populations and GSI reporting units for PIT-tagged Chinook Salmon from SY2021 using Chinook Salmon baseline v3.1. The GSI reporting unit of each population is highlighted in gray.

TRT	n	HELLSC	SFSALM	MFSALM	UPSALM	FALL	CHMBLN	TUCANO
CRLOC	52	0.423	0.423	0.058	0.096	0	0	0
CRLOL	12	1.000	0	0	0	0	0	0
GRCAT	24	0.958	0	0.042	0	0	0	0
GRLOO	7	0.857	0.143	0	0	0	0	0
GRLOS	39	0.872	0.077	0	0.051	0	0	0
GRMIN	68	0.882	0.059	0	0.059	0	0	0
GRUMA	7	0.857	0	0.143	0	0	0	0
GRWEN	25	0.920	0	0	0	0.08	0	0
IRBSH	11	0.818	0	0.091	0.091	0	0	0
IRMAI	82	0.866	0.049	0.049	0.037	0	0	0
SCUMA	3	0.333	0.667	0	0	0	0	0
SFMAI	143	0.112	0.776	0.056	0.056	0	0	0
SFEFS	93	0.097	0.839	0.032	0.032	0	0	0
SFSEC	101	0.069	0.891	0.020	0.020	0	0	0
MFBEA	53	0.075	0.038	0.830	0.057	0	0	0
MFBIG	98	0.265	0.235	0.327	0.143	0	0.031	0
MFMAR	44	0.045	0.045	0.818	0.091	0	0	0
SRLEM	40	0.250	0.125	0.025	0.600	0	0	0
SRPAH	23	0.130	0.130	0	0.739	0	0	0
SRPAN	18	0.333	0.611	0	0	0	0	0.056
SRUMA	57	0.158	0.105	0	0.737	0	0	0
SRVAL	19	0.053	0.158	0	0.789	0	0	0
SRYFS	8	0.250	0	0	0.750	0	0	0

FIGURES

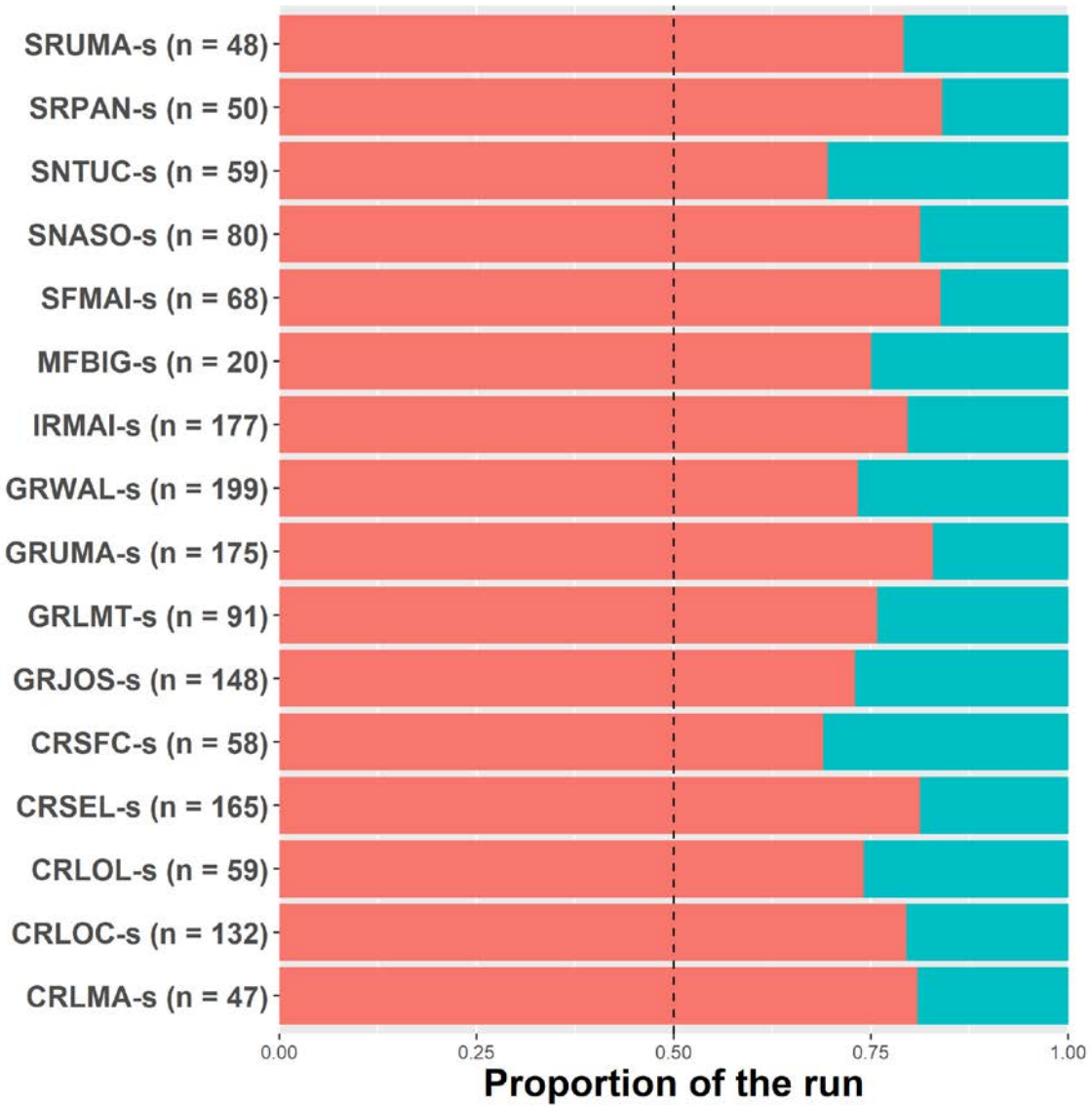


Figure 1. Sex ratios for Snake River steelhead populations (see Table 2 for a list of population names, codes, and composite Instream PIT Tag Detection Systems sites). Sample sizes are shown in the y-axis labels. The dotted vertical line indicates a 50:50 sex ratio and the proportion of females and males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

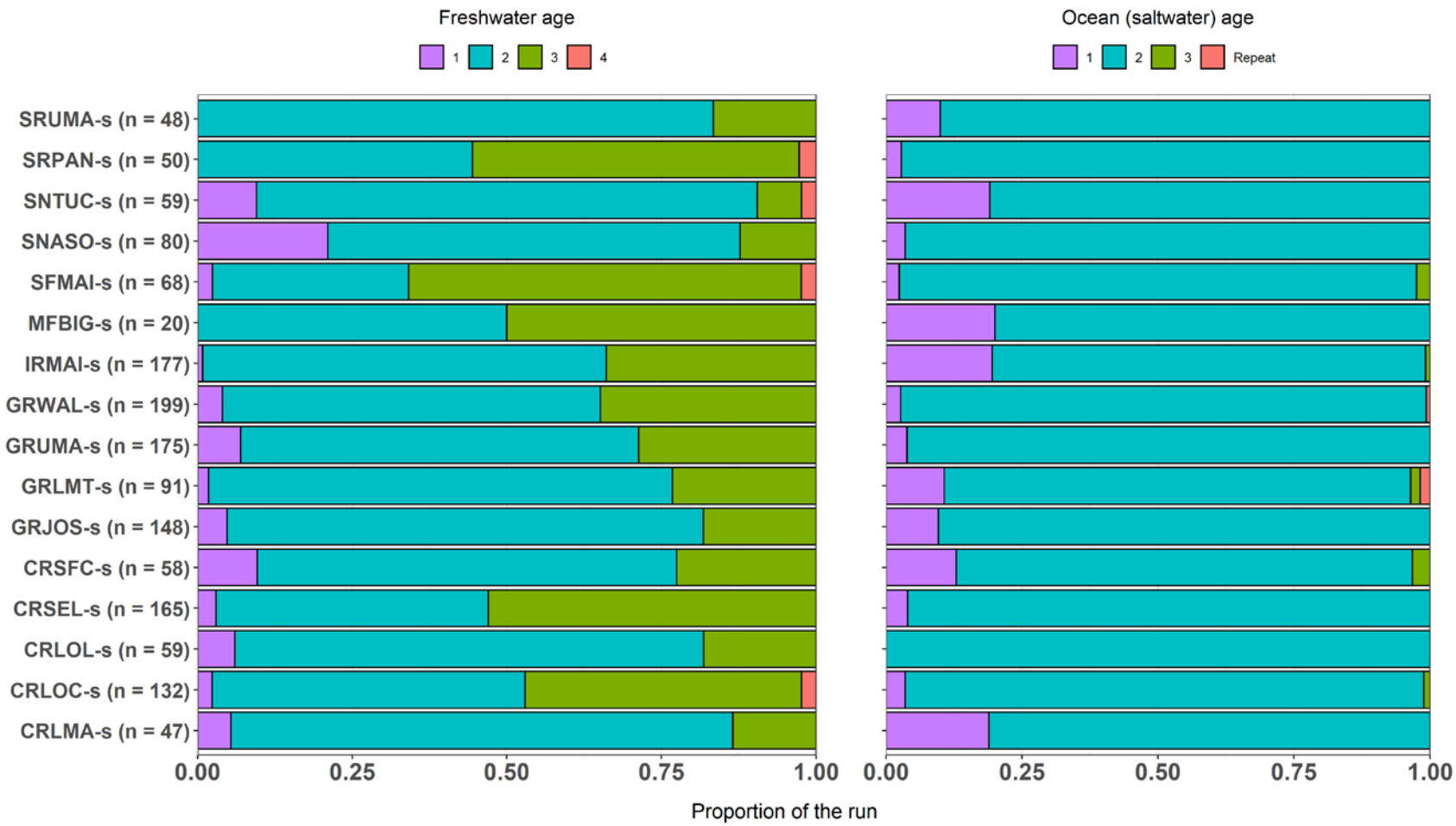


Figure 2. Distribution of freshwater and ocean (saltwater) ages for Snake River steelhead populations (see Table 2 for a list of population names, codes, and composite Instream PIT Tag Detection Systems sites). Sample sizes are shown in y-axis labels.

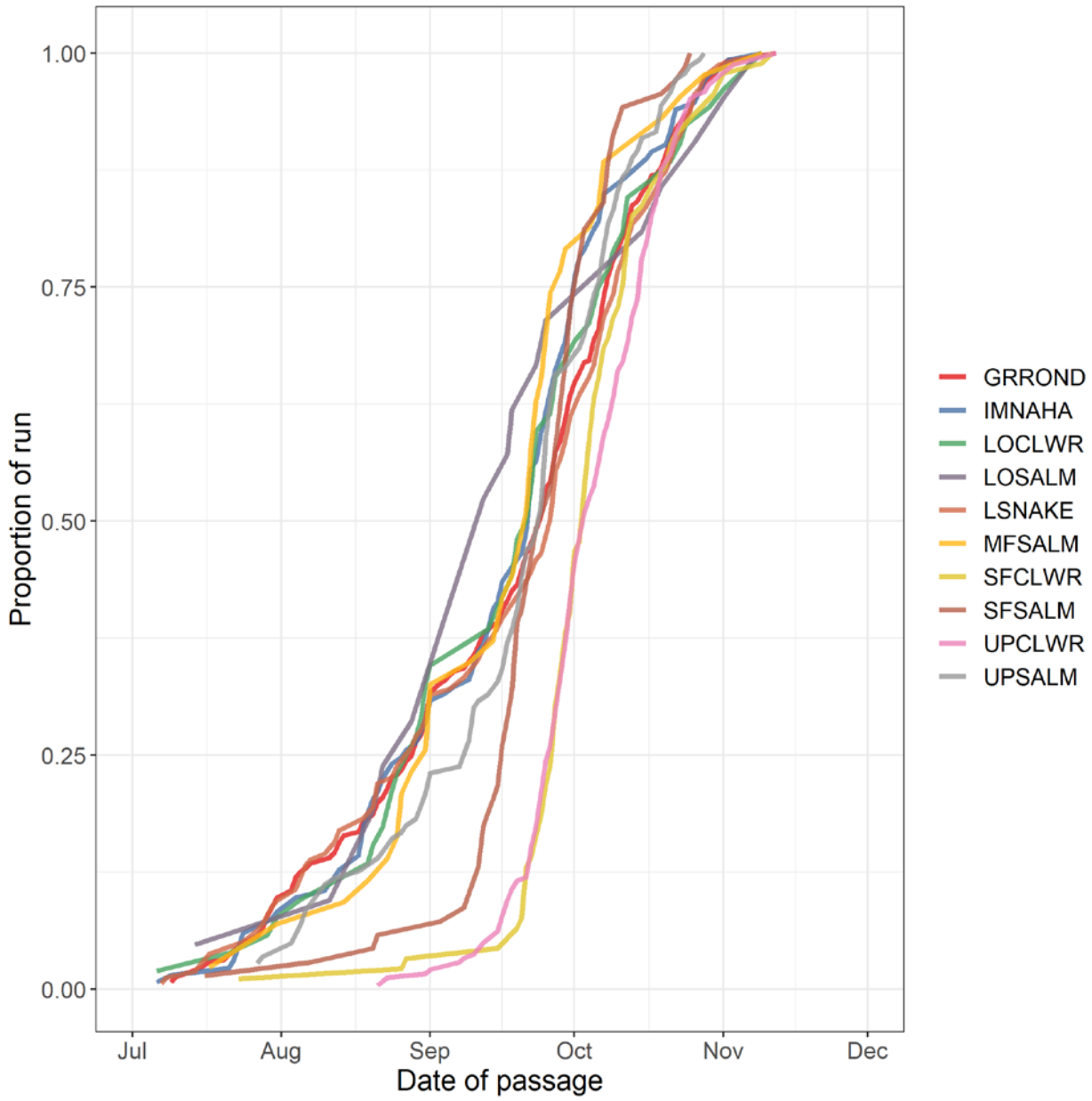


Figure 3. Date of passage for adult steelhead PIT tagged at Lower Granite Dam (LGR), Washington and later detected at Snake River Instream PIT Tag Detection Systems by GSI reporting unit. Steelhead migrating past LGR during the spring portion of the migration were removed from the analysis.

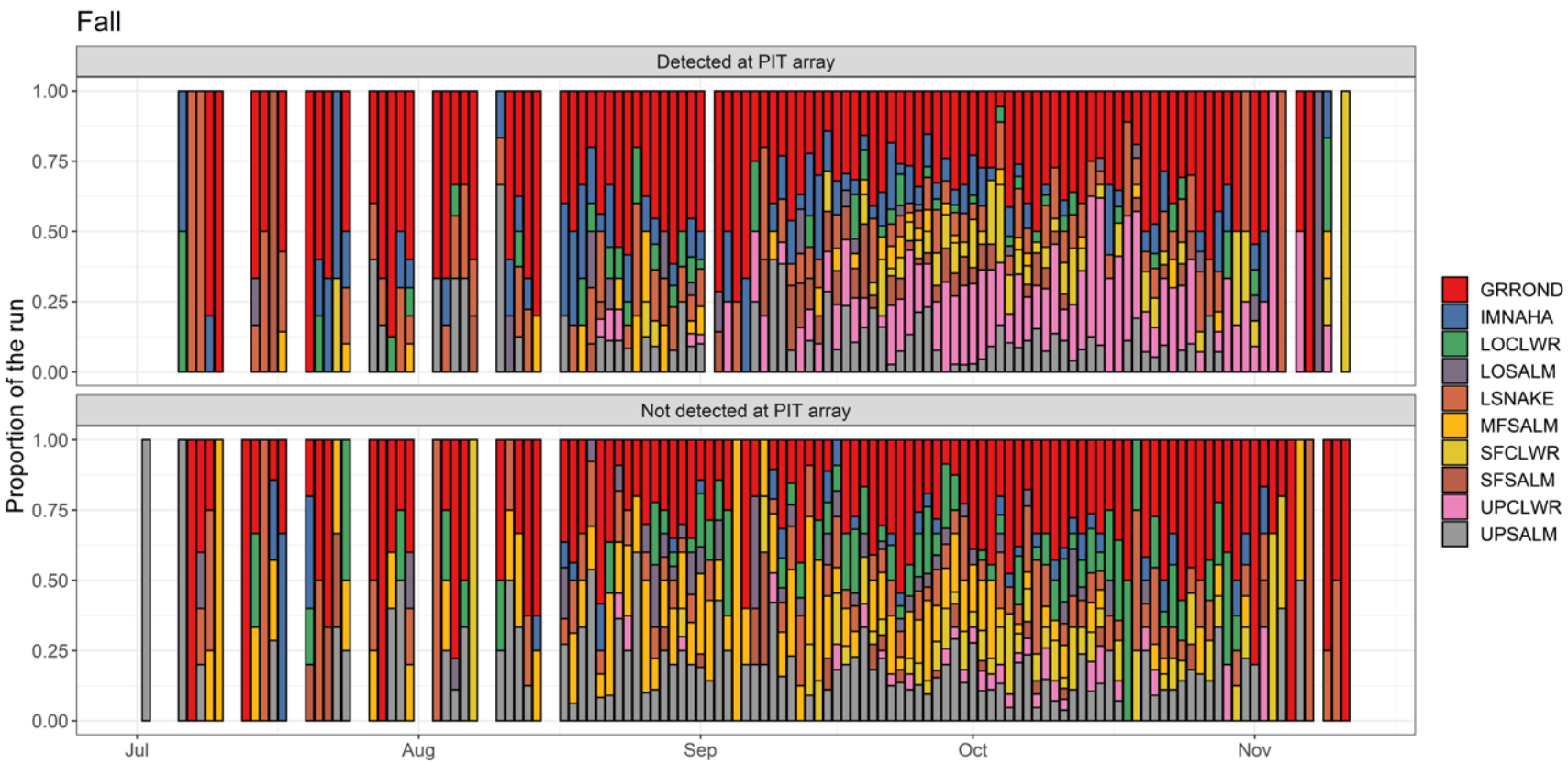


Figure 4. Relative contribution of genetic stocks to the weekly SY2021 steelhead run at Lower Granite Dam that were or were not detected at a PIT tag array in the Snake River basin for the fall portion of the run (prior to trap closure in November).

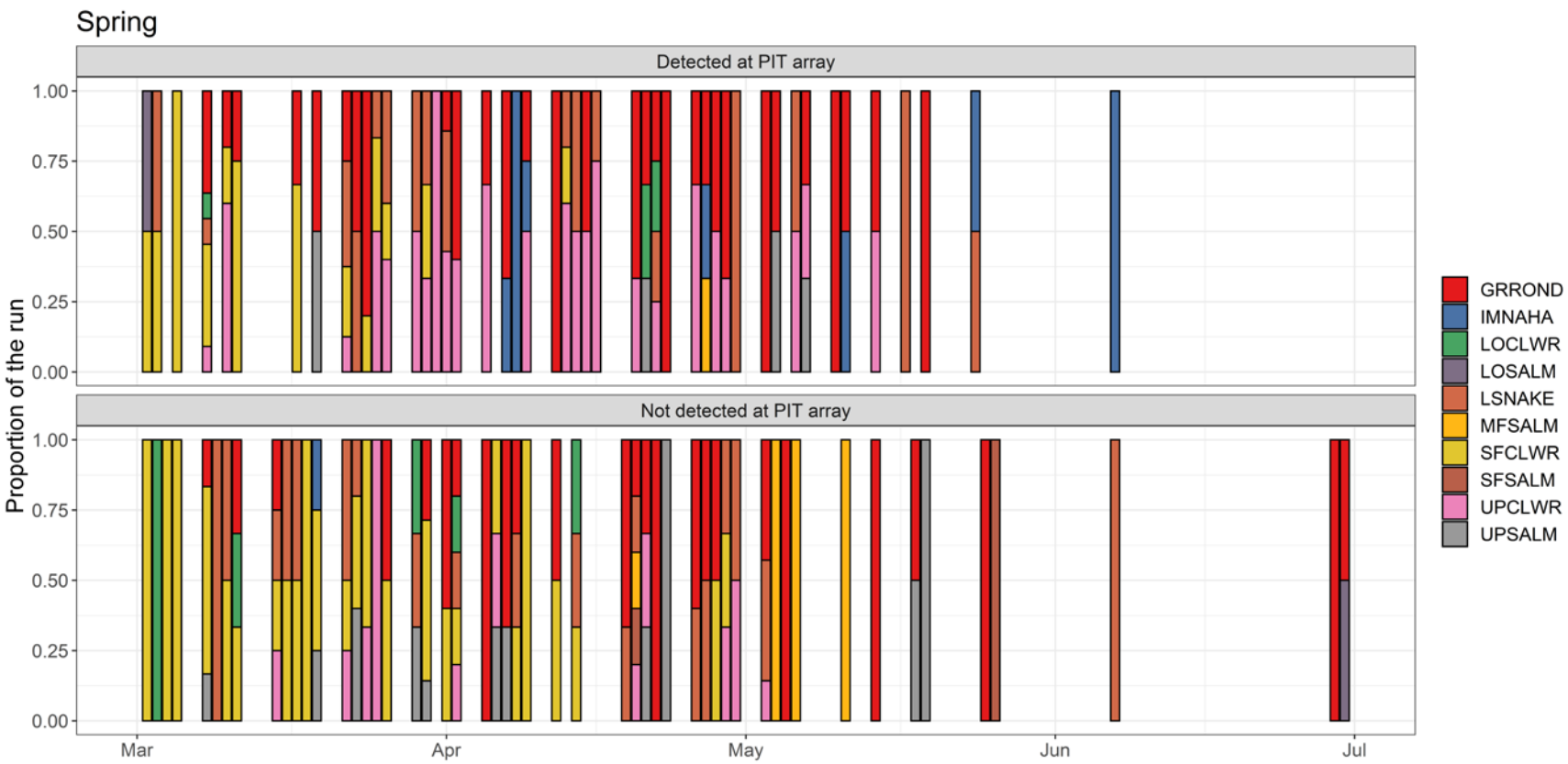


Figure 5. Relative contribution of genetic stocks to the weekly SY2021 steelhead run at Lower Granite Dam that were or were not detected at a PIT tag array in the Snake River basin during the spring portion of the run.

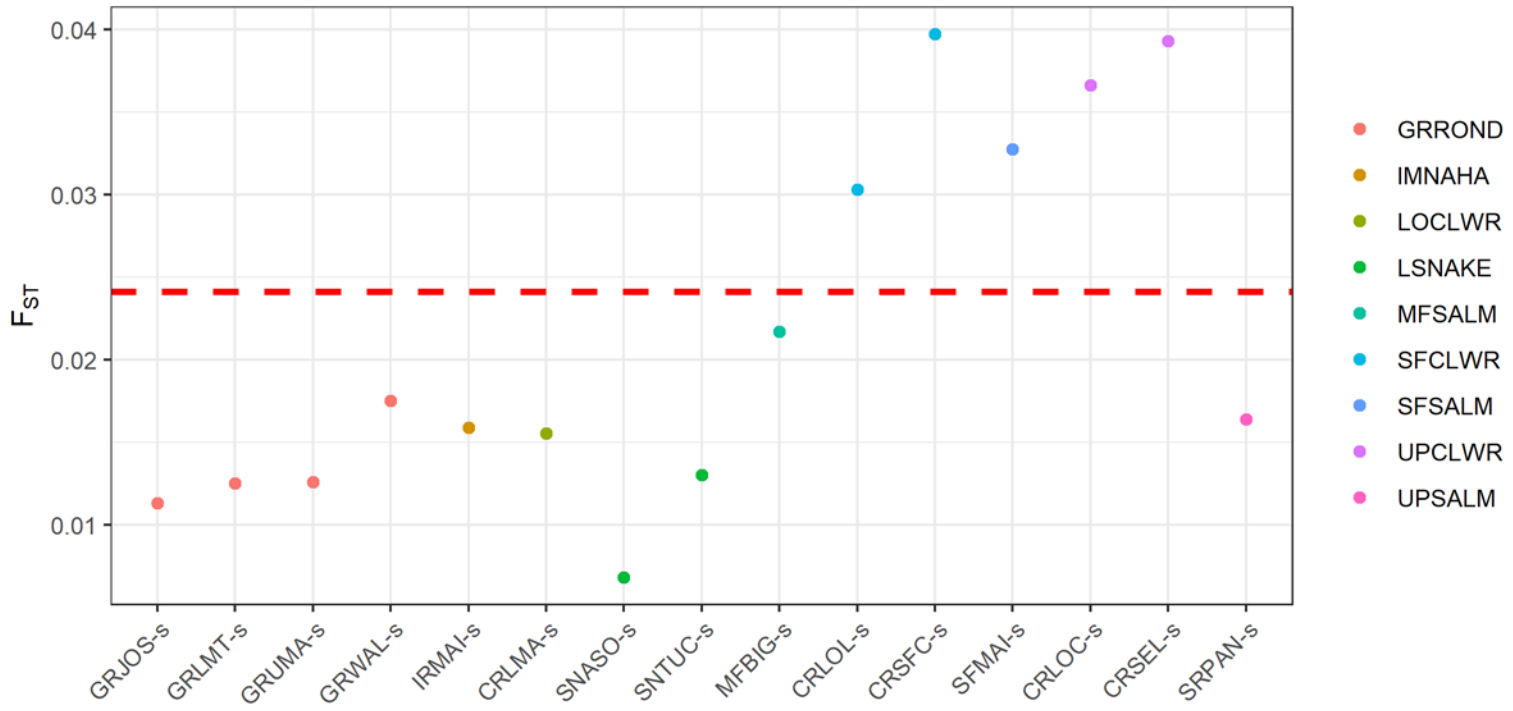


Figure 6. Estimates of mean pairwise F_{ST} for Snake River steelhead populations with ≥20 samples detected at In-Stream PIT Detection Systems sites for SY2021. The dashed line is the average pairwise F_{ST} estimate across all populations. Genetic stocks are coded by color and population descriptions can be found in Table 2.

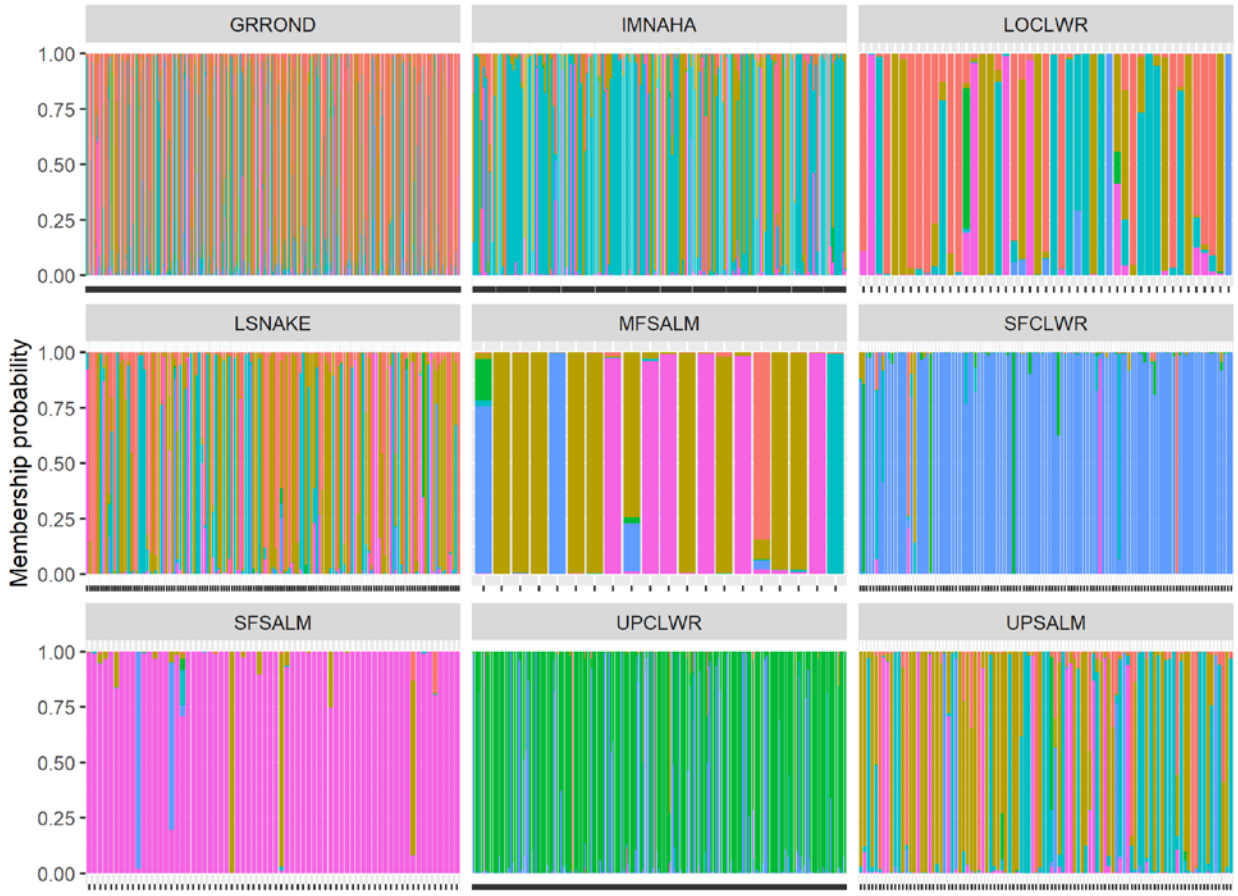


Figure 7. Bar charts of individual membership probability to six genetic clusters for Snake River steelhead populations with ≥20 samples detected at In-Stream PIT Detection Systems sites organized by genetic reporting unit for SY2021. The number of clusters and associated memberships were identified by discriminant analysis of principal components. Each vertical line represents an individual fish and colors correspond to different genetic clusters. Individuals are grouped based on the location of the Snake River steelhead population within a GSI reporting unit.

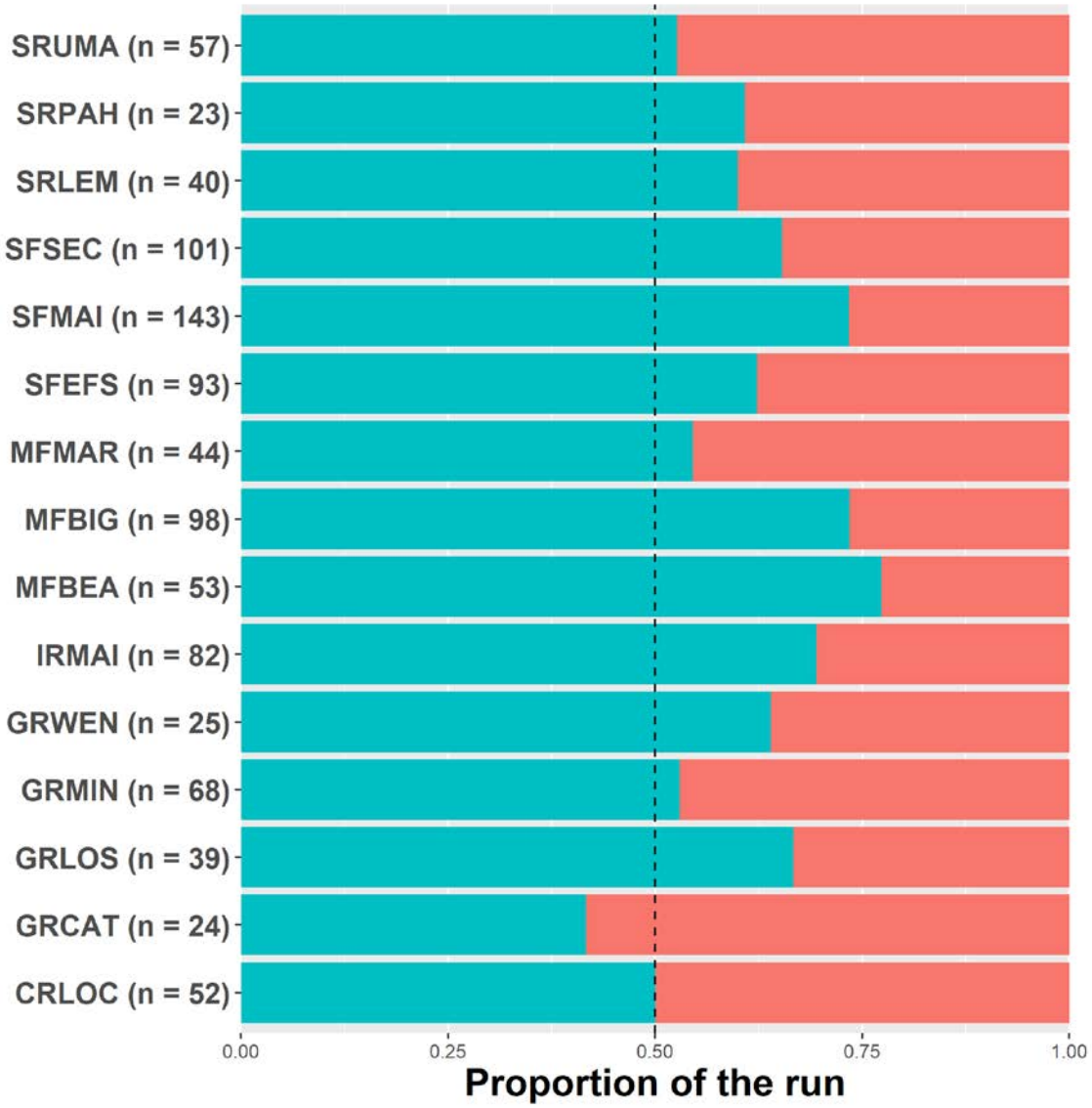


Figure 8. Sex ratios for Snake River Chinook Salmon populations (see Table 3 for a list of population names, codes, and composite IPTDS sites). Sample sizes are shown in the y-axis labels. The dotted vertical line indicates a 50:50 sex ratio and the proportion of females and males is given in red and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

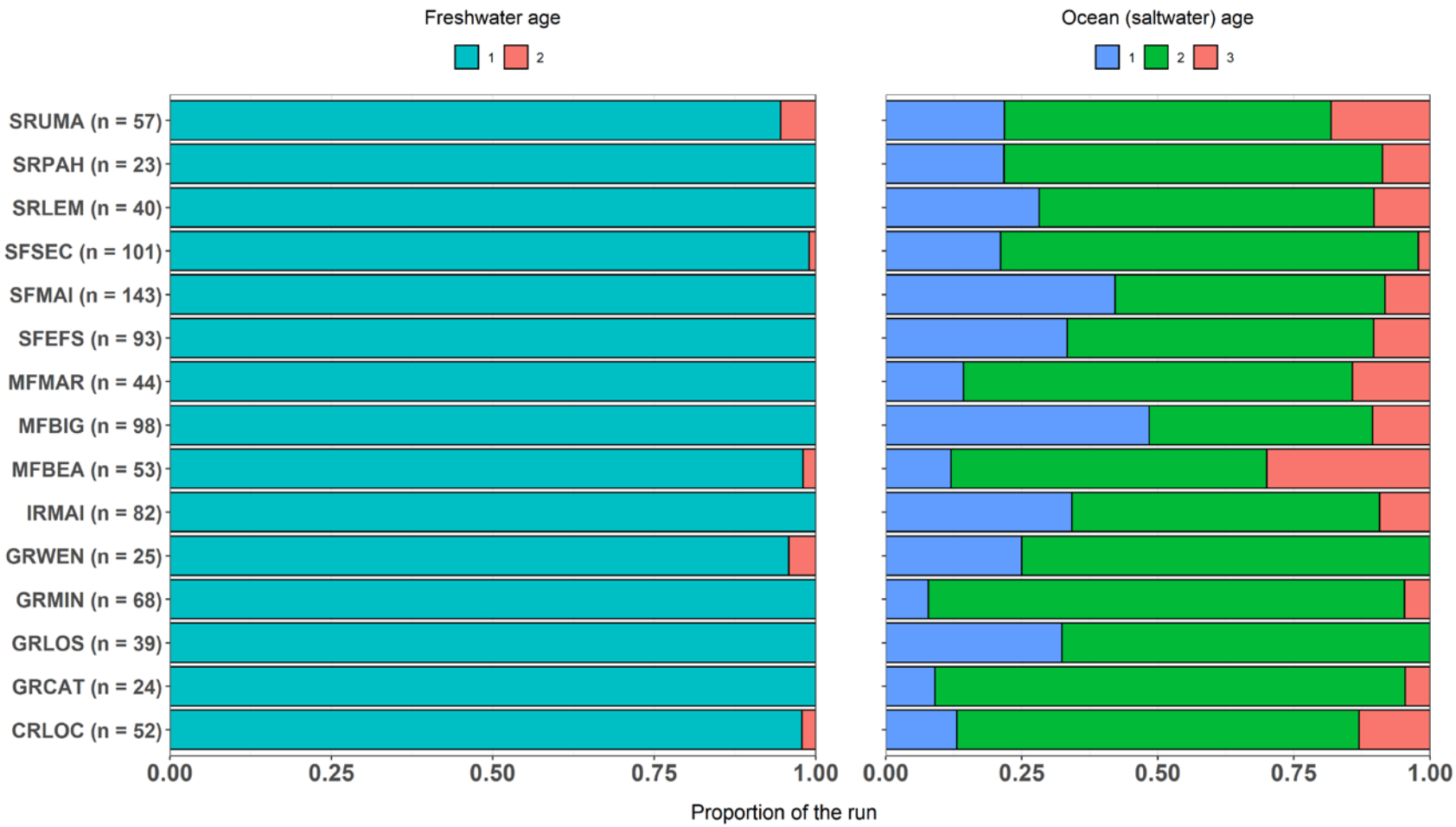


Figure 9. Distribution of freshwater and ocean (saltwater) ages for Snake River Chinook Salmon populations (see Table 3 for a list of population names, codes, and composite IPTDS sites). Sample sizes are shown in y-axis labels.

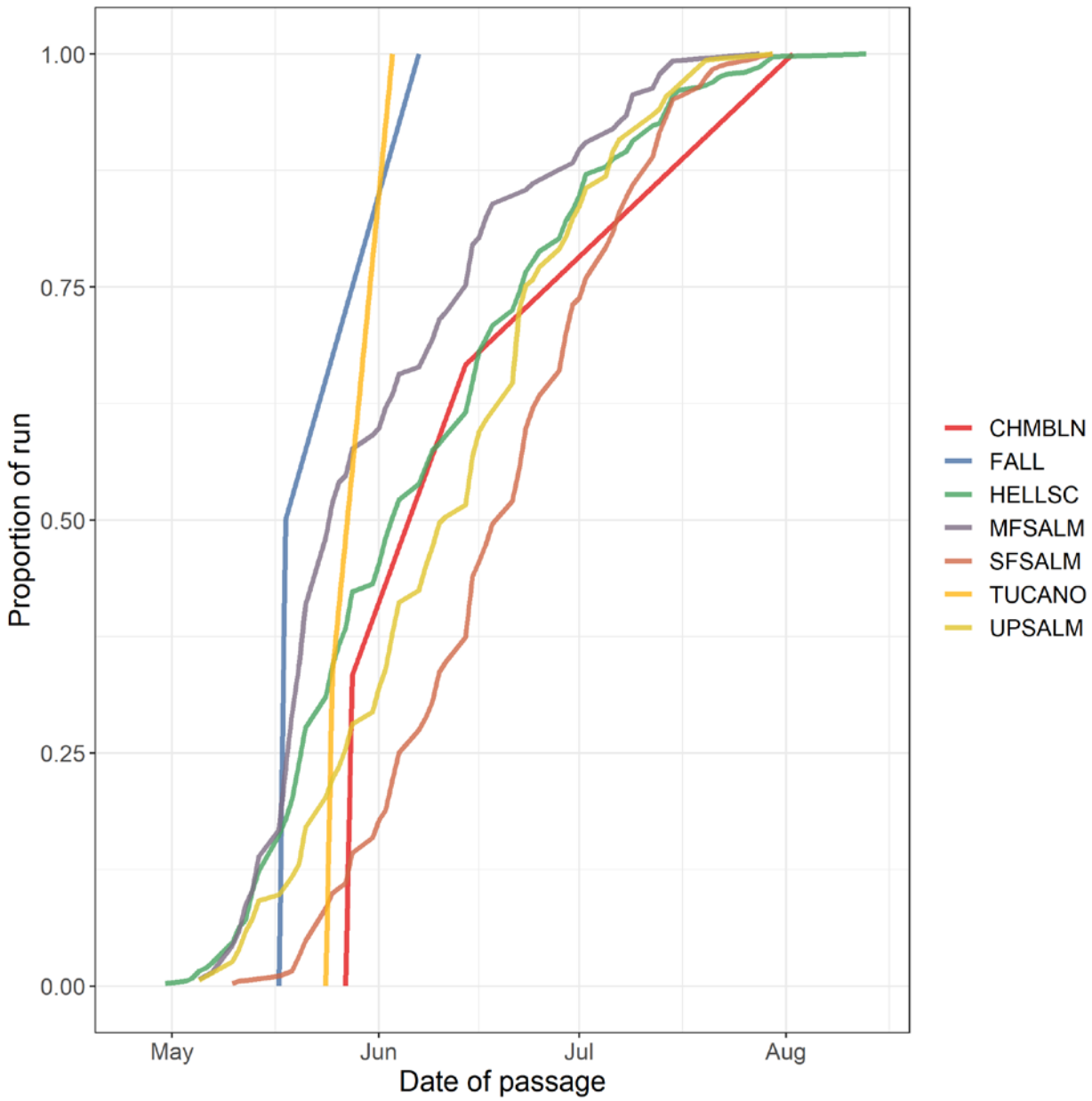


Figure 10. Date of passage for adult Chinook Salmon PIT-tagged at Lower Granite Dam (LGR), Washington and later detected at Snake River Instream PIT Tag Detection Systems site by GSI reporting unit.

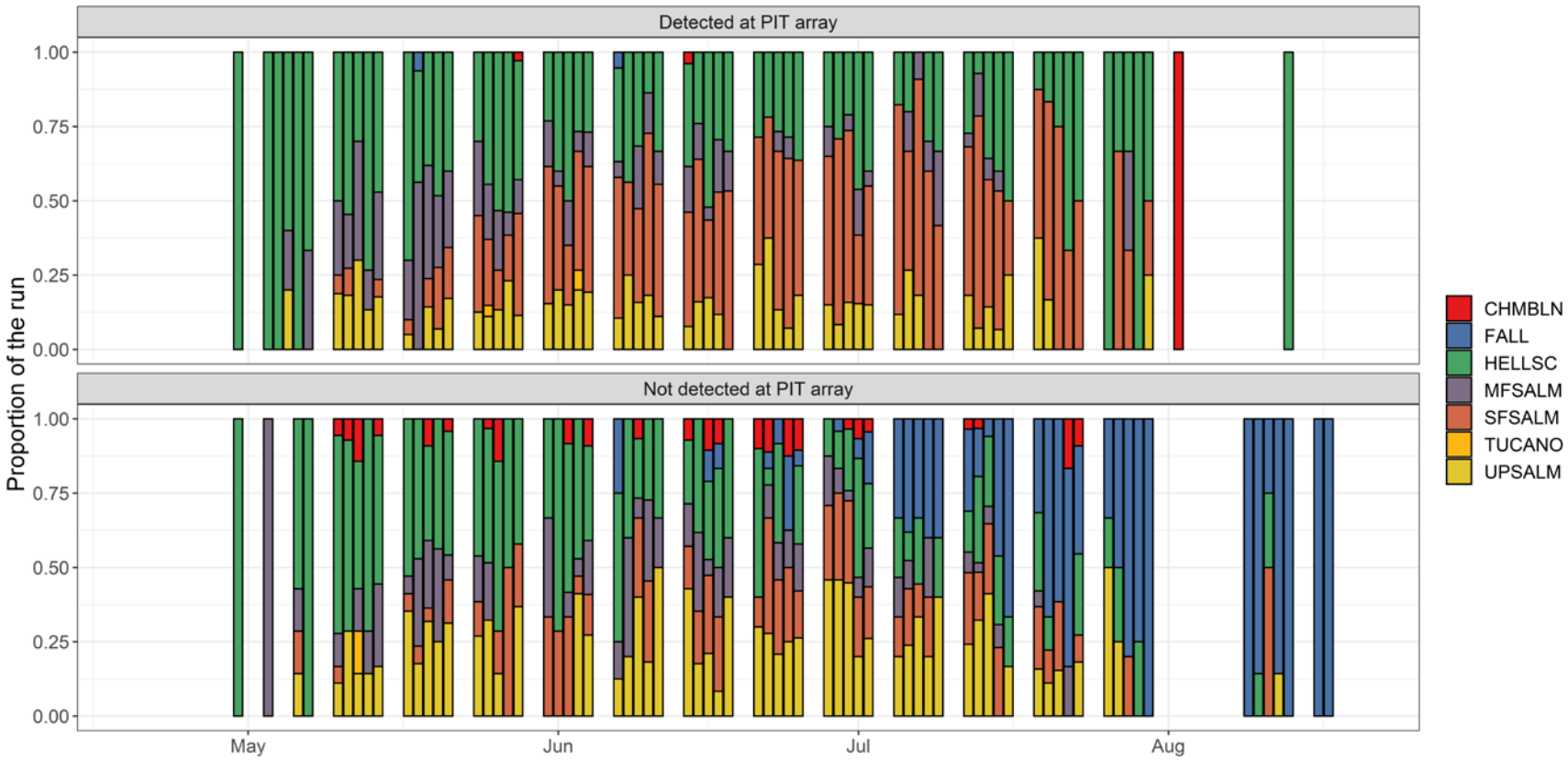


Figure 11. Relative contribution of genetic stocks to the weekly SY2021 Chinook Salmon run at Lower Granite Dam that were or were not detected at a PIT tag array in the Snake River basin.

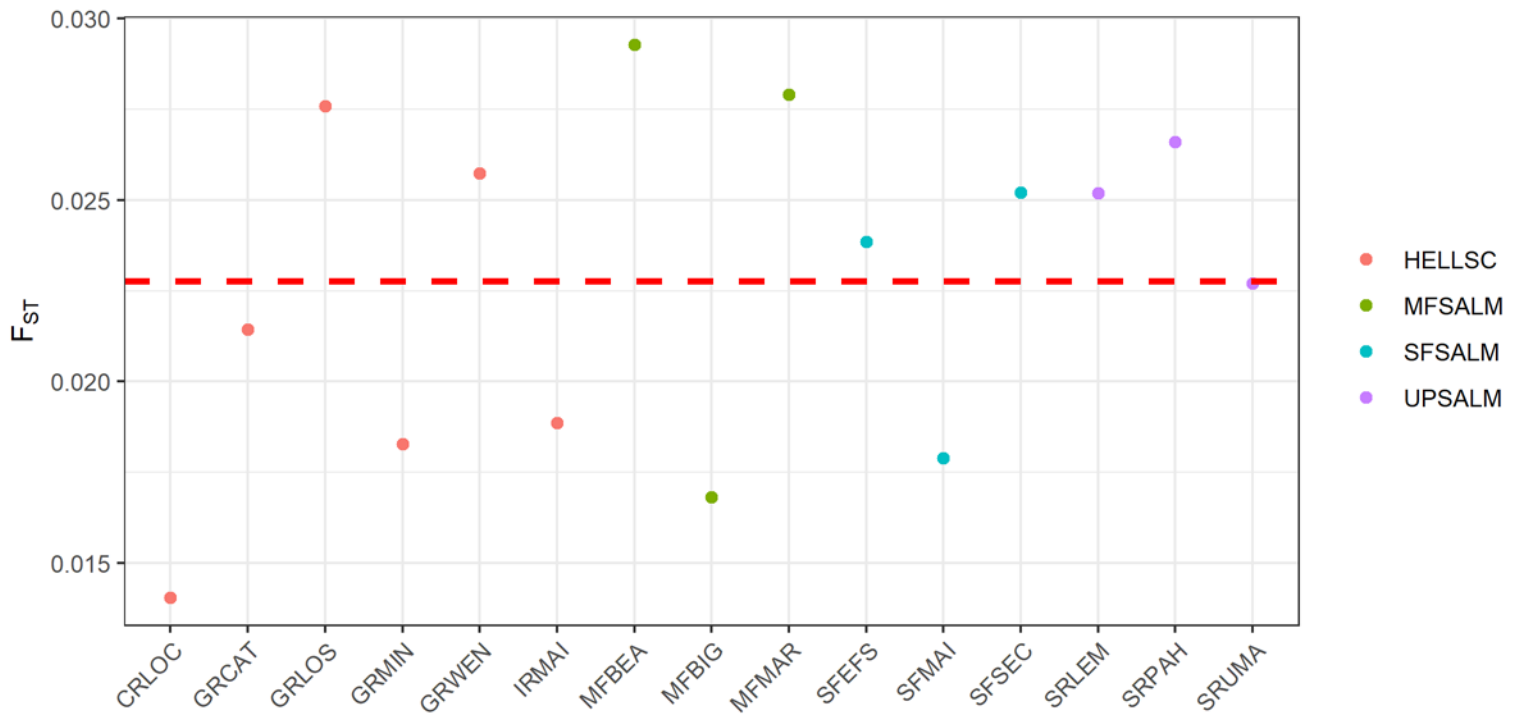


Figure 12. Estimates of mean pairwise F_{ST} for Snake River Chinook Salmon populations with ≥20 samples detected at In-Stream PIT Detection Systems sites for SY2021. The dashed line is the average pairwise F_{ST} estimate across all populations. Genetic stocks are coded by color and population names can be found in Table 3.

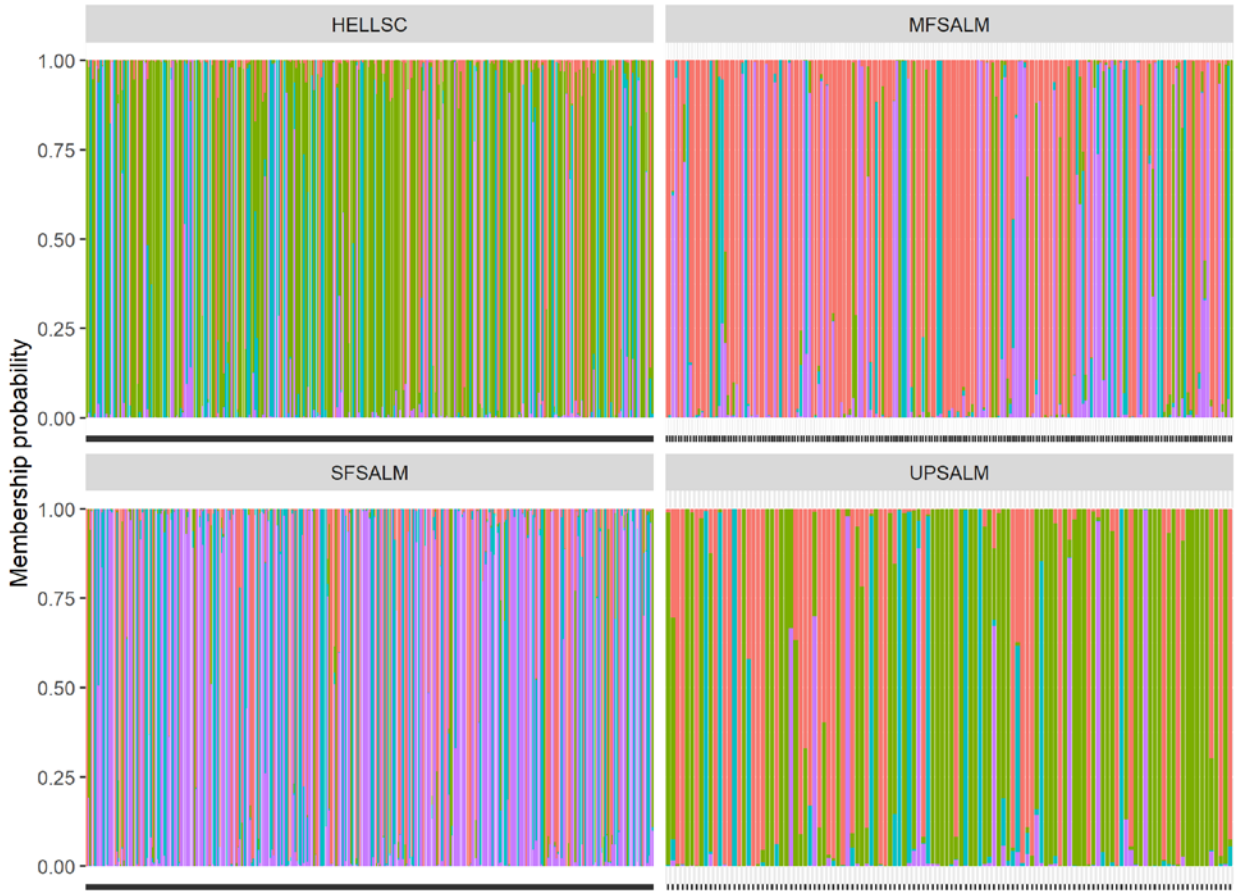


Figure 13. Bar charts of individual membership probability to four genetic clusters for Snake River Chinook Salmon populations with ≥20 samples detected at In-Stream PIT Detection Systems sites organized by genetic reporting unit for SY2021. The number of clusters and associated memberships were identified by discriminant analysis of principal components. Vertical lines correspond to individuals and colors represent different genetic clusters. Individuals are grouped based on the location of the Snake River steelhead population within a GSI reporting unit.

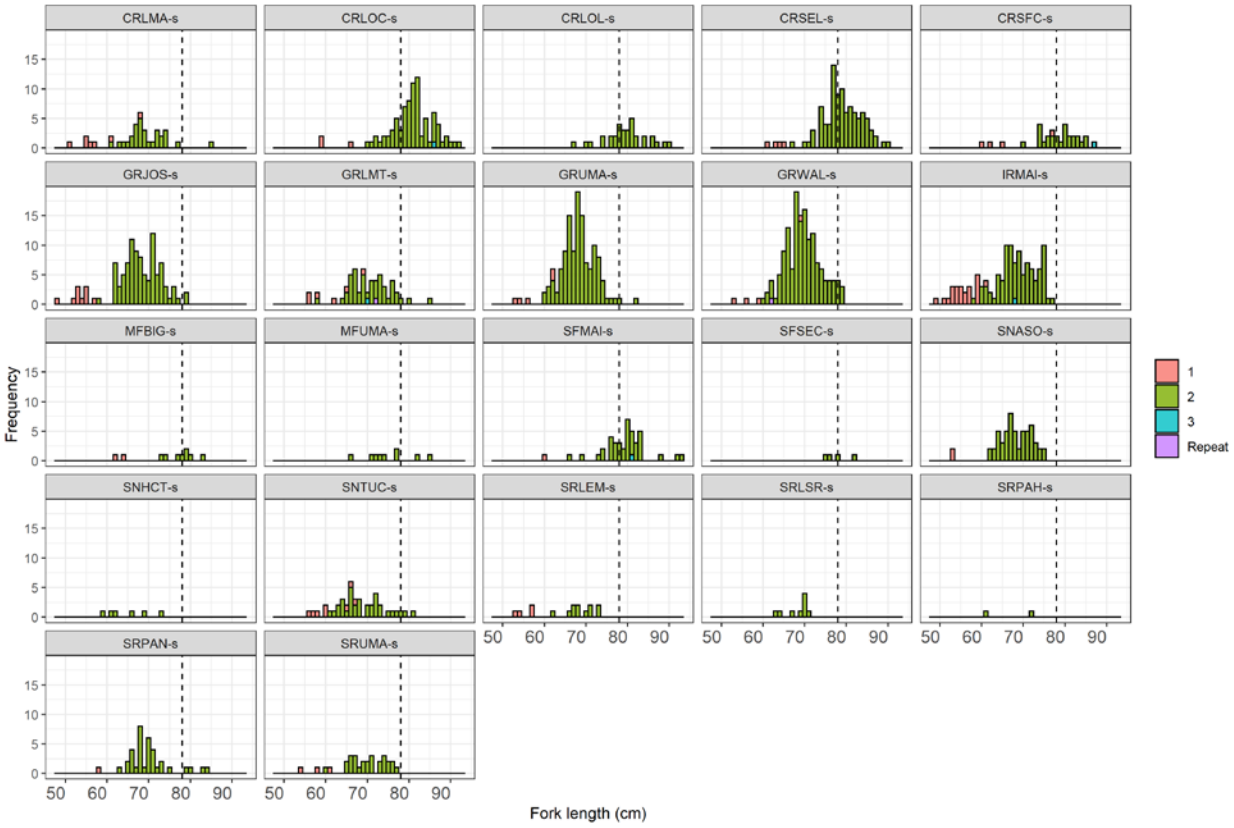
APPENDICES

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 SY2021.

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															
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	WEB, LAP, SWT, EPR, JA1	47	38	9	-	81	19	67.7	46	1	98	2	7	30	-	-	19	81	-	-	-	7	27	3	-	10	-	15	57	6	-	7/31/2020	9/5/2020	9/25/2020	10/9/2020	3/22/2021	0	0.296	0.306	98.3
CRLOC-s	LRU, FISTRP, LRL	132	105	27	-	80	20	80.7	25	98	20	80	3	81	1	-	4	95	1	-	-	2	44	38	1	47	-	2	33	29	1	9/17/2020	9/30/2020	10/13/2020	10/23/2020	4/22/2021	2	0.280	0.284	95.5
CRLOL-s	LC2, LC1	59	43	15	1	73	25	80.1	13	41	24	76	-	33	-	-	-	100	-	-	-	2	25	6	-	26	-	3	42	10	-	9/18/2020	9/27/2020	10/5/2020	10/26/2020	3/25/2021	1	0.277	0.281	96
CRSEL-s	SW2, SW1	165	134	31	-	81	19	78.9	59	91	39	61	4	96	-	-	4	96	-	-	-	3	48	49	-	65	-	2	29	30	-	9/12/2020	9/25/2020	10/2/2020	10/15/2020	3/10/2021	3	0.285	0.292	94.9
CRSFC-s	SC2, SC1	58	40	18	-	69	31	79.3	20	36	36	64	4	26	1	-	13	84	3	-	-	5	21	4	1	27	-	9	36	7	2	9/18/2020	9/27/2020	10/7/2020	11/9/2020	3/22/2021	1	0.274	0.281	96
GRJOS-s	JOC	148	108	40	-	73	27	67.8	143	4	97	3	10	94	-	-	10	90	-	-	-	11	78	15	-	44	-	7	53	10	-	7/24/2020	8/23/2020	9/24/2020	10/10/2020	3/22/2021	4	0.300	0.304	99.4
GRLMT-s	WEN	91	69	22	-	76	24	70.1	84	4	95	5	6	48	1	1	11	86	2	2	-	6	36	13	1	35	-	7	40	14	1	7/30/2020	8/27/2020	9/18/2020	10/8/2020	11/12/2020	2	0.295	0.302	99.4
GRUMA-s	UGR, LOOH, UGS, CATHEW, CCW, CCU	175	145	30	-	83	17	68.3	171	3	98	2	5	124	-	-	4	96	-	-	-	13	80	36	-	46	-	7	46	21	-	7/21/2020	8/20/2020	9/21/2020	10/8/2020	11/1/2020	1	0.306	0.309	100
GRWAL-s	WR2, MR1, BCANF, WR1, LOSTIW, WALH	199	146	53	-	73	27	69.4	190	5	97	3	4	144	-	1	3	97	-	1	1	7	89	52	-	50	1	4	45	26	-	7/24/2020	8/30/2020	9/30/2020	10/22/2020	4/28/2021	6	0.304	0.311	100
IRMAI-s	IR2, BSC, GCM, IR3, IR5, LSHEEF, COC, IR1, CZY, CAMP4C	177	141	36	-	80	20	67.1	175	1	99	1	23	94	1	-	19	80	1	-	-	9	83	26	-	59	-	5	47	15	-	8/3/2020	9/10/2020	9/25/2020	10/5/2020	4/8/2021	3	0.294	0.299	99.4
MFBIG-s	TAY	20	15	5	-	75	25	73	14	5	74	26	2	8	-	-	20	80	-	-	-	-	7	3	-	10	-	-	35	15	-	8/28/2020	9/7/2020	9/21/2020	9/29/2020	10/19/2020	2	0.293	0.287	89.2
MFUMA-s	MAR	13	9	4	-	69	31	76.9	9	4	69	31	-	9	-	-	-	100	-	-	-	-	2	7	-	4	-	-	15	54	-	8/20/2020	9/5/2020	9/20/2020	9/25/2020	10/7/2020	-	-	-	-
SFMAI-s	ESS, KRS, YPP	68	57	11	-	84	16	78.3	27	37	42	58	1	39	1	-	2	95	2	-	-	2	11	27	1	27	-	3	16	40	1	9/3/2020	9/17/2020	9/23/2020	10/1/2020	10/19/2020	2	0.291	0.298	96.6
SFSEC-s	ZEN	6	6	-	-	100	-	78.2	2	3	40	60	-	4	-	-	-	100	-	-	-	-	-	4	-	2	-	-	-	67	-	9/18/2020	9/23/2020	9/29/2020	9/30/2020	10/8/2020	-	-	-	-
SNASO-s	ACM, AFC, ACB, TENMC2, GEORGC, ALPOWC	80	65	15	-	81	19	67.6	80	0	100	0	2	55	-	-	4	96	-	-	-	13	38	6	-	23	-	16	48	8	-	7/14/2020	9/10/2020	9/27/2020	10/22/2020	4/1/2021	1	0.306	0.311	98.9
SNHCT-s	OXBO	9	7	2	-	78	22	66.3	9	0	100	0	-	6	-	-	-	100	-	-	-	2	4	-	-	3	-	22	44	-	-	8/12/2020	9/10/2020	9/17/2020	9/26/2020	10/5/2020	-	-	-	-
SNTUC-s	MTR, UTR, LTR, TFH, TPJ	59	41	18	-	69	31	68.6	55	3	95	5	8	34	-	-	19	81	-	-	1	8	30	3	-	17	2	14	51	5	-	7/29/2020	9/26/2020	10/10/2020	10/19/2020	4/9/2021	1	0.307	0.312	99.4
SRLEM-s	HYC, EVU, LLR, KEN, LRW	19	15	4	-	79	21	65.3	19	0	100	0	4	11	-	-	27	73	-	-	-	4	9	2	-	4	-	21	47	11	-	7/27/2020	8/31/2020	9/25/2020	10/6/2020	10/19/2020	-	-	-	-
SRLSR-s	WB1	17	11	6	-	65	35	67.1	17	0	100	0	-	9	-	-	-	100	-	-	-	1	6	2	-	8	-	6	35	12	-	7/30/2020	9/30/2020	10/6/2020	10/27/2020	4/27/2021	-	-	-	-
SRPAH-s	PAHH	4	4	-	-	100	-	66.2	4	0	100	0	-	2	-	-	-	100	-	-	-	-	2	-	-	2	-	-	50	-	-	9/23/2020	9/23/2020	9/27/2020	10/6/2020	10/10/2020	-	-	-	-
SRPAN-s	PCA	50	42	8	-	84	16	70.2	45	5	90	10	1	35	-	-	3	97	-	-	-	-	17	18	1	14	-	-	34	36	2	7/24/2020	8/19/2020	8/28/2020	9/12/2020	10/7/2020	1	0.299	0.299	98.9
SRUMA-s	VC2, YFK, SAWT	48	38	10	-	79	21	68.6	48	0	100	0	3	27	-	-	10	90	-	-	-	1	26	3	-	18	-	2	54	6	-	8/27/2020	9/16/2020	9/27/2020	10/7/2020	10/22/2020	1	0.293	0.295	97.7

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 SY2021 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 SY2021.

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	52	26	26	-	50	50	72.3	75.3	-	6	34	6	6	12	65	12	12	6	33	7	6	12	63	13	12	5/24/2021	6/7/2021	6/18/2021	7/7/2021	7/20/2021	1	0.22754	0.235	92.4
CRLOL	LC2	12	5	7	-	42	58	73.8	73.8	-	-	7	1	4	-	58	8	33	-	6	2	4	-	50	17	33	5/5/2021	5/7/2021	5/17/2021	5/21/2021	5/25/2021	-	-	-	-
GRCAT	CCW, CATHEW	24	14	10	-	58	42	66.9	68.2	-	2	19	1	2	8	79	4	8	2	19	1	2	8	79	4	8	5/4/2021	5/11/2021	5/17/2021	5/20/2021	5/27/2021	1	0.25174	0.246	84.7
GRLOO	LOOH	7	4	3	-	57	43	68.3	68.3	-	-	6	-	1	-	86	-	14	-	6	-	1	-	86	-	14	5/3/2021	5/5/2021	5/13/2021	6/3/2021	6/14/2021	-	-	-	-
GRLOS	LOSTIW	39	13	26	-	33	67	67.3	72.2	-	11	23	-	5	28	59	-	13	11	23	-	5	28	59	-	13	5/21/2021	6/3/2021	6/17/2021	7/8/2021	7/28/2021	1	0.23425	0.228	88.8
GRMIN	MR1	68	32	36	-	47	53	70.1	71.9	-	5	56	3	4	7	82	4	6	5	56	3	4	7	82	4	6	5/13/2021	5/20/2021	6/9/2021	6/22/2021	7/9/2021	-	0.24331	0.243	94.7
GRUMA	GRANDW, UGS	7	3	4	-	43	57	67.9	67.9	-	-	6	1	-	-	86	14	-	-	6	1	-	-	86	14	-	5/7/2021	5/7/2021	5/13/2021	5/18/2021	5/19/2021	-	-	-	-
GRWEN	WEN	25	9	16	-	36	64	62.7	67.1	-	6	18	-	1	24	72	-	4	6	17	1	1	24	68	4	4	5/10/2021	5/13/2021	5/18/2021	5/20/2021	6/7/2021	2	0.26445	0.271	92.9
IRBSH	BSC	11	7	4	-	64	36	76.6	78.4	-	1	4	6	-	9	36	55	-	1	4	6	-	9	36	55	-	5/5/2021	5/24/2021	5/28/2021	6/15/2021	7/1/2021	-	-	-	-
IRMAI	IMNAHW, IML, IR4, IR5, IR3	82	25	57	-	30	70	67.9	74.4	-	26	43	7	6	32	52	9	7	26	43	7	6	32	52	9	7	5/26/2021	6/11/2021	6/23/2021	7/9/2021	7/27/2021	1	0.23753	0.237	90.6
MFBEA	BRC	53	12	41	-	23	77	73.8	77.1	-	6	29	15	3	11	55	28	6	6	28	16	3	11	53	30	6	5/12/2021	5/19/2021	5/21/2021	5/28/2021	6/9/2021	-	0.21205	0.21	80
MFBIG	TAY	98	26	72	-	27	73	63.3	75.6	-	46	39	10	3	47	40	10	3	46	39	10	3	47	40	10	3	5/17/2021	6/2/2021	6/15/2021	6/30/2021	7/14/2021	2	0.21454	0.221	91.2
MFMAR	MAR	44	20	24	-	45	55	70.9	74.8	-	6	30	6	2	14	68	14	5	6	30	6	2	14	68	14	5	5/10/2021	5/17/2021	5/21/2021	5/28/2021	6/22/2021	-	0.22524	0.22	82.9
SCUMA	SC3, SC4	3	-	3	-	-	100	74.3	74.3	-	-	2	-	1	-	67	-	33	-	2	-	1	-	67	-	33	5/13/2021	5/13/2021	6/9/2021	6/15/2021	6/15/2021	-	-	-	-
SFEFS	JOHNSC, ESS, YPP	93	35	58	-	38	62	68.3	75.2	-	29	49	9	6	31	53	10	6	29	49	9	6	31	53	10	6	5/21/2021	6/3/2021	6/18/2021	6/29/2021	7/14/2021	2	0.22158	0.224	89.4
SFMAI	KRS, SALSFW	143	38	105	-	27	73	66.7	74.1	-	51	60	10	22	36	42	7	15	51	60	10	22	36	42	7	15	5/24/2021	6/4/2021	6/24/2021	7/8/2021	7/20/2021	2	0.22306	0.225	94.1
SFSEC	ZEN	101	35	66	-	35	65	69.1	72.9	-	20	73	2	6	20	72	2	6	19	74	2	6	19	73	2	6	5/25/2021	6/7/2021	6/15/2021	6/28/2021	7/13/2021	2	0.22345	0.222	88.8
SNTUC	UTR, TFH, LTR	6	5	1	-	83	17	70	70	-	-	5	-	1	-	83	-	17	-	5	-	1	-	83	-	17	5/10/2021	5/25/2021	6/3/2021	7/5/2021	7/14/2021	-	-	-	-
SRLEM	EVU, LRW, EVL, HYC, LLR	40	16	24	-	40	60	67.5	73.7	-	11	24	4	1	28	60	10	2	11	24	4	1	28	60	10	2	5/11/2021	5/19/2021	6/1/2021	6/22/2021	7/13/2021	-	0.22352	0.225	81.8
SRPAH	PAHH	23	9	14	-	39	61	69.7	74.7	-	5	16	2	-	22	70	9	-	5	16	2	-	22	70	9	-	5/31/2021	6/15/2021	6/22/2021	7/1/2021	7/6/2021	-	0.22615	0.228	75.9
SRPAN	PCA	18	7	11	-	39	61	68.1	73.3	-	6	9	3	-	33	50	17	-	6	9	3	-	33	50	17	-	5/13/2021	5/21/2021	6/2/2021	6/16/2021	7/1/2021	-	-	-	-
SRUMA	SAWT, RFL	57	27	30	-	47	53	71.1	76.2	-	12	33	10	2	21	58	18	4	10	34	11	2	18	60	19	4	5/19/2021	5/28/2021	6/3/2021	6/14/2021	7/2/2021	5	0.22152	0.229	85.3
SRVAL	VC2	19	1	18	-	5	95	71.1	71.1	-	-	16	1	2	-	84	5	11	-	16	1	2	-	84	5	11	5/5/2021	5/14/2021	6/15/2021	6/21/2021	6/24/2021	-	-	-	-
SRYFS	YFK	8	3	5	-	38	62	74.5	77.6	-	1	3	1	3	12	38	12	38	1	3	1	3	12	38	12	38	5/11/2021	5/12/2021	5/21/2021	6/30/2021	7/7/2021	-	-	-	-

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 SY2021 individuals with ocean age and length data are shown. A description of population names and associated details can be found in Table 3.

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