FISHERY RESEARCH

WILD JUVENILE STEELHEAD AND CHINOOK SALMON ABUNDANCE AND COMPOSITION AT LOWER GRANITE DAM, MIGRATORY YEAR 2022

ANNUAL REPORT

Photo: IDFG

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ABBREVIATIONS AND ACRONYMS

BPA	Bonneville Power Administration
CHMBLN	Chamberlain Creek Genetic Stock
CI	Confidence Interval
DPS	Distinct Population Segment
EFGL	Eagle Fish Genetics Lab
ESA	Endangered Species Act
ESU	Evolutionarily Significant Unit
FALL	Snake River Fall Chinook Salmon Genetic Stock
GRROND	Grande Ronde River Genetic Stock
GSI	Genetic Stock Identification
GT-seq	Genotyping-in-Thousands by Sequencing
HELLSC	Hells Canyon Genetic Stock
IDFG	Idaho Department of Fish and Game
IMNAHA	Imnaha River Genetic Stock
LGR	Lower Granite Dam
LOCLWR	Lower Clearwater River Genetic Stock
LOSALM	Lower Salmon River Genetic Stock
LSNAKE	Lower Snake River Genetic Stock
MFSALM	Middle Fork Salmon River Genetic Stock
MPG	Major Population Group
MY	Smolt Migration Year
NMFS	National Marine Fisheries Service
NOAA	National Oceanic and Atmospheric Administration
NWFSC	Northwest Fisheries Science Center
PBT	Parentage Based Tagging
PIT	Passive Integrated Transponder
PSMFC	Pacific States Marine Fisheries Commission
QCI	Quantitative Consultants, Inc.
SFCLWR	South Fork Clearwater River Genetic Stock
SFSALM	South Fork Salmon River Genetic Stock
SNP	Single Nucleotide Polymorphism
TUCANO	Tucannon River Genetic Stock
UPCLWR	Upper Clearwater River Genetic Stock
UPSALM	Upper Salmon River Genetic Stock
WDFW	Washington Department of Fish and Wildlife

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ABSTRACT

This report summarizes the abundance and composition of wild juvenile steelhead and yearling spring-summer Chinook Salmon emigrating at Lower Granite Dam in migration year 2022. We used systematic biological samples from the Juvenile Fish Facility to decompose each species by origin, age, sex, and genetic stock. We were unable to estimate the abundance of steelhead and yearling Chinook Salmon smolts in migration year 2020 due to no sampling during the Covid pandemic. Also, higher spill and low collection efficiencies in the juvenile trap in migration year 2021 contributed to analytical issues, resulting in unreliable abundance estimates. In migration year 2022, estimated wild steelhead emigration was 586,605 smolts which was below the 10-yr average and the lowest abundance estimate in the timeseries. The Grande Ronde River genetic stock had the highest relative abundance (29%) followed by the Upper Salmon River (15%). Sex ratios were female biased in six genetic stocks, contributing to the 69% female bias for the aggregate juvenile emigration. Ages ranged from one to five years with most smolts showing ages of 2 and 3 years. Estimated wild Chinook Salmon emigration was 659,961 yearling smolts which was below the 10-yr average and the second lowest abundance estimate in the timeseries. The Hells Canyon genetic stock had the highest relative abundance (48%) followed by the South Fork Salmon River (21%). Sex ratios were unbiased at the stock and aggregate levels.

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INTRODUCTION

Populations of steelhead *Oncorhynchus mykiss* and Chinook Salmon *O. tshawytscha* in the Snake River basin declined substantially following the construction of hydroelectric dams in the Snake and Columbia rivers. Raymond (1988) documented a decrease in the survival of emigrating steelhead and Chinook Salmon from the Snake River following the construction of dams on the lower Snake River during the late 1960s and early 1970s. Abundance rebounded slightly in the 1980s, but then adult escapement over Lower Granite Dam (LGR) into the Snake River basin declined again (Matthews and Waples 1991; Busby et al. 1996). Hatchery-origin steelhead and Chinook Salmon comprise most of the returning adults while returns of naturally produced fish remain critically low.

Snake River summer steelhead and spring-summer Chinook Salmon were classified as threatened under the Endangered Species Act (ESA) in 1997 and 1992, respectively. Within the Snake River steelhead distinct population segment (DPS), there are six major population groups (MPGs): Lower Snake River, Grande Ronde River, Imnaha River, Clearwater River, Salmon River, and Hells Canyon Tributaries (Table 1; ICBTRT 2003, 2005). The Hells Canyon MPG is considered extirpated. Twenty-four extant demographically independent populations have been identified within the DPS. Within the Snake River spring-summer Chinook Salmon evolutionarily significant unit (ESU), there are five MPGs: Lower Snake River, Grande Ronde/Imnaha Rivers, South Fork Salmon River, Middle Fork Salmon River, and Upper Salmon River (Table 1; ICBTRT 2003, 2005). Twenty-eight extant demographically independent populations have been identified within the ESU. Spring-summer Chinook Salmon from the Clearwater River basin are considered a re-introduced stock that is not protected under the ESA. There are two MPGs that comprise the Clearwater River basin: the Dry and Wet Clearwater. A population structure for the Clearwater has been proposed but not all are currently occupied (ICBTRT 2005).

Anadromous fish management programs in the Snake River basin include 1) large-scale hatchery programs intended to mitigate the impacts of hydroelectric dam construction and operation, and 2) recovery planning and implementation efforts aimed at recovering ESA-listed wild steelhead and salmon stocks. The long-range goal of the Idaho Department of Fish and Game (IDFG) anadromous fish program, consistent with basin-wide mitigation and recovery programs, is to preserve Idaho's salmon and steelhead runs and recover them to provide benefit to all users (IDFG 2019). Management to achieve these goals requires an understanding of how salmonid populations function as well as regular status assessments (McElhany et al. 2000). However, specific data on Snake River summer steelhead and spring-summer Chinook Salmon populations were lacking during ESA listing and in the first status reviews, particularly in key parameters such as population abundance, age structure, genetic diversity, recruits per spawner, and survival rates (ICBTRT 2003). Idaho Department of Fish and Game provides research, monitoring, and evaluation of the status of the state's populations of anadromous salmon and steelhead. Recommendations for monitoring populations across the Columbia River basin include: 1) annual estimation of juvenile emigrant abundance across major populations, and 2) estimation of the adult-to-juvenile productivity of emigrants (Crawford and Rumsey 2011).

The aggregate emigration of juvenile summer steelhead and spring-summer Chinook Salmon from the Snake River populations is sampled at LGR, except for the Tucannon River (Washington) populations. Some wild fish originate from Washington or Oregon tributaries, but the majority are from Idaho. Age, sex, and genetic stock composition data, obtained at the LGR juvenile fish trap, facilitate estimation of productivity and survival metrics that are important for monitoring the recovery of wild populations of both species.

We summarize the composition of wild juvenile Snake River summer steelhead (hereafter steelhead) and wild juvenile spring-summer Chinook Salmon (hereafter Chinook Salmon) emigrating at LGR during migration year (MY) 2022. The objectives of this report are to 1) estimate the total and stock-specific abundance of wild juvenile steelhead and yearling Chinook Salmon at LGR, 2) estimate age class- and sex-specific abundance within genetic stocks of wild juvenile steelhead and yearling Chinook Salmon at LGR, and 3) compare the aggregate and stock-specific abundance estimated in migration year 2022 to previous years. Abundance estimates in migration years 2020 and 2021 were excluded from the timeseries figures due to no sampling during the COVID pandemic and unreliable estimates (Copeland et al. 2024 in preparation), respectively. The productivity calculations were discontinued in this report since the methods need clarified and standardized across brood years. We plan to continue the productivity analysis in future reports once we establish a standard method.

METHODS

Juvenile Trap Operations at Lower Granite Dam

Samples of juvenile steelhead and Chinook Salmon passing LGR were collected during daily operation of the Juvenile Fish Facility by IDFG in cooperation with the Smolt Monitoring Program. The juvenile trap is located on the LGR juvenile bypass system, and it is operated annually from late March to late October. The trap captured a systematic sample of fish passing through the Juvenile Fish Facility by operating two trap gates according to a predetermined sample rate. The sample rate regulated how long the trap gates remain open, up to six times per hour. Although the trap was operational 24 hours per day, and fish were processed every morning seven days a week, we only took biological samples during the weekdays from March 28 to June 30. Additional details on the juvenile trap can be found in Mensik et al. (2010). Our weekday sample rate was predetermined daily to collect 250-750 fish per day (all species combined), depending on the expected daily number of fish entrained in the bypass system. Sample rates were not determined for weekend days because samples were not collected on weekends.

Standard methods found in Mensik et al. 2010 were used by PSMFC and IDFG staff to process juvenile fish. All captured fish were anesthetized, identified to species, examined for external marks, tags, and injuries, and scanned for an internal coded wire tag and passive integrated transponder tag. All fish were classified by origin (wild or hatchery) and the presence or absence of the adipose fin (hereafter ad-intact or ad-clipped). Wild fish have an intact adipose fin. Most hatchery-origin steelhead and Chinook Salmon have a clipped adipose fin, but some are released ad-intact for population supplementation purposes. Captured fish determined to be potentially wild were sampled for tissue (both species) and scales (steelhead only). The trap sample was sorted and processed by Smolt Monitoring Program personnel and fish deemed wild were passed to IDFG technicians. Fish that were PIT tagged, diseased or injured, or identified as fall Chinook Salmon (based on external morphology, Tiffan et al. 2000) were omitted. Target sample sizes were 2,000 per species for steelhead and yearling Chinook Salmon for the trapping season. All sampled fish were measured for fork length (FL, to the nearest millimeter). After processing, fish were returned to the bypass system to resume downstream migration or diverted to holding tanks for transportation downriver as part of the hydropower mitigation effort.

Scale samples were taken from juvenile steelhead above the lateral line and posterior to the dorsal fin (Wright et al. 2015). Scales were stored in coin envelopes for transport to the IDFG Nampa Research Anadromous Ageing Laboratory in Nampa, Idaho. Estimated ages were used to assign steelhead to a brood year for cohort analysis. Age of Chinook Salmon was estimated

as either age-1 yearlings or age-0 subyearlings based on length and external morphology, so scales were not needed to determine brood year (Camacho et al. 2017). Only age-1 yearlings were sampled. Tissue samples from both species were taken via a small clip of the caudal fin. Tissues were stored on Whatman sheets for transport to the IDFG Eagle Fish Genetics Laboratory (EFGL) in Eagle, Idaho. Lower Granite Dam juvenile trapping data were stored in and accessed from the Lower Granite Dam Trapping database. Scale ageing data were stored in and accessed from the BioSamples database.

Scale and Genetic Tissue Processing and Analysis

Technicians processed scale samples in the IDFG Nampa Research Anadromous Ageing Laboratory according to protocols detailed in Wright et al. (2015). Briefly, 6-10 non-regenerated scales from each sampled fish were cleaned and mounted between two glass microscope slides. The best scales were imaged at 40x magnification on a computer video monitor using a Leica DM4000B microscope and a Jenoptik Gryphax Arktur digital camera. Two technicians independently viewed each image to assign ages without reference to fish length. If there was no age consensus among the readers, a third reader viewed the image, and all readers collectively examined the image to resolve their differences before a final age was assigned. If a consensus age was not attained, the sample was excluded from further analysis. In this report, total age equals freshwater age, so we did not use the ageing designation developed for anadromous salmonids, which also accounts for time spent in the ocean, and instead reported age as an integer.

The EFGL used a methodology developed by scientists at the Columbia River Inter-Tribal Fish Commission (CRITFC) known as "Genotyping-in-Thousands by sequencing" (GT-seq). This involved the genotyping of single nucleotide polymorphism (SNP) genetic marker panels (50-500) on thousands of pooled individuals at a time (Campbell et al. 2015). These pooled reactions were made possible with sample-specific barcodes that were incorporated during the polymerase chain reaction (PCR) process. Following PCR, SNP amplicons were sequenced on an Illumina NextSeq DNA sequencer. Detailed methods for GT-seq library preparation and genotyping are provided in Campbell et al. (2015). The GT-seq panels consisted of 368 SNP markers for steelhead and 343 SNP markers for Chinook Salmon. Data for the SNP marker panels described above ('CRITFC/IDFG steelhead GTseq v5.0 368', 'CRITFC IDFG Chinook GTseq v4.0 343') can be accessed via the FishGen webpage (https://www.fishgen.net/Home.aspx). Detailed methods for DNA extraction, DNA amplification, and SNP genotyping are detailed in section 2 of Vu et al. (2015). Samples were processed at either the EFGL or the CRITFC's genetics laboratory in Hagerman, Idaho (BPA project 2010-026-00).

Parentage-based tagging (PBT) involves sampling and genotyping hatchery broodstock on an annual basis, with the resulting parental genotypes added to a genetic database (Steele et al. 2013; 2019). Subsequently, progeny of these parents (collected either as juveniles or adults) that are genotyped can be assigned back to their parents via parentage analysis. Beginning in MY 2012, parentage analysis was conducted on unmarked juveniles sampled at the LGR trap to identify hatchery fish that were phenotypically wild since they had no internal tags or external marks detected. Fin tissue was sampled from nearly all steelhead and spring-summer Chinook Salmon broodstock spawned at Snake River hatcheries in Idaho, Oregon, and Washington since 2008 (Steele et al. 2019). The near-complete sampling of all hatchery broodstock in the Snake River basin effectively "tagged" all hatchery-origin steelhead and Chinook Salmon. Parentage assignment using SNP genotypes was performed using the program SNPPIT (Anderson 2010). Fish assigning to hatchery parents were removed from analysis. The remainder were subjected to genetic stock identification.

Genetic stock identification (GSI) is a complimentary genetic technique to PBT that seeks to identify the source of origin of wild fish. Briefly, this technique involves genotyping wild fish sampled on the landscape and using these population-level allele frequencies to assign individual fish of unknown origin (e.g., juveniles sampled at LGR) to reporting groups (hereafter genetic stocks). Juvenile genotypes were analyzed against genetic baseline populations to assign each individual to the genetic stock in which the probability of its genotype occurring is the greatest (i.e., maximum probability of membership). A detailed description of the Chinook Salmon genetic baseline (v3.1) used can be found in Hargrove et al. (2022). The steelhead genetic baseline (v3.1) was developed by Vu et al. (2015), refined by Powell et al. (2018), and described in Hargrove et al. (2021) (Figure 1; Figure 2). Genetic stocks are assemblages of baseline populations grouped primarily by genetic and geographic similarities and secondarily by political boundaries and management units (Ackerman et al. 2012). Individuals were assigned to genetic stocks using the algorithms implemented in the R package rubias (Moran and Anderson 2019). Ten wild steelhead genetic stocks were used (Figure 1). The genetic stocks included: 1) UPSALM: Upper Salmon River (including Panther Creek and upstream); 2) MFSALM: Middle Fork Salmon River (including Chamberlain and Bargamin creeks); 3) SFSALM: South Fork Salmon River; 4) LOSALM: Little Salmon River and tributaries of the 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: tributaries of the Lower Snake River both above (e.g., Alpowa and Asotin creeks) and below (primarily Tucannon River) LGR. Some Tucannon River steelhead ascended LGR Dam and either stayed upriver to spawn or fell back and spawned downriver. Seven wild Chinook Salmon genetic stocks were used (Figure 2). The genetic stocks included: 1) UPSALM: Upper Salmon River (including North Fork Salmon River and upstream); 2) MFSALM: Middle Fork Salmon River; 3) CHMBLN: Chamberlain Creek; 4) SFSALM: South Fork Salmon River; 5) HELLSC: Hells Canyon stock, an aggregate genetic stock that includes the Clearwater, Little Salmon, Lower Salmon, Grande Ronde, Imnaha, and Lower Snake rivers; 6) TUCANO: Tucannon River; and 7) FALL: Snake River fall Chinook Salmon. Chinook Salmon populations in TUCANO can be distinguished from HELLSC in GSI analyses because they exhibit low levels of introgression with fall Chinook Salmon (Narum et al. 2010). The TUCANO genetic stock was included in the baseline to represent fish that originated below LGR which may be the progeny of Tucannon River adults that ascended the dam and stayed upriver to spawn. Except for the FALL and CHMBLN stocks, these genetic stocks largely correspond to Snake River spring-summer Chinook Salmon MPGs (Table 1). Three collections of Snake River fall Chinook Salmon (Clearwater River, Nez Perce Tribal Hatchery, and Lyons Ferry Hatchery) were included in the genetic baseline to distinguish fall Chinook Salmon from spring-summer Chinook Salmon (Ackerman et al. 2012). The CHMBLN stock is considered to be part of the Middle Fork Salmon River MPG.

The Genetic Monitoring of Snake River Salmonids project (2010-031-00) will continue to update the genetic baselines periodically, aiming to improve resolution. For example, Hargrove et al. *in press* described a new genetic baseline for steelhead which correctly assigned a higher percentage of individuals to their genetic stock of origin compared to the previous version. Further, the GSI project will continue to develop methods and evaluate available tools to assess and improve the accuracy and precision of genetic stock proportion and abundance estimates in the future. These efforts are reported separately in the annual progress reports (e.g., Harris et al. 2023). The accuracy of the sex-specific genetic assays was evaluated in Steele et al. (2016). Sex was not and generally cannot be reliably determined by personnel at the LGR trap; thus, a direct comparison between the sex identified at the trap and by the genetic assay was not attempted. Campbell et al. (2012) and references therein described in more detail the methods of sex-determination using genetic assays.

Emigration by Origin, Age, Sex, and Genetic Stock

Abundance estimates were made by modifying the methods in Steinhorst et al. (2017) to incorporate a hierarchical structure (Figure 3) and to quantify variance in the initial point estimate. Juvenile emigration abundance was estimated using 1) daily counts of putative wild juveniles collected in the LGR juvenile fish trap, 2) the trap sample rate (the proportion of time the trap is open), and 3) estimated daily collection efficiencies (probability of entrainment in the juvenile bypass system at the dam). The daily counts of all steelhead and Chinook Salmon juveniles at LGR during March-July as well as the daily trap sample rates were obtained from the Fish Passage Center (FPC, B. Chockley, personal communication). DeHart (2019) described juvenile collection procedures at LGR (also see http://www.fpc.org/documents/metadata/FPC_SMP_Metadata.html). The estimated daily juvenile collection (guidance) efficiencies were obtained from the Northwest Fisheries Science Center (NWFSC, Steve Smith, personal communication). Collection efficiencies for steelhead and yearling Chinook Salmon were estimated using procedures detailed in Sandford and Smith (2002).

First, an estimate of the total number of ad-intact juveniles emigrating past LGR was found by expanding the number of ad-intact juveniles caught in the trap each day by the probability that a juvenile was sampled. The total number of ad-intact juveniles were estimated as

$$N_s = \sum_{d=1}^{D} \frac{c_{sd}}{t_d \times e_{sd}} = \sum_{d=1}^{D} N_{sd}$$

where s is species (steelhead, yearling Chinook Salmon), d is day of the year, N_s is total abundance by species, c_{sd} is number of smolts collected in the trap by species and day, t_d is trap rate by day, e_{sd} is estimated guidance efficiency by species and day, N_{sd} is abundance by species and day, and D indicates the summation across days. Total abundance for each species during a MY was then estimated from the sums of daily estimates beginning at initiation of trapping until the date of last recorded passage. Note that the realized population sampling rate was the product of t_d and e_{sd} and changes almost daily. The t_d and c_{sd} estimates were obtained from the Fish Passage Center (B. Chockley, *pers. comm.*) and the e_{sd} estimates were obtained from the Northwest Fisheries Science Center (S. Smith, *pers. comm.*)

The total estimate of unmarked, untagged juveniles was then decomposed into estimates of wild (W) and ad-intact hatchery (HNC) juveniles using PBT analysis. Abundance estimates of HNC juveniles were included in Camacho et al. (2018b) but were excluded from the present report. The abundance of W juveniles was calculated by grouping the daily abundance estimates, N_{sd}, into strata consisting of T "statistical weeks" formed by combining adjacent weeks (if needed to obtain sufficient sample sizes). The weekly species abundance estimates were $(N_{s1}, N_{s2}, ..., N_{sT})$ where species abundance within a stratum t is calculated as: $N_{st} = \sum_{d \in t} N_{sd}$.

The rearing data were

$$R_{s1}, R_{s2}, ..., R_{sM}$$
$$t_1 e_{s1}, t_2 e_{s2}, ..., t_M e_{sM}$$

where R_s is the proportion of smolts of rear type R and species s, e_s is the species-specific guidance efficiency, t is the trap rate, and M is the number of juveniles trapped. The numbers 1, 2, and so forth indicate the stratum number. We divided the data into strata and obtained the expanded number of wild juveniles by dividing each juvenile k of species s by its daily probability of being sampled, p_{sk}, which is calculated as $t_k e_{sk}$. Note that we assume that each juvenile k of

species s trapped on day d have the same trap rate and guidance efficiency so $t_k e_{sk} = t_d e_{sd}$. Further, p_{sk} equals the probability of species s being sampled on day d (p_{sd}). The expanded number of juveniles f of species s that were W in stratum t was

$$f_{sWt} = \sum_{k \in t} \frac{\delta_{Rk}}{t_k e_{sk}}$$

where δ_{Rk} is 1 if R is wild and 0 otherwise giving the table:

Rear/Stratum	1	2	…	T	
HNC	f_{sHNC1}	f_{sHNC2}	…	f_{sHNCT}	#HNC#
W	f_{sW1}	f_{sW2}		f_{sWT}	#W#
Column total	#1	#2	…	#T	#

Dividing by the marginal column totals, #1, #2,…,#T yielded proportions HNC and W by strata, p_{sRt}. If we wanted a pooled proportion, then we would use #HNC/# and #W/#.

For each stratum, we multiplied the proportion W (or HNC) by the estimate of total juveniles of species to yield the abundance of W and HNC within each stratum. We summed abundances across strata to yield total abundance of W and HNC as

$$W = \sum_{t=1}^{T} p_{sWt} N_{st} \text{ and } HNC = \sum_{t=1}^{T} p_{sHNCt} N_{st}$$

where T is the number of strata, t is an individual stratum, p_{sWt} is the proportion of species s that is W in stratum t, p_{sHNCt} is the proportion of species s that is HNC in stratum t, and N_{st} is the total number of juveniles of species s in stratum t.

This method to estimate total W and HNC emigration was preferred if proportion W (or HNC) varies over the season and if there were sufficient samples to get stable estimates of proportion W (or HNC) by strata. Otherwise, one might use the pooled estimates of proportion wild.

The W emigration estimates of species s by stratum $(W_{s1}, W_{s2}, …, W_{sT})$ were then decomposed by a PRIMARY category (usually genetic stock). Genetic stock proportions may change throughout the trapping season, but we assumed the genetic stock proportions were roughly equal within a stratum. We would like to know the true proportions, e.g., of genetic stocks A to E $(\pi_{At}, \pi_{Bt}, \pi_{Ct}, \pi_{Dt}, \pi_{Et})$ for t = 1, where T is the number of strata. If all W trapped juveniles were analyzed, then we could compute estimates of the proportions $(\pi_{At}, \pi_{Bt}, \pi_{Ct}, \pi_{Dt}, \pi_{Et})$ as above for W and HNC. However, not all trapped juveniles were analyzed every day so the realized capture rate of a group of fish analyzed on day d is $t_d \times e_{sd} \times \frac{a_{sd}}{c_{sd}}$ where c_{sd} is number of smolts collected in the trap by species and day, and a_{sd} is the species-specific number of juveniles analyzed on day d. If a_{jd} is the number of W fish of group j on day d, we get an estimate of the number of Wild juveniles of each group for stratum t as

$$A_{jt} = \sum_{d \text{ in } t} \frac{a_{jd}}{t_d \times e_{sd} \times \frac{a_{sd}}{c_{sd}}} = \sum_{d \text{ in } t} \sum_{fish\, k \text{ on } day\, d} \frac{\delta_j}{t_k \times e_{sk} \times \frac{a_{sd}}{c_{sd}}}$$

where $\delta_j = 0$ except for fish of group A_j when $\delta_j = 1$. Note that we assumed that all fish of species s analyzed on a given day had the same trapping rate and collection efficiency so $t_k \times e_{sk} = t_d \times e_{sd}$ and the second summation on the right sums to $a_{jd}/(t_d \times e_{sd} \times \frac{a_{sd}}{c_{sd}})$ as indicated.

Except for the addition of the realized tissue sampling rate, $\frac{a_{sd}}{c_{sd}}$, we obtained the expanded group by stratum table as above for W and HNC,

Group/Stratum	1	2	…	T
A	A_{11}	A_{12}	…	A_{1T}
B	A_{21}	A_{22}	…	A_{2T}
...	…	…	…	…
E	A_{51}	A_{52}	…	A_{5T}
Column total	#1	#2	…	#T

Dividing by the column totals, we obtained estimates of the group proportions, π_{jt}, by stratum. The strata proportions were applied to the estimated total W emigration estimate for each week. Summing over strata provided an estimate of the numbers of W fish for each group $(A_A, \dots, A_E)$. Note that strata were formed to try to provide a minimum sample size of approximately 100 analyzed fish per stratum. If there is a SECONDARY classification variable, then the A_{jt} expanded frequency table above is 3-dimensional where A_{ijt} is calculated as A_{jt} above with SECONDARY dimension i. For a given stratum and primary category, there may be no data for the secondary category. In this case the expanded frequencies were pooled over strata and a pooled estimate of the SECONDARY proportions was computed for each level of the PRIMARY variable. Using this hierarchical structure constrained point estimates for each subsequent variable to sum to its relevant parent class. For example, all abundance estimates by age for a given stock will sum to the abundance of that stock. Similarly, all stock estimates will sum to the relevant rear-type abundance and W and HNC rear types will sum to the total estimate of ad-intact smolts at LGR (Figure 3).

Confidence intervals for all point estimates were computed using a bootstrapping algorithm (Manly 1997). There were three sources of sampling error in the decomposed emigration estimates: variance in the estimated number of fish trapped each day, variance in the proportion W by stratum, and variance in estimates of age, sex, and genetic stock proportions. To account for these sources of variability when estimating abundance by age, sex, and genetic stock, we used a compound bootstrap routine: a parametric bootstrap by stratum, and a weighted nonparametric bootstrap by stratum of the biological sample data (age, sex, and genetic stock). The number of juveniles trapped per day was considered a series of Bernoulli trials, where N_d was the true number of juveniles passing the trap for day d and each juvenile was trapped with probability $t_d e_{sd}$. A bootstrap value of trap catch c for day d was generated by taking a random value from $c_d^* \sim Binomial(N_{sd}, p_{sd})$, where $p_{sd} = t_d \times e_{sd}$ as above. Given a bootstrap value for the number of juveniles trapped on day d, we got a bootstrap value for the number of juveniles arriving on day d as $N_{sd}^* = c_{sd}^*/p_{sd}$. Summing over days in a stratum, we got a bootstrap value for the total number of juveniles emigrating during each stratum $(N_{s1}^*, N_{s2}^*, \dots, N_{sT}^*)$. For each stratum, we got a bootstrap estimate of the proportion W in the stratum using a weighted nonparametric bootstrap for the data for that stratum with weights p_k where k indexes fish in stratum t. Note that $p_{sk} = p_{sd}$ for all trapped fish on day d. This led to bootstrap values f_{sWt}^* and hence bootstrap proportion W for each stratum. Multiplying these proportions by the bootstrap

estimates of total juveniles emigrating during each stratum yielded bootstrap estimates of number W by stratum. Summing across strata, we obtained bootstrap estimates of total W.

Given the bootstrap values for total W juveniles, we generated bootstrap values for the *numbers* of juveniles of each age, sex, and genetic stock if we generated bootstrap values for the *proportions* of juveniles in each respective group for each stratum. We did this by producing bootstrap values A_{jt}^* (or A_{ijt}^*) via a weighted bootstrap of the age, sex, or genetic stock data for that stratum with weights $t_k \times e_{sk} \times \frac{a_d}{c_{sd}}$. These were converted to proportions and bootstrap estimates of numbers of W fish by age, sex, or genetic stock by stratum were found by multiplying these proportions by the bootstrap estimates of total W juveniles for each stratum. We then summed over strata to obtain season-long bootstrap estimates of numbers of juveniles by age, sex, and genetic stock. We conducted the compound bootstrap procedure 5,000 times. For each iteration, the numbers of W fish of various ages, sex, or stock were computed. The one-at-a-time bootstrap intervals were found by finding the 5th and 95th percentiles of the 5,000 ordered bootstrap values for each group (i.e., α = 0.10). The algorithm was written and implemented in the R programming environment (R Development Core Team 2021) by Kirk Steinhorst (University of Idaho) and can be found within the SCOBI package (https://github.com/mackerman44/SCOBI) as the SCRAPI function. If the reader is interested in accessing these data, please submit a data request at https://idfg.idaho.gov/species/request-data.

RESULTS

Wild Steelhead Emigration

The first and last wild steelhead smolt were captured on March 28 and June 30, 2022, respectively. There were 1,221 wild steelhead smolts sampled for analysis, of which 1,154 (95%) yielded a genetic stock, sex, and age. An additional 20 ad-intact hatchery-origin smolts were sampled but not used. Estimated wild steelhead emigration was 586,605 smolts (549,501–623,929 90% confidence interval (CI); Figure 4; Appendix A-1 and B-1). This aggregate abundance estimate was below the 10-yr average (MY2010-2019) and the lowest in the timeseries (Figure 4).

The Grande Ronde River stock had the highest abundance at 171,841 smolts (147,607–194,418 90% CI) or 29% of the total, followed by the Upper Salmon River stock at 86,085 smolts (63,662–98,069 90% CI) or 15% of the total (Appendix B-1 and B-2). The Lower Salmon River stock had the lowest abundance at 9,872 smolts (3,677–18,368 90% CI) or 2% of the total (Appendix B-1). Six of the ten stocks (i.e, LOCLWR, LOSALM, MFSALM, SFCLWR, UPCLWR, and UPSALM) showed the lowest abundance in MY2022 compared to other migration years in the timeseries (Appendix B-2).

Females comprised 69% of the total wild steelhead smolts (Appendix B-1 and B-3). Within genetic stocks, female sex ratios ranged from 62% in the Grande Ronde River stock to 81% in the South Fork Salmon River stock (Appendix B-1 and B-4).

Overall, smolt ages ranged from 1 to 5 years. Age-2 was the most abundant age class followed by age-3, comprising 60% and 29% of smolts, respectively (Appendix B-5). This latter trend occurred in all stocks except the Middle Fork Salmon River and Upper Clearwater River in which age-3 was the most abundant age class followed by age-2 (Appendix B-6).

Wild Yearling Chinook Salmon Emigration

Like steelhead, the first and last wild Chinook Salmon smolt were captured on March 28 and June 30, 2022, respectively. There were 1,071 wild Chinook Salmon smolts sampled for analysis, of which 1,040 (97%) yielded a genetic stock and sex. An additional 525 ad-intact hatchery-origin smolts were sampled but not used. Estimated emigration of wild Chinook Salmon was 659,961 yearling smolts (628,530–691,997 90% CI; Appendix A-2). This aggregate abundance estimate was below the 10-yr average (MY2010-2019) and the second lowest in the timeseries (Figure 4).

The Hells Canyon stock had the highest abundance at 319,715 smolts (291,611–347,311 90% CI) or 48% of the total, followed by the South Fork Salmon River stock at 136,087 smolts (127,815–167,943 90% CI) or 21% of the total (Appendix C-1 and C-2). The Chamberlain Creek stock had the lowest abundance at 13,863 smolts (5,592–19,064 90% CI) or 2% of the total. In previous years, juveniles produced from Tucannon River adults that strayed and spawned above LGR were detected at LGR, but juveniles from the Tucannon River stock were not detected in MY2022. The Upper Salmon River stock showed the lowest abundance in MY2022 compared to other migration years in the timeseries (Appendix C-2). The difference in juvenile male and female abundance within each genetic stock and at the aggregate level was statistically insignificant (i.e. 90% CIs overlapped; Appendix C-1 and C-4).

DISCUSSION

We provide a stock assessment of wild juveniles emigrating in 2022 using genetic stock identification for the Snake River steelhead DPS and spring-summer Chinook Salmon ESU (exclusive of the Tucannon River). This report continues the data series developed in Camacho et al. (2018b) which included juvenile emigration estimates within and across genetic stocks, and the implementation of PBT to distinguish ad-intact hatchery fish from wild fish (Steele et al. 2018).

In this analysis, we assumed that the realized sampling rate adequately described the probability that any fish passing Lower Granite Dam (LGR) could be sampled. There are three possible exceptions to this assumption. First, we assumed there was no size bias in collection at LGR (i.e., larger juveniles were less likely to enter the juvenile by-pass system); however, evidence for and against size bias has been presented in the peer-reviewed literature (e.g., see Faulkner et al. 2019 and Storch et al. 2021). Second, PIT-tagged fish were counted but not sampled so populations with a high rate of PIT tagging may be underrepresented in this analysis. Third, sub-yearling and holdover yearling fall Chinook Salmon smolts that were phenotypically distinct from spring-summer Chinook Salmon smolts (Tiffan et al. 2000) were not sampled at the trap. Further, Fall Chinook Salmon estimates presented here do not represent their total emigration.

The 2020 Record of Decision for operations on the Columbia River System set dam-specific spill levels at a higher proportion of total flow than in the past. The increased spill proportion at LGR has greatly decreased collection efficiencies in the juvenile bypass system. Further, the spill proportion in MY2021 was considerably higher than the 10-yr average, contributing to below average daily collection efficiencies (Copeland et al. 2024 in preparation). The model described in Sandford and Smith (2002) could be substantially overestimating collection efficiencies during higher spill, resulting in underestimations of abundance (Copeland et al. 2024 in preparation). Recent modeling efforts show that the probability of smolt passage in the powerhouse (turbines and juvenile bypass system) was generally affected by discharge,

forebay temperature, smolt size, diel period, and approach location (Harnish et al. 2023). The accuracy of collection efficiencies was improved by models that account for the effects of variation in spill proportion and flow on the probability of smolt passage in bypass systems on the Columbia River (McCann et al. 2015). The McCann models were updated with new data for many sites, including data collected during years with high spill (i.e., 2019-2022; McCann et al. 2023).

Most Snake River steelhead and Chinook Salmon stocks spawn above LGR with three notable exceptions. First, Snake River fall Chinook Salmon spawn upstream and downstream of LGR. Most fall Chinook Salmon emigrate as subyearling smolts and although they are counted, they are not sampled at LGR. Morphological traits are used to distinguish yearling and subyearling Chinook Salmon. Second, the Tucannon River population of spring-summer Chinook Salmon originates downstream of LGR. Emigration estimates of yearling Chinook Salmon from the Tucannon River stock reported for earlier years represented the number of offspring that were produced from adults originating from the Tucannon River that strayed and reproduced upstream of LGR. Tucannon River populations demonstrate slight evidence for introgression (5.3%) with fall Chinook Salmon (Narum et al. 2010) and are generally highly identifiable (Ackerman et al. 2012). Third, some wild steelhead belonging to the Lower Snake River genetic stock spawn in Asotin Creek (61 rkm upstream from LGR) and in minor tributaries of the LGR reservoir (e.g., Alpowa Creek). Further, many steelhead from the Tucannon River stray far above LGR to spawn (Bumgarner and Dedloff 2011). The production of steelhead and Chinook Salmon populations that do not spawn exclusively above LGR is incomplete in this report, but they must be identified for accurate assessment of the other Snake River stocks.

Quantifying spatiotemporal and biological variation in freshwater production of salmon and steelhead is important to understanding population dynamics. Steelhead and Chinook Salmon exhibit variable life history strategies both in freshwater and saltwater environments. The increased diversity of life history traits such as age-at-migration and sex bias in anadromy increases resiliency and can benefit a species' persistence by spreading risk across space and time (Copeland et al. 2017; Quinn 2018; Dobos et al. 2020). Further, spatiotemporal diversity in juvenile habitat use and life history traits buffers against the risk of stochastic events such as droughts, fire, and erosion that could lead to year class failures. For example, a cohort of spring-summer Chinook Salmon juveniles typically emigrates in a single year, making them potentially more susceptible to stochastic events. We found that Snake River steelhead juveniles can rear in freshwater environments for one to five years prior to emigrating to the ocean, making ontogenetic shifts in habitat use during their freshwater rearing stage (e.g., from tributary to mainstem rivers, Dobos et al. 2020). Also, sex can impact whether a fish undergoes an anadromous life history strategy. Theory suggests that females benefit from anadromy by attaining larger adult body sizes and higher fecundity while males can successfully mature and reproductively compete in a non-anadromous form (Hendry et al. 2004). Given this, we expected a female bias in juvenile emigration and found evidence for this in steelhead juveniles. The fitness of a particular life history strategy may vary with fish density, frequency of other life history types, and condition of individuals (Hendry et al. 2004) which can change with time and location. Juvenile sex ratios varied among stocks and could be impacted by rearing habitat. For example, some tributaries can produce more female emigrants than others within the same watershed (Mills et al. 2012). Further, analyses at smaller spatial scales could determine these mechanisms for emigrating juveniles which is a convenient and meaningful life stage to consider recruitment (Solomon 1985).

Accurately quantifying the abundance of a juvenile steelhead cohort is difficult due to their life history diversity. We found a maximum age at juvenile emigration to be five years, but age estimates from adult scales show that juveniles can emigrate at age-6 (Camacho et al. 2017). Extended freshwater rearing times elongate the timeframe to consider a juvenile abundance

estimate complete for a single brood year. The aggregate emigration at LGR was composed of mostly age-2 smolts followed by age-3 smolts. The abundance of age-2 and age-3 smolts across stocks was driven by the two most abundant genetic stocks, the Grand Ronde River and the Upper Salmon River, that produce relatively stable numbers of age-3 smolts, but variable numbers of age-2 smolts across migration years (Appendix B-6). Higher interannual variability in the abundance of age-2 smolts than in age-3 smolts at the aggregate level is an emerging pattern (Appendix B-5). Also, an unknown portion of steelhead remain in their natal stream (i.e., residualize) and are never quantified, reducing the juvenile abundance estimates for a single cohort. Resident *O. mykiss* females could affect the true stock-recruitment relationship (Berntson et al. 2011 and Courter et al. 2013). Unfortunately, feasible methods to assess the rate of residualization for steelhead in the Snake River basin are lacking.

The juvenile emigration estimates reported here will be used to assess the abundance, productivity, and status of wild steelhead and spring-summer Chinook Salmon across the Snake River basin. We aimed to measure juvenile emigration at a basin-wide scale which should be considered complementary to the intensive smaller scale juvenile sampling with rotary screw traps (e.g., Young et al. 2023) in the Snake River basin. We found that the aggregate abundance of steelhead and spring-summer Chinook Salmon in MY2022 was below the 10-yr average (MY2010-2019). This is probably related to recent adult returns that are also below the 10-year average (NPT 2022). The combination of juvenile and adult compositional analyses at LGR (Camacho et al. 2017, 2018a, 2019b) can allow us to assess the status and productivity of specific reporting groups (e.g., MPGs and genetic stocks) at the juvenile and adult life stages. In the future, estimates within this report will be combined with those in other datasets to explore relationships leading to a better understanding of how Snake River steelhead and spring-summer Chinook Salmon populations function.

RECOMMENDATIONS

- Adopt a standardized method to calculate productivity (the number of smolts per female available for natural reproduction) within brood years. Apply this method to prior and future productivity analyses
  - Consider variable productivity and pre-spawn mortality by rear-type (wild vs. hatchery)
  - Assess stock-recruit relationships at the aggregate and stock level for spring-summer Chinook Salmon (exclude MY2020 and MY2021)

- Continue scale and tissue sampling at LGR for age and stock composition estimates

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TABLES

Table 1.   Major population groups and independent populations within the Snake River steelhead distinct population segment (DPS) and spring-summer Chinook Salmon evolutionary significant unit (ESU; ICBTRT 2003, 2005).

Snake River steelhead DPS	
Major population group	**Population name**
Lower Snake River	1. Tucannon River 2. Asotin Creek
Grande Ronde River	3. Lower Grande Ronde River 4. Joseph Creek 5. Wallowa River 6. Upper Grande Ronde River
Imnaha River	7. Imnaha River
Clearwater River	8. Lower Clearwater River 9. North Fork Clearwater River (extirpated) 10. Lolo Creek 11. Lochsa River 12. Selway River 13. South Fork Clearwater River
Salmon River	14. Little Salmon River 15. Chamberlain Creek 16. South Fork Salmon River 17. Secesh River 18. Panther Creek 19. Lower Middle Fork Salmon River 20. Upper Middle Fork Salmon River 21. North Fork Salmon River 22. Lemhi River 23. Pahsimeroi River 24. East Fork Salmon River 25. Upper Salmon River
Hells Canyon Tributaries (extirpated)	

Table 1. Continued.

Snake River spring-summer Chinook Salmon ESU	
Major population group	**Population name**
Lower Snake River	1. Tucannon River
	2. Asotin Creek (extirpated) [a]
Grande Ronde/Imnaha Rivers	3. Wenaha River
	4. Lostine River
	5. Minam River
	6. Catherine Creek
	7. Upper Grande Ronde River
	8. Imnaha River
	9. Big Sheep Creek (extirpated) [a]
	10. Lookinglass Creek (extirpated) [a]
South Fork Salmon River	11. Little Salmon River
	12. South Fork Salmon River
	13. Secesh River
	14. East Fork South Fork Salmon River
Middle Fork Salmon River	15. Chamberlain Creek
	16. Lower Middle Fork Salmon River
	17. Big Creek
	18. Camas Creek
	19. Loon Creek
	20. Upper Middle Fork Salmon River
	21. Sulphur Creek
	22. Bear Valley Creek
	23. Marsh Creek
Upper Salmon River	24. North Fork Salmon River
	25. Lemhi River
	26. Upper Salmon River Lower Mainstem
	27. Pahsimeroi River
	28. East Fork Salmon River
	29. Yankee Fork Salmon River
	30. Valley Creek
	31. Upper Salmon River Upper Mainstem
	32. Panther Creek (extirpated) [a]
Dry Clearwater River (extirpated) [a]	33. Potlatch River (extirpated) [a]
	34. Lapwai Creek (extirpated) [a]
	35. Lawyer Creek (extirpated) [a]
	36. Upper South Fork Clearwater River (extirpated) [a]
Wet Clearwater River (extirpated) [a]	37. Lower North Fork Clearwater River (extirpated)
	38. Upper North Fork Clearwater River (extirpated)
	39. Lolo Creek (extirpated) [a]
	40. Lochsa River (extirpated) [a]
	41. Meadow Creek (extirpated) [a]
	42. Moose Creek (extirpated) [a]
	43. Upper Selway River (extirpated) [a]

[a]   Reintroduced fish exist in extirpated areas except the North Fork Clearwater River.
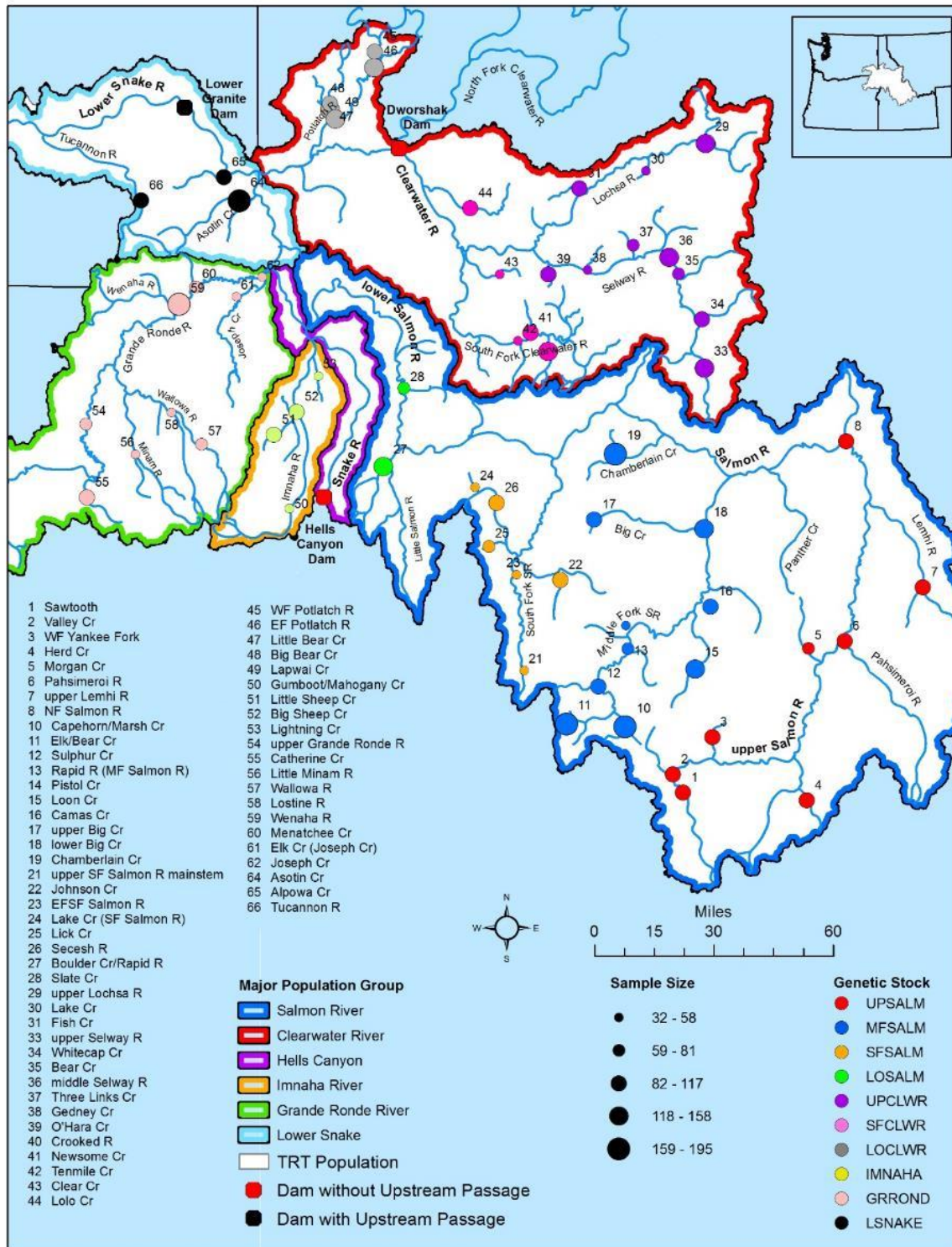
FIGURES

Figure 1. Genetic stocks and baseline collections used for steelhead mixed stock analysis at Lower Granite Dam since 2016 (Powell et al. 2018). The Hells Canyon Tributaries major population group (shaded purple) does not support independent populations and is considered extirpated (NMFS 2011). See text for genetic stock abbreviations.
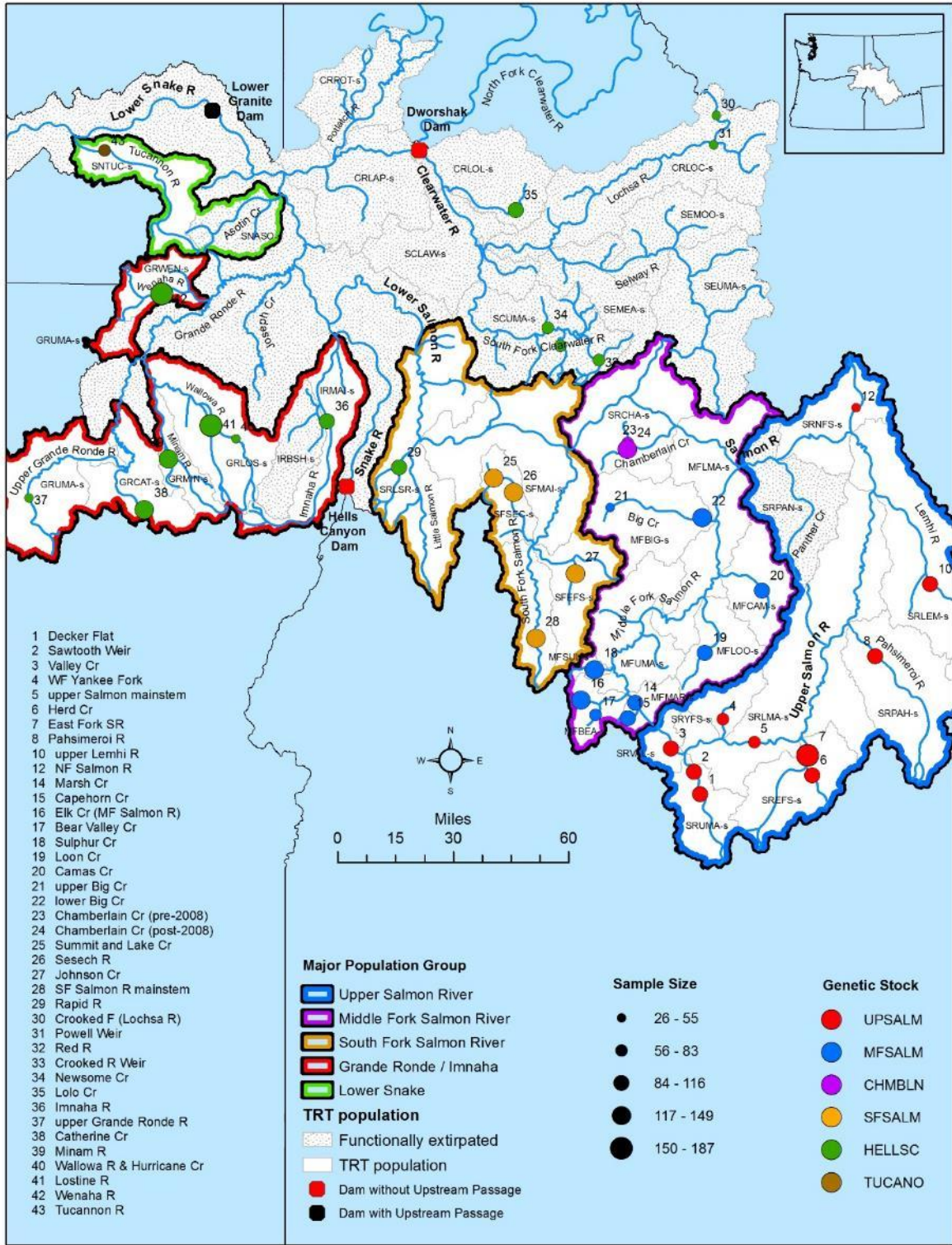
Figure 2.   Genetic stocks and baseline collections used for Chinook Salmon mixed stock analysis at Lower Granite Dam since 2016 (Powell et al. 2018). Reintroduced fish exist in functionally extirpated populations as mapped. See text for genetic stock abbreviations.
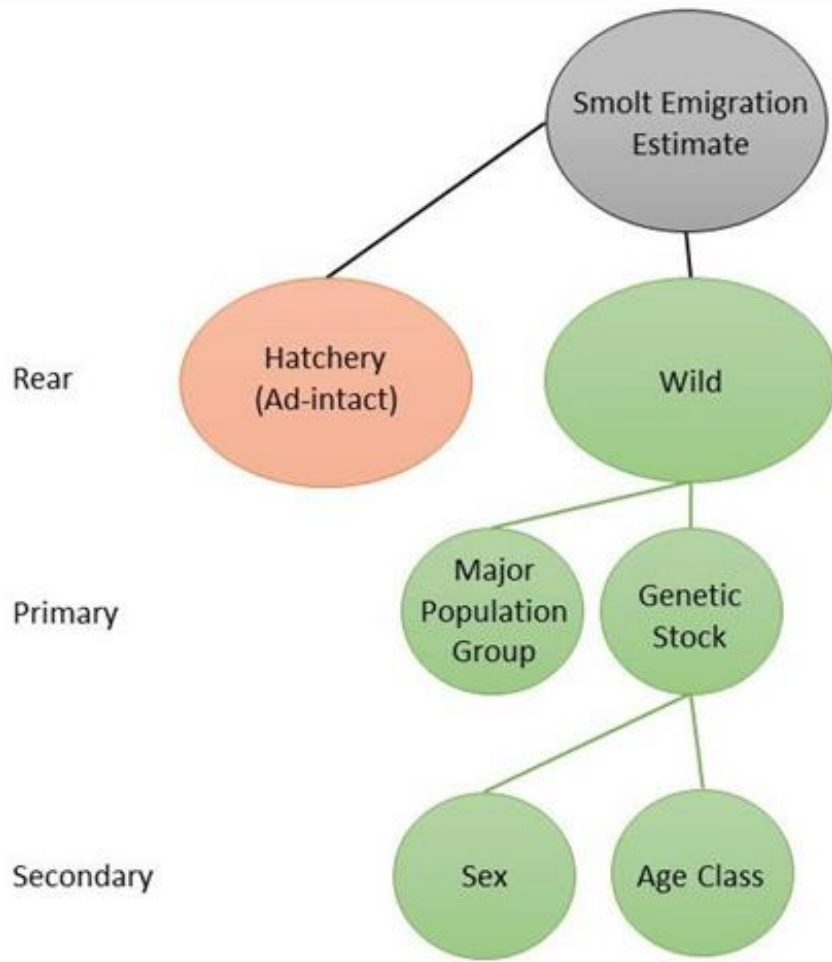
Figure 3. Schematic of the juvenile companion model (SCRAPI) to the adult Salmonid Compositional Bootstrap Intervals (SCOBI) decomposition model for Lower Granite Dam.
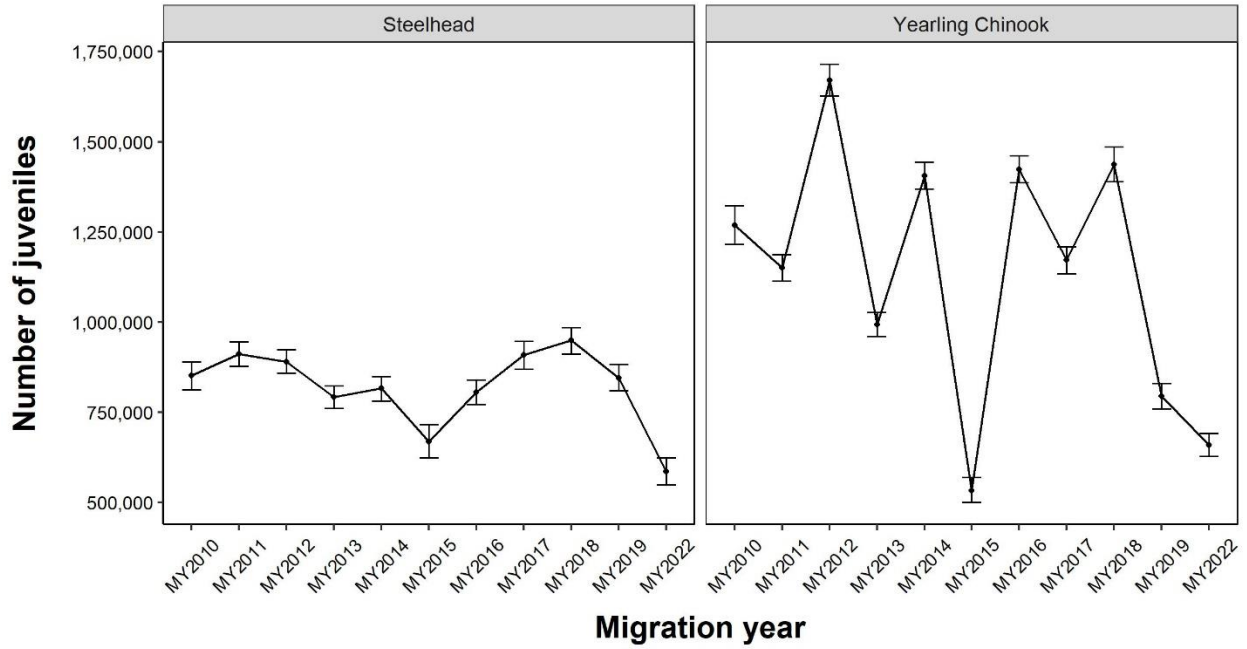
Figure 4.   Abundance of wild juvenile steelhead and yearling Chinook Salmon emigrating at Lower Granite Dam from 2010 to 2022. Confidence intervals are at 90%. Abundance estimates in migration years 2020 and 2021 were excluded from the timeseries figures due to no sampling during the COVID pandemic and unreliable estimates (Copeland et al. 2024 in preparation), respectively.

APPENDICES

Appendix A: Juvenile trapping operations at Lower Granite Dam in migration year 2022.

Appendix A-1. Weekly Fish Passage Center trap collection details and valid trap samples of juvenile steelhead at Lower Granite Dam in migration year 2022.

SCRAPI strata	Statistical week	Sampling period	Days trap open	Days bio sample taken	Wild estimate	Wild fish trapped	Genetic stock	Sex	Age
						Number of valid samples used in SCRAPI analysis			
1	13-19[a]	3/26-5/8	32	27	147,908	351	198	198	186
2	20	5/9-5/15	5	5	235,247	263	226	226	220
3	21	5/16-5/22	5	5	61,975	224	157	157	146
4	22	5/23-5/29	5	5	52,590	285	172	172	169
5	23	5/30-6/5	5	5	49,000	226	157	157	153
6	24	6/6-6/12	5	5	23,612	207	150	150	146
7	25-27[a]	6/13-6/30	14	14	16,273	192	142[a]	142	134
Total			71	66	586,605	1,748	1,202	1,202	1,154

[a] Statistical weeks are grouped to try to provide a minimum sample size of 100 valid fish with a genotype, sex, and age while maintaining relatively similar sample sizes among strata.

Appendix A-2. Weekly Fish Passage Center trap collection details and valid trap samples of yearling Chinook Salmon at Lower Granite Dam in migration year 2022.

SCRAPI strata	Statistical week	Sampling period	Days trap open	Days bio sample taken	Number of valid samples used in SCRAPI analysis			
					Wild estimate	Wild fish trapped	Genetic stock	Sex
1	13-15[a]	3/26-4/10	10	10	22,677	760	120	120
2	16	4/11-4/17	5	5	19,074	311	112	112
3	17-19[a]	4/18-5/8	17	15	191,878	556	180	179
4	20	5/9-5/15	5	5	230,705	273	159	159
5	21	5/16-5/22	5	5	69,461	240	124	124
6	22	5/23-5/29	5	4	72,437	397	137	137
7	23-24[a]	5/30-6/12	10	10	45,295	215	124	124
8	25-27[a]	6/13-6/30	14	13	8,434	121	85	85
Total			71	67	659,961	2,873	1,041	1,040

[a] Statistical weeks are grouped to try to provide a minimum sample size of 100 valid fish with a genotype and sex while maintaining relatively similar sample sizes among strata.
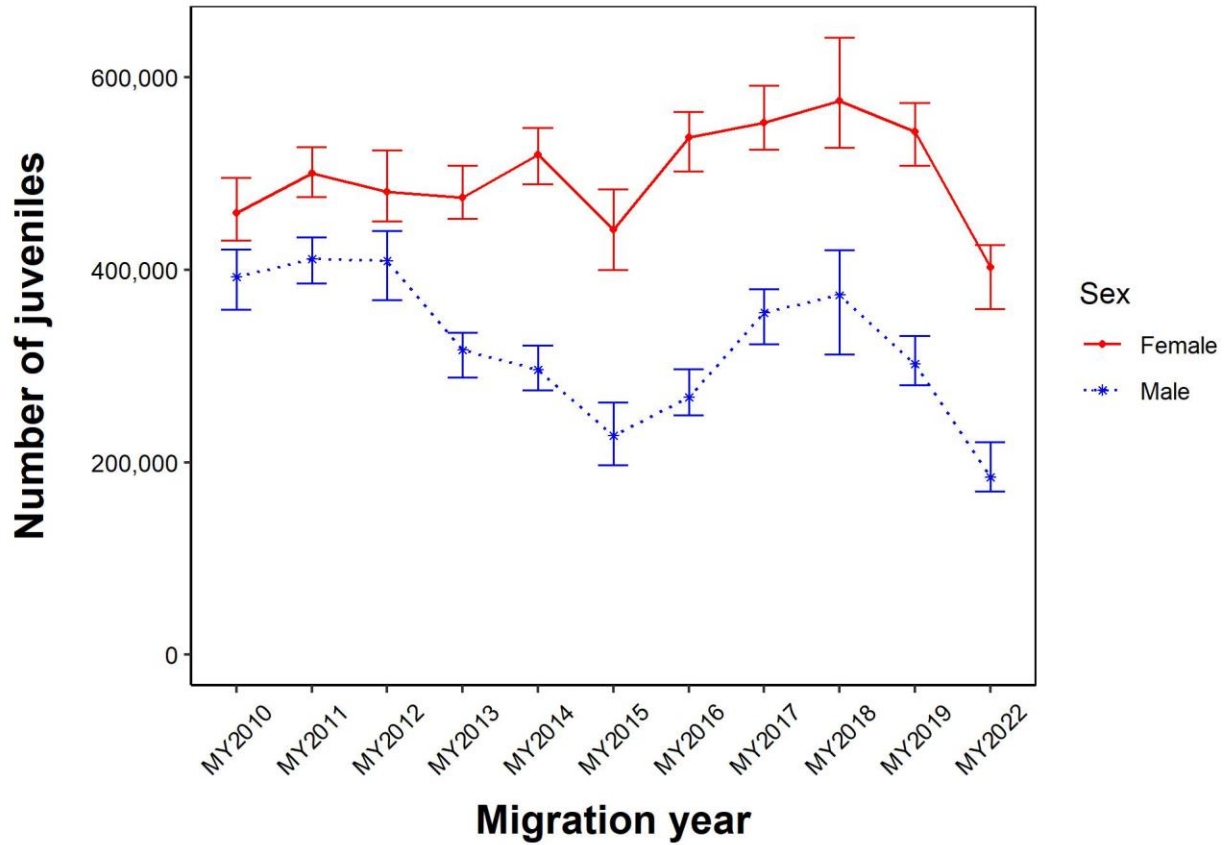
Appendix B: Wild juvenile steelhead at Lower Granite Dam in migration year 2022.

Appendix B-1. Wild juvenile steelhead emigration estimates by sex for each genetic stock at Lower Granite Dam in migration year 2022. L = lower bound and U = upper bound of 90% confidence intervals. See text for stock abbreviations.

| Genetic stock	Estimated number of wild juvenile steelhead at Lower Granite Dam								
	Female			Male			Total		
	Estimate	L	U	Estimate	L	U	Estimate	L	U
UPSALM	60,372	44,542	73,289	25,713	13,715	33,672	86,085	63,662	98,069
MFSALM	26,545	17,700	35,973	10,288	5,008	16,664	36,833	26,100	47,918
SFSALM	25,274	13,393	31,223	6,081	3,476	13,302	31,355	19,728	40,306
LOSALM	6,872	684	13,840	3,000	1,707	7,723	9,872	3,677	18,368
UPCLWR	40,307	23,914	53,218	12,726	7,980	25,433	53,033	36,473	70,750
SFCLWR	38,088	26,972	55,634	12,416	13,641	28,998	50,504	45,281	78,733
LOCLWR	12,854	8,902	19,222	5,283	3,583	9,486	18,137	14,637	26,407
IMNAHA	33,017	20,065	41,380	11,603	8,229	19,264	44,620	31,759	55,200
GRROND	105,839	88,099	124,175	66,002	51,599	82,829	171,841	147,607	194,418
LSNAKE	53,321	46,372	75,338	31,004	20,956	41,681	84,325	72,518	108,013
Total	402,489	359,421	425,636	184,116	169,886	221,159	586,605	549,501	623,929
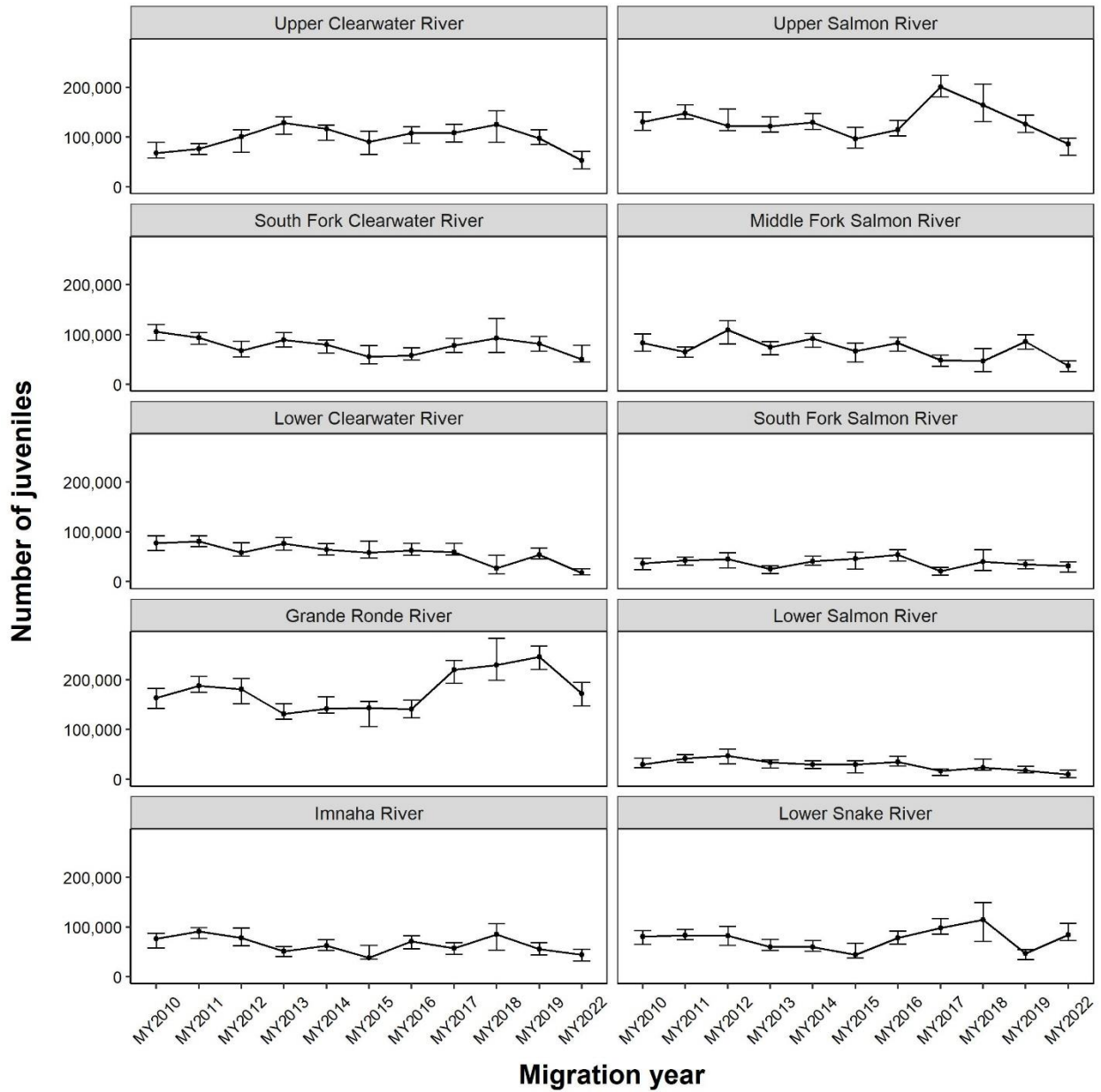
Appendix B-2. Wild juvenile steelhead emigration estimates by genetic stock at Lower Granite Dam from 2010 to 2022. Confidence intervals are at 90%. Abundance estimates in migration years 2020 and 2021 were excluded from the timeseries figures due to no sampling during the COVID pandemic and unreliable estimates (Copeland et al. 2024 in preparation), respectively.
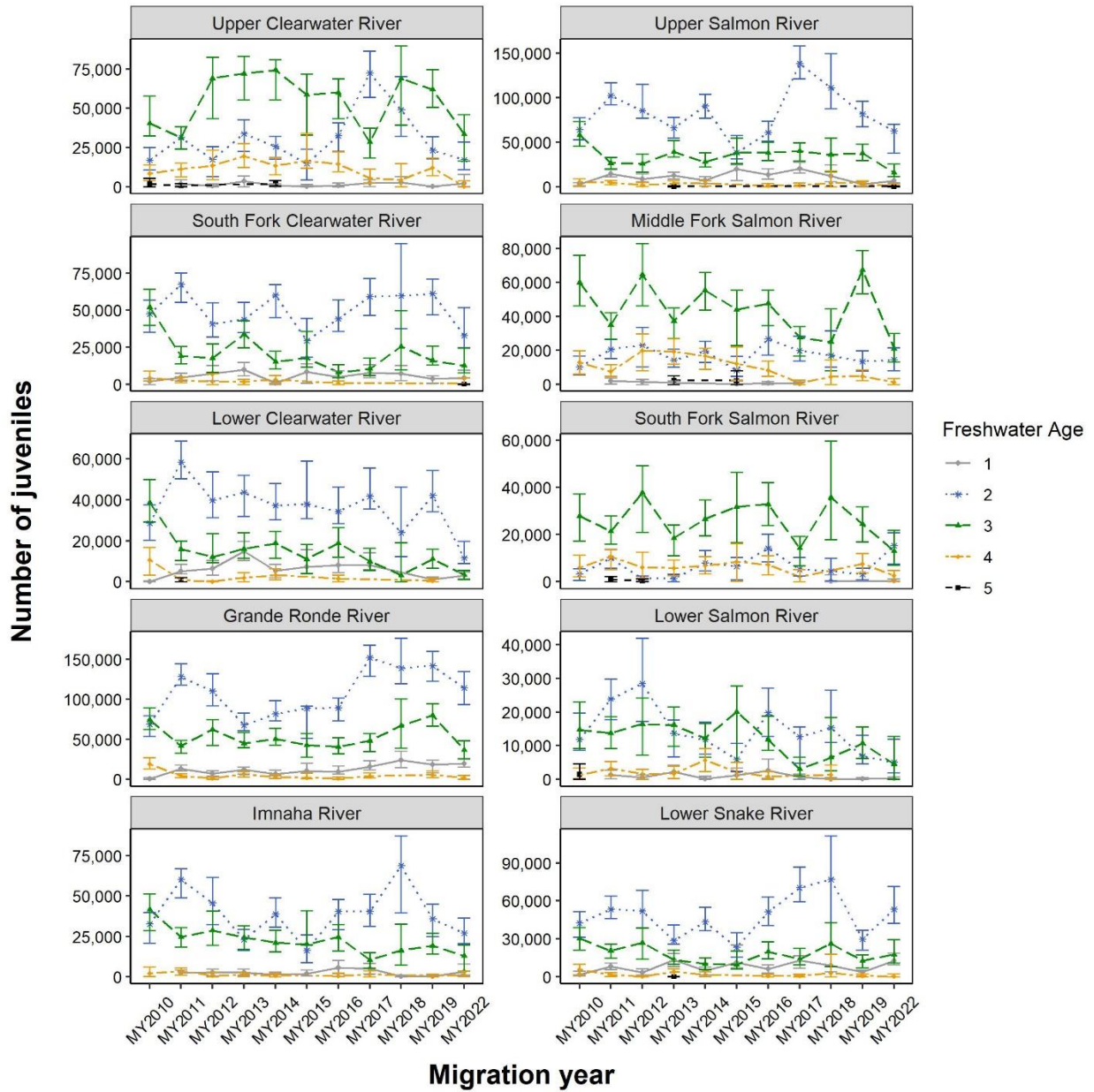
Appendix B-3. Wild juvenile steelhead emigration estimates by sex at Lower Granite Dam from 2010 to 2022. Confidence intervals are at 90%. Abundance estimates in migration years 2020 and 2021 were excluded from the timeseries figures due to no sampling during the COVID pandemic and unreliable estimates (Copeland et al. 2024 in preparation), respectively.
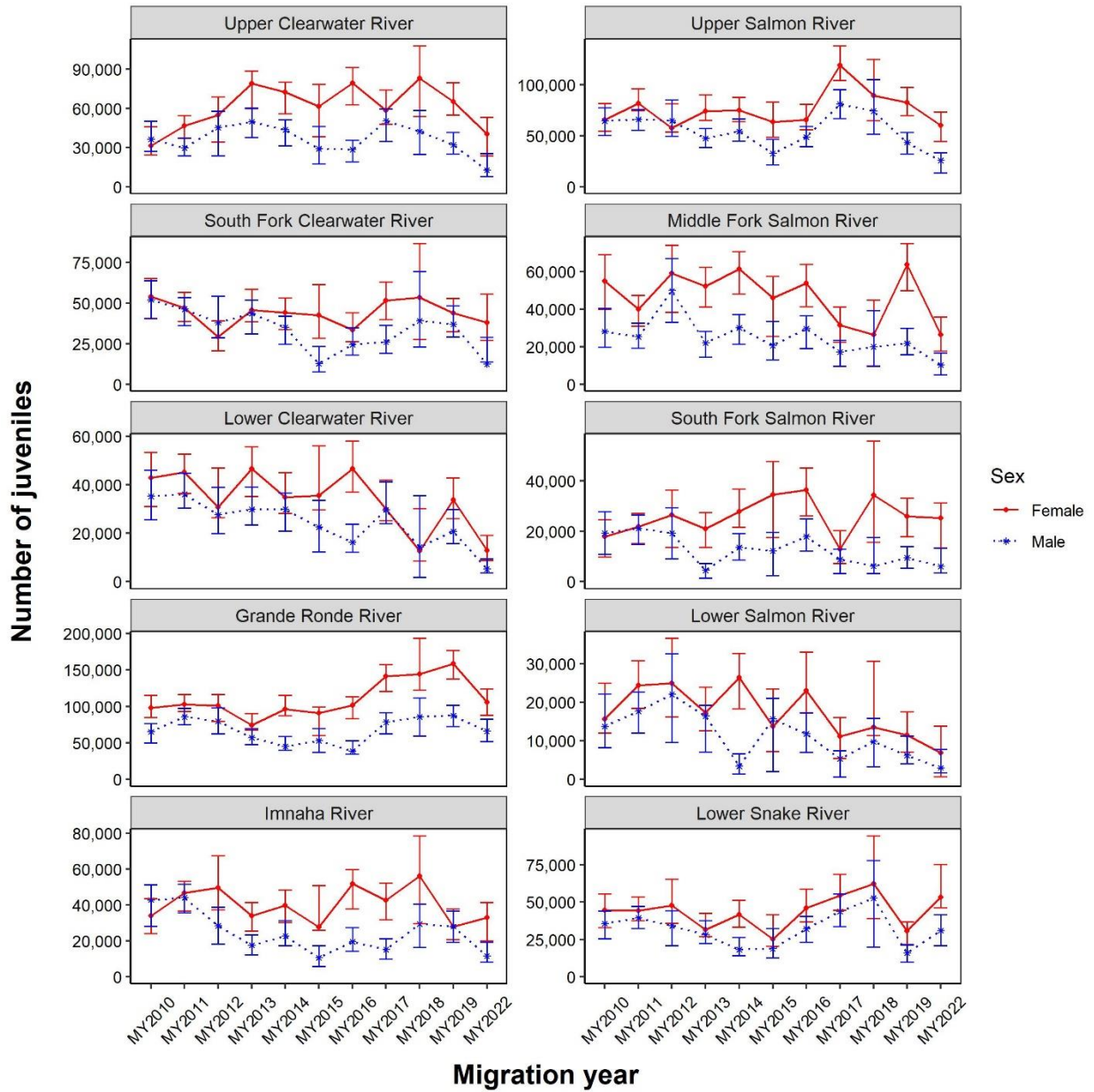
Appendix B-4. Wild juvenile steelhead emigration estimates by sex for each genetic stock at Lower Granite Dam from 2010 to 2022. Confidence intervals are at 90%. Abundance estimates in migration years 2020 and 2021 were excluded from the timeseries figures due to no sampling during the COVID pandemic and unreliable estimates (Copeland et al. 2024 in preparation), respectively.
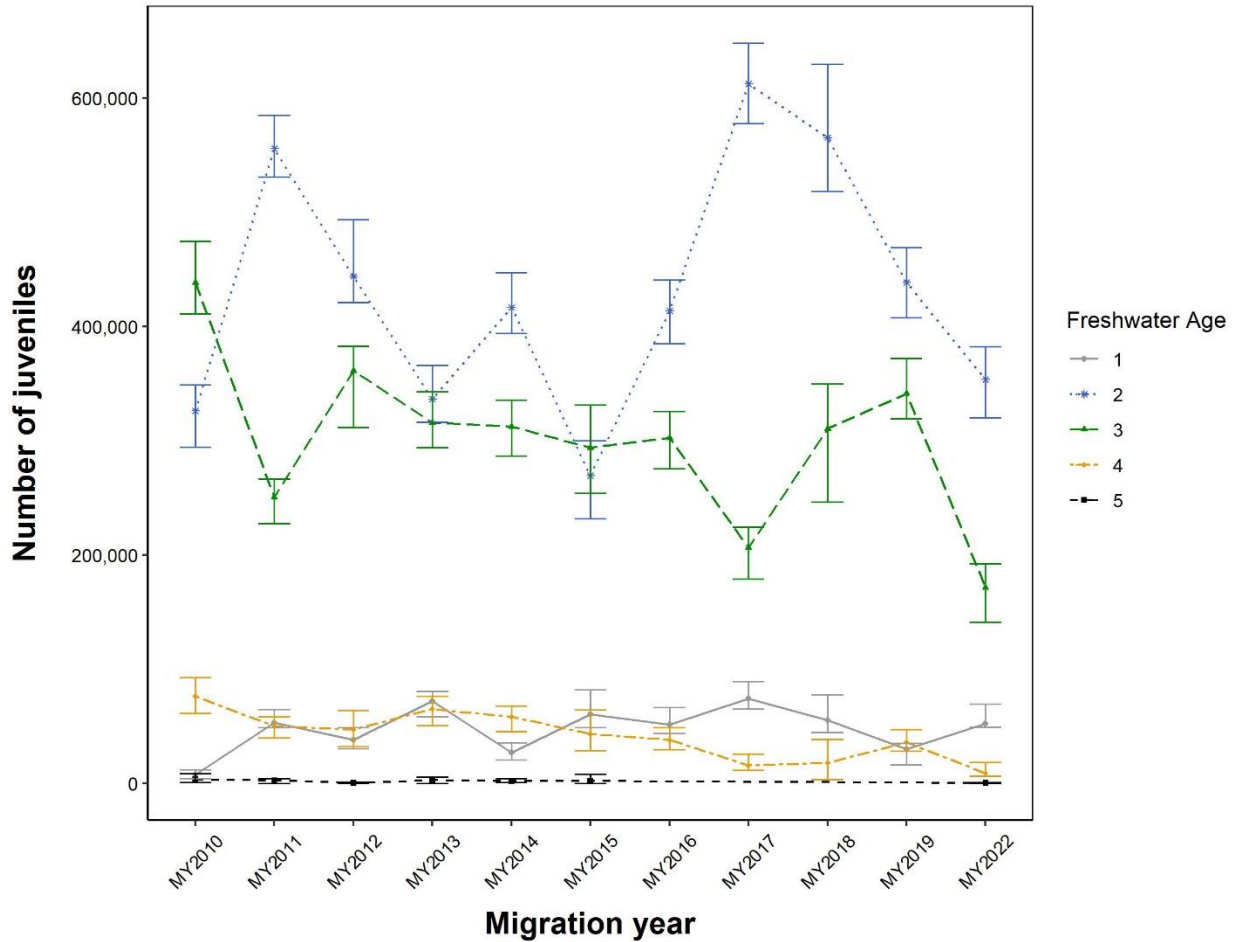
Appendix B-5. Wild juvenile steelhead emigration estimates by freshwater age at Lower Granite Dam from 2010 to 2022. Confidence intervals are at 90%. Abundance estimates in migration years 2020 and 2021 were excluded from the timeseries figures due to no sampling during the COVID pandemic and unreliable estimates (Copeland et al. 2024 in preparation), respectively.
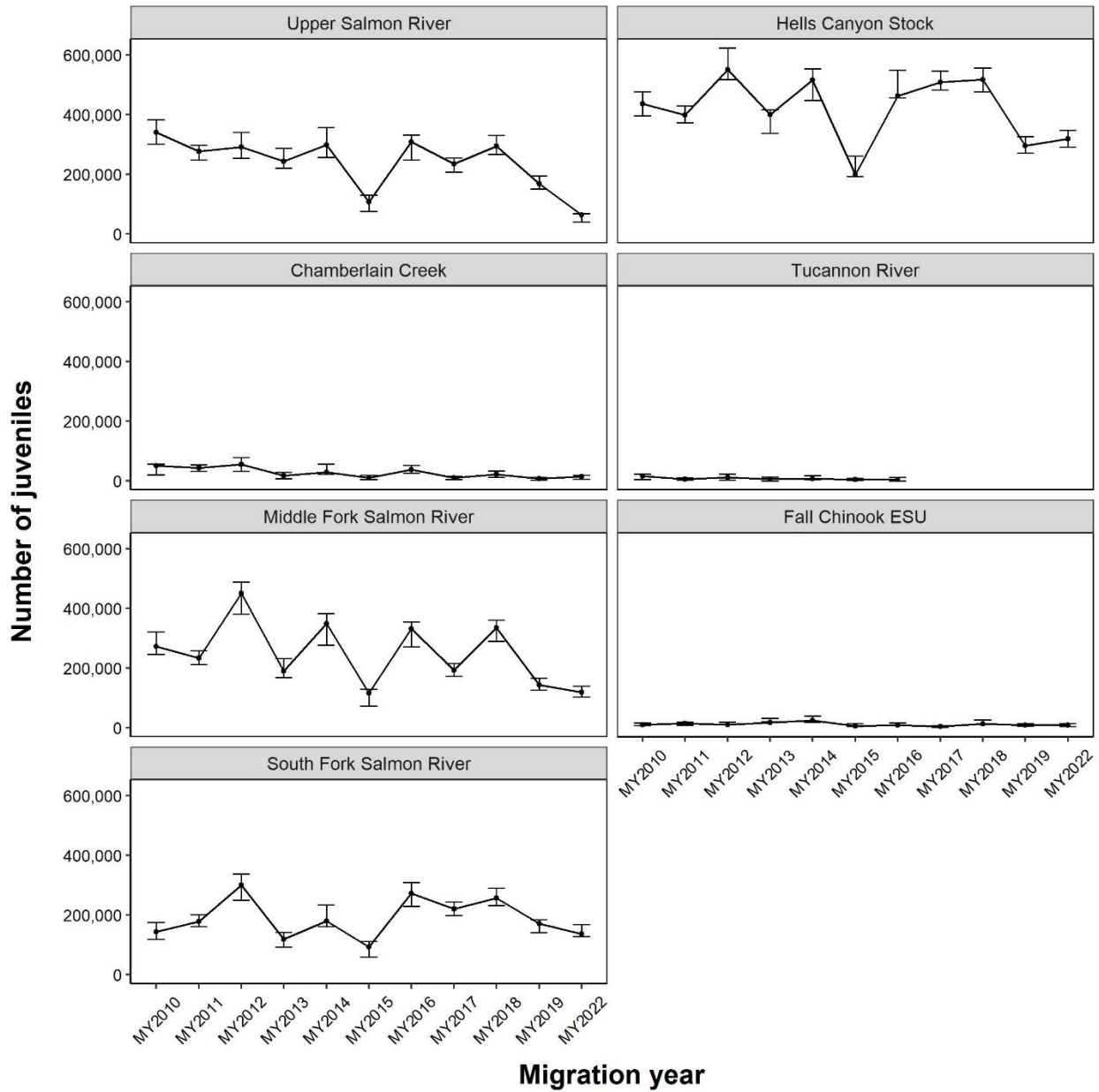
Appendix B-6. Wild juvenile steelhead emigration estimates by freshwater age for each genetic
stock at Lower Granite Dam from 2010 to 2022. Confidence intervals are at 90%.
Abundance estimates in migration years 2020 and 2021 were excluded from the
timeseries figures due to no sampling during the COVID pandemic and unreliable
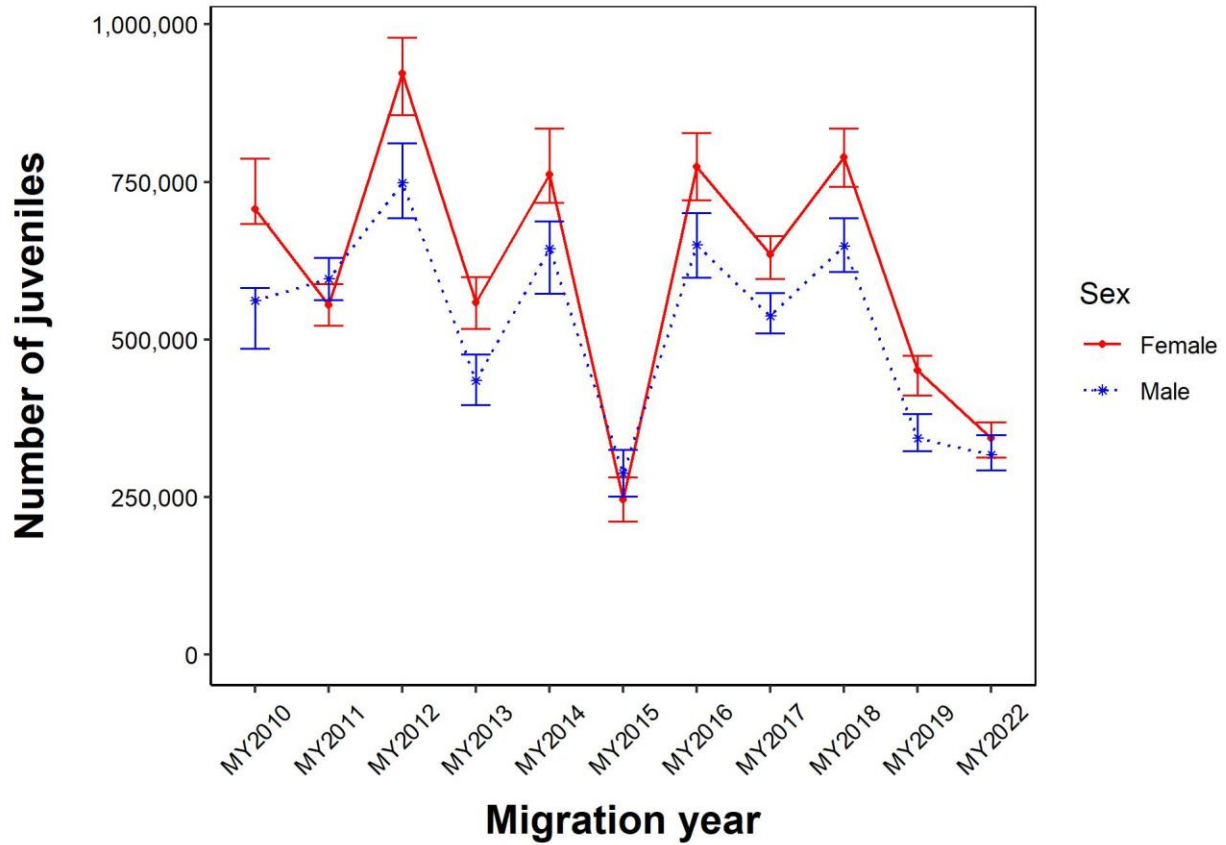estimates (Copeland et al. 2024 in preparation), respectively.

Appendix C: Wild yearling Chinook Salmon at Lower Granite Dam in migration year 2022.

Appendix C-1. Wild yearling Chinook Salmon emigration estimates by sex for each genetic stock at Lower Granite Dam in migration year 2022. L = lower bound and U = upper bound of 90% confidence intervals. See text for stock abbreviations.
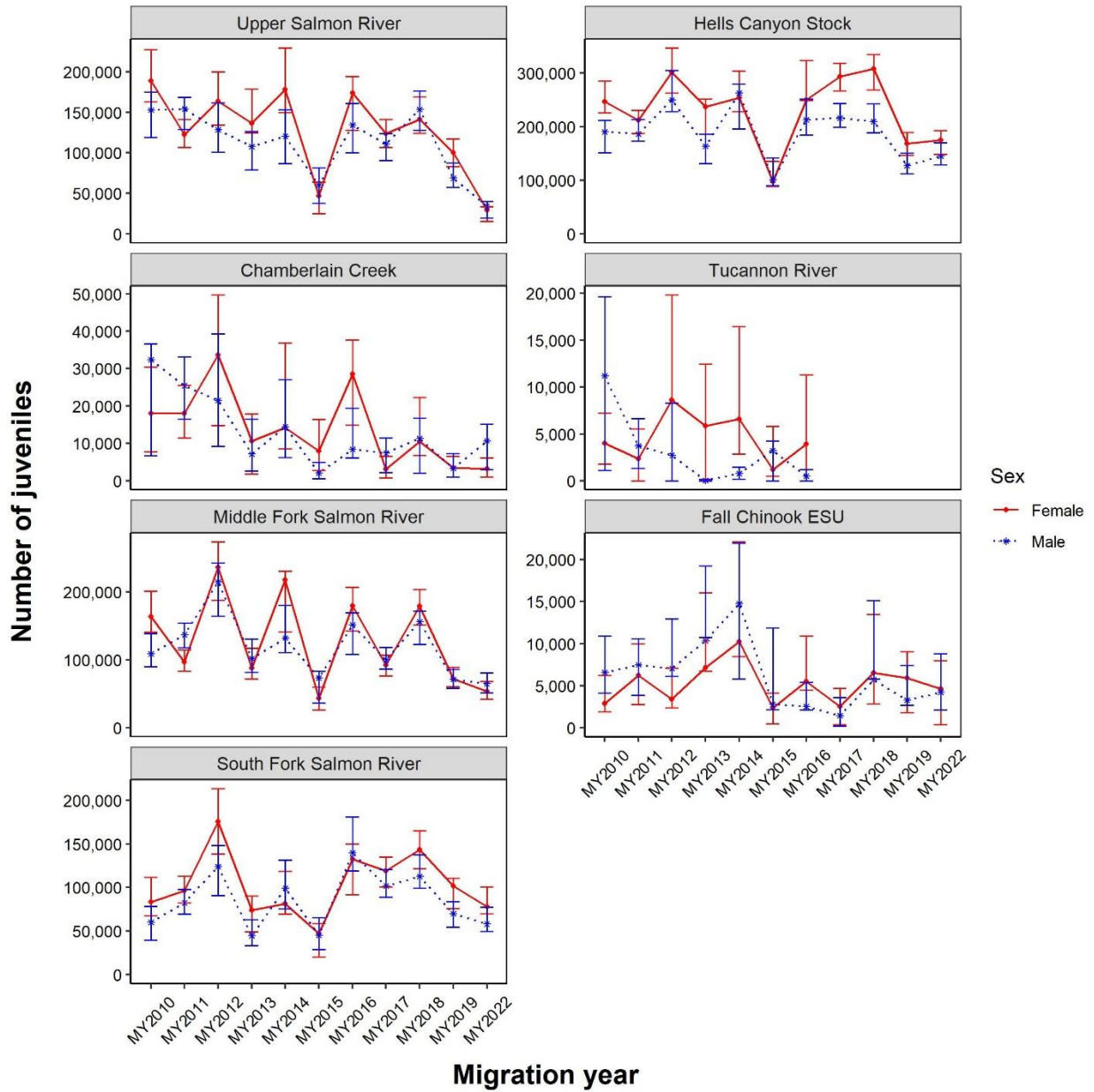
| | Estimated number of wild yearling Chinook Salmon at Lower Granite Dam | | | | | | | | |
| | Female | | | Male | | | Total | | |
Genetic stock	Estimate	L	U	Estimate	L	U	Estimate	L	U
UPSALM	29,200	15,654	33,842	33,918	19,780	40,020	63,118	40,737	67,426
CHMBLN	3,177	1,067	6,068	10,686	2,945	15,151	13,863	5,592	19,064
MFSALM	53,669	41,885	68,316	64,657	51,716	81,163	118,326	102,276	139,672
SFSALM	77,931	69,833	100,695	58,156	49,609	77,084	136,087	127,815	167,943
HELLSC	174,512	148,582	192,620	145,203	129,139	170,008	319,715	291,611	347,311
TUCANO	0	0	0	0	0	0	0	0	0
FALL	4,633	349	7,951	4,219	2,103	8,782	8,852	3,627	14,171
Total	343,122	312,474	368,437	316,839	292,383	348,017	659,961	628,530	691,997

Appendix C-2. Wild yearling Chinook Salmon emigration estimates by genetic stock at Lower Granite Dam from 2010 to 2022. The Tucannon River stock was absent in 2017 to 2019 and 2022. Confidence intervals are at 90%. Abundance estimates in migration years 2020 and 2021 were excluded from the timeseries figures due to no sampling during the COVID pandemic and unreliable estimates (Copeland et al. 2024 in preparation), respectively.

Appendix C-3. Wild yearling Chinook Salmon emigration estimates by sex at Lower Granite Dam from 2010 to 2022. Confidence intervals are at 90%. Abundance estimates in migration years 2020 and 2021 were excluded from the timeseries figures due to no sampling during the COVID pandemic and unreliable estimates (Copeland et al. 2024 in preparation), respectively.

Appendix C-4. Wild yearling Chinook Salmon emigration estimates by sex for each genetic stock at Lower Granite Dam from 2010 to 2022. The Tucannon River stock was absent in 2017 to 2019 and 2022. Confidence intervals are at 90%. Abundance estimates in migration years 2020 and 2021 were excluded from the timeseries figures due to no sampling during the COVID pandemic and unreliable estimates (Copeland et al. 2024 in preparation), respectively.

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