FISHERY RESEARCH

WILD ADULT STEELHEAD AND CHINOOK SALMON ABUNDANCE AND COMPOSITION AT LOWER GRANITE DAM, SPAWN YEAR 2023

ANNUAL PROGRESS REPORT

Photo: IDFG

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2023 Annual Report

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ACKNOWLEDGMENTS

Suggested citation:

Beeken, N. B., J. S. Hargrove, A. C. Harris, M. Davison, T. Copeland, L. Chiaramonte, and N. R. Smith. 2024. Wild adult steelhead and Chinook Salmon abundance and composition at Lower Granite Dam, spawn year 2023. Annual report 2023. Idaho Department of Fish and Game Report 24-12

ABBREVIATIONS AND ACRONYMS

BPA	Bonneville Power Administration
BY	Brood Year
CI	Confidence Interval
CHMBLN	Chamberlain Creek Genetic Stock
CLRWTR	Clearwater River Genetic Stock
CWT	Coded Wire Tag
DPS	Distinct Population Segment
EFGL	Eagle Fish Genetics Laboratory
ESA	Endangered Species Act
ESU	Evolutionarily Significant Unit
FALL	Snake River Fall Chinook Salmon
FL	Fork Length
FPC	Fish Passage Center
GRROND	Grande Ronde River Genetic Stock
GSI	Genetic Stock Identification
GT-seq	Genotyping-in-Thousands by Sequencing
H	Adipose Fin Clipped Hatchery
HELLSC	Hells Canyon Genetic Stock
HNC	Adipose Fin Intact Hatchery
ICBTRT	Interior Columbia Basin Technical Recovery Team
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
NPCC	Northwest Power Conservation Council
NRAAL	Nampa Research Anadromous Ageing Laboratory
NWFSC	Northwest Fisheries Science Center
PBT	Parentage Based Tag
PIT	Passive Integrated Transponder
PSMFC	Pacific States Marine Fisheries Commission
SALMON	Salmon River Major Population Group
SAR	Smolt-to-adult return rate
SCOBI	Salmonid Compositional Bootstrap Intervals
SFCLWR	South Fork Clearwater River Genetic Stock
SFSALM	South Fork Salmon River Genetic Stock

SNP	Single Nucleotide Polymorphism
SY	Spawn Year
TUCANO	Tucannon River Genetic Stock
UPCLWR	Upper Clearwater River Genetic Stock
UPSALM	Upper Salmon River Genetic Stock
USACE	U. S. Army Corps of Engineers
W	Wild
WDFW	Washington Department of Fish and Wildlife

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ABSTRACT

This report summarizes the abundance and composition of wild adult steelhead *Oncorhynchus mykiss* and spring-summer Chinook Salmon *O. tshawytscha* migrating upstream of Lower Granite Dam in spawn year (SY) 2023. We used a combination of window counts, nighttime passage rates, fallback-reascension rates, and biological samples collected using a systematic random sample design from the fish trap at Lower Granite Dam to estimate abundance of each species by origin, body size, sex, age, and genetic stock. The time series of abundance and composition was used to calculate adult-to-adult productivity, expressed as recruits per spawner, and smolt-to-adult return rate for each species.

The estimated total escapement for hatchery and wild steelhead was 76,203 (74,953–77,589 95% CI). The estimated wild steelhead escapement was 13,631 fish (13,104–14,201 95% CI), comprising 18% of the total escapement estimate. The Grande Ronde River genetic stock was the most abundant (3,670 fish [3,334–4,030 95% CI]) followed by the Lower Snake River stock (2,083 fish [1,738–2,431 95% CI]). Small steelhead (<78 cm fork length [FL]) comprised 59% of the adipose fin-clipped hatchery run and large steelhead (≥78 cm FL) comprised 63% of the adipose fin-intact hatchery run. The wild run had a higher percentage of small steelhead at 79% compared to either hatchery group. Female steelhead comprised 76% of the wild steelhead run at Lower Granite Dam with female percentages within genetic stocks ranging from 72% for the South Fork Clearwater River to 83% for the Middle Fork Salmon River. We observed 20 different steelhead age classes. Total age for adult steelhead ranged from three to eight years. Freshwater ages ranged from one to four years. Saltwater ages ranged from one to three years, with additional fish that were observed to be repeat spawners. In SY2023, adult-to-adult productivity was completed for brood year 2015 and was 0.26 returning recruits per spawner. Productivities for all genetic stocks were below replacement. The smolt-to-adult return rate for wild steelhead was 0.68% for smolts passing Lower Granite Dam in migration year 2019. The average wild escapement from 2019-2023 is approximately 43% of the average wild escapement from 2014-2018 (11,367 fish and 26,275 fish, respectively).

The estimated total escapement for hatchery and wild spring-summer Chinook Salmon was 60,312 fish (59,362–61,292 95% CI). The estimated wild Chinook Salmon escapement was 8,028 fish (7,642–8,438 95% CI), comprising 13% of the total escapement estimate. The Hells Canyon genetic stock was the most abundant (2,678 fish [2,409–2,990 95% CI]) followed by the South Fork Salmon River stock (2,131 fish [1,907–2,427 95% CI]). Large Chinook Salmon (≥57 cm FL) comprised 84% of the ad-clipped hatchery run, 81% of the adipose fin-intact hatchery run, and 94% of the wild run. Male Chinook Salmon comprised 56% of the wild Chinook Salmon run at Lower Granite Dam with male percentages within genetic stocks ranging from 53% for the Fall stock to 69% for the Chamberlain Creek stock. We observed seven different Chinook Salmon age classes. Total age for adult Chinook Salmon ranged from three to six years. Freshwater ages ranged from one to two years, and saltwater ages ranged from zero to three years. Mini-jack Chinook Salmon are defined as having a saltwater age of 0 while jack Chinook Salmon are defined as having a saltwater age of 1. All the minijacks sampled have been assigned to the Fall Chinook Salmon stock. In SY2023, adult-to-adult productivity was completed for brood year 2017 and was 1.39 returning recruits per spawner. Productivities for the South Fork Salmon River, Upper Salmon River, and Hells Canyon stocks were above replacement. The smolt-to-adult return rate for wild Chinook Salmon was 1.02% for smolts passing Lower Granite Dam in migration year 2019. The current 5-year average of wild escapement (9,716 fish; 2019–2023) is approximately 58% of the previous 5-year average (16,735 fish; 2014–2018).

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INTRODUCTION

Populations of steelhead trout *Oncorhynchus mykiss* and Chinook Salmon *O. tshawytscha* in the Snake River basin have declined following the construction of hydroelectric dams in the Snake and Columbia rivers. Raymond (1988) documented a decrease in 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. Snake River spring-summer Chinook Salmon (hereafter Chinook Salmon) were classified as threatened under the Endangered Species Act (ESA) in 1992, and Snake River steelhead were classified as threatened under the ESA in 1997.

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, 2009; Ford 2011, 2015; NMFS 2016). The Hells Canyon MPG is considered functionally extirpated. In total, 24 extant populations have been identified in the DPS.

Within the Snake River spring-summer Chinook Salmon evolutionarily significant unit (ESU), there are seven MPGs: Lower Snake River, Grande Ronde/Imnaha Rivers, South Fork Salmon River, Middle Fork Salmon River, Upper Salmon River, Dry Clearwater River, and Wet Clearwater River (Table 1; ICBTRT 2003, 2005, 2009; Ford 2011, 2015; NMFS 2016). The Dry Clearwater River and Wet Clearwater River MPGs are considered extirpated, but natural populations have been established by stocking individuals from other Snake River MPGs. In total, 28 extant populations have been identified in the ESU.

The 2019-2024 Idaho department of Fish and Game (IDFG) Fisheries Management Plan defines wild-origin salmon and steelhead as native fish produced from populations which have no history of reproductive introgression with hatchery or non-native fish. The plan defines natural-origin fish as those produced from natural spawning and rearing but may be the offspring of either hatchery or wild parents, or an introduced stock. For the purposes of this report, all naturally produced salmon and steelhead are classified and referred to as "wild".

Anadromous fish management programs in the Snake River basin include large-scale hatchery programs intended to mitigate the impacts of hydroelectric dam construction and operation as well as recovery planning and implementation efforts for ESA-listed wild steelhead and salmon stocks. The IDFG anadromous fish program's long-term goals, consistent with basin-wide mitigation and recovery programs, are 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 (McElhany et al. 2000) as well as regular status assessments. The key metrics to assessing viability of salmonid populations are abundance, productivity, spatial structure, and diversity (McElhany et al. 2000).

The aggregate escapement of Snake River steelhead and Chinook Salmon is estimated at LGR, except for the Tucannon River population in Washington, which is downstream of LGR. Age, sex, and stock composition data are important for monitoring recovery of wild fish for both species. Age data from scales collected at LGR are used to assign returning adults to specific brood years, for cohort analysis, and to estimate productivity and survival rates (Camacho et al. 2017; 2018a; 2018b; 2019a; 2019b; Lawry et al. 2020; Baum et al. 2022a; 2022b). In addition, escapement estimates by cohort are used to forecast run sizes in subsequent years, and these forecasts are the basis for preliminary fisheries management plans in the Columbia River basin.

At Columbia River dams, U.S. Army Corps of Engineers (USACE) counts fish at viewing windows and designates Chinook Salmon between 30 and 57 cm (12 and 22 in) in fork length as jacks. Salmonids under 30 cm (12 in) in fork length are not identified to species. Mini-jacks are precocious salmon generally under 30 cm in fork length and thus are not counted (Steve Richards, WDFW, personal communication). Throughout this report, unless otherwise stated, adult Chinook Salmon refers to reproductively mature fish returning to spawn, including jacks but excluding mini-jacks.

Additionally, the USACE defines the Chinook Salmon run type by calendar date. Any Chinook Salmon counted at the LGR window from March 1 to June 17 is considered spring run, June 18 to August 17 is considered summer run, and August 18 to December 31 is considered fall run. Fall-run Chinook Salmon passing LGR during the March 1 to August 17 period are presented in this report for accounting purposes only and do not represent the entirety of fall-run Chinook Salmon. For steelhead, the run year at LGR is defined to be from July 1 of the previous year to June 30 of the current year, and most steelhead pass LGR in the fall. The steelhead run year dates were chosen to be consistent with the upriver steelhead run year at Bonneville Dam as defined in the *U.S. v. Oregon* management agreement (Joint Columbia River Management Staff 2023).

The goal of this report is to summarize the abundance and composition of wild adult steelhead and spring-summer Chinook Salmon returning to LGR during spawn year (SY) 2023. We also update the time series for adult-to-adult productivity and smolt-to-adult return (SAR) rate for both species, last described by Baum et al. (2023). The objectives of this report are to:

1. Describe LGR adult trap operations and data collection during 2022–2023, which is the timeframe encompassing all steelhead and Chinook Salmon passing LGR for SY2023.

2. Estimate wild steelhead and Chinook Salmon escapement and size, sex, and age composition in aggregate and by genetic stock.

3. Evaluate wild steelhead and Chinook Salmon status using adult-to-adult productivity and replacement rates in aggregate and by genetic stock.

4. Estimate survival using SAR rate for the aggregate return of wild steelhead and Chinook Salmon.

METHODS

Adult Trap Operations at Lower Granite Dam

Systematic samples of adult steelhead and Chinook Salmon ascending LGR were collected during daily operation of the adult fish trap by National Marine Fisheries Service (NMFS). The trap is located in the LGR fish ladder and is upstream of the fish-counting window. The trap captured a systematic random sample of fish by operating a computerized trap gate according to a predetermined sample rate. The trap gate was opened four times per hour for a length of time directed by the programmed sample rate; the trap was operational 24 hours per day. The sample rate is determined based on sample size goals of the various projects using the adult trapping data combined with forecasted abundance of the targeted species, run, and rear type. Ideally, the sample rate is apportioned equally across the entire sampling season. However, the trap did not

operate during weekends from March 2 to August 17, and the trap rate was adjusted to continue achieving the sample rate goal by compensating for the two non-trapping weekend days. In-season adjustments to the sample rate were sometimes needed to accommodate limitations at the trapping facility, changes to the forecast, or sample size goal modifications. Additionally, high (≥21°C or ≥70°F) and low (≤0°C or ≤32°F) water temperatures require the trapping facility to temporarily modify or cease operations.

During SY2023, the trap was closed November 16, 2022 through February 28, 2023 for the winter (Appendix A-1). When the trap was operating, daily trapping rates generally varied from 18% to 25% for the SY2023 season (Appendix A-2 and A-3). While the trap was operating, 96.3% of the steelhead run passed the counting window (Appendix A-2). Most of the steelhead run passed LGR in the fall of 2022 (Appendix A-2). While the trap was operating, 72.5% of the Chinook Salmon run passed the counting window. A reduced percentage of Chinook Salmon pass during trap operation since the trap is non-operational on the weekends during the Chinook Salmon spring-summer run period (Appendix A-3). More information about trap logistics can be found in Harmon (2003), Steinhorst et al. (2010), and USACE (2021, 2022).

Standard methods were used by NMFS and IDFG staff to process and biologically sample fish at the trap. All fish captured were anesthetized; examined for external marks, tags, and injuries; scanned for a coded wire tag (CWT) and passive integrated transponder (PIT) tag; and measured for fork length (FL, nearest cm). The number of fish processed each day at the LGR trap in SY2023 ranged from one fish to 967 fish. Each fish was directly handled for a minimum of 15 seconds to a maximum of 1 minute and 15 seconds (Nolan Smith, PSMFC, personal communication).

All fish were classified by origin (hatchery or wild) based on a hierarchical key of external marks and internal tags identified at LGR and after post-hoc genetic analysis conducted in the laboratory (Appendix A-4). At the LGR trap, the presence or absence of an adipose fin was determined first. All fish considered to have a clipped adipose fin (absent or partial clip evident by a healed scar) were classified as ad-clipped hatchery fish. Although most hatchery steelhead and Chinook Salmon have a clipped adipose fin (hereafter ad-clipped), some were released with an unclipped adipose fin (hereafter ad-intact) for supplementation or broodstock management purposes (Venditti et al. 2022). All ad-intact fish were subsequently scanned for a CWT and examined for ventral fin clips or other external marks and tags. Any ad-intact fish with the presence of a CWT or ventral fin clip were classified as ad-intact hatchery fish. The trap crew sampled fin tissue from all ad-intact fish; genotyping for parentage-based tagging (PBT) analysis was conducted post hoc to further classify ad-intact hatchery fish (Hargrove et al. 2021a). In summary, final classification of hatchery fish was made using any of four marks or tags: adipose fin clip (complete removal or partial clip), CWT, ventral fin clip, or PBT. Information associated with previous PIT tagging events was not used to determine origin.

For all ad-intact fish, scale samples were taken from above the lateral line and posterior to the dorsal fin. Samples were stored in coin envelopes for transport to the IDFG Nampa Research Anadromous Ageing Laboratory (NRAAL). For all ad-intact fish, tissue samples for genetic analysis were taken from a small clip of the anal fin. Tissues were stored on a dry Whatman paper medium (LaHood et al. 2008) for transport to the IDFG Eagle Fish Genetics Laboratory (EFGL). All ad-intact fish captured were also PIT tagged (if not previously tagged) for abundance estimation at instream PIT tag detectors upstream of LGR (IPTDSW 2020; See et al. 2021). After processing, all fish were returned to the adult fish ladder to resume their upstream migration.

Trap Data Management

All data were entered into a NMFS cloud-based database via touch-screen computer systems located in the trap work area. Initiated in 2012, this system allowed interested parties to access the data they needed at the end of each day and eliminated transcription errors from paper data sheets to electronic form. The IDFG LGR SQL server database automatically queries the NMFS database daily to populate tables used by IDFG for reporting purposes. The IDFG LGR SQL server database also queries and combines ageing data from the NRAAL BioSamples database to the associated trap records. Genetic data from the EFGL Progeny database is manually uploaded to the IDFG LGR SQL database.

Valid Sample Selection

Not all trapped fish were deemed valid by IDFG for sample processing and analysis. Trapped fish that were missing data for any of the following five fields were considered invalid: date of collection, species, FL, origin (hatchery or wild), or adipose fin status (ad-clipped or ad-intact). Trapped fish less than 30 cm FL were considered invalid as they are not identified to species at the USACE fish-counting window. Further, the trap was not designed to efficiently trap these smaller fish (Darren Ogden, NMFS, personal communication); for Chinook Salmon, this includes all mini-jacks less than 30 cm FL.

Our sampling target was to age and genotype approximately 2,000 wild steelhead and 2,000 wild Chinook Salmon. In collaboration with our work, a second sampling goal was to PIT tag, age, and genotype approximately 4,000 wild steelhead and 4,000 wild Chinook Salmon to estimate abundance at instream PIT detectors. We emphasize that both objectives were complimentary and not mutually exclusive. Every ad-intact steelhead and Chinook Salmon trapped at LGR was genotyped to simplify collaborative logistics and to increase accuracy and precision of abundance estimates using genetic stock identification (GSI) and PBT. All valid samples from wild fish were systematically subsampled if more than approximately 2,000 samples were available for each species. The result was a pool of samples collected systematically across the spawning run of each species and generally in constant proportion to their abundance. Hence, for either species, the sample pool can be considered a daily systematic sample (Steinhorst et al. 2017).

Scale Processing, Analysis, and Age Validation

Technicians processed scale samples in the NRAAL according to protocols detailed in Wright et al. (2015). Ages were formatted using the European system where freshwater age was separated from saltwater age by a decimal. For steelhead repeat spawners, an 'R' is added to the saltwater age to indicate the winter spent in freshwater during the second spawning migration (see Copeland et al. 2018 for ageing repeat spawners). Age classes are defined as the unique combinations of freshwater, saltwater, and repeat spawning ages. Brood year (BY) is the spawn year minus the total age at spawning (total age = freshwater age + saltwater age + 1). One year is added to scale age estimations for steelhead and Chinook Salmon because a visible annulus is not formed during growth but is assumed to have occurred. For steelhead, no visible annulus forms during the adult period of the lifecycle spent in freshwater over winter, when mineral deposits that form on scales are metabolized for gonad and gamete growth (Persson et al. 1998; Witten and Huysseune 2009). For Chinook Salmon, no visible annulus is formed on scales during their first winter of juvenile development. Fish lacking either a freshwater or saltwater age were not used for analysis.

Steelhead and Chinook Salmon with known saltwater ages were used to compute aging accuracy rates for both species. We validated wild fish saltwater age assignments using known saltwater ages from wild fish that were PIT tagged as juveniles and from hatchery fish with a CWT. Accuracy of age assignments was estimated by percent agreement between scale-based saltwater age and known saltwater age. The estimation of age using scales is sufficiently accurate to produce age compositions (Copeland et al. 2018; Reinhardt et al. 2022).

Genetic Tissue Processing and Analysis

Detailed methods for extraction of genomic DNA from tissue samples, DNA amplification, and single nucleotide polymorphism (SNP) genotyping are described in Vu et al. (2015) and Campbell et al. (2015). Briefly, samples were processed using "Genotyping-in-Thousands by sequencing" (GT-seq) protocols at either the EFGL in Eagle, Idaho, or the Columbia River Inter-Tribal Fish Commission's genetics laboratory in Hagerman, Idaho. Steelhead were examined at a 379 SNP marker panel, and Chinook Salmon were examined at a 349 SNP marker panel. Each panel contains SNPs for PBT, GSI, and genetic sex-determination.

Parentage-based tagging involves annual sampling and genotyping of hatchery broodstock that are used to create a database of parental genotypes. Subsequently, progeny of these genotyped parents (collected either as juveniles or adults) can be assigned back to their parents via parentage analysis. Parentage assignments were performed on all ad-intact adults returning to LGR to identify hatchery fish that were phenotypically wild (unclipped/unmarked) using the program SNPPIT (Anderson 2010, available at: https://github.com/eriqande/snppit). Since 2008, fin tissue has been sampled from nearly all adult steelhead and spring-summer Chinook Salmon broodstock spawned at Snake River hatcheries in Idaho, Oregon, and Washington (Delomas et al. 2020). The PBT project essentially "tags" all hatchery steelhead, spring-summer Chinook Salmon, and fall Chinook Salmon smolts released in the Snake River basin. This allows researchers to identify the exact parents of an individual, and thus its hatchery of origin and total age (Steele et al. 2013). Parentage Based Tagging is a critical tool to differentiate hatchery fish when no other physical tags (e.g., CWT and fin clips) are present and can significantly improve escapement estimates for wild Chinook Salmon and steelhead (Hargrove et al. 2021b).

Genetic stock identification is a complimentary genetic technique to PBT that seeks to identify the 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 (adults sampled at LGR) to unique groups (i.e., genetic stocks). 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. Vu et al. (2015) and Powell et al. (2018) provide a detailed description of the Snake River genetic baselines used for both steelhead and Chinook Salmon GSI analyses (Figure 1; Figure 2). Genetic stocks were 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. The genetic stocks include: 1) UPSALM: upper Salmon River (including North Fork Salmon River 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 upstream (e.g., Alpowa and Asotin creeks) and downstream (primarily Tucannon River) of LGR. Some Tucannon River steelhead ascend the dam and either stay upriver to spawn or fall back and spawn downriver. Results from some genetic stocks are aggregated to report by Snake River steelhead MPGs (Table 1).

Seven wild Chinook Salmon genetic stocks were used. The genetic stocks include: 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 account for returning adults that originated from populations below LGR but ascended the dam and either stay upriver to spawn or fall back and spawn downriver. Except for fall Chinook Salmon, these genetic stocks largely correspond to Snake River spring-summer Chinook Salmon MPGs (Table 1). The MFSALM and CHMBLN genetic stock results were aggregated to report the Middle Fork Salmon River MPG. Three collections of Snake River fall Chinook Salmon (Clearwater River, Nez Perce Tribal Hatchery, and Lyons Ferry Hatchery) were included in the genetic stock identification baseline to distinguish wild fall Chinook Salmon trapped prior to August 18 from wild spring-summer Chinook Salmon (Ackerman et al. 2014).

The resolution of the Snake River genetic baselines was evaluated in Vu et al. (2015). The GSI project (BPA Project 2010-031-00) continues to update the genetic baselines periodically in an effort to improve resolution. Further, the GSI project continues to develop methods and evaluate available tools to assess and improve the accuracy and precision of genetic stock proportion and abundance estimates. These efforts are reported separately in the annual progress reports for the GSI project (Hargrove et al. 2022).

Phenotypic sex was not, and generally cannot be, reliably determined by personnel at the LGR trap, as most adult anadromous fish typically do not exhibit sexually dimorphic characteristics at the time when they ascend LGR. A sex-determination assay developed by Campbell et al. (2012) was used and included in the genotyping process. The accuracy of the sex-determination assays was evaluated in Steele et al. (2016). Further details can be found in Campbell et al. (2012).

Wild Escapement by Origin, Genetic Stock, Size, Sex, and Age

Total aggregate escapement of steelhead and Chinook Salmon in SY2023 was estimated using the statistical model EASE (Estimating Adult Salmonid Escapement) developed by Thomas Delomas (GitHub - delomast/escapeLGD: Escapement Estimation at Lower Granite Dam; R Development Core Team 2021). The EASE model was first implemented in SY2021 (Baum et al. 2022b). The general process of EASE involves obtaining the total number of fish ladder ascensions (nighttime and daytime ascensions) by adult salmonids, estimating the composition of ascensions (relative to genetic stock groups; Figure 3), defining strata sets, then applying the stock-specific (upper or lower) fallback-reascension rates to the composition of ascensions to obtain the adjusted escapement estimates (hereafter referred to as total adjusted escapement). Uncertainty surrounding GSI is quantified among time-steps by bootstrapping. A more detailed description of EASE methods can be found in Appendix B-1.

To estimate total number of ascensions, EASE began with the USACE daily window counts which is the number of salmonids identified to species (>30 cm FL) as they swim past the viewing window during counting hours (0400–2000). Prior to SY2021, the window counts, which occur in the fish ladder downstream of the trap, were assumed to be the daily aggregate escapement to LGR for each species. However, for EASE, the window counts were treated as a measure of the number of daytime ascensions (Appendix B-1, Daytime Ascensions, Nighttime Passage, and Total Number of Ascensions section). Window count data were downloaded from the Fish Passage Center (FPC) website: Adult Daily Dam Counts - Data Query (fpc.org). The total number of daytime ascensions was estimated by expanding the window counts for the sampling rate (historically $\frac{5}{6}$, or 50 minutes out of every hour). The counts were only performed during the daytime (0400–2000); therefore, the frequency of nighttime ascensions (nighttime passage) also needed to be estimated (Appendix B-1, Daytime Ascensions, Nighttime Passage, and Total Number of Ascensions section). The proportion of ascensions occurring at night was estimated using PIT tag detections in the ladder and was used to estimate the total number of ascensions (Columbia River Data Access in Real Time [DART]; DART PIT Tag Adult Lower Granite Ladder Window Count Hour Summary and Detection Details | Columbia Basin Research [washington.edu]). After accounting for sampling rate and nighttime passage, the resulting estimate represents the total number of ascensions.

To estimate the composition of ascensions, the total number of ascensions were then decomposed into escapement estimates for reporting groups of interest with 95% confidence intervals (CI) so the fallback-reascension rates (proportion of fish that fell back below the dam and later reascended) can be proportionally applied (Appendix B-1, Fallback Rates and Composition of Ascensions sections). The total number of ascensions initially includes repeat ascensions, so the fallback-reascension rates were applied to the total number of ascensions after decomposition, assuming every fish that fell back reascended. Fallback-reascension rate was calculated separately for upper stocks (originating upstream of LGR) and lower stocks (originating downstream of LGR) to account for differences in fallback-reascension rates between stocks. For steelhead, the LSNAKE stock was defined as "lower" and the other nine stocks were "upper". For Chinook Salmon, all stocks were defined as "upper". Fallback-reascension rates were also calculated using PIT tag detections from DART (excluding fish tagged as adults at LGR). The basic methods for estimating the composition of ascensions were developed by Delomas and Hess (2021) and implemented in the EASE R package (GitHub - delomast/escapeLGD: Escapement Estimation at Lower Granite Dam; R Development Core Team 2021). The EASE model combined the number of ascensions with the adult trap sample data on a temporally stratified basis to account for changes in the trapping rate and run characteristics through time. Some valid wild fish were removed from the trap sample due to analytical complications. Further, an error occurs in the EASE model when there is only one fish from a genetic stock within a stratum that also does not have an age estimate. These removed fish are still used to calculate the origin proportions in the trap sample, but they are excluded from the calculation of stock proportions in the trap sample (Appendix A-5, Appendix A-6). The spawn year for each species was divided into "statistical week" strata with each stratum defined as a week (starts on Monday and ends on Sunday) or a series of adjacent weeks with sufficient trap numbers (n ≥100 wild fish for each species) to adequately estimate all group proportions. In addition to the defined strata for composition estimates, two other sets of strata were defined for fallback-reascension and nighttime passage estimates through time. Criteria for these strata sets can be found in the Stratification section of Appendix B-1. Escapement by stratum was estimated by 1) calculating the total number of ascensions (i.e., account for daytime sample rate and night passage rates) in each stratum, 2) multiplying the ascensions by the trap proportions to yield composition, and 3) applying stock-specific fallback-reascension rates to the composition point estimates. The total

adjusted escapement of a species to LGR for the spawn year was the sum of escapement estimates across strata. In essence, the stratum-specific trap proportions for a reporting group were weighted by the species run size within each stratum. We assumed that 1) the total number of ascensions represents true abundance, 2) fish ascend LGR only by the ladder, 3) window counts by species are accurate, 4) PIT-tagged fish represent the behavior of untagged fish regarding fallback-reascension and nighttime passage, and 5) group-specific trap proportions are constant within each stratum.

The composition of ascensions decomposes the total adjusted escapement into rearing type, primary, and secondary categories (Figure 3; Appendix B-1, Composition of Ascensions section). These are hierarchical and each category is nested within the previous category, thus point estimates of nested categories must sum to the parent category total. First, the total adjusted escapement is decomposed into rearing type (ad-intact hatchery, ad-clipped hatchery, and wild). Fish from each rearing type are then divided into primary categories. Hatchery-reared fish (ad-clipped and ad-intact) are divided into primary size categories (large and small). Wild-reared fish are divided into primary categories by genetic stock and Major Population Group. Wild fish genetic stocks are then further decomposed into secondary categories (size, sex, brood year, saltwater age, and age class). Reporting groups for each of the primary and secondary categories were defined based on criteria important for fishery management and monitoring and evaluation. Genetic stock encompassed the species-specific reporting groups (ten for steelhead and seven for Chinook Salmon) described in the Genetics Tissue Processing and Analysis section above. Sex included a male and a female reporting group. Age class, brood year, and saltwater age reporting groups vary in number based on the freshwater and saltwater age structure observed from scale samples of trapped fish during the spawn year. Lastly, size included two length-reporting groups (large, small); however, length cutoffs differ for each species. Large steelhead are greater than or equal to 78 cm FL (B-Index), whereas small steelhead are less than 78 cm FL (A-Index), for fisheries managed under the U.S. v. Oregon Management Agreement (Joint Columbia River Management Staff 2023). For Chinook Salmon, large fish are greater than or equal to 57 cm FL corresponding to adult-sized fish, whereas small fish from 30–57 cm FL correspond to jack-sized fish. A linear regression equation for saltwater-caught Chinook Salmon in Southeast Alaska was used to convert the 24-inch (61 cm) total length cutoff to a FL equivalent of 57 cm (Conrad and Gutmann 1996).

To obtain abundance estimates for each category of interest, the composition proportions were multiplied by the total number of ascensions. Escapement in each category was then calculated by multiplying the ascension estimates by $1 - p_f$, where p_f is the corresponding fallback rate for that category of interest. A small minority of hatchery steelhead groups are split between release sites and have ambiguous PBT groups, so PIT tag detections were used to split the composition estimate into separate release groups and assign the appropriate fallback-reascension rate (Appendix B-1, Non-specific PBT Groups section). To obtain estimates at higher levels (e.g., total number of wild fish), the estimates for the relevant categories are summed. A parametric bootstrap is used to find 95% CIs on the estimated abundance of wild (W), ad-clipped hatchery (H), and ad-intact hatchery (HNC). The parametric bootstrap uses the number of adults trapped in each stratum along with the three estimated multinomial proportions for W, H, and HNC in that stratum to produce bootstrap pseudo values for numbers of fish by rearing category. These are converted to pseudo proportions by stratum and multiplied by weekly ascensions to produce bootstrap estimates of totals by W, H, and HNC. The three bootstrap series of estimates are ordered and the 2.5[th] and 97.5[th] percentiles give the three one-at-a-time confidence intervals. All CIs are generated for the spawn year total rather than for individual strata.

Further, for each stratum a two-way table of proportions was calculated for combinations of the primary and secondary variable categories. For each stratum, these proportions are applied to estimated numbers of fish of the given rearing type and primary category to get estimates of numbers of fish for each level of the secondary category. That is, if one fixes a primary category, then the estimated number of fish of that primary category is decomposed into estimates for each of the secondary categories. Summing over primary categories, the resulting estimate of fish in each secondary category is constrained to sum to the total fish found in the primary categories. Each row of a table of proportions for fixed stratum and primary category was used to produce multinomial parametric bootstrap pseudo values for numbers of fish in each secondary category leading to confidence intervals for the corresponding estimates.

In the model, whole fish numbers are being multiplied or divided by fractions, therefore additional rounding steps were needed to adjust point estimates in the final output of data. First, all rear types must sum to the total adjusted escapement (Figure 3). If rear types do not sum to the total adjusted escapement, fish were added or subtracted from the rear type with the largest number of fish. Second, genetic stock estimates must sum to the wild fish estimate. If not, fish were added or subtracted from the genetic stock with the largest number of fish. The adjusted estimates for the genetic stocks were used to further adjust the MPG and composition estimates. Estimates for MPGs were adjusted to match the summation of corresponding genetic stocks (e.g., for steelhead, all genetic stocks with suffix CLWR combine into the Clearwater MPG (CLRWTR), and all genetic stocks with suffix SALM combine into the Salmon MPG [SALMON]). For composition estimates (size, sex, age class), fish were added or subtracted from the group with the largest number of fish (e.g., male and female CHMBLN need to add up to the total genetic stock estimate for CHMBLN). For total age and saltwater age composition estimates within each genetic stock, estimates must sum to the corresponding aggregation of age class composition estimates within each genetic stock. Fish were added or subtracted from each total age and saltwater age group to match the corresponding aggregation of age classes, (e.g., two-saltwater age CHMBLN must sum to the aggregated total estimate from age classes F1S2 and F2S2 for CHMBLN). After adjusting composition groups within each genetic stock, individual composition group estimates over all genetic stocks were summed to obtain aggregate estimates (e.g., male aggregate estimate is the sum of all male estimates from each genetic stock). All aggregate composition estimates must add up to the rear-type estimate. In general, adjustments involved adding or subtracting fewer than five fish.

Adult-to-Adult Productivity

Adult-to-adult productivity is the number of returning recruits (i.e, adults) per parent spawner, and it is calculated for the entire run and for each genetic stock. Final adult-to-adult productivities are calculated for the completed brood while preliminary productivities are calculated for the following brood year. A brood year cohort of steelhead and Chinook Salmon is considered complete when we check if any adult fish from this brood year with a total age of 8 and 6 years, respectively, are observed at LGR in the spawn year (here it is 2023) undergoing analysis. However, as age structure shifts though time we can use proportions of total age classes to adjust the rate at which a brood year is complete for either species. A completed brood year comprises multiple spawn years given the variation in the total age of adult fish at LGR. Productivity is calculated by dividing the number of returning recruits for the completed brood year by the number of parent spawners in this brood year. The replacement rate is 1 returning recruit per parent spawner. For SY2023 steelhead, brood year 2015 is completed for which final productivities are calculated while preliminary productivities are calculated for brood year 2016. For SY2023 Chinook Salmon, brood year 2017 is completed for which final productivities are calculated while preliminary productivities are calculated for brood year 2018. We exclude the

Lower Snake River stock (steelhead) and the Tucannon River and Fall stocks (Chinook Salmon) from the productivity calculations.

Smolt-to-Adult Return Rate

To estimate the aggregate SAR rate for wild steelhead and Chinook Salmon, the age composition of adults at LGR was combined with estimates of emigrating wild smolt cohorts at LGR. Smolt production estimates for both species were acquired from Ebel et al. (2022). For steelhead, we continue the SAR series that began with smolt migration year (MY) 2010. Repeat spawning steelhead were excluded from the SAR estimates because they were already accounted for on their maiden spawning migration. Further, repeat spawners likely have different downstream survival rates than smolts. For Chinook Salmon, we continue the SAR series that began with MY1996. No smolt estimates were available for MY2020 due to COVID-19 closures; IDFG and FPC personnel are collaborating to develop the best approach to address the data gap implications.

Smolt-to-adult return rates (SAR_k) for a particular smolt migration year (k) were calculated using this equation:

$$SAR_k = \frac{\sum_{l-1}^{4} r_{k+l}}{S_k},$$

where r_{k+l} is the adult return from that cohort in year $k + l$; l is saltwater age; and S_k is the estimate of smolts migrating in year k. The maximum value of l was four because that was the maximum saltwater age observed for steelhead and spring-summer Chinook Salmon at LGR (Copeland et al. 2004). Formulas from Fleiss (1981) were used to estimate the 95% confidence limits on SAR values. The lower limit is given by

$$\frac{\left(2np + t_{\alpha/2}^2 - 1\right) - t_{\alpha/2}\sqrt{t_{\alpha/2}^2 - (2 + 1/n) + 4p(nq + 1)}}{2\left(n + t_{\alpha/2}^2\right)},$$

and the upper limit by

$$\frac{\left(2np + t_{\alpha/2}^2 + 1\right) + t_{\alpha/2}\sqrt{t_{\alpha/2}^2 + (2 + 1/n) + 4p(nq + 1)}}{2\left(n + t_{\alpha/2}^2\right)},$$

where n is the number of smolts, p is the SAR value as a proportion, q is 1-SAR, and $t_{\alpha/2}$ is 1.96.

RESULTS

Steelhead Escapement

The total escapement estimate of steelhead for SY2023 was 76,203 fish (74,953–77,589 95% CI) based on a window count of 75,015 fish (Table 2). The fallback-reascension rate was 6.77% (5.68–7.88% 95% CI) for upper stock groups (upstream of LGR) and 9.29% (5.93–13.59% 95% CI) for the lower stock group (downstream of LGR). The overall nighttime passage rate for

the entire run was 8.34% (7.22–9.67% 95% CI). Of the 76,203 fish, the LGR trap captured 14,531 of them, of which 2,760 were valid wild fish (Appendix A-5). Our estimate of wild escapement was 13,631 fish (13,104–14,201 95% CI), which comprised approximately 18% of the total estimate (Table 2). The remaining 62,572 fish were of hatchery origin. We estimate ad-clipped hatchery escapement was 57,241 fish (56,181–58,399 95% CI) and ad-intact hatchery escapement was 5,331 fish (4,998–5,661 95% CI). External marks, internal tags, and genetics were used to determine that 9% of the total hatchery fish and 7% of the total steelhead run were ad-intact hatchery fish. Hatchery fish comprised 28% of all ad-intact steelhead.

Steelhead by Genetic Stock, Size, Sex, and Age

Relative abundance of wild steelhead among genetic stocks varied greatly in SY2023. The Grande Ronde River stock had the highest abundance, and the Lower Clearwater River stock had the lowest abundance, comprising 27% and 2% of the total wild escapement, respectively (Appendix D-1). Escapement estimates for each genetic stock were as follows (Appendix D-2): UPSALM 1,973 (1,700–2,264 95% CI); MFSALM 1,083 (920–1,256 95% CI); SFSALM 390 (291–493 95% CI); LOSALM 370 (198–542 95% CI); UPCLWR 1,716 (1,515–1,929 95% CI); SFCLWR 1,094 (936–1,259 95% CI); LOCLWR 282 (146–427 95% CI); IMNAHA 970 (782–1,168 95% CI); GRROND 3,670 (3,334–4,030 95% CI); and LSNAKE 2,083 (1,738–2,431 95% CI).

Small steelhead (<78 cm fork length [FL]) comprised 59% of the adipose fin-clipped hatchery run and large steelhead (≥78 cm FL) comprised 63% of the adipose fin-intact hatchery run. The highest percentage of small steelhead was found in the wild run at 79%. Estimated escapement for small wild steelhead was 10,701 fish (10,210–11,160 95% CI), for small ad-clipped hatchery steelhead was 33,589 fish (32,310–34,940 95% CI), and for small ad-intact hatchery steelhead was 1,953 fish (1,757–2,170 95% CI). Estimated escapement for large wild steelhead was 2,930 fish (2,677–3,219 95% CI), for large ad-clipped hatchery steelhead was 23,652 fish (22,435–24,933 95% CI), and for large ad-intact hatchery steelhead was 3,378 fish (3,105–3,650 95% CI). The highest percentage of large steelhead (≥78 cm FL) was found within the ad-intact hatchery fish, likely driven by the Dworshak hatchery stock, of which many are intentionally released as ad-intact. Stock-specific estimates for wild fish by size are reported in Appendix D-2.

Wild female steelhead comprised 76% of the total wild steelhead escapement at LGR (Appendix D-3). Sex-specific escapement was estimated to be 10,418 females (9,983–10,888 95% CI) and 3,213 males (2,948–3,487 95% CI). Sex ratios for each genetic stock mirrored the aggregate wild run and ranged from 72% for the South Fork Clearwater River to 83% for the Middle Fork Salmon River (Appendix D-2).

Twenty different age classes were observed from the 2,161 wild fish that were assigned a genetic stock and a total age (Appendix D-4). Total age at spawning ranged from 3-8 years with freshwater age ranging from 1-4 years and saltwater age ranging from 1-3 years. Some steelhead returned as repeat spawners. Repeat spawning fish made up 0.9% of the total wild steelhead ascending LGR. Repeat spawners were observed in all genetic stocks except for the LOCLWR. Repeat spawners within each genetic stock ranged from 0.23% (UPCLWR) to 2% (SFSALM).

For seven of the ten genetic stocks of steelhead, the most abundant total age cohort was age-5 fish (hatched in BY2018; Appendix D-4). The most abundant total age cohort of the remaining three stocks was age-6 fish (BY2017; MFSALM, UPCLWR, and SFSALM). We estimated that 103 (55–157 95% CI) of the returning adults were age-3 fish (BY2020); 1,986 (1,763–2,203 95% CI) were age-4 fish (BY2019); 6,768 (6,385–7,200 95% CI) were age-5 fish

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(BY2018); 4,427 (4,106–4,777 95% CI) were age-6 fish (BY2017); 327 (242–426 95% CI) were age-7 fish (BY2016); and 20 (0-48 95% CI) were age-8 fish (BY2015).

Most of the wild return (57%) emigrated to the ocean as age-2 smolts and, excluding repeat spawners, 81% of these spent 2 years in saltwater (Appendix D-5). We estimated that 2,395 fish (2,132–2,632 95% CI) were saltwater age-1 (MY2021); 10,894 fish (10,406–11,413 95% CI) were saltwater age-2 (MY2020); 221 fish (143–303 95% CI) were saltwater age-3 (MY2019); and 121 fish (67–180 95% CI) were repeat spawners regardless of their migratory year. Saltwater age 2 was the most abundant age class within each stock (Appendix D-6). The mean fork lengths of saltwater age-1 and saltwater age-2 steelhead were less than the 78 cm FL threshold for large steelhead while the mean fork length of saltwater age-3 steelhead was greater than this threshold (Appendix D-7).

Readers accurately determined the saltwater age of 96.8% of the scale samples (n = 32) from steelhead with known saltwater ages that were collected during SY2023 (Appendix C-1). The known saltwater age sample was 28% saltwater age-1 steelhead and 72% saltwater age-2 steelhead. There were no saltwater age-3, saltwater age-4, or repeat spawners in the known saltwater age sample.

Steelhead Adult-to-Adult Productivity

Wild steelhead returning to LGR in SY2023 completed the BY2015 cohort, allowing an adult-to-adult productivity estimate. Brood year 2015 returned 11,823 adults from 45,789 parents, resulting in an overall adult-to-adult productivity estimate of 0.26 recruits per spawner, which is well below the 1.0 recruit per spawner necessary for replacement (Figure 5). A preliminary estimate of an overall adult-to-adult productivity for the BY2016 cohort also placed it below replacement (0.47 recruits per spawner). Although unlikely to change significantly, the estimate for BY2016 is preliminary and will be completed with the SY2024 return.

None of the genetic stocks had BY2015 adult-to-adult productivity estimates that were above replacement (Figure 6). The recruits per spawner estimates for each stock were as follows: UPSALM 0.26, MFSALM 0.23, SFSALM 0.18, LOSALM 0.13, UPCLWR 0.21, SFCLWR 0.23, LOCLWR 0.14, IMNAHA 0.20, and GRROND 0.36. Estimates for LSNAKE were excluded because the fish from this stock recorded at LGR were only a proportion of the total returning adults; therefore, productivity estimates for LSNAKE were not representative of the entire stock. Preliminary estimates of adult-to-adult productivity by genetic stock for BY2016 placed all genetic stocks below replacement. The estimates for BY2016 are preliminary and will be completed with the SY2024 return.

Steelhead Smolt-to-Adult Return Rate

This report continued the SAR rate series that began with smolt MY2010 (Table 3; Figure 7). With adult returns from SY2023, the SAR time series was completed for MY2010–MY2019. The most recently completed cohort, MY2019, returned 5,723 fish from 845,815 emigrants for a SAR estimate of 0.68% (0.66–0.69% 95% CI). The 5-year geometric mean SAR was 1.01%.

Chinook Salmon Escapement

The total escapement estimate for Chinook Salmon in SY2023 was 60,312 fish (59,362–61,292 95% CI) based on a window count of 63,368 fish (Table 4). The overall fallback-reascension rate for the entire run was 8.68% (7.46–9.80% 95% CI) and the overall nighttime

passage rate was 4.06% (3.26–4.98% 95% CI). Of the 60,312 fish, the LGR trap captured 11,300 of them, of which 1,603 were valid wild fish (Appendix A-6). Our estimate of wild escapement was 8,028 fish (7,642–8,438 95% CI), which comprised approximately 13% of the total estimate (Table 4). The remaining 52,284 fish were of hatchery origin. We estimated that ad-clipped hatchery escapement was 46,766 fish (45,883–47,687 95% CI) and ad-intact hatchery escapement was 5,518 fish (5,185–5,822 95% CI). External marks, internal tags, and genetics were used to determine that 11% of the total hatchery fish and 9% of the total Chinook Salmon run were ad-intact hatchery fish. Hatchery fish comprised 41% of all ad-intact Chinook Salmon.

Chinook Salmon by Genetic Stock, Size, Sex, and Age

Relative abundance of wild Chinook Salmon by genetic stock varied greatly in SY2023. The Hells Canyon stock had the highest abundance and the Tucannon River stock had the lowest abundance, comprising 33% and 0% of the total wild escapement, respectively (Figure 8; Appendix E-1). Escapement estimates for each genetic stock were as follows (Appendix E-2): UPSALM 1,092 (932–1,303 95% CI); CHMBLN 116 (64-171 95% CI); MFSALM 934 (772–1,125 95% CI); SFSALM 2,131 (1,907–2,427 95% CI); HELLSC 2,678 (2,409–2,990 95% CI); TUCANO 0 (0–0 95% CI); and FALL 1,077 (719–1,206 95% CI).

Large Chinook Salmon (≥57 cm FL) comprised 84% of the ad-clipped hatchery run, 81% of the adipose fin-intact hatchery run, and 94% of the wild run. Estimated escapement for large wild Chinook Salmon was 7,572 fish (7,114–7,900 95% CI), for large ad-clipped hatchery Chinook Salmon was 39,432 fish (38,612–40,285 95% CI), and for large ad-intact hatchery Chinook Salmon was 4,474 fish (4,189–4,779 95% CI). Estimated escapement for small wild Chinook Salmon was 456 fish (358–703 95% CI), for small ad-clipped hatchery Chinook Salmon was 7,334 fish (6,956–7,708 95% CI), and for small ad-intact hatchery Chinook Salmon was 1,044 fish (878–1,161 95% CI). Stock-specific estimates for wild fish by size are reported in Appendix E-2.

Wild male Chinook Salmon comprised 56% of the total wild Chinook Salmon escapement at LGR (Appendix E-3). Sex-specific escapement was estimated to be 4,467 males (4,177–4,777 95% CI) and 3,561 females (3,273–3,829 95% CI). Male sex ratios within genetic stocks ranged from 53% for the Fall stock to 69% for the Chamberlain Creek stock (Appendix E-2).

Seven different age classes were observed from the 1,368 wild fish that were assigned a genetic stock and a total age (Appendix E-4). Age at spawning (i.e, total age) ranged from 3-6 years, with freshwater age ranging from 1-2 years and saltwater age ranging from 0-3 years.

For all but one genetic stock, age-4 fish (hatched in BY2019) were the most abundant total age cohort; age-5 (BY2018) fish were most abundant in the Fall Chinook stock (Appendix E-4). We estimated that 783 (661–969 95% CI) of the returning adults were age-3 fish (BY2020); 4,912 (4,593–5,259 95% CI) were age-4 fish (BY2019); 2,297 (2,017–2,517 95% CI) were age-5 fish (BY2018); and 36 (7–69 95% CI) were age-6 fish (BY2017).

Most of the wild return (94%) emigrated to the ocean as age-1 smolts and 66% spent 2 years in saltwater (Appendix E-5). Further, these fish have a total age of 4 years since they were brooded in 2019. We estimated that 8 fish (0–28 95% CI) were saltwater age zero (minijacks from MY2023); 801 fish (674-971 95% CI) were saltwater age-1 (i.e., jacks) (MY2022); 5,271 fish (4,929–5,568 95% CI) were saltwater age-2 (MY2021); and 1,948 fish (1,753–2,155 95% CI) were saltwater age-3 (MY2020). Further, saltwater age-2 was the most abundant age class in all the returning Chinook Salmon genetic stocks (Appendix E-6). The mean FL for saltwater age-1 Chinook Salmon was less than the 57-cm FL threshold for large Chinook Salmon while the mean

FL for saltwater age-2 and saltwater age-3 Chinook Salmon was greater than this threshold (Appendix E-7).

Readers accurately determined the saltwater age of 91.2% of the scale samples (n = 57) from Chinook Salmon with a known saltwater age that were collected in SY2023 (Appendix C-2). The known saltwater age sample was 9% saltwater age-1, 82% saltwater age-2, and 9% saltwater age-3. There were no saltwater age-4 fish in the known saltwater age sample.

Chinook Salmon Adult-to-Adult Productivity

Wild Chinook Salmon returning to LGR in SY2023 completed the BY2017 cohort, allowing an adult-to-adult productivity estimate. Brood year 2017 returned 8,037 adults from 5,793 parents, resulting in an overall adult-to-adult productivity estimate of 1.39 recruits per spawner, which is slightly above the 1.0 recruit per spawner necessary for replacement (Figure 9). A preliminary estimate of adult-to-adult productivity for the BY2018 cohort (2.58 recruits per spawner) placed it above replacement. Although unlikely to change significantly, the estimate for BY2018 is preliminary and will be completed with the SY2024 return.

Adult-to-adult productivity estimates for BY2017 were at or slightly above replacement for four stocks. Recruits per spawner for each genetic stock were as follows: UPSALM 1.47; CHMBLN 0.58; MFSALM 0.97; SFSALM 1.78; and HELLSC 1.07 (Figure 10). Estimates for TUCANO and FALL stocks were excluded because the fish from these stocks recorded at LGR were only a proportion of the total returning adults so productivity estimates for these two stocks were not representative of the entire stock. Preliminary estimates of adult-to-adult productivity by genetic stock for BY2018 placed all stocks above replacement. The estimates for BY2018 are preliminary and will be completed with the SY2024 return.

Chinook Salmon Smolt-to-Adult Return Rate

This report continued the SAR rate series that began with smolt migration year 1996 (Table 5;Figure 11). With adult returns from SY2023, the SAR time series was completed for MY1996–2019. The most recently completed cohort, MY2019, returned 8,145 adults from 794,695 yearling emigrants for a SAR estimate of 1.02% (1.0–1.05% 95% CI). The 10-year geometric mean SAR was 1%, and the 5-year geometric mean SAR was 0.66%.

DISCUSSION

The total escapement of returning SY2023 steelhead at Lower Granite Dam increased by 31,482 fish compared to SY2022 (Table 2). Wild steelhead escapement was 13% of the proposed escapement goal of 104,500 fish and 65% of NMFS' minimum abundance threshold of 21,000 fish, to the Snake River basin (NMFS 2017; IDFG 2019; Columbia Basin Partnership Task Force 2020). We noted the 5-year geometric mean of wild steelhead escapement (11,367 fish for SY2019–2023) was 43% of the previous 5-year geometric mean (26,275 fish for SY2014–2018). In four of the ten wild steelhead stocks (Upper Salmon River, Upper Clearwater River, South Fork Clearwater River, and Grande Ronde River), escapement estimates increased significantly from SY2022 to SY2023 as evidenced by non-overlapping confidence intervals (Figure 4). The abundance of the remaining steelhead genetic stocks did not change significantly from last year (i.e., confidence intervals overlapped).

The total escapement of returning SY2023 spring-summer Chinook Salmon at Lower Granite Dam decreased by 22,788 fish compared to SY2022 (Table 4). Wild Chinook Salmon escapement was 6% of the proposed escapement goal of 127,000 fish and 25% of NMFS' minimum abundance threshold of 31,500 fish, to the Snake River basin (NMFS 2017; IDFG 2019; Columbia Basin Partnership Task Force 2020). We noted the 5-year geometric mean of wild Chinook Salmon escapement (9,716 fish for SY2019–2023) was 58% of the previous 5-year geometric mean (16,735 fish for SY2014–2018). In five of the seven wild Chinook Salmon stocks (Upper Salmon River, Chamberlain Creek, Middle Fork Salmon River, South Fork Salmon River, and Hells Canyon), escapement estimates decreased significantly from SY2022 to SY2023 as evidenced by non-overlapping confidence intervals (Figure 8). The abundance of the remaining genetic stocks (Tucannon River and Fall Chinook) which are not representative, did not change significantly from last year.

Regardless of abundance, low adult-to-adult productivity estimates are a major cause for concern because steelhead and Chinook Salmon populations with productivities far below one recruit per spawner (replacement) are at risk of severe population declines or extirpation. The 5-year average of overall adult-to-adult productivity for steelhead (BY2011-2015) and Chinook Salmon (BY2013-2017) was below replacement at 0.48 and 0.54 recruits per spawner, respectively (Figures 5 and 9). Also, all stocks of each species showed productivities that were below replacement when averaged across the last five completed brood years (Figures 6 and 10). The most recently completed brood year for Chinook Salmon (i.e., 2017) showed an overall productivity that was above replacement which had not occurred since BY2011 (Figure 9). However, the overall spawner abundance of Chinook Salmon in BY2017 was only 5,793 fish compared to 26,583 fish in BY2011. Further, the preliminary BY2018 adult-to-adult productivity estimates for all wild Chinook Salmon stocks are projected to be above replacement (i.e., ranging from 2.18-4.46; Figure 10). In contrast, the preliminary BY2016 productivity estimates for all wild steelhead stocks are projected to be below replacement (Figure 6). Small stocks with dwindling productivities (such as the LOSALM steelhead stock or CHMBLN Chinook Salmon stock) are particularly vulnerable to extirpation, and their extinction would be a big loss for the overall genetic diversity of both species in the Snake River basin.

Adult-to-adult productivity is directly linked to smolt-to-adult return rates, which have also remained below management goals. The 5-year geometric mean SAR for both species was below the NPCC fish and wildlife program objective to achieve a range of 2–6% (mean of 4%; NPCC 2014, 2020; Figures 7 and 11). The most recently completed migration year cohort of steelhead and Chinook Salmon (MY2019) showed SAR rates below the objective range (Figures 7 and 11). Further, the SAR rate from MY2018 to MY2019 decreased by 1.38% for steelhead and increased by 0.31% for Chinook Salmon (Figures 7 and 11). Estimated Chinook Salmon SARs using our analysis have been slightly higher but closely track the estimates provided by the Comparative Survival Study (CSS; McCann et al. 2015). Smolt-to-adult returns rates are affected by environmental conditions, predation, and other factors that vary among years but are also directly influenced by the marine environment and passage conditions at hydropower dams during smolt outmigration (Petrosky et al. 2020). Although ocean conditions are becoming increasingly variable and unfeasible to regulate, managers may be able to improve SARs by altering passage conditions at hydropower dams. For example, managers have increased the proportion of water flowing through spillways at mainstem dams (including Lower Granite Dam) which may prove beneficial for outmigrating smolts.

Continuous monitoring of population metrics, such as size and age, is essential for adaptive management and tracking trends over time. Steelhead fisheries management in the Columbia and Snake rivers is partially driven by the abundance of large steelhead, often called

B-run steelhead in fisheries regulations, counted at Bonneville and Lower Granite dams. B-run steelhead are defined as fish ≥78 cm FL and are often associated with having a saltwater age of 2 years. A-run steelhead (<78 cm FL) can also return as saltwater age-2 but are smaller in size than the B-run dominated stocks. The mean length for saltwater age-2 steelhead in SY2023 was 6 cm less than the length cutoff for the B-run/large size classification. In SY2023, the mean fork length of steelhead with a saltwater age of 2 was 70 cm for the A-run group and 81 cm for the B-run group. Also, SY2023 saltwater age-2 steelhead were on average 1 cm smaller than SY2022 saltwater age-2 steelhead (Appendix D-7). The depressed returns of steelhead populations that typically produce larger saltwater age-2 and age-3 fish (i.e., the Upper Clearwater, South Fork Clearwater, Middle Fork Salmon, and South Fork Salmon river wild populations and the Dworshak hatchery stock) may have contributed to the greater return of small (i.e., A-run) steelhead in the aggregate SY2023 escapement (Appendix D-2, Table 2). This poses a challenge to fisheries managers because it has impacted fishing regulations and public perception of fewer returning B-run steelhead (Copeland et al. 2017; Bowersox et al. 2019). It is also important to recognize that size and age trends could behave differently between A-run dominant and B-run dominant stocks; therefore, fisheries managers must be cautious in their data interpretation and instead look at stock-specific trends to better inform their conclusions. Interspecific interactions with other Pacific salmonids can impact the abundance of B-run steelhead. Pink Salmon are often substantially more abundant in odd-numbered calendar years, and a negative correlation between the interannual change in abundance of Pink Salmon and B-run steelhead has been shown across 38 years (Ruggerone et al. 2023). In contrast, A-run steelhead do not show a significant difference in abundance between odd and even years, suggesting less interaction or competition with Pink Salmon compared to B-run steelhead (Ruggerone et al. 2023). Further, we expect to see large interannual variation in the overall and stock-specific abundance of A- and B-run steelhead. Overall, several factors such as hydropower passage and ocean conditions influence anadromous salmonid survival in river and ocean systems (Lawson et al. 2004; Schaller et al. 2014), and fisheries managers must consider the relationships between these factors in the context of life history and survival.

In this report, we omitted the productivity estimates for three genetic stocks because only a portion of the stock population could be accounted for at LGR. In these data, a genetic stock can have an incomplete estimate in two ways. The first is that the genetic stock, fully or partially, contains populations that originate downstream of LGR. The LSNAKE (steelhead) and TUCANO (Chinook Salmon) stocks contain the Tucannon River population located downstream of LGR. Some returning adults that are born in the Tucannon River overshoot their natal stream and stray upstream of LGR (Boggs et al. 2004; Richins and Skalski 2018). Without abundance information from the Tucannon River for each species, estimates for the LSNAKE and TUCANO should be considered minimum returns to the Snake River basin. The second way is that a genetic stock overlaps run designations defined by USACE calendar dates. The FALL (Chinook Salmon) genetic stock reported here only includes fall-run Chinook Salmon that cross LGR during the spring-summer Chinook Salmon run period (March 1–August 17): fish from the FALL stock that cross LGR after August 17 and the few fish from the FALL stock that spawn downstream of LGR are unaccounted for. Most of the FALL genetic stock ascend LGR after August 17. However, by accounting for FALL Chinook Salmon trapped on August 17 and earlier, we get a better estimate of the true spring-summer stocks returning to the Snake River. Also, only a small amount (<30 PIT-tagged fish in any given year) of spring-summer Chinook Salmon ascend LGR after August 17 (unpublished data). However, quantifying abundances of spring-summer Chinook Salmon during the USACE fall-run period designation is not within the scope of this report. Reporting estimates from the incomplete genetic stocks is conducted for accounting purposes and inferences should not be made using the associated results. The inclusion of these stocks

provides critical information for a more refined decomposition of the aggregate run at LGR into desired reporting groups.

The recently developed EASE model (first implemented in SY2021) estimated escapement of steelhead and Chinook Salmon at LGR by using the same basic principles of previous methods but combined their strengths and addressed biases (steelhead run reconstruction [Stark et al. 2021], fall Chinook run reconstruction [Steinhorst et al. 2010], SCOBI [Steinhorst et al. 2017], STADEM [See et al. 2021]). Prior to the SY2021 report (Baum et al. 2022b), wild and hatchery escapement estimates were based on unadjusted window counts (i.e. the counts were treated as a complete census). However, there were a couple of potential biases when estimating total adult escapement at LGR using unadjusted window counts. First, some returning fish were known to fallback downstream of LGR after successfully crossing to the upstream side. The fallback fish that re-ascend the LGR ladder were essentially counted twice at the window. Second, the window was not used to count fish 24 hours a day throughout the season; therefore, the daily counts excluded nighttime passage (USACE 2021, 2022). The EASE model is fundamentally similar to the previously implemented SCOBI model; however, it accounts for nighttime passage rates and stock-specific fallback/reascension rates to inform the total daily counts. Window counts are a critical component of the ESA listing and have been used for decades to evaluate population performance in the hydrosystem (Joint Columbia River Management Staff 2023); therefore, the adjusted EASE escapement estimates are still directly related to and maintain a transparent relationship with window count data. Steelhead and Chinook Salmon window counts at LGR are reported in Tables 2 and 4, respectively. The EASE model also provides a measure of GSI uncertainty when assigning stocks and does not use the number of trapped fish to inform the total number of fish that ascended the ladder. Accounting for all the above issues increases the value of the time series to address multiple management and assessment needs.

This report provides valuable basin-wide escapement information for assessing the status of Snake River steelhead and spring-summer Chinook Salmon. We summarized the abundance and composition of wild adult steelhead and Chinook Salmon returning to LGR in SY2023 and compared these metrics to previous years. Since SY1998, wild steelhead and Chinook Salmon abundance estimates have failed to exceed their species-specific minimum abundance thresholds in most years. Wild steelhead abundance has only exceeded 21,000 fish twelve times in the past 26 years. Wild Chinook Salmon abundance has only exceeded 31,500 fish twice in the past 26 years. Neither species has exceeded their minimum abundance threshold in the past five years. We also updated the adult-to-adult productivity and the SAR rate series for both species. These long-term escapement patterns of steelhead and Chinook Salmon are the result of how each species is responding to different environmental and anthropogenic conditions at various life stages, and we must consider each of these interacting factors to best manage both species.

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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, 2009; Ford 2011, 2015; NMFS 2016). Extirpated populations are shaded.

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 basin upstream of Dworshak Dam.

Table 2. Estimated annual escapement of steelhead by size and origin, spawn years 1998–2023. Large fish were greater than or equal to 78 cm fork length (FL) and small fish were less than 78 cm FL. Ad-clipped and ad-intact refer to the adipose fin. Estimates from 1998–2020 were generated by IDFG and are the USACE window counts decomposed using adult trap data (Alan Byrne, IDFG, personal communication; Camacho et al. 2017, 2018a, 2019a; Lawry et al. 2020; Baum et al. 2022a). Starting in SY2021 (below the dashed line), estimates were generated by IDFG using the USACE window counts, PIT tag detections, and adult trap data in the EASE model (Baum et al. 2022b).

			Estimated number of steelhead at LGR that were:							
Spawn year[a]	EASE escapement estimate	LGR window count	Large wild	Large hatchery ad-clipped	Large hatchery ad-intact	Small wild	Small hatchery ad-clipped	Small hatchery ad-intact	Total hatchery	Total wild
1998	-	86,646	1,325	10,878	0	7,424	67,019	0	77,897	8,749
1999	-	70,662	2,301	17,455	0	7,074	43,832	0	61,287	9,375
2000	-	74,051	914	8,834	0	10,184	54,119	0	62,953	11,098
2001	-	117,302	2,886	17,128	0	17,689	79,589	10	96,727	20,575
2002	-	268,466	3,174	30,677	0	37,545	191,091	5,979	227,747	40,719
2003	-	222,176	13,623	51,358	6,618	28,308	110,535	11,734	180,245	41,931
2004	-	172,510	7,254	23,058	2,132	21,892	106,334	11,840	143,364	29,146
2005	-	151,646	4,774	23,179	2,005	18,297	94,225	9,166	128,575	23,071
2006	-	158,165	3,544	26,143	3,345	14,586	96,644	13,903	140,035	18,130
2007	-	149,166	1,633	33,332	5,880	7,877	85,210	15,234	139,656	9,510
2008	-	155,142	2,924	20,513	3,446	11,242	102,374	14,643	140,976	14,166
2009	-	178,870	5,659	40,713	6,998	18,216	94,205	13,079	154,995	23,875
2010	-	323,382	4,529	16,555	2,700	38,210	231,003	30,385	280,643	42,739
2011[b]	-	208,296	9,584	31,574	4,118	34,549	110,750	17,721	164,163	44,133
2012	-	180,320	4,198	17,801	2,113	35,240	113,038	7,930	140,882	39,438
2013	-	109,186	3,337	13,695	3,970	19,806	63,611	4,767	86,043	23,143
2014	-	108,154	1,885	5,546	1,593	23,470	70,332	5,328	82,799	25,355
2015	-	165,591	6,928	21,067	3,639	38,861	89,341	5,755	119,802	45,789
2016	-	136,150	3,130	8,465	1,408	30,806	88,296	4,045	102,214	33,936
2017	-	101,826	3,001	25,724	4,145	12,575	52,825	3,556	86,250	15,576
2018	-	74,097	263	3,845	539	10,454	56,738	2,258	63,380	10,717
2019	-	51,818	1,232	13,119	2,223	7,055	26,776	1,413	43,531	8,287
2020	-	34,410	400	2,194	871	9,234	20,259	1,452	24,776	9,634
2021[c]	61,315	59,126	3,265	14,181	3,880	12,213	26,248	1,528	45,837	15,478
2022	44,721	42,586	1,292	5,823	1,174	8,515	26,890	1,027	34,914	9,807
2023	76,203	75,015	2,930	23,652	3,378	10,701	33,589	1,953	62,572	13,631

[a] Steelhead at Lower Granite Dam are considered fish passing July 1 through June 30; most steelhead pass the dam in the fall but are assigned to their spawn year the following spring.

[b] Spawn year 2011 was the first year of adult Parentage Based Tagging returns used to adjust wild and hatchery ad-intact fish estimates.

[c] Escapement estimates using EASE model began in SY2021. EASE estimate does not exactly match the LGR window counts. Decomposition estimates add up to EASE escapement estimate, not the LGR window count.

Table 3. Estimated number of wild steelhead smolts, number of wild returning adult steelhead by saltwater age, and percent smolt-to-adult return (% SAR) rate at Lower Granite Dam. Scale samples were used for all smolt migration years. Repeat spawners (shaded) were not used to estimate SARs. The SAR 95% confidence intervals (CI) are in parentheses.

Smolt migration year	Estimated number of smolts[a]	Adults returning to Lower Granite Dam by saltwater age			Repeat spawners	% SAR (95% CI)
		1	2	3		
2005	n/a	n/a	n/a	902	n/a	n/a
2006	n/a	n/a	12,129	869	270	n/a
2007	n/a	10,844	16,404	252	441	n/a
2008	n/a	25,175	32,096	345	643	n/a
2009	n/a	11,360	24,538	157	555	n/a
2010	851,481	14,051	14,596	317	386	3.40 (3.36–3.44)
2011	911,602	7,785	7,750	364	278	1.74 (1.72–1.77)
2012	890,665	16,936	30,450	124	484	5.33 (5.29–5.38)
2013	792,037	14,482	21,839	121	222	4.60 (4.56–4.65)
2014	816,219	11,598	13,499	71	124	3.08 (3.05–3.12)
2015	669,442	1,706	2,040	30	257	0.56 (0.54–0.58)
2016	805,433	8,498	4,169	53	48	1.58 (1.55–1.61)
2017	908,556	3,804	3,993	25	96	0.86 (0.84-0.88)
2018	949,098	5,511	13,988	19	134	2.06 (2.03–2.09)
2019	845,815	1,354	4,148	221	121	0.68 (0.66–0.69)
2020[b]	n/a	5,506	10,894	-	-	-

[a] Smolt abundance for 2010–2019 derived from SCRAPI program (Camacho et al. 2018b, 2019b; Ebel et al. 2022).

[b] Smolt abundance and %SAR unavailable due to COVID-19 trap closures.

Table 4. Estimated annual escapement of Chinook Salmon by origin and saltwater age, spawn years 1998–2023. Jacks were one-saltwater age and include zero-saltwater age mini-jacks; adults were two-saltwater age and older. Estimates from 1998–2020 were generated by IDFG and are the USACE window counts decomposed using adult trap data (Alan Byrne, IDFG, personal communication; Camacho et al. 2017, 2018a, 2019a; Lawry et al. 2020; Baum et al. 2022a). Starting in SY2021 (below the dashed line), estimates were generated by IDFG using a combination of the USACE window counts, PIT tag detections, and adult trap data in the EASE model (Baum et al. 2022b).

Spawn year[a]	EASE escapement estimate	LGR window count	Estimated number of Chinook Salmon at Lower Granite Dam that were:							
			Wild adults[b]	Wild jacks[b]	Total wild	Hatchery adults[b]	Hatchery jacks[b]	Total hatchery	Total adults[b]	Total jacks[b]
1998	-	14,646	5,378	122	5,500	8,831	315	9,146	14,209	437
1999	-	10,647	2,695	236	2,931	3,861	3,855	7,716	6,556	4,091
2000	-	51,835	7,347	1,500	8,847	30,414	12,574	42,988	37,761	14,074
2001	-	192,632	37,063	1,621	38,684	148,630	5,318	153,948	185,693	6,939
2002	-	101,226	27,743	340	28,083	69,441	3,702	73,143	97,184	4,042
2003	-	99,463	29,270	2,349	31,619	57,761	10,083	67,844	87,031	12,432
2004	-	86,501	16,808	982	17,790	62,701	6,010	68,711	79,509	6,992
2005	-	35,100	8,691	386	9,077	25,118	905	26,023	33,809	1,291
2006	-	31,223	8,775	292	9,067	21,312	844	22,156	30,087	1,136
2007	-	42,551	7,694	1,114	8,808	21,034	12,709	33,743	28,728	13,823
2008	-	88,776	14,046	2,333	16,379	53,027	19,370	72,397	67,073	21,703
2009	-	111,580	12,963	3,454	16,417	45,477	49,686	95,163	58,440	53,140
2010	-	134,684	26,281	1,368	27,649	97,273	9,762	107,035	123,554	11,130
2011	-	134,594	22,407	4,176	26,583	69,636	38,375	108,011	92,043	42,551
2012	-	84,771	20,298	1,242	21,540	59,221	4,010	63,231	79,519	5,252
2013	-	70,966	12,407	6,856	19,263	30,556	21,147	51,703	42,963	28,003
2014	-	114,673	26,351	3,987	30,338	65,415	18,920	84,335	91,766	22,907
2015	-	132,432	21,499	1,910	23,409	96,163	12,860	109,023	117,662	14,770
2016	-	81,753	15,939	813	16,752	58,187	6,814	65,001	74,126	7,627
2017	-	48,192	4,108	1,685	5,793	30,180	12,219	42,399	34,288	13,904
2018	-	42,232	6,863	519	7,382	31,820	3,030	34,850	38,683	3,549
2019	-	29,617	4,152	1,010	5,162	19,528	4,927	24,455	23,680	5,937
2020[c]	-	34,786	8,565	1,209	9,774	21,564	3,448	25,012	30,129	4,657
2021[d]	46,429	47,251	6,563	2,041	8,604	29,252	8,573	37,825	35,815	10,614
2022	83,100	92,283	16,048	964	17,012	54,514	11,574	66,088	70,562	12,538
2023	60,312	63,368	7,219	809	8,028	43,621	8,663	52,284	50,840	9,472

a   Spring-summer Chinook Salmon at Lower Granite Dam are considered fish passing March 1 through August 17.

b   For spawn years 2005–2019, the wild vs. hatchery and adults vs. jacks splits were estimated using scale samples, other biological data, and starting in 2011 parentage based tagging (PBT) samples collected at the LGR adult trap. Due to COVID-19 trap closures in SY2020, few scale samples were taken, so adults and jacks were estimated using length at the LGR counting window (adult ≥57 cm FL; jack <57 cm FL). For spawn years 1998–2004 (shaded gray), the splits were estimated using fin ray samples collected on the spawning grounds and biological samples collected at the adult trap. The saltwater ages of hatchery fish were calculated with this formula: spawn year - brood year - freshwater age 2. Hatchery fish that did not assign to a PBT group were proportionally assigned to saltwater ages.

c   Window count, total adult, and total jack numbers for SY2020 are from actual LGR window count data. All other SY2020 estimates were calculated using run reconstruction methods described in Baum et al. (2022a).

Table 4. Continued

[d]   Escapement estimates using EASE model began in SY2021. EASE estimate does not exactly match the LGR window counts. Decomposition estimates add up to EASE escapement estimate, not the LGR window count.

Table 5. Estimated number of wild Chinook Salmon smolts, number of wild returning adult Chinook Salmon by saltwater age, and percent smolt-to-adult return (% SAR) rate at Lower Granite Dam. Fin ray samples were used to estimate age composition for adults returning from smolt migration years 1996–2004 (above the dashed line) whereas scale samples were used in smolt migration year 2005 and after (below the dashed line). SAR 95% confidence intervals (CI) are in parentheses.

Smolt migration year	Estimated number of smolts[a]	Adults returning to Lower Granite Dam by saltwater age					% SAR (95% CI)
		0[b]	1	2	3	4	
1996	419,826	n/a	n/a[c]	628	451	0	0.26 (0.24–0.27)
1997	161,157	n/a	122	2,162	409	23	1.69 (1.62–1.75)
1998	599,159	n/a	236	6,938	1,056	281	1.42 (1.39–1.45)
1999	1,560,298	n/a	1,500	35,984	12,455	481	3.23 (3.20–3.26)
2000	1,344,382	n/a	1,621	15,007	22,724	43	2.93 (2.90–2.96)
2001	490,534	n/a	340	6,065	1,799	53	1.68 (1.65–1.72)
2002	1,128,582	n/a	2,349	14,966	2,739	24	1.78 (1.75–1.80)
2003	1,455,786	n/a	982	5,899	1,886	10	0.60 (0.59–0.62)
2004	1,517,951	n/a	351	6,865	3,903	27	0.73 (0.72–0.75)
2005	1,734,464	35	280	3,781	2,703	22	0.39 (0.38–0.40)
2006	1,227,474	12	1,104	11,316	2,937	0	1.25 (1.23–1.27)
2007	787,150	10	2,306	10,004	1,368	0	1.74 (1.71–1.77)
2008	856,556	27	3,431	24,914	7,658	59	4.21 (4.17–4.26)
2009	894,629	23	1,344	14,751	6,258	14	2.50 (2.47–2.54)
2010	1,268,659	23	3,985	13,980	4,523	0	1.77 (1.75–1.80)
2011	1,184,839	189	1,194	7,870	1,408	0	0.90 (0.88–0.92)
2012	1,674,268	49	6,780	24,942	2,866	27	2.07 (2.05–2.09)
2013	1,006,960	76	3,921	18,633	5,709	33	2.82 (2.79–2.85)
2014	1,406,596	67	1,894	10,203	1,258	0	0.95 (0.94–0.97)
2015	525,743	16	766	2,817	333	5	0.75 (0.73–0.77)
2016	1,424,036	47	1,651	6,530	956	0	0.64 (0.63–0.66)
2017	1,171,926	34	490	3,191	393	5	0.35 (0.34–0.36)
2018	1,437,312	29	992	8,172	929	19	0.71 (0.69–0.72)
2019	794,695	18	1,209	5,629	1,289	0	1.02 (1.00–1.05)
2020[d]	n/a	0	2,009	14,740	1,948	-	n/a

[a]   Smolt abundance for 2010–2023 derived from SCRAPI program (Camacho et al. 2018b, 2019b; Ebel et al. 2022).

[b]   Mini-jack (zero-saltwater age) samples were not sampled on the spawning grounds, thus mini-jack fin rays are not available for smolt migration years 1996–2004; only mini-jacks ≥30 cm FL, were sampled for scales at Lower Granite Dam for smolt migration years 2005–2023.

[c]   Jack (saltwater age-1) fin ray samples were not collected on the spawning grounds and are not available (n/a) for smolt migration year 1996.

[d]   MY2020 smolt estimate and %SAR unavailable due to COVID-19 trap closures.

FIGURES
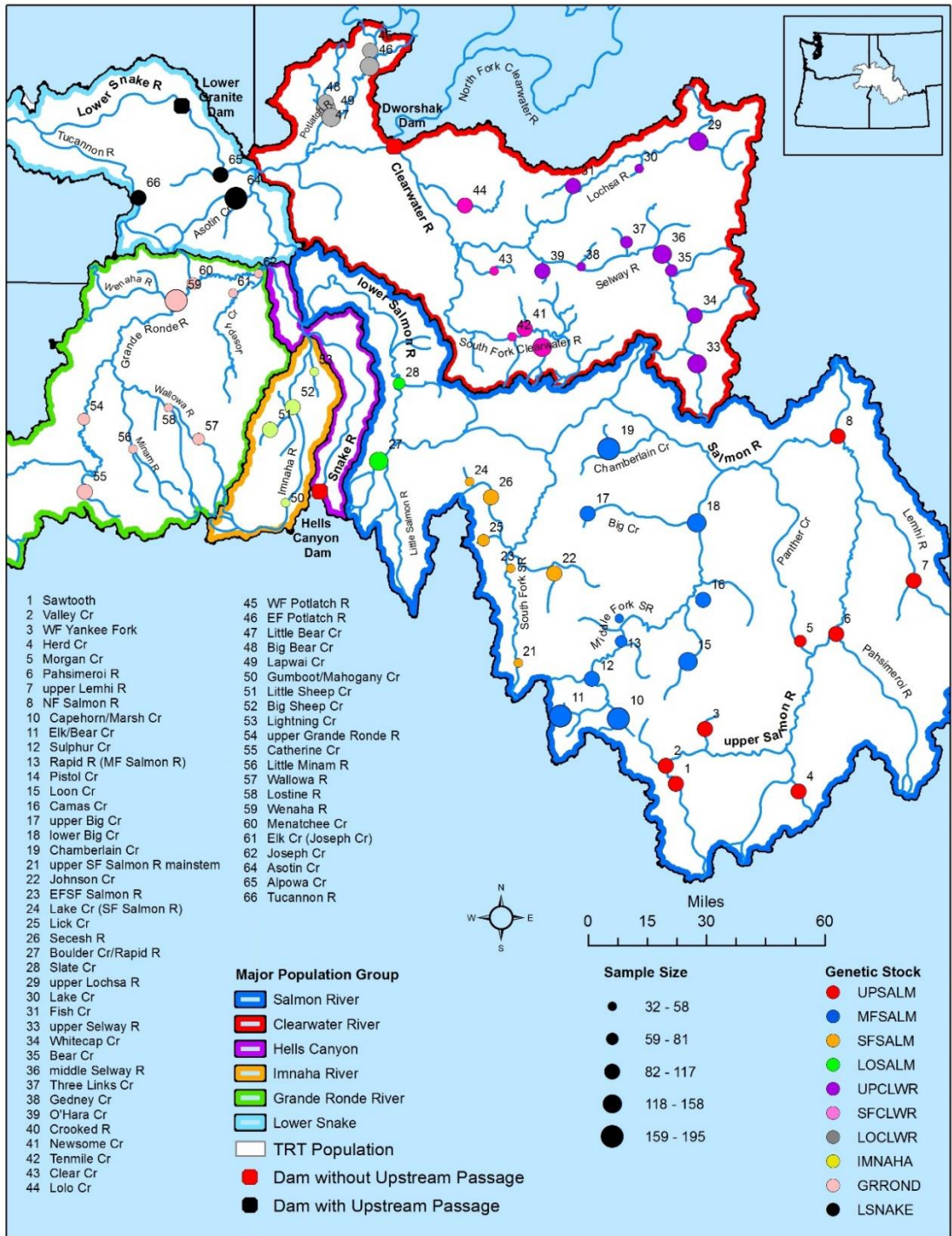
Figure 1.   Map of steelhead genetic stocks and sample collections included in the Snake River basin SNP baseline version 3.1 (Powell et al. 2018) used for genetic stock identification at Lower Granite Dam. A detailed description of collections can be found in Hargrove et al. (2021a). The Hells Canyon Tributaries major population group does not support independent populations and is considered extirpated (NMFS 2016). See Genetic Tissue Processing and Analysis section for definition of genetic stock abbreviations.
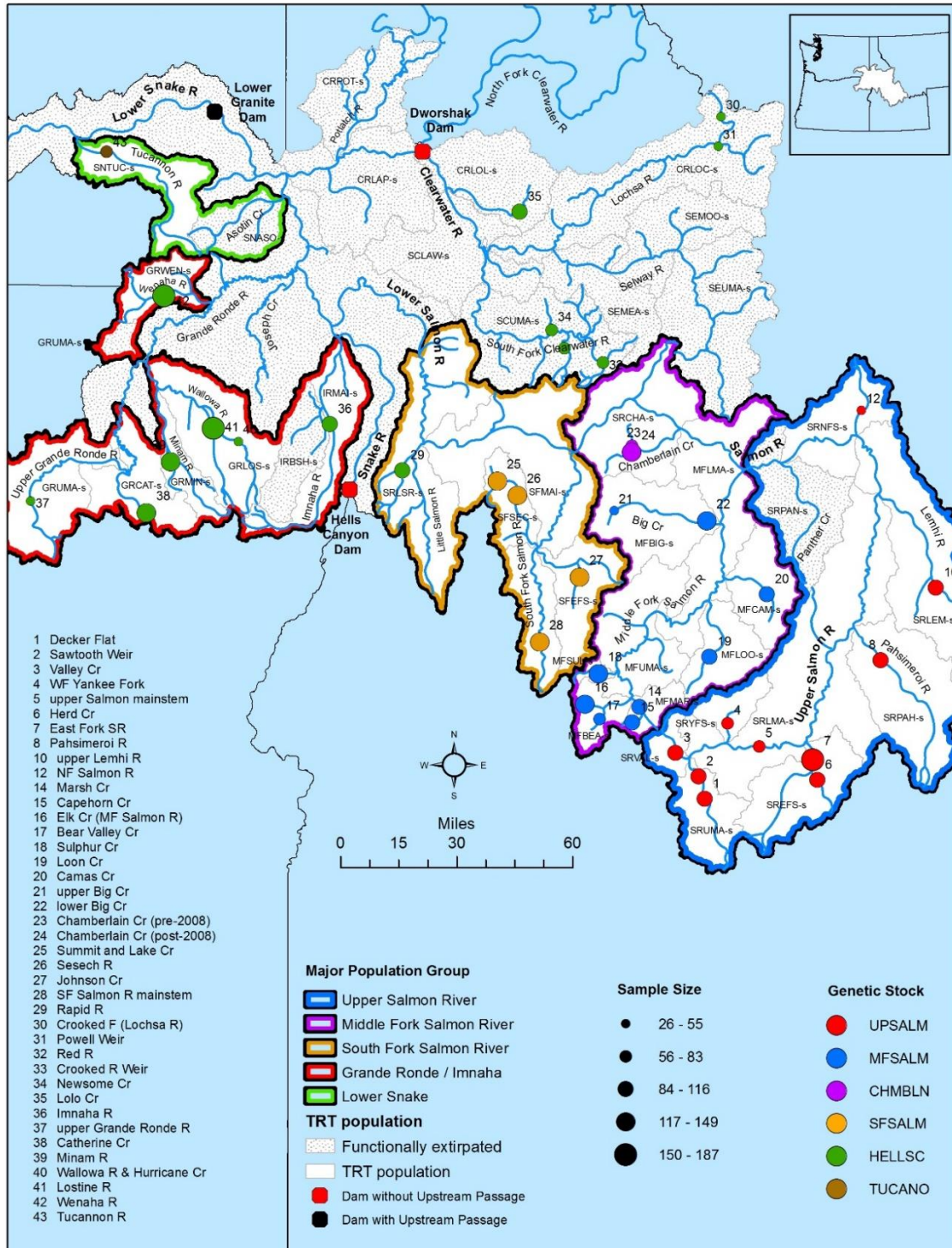
Figure 2. Map of Chinook Salmon genetic stocks and sample collections included in the Snake River basin SNP baseline version 3.1 (Powell et al. 2018) used for genetic stock identification at Lower Granite Dam. A detailed description of collections can be found in Hargrove et al. (2022). Reintroduced fish exist in functionally extirpated TRT populations as mapped. See Genetic Tissue Processing and Analysis section for definition of genetic stock abbreviations.
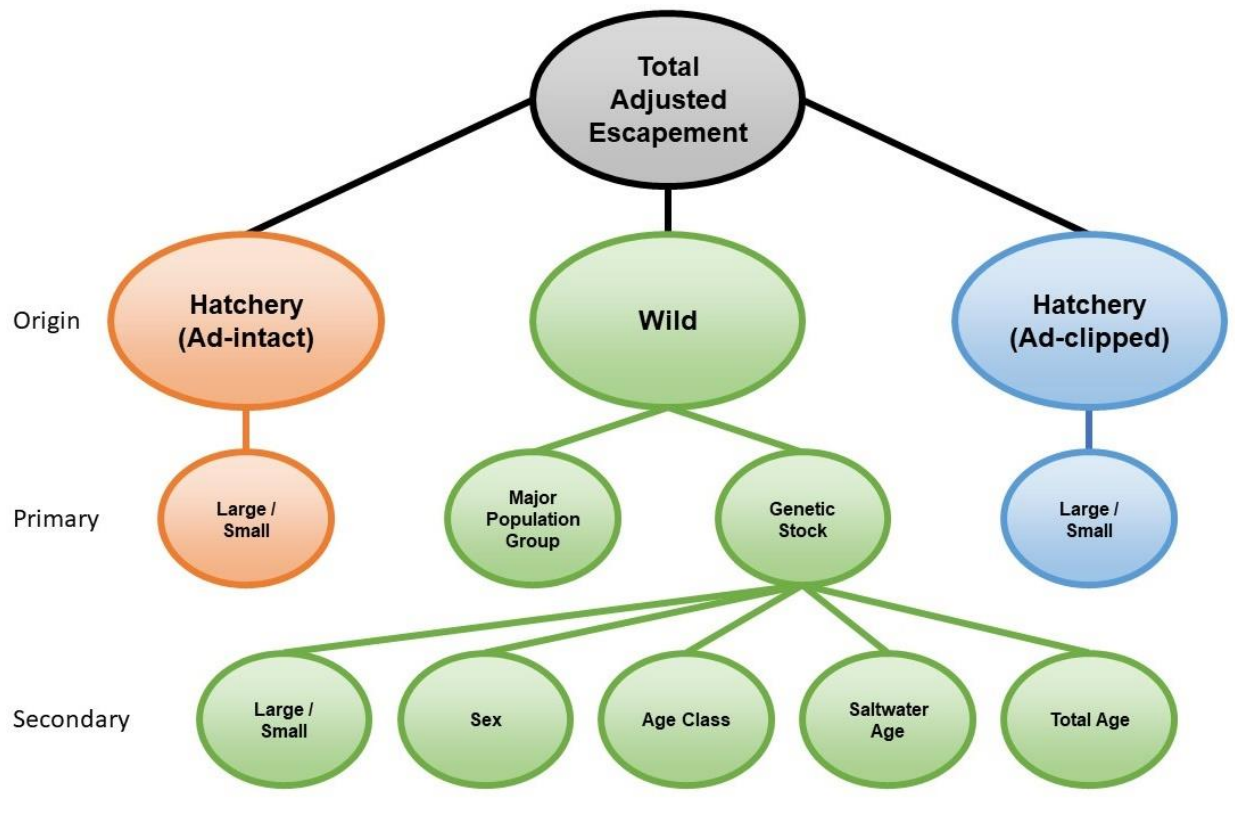
Figure 3.   Schematic of the Lower Granite Dam Estimating Adult Salmonid Escapement (EASE) decomposition model. Total adjusted escapement refers to the LGR window counts with nighttime passage and fallback-reascension rates incorporated. Large/Small refer to fork length (FL) designations for Chinook Salmon where large is ≥57 cm FL and small is <57 cm FL and steelhead where large is ≥78 cm FL and small is <78 cm FL. Fish <30 cm FL are not designated to species and are ignored.
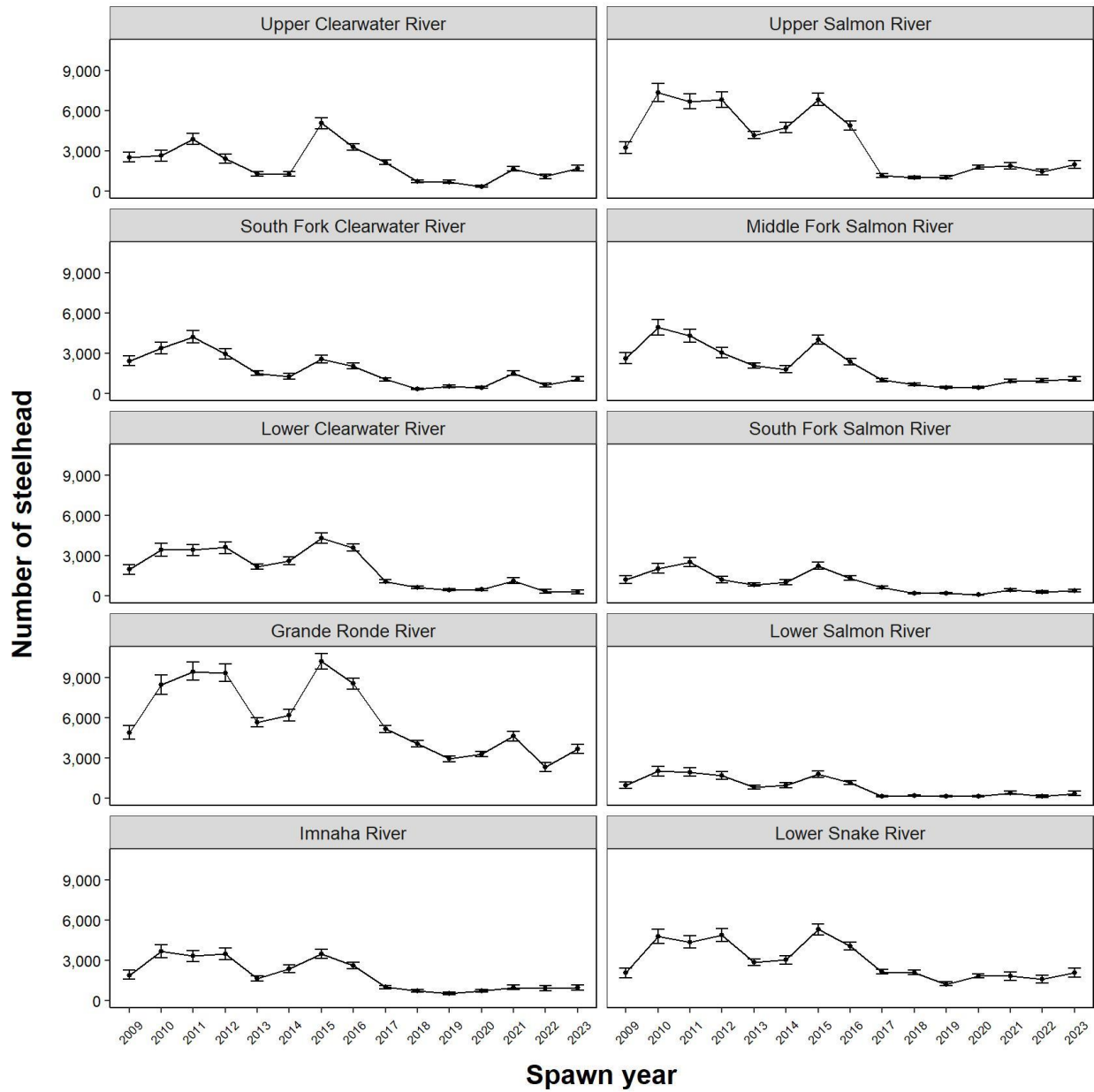
Figure 4.   Estimated escapement of wild steelhead by genetic stock at Lower Granite Dam for spawn years 2009–2023. From SY2009–2021, confidence intervals are at 90%. Starting in SY2022, confidence intervals are at 95%.
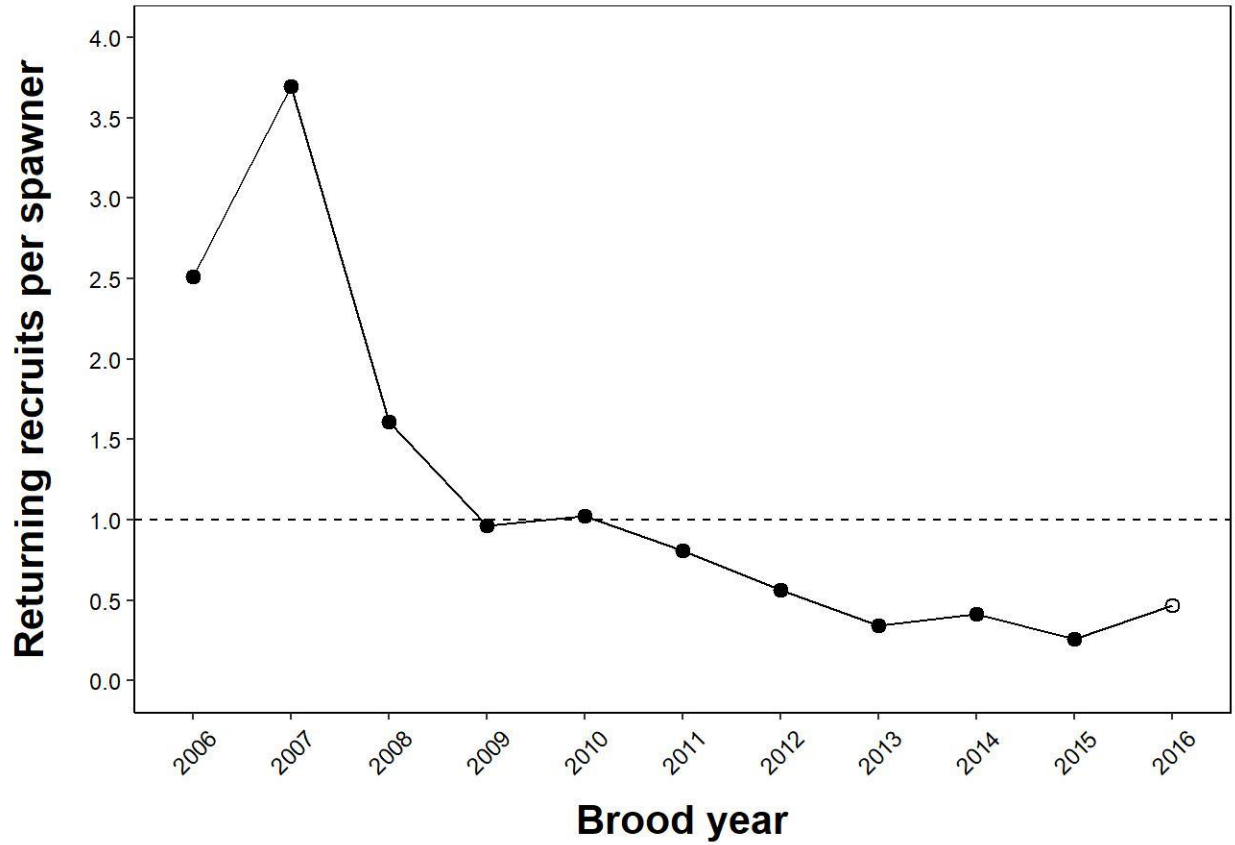
Figure 5.   Adult-to-adult productivity (returning recruits per parent spawner) of wild steelhead at Lower Granite Dam. The dashed line at 1.0 recruit per spawner represents replacement. Spawn year 2023 completed brood year 2015. Brood year 2016 (hollow dot) was shown for reference but represents a preliminary result that will be completed in SY2024.
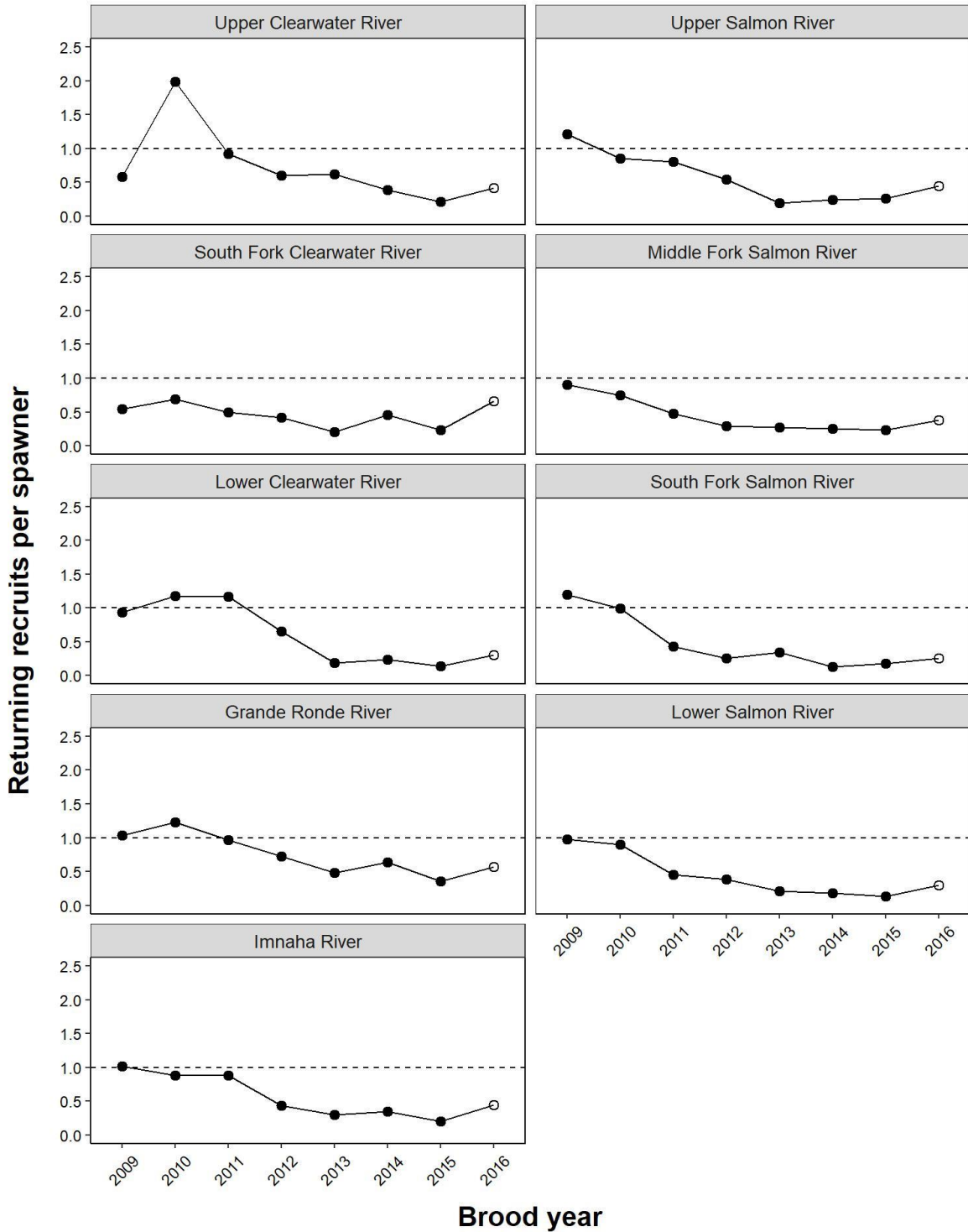
Figure 6.   Adult-to-adult productivity (returning recruits per parent spawner) for each genetic stock of wild steelhead at Lower Granite Dam. The dashed line at 1.0 recruit per spawner represents replacement. Spawn year 2023 completed brood year 2015. Brood year 2016 (hollow dot) was shown for reference but represents a preliminary result that will be completed in SY2024.
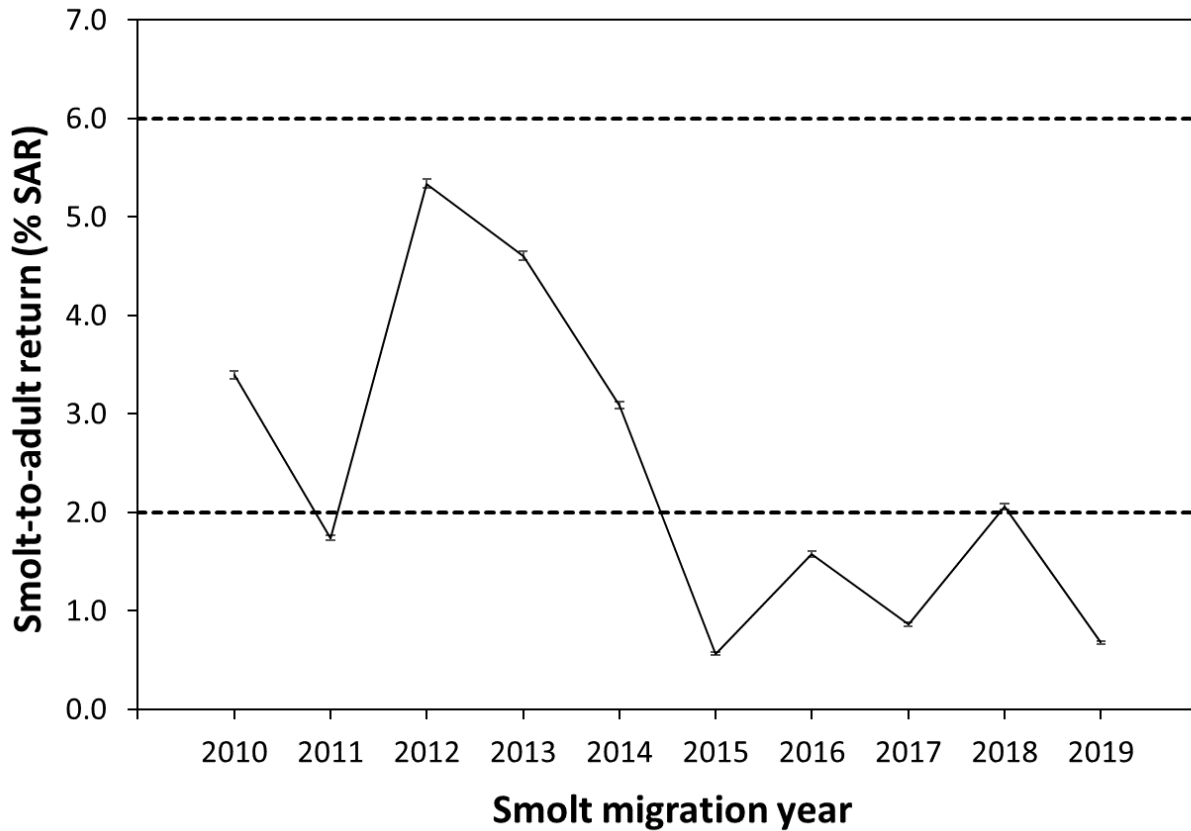
Figure 7.   Estimated wild steelhead smolt-to-adult return (% SAR) rate of emigrant smolts and adult returns to Lower Granite Dam for smolt migration years 2010–2019. Confidence intervals are at 95%. The dashed lines represent the lower and upper range of SAR objectives for wild steelhead established by the Northwest Power and Conservation Council (NPCC 2014, 2020). See Table 3 for more data.
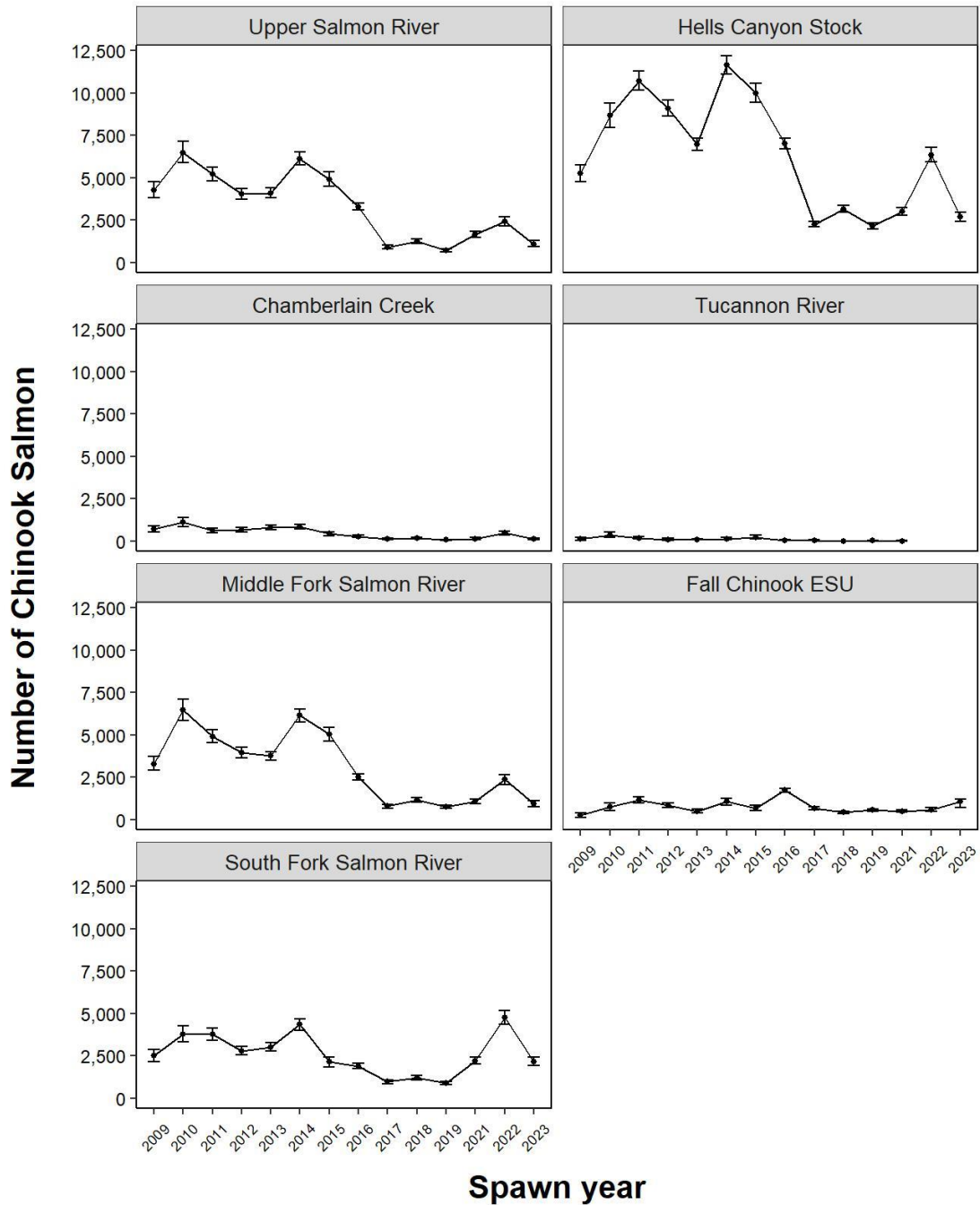
Figure 8.   Estimated escapement of wild Chinook Salmon by genetic stock at Lower Granite Dam from March 1 to August 17 of spawn years 2009–2023. From SY2009–2021, confidence intervals are at 90%. Starting in SY2022, confidence intervals are at 95%. Spawn year 2020 stock-specific estimates exclude jacks and were generated using run reconstruction, so confidence intervals are absent. Hells Canyon stock is an aggregate genetic stock that includes the Clearwater, Little Salmon, Lower Salmon, Grande Ronde, Imnaha, and Lower Snake rivers. Zero Chinook Salmon from the Tucannon River stock were trapped in SY2022 and SY2023.
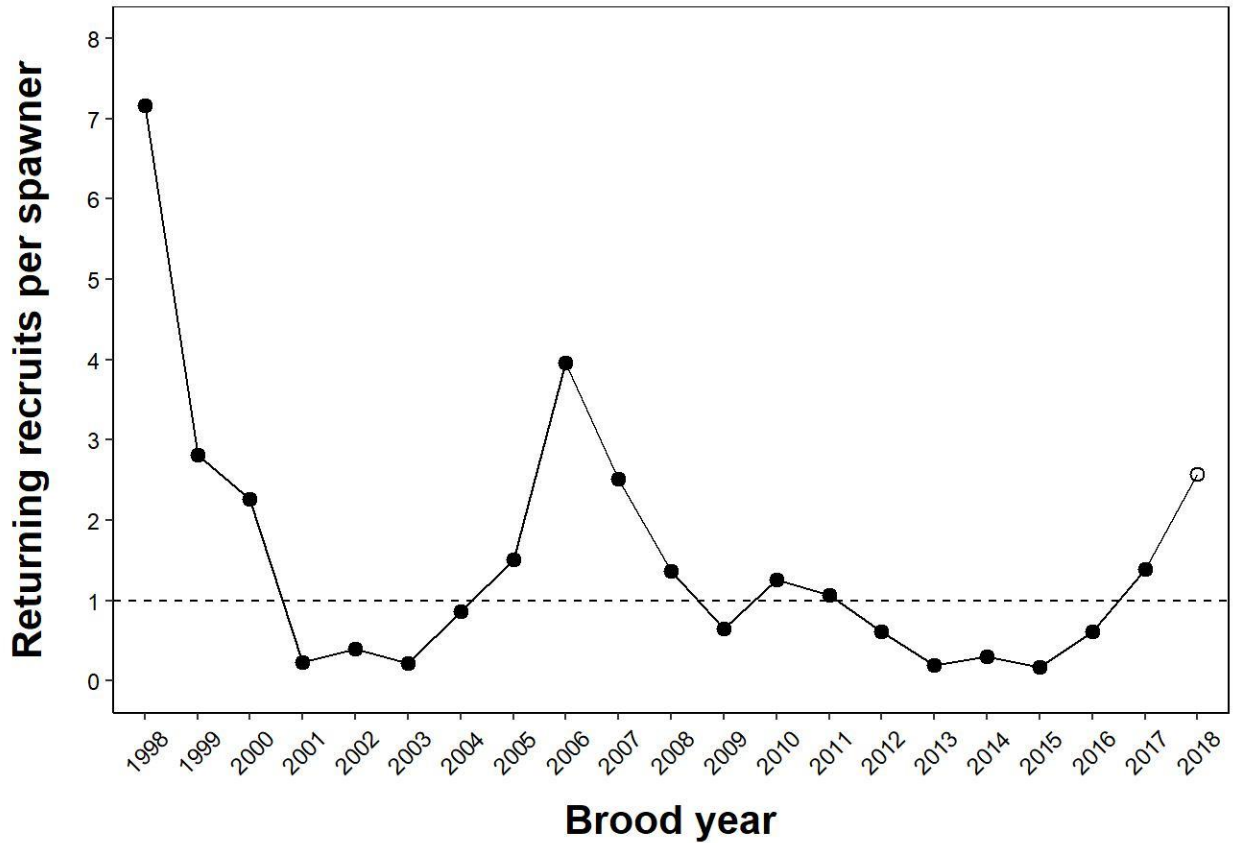
Figure 9.   Adult-to-adult productivity (returning recruits per parent spawner) of wild Chinook Salmon at Lower Granite Dam. The dashed line at 1.0 recruit per spawner represents replacement. Spawn year 2023 completed brood year 2017. Brood year 2018 (hollow dot) was shown for reference but represents a preliminary result that will be completed in SY2024.
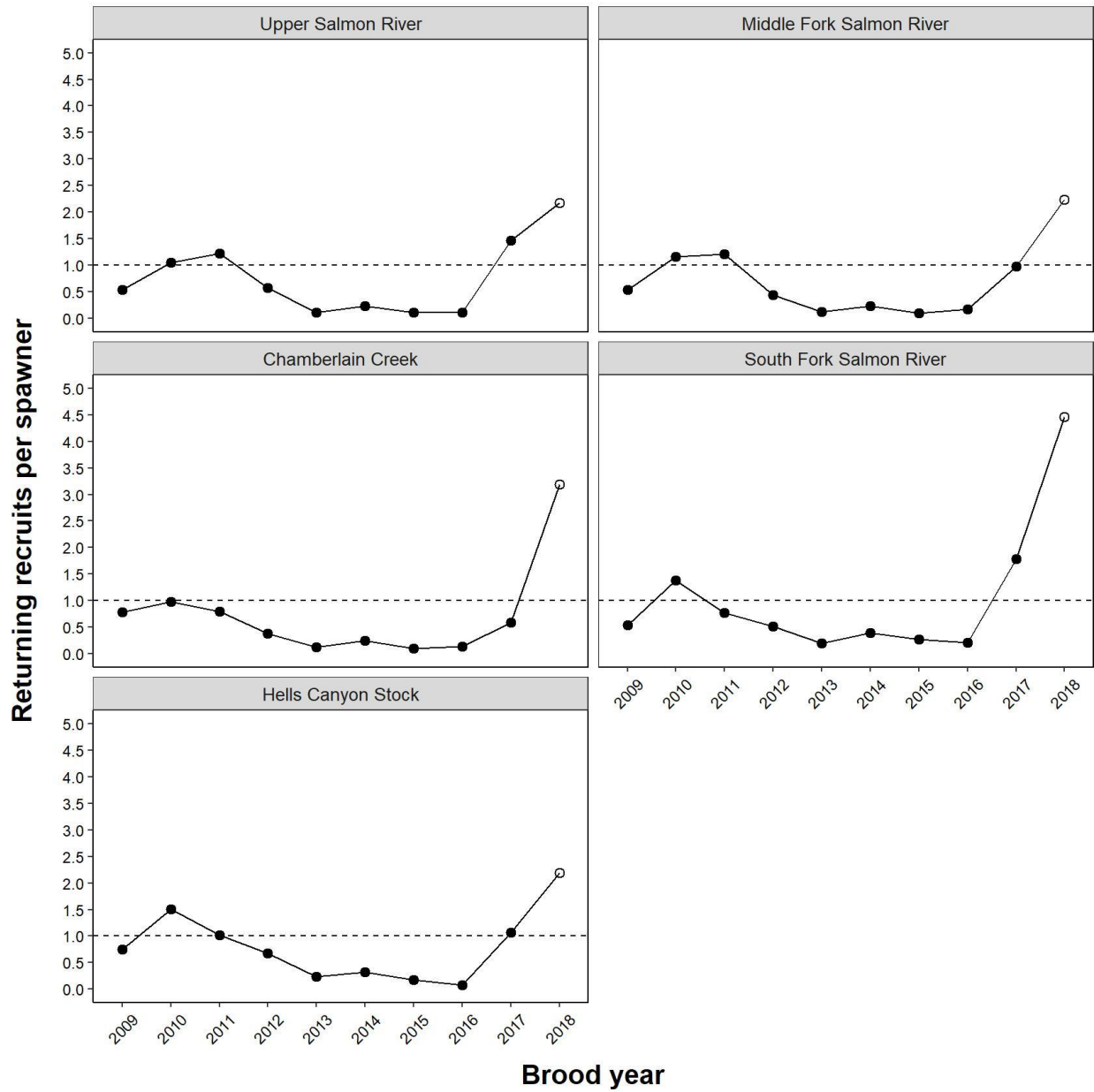
Figure 10.   Adult-to-adult productivity (returning recruits per parent spawner) for each genetic stock of wild Chinook Salmon at Lower Granite Dam. The dashed line at 1.0 recruit per spawner represents replacement. Spawn year 2023 completed brood year 2017. Brood year 2018 (hollow dot) was shown for reference but represents a preliminary result that will be completed in SY2024.
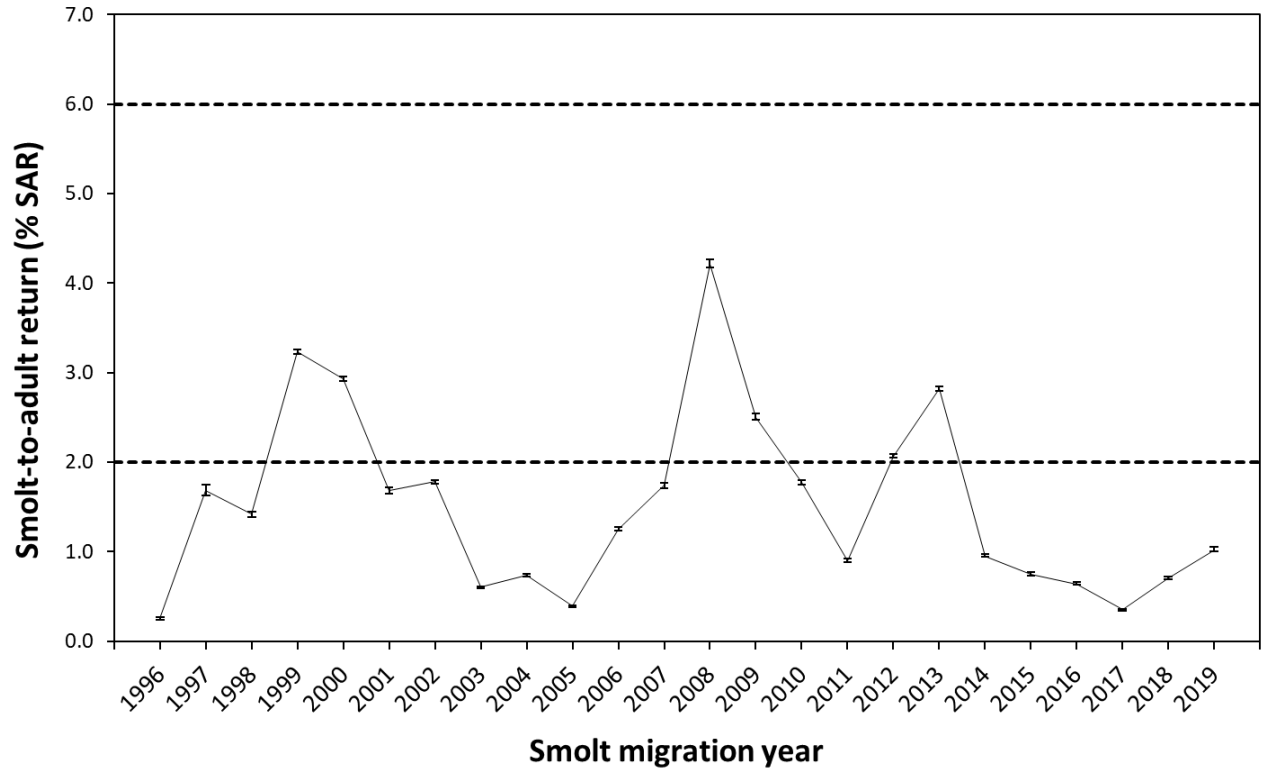
Figure 11.   Estimated wild Chinook Salmon smolt-to-adult return (% SAR) rate of emigrant smolts and adult returns to Lower Granite Dam for smolt migrations years 1996-2019. Confidence intervals are at 95%. The dashed lines represent the lower and upper range of SAR objectives for wild Chinook Salmon established by the Northwest Power and Conservation Council (NPCC 2014, 2020). See Table 5 for more data.

APPENDICES

Appendix A: Annual Lower Granite Dam trapping operations, 2022–2023.

Appendix A-1. Annual Lower Granite Dam trapping operations, 2022–2023. Shaded areas were outside the 2023 spawn year (July 1, 2022 to June 30, 2023 for steelhead and March 1 to August 17, 2023 for Chinook Salmon).

Calendar date	Trap operation	Comments
Calendar year 2022		
January 1–March 1	Closed	Winter closure
March 2–May 8	5 days/week, 25% Daily Rate	
May 9–August 17	5 days/week, 20% Daily Rate	
August 18–August 29	7 days/week, 60% Daily Rate[a]	
August 30–November 15	7 days/week, 18% Daily Rate	
November 16–December 31	Closed	Winter closure
	Calendar year 2023	
January 1–February 28	Closed	Winter closure
March 1–June 29	5 days/week, 25% Daily Rate	
June 30	100% Daily Rate[b]	Programming error
July 1–August 17	5 days/week, 25% Daily Rate	
August 18–August 30	7 days/week, 70% Daily Rate[a]	
August 31–November 15	7 days/week, 18% Daily Rate	
November 16–December 31	Closed	Winter closure

[a] Trap rate exceeded co-manager agreement for a trap rate maximum of 20% (7 days/week) to accommodate fall-run Chinook Salmon broodstock collection at the LGR trap.
[b] After the trap was flushed on June 29, it was not set to the correct program setting when turned back on. The error was caught the afternoon of June 30, resulting in a trap rate of 100% for about 17 hours.

Appendix A-2. Daily number of steelhead counted at the Lower Granite Dam window, spawn year 2023. Vertical gray bars indicate when the trap was open and daily trapping rate. 96.3% of the steelhead run passed LGR when the trap was open. See Appendix A-1 and text for explanation of various trap closures.
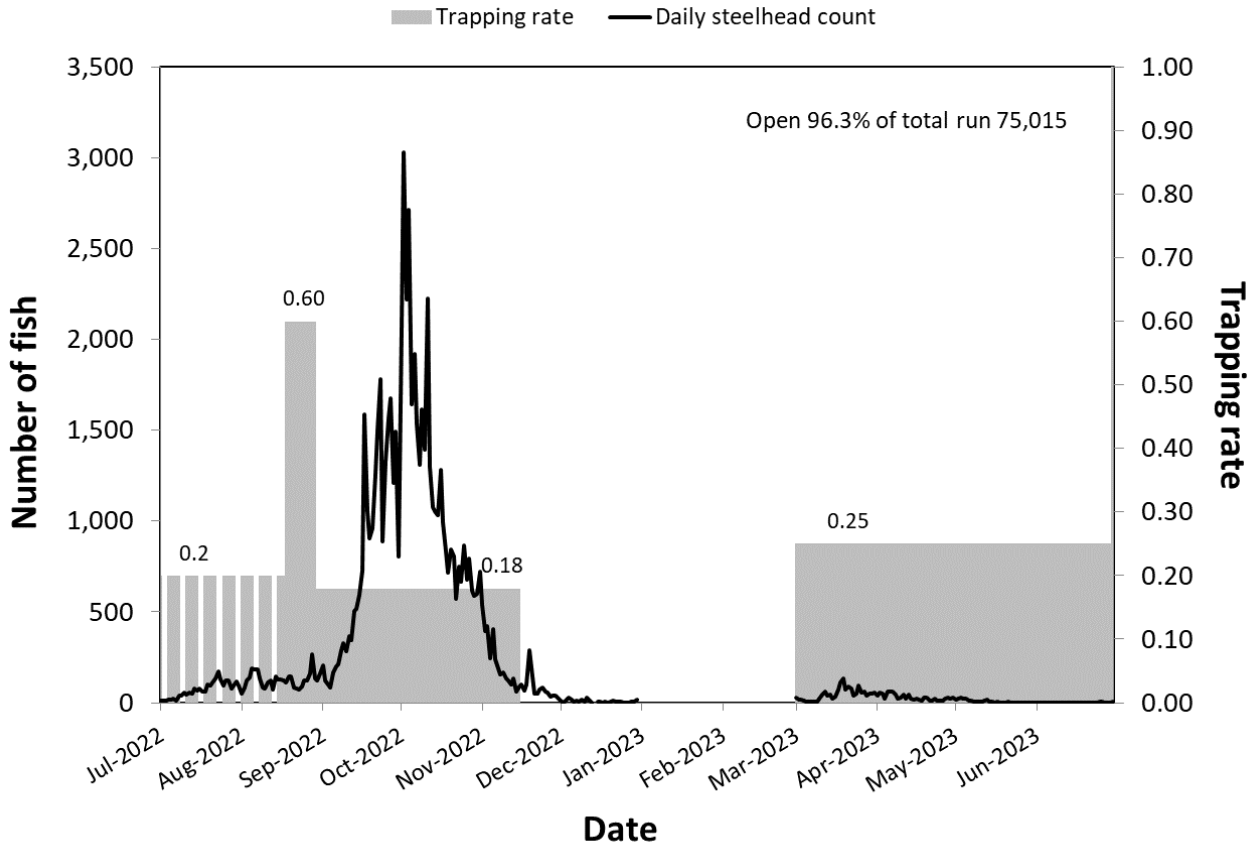
Appendix A-3. Daily number of Chinook Salmon counted at the Lower Granite Dam window, spawn year 2023. Vertical gray bars indicate when the trap was open and daily trapping rate. 72.5% of the Chinook Salmon run passed LGR when the trap was open. See Appendix A-1 and text for explanation of various trap closures.

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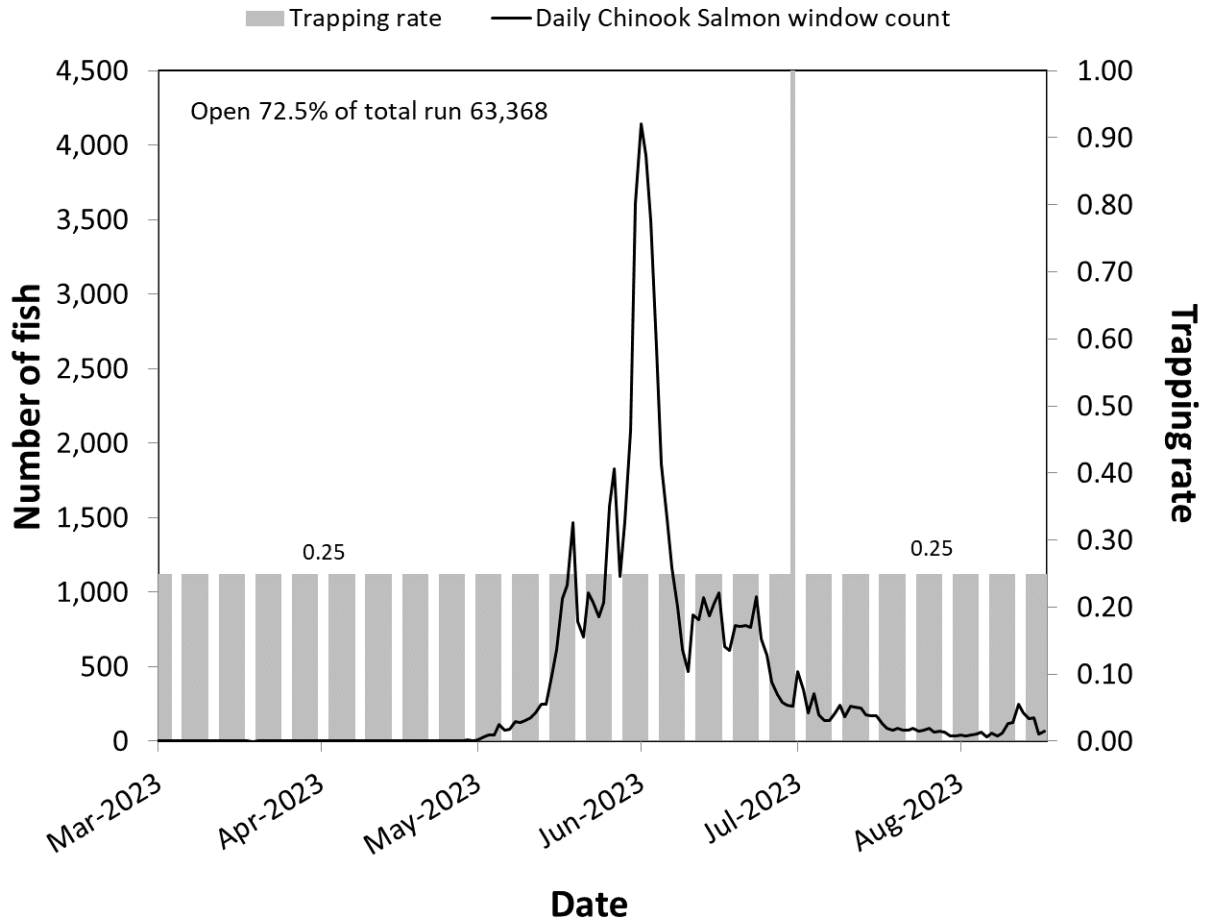
Appendix A-4. A hierarchical (top to bottom) key of external marks and internal tags used to determine hatchery origin steelhead and Chinook Salmon at Lower Granite Dam (LGR), spawn years 2009–2023. Only fish failing to meet criteria were considered wild.

If the LGR mark or tag is:	Then the origin at window is:	Then the origin at trap is:	And the final origin is:
Adipose fin clip[a]	Hatchery	Hatchery	Hatchery
Coded wire tag (CWT)	N/A	Hatchery	Hatchery
Ventral fin clip[b]	N/A	Hatchery	Hatchery
Parentage based tag (PBT)[c]	N/A	N/A	Hatchery
Passive integrated transponder (PIT)[d]	N/A	N/A	N/A

[a] Fish with a partial adipose fin clip (potential mis-clip) are genetically sampled to confirm origin.
[b] All ventral fin clip fish should also be adipose fin clipped.
[c] Used as final origin determination for fish with an intact adipose fin (unclipped). Began assigning Chinook Salmon and steelhead to release groups in SY2011 and SY2012, respectively.
[d] Minor discrepancies occurred between the PIT-tag database (PTAGIS) and LGR trap databases (LGTrappingDB, BioSamples, and Progeny) that prevent the use of PIT-tags to determine origin at this time.

Appendix A-5. Weekly window counts and valid adult trap samples of steelhead at Lower Granite Dam, spawn year 2023. Data were summarized by weekly strata for analysis using the Estimating Adult Salmonid Escapement (EASE) model.

Time strata	Statistical week[a]	Window sampling period	Number of days	Days trap open[b]	Window count	Total valid fish trapped	Valid wild fish trapped	Number of valid wild fish samples used in EASE analysis			
								Genetic stock	Size[c]	Sex[c]	Age[c]
						Fall 2022					
1	27A–31	7/1–7/31	31	21	2,194	323	132	130	130	130	104
2	32-34	8/1-8/21	21	17	2,549	634	251	243	243	243	216
3	35-36	8/22-9/4	14	14	1,835	775	276	254	254	254	219
4	37-38	9/5-9/18	14	14	7,178	1,222	270	258	258	258	210
5	39	9/19-9/25	7	7	8,627	1,622	309	306	306	306	252
6	40	9/26-10/2	7	7	11,842	2,208	334	325	325	325	252
7	41	10/3-10/9	7	7	12,965	2,532	324	321	321	321	248
8	42	10/10-10/16	7	7	9,369	1,752	203	201	201	201	154
9	43	10/17-10/23	7	7	5,508	1,148	148	147	147	147	122
10	44	10/24-10/30	7	7	4,807	921	128	125	125	125	107
11	45-53	10/31-12/30	61	16	5,568	854	167	163	163	163	140
						Spring 2023					
12	1-27B	3/1-6/30	122	122	2,573	540	218	190	190	190	137
Total:			305	246	75,015	14,531	2,760	2,663[c]	2,663[c]	2,663[c]	2,161

a   Statistical weeks are grouped to try to provide a minimum sample size of 100 valid wild fish per stratum.

b   See Appendix A-1 for trapping operation details

c   The counts in the size, sex, and age columns refer to fish with a genetic stock assignment and assignment for the respective variables. Ninety fish without ages were removed from the genetic stock, size, and sex sample due to analytical complications in EASE, reducing the total sample size to 2,573 fish.

Appendix A-6. Weekly window counts and valid adult trap samples of Chinook Salmon at Lower Granite Dam, spawn year 2023. Data were summarized by weekly strata for analysis using the Estimating Adult Salmonid Escapement (EASE) model.

Time strata	Statistical week[a]	Window sampling period	Number of days	Days trap open[b]	Window count	Total valid fish trapped	Valid wild fish trapped	Number of valid wild fish samples used in EASE analysis			
								Genetic stock	Size[c]	Sex[c]	Age[c]
1	1-22	3/1-5/28	89	63	15,906	2,539	162	144	144	144	120
2	23	5/29-6/4	7	5	21,377	3,447	287	281	281	281	252
3	24	6/5-6/11	7	5	7,353	1,659	247	242	242	242	207
4	25	6/12-6/18	7	5	5,788	1,131	247	238	238	238	207
5	26	6/19-6/25	7	5	5,331	938	202	195	195	195	178
6	27	6/26-7/2	7	5	2,256	552	143	138	138	138	129
7	28-29	7/3-7/16	14	10	2,752	533	153	150	150	150	132
8	30-53	7/17-8/17	32	24	2,605	501	162	158	158	158	143
Total:			170	122	63,368	11,300	1,603	1,546[c]	1,546[c]	1,546[c]	1,368

a   Statistical weeks are grouped to try to provide a minimum sample size of 100 valid wild fish per stratum.

b   See Appendix A-1 for trapping operation details.

c   The counts in the size, sex, and age columns refer to fish with a genetic stock assignment and assignment for the respective variables. Two fish without ages were removed from the genetic stock, size, and sex sample due to analytical complications in EASE, reducing the sample size to 1,544 fish.

Appendix B. Methods description of Estimating Adult Salmonid Escapement (EASE) model used for all steelhead and spring-summer Chinook Salmon estimates, spawn year 2023.

Appendix B-1. Methods description of Estimating Adult Salmonid Escapement (EASE) model used for all steelhead and spring-summer Chinook Salmon estimates, spawn year 2023.

The following methods provide detailed information about the Estimating Adult Salmonid Escapement model (EASE; escapeLGD R package; GitHub - delomast/escapeLGD: Escapement Estimation at Lower Granite Dam; R Development Core Team 2021) used for all escapement estimates of steelhead and spring-summer Chinook Salmon at Lower Granite Dam in SY2023.

Daytime Ascensions, Nighttime Passage, and Total Number of Ascensions

For daytime ascensions, the window count, w, is considered a binomial random variable

$$w \sim \text{bin}(r, a_d), \tag{1}$$

where r is the proportion of time counting was performed and a_d is the number of daytime ascensions. The point estimate of a_d is therefore $\frac{w}{r}$. Bootstrap estimates are generated by parametric bootstrapping. Random binomials are generated using a probability of success of r and number of trials of a_d. These random binomials are then divided by r to yield bootstrap estimates of a_d.

For nighttime passage, the probability a given ascension occurs at night is estimated using PIT tag detections in the ladder. The number of PIT ascensions at night, d_n, is treated as a binomial random variable

$$d_n \sim \text{bin}(p_n, d_a), \tag{2}$$

where p_n is the probability a given ascension occurs at night and d_a is the total number of PIT ascensions. The maximum likelihood estimate of p_n is therefore $\frac{d_n}{d_a}$. Bootstrap estimates are generated by parametric bootstrapping. Random binomials are generated using a probability of success of the maximum likelihood estimate of p_n and number of trials of d_a. These random binomials are then divided by d_a to yield bootstrap estimates of p_n.

Using the estimates of a_d and p_n, the total number of ascensions, a_t, is calculated as

$$a_t = a_d / (1 - p_n). \tag{3}$$

To generate d_n for input to the model, a user must categorize PIT ascensions as occurring during the day or night. This is currently performed by Columbia River DART. Detection histories are broken into ascensions with each ascension beginning with a detection at the viewing window array and ending with a detection at the ladder exit array. We then exclude any fish that were PIT tagged as adults in the Lower Granite trap. Ascensions whose first detection at the viewing window is outside of counting hours are assigned to the night. Detection efficiency of PIT tags in the ladder is assumed to be 100%, and if any fish are not detected at the viewing window and subsequently at the ladder exit, they are excluded.

Fallback Rates

Fallback rates have previously been observed to vary between groups of steelhead stocks, specifically between stocks upstream and downstream of LGR. To estimate escapement to the level of these stocks, fallback rates must be estimated separately for each group. The method described here is applied separately to each group to yield group-specific estimates of fallback rates.

The probability that a given ascension results in fallback (e.g., the fish that ascended later fell back below the dam) is estimated using PIT tag detections. The number of PIT ascensions that later reascended, d_f, is treated as a binomial random variable

$$d_f \sim \text{bin}(p_f, d_{as}), \tag{4}$$

where p_f is the probability that a given ascension results in fallback and d_{as} is the total number of ascensions from the given stock group. The maximum likelihood estimate of p_f is therefore $\frac{d_f}{d_{as}}$. Bootstrap estimates are generated by parametric bootstrapping. Random binomials are generated using a probability of success of the maximum likelihood estimate of p_f and number of trials of d_{as}. These random binomials are then divided by d_{as} to yield bootstrap estimates of p_f.

It is important to realize that because fish are only detected as having fallen back if they later reascend, this assumes that the rate of fallback without reascension is 0.

To generate d_f for input to the model, a user must categorize PIT ascensions as being first ascensions or reascensions. This is currently performed by Columbia River DART by breaking detection histories into unique ascensions as described in the previous section. We then exclude any fish that were PIT tagged as adults in the Lower Granite trap. By only using fish PIT tagged prior to arrival at the dam, we ensure that sampling is not biased with respect to whether a fish is trapped or not.

Composition of Ascensions

The trap provides a sample of all fish ascending the ladder as it traps fish 24 hours a day during the days it is operational. We used this sample to estimate the composition of fish ascending the ladder by adipose fin status (ad-clipped or ad-intact), origin (hatchery or wild), and one or two additional categorical variables (e.g. PBT, GSI, genetic sex). Composition is estimated using the methods developed by Delomas and Hess (2021) and implementing the approach discussed therein for integrating GSI uncertainty into the estimates. Inputs required for this step are the attributes recorded for trapped fish and parentage-based tagging (PBT) tag rates.

Composition is estimated in a hierarchical, step-wise manner (Steinhorst et al. 2017) to accommodate the desire for marginal totals for some variables to be the same regardless of the other variables being estimated in a given run of the model. For example, the number of ad-intact hatchery fish estimated should be the same regardless of whether the wild component is being estimated by genetic stock and sex or by genetic stock and size. The proportions of ad-clipped and ad-intact fish are first estimated using clip information recorded at the trap. The proportion of fish that are ad-clipped, p_{AD}, is estimated as $\frac{Number\ of\ ad-clipped\ fish}{Total\ number\ of\ fish}$. The ad-intact portion is then split further into fish with physical tags denoting them of hatchery origin (e.g. CWT, ventral fin clips) and fish without such physical tags. The proportion of ad-intact fish with physical tags, p_{phys},

is estimated as $\frac{Number\ of\ physically\ tagged\ ad-intact\ fish}{Total\ number\ of\ ad-intact\ fish}$. The unmarked (ad-intact, no physical tags), genotyped fish are then used to estimate the proportion of unmarked fish that are hatchery origin, p_{PBT}, and wild using PBT assignments and tag rates. This is done using a maximum likelihood method (Delomas and Hess 2021). The proportions of fish that are ad-clipped hatchery-origin (H), ad-intact hatchery-origin (HNC), and wild-origin (W) can then be calculated as

$$H = p_{AD}, \tag{5}$$

$$HNC = (1 - p_{AD})(p_{phys} + (1 - p_{phys})\,p_{PBT}), \tag{6}$$

$$W = (1 - p_{AD})(1 - p_{phys})(1 - p_{PBT}). \tag{7}$$

Composition within each group (H, HNC, W) is then estimated for one or two additional variables.

For the H group, composition of the first variable is estimated using all ad-clipped fish with data for the first variable. Composition of a second variable (if included) within the categories of the first variable is then estimated using all ad-clipped fish with data for both the first and second variables and with marginal proportions for the first variable constrained to their estimated values. The composition of the PBT grouping variable (groups for which PBT tag rates are defined) and the composition of the second variable if the first variable is the PBT grouping variable are estimated using the maximum likelihood method described by Delomas and Hess (2021). Other variables are treated as multinomial random variables and maximum likelihood estimates (observed proportions in the sample) are calculated (ex: size category).

For the HNC group, composition is estimated using the maximum likelihood method described by Delomas and Hess (2021) applied separately to the ad-intact, physically tagged fish and the unmarked fish and then summed together. If the variable of interest is not the PBT grouping variable, the estimates for the ad-intact, physically tagged fish are simply the observed proportions in the sample. For the unmarked fish, the proportions of the PBT grouping variable are constrained to the values estimated during the previous estimation of p_{PBT}.

For the W group, composition for the first variable is estimated using the maximum likelihood method described by Delomas and Hess (2021) and using data from all ad-intact, genotyped samples with data for the first variable. The W group is a mixture of different genetic stocks and so the first variable should always be genetic stock. Composition of a second variable (if included) within the categories of the first variable is then estimated using all ad-intact, genotyped fish with data for both the first and second variables and with marginal proportions for the first variable constrained to their estimated values. Secondary variables for this analysis include size, sex, age class, saltwater age, and brood year (Figure 3). The proportions of the PBT grouping variable within the ad-intact, unmarked fish are constrained to the values estimated during the previous estimation of p_{PBT}. It is important that the variables of interest for the W group (e.g. GSI) are recorded for ad-intact, unmarked samples regardless of PBT assignment. This is because the composition of the ad-intact, unmarked, PBT assigned samples contributes to the likelihood used to calculate composition of the W group. For estimating composition of the second variable, it is assumed that within the PBT groups of the unmarked HNC fish, the first and second variables are independent. This is expected to be the case as one variable is typically GSI assignment, and within an HNC PBT group, variation in GSI assignment is not expected to reflect meaningful genetic structure.

The uncertainty in GSI assignments is incorporated into the composition point estimates by estimating composition iteratively while replacing GSI assignments with draws from the joint posterior distribution of all GSI assignments in the dataset (Delomas and Hess 2021). Point estimates are then calculated as the means across iterations. Bootstrap estimates are obtained by non-parametric bootstrapping and simultaneously replacing GSI assignments with draws from the posterior of GSI assignments.

Stratification

When estimating escapement over an extended period, a stratified approach has been previously demonstrated to be superior to a pooled approach as many parameters change over time and the trap (sampling) rate can also change during the run (Steinhorst et al. 2017). As such, this model is implemented using a stratified approach and estimates are obtained by summing results across strata. Confidence intervals are then calculated as the quantiles ($\frac{\alpha}{2}$ and $1 - \frac{\alpha}{2}$) of the bootstrap estimates.

As multiple datasets are used to estimate different parameters, several sets of strata are defined. One set is defined for nighttime passage estimates. Separate sets of strata are defined for fallback rates for each stock group. This allows strata to be shorter in duration for stock groups with more PIT tag detections. Finally, a set of strata is defined for the composition estimates. The one interdependency between strata is that every composition estimate stratum must correspond to one and only one fallback stratum for each stock group. When defining strata, several criteria are kept in mind. The model must be able to estimate parameters in each time step, so there must be at least one sample informing each parameter. The parameters being estimated should be approximately constant in each stratum, so strata should not span changes in environmental conditions that could affect the underlying parameters (e.g., for estimating steelhead escapement, fall and spring periods should not be combined). Additionally, while a minimum of one sample is required for each stratum, it is recommended that there be sufficient samples to provide a reasonable estimate of the underlying parameters. For example, if composition of the W portion of the run is being estimated by genetic stock, approximately 45 genotyped, unmarked, untagged samples per stratum (Given more than three possible categories, a sample size of 45 indicates a maximum error of any estimated multinomial proportion within that stratum of 0.15 with α = 0.10) for the composition estimates can be recommended (Thompson 1987).

Based on data for previous years, for the bulk of the run, a stratum corresponds to a week, but for the tails of the run several weeks may be combined into one stratum. The exception to this may be the fallback estimates for steelhead released below Lower Granite Dam. Since there are fewer PIT tagged fish in this group, combining weeks into a single stratum may be a more frequent occurrence.

Non-specific PBT Groups

For a small minority of hatchery releases, PBT assignments do not definitively indicate which stock group (upper or lower) a fish belongs to for application of fallback rates. This occurs when fish from the same family are split (and not differentially marked) between two release groups. In these scenarios, the release groups are typically PIT tagged separately, and so PIT tag detections can be used to split the composition estimate for the PBT group into separate release groups. Consider a PBT group that is composed of two release groups (release A and B), and the PIT tagging rates at release are t_A and t_B. The number of detections of PIT tags from each group, d_A and d_B, can be considered binomial random variables

$$d_A \sim \text{bin}(t_A, N_A), \tag{8}$$

$$d_B \sim \text{bin}(t_B, N_B), \tag{9}$$

where N_A and N_B are the total numbers of fish in each release. An estimate of N_A is simply $\frac{d_A}{t_A}$, and similarly for N_B. The proportion of fish in the PBT group that belong to each release group is then calculated and used to split the PBT group composition estimate. Bootstrap estimates of N_A and N_B are obtained by parametric bootstrapping. Random binomials are generated using a probability of success of t_A and t_B and number of trials of N_A and N_B. These random binomials are then divided by the tag rates to yield bootstrap estimates of N_A and N_B. This procedure is extendable to PBT groups containing more than two separately PIT tagged release groups.

Appendix C: Steelhead and Chinook Salmon age validation.

Appendix C-1. Age bias plot illustrating pairwise comparisons of scale-based saltwater age with known age for steelhead at Lower Granite Dam, spawn year 2023 (Micah Davison, IDFG, scale data; PTAGIS, PIT-tag data). Dashed line represents the 1:1 relationship. Values adjacent to the circles are the sample sizes in each group. PA = percent agreement and n = total sample size.
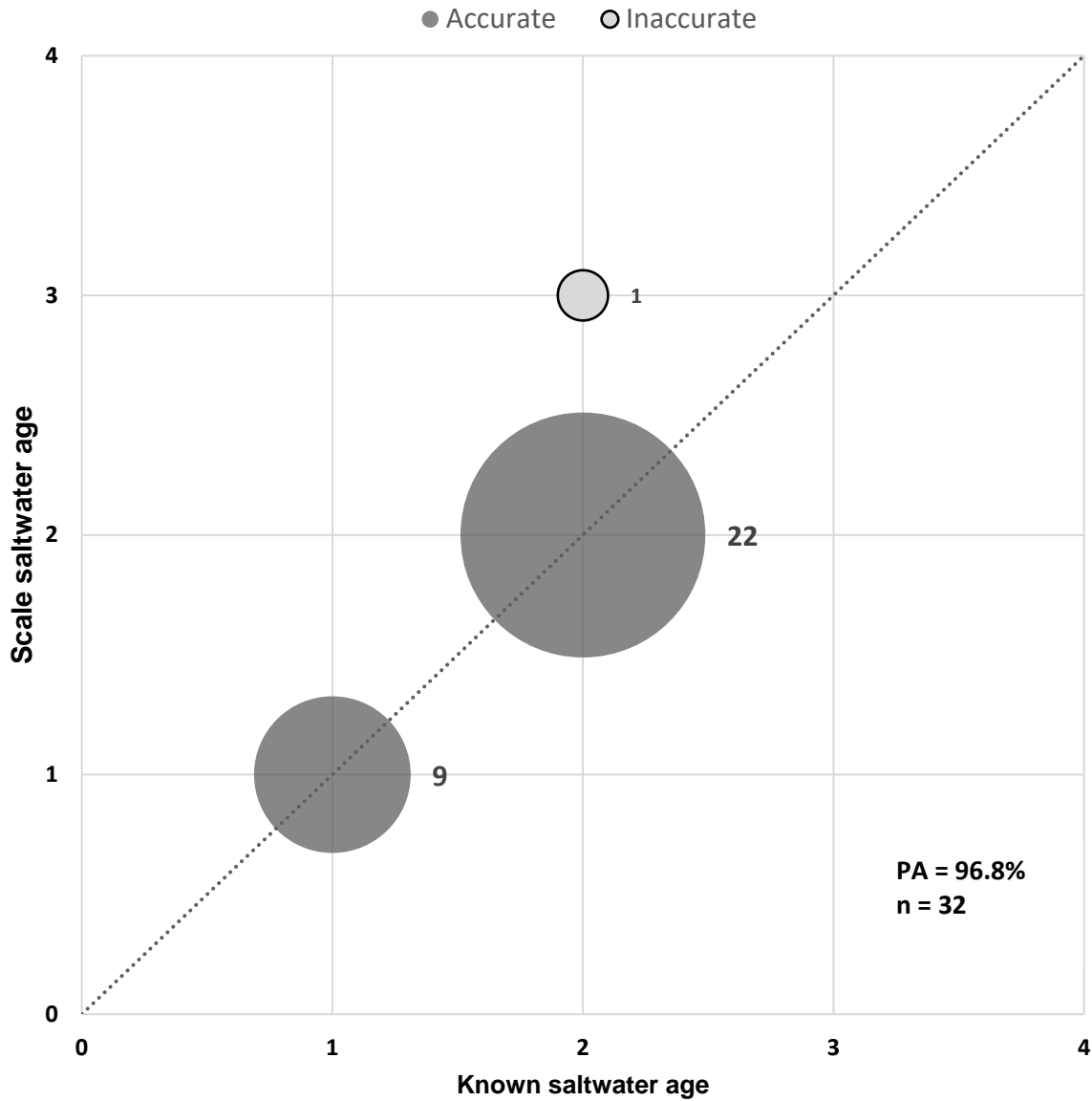
Appendix C-2. Age bias plot illustrating pairwise comparisons of scale-based saltwater age with known age for Chinook Salmon at Lower Granite Dam, spawn year 2023 (Micah Davison, IDFG, scale data; PTAGIS, PIT-tag data). Dashed line represents the 1:1 relationship. Values adjacent to the circles are the sample sizes in each group. PA = percent agreement and n = total sample size.
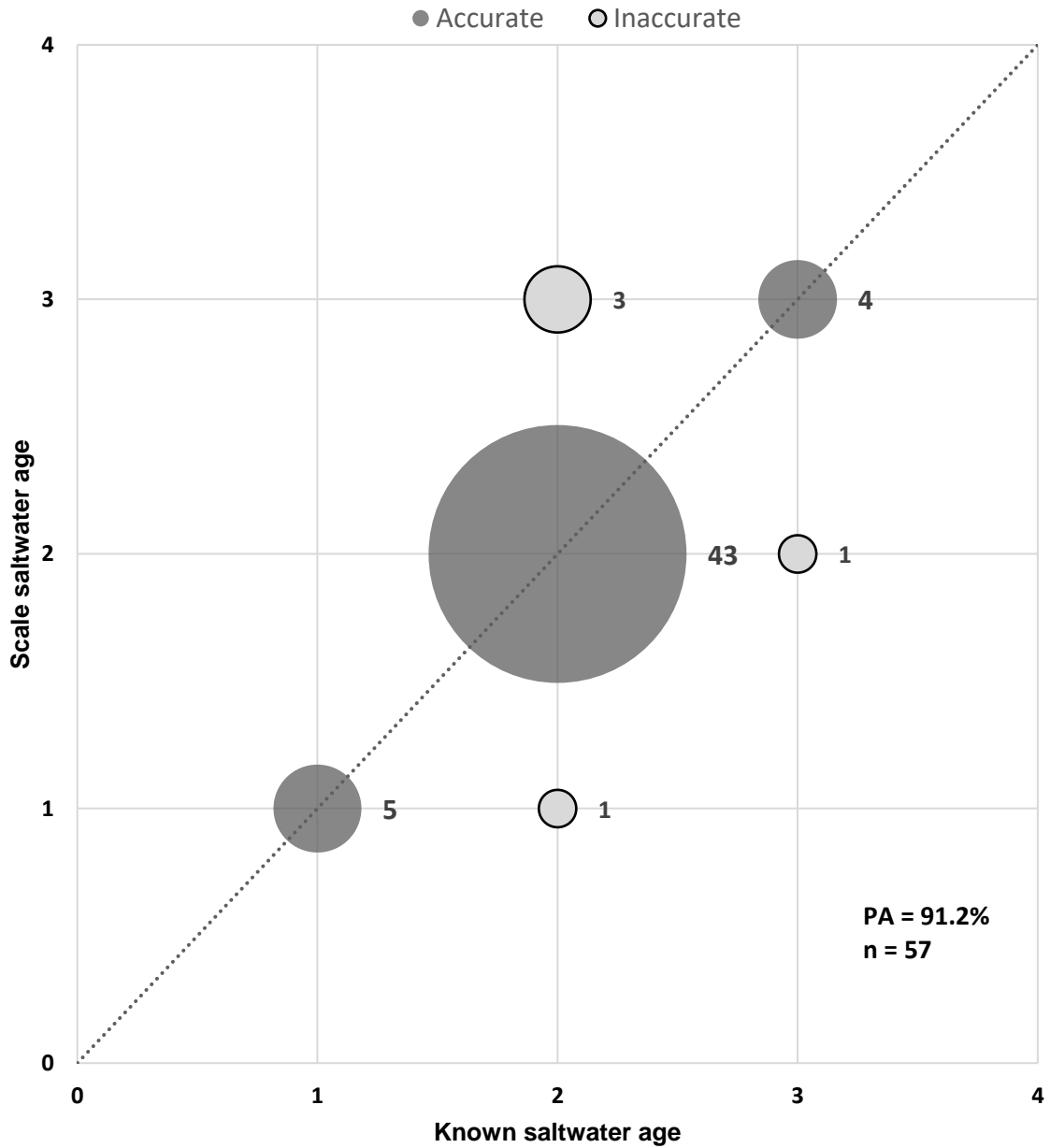
Appendix D: Wild steelhead at Lower Granite Dam, spawn year 2023.

Appendix D-1. Percent estimated escapement of wild steelhead by genetic stock relative to the total estimated wild escapement at Lower Granite Dam, spawn years 2009–2023. See Genetic Tissue Processing and Analysis section for definition of stock abbreviations.
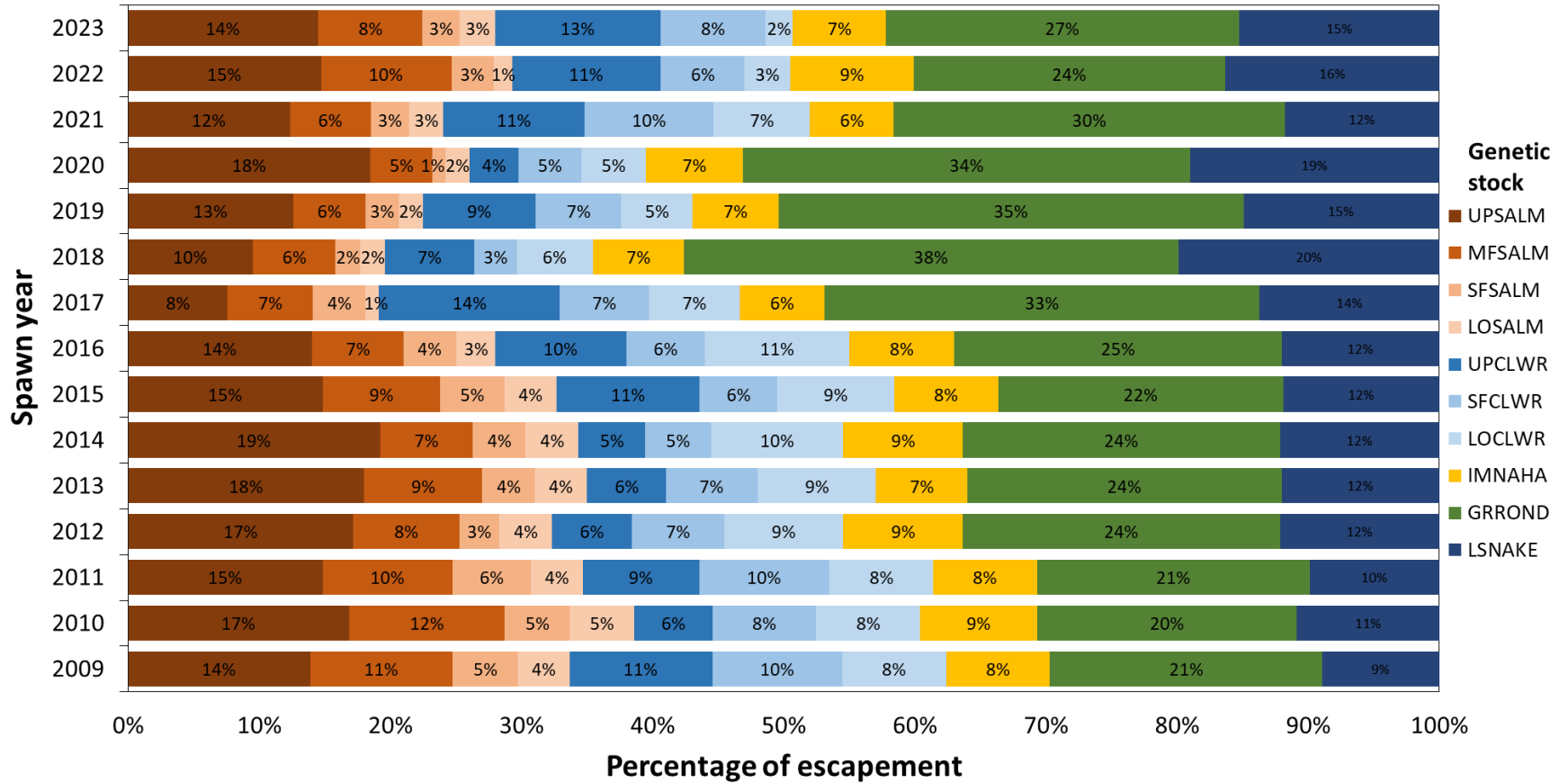
Appendix D-2. Estimated escapement of wild steelhead by sex and size for each genetic stock at Lower Granite Dam, spawn year 2023. L = lower bound and U = upper bound of 95% confidence intervals. See Genetic Tissue Processing and Analysis section for definition of stock abbreviations.

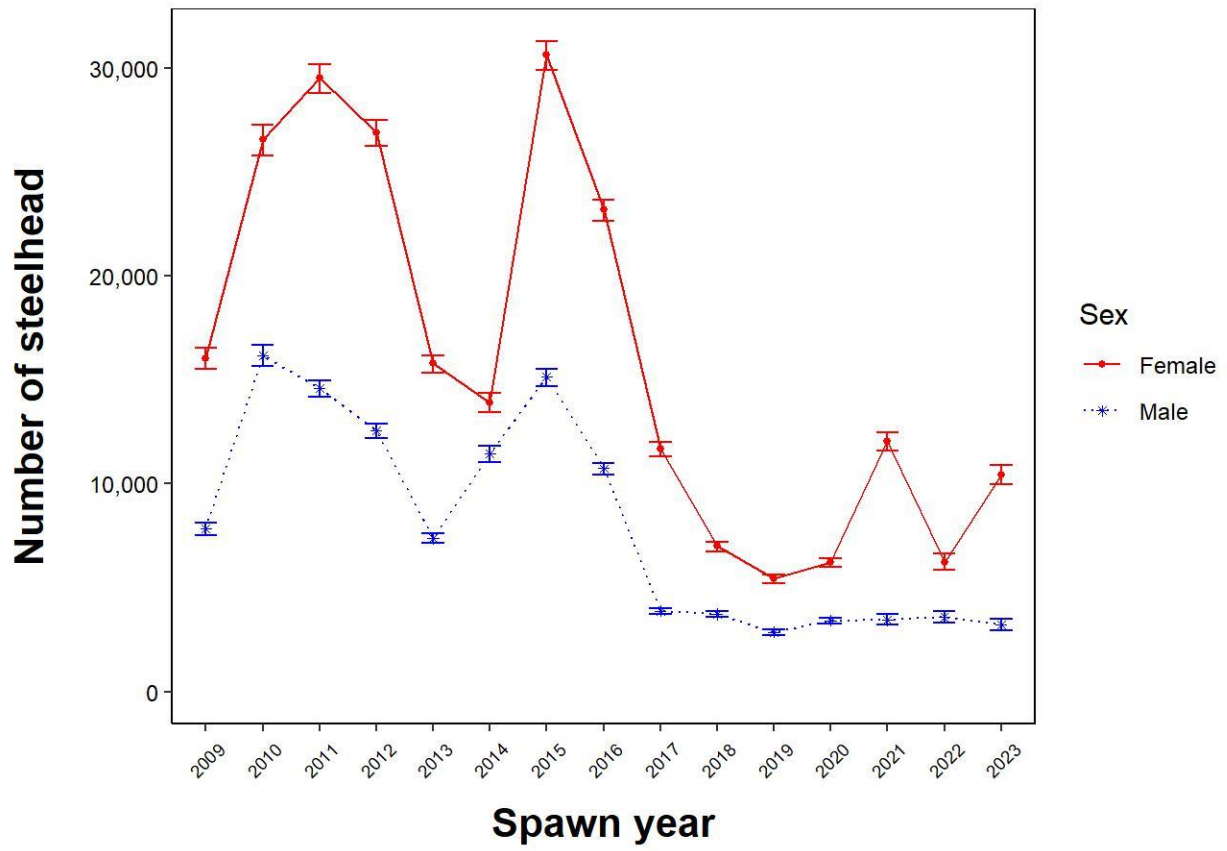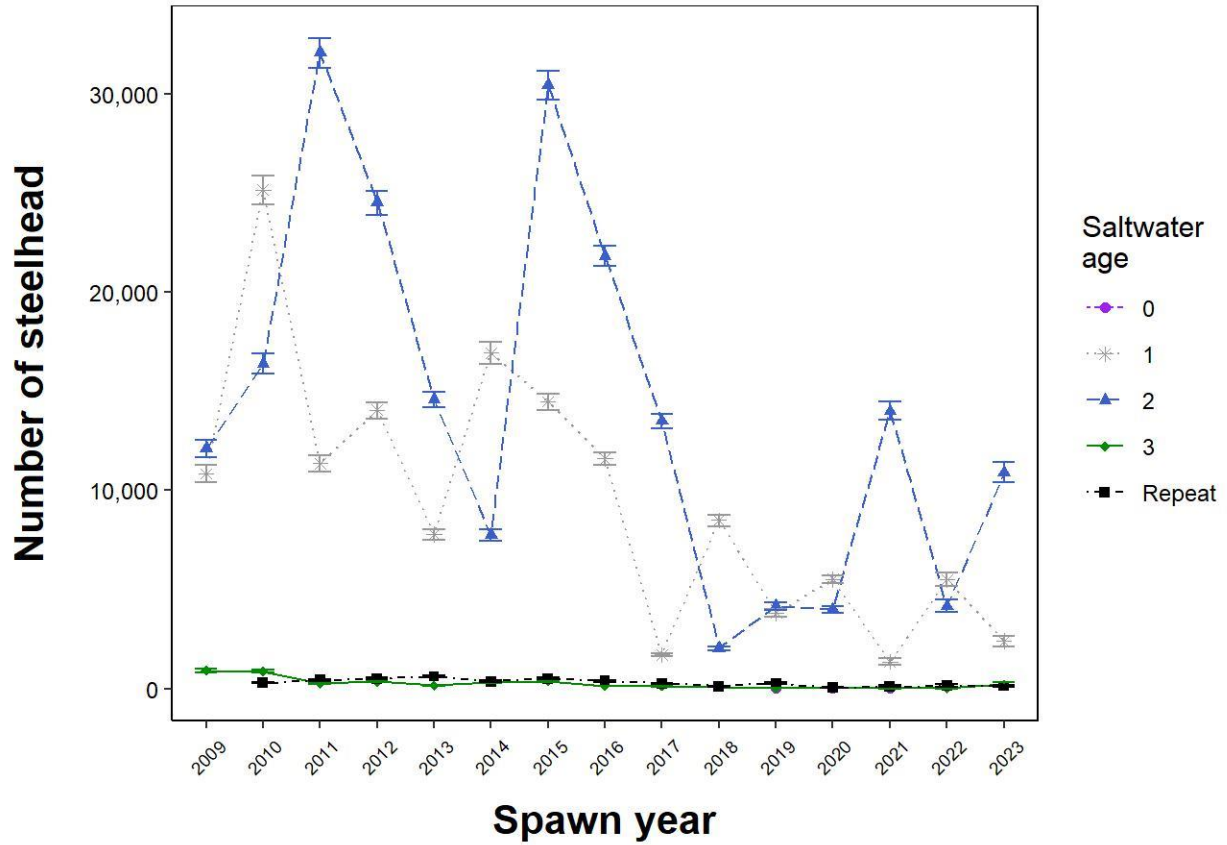| Genetic stock | Estimated number of wild steelhead at Lower Granite Dam that were: | | | | | | | | | | | | | | |
| | Female | | | Male | | | Large | | | Small | | | Total wild | | |
	Estimate	L	U	Estimate	L	U	Estimate	L	U	Estimate	L	U	Estimate	L	U
UPSALM	1,447	1,230	1,680	526	401	656	91	41	155	1,882	1,616	2,150	1,973	1,700	2,264
MFSALM	903	764	1,056	180	117	245	319	242	411	764	621	915	1,083	920	1,256
SFSALM	302	218	390	88	43	143	218	150	300	172	105	246	390	291	493
LOSALM	292	155	446	78	22	145	40	11	85	330	173	499	370	198	542
UPCLWR	1,415	1,225	1,603	301	227	394	1,266	1,093	1,440	450	343	568	1,716	1,515	1,929
SFCLWR	783	627	937	311	224	410	698	567	840	396	302	498	1,094	936	1,259
LOCLWR	221	112	342	61	16	117	38	5	85	244	127	386	282	146	427
IMNAHA	714	562	896	256	167	360	46	11	88	924	747	1,112	970	782	1,168
GRROND	2,787	2,475	3,113	883	737	1,056	116	65	217	3,554	3,202	3,898	3,670	3,334	4,030
LSNAKE	1,554	1,278	1,824	529	380	682	98	42	157	1,985	1,657	2,331	2,083	1,738	2,431
Total	10,418	9,983	10,888	3,213	2,948	3,487	2,930	2,677	3,219	10,701	10,210	11,160	13,631	13,104	14,201

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Appendix D-3. Estimated escapement of wild steelhead by sex at Lower Granite Dam, spawn years 2009–2023. From SY2009–2021, confidence intervals are at 90%. Starting in SY2022, confidence intervals are at 95%.

Appendix D-4. Estimated escapement of wild steelhead by smolt migration year (MY), brood year (BY), and age class for each genetic stock at Lower Granite Dam, spawn year 2023. Only individual fish that had both a total age and an assigned stock were used (n = 2,161). Age class format is European: freshwater age.saltwater age. R indicates consecutive year repeat spawners who spawned two years in a row. R1 indicates skip spawners who spent one year in saltwater between spawning years while R2 indicates skip spawners who spent two years in saltwater between spawning years. See Genetic Tissue Processing and Analysis section for definition of stock abbreviations.

| | MY2018 | | | MY2019 | | | | | | | | MY2020 | | | | | MY2021 | | | | |
| | BY15 | BY16 | BY17 | BY15 | BY16 | BY16 | BY16 | BY17 | BY17 | BY17 | BY18 | BY16 | BY17 | BY18 | BY18 | BY19 | BY17 | BY18 | BY19 | BY20 | |
Genetic stock	3.2R1	2.2R1	1.1R2	4.3	3.1R1	3.2R	3.3	2.1R1	2.2R	2.3	1.1R1	4.2	3.2	2.1R	2.2	1.2	4.1	3.1	2.1	1.1	Total wild
UPSALM	0	0	0	0	1	0	2	7	1	5	2	15	434	1	984	61	8	117	320	15	1,973
MFSALM	0	0	0	0	0	3	30	0	0	5	0	59	580	0	277	4	7	88	30	0	1,083
SFSALM	0	0	0	0	0	8	0	0	0	5	0	43	217	0	88	3	0	10	16	0	390
LOSALM	0	0	1	0	0	0	0	1	0	0	2	6	99	0	162	29	4	21	42	3	370
UPCLWR	4	0	0	8	0	0	39	0	0	25	0	36	1,127	0	444	7	6	9	11	0	1,716
SFCLWR	2	8	0	0	0	0	17	0	0	64	0	7	314	0	535	45	0	19	70	13	1,094
LOCLWR	0	0	0	0	0	0	0	0	0	3	0	2	68	0	154	6	0	18	29	2	282
IMNAHA	0	0	0	0	0	0	5	1	1	1	1	3	220	0	466	30	8	74	155	5	970
GRROND	6	0	0	0	9	0	1	14	16	3	6	23	763	11	1,850	144	17	203	573	31	3,670
LSNAKE	0	0	1	0	0	0	2	8	1	4	2	7	388	0	1,098	102	2	126	308	34	2,083
Total wild	12	8	2	8	10	11	96	31	19	115	13	201	4,210	12	6,058	431	52	685	1,554	103	13,631

Appendix D-5. Estimated escapement of wild steelhead by saltwater age at Lower Granite Dam, spawn years 2009–2023. From SY2009–2021, confidence intervals are at 90%. Starting in SY2022, confidence intervals are at 95%. Repeat refers to steelhead showing evidence of previous spawning events.

Appendix D-6. Estimated escapement of wild steelhead by saltwater age for each genetic stock at Lower Granite Dam, spawn years 2009–2023. From SY2009–2021, confidence intervals are at 90%. Starting in SY2022, confidence intervals are at 95%. Repeat refers to steelhead showing evidence of previous spawning events.
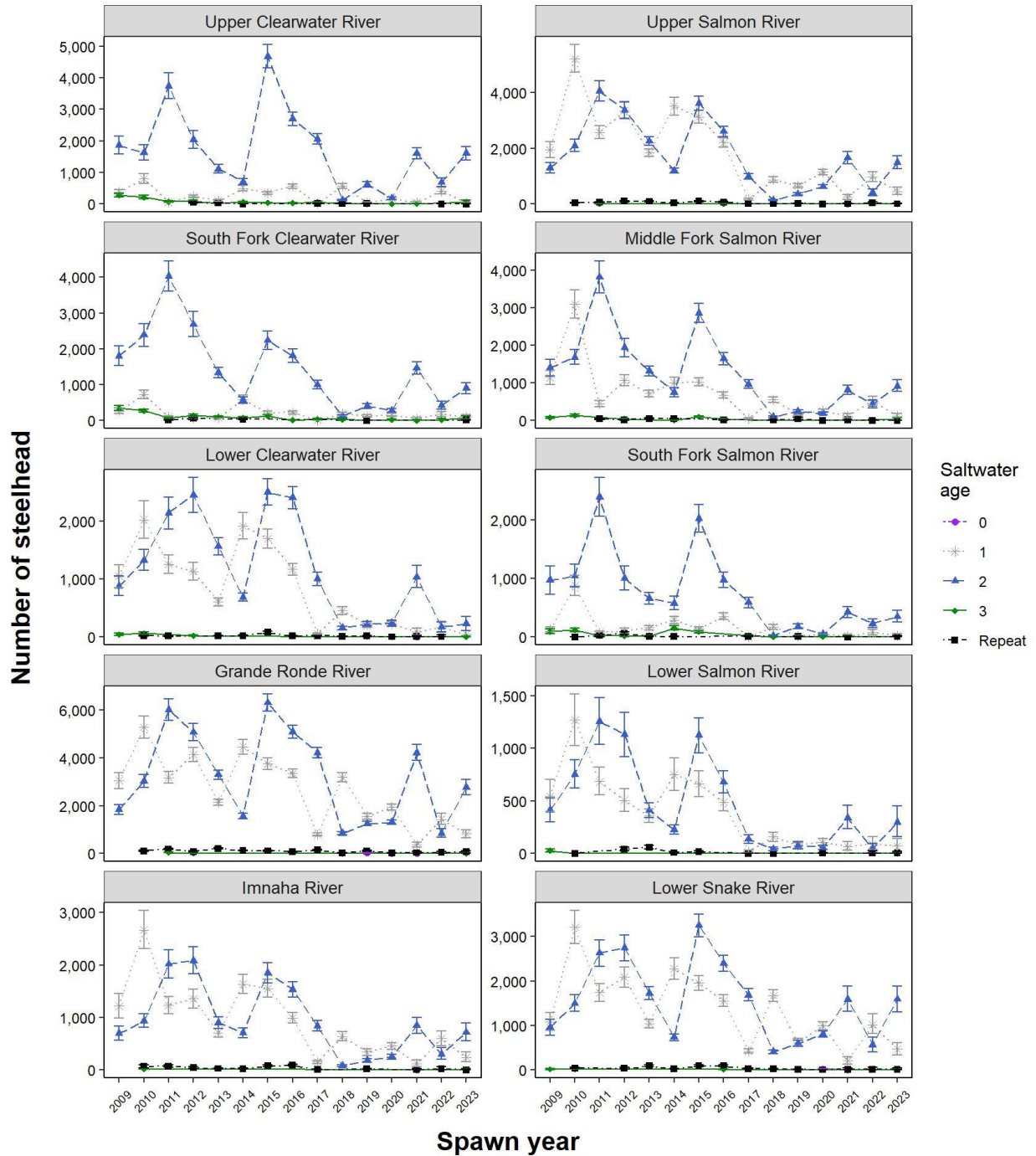
Appendix D-7. Length frequency distribution of trapped wild steelhead by saltwater age at Lower Granite Dam, spawn year 2023. Solid black vertical lines represent the mean fork length (FL) for saltwater age 1 (58 cm, n = 395), saltwater age 2 (72 cm, n = 1,717), and saltwater age 3 (83 cm, n = 33). Dashed vertical red line represents the 78 cm FL cutoff for determining large-sized steelhead.
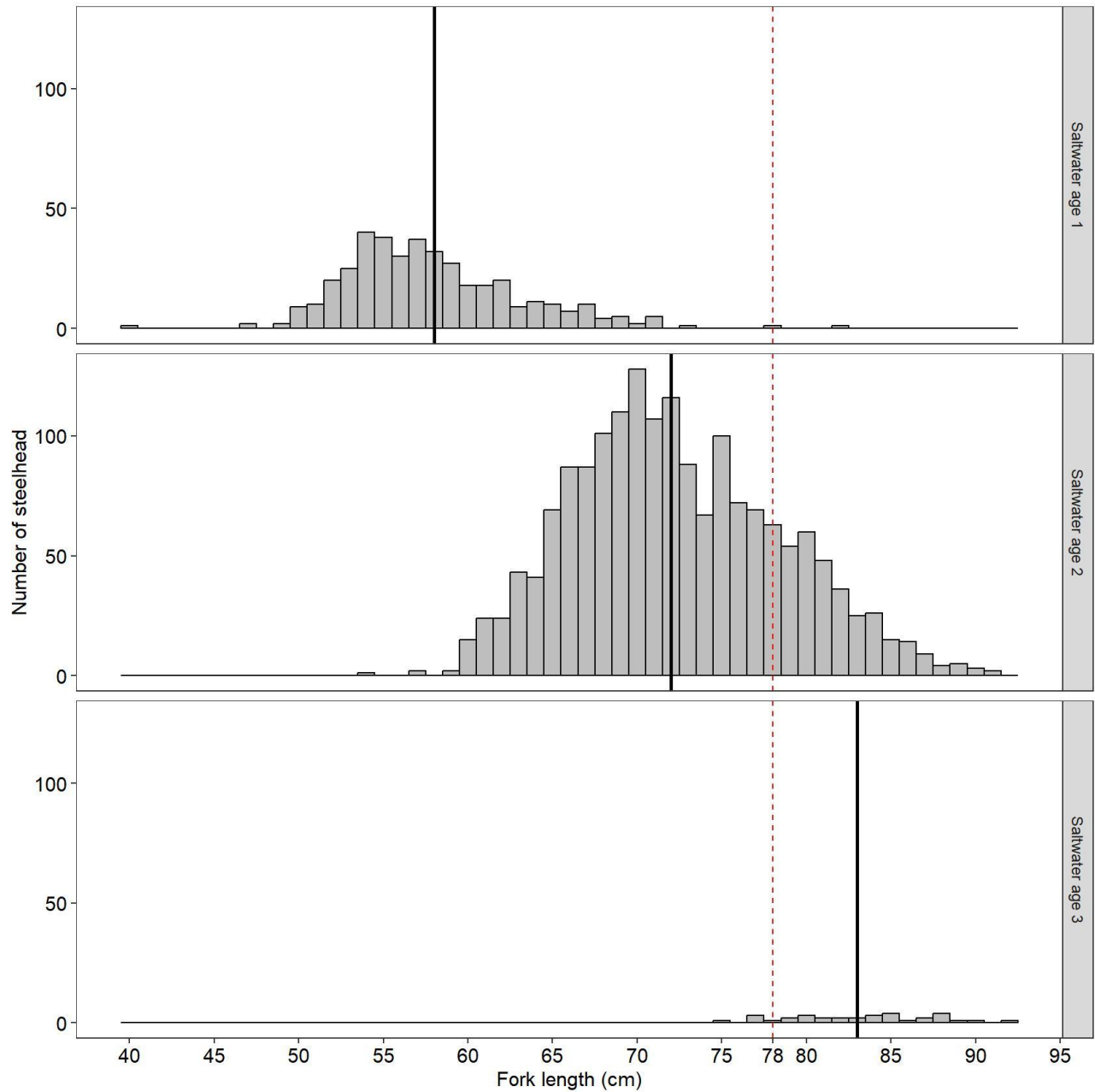
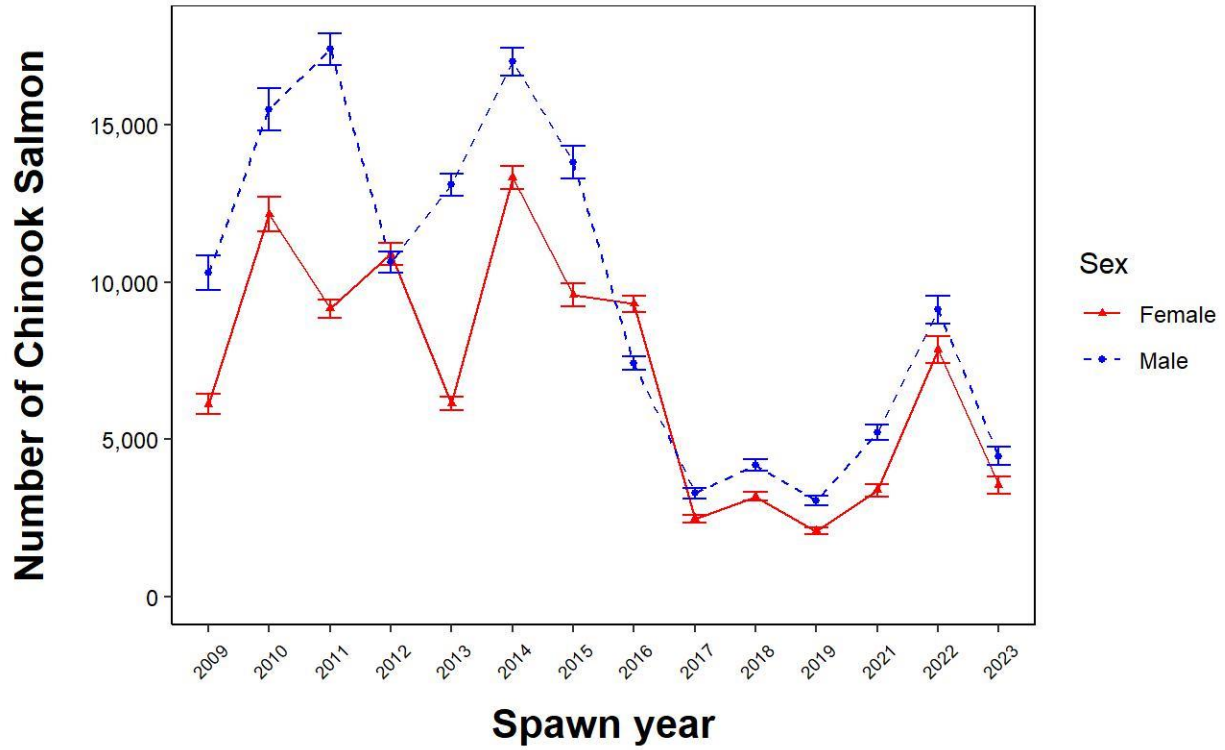Appendix E: Wild Chinook Salmon at Lower Granite Dam, spawn year 2023.

Appendix E-1. Percent estimated escapement of wild Chinook Salmon by genetic stock relative to the total estimated wild escapement at Lower Granite Dam, spawn years 2009–2023. Spawn year 2020 stock-specific estimates were generated using run reconstruction methods and exclude jacks in the total wild count. See Genetic Tissue Processing and Analysis section for definition of stock abbreviations.
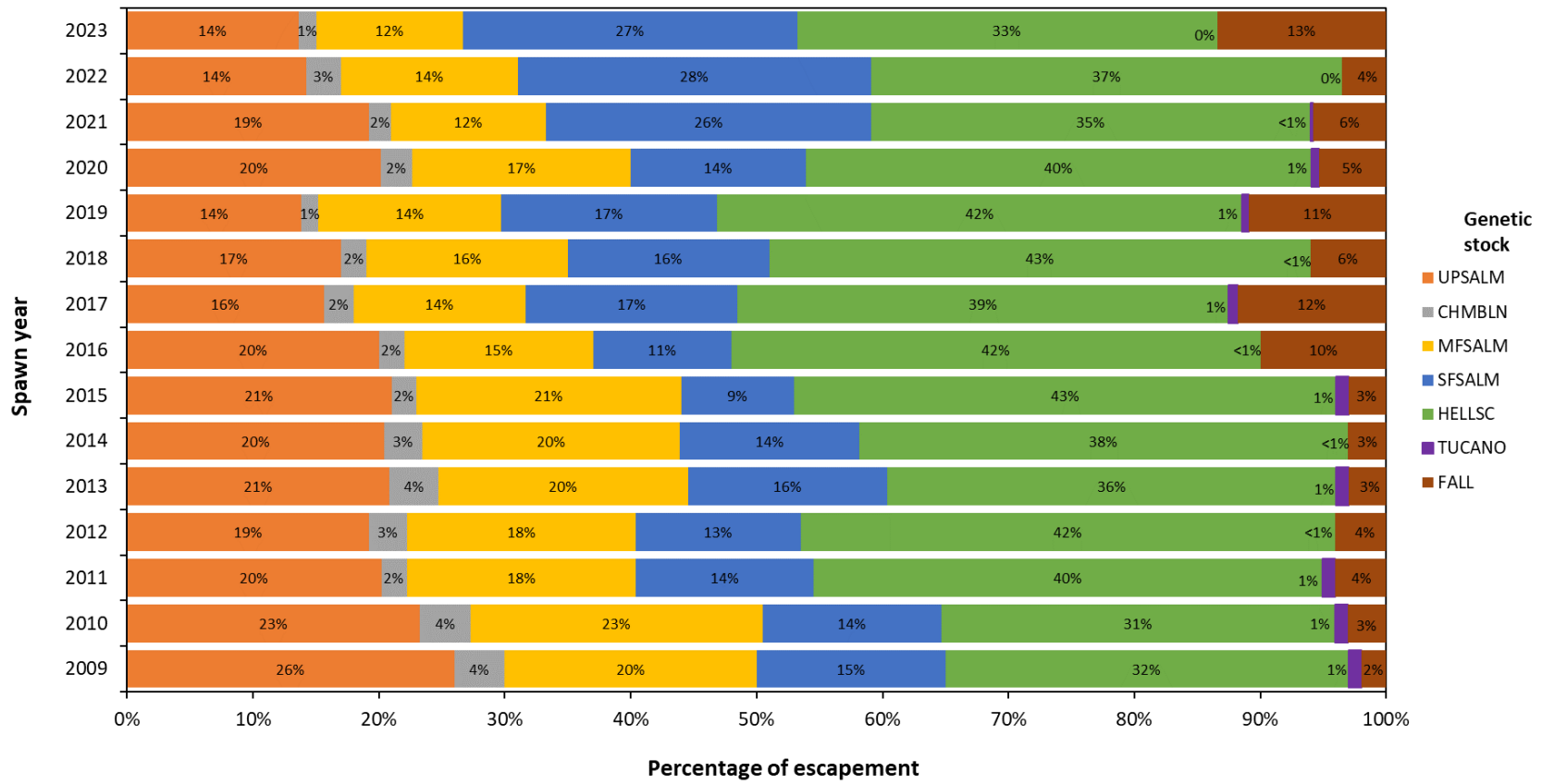
Appendix E-2. Estimated escapement of wild Chinook Salmon by sex and size for each genetic stock at Lower Granite Dam, spawn year 2023. L = lower bound and U = upper bound of 95% confidence intervals. See Genetic Tissue Processing and Analysis section for definition of stock abbreviations.

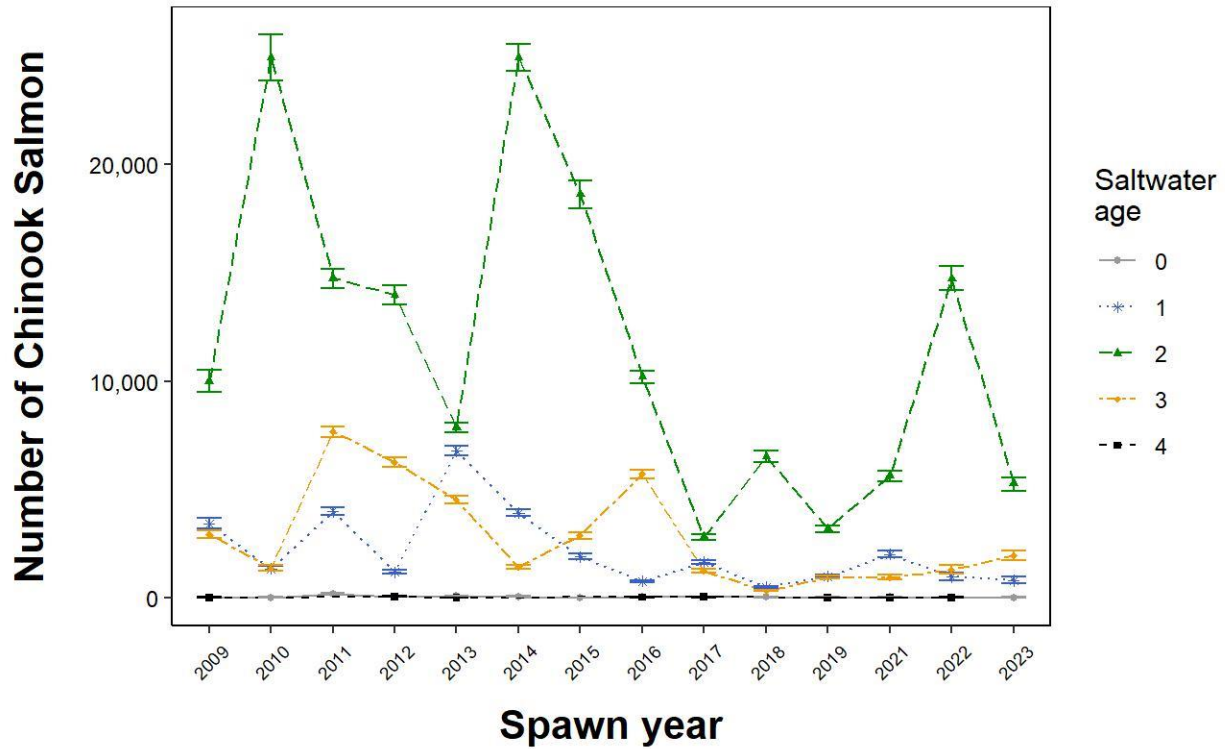| Genetic stock | Estimated number of wild Chinook Salmon at Lower Granite Dam that were: | | | | | | | | | | | | | | |
| | Female | | | Male | | | Large | | | Small | | | Total wild | | |
	Estimate	L	U	Estimate	L	U	Estimate	L	U	Estimate	L	U	Estimate	L	U
UPSALM	476	367	607	616	501	763	1,057	886	1,252	35	11	99	1,092	932	1,303
CHMBLN	36	10	74	80	37	125	80	37	128	36	11	71	116	64	171
MFSALM	382	284	504	552	436	688	887	711	1,053	47	21	125	934	772	1,125
SFSALM	906	768	1,069	1,225	1,059	1,435	1,958	1,715	2,232	173	109	282	2,131	1,907	2,427
HELLSC	1,252	1,090	1,447	1,426	1,232	1,628	2,560	2,290	2,863	118	61	207	2,678	2,409	2,990
TUCANO	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FALL	509	306	615	568	372	676	1,030	652	1,158	47	21	119	1,077	719	1,206
Total	3,561	3,273	3,829	4,467	4,177	4,777	7,572	7,114	7,900	456	358	703	8,028	7,642	8,438

Appendix E-3. Estimated escapement of wild Chinook Salmon by sex at Lower Granite Dam, spawn years 2009–2023. From SY2009–2021, confidence intervals are at 90%. Starting in SY2022, confidence intervals are at 95%. Spawn year 2020 sex estimates are unavailable because the trap was closed due to COVID-19 restrictions.

Appendix E-4. Estimated escapement of wild Chinook Salmon by smolt migration year (MY), brood year (BY), and age class for each genetic stock at Lower Granite Dam, spawn year 2023. Only individual fish that had both a total age and an assigned stock were used (n = 1,368). Age class format is European: freshwater age.saltwater age. See Genetic Tissue Processing and Analysis section for definition of stock abbreviations.

|	MY2020		MY2021		MY2022		MY2023	
	BY17	BY18	BY18	BY19	BY19	BY20	BY20	
Genetic stock	2.3	1.3	2.2	1.2	2.1	1.1	2.0	Total wild
UPSALM	0	337	1	686	0	68	0	1,092
CHMBLN	0	31	0	53	0	32	0	116
MFSALM	0	242	1	591	0	100	0	934
SFSALM	0	510	3	1,373	0	245	0	2,131
HELLSC	0	575	1	1,841	0	261	0	2,678
TUCANO	0	0	0	0	0	0	0	0
FALL	36	217	379	342	26	69	8	1,077
Total wild	36	1,912	385	4,886	26	775	8	8,028

Appendix E-5. Estimated escapement of wild Chinook Salmon by saltwater age at Lower Granite Dam, spawn years 2009–2023. From SY2009–2021, confidence intervals are at 90%. Starting in SY2022, confidence intervals are at 95%. Spawn year 2020 saltwater age estimates were generated using run reconstruction and do not have confidence intervals. Saltwater age-0 refers to mini-jacks and saltwater age-1 refers to jacks.

Appendix E-6. Estimated escapement of wild Chinook Salmon by saltwater age for each genetic stock at Lower Granite Dam, spawn years 2009–2023. Spawn year 2020 saltwater age estimates were unavailable at the stock level because the trap was closed due to COVID-19 restrictions. From SY2009–2021, confidence intervals are at 90%. Starting in SY2022, confidence intervals are at 95%. Saltwater age-0 refers to mini-jacks and saltwater age-1 refers to jacks. No Chinook Salmon from the Tucannon River stock were captured in SY2022 and SY2023.
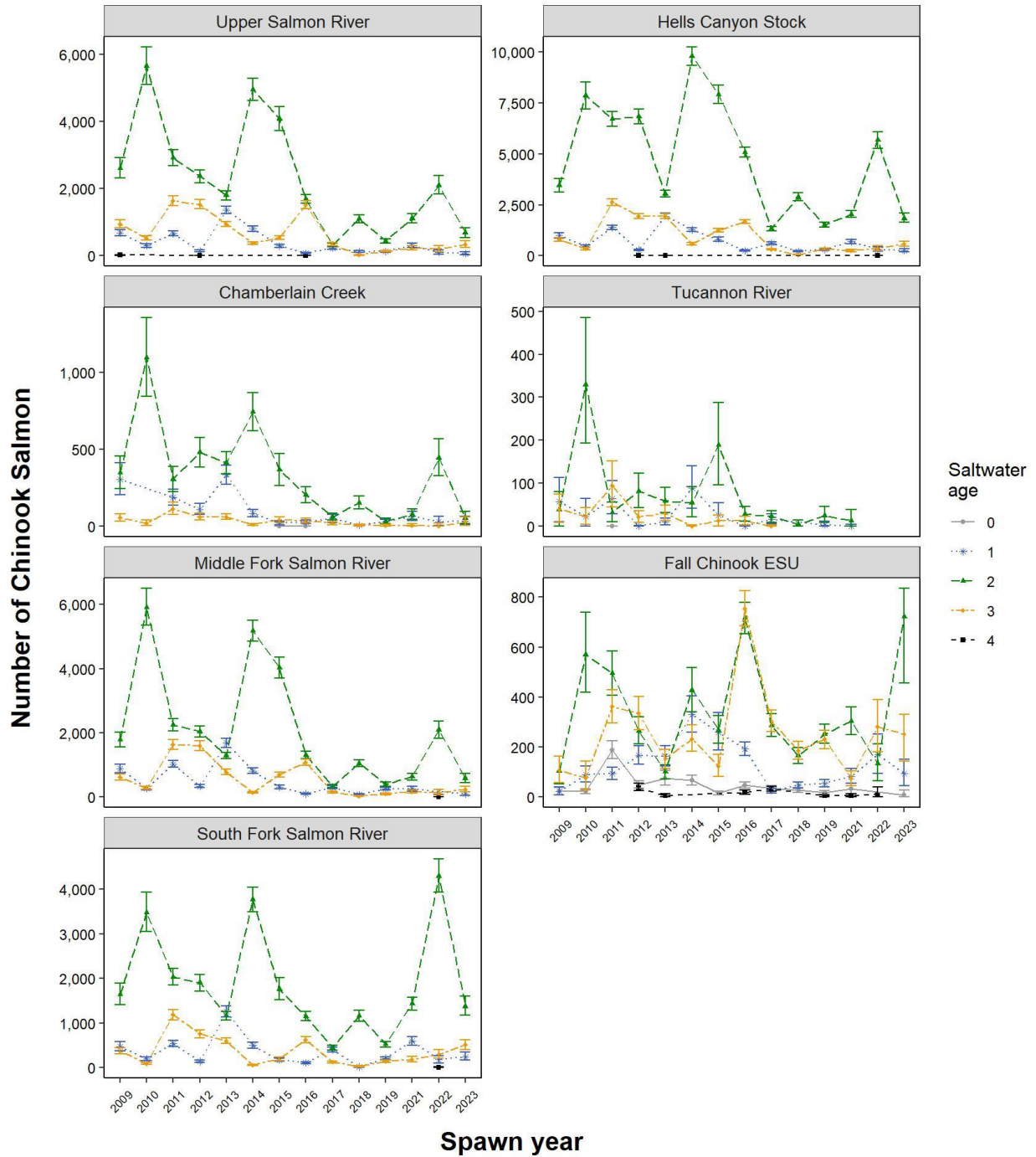
Appendix E-7. Length frequency distribution of trapped wild Chinook Salmon by saltwater age at Lower Granite Dam, spawn year 2023. Solid black vertical lines represent the mean fork length (FL) for saltwater age 0 (33 cm, n = 1), saltwater age 1 (50 cm, n = 159), saltwater age 2 (71 cm, n = 887), and saltwater age 3 (81 cm, n = 340). Dashed vertical red line represents the 57 cm FL cutoff for determining large-sized Chinook Salmon.
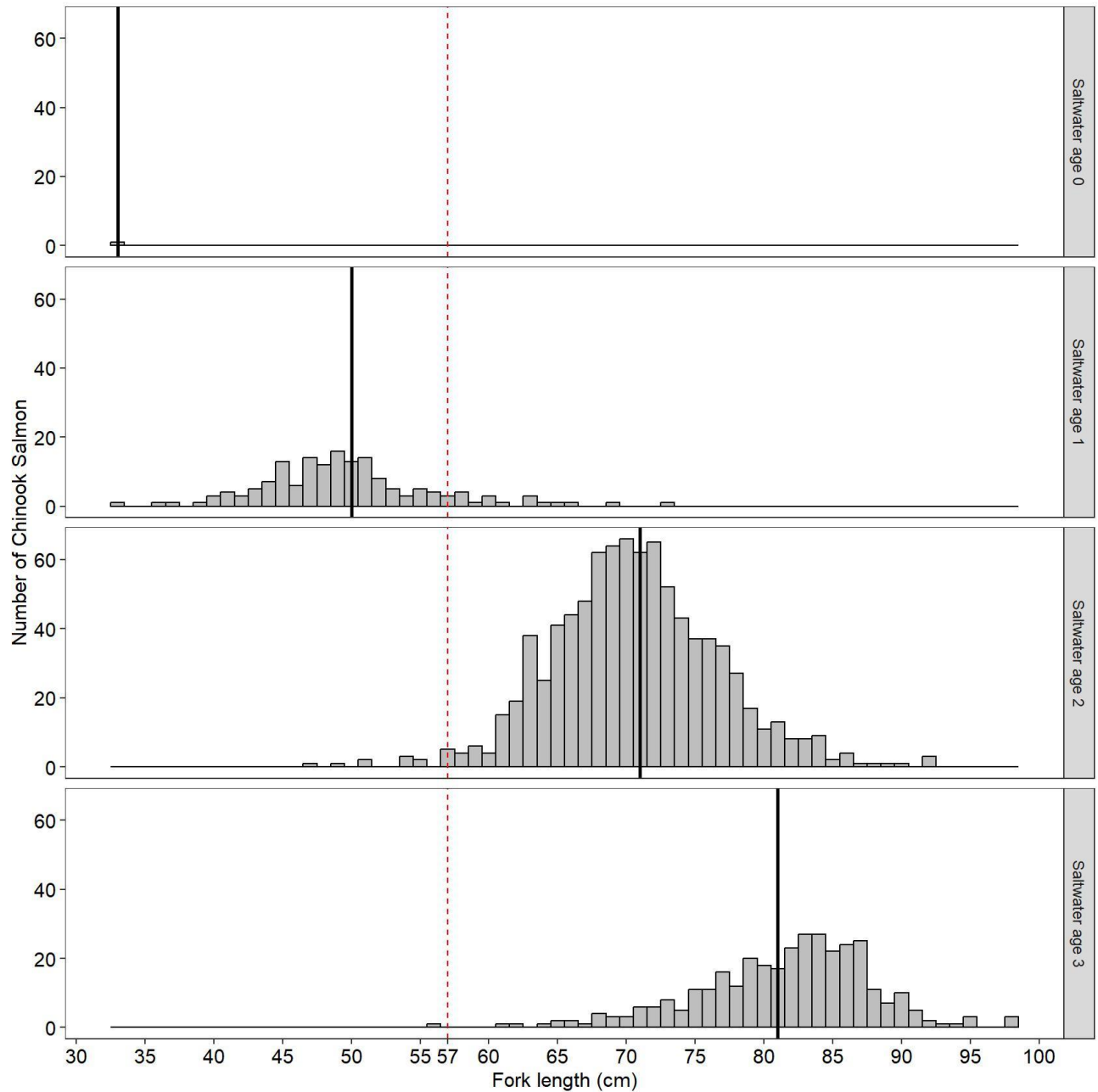
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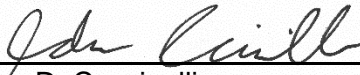Supervisory Fisheries Biologist

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